

Additional file 1. Differently expressed gene between uni

Probe_Set_ID	Gene_Symbol
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Gga.10.1.S1_at	OTX2
Gga.100.1.S1_a_at	FAS
Gga.10003.1.S1_at	MKL2
Gga.10004.1.S1_at	LOC416212
Gga.10008.1.S1_at	ZNF512B
Gga.10012.1.S1_s_at	SLC30A1
Gga.10017.1.S1_at	LOC777533
Gga.10021.2.S1_s_at	AGL
Gga.10022.1.S1_at	PCTP
Gga.10025.1.S1_at	CHGB
Gga.10026.1.S1_at	VPS37B
Gga.10027.2.S1_at	CPSF3
Gga.10029.1.S1_at	SCRN3
Gga.10032.1.A1_at	POLR1B
Gga.10033.1.S1_at	C20orf58
Gga.10034.1.S1_at	SERPINB2
Gga.10034.2.S1_a_at	SERPINB2
Gga.10034.2.S1_s_at	SERPINB2
Gga.10036.2.S1_a_at	DSCR2
Gga.10037.1.S1_s_at	NOXO1
Gga.10042.1.S1_a_at	CD200R1
Gga.10045.1.S1_at	VCP
Gga.10051.1.S1_at	RCBTB1
Gga.10056.1.S1_at	PHF20L1
Gga.10057.1.S1_s_at	TCP11L1
Gga.1006.1.S1_at	TBP
Gga.1006.2.S1_a_at	TBP
Gga.10060.1.S1_s_at	UBE1L2
Gga.10061.1.S1_s_at	SLC16A6
Gga.10062.1.S1_s_at	TTF2
Gga.10065.1.S1_at	USP54
Gga.10066.1.S1_at	MTMR7
Gga.10067.1.S1_at	KANK4

Gga.10068.1.S1_at	KLHDC10
Gga.10069.1.S1_at	CBFA2T3
Gga.10077.1.S1_at	WDR35
Gga.10077.2.S1_s_at	WDR35
Gga.10078.2.S1_x_at	LOC419724
Gga.10096.1.S1_at	FBLN5
Gga.10098.1.S1_s_at	FAP
Gga.10100.1.S1_at	IFT80
Gga.10103.1.S1_s_at	COBL
Gga.10107.1.S1_s_at	RCJMB04_18i2
Gga.10108.1.S1_at	ANXA8
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Gga.10114.2.S1_at	RNPEPL1
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Gga.10124.2.S1_a_at	SETBP1
Gga.10125.1.S1_a_at	FAIM
Gga.10129.1.S1_at	ECHDC1
Gga.10131.2.S1_a_at	TM4SF4
Gga.10133.1.S1_s_at	TBC1D8B
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Gga.10139.1.S1_s_at	LOC421693
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Gga.10146.1.S1_at	C3orf26
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Gga.10155.1.S1_at	EREG
Gga.10156.2.S1_a_at	ERP27
Gga.1016.1.S1_s_at	RCJMB04_34i9
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Gga.10172.2.S1_at	RERGL
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Gga.10224.1.S1_at	TRIM65
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Gga.10226.1.S1_s_at	LOC418990
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Gga.1029.3.S1_a_at	RBBP4
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Gga.10323.1.S1_at	RBM14

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Gga.10392.1.S1_at	TIMM10
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Gga.10406.2.S1_s_at	CYLD
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Gga.1043.1.S1_s_at	NUDT19
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Gga.10535.2.S1_s_at	CNOT1
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Gga.10877.1.S1_s_at	TBC1D8
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Gga.10988.1.S1_x_at	EFCAB1
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Gga.11026.1.S1_at	PKHD1
Gga.11028.2.S1_s_at	METTL8
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Gga.1108.1.S1_s_at	RCJMB04_3c23
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Gga.11372.1.S1_s_at	TTL7
Gga.11377.1.S1_at	UPK3A
Gga.11378.1.S1_s_at	PMP2
Gga.1138.1.S1_s_at	AARS
Gga.11380.1.S1_at	FRMD3
Gga.11383.1.S1_at	DUPD1
Gga.11384.2.S1_s_at	SMPX
Gga.11386.1.S1_at	ALG13
Gga.11387.1.A1_at	LOC769163
Gga.11387.1.S1_s_at	FILIP1L
Gga.11391.1.S1_at	LMOD3
Gga.11394.1.S1_at	ERICH1

Gga.11399.2.S1_a_at	MECR
Gga.1140.1.S1_at	RCJMB04_11e18
Gga.11405.1.S1_at	CCNJ
Gga.11406.1.S1_a_at	LOC426545
Gga.11407.1.S1_at	FAM3B
Gga.11410.1.A1_s_at	SEC24D
Gga.11429.1.S1_s_at	DCLK1
Gga.11430.1.S1_at	PENK
Gga.11431.2.S1_at	TXNDC15
Gga.11436.1.S1_a_at	STARD3NL
Gga.11441.1.S1_s_at	TINP1
Gga.11443.1.S1_at	C10orf26
Gga.11444.1.S1_s_at	C9orf64
Gga.11445.1.S1_at	STYK1
Gga.11447.1.S1_a_at	PLA2G10
Gga.11449.1.S1_at	MLLT6
Gga.11450.1.S1_at	ETNK1
Gga.11451.1.S1_s_at	ELP2
Gga.11452.2.S1_a_at	OFD1
Gga.11453.1.S1_at	TMOD3
Gga.11454.1.S1_at	ALDH7A1
Gga.11456.1.S1_at	CSTA
Gga.1146.2.S1_at	SSB
Gga.11463.2.S1_s_at	ENPP2
Gga.11466.1.S1_at	GPR23
Gga.11466.2.S1_a_at	GPR23
Gga.11468.1.S1_a_at	PPIC
Gga.11469.2.S1_at	KCTD20
Gga.11469.3.S1_a_at	KCTD20
Gga.1147.1.S1_s_at	MAPK8
Gga.11470.1.S1_at	NUP153
Gga.11472.1.S1_s_at	TEX2
Gga.11474.1.S1_a_at	RFESD
Gga.11477.1.S1_at	LOC418095
Gga.11478.1.S1_s_at	RCJMB04_10o8
Gga.11478.2.S1_s_at	RCJMB04_10o8
Gga.1148.1.S2_at	ST6GAL1
Gga.11481.1.S1_at	BRI3BP
Gga.11484.1.S1_at	CCDC18 /// LOC424498
Gga.11486.1.S1_at	LOC771147 /// RPL9

Gga.11492.1.S1_at	ZAK
Gga.1150.2.S1_a_at	OLFML3
Gga.11516.1.S1_at	P2RY6
Gga.11522.1.S1_at	LOC775993 /// RCJMB04_19p13
Gga.11522.1.S1_x_at	LOC775993 /// RCJMB04_19p13
Gga.1153.1.S1_at	DLG7
Gga.11534.1.A1_at	ADCY7 /// LOC769333
Gga.11539.1.S1_at	LOC420129
Gga.11576.1.S1_at	DNAJC19
Gga.11577.1.S1_at	ABHD11
Gga.11578.1.S1_s_at	GDI2
Gga.11579.1.S1_at	LOC415661
Gga.1158.3.S1_a_at	HOPX
Gga.1158.3.S1_s_at	HOPX
Gga.11580.1.S1_at	STK16
Gga.11581.1.S1_at	TMEM35
Gga.11584.1.S1_at	LOC417722
Gga.11591.1.S1_at	FGD3
Gga.11597.1.S1_s_at	RCJMB04_17i9
Gga.11597.2.S1_at	RCJMB04_17i9
Gga.11597.2.S1_s_at	RCJMB04_17i9
Gga.11599.1.S1_s_at	TRIM65
Gga.11604.2.S1_a_at	LOC428877
Gga.1161.1.S1_at	SDHD
Gga.11611.1.S1_at	WIF1
Gga.11620.1.S1_at	POT1
Gga.11623.1.S1_at	LOC415787
Gga.11623.2.S1_s_at	LOC415787
Gga.11628.2.S1_a_at	POLB
Gga.1163.1.S1_at	CYP3A37
Gga.11630.1.S1_x_at	LOC426615
Gga.11630.2.S1_a_at	LOC426615
Gga.11630.2.S1_at	LOC426615
Gga.11631.1.S1_at	PRAM1
Gga.11635.1.S1_at	RACGAP1
Gga.11640.1.S1_at	SUCNR1
Gga.11641.1.S1_at	DCI
Gga.11643.2.S1_s_at	C20orf42
Gga.11646.1.S1_at	FAM20A
Gga.11648.1.S1_at	PHCA

Gga.1165.1.S1_at	FGG
Gga.11650.2.S1_at	GCNT7
Gga.11655.1.S1_at	GPR56
Gga.11658.1.S1_at	BPI
Gga.11660.1.S1_at	TRAF2
Gga.11662.1.S1_at	CHMP4C
Gga.11662.2.S1_a_at	CHMP4C
Gga.11665.1.S1_s_at	BHLHB2
Gga.11672.1.S1_at	RCJMB04_13a21
Gga.11675.1.S1_at	TTLL11
Gga.11677.1.S1_at	TOX3
Gga.11677.1.S1_s_at	TOX3
Gga.11678.4.S1_a_at	SPG21
Gga.11681.1.S1_s_at	SSX2IP
Gga.11687.1.S1_s_at	DENND4A
Gga.11689.1.S1_at	SYNGR1
Gga.1169.1.S1_at	AADACL2
Gga.11690.1.S1_at	PHOSPHO2
Gga.11692.1.S1_at	LOC418120
Gga.11703.1.S1_at	AARSD1
Gga.11708.1.S1_at	CARKL
Gga.1171.1.S1_at	LY6E
Gga.11710.1.S1_at	LOC769608 /// LOC769668
Gga.11713.1.S1_at	LOC426179
Gga.11713.1.S1_s_at	LOC426179
Gga.11714.1.S1_at	HOXB7
Gga.11721.1.S1_s_at	DAAM2
Gga.11723.1.S1_s_at	TNRC6B
Gga.11726.1.S1_a_at	GADD45G
Gga.11730.1.S1_at	SLC2A10
Gga.11740.1.S1_at	LOC415459
Gga.11741.1.S1_a_at	TFPI
Gga.11741.3.S1_a_at	TFPI
Gga.11741.4.A1_at	TFPI
Gga.11741.4.S1_a_at	TFPI
Gga.11749.1.S1_a_at	CDC42EP3
Gga.11751.1.S1_at	WAPAL
Gga.11755.1.S1_at	TERT
Gga.11758.1.S1_at	ANKRD13A
Gga.1176.2.S1_a_at	RFWD2

Gga.11760.1.S1_at	TMEM103
Gga.11761.2.S1_a_at	PFTK1
Gga.11762.1.S1_at	LOC419391
Gga.11764.2.S1_a_at	GCHFR
Gga.11766.2.S1_a_at	NDP
Gga.11776.1.S1_s_at	RACGAP1
Gga.11781.1.S1_at	TM6SF1
Gga.11782.1.S1_at	CAST
Gga.11783.1.S1_at	IL28RA
Gga.11787.2.S1_s_at	SH3BGR
Gga.11789.1.S1_a_at	ODZ4
Gga.11791.1.S1_at	C1QTNF7
Gga.11792.1.S1_at	NMT1
Gga.11795.1.S1_s_at	RCJMB04_20k13
Gga.11796.1.S1_a_at	SPCS1
Gga.11797.1.S1_s_at	VRK1
Gga.11799.1.S1_at	SEPN1
Gga.11799.2.S1_a_at	SEPN1
Gga.11801.1.S1_a_at	JMJD2C
Gga.11811.1.S1_at	CXorf41
Gga.11819.1.S1_at	CENPQ
Gga.1182.1.S1_s_at	RCJMB04_11i10
Gga.11822.1.S1_at	PPP1R3B
Gga.11825.1.S1_s_at	GK
Gga.11826.2.S1_at	WAC
Gga.11827.2.S1_a_at	LOC415531
Gga.11828.1.S1_at	NINJ1
Gga.11828.2.S1_a_at	NINJ1
Gga.11830.1.S1_at	DNASE1L3
Gga.11832.1.S1_at	EGLN3
Gga.11834.3.S1_a_at	NAPRT1
Gga.11836.1.S1_s_at	COBLL1
Gga.11841.1.S1_s_at	KLF6
Gga.11842.1.S1_s_at	SYDE2
Gga.11845.1.S1_at	TMEM16A
Gga.11847.1.S1_at	BTD
Gga.11850.2.A1_a_at	LOC770664
Gga.11850.2.S1_a_at	LOC770664
Gga.11851.1.S1_at	NTHL1
Gga.11853.2.S1_a_at	LOC771706

Gga.11854.1.S1_at	TSPAN6
Gga.11855.1.S1_at	LOC421956
Gga.11859.1.S1_at	ARHGAP1
Gga.1187.2.S1_s_at	LIMS1 /// LOC771176
Gga.11874.1.S1_at	SLC7A6OS
Gga.11876.1.S1_a_at	C9orf19
Gga.11876.2.S1_at	C9orf19
Gga.11876.3.S1_a_at	C9orf19
Gga.11878.1.S1_at	SFXN5
Gga.11879.1.S1_at	LOC424258
Gga.1188.1.S1_at	CIAO1
Gga.11883.3.S1_at	ASPH
Gga.11883.4.S1_a_at	ASPH
Gga.1189.2.S1_a_at	HMGN1
Gga.11890.1.S1_at	NARF
Gga.11900.1.S1_at	FAM129A
Gga.11901.1.S1_at	SLC4A7
Gga.11902.1.A1_at	TMEM57
Gga.11908.1.S1_at	CMC1
Gga.11908.2.S1_a_at	CMC1
Gga.11908.3.S1_at	CMC1
Gga.11909.1.S1_s_at	MPP7
Gga.11911.2.S1_a_at	ZMYND11
Gga.11914.2.S1_a_at	WAPAL
Gga.11915.2.S1_a_at	CD99L2
Gga.11917.1.S1_at	TROVE2
Gga.11918.1.S1_at	NSUN3
Gga.11920.2.S1_a_at	RG9MTD2
Gga.11922.1.S1_at	BTF3
Gga.11927.1.S1_s_at	CPM
Gga.11929.1.S1_at	KLHDC8A
Gga.1193.1.S1_at	PTPRC
Gga.1193.1.S2_at	PTPRC
Gga.11930.1.S1_s_at	FLRT2
Gga.11938.3.S1_s_at	ASTE1
Gga.11941.1.S1_at	AK5
Gga.11945.1.S1_at	CNRIP1
Gga.11947.3.S1_at	ISCA2
Gga.11948.1.S1_at	KLC1
Gga.11948.2.S1_a_at	KLC1

Gga.11950.1.S1_s_at	KCNK5
Gga.11955.1.S1_at	IGSF6
Gga.11957.1.S1_s_at	WHSC1L1
Gga.11958.1.S1_a_at	C1orf35
Gga.11959.1.S1_at	ZCCHC4
Gga.11961.1.S1_at	MRPL53
Gga.11963.1.S1_at	BLZF1
Gga.11965.1.S1_at	TRAPPC2L
Gga.11966.1.S1_a_at	RCAN2
Gga.11967.1.S1_at	GPC5
Gga.11968.1.S1_at	QRSL1
Gga.11971.2.S1_at	IKZF5
Gga.11985.1.S1_at	ELMOD1
Gga.11991.1.S1_at	POLR2C
Gga.11993.1.S1_s_at	RNF11
Gga.11996.1.S1_at	RASD2
Gga.11997.1.S1_a_at	LOC419483
Gga.11999.1.A1_at	SCG2
Gga.11999.1.S1_at	SCG2
Gga.12002.1.S1_a_at	CAPSL
Gga.12003.1.S1_at	THOC2
Gga.12004.1.S1_s_at	DICER1
Gga.12006.1.S1_at	ADM
Gga.12007.1.S1_at	C3orf34
Gga.1201.1.S1_s_at	GYG1
Gga.12011.1.S1_x_at	CEP290
Gga.12012.1.S1_at	FAM118B
Gga.12022.1.S1_s_at	BYSL
Gga.12024.1.S1_at	BPHL
Gga.12026.2.S1_at	NENF
Gga.12028.1.S1_a_at	LOC416518
Gga.12029.1.S1_at	MRPS27
Gga.12030.4.S1_a_at	PEX16
Gga.12030.4.S1_x_at	PEX16
Gga.12034.1.S1_at	LOC769277
Gga.12035.2.S1_a_at	OXNAD1
Gga.1204.1.S1_s_at	LOC425529
Gga.12040.2.S1_a_at	TSPAN8
Gga.12043.1.S1_at	PALMD
Gga.12048.1.S1_a_at	ZFAND1

Gga.12055.1.S1_s_at	PRAGMIN
Gga.12057.1.S1_at	LRAT
Gga.12058.1.S1_at	LOC420294
Gga.1207.1.S1_at	LOC426515
Gga.12072.2.S1_a_at	MED31
Gga.12074.1.S1_s_at	CP
Gga.12075.1.S1_at	LOC420592
Gga.12076.1.S1_at	P2RX5
Gga.12079.2.S1_a_at	PAP2D
Gga.1208.2.S1_a_at	SLC25A16
Gga.12080.1.S1_at	RRAD
Gga.12085.1.S1_at	LOC418836
Gga.12088.2.S1_a_at	FLRT3
Gga.12089.1.S1_a_at	LOC424430
Gga.12095.1.S1_at	C6orf57
Gga.12097.1.S1_s_at	POLA1
Gga.12098.1.S1_a_at	LOC415756
Gga.121.1.S1_at	UCP3
Gga.1210.1.S1_at	CCRN4L
Gga.12104.1.S1_at	RAMP2
Gga.12105.2.S1_a_at	C2orf34
Gga.12106.1.S1_a_at	RCJMB04_8b16
Gga.12110.2.S1_a_at	OLFM3
Gga.12112.1.S1_at	APOBEC2
Gga.12113.1.A1_at	SH3BGRL2
Gga.12115.1.S1_s_at	ZNF207
Gga.12116.1.S1_s_at	MYST4
Gga.12119.2.S1_a_at	LOC416419
Gga.12120.1.S1_at	PACSIN3
Gga.12121.1.S1_at	SUSD3
Gga.12127.1.S1_s_at	RBM26
Gga.12132.2.S1_a_at	SRD5A2L2
Gga.12133.1.S1_s_at	TTC14
Gga.12136.1.S1_at	CHCHD1
Gga.1214.1.S1_at	ZNF294
Gga.12140.2.S1_a_at	EGFL7
Gga.12140.2.S1_s_at	EGFL7
Gga.12144.1.S1_s_at	RAPGEF1
Gga.12148.1.S1_at	ICK
Gga.12149.1.S1_s_at	HNRPLL

Gga.12149.2.S1_at	HNRPLL
Gga.1216.1.S1_at	C12orf57
Gga.12160.3.S1_a_at	UBXD1
Gga.12162.1.S1_at	CXorf36
Gga.12165.1.S1_at	FAM62B /// NCAPG2
Gga.12166.1.S1_at	ZEB2
Gga.12169.1.S1_at	C16orf42
Gga.12171.1.S1_s_at	DDX24
Gga.12183.3.S1_a_at	DHR SX
Gga.12186.1.S1_at	LYVE1
Gga.12192.1.S1_at	OSMR
Gga.12192.2.S1_a_at	OSMR
Gga.12193.1.S1_a_at	C7orf16
Gga.12197.2.S1_s_at	AKAP12
Gga.122.2.S1_a_at	CFDP1
Gga.12201.1.S1_at	C7orf36
Gga.12201.2.S1_a_at	C7orf36
Gga.12203.1.S1_at	SPC25
Gga.12204.1.S1_at	KATNA1
Gga.12205.1.S1_at	C13orf7
Gga.12207.1.S1_s_at	RTTN
Gga.12208.2.S1_at	GINS1
Gga.12209.1.S1_at	C4orf31
Gga.1221.1.S1_at	WHSC1
Gga.12211.1.S1_at	LOC426086
Gga.12212.1.S1_a_at	CENPK
Gga.12213.1.S1_s_at	ZMAT5
Gga.12218.1.S1_at	KDEL R3
Gga.12224.1.S1_a_at	NT5DC1
Gga.12225.1.S1_at	SFRS17A
Gga.12229.1.S1_at	CAMK4
Gga.12232.1.S1_at	KLF3
Gga.12233.1.S1_at	AS A HL
Gga.12234.1.S1_at	TYMS
Gga.12237.1.S1_at	STX18
Gga.12240.1.S1_at	ACSBG1
Gga.12241.1.S1_at	PPFIA1
Gga.12241.1.S1_s_at	PPFIA1
Gga.12242.2.S1_at	NUDT7
Gga.12243.1.S1_at	RWDD2B

Gga.12249.1.S1_at	DBX2
Gga.12255.1.S1_at	WASL
Gga.12255.1.S1_s_at	WASL
Gga.12256.1.S1_at	LOC771073
Gga.1226.1.S1_s_at	KIAA1274
Gga.1226.2.S1_s_at	KIAA1274
Gga.12260.1.S1_at	IRAK1BP1
Gga.12261.1.S1_at	SNN
Gga.12264.2.S1_a_at	COR4
Gga.12266.1.S1_at	FABP3
Gga.12267.1.S1_s_at	NDUFAF1
Gga.12272.1.S1_at	C15orf40
Gga.12278.1.S1_a_at	ADAT2
Gga.12280.1.S1_at	SUV420H1
Gga.12280.2.S1_a_at	SUV420H1
Gga.12294.1.S1_a_at	CYBASC3
Gga.12298.1.S1_at	VSTM2A
Gga.123.1.S1_at	MUSK
Gga.12301.1.S1_at	PSCD3
Gga.12302.1.S1_at	IMPAD1
Gga.12304.1.S1_at	C18orf55
Gga.12305.1.S1_at	LOC423054
Gga.12307.3.S1_a_at	SORBS2
Gga.12309.1.S1_at	AIFM2
Gga.12310.1.S1_at	BBOX1
Gga.12311.2.S1_x_at	TIRAP
Gga.12315.1.S1_s_at	CDKL2
Gga.1232.1.S1_at	CALCA
Gga.1232.2.S1_a_at	CALCA
Gga.12326.1.S1_s_at	MXI1
Gga.1233.3.S1_at	AP3B1
Gga.12331.2.S1_a_at	PCMTD2
Gga.12332.1.S1_at	GOLPH3
Gga.12334.1.S1_at	ANKRD16
Gga.12335.2.S1_s_at	RCJMB04_26f20
Gga.12337.3.S1_a_at	GTF2E2
Gga.12337.3.S1_s_at	WRN
Gga.12338.1.S1_at	PTPRF
Gga.12341.1.S1_s_at	SLC13A5
Gga.12346.1.S1_at	LOC424919

Gga.12348.1.S1_at	C3orf39
Gga.12349.1.S1_at	ASAM
Gga.1235.2.S1_at	KCNAB2
Gga.12350.1.S1_at	LOC426886
Gga.12352.1.S1_s_at	UACA
Gga.12360.1.S1_at	TMEM213
Gga.12364.1.S1_at	ZNF330
Gga.12370.1.S1_at	TFB1M
Gga.12370.3.S1_a_at	TFB1M
Gga.12370.3.S1_x_at	TFB1M
Gga.12371.1.S1_at	RCJMB04_9f20
Gga.1238.1.S1_at	ADD1
Gga.12381.1.S1_s_at	LOC427449
Gga.12383.1.S1_at	CRHBP
Gga.12388.1.S1_at	FANCL
Gga.12391.1.S1_at	LOC422172
Gga.12393.1.S1_at	CHST6
Gga.12396.2.S1_at	TMEM164
Gga.124.1.S1_at	FBP2
Gga.12401.1.S1_at	PRRG4
Gga.12407.1.S1_at	LOC422654
Gga.12408.3.S1_a_at	ATXN3
Gga.12412.1.S1_at	ITGB1BP1
Gga.12413.1.S1_s_at	UBXD7
Gga.12417.1.S1_at	LOC776125
Gga.12423.1.S1_at	EFR3A
Gga.12424.1.S1_at	KIF21A
Gga.12428.1.S1_s_at	ANKRD10
Gga.12432.2.S1_a_at	C10orf57
Gga.12434.1.S1_at	MAP3K7
Gga.12437.1.S1_at	SFRS11
Gga.12437.2.S1_at	CHGA
Gga.12438.1.S1_at	EXOSC7
Gga.12439.1.S1_s_at	UBXD2
Gga.1244.1.S1_at	RCJMB04_8o21
Gga.12440.1.S1_a_at	LYRM1
Gga.12443.1.S1_at	GALNTL4
Gga.12454.1.S1_at	RLN3
Gga.12456.1.S1_at	SIRT5
Gga.12458.1.S1_s_at	MLLT4

Gga.12459.1.S1_at	RBM17
Gga.1246.1.S1_at	C3orf37
Gga.12461.3.A1_at	SNRNP35
Gga.12463.1.S1_at	PPP2R3B
Gga.12466.2.S1_a_at	KCNE3
Gga.12468.1.S1_at	SUMF2
Gga.1247.1.S1_at	LOC396098
Gga.1247.1.S2_at	LOC396098
Gga.12470.1.S1_at	LOC426994
Gga.12471.1.S1_at	VASH2
Gga.12472.1.S1_s_at	LOC422745
Gga.12475.1.S1_at	TTYH3
Gga.12477.1.S1_at	LOC776632 /// NAPG
Gga.12478.1.S1_at	JSRP1
Gga.12486.1.S1_at	TSPAN13
Gga.1249.1.S1_at	GRPEL1
Gga.12491.1.S1_a_at	DNTTIP1
Gga.12492.1.S1_at	C9orf30
Gga.12493.2.S1_s_at	ZNF451
Gga.12502.1.S1_at	NAF1
Gga.12503.2.S1_at	NXNL2
Gga.12504.1.S1_at	COMMD4
Gga.12506.1.S1_at	EML4
Gga.12507.1.S1_s_at	ZDHHC20
Gga.12510.1.S1_at	LOC420043
Gga.12512.1.S1_at	PLXDC2
Gga.12515.1.S1_at	LHX8
Gga.12516.1.S1_s_at	IL20RA
Gga.12519.1.S1_at	ZCCHC2
Gga.12523.1.S1_at	CPPED1
Gga.12525.1.S1_at	FREM1
Gga.12535.1.S1_at	LOC424152
Gga.12537.1.S1_at	MPHOSPH9
Gga.12539.2.S1_at	NPLOC4
Gga.12541.1.S1_at	NUDT2
Gga.12545.1.S1_s_at	VPS8
Gga.12546.1.S1_s_at	INPP4B
Gga.12557.1.S1_at	TMEFF2
Gga.12560.1.S1_s_at	RCJMB04_9o2
Gga.12561.1.A1_at	DSE

Gga.12562.1.S1_at	C14orf153
Gga.12562.2.S1_a_at	C14orf153
Gga.12562.2.S1_x_at	C14orf153
Gga.12563.1.S1_at	RGS7
Gga.12564.1.S1_at	LATS1
Gga.12565.1.S1_s_at	CACNA2D1
Gga.12566.1.S1_at	LRRC42
Gga.12569.1.S1_at	FNBP1L
Gga.1257.1.S1_s_at	GLCCI1
Gga.12570.1.S1_s_at	LOC424004
Gga.12574.1.S1_at	LOC418549
Gga.12576.1.S1_at	PARD6B
Gga.1258.1.S1_at	CANX
Gga.12582.1.S1_at	LOC430620
Gga.12588.2.S1_a_at	LOC415770
Gga.12588.3.S1_a_at	C19orf40
Gga.12593.1.S1_at	PDCD6
Gga.12594.1.S1_at	LOC424261
Gga.12596.1.S1_at	STK11
Gga.12597.1.S1_at	LOC419381
Gga.12598.1.S1_at	RHOJ
Gga.12599.1.S1_s_at	WDR12
Gga.126.1.S1_at	TLE4
Gga.12600.1.S1_s_at	C7
Gga.12603.1.S1_at	TRIM23
Gga.12604.1.S1_a_at	MS4A15
Gga.12606.1.S1_at	RAI14
Gga.12606.1.S1_s_at	RAI14
Gga.12609.1.S1_at	AGGF1
Gga.1262.2.S1_at	RCJMB04_10f20
Gga.12624.1.S1_at	NDUFS5
Gga.12625.1.S1_at	CD99
Gga.12626.1.S1_at	HCFC2
Gga.12626.2.S1_s_at	HCFC2
Gga.12630.1.S1_s_at	WDR12
Gga.12631.2.S1_at	LOC417712
Gga.12632.1.S1_at	SLC45A1
Gga.12635.1.S1_at	LOC428459
Gga.12635.2.S1_a_at	LOC428459
Gga.12636.1.A1_at	NPM1

Gga.12637.2.S1_a_at	UTP18
Gga.12640.1.S1_s_at	WDR33
Gga.12642.2.S1_a_at	LOC424434
Gga.12648.1.S1_at	STEAP1
Gga.1265.3.S1_at	PDPK1
Gga.1266.2.S1_a_at	TXLNA
Gga.12660.2.S1_a_at	PCSK5
Gga.12661.1.S1_at	PNPLA8
Gga.12662.1.S1_at	RCJMB04_17i9
Gga.12663.2.S1_a_at	RFXDC2
Gga.12667.2.S1_s_at	FILIP1
Gga.12668.1.S1_at	SUV420H1
Gga.12669.1.S1_at	RAD1
Gga.12674.3.A1_a_at	TMEM131
Gga.12675.1.S1_at	LOC427367
Gga.12678.1.S1_at	C12orf43
Gga.1268.1.S1_a_at	RHOG
Gga.12682.1.S1_s_at	CASC5
Gga.12683.1.S1_at	RCJMB04_21o24
Gga.12684.2.S1_s_at	EXOSC2
Gga.12688.1.S1_at	SEPX1
Gga.12697.1.S1_at	GPR143
Gga.12705.1.A1_at	CHMP5
Gga.12707.1.S1_s_at	DDEF1
Gga.12730.1.S1_s_at	JMJD2B
Gga.12733.1.S1_a_at	TRAF3IP1 /// USP40
Gga.12737.1.S1_at	LOC426031
Gga.12738.1.S1_at	DYNLRB2
Gga.12741.1.S1_at	SCN8A
Gga.12741.1.S1_s_at	SCN8A
Gga.12743.1.S1_at	ETV7
Gga.12750.1.S1_at	HEATR5B
Gga.12755.1.S1_s_at	OTUD7A
Gga.12759.1.S1_at	CPNE8
Gga.12764.1.S1_s_at	SRGAP1
Gga.12774.1.S1_at	OPRL1
Gga.12781.1.S1_at	LSM11
Gga.12788.1.S1_at	NDUFA2
Gga.12797.1.A1_at	LOC422427
Gga.128.1.S1_at	NR3C1

Gga.12800.1.S1_at	MMP3
Gga.12802.1.S1_s_at	KIF1B
Gga.12811.1.S1_s_at	NUAK2
Gga.12818.1.S1_at	PTPN13
Gga.12830.1.S1_at	TBC1D14
Gga.12834.1.S1_s_at	LOC769019
Gga.12839.1.S1_at	C14orf79
Gga.12842.1.S1_at	HABP2
Gga.12843.1.S1_at	PPTC7
Gga.12846.1.S1_at	SMG7
Gga.12847.1.S1_s_at	PASK
Gga.12849.1.S1_at	SMOC2
Gga.12855.1.S1_at	IQCK
Gga.12858.1.S1_at	GATSL1
Gga.12861.1.S1_at	LOC415708
Gga.12862.1.S1_s_at	GNPTAB
Gga.12864.1.S1_at	TEKT1
Gga.12864.1.S1_s_at	TEKT1
Gga.12866.1.A1_at	UGP2
Gga.12867.1.S1_at	NR2C1
Gga.12870.1.S1_at	KCNIP1
Gga.12873.1.S1_at	CHMP1A
Gga.12881.1.S1_s_at	ATP11B
Gga.12884.1.S1_at	PLA2R1
Gga.12886.1.S1_at	ST6GAL2
Gga.1289.1.S1_at	CCNT2
Gga.12890.2.S1_a_at	SLC35B3
Gga.1290.1.S1_at	NDUFS3
Gga.12909.1.S1_at	RHPN2
Gga.12911.1.S1_at	RASL11B
Gga.12914.1.S1_at	C12orf11
Gga.12916.1.S1_at	NARG1L
Gga.12917.1.S1_at	SLC35B3
Gga.12922.1.S1_s_at	SLC12A7
Gga.12924.1.S1_at	SGCE
Gga.12925.1.S1_at	SMCHD1
Gga.12928.1.S1_at	VCAM1
Gga.1293.1.S1_at	LOC420252 /// LOC771634
Gga.12931.1.S1_s_at	ELL
Gga.12933.1.S1_at	RCJMB04_3f10

Gga.12938.1.S1_at	NPBWR1
Gga.12939.1.S1_at	KIAA1826
Gga.1294.1.S1_at	MYO1F
Gga.12941.1.S1_at	SDCCAG10
Gga.12943.1.S1_s_at	CD8A
Gga.12944.1.S1_at	RGS19
Gga.12945.1.S1_at	GCK
Gga.12946.1.S1_at	RCJMB04_11p1
Gga.12947.1.S1_at	LONP2
Gga.12949.1.S1_at	SPAG9
Gga.1295.1.S1_at	UBE2A
Gga.1295.1.S2_at	UBE2A
Gga.12952.1.S1_at	INPP5B
Gga.12953.1.S1_at	ASB2
Gga.12955.1.S1_at	RCJMB04_3p2
Gga.12956.1.S1_s_at	C14orf129
Gga.12965.1.S1_s_at	C21orf45
Gga.12968.1.S1_s_at	DBF4
Gga.12985.1.S1_at	AP4E1
Gga.12986.1.S1_at	NKTR
Gga.12988.1.S1_at	COL24A1
Gga.12993.1.S1_at	RCJMB04_4k2
Gga.12995.1.S1_s_at	CLIC4
Gga.12997.1.S1_s_at	PRRX2
Gga.12999.1.S1_at	TMEM214
Gga.13000.1.S1_at	RAB2A
Gga.13002.1.S1_at	LOC417445
Gga.1301.1.S1_at	LRPPRC
Gga.13012.1.S1_s_at	ASCC3
Gga.13017.1.S1_s_at	RCJMB04_23i18
Gga.13018.1.S1_s_at	C1orf77
Gga.13022.1.A1_at	DNAJB4
Gga.13027.1.S1_at	KCNH7
Gga.13028.1.S1_at	ELF1
Gga.1303.1.S1_s_at	FAM53A
Gga.13036.1.S1_at	SORBS2
Gga.13038.1.S1_at	CYB5R4
Gga.13038.1.S1_s_at	CYB5R4
Gga.13049.2.S1_s_at	KIAA1467
Gga.13052.1.S1_s_at	DPP9

Gga.1306.1.S1_at	NCAPG2
Gga.13062.1.S1_at	MVK
Gga.13064.1.S1_at	SEMA4G
Gga.13076.1.S1_at	OMA1
Gga.13077.1.S1_s_at	PHLDB2
Gga.1308.1.S1_at	KIF20A /// RCJMB04_10113
Gga.13084.2.S1_a_at	LOC417981
Gga.13091.1.S1_at	TMEM41B
Gga.13099.1.S1_at	LOC418364
Gga.131.1.S1_at	MX1
Gga.13100.1.S1_s_at	D2HGDH
Gga.13104.1.S1_at	GAD2
Gga.1311.3.S1_at	LOC418309
Gga.1311.8.S1_at	LOC768776
Gga.13115.1.S1_at	TMEM62
Gga.13118.1.S1_at	LOC771481
Gga.13129.1.S1_s_at	LOC419204
Gga.1313.1.S1_s_at	SPI1
Gga.13135.1.S1_at	ZCRB1
Gga.13140.1.S1_s_at	IVNS1ABP
Gga.13141.3.A1_at	ZNF512B
Gga.13141.3.S1_s_at	UCKL1 /// ZNF512B
Gga.13144.1.S1_at	C14orf32
Gga.13146.1.S1_at	EPSTI1
Gga.13148.1.S1_at	LOC416052
Gga.13150.1.S1_at	PRICKLE2
Gga.13153.1.S1_at	TECPR1
Gga.13158.1.S1_at	MAP3K7
Gga.13159.1.S1_s_at	LOC426100
Gga.13163.1.S1_at	TIPRL
Gga.13173.1.S1_at	PTER
Gga.13174.1.S1_at	TUBD1
Gga.1318.1.S1_s_at	SF3B3
Gga.13183.1.S1_at	ANK2
Gga.13185.1.S1_at	LOC768612
Gga.13193.1.S1_at	APBB2
Gga.13197.1.A1_at	MAST3
Gga.13197.1.S1_at	MAST3
Gga.13205.1.S1_at	RPS6KL1
Gga.13210.1.S1_at	DTNBP1

Gga.13211.1.S1_at	RFXAP
Gga.13215.1.S1_at	NUDT4
Gga.13218.1.A1_at	CDC37L1
Gga.13218.1.S1_at	CDC37L1
Gga.1322.1.S1_a_at	PPP3CA
Gga.1322.2.A1_at	PPP3CA
Gga.13223.1.S1_at	TTC33
Gga.13224.1.S1_at	TMEM63A
Gga.13225.1.S1_at	LOC428366
Gga.1323.1.S1_at	EXOD1
Gga.13245.1.S1_at	TATDN1
Gga.13247.1.S1_at	KIAA1841
Gga.1325.1.S1_at	TES
Gga.13257.1.S1_at	LOC421552
Gga.13267.1.S1_at	TOM1L1
Gga.13269.1.S1_at	S1PR1
Gga.13271.1.S1_at	RABGEF1
Gga.13277.1.S1_s_at	SNX8
Gga.1328.1.S2_at	B2M
Gga.1328.2.A1_at	B2M
Gga.13280.1.S1_at	LOC768499
Gga.13283.1.S1_at	TXNDC13
Gga.13289.1.S1_at	ASXL3
Gga.1329.1.S2_at	ARNTL
Gga.13290.1.S1_at	RNFT1
Gga.13291.1.S1_at	OIT3
Gga.13298.1.S1_at	B4GALT6
Gga.13300.1.S1_at	ODF2
Gga.13310.1.S1_at	B4GALNT3
Gga.13311.1.S1_s_at	VPS26B
Gga.13312.1.S1_at	RCJMB04_7b15
Gga.13315.1.S1_at	C1orf9
Gga.13321.2.S1_a_at	PHB
Gga.13323.2.A1_at	IGF2BP3
Gga.13324.1.S1_at	BBS12
Gga.13327.1.S1_s_at	C4orf18
Gga.13338.1.S1_s_at	HIAT1
Gga.13339.1.S1_at	ST8SIA6
Gga.13340.2.S1_a_at	COMMD9
Gga.13341.1.S1_at	LOC423270

Gga.13342.1.S1_at	TST
Gga.13343.1.S1_at	MESDC2
Gga.1335.1.S1_at	SLC4A2
Gga.13352.1.S1_at	ZCCHC7
Gga.13354.1.S1_at	GARNL3
Gga.13354.2.S1_at	GARNL3
Gga.13356.1.S1_at	C1orf41
Gga.1336.1.S1_at	ISG20L2
Gga.13367.1.S1_at	AMOTL2
Gga.1337.1.S1_at	LOC395787
Gga.1337.2.S1_a_at	LOC395787
Gga.13373.1.S1_at	CSGALNACT1
Gga.13374.1.S1_at	INPP5F
Gga.13385.1.S1_at	LOC430303
Gga.13391.2.S1_at	LOC417234
Gga.13392.1.S1_at	LOC415987
Gga.13393.1.S1_s_at	LRCH2
Gga.13399.2.S1_s_at	RCJMB04_7g14
Gga.13400.1.S1_at	ZCCHC11
Gga.13403.1.S1_at	CPSF3L
Gga.13412.1.S1_at	OSBPL2
Gga.13415.1.S1_at	ADD3
Gga.1342.1.S1_at	KIF5B
Gga.13424.1.S1_at	SCLT1
Gga.13432.1.S1_s_at	R3HDM1
Gga.13436.1.S1_s_at	PMM2
Gga.13438.1.S1_s_at	RBM5
Gga.13439.1.S1_at	ARV1
Gga.13440.1.S1_at	RGS9
Gga.13442.1.S1_at	RDX
Gga.13445.1.S1_a_at	NEXN
Gga.13445.1.S1_at	NEXN
Gga.13448.1.S1_at	OSTN
Gga.1345.2.A1_at	YTHDC2
Gga.1345.2.S1_at	YTHDC2
Gga.13450.1.S1_at	RCJMB04_5f7
Gga.13466.1.S1_at	HNRNPH3
Gga.13469.1.S1_at	LOC771290
Gga.1348.1.S1_at	ARHGAP24
Gga.13481.1.S1_at	FBXL22

Gga.13484.1.S1_at	IL15
Gga.13489.1.S1_at	C2CD2
Gga.13490.1.S1_at	CKMT1A
Gga.13491.1.S1_at	LOC770869
Gga.13493.1.S1_s_at	CEP152
Gga.135.3.S1_a_at	NRG1
Gga.13500.1.S1_at	SFRS3
Gga.13502.1.S1_at	PHF11
Gga.13507.1.S1_at	LOC768787
Gga.13513.1.A1_at	RAB21
Gga.13513.1.S1_at	RAB21
Gga.13515.1.S1_at	RCJMB04_11a8
Gga.13519.1.S1_s_at	RCJMB04_25m5
Gga.13529.1.S1_s_at	SLC31A1
Gga.1353.1.S1_at	ROCK1
Gga.13530.1.S1_s_at	NANP
Gga.13531.1.S1_s_at	CCDC47
Gga.13539.1.S1_at	NPEPPS
Gga.13542.1.S1_s_at	RCJMB04_1f5
Gga.13544.1.S1_at	FNDC3B
Gga.1356.1.S1_at	RDM1
Gga.13564.1.S1_at	KIAA1946
Gga.13569.1.S1_at	LOC422347
Gga.13574.1.S1_at	FSTL4
Gga.13579.1.S1_at	RCJMB04_1919
Gga.13579.1.S1_s_at	RCJMB04_1919
Gga.13580.1.S1_at	NEK1
Gga.13583.1.S1_at	CD36
Gga.13584.1.S1_at	TRIO
Gga.13585.1.S1_at	FAM20A
Gga.13585.1.S1_s_at	FAM20A
Gga.13586.1.S1_at	NPLOC4
Gga.13589.1.S1_at	LOC415605 /// REEP5
Gga.13594.1.S1_at	RAB31
Gga.13595.1.S1_at	MUC
Gga.13605.1.A1_at	RPL9
Gga.1361.1.S1_at	PARP11
Gga.13611.1.S1_s_at	TVA
Gga.1362.2.S1_a_at	ZMYND8
Gga.13627.1.S1_s_at	ACBD7

Gga.1363.1.S1_at	CD38
Gga.13657.1.S1_s_at	UTRN
Gga.1366.2.S1_a_at	SGK269 /// TSPAN3
Gga.13662.1.S1_s_at	PDCD6IP
Gga.13663.1.S1_at	FAM40B
Gga.13672.1.S1_at	RCJMB04_7n4
Gga.13676.1.S1_at	ACSM5
Gga.13680.1.S1_at	NSMCE1
Gga.1369.1.S1_at	P2RX4
Gga.13691.1.S1_at	CMTM4
Gga.137.1.S1_at	EDNRA
Gga.13704.1.A1_s_at	PTPN3
Gga.13708.1.S1_at	EFHA2
Gga.13730.1.S1_at	MMP23B
Gga.13736.1.S1_at	TMEM14C
Gga.1374.4.S1_x_at	GAPDH
Gga.13740.1.S1_at	GULP1
Gga.13749.1.A1_at	HAUS8
Gga.1375.2.S1_s_at	SRP54
Gga.1378.1.S1_s_at	RCJMB04_10m2
Gga.13785.1.S1_at	HNRPLL
Gga.138.1.S1_at	EDNRB2
Gga.13803.1.S1_s_at	CPA6
Gga.1382.1.S1_at	GPD1L
Gga.13823.1.S1_at	LOC425001
Gga.13824.1.S1_at	DNAH10
Gga.13840.1.S1_at	GALNT7
Gga.13846.1.S1_s_at	XPO4
Gga.13848.1.S1_s_at	TANC1
Gga.1385.2.S1_at	DEAF1
Gga.1385.3.S1_at	DEAF1
Gga.13852.1.S1_at	FAM73B
Gga.13858.1.S1_at	FAM69B
Gga.13861.1.S1_s_at	ARMC8
Gga.13865.1.S1_s_at	AHCTF1P
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Gga.13872.1.S1_s_at	KIAA1841
Gga.13879.1.S1_s_at	ZNF532
Gga.13883.1.S1_at	BBS5
Gga.13883.1.S1_s_at	BBS5

Gga.13887.1.S1_s_at	CCDC111
Gga.13891.1.S1_s_at	GLT1D1
Gga.13894.1.S1_s_at	LOC415859
Gga.13895.1.S1_at	TRAK1
Gga.13897.1.S1_x_at	XPC
Gga.139.1.S1_at	TCF7
Gga.13902.1.S1_at	PWWP2A
Gga.13903.1.S1_at	PITX1
Gga.13908.1.S1_at	LOC769056
Gga.13911.1.S1_at	CD93
Gga.13917.1.S1_at	TBC1D9
Gga.13935.1.S1_at	CBS
Gga.13957.1.S1_at	LOC417755
Gga.1396.1.S1_at	GAL8
Gga.1396.2.S1_s_at	GAL8
Gga.13963.1.S1_s_at	C13orf24
Gga.13970.1.S1_s_at	RBM46
Gga.13978.1.S1_s_at	LHFPL5
Gga.13979.1.S1_s_at	SCAPER
Gga.13984.1.S1_s_at	LOC768338 /// MTFR1
Gga.14.1.S1_at	SEMA3F
Gga.140.1.S1_at	TCF7L1
Gga.14001.1.S1_at	SPAST
Gga.14002.2.S1_at	DENND4C
Gga.14016.1.S1_x_at	LTBP3
Gga.14021.1.S1_s_at	SCN8A
Gga.14025.1.S1_at	SAP30L
Gga.14029.1.S1_at	SLC16A12
Gga.1403.1.S1_a_at	THRSP
Gga.14038.1.S1_at	LOC419322
Gga.1404.1.S1_at	MCFD2
Gga.14055.1.S1_at	LIN28B
Gga.14057.1.S1_a_at	LOC418554
Gga.14064.1.S1_at	LOC418782
Gga.14068.1.S1_at	DEPDC6
Gga.14074.1.S1_s_at	MTMR12
Gga.14078.1.S1_s_at	RCJMB04_34c15
Gga.14081.1.S1_at	DHCR7
Gga.14122.1.S1_s_at	AHNAK2
Gga.14132.1.S1_at	ATF7IP

Gga.14146.1.S1_at	LOC426031
Gga.14152.1.S1_at	LOC771290
Gga.14154.1.S1_at	NOM1
Gga.14157.1.S1_at	CABLES2
Gga.14169.1.S1_at	NHS
Gga.14179.1.S1_at	DDEF1
Gga.14180.1.S1_at	TNS3
Gga.14180.1.S1_s_at	TNS3
Gga.14192.1.S1_at	LOC769469
Gga.14193.1.S1_s_at	CNTNAP5
Gga.14196.1.S1_at	ANKRD34A
Gga.142.1.S1_at	PTPRO
Gga.14209.1.S1_at	LOC425403
Gga.14210.1.S1_a_at	MLF1IP
Gga.14210.2.S1_at	MLF1IP
Gga.14211.1.S1_at	NOTCH2
Gga.14213.1.S1_at	LDLRAD1
Gga.14215.1.S1_s_at	FANCB
Gga.14220.1.A1_at	MAP1A
Gga.14225.1.S1_at	LOC427029
Gga.14226.1.S1_s_at	PDE5A
Gga.14227.1.S1_at	LOC423015
Gga.14253.1.S1_at	DUSP22
Gga.14265.1.A1_at	RASA1
Gga.14272.1.S1_at	MC5R
Gga.143.1.S1_at	TGFBR1
Gga.14303.2.S1_at	GAB2
Gga.14314.1.S1_s_at	MTMR6
Gga.14335.1.S1_at	LOC421901
Gga.14338.1.S1_at	FGFR2
Gga.14339.1.S1_s_at	C13orf15
Gga.14346.1.S1_at	GOLGB1
Gga.14359.1.S1_a_at	LOC771050 /// LOC772231
Gga.14362.1.S1_at	RAGE
Gga.14367.1.A1_s_at	PYROXD1
Gga.14368.1.S1_at	GNAZ
Gga.14368.2.S1_a_at	GNAZ
Gga.14388.1.S1_at	UTS2
Gga.14392.1.S1_at	ADCY5
Gga.14393.1.S1_s_at	PDE7B

Gga.14394.1.S1_at	CYP2R1
Gga.14397.1.S1_s_at	SPRED2 /// TNRC6A
Gga.14399.1.S1_at	GTF3C4
Gga.144.1.S1_at	ENTPD8
Gga.14400.1.S1_at	IFT122
Gga.14403.1.S1_s_at	DYRK2
Gga.14404.1.S1_s_at	FNBP4
Gga.14406.2.S1_a_at	LOC426829 /// LOC769984 /// LOC
Gga.14411.1.S1_at	RBM12
Gga.14412.1.S1_at	LOC422694
Gga.14413.1.S1_at	LTV1
Gga.14416.1.S1_at	PTEN
Gga.14417.2.S1_a_at	SLC41A1
Gga.14419.1.S1_s_at	CHORDC1
Gga.14426.1.S1_at	LIPA
Gga.14427.1.S1_at	LOC772054
Gga.14429.1.S1_at	LOC776315
Gga.1443.2.S1_s_at	MAP2K1
Gga.14432.1.S1_s_at	HMX1
Gga.14435.1.A1_at	RCJMB04_3o20
Gga.14445.1.S1_s_at	SLC1A6
Gga.14449.1.S1_at	PLEKHB1
Gga.14450.1.S1_at	ARL8B
Gga.14452.1.S1_at	CCT8
Gga.14453.1.S1_at	LOC407087
Gga.14455.1.S1_at	GEM
Gga.14455.1.S2_at	GEM
Gga.14456.1.S1_at	CLEC2D
Gga.14461.1.S1_at	LOC426827
Gga.14463.1.S1_at	SETD8
Gga.14466.1.S1_at	PCDH17
Gga.14472.1.S1_at	ACSS3
Gga.14489.1.S1_at	LOC419032
Gga.14492.1.S1_at	NT5C1B
Gga.145.1.S1_at	NR2C1
Gga.14502.1.A1_at	LOC424525
Gga.14502.1.S1_at	COL24A1 /// LOC424525
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Gga.14509.1.S1_s_at	HERC2
Gga.14520.1.S1_at	LOC427227

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Gga.14535.1.S1_at	FUK
Gga.1454.1.S1_at	LSM5
Gga.14549.1.S1_at	RCJMB04_5a10
Gga.1457.1.S1_at	HFM1
Gga.14571.1.S1_s_at	HPS5
Gga.14573.1.S1_at	PPM1J
Gga.14579.1.S1_at	CUBN
Gga.146.1.S2_at	DYRK1A
Gga.14605.1.S1_at	FGD6
Gga.14608.1.S1_at	GALNT3
Gga.14609.1.S1_at	HERC4
Gga.14618.1.S1_at	DTX3L
Gga.14622.1.S1_s_at	DDX51
Gga.14646.1.A1_at	DPY19L1
Gga.14655.1.S1_at	USP16
Gga.14659.1.S1_at	PMCH
Gga.14664.1.S1_at	TECPR1
Gga.14683.1.S1_s_at	ADAMTSL1
Gga.14691.1.S1_at	TUFT1
Gga.14700.1.A1_at	ACTBL2
Gga.14700.1.S1_at	ACTBL2
Gga.14717.1.S1_at	TAP1
Gga.14719.1.S1_at	LOC421768
Gga.14725.1.S1_at	B4GALT6
Gga.14728.1.S1_at	LOC424623
Gga.1473.1.S1_at	JUN
Gga.1475.1.S1_at	DPM1
Gga.14779.2.S1_a_at	LOC426092
Gga.14784.1.S1_at	AGPAT6
Gga.1479.1.S1_at	PTN
Gga.1479.2.S1_a_at	PTN
Gga.14801.1.S1_s_at	BRWD2
Gga.1482.1.S1_at	KPNA3
Gga.14834.1.S1_s_at	BRCA1
Gga.14857.1.S1_at	ATP5C1
Gga.1486.1.S1_at	GNS
Gga.14869.1.S1_at	VPS13B
Gga.1487.1.S2_at	EIF2S2
Gga.14876.1.S1_s_at	SMURF2

Gga.14884.1.S1_at	CCDC88A
Gga.14884.1.S1_s_at	CCDC88A
Gga.14890.1.S1_at	GPR1
Gga.14901.1.S1_at	LOC770649
Gga.14902.1.S1_at	KHDRBS2
Gga.1491.1.S1_at	RREB1
Gga.14911.1.S1_at	OXTR
Gga.14915.1.A1_at	KIF14
Gga.14915.1.A1_s_at	KIF14
Gga.14936.1.S1_at	IL23R
Gga.14951.1.S1_at	PCGF5
Gga.14952.1.A1_at	SCLT1
Gga.14954.1.S1_at	NAALADL2
Gga.14959.1.S1_s_at	FAM123B
Gga.14960.1.A1_at	TANC2
Gga.14960.1.S1_at	TANC2
Gga.14967.1.S1_s_at	LRRC48
Gga.14969.1.A1_at	ABHD7
Gga.14969.1.S1_at	ABHD7
Gga.1497.2.S1_a_at	C21orf70
Gga.14970.1.S1_at	AGXT2L1
Gga.1498.1.S1_at	GLRX3
Gga.14982.1.S1_at	KIAA1109
Gga.14983.1.S1_at	GDE1
Gga.14999.1.S1_at	PXDN
Gga.150.2.S2_at	FLT1
Gga.15002.1.S1_s_at	ZNF509
Gga.15006.1.S1_at	KIAA1333
Gga.15017.1.S1_at	ACPL2
Gga.15019.1.S1_s_at	TUFT1
Gga.15024.1.A1_at	IL6
Gga.15027.1.S1_at	SLAMF1
Gga.15036.1.S1_at	LOC419276
Gga.15049.1.S1_s_at	LIMS1 /// LOC771176
Gga.15061.1.S1_at	MRGPRH
Gga.1507.1.S1_at	ISL1
Gga.1507.1.S2_at	ISL1
Gga.15070.1.S1_s_at	KIAA1109
Gga.15081.1.S1_at	LOC423113
Gga.15083.1.S1_at	SLC23A3

Gga.15090.1.S1_s_at	TSHZ2
Gga.1510.1.S1_s_at	PSAT1
Gga.15111.1.S1_s_at	SYNE2
Gga.15114.1.S1_s_at	MYST3
Gga.15119.1.S1_at	FAM38B
Gga.15137.1.S1_at	LOC769469
Gga.15140.1.S1_at	LOC423899
Gga.15142.1.S1_s_at	PGDS
Gga.15143.1.A1_at	TTN
Gga.15157.1.S1_at	MYO6
Gga.15163.1.S1_at	C7orf46
Gga.15188.1.S1_at	CNTN4
Gga.15195.1.S1_at	PPP1R10
Gga.15205.1.S1_at	TCF25
Gga.15218.1.S1_at	MFN2
Gga.15221.1.S1_s_at	C17orf85
Gga.15226.1.S1_s_at	C16orf14
Gga.15231.1.S1_at	C21orf70
Gga.15233.1.S1_s_at	IFT88
Gga.15247.1.S1_at	PHF15
Gga.15255.1.S1_s_at	JMJD1C
Gga.15266.1.S1_at	TCP11L1
Gga.15268.1.S1_at	SLC6A6
Gga.15269.1.S1_at	PKHD1
Gga.1527.1.S1_at	METTL7A
Gga.15288.1.S1_at	MYCN
Gga.15296.1.S1_s_at	ERC1
Gga.15305.1.S1_at	PALLD
Gga.15311.1.S1_at	ST6GALNAC3
Gga.15312.1.S1_a_at	UBAP2
Gga.15313.1.S1_at	SFRS4
Gga.15314.1.S1_at	FAM134C
Gga.15314.1.S1_s_at	FAM134C
Gga.15316.1.S1_s_at	STARD4
Gga.15317.1.S1_at	RAP2C
Gga.15318.1.S1_x_at	RPSA
Gga.15320.1.S1_at	GNG11
Gga.15322.1.S1_s_at	MAPT
Gga.15327.1.S1_at	SPG3A
Gga.1533.1.S1_s_at	RACGAP1

Gga.15330.1.S1_at	COL4A3BP
Gga.15332.1.S1_at	C14orf121
Gga.15344.1.S1_s_at	LOC425659
Gga.15345.1.S1_s_at	TMEM175
Gga.1535.1.S1_a_at	NCAPH2
Gga.15350.1.S1_at	CEP55
Gga.15354.1.S1_at	UGCG
Gga.1536.1.S1_at	VPS54
Gga.15365.1.S1_s_at	AP2M1
Gga.15371.1.S1_at	LOC768772
Gga.15388.1.S1_at	SLC24A6
Gga.15399.1.S1_s_at	EVL
Gga.15411.1.S1_at	FAIM2
Gga.15420.1.S1_at	SIPA1L2
Gga.15424.1.S1_at	WDSOF1
Gga.15427.2.S1_a_at	LOC420734
Gga.15457.1.S1_at	KIF27
Gga.1546.1.S1_at	PRRX1
Gga.1546.1.S2_a_at	PRRX1
Gga.15467.1.S1_s_at	DPH3
Gga.15490.1.S1_at	LOC416390
Gga.155.1.S1_s_at	LGALS3
Gga.1551.2.S1_a_at	BIRC5
Gga.15510.1.S1_at	TCP11
Gga.15518.1.S1_at	KLHL10
Gga.15543.2.S1_at	LOC421495
Gga.15567.1.S1_at	TMPRSS2
Gga.15578.1.S1_a_at	FOXN4
Gga.15580.1.S1_at	SLC24A4
Gga.15588.1.S1_at	LOC416618
Gga.15601.1.A1_at	LOC426161
Gga.15620.1.A1_at	LOC426985
Gga.1567.1.S1_a_at	LOC772356
Gga.15677.1.S1_at	API5 /// RCJMB04_17g4
Gga.157.1.S1_at	RUNX2
Gga.15700.1.S1_at	BHLHB2
Gga.15703.1.S1_at	NR2C2
Gga.15703.2.S1_at	NR2C2
Gga.15703.2.S1_s_at	NR2C2
Gga.15708.1.S1_at	TMEM184B

Gga.15709.1.S1_s_at	RCJMB04_30a20
Gga.15719.1.S1_at	THAP7
Gga.15728.1.S1_at	RCJMB04_7f20
Gga.1573.1.S1_at	HPD
Gga.15744.1.S1_at	SNX3
Gga.15745.1.S1_at	PNPT1
Gga.15746.1.S1_at	JMJD1C
Gga.15754.1.S1_at	AMD1
Gga.15762.1.S1_at	LOC416415
Gga.15772.1.S1_at	KIF24
Gga.15784.2.S1_a_at	C6orf186
Gga.15785.1.S1_at	LYSMD2
Gga.15795.1.S1_at	UBE2V2
Gga.158.1.S1_a_at	IRF10
Gga.15801.1.S1_s_at	DTL
Gga.15803.1.S1_at	TXNDC16
Gga.15805.1.S1_at	FLT4
Gga.15811.2.S1_s_at	N-PAC
Gga.15811.3.S1_s_at	N-PAC
Gga.15815.1.A1_at	TRAIP
Gga.15821.1.S1_at	LASP1
Gga.15822.1.S1_at	ZNF318
Gga.15826.1.S1_at	RNF149
Gga.15833.1.S1_at	CEP63
Gga.1584.1.S1_s_at	RCJMB04_25a7
Gga.15842.1.S1_at	C6orf98
Gga.15843.1.S1_at	EME1
Gga.1585.1.S2_at	STMN2
Gga.15860.1.A1_at	CCDC117 /// LOC769136
Gga.15860.1.S1_at	LOC416916
Gga.15868.1.S1_s_at	TMEM37
Gga.15873.1.S1_at	LETM2
Gga.1588.1.S1_at	ZDHHC14
Gga.15881.1.S1_at	ZFP106
Gga.15885.1.S1_at	SACS
Gga.15892.1.S1_at	HMG20A
Gga.159.1.S1_at	MID1
Gga.15900.1.S1_s_at	RCJMB04_11k6
Gga.15902.1.S1_s_at	ASCC3L1
Gga.15903.1.S1_s_at	PDZRN3

Gga.1591.2.S1_at	TBCCD1
Gga.15918.1.S1_at	PPP1R14C
Gga.15934.1.S1_at	LOC428586
Gga.15935.1.S1_s_at	NUP153
Gga.15943.1.S1_at	FAM46D
Gga.15948.1.S1_at	PATZ1
Gga.15954.1.S1_at	GAB1
Gga.15956.1.S1_at	LOC426275
Gga.15957.1.S1_s_at	KIAA0664
Gga.15961.2.S1_x_at	CEP76 /// LOC768721
Gga.15975.1.S1_at	DAK
Gga.15981.1.S1_at	RCJMB04_6p13
Gga.15982.1.S1_at	MANBA
Gga.15983.1.S1_s_at	FXN
Gga.1599.1.S1_s_at	PARP6
Gga.15991.1.S1_at	LOC420501
Gga.15996.1.S1_at	LOC431243 /// LOC431477
Gga.15998.1.S1_at	COLEC12
Gga.16.1.S1_at	GHRL
Gga.160.1.S2_at	FSHB
Gga.16002.1.S1_at	ENOX1
Gga.16007.1.S1_at	TDP1
Gga.16012.1.S1_s_at	RCJMB04_20f16
Gga.16014.1.S1_at	LOC425209
Gga.16019.1.S1_at	P4HA3
Gga.16025.1.S1_at	C3orf14
Gga.16030.1.S1_at	TMEM220
Gga.16032.1.A1_at	YTHDC1
Gga.16033.1.S1_at	CHAD
Gga.16036.1.S1_at	UACA
Gga.16038.1.S1_at	ADIPOQ
Gga.16040.1.S1_at	TRIO
Gga.16042.1.S1_at	C5orf24
Gga.16045.1.S1_at	LOC423899
Gga.1605.1.S1_s_at	RSPO3
Gga.16050.1.S1_s_at	DNAJC3
Gga.16053.1.S1_at	RCOR3
Gga.16057.1.S1_s_at	E2F8
Gga.16063.1.S1_s_at	ABTB1
Gga.16065.1.S1_at	SLC1A4

Gga.16067.1.S1_at	CD55
Gga.16080.1.S1_at	FDXR
Gga.16081.1.S1_at	LOC769756
Gga.16086.1.S1_s_at	ERCC5
Gga.16087.1.S1_at	LOC427191
Gga.16089.1.S1_s_at	BTBD12
Gga.1609.1.S1_at	APOH
Gga.16098.1.S1_at	SOX5
Gga.16099.1.S1_s_at	LOC426499
Gga.16103.1.S1_at	C3orf59
Gga.16111.1.S1_at	RCJMB04_5k12
Gga.16115.1.S1_s_at	GPR153
Gga.16117.1.A1_at	CP
Gga.16123.1.S1_at	RAD51
Gga.16126.1.S1_at	CADPS
Gga.16138.1.S1_at	LOC421716
Gga.16139.1.S1_s_at	RCJMB04_8n14
Gga.16147.1.S1_at	PITPNM3
Gga.16149.1.S1_a_at	ANKMY1
Gga.1615.1.S1_at	TMTC1
Gga.16164.1.S1_s_at	RAB14
Gga.16181.1.S1_at	KIAA1310
Gga.16181.1.S1_s_at	KIAA1310
Gga.16189.2.S1_a_at	TMCO7
Gga.16194.1.S1_at	PTPRK
Gga.16196.1.S1_at	KRT14
Gga.16198.1.S1_at	FUCA1
Gga.16202.1.S1_at	LOC415665
Gga.16207.1.S1_s_at	PPP2R3A
Gga.16219.1.S1_at	RNF19B
Gga.1622.1.S1_at	MANEA
Gga.16228.1.S1_at	FAM81A
Gga.16229.1.A1_at	PDAP1
Gga.1623.1.S1_at	N6AMT2
Gga.16230.2.S1_a_at	KCTD3
Gga.16233.1.S1_x_at	MYO9A
Gga.16242.1.S1_at	CPEB2
Gga.16243.1.S1_at	SCOC
Gga.16250.1.S1_a_at	LOC418218
Gga.16252.1.S1_at	RCBTB1

Gga.16258.1.S1_at	CTTN
Gga.16267.1.S1_at	LOC769497
Gga.16267.1.S1_s_at	LOC417053 /// LOC417057 /// LOC
Gga.16272.1.S1_s_at	C6orf62
Gga.16281.1.S1_s_at	VPS8
Gga.16282.1.S1_at	LOC769088
Gga.16287.1.S1_at	PHF14
Gga.16288.1.S1_at	LOC427227
Gga.16290.1.S1_at	LOC425011
Gga.16294.1.S1_a_at	SEC61A2
Gga.16294.2.S1_s_at	SEC61A2
Gga.16296.1.S1_at	AGPAT3 /// LOC777139
Gga.16298.1.S1_s_at	SECISBP2
Gga.1630.1.S1_x_at	MAPK10
Gga.16301.1.S1_at	LOC419693
Gga.16302.2.S1_s_at	STK10
Gga.16307.1.S1_at	MTMR9
Gga.16313.1.S1_s_at	DIP2B
Gga.16314.1.S1_at	KIAA1913
Gga.16320.1.S1_s_at	WDFY1
Gga.16321.2.S1_at	LOC420382
Gga.16325.1.S1_at	LOC426128
Gga.16334.1.S1_s_at	ABHD13
Gga.16335.1.S1_s_at	DENND4C
Gga.16336.1.S1_at	CDC2L2
Gga.16339.1.S1_at	LOC422221
Gga.16349.2.S1_a_at	LOC415511
Gga.16350.1.S1_at	TLOC1
Gga.16352.1.S1_at	LOC427301
Gga.16354.1.S1_s_at	ATG4B
Gga.16354.1.S2_s_at	ATG4B
Gga.16356.1.S1_at	NOTCH1
Gga.1636.1.A1_s_at	RCJMB04_23h2
Gga.16365.1.S1_at	SPIRE1
Gga.16366.1.S1_s_at	AMDHD2
Gga.16369.1.S1_at	KIAA1109
Gga.16370.1.S1_s_at	TMEM220
Gga.16371.1.S1_s_at	STT3A
Gga.16378.1.S1_at	ASB5
Gga.16385.1.S1_s_at	KIAA0368

Gga.16394.1.S1_at	C4 /// CYP21
Gga.164.1.S1_s_at	NR2C2
Gga.16416.1.S1_at	RCJMB04_11d23
Gga.16417.1.S1_at	USP24
Gga.16420.1.S1_at	RCJMB04_6i4
Gga.16422.1.S1_at	C10orf72
Gga.16425.1.S1_at	IRF2BP2
Gga.16427.1.S1_at	USP14
Gga.16429.1.S1_s_at	TRIM35
Gga.16430.1.S1_at	LOC423474
Gga.16439.1.S1_at	SMOC1
Gga.16442.1.S1_at	LOC771481
Gga.16443.1.S1_s_at	PRDM11
Gga.16444.1.S1_at	PDK4
Gga.16445.1.S1_a_at	LOC769733
Gga.16446.1.S1_s_at	NHEDC2
Gga.1645.1.S1_s_at	RCJMB04_5m7
Gga.16457.1.S1_s_at	IFIH1
Gga.16458.1.S1_at	SPATA17
Gga.16461.3.S1_s_at	RBM7
Gga.16476.1.S1_at	DYNLT3
Gga.16484.1.S1_at	CISD2
Gga.16487.1.S1_s_at	RASA3
Gga.16489.1.S1_at	C5orf30
Gga.16491.2.S1_at	LOC769173 /// RCJMB04_1o21
Gga.16494.1.S1_at	LOC768787
Gga.16494.1.S1_s_at	LOC768787
Gga.16497.1.S1_at	LOC421506
Gga.165.1.S1_at	SOX1
Gga.1650.1.S1_at	LOC428459
Gga.16501.1.S1_at	DNASE2B
Gga.16512.1.S1_at	FAM65A
Gga.1652.1.S1_at	SMPD3
Gga.16521.1.S1_s_at	WDR44
Gga.16523.1.S2_s_at	ATP2A3
Gga.16527.1.S1_at	MTX3
Gga.16533.1.S1_at	DBNL
Gga.16546.1.A1_at	MIA3
Gga.16546.1.S1_at	MIA3
Gga.16550.1.S1_at	LOC416500

Gga.16552.1.S1_a_at	LOC421780
Gga.16552.2.S1_a_at	LOC421780
Gga.16553.1.S1_at	CD81
Gga.16554.2.S1_a_at	LAPTM4B
Gga.16556.1.S1_at	SPATA18
Gga.16559.1.S1_at	SUCLG1
Gga.16560.2.S1_a_at	MCL1
Gga.16563.1.S1_at	ATRX
Gga.16574.1.S1_at	RCJMB04_11a3
Gga.16577.1.S1_at	HEPH
Gga.16581.1.S1_at	GRAMD3
Gga.16583.1.S1_at	CUL1
Gga.16585.1.S1_at	C15orf41
Gga.16586.1.S1_at	BAAT
Gga.16596.1.S1_at	PID1
Gga.16601.1.S1_at	TCBA1
Gga.16601.1.S1_at	TCBA1
Gga.16606.1.S1_at	ARL4C
Gga.1661.1.S1_at	RCJMB04_7b13
Gga.16616.1.S1_at	ODF1
Gga.16621.1.S1_at	LOC417168
Gga.16624.1.S1_at	BRD8
Gga.16625.1.S1_at	TPPP2
Gga.1663.1.S1_s_at	LHFP
Gga.16632.1.S1_at	LRRC67
Gga.16633.1.S1_at	LOC419830
Gga.16635.1.S1_at	SPAG4
Gga.16637.1.S1_at	CYB5D2
Gga.16651.1.S1_s_at	LOC415795
Gga.16656.1.S1_at	LOC416530 /// LOC770733
Gga.16660.2.S1_at	PHF5A
Gga.16660.3.S1_at	PHF5A
Gga.16660.3.S1_s_at	PHF5A
Gga.16663.1.S1_at	C4
Gga.16663.1.S1_s_at	C4
Gga.16665.1.S1_at	EEPD1
Gga.16670.2.S1_s_at	DCK
Gga.16674.1.S1_at	LOC427419
Gga.16679.1.S1_at	RCJMB04_9b7
Gga.16682.1.S1_at	MAGI2

Gga.16685.1.S1_at	FNTA
Gga.16689.1.S1_s_at	PARVB
Gga.16697.1.S1_s_at	CLDND1
Gga.16702.1.S1_at	PTPN5
Gga.16708.1.S1_at	NOL11
Gga.16715.1.S1_at	EVI5
Gga.16721.1.S1_at	LOC423369
Gga.16722.1.S1_at	SRGAP1
Gga.16731.1.S1_at	LOC769088
Gga.16732.1.S1_at	NOVA1
Gga.16744.1.S1_at	GCAT
Gga.1675.1.S1_at	MEGF9
Gga.16752.1.S1_at	TUSC2
Gga.16753.1.S1_s_at	TARDBP
Gga.16754.1.S1_at	LOC427412
Gga.16755.1.S1_s_at	LOC770146 /// TAF3
Gga.16767.1.S1_s_at	KLF6
Gga.16768.1.S1_at	LOC769351
Gga.16786.1.S1_at	ELF1
Gga.16788.1.S1_at	KIAA0082
Gga.16793.1.S1_s_at	PDS5A
Gga.16794.1.S1_s_at	RCJMB04_1f5
Gga.1680.1.A1_at	FGFR2
Gga.16806.3.S1_at	HOMER3
Gga.16806.4.S1_a_at	HOMER3
Gga.16807.1.S1_at	CREB3L2
Gga.16807.1.S1_s_at	CREB3L2
Gga.1682.1.S1_a_at	LOC417447
Gga.16827.1.S1_at	LOC771158
Gga.16830.1.S1_at	MASP2
Gga.16831.1.S1_at	CDH8
Gga.16837.1.S1_at	NIPBL
Gga.16838.1.S1_at	SPCS2
Gga.16839.1.S1_at	STX1A
Gga.1684.1.S1_at	C14orf149
Gga.16840.1.S1_s_at	RCJMB04_32c9
Gga.16843.1.S1_s_at	LOC769938 /// SEPHS1
Gga.16844.2.S1_s_at	COL3A1
Gga.16846.1.S1_s_at	C20orf194
Gga.16852.1.S1_at	ZADH1

Gga.16860.1.S1_at	LOC417345
Gga.16863.1.S1_s_at	GAL10
Gga.1687.1.S1_at	ALS2CR4
Gga.16870.1.S1_at	ATAD5
Gga.1688.1.S1_at	BRUNOL6
Gga.16880.1.S1_at	GANC
Gga.16893.1.S1_at	GLT25D2
Gga.16894.1.S1_at	SEL1L
Gga.16903.1.S1_at	FAM122B
Gga.16910.1.S1_at	CHD9
Gga.16916.1.S1_at	GLA
Gga.16916.2.S1_at	GLA
Gga.16934.1.S1_at	OBFC2A
Gga.16936.1.S1_at	EPS8L2
Gga.16937.1.S1_at	JAKMIP1
Gga.1694.1.S1_at	TTC9
Gga.16962.1.S1_at	PIWIL1
Gga.16970.1.S1_at	GEN1
Gga.16971.1.S1_at	LAMC1
Gga.16974.1.S1_at	CABP1
Gga.16978.1.S1_at	KLHL29
Gga.16986.1.S1_at	LOC415871
Gga.16991.2.S1_a_at	ADHFE1
Gga.16992.1.S1_at	SMC6
Gga.16995.1.S1_at	LOC424473
Gga.16998.1.S1_at	SLC24A5
Gga.17001.1.S1_at	OXR1
Gga.17002.1.S1_at	LOC418362
Gga.17004.1.S1_at	ST3GAL5
Gga.17006.1.S1_s_at	ARHGEF10
Gga.17007.1.A1_at	HIAT1
Gga.17007.1.S1_at	HIAT1
Gga.17013.1.S1_at	FAM136A /// LOC426296
Gga.17017.1.S1_at	KIAA0753
Gga.17025.1.S1_at	GPM6B
Gga.17034.1.S1_s_at	YPEL2
Gga.17040.2.S1_a_at	FGF2
Gga.17046.1.S1_at	LONRF3
Gga.17051.1.S1_at	GALNTL1
Gga.17053.1.S1_s_at	RCJMB04_27114

Gga.17061.1.S1_s_at	ABCC1
Gga.17062.1.S1_s_at	ZNF644
Gga.17063.1.S1_s_at	RCJMB04_27k21
Gga.17067.1.S1_at	ALG9
Gga.1707.1.S1_at	CAPN1
Gga.17073.1.S1_at	SLC25A32
Gga.17077.1.S1_s_at	SYNE2
Gga.17086.1.S1_at	LOC771537
Gga.17089.1.S1_at	C8orf41
Gga.17090.1.S1_s_at	SCIN
Gga.171.1.S1_s_at	NR3C1
Gga.17104.1.S1_at	BCL2L15
Gga.17114.2.S1_a_at	HLF
Gga.17129.1.S1_at	PRMT8
Gga.17133.1.S1_s_at	DOCK3
Gga.17143.1.S1_s_at	MESDC2
Gga.17144.1.S1_s_at	TMED2
Gga.17147.1.S1_s_at	CCDC127
Gga.17156.1.S1_at	ALG14
Gga.17166.1.S1_at	TRAIL-LIKE
Gga.1717.1.S1_at	IFITM5
Gga.17174.1.S1_at	FN3K
Gga.17178.1.S1_at	LOC416622
Gga.17186.1.S1_at	PLEKHK1
Gga.172.1.S1_a_at	EPHA1
Gga.1720.1.S1_at	BCAR1
Gga.17202.1.S1_s_at	WWC1
Gga.17216.1.S1_s_at	RRAGC
Gga.17219.1.S1_at	EFHA2
Gga.1722.1.S1_at	TMEM49
Gga.17228.2.S1_s_at	SLC25A24
Gga.17232.1.S1_at	SGK269
Gga.17234.1.S1_at	LOC421419
Gga.17240.1.A1_at	LEF1
Gga.17249.1.S1_at	ZNF827
Gga.17253.1.S1_at	CHPT1
Gga.17263.1.S1_at	LOC424155
Gga.17269.1.S1_at	ST6GALNAC5
Gga.17276.1.S1_at	ERBB2IP
Gga.17279.1.S1_at	ARFGAP2

Gga.17290.1.S1_at	BTBD3
Gga.17291.1.S1_at	C1orf168
Gga.1730.1.S1_at	SLC26A11
Gga.17301.1.S1_at	SMPDL3B
Gga.17305.1.S1_s_at	SGMS1
Gga.17307.1.S1_at	NFIB
Gga.17308.1.S1_s_at	DYNLL2
Gga.17309.1.S1_at	CNO
Gga.17312.1.S1_at	ZNF292
Gga.17314.1.S1_at	RCJMB04_16k12
Gga.17317.1.S1_s_at	TRPV6
Gga.17327.1.S1_at	TOR1AIP1
Gga.1733.1.S1_at	DHRS2
Gga.17331.2.S1_at	LOC416414
Gga.17339.1.S1_s_at	SPEN
Gga.17356.1.S1_at	SFRS8
Gga.1737.1.S1_at	SLC27A4
Gga.17380.1.S1_at	DCUN1D1
Gga.17383.1.S1_at	RCJMB04_8f10
Gga.17392.1.S1_at	TMEM215
Gga.17395.1.S1_s_at	LOC770202
Gga.1740.1.S1_at	LOC420679
Gga.17410.1.S1_at	GLCCI1
Gga.17424.1.S1_at	RLBP1L1
Gga.17425.1.A1_at	POM121
Gga.17432.1.A1_at	TBC1D22B
Gga.17437.1.S1_at	MTUS1
Gga.17441.1.S1_at	FAM101A
Gga.17442.1.S1_at	NRF1
Gga.17448.1.S1_at	USP30
Gga.1746.1.S1_s_at	LOC420108
Gga.17467.1.S1_s_at	TTN
Gga.17471.1.S1_at	KIAA0319L
Gga.17473.1.S1_at	TXNDC10
Gga.17473.1.S1_s_at	TXNDC10
Gga.17477.1.S1_at	ATP13A3
Gga.17479.1.S1_s_at	LOC416668
Gga.1748.1.S1_at	PNPLA2
Gga.17483.1.S1_at	CABLES1
Gga.17484.1.S1_at	ANKRD13C

Gga.17488.1.S1_at	FBLN2
Gga.17492.1.S1_at	ARL13B
Gga.17494.1.S1_at	RNF14
Gga.17495.1.S1_at	ADAMTS13
Gga.1750.1.S1_at	SLC16A2
Gga.17508.1.S2_at	FSTL1
Gga.17512.1.S1_at	RCJMB04_8p1
Gga.17513.1.S1_at	PLEKHC1
Gga.17515.1.S1_at	ADNP
Gga.17517.1.S1_at	NUDT9
Gga.17518.1.S1_at	NKTR
Gga.17519.1.S1_at	UBR2
Gga.17532.1.S1_at	UPK1B
Gga.17535.1.S1_at	RHOC
Gga.1754.1.S1_s_at	YAF2
Gga.17540.1.S1_at	ACOT9
Gga.1755.1.S1_at	NEB
Gga.1755.3.S1_a_at	LOC771699 /// NEB
Gga.17563.1.S1_s_at	FAM76B
Gga.17572.1.S1_at	KTI12
Gga.1758.1.S1_at	ALOX5AP
Gga.17580.1.S1_at	SLAIN2
Gga.17585.2.S1_a_at	HDGF
Gga.17590.1.S1_s_at	RCJMB04_10k5
Gga.17594.1.S1_a_at	CADM1
Gga.176.1.S1_a_at	GAL1
Gga.17602.1.S1_s_at	IPO5
Gga.1761.1.S1_at	GPR116
Gga.17610.1.S1_at	CAMK2G
Gga.17621.1.S1_s_at	RP2
Gga.1763.1.S1_at	WFDC1
Gga.17637.1.S1_at	LOC771258
Gga.17638.1.S1_at	ATF3
Gga.17639.1.S1_s_at	GLS
Gga.17642.1.S1_at	RNF213
Gga.17643.2.S1_at	POLRMT
Gga.17645.1.S1_at	TRIP12
Gga.17647.1.S1_at	NCF2
Gga.17647.1.S1_s_at	NCF2
Gga.17648.1.S1_s_at	JMJD1A

Gga.17649.1.S1_s_at	SLC30A6
Gga.1765.1.S1_s_at	LOC420411
Gga.17651.1.S1_s_at	SLC33A1
Gga.17653.1.S1_s_at	TMEM131
Gga.17654.1.S1_at	LRRC40
Gga.17664.1.S1_at	UGCG
Gga.17665.1.S1_s_at	KIAA1324L
Gga.17671.1.S1_at	FRMD5
Gga.17676.1.S1_at	C16orf68
Gga.17678.1.S1_x_at	LOC770627
Gga.17679.1.S1_s_at	CHIR-B5 /// CHIR-B6 /// LOC4254
Gga.1768.1.S1_at	MGAT3
Gga.177.1.A1_at	GLIS2
Gga.17704.1.S1_at	WFIKK2
Gga.17706.1.S1_at	LOC770209
Gga.17720.1.A1_at	SPEN
Gga.17726.1.S1_at	RCJMB04_5h22
Gga.17727.1.S1_at	SPAG16
Gga.1773.1.S1_at	ADCY9
Gga.17731.1.S1_s_at	PPAT
Gga.1774.1.S1_at	C9orf82
Gga.17745.1.S1_s_at	TSR1
Gga.17750.1.S1_at	LOC421727
Gga.17752.1.A1_at	LOC420030
Gga.17761.1.S1_at	C6orf60
Gga.17774.1.S1_s_at	KIF5C
Gga.17782.1.S1_at	TNFRSF13B
Gga.17799.1.S1_at	MAGI2
Gga.178.1.S1_s_at	GBP
Gga.1780.1.S1_at	PUM2
Gga.17805.1.S1_at	HNRPA3
Gga.17811.1.A1_at	C10orf47
Gga.17821.1.A1_at	NDFIP1
Gga.17822.1.S1_at	KIAA1217
Gga.1783.1.S1_at	SLCO2B1
Gga.1784.1.S1_at	ITGA8
Gga.1784.1.S2_at	ITGA8
Gga.17845.1.S1_at	LOC418204
Gga.17847.1.S1_at	LOC427288
Gga.17860.1.S1_at	DOK7

Gga.17880.1.S1_at	TSPAN12
Gga.17888.1.S1_s_at	SH3RF1
Gga.17898.1.S1_s_at	SYNE2
Gga.179.1.S1_s_at	AVR2 /// LOC427416
Gga.17912.1.A1_at	FANCA
Gga.17917.1.S1_s_at	NSD1
Gga.17928.1.S1_at	SFRS11
Gga.17938.1.S1_at	CCDC91
Gga.1794.1.S1_at	NCAM1
Gga.17940.1.S1_at	ANAPC4
Gga.1796.1.S1_s_at	PLEKHB1
Gga.17961.1.S1_at	SMPD4
Gga.17964.1.S1_at	LOC418414
Gga.1798.1.S1_a_at	TSC22D1
Gga.1798.3.A1_at	TSC22D1
Gga.17980.1.S1_at	RCJMB04_3e14
Gga.17980.1.S1_s_at	RCJMB04_3e14
Gga.17986.1.S1_at	FRMD4B
Gga.17987.1.S1_at	JAKMIP2
Gga.1799.1.S2_at	RPL29
Gga.17993.1.S1_at	ZC3HAV1
Gga.18001.1.S1_at	ABCB10
Gga.18003.1.S1_at	PRKACB
Gga.18007.1.S1_at	DDX49
Gga.18023.1.S1_at	LOC419171
Gga.18029.1.S1_at	LOC423731
Gga.1804.1.S1_at	SLC35B4
Gga.1804.1.S1_s_at	SLC35B4
Gga.18051.1.S1_s_at	E4F1
Gga.18059.1.S1_at	PTPLA
Gga.1806.1.S1_at	SOUL
Gga.18068.1.S1_s_at	FRMD1
Gga.18073.1.S1_at	ASPM
Gga.18088.1.S1_at	FKBP6
Gga.1809.1.S1_at	HSPB1
Gga.18091.1.S1_at	MTMR8
Gga.18109.1.S1_at	CNOT2
Gga.18117.1.S1_at	LCT
Gga.18121.1.S1_s_at	NARG2
Gga.18122.1.S1_s_at	PLXNC1

Gga.18131.1.S1_at	LOC429096
Gga.18135.1.S1_at	LOC426586
Gga.18136.1.S1_at	ZDHHC21
Gga.1814.1.S1_at	PUNC
Gga.1815.1.S1_at	TUBB2B
Gga.18151.1.S1_at	BNC1
Gga.18156.1.S1_s_at	BCOR
Gga.1816.1.S1_at	TMEM59
Gga.18161.1.S1_at	AP3D1
Gga.18163.1.S1_at	PEX1
Gga.1817.1.S1_at	SALL1
Gga.1817.1.S2_at	SALL1
Gga.1819.1.S1_at	DIO2
Gga.18194.1.S1_at	RTEL1
Gga.18195.1.S1_at	C9orf75
Gga.182.1.S1_at	NOTCH1
Gga.18223.1.S1_at	NCOR1
Gga.18227.1.S1_at	LOC426196
Gga.1823.1.S1_at	PET112L
Gga.18232.1.S1_at	LOC768462
Gga.18236.1.A1_at	GGA2
Gga.18236.1.S1_at	GGA2
Gga.1824.1.S1_at	PGRMC1
Gga.18246.1.S1_at	KIAA2018
Gga.1825.2.A1_at	PTPLAD1
Gga.18251.1.S1_at	MSH6
Gga.18251.1.S1_s_at	MSH6
Gga.18266.1.S1_at	ANKRD26
Gga.18271.1.A1_at	LOC422606
Gga.18271.1.S1_at	LOC422606
Gga.18271.1.S1_s_at	HELQ
Gga.1828.1.S1_at	RAB11B
Gga.18287.1.S1_at	C14orf135
Gga.183.1.S1_at	UGT8
Gga.18300.1.S1_at	SLITRK2
Gga.18316.1.S1_at	SLC16A10
Gga.18328.1.S1_at	LOC422400
Gga.18338.1.S1_s_at	OGFRL1
Gga.18351.1.A1_at	SULF1
Gga.18355.1.S1_at	LOC771883

Gga.18365.1.S1_s_at	SOX30
Gga.18391.1.S1_at	LOC424998
Gga.18393.1.S1_s_at	CADPS
Gga.18398.1.S1_at	SCUBE2
Gga.184.1.S1_a_at	CSPG5
Gga.18423.1.S1_s_at	C16orf62
Gga.18425.1.S1_at	RCJMB04_9o17
Gga.18429.1.S1_at	UBASH3B
Gga.18435.1.S1_at	C10orf54
Gga.18437.1.S1_at	LOC423545
Gga.1845.1.S1_at	SPIN1
Gga.18455.1.S1_at	ABCD3
Gga.18461.1.S1_s_at	PTPRF
Gga.18467.1.S1_at	MTX3
Gga.18469.1.S1_s_at	DOCK8
Gga.18479.1.S1_at	RILP
Gga.18492.1.A1_at	LOC429131
Gga.18496.1.S1_at	XKR6
Gga.18499.1.A1_at	PTPRS
Gga.18504.1.S1_at	PARVA
Gga.18514.1.S1_s_at	LOC422151
Gga.1852.1.S1_at	AAK1
Gga.18526.1.S1_at	ANKRD50
Gga.1853.1.S1_s_at	TCEA1
Gga.18531.1.S1_s_at	LARS
Gga.18533.1.S1_s_at	PLA2R1
Gga.18542.1.S1_at	MSH3
Gga.18545.1.S1_at	ADAMTS17
Gga.18573.1.S1_at	C22orf30
Gga.18576.1.S1_at	SPTLC3
Gga.18579.1.S1_at	VPS53
Gga.1858.1.S1_at	MRPL41
Gga.18596.1.S1_s_at	CCDC125
Gga.18602.1.S1_s_at	LCORL
Gga.18613.1.S1_at	LOC422956
Gga.18623.1.S1_at	SIRT4
Gga.18629.1.S1_at	TMCC3
Gga.18647.1.S1_s_at	LOC427447
Gga.18655.1.S1_at	LOC419741
Gga.18661.1.S1_at	RCJMB04_22p10

Gga.18667.1.S1_at	LOC777388
Gga.18677.1.S1_at	MUC1
Gga.18678.1.S1_at	LOC426456
Gga.18688.1.S1_at	LL
Gga.1869.1.S1_at	FAM84A
Gga.18694.1.S1_at	LOC769331
Gga.18696.1.S1_s_at	TMCO3
Gga.18697.1.S1_s_at	FBXL10
Gga.187.2.S1_a_at	DBT
Gga.18709.1.S1_at	ARHGAP5
Gga.1871.1.S1_at	FAM96B
Gga.18711.1.S1_s_at	ASPSCR1
Gga.18728.1.S1_s_at	CEP192
Gga.18750.1.A1_at	CCNYL1
Gga.18756.1.S1_s_at	EML1
Gga.18766.1.S1_at	FIGNL1
Gga.1877.1.S1_at	ELAVL1
Gga.18770.1.S1_at	NEIL3
Gga.18773.1.A1_at	ADAMTS15
Gga.18777.1.S1_at	LOC416689
Gga.1878.1.S1_s_at	ARCN1
Gga.1879.1.S1_at	LANCL2
Gga.18814.1.S1_at	LOC418298
Gga.18831.1.S1_s_at	SLC25A28
Gga.18837.1.S1_at	SMC6
Gga.1884.2.S1_s_at	RCJMB04_16e10
Gga.18854.1.S1_s_at	LOC422540
Gga.18859.1.S1_at	ACLY
Gga.18862.1.S1_at	LOC417726
Gga.18880.2.S1_a_at	HSD11B1L
Gga.18891.1.S1_s_at	RAB39B
Gga.18894.1.S1_s_at	PDCD1
Gga.18895.1.S1_s_at	SNRPD3
Gga.18900.1.S1_s_at	GLCCI1
Gga.18909.1.S1_s_at	MYL1
Gga.1891.1.S1_at	YES1
Gga.1891.1.S2_at	YES1
Gga.18910.1.S1_at	GNAI1
Gga.18910.1.S1_s_at	GNAI1
Gga.18916.1.S1_at	NOTCH2

Gga.18918.1.S1_at	PARD3
Gga.18926.2.S1_a_at	PTP4A3
Gga.18928.1.S1_s_at	TNRC15
Gga.18931.1.S1_at	PTP4A1
Gga.18933.1.S1_s_at	RASSF5
Gga.18939.1.S1_at	SCPEP1
Gga.18942.1.S1_at	ACSL1
Gga.18945.1.S1_at	PREX1
Gga.18947.1.S1_at	ADNP2
Gga.18948.1.S1_at	TACC1
Gga.18949.1.A1_at	USP9X
Gga.1895.1.S2_at	GABRG2
Gga.18950.1.S1_s_at	VPRBP
Gga.18956.1.S1_s_at	POLL
Gga.18957.1.S1_at	MKI67
Gga.18959.1.S1_at	RCJMB04_4e14
Gga.18965.1.S1_at	GBP6
Gga.18969.1.S1_s_at	TMBIM1
Gga.18970.1.S1_s_at	RBM16
Gga.18974.1.S1_at	ITPK1
Gga.18980.1.S1_at	NUAK1
Gga.1899.1.S1_a_at	NES
Gga.18993.1.S1_at	DGKI
Gga.19.1.S1_at	IL1B
Gga.19002.1.S1_at	SFRS11
Gga.1901.1.S1_at	SLC29A3
Gga.19011.1.S1_at	FAM134C
Gga.19015.1.S1_at	ZBTB1
Gga.19016.1.S1_s_at	LOC771498 /// USP6NL
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Gga.19025.1.S1_at	DUSP5
Gga.19030.2.A1_a_at	ZDHHC23
Gga.19037.1.S1_at	RCJMB04_3m6
Gga.19042.1.S1_s_at	CDC5L
Gga.19046.1.S1_at	IDH3A
Gga.19049.1.S1_at	IL18
Gga.19056.1.S1_at	GAPVD1
Gga.19057.1.S1_s_at	C11orf46
Gga.19059.2.S1_a_at	SCRN1
Gga.1906.1.S2_at	CRISPLD1

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Gga.19081.1.A1_at	TELO2
Gga.19084.1.S1_s_at	VT A1
Gga.19087.1.S1_at	RALB
Gga.19093.1.S1_s_at	CDYL
Gga.19094.1.S1_s_at	SLC39A6
Gga.19096.1.A1_at	ARL2BP
Gga.191.3.S1_a_at	GHSR
Gga.1910.1.S1_a_at	C6orf192
Gga.19100.1.S1_at	DGKD
Gga.19105.1.S1_s_at	RCJMB04_21j12
Gga.19119.1.S1_at	ANKRD28
Gga.19121.1.S1_at	UQCC
Gga.19126.1.S1_at	METTL5
Gga.1913.1.S1_s_at	RFC1
Gga.19136.1.A1_a_at	MURC
Gga.19140.1.S1_at	RBBP6
Gga.19141.1.S1_at	SNX21
Gga.19142.1.S1_at	CCNJ
Gga.19146.1.S1_at	LOC417822
Gga.19150.1.S1_s_at	LOC777560
Gga.19159.1.S1_at	CACHD1
Gga.19160.1.S1_s_at	SLC10A7
Gga.19162.1.S1_at	RET
Gga.1917.1.S1_at	CDH2
Gga.19172.1.S1_s_at	MYNN
Gga.19177.2.S1_at	LOC425502
Gga.1918.1.S2_at	LMBR1
Gga.19180.1.S1_s_at	MXI1
Gga.19184.1.S1_at	LOC427095
Gga.19187.1.S1_at	RCJMB04_21i6
Gga.19188.1.S1_at	KBTBD10
Gga.19191.1.A1_at	SEZ6L
Gga.19192.1.S1_at	LOC420915
Gga.19202.1.S1_at	LOC421229
Gga.19209.1.S1_at	LOC423724
Gga.19214.1.S1_at	ST8SIA5
Gga.19219.1.S1_at	GABPB2
Gga.19224.1.S1_at	ZXDC
Gga.19228.1.S1_at	RABGAP1

Gga.19241.1.S1_s_at	BRWD1
Gga.1925.1.S1_at	PRRX2
Gga.19251.1.S1_at	TBC1D1
Gga.1926.1.S1_at	RANBP1
Gga.19267.1.S1_s_at	RBBP6
Gga.1927.1.S1_at	GADD45A
Gga.19271.1.S1_at	LOC427192
Gga.19274.1.S1_s_at	LOC418221
Gga.19276.1.S1_s_at	LOC422177
Gga.19278.1.S1_s_at	ALDH9A1
Gga.19279.1.S1_at	CLPTM1L
Gga.19287.1.S1_at	PRPS1
Gga.19288.1.S1_at	TMEM57
Gga.19294.1.S1_at	SLC35E3
Gga.19300.1.S1_at	SLC16A2
Gga.19305.1.S1_at	RSPO3
Gga.19311.1.S1_s_at	ST8SIA3
Gga.19316.1.S1_at	LOC772031
Gga.19319.1.S1_at	NELF
Gga.1932.1.S1_at	CRK
Gga.19320.1.S1_at	LOC426510
Gga.19325.1.S1_at	EPHX2
Gga.19326.1.S1_at	ZNF704
Gga.19329.1.S1_at	C10orf38
Gga.1933.3.S1_at	MRPL20
Gga.19332.1.S1_s_at	MIA3
Gga.19333.1.S1_at	ST6GALNAC3
Gga.19339.1.S1_at	LOC419841
Gga.1935.1.S1_at	FADS2
Gga.19350.1.S1_at	TOR1AIP2
Gga.19361.1.S1_s_at	TNRC6C
Gga.19362.1.S1_at	MYSM1
Gga.19364.1.S1_at	BMP2K
Gga.19381.1.S1_s_at	NIN
Gga.19387.1.S1_at	ATXN7
Gga.1939.1.S1_at	EMP1
Gga.19390.1.S1_at	MED13
Gga.19393.1.S1_s_at	CYP26C1
Gga.19396.1.S1_s_at	RAB22A
Gga.19397.1.S1_at	NOL12

Gga.194.1.S1_at	CBL
Gga.19402.1.S1_at	LOXL3
Gga.19405.1.S1_at	LOC771307
Gga.19408.1.S1_s_at	ACOT9
Gga.19409.1.S1_s_at	COL4A2
Gga.1941.1.S1_at	FZD4
Gga.19410.1.S1_at	LOC772356
Gga.19418.1.S1_at	LOC418786
Gga.19425.1.S1_at	TLE3
Gga.1943.1.S1_a_at	KIAA0368
Gga.19447.2.S1_s_at	LOC770705
Gga.19451.1.S1_at	RCJMB04_17j13
Gga.19452.1.S1_at	CD44
Gga.19455.1.S1_at	LOC417937
Gga.19459.1.S1_s_at	CHST10
Gga.19460.1.S1_at	ANKRD32
Gga.19462.1.S1_at	SLC25A39
Gga.19467.1.S1_at	RNF34
Gga.19467.1.S1_s_at	RNF34
Gga.19470.1.A1_at	CCDC73
Gga.19474.1.S1_at	MAP7D3
Gga.1948.1.S1_at	TMEM106C
Gga.19481.1.S1_at	TTN
Gga.19481.2.S1_at	TTN
Gga.19481.5.S1_a_at	TTN
Gga.19481.6.S1_at	TTN
Gga.19484.1.S1_at	ERGIC2
Gga.1949.1.S1_s_at	NFYA
Gga.19490.1.S1_at	LOC777560
Gga.195.1.S1_at	GPR149
Gga.1950.1.S1_at	FAT3
Gga.19507.1.S1_at	LOC419269
Gga.19508.1.S1_s_at	GAB1
Gga.19511.1.S1_at	C14orf143
Gga.19514.1.S1_s_at	C20orf58
Gga.19526.1.S1_at	LOC421238
Gga.1955.1.S1_s_at	C15orf23
Gga.19553.1.S1_at	TMTC1
Gga.19553.1.S1_s_at	TMTC1
Gga.19558.1.S1_s_at	P2RY8

Gga.19570.1.A1_at	PRIC285
Gga.19571.1.S1_at	FRMPD2
Gga.19575.1.A1_at	HNRPK
Gga.19575.1.S1_at	HNRPK
Gga.1958.1.S1_a_at	CKS2
Gga.19589.1.S1_at	CCDC103
Gga.19592.1.S1_at	IVNS1ABP
Gga.19593.1.S1_s_at	UQCRB
Gga.1960.2.S1_a_at	MB
Gga.19602.1.S1_at	LOC428436
Gga.19613.1.S1_at	LOC417507
Gga.19619.1.S1_at	PHF2
Gga.19628.1.S1_at	TMEM179
Gga.19632.1.S1_at	LOC777116
Gga.1964.1.S1_at	MYO10
Gga.1964.1.S1_s_at	MYO10
Gga.19650.1.S1_at	IDUA
Gga.19651.1.S1_at	PKN2
Gga.19654.1.S1_at	DCLK1
Gga.19655.1.S1_at	NOTUM
Gga.19662.1.S1_at	LOC415615
Gga.19667.1.S1_at	PREX1
Gga.19669.1.S1_at	RCJMB04_2115
Gga.1967.1.S1_s_at	FAM107B
Gga.19677.1.S1_at	DCUN1D3
Gga.19678.1.A1_at	EVL
Gga.19693.1.A1_at	LOC427846
Gga.19693.1.S1_at	LOC427846
Gga.19700.1.S1_at	FOXO3
Gga.19702.1.S1_at	ATG2B
Gga.19706.1.S1_at	UPP2
Gga.19709.1.S1_s_at	F5
Gga.19738.1.S1_s_at	DIAPH3
Gga.19755.1.S1_at	MOCOS
Gga.19759.1.S1_at	LOC421215
Gga.19760.1.S1_at	GPR97
Gga.19774.1.A1_at	VPS41
Gga.19774.1.S1_at	VPS41
Gga.19785.1.S1_at	CLDN15
Gga.19791.1.S1_s_at	LRP12

Gga.19797.1.S1_at	C14orf32
Gga.198.1.S1_at	MMP9
Gga.19815.1.S1_at	ZZEF1
Gga.19833.1.S1_at	DIP2A
Gga.1984.2.A1_a_at	MAD2L1
Gga.19866.1.S1_at	LOC422067
Gga.19867.1.S1_at	TOX3
Gga.19869.1.S1_s_at	TOE1
Gga.19872.1.S1_s_at	ANAPC2
Gga.19875.1.S1_at	PLXNA2
Gga.19877.1.S1_at	MDH2
Gga.19878.1.S1_at	ARID1A
Gga.19885.1.S1_at	CCDC112
Gga.1990.1.S1_at	MRPL35
Gga.19902.1.S1_at	FAF1
Gga.1991.1.S1_at	PIGS
Gga.19912.1.S1_at	LOC427010
Gga.19927.1.S1_at	C20orf7
Gga.19934.1.S1_at	SNAI2
Gga.19937.1.S1_at	RNF207
Gga.19938.1.A1_at	MED31
Gga.19939.1.S1_at	TFF2
Gga.19941.1.A1_at	LOC769949
Gga.19944.1.S1_at	CCDC60
Gga.19950.1.S1_s_at	F13A1
Gga.19953.1.S1_at	C10orf63
Gga.19953.1.S1_s_at	C10orf63
Gga.19955.1.S1_at	ZDHHC3
Gga.19956.1.S1_s_at	CHIA /// LOC768786
Gga.19969.1.S1_at	KIAA0430
Gga.19977.1.S1_s_at	DOCK9
Gga.200.2.S1_a_at	FBN2
Gga.20011.1.S1_at	CCDC84
Gga.20011.2.S1_s_at	RNF19A
Gga.20014.1.S1_s_at	DNER
Gga.20016.1.S1_at	ST3GAL5
Gga.20017.1.S1_s_at	TEC
Gga.20018.1.S1_at	LOC395756
Gga.20038.1.S1_at	EXOC3L
Gga.20040.1.S1_at	LOC417113

Gga.20041.1.S1_at	PCSK6
Gga.20043.1.S1_at	LATS1
Gga.20046.1.S1_s_at	C20orf11
Gga.20056.1.S1_at	PALM2
Gga.20060.1.S1_at	ABAT
Gga.20061.1.S1_at	NINJ2
Gga.20062.1.S1_s_at	SIPA1L2
Gga.20064.1.S1_s_at	UNC119B
Gga.20070.1.S1_at	MAN1A1
Gga.2008.2.S1_a_at	BNIP3
Gga.2010.2.S1_a_at	TOP2A
Gga.2015.1.S1_at	ITGB1
Gga.2024.1.S1_at	MSI1
Gga.2025.1.S1_at	DNTTIP2
Gga.2026.1.S1_at	PLEKHM2
Gga.2029.1.S1_at	C13orf34
Gga.2032.1.S1_at	CDCA2
Gga.2038.1.S1_at	MAB21L2
Gga.2039.1.S1_at	HMOX1
Gga.204.1.S1_at	TMOD4
Gga.2049.1.S1_at	ERGIC1
Gga.2052.2.S1_at	PDHA1
Gga.2057.1.S1_at	C1orf83
Gga.2057.2.S1_a_at	C1orf83
Gga.2058.1.S1_at	GLS
Gga.2058.1.S1_s_at	GLS
Gga.2061.1.S1_at	GATA6
Gga.2064.1.S1_a_at	ERG
Gga.2064.1.S2_at	ERG
Gga.2067.1.S1_at	RCJMB04_9a7
Gga.2070.2.S1_a_at	ID4
Gga.2081.1.S2_at	GATA5
Gga.2083.1.S1_at	TXNL1
Gga.2085.1.S1_at	USP25
Gga.2087.1.S1_s_at	CSNK1E
Gga.2087.1.S2_at	CSNK1E
Gga.2100.1.S1_s_at	DNA2L
Gga.2105.2.S1_a_at	MPRIP
Gga.2117.1.S1_at	WDR5
Gga.2119.1.S1_a_at	LOC426015

Gga.2119.2.A1_x_at	LOC426015 /// LOC768441
Gga.212.1.S1_at	NRXN1
Gga.2124.1.S1_at	ST14
Gga.2128.1.S1_at	LOC768920
Gga.2129.1.S1_s_at	MAP1B
Gga.2136.1.S1_at	LOC429716
Gga.2137.1.S1_s_at	ADARB1
Gga.2141.2.S1_at	C5orf21
Gga.2144.2.S1_a_at	HSF2
Gga.2148.1.S1_at	SLC31A1
Gga.2152.1.S1_at	LOC395762
Gga.2156.2.S1_at	SLIT1
Gga.2163.1.S1_at	MAPK1
Gga.2167.1.S1_at	GNAI1
Gga.217.1.S1_x_at	BLB1
Gga.2171.1.S1_at	FER1L3
Gga.2172.1.S2_at	PPP1R12B
Gga.2178.2.S1_a_at	DOT1L
Gga.218.1.S1_at	TWIST2
Gga.2183.1.S1_at	GRTP1
Gga.2184.1.S1_at	C5orf13
Gga.2186.1.S1_at	GPN2
Gga.2190.2.S1_a_at	SOCS2
Gga.2200.1.S1_at	CYR61
Gga.2210.1.S1_a_at	FKBP1B
Gga.2225.1.S1_at	IL6ST
Gga.2239.1.S1_at	LOC419136
Gga.224.1.S1_at	ZP1
Gga.2240.2.S1_a_at	FREQ
Gga.2250.1.S1_at	HIRA
Gga.2253.1.S1_at	TMEM163
Gga.226.1.S1_at	F13A1
Gga.226.2.S1_a_at	F13A1
Gga.227.1.S1_at	STAR
Gga.2278.1.S1_at	KIAA1529 /// LOC772014
Gga.2283.1.S2_at	DLL1
Gga.229.1.S1_at	HINT1
Gga.2292.2.S1_at	CDC37
Gga.230.1.S1_at	LOC395425
Gga.2301.1.S1_at	APCDD1

Gga.2302.2.S1_at	NVL
Gga.2303.1.S1_at	RAD51
Gga.2305.1.S1_at	CXCR4
Gga.2307.1.S1_at	SETD3
Gga.2309.1.S1_at	DNAJC9
Gga.2309.2.A1_s_at	DNAJC9
Gga.2311.1.S1_s_at	TMCO1
Gga.2320.2.S1_a_at	CENPC1
Gga.2324.2.S1_at	LAP3
Gga.2325.2.S1_s_at	NUPL1
Gga.2329.1.S1_at	EYA1
Gga.2330.1.S1_at	LOC415822
Gga.2337.1.S2_s_at	SP3
Gga.2345.2.S1_a_at	TRIAP1
Gga.2348.1.S1_at	LHX9
Gga.2348.3.S1_a_at	LHX9
Gga.2352.1.S2_at	DAB1
Gga.2356.1.S1_at	SYBL1
Gga.2356.2.S1_at	SYBL1
Gga.2361.1.S1_at	RIC3
Gga.2361.2.S1_a_at	RIC3
Gga.2362.1.S1_s_at	SMCR8
Gga.2364.1.S1_at	LOC423793
Gga.2364.1.S1_s_at	LOC423793
Gga.2368.1.S1_at	CCNE1 /// LOC776873
Gga.2379.1.S1_at	LOC426582
Gga.238.1.S1_at	LRRC17
Gga.2381.1.S1_at	RCJMB04_7i20
Gga.2381.3.S1_at	RCJMB04_7i20
Gga.2383.1.S1_at	ZFX
Gga.2402.1.S1_at	CRY2
Gga.2402.1.S2_at	CRY2
Gga.2402.1.S2_s_at	CRY2
Gga.2406.2.S1_at	DPY19L1
Gga.2409.1.S1_at	WDR1
Gga.2422.2.S2_x_at	LOC772322
Gga.2424.2.S1_a_at	B4GALT2
Gga.2427.1.S1_at	TANC1
Gga.243.3.S1_a_at	NTM
Gga.2431.1.S1_at	C1orf115

Gga.2437.1.S1_at	GSTT1
Gga.2437.1.S2_at	GSTT1
Gga.2444.1.S1_at	MOBKL1A
Gga.2449.3.S1_a_at	RANBP9
Gga.245.1.S1_at	FGF18
Gga.2455.2.A1_at	LOC421802
Gga.2458.1.S1_at	IFRD1
Gga.2462.1.S1_at	TIE1
Gga.2464.1.S1_at	GLUL
Gga.2464.1.S2_at	GLUL
Gga.2467.1.S1_at	IGJ
Gga.2469.1.A1_at	RCJMB04_14o23
Gga.247.1.S1_at	PCSK5
Gga.2475.1.S1_at	PON2
Gga.2479.1.S1_at	ING1
Gga.2485.1.S1_s_at	PRIM2
Gga.2493.2.S1_s_at	NCDN
Gga.2494.1.S2_at	XDH
Gga.2499.1.S1_at	CCBL2
Gga.2501.2.S1_at	UBB
Gga.2501.2.S1_x_at	UBB
Gga.2505.1.S1_s_at	RCJMB04_8l16
Gga.2509.1.S1_at	P2RY1
Gga.2510.1.S1_at	C3
Gga.2516.1.S1_at	PTPRG
Gga.2517.1.S1_at	CHEK2
Gga.2518.1.S1_at	HSBP1
Gga.252.1.S1_at	FOXK1
Gga.2523.1.S1_at	HMGCS2
Gga.2529.1.S1_a_at	IL1RL1
Gga.2529.2.S1_a_at	IL1RL1
Gga.253.1.S1_at	CBF-2
Gga.2531.1.S1_at	LHFPL2 /// LOC395628
Gga.2533.1.S1_s_at	GSTA3
Gga.2535.2.S1_a_at	LTBP1
Gga.2538.2.S1_a_at	NRP2
Gga.2543.1.S1_s_at	REPS2
Gga.2547.1.S1_at	LOC771567
Gga.2549.1.S1_at	LOC416592
Gga.255.1.S1_at	CCL4

Gga.2551.2.S1_a_at	LTF
Gga.2551.2.S1_s_at	LTF
Gga.2557.1.S1_at	SUCLG2
Gga.2558.1.S1_a_at	COL14A1
Gga.256.1.S2_at	TPD52L1
Gga.2565.2.S1_s_at	UTP6
Gga.2572.1.S1_at	LAMP2
Gga.2573.1.S1_at	NRIP3
Gga.2575.1.S1_at	MFSD10
Gga.2589.1.S1_at	LOC419175
Gga.260.1.S1_a_at	CCDC86
Gga.260.2.S1_a_at	DMRT1
Gga.2603.1.S1_at	MAFB
Gga.2608.1.S1_at	DCX
Gga.2609.1.S1_at	THEX1
Gga.2612.1.S1_at	KRT19
Gga.2612.2.S1_a_at	KRT19
Gga.2612.2.S1_s_at	KRT19
Gga.2613.1.S1_s_at	SPARC
Gga.2614.1.A1_at	TMOD1
Gga.2628.1.S1_s_at	ABAT
Gga.2637.1.S1_at	MCOLN2
Gga.2640.1.S1_at	CFC1B
Gga.2641.1.S1_at	LOC424283
Gga.2645.1.S1_at	TGFBR2
Gga.2647.1.S1_at	MTMR2
Gga.2648.1.S2_at	HOXB3
Gga.265.1.S1_at	MARCO
Gga.2657.1.A1_at	LOC420153
Gga.2663.1.S1_at	FKBP9
Gga.2667.1.S1_at	SULT1C3
Gga.2668.2.S1_at	RARB
Gga.2672.2.S1_s_at	RCJMB04_12b8
Gga.2674.2.S1_a_at	FAM69B
Gga.2674.2.S1_at	FAM69B
Gga.2679.1.S1_at	FBLN1
Gga.2680.1.S1_at	AQP1
Gga.2685.1.S2_at	FGF13
Gga.269.1.S1_at	RUNX1T1
Gga.2690.1.S1_a_at	FZD6

Gga.2690.2.S1_a_at	FZD6
Gga.2693.1.S1_at	LARP4
Gga.2694.1.S1_at	LEF1
Gga.2694.1.S2_s_at	LEF1
Gga.2695.1.S1_at	BPMS2
Gga.27.1.S1_at	RAX
Gga.2700.1.S1_at	NR6A1
Gga.2707.2.S1_a_at	CLOCK
Gga.2708.1.S1_at	CLGN
Gga.271.1.A1_at	BMP1
Gga.271.1.S1_at	BMP1
Gga.2713.1.S1_at	KCNG2
Gga.2715.1.S1_at	FBXO5
Gga.2722.1.S1_a_at	CKB
Gga.2726.1.S1_at	SNCA
Gga.273.1.A1_at	TCF7L2
Gga.2733.1.S1_at	CNR1
Gga.2734.1.S2_at	ALCAM
Gga.2737.2.S1_at	INTS6
Gga.2741.1.S2_at	GRIA4
Gga.2742.1.S1_at	FAM96A
Gga.2743.1.S1_at	ARHGAP21
Gga.2745.1.S1_at	COX11
Gga.2747.2.S1_s_at	ZCCHC4
Gga.275.2.S1_a_at	MITF
Gga.2754.1.S1_at	ZWILCH
Gga.2756.1.S1_at	LGI1
Gga.2757.1.S1_at	SIAH1
Gga.2759.1.S1_at	ADD3
Gga.276.1.S1_at	EBF1
Gga.2762.1.S1_s_at	DHX30
Gga.2763.3.S1_a_at	SF3A3
Gga.2764.1.S1_at	SLC35F1
Gga.2769.1.S1_at	IL6
Gga.277.1.S1_at	SRC
Gga.2770.1.S1_at	RCJMB04_16e8
Gga.2770.2.S1_s_at	RCJMB04_16e8
Gga.2775.2.S1_a_at	MYO9A
Gga.2776.1.S1_at	TMEM192
Gga.280.1.S1_at	MAFK

Gga.2808.1.S1_at	C1orf102
Gga.281.1.S1_at	MAFF
Gga.2810.1.S1_at	PFKM
Gga.2810.2.S1_at	PFKL
Gga.2818.1.S1_at	ARNTL2
Gga.2827.2.S1_a_at	TIMP3
Gga.283.1.S1_at	CHRNA9
Gga.2830.1.S1_at	LOC776660
Gga.2832.1.S1_at	RCJMB04_3o20
Gga.2838.1.S1_at	LOC771160
Gga.2838.2.S1_a_at	CUX1 /// LOC771160
Gga.284.1.S1_at	ARBP
Gga.2840.1.S1_at	B4GALT1
Gga.2841.1.S1_at	LRRC8D
Gga.2844.2.S1_s_at	STMN1
Gga.2852.1.S2_at	ACVR2A
Gga.2855.1.S1_at	HABP4
Gga.2858.1.S1_s_at	PTEN
Gga.2860.1.S1_a_at	SLC12A3
Gga.2865.1.S1_at	TAP2
Gga.2876.1.S2_a_at	VAV3
Gga.2876.2.S1_x_at	VAV3
Gga.2877.2.S1_a_at	DNAJC18
Gga.2877.2.S1_at	DNAJC18
Gga.2877.3.S1_s_at	DNAJC18
Gga.2883.1.S1_at	DHFR
Gga.2888.1.S1_at	FBN1
Gga.2891.1.S1_s_at	RCJMB04_13h15
Gga.2893.1.S1_a_at	MERTK
Gga.2896.1.S1_at	CBR1
Gga.2898.1.S1_at	SMTN
Gga.2901.1.S1_s_at	ARHGAP26
Gga.2901.1.S2_at	ARHGAP26
Gga.2902.1.S1_a_at	HBA2
Gga.2902.1.S1_s_at	HBA2
Gga.2905.1.S1_s_at	RCJMB04_18a16
Gga.2909.1.S1_a_at	HBA1
Gga.2909.1.S1_at	HBA1
Gga.2914.1.S1_at	GPC4
Gga.292.1.S1_at	CENPF

Gga.2922.1.S1_at	LOC415303
Gga.2924.3.S1_s_at	MTF1
Gga.2931.1.S1_at	RRBP1
Gga.294.1.S1_at	PHOX2B
Gga.2942.2.S1_at	LAMP2
Gga.2952.1.S1_at	CLDN3
Gga.2956.1.S1_at	IL22RA1
Gga.296.1.S1_at	CCL1
Gga.2960.1.S1_at	CASP6
Gga.2964.3.S1_a_at	CCT6A
Gga.2965.1.S1_at	TIMP2
Gga.2971.2.S1_at	C3orf64
Gga.2971.2.S1_s_at	AER61
Gga.2977.1.S1_at	PTPRZ1
Gga.2980.1.S1_at	IRX2
Gga.2983.1.S1_at	ODZ2
Gga.2986.3.S1_a_at	RB1
Gga.2992.2.S1_at	C18orf37
Gga.2996.1.S2_at	ALDH1A2
Gga.2996.2.S1_a_at	ALDH1A2
Gga.3001.1.S1_at	NISCH
Gga.3003.1.S1_s_at	PRKRIP1
Gga.3009.1.S1_s_at	RCJMB04_2p15
Gga.302.2.S1_a_at	FGF14
Gga.3020.1.S1_at	ACTR2
Gga.3025.1.S1_at	CREB1
Gga.3029.1.S1_at	LOC425350
Gga.3030.1.S1_at	RETSAT
Gga.3033.1.S1_at	LOC417533
Gga.3037.1.S1_s_at	CHRD1
Gga.3043.1.S1_at	FNBP1L
Gga.3047.1.S1_at	EPHA5
Gga.3052.1.S1_s_at	YTHDF1
Gga.3053.1.S1_at	EPHB3
Gga.3060.1.S1_at	BARX2
Gga.3062.2.S1_at	LOC423006
Gga.3063.1.S1_at	MYBPC1
Gga.3066.1.S1_at	HS1BP3
Gga.3074.1.S1_a_at	C-16
Gga.3074.2.S1_at	C-16

Gga.3075.1.S1_at	ADAMTSL3
Gga.3078.1.S1_at	LOC430910
Gga.3080.1.S1_a_at	GLG1
Gga.3080.1.S2_at	GLG1
Gga.3095.1.S1_a_at	PLBD1
Gga.3104.1.S1_at	COL4A2
Gga.311.1.S1_at	FZ-8
Gga.3110.1.S1_x_at	COL6A1
Gga.3111.1.S2_at	CLDN5
Gga.3113.1.S1_at	NCALD
Gga.3118.1.S1_at	DBI
Gga.312.2.S1_a_at	PRR11
Gga.3125.1.S1_at	ID2
Gga.3130.2.S1_a_at	CLIP1
Gga.3136.1.S1_at	SDC3
Gga.3137.1.S1_at	PGDS
Gga.3140.1.A1_at	THSD7A
Gga.3141.1.S1_at	CNR1
Gga.3143.2.S1_s_at	RCJMB04_5g5
Gga.3145.3.S1_at	RCJMB04_34k20
Gga.3146.1.S1_at	CCNB2
Gga.3148.1.S1_at	EXOC5
Gga.3149.1.S1_at	LOC395095
Gga.3157.1.S1_at	MRE11A
Gga.3164.1.S1_at	ORMDL3
Gga.3168.2.S2_at	QKI
Gga.3169.1.S1_at	CDCA3
Gga.3178.1.S2_at	DACH2
Gga.318.1.S1_at	KCNN2
Gga.3180.1.S2_a_at	LFNG
Gga.3185.1.S1_at	MRPL21
Gga.3187.1.S1_at	HOXD8
Gga.3193.3.S1_at	USP10
Gga.3198.1.S1_at	RCJMB04_19f9
Gga.3200.1.S1_s_at	SMC4
Gga.3202.1.S1_a_at	LOC420716
Gga.3204.1.S1_at	C7orf23
Gga.3209.3.S1_at	IPMK
Gga.3212.1.S1_at	ANLN
Gga.3212.2.S1_s_at	ANLN

Gga.3214.1.S1_at	XRCC5
Gga.3216.1.S1_at	RMND1
Gga.3217.1.S1_at	MAN1B1
Gga.3219.1.S1_at	FIGF
Gga.322.1.S1_at	SPRY1
Gga.3220.1.S1_at	HEMK1
Gga.3225.1.S1_at	MYH11
Gga.3232.1.S1_at	NDUFS4
Gga.3236.1.S1_at	PHF11
Gga.3238.2.S1_a_at	NEGR1
Gga.3242.3.S1_at	LOC769185
Gga.3247.1.S1_at	ABL2
Gga.3250.1.S1_at	VSNL1
Gga.3257.1.S1_at	LCAT
Gga.3259.1.S1_at	ANGPT2
Gga.3266.1.S1_at	LOC425605
Gga.3271.1.S1_at	LOC769726
Gga.3273.5.S1_x_at	B-G
Gga.3273.6.S1_a_at	B-G
Gga.3280.1.S1_at	CBLN1
Gga.3282.5.S1_at	MRPS16
Gga.329.1.S1_at	HAS2
Gga.3301.1.S1_at	ATP1B1
Gga.3303.1.S1_s_at	LOC425172 /// RCJMB04_8p20
Gga.3306.1.S1_s_at	EDNRB
Gga.3309.1.S1_at	ANKRD38
Gga.331.1.S1_at	CYP26A1
Gga.3315.1.S1_a_at	MRPL17
Gga.3315.2.S1_a_at	MRPL17
Gga.3315.2.S1_x_at	MRPL17
Gga.3316.1.S1_s_at	HHEX
Gga.3317.1.S1_s_at	NCOA1
Gga.3323.1.S1_s_at	FABP5
Gga.3328.2.S1_a_at	C18orf21
Gga.3330.1.S1_at	SPON1
Gga.3332.1.S1_at	MXRA8
Gga.3337.1.S1_at	MUC5B
Gga.3338.1.S1_at	CAPZA2
Gga.3339.1.S1_at	ARSH
Gga.3341.1.S1_at	PODXL

Gga.3345.1.S1_at	ATP2B1
Gga.3348.2.S1_s_at	PCDH9
Gga.3349.1.S2_at	C4BPA
Gga.3357.2.S1_a_at	LYG2
Gga.3360.1.S1_at	LOC776932
Gga.3363.3.S1_a_at	IRF2
Gga.3371.1.S1_s_at	RCJMB04_18h18
Gga.3373.1.S1_at	POPDC3
Gga.3373.2.S1_at	POPDC3
Gga.3373.7.S1_a_at	POPDC3
Gga.3379.2.S1_at	SH3KBP1
Gga.3379.3.S1_at	SH3KBP1
Gga.3379.3.S1_s_at	SH3KBP1
Gga.3380.1.S1_at	TRA@
Gga.3383.1.S1_at	LITAF
Gga.3383.1.S2_at	LITAF
Gga.3387.1.S1_at	ADRA1B
Gga.3388.3.S1_at	SLC34A1
Gga.3398.2.S1_a_at	PITX2
Gga.3399.1.S1_s_at	FCHSD2
Gga.34.1.S1_at	CACNG4
Gga.3402.1.S1_a_at	OLFM1
Gga.3403.1.S2_at	GDF5
Gga.3405.1.S1_at	EPHB2
Gga.341.1.S1_at	CHRNA4
Gga.3411.1.S1_at	RCJMB04_5i17
Gga.3412.1.S1_at	CITED4
Gga.3416.4.S1_a_at	HESX1
Gga.3419.1.S1_at	NRXN3
Gga.3420.1.S1_at	ZNF609
Gga.3425.1.S1_at	SCP2
Gga.3427.1.S1_at	ELAVL4
Gga.343.1.S1_at	PDLIM3
Gga.344.1.S1_s_at	PDLIM3
Gga.3441.2.S1_s_at	TMEM167
Gga.3441.3.S1_at	TMEM167
Gga.3444.1.S1_at	FZD9
Gga.3447.1.S1_at	PLCD1
Gga.3459.1.S1_at	COL9A3
Gga.3459.1.S2_at	COL9A3

Gga.3476.1.S1_at	ETV6
Gga.3477.1.S1_at	FGFR2
Gga.3477.1.S2_at	FGFR2
Gga.3500.1.S1_at	ROCK2
Gga.352.1.S1_at	RGS20
Gga.3524.2.S1_a_at	MRPL27
Gga.3550.1.S1_at	MYO5A
Gga.3550.1.S2_at	LOC426524 /// LOC771580 /// MY
Gga.3551.1.S1_at	SPP1
Gga.3555.1.S1_at	SLC16A3
Gga.3572.1.S2_at	CD44
Gga.3572.1.S2_s_at	CD44
Gga.3573.2.S1_a_at	DKK3
Gga.3575.1.S1_at	LOC422926
Gga.358.1.S1_at	TCRA
Gga.3580.1.S1_at	INSR
Gga.3585.1.S2_at	KAT2A
Gga.3595.1.S1_at	EIF4E
Gga.3599.1.S1_at	SEC23A
Gga.3599.2.S1_a_at	SEC23A
Gga.3599.2.S1_s_at	SEC23A
Gga.3599.3.S1_a_at	SEC23A
Gga.3599.3.S1_at	SEC23A
Gga.3602.3.S1_x_at	LOC426458 /// LOC770857
Gga.3606.1.S1_s_at	E2F4
Gga.3615.1.S1_at	FST
Gga.3615.1.S2_at	FST
Gga.3617.1.S1_at	LOC415913
Gga.3621.1.S1_at	CRYZ
Gga.3635.1.S1_at	CTTN
Gga.3640.2.S1_a_at	KTN1
Gga.3652.1.S1_at	CLEC3B
Gga.3659.1.S1_at	NFE2L2
Gga.3659.1.S2_at	NFE2L2
Gga.3665.1.S2_at	CDH20
Gga.367.1.S1_x_at	TRA@
Gga.3670.1.S1_at	LOC395978
Gga.3670.2.S1_at	TNRC15
Gga.3671.1.S1_at	LOC396371
Gga.3672.1.S1_at	ST3GAL1

Gga.3677.1.S1_at	CAPN2
Gga.3678.2.S1_a_at	TAF1A
Gga.3685.1.S1_at	MYH1 /// MYH2 /// MYH3 /// MYH4
Gga.3688.1.S1_at	FABP1
Gga.3689.2.S1_a_at	HDAC4
Gga.3690.1.A1_at	ZNF207
Gga.3690.1.S1_at	ZNF207
Gga.3693.1.A1_at	B-G /// LOC425214 /// LOC768349
Gga.3697.1.S1_at	LOC418200
Gga.3698.1.A1_s_at	LOC416899
Gga.3705.1.S1_at	CENPF
Gga.3713.1.S1_at	MBNL2
Gga.3729.1.S1_at	CAMKK2
Gga.3738.1.S1_at	BLNK
Gga.3739.1.S1_at	INTS6
Gga.3743.1.S1_at	TRIP13
Gga.3745.1.S1_at	CPZ
Gga.375.1.S1_x_at	TRA@
Gga.3751.1.S1_at	RYK
Gga.3754.1.S1_a_at	HES1
Gga.3757.1.S2_at	KCNT1
Gga.3768.1.S1_s_at	RQCD1
Gga.3773.1.S1_a_at	IL17RD
Gga.3777.1.S1_at	SCP2
Gga.3781.1.S1_at	ACE
Gga.3792.2.S1_a_at	TOM1
Gga.3807.1.S2_s_at	ALDH1A3
Gga.3811.1.S1_at	BOK
Gga.3818.1.S1_at	TNC
Gga.3820.3.S1_s_at	NASP
Gga.3823.1.S2_at	PER2
Gga.3823.2.S1_a_at	PER2
Gga.3823.2.S1_at	PER2
Gga.3828.1.S1_at	EMB
Gga.3833.1.S1_s_at	PPP3R1
Gga.3834.1.S2_at	PLEKHA2
Gga.3839.1.S1_s_at	FZD3
Gga.384.1.S1_at	LOC395641
Gga.3848.1.S1_s_at	RCJMB04_1b4
Gga.3852.1.S2_s_at	RHOB

Gga.3853.1.S2_at	ZNF622
Gga.3854.1.S2_at	CTSB
Gga.3858.2.S1_a_at	PPARG
Gga.3858.3.S1_a_at	PPARG
Gga.386.1.S1_at	RGS17
Gga.3864.1.S1_at	PSEN1
Gga.3866.1.S1_at	RASSF8
Gga.3870.1.S1_at	CHST10
Gga.3871.1.S1_at	GTF2H1
Gga.3875.1.S1_at	AKT1
Gga.3886.1.S1_at	DTX3L
Gga.3899.1.S1_a_at	PDGFA
Gga.390.1.S1_at	CHAT2
Gga.3903.1.S1_at	CDH13
Gga.3903.1.S2_at	CDH13
Gga.3904.1.S1_at	RCJMB04_8a2
Gga.3908.1.S1_at	TAGLN
Gga.391.1.S1_at	IL10RB
Gga.392.1.S1_at	PLEK
Gga.392.2.S1_a_at	PLEK
Gga.3921.1.S1_at	EIF5B
Gga.3928.1.S1_at	HAPLN1
Gga.393.1.S1_at	ERBB4
Gga.394.1.S1_at	TMCO3
Gga.3950.1.S1_at	BMP2
Gga.3952.1.S1_at	TFDP1
Gga.3953.2.S1_a_at	GPBP1L1
Gga.3957.2.S1_a_at	ENAH
Gga.396.1.S1_at	TACR1
Gga.3961.1.S1_at	SMN
Gga.3972.1.S1_at	SEMA3D
Gga.3972.1.S2_at	SEMA3D
Gga.3973.1.S1_at	TWIST1
Gga.3975.1.S1_at	MINPP1
Gga.398.1.S1_at	MMP-13
Gga.3982.1.S2_at	INHBA
Gga.3986.2.S1_a_at	CA2
Gga.3994.3.S1_x_at	FN1
Gga.40.1.S1_at	LOC395345
Gga.4003.1.S1_at	CHAC1

Gga.4006.1.S1_at	PPARA
Gga.4007.1.S1_at	TCF12
Gga.4012.1.S1_at	IKZF5
Gga.4017.1.S2_at	EZR
Gga.4019.1.S1_at	TP63
Gga.402.1.S1_at	PGA5
Gga.4024.1.S1_at	MAPKAPK5
Gga.403.1.S1_at	ZP4
Gga.4035.1.S1_at	K123
Gga.4037.2.A1_s_at	B-LA
Gga.4037.3.S1_at	RCJMB04_17a7
Gga.4041.1.S1_a_at	TXN
Gga.4041.2.S1_a_at	LOC418811
Gga.4048.1.S1_at	ID3
Gga.405.1.S1_a_at	ITPKA
Gga.4051.1.S1_at	CTGF
Gga.4052.1.S1_at	MYL9
Gga.4053.1.S1_at	EEF1A2
Gga.4057.1.S1_at	SSBP3
Gga.4057.2.S1_a_at	SSBP3
Gga.4061.2.S1_a_at	HMGB2
Gga.4066.1.S1_at	SMC2
Gga.4067.1.S1_at	TSN
Gga.4068.1.S2_at	RANP1
Gga.4070.1.S1_at	CSF1R
Gga.4074.1.S1_s_at	KIAA1143
Gga.4078.1.S1_at	LUM
Gga.4082.1.S1_at	SMO
Gga.4083.1.S1_at	NKX-6.1
Gga.4087.1.S2_at	FZD1
Gga.4088.1.S1_at	SLITRK4
Gga.409.1.S1_at	WNT5A
Gga.4090.1.S1_a_at	TNNT3
Gga.4091.1.S2_a_at	MYLK
Gga.4091.2.S1_a_at	MYLK
Gga.4092.2.S1_at	RCJMB04_1d5
Gga.4092.2.S1_x_at	RCJMB04_1d5
Gga.4094.1.A1_at	LOC768569
Gga.4094.1.S1_at	LOC768569
Gga.4096.3.S1_a_at	PVALB

Gga.4098.1.S1_at	CNP
Gga.4099.1.S1_s_at	LOC771156
Gga.41.1.S1_at	BCMO1
Gga.4101.1.S1_at	TM9SF3
Gga.4106.1.S1_at	SLC15A1
Gga.4108.1.S2_at	TPM1
Gga.4108.4.S1_s_at	TPM1
Gga.4109.1.S1_at	ABCB1
Gga.4109.1.S2_at	ABCB1
Gga.4110.10.S1_x_at	IGLL1
Gga.4110.11.S1_x_at	IGLL1
Gga.4110.12.S1_a_at	IGLL1
Gga.4110.4.S1_a_at	IGLL1
Gga.4110.4.S1_x_at	IGLL1
Gga.4112.1.S1_at	APOB
Gga.4114.1.S1_at	PLG
Gga.4116.1.S1_at	CASP9
Gga.4119.1.S1_at	ALDH1A1
Gga.4128.1.S2_at	TNS1
Gga.4128.3.S1_a_at	TNS1
Gga.4129.1.S1_at	CCNA2
Gga.4132.1.S1_at	ENO2
Gga.4133.1.S1_s_at	SMAD5
Gga.4134.1.S1_at	CHRNA1
Gga.4138.2.S1_at	EIF4G2
Gga.4141.1.S1_at	MATN1
Gga.4144.2.S1_at	COPS5
Gga.4144.2.S1_s_at	COPS5
Gga.415.1.S1_at	SERPINB10
Gga.4150.2.S1_a_at	BSG
Gga.4150.7.A1_a_at	LOC770363
Gga.4153.1.S2_a_at	THY1
Gga.4166.2.S1_a_at	HMGN2
Gga.4167.1.S1_x_at	XPO7
Gga.4170.1.S1_at	AKR1B10
Gga.4179.1.S1_at	NEFM
Gga.418.1.S1_x_at	BF2
Gga.4185.1.S2_at	IFNAR1
Gga.4194.1.S1_at	OGN
Gga.4195.1.A1_at	C20orf11

Gga.4196.1.S1_a_at	ABLIM2
Gga.4196.1.S1_at	ABLIM2
Gga.4196.2.S1_at	ABLIM2
Gga.4205.2.S1_at	RTN4
Gga.421.2.S1_a_at	TK1
Gga.4210.1.S1_at	MT4
Gga.4211.1.S1_at	CRTAP
Gga.4216.1.S1_at	MYOM2
Gga.4217.1.S1_a_at	MYH1 /// MYH2 /// MYH3
Gga.4217.3.S1_at	MYH6
Gga.4217.3.S1_x_at	MYH6
Gga.4217.4.S1_x_at	MYH2
Gga.4217.5.S1_at	MYH2
Gga.4217.5.S1_x_at	MYH2
Gga.4217.6.S1_x_at	MYH3
Gga.4225.1.S1_at	LECT2
Gga.424.1.S1_s_at	VSIG1
Gga.4243.1.S1_at	HOXA4
Gga.4257.1.S1_at	COL6A2
Gga.427.1.S1_at	PCBD1
Gga.4279.1.S1_s_at	LOC768616 /// LOC768663 /// PRS
Gga.4279.3.S1_a_at	LOC768616 /// LOC768663 /// PRS
Gga.4279.4.S1_a_at	LOC768616 /// LOC768663 /// PRS
Gga.4285.1.S1_at	CEBPB
Gga.4288.1.S1_at	STT3A
Gga.4291.1.S1_at	TPH1
Gga.4292.1.S1_at	LAMC1
Gga.4293.1.S1_at	ASL
Gga.4296.2.S1_a_at	CLK3
Gga.4296.3.S1_a_at	CLK3
Gga.4301.1.S1_at	CHD1
Gga.4306.1.S1_at	DMN
Gga.4307.1.S1_at	PVALB
Gga.4308.1.S1_at	LOC396507
Gga.4309.1.S1_at	SOX8
Gga.4316.1.S1_at	PAPOLA
Gga.4317.1.S1_a_at	CACNA1B
Gga.4320.1.S1_a_at	LOC777119
Gga.4321.2.S1_s_at	NT5C3L
Gga.4329.1.S2_at	GHR

Gga.4332.1.S1_at	HSPCB
Gga.4338.3.S1_a_at	UQCRC1
Gga.4343.1.S1_s_at	MYSM1
Gga.4348.1.S1_at	LOC417822
Gga.4349.1.S1_s_at	SMARCB1
Gga.4349.2.S1_s_at	SMARCB1
Gga.4350.1.S2_at	FYN
Gga.4359.1.S1_s_at	TNFSF13B
Gga.4359.1.S2_s_at	TNFSF13B
Gga.4362.1.S1_at	IKZF3
Gga.4369.1.S1_at	NAGA
Gga.437.1.S1_at	TYK2
Gga.4370.2.S1_s_at	MCM6
Gga.4371.1.S1_s_at	PHTF2
Gga.4373.1.S1_s_at	CYB5R2
Gga.4374.1.S1_a_at	IRF4
Gga.4375.1.S1_at	GTF3C3
Gga.4383.1.S1_at	RAP1A
Gga.4384.1.S1_at	BIRC2
Gga.4384.1.S2_at	BIRC2
Gga.4384.1.S2_s_at	BIRC2
Gga.4390.2.S1_a_at	FTH1
Gga.4390.4.S1_a_at	FTH1
Gga.4390.4.S1_s_at	FTH1
Gga.4394.1.S1_at	BCL2
Gga.4403.1.S1_at	PSAP
Gga.4403.1.S2_at	PSAP
Gga.4409.1.S1_a_at	CCL4
Gga.4412.1.S1_a_at	TAPBP
Gga.4414.1.S1_s_at	CD74
Gga.4416.1.S1_at	SERPINI1
Gga.442.1.S1_at	LOC395744
Gga.4420.2.S1_a_at	RTN1
Gga.4421.1.S1_x_at	UBC
Gga.4424.1.S1_at	SH3GL3
Gga.443.1.S1_at	LOC419978 /// LOC426838 /// LOC
Gga.4430.2.S1_at	SLC35A1
Gga.4439.2.S1_at	MAP6
Gga.444.1.S1_at	LOC419978 /// LOC426838 /// LOC
Gga.4442.1.S1_at	LOC768632 /// LOC768817 /// LOC

Gga.4445.1.S1_at	NR2F2	
Gga.4446.1.S3_at	GIT2	
Gga.4447.1.S1_at	PCK1	
Gga.445.2.S1_a_at	LOC769232	
Gga.445.2.S1_at	LOC769232	
Gga.4450.1.S1_s_at	C11orf61	
Gga.4454.2.S1_s_at	RCJMB04_24e7	
Gga.4459.4.S1_a_at	RPL35A	
Gga.446.1.S1_at	ETV4	
Gga.4469.3.S1_at	SET	
Gga.447.1.S1_s_at	ETV5	
Gga.4471.1.S1_at	USPL1	
Gga.4474.1.S1_s_at	RAD21	
Gga.4478.1.S1_at	UBE2J1	
Gga.448.1.S1_at	TJP2	
Gga.4485.2.S1_s_at	RPN2	
Gga.4485.3.S1_at	RPN2	
Gga.449.1.S1_at	NOG	
Gga.4493.1.S1_at	BRCA1	
Gga.4493.1.S2_at	BRCA1	
Gga.450.1.S1_at	CD5	
Gga.4500.1.S2_at	RPS28	
Gga.4511.1.S1_at	TCIRG1	
Gga.4512.1.S1_at	RPS14	
Gga.4514.2.S1_s_at	RRM1	
Gga.4514.3.S1_s_at	RRM1	
Gga.4515.2.S1_at	PRDX3	
Gga.4516.2.S1_at		41163
Gga.4522.2.S1_a_at	DHX15	
Gga.4533.6.A1_at	DYNLT1	
Gga.4535.1.S1_at	AKAP12	
Gga.4535.2.S1_a_at	AKAP12	
Gga.4536.2.S1_a_at	AKR1D1	
Gga.4544.1.S1_at	BRG1	
Gga.4547.2.S1_a_at	MYH10	
Gga.4557.1.S1_at	FGB	
Gga.4558.2.S1_s_at	MXD4	
Gga.4561.1.S1_at	SEPX1	
Gga.4562.1.S1_s_at	GAL9	
Gga.4564.1.S1_a_at	FMO6P	

Gga.4565.3.S1_a_at	TEX264
Gga.4567.1.S1_a_at	ATP5J2
Gga.4567.3.S1_a_at	ATP5J2
Gga.4567.4.S1_x_at	ATP5J2
Gga.4577.2.S1_at	RCJMB04_1112
Gga.4579.1.S1_x_at	TUBB2A
Gga.458.1.S1_at	CDD
Gga.4582.1.S1_at	ARGLU1
Gga.4583.2.S1_x_at	RPL24
Gga.4583.4.A1_at	RPL24
Gga.4589.1.S1_at	RHOBTB2
Gga.4590.1.S1_s_at	LOC422090
Gga.4594.1.S2_at	ATP1B3
Gga.4596.1.S1_at	PTMS
Gga.4597.1.S1_at	TAF13
Gga.4598.5.S1_a_at	PFDN1
Gga.460.1.S1_at	LHCGR
Gga.4600.2.S1_at	LOC770937
Gga.4604.1.S1_at	C10orf84
Gga.4608.1.S1_at	LOC425539
Gga.4609.3.S1_a_at	PHPT1
Gga.4611.1.S1_at	METT10D
Gga.462.1.S1_x_at	APOA4
Gga.462.2.S1_a_at	APOA4
Gga.4621.1.S1_s_at	TRAP1
Gga.4629.1.S1_at	LOC768360
Gga.4637.1.S1_s_at	YARS
Gga.464.2.A1_at	AXIN1
Gga.464.2.S1_a_at	AXIN1
Gga.4640.1.S1_at	C19orf6
Gga.4649.1.S1_s_at	PSMC3
Gga.4657.1.S1_at	RPL31
Gga.4659.1.S1_at	C19orf12
Gga.4661.1.S1_x_at	TUBA1C
Gga.4661.2.S1_at	TUBA1C
Gga.4663.1.S1_at	PSPH
Gga.4664.2.S1_a_at	LOC769329
Gga.4668.1.S1_at	DNER
Gga.4668.2.S1_a_at	DNER
Gga.467.1.S1_at	TBX19

Gga.4672.1.S2_at	ATP6V0A1
Gga.4675.1.S1_at	SDC2
Gga.4675.1.S2_at	SDC2
Gga.4682.1.S1_at	UNG
Gga.4682.1.S2_at	UNG
Gga.4688.1.S1_at	ACOT8
Gga.469.1.S1_at	FOXC2
Gga.4693.1.S1_s_at	MLX
Gga.4699.2.S1_s_at	LOC415641 /// LOC423151
Gga.4703.1.S1_s_at	NDFIP1
Gga.4705.2.S1_s_at	DHODH
Gga.4706.1.S1_at	CALCOCO2
Gga.4707.1.S1_at	RNPC3
Gga.4712.2.S1_at	OXCT1
Gga.4718.1.S1_at	SFRS3
Gga.4719.1.S1_a_at	APOA1
Gga.4719.1.S1_s_at	APOA1
Gga.4723.1.S1_at	LECT1
Gga.4724.1.S1_at	HSP90B1
Gga.4724.1.S2_at	HSP90B1
Gga.4727.1.S1_at	RCJMB04_4k2
Gga.4728.1.S1_at	C6orf72
Gga.4729.2.S1_at	RPL18A
Gga.4730.1.S1_at	NAPB
Gga.4731.3.S1_at	RCJMB04_35e13
Gga.4732.1.S1_at	LRP11
Gga.4732.3.S1_a_at	LRP11
Gga.4732.3.S1_at	LRP11
Gga.4738.1.S1_at	NEO1
Gga.4744.3.S1_a_at	PMPCA
Gga.4746.1.S1_a_at	NDUFB1
Gga.4747.1.S1_at	SLC25A3
Gga.4749.1.S1_at	HADH
Gga.475.1.S2_at	FSHR
Gga.4750.1.S1_s_at	FKBP5
Gga.4755.2.S1_at	HP1BP3
Gga.4755.2.S1_s_at	HP1BP3
Gga.4756.1.S1_a_at	CIRBP
Gga.4757.1.S1_at	MAP4K4
Gga.476.1.S1_at	TEAD3

Gga.4764.1.S1_at	ARL1
Gga.4767.1.S1_at	NAT11
Gga.4768.1.S1_at	ETS2
Gga.4769.1.S1_s_at	CUL3
Gga.4773.1.S1_at	RCJMB04_1i20
Gga.4773.2.S1_s_at	RCJMB04_1i20
Gga.4774.2.S1_a_at	LOC422278
Gga.4776.1.S2_at	LOC771147 /// RPL9
Gga.4782.1.S1_a_at	HNRNPAB
Gga.4782.1.S2_at	HNRNPAB
Gga.4785.2.S1_at	NIT2
Gga.4788.1.S1_at	RCJMB04_8a2
Gga.4789.1.S1_at	FAM70A
Gga.4791.1.S1_at	IFI35
Gga.4792.2.S1_at	NFS1
Gga.4795.2.S1_a_at	KLHDC2
Gga.4798.1.S1_at	GPM6A
Gga.4799.1.S1_s_at	PPM1M
Gga.48.1.S1_at	DPF2
Gga.4804.1.S1_at	EIF3E
Gga.4807.2.A1_at	SNAP25
Gga.4808.1.S1_s_at	KDM6A
Gga.481.1.S1_at	FMOD
Gga.4811.3.S1_s_at	HNRPK
Gga.4826.1.A1_at	FBXO45
Gga.4827.1.S2_at	SLC25A6
Gga.483.1.S1_at	CTSK
Gga.4830.1.S1_at	SFRP1
Gga.4830.1.S2_at	SFRP1
Gga.4832.1.S1_at	LOC770612
Gga.4834.3.S1_at	RCJMB04_33p3
Gga.4836.1.S1_a_at	TMEM141
Gga.4836.2.S1_x_at	TMEM141
Gga.4837.1.S1_at	KERA
Gga.4838.2.S1_s_at	C19orf10
Gga.4839.1.S1_a_at	MDH2
Gga.4842.2.S1_a_at	SLC4A1
Gga.4845.1.S1_at	LOC423265
Gga.4845.3.S1_at	LOC423265
Gga.4845.3.S1_s_at	LOC423265

Gga.4846.1.S1_at	LOC395193
Gga.4846.1.S2_at	LOC395193
Gga.4849.1.S1_at	ELF1
Gga.485.1.S1_a_at	TEAD4
Gga.485.4.S1_a_at	TEAD4
Gga.4850.2.S1_at	GRIP1
Gga.4851.1.A1_at	COL3A1
Gga.4851.1.S1_at	COL3A1
Gga.4853.1.S1_at	C20orf149
Gga.4854.1.S1_at	LOC769345
Gga.4856.1.S1_s_at	PMP22
Gga.4866.2.S1_at	RNF185
Gga.4867.1.S1_a_at	TXNDC17
Gga.4867.3.S1_a_at	TXNDC17
Gga.4868.1.S1_a_at	PNLIP
Gga.4870.3.S1_a_at	ACTC1
Gga.4871.1.S1_at	PSMC5
Gga.4873.1.S1_a_at	HSPE1
Gga.4874.2.S1_at	TUBB2C
Gga.4878.1.S1_at	RPL7
Gga.4879.2.S1_at	HSP90AA1
Gga.4882.1.S1_at	ASB7
Gga.4884.1.S1_at	ANXA1
Gga.4888.1.S1_s_at	PTP4A1
Gga.4889.1.S1_s_at	NFASC
Gga.4891.1.S1_s_at	RCJMB04_2g17
Gga.4896.1.S1_at	LOC427638
Gga.49.1.S1_at	CBX4
Gga.4900.3.S1_s_at	LOC425783
Gga.4900.4.S1_at	LOC776458
Gga.4900.7.S1_at	LOC776458
Gga.4907.1.S1_s_at	POU2AF1
Gga.4912.1.S1_at	G3BP1
Gga.4929.1.S1_s_at	GABPB2
Gga.4930.2.S1_a_at	LOC424773
Gga.4931.1.S1_at	PMS1
Gga.4933.1.S1_at	HIF1A
Gga.4938.1.S1_s_at	AMY2A
Gga.4939.1.S1_s_at	FABP4
Gga.4940.2.S1_a_at	UBE2I

Gga.4942.1.S1_at	HSP70
Gga.4948.1.S1_at	FKBP1A
Gga.4949.1.S1_at	SREBF2
Gga.495.1.S1_at	GAL2
Gga.4955.1.S1_at	FRZB
Gga.4956.1.S1_at	LEFTY2
Gga.4958.1.S1_at	XIRP2
Gga.4964.1.S1_a_at	LOC776590
Gga.4964.1.S1_x_at	LOC776590
Gga.4964.11.S1_a_at	LOC776309 /// LOC776590
Gga.4964.11.S1_x_at	LOC776309 /// LOC776590
Gga.4964.17.S1_x_at	LOC776590
Gga.4964.2.S1_a_at	LOC776306 /// LOC776590
Gga.4964.20.S1_x_at	LOC776590 /// LOC777160
Gga.4964.22.S1_x_at	LOC776593
Gga.4964.25.S1_x_at	LOC776574 /// LOC776590 /// LOC776593
Gga.4964.3.S1_x_at	LOC776590
Gga.4964.30.A1_at	LOC776574
Gga.4964.35.S1_x_at	LOC776574 /// LOC776590
Gga.4964.36.S1_x_at	LOC776574 /// LOC776590
Gga.4964.4.S1_at	LOC428465 /// LOC776593
Gga.4964.4.S1_x_at	LOC428465 /// LOC776593
Gga.4964.47.S1_x_at	LOC776590 /// LOC777160
Gga.4964.5.S1_a_at	LOC776306 /// LOC776590
Gga.4964.54.A1_x_at	LOC776574
Gga.4964.54.S1_x_at	LOC776574 /// LOC776590 /// LOC776593
Gga.4965.1.S1_a_at	COL12A1
Gga.4972.1.S1_at	PTPRA
Gga.4972.1.S1_s_at	PTPRA
Gga.4973.1.S1_x_at	BF2
Gga.4973.2.S1_x_at	BF1 /// BF2 /// HLA-G
Gga.4973.3.S1_x_at	BF1 /// BF2 /// HLA-G
Gga.4974.1.S1_at	VCAN
Gga.4974.1.S2_at	VCAN
Gga.4975.1.S1_a_at	TPM3
Gga.4975.2.S1_a_at	TPM3
Gga.4975.5.S1_a_at	TPM3
Gga.4975.5.S1_x_at	TPM3
Gga.4977.1.S1_at	MSX2
Gga.4978.2.S1_a_at	CALB2

Gga.4979.1.S1_at	TCF3
Gga.4980.1.S1_at	ADORA1
Gga.4981.1.S1_s_at	HBG1 /// HBG2
Gga.4981.2.S1_at	HBE1 /// HBG2
Gga.4982.1.S1_at	LOC395492
Gga.4984.1.S1_at	TNNT2
Gga.4985.1.S1_a_at	HDAC1
Gga.4986.1.S1_at	MYBPC2
Gga.4988.1.S1_at	CALD1
Gga.4988.2.S1_a_at	CALD1
Gga.4995.1.A1_at	LOC776570
Gga.4995.1.S1_s_at	LOC776570
Gga.4999.1.S1_a_at	ITGA4
Gga.4999.2.S1_at	ITGA4
Gga.5002.1.S1_at	MDK
Gga.5005.1.S1_at	CHIA
Gga.5005.1.S1_s_at	CHIA
Gga.5007.1.S1_at	CDKN2B
Gga.5008.1.S1_at	CDKN2A
Gga.501.1.S1_at	MMP27
Gga.5018.1.A1_s_at	ZFX
Gga.502.1.S1_at	HMGA2
Gga.5028.1.S1_at	LOC404298
Gga.5031.1.S1_s_at	NT5C3
Gga.506.1.S1_at	ST8SIA1
Gga.5073.1.S1_at	LOC428141
Gga.5085.1.S1_at	OVM
Gga.5087.1.S1_x_at	LOC769327
Gga.5091.1.S1_at	CAV1
Gga.5092.1.A1_at	ANXA2
Gga.5095.1.S1_at	CHRNA3
Gga.5101.1.S1_at	ZBTB16
Gga.5109.1.S1_s_at	MYCN
Gga.511.1.S1_at	TLX1
Gga.5111.1.S1_at	CCDC80
Gga.512.1.S1_at	IL8
Gga.5122.1.S1_at	HOXA7
Gga.5126.1.S1_s_at	GRIA2
Gga.513.1.S1_s_at	LOC776572 /// LOC776580 /// LOC
Gga.5130.1.S1_at	F8

Gga.5132.1.S1_at	F7
Gga.5133.1.S1_at	DAZL
Gga.5136.1.S1_x_at	BLB2
Gga.514.1.S1_at	F10
Gga.5144.1.A1_at	SEPHS1
Gga.5144.1.S1_at	SEPHS1
Gga.5146.1.S1_at	DDB1
Gga.5147.1.S1_x_at	BLB2
Gga.5148.1.S1_at	TNFRSF1B
Gga.5148.1.S1_s_at	TNFRSF1B
Gga.5148.1.S2_s_at	TNFRSF1B
Gga.5154.1.S1_at	POSTN
Gga.5160.1.S1_at	CACNB4
Gga.5161.2.S1_s_at	ANK3
Gga.5162.1.S1_at	F5
Gga.5163.1.S1_at	NGFB
Gga.5164.1.S1_at	BCL2A1
Gga.5164.1.S2_at	BCL2A1
Gga.5166.1.S1_at	TSPAN32
Gga.5167.1.S1_at	CD81
Gga.5168.2.S1_s_at	UBE2G2
Gga.517.1.S1_x_at	BLB1
Gga.5170.1.S1_s_at	PODXL
Gga.5171.1.S1_at	CDH5
Gga.5174.1.S1_at	PHF20L1
Gga.5175.1.S1_s_at	RCJMB04_30a17
Gga.5178.1.S1_at	PTPRF
Gga.518.1.S1_x_at	BLB1
Gga.5180.1.S1_at	TNFRSF8
Gga.5187.1.S1_at	SQSTM1
Gga.5187.1.S1_s_at	SQSTM1
Gga.5190.2.S1_at	ELFN1
Gga.5196.1.S1_at	SAP30
Gga.5200.3.S1_s_at	RCJMB04_25c5
Gga.5205.1.S1_at	BZRPL1
Gga.5208.1.S1_a_at	UBQLN1
Gga.5218.1.S1_at	GKAP1
Gga.5221.2.S1_at	NUP98
Gga.5226.2.S1_s_at	KIAA1609
Gga.5229.1.S1_s_at	C18orf22

Gga.5231.1.S1_at	PPP4R2
Gga.5231.2.A1_at	PPP4R2
Gga.5236.1.S1_at	CWC15
Gga.5237.2.S1_at	IPO7
Gga.5242.2.S1_a_at	HSD17B11
Gga.5244.1.S1_at	RCJMB04_5e8
Gga.5244.2.S1_a_at	RCJMB04_5e8
Gga.5245.1.S1_a_at	KIAA0317
Gga.5245.2.A1_at	KIAA0317
Gga.5255.1.S1_at	EFEMP1
Gga.5256.1.S1_at	REXO1
Gga.5262.3.S1_s_at	ACAT2
Gga.5270.1.S1_at	LOC422270
Gga.5278.2.S1_a_at	TARSL2
Gga.5281.1.S1_at	ACYP2
Gga.5283.1.S1_at	SCARB2
Gga.5285.1.A1_at	LANCL1
Gga.5288.1.S1_at	TEF
Gga.5289.1.S1_at	GPD1
Gga.5291.1.S1_at	CADM1
Gga.5293.2.S1_a_at	LOC424892
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Gga.5300.1.S1_at	PDE6D
Gga.5305.1.S1_at	SPRED1
Gga.5313.2.S1_a_at	AMFR
Gga.5313.2.S1_at	AMFR
Gga.5316.2.S1_s_at	LRFN5
Gga.5323.1.S1_s_at	MEF2C
Gga.5325.1.S1_at	BCL7A
Gga.5327.3.S1_a_at	LOC419508
Gga.5341.1.S1_at	SHANK2
Gga.5345.2.S1_a_at	ALKBH2
Gga.5347.1.S1_s_at	RCJMB04_25m4
Gga.5350.1.S1_a_at	OSGEPL1
Gga.5356.1.S1_at	DPP7
Gga.5359.1.S1_at	LOC417676
Gga.536.1.S1_a_at	OASL
Gga.5360.2.S1_a_at	TSC22D3
Gga.5361.2.S1_at	ADH5
Gga.5369.1.S1_at	SCNN1G

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Gga.5378.1.S1_at	HNRNPU
Gga.5383.2.S1_at	PDCD2L /// RCJMB04_27n18
Gga.5384.2.S1_at	NEK4
Gga.5385.1.S1_s_at	RCJMB04_21j5
Gga.5386.1.S1_at	TNFRSF6B
Gga.539.1.S1_at	CD247
Gga.5393.1.S1_at	LOC423941
Gga.5394.1.S1_a_at	STK40
Gga.5396.1.S1_at	C1QB
Gga.5397.1.S1_at	CYP2J2
Gga.5397.1.S1_s_at	CYP2J2
Gga.5398.1.S1_at	AGAP1
Gga.540.1.S1_at	MGP
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Gga.5407.1.S1_at	TCEA2
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Gga.542.1.S1_at	LOC395914
Gga.5427.1.S1_at	EFHA1
Gga.5435.1.S1_at	RRAGB
Gga.5440.1.S1_s_at	BCL7A
Gga.5441.2.S1_a_at	HTATIP2
Gga.5444.2.A1_at	BDH1
Gga.5444.2.S1_a_at	BDH1
Gga.5447.1.S1_at	AP4B1
Gga.5451.2.S1_a_at	CDKAL1
Gga.5455.2.S1_s_at	CIAPIN1
Gga.5465.1.S1_at	RCAN1
Gga.5484.1.S1_at	DYNC2LI1
Gga.5487.1.S1_at	POLE3
Gga.5489.1.S1_at	MRPL42
Gga.5492.2.S1_s_at	SUGT1
Gga.5500.2.S1_a_at	MRAS
Gga.5501.1.S1_at	DUS1L
Gga.5506.1.S1_a_at	LOC415950
Gga.5517.1.S1_s_at	RCJMB04_33m12
Gga.552.1.S1_at	DIO3
Gga.5522.2.S1_a_at	SLC25A1

Gga.5527.1.S1_at	TSPAN1
Gga.5529.1.S1_at	MAPK14
Gga.553.1.S1_at	DIO1
Gga.5532.1.S1_at	SMU1
Gga.5533.1.S1_at	LATS1
Gga.5537.1.S1_at	FUNDC1
Gga.554.1.S1_at	HGF
Gga.5540.1.S1_at	DAGLB
Gga.5541.1.S1_at	PECAM1
Gga.5545.1.S1_at	LEPROTL1
Gga.5546.1.S1_at	SCYL3
Gga.5548.1.S1_at	NPM3
Gga.5551.1.S1_a_at	GPR153
Gga.5553.2.S1_s_at	GPS1
Gga.5554.1.S1_at	CSRP3
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Gga.5559.1.S1_at	DYNLRB1
Gga.556.1.S1_at	PAX6
Gga.5566.1.S1_at	SLC25A4
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Gga.5573.1.S1_at	RCJMB04_3k21
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Gga.5580.1.S1_at	FBXL18
Gga.5588.1.S1_at	PDZK1IP1
Gga.5594.1.S1_at	TRPV2
Gga.5601.1.S1_at	SRP14
Gga.5601.2.S1_s_at	SRP14
Gga.561.1.S1_s_at	LOC395944
Gga.5612.1.S1_at	AK3L2
Gga.5613.1.S1_at	BANP
Gga.5616.2.S1_a_at	LOC770126
Gga.5625.1.S1_s_at	RCJMB04_1e2
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Gga.5627.1.S1_at	LIPG
Gga.5629.1.S1_at	LOC415671
Gga.563.1.S1_at	SCN9A
Gga.5631.2.S1_at	IKIP
Gga.5631.3.S1_at	IKIP
Gga.5635.1.S1_at	ABCC5
Gga.5636.1.S1_at	CAPRIN1

Gga.5637.1.S1_at	IL4
Gga.5644.1.S1_s_at	RCJMB04_15h2
Gga.5644.2.S1_s_at	RCJMB04_15h2
Gga.5648.2.S1_a_at	ISLR
Gga.5671.1.S1_at	KRAS
Gga.568.1.S1_at	LOC395957
Gga.5680.1.S1_at	GRID2
Gga.5687.2.S1_a_at	KIF2C
Gga.5687.3.S1_a_at	KIF2C
Gga.5687.4.S1_a_at	KIF2C
Gga.5692.1.S1_at	NDUFB4
Gga.5707.2.S1_a_at	C7orf26
Gga.5713.3.S1_a_at	RTN4IP1
Gga.572.1.S1_at	NR5A2
Gga.572.1.S2_at	NR5A2
Gga.574.1.S1_at	CD8B
Gga.5743.1.S1_at	LY96
Gga.5744.1.S1_at	HDDC2
Gga.5747.1.S1_a_at	SAV1
Gga.5748.1.S1_at	IL13RA2
Gga.575.1.S1_at	CD8A
Gga.5751.1.S1_at	ANKRD1
Gga.5751.1.S2_at	ANKRD1
Gga.5753.1.S1_s_at	RCJMB04_33d2
Gga.5755.2.S1_a_at	TSPAN4
Gga.576.1.S1_at	ICOSLG
Gga.5764.1.S1_s_at	PUM1
Gga.5776.1.S1_at	CD34
Gga.5777.1.S1_at	CREB3
Gga.5778.2.A1_at	LOC769246
Gga.5779.2.S1_a_at	CUTC
Gga.5782.1.S1_at	RCJMB04_19e2
Gga.5784.1.S1_at	TMEM121
Gga.5793.1.S1_at	LOC777261
Gga.5799.1.S1_s_at	P4HA2
Gga.5803.2.S1_s_at	RCJMB04_5b12
Gga.5805.1.S1_s_at	RCJMB04_2h17
Gga.5808.2.S1_a_at	SSNA1
Gga.5810.1.S1_at	MED10
Gga.5814.1.S1_at	SI

Gga.5816.1.S1_at	RBPM5
Gga.5816.2.S1_a_at	RBPM5
Gga.5824.1.S1_at	LOC770695
Gga.5826.1.S1_at	MAPT
Gga.5827.1.S1_at	DSCAM
Gga.583.1.A1_at	SI
Gga.5830.1.S1_at	RWDD2B
Gga.5838.1.A1_at	LOC426624
Gga.5838.1.S1_s_at	CHIR-B3 /// LOC770720 /// LOC7'
Gga.584.1.S1_at	VDR
Gga.5846.1.S1_at	LOC771291
Gga.5847.1.S1_at	PROSAPIP1
Gga.5848.3.S1_a_at	CLDN10
Gga.5850.1.S1_at	MED21
Gga.5851.1.S1_at	UGT1A1
Gga.5853.1.S1_at	PEPD
Gga.5854.1.S1_at	ENPP7
Gga.5860.1.S1_at	GPA33
Gga.5865.1.S1_at	TBCA
Gga.5869.1.S1_s_at	OLFML2B
Gga.5876.3.S1_at	DAZAP1
Gga.5877.1.S1_at	MRPL1
Gga.5878.1.S1_at	MICALL2
Gga.588.1.S1_at	GFRA1
Gga.5888.2.S1_a_at	MLL3
Gga.5890.2.S1_at	WDR77
Gga.5891.1.S1_at	PDCD6
Gga.5897.1.S1_at	AGPS
Gga.5899.1.S1_at	FAM125B
Gga.59.1.S1_at	LOC395260
Gga.5900.1.S1_a_at	DNAJA4
Gga.5900.3.S1_a_at	DNAJA4
Gga.5901.1.S1_s_at	BRP44L
Gga.5901.2.S1_s_at	BRP44L
Gga.5905.1.S1_at	C1orf123
Gga.5906.1.S1_at	SYNGR3
Gga.591.1.S1_s_at	CYP11A1
Gga.5917.1.S1_at	LOC769799
Gga.5919.1.S1_at	CYCS
Gga.5919.2.S1_a_at	CYCS

Gga.5928.1.S1_at	LOXL1
Gga.5929.1.S1_at	LOC769360
Gga.593.1.S1_at	CHAT1
Gga.593.1.S1_s_at	CHAT1 /// CHAT2
Gga.5932.1.S1_s_at	CLCN7
Gga.5935.1.S1_s_at	SNTB1
Gga.5946.3.S1_a_at	CPA2
Gga.595.1.S1_at	NELL2
Gga.5953.1.S1_s_at	SLC43A3
Gga.5955.1.S1_at	LOC425935
Gga.5957.1.S1_a_at	CREB3L2
Gga.5957.2.A1_at	CREB3L2
Gga.5958.1.S1_at	NLK
Gga.596.1.S2_at	HSD3B1
Gga.5964.1.S1_at	UROS
Gga.5969.2.S1_a_at	PAQR7
Gga.5972.1.S1_at	MBD2
Gga.5982.1.S1_s_at	RCJMB04_13d22
Gga.5984.2.S1_a_at	LOC424383
Gga.5986.1.S1_at	LOC419782
Gga.5993.1.S1_at	OAF
Gga.5999.2.S1_at	PSME3
Gga.6003.1.S1_a_at	ME3
Gga.6007.1.S1_at	RNF128
Gga.6008.1.S1_at	CDC45L
Gga.6011.1.S1_s_at	UHRF2
Gga.6012.2.S1_a_at	LOC418426
Gga.6024.3.S1_s_at	PNRC1
Gga.6025.1.S1_s_at	CTSS
Gga.6027.1.S1_at	SUCLG1
Gga.6027.1.S1_s_at	SUCLG1
Gga.6030.1.S1_s_at	RCJMB04_31h10
Gga.6031.1.S1_at	RCJMB04_10h2
Gga.6034.1.S1_at	NEK6
Gga.6042.1.S1_at	C20orf54
Gga.6042.2.S1_s_at	GARNL3
Gga.6044.3.S1_a_at	MRPS18C
Gga.6048.1.S1_a_at	CLK4
Gga.6049.1.S1_at	ATP5J
Gga.6052.2.S1_a_at	SCD5

Gga.6054.1.S1_at	PKD2
Gga.6054.2.S1_s_at	PKD2
Gga.6057.1.S1_at	HNRNPA0
Gga.606.1.S1_at	KIT
Gga.6065.3.S1_at	SEC11A
Gga.6066.1.S1_at	TCF7
Gga.6068.3.S1_at	DNALI1
Gga.607.1.S1_at	BMPR1B
Gga.6070.1.S1_at	PSCA
Gga.6072.2.S1_at	SRGN
Gga.6076.1.S1_at	LOC771972
Gga.6077.1.S1_at	TMIGD1
Gga.6086.2.S1_a_at	LOC419498
Gga.6089.1.S1_at	SLC27A2
Gga.609.1.S1_at	CTR BETA 2
Gga.6090.2.S1_a_at	NT5DC2
Gga.6091.1.S1_s_at	ATP5I
Gga.6093.1.S1_at	C9orf91
Gga.6098.1.S1_at	LOC428309
Gga.6099.1.S1_at	LOC771753
Gga.6103.1.S1_at	H3F3A /// LOC769809 /// LOC770
Gga.6103.1.S1_x_at	H3F3A /// LOC769809 /// LOC770
Gga.6104.1.S1_at	C6orf86
Gga.6104.1.S1_s_at	C6orf86
Gga.6106.1.S1_a_at	RARRES2
Gga.6122.1.S1_a_at	TSPO
Gga.613.1.A1_at	UBXD2
Gga.6131.1.S1_at	DNAJC8
Gga.6146.2.S1_a_at	LGALS2
Gga.6147.1.S1_at	ABLIM3
Gga.6159.1.S1_s_at	ACADL
Gga.6162.1.S1_s_at	LOC423224 /// SPTBN5
Gga.6165.1.S1_at	KIF9
Gga.6169.1.S1_at	LYRM2
Gga.617.1.S1_at	CYP1A1
Gga.6171.1.S1_a_at	COX7C
Gga.6175.2.S1_a_at	C12orf31
Gga.6177.1.S1_at	SIL1
Gga.618.1.S1_at	CYP1A4
Gga.6181.1.S1_at	HSD11B1

Gga.6182.1.S1_at	LOC771784
Gga.6183.1.S1_at	REG4
Gga.6185.1.S1_a_at	LOC770190
Gga.6201.1.S1_at	ISG12-2
Gga.6203.1.S1_at	BTBD11
Gga.6203.2.S1_a_at	BTBD11
Gga.621.1.S1_at	HOXA2
Gga.6214.1.S1_a_at	PLA2G1B
Gga.622.1.S1_at	BFSP1
Gga.623.1.S1_at	LOC396058
Gga.6236.1.S1_at	RCJMB04_1e1
Gga.6240.1.S1_at	RCJMB04_18p19
Gga.6250.1.S1_at	SELENBP1
Gga.6252.1.S1_at	TMEM16A
Gga.6256.2.S1_a_at	GNMT
Gga.6260.1.S1_at	LOC770490
Gga.6263.2.S1_s_at	LOC424014
Gga.6265.1.S1_at	GSTT1
Gga.6267.1.S1_at	STOM
Gga.6269.2.S1_s_at	FARSB
Gga.6276.2.S1_a_at	PES1
Gga.6276.3.S1_at	PES1
Gga.6279.3.S1_a_at	C16orf57
Gga.6289.2.S1_at	CAB39L
Gga.6289.2.S1_s_at	CAB39L
Gga.6292.1.S1_a_at	TM4SF4
Gga.6294.1.S1_at	SH3PX3
Gga.6299.2.S1_s_at	PRPSAP2
Gga.6311.1.S1_at	HEY1
Gga.6314.1.S1_at	LOC422151
Gga.6318.1.S1_at	ADRBK2
Gga.632.1.S1_at	AGTR1
Gga.6324.1.S1_at	RBP2
Gga.6328.2.S1_at	TIMM17A
Gga.6329.1.S1_at	LOC420860
Gga.633.1.S1_at	EPHB6
Gga.6330.2.S1_s_at	RNF7
Gga.6338.1.S1_s_at	BRD7
Gga.6340.2.S1_a_at	TNNI1
Gga.6342.1.S1_s_at	DFNA5

Gga.6343.4.S1_a_at	CDKN3
Gga.6344.3.S1_a_at	IWS1
Gga.6347.2.A1_at	C7orf30
Gga.635.1.S1_at	GLRX
Gga.6356.2.S1_s_at	LOC422214
Gga.636.1.S1_at	IBSP
Gga.6363.1.S1_at	DEPDC7
Gga.6368.1.S1_at	DUSP14
Gga.6369.1.S1_at	ENTPD8
Gga.6371.2.S1_a_at	BTG2
Gga.6375.1.S1_at	BHLHB8
Gga.6383.1.S1_at	PPP2R1B
Gga.639.1.S1_at	S100A11
Gga.6390.3.S1_a_at	CTSC
Gga.6394.1.S1_a_at	RAPSN
Gga.6399.1.S1_at	MALL
Gga.64.1.S1_at	LOC776572 /// LOC776580 /// LOC776581
Gga.6402.1.S1_at	C1orf190
Gga.6408.1.S1_at	DGKE
Gga.6446.1.S1_x_at	RPL38
Gga.645.1.S1_s_at	SKIL
Gga.6457.2.S1_at	MTERFD1
Gga.6460.1.S1_at	LOC770251
Gga.6470.1.S1_at	TMEM104
Gga.6474.1.S1_at	CXorf39
Gga.648.1.S2_at	FGF1
Gga.6487.1.S1_at	CAPN8
Gga.6492.1.S1_at	LOC422510
Gga.6496.1.S1_at	GAL11
Gga.6504.1.S1_at	LOC422993
Gga.6514.1.S1_a_at	LYPLA2P1
Gga.6516.1.S1_at	FABP2
Gga.6523.1.S1_at	TMEM173
Gga.6529.1.S1_at	FCER1G
Gga.653.1.S1_at	TNXB
Gga.6535.1.S1_at	KBTBD8
Gga.6548.1.S1_at	GPR87
Gga.6559.1.A1_at	SEMA3G
Gga.657.1.S1_at	FOXG1
Gga.658.1.S1_at	RYR3

Gga.659.1.S1_at	RYR1
Gga.6597.1.S1_at	SDC1
Gga.660.1.S1_at	P2RY6
Gga.6612.2.A1_at	LOC693257
Gga.6614.1.S1_at	C1orf66
Gga.663.1.S1_at	P2RY5
Gga.6642.1.A1_at	LOC769242
Gga.6650.3.S1_a_at	PDCD1LG2
Gga.6653.1.S1_at	HNF4beta
Gga.666.1.S1_a_at	VIP
Gga.67.1.S1_at	MIP
Gga.670.1.S1_at	MST1
Gga.6700.1.S1_s_at	ABCG1
Gga.6712.1.S1_at	LOC425525 /// LOC427060 /// LOC
Gga.6713.1.S1_at	GZMA
Gga.6714.1.S1_at	RAD9A
Gga.6718.1.S1_s_at	VPS16
Gga.6726.1.S1_at	RAB40C
Gga.6729.2.S1_at	DHX57 /// LOC429336
Gga.674.1.S1_at	GCH1
Gga.6762.1.A1_at	DDOST
Gga.6763.1.S1_s_at	KIAA1244
Gga.6765.1.S1_at	RGS12
Gga.677.1.S1_at	GNOT1
Gga.6773.1.S1_at	SLC10A4
Gga.6778.1.S1_x_at	LOC426912
Gga.6778.2.S1_a_at	LOC431317
Gga.6778.2.S1_at	LOC426912
Gga.679.1.S1_at	VLDLR
Gga.6791.1.A1_at	NFIB
Gga.6791.1.A1_s_at	NFIB
Gga.6792.1.A1_x_at	KLHL8
Gga.6795.1.A1_at	KIFC1
Gga.6804.1.A1_s_at	RCJMB04_21h11
Gga.681.2.S1_a_at	NTRK2
Gga.682.1.S1_a_at	ST6GALNAC2
Gga.6823.1.A1_at	PSMC3
Gga.6825.1.S1_at	LOC419812
Gga.6838.1.S1_at	C2orf43
Gga.6842.2.S1_s_at	CNOT4

Gga.6847.1.S1_at	LOC425364 /// LOC425625 /// LOC
Gga.6848.2.S1_at	RCJMB04_20n13
Gga.685.1.S1_at	RAF1
Gga.6851.1.S1_at	SLC26A9
Gga.6853.1.A1_at	LOC425311
Gga.6868.1.S1_at	LOC417458
Gga.6870.1.S1_at	FBXO39
Gga.6870.1.S1_s_at	LOC776097
Gga.6877.1.S1_at	ROBO2
Gga.6878.1.S1_s_at	ADCY7
Gga.6910.1.A1_at	RCJMB04_38d18
Gga.6917.1.A1_at	RNASEH1
Gga.6919.1.A1_at	CXXC5
Gga.692.1.S2_at	LOC396173
Gga.6922.1.S1_at	MYSM1
Gga.693.1.S1_at	CSRP1
Gga.6939.1.A1_at	DNAH9
Gga.694.1.S1_at	EPHB1
Gga.6941.1.S1_at	LOC771156
Gga.6959.1.S1_at	IL4R
Gga.6972.1.S1_at	ABI3
Gga.698.1.S2_at	VCL
Gga.6982.1.S1_at	LOC415553
Gga.6982.2.S1_a_at	LOC415553
Gga.6983.1.S1_at	MGRN1
Gga.6984.1.S1_at	HN1
Gga.6984.2.S1_s_at	HN1
Gga.6987.2.S1_at	PDCD5
Gga.699.1.S1_at	THRB
Gga.6993.1.S1_at	LOC415683
Gga.70.1.S1_at	NKX3-2
Gga.700.1.S1_at	TNNI2
Gga.7002.1.S1_at	FBXW8
Gga.7004.1.S1_at	LOC420301
Gga.7009.2.S1_a_at	GNB4
Gga.701.1.S1_at	RSFR
Gga.701.1.S1_s_at	LOC396194 /// RSFR
Gga.7011.1.S1_a_at	LOC419195
Gga.7013.1.S1_at	CHPF
Gga.7017.1.S1_at	GDA /// LOC770483

Gga.7018.1.S1_s_at	FGD3
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Gga.7024.1.S1_s_at	SIRT2
Gga.703.1.S1_at	LOC396194
Gga.7035.1.S1_x_at	LOC769722
Gga.7035.4.S1_a_at	LOC769722
Gga.7035.4.S1_x_at	LOC769722
Gga.7037.1.S1_s_at	SUPT5H
Gga.7037.2.S1_s_at	SUPT5H
Gga.7040.1.S1_at	CTSH
Gga.7041.3.S1_a_at	LOC422046
Gga.7044.1.S1_s_at	SEPP1
Gga.7044.3.S1_s_at	SEPP1
Gga.7046.1.S1_s_at	DMBT1
Gga.7048.1.S1_at	MIZF
Gga.705.1.S1_at	PGR
Gga.7055.2.S1_a_at	LOC776812
Gga.706.1.S1_at	TP53
Gga.7061.1.S1_s_at	SH3GLB1
Gga.7064.1.S1_at	IGSF1
Gga.7066.1.S1_at	SIPA1L1
Gga.707.1.S1_at	LOC396207
Gga.7074.1.S1_at	PPIH
Gga.7079.1.S1_at	FOXK2
Gga.708.1.S1_x_at	NFIC
Gga.708.3.S1_a_at	NFIC
Gga.7084.1.S1_at	SOS2
Gga.7086.1.S1_at	LOC420010
Gga.7087.1.S1_at	CKAP5
Gga.7089.1.S1_at	TMEM22
Gga.709.2.S1_a_at	NFIB
Gga.7097.1.S1_at	FAM120A
Gga.71.1.S1_at	PDGFB
Gga.710.1.S1_a_at	NFIA
Gga.710.6.S1_a_at	NFIA
Gga.7100.1.S1_at	LOC422509
Gga.7102.1.S1_at	UBOX5
Gga.7104.1.S1_s_at	CRIP1
Gga.7109.1.S1_s_at	INPP5K
Gga.711.1.S1_at	TNR

Gga.7115.1.S1_a_at	AGTRAP
Gga.7117.1.S1_at	LGTN
Gga.7118.2.S1_s_at	METT9
Gga.713.1.S1_at	LYZ
Gga.7130.1.S1_at	OSBPL10
Gga.7139.2.S1_s_at	C14orf32
Gga.714.1.S2_at	FMN1
Gga.7140.2.S1_s_at	RCJMB04_3a16
Gga.7144.1.S1_at	C19orf28
Gga.7147.1.S1_at	IFT172
Gga.7148.2.A1_at	PLCG2
Gga.7149.2.S1_a_at	LPXN
Gga.715.1.S1_at	LMNA
Gga.7164.1.S1_at	LOC421110
Gga.7176.1.S1_at	MECR
Gga.718.1.S1_at	DMD
Gga.718.2.S1_a_at	DMD
Gga.718.3.S1_x_at	DMD
Gga.7180.1.S1_s_at	BUB1
Gga.7186.1.S1_at	BPNT1
Gga.7186.2.S1_a_at	BPNT1
Gga.7194.1.S1_at	SPATA13
Gga.7197.1.S1_at	LOC771974
Gga.7199.1.S1_s_at	COMT
Gga.72.1.S1_at	CAPN3
Gga.7201.2.S1_a_at	PXMP4
Gga.7203.1.S1_at	STK10
Gga.7204.1.S1_at	LOC769044
Gga.721.1.S1_at	MYB
Gga.7210.1.S1_at	ZP3
Gga.7211.1.S1_at	TMBIM1
Gga.7212.1.S1_at	LOC421447
Gga.7213.1.S1_at	LOC423256
Gga.722.1.S1_x_at	LOC396247
Gga.7223.1.A1_at	AP1G1
Gga.7224.2.S1_s_at	NRBP1
Gga.7225.1.S1_at	LOC418040
Gga.7228.1.S1_at	CMBL
Gga.723.1.S1_a_at	CD28
Gga.7230.1.S1_at	LOC770869

Gga.7231.1.S1_at	SOX17
Gga.7235.1.S1_at	DHRS3
Gga.7237.1.S1_at	LOC425086
Gga.724.1.S1_at	HOXD4
Gga.7240.1.S1_s_at	PLTP
Gga.7242.1.S1_at	LOC428693
Gga.7244.1.S1_at	LOC426184
Gga.7247.1.S1_at	CREB3L3
Gga.7252.1.S1_at	MRPS12
Gga.7254.2.S1_a_at	LOC769737
Gga.7256.1.S1_at	SEC14L2
Gga.7259.1.A1_at	LOC769608
Gga.726.2.S1_a_at	CDC2
Gga.7260.1.S1_at	SCARF1
Gga.7262.1.S1_at	MRRF
Gga.7262.3.S1_at	MRRF
Gga.7266.1.S1_at	C7orf55
Gga.7267.2.S1_at	WDR13
Gga.7268.2.S1_s_at	RCJMB04_7e11
Gga.7271.1.S1_s_at	MPP1
Gga.7275.1.S1_at	MOSPD1
Gga.7276.1.S1_at	PIGC
Gga.7278.1.S1_at	SLC25A29
Gga.7281.1.S1_at	FBXL21
Gga.7281.2.S1_a_at	FBXL21
Gga.7282.1.S1_at	C20orf116
Gga.7285.1.S1_at	LOC770952
Gga.729.1.S1_at	LOC396260
Gga.7296.3.S1_s_at	IFNGR2
Gga.7298.1.S1_at	C1QA
Gga.7309.1.S1_at	LOC431003
Gga.7310.2.A1_at	PRKAB1
Gga.7317.1.S1_at	GFAP
Gga.7319.2.S1_a_at	LOC426622
Gga.7319.2.S1_s_at	LOC426622
Gga.7320.1.S1_at	TXNRD3
Gga.7320.1.S1_s_at	TXNRD3
Gga.7324.1.S1_at	ARFGAP3
Gga.7331.1.S1_at	RAI2
Gga.7337.1.S1_at	SSBP2

Gga.7337.2.S1_a_at	SSBP2
Gga.735.1.S1_at	SRL
Gga.7351.1.S1_at	C6orf161
Gga.7354.1.S1_at	IKZF2
Gga.7355.1.S1_at	MIS12
Gga.7356.1.S1_at	PANK3
Gga.7360.1.S1_a_at	LOC769609
Gga.7367.1.S1_at	NHEJ1
Gga.7373.2.S1_at	NDUFB3
Gga.7374.2.S1_a_at	RBM41
Gga.7376.1.S1_at	RCJMB04_16d24
Gga.738.1.S1_at	GSC
Gga.7381.3.S1_s_at	WDR45L
Gga.7382.1.S1_at	NOM1
Gga.7388.2.S1_s_at	TOR1A
Gga.739.1.S1_at	P20K
Gga.7391.1.S1_at	C11orf77
Gga.7396.1.S1_at	C9orf167
Gga.74.1.S1_at	LMO2
Gga.740.1.S1_at	S100A9
Gga.7412.1.S1_s_at	RCJMB04_2h7
Gga.7415.1.S1_at	TPP1
Gga.742.1.S1_at	SST
Gga.7424.1.S1_at	SYNJ2
Gga.7425.1.S1_at	ANXA8L1
Gga.7428.1.S1_at	CMYA5
Gga.7430.1.S1_at	SYT11
Gga.7435.3.S1_a_at	OSBPL1A
Gga.7438.1.S1_at	TSHZ2
Gga.7442.1.S1_at	PTGER3
Gga.7447.1.S1_at	LOC772080
Gga.7447.2.S1_at	LOC772080
Gga.7447.2.S1_s_at	LOC772080
Gga.7448.1.S1_at	MED24
Gga.7449.1.S1_at	LOC416335
Gga.7460.1.S1_a_at	C9orf151
Gga.7460.1.S1_at	C9orf151
Gga.7466.1.S1_at	FAM123A
Gga.7467.1.S1_at	PDLIM4
Gga.7468.1.S1_at	PERP

Gga.7471.1.S1_at	HSPG2
Gga.7471.2.A1_s_at	HSPG2
Gga.7476.1.S1_at	TMEM108
Gga.7477.1.S1_s_at	MSH6
Gga.7482.1.S1_s_at	SETD4
Gga.749.1.S1_at	PLS1
Gga.7492.2.S1_a_at	RASL11B
Gga.7494.1.S1_at	RCJMB04_4p22
Gga.750.1.S1_at	MYOD1
Gga.7508.2.S1_at	LOC428674
Gga.751.1.S1_at	LOC396296
Gga.7514.1.S1_at	CAD
Gga.7514.2.S1_at	CAD
Gga.7518.1.S1_s_at	RCJMB04_1g4
Gga.752.1.S1_at	TAL1
Gga.7528.1.S1_at	KLF2
Gga.7529.1.S1_at	NPAT
Gga.7535.1.S1_at	NSD1
Gga.7545.1.S1_at	MORN2
Gga.7551.1.S1_at	WISP1
Gga.7557.1.S1_at	LOC768734
Gga.756.1.S1_s_at	ANK2
Gga.7562.1.S1_a_at	LOC770202
Gga.7566.1.S1_at	LOC424918
Gga.7571.1.S1_at	SNRPA1
Gga.7584.1.S1_s_at	KLHL18
Gga.7588.1.S1_at	GGTL3
Gga.759.1.S1_at	IGFBP2
Gga.7598.1.S1_at	LOC425545
Gga.7599.1.S1_at	LOC420810
Gga.7604.1.S1_at	PLSCR1
Gga.7604.2.S1_a_at	PLSCR1
Gga.7618.1.S1_at	PSCD3
Gga.7619.1.S1_at	COG7
Gga.7620.2.S1_a_at	C11orf54
Gga.7623.1.S1_at	C6orf129
Gga.7633.1.S1_s_at	MYO9A
Gga.7639.2.S1_a_at	C8orf80
Gga.764.1.S1_at	ACVR2B
Gga.7644.1.S1_at	LOC772187

Gga.7650.1.S1_at	GSK3B
Gga.7653.2.S1_a_at	PRR6
Gga.7656.2.S1_s_at	RCJMB04_17e23
Gga.766.1.S1_at	SEMA4D
Gga.7672.2.S1_a_at	RCJMB04_2j4
Gga.7673.1.S1_at	C9orf18
Gga.7674.2.S1_at	MYCBP
Gga.7677.1.S1_at	LOC768603
Gga.7679.1.S1_at	GPSM2
Gga.7685.3.S1_a_at	ANAPC2
Gga.7686.1.S1_at	C20orf72
Gga.7689.2.S1_at	CASK
Gga.7689.2.S1_x_at	CASK
Gga.7692.2.S1_a_at	TAGLN3
Gga.7697.3.S1_a_at	LOC423257
Gga.7708.1.S1_at	RCJMB04_1d13
Gga.7715.2.S1_at	LOC415966
Gga.7721.1.S1_at	VILL
Gga.7725.1.S1_at	LOC426422
Gga.7730.2.S1_at	ARSI
Gga.7733.1.S1_at	ENTPD7
Gga.774.1.S1_at	DNTT
Gga.7741.1.S1_at	PTCD1
Gga.7743.1.S1_at	MRPL33
Gga.7748.1.S1_at	OSBPL10
Gga.775.1.S1_at	P22
Gga.7750.1.S1_at	LOC422459
Gga.7752.1.S1_at	LOC770248
Gga.7757.1.S1_at	UNC50
Gga.7759.1.S1_a_at	CCT2
Gga.7774.1.S1_at	LOC427414
Gga.7775.1.S1_at	LOC417013
Gga.7778.1.S1_at	TM2D2
Gga.778.1.S1_at	LOC396357
Gga.7784.1.S1_s_at	C4orf8
Gga.7785.1.S1_at	ADAMTS13
Gga.7790.1.S1_at	NR0B2
Gga.7792.1.S1_s_at	RCJMB04_9i11
Gga.7799.3.S1_at	ING4
Gga.780.1.S1_at	IAPP

Gga.7800.1.S1_at	LOC428660
Gga.7802.1.S1_at	CCDC28A
Gga.7802.2.S1_at	CCDC28A
Gga.7803.1.S1_at	C6orf89
Gga.7807.1.S1_at	MFGE8
Gga.7809.1.S1_at	LOC771069
Gga.7811.1.S1_at	NME6
Gga.7812.1.S1_at	ORC6L
Gga.7812.2.S1_a_at	ORC6L
Gga.7815.2.S1_a_at	LOC418170
Gga.7818.1.S1_at	NELF
Gga.7823.1.S1_at	RCJMB04_19g9
Gga.7828.2.S1_a_at	LOC425901
Gga.7829.2.S1_a_at	C15orf48
Gga.7833.3.S1_at	CCDC12
Gga.7835.1.S1_at	KLHL8
Gga.7838.1.S1_at	CSF2RA
Gga.784.1.S1_s_at	PTPRS
Gga.7840.1.S1_at	MASP1
Gga.7842.1.S1_at	ARRDC2
Gga.7843.1.S1_at	SYPL1
Gga.7849.1.S1_at	LOC769446
Gga.7851.1.S1_at	GLO1
Gga.7855.1.S1_at	BMPER
Gga.7860.1.S1_at	XPO6
Gga.7865.1.S1_at	IRAK2
Gga.787.2.S1_a_at	CFL2
Gga.7877.1.S1_at	PIGL
Gga.7879.1.S1_a_at	PEX10
Gga.7879.2.S1_at	PEX10
Gga.788.1.S1_at	LOC396380
Gga.7880.1.S1_at	BCL9
Gga.7881.1.S1_at	POLR2E
Gga.7885.2.S1_at	MSH4
Gga.7886.1.S1_at	C1QTNF2
Gga.7890.1.S1_at	SFRP4
Gga.7892.1.S1_at	LOC769992
Gga.7897.1.S1_s_at	LRSAM1
Gga.790.1.S1_at	ISLET-2
Gga.7900.2.S1_a_at	FIBIN

Gga.7901.1.S1_at	BOC
Gga.7907.1.S1_at	LRRC16A
Gga.7908.1.S1_at	C16orf61
Gga.7908.1.S1_s_at	C16orf61
Gga.791.1.S1_at	IRF1
Gga.7917.2.S1_a_at	GRAMD2
Gga.7918.1.S1_at	LOC423448
Gga.7918.1.S1_s_at	LOC423448
Gga.7920.1.S1_at	C11orf52
Gga.7921.1.S1_at	CKAP5
Gga.7921.1.S1_s_at	CKAP5
Gga.7924.1.S1_s_at	FAM108C1
Gga.7925.1.S1_s_at	RNF34
Gga.793.1.S1_s_at	ACHE
Gga.7932.1.S1_s_at	ATG12
Gga.7936.1.S1_at	WWC3
Gga.7937.1.S1_at	CDS2
Gga.7942.1.S1_at	SAMD4A
Gga.795.1.S1_at	GATA4
Gga.7953.1.S1_at	RPL27A
Gga.7955.1.S1_at	SLC14A2
Gga.7960.1.S1_at	WNT5B
Gga.7961.2.S1_a_at	C1orf128
Gga.7966.1.S1_s_at	RNF4
Gga.7970.1.S1_at	LOC769783
Gga.7997.1.S1_at	C20orf177
Gga.7997.2.S1_at	C20orf177
Gga.8001.2.S1_a_at	ATPAF1
Gga.8001.3.S1_a_at	ATPAF1
Gga.8001.3.S1_at	ATPAF1
Gga.8002.1.S1_a_at	C2orf33
Gga.8003.1.S1_at	C20orf30
Gga.8004.1.S1_s_at	PEMT
Gga.8004.3.S1_at	PEMT
Gga.801.1.S1_at	IFNA
Gga.8020.2.S1_a_at	C5orf32
Gga.8021.3.S1_at	IMMP1L
Gga.8030.1.S1_at	TFPI2
Gga.8036.1.S1_s_at	C6orf154
Gga.8038.1.S1_at	RFC4

Gga.804.1.S1_at	TGFBR3
Gga.8043.1.S1_at	C6orf32
Gga.8046.2.S1_a_at	LYRM5
Gga.805.1.S1_at	EPHA3
Gga.8061.1.S1_at	HSCB
Gga.8062.2.S1_at	ARL6IP1
Gga.8069.1.S1_at	MGAT4B
Gga.8069.2.S1_a_at	MGAT4B
Gga.8076.2.S1_a_at	GNAL
Gga.8078.1.S1_at	GAS6
Gga.8081.1.S1_at	FSTL4
Gga.8088.1.S1_at	CASP8AP2
Gga.8089.1.S1_at	KLF1
Gga.8090.1.S1_at	TAF3
Gga.8101.1.A1_a_at	TOMM7
Gga.8102.1.S1_at	LOC415871
Gga.8103.2.S1_at	ARIH2
Gga.8103.3.S1_a_at	ARIH2
Gga.8104.1.S1_at	HCK
Gga.8109.1.S1_s_at	KIAA0020
Gga.8116.1.S1_at	SLC46A3
Gga.812.1.S1_at	HSF1
Gga.8124.1.S1_at	MUSTN1
Gga.8125.1.S1_at	GJB1
Gga.8127.1.S1_at	PUS7
Gga.8128.1.S1_at	LOC416149
Gga.8129.1.S1_at	LOC770818
Gga.813.2.S1_at	LOC396417
Gga.813.3.S1_at	LOC396417
Gga.8133.1.S1_at	C10orf65
Gga.8134.1.S1_at	KLHDC4
Gga.8135.1.S1_at	COQ10B
Gga.8138.1.S1_at	ELF3
Gga.8139.1.S1_at	LOC419389
Gga.8140.1.S1_at	FGFBP1
Gga.8141.1.S1_at	EVPL
Gga.8144.2.S1_at	FAM70A
Gga.815.1.S1_at	ITGAV
Gga.8154.1.S1_at	RAB17
Gga.8155.1.S1_at	AR

Gga.8159.1.S1_at	LOC422298
Gga.816.1.S1_at	VIL1
Gga.8163.1.S1_s_at	AGA
Gga.8164.1.S1_a_at	LOC421099
Gga.8164.2.S1_at	LOC421099
Gga.8173.1.S1_at	C11orf34
Gga.8174.1.S1_at	RAB20
Gga.8178.1.S1_at	C16orf14
Gga.8181.2.S1_a_at	IVNS1ABP
Gga.819.1.S1_at	TUBB1
Gga.8193.2.S1_x_at	RCCD1
Gga.8194.1.S1_a_at	CEP192
Gga.8199.1.S1_at	LAD1
Gga.820.1.S1_at	TNNI3
Gga.8213.1.S1_at	RCJMB04_10i2
Gga.8216.1.S1_at	LOC424257
Gga.8218.1.S1_at	SLC7A9
Gga.8219.1.S1_at	NDUFA12L
Gga.822.1.S1_a_at	ELN
Gga.8224.1.S1_at	LOC422694
Gga.8226.1.S1_at	LOC431580
Gga.8227.1.S1_s_at	ISG12-1
Gga.823.1.S1_at	TNNC2
Gga.8232.1.S1_at	FBXO31
Gga.8237.1.S1_a_at	LOC770630
Gga.8238.1.S1_at	EDN2
Gga.8239.1.S1_at	LOC427229
Gga.8241.1.S1_at	TCF21
Gga.8242.1.S1_at	PEX12
Gga.8244.1.S1_at	CMPK2
Gga.8249.1.S1_at	RPL7L1
Gga.826.1.S1_s_at	IL8
Gga.8260.1.S1_at	C8orf80
Gga.8267.2.S1_a_at	C13orf18
Gga.8269.1.S2_at	TIAL1
Gga.8275.1.S1_at	LOC417387
Gga.8280.2.S1_a_at	PGAM5
Gga.8287.1.S1_at	TIPRL
Gga.8290.1.S1_s_at	ANKRD40
Gga.8292.1.S1_at	CAMTA1

Gga.8293.1.S1_at	LOC421740
Gga.8296.2.S1_a_at	LOC424241
Gga.8310.2.S1_s_at	C1orf9
Gga.8312.1.S1_at	LOC769704
Gga.8312.1.S1_s_at	LOC415787
Gga.8312.2.S1_at	CES1
Gga.8312.3.S1_at	LOC771300
Gga.8312.4.S1_a_at	LOC769339 /// LOC769704
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Gga.8313.2.S1_s_at	AGK
Gga.8327.3.S1_a_at	FXR1
Gga.8329.1.S1_at	PRKCH
Gga.8335.1.S1_at	TMEM120A
Gga.8336.1.S1_s_at	RCJMB04_21h11
Gga.8342.1.S1_at	LOC777560
Gga.8352.1.S1_at	LAMA2
Gga.8357.1.S1_at	KIF13A
Gga.8359.1.S1_at	GSTA3
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Gga.8363.1.S1_at	AXIN2
Gga.8363.1.S2_at	AXIN2
Gga.8365.1.A1_at	RCJMB04_28l23
Gga.8366.1.S1_at	ALDH2
Gga.8368.1.S1_at	TC2N
Gga.837.1.S1_a_at	NPY
Gga.8373.1.S1_at	RAPGEF3
Gga.8374.1.S1_at	RNF122
Gga.8376.1.S1_s_at	SNRPD3
Gga.8379.1.S1_at	RCJMB04_1g4
Gga.838.1.S1_at	ATP1A3
Gga.8382.1.S1_at	SCAMP5
Gga.8389.1.S1_at	LATS1
Gga.8391.2.S1_at	LOC423772
Gga.8392.1.S1_at	EMP1
Gga.8393.2.S1_a_at	CEP57
Gga.8394.1.S1_at	FUNDC2
Gga.8395.1.S1_at	LOC769366
Gga.84.1.A1_at	LOC430062
Gga.84.1.S1_at	LOC430062
Gga.8400.2.S1_at	UBE2F

Gga.8401.1.S1_at	JTB
Gga.8407.1.S1_s_at	C20orf42
Gga.841.1.S1_at	MYL2
Gga.8417.3.S1_s_at	RCJMB04_34k12
Gga.842.1.S1_at	FBXL12
Gga.8423.2.S1_a_at	C18orf45
Gga.8424.1.S1_at	C9orf21
Gga.8429.2.S1_a_at	LOC420849
Gga.8432.1.S1_at	C9orf80
Gga.8433.1.S1_a_at	PHACTR1
Gga.8434.1.S1_at	IGFBP4
Gga.8435.1.S1_at	LOC771055
Gga.8436.2.A1_at	C4orf33
Gga.8436.2.S1_a_at	C4orf33
Gga.8445.1.S1_at	DUSP6
Gga.8446.1.S1_at	GSR
Gga.8447.1.S1_at	FGFBP2
Gga.8448.1.S1_at	HAL
Gga.845.1.S1_at	LOC426910
Gga.8451.1.S1_a_at	TERF1
Gga.8454.1.S1_at	LOC426624
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Gga.8462.1.S1_at	BUB1B
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Gga.8466.1.S1_s_at	SUMO1
Gga.8467.1.S1_a_at	NCAPG
Gga.8468.1.S1_at	PEX10
Gga.8479.1.S1_at	FUBP1
Gga.8479.1.S2_at	FUBP1
Gga.8487.1.S1_at	SRP72
Gga.8487.2.S1_at	SRP72
Gga.8488.1.S1_s_at	NDUFV1
Gga.8489.1.S1_at	FGF9
Gga.8499.2.S1_at	RPS13
Gga.8499.4.A1_at	RPS13
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Gga.8506.1.S2_s_at	TRIB2
Gga.8508.1.S1_s_at	SLA

Gga.8508.1.S2_s_at	SLA
Gga.8509.1.S1_s_at	DNPEP
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Gga.8517.1.S1_at	LDLR
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Gga.8529.1.S2_at	CREB1
Gga.8535.1.S2_at	UNC5C
Gga.8537.1.S1_at	TNKS2
Gga.854.1.S1_a_at	LGALS1
Gga.8542.3.S1_a_at	ATP5O
Gga.8548.3.S1_s_at	BTF3L4
Gga.8557.1.S1_at	IL17F
Gga.8559.2.S1_a_at	LOC769871 /// TADA1L
Gga.8563.1.A1_at	SDC1
Gga.8567.1.S1_at	STAT3
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Gga.8594.1.S1_at	SLC5A1
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Gga.8622.1.S1_at	LOC770708
Gga.863.1.S1_at	GJA5
Gga.8635.1.S1_at	SLC5A1
Gga.866.1.S1_at	COL17A1
Gga.8674.1.S1_s_at	RCJMB04_26f20
Gga.8676.1.S1_at	C14orf83
Gga.870.2.S1_a_at	FGFR1
Gga.8702.1.S1_at	DUSP15
Gga.871.1.S1_at	SLC2A3
Gga.873.2.S1_a_at	LOC396522
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Gga.8732.1.S1_at	PLK3
Gga.8736.1.S1_at	MICAL1
Gga.8737.1.S1_at	MAL2
Gga.8747.1.S1_at	LOC429710
Gga.876.1.S1_s_at	B-G
Gga.8763.1.S1_at	YTHDC1
Gga.877.1.S1_at	ATP2A1
Gga.8771.1.S1_at	FGFRL1
Gga.8774.1.S1_s_at	TNFSF10
Gga.8774.1.S2_s_at	TNFSF10
Gga.8779.2.S1_a_at	E4F1

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Gga.8817.1.S1_s_at	FDFT1
Gga.882.1.S1_at	MYBPH
Gga.8829.1.S1_s_at	WASL
Gga.8836.1.S1_at	FAM100A
Gga.8837.1.S1_at	LOC771289
Gga.8838.1.S1_at	LOC427079
Gga.8839.1.S1_at	TUBD1
Gga.8839.2.S1_a_at	TUBD1
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Gga.8850.1.S1_at	KBTBD2
Gga.8851.1.S1_a_at	IDI1
Gga.8853.3.S1_s_at	SULT1B1
Gga.8854.1.S1_at	ZBTB43
Gga.8858.1.S1_s_at	FKBP7
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Gga.8861.1.S1_at	MAP3K8
Gga.8864.1.S1_at	AMD1
Gga.8868.1.S1_at	GDE1
Gga.887.1.S1_at	OCM2
Gga.8873.1.S1_a_at	NMI
Gga.8876.1.S1_at	AQP11
Gga.8877.1.S1_at	ATXN7L1
Gga.8878.1.S1_at	DGKD
Gga.888.1.S1_at	COL6A3
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Gga.8880.2.S1_s_at	MME
Gga.8886.2.S1_at	DPP4
Gga.889.1.S1_at	ITGA3
Gga.8898.1.S1_at	PARL
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Gga.8906.2.S1_s_at	EIF5
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Gga.8931.1.S1_at	PLIN
Gga.8932.1.S1_at	CRHR2
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Gga.8944.3.S1_s_at	LOC424393 /// LOC776927
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Gga.8962.1.S1_at	LOC769755
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Gga.8975.1.S1_s_at	LOC420381
Gga.8977.1.S1_at	C1orf58
Gga.8980.1.S1_s_at	ACAD11
Gga.8981.1.S1_at	LOC424832
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Gga.8986.1.S1_at	THOC7
Gga.8990.2.S1_s_at	RCJMB04_31e20
Gga.8996.1.S1_at	PCDH24
Gga.8999.1.S1_at	AKAP13
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Gga.900.1.S1_at	ADORA3
Gga.901.1.S1_at	KRTAP10-4
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Gga.9013.2.S1_s_at	FKBP4
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Gga.9023.2.S1_a_at	SNX4
Gga.9025.1.S1_at	C1R
Gga.9027.1.S1_at	SCARB1
Gga.9028.1.S1_s_at	RCJMB04_1d11
Gga.9029.1.S1_at	BECN1
Gga.9033.1.S1_at	RCJMB04_13d16
Gga.9036.1.S1_a_at	ETHE1
Gga.9037.1.S1_at	DOCK9
Gga.9039.1.S1_at	GOLM1
Gga.9043.1.S1_at	WHSC2
Gga.9052.1.S1_at	LOC768655
Gga.9060.1.S1_at	LOC770392

Gga.9062.1.S1_at	ENPP3
Gga.9074.2.S1_s_at	C12orf10
Gga.9075.1.S1_at	TCN2
Gga.9077.1.S1_at	HVCN1
Gga.9079.1.S1_at	ABI2
Gga.9081.1.S1_at	DNAJC3
Gga.9083.1.S1_at	KCNA2
Gga.9086.1.S1_at	RHAG
Gga.9086.1.S2_at	RHAG
Gga.9088.1.S1_at	SS2
Gga.909.1.S1_at	SLIT2
Gga.9103.1.S1_at	LYG2
Gga.9126.2.S1_at	CHIR-A2 /// LOC425308 /// LOC4.
Gga.9127.1.S1_at	ATP10D
Gga.913.1.S1_at	FZR1
Gga.9132.1.S1_s_at	AARS
Gga.9133.1.S1_at	LOC417536
Gga.9136.1.S1_at	TACSTD1
Gga.9136.2.S1_a_at	TACSTD1
Gga.9136.2.S1_x_at	TACSTD1
Gga.9138.1.S1_at	GMIP
Gga.914.2.S1_at	CDH1-A
Gga.9147.1.S1_at	LOC424588
Gga.9149.1.S1_at	HDHD2
Gga.915.1.S1_at	SOCS3
Gga.9152.1.S1_at	TMEM169
Gga.9154.3.S1_x_at	PACS2
Gga.9156.1.S1_s_at	TMEM57
Gga.9157.2.S1_a_at	COX19
Gga.9158.1.S1_at	AHSA2
Gga.916.1.S2_at	IFNG
Gga.9160.2.S1_a_at	DNAJB6
Gga.9160.3.S1_at	DNAJB6
Gga.9161.1.S1_at	PANK3
Gga.9165.2.S1_at	C6orf163
Gga.9168.1.S1_at	S100B
Gga.9174.1.S1_at	KCTD10
Gga.9174.3.S1_a_at	KCTD10
Gga.9174.3.S1_x_at	KCTD10
Gga.918.1.S1_at	KCNMB1

Gga.9181.5.A1_at	RPS25
Gga.9185.1.S1_at	LOC427196
Gga.9186.1.S1_s_at	NEURL
Gga.9187.1.S1_s_at	PRPSAP1
Gga.92.1.S1_at	AGMAT /// LOC771697
Gga.920.1.S1_at	SP1
Gga.9203.1.S1_s_at	RCJMB04_16e10
Gga.9205.1.S1_at	PLAC8
Gga.9211.3.S1_at	LOC426157 /// PCF11
Gga.9212.1.S1_s_at	NOL14
Gga.9219.1.S1_at	MPHOSPH10
Gga.9224.2.S1_a_at	MRPS10
Gga.9229.2.S1_a_at	ATRX
Gga.9235.1.S1_at	ELMOD2
Gga.9238.1.S1_at	LEPR
Gga.9239.1.S1_s_at	HLA-G /// LOC417056 /// LOC417
Gga.924.1.S1_at	BF2
Gga.9244.2.S1_a_at	TEKT4
Gga.9260.1.S1_at	LOC417053 /// LOC417057 /// LOC
Gga.9262.1.S1_at	HMGA1
Gga.9263.1.S1_at	JMJD2C
Gga.9265.1.S1_at	MSH2
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Gga.927.1.S1_at	ANPEP
Gga.9270.2.S1_a_at	SERHL2
Gga.9276.2.S1_s_at	LOC772074
Gga.9278.1.S1_at	CETN3
Gga.9282.1.S1_s_at	EIF2AK4
Gga.9290.1.S1_at	HS2ST1
Gga.9290.1.S2_at	HS2ST1
Gga.9293.1.S1_at	FN1
Gga.9294.1.S1_at	IMP3
Gga.9299.1.S1_at	CPT1A
Gga.930.1.S1_at	AKT2
Gga.9303.1.S1_at	RCJMB04_5h14
Gga.9305.1.S1_at	LOC416033
Gga.9307.1.S1_at	NPTX2
Gga.931.1.A1_at	PLAT
Gga.9311.1.S1_at	FASTKD2
Gga.9313.1.S1_at	GRRP1

Gga.9314.1.S1_at	SOX4
Gga.9315.1.S1_at	KRT222P
Gga.9319.1.S1_at	ADPRHL1
Gga.9320.1.S1_at	WEE1
Gga.9327.1.S1_at	C4orf34
Gga.9334.1.S1_at	SGK1
Gga.9334.2.S1_a_at	SGK1
Gga.9336.1.S1_at	GSPT1
Gga.9338.1.S1_at	HINTW
Gga.9341.1.S1_at	USP7
Gga.9341.3.S1_a_at	USP7
Gga.9342.1.S1_at	AVEN
Gga.9346.3.S1_a_at	VIM
Gga.9347.2.S1_s_at	NFRKB
Gga.9347.3.S1_a_at	NFRKB
Gga.936.1.S1_at	SFTPA1
Gga.9362.2.S1_at	LOC423783
Gga.9364.1.S1_at	IGFBP5
Gga.9366.3.S1_a_at	RIOK1
Gga.9367.2.S1_s_at	TDRD3
Gga.937.1.S1_at	SOD2
Gga.9376.3.S1_at	GARS
Gga.9378.1.S1_s_at	RCJMB04_1j7
Gga.9378.2.S1_at	RCJMB04_1j7
Gga.938.1.S1_at	IKZF2
Gga.9382.1.A1_at	GEMIN4
Gga.9385.1.S1_a_at	SIVA1
Gga.9386.1.S1_at	RBP7
Gga.9387.1.S1_at	GGT1
Gga.939.1.S1_at	LOC395310
Gga.9390.1.S1_at	RCJMB04_4h19
Gga.94.1.S1_at	KHSRP
Gga.9403.1.S1_a_at	CCDC109B
Gga.9404.1.S1_at	PCSK2
Gga.9414.1.S1_at	FAM101B
Gga.9423.3.S1_s_at	SELT
Gga.943.1.S1_s_at	GRIA1
Gga.944.1.S1_at	CENPH
Gga.9457.1.S1_at	LOC416888
Gga.9466.1.S1_s_at	C17orf63

Gga.9467.1.S1_at	ITM2B
Gga.9471.1.S1_at	ANGPT1
Gga.9472.1.S1_s_at	LIN52
Gga.9473.1.S1_at	ITGB5
Gga.9475.1.A1_at	DAG1
Gga.9475.1.S1_at	DAG1
Gga.9475.1.S1_x_at	DAG1
Gga.9476.1.S1_at	ROR1
Gga.9478.1.S1_at	BSX
Gga.9483.1.S1_at	LOC414835
Gga.9495.2.S1_a_at	RIPK5
Gga.9499.1.S1_s_at	HS6ST2
Gga.950.1.S1_at	HPSE
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Gga.9503.1.S1_s_at	PCDH17
Gga.9505.1.A1_at	PCDHGC5
Gga.9507.1.A1_at	FAT3
Gga.9509.1.S1_at	BMP10
Gga.951.1.S1_at	TULP1
Gga.9510.1.S1_at	RCJMB04_5f2
Gga.9512.1.S1_s_at	HIBCH
Gga.9513.1.S1_a_at	CXCL12
Gga.9513.1.S2_at	CXCL12
Gga.9514.1.S1_at	HAAO
Gga.9517.1.S1_at	DENND4A
Gga.9518.1.S1_at	C6orf117
Gga.952.1.S1_at	NKX2-1
Gga.9525.1.S1_s_at	KIAA1946
Gga.9528.1.S1_at	EFCBP1
Gga.9530.1.S1_s_at	C14orf143
Gga.9531.1.S1_at	CAMP
Gga.9534.1.S1_at	ZDHHC6
Gga.9536.1.S1_s_at	CCDC131
Gga.9540.1.S1_s_at	MOSPD2
Gga.9547.1.S1_at	SLC7A3
Gga.9554.1.S1_at	FAM120A
Gga.9556.1.S1_at	ZBTB34
Gga.9563.1.S1_at	CCL4 /// CCL5
Gga.9565.1.S1_at	C1orf55
Gga.9566.1.S1_at	SLC25A37

Gga.9566.2.S1_s_at	SLC25A37
Gga.9567.1.S1_at	B3GNT7
Gga.9573.1.S1_at	ECM2
Gga.9574.1.S1_at	LOC419390
Gga.9577.1.S1_at	TUBGCP4
Gga.9580.1.S1_at	AKR1B1 /// LOC425137 /// LOC75
Gga.9582.1.S1_at	RNPC3
Gga.9582.2.S1_a_at	RNPC3
Gga.9587.2.S1_at	CCDC141
Gga.959.1.S1_at	SOX18
Gga.9591.1.S1_s_at	AGAP1
Gga.9592.1.S1_at	DOK5
Gga.9593.1.S1_at	EMP2
Gga.9597.1.S1_at	UBAC2
Gga.96.2.S1_at	GJD2
Gga.960.1.S1_at	VIPR1
Gga.9600.2.S1_at	DCTN5
Gga.9605.1.S1_s_at	PARP4
Gga.9608.1.S1_at	HSPA4
Gga.961.2.S1_at	TBX5
Gga.9610.1.S1_at	BMS1
Gga.9610.1.S1_s_at	BMS1
Gga.9614.1.S1_at	SYN2
Gga.9616.1.S1_at	DCUN1D4
Gga.9617.1.S1_at	PRR5
Gga.9617.2.S1_at	PRR5
Gga.9619.1.S1_at	LOC769963
Gga.9619.2.S1_s_at	PAFAH2
Gga.962.1.S1_a_at	PITX1
Gga.9623.1.S1_a_at	CAMK2A
Gga.9624.1.S1_at	GLTPD1
Gga.9626.1.S1_s_at	RCJMB04_8d19
Gga.9626.3.S1_s_at	RCJMB04_8d19
Gga.9632.1.S1_at	RPAP2
Gga.9632.2.S1_a_at	RPAP2
Gga.9634.1.S1_at	DECR1
Gga.9635.3.S1_at	LOC769384
Gga.9636.1.S1_at	SNORA32
Gga.9637.2.S1_a_at	SAT1
Gga.9639.1.S1_at	HPGD

Gga.9641.1.S1_at	CYP3A80
Gga.9643.1.S1_at	ANXA13
Gga.9646.1.S1_at	YIPF5
Gga.9651.1.S1_at	ZBTB25
Gga.9652.1.S1_at	SERPINA4
Gga.9654.1.S1_at	C9orf100
Gga.9655.1.S1_at	MND1 /// TRIM2
Gga.9659.1.S1_s_at	SPTBN1
Gga.9662.2.S1_a_at	C15orf42
Gga.9663.2.S1_a_at	DALRD3
Gga.9663.3.S1_a_at	DALRD3
Gga.9667.1.S1_s_at	CHODL
Gga.9668.1.S1_s_at	ATRX
Gga.9670.1.S1_at	FAH
Gga.9674.1.S1_at	TRIM55
Gga.9675.1.S1_at	PDGFD
Gga.9676.1.S1_s_at	HCFC2
Gga.9677.1.S1_at	C17orf39
Gga.9680.3.S1_a_at	RAD51L3
Gga.9681.1.S1_at	FAM77D
Gga.9682.1.S1_at	BCLAF1
Gga.9686.2.S1_a_at	RDH10
Gga.9687.1.S1_at	FAM149A
Gga.969.1.S1_at	MOXD1
Gga.9692.1.S1_at	LOC770574
Gga.9693.1.S1_at	HEATR2
Gga.9693.2.S1_a_at	HEATR2
Gga.9697.1.S1_s_at	PNN
Gga.9699.4.S1_x_at	JMJD7-PLA2G4B
Gga.970.1.S2_at	LOC395334
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Gga.9700.2.S1_a_at	TSPAN7
Gga.9701.1.S1_at	DPAGT1
Gga.9701.2.S1_a_at	DPAGT1
Gga.9705.1.S1_at	EIF1B
Gga.9708.1.S1_at	PPAP2A
Gga.9708.2.S1_a_at	PPAP2A
Gga.9710.1.S1_at	SH2D4A
Gga.9711.1.S1_at	LOC416827
Gga.9713.2.S1_a_at	HINTW

Gga.9721.1.S1_a_at	LOC770114
Gga.9721.2.S1_at	LOC770050
Gga.9723.2.S1_a_at	LOC422005
Gga.9723.3.S1_a_at	LOC422005
Gga.9731.2.S1_a_at	SPON2
Gga.9740.1.S1_at	PPCDC
Gga.9740.2.S1_s_at	PPCDC
Gga.9742.1.S1_s_at	SF3A1
Gga.9745.1.S1_at	LOC418817
Gga.9747.1.S1_a_at	IFT80
Gga.9750.1.S1_s_at	ITCH
Gga.9757.1.S1_at	RGS5
Gga.976.1.S1_at	CIRBP
Gga.9760.1.S1_at	C12orf5
Gga.9763.1.S1_s_at	CDA
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Gga.9766.1.S1_s_at	LEPRE1
Gga.9767.1.S1_at	MTMR14
Gga.9768.1.S1_at	PSCDBP
Gga.977.1.S1_at	PTRF
Gga.977.2.S1_at	PTRF
Gga.9770.2.S1_at	C5orf3
Gga.9770.3.S1_a_at	C5orf3
Gga.9773.1.S1_s_at	RBM24
Gga.9778.1.S1_at	IGHMBP2
Gga.9784.1.S1_at	POF1B
Gga.9784.2.A1_at	POF1B
Gga.979.1.S1_at	PEPCK-M
Gga.9791.1.S1_at	LOC427134
Gga.9796.1.S1_at	RUFY1
Gga.9797.1.S1_at	CBX7
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Gga.98.2.S1_a_at	TLR2
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Gga.9803.1.S1_at	IMPA1
Gga.9806.1.S1_at	A2LD1
Gga.9809.1.S1_at	BRD3
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Gga.9815.1.S1_at	PEX13
Gga.9816.1.S1_s_at	RCJMB04_10k5

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Gga.9826.1.S1_at	RPP30	
Gga.9827.1.S1_s_at	GOLIM4	
Gga.9829.1.S1_at	CA5B	
Gga.9837.2.S1_a_at	WDR21A	
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Gga.9862.1.S1_at	USP38	
Gga.9863.1.S1_at	LOC768982	
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Gga.9872.1.S1_at	HERPUD1	
Gga.9873.1.S1_at	C1QC	
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Gga.9882.1.S1_at	CSF2RA	
Gga.9887.1.S1_s_at	TACC3	
Gga.9889.1.S1_at	OXR1	
Gga.9892.1.S1_at	IRG1	
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Gga.9899.1.S1_at	SLC7A3	
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Gga.9906.1.S1_at	METRNL	
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Gga.9910.1.S1_at	C10orf118	
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Gga.9915.1.S1_s_at	PECAM1 /// PECAM1	
Gga.9915.2.S1_at	PECAM1	
Gga.9918.1.S1_at	NOB1	
Gga.9923.1.S1_at	LOC417353	
Gga.9926.1.S1_at	C17orf62	
Gga.9931.1.S1_at	LOC425332	
Gga.9935.1.S1_at	DMBT1	
Gga.9941.1.S1_s_at	THSD7A	

Gga.9949.1.S1_at	NSDHL
Gga.9959.1.S1_s_at	PAN3
Gga.9961.2.S1_s_at	ZNF652
Gga.9962.1.S1_at	RCJMB04_16e10
Gga.9963.1.S1_at	TBC1D13
Gga.9971.1.S1_at	ANXA10
Gga.9972.1.S1_at	RASD1
Gga.9976.1.S1_at	WDR51A
Gga.9980.2.S1_a_at	LOC771191
Gga.9986.1.S1_at	FSCN1
Gga.9987.1.S1_at	UQCRB
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Gga.9997.1.S1_at	KIAA1712
Gga.9999.1.S1_at	RASA3
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GgaAffx.10003.1.S1_s_at	ZFYVE28
GgaAffx.10004.1.S1_at	C4orf15
GgaAffx.10005.1.S1_at	POLN
GgaAffx.10011.1.S1_at	WHSC2
GgaAffx.10012.1.S1_at	CXADR
GgaAffx.10015.3.S1_s_at	LETM1
GgaAffx.10018.2.S1_s_at	SLBP
GgaAffx.10030.1.S1_at	MDN1
GgaAffx.10042.3.S1_s_at	ZNF704
GgaAffx.10052.2.S1_at	GABRR1
GgaAffx.10053.1.S1_at	ACY1L2
GgaAffx.10057.1.S1_at	ADAMTS1
GgaAffx.10059.1.S1_at	ADAMTS5
GgaAffx.10063.1.S1_at	C6orf165
GgaAffx.10065.1.S1_at	SLC7A13
GgaAffx.10066.1.S1_s_at	RCJMB04_30p22
GgaAffx.10076.1.S1_at	NT5E
GgaAffx.10088.2.A1_at	PRSS35
GgaAffx.10096.1.S1_at	C6orf157
GgaAffx.10104.2.S1_s_at	ATP6V0D2
GgaAffx.10105.1.S1_s_at	LOC771856
GgaAffx.10108.1.S1_at	TTK
GgaAffx.10110.1.S1_at	LCA5

GgaAffx.10124.2.S1_s_at	RIPK2
GgaAffx.10125.2.S1_at	LOC422922 /// LOC771804
GgaAffx.10125.3.S1_at	LOC422923 /// LOC422924 /// LOC
GgaAffx.10125.4.S1_at	LOC422922 /// LOC771804 /// LOC
GgaAffx.10125.4.S1_x_at	LOC422922 /// LOC771804 /// LOC
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GgaAffx.10163.1.S1_s_at	RIMS1
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GgaAffx.10187.2.S1_s_at	DPY19L4
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GgaAffx.10223.1.S1_s_at	SPAG1
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GgaAffx.10245.1.S1_at	BAALC
GgaAffx.10252.1.S1_s_at	RIMS2
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GgaAffx.10256.2.S1_at	ZFPM2
GgaAffx.10257.1.S1_at	OXR1
GgaAffx.10266.1.S1_at	EXOC6B
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GgaAffx.10287.1.S1_at	BACE2
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GgaAffx.10298.1.S1_at	C2CD2
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GgaAffx.1032.3.S1_s_at	INPP5D
GgaAffx.10324.1.S1_s_at	UBASH3A

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GgaAfx.10347.1.S1_at	LOC418544
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GgaAfx.10353.1.S1_at	CRYAA
GgaAfx.10358.2.S1_s_at	ZFAT1
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GgaAfx.10363.2.S1_s_at	MAOB
GgaAfx.10378.1.S1_at	PHF20L1
GgaAfx.10380.2.S1_at	KCNQ3
GgaAfx.10387.2.S1_at	OC90
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GgaAfx.10395.1.S1_at	LOC428640
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GgaAfx.10425.1.S1_at	HCRTR2
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GgaAfx.10438.1.S1_at	C6orf142
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GgaAfx.10451.1.S1_at	LOC772218
GgaAfx.10460.1.S1_at	KLHL15
GgaAfx.10460.2.S1_s_at	KLHL15
GgaAfx.10472.1.S1_at	FAM91A1
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GgaAfx.10482.1.S1_at	C8orf32
GgaAfx.10484.1.S1_at	ATAD2
GgaAfx.10492.1.S1_s_at	TSSC1
GgaAfx.10494.2.S1_s_at	TTC15
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GgaAfx.10499.1.S1_at	RNF144A
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GgaAfx.10509.2.S1_at	TAF2
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GgaAfx.10522.1.S1_at	LOC421935
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GgaAfx.10526.2.S1_s_at	ATP6V1C2

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GgaAffx.10538.1.S1_s_at	LOC421952
GgaAffx.10540.1.S1_at	KCNS3
GgaAffx.10553.2.S1_s_at	ATAD2B
GgaAffx.10555.1.S1_at	LOC421978
GgaAffx.10556.1.S1_s_at	RCJMB04_19g9
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GgaAffx.10650.3.S1_s_at	EXTL3
GgaAffx.10653.1.S1_s_at	INTS9
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GgaAffx.10684.1.S1_at	MUT
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GgaAffx.10704.2.S1_at	TMEM166

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GgaAffx.10727.3.S1_s_at	ATP10A
GgaAffx.10727.5.S1_s_at	ATP10A
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GgaAffx.10807.1.S1_at	EBI2
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GgaAffx.10840.1.S1_at	CLN5
GgaAffx.10842.3.S1_s_at	TBC1D4
GgaAffx.10846.1.S1_at	PCDH20
GgaAffx.10847.1.S1_at	DIAPH3
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GgaAffx.10853.2.S1_s_at	NARG1L
GgaAffx.10856.1.S1_at	LOC428066
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GgaAffx.10860.2.S1_s_at	DGKH
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GgaAffx.10869.1.S1_at	SLC25A30
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GgaAffx.10885.1.S1_at	SETDB2

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GgaAfx.10913.1.S1_at	STOML3
GgaAfx.10919.1.S1_at	CCNA1
GgaAfx.10923.1.S1_at	DCLK1
GgaAfx.10930.1.S1_at	STARD13
GgaAfx.10933.1.S1_s_at	FRY
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GgaAfx.10937.3.S1_s_at	HSPH1
GgaAfx.10939.1.S1_at	SLC7A1
GgaAfx.10945.1.S1_s_at	SLC46A3
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GgaAfx.10954.1.S1_at	USP12
GgaAfx.10968.4.S1_s_at	ATP8A2
GgaAfx.1097.1.S1_at	SETBP1
GgaAfx.10975.1.S1_at	MIPEP
GgaAfx.10975.2.S1_s_at	MIPEP
GgaAfx.1098.1.S1_s_at	PRKAB2
GgaAfx.10983.1.S1_at	RCJMB04_9b21
GgaAfx.10985.1.S1_at	CENPJ
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GgaAfx.10997.2.S1_s_at	EXPH5 /// KDELC2
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GgaAfx.11003.1.S1_at	RAB39
GgaAfx.11009.3.S1_s_at	GUCY1A2
GgaAfx.11012.1.S1_at	AASDHPPT
GgaAfx.11012.2.S1_s_at	AASDHPPT
GgaAfx.11017.1.S1_s_at	DYNC2H1
GgaAfx.11017.4.S1_s_at	DYNC2H1
GgaAfx.11018.1.S1_s_at	MMP1
GgaAfx.11032.1.S1_at	LOC418990
GgaAfx.11035.1.S1_s_at	FAM76B
GgaAfx.1104.1.S1_s_at	PPP2R4
GgaAfx.11051.1.S1_at	CCDC67
GgaAfx.11053.2.S1_s_at	SLC36A4

GgaAffx.11079.1.S1_at	ARHGEF19
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GgaAffx.11090.1.S1_at	LOC419050
GgaAffx.11092.1.S1_s_at	POLD3
GgaAffx.11103.1.S1_at	DNAJB13
GgaAffx.11124.1.S1_s_at	LOC769317 /// OR52R1
GgaAffx.11131.1.S1_at	REEP2
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GgaAffx.11133.1.S1_s_at	RCJMB04_4f12
GgaAffx.11145.1.S1_at	LOC429723
GgaAffx.11152.1.S1_at	CHCHD8
GgaAffx.11161.1.S1_at	LOC429831
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GgaAffx.11180.1.S1_at	C16orf35
GgaAffx.11181.1.S1_at	TDRKH
GgaAffx.1120.1.S1_at	DDEFL1
GgaAffx.11201.1.S1_s_at	TLR6
GgaAffx.11201.2.S1_s_at	LOC768669 /// TLR16 /// TLR6
GgaAffx.11201.3.S1_s_at	LOC768669 /// TLR16 /// TLR6
GgaAffx.11212.1.S1_s_at	LCORL
GgaAffx.11214.1.S1_at	LOC776768
GgaAffx.11214.1.S1_x_at	LOC776768
GgaAffx.11214.2.S1_at	LOC427569
GgaAffx.11221.1.S1_s_at	WDSOF1
GgaAffx.11239.1.S1_at	TSC1
GgaAffx.11240.1.S1_at	LOC772235
GgaAffx.11249.1.S1_at	CCDC83
GgaAffx.11257.1.S1_at	THUMPD2
GgaAffx.11258.2.S1_s_at	ATRN
GgaAffx.11258.4.S1_s_at	ATRN
GgaAffx.11259.2.S1_at	LOC776280
GgaAffx.11259.3.S1_s_at	CD5L /// LOC425218 /// LOC4258
GgaAffx.11274.1.S1_at	FBN2
GgaAffx.11281.1.S1_at	LOC425564
GgaAffx.11284.1.S1_at	QPCTL
GgaAffx.11288.1.S1_s_at	PEO1
GgaAffx.11292.2.S1_s_at	LOC425334 /// RHBDF1
GgaAffx.11293.1.S1_s_at	WWC3
GgaAffx.11302.1.S1_at	LOC417738 /// LOC776729

GgaAffx.11302.2.S1_at	LOC417738 /// LOC776729
GgaAffx.11320.2.S1_at	FBXO38 /// LOC426479 /// LOC42
GgaAffx.11324.1.S1_at	CDC42SE2
GgaAffx.11325.1.S1_at	LOC425984
GgaAffx.11327.1.S1_at	KCNS2
GgaAffx.11331.1.S1_at	KIAA1324L
GgaAffx.11335.1.S1_at	CYLD
GgaAffx.11352.1.S1_at	KIAA0802
GgaAffx.11357.1.S1_at	LOC430965
GgaAffx.11358.1.S1_s_at	ZC3HAV1
GgaAffx.11359.7.S1_at	SGSM1
GgaAffx.11364.2.S1_s_at	MTBP
GgaAffx.11368.1.S1_at	PRIM1
GgaAffx.11375.1.S1_at	RCJMB04_1a13
GgaAffx.11396.1.S1_s_at	C20orf59
GgaAffx.114.1.S1_s_at	SLC27A6
GgaAffx.11402.1.S1_at	NEK2
GgaAffx.11404.1.S1_at	MXI1
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GgaAffx.11416.1.S1_s_at	TAF8
GgaAffx.11417.1.S1_at	KIF11
GgaAffx.11418.1.S1_at	XPO4
GgaAffx.11423.1.S1_at	RCJMB04_1g4
GgaAffx.11425.1.S1_at	UMPS
GgaAffx.11426.1.S1_at	TNFRSF18
GgaAffx.11429.1.S1_s_at	MMP7
GgaAffx.11430.1.S1_s_at	SH3KBP1
GgaAffx.11431.1.S1_at	SNX13
GgaAffx.11433.1.S1_s_at	RCJMB04_1g23
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GgaAffx.11440.1.S1_s_at	RCJMB04_1h22
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GgaAffx.11459.1.S1_s_at	RCJMB04_1j12
GgaAffx.11462.1.S1_at	ZNF706
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GgaAffx.11470.1.S1_s_at	LAPTM4A
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GgaAffx.11480.1.S1_s_at	UFM1
GgaAffx.11481.1.S1_s_at	USP6NL
GgaAffx.11486.1.S1_at	C9orf41
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GgaAffx.11491.1.S1_s_at	SLC25A4
GgaAffx.11494.1.S1_s_at	C20orf24
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GgaAffx.11513.1.S1_at	CCNE2
GgaAffx.11513.1.S1_s_at	CCNE2
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GgaAffx.11578.1.S1_s_at	KPNA2
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GgaAffx.11584.1.S1_s_at	RBM24
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GgaAffx.11649.1.S1_at	RCJMB04_3e14
GgaAffx.11650.1.S1_s_at	PCID2
GgaAffx.11660.1.S1_s_at	ZNF384
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GgaAffx.11665.1.S1_at	ITGA9
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GgaAffx.11702.1.S1_s_at	PLEKHF2
GgaAffx.11707.1.S1_s_at	RNUXA
GgaAffx.11713.1.S1_s_at	ARHGEF3
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GgaAffx.11747.1.S1_at	SLBP
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GgaAffx.11782.1.S1_s_at	CEP55
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GgaAffx.11790.1.S1_at	GUF1
GgaAffx.11792.1.S1_at	RCJMB04_3i4
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GgaAffx.11825.1.S1_s_at	CORO7 /// MAGMAS
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GgaAffx.11839.1.S1_s_at	TMEM59
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GgaAffx.11986.1.S1_s_at	VPS35
GgaAffx.11989.1.S1_at	STAU2
GgaAffx.11992.1.S1_at	RCJMB04_7n24
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GgaAffx.12029.1.S1_at	TNFRSF1B
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GgaAffx.12077.1.S1_at	RCJMB04_8p20
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GgaAffx.12087.1.S1_s_at	CENPL
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GgaAffx.12115.1.S1_at	RCJMB04_9g24
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GgaAffx.12525.1.S1_s_at	ORC2L
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GgaAffx.12549.1.S1_at	CCDC13
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GgaAffx.12568.1.S1_at	CCDC5
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GgaAffx.12577.1.S1_at	AGA
GgaAffx.12579.1.S1_at	DUSP10
GgaAffx.12587.1.S1_s_at	CKAP2
GgaAffx.12588.1.S1_at	RCJMB04_18m15
GgaAffx.12592.1.S1_at	SERTAD2
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GgaAffx.12601.1.S1_s_at	RCJMB04_113
GgaAffx.12605.1.S1_at	RANGAP1
GgaAffx.12619.1.S1_at	ADRBK1
GgaAffx.12628.1.S1_at	LOH12CR1
GgaAffx.12634.1.S1_at	CDR2
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GgaAffx.12647.1.S1_at	RCJMB04_19p13

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GgaAfx.12658.1.S1_at	NCF4
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GgaAfx.12670.1.S1_s_at	NUDT14
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GgaAfx.12672.1.S1_at	RCJMB04_20f16
GgaAfx.12678.1.S1_s_at	SFRS6
GgaAfx.12680.1.S1_at	NDUFS1
GgaAfx.12686.1.S1_at	RCJMB04_20k13
GgaAfx.12691.1.S1_at	GABPA
GgaAfx.12693.1.S1_at	RIOK2
GgaAfx.12697.1.S1_s_at	RCOR3
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GgaAfx.12736.1.S1_at	RCJMB04_22d6
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GgaAffx.13241.1.S1_at	SLC16A1
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GgaAfx.20499.1.S1_s_at	C12orf10
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GgaAfx.22290.3.S1_at	LRCH3
GgaAfx.22293.1.S1_s_at	MGRN1
GgaAfx.22296.1.S1_s_at	AOF2
GgaAfx.223.2.S1_s_at	RCJMB04_17j13
GgaAfx.22303.1.S1_at	DOT1L
GgaAfx.22308.1.S1_s_at	BTBD12
GgaAfx.22312.2.S1_s_at	MYO3A
GgaAfx.22313.1.S1_s_at	RCJMB04_17i9
GgaAfx.22314.1.S1_at	RAE1
GgaAfx.22329.1.S1_at	BCL9L
GgaAfx.22331.1.S1_at	ARMC9
GgaAfx.22337.2.S1_s_at	MYO1B
GgaAfx.22337.3.S1_s_at	MYO1B
GgaAfx.22338.1.S1_at	FBXW4
GgaAfx.22343.1.S1_s_at	ARHGAP21
GgaAfx.22351.1.S1_at	KIAA2022
GgaAfx.22356.4.S1_s_at	KIAA1217
GgaAfx.22356.5.S1_s_at	LOC420501
GgaAfx.22360.1.S1_at	DOK5
GgaAfx.22364.1.S1_at	LOC415641 /// LOC423151
GgaAfx.22370.3.S1_at	C17orf28
GgaAfx.22376.1.S1_at	KIAA1841
GgaAfx.22377.1.S1_at	LOC770784
GgaAfx.22383.1.S1_at	LOC771302
GgaAfx.22384.1.S1_s_at	ATRX
GgaAfx.22392.1.S1_at	C11orf57
GgaAfx.22396.2.S1_at	SPAG6
GgaAfx.22396.2.S1_s_at	SPAG6
GgaAfx.22413.1.S1_at	MLLT10
GgaAfx.22417.1.S1_at	RCJMB04_36h7
GgaAfx.22418.1.S1_at	PHLPPL
GgaAfx.22425.1.S1_s_at	SLC16A5
GgaAfx.2243.1.S1_s_at	ATP2B4
GgaAfx.22440.1.S1_at	TMEM209
GgaAfx.22440.3.S1_s_at	TMEM209
GgaAfx.22444.1.S1_at	TSEN54
GgaAfx.22445.1.S1_s_at	MTMR3
GgaAfx.22446.1.S1_at	HBP1
GgaAfx.22450.1.S1_at	PRDM11

GgaAfx.2246.2.S1_s_at	LOC770890
GgaAfx.22460.1.S1_at	MEST
GgaAfx.2247.1.A1_at	LOC428815
GgaAfx.22476.1.S1_at	C2orf60
GgaAfx.2248.1.S1_at	LOC428816
GgaAfx.22486.1.S1_s_at	SRPK2
GgaAfx.22486.2.S1_at	SRPK2
GgaAfx.22491.2.S1_s_at	SPTBN1
GgaAfx.22513.1.S1_at	ANKRD34A
GgaAfx.22516.2.S1_s_at	LOC424944
GgaAfx.22524.1.S1_at	CCDC146
GgaAfx.2253.2.S1_s_at	ADC
GgaAfx.22530.1.S1_at	RNPEPL1
GgaAfx.22530.1.S1_s_at	RNPEPL1
GgaAfx.22534.1.S1_s_at	CKAP5
GgaAfx.22534.3.S1_s_at	CKAP5
GgaAfx.22537.1.S1_at	SLC24A6
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GgaAfx.22547.3.S1_at	GZF1 /// ZNF605
GgaAfx.22547.6.S1_s_at	GZF1
GgaAfx.22553.1.S1_at	ALS2CR2
GgaAfx.22558.1.S1_at	C20orf19
GgaAfx.22560.1.S1_s_at	ANKRD12
GgaAfx.22565.2.S1_s_at	ALS2
GgaAfx.22572.1.S1_s_at	ZBTB34
GgaAfx.22578.1.S1_at	GNAT3
GgaAfx.22590.2.S1_at	SLC35B4
GgaAfx.22590.3.S1_s_at	SLC35B4
GgaAfx.22607.1.S1_s_at	HNRPLL
GgaAfx.2261.5.S1_s_at	DARS2
GgaAfx.22611.1.S1_at	DLL4
GgaAfx.22614.1.A1_at	FAM125B
GgaAfx.22615.2.S1_s_at	NR2C2
GgaAfx.22617.1.S1_at	BRD1
GgaAfx.22617.1.S1_s_at	BRD1
GgaAfx.22619.1.S1_at	ALG12 /// RCJMB04_1n22
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GgaAfx.22623.1.S1_at	ZBED4
GgaAfx.22627.1.S1_at	INOC1

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GgaAffx.22643.1.S1_at	FAM125B
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GgaAffx.22647.2.S1_s_at	MAPK11
GgaAffx.22650.2.S1_s_at	LTK
GgaAffx.22651.1.S1_at	RCJMB04_4p22
GgaAffx.22659.1.S1_at	MGA
GgaAffx.22660.1.S1_at	ATF2
GgaAffx.22661.1.S1_at	RAPH1
GgaAffx.22664.1.S1_s_at	SLC25A43
GgaAffx.22672.1.S1_at	CUBN
GgaAffx.22675.1.S1_at	C20orf23
GgaAffx.22675.2.S1_at	C20orf23
GgaAffx.22680.1.S1_at	WDR85
GgaAffx.22681.1.S1_at	SSX2IP
GgaAffx.22683.1.S1_at	SSX2IP
GgaAffx.22684.1.S1_at	C10orf38
GgaAffx.22686.1.S1_at	SPATA1
GgaAffx.22689.1.S1_s_at	LRSAM1
GgaAffx.22694.1.S1_s_at	AFTPH
GgaAffx.22694.3.S1_at	AFTPH
GgaAffx.22699.1.S1_at	ATP11B
GgaAffx.22699.3.S1_s_at	ATP11B
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GgaAffx.22704.1.S1_at	WDR31
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GgaAffx.22718.1.S1_s_at	ELTD1
GgaAffx.22721.1.S1_at	RNF208
GgaAffx.22723.1.S1_at	EHBP1
GgaAffx.22732.1.S1_s_at	FBXO11
GgaAffx.22738.1.S1_s_at	PAK7
GgaAffx.22748.1.S1_at	MAP4K4
GgaAffx.22749.2.S1_s_at	EFTUD2
GgaAffx.2275.1.S1_at	TMEM16C
GgaAffx.22758.1.S1_s_at	CXorf57
GgaAffx.22766.1.S1_at	MKKS
GgaAffx.22773.2.S1_at	TMEM87A
GgaAffx.22776.2.S1_s_at	LCN15

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GgaAfx.22779.2.S1_s_at	LOC420542
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GgaAfx.22795.1.S1_s_at	TTN
GgaAfx.22799.1.S1_at	MTM1
GgaAfx.2280.1.S1_at	FOXN1
GgaAfx.22805.1.S1_at	ANKRD26
GgaAfx.22805.3.S1_s_at	ANKRD26
GgaAfx.22807.1.S1_s_at	CEP27
GgaAfx.22808.1.S1_at	DGAT2
GgaAfx.2281.1.S1_at	UNC119
GgaAfx.22817.1.S1_s_at	ATRNL1
GgaAfx.22819.1.S1_at	ECT2
GgaAfx.22822.1.S1_s_at	CDC42BPA
GgaAfx.22831.1.S1_at	CCNF
GgaAfx.22835.1.S1_at	LOC770184
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GgaAfx.22849.1.S1_at	UBR1
GgaAfx.22849.2.S1_s_at	UBR1
GgaAfx.22854.1.S1_s_at	PLD1
GgaAfx.22861.1.S1_s_at	BZRAP1
GgaAfx.22861.2.S1_s_at	BZRAP1
GgaAfx.2287.1.S1_at	FANCF
GgaAfx.22872.2.S1_s_at	TNIK
GgaAfx.22873.1.S1_at	CNIH3
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GgaAfx.22889.1.S1_s_at	EIF3A
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GgaAfx.22895.1.S1_at	EPB41L1
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GgaAfx.22909.1.S1_at	ANKIB1
GgaAfx.22913.1.S1_at	LRRC34
GgaAfx.22916.2.S1_s_at	DISP1
GgaAfx.22926.1.S1_at	EVI1
GgaAfx.22932.2.S1_s_at	GOLIM4
GgaAfx.22938.1.S1_s_at	RAPGEF2
GgaAfx.22938.4.S1_s_at	FNIP2
GgaAfx.22943.1.S1_at	NPY5R
GgaAfx.22945.2.S1_s_at	RAB3GAP2

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GgaAffx.22954.3.S1_s_at	TACC2
GgaAffx.22955.1.S1_at	LOC416375 /// LOC425481
GgaAffx.22965.1.S1_s_at	TLK1
GgaAffx.22965.2.S1_at	TLK1
GgaAffx.2297.2.S1_s_at	UBLCP1
GgaAffx.22971.1.S1_s_at	MPP5
GgaAffx.22987.1.S1_at	THBS1
GgaAffx.22996.1.S1_at	LOC422427
GgaAffx.22997.1.S1_at	CHRM5
GgaAffx.22999.1.S1_s_at	COL1A2
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GgaAffx.23004.1.S1_at	RSRC1
GgaAffx.23028.1.S1_s_at	SPRED1
GgaAffx.23033.1.S1_at	HCLS1
GgaAffx.23034.1.S1_at	LOC770879
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GgaAffx.23045.2.S1_s_at	ZNF770
GgaAffx.23064.2.S1_s_at	INPP4B
GgaAffx.23068.1.S1_s_at	TRERF1
GgaAffx.23072.2.S1_s_at	EML4
GgaAffx.23076.1.S1_s_at	STRN3
GgaAffx.23081.2.S1_s_at	PLEKHH2
GgaAffx.23084.1.S1_s_at	TIE1
GgaAffx.23085.1.S1_s_at	RAB3IP
GgaAffx.23089.1.S1_at	ELOVL1
GgaAffx.23093.1.S1_s_at	BAZ1A
GgaAffx.231.1.S1_at	GAS7
GgaAffx.2310.1.S1_at	INSR
GgaAffx.23114.3.S1_s_at	DAAM2
GgaAffx.23122.1.S1_s_at	JMJD2A
GgaAffx.23140.1.S1_at	KIAA0082
GgaAffx.23142.1.S1_at	CYP21
GgaAffx.23149.2.S1_s_at	LGR5
GgaAffx.23153.1.S1_s_at	CCDC131
GgaAffx.23155.1.S1_at	RAB21
GgaAffx.23159.1.S1_at	FBXO33
GgaAffx.2316.1.S1_at	VPS13C
GgaAffx.23160.1.S1_at	C14orf44

GgaAfx.23163.3.S1_s_at	MFSD8
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GgaAfx.23174.3.S1_at	LOC423347
GgaAfx.23174.3.S1_s_at	LOC423347
GgaAfx.23180.1.S1_at	KRT79
GgaAfx.23183.1.S1_s_at	LTBP3
GgaAfx.23187.1.S1_s_at	YLPM1
GgaAfx.23188.1.A1_s_at	NPM3
GgaAfx.2319.1.S1_s_at	HELZ
GgaAfx.23190.1.S1_s_at	RPS6KL1
GgaAfx.23192.1.S1_s_at	SLC33A1
GgaAfx.23227.1.S1_at	LOC425588
GgaAfx.23229.1.S1_s_at	CP
GgaAfx.23230.1.S1_s_at	HPS3
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GgaAfx.23235.1.S1_at	EBF3
GgaAfx.23236.1.S1_at	AHSA1
GgaAfx.23240.1.S1_at	STIL
GgaAfx.23241.1.S1_at	SLC5A9
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GgaAfx.23243.1.S1_at	FCR/L
GgaAfx.23246.2.S1_s_at	AGXT2L1
GgaAfx.23247.1.S1_s_at	HES5
GgaAfx.23250.1.S1_s_at	PAPSS1
GgaAfx.23253.1.S1_at	FAM82A
GgaAfx.23253.1.S1_s_at	FAM82A
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GgaAfx.23256.1.S1_at	FLRT2
GgaAfx.23258.1.S1_at	FEZ2
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GgaAfx.23262.1.A1_at	GPR65
GgaAfx.23262.1.S1_at	GPR65
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GgaAfx.23270.3.S1_at	CC2D1B
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GgaAfx.23276.1.S1_at	ZCCHC11
GgaAfx.23280.1.S1_at	CCDC111
GgaAfx.23286.1.S1_at	TFB2M
GgaAfx.23288.1.S1_at	SCP2
GgaAfx.23290.2.S1_at	EML5

GgaAfx.23294.1.S1_s_at	WWC2
GgaAfx.23300.1.S1_at	MIOS
GgaAfx.23308.1.S1_s_at	CCDC88C
GgaAfx.23315.1.S1_s_at	GALNT7
GgaAfx.23316.1.S1_at	LOC772308
GgaAfx.23316.1.S1_x_at	LOC772308
GgaAfx.23319.1.S1_s_at	FMN2
GgaAfx.23329.1.S1_at	GOLGA5
GgaAfx.2333.1.S1_at	FANCD2
GgaAfx.23330.1.S1_at	PPAP2B
GgaAfx.23333.1.S1_at	SPATA4
GgaAfx.23341.5.S1_s_at	RCJMB04_31a4
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GgaAfx.23359.2.S1_at	RDH5
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GgaAfx.23386.2.S1_at	INADL
GgaAfx.23386.3.S1_s_at	INADL
GgaAfx.23390.1.S1_s_at	ANKRD38
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GgaAfx.23401.4.S1_s_at	DOCK7
GgaAfx.23405.1.S1_at	SERPINA4
GgaAfx.23422.1.S1_at	LOC425645 /// LOC777099 /// PW
GgaAfx.23422.2.S1_s_at	LOC425645 /// LOC777099
GgaAfx.23427.1.S1_at	SIPA1L2
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GgaAfx.23440.5.A1_at	HOXA10
GgaAfx.23445.1.S1_s_at	PTPN13
GgaAfx.23449.1.S1_at	IFIH1
GgaAfx.23460.3.S1_s_at	ARHGAP24
GgaAfx.23461.1.S1_s_at	LIN54
GgaAfx.2347.1.S1_at	LOC427447
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GgaAffx.23485.2.S1_s_at	C6orf70	
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GgaAffx.23494.2.S1_at	PLCH2	
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GgaAffx.23540.1.S1_at	PRKAG3 /// TTLL4	
GgaAffx.23541.1.S1_at	C14orf131	
GgaAffx.23543.1.S1_at	RABGGTB	
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GgaAffx.23558.1.S1_at	C17orf38	
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GgaAffx.23632.1.S1_at	PDIA5	
GgaAffx.23636.1.S1_at	AGBL3	
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GgaAfx.2370.1.S1_at	FYB
GgaAfx.2370.1.S1_s_at	FYB
GgaAfx.23700.2.S1_s_at	KIF15
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GgaAfx.23716.1.S1_at	FBXL2
GgaAfx.2372.1.S1_s_at	RCJMB04_14f2
GgaAfx.23721.2.S1_s_at	PDE5A
GgaAfx.23729.1.S1_at	SEC24D
GgaAfx.23729.2.S1_s_at	SEC24D
GgaAfx.2373.1.S1_s_at	FYB
GgaAfx.23731.1.S1_at	PRSS12
GgaAfx.23736.1.S1_s_at	SLC25A17
GgaAfx.23737.1.S1_at	LOC430152
GgaAfx.23739.1.S1_at	ARSJ
GgaAfx.23763.1.S1_at	SLC12A8
GgaAfx.23767.1.S1_at	LBA1
GgaAfx.2377.1.S1_at	IL28B
GgaAfx.23776.1.S1_at	FAIM
GgaAfx.23778.1.S1_s_at	NAT12
GgaAfx.23779.1.S1_at	C14orf108
GgaAfx.23783.1.S1_at	ANLN
GgaAfx.23792.1.S1_at	RCN1
GgaAfx.23793.1.S1_s_at	C1orf130
GgaAfx.23800.1.S1_at	SLC35F5
GgaAfx.23801.1.S1_s_at	LOC769503 /// LOC770605 /// LOC
GgaAfx.23809.1.S1_at	BBS9
GgaAfx.23813.1.S1_s_at	SAMD4A
GgaAfx.23815.1.S1_at	KIAA0241
GgaAfx.23815.2.S1_s_at	KIAA0241
GgaAfx.23816.1.S1_at	CGRRF1
GgaAfx.23819.3.S1_s_at	CCNT2
GgaAfx.23830.1.S1_at	KLHDC1
GgaAfx.23837.4.S1_s_at	R3HDM1
GgaAfx.23838.1.S1_s_at	DDX17
GgaAfx.23840.1.S1_s_at	ADH1C
GgaAfx.23844.1.S1_s_at	UTRN

GgaAffx.23852.1.S1_at	MTTP
GgaAffx.23859.1.S1_s_at	PLA2G6
GgaAffx.23860.1.S1_at	LOC776580
GgaAffx.23862.1.S1_at	POU6F2
GgaAffx.23866.1.S1_at	C7orf11
GgaAffx.23867.1.S1_at	NHEDC2
GgaAffx.23870.1.S1_at	SAV1
GgaAffx.23874.1.S1_s_at	MAP3K7IP2
GgaAffx.23874.2.S1_at	MAP3K7IP2
GgaAffx.23878.1.S1_at	NIN
GgaAffx.23880.1.S1_at	C6orf72
GgaAffx.23882.1.S1_at	SPOPL
GgaAffx.23883.1.S1_at	PPP1R14C
GgaAffx.23887.1.S1_at	TXNDC16
GgaAffx.23903.1.S1_s_at	GGA1
GgaAffx.23909.4.S1_at	ADCY1 /// LOC420787
GgaAffx.23912.2.S1_s_at	ZEB2
GgaAffx.23916.1.S1_at	HUS1
GgaAffx.23924.2.S1_s_at	KIF5C
GgaAffx.23925.1.S1_at	LOC420793
GgaAffx.23927.4.S1_s_at	RBL1
GgaAffx.23929.1.S1_at	NFX1
GgaAffx.23934.2.S1_at	SLC12A7
GgaAffx.23934.3.S1_at	SLC12A7
GgaAffx.23936.1.S1_at	RCJMB04_10a6
GgaAffx.23937.1.S1_s_at	MYH9
GgaAffx.23939.1.S1_s_at	GPD2
GgaAffx.23940.1.S1_at	UPP2
GgaAffx.23944.1.S1_at	TANC1
GgaAffx.23946.1.S1_s_at	ZCCHC6
GgaAffx.23947.1.S1_at	PRDM4
GgaAffx.23950.1.S1_at	CDC14C
GgaAffx.23970.1.S1_s_at	NUAK1
GgaAffx.23972.1.S1_at	GPLD1
GgaAffx.23973.1.S1_at	KIAA1033
GgaAffx.23974.1.S1_at	CDKAL1
GgaAffx.23974.1.S1_s_at	CDKAL1
GgaAffx.23976.1.S1_at	RCJMB04_11d23
GgaAffx.23986.1.S1_at	GFOD1
GgaAffx.23993.1.S1_at	GNPTAB

GgaAfx.23993.3.S1_s_at	GNPTAB
GgaAfx.23994.1.S1_at	LIAS
GgaAfx.240.5.S1_s_at	RCJMB04_7e17
GgaAfx.24000.1.S1_at	DSP
GgaAfx.24000.1.S1_s_at	DSP
GgaAfx.24000.2.S1_s_at	DSP
GgaAfx.24003.1.S1_x_at	LYRM4
GgaAfx.24004.1.S1_at	CDYL
GgaAfx.24005.1.S1_at	PRPF4B
GgaAfx.24006.1.A1_at	C6orf86
GgaAfx.24015.3.S1_s_at	SLC37A3
GgaAfx.24019.2.S1_at	DENND2A
GgaAfx.24028.1.S1_s_at	CREB3L2
GgaAfx.24033.1.S1_at	DGKI
GgaAfx.24033.1.S1_s_at	DGKI
GgaAfx.24039.1.S1_s_at	TTLL11
GgaAfx.24044.3.S1_s_at	YARS2
GgaAfx.24049.1.S1_at	DNM1L
GgaAfx.24053.1.S1_s_at	RCJMB04_9b7
GgaAfx.24061.1.S1_at	MYO10
GgaAfx.24061.2.S1_s_at	MYO10
GgaAfx.24065.1.S1_at	TTLL11
GgaAfx.24065.1.S1_s_at	TTLL11
GgaAfx.24070.1.S1_at	C6orf97
GgaAfx.24072.1.S1_at	C6orf98
GgaAfx.24073.1.S1_at	CDYL2
GgaAfx.24078.1.S1_s_at	TRIO
GgaAfx.24078.5.S1_s_at	TRIO
GgaAfx.2408.1.S1_at	MID2
GgaAfx.24089.1.S1_s_at	ERC1
GgaAfx.24090.1.S1_at	FBXL14
GgaAfx.24095.2.S1_at	LOC430333
GgaAfx.24097.1.S1_s_at	MICAL3
GgaAfx.24100.1.S1_s_at	SEMA5A
GgaAfx.24101.1.S1_at	MTRR
GgaAfx.24104.1.S1_at	MGST1
GgaAfx.24111.1.S1_s_at	LOC768469 /// LOC770493 /// LOC
GgaAfx.24116.1.S1_at	ADAMTS15
GgaAfx.24122.1.S1_s_at	C9orf4
GgaAfx.24123.1.S1_at	PDE3A

GgaAfx.24128.1.S1_at	LOC430333 /// LOC772321 /// LOC
GgaAfx.24135.1.S1_s_at	SEMA7A
GgaAfx.24149.1.S1_at	KIAA0528
GgaAfx.24149.3.S1_s_at	KIAA0528
GgaAfx.24149.4.S1_s_at	KIAA0528
GgaAfx.2416.1.S1_at	HELZ
GgaAfx.24163.1.S1_at	PRMT8
GgaAfx.24163.2.S1_s_at	PRMT8
GgaAfx.24166.1.S1_s_at	KIAA1219
GgaAfx.24166.3.S1_s_at	KIAA1219
GgaAfx.24166.4.S1_s_at	KIAA1219
GgaAfx.24185.1.S1_at	IL7R
GgaAfx.24191.1.S1_s_at	PWWP2A
GgaAfx.24200.1.S1_at	LOC426100
GgaAfx.24202.1.S1_at	RANBP10
GgaAfx.2421.1.S1_s_at	TIMD4
GgaAfx.24216.1.S1_at	LOC415891
GgaAfx.24232.3.S1_s_at	LRRC16A
GgaAfx.24236.1.S1_at	RBM16
GgaAfx.24240.1.S1_s_at	TFB1M
GgaAfx.24242.1.S1_at	ZNF236
GgaAfx.24242.2.S1_s_at	ZNF236
GgaAfx.24245.1.S1_at	TSHZ1
GgaAfx.2425.1.S1_at	CCR7
GgaAfx.24252.1.S1_at	C10orf137
GgaAfx.24252.1.S1_s_at	C10orf137
GgaAfx.24253.1.S1_at	KPNB1
GgaAfx.24269.1.S1_at	AASDH
GgaAfx.24271.1.S1_at	LOC422745
GgaAfx.24272.1.S1_at	FUCA2
GgaAfx.24275.2.S1_s_at	CEP135
GgaAfx.24277.1.S1_s_at	EXOC1
GgaAfx.24279.1.S1_at	LSMD1
GgaAfx.24281.1.S1_s_at	HIVEP2
GgaAfx.24282.1.S1_at	SRD5A3 /// TMEM165
GgaAfx.24283.1.S1_at	UBAP2
GgaAfx.24287.1.S1_s_at	PML
GgaAfx.24289.1.S1_at	SYNJ2BP
GgaAfx.24290.1.S1_at	DUSP16
GgaAfx.24294.1.S1_at	AFG3L2 /// LOC425565

GgaAfx.243.1.S1_s_at	DHDDS
GgaAfx.24300.1.S1_s_at	PCYOX1
GgaAfx.24301.1.S1_s_at	CEP192
GgaAfx.24305.1.S1_at	MAP3K5
GgaAfx.24329.1.A1_at	FBXO40
GgaAfx.24331.1.S1_s_at	HNRPA3P2
GgaAfx.24337.1.S1_at	C1orf77
GgaAfx.24339.1.S1_x_at	CHIR2D-956 /// LOC425235 /// LC
GgaAfx.24344.1.S1_s_at	NISCH
GgaAfx.24355.1.S1_at	NRBP2
GgaAfx.2436.4.S1_at	SLC6A5
GgaAfx.2436.4.S1_s_at	SLC6A5
GgaAfx.24375.2.S1_at	PLA2G5
GgaAfx.24377.2.S1_s_at	PARVB
GgaAfx.24380.1.S1_at	ARHGAP8
GgaAfx.24381.1.S1_at	TBC1D1
GgaAfx.24388.1.S1_at	MFAP5
GgaAfx.24389.1.S1_at	LOC772329
GgaAfx.2440.4.S1_s_at	PIGT
GgaAfx.24406.1.S1_at	LOC422804
GgaAfx.24424.1.S1_at	CDC37L1
GgaAfx.24426.1.S1_at	STAB1
GgaAfx.24428.1.S1_at	RCJMB04_1p22
GgaAfx.24429.1.A1_at	LOC426599
GgaAfx.24433.1.S1_at	VPS16
GgaAfx.24435.1.S1_at	CDCA3
GgaAfx.24435.1.S1_s_at	CDCA3
GgaAfx.24437.2.S1_s_at	CC2D2A
GgaAfx.24452.1.S1_s_at	ATN1
GgaAfx.24457.1.S1_s_at	PNPLA2
GgaAfx.24459.2.S1_s_at	MBOAT5
GgaAfx.24462.1.S1_at	ZZEF1
GgaAfx.24471.1.S1_at	LMOD3 /// LOC426075
GgaAfx.24484.2.S1_s_at	C1R
GgaAfx.24485.1.S1_s_at	RCJMB04_11e18
GgaAfx.24486.1.S1_at	FBN2
GgaAfx.24487.1.S1_at	PRRC1
GgaAfx.24491.1.S1_at	MIER3
GgaAfx.24492.1.S1_at	GABARAPL3
GgaAfx.24497.1.S1_at	TRPV6

GgaAfx.24513.8.S1_at	EPB41L3
GgaAfx.24516.1.S1_s_at	ERBB2IP
GgaAfx.24516.2.S1_s_at	ERBB2IP
GgaAfx.2452.1.S1_s_at	APBA2
GgaAfx.24520.2.S1_s_at	SFRS12
GgaAfx.24534.1.S1_at	C7
GgaAfx.24538.1.S1_at	C6orf60
GgaAfx.24540.1.S1_s_at	DCBLD1
GgaAfx.24545.1.S1_at	ENC1
GgaAfx.24548.1.S1_at	ESCO1
GgaAfx.24549.1.S1_at	ANKRD31
GgaAfx.24553.1.S1_at	DSE
GgaAfx.24555.1.S1_s_at	COL10A1
GgaAfx.2456.1.S1_at	LONP2
GgaAfx.24566.1.S1_at	LAMA4
GgaAfx.24574.1.S1_at	CD274
GgaAfx.24577.1.S1_s_at	REV3L
GgaAfx.24579.2.S1_s_at	ANKRD29
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GgaAfx.24583.1.S1_at	LOC418339
GgaAfx.24584.1.S1_at	LOC427229
GgaAfx.24591.1.S1_at	LOC418339
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GgaAfx.24611.2.S1_s_at	LOC428525
GgaAfx.24613.1.S1_at	ZNF521
GgaAfx.24617.1.S1_at	LOC418360
GgaAfx.24618.1.S1_s_at	ZFAND5
GgaAfx.2462.1.S1_at	LOC422137
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GgaAfx.24633.1.S1_at	TTF2
GgaAfx.24638.1.S1_at	HISPPD1
GgaAfx.24638.1.S1_s_at	HISPPD1
GgaAfx.24639.1.S1_at	FILIP1L
GgaAfx.24643.1.S1_at	SESN1
GgaAfx.24644.1.S1_at	FOXO3
GgaAfx.24648.1.S1_at	RNF38
GgaAfx.24654.1.S1_at	PCGF3
GgaAfx.24656.1.S1_s_at	ATG16L1
GgaAfx.24673.1.S1_at	ARL13B
GgaAfx.24674.1.A1_at	STX19

GgaAfx.24674.1.S1_at	STX19
GgaAfx.24676.1.S1_at	EPHA6
GgaAfx.24681.1.S1_at	NSMAF
GgaAfx.24683.1.S1_s_at	ILDR2
GgaAfx.24689.1.S1_at	CHD7
GgaAfx.2469.1.S1_at	C5orf4
GgaAfx.24692.2.S1_s_at	PDZK1
GgaAfx.24694.1.S1_s_at	GBE1
GgaAfx.247.1.S1_at	ENTPD4
GgaAfx.247.2.S1_s_at	ENTPD4
GgaAfx.24703.2.S1_at	JAKMIP1
GgaAfx.24709.1.S1_s_at	LOC771304
GgaAfx.24711.1.S1_at	SH3TC1
GgaAfx.24718.5.S1_at	SLCO5A1
GgaAfx.24720.1.S1_at	LOC768383
GgaAfx.24722.1.S1_at	MAP3K7
GgaAfx.24729.2.S1_s_at	NCOA2
GgaAfx.24733.1.S1_at	XRCC4
GgaAfx.24733.1.S1_s_at	XRCC4
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GgaAfx.24735.1.S1_at	LOC420181
GgaAfx.2474.1.S1_s_at	BCORL1
GgaAfx.2474.3.S1_s_at	BCORL1
GgaAfx.24752.1.S1_at	KIAA0368
GgaAfx.24753.1.S1_s_at	WHSC1
GgaAfx.24769.1.S1_s_at	ANKRD6
GgaAfx.24771.1.S1_at	RRAGD
GgaAfx.24772.1.S1_at	C17orf59
GgaAfx.24775.1.S1_at	SNX16
GgaAfx.24784.1.S1_at	TIAM1
GgaAfx.24796.1.S1_at	WWP1
GgaAfx.24804.1.S1_at	FILIP1
GgaAfx.24805.1.S1_at	SLC7A7
GgaAfx.24812.1.S1_s_at	C21orf66
GgaAfx.24815.2.S1_at	ASRGL1
GgaAfx.24816.1.S1_at	OGFRL1
GgaAfx.24817.1.S1_s_at	KIAA1429
GgaAfx.24819.1.S1_at	TMEM50B
GgaAfx.24824.1.S1_at	FASTKD5
GgaAfx.24833.1.S1_at	ALMS1

GgaAffx.24835.2.S1_s_at	RNF19A
GgaAffx.24836.1.S1_at	HLCS
GgaAffx.24837.1.S1_at	KLF10
GgaAffx.24840.3.S1_s_at	BRWD1
GgaAffx.24843.1.S1_s_at	RIMS2
GgaAffx.24845.1.S1_at	ALMS1
GgaAffx.24849.1.S1_at	LOC428379 /// LOC772340
GgaAffx.2485.2.S1_at	PHKB
GgaAffx.2485.3.S1_s_at	PHKB
GgaAffx.24855.3.S1_s_at	CSMD3
GgaAffx.2486.1.S1_at	SAP30L
GgaAffx.24867.1.S1_s_at	PRDM15
GgaAffx.24867.3.S1_s_at	PRDM15
GgaAffx.24869.1.S1_at	PTP4A3
GgaAffx.24869.1.S1_s_at	PTP4A3
GgaAffx.24887.1.S1_at	CXorf36
GgaAffx.24893.1.S1_s_at	KDM6A
GgaAffx.24895.1.S1_at	FUNDC1
GgaAffx.24898.2.S1_s_at	EFHC2
GgaAffx.24899.1.S1_at	RCJMB04_1d13
GgaAffx.24899.1.S1_s_at	RCJMB04_1d13
GgaAffx.24912.1.S1_s_at	BCOR
GgaAffx.24917.1.S1_s_at	EFR3A
GgaAffx.24921.2.S1_s_at	MAP3K7IP3
GgaAffx.24932.3.S1_s_at	POLA1
GgaAffx.24934.1.S1_at	GCLC
GgaAffx.24935.1.S1_at	ELOVL5
GgaAffx.24936.1.S1_at	PCYT1B
GgaAffx.24937.1.S1_s_at	MCPH1
GgaAffx.24946.2.S1_at	ZHX1
GgaAffx.24953.1.S1_at	KIDINS220
GgaAffx.24956.1.S1_s_at	MAP7D2
GgaAffx.24956.3.S1_s_at	MAP7D2
GgaAffx.24967.1.S1_at	SMC6
GgaAffx.24973.1.S1_at	APOB
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GgaAffx.24992.1.S1_s_at	DTNB
GgaAffx.24999.1.S1_s_at	EPHX2
GgaAffx.2501.2.S1_s_at	LOC424420
GgaAffx.25017.1.S1_at	FZD3

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GgaAffx.25022.1.S1_at	XKR6	
GgaAffx.25044.1.S1_at	PHF16	
GgaAffx.25048.1.S1_s_at	CYFIP1	
GgaAffx.25050.1.S1_at	HERC2	
GgaAffx.25059.1.S1_at	LYG2	
GgaAffx.25060.1.S1_at	EIF5B	
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GgaAffx.25078.1.S1_at		41162
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GgaAffx.25081.1.S1_s_at	RASA3	
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GgaAffx.25088.2.S1_at	MYO16	
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GgaAffx.2511.1.S1_at	MICALL2	
GgaAffx.25114.3.S1_s_at	MBNL2	
GgaAffx.25117.1.S1_s_at	DZIP1	
GgaAffx.25119.1.A1_at	SLITRK1	
GgaAffx.25124.1.S1_s_at	RBM26	
GgaAffx.25124.2.S1_at	RBM26	
GgaAffx.25124.3.S1_s_at	RBM26	
GgaAffx.25126.1.S1_s_at	C13orf7	
GgaAffx.25129.1.S1_at	COMMD6	
GgaAffx.2513.1.S1_at	TET1	
GgaAffx.25134.1.S1_s_at	DIS3	
GgaAffx.25138.1.S1_at	OLFM4	
GgaAffx.25142.1.S1_s_at	COG3	
GgaAffx.25143.1.S1_s_at	ZC3H13	
GgaAffx.25146.1.S1_at	LRCH1	
GgaAffx.25146.2.S1_at	LRCH1	
GgaAffx.25146.2.S1_s_at	LRCH1	
GgaAffx.25150.1.S1_at	KCNRG	
GgaAffx.25151.1.S1_at	DHRS12	
GgaAffx.25155.1.S1_at	DCLK1	
GgaAffx.25166.1.S1_s_at	PAN3	
GgaAffx.25168.2.S1_s_at	LOC415664 /// LOC427532	
GgaAffx.25173.1.S1_at	TNFRSF19	
GgaAffx.2518.1.S1_at	THSD4	

GgaAfx.25180.2.A1_at	LOC771527
GgaAfx.25196.2.S1_s_at	LOC418990
GgaAfx.25198.2.S1_at	FAM76B
GgaAfx.25199.1.S1_at	DUS3L
GgaAfx.25200.1.S1_at	PANX1
GgaAfx.25213.2.S1_s_at	RAB30
GgaAfx.25215.2.S1_s_at	PCF11
GgaAfx.2522.1.S1_at	TMCO4
GgaAfx.2522.2.S1_s_at	TMCO4
GgaAfx.25227.8.S1_s_at	NARS2
GgaAfx.25229.1.S1_at	VWF
GgaAfx.25232.1.S1_s_at	GADD45B
GgaAfx.25233.1.S1_at	CUX1
GgaAfx.25237.1.S1_at	SLCO2B1
GgaAfx.25241.1.S1_at	KIAA0280
GgaAfx.25253.1.S1_at	SPDYA
GgaAfx.25254.1.A1_at	TXNL4A
GgaAfx.25256.1.S1_at	TBC1D1
GgaAfx.25266.1.S1_at	LOC426599
GgaAfx.2527.3.S1_at	ZDHHC13
GgaAfx.25274.1.S1_s_at	DNASE1 /// LOC768347
GgaAfx.25278.1.S1_at	LOC426179
GgaAfx.25280.1.S1_at	COTL1
GgaAfx.25285.1.S1_s_at	RCJMB04_20b24
GgaAfx.25290.1.S1_s_at	LOC426125
GgaAfx.25291.1.S1_at	RCJMB04_3m23
GgaAfx.25293.1.S1_at	SCRIB
GgaAfx.25309.1.S1_s_at	PRPSAP1
GgaAfx.25314.1.S1_at	VIT2
GgaAfx.25317.2.S1_at	C9orf72
GgaAfx.25322.1.S1_at	LOC419425
GgaAfx.25325.3.S1_s_at	NTNG1
GgaAfx.25331.1.S1_at	SAFB2
GgaAfx.25344.1.S1_s_at	ABCA3
GgaAfx.25349.1.S1_at	LOC776973 /// RSF1
GgaAfx.25349.2.S1_s_at	LOC776973 /// RSF1
GgaAfx.25355.1.A1_at	C19orf22
GgaAfx.25358.2.S1_s_at	LIMS2
GgaAfx.25361.1.A1_at	GPR17
GgaAfx.25365.1.S1_at	COMT

GgaAffx.25369.2.S1_s_at	AHCY
GgaAffx.2537.1.S1_at	SSH2
GgaAffx.25371.2.S1_at	LOC423613
GgaAffx.25372.1.S1_at	DENND2C
GgaAffx.25374.2.S1_at	WDR33
GgaAffx.25376.1.S1_at	CAMK4
GgaAffx.25377.1.S1_s_at	DGCR8
GgaAffx.25386.1.S1_at	DOCK2
GgaAffx.25388.1.S1_at	NAGPA
GgaAffx.25392.2.S1_s_at	PFKFB4
GgaAffx.25418.1.S1_at	KIF14
GgaAffx.25432.1.S1_at	KLHL6
GgaAffx.25432.1.S1_s_at	KLHL6
GgaAffx.2544.1.S1_at	DNAJA2
GgaAffx.25442.4.S1_at	SEMA6A
GgaAffx.25443.1.S1_s_at	CNOT1
GgaAffx.25446.3.S1_s_at	YEATS2
GgaAffx.25465.1.S1_s_at	CLSPN
GgaAffx.25485.1.S1_at	ORMDL1 /// RCJMB04_14o23
GgaAffx.25487.1.S1_at	AVR2 /// LOC427416
GgaAffx.25493.1.S1_at	SIL1
GgaAffx.25502.2.S1_at	SLC2A5
GgaAffx.25507.1.S1_at	GLRX2
GgaAffx.25510.1.S1_at	SFRS8
GgaAffx.25510.3.S1_at	SFRS8
GgaAffx.25521.1.S1_s_at	COL5A2
GgaAffx.25534.1.S1_s_at	COL3A1
GgaAffx.25542.1.S1_at	GULP1
GgaAffx.25548.1.S1_s_at	RABGEF1
GgaAffx.2556.3.S1_at	LOC768580
GgaAffx.25560.1.S1_s_at	LOC419703 /// SIK2
GgaAffx.25561.1.S1_s_at	PIWIL1
GgaAffx.25563.1.S1_s_at	UBE4B
GgaAffx.25567.1.S1_at	NEFL
GgaAffx.25575.1.S1_at	SBNO2
GgaAffx.25575.1.S1_s_at	SBNO2
GgaAffx.25575.5.S1_s_at	SBNO2
GgaAffx.25584.4.S1_s_at	LOC415683
GgaAffx.25592.1.S1_at	LOC415345
GgaAffx.25594.1.S1_at	CSNK1D

GgaAffx.25595.1.S1_s_at	AQP5
GgaAffx.25603.1.S1_at	AKAP7 /// LOC768867
GgaAffx.2561.1.S1_at	CYSLTR1
GgaAffx.25616.3.S1_at	NBR1
GgaAffx.25617.1.S1_at	SNRPC
GgaAffx.25618.1.S1_at	FA2H
GgaAffx.25622.3.S1_at	USP52
GgaAffx.25626.2.S1_s_at	MED23
GgaAffx.25630.2.S1_s_at	MAP2
GgaAffx.25640.1.S1_at	RND2
GgaAffx.25641.1.S1_at	STK10
GgaAffx.25642.1.S1_at	VAT1
GgaAffx.25648.1.S1_at	PEX14
GgaAffx.25653.1.S1_at	LOC425347
GgaAffx.25653.2.S1_at	ZNF532
GgaAffx.25672.1.S1_s_at	ASPCR1
GgaAffx.25686.1.S1_at	CLEC2B /// CLEC2D /// LOC4170
GgaAffx.25686.1.S1_x_at	CLEC2B /// CLEC2D /// LOC4170
GgaAffx.25695.2.S1_s_at	LOC426235 /// LOC772002
GgaAffx.25695.3.S1_s_at	LOC426235
GgaAffx.25699.1.S1_at	DHX37
GgaAffx.25709.1.S1_s_at	SERPINF2
GgaAffx.2571.1.S1_at	KCNK15
GgaAffx.25710.1.S1_at	CA10
GgaAffx.25716.1.S1_at	WDR7
GgaAffx.25719.2.S1_s_at	RCJMB04_22m21
GgaAffx.2572.1.S1_at	MYO1E
GgaAffx.25721.1.S1_at	DDX41
GgaAffx.25722.2.S1_s_at	SLC37A2
GgaAffx.25739.2.S1_s_at	EXOSC10
GgaAffx.25755.1.S1_s_at	NCOR2
GgaAffx.25755.4.S1_s_at	NCOR2
GgaAffx.25763.1.S1_at	TRIM25
GgaAffx.25763.1.S1_s_at	TRIM25
GgaAffx.25763.2.S1_at	TRIM25
GgaAffx.25775.1.S1_at	RCJMB04_3p2
GgaAffx.25776.1.S1_at	NFYC
GgaAffx.25782.2.S1_at	LOC427010
GgaAffx.25782.2.S1_s_at	ZFR
GgaAffx.25782.3.S1_s_at	LOC427010

GgaAffx.25796.1.S1_at	PCDH24
GgaAffx.25800.1.S1_s_at	LOC776927
GgaAffx.25800.5.S1_s_at	LOC424393 /// LOC776927
GgaAffx.25810.1.S1_at	CRTC1
GgaAffx.25810.2.S1_s_at	CRTC1
GgaAffx.25810.3.S1_s_at	CRTC1
GgaAffx.25811.1.S1_s_at	LZTR1
GgaAffx.25813.2.S1_s_at	RCJMB04_21i6
GgaAffx.2583.1.S1_at	ATOX1
GgaAffx.25830.1.S1_at	KAT2A
GgaAffx.25833.1.S1_at	DNAJC21
GgaAffx.25839.2.S1_s_at	RCJMB04_30k7
GgaAffx.25854.1.S1_at	DHX57 /// LOC429336
GgaAffx.25857.1.S1_at	IPO9
GgaAffx.25860.1.S1_at	LOC428272
GgaAffx.25864.1.S1_at	MCM10
GgaAffx.25869.1.S1_at	LOXL2
GgaAffx.25873.1.S1_at	KLHL5
GgaAffx.25875.1.S1_s_at	ALDH9A1
GgaAffx.25879.1.S1_s_at	MAST3
GgaAffx.25881.1.S1_at	PECAM1
GgaAffx.25881.1.S1_s_at	PECAM1 /// PECAM1
GgaAffx.25884.1.S1_at	ARRDC2
GgaAffx.25890.1.S1_at	RCJMB04_20c20
GgaAffx.25890.4.S1_s_at	RCJMB04_20c20
GgaAffx.25896.1.S1_s_at	SLC1A3
GgaAffx.25899.1.S1_s_at	TRRAP
GgaAffx.25904.1.S1_s_at	RPGRIP1L
GgaAffx.25906.1.S1_at	TTF1
GgaAffx.25917.1.S1_s_at	MYST3
GgaAffx.25929.1.S1_at	RBL2
GgaAffx.25933.3.S1_s_at	PITPNC1
GgaAffx.25937.3.S1_s_at	RCJMB04_9d3
GgaAffx.25941.1.S1_at	RNF145
GgaAffx.25948.2.S1_s_at	MACF1
GgaAffx.25950.1.S1_at	HELZ
GgaAffx.25958.1.S1_at	SOX30
GgaAffx.25960.1.S1_s_at	FBXO42
GgaAffx.25962.2.S1_s_at	TOX3
GgaAffx.25969.1.S1_at	MREG

GgaAffx.25979.1.S1_s_at	BNIP2
GgaAffx.25985.1.S1_at	OTUD7A
GgaAffx.26023.5.S1_s_at	KRT15
GgaAffx.26025.1.S1_at	TRIT1
GgaAffx.26026.1.S1_at	IFT81
GgaAffx.26037.1.S1_at	P2RX7
GgaAffx.2604.3.S1_s_at	SERINC3
GgaAffx.26045.1.S1_at	ZNF423
GgaAffx.26046.1.S1_at	XPR1
GgaAffx.26047.1.S1_s_at	PRDM12
GgaAffx.26061.1.S1_s_at	OCRL
GgaAffx.26062.1.S1_s_at	CHIR-B3 /// LOC770720
GgaAffx.26064.1.S1_at	MYPN
GgaAffx.26068.1.S1_at	HNRNPH3
GgaAffx.26072.2.S1_s_at	TJP1
GgaAffx.26074.1.S1_at	CCDC46
GgaAffx.26075.1.S1_s_at	RCJMB04_3e19 /// WDR82P1
GgaAffx.26076.1.S1_at	NEK8
GgaAffx.2608.1.S1_at	MAD1L1
GgaAffx.26081.1.S1_s_at	RUFY2
GgaAffx.26081.2.S1_at	RUFY2
GgaAffx.26090.1.S1_at	LYPLA2P1
GgaAffx.26106.6.S1_s_at	JMJD2B
GgaAffx.26108.1.S1_at	FAM81A
GgaAffx.2611.1.S1_at	FBXL10
GgaAffx.2611.2.S1_s_at	FBXL10
GgaAffx.26111.2.S1_s_at	CCAR1
GgaAffx.26128.1.S1_at	GAA
GgaAffx.26129.1.S1_at	FAM20A
GgaAffx.26133.1.S1_s_at	UGT1A1 /// UGT1A9
GgaAffx.26139.2.S1_at	LOC422990 /// PSMD13
GgaAffx.26141.1.S1_s_at	HKDC1
GgaAffx.26156.1.S1_at	VPS13D
GgaAffx.2616.1.S1_at	LOC768647
GgaAffx.26161.1.S1_at	CGNL1
GgaAffx.26175.1.S1_at	ABCA5
GgaAffx.26183.1.S1_at	C7orf27
GgaAffx.26187.1.S1_s_at	WDR66
GgaAffx.26190.1.S1_at	LOC417445
GgaAffx.26195.1.S1_s_at	XPO1

GgaAfx.26199.2.S1_s_at	RCJMB04_13a9
GgaAfx.26203.1.S1_at	SPECC1
GgaAfx.26205.1.S1_s_at	SLC39A11
GgaAfx.26210.1.A1_s_at	LOC770343
GgaAfx.26213.1.S1_at	SHCBP1
GgaAfx.26220.2.S1_at	SEMA3G
GgaAfx.26220.2.S1_s_at	SEMA3G
GgaAfx.26232.1.S1_at	EFNB1
GgaAfx.26234.1.S1_s_at	KNTC1
GgaAfx.26236.1.S1_at	STK38
GgaAfx.26244.4.S1_s_at	PPFIA1
GgaAfx.26246.1.S1_at	SEPHS1
GgaAfx.26247.1.S1_at	LRRC8A
GgaAfx.26254.1.S1_at	FAAP100 /// NPLOC4
GgaAfx.26256.1.S1_at	RBM5
GgaAfx.26257.1.S1_at	SLC45A1
GgaAfx.26262.1.S1_at	LOC423006
GgaAfx.26265.1.S1_at	ATXN2
GgaAfx.26265.2.S1_s_at	ATXN2
GgaAfx.26265.3.S1_s_at	ATXN2
GgaAfx.26266.1.S1_at	RBM5
GgaAfx.26268.1.S1_at	RNF216
GgaAfx.26278.1.S1_at	PTCHD2
GgaAfx.26281.1.S1_s_at	ARFGEF2
GgaAfx.26281.3.S1_s_at	ARFGEF2
GgaAfx.26282.1.S1_at	ZDHHC12
GgaAfx.26285.1.S1_at	AKAP10
GgaAfx.26291.1.S1_at	CCDC21
GgaAfx.26296.1.S1_at	SLC7A9
GgaAfx.26305.1.S1_at	OBSCN
GgaAfx.26327.1.S1_x_at	CHIR-AB3 /// LOC425309 /// LOC
GgaAfx.26344.1.S1_at	ZNFX1
GgaAfx.26345.1.S1_at	RASD1
GgaAfx.26355.1.S1_at	SLC10A4
GgaAfx.26357.1.S1_at	SLC6A1
GgaAfx.26357.2.S1_s_at	SLC6A1
GgaAfx.26361.2.S1_at	GLRA4
GgaAfx.26363.1.A1_at	VGLL4
GgaAfx.26365.1.S1_at	C3orf31
GgaAfx.26372.1.S1_at	KIAA0355

GgaAfx.26374.1.S1_at	TIMP4
GgaAfx.26375.1.S1_at	DLG5
GgaAfx.26383.1.S1_at	LOC415969
GgaAfx.26385.1.S1_s_at	RCJMB04_33h8
GgaAfx.26395.1.S1_s_at	DEAF1
GgaAfx.2640.1.S1_at	NPAL3
GgaAfx.26401.1.S1_at	CEP152
GgaAfx.26403.1.S1_at	TPR
GgaAfx.26414.1.S1_s_at	CES1 /// LOC769704
GgaAfx.26416.1.S1_at	LOC416899
GgaAfx.2642.1.A1_at	CHST12
GgaAfx.2642.1.S1_at	CHST12
GgaAfx.26426.1.S1_s_at	SCG2
GgaAfx.26432.1.S1_s_at	COL11A1
GgaAfx.26442.1.S1_s_at	CD72
GgaAfx.26446.2.S1_s_at	GSTT1
GgaAfx.26459.1.S1_s_at	USP54
GgaAfx.26461.1.S1_at	CDC14A
GgaAfx.26461.2.S1_s_at	CDC14A
GgaAfx.26462.1.A1_at	GPR88
GgaAfx.26463.1.S1_at	ACPL2
GgaAfx.26464.1.S1_at	BRIP1
GgaAfx.26476.1.S1_at	DCP1A
GgaAfx.26486.1.S1_at	ZNF232
GgaAfx.26489.1.S1_at	POLR1E
GgaAfx.26492.1.S1_s_at	AGL
GgaAfx.26498.1.S1_s_at	PDLIM1
GgaAfx.26501.1.S1_s_at	OGT
GgaAfx.26502.1.S1_at	FREM1
GgaAfx.26505.1.S1_s_at	C3orf63
GgaAfx.26508.2.S1_at	TAF1
GgaAfx.26508.2.S1_s_at	TAF1
GgaAfx.26509.1.A1_at	LOC771941
GgaAfx.26509.1.S1_s_at	LOC771941 /// MLYCD
GgaAfx.26511.1.S1_s_at	MPZL1
GgaAfx.26516.1.S1_at	KIF9
GgaAfx.26516.1.S1_s_at	KIF9
GgaAfx.26527.1.S1_at	TCOF1
GgaAfx.26530.1.A1_at	LOC424832
GgaAfx.26530.1.S1_at	LOC424832

GgaAfx.26540.2.S1_s_at	LOC425155
GgaAfx.26541.1.S1_at	GFER
GgaAfx.2655.1.S1_x_at	COL13A1
GgaAfx.2655.6.S1_at	COL13A1
GgaAfx.26560.1.S1_at	ARHGAP29
GgaAfx.26564.1.S1_at	KSR1
GgaAfx.26564.1.S1_s_at	KSR1
GgaAfx.26564.2.S1_s_at	KSR1
GgaAfx.26573.1.S1_at	ZDHHC7
GgaAfx.26579.1.S1_s_at	CSF1R
GgaAfx.26586.1.S1_s_at	SLC7A3
GgaAfx.26587.1.S1_at	RCJMB04_1e1
GgaAfx.26599.1.S1_s_at	LOC416916
GgaAfx.26601.1.S1_s_at	ARFGAP1
GgaAfx.26607.5.S1_s_at	ZNF143
GgaAfx.26616.1.S1_s_at	DLG3
GgaAfx.26624.6.S1_s_at	TRPM7
GgaAfx.26629.2.S1_at	KIAA0664
GgaAfx.26630.1.S1_at	TBC1D9B
GgaAfx.26637.1.S1_at	ERF
GgaAfx.26643.1.S1_at	LRCH2
GgaAfx.26643.2.S1_s_at	LRCH2
GgaAfx.26643.4.S1_at	LRCH2
GgaAfx.26643.4.S1_s_at	LRCH2
GgaAfx.26643.6.S1_at	LRCH2
GgaAfx.26644.1.S1_at	WSCD1
GgaAfx.26651.3.S1_at	SCUBE2
GgaAfx.26651.6.S1_s_at	SCUBE2
GgaAfx.26653.1.S1_at	ANUBL1
GgaAfx.26656.1.S1_at	SQSTM1
GgaAfx.26656.2.S1_at	SQSTM1
GgaAfx.26666.1.S1_s_at	MYO1D
GgaAfx.26668.2.S1_s_at	ST5
GgaAfx.26669.1.S1_s_at	MAML1
GgaAfx.26670.1.S1_at	SLC5A11
GgaAfx.26671.1.S1_at	EVI5
GgaAfx.26671.1.S1_s_at	EVI5
GgaAfx.26677.1.S1_at	LOC423775
GgaAfx.2668.1.S1_at	PTDSS2
GgaAfx.26683.1.S1_s_at	LOC777076 /// RUFY1

GgaAffx.26692.1.S1_at	SLC13A5
GgaAffx.26694.1.S1_at	ADAMTS2
GgaAffx.26697.2.S1_s_at	PRPF6
GgaAffx.26702.1.S1_s_at	LOC422229
GgaAffx.26704.1.S1_at	ABHD7
GgaAffx.26704.1.S1_s_at	ABHD7
GgaAffx.26714.1.S1_s_at	RBBP6
GgaAffx.26725.1.S1_at	ZBTB46
GgaAffx.26729.1.S1_s_at	TNRC6A
GgaAffx.26737.1.S1_at	PLEKHA7
GgaAffx.26741.1.S1_s_at	ZNF644
GgaAffx.2675.1.S1_at	LOC424033
GgaAffx.26752.1.S1_s_at	PIK3C2A
GgaAffx.26766.1.S1_at	TMEM32
GgaAffx.2677.1.S1_at	MYLK3
GgaAffx.26771.1.S1_s_at	LIMA1
GgaAffx.26772.1.S1_at	LRRC8C
GgaAffx.26774.2.S1_s_at	SLC9A6
GgaAffx.26777.1.S1_s_at	TXNRD3
GgaAffx.2684.1.S1_s_at	FAT2
GgaAffx.269.1.S1_at	KLHL12
GgaAffx.2690.1.S1_at	RASAL2
GgaAffx.2690.3.S1_s_at	RASAL2
GgaAffx.2698.4.S1_s_at	ABCA8
GgaAffx.2699.1.S1_s_at	ABCA5
GgaAffx.270.1.S1_at	ERMP1
GgaAffx.2700.1.S1_at	MYLK3
GgaAffx.2701.1.S1_at	INPPL1
GgaAffx.2710.1.S1_at	WDR41
GgaAffx.2714.2.S1_s_at	CCDC109A
GgaAffx.2732.1.S1_at	LOC428824
GgaAffx.2735.1.S1_s_at	RCJMB04_3a3
GgaAffx.2736.1.S1_at	WNT11B
GgaAffx.2744.1.S1_at	LUZP2
GgaAffx.2749.1.S1_at	COR4
GgaAffx.2750.1.S1_s_at	RAB27A
GgaAffx.2751.1.S1_at	ARSB
GgaAffx.2766.1.S1_s_at	ASTN1
GgaAffx.2767.1.A1_at	PLEKHF1
GgaAffx.2773.1.S1_at	ZCCHC8

GgaAffx.2785.1.S1_at	CCDC137
GgaAffx.2789.1.S1_at	BHMT
GgaAffx.2815.1.S1_at	RBM22
GgaAffx.2816.1.S1_s_at	TCTN1
GgaAffx.2820.1.S1_at	RCJMB04_19e2
GgaAffx.2824.1.S1_s_at	KIAA1370
GgaAffx.2824.2.S1_s_at	KIAA1370
GgaAffx.2826.1.S1_at	PHYHD1
GgaAffx.2831.1.S1_at	NDST1
GgaAffx.2832.1.S1_s_at	NPLOC4
GgaAffx.2853.1.S1_at	RCJMB04_19e2
GgaAffx.2862.1.S1_s_at	MTHFR
GgaAffx.2862.3.S1_s_at	MTHFR
GgaAffx.2867.1.S1_s_at	LOC428696
GgaAffx.2874.5.S1_at	LOC427547
GgaAffx.2874.7.S1_s_at	LOC427547
GgaAffx.2876.1.S1_at	LOC772274 /// MYO5C
GgaAffx.2879.2.S1_at	NMNAT2
GgaAffx.288.1.S1_at	DDX25
GgaAffx.2884.1.S1_at	FBXO2
GgaAffx.2887.1.S1_at	TRPV3
GgaAffx.2890.1.S1_s_at	LOC416488
GgaAffx.2893.1.S1_at	ASPA
GgaAffx.2903.1.A1_at	GDPD2
GgaAffx.2907.1.S1_at	IVD
GgaAffx.2912.1.S1_s_at	NLE1
GgaAffx.2918.1.S1_s_at	WDR34
GgaAffx.2927.1.A1_at	KCNJ12
GgaAffx.2936.1.S1_at	SLC7A10
GgaAffx.2958.1.S1_at	SCG3
GgaAffx.2959.1.S1_x_at	LOC420363
GgaAffx.2960.1.S1_s_at	C1QB
GgaAffx.2968.1.S1_s_at	RCJMB04_13e7
GgaAffx.2968.3.S1_s_at	SLC47A2
GgaAffx.2975.1.S1_at	DMXL2 /// LOC776238
GgaAffx.2978.1.S1_at	PLCB2
GgaAffx.2978.2.S1_s_at	PLCB2
GgaAffx.2978.3.S1_at	PLCB2
GgaAffx.2979.1.S1_at	C12orf51
GgaAffx.2984.1.S1_s_at	PHKA1

GgaAfx.2985.1.S1_s_at	TRAFD1
GgaAfx.2986.1.S1_at	C10orf56
GgaAfx.2993.1.S1_at	EPB42
GgaAfx.2993.5.S1_at	LOC771136 /// TGM3
GgaAfx.2993.7.S1_at	LOC771136
GgaAfx.3004.1.S1_at	ATP2B2
GgaAfx.3009.1.S1_s_at	SEMA6D
GgaAfx.3022.1.S1_at	PHACTR3
GgaAfx.3027.1.S1_at	SLC6A11
GgaAfx.3028.1.S1_at	SYCP2
GgaAfx.3035.1.S1_s_at	RCJMB04_4l2
GgaAfx.3051.1.S1_at	LOC415780
GgaAfx.3052.1.S1_at	LOC415780
GgaAfx.3074.1.S1_at	ATG7
GgaAfx.3074.1.S1_s_at	ATG7
GgaAfx.3077.1.S1_at	RCJMB04_8b16
GgaAfx.3077.1.S1_s_at	RCJMB04_8b16
GgaAfx.3088.1.A1_at	IRS1
GgaAfx.3094.1.S1_at	LOC424802
GgaAfx.3105.2.S1_s_at	TSEN2
GgaAfx.3109.1.S1_at	C10orf11
GgaAfx.311.1.S1_at	PADI2
GgaAfx.3113.1.S1_at	COMTD1
GgaAfx.3119.1.S1_at	SHC4
GgaAfx.3119.2.S1_at	SHC4
GgaAfx.3119.2.S1_s_at	SHC4
GgaAfx.3130.1.S1_at	LOC415973
GgaAfx.3132.1.S1_s_at	DHX30
GgaAfx.3134.1.S1_at	RCJMB04_1f9
GgaAfx.3145.1.S1_s_at	MYST4
GgaAfx.3147.1.S1_at	TEX14
GgaAfx.318.1.S1_at	FANCA
GgaAfx.3180.1.S1_s_at	C1orf27
GgaAfx.3180.2.S1_s_at	C1orf27
GgaAfx.3186.1.S1_at	DRD4
GgaAfx.3192.1.S1_at	C1orf26
GgaAfx.3196.1.S1_at	FAM124B
GgaAfx.3200.1.S1_s_at	FBLN2
GgaAfx.3201.1.S1_at	TAF4
GgaAfx.3202.2.S1_s_at	LOC416899 /// LOC768372

GgaAffx.3206.1.S1_s_at	KIAA0913
GgaAffx.3214.1.S1_at	LOC425228
GgaAffx.3235.1.S1_s_at	PHF2
GgaAffx.3235.3.S1_s_at	PHF2
GgaAffx.3236.1.S1_at	GTPBP5
GgaAffx.3241.1.S1_at	LOC769184
GgaAffx.3241.1.S1_x_at	LOC769184
GgaAffx.3247.1.S1_at	KIAA0423
GgaAffx.325.7.S1_s_at	KLHL12
GgaAffx.3251.1.S1_s_at	LOC422804
GgaAffx.3254.1.S1_at	SYNPO2L
GgaAffx.3255.1.S1_at	WNK2
GgaAffx.3255.1.S1_s_at	WNK2
GgaAffx.3257.1.S1_at	WNK2
GgaAffx.3264.1.S1_at	MOGAT1
GgaAffx.3269.2.S1_s_at	ADCYAP1R1
GgaAffx.327.1.S1_at	UBXD5
GgaAffx.3270.1.S1_at	ADCYAP1R1
GgaAffx.3275.1.S1_at	USP54
GgaAffx.3277.1.S1_at	EXTL2
GgaAffx.3282.1.S1_s_at	LOC428397
GgaAffx.3282.3.S1_at	LOC428397
GgaAffx.3284.1.S1_at	BICD2
GgaAffx.3290.1.S1_at	SPATA2L
GgaAffx.3294.1.S1_at	LOC423026
GgaAffx.3295.1.S1_at	LOC424816
GgaAffx.3296.1.S1_at	OLFML1
GgaAffx.3297.1.S1_s_at	LMF1
GgaAffx.3298.1.S1_s_at	SLC25A36
GgaAffx.3299.1.S1_at	TBX2 /// TBX4
GgaAffx.3301.1.S1_at	ZBTB47
GgaAffx.3306.1.S1_s_at	KBTBD5
GgaAffx.3306.2.S1_at	KBTBD5
GgaAffx.3306.3.S1_at	KBTBD5
GgaAffx.3307.1.S1_at	PPFIBP2
GgaAffx.331.2.S1_s_at	SPIRE2
GgaAffx.3310.1.S1_s_at	CA7
GgaAffx.3321.1.S1_s_at	OVCH2
GgaAffx.3345.1.S1_at	C20orf151
GgaAffx.335.1.S1_s_at	SARS

GgaAffx.3350.1.S1_at	USP32
GgaAffx.3352.1.S1_at	RCJMB04_2p4
GgaAffx.3366.1.S1_s_at	SORBS1
GgaAffx.3366.5.S1_at	SORBS1
GgaAffx.3368.1.S1_at	LOC772204
GgaAffx.338.1.S1_at	TNFRSF9
GgaAffx.338.2.S1_s_at	TNFRSF9
GgaAffx.3387.1.S1_at	LOC425324 /// LOC426333
GgaAffx.3396.1.S1_at	MRM1
GgaAffx.34.1.S1_at	COPS5
GgaAffx.3404.1.S1_s_at	AATF
GgaAffx.3405.1.S1_at	FREM1
GgaAffx.3407.1.S1_at	FREM1
GgaAffx.3415.1.S1_at	ZDHC21
GgaAffx.3419.1.S1_at	CCDC66
GgaAffx.3431.1.S1_at	HSD17B2
GgaAffx.3434.1.S1_s_at	AP1GBP1
GgaAffx.3437.2.S1_s_at	PTH1R
GgaAffx.3442.2.S1_s_at	ARHGEF3
GgaAffx.3443.1.S1_at	LOC769642
GgaAffx.345.1.S1_at	LOC771297
GgaAffx.3455.1.S1_at	PIK3CB
GgaAffx.3464.1.S1_at	APPL1
GgaAffx.3468.1.S1_at	MYO18B
GgaAffx.3469.1.S1_at	ITM2C
GgaAffx.3475.1.S1_at	GPR55
GgaAffx.3477.1.A1_at	GPR35
GgaAffx.3477.1.S1_at	GPR35
GgaAffx.349.2.S1_s_at	PER3
GgaAffx.349.3.S1_at	PER3
GgaAffx.3490.1.S1_s_at	TBL3
GgaAffx.3505.1.S1_at	NF1
GgaAffx.3510.1.S1_s_at	HPS4
GgaAffx.3513.1.S1_at	DNHD2
GgaAffx.3518.1.S1_at	OGFR
GgaAffx.3519.1.S1_at	SLC44A3
GgaAffx.3525.1.S1_at	F3
GgaAffx.3534.2.S1_s_at	TRPM2
GgaAffx.3542.1.S1_s_at	RCJMB04_2i22
GgaAffx.3545.1.S1_at	TSC2

GgaAffx.3547.1.S1_s_at	LOC422211
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GgaAffx.3553.2.S1_at	LOC428402
GgaAffx.3561.1.S1_at	LOC416914
GgaAffx.3568.1.S1_at	CRISPLD2
GgaAffx.3574.1.S1_at	RCJMB04_19f9
GgaAffx.3582.1.S1_s_at	SQRDL
GgaAffx.3582.2.S1_at	SQRDL
GgaAffx.3588.2.S1_at	CELSR3
GgaAffx.3595.5.S1_at	SGSM2
GgaAffx.3598.1.A1_at	LOC428705
GgaAffx.3603.1.S1_at	LOC768665
GgaAffx.3610.2.S1_s_at	BIRC7
GgaAffx.3613.1.S1_at	PKD2L1
GgaAffx.3615.1.S1_at	HMGXB3
GgaAffx.3620.1.S1_at	JPH3
GgaAffx.3622.1.S1_at	ABCG2
GgaAffx.3622.2.S1_s_at	ABCG2
GgaAffx.3623.1.S1_at	ALOX5
GgaAffx.3624.1.S1_at	WDR40A
GgaAffx.3635.1.S1_at	LOC427400
GgaAffx.3640.1.S1_at	LOC772338
GgaAffx.3644.4.S1_at	KCNQ2
GgaAffx.365.1.S1_at	SOX13
GgaAffx.3660.1.S1_at	SRMS
GgaAffx.3660.1.S1_x_at	SRMS
GgaAffx.3663.1.S1_at	HEXDC
GgaAffx.3684.2.S1_at	EEFSEC
GgaAffx.3689.1.S1_at	FAM69A
GgaAffx.3690.1.S1_at	PPYR1
GgaAffx.3705.2.S1_s_at	HDC
GgaAffx.3712.1.S1_s_at	DAK
GgaAffx.3713.1.S1_s_at	SEC61A1
GgaAffx.3716.1.S1_s_at	LCMT1
GgaAffx.3719.1.S1_s_at	BTBD8
GgaAffx.3719.3.S1_s_at	BTBD8
GgaAffx.372.1.S1_at	PTPN7
GgaAffx.3720.1.S1_at	GDF10
GgaAffx.3726.1.S1_s_at	ABTB1
GgaAffx.3729.3.S1_s_at	WHDC1

GgaAffx.373.1.S1_at	PCNX	
GgaAffx.3730.1.S1_at	BTBD8	
GgaAffx.3732.1.S1_at	SAMD10	
GgaAffx.3734.1.S1_s_at	HOMER2	
GgaAffx.3741.1.S1_s_at	LOC422229	
GgaAffx.3750.1.S1_at	AXUD1	
GgaAffx.3756.4.S1_s_at	PITPNM3	
GgaAffx.3765.1.S1_s_at	CDC7	
GgaAffx.377.1.S1_at		40970
GgaAffx.3777.1.S1_s_at	ZBTB46	
GgaAffx.3779.1.S1_at	TEKT1	
GgaAffx.3787.1.S1_at	PALB2	
GgaAffx.3795.1.S1_at	GPC3	
GgaAffx.3813.1.S1_at	ZC3H18	
GgaAffx.3838.1.S1_at	PLXNA1	
GgaAffx.3841.1.S1_at	ENDOGL1	
GgaAffx.3847.1.S1_at	HNRNPA0	
GgaAffx.3865.1.S1_at	RHEB	
GgaAffx.3871.1.S1_at	OTOG	
GgaAffx.3874.1.S1_at	ACSF3	
GgaAffx.3883.1.S1_at	MAP7D3	
GgaAffx.3887.1.S1_at	KLF15	
GgaAffx.3892.1.S1_s_at	PGBD3	
GgaAffx.3894.1.S1_s_at	MAP7D3	
GgaAffx.3898.1.A1_at	ESPNL	
GgaAffx.3906.1.S1_s_at	GALNS	
GgaAffx.3919.1.S1_s_at	JMJD5	
GgaAffx.3927.4.S1_s_at	LOC428958	
GgaAffx.3929.1.S1_at	GPR112	
GgaAffx.3937.1.S1_at	IL4R	
GgaAffx.3939.2.S1_s_at	DPP6	
GgaAffx.3941.1.S1_at	IL21R	
GgaAffx.3948.2.S1_at	CLCA2	
GgaAffx.3948.4.S1_s_at	LOC424523	
GgaAffx.3954.1.S1_at	FAM38A	
GgaAffx.3956.1.S1_s_at	PAXIP1	
GgaAffx.396.1.S1_at	ANKRD47	
GgaAffx.3985.1.S1_at	KCTD5	
GgaAffx.3989.1.S1_at	SLC6A6	
GgaAffx.3992.1.S1_s_at	PAK2	

GgaAfx.3997.1.S1_s_at	ART1 /// ART7B
GgaAfx.3997.2.A1_at	ART1
GgaAfx.3997.2.S1_at	ART1
GgaAfx.4000.1.S1_at	ARNT2
GgaAfx.4004.2.S1_at	C16orf45
GgaAfx.4004.2.S1_s_at	C16orf45
GgaAfx.4006.1.S1_at	KCNQ1
GgaAfx.401.1.S1_at	PHF13
GgaAfx.4011.1.S1_at	TTLL9
GgaAfx.4011.3.S1_s_at	TTLL9
GgaAfx.4014.1.S1_at	XKR7
GgaAfx.4028.1.S1_at	PLXNA4B
GgaAfx.4030.2.S1_s_at	KIAA0430
GgaAfx.4033.1.S1_at	HTR7
GgaAfx.4038.1.S1_s_at	RCJMB04_5h24
GgaAfx.4044.1.S1_s_at	PTPRN2
GgaAfx.4053.2.S1_at	ZFAND6
GgaAfx.407.4.S1_s_at	HIVEP3
GgaAfx.4076.1.S1_s_at	FAM62B
GgaAfx.408.1.S1_at	CIRH1A
GgaAfx.4089.1.S1_s_at	UBASH3B
GgaAfx.4108.1.S1_at	RCJMB04_3m6
GgaAfx.4109.1.S1_at	LOC770392
GgaAfx.411.1.S1_at	COG8
GgaAfx.4115.3.S1_s_at	ATP11C
GgaAfx.4123.1.S1_at	XKRX
GgaAfx.4124.1.S1_at	GRIK4
GgaAfx.4128.1.S1_at	ADORA2A
GgaAfx.4130.1.S1_s_at	LIPH
GgaAfx.4138.1.S1_s_at	ABCC1
GgaAfx.4150.1.S1_at	ARHGEF12
GgaAfx.4161.1.S1_at	BRSK2
GgaAfx.4164.1.S1_at	TADA3L
GgaAfx.4176.3.S1_s_at	RAB36
GgaAfx.4177.1.S1_at	POU2F3
GgaAfx.4195.1.S1_at	TRIM29
GgaAfx.420.1.S1_at	RCJMB04_29f20
GgaAfx.4203.1.S1_s_at	XYLT1
GgaAfx.4203.2.S1_s_at	XYLT1
GgaAfx.4208.1.S1_s_at	RCJMB04_22b21

GgaAfx.4209.1.S1_s_at	MCAM
GgaAfx.4215.2.S1_at	KIN
GgaAfx.4217.2.S1_at	PDZD3
GgaAfx.4222.1.S1_at	RCJMB04_1d17
GgaAfx.4226.1.S1_at	ABCG4
GgaAfx.4227.1.S1_at	SRPX2
GgaAfx.4245.1.S1_at	KLHL25
GgaAfx.4264.2.S1_at	LOC416959
GgaAfx.4283.1.S1_at	LOC771371
GgaAfx.4294.1.S1_at	SLCO3A1
GgaAfx.4303.1.S1_at	LOC415505
GgaAfx.4305.1.S1_at	TMC7
GgaAfx.4314.1.S1_at	LOC422075
GgaAfx.4325.1.S1_at	BAIAP2
GgaAfx.4329.1.S1_s_at	MCM10
GgaAfx.4331.2.S1_s_at	LOC416613
GgaAfx.4332.1.A1_at	CLDN22
GgaAfx.4338.1.S1_at	RCJMB04_33d2
GgaAfx.4340.1.S1_at	DUSP11
GgaAfx.4341.1.S1_at	DUSP11
GgaAfx.4348.1.S1_at	LOC423820
GgaAfx.4352.1.S1_s_at	VWA3A
GgaAfx.4353.1.S1_at	LOC777252
GgaAfx.4355.1.S1_at	LOC416618
GgaAfx.4361.4.S1_s_at	USP28
GgaAfx.4368.2.S1_s_at	MCTP2
GgaAfx.4379.1.S1_at	TLR4
GgaAfx.4384.1.S1_at	RNF213
GgaAfx.4387.1.S1_at	ARRDC4
GgaAfx.4389.1.S1_at	LOC427509
GgaAfx.4393.3.S1_s_at	LOC771298
GgaAfx.4394.1.S1_at	LOC416622
GgaAfx.4397.1.S1_at	LOC422082
GgaAfx.4409.1.S1_at	LOC428967
GgaAfx.4411.2.S1_s_at	LRRC28
GgaAfx.4428.1.S1_at	ATP13A3
GgaAfx.4428.2.S1_s_at	ATP13A3
GgaAfx.4444.2.S1_s_at	KIAA0152
GgaAfx.4456.1.S1_at	LINS1
GgaAfx.446.1.S1_at	RNF207

GgaAffx.4460.3.S1_s_at	PARD3
GgaAffx.4463.1.S1_at	AFF4
GgaAffx.4463.2.S1_s_at	AFF4
GgaAffx.4468.1.S1_at	ACOX2
GgaAffx.4468.2.S1_s_at	ACOX2
GgaAffx.4480.1.S1_at	CLEC16A
GgaAffx.4484.1.S1_at	LOC427844
GgaAffx.4487.1.S1_s_at	PGS1
GgaAffx.4487.3.S1_s_at	PGS1
GgaAffx.4490.1.S1_s_at	EPC1
GgaAffx.4497.3.S1_s_at	ATP13A4
GgaAffx.4506.2.S1_s_at	RAB3IL1
GgaAffx.4520.1.S1_s_at	KIF5B
GgaAffx.4524.1.S1_s_at	MSI1
GgaAffx.4528.1.S1_at	PCSK6
GgaAffx.4531.1.S1_s_at	LOC769198
GgaAffx.4536.1.S1_s_at	ARHGAP12
GgaAffx.4549.1.S1_at	ZNF438
GgaAffx.4554.1.S1_at	LOC416638
GgaAffx.4563.1.S1_at	LOC428249
GgaAffx.4569.1.S1_at	LOC771141
GgaAffx.4571.1.A1_at	RCJMB04_2120
GgaAffx.4573.1.S1_at	LOC427511
GgaAffx.4575.1.S1_at	RCJMB04_2120
GgaAffx.4580.1.S1_s_at	MED19
GgaAffx.4581.1.S1_at	LOC424525
GgaAffx.4584.1.S1_at	RASL12
GgaAffx.4585.1.S1_at	LOC422293
GgaAffx.4587.1.S1_at	LOC429557
GgaAffx.460.1.S1_at	STX12
GgaAffx.4601.1.S1_at	SUDS3
GgaAffx.4606.2.S1_s_at	ABCC2
GgaAffx.4626.1.S1_at	C20orf174
GgaAffx.4634.4.S1_at	MAGI1
GgaAffx.4635.1.A1_at	LOC771647
GgaAffx.4644.1.S1_at	SSH1
GgaAffx.4644.2.S1_s_at	SSH1
GgaAffx.4650.1.S1_s_at	SELE
GgaAffx.4651.1.S1_at	LOC420485
GgaAffx.4652.2.S1_s_at	LOC769505 /// LOC769630

GgaAfx.4655.1.S1_at	TMEM8
GgaAfx.4661.1.S1_at	LOC422301
GgaAfx.4662.1.S1_at	LOC422301
GgaAfx.4665.1.S1_at	CNNM1
GgaAfx.4666.1.S1_at	LARS
GgaAfx.4666.1.S1_s_at	LARS
GgaAfx.4677.2.S1_s_at	MASTL
GgaAfx.4681.1.S1_at	ITFG3
GgaAfx.4687.1.S1_at	DENND4A
GgaAfx.4700.1.S1_s_at	ZFYVE27
GgaAfx.4703.1.S1_at	ANKRD2
GgaAfx.471.1.S1_s_at	LOC415660 /// LOC415663
GgaAfx.4715.1.S1_at	LOC428715
GgaAfx.4717.1.S1_at	LOC420491
GgaAfx.4726.1.S1_s_at	KBTBD8
GgaAfx.4733.1.S1_at	MTMR8
GgaAfx.4746.1.S1_at	NAT15
GgaAfx.4748.1.S1_at	ARHGEF9
GgaAfx.4754.2.S1_s_at	SLIT1
GgaAfx.4763.7.S1_s_at	CACNA1G
GgaAfx.4764.1.S1_at	C20orf86
GgaAfx.4768.3.S1_s_at	MEGF11
GgaAfx.4776.1.S1_s_at	MYO3A
GgaAfx.4777.1.S1_at	TIPIN
GgaAfx.4789.1.S1_at	C10orf63
GgaAfx.4800.1.S1_s_at	MYO1B
GgaAfx.4802.1.S1_at	NMUR1
GgaAfx.4816.3.S1_s_at	LOC427595
GgaAfx.4817.1.S1_at	PRODH
GgaAfx.4819.2.S1_at	LOC422323
GgaAfx.4820.1.S1_at	LOC416090
GgaAfx.4823.1.S1_at	TMEM104
GgaAfx.4824.1.S1_s_at	PHLDB1
GgaAfx.4835.1.S1_at	FBXO3
GgaAfx.4837.1.S1_s_at	KIAA1217
GgaAfx.4840.2.S1_s_at	DIS3L2
GgaAfx.4846.4.S1_s_at	FOXP1
GgaAfx.4847.1.S1_at	FADS6
GgaAfx.4848.1.S1_s_at	CBLN4
GgaAfx.4851.1.S1_at	EIF4E3

GgaAfx.4864.1.S1_at	SHQ1
GgaAfx.4867.1.S1_at	ZDHC15
GgaAfx.4872.3.S1_s_at	LOC415641 /// LOC423151
GgaAfx.4872.4.S1_s_at	LOC415641 /// LOC423151
GgaAfx.488.1.S1_at	KCNAB2
GgaAfx.4881.1.S1_at	ALPI
GgaAfx.4891.2.S1_s_at	BTRC
GgaAfx.4894.1.S1_at	LOC417007
GgaAfx.4928.3.S1_s_at	BCDO2
GgaAfx.493.1.S1_s_at	LOC420070
GgaAfx.4936.3.S1_s_at	ECEL1
GgaAfx.4940.1.S1_s_at	LOC776539
GgaAfx.4941.1.S1_at	PAMR1
GgaAfx.4945.1.S1_at	LDLRAD3
GgaAfx.4948.1.S1_at	LDLRAD3
GgaAfx.4950.1.S1_at	CHRND
GgaAfx.4955.1.S1_at	LAMB1
GgaAfx.4956.1.S1_at	CHRNA
GgaAfx.496.1.S1_at	CAPN5
GgaAfx.4960.3.S1_at	IQCH
GgaAfx.4973.1.S1_at	TRAF6
GgaAfx.4973.2.S1_s_at	TRAF6
GgaAfx.4975.1.A1_at	RAG1
GgaAfx.4975.1.S1_at	RAG1
GgaAfx.4976.1.S1_at	RAG2
GgaAfx.4982.1.S1_at	NFATC2
GgaAfx.4984.2.S1_s_at	SLC26A3
GgaAfx.4985.1.S1_at	C10orf112
GgaAfx.4988.1.S1_at	LOC424054
GgaAfx.5009.1.S1_at	RCJMB04_7p22
GgaAfx.5013.1.S1_at	C20orf175
GgaAfx.5026.1.S1_at	LIF
GgaAfx.5027.1.S1_at	COG5
GgaAfx.503.1.S1_at	CREG2
GgaAfx.5030.1.S1_at	COG5
GgaAfx.5039.1.S1_at	CORO2B
GgaAfx.5048.1.S1_s_at	PAK3
GgaAfx.5056.1.S1_at	ASTL
GgaAfx.5077.1.S1_s_at	KIF23
GgaAfx.508.1.S1_at	EYA3

GgaAfx.5084.1.S1_at	CCDC88A
GgaAfx.5084.2.S1_s_at	CCDC88A
GgaAfx.5084.3.S1_s_at	CCDC88A
GgaAfx.5091.1.S1_at	ATXN7L1
GgaAfx.511.1.S1_at	MYH13
GgaAfx.5111.1.S1_at	C10orf112
GgaAfx.5114.1.S1_at	SGOL2
GgaAfx.5116.1.S1_at	FBXO18
GgaAfx.5126.1.S1_at	TLR15
GgaAfx.5144.1.S1_s_at	LOC424943
GgaAfx.5146.1.S1_s_at	NT5C2
GgaAfx.515.2.S1_s_at	PIP5K1C
GgaAfx.517.2.S1_s_at	HYAL1
GgaAfx.5185.2.S1_s_at	RCJMB04_28i17
GgaAfx.5200.1.S1_at	CFLAR
GgaAfx.5200.2.S1_s_at	CFLAR
GgaAfx.5207.1.S1_s_at	CDCA8
GgaAfx.5217.1.S1_at	IL5RA
GgaAfx.5222.1.S1_at	FAM26B
GgaAfx.5224.1.S1_at	FAM26A
GgaAfx.5228.1.S1_at	LOC416107
GgaAfx.5229.1.S1_at	LRCH4
GgaAfx.5239.1.S1_at	ITPR1
GgaAfx.5245.1.S1_at	OBFC1
GgaAfx.5245.1.S1_s_at	OBFC1
GgaAfx.5246.1.S1_at	CASP10
GgaAfx.5247.1.S1_at	FGL2
GgaAfx.5249.1.S1_at	CAPN10
GgaAfx.5249.2.S1_s_at	CAPN10
GgaAfx.5251.1.S1_at	PION
GgaAfx.5255.1.S1_at	LOC422353
GgaAfx.5257.1.S1_at	RSBN1L
GgaAfx.5263.1.S1_at	FES
GgaAfx.5264.1.S1_at	CASP18
GgaAfx.5267.1.S1_at	LMCD1
GgaAfx.5278.1.S1_at	LOC422353
GgaAfx.5281.1.S1_s_at	C10orf78
GgaAfx.5286.3.S1_s_at	HISPPD2A
GgaAfx.5293.1.S1_at	C20orf74
GgaAfx.5294.1.S1_at	VHL

GgaAfx.5297.1.S1_at	RCJMB04_15j12
GgaAfx.5299.1.S1_s_at	IRAK2
GgaAfx.5303.1.A1_at	KIAA1754
GgaAfx.5306.3.S1_s_at	DVL3
GgaAfx.5311.1.S1_at	PFTK2
GgaAfx.5316.1.S1_at	CHST1
GgaAfx.5323.2.S1_at	DHX8
GgaAfx.5323.3.S1_s_at	DHX8
GgaAfx.5330.1.S1_at	CDK3
GgaAfx.5335.2.S1_s_at	PLXND1
GgaAfx.5336.1.S1_at	ALS2CR8
GgaAfx.534.2.S1_s_at	GUCY2F
GgaAfx.5340.1.S1_at	PLEKHM3
GgaAfx.5352.3.S1_s_at	VPS18
GgaAfx.5355.1.S1_at	KLF7
GgaAfx.5357.2.S1_at	ALG3
GgaAfx.5359.1.S1_at	CPO
GgaAfx.5362.2.S1_s_at	LOC417253
GgaAfx.5365.1.S1_s_at	EIF4G1
GgaAfx.5379.2.S1_at	BRD1
GgaAfx.5379.2.S1_s_at	BRD1
GgaAfx.538.1.A1_at	LRRC32
GgaAfx.5380.1.S1_at	PPP2R5D
GgaAfx.5385.1.S1_at	MDH1B
GgaAfx.5385.2.S1_s_at	MDH1B
GgaAfx.5387.1.S1_at	MAL
GgaAfx.5388.1.S1_s_at	INOC1
GgaAfx.5390.1.S1_at	SMNDC1
GgaAfx.5394.1.S1_at	NSUN6
GgaAfx.5399.1.S1_at	OIP5
GgaAfx.54.1.S1_at	KLHL5
GgaAfx.5402.1.S1_at	ADAM23
GgaAfx.5404.1.S1_s_at	NUSAP1
GgaAfx.5406.1.S1_at	GPR1
GgaAfx.5413.1.S1_at	LOC771098
GgaAfx.5413.1.S1_x_at	LOC771098
GgaAfx.5416.2.S1_s_at	RTF1
GgaAfx.5418.1.S1_at	LOC771349
GgaAfx.5419.1.A1_at	LOC771361
GgaAfx.5423.1.S1_at	ZBTB33

GgaAffx.5427.1.S1_at	CUL9
GgaAffx.5433.1.S1_at	LOC771422
GgaAffx.5453.1.S1_at	MGA
GgaAffx.5458.1.S1_at	CTLA4
GgaAffx.5467.1.S1_at	RBM20
GgaAffx.5472.1.S1_at	SELO
GgaAffx.5473.1.S1_at	RAPH1
GgaAffx.5474.1.S1_at	WDR63
GgaAffx.5477.1.S1_at	TRABD
GgaAffx.5482.2.S1_s_at	ZNF800
GgaAffx.549.3.S1_at	MAPK14
GgaAffx.5492.1.S1_at	C1QL3
GgaAffx.5495.2.S1_s_at	JMJD7-PLA2G4B
GgaAffx.5499.1.S1_s_at	PNPLA7
GgaAffx.5500.1.S1_at	LOC420526
GgaAffx.5501.1.S1_at	C2orf13
GgaAffx.5508.6.S1_s_at	MCF2L2
GgaAffx.5512.1.S1_at	LAMP3
GgaAffx.5519.1.S1_at	LOC421270
GgaAffx.5529.1.S1_at	GPAM
GgaAffx.553.2.S1_s_at	RASSF5
GgaAffx.5539.1.S1_s_at	SLC1A4
GgaAffx.5541.1.S1_at	IDH1
GgaAffx.5543.1.S1_at	IQUB
GgaAffx.5547.2.S1_at	LOC771293
GgaAffx.5548.1.S1_at	RCJMB04_9o17
GgaAffx.5549.1.S1_at	ATP6AP1
GgaAffx.555.1.S1_s_at	PRKRIR
GgaAffx.5556.1.S1_at	HAO1
GgaAffx.5560.1.S1_s_at	DNAJC10
GgaAffx.5573.1.S1_s_at	PLCB1
GgaAffx.5573.2.S1_s_at	PLCB1
GgaAffx.5577.1.S1_at	VTI1A
GgaAffx.558.1.S1_s_at	SLC26A8
GgaAffx.5584.1.S1_at	IL1RAPL2
GgaAffx.5584.2.S1_s_at	IL1RAPL2
GgaAffx.5585.1.S1_at	LOC427775
GgaAffx.5586.1.S1_at	SYT4
GgaAffx.5598.1.S1_at	LRRC26
GgaAffx.5600.1.S1_at	EHBP1

GgaAfx.5604.2.S1_at	PLCB4
GgaAfx.5612.1.S1_at	GIMAP1
GgaAfx.5616.1.S1_at	TMEM17
GgaAfx.5617.1.S1_at	PEX5L
GgaAfx.562.1.S1_at	RLF
GgaAfx.5630.2.S1_s_at	SPTBN5
GgaAfx.5630.6.S1_s_at	SPTBN5
GgaAfx.5634.1.S1_s_at	FOXN2
GgaAfx.5641.1.S1_s_at	FAM73A
GgaAfx.5647.1.S1_at	EXD3
GgaAfx.5648.1.S1_at	LOC428554
GgaAfx.5653.2.S1_at	PLA2G4F
GgaAfx.5663.1.S1_at	SMAD7
GgaAfx.5667.1.S1_at	LOC768788
GgaAfx.5668.1.S1_at	GNB4
GgaAfx.5670.1.S1_at	WNT16
GgaAfx.5672.1.S1_at	ZZZ3
GgaAfx.5682.2.S1_s_at	STEAP4
GgaAfx.5692.3.S1_s_at	RCJMB04_12b15
GgaAfx.5695.1.S1_at	PIGK
GgaAfx.5704.1.S1_at	LOC417291
GgaAfx.5712.2.S1_s_at	TBC1D8B
GgaAfx.5713.1.A1_at	ANKRD9
GgaAfx.5714.1.S1_at	FUT7
GgaAfx.5721.1.S1_at	LYCAT
GgaAfx.5725.3.S1_at	ACTL6A
GgaAfx.5729.1.S1_at	CAPN13
GgaAfx.5730.1.S1_at	CAPN13
GgaAfx.5734.2.S1_at	GALNT14
GgaAfx.5743.4.S1_at	GTF2A1L
GgaAfx.5743.4.S1_s_at	GTF2A1L
GgaAfx.5745.1.S1_at	TTN
GgaAfx.575.1.S1_at	MARVELD3
GgaAfx.5758.1.S1_at	TTN
GgaAfx.5786.1.S1_at	CDAN1
GgaAfx.5788.1.S1_s_at	CDC42BPA
GgaAfx.579.1.S1_s_at	SRPK1
GgaAfx.5791.1.S1_at	LOC422394
GgaAfx.5795.1.S1_at	TRMT6
GgaAfx.5808.1.S1_at	C10orf96

GgaAfx.5811.1.A1_x_at	LOC431318
GgaAfx.5812.1.S1_at	LOC416752
GgaAfx.5816.1.S1_s_at	LOC770919
GgaAfx.5818.1.S1_at	LOC426835 /// LOC770105
GgaAfx.5823.1.S1_s_at	AMDHD2
GgaAfx.5824.1.S1_at	PNLIPRP3
GgaAfx.5832.1.S1_s_at	PLD1
GgaAfx.5833.1.S1_at	LOC423918
GgaAfx.5835.1.S1_at	TMEM62
GgaAfx.5841.1.S1_at	RBM46
GgaAfx.5846.1.S1_s_at	LOC429837 /// SFMBT2
GgaAfx.5847.1.A1_at	NPY2R
GgaAfx.5850.1.S1_at	DNAL1
GgaAfx.5852.1.S1_at	RNPS1
GgaAfx.5856.1.S1_s_at	SLC18A2
GgaAfx.5859.1.S1_at	PDZD8
GgaAfx.5862.1.S1_s_at	NUMB
GgaAfx.5869.1.S1_s_at	NVL
GgaAfx.5884.2.S1_at	RBM25
GgaAfx.5884.3.S1_at	RBM25
GgaAfx.5888.1.S1_at	ZFYVE1
GgaAfx.5895.2.S1_at	RCJMB04_3a1
GgaAfx.5895.2.S1_s_at	RCJMB04_3a1
GgaAfx.5911.2.S1_at	WNT2
GgaAfx.5916.1.S1_at	PHC3
GgaAfx.5916.2.S1_s_at	PHC3
GgaAfx.5923.1.S1_s_at	LRRC31
GgaAfx.5930.1.S1_at	GRK5
GgaAfx.5936.1.S1_at	SMOC1
GgaAfx.5947.1.S1_s_at	BAG3
GgaAfx.5949.1.S1_s_at	PPP1R3A
GgaAfx.5954.1.S1_at	KIAA1822L
GgaAfx.5958.1.A1_at	PFN3
GgaAfx.5960.2.S1_s_at	LOC424998
GgaAfx.5963.1.S1_at	RCJMB04_7n4
GgaAfx.5965.1.S1_at	PPAPDC1A
GgaAfx.5966.1.S1_at	CDK6
GgaAfx.5967.1.S1_at	SAMD9L
GgaAfx.5969.1.S1_at	DOCK4
GgaAfx.5970.1.S1_at	HEPACAM2

GgaAfx.5977.1.A1_at	C14orf83
GgaAfx.5983.1.S1_at	ATE1
GgaAfx.5987.1.S1_at	PIGH
GgaAfx.599.1.S1_at	LOC776459
GgaAfx.6002.2.S1_s_at	DYNC1I2
GgaAfx.6003.1.S1_at	PRICKLE1
GgaAfx.6008.1.S1_at	SPOCK3
GgaAfx.6011.1.S1_s_at	ADAMTS20
GgaAfx.6024.1.S1_at	TMEM117
GgaAfx.6026.1.S1_s_at	PEPCK-M
GgaAfx.6031.4.S1_at	MYO3B
GgaAfx.6046.1.S1_at	GPATCH2
GgaAfx.605.5.S1_at	NRG2
GgaAfx.6052.1.S1_s_at	LOC422427
GgaAfx.6053.1.A1_at	COL1A2
GgaAfx.6057.2.S1_s_at	RCJMB04_14m6
GgaAfx.6062.1.A1_at	USH2A
GgaAfx.6062.1.S1_at	USH2A
GgaAfx.6064.1.S1_at	USH2A
GgaAfx.6065.1.S1_at	LOC771944
GgaAfx.6069.3.S1_at	ARID2
GgaAfx.6091.1.S1_at	SART3
GgaAfx.6093.1.S1_at	KIAA0157
GgaAfx.6110.1.S1_s_at	ARHGAP11A
GgaAfx.6114.1.S1_at	RASGRP1
GgaAfx.6125.1.S1_at	CENPF
GgaAfx.6128.1.S1_at	SLC7A11
GgaAfx.6128.3.S1_at	SLC7A11
GgaAfx.6133.1.S1_at	ELF2
GgaAfx.6135.1.S1_at	CENPF
GgaAfx.6147.1.S1_at	RPS6KC1
GgaAfx.6154.1.S1_at	FLVCR1
GgaAfx.6156.1.S1_at	NSL1
GgaAfx.6162.1.S1_at	LOC424161
GgaAfx.6163.1.S1_at	CLGN
GgaAfx.6164.1.S1_at	LOC422448
GgaAfx.6169.1.S1_at	TBK1
GgaAfx.6171.1.S1_at	FASTKD1
GgaAfx.6177.1.S1_at	GNS
GgaAfx.6182.1.S1_at	LOC421379

GgaAfx.6185.1.S1_at	LOC425522 /// LOC776113
GgaAfx.6186.1.S1_at	CCDC3
GgaAfx.6190.1.S1_at	LEMD3
GgaAfx.6196.1.S1_at	SERTAD4
GgaAfx.6197.1.S1_at	SYT14
GgaAfx.6199.1.S1_at	C1orf107
GgaAfx.6199.1.S1_s_at	C1orf107
GgaAfx.621.1.S1_at	C1orf160
GgaAfx.622.1.S1_at	ESAM
GgaAfx.6223.1.S1_at	KIAA1333
GgaAfx.6228.1.S1_s_at	CYLD
GgaAfx.6233.1.S1_at	KCNG3
GgaAfx.6236.1.S1_at	LOC421394
GgaAfx.6243.1.S1_s_at	THADA
GgaAfx.6243.3.S1_s_at	THADA
GgaAfx.625.1.S1_at	LOC772366
GgaAfx.6251.1.S1_at	ABCG5
GgaAfx.6252.1.S1_at	ABCG8
GgaAfx.626.1.A1_at	PANX3
GgaAfx.627.1.S1_s_at	NPHP4
GgaAfx.6271.1.S1_at	ZNF827
GgaAfx.6274.1.S1_at	SRBD1
GgaAfx.6275.1.S1_at	SRBD1
GgaAfx.6276.1.S1_at	ARHGAP5
GgaAfx.6282.1.S1_at	KIAA0467
GgaAfx.6286.1.S1_s_at	PRKCE
GgaAfx.6286.3.S1_s_at	PRKCE
GgaAfx.6287.1.S1_at	LOC423317
GgaAfx.6293.1.S1_at	KIAA0467
GgaAfx.6294.1.S1_at	SOCS5
GgaAfx.6295.1.S1_at	TMEM34
GgaAfx.6297.1.S1_at	TTC7A
GgaAfx.630.1.S1_s_at	C1orf174
GgaAfx.6308.4.S1_s_at	PLB1
GgaAfx.6316.1.S1_at	SUPT7L
GgaAfx.6328.1.S1_at	DDI2
GgaAfx.634.1.S1_at	LPO
GgaAfx.6369.2.S1_s_at	PLK3
GgaAfx.6384.2.S1_s_at	RCJMB04_13c10
GgaAfx.6386.1.S1_at	RNF8

GgaAfx.6391.2.S1_s_at	ANKRD15
GgaAfx.6392.1.S1_at	DMRT3
GgaAfx.6396.1.S1_at	INTU
GgaAfx.6397.1.S1_at	LOC421438
GgaAfx.640.1.S1_at	TDRKH
GgaAfx.6403.1.S1_at	SLC29A1
GgaAfx.6405.1.S1_at	HSPA4L
GgaAfx.6405.2.S1_s_at	HSPA4L
GgaAfx.641.1.S1_at	AP3D1
GgaAfx.6410.1.S1_at	ZNF410
GgaAfx.6413.1.S1_s_at	LOC422497
GgaAfx.6416.1.S1_at	TRHDE
GgaAfx.6416.2.S1_s_at	TRHDE
GgaAfx.6418.2.S1_s_at	C4orf29
GgaAfx.6425.1.S1_at	LARP2
GgaAfx.6433.3.S1_s_at	UROD
GgaAfx.6437.1.S1_at	GLIPR1L2
GgaAfx.644.2.S1_s_at	MAP2K4
GgaAfx.6443.1.S1_s_at	ABCD4
GgaAfx.645.1.S1_at	MPO
GgaAfx.6467.1.S1_s_at	ZDHHC17
GgaAfx.6470.1.S1_at	COL28A1
GgaAfx.6475.1.S1_at	E2F7
GgaAfx.6478.1.S1_s_at	KIAA0317
GgaAfx.65.1.S1_at	FER1L5
GgaAfx.6518.1.S1_at	CNOT6L
GgaAfx.6518.2.S1_s_at	CNOT6L
GgaAfx.6519.1.S1_at	TAS2R7
GgaAfx.6526.1.S1_s_at	PIK3R3
GgaAfx.6526.7.S1_s_at	PIK3R3
GgaAfx.6528.2.S1_at	LOC772154
GgaAfx.653.1.S1_at	DBF4B
GgaAfx.6535.1.S1_s_at	POMGNT1
GgaAfx.6545.4.S1_x_at	RCJMB04_n15
GgaAfx.6552.5.S1_s_at	ESRRB
GgaAfx.6562.1.S1_at	GPR171
GgaAfx.6566.1.S1_at	MMRN1
GgaAfx.6567.1.S1_at	KIAA1737
GgaAfx.6591.2.S1_s_at	ABCC10
GgaAfx.660.1.S1_at	GOLGA1

GgaAfx.662.1.S1_at	LOC771115
GgaAfx.6626.1.S1_s_at	PPP2R2D
GgaAfx.6632.1.S1_at	ALKBH1
GgaAfx.6638.1.A1_at	PWWP2
GgaAfx.6647.1.S1_at	LOC772154
GgaAfx.6655.1.S1_at	COL25A1
GgaAfx.6656.1.S1_at	LTBP1
GgaAfx.6665.1.S1_s_at	RCJMB04_1d5
GgaAfx.6666.1.S1_s_at	YIPF4
GgaAfx.6671.1.S1_at	ALOXE3 /// LOC429674
GgaAfx.6675.3.S1_s_at	TBCKL
GgaAfx.6684.1.S1_s_at	GSTCD
GgaAfx.6685.1.S1_at	GTF2A1
GgaAfx.6689.1.S1_at	STON2
GgaAfx.6694.1.S1_at	VIT
GgaAfx.6707.1.S1_at	SULT6B1
GgaAfx.6708.1.S1_at	LRP2BP
GgaAfx.6712.1.S1_at	PRKD3
GgaAfx.6712.2.S1_s_at	PRKD3
GgaAfx.6715.1.S1_s_at	PTPN21
GgaAfx.6720.3.S1_s_at	ZC3H14
GgaAfx.6720.5.S1_s_at	ZC3H14
GgaAfx.6727.2.S1_s_at	EML5
GgaAfx.6729.1.S1_at	STOX2
GgaAfx.673.1.S1_s_at	MAN1C1
GgaAfx.6735.1.S1_s_at	CDKN2AIP /// LOC422554
GgaAfx.6738.1.S1_at	TTC8
GgaAfx.6740.1.S1_s_at	FOXN3
GgaAfx.6757.1.S1_at	LOC421495
GgaAfx.6764.1.S1_at	ZNF238
GgaAfx.6773.1.S1_at	TMEM106B
GgaAfx.6774.1.S1_at	TMEM16H
GgaAfx.6779.1.S1_s_at	RCJMB04_16f17
GgaAfx.6783.2.S1_s_at	SMEK1
GgaAfx.6785.1.S1_at	EXO1
GgaAfx.6789.1.S1_at	WDR64
GgaAfx.6791.1.S1_at	WDR64
GgaAfx.6796.1.S1_s_at	TRIP11
GgaAfx.6799.1.S1_s_at	FBXO8
GgaAfx.6802.1.S1_s_at	PIGM

GgaAfx.681.3.S1_s_at	MTMR4
GgaAfx.6810.2.S1_s_at	CPSF2
GgaAfx.6812.1.S1_at	ACOT11
GgaAfx.6816.2.S1_s_at	DGKB
GgaAfx.6821.1.S1_s_at	SLC24A4
GgaAfx.6826.1.S1_at	TMEM61
GgaAfx.6834.4.S1_s_at	RYR2
GgaAfx.6835.1.S1_at	USP24
GgaAfx.6836.1.S1_at	WDR17
GgaAfx.6837.1.S1_at	USP24
GgaAfx.6839.1.S1_at	AGR3
GgaAfx.6844.1.S1_at	LOC429936
GgaAfx.6847.2.S1_s_at	RCJMB04_27p10
GgaAfx.6849.1.S1_at	ERO1LB
GgaAfx.6849.2.S1_s_at	ERO1LB
GgaAfx.6855.1.S1_at	KIAA1409
GgaAfx.6859.1.S1_at	MTHFD2L
GgaAfx.6859.2.S1_s_at	MTHFD2L
GgaAfx.6868.1.S1_at	TACSTD2
GgaAfx.6875.2.S1_at	USO1
GgaAfx.6884.1.S1_at	ANTXR2
GgaAfx.6885.1.S1_at	ANTXR2
GgaAfx.6887.1.S1_at	FGF5
GgaAfx.6890.1.S1_at	TMEM161B
GgaAfx.6896.1.S1_at	LOC776184
GgaAfx.6898.1.S1_at	SP4
GgaAfx.6898.2.S1_s_at	SP4
GgaAfx.6916.1.S1_at	B3GALT1
GgaAfx.6931.1.S1_at	GPNMB
GgaAfx.6933.1.S1_s_at	C7orf30
GgaAfx.6935.1.S1_at	TTC21B
GgaAfx.6936.1.S1_s_at	USP1
GgaAfx.6939.2.S1_s_at	PPFIA2
GgaAfx.6945.1.S1_at	SERPINA5
GgaAfx.6948.1.S1_at	TMTC2
GgaAfx.6948.2.S1_s_at	TMTC2
GgaAfx.6955.1.S1_s_at	MPP6
GgaAfx.6968.1.S1_s_at	OSBPL3
GgaAfx.6970.1.S1_s_at	LOC771163
GgaAfx.6975.1.S1_at	LOC776434 /// PCNXL2

GgaAffx.6978.1.S1_s_at	KLHL8
GgaAffx.6986.1.S1_at	PRCP
GgaAffx.6995.1.S1_s_at	LOC424180 /// SCN1A /// SCN2A
GgaAffx.6995.2.S1_at	SCN1A
GgaAffx.700.1.S1_at	ACTRT2
GgaAffx.7006.1.S1_s_at	FIGN
GgaAffx.7016.1.S1_at	C14orf49
GgaAffx.7026.1.S1_at	C1orf96
GgaAffx.7034.1.S1_at	TAF5L
GgaAffx.7038.2.S1_s_at	GALNT2
GgaAffx.7045.1.S1_at	COG2
GgaAffx.7049.3.S1_s_at	WDR78
GgaAffx.7063.1.S1_at	BCL11B
GgaAffx.7063.2.S1_s_at	BCL11B
GgaAffx.7065.1.S1_at	THAP9
GgaAffx.7088.1.S1_at	C12orf50
GgaAffx.7095.1.S1_at	PDCD2
GgaAffx.7098.1.S1_at	LOC422599
GgaAffx.7100.2.S1_s_at	CEP290
GgaAffx.7101.1.S1_s_at	CEP290
GgaAffx.7109.1.S1_s_at	EML1
GgaAffx.711.1.A1_at	ST3GAL4
GgaAffx.7118.1.S1_s_at	COLQ
GgaAffx.7118.4.S1_at	COLQ
GgaAffx.7120.1.S1_at	HACL1
GgaAffx.7132.1.S1_at	WDR25
GgaAffx.7149.1.S1_at	PLCL2
GgaAffx.7161.1.S1_s_at	RCJMB04_1f4
GgaAffx.7162.1.S1_s_at	WDFY3
GgaAffx.7169.2.S1_at	PPM1K
GgaAffx.7174.1.S1_at	SGOL1
GgaAffx.7182.1.S1_at	KIF25
GgaAffx.7188.1.S1_s_at	NGLY1
GgaAffx.7188.2.S1_s_at	NGLY1
GgaAffx.7188.3.S1_s_at	NGLY1
GgaAffx.7190.1.S1_s_at	PLXNC1
GgaAffx.7193.1.S1_at	CCDC41
GgaAffx.7202.1.S1_at	CRELD2
GgaAffx.7211.1.S1_at	LOC421567
GgaAffx.7215.1.S1_at	C1orf173

GgaAfx.7220.1.S1_at	WDR20
GgaAfx.7221.1.S1_at	C14orf131
GgaAfx.7226.1.S1_at	RNF25
GgaAfx.7239.1.S1_s_at	ZNF142
GgaAfx.7245.1.S1_at	LOC421567
GgaAfx.7251.1.S1_at	CCR6
GgaAfx.7257.1.S1_s_at	RBMS3
GgaAfx.7261.2.S1_s_at	MFHAS1
GgaAfx.7269.1.S1_at	LOC417921
GgaAfx.7275.3.S1_s_at	RPS6KA2
GgaAfx.7278.1.S1_at	SMARCAL1
GgaAfx.7278.2.S1_at	SMARCAL1
GgaAfx.7278.2.S1_s_at	SMARCAL1
GgaAfx.7282.1.S1_at	GPD1L
GgaAfx.7286.1.S1_s_at	PECR
GgaAfx.7307.1.S1_at	CYP27C1
GgaAfx.7309.1.S1_at	NOD1
GgaAfx.7313.1.S1_at	LOC419095
GgaAfx.732.1.S1_at	MEX3D
GgaAfx.7320.1.S1_at	CAPN7
GgaAfx.7330.2.S1_s_at	SCYL2
GgaAfx.7334.1.S1_s_at	PIK3R4
GgaAfx.7345.1.S1_at	ATP2C1
GgaAfx.7345.3.S1_s_at	ATP2C1
GgaAfx.7353.2.S1_s_at	SLC17A8
GgaAfx.7353.6.S1_s_at	SLC17A8
GgaAfx.7355.1.S1_at	SPOP
GgaAfx.736.3.S1_s_at	TYW1
GgaAfx.7375.2.S1_s_at	SLC4A4
GgaAfx.7380.1.S1_s_at	CPNE4
GgaAfx.7391.2.S1_s_at	NPFFR2
GgaAfx.7394.1.S1_at	ADAMTS3
GgaAfx.7395.1.S1_at	PNLDC1
GgaAfx.7403.1.S1_at	SLC5A8
GgaAfx.7403.2.S1_s_at	SLC5A8
GgaAfx.7407.1.S1_s_at	TFCP2L1
GgaAfx.7409.1.S1_at	UTP20
GgaAfx.7415.1.S1_s_at	KIAA0284
GgaAfx.7416.1.S1_at	PLD4
GgaAfx.7420.1.S1_at	PLD4

GgaAfx.7423.1.S1_at	ATG9A	
GgaAfx.7428.2.S1_s_at	ACPP	
GgaAfx.7431.1.S1_at	NUP205	
GgaAfx.7438.1.A1_at	STX11	
GgaAfx.7438.1.S1_at	STX11	
GgaAfx.7445.1.S1_at	CSTF3	
GgaAfx.7458.1.S1_at	CCDC14	
GgaAfx.746.3.S1_at	DNAH9	
GgaAfx.7466.1.A1_at	CCR2	
GgaAfx.7468.1.A1_at	XCR1	
GgaAfx.7468.1.S1_at	XCR1	
GgaAfx.7469.1.S1_at	FYCO1	
GgaAfx.7470.1.S1_at	FYCO1	
GgaAfx.7472.1.A1_at	LOC769813	
GgaAfx.7493.1.S1_s_at	UGT2A3	
GgaAfx.7508.1.S1_at	SGPP1	
GgaAfx.7514.1.S1_at	SPATA5	
GgaAfx.7522.1.S1_at	GUCY2C	
GgaAfx.7522.1.S1_s_at	GUCY2C	
GgaAfx.7538.1.S1_at	KIAA1109	
GgaAfx.7539.1.S1_at	KIAA1109	
GgaAfx.7543.1.S1_at	KIAA1109	
GgaAfx.7556.1.S1_at	CDCP1	
GgaAfx.7559.1.S1_s_at	PRKCH	
GgaAfx.7561.1.S1_at	SLC38A6	
GgaAfx.7563.1.S1_at	ULK4	
GgaAfx.7570.1.S1_s_at		41155
GgaAfx.7575.1.S1_at	MEI1	
GgaAfx.7577.1.S1_at	LOC425756	
GgaAfx.7588.1.S1_at	SLC25A38	
GgaAfx.7589.1.A1_at	CX3CR1	
GgaAfx.7589.1.S1_at	CX3CR1	
GgaAfx.7590.1.S1_at	TNIP3	
GgaAfx.7591.1.S1_at	TOB2	
GgaAfx.7592.1.S1_at	CCR4	
GgaAfx.7593.1.S1_at	TNIP3	
GgaAfx.7600.1.S1_at	LOC429569 /// LOC776078 /// PCI	
GgaAfx.761.1.S1_at	GPR114	
GgaAfx.7611.2.S1_at	CLASP2	
GgaAfx.7629.1.S1_s_at	MKL1	

GgaAffx.7631.1.S1_at	QSER1
GgaAffx.7635.1.S1_s_at	RCJMB04_23o7
GgaAffx.7637.1.S1_at	LARP7
GgaAffx.7642.1.S1_at	DCLK3
GgaAffx.7644.1.S1_at	GRAP2
GgaAffx.7645.1.S1_s_at	LBA1
GgaAffx.7654.1.S1_s_at	LOC424265
GgaAffx.7654.2.S1_s_at	PARP14
GgaAffx.7657.1.A1_at	TIFA
GgaAffx.7657.1.S1_at	TIFA
GgaAffx.7658.1.S1_at	PARP9
GgaAffx.7663.1.S1_at	C4orf16
GgaAffx.7663.2.S1_s_at	C4orf16
GgaAffx.7665.1.S1_at	GPR141
GgaAffx.7666.1.S1_at	LOC422694
GgaAffx.7671.2.S1_at	FAM62C
GgaAffx.7671.3.S1_s_at	FAM62C
GgaAffx.7673.1.S1_at	CCDC73
GgaAffx.7674.1.S1_at	AOAH
GgaAffx.7682.1.S1_at	EN1
GgaAffx.7693.2.S1_at	ELP4
GgaAffx.7704.1.S1_at	HERPUD2
GgaAffx.7717.1.S1_at	RCJMB04_3l24
GgaAffx.7727.2.S1_s_at	BBS9
GgaAffx.7730.2.S1_s_at	ACMSD
GgaAffx.7741.1.S1_s_at	ZRANB3
GgaAffx.7745.3.S1_s_at	PDE1C
GgaAffx.7751.1.S1_at	C14orf104
GgaAffx.7759.1.S1_at	UTRN
GgaAffx.776.2.S1_s_at	WBSCR16
GgaAffx.7763.1.A1_at	LOC770975
GgaAffx.7766.2.S1_s_at	GOLGA4
GgaAffx.7775.1.S1_at	TMEM184B
GgaAffx.7781.1.S1_s_at	L2HGDH
GgaAffx.7782.1.S1_at	SHPRH
GgaAffx.7787.1.S1_at	CDKL1
GgaAffx.7796.1.S1_s_at	SLC39A8
GgaAffx.7799.2.S1_s_at	C6orf103
GgaAffx.7801.1.S1_at	C6orf103
GgaAffx.7802.1.S1_at	MAP4K5

GgaAffx.7805.2.S1_s_at	C7orf10
GgaAffx.7814.1.S1_at	UST
GgaAffx.7819.1.S1_s_at	HECW1
GgaAffx.7819.3.S1_s_at	HECW1
GgaAffx.7822.1.S1_at	TDRD7
GgaAffx.7823.1.S1_s_at	STK17A
GgaAffx.7832.2.S1_s_at	FRMD6
GgaAffx.7834.1.S1_at	NXPH2
GgaAffx.7836.1.S1_at	LOC424300
GgaAffx.7851.2.S1_s_at	NID2
GgaAffx.7854.1.S1_at	GPR137C
GgaAffx.7866.8.S1_s_at	LRP1B
GgaAffx.787.1.S1_s_at	DBR1
GgaAffx.7876.7.S1_at	MTHFD1L
GgaAffx.7879.1.S1_at	LOC418038
GgaAffx.7885.1.S1_at	DDHD1
GgaAffx.7898.1.S1_at	ELFN2
GgaAffx.7901.1.S1_at	C14orf106
GgaAffx.7903.1.S1_s_at	EPC2
GgaAffx.7908.1.S1_at	EIF2B4
GgaAffx.7909.1.S1_at	TMPRSS6
GgaAffx.7916.1.S1_at	RBM43
GgaAffx.7919.2.S1_at	TMPRSS6
GgaAffx.7928.1.S1_s_at	SLC12A7
GgaAffx.7930.2.S1_at	CD1C
GgaAffx.7936.1.S1_at	BRD9
GgaAffx.7939.2.S1_at	SLC9A3
GgaAffx.7949.1.S1_s_at	FMNL2
GgaAffx.7951.1.S1_at	COL15A1
GgaAffx.7957.1.S1_at	NR4A2
GgaAffx.797.1.S1_at	C16orf48
GgaAffx.7983.1.S1_s_at	TLE1
GgaAffx.7989.1.S1_at	
GgaAffx.7992.1.S1_at	SLC28A3
GgaAffx.7993.1.S1_at	AGTPBP1
GgaAffx.800.1.S1_s_at	PLCH2
GgaAffx.8002.1.S1_at	C22orf28
GgaAffx.8007.1.S1_at	FANCC
GgaAffx.8009.1.S1_at	RECK
GgaAffx.801.1.S1_at	TP53INP2

GgaAfx.8014.1.S1_at	RIC8B	
GgaAfx.8019.1.S1_s_at	ATP9B	
GgaAfx.8023.1.S1_s_at	ALDH5A1	
GgaAfx.8023.3.S1_at	ALDH5A1	
GgaAfx.8024.1.S1_at	LOC771624	
GgaAfx.8027.1.S1_at	LOC420821	
GgaAfx.8037.1.S1_s_at	KIF13A	
GgaAfx.8040.1.S1_s_at	ALDH1L2	
GgaAfx.8041.1.S1_at	C12orf45	
GgaAfx.8042.1.S1_at	RANBP9	
GgaAfx.8042.1.S1_s_at	RANBP9	
GgaAfx.8049.3.S1_s_at	CCDC90A	
GgaAfx.8055.1.S1_s_at	RCJMB04_19j20	
GgaAfx.8069.1.S1_s_at	NT5DC3	
GgaAfx.8072.2.S1_s_at	HIVEP1	
GgaAfx.8079.1.S1_at	ADAM12	
GgaAfx.8092.1.S1_s_at	C12orf48	
GgaAfx.8095.1.S1_at	GNPTAB	
GgaAfx.8097.1.S1_at	SYCP3	
GgaAfx.8101.3.S1_at	LOC428479	
GgaAfx.8107.1.S1_s_at	UBR4	
GgaAfx.8109.1.S1_at	PARP12	
GgaAfx.8112.3.S1_s_at	TBXAS1	
GgaAfx.8115.3.S1_at	ATP6V0A4	
GgaAfx.8118.1.S1_s_at	SVOPL	
GgaAfx.8122.1.S1_at	C6orf85	
GgaAfx.8129.1.S1_at	EXOC2	
GgaAfx.8131.1.S1_s_at	LOC418108	
GgaAfx.8143.1.S1_s_at	ADCK2	
GgaAfx.8144.1.S1_at	SERPINB1	
GgaAfx.8148.1.S1_at	SERPINB5	
GgaAfx.8156.1.S1_at	LOC429942	
GgaAfx.8182.2.S1_s_at	FGD4	
GgaAfx.8201.1.S1_s_at		40979
GgaAfx.8202.1.S1_at	RCJMB04_12m23	
GgaAfx.8211.1.S1_s_at	WASH2P	
GgaAfx.8215.1.S1_at	C6orf98	
GgaAfx.8228.8.S1_at	SLC6A13	
GgaAfx.8232.1.S1_s_at	WNK1	
GgaAfx.8244.1.S1_at	ANKRD33B	

GgaAfx.8261.1.S1_at	IL17RA
GgaAfx.8268.1.S1_at	SBK2
GgaAfx.8270.1.S1_at	CCT5
GgaAfx.8273.1.S1_at	LOC425916
GgaAfx.8273.1.S1_x_at	LOC425916
GgaAfx.830.1.S1_at	LOC426958
GgaAfx.8301.1.S1_at	LOC420943
GgaAfx.8311.1.S1_s_at	FIGNL1
GgaAfx.8313.1.S1_s_at	EPS8
GgaAfx.8317.2.S1_s_at	DDC
GgaAfx.8318.1.S1_at	CHD2
GgaAfx.8324.1.S1_s_at	GRB10
GgaAfx.8324.2.S1_at	GRB10
GgaAfx.8327.4.S1_s_at	TRIM27.2
GgaAfx.8335.1.S1_at	PIK3C2G
GgaAfx.8337.1.S1_s_at	PLCZ1
GgaAfx.8339.1.A1_at	CAPZA3
GgaAfx.8349.1.S1_at	C18orf37
GgaAfx.8350.1.S1_at	C9orf5
GgaAfx.8356.1.S1_s_at	MOCOS
GgaAfx.8358.1.S1_s_at	TUBGCP6
GgaAfx.8374.1.S1_s_at	SLCO1A2
GgaAfx.8389.2.S1_s_at	SLC6A19
GgaAfx.8389.7.S1_at	SLC6A19
GgaAfx.8393.2.S1_at	GRAMD4 /// LOC425953
GgaAfx.8393.3.S1_s_at	GRAMD4 /// LOC425953
GgaAfx.8405.1.S1_at	GABBR2
GgaAfx.8409.1.S1_at	CENPE
GgaAfx.8414.2.S1_s_at	C3AR1
GgaAfx.8419.5.S1_s_at	LOC431192
GgaAfx.8421.1.S1_at	LOC427933
GgaAfx.8426.1.S1_s_at	RCJMB04_4o20
GgaAfx.8442.1.S1_at	LOC425987
GgaAfx.845.1.S1_s_at	MAP2K2
GgaAfx.8456.1.S1_at	CEP152
GgaAfx.8463.1.S1_at	DMXL2 /// LOC776238
GgaAfx.8477.2.S1_s_at	SLC5A12
GgaAfx.8480.1.S1_at	GMIP
GgaAfx.8481.1.S1_at	GMIP
GgaAfx.8485.1.S1_at	SECISBP2L

GgaAfx.8485.2.S1_s_at	SECISBP2L
GgaAfx.8487.1.S1_at	LOC425493 /// LOC425497 /// LOC
GgaAfx.8497.1.S1_at	OTUD7B
GgaAfx.851.1.S1_at	PDCL
GgaAfx.8518.1.S1_at	LMBRD2
GgaAfx.8524.2.S1_s_at	LOC430516
GgaAfx.8525.3.S1_s_at	IDE
GgaAfx.8525.8.S1_s_at	IDE
GgaAfx.8530.1.S1_at	LOC772153
GgaAfx.8541.1.S1_at	C9orf98
GgaAfx.8547.1.S1_at	LOC425235 /// LOC429547 /// LOC
GgaAfx.855.1.S1_at	STAG1
GgaAfx.8553.3.S1_at	PBX4
GgaAfx.8554.1.S1_x_at	LOC396003
GgaAfx.8558.1.S1_s_at	SORBS2
GgaAfx.8560.1.S1_at	LOC420992
GgaAfx.8568.1.S1_at	PARD3B
GgaAfx.8571.1.S1_at	PARD3B
GgaAfx.8574.1.S1_at	TXNDC4
GgaAfx.8577.1.S1_s_at	PLEKHO1
GgaAfx.8585.3.S1_s_at	TLR3
GgaAfx.8586.1.S1_s_at	LOC416322
GgaAfx.8586.3.S1_s_at	LOC416322
GgaAfx.8588.1.S1_at	S100A13
GgaAfx.859.1.S1_at	CLIP2
GgaAfx.8591.1.S1_at	CCDC82
GgaAfx.8595.2.S1_s_at	CENPN
GgaAfx.8602.2.S1_s_at	CASC3
GgaAfx.8616.1.S1_x_at	LOC429920 /// LOC429942 /// LOC
GgaAfx.8628.1.S1_at	GZMK
GgaAfx.8631.1.S1_at	CDC20B
GgaAfx.8637.1.S1_at	LOC769442
GgaAfx.8649.1.S1_s_at	F11
GgaAfx.8655.1.S1_s_at	FAT
GgaAfx.866.1.S1_at	CLIP2
GgaAfx.8661.1.S1_at	FRG1
GgaAfx.8667.1.S1_at	C6orf98
GgaAfx.8668.1.S1_at	MYCT1
GgaAfx.8673.1.S1_at	LOC421644
GgaAfx.8681.1.S1_s_at	CNKSR3

GgaAffx.8685.1.S1_s_at	C6orf62
GgaAffx.8691.1.S1_at	PNKD
GgaAffx.8692.1.A1_at	CLDN20
GgaAffx.8698.2.S1_s_at	ZNF236
GgaAffx.8698.3.S1_s_at	ZNF236
GgaAffx.8698.4.S1_s_at	ZNF236
GgaAffx.8699.1.S1_at	CLEC2B /// CLEC2D /// LOC4170
GgaAffx.870.1.S1_s_at	RCJMB04_8m14
GgaAffx.8701.1.S1_s_at	NOX3
GgaAffx.8715.1.S1_s_at	C10orf137
GgaAffx.8716.1.S1_s_at	C10orf137
GgaAffx.8719.1.S1_at	DLC1
GgaAffx.8720.1.S1_at	LOC771735
GgaAffx.8722.1.S1_at	ZDHHC14
GgaAffx.8722.1.S1_s_at	ZDHHC14
GgaAffx.8725.1.S1_s_at	CNDP2
GgaAffx.8727.1.S1_at	C18orf51
GgaAffx.8733.1.S1_at	PCNX
GgaAffx.8736.1.S1_at	LOC770831
GgaAffx.8737.1.S1_at	DLC1
GgaAffx.8738.1.S1_at	PRDM2
GgaAffx.874.1.S1_at	TRSPAP1
GgaAffx.8741.1.S1_at	LONRF1
GgaAffx.8745.1.S1_at	CBLN2
GgaAffx.8755.1.A1_at	ENPP7
GgaAffx.8756.1.S1_at	LOC769836
GgaAffx.8757.1.S1_at	CD226
GgaAffx.876.1.S1_s_at	SNAP29
GgaAffx.8761.1.S1_at	LOC769676
GgaAffx.8763.1.S1_s_at	DOK6
GgaAffx.8765.1.S1_at	GFPT2 /// LOC416372
GgaAffx.8771.1.S1_s_at	GALK2
GgaAffx.8774.8.S1_x_at	LOC429898
GgaAffx.8775.1.S1_s_at	HIVEP2
GgaAffx.8779.1.S1_at	LOC768893
GgaAffx.8785.1.S1_at	IMPA2
GgaAffx.8788.1.S1_at	TNPO3
GgaAffx.879.2.S1_s_at	PTGS1
GgaAffx.8810.1.S1_at	SLC35D3
GgaAffx.882.2.S1_s_at	COX10

GgaAffx.8820.1.S1_at	RNMT
GgaAffx.8821.1.S1_at	MC2R
GgaAffx.8823.2.S1_at	LOC426295 /// LOC770658
GgaAffx.8828.2.S1_at	RCJMB04_18g1
GgaAffx.8837.1.S1_at	GIMAP1
GgaAffx.8840.1.S1_at	LOC421690
GgaAffx.8842.1.S1_s_at	LOC421049
GgaAffx.8846.1.S1_at	LOC421049 /// LOC769555
GgaAffx.8847.1.S1_at	RCJMB04_5f7
GgaAffx.8861.1.S1_at	SCFD2
GgaAffx.8868.2.S1_s_at	FAM38B
GgaAffx.8875.1.S1_at	GNG4
GgaAffx.8878.1.S1_s_at	QDPR
GgaAffx.8887.1.S1_s_at	RCJMB04_35g11 /// VNN1
GgaAffx.8889.1.S1_at	TAAR1
GgaAffx.889.1.S1_at	ZBTB44
GgaAffx.8892.1.S1_at	LOC426330
GgaAffx.8892.1.S1_x_at	LOC426330
GgaAffx.8894.1.S1_at	EPB41L2
GgaAffx.8900.1.S1_at	RCJMB04_14c24
GgaAffx.8901.1.S1_at	LRMP
GgaAffx.8903.1.S1_s_at	ARHGAP18
GgaAffx.8910.1.S1_at	RCJMB04_9e6
GgaAffx.8910.2.S1_s_at	RCJMB04_9e6
GgaAffx.8913.1.S1_at	CASC1
GgaAffx.8921.1.S1_at	RCJMB04_21o24
GgaAffx.8928.1.S1_at	KIAA0802
GgaAffx.8939.1.S1_s_at	LOC422763
GgaAffx.8941.1.S1_at	LOC420252
GgaAffx.896.1.S1_at	LOC419599
GgaAffx.8960.1.S1_at	TXK
GgaAffx.8962.4.S1_at	LOC426333 /// LOC769807
GgaAffx.8962.6.S1_at	LOC425324 /// LOC426333 /// LOC
GgaAffx.8964.1.S1_at	NPAL1
GgaAffx.8965.1.S1_at	LOC769475
GgaAffx.8969.1.S1_at	LOC776064
GgaAffx.8972.1.S1_s_at	RCJMB04_8k11
GgaAffx.8978.2.S1_s_at	TTLL1
GgaAffx.8990.1.S1_at	CAPRIN1
GgaAffx.9002.1.S1_s_at	ATP10D

GgaAffx.9002.3.S1_s_at	ATP10D
GgaAffx.9008.1.S1_at	PARVG
GgaAffx.9008.1.S1_s_at	PARVG
GgaAffx.9013.1.S1_at	GNPDA2
GgaAffx.9014.1.S1_at	EFCAB4B
GgaAffx.9022.1.S1_at	RCJMB04_3j12
GgaAffx.9023.1.S1_at	ATXN10
GgaAffx.9032.4.S1_s_at	ATP8A1
GgaAffx.9032.5.S1_s_at	ATP8A1
GgaAffx.9033.1.S1_s_at	RCJMB04_11o5
GgaAffx.9036.1.S1_at	CCDC4
GgaAffx.9045.1.S1_at	A2M
GgaAffx.9051.1.S1_s_at	APBB2
GgaAffx.9058.2.S1_s_at	RBM47
GgaAffx.9064.1.S1_at	RHOH
GgaAffx.907.1.S1_at	NADK
GgaAffx.9070.1.S1_s_at	NMRAL1
GgaAffx.9083.1.S1_at	UGDH
GgaAffx.9087.2.S1_s_at	ARL2BP
GgaAffx.9093.1.S1_at	ITFG2
GgaAffx.9094.1.S1_s_at	RELL1
GgaAffx.9098.1.S1_at	CENTD1
GgaAffx.9104.2.S1_at	LOC426508 /// LOC776720
GgaAffx.9105.1.S1_at	STIM2
GgaAffx.9109.1.S1_s_at	R3HDM2
GgaAffx.911.1.S1_at	MYBBP1A
GgaAffx.9117.2.S1_s_at	MAN1A2
GgaAffx.9117.5.S1_s_at	MAN1A2
GgaAffx.9120.1.S1_at	CCKAR
GgaAffx.9120.2.S1_s_at	CCKAR
GgaAffx.9121.1.S1_at	APOA5
GgaAffx.9126.1.S1_at	LGALS8
GgaAffx.9126.5.S1_s_at	LGALS8
GgaAffx.9126.6.S1_at	LGALS8
GgaAffx.9126.6.S1_x_at	LGALS8
GgaAffx.9134.1.S1_at	SEPSECS
GgaAffx.9142.1.S1_at	PPARGC1A
GgaAffx.9143.2.S1_at	LOC430964
GgaAffx.9152.2.S1_s_at	CASR
GgaAffx.916.1.S1_at	HS3ST3A1 /// LOC769421

GgaAffx.9160.1.S1_at	NCAPG	
GgaAffx.9166.2.S1_at	DHX32	
GgaAffx.9173.1.A1_at	FAM46C	
GgaAffx.9174.2.S1_at	CHD4 /// LOC426176	
GgaAffx.9174.2.S1_s_at	CHD4 /// LOC426176	
GgaAffx.9175.1.A1_at	GPR92	
GgaAffx.9175.1.S1_at	GPR92	
GgaAffx.9185.1.A1_at	C12orf53	
GgaAffx.9194.1.S1_at	LAG3	
GgaAffx.9196.1.S1_s_at	LOC429336	
GgaAffx.9197.1.S1_at	RCJMB04_7120	
GgaAffx.9212.1.S1_s_at	PROM1	
GgaAffx.9231.1.S1_at	CSPP1	
GgaAffx.9231.2.S1_s_at	CSPP1	
GgaAffx.9238.1.S1_at	LOC426620	
GgaAffx.9241.3.S1_s_at	SH3TC2	
GgaAffx.9243.1.S1_s_at	CNOT6 /// LOC772253	
GgaAffx.9243.3.S1_s_at	CNOT6	
GgaAffx.9256.1.S1_s_at	C1S	
GgaAffx.9257.1.S1_at	AGBL2	
GgaAffx.9262.1.S1_at	MT3	
GgaAffx.9263.1.S1_s_at	SUPT5H	
GgaAffx.9268.1.S1_at	LASS3	
GgaAffx.9268.2.S1_s_at	LASS3	
GgaAffx.927.3.S1_s_at	SPNS2	
GgaAffx.9275.1.S1_at	CHD1	
GgaAffx.9281.1.S1_at	LOC427110	
GgaAffx.9283.1.S1_at	LOC427110	
GgaAffx.9284.1.S1_at	MCTP1	
GgaAffx.9290.2.S1_s_at	CLSTN3	
GgaAffx.9296.3.S1_s_at	ELL2	
GgaAffx.9299.2.S1_at	LOC769230 /// PC1	
GgaAffx.9300.1.S1_at	CAST	
GgaAffx.9312.1.S1_at		40971
GgaAffx.9324.5.S1_s_at	MEGF10	
GgaAffx.9336.1.S1_at	IL31RA	
GgaAffx.9342.1.S1_at	LOC769174	
GgaAffx.9345.1.S1_at	LOC770348	
GgaAffx.9346.1.S1_s_at	DEPDC1B	
GgaAffx.9347.1.S1_at	ELOVL7	

GgaAffx.9350.2.S1_s_at	LOC770670
GgaAffx.9351.1.S1_at	LOC425720
GgaAffx.9361.2.S1_s_at	RNF180
GgaAffx.9364.1.S1_at	SFRS12IP1
GgaAffx.9368.2.S1_at	ADAMTS6
GgaAffx.9368.2.S1_s_at	ADAMTS6
GgaAffx.9392.1.S1_at	LOC427170
GgaAffx.9401.1.S1_at	LOC770116
GgaAffx.9404.1.S1_at	KIAA2018
GgaAffx.9411.1.S1_at	HOMER1
GgaAffx.9412.1.S1_at	LOC427182
GgaAffx.9414.2.S1_s_at	EMILIN2
GgaAffx.9415.1.S1_at	PTPRK
GgaAffx.9416.1.S1_at	TRIM45
GgaAffx.9419.1.S1_at	C6orf190
GgaAffx.9422.1.S1_at	PTGER4
GgaAffx.9422.2.S1_s_at	PTGER4
GgaAffx.9423.1.S1_at	C6orf174
GgaAffx.9426.1.S1_at	PRKAA1
GgaAffx.9429.4.S1_at	LPIN2
GgaAffx.9435.1.S1_at	FBXO4
GgaAffx.9441.2.S1_s_at	LOC776223
GgaAffx.945.1.S1_at	AIRE
GgaAffx.9464.1.S1_at	DCBLD1
GgaAffx.9472.1.S1_at	LOC427201
GgaAffx.9473.1.S1_s_at	POLQ
GgaAffx.9478.1.S1_s_at	LOC427201
GgaAffx.9484.1.S1_at	KPNA5
GgaAffx.9484.1.S1_s_at	KPNA5
GgaAffx.9493.1.S1_s_at	STXBP5L
GgaAffx.9494.1.S1_at	LOC431595
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GgaAffx.9504.1.S1_at	C5orf37
GgaAffx.9506.1.S1_at	SV2C
GgaAffx.9512.2.S1_at	MIB1
GgaAffx.9512.2.S1_s_at	MIB1
GgaAffx.9515.1.S1_at	F2R
GgaAffx.9520.1.S1_at	TMEM128
GgaAffx.9520.1.S1_s_at	TMEM128
GgaAffx.9525.1.S1_at	LYAR

GgaAffx.9530.1.S1_at	SLC22A15
GgaAffx.9542.1.S1_at	EVC
GgaAffx.9549.1.S1_at	CDC2L6
GgaAffx.9557.1.S1_s_at	LAMA3
GgaAffx.9565.2.S1_s_at	PTPRD
GgaAffx.9568.1.S1_s_at	CDC40
GgaAffx.9578.1.S1_s_at	LOC418344
GgaAffx.9580.1.S1_at	MLLT3
GgaAffx.9580.2.S1_s_at	MLLT3
GgaAffx.9581.1.S1_at	ASAH3L
GgaAffx.9582.1.S1_s_at	DENND4C
GgaAffx.9583.1.S1_at	OSBPL1A
GgaAffx.9585.1.S1_s_at	LOC427239 /// RCJMB04_9g9
GgaAffx.9593.1.S1_at	C9orf39
GgaAffx.9597.1.S1_at	LOC431604
GgaAffx.9599.1.S1_at	LOC421081
GgaAffx.9602.1.S1_at	APBA1
GgaAffx.9611.1.S1_at	TAF4B
GgaAffx.9611.2.S1_s_at	TAF4B
GgaAffx.9617.1.A1_at	GPR15
GgaAffx.9617.1.S1_at	GPR15
GgaAffx.9622.1.S1_s_at	ILDR1
GgaAffx.9623.1.S1_at	WDR52
GgaAffx.9628.1.S1_at	GDA
GgaAffx.9629.1.S1_at	DSG2
GgaAffx.9633.1.S1_s_at	B4GALT6
GgaAffx.9635.2.S1_s_at	LOC421093
GgaAffx.9649.1.S1_at	LOC431610
GgaAffx.9650.1.S1_at	LOC431610
GgaAffx.9660.1.S1_at	GNA14
GgaAffx.9661.1.S1_at	RCJMB04_23b22
GgaAffx.9662.1.S1_at	RCJMB04_23b22
GgaAffx.9678.2.S1_at	DTNA
GgaAffx.968.3.S1_s_at	ZAP70
GgaAffx.9694.1.S1_at	LOC421107
GgaAffx.9704.1.S1_at	TMEM157
GgaAffx.9710.2.S1_s_at	LOC769132
GgaAffx.9719.1.S1_at	GIN1
GgaAffx.972.2.S1_s_at	NCAPD3
GgaAffx.9720.1.A1_at	RB1CC1

GgaAffx.973.1.S1_at	PPM1F
GgaAffx.9731.1.S1_s_at	TBC1D23
GgaAffx.9731.3.S1_s_at	TBC1D23
GgaAffx.9740.1.S1_at	ARMC2
GgaAffx.9743.1.S1_s_at	GPR128
GgaAffx.9750.2.S1_s_at	LNPEP
GgaAffx.9753.1.S1_at	LACE1
GgaAffx.9753.2.S1_at	LACE1
GgaAffx.9757.3.S1_s_at	ABI3BP
GgaAffx.9758.1.S1_at	SCML4
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GgaAffx.9763.2.S1_s_at	RCJMB04_24g5
GgaAffx.9767.1.S1_at	LOC776393
GgaAffx.9770.3.S1_s_at	IMPG2
GgaAffx.9771.1.S1_at	SENP7
GgaAffx.9774.1.S1_at	LOC421125
GgaAffx.9782.1.S1_at	AIM1
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GgaAffx.9788.1.S1_at	SH2D1B
GgaAffx.9789.1.S1_at	TRAT1
GgaAffx.9801.1.S1_at	THAP1
GgaAffx.9802.1.S1_at	PRDM1
GgaAffx.9805.1.S1_s_at	TMPRSS7
GgaAffx.9807.1.S1_at	HOOK3
GgaAffx.9812.1.A1_at	CGGBP1
GgaAffx.9813.1.S1_at	LOC430761 /// LOC776461
GgaAffx.9818.5.S1_s_at	PREP
GgaAffx.9822.1.S1_at	HACE1
GgaAffx.9822.2.S1_at	HACE1
GgaAffx.9824.3.S1_s_at	MINA /// RCJMB04_19e21
GgaAffx.9826.1.S1_at	PSD3
GgaAffx.983.1.S1_at	SLC12A1
GgaAffx.9831.1.S1_at	FSD1L
GgaAffx.9837.1.S1_at	CD2
GgaAffx.9848.1.S1_s_at	IGSF3
GgaAffx.9854.2.S1_s_at	CHD7
GgaAffx.9859.1.S1_at	KTELC1
GgaAffx.9870.1.S1_at	GGH
GgaAffx.9875.1.S1_s_at	ARMC1
GgaAffx.9878.1.S1_at	KLHL32

GgaAffx.9878.2.S1_s_at	KLHL32
GgaAffx.988.3.S1_s_at	CEP110
GgaAffx.9882.3.S1_at	ROBO2
GgaAffx.9887.1.S1_s_at	SGK3
GgaAffx.9910.1.S1_s_at	GRIN3A
GgaAffx.9911.1.S1_at	GRIN3A
GgaAffx.9927.1.S1_at	LOC427316
GgaAffx.9928.1.A1_at	ANKRD34B
GgaAffx.9931.3.S1_s_at	KIAA0776
GgaAffx.9935.1.S1_at	SLCO5A1
GgaAffx.9938.1.S1_at	LOC427318
GgaAffx.9956.3.S1_s_at	HGFAC
GgaAffx.9957.1.S1_at	LACTB2
GgaAffx.9957.1.S1_s_at	LACTB2
GgaAffx.9960.1.S1_at	HTT
GgaAffx.998.1.S1_at	VWA1
GgaAffx.9985.1.S1_s_at	ROD1
GgaAffx.9996.1.S1_s_at	SUSD1

The different number of asterisks (*) indicates statistically significant d

nfected and RB1B infected chicken thymus tissues at 7, 14 21 and 28 dpi

Gene_Title	Fold Change (Mean)		
	7dpi	14dpi	21dpi
breast cancer 2, early onset	1.015492	1.002534	0.968901
orthodenticle homeobox 2			2.372843
Fas (TNF receptor superfamily, member 6)	2.093793	2.20886	2.301005
MKL/myocardin-like 2	2.49162	0.890158	1.224265
hypothetical LOC416212	0.854166	2.28451	
zinc finger protein 512B	1.18886	0.730429	1.923972
Solute carrier family 30 (zinc transporter), member 1	1.052566	1.235698	1.530342
hypothetical protein LOC777533	0.829933	0.909606	1.142019
amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycoge	0.643951	1.101461	0.439414
phosphatidylcholine transfer protein	0.851164	1.224057	2.356533
chromogranin B (secretogranin 1)	1.301589		
vacuolar protein sorting 37 homolog B (S. cerevisiae)			
cleavage and polyadenylation specific factor 3, 73kDa		3.888355	
secernin 3	1.716606	1.056959	0.338347
Polymerase (RNA) I polypeptide B, 128kDa	0.954794	0.874226	0.158632
chromosome 20 open reading frame 58	3.648778	1.426398	4.267167
serpin peptidase inhibitor, clade B (ovalbumin), member 2	1.743185	3.425903	0.754401
Serpin peptidase inhibitor, clade B (ovalbumin), member 2	3.926374	8.799125	0.969519
serpin peptidase inhibitor, clade B (ovalbumin), member 2	1.883896	2.08595	1.025533
Down syndrome critical region gene 2	0.69904	1.154573	0.376312
NADPH oxidase organizer 1			0.04199
CD200 receptor 1	2.218277	1.60943	5.400762
Valosin-containing protein	2.26975		0.33704
regulator of chromosome condensation (RCC1) and BTB (P	0.401577	1.654566	0.664966
PHD finger protein 20-like 1	1.154789	1.216548	1.102787
t-complex 11 (mouse)-like 1			
TATA box binding protein	1.10323	1.066117	0.878966
TATA box binding protein	1.086252	0.989085	0.42972
ubiquitin-activating enzyme E1-like 2	0.530471	0.498726	
solute carrier family 16, member 6 (monocarboxylic acid tra	0.858615	1.32397	0.193521
transcription termination factor, RNA polymerase II			0.182243
ubiquitin specific peptidase 54			
Myotubularin related protein 7	1.407102	0.668203	2.812147
KN motif and ankyrin repeat domains 4	1.76584	1.597441	2.941288

kelch domain containing 10	0.401871	0.844281	0.539734
Core-binding factor, runt domain, alpha subunit 2; translocated to, 3			0.457757
WD repeat domain 35	0.314886	2.886201	2.433113
WD repeat domain 35		3.988382	
Similar to KIAA0712 protein	0.684272	0.304815	0.714333
fibulin 5	1.659269	1.751496	3.267515
fibroblast activation protein, alpha			0.794608
intraflagellar transport 80 homolog (Chlamydomonas)	0.948325	0.844586	0.405309
cordon-bleu homolog (mouse)	0.902538	0.856739	0.441963
NLR family, CARD domain containing 5	0.637405	2.100674	0.602615
annexin A8	0.418762	1.133532	0.151639
arginyl aminopeptidase (aminopeptidase B)-like 1	1.10867	0.283937	0.991528
arginyl aminopeptidase (aminopeptidase B)-like 1	0.606356	1.271502	2.023698
SET binding protein 1			40.17753
SET binding protein 1		0.673571	
Fas apoptotic inhibitory molecule	1.096464	0.898013	0.320386
enoyl Coenzyme A hydratase domain containing 1			
transmembrane 4 L six family member 4			0.135321
TBC1 domain family, member 8B (with GRAM domain)	1.560444	1.522277	0.732416
Similar to AHI1 protein	0.433109	1.046426	0.575256
Similar to AHI1 protein	0.560592	1.058862	1.818079
DnaJ (Hsp40) homolog, subfamily C, member 28	0.991982	1.008099	1.619541
chromosome 3 open reading frame 26	1.972657	2.746603	0.331597
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosami		1.350184	0.051293
epiregulin	2.598501	0.598287	
endoplasmic reticulum protein 27 kDa		4.965324	
flotillin 2	0.719506	1.110647	2.731668
neurotensin	6.367449	6.33206	2.836062
RERG/RAS-like	6.405937		
RERG/RAS-like			5.078518
recombination signal binding protein for immunoglobulin ka	1.370788	1.531251	0.374079
recombination signal binding protein for immunoglobulin ka	1.473147	1.09733	0.390764
serine/threonine/tyrosine interacting-like 1	0.510732	1.212054	0.279896
Cytidine deaminase		0.331433	
Splicing factor 3b, subunit 1, 155kDa		4.39717	0.055953
cell adhesion molecule 2	1.860217		0.400049
similar to FLJ12476 protein	0.44564		
Solute carrier family 18 (vesicular monoamine), member 1	1.007566	0.774004	1.758814
additional sex combs like 3 (Drosophila)	0.661744	0.671096	0.23132
TOX high mobility group box family member 3			

chemokine (C-C motif) ligand 17	0.54175	1.464508	6.736172
mannan-binding lectin serine peptidase 2		11.52892	
intestinal zipper protein /// similar to zipper protein	10.4874	1.024669	0.369629
mitogen-activated protein kinase 12	3.086698	1.632821	1.010218
enhancer of zeste homolog 1 (Drosophila)	0.694745		4.534922
alkB, alkylation repair homolog 4 (E. coli)	0.851821	1.117418	1.852513
ATP-binding cassette, sub-family A (ABC1), member 5		1.01345	0.013773
tripartite motif-containing 65	0.698022	0.849294	1.562876
hypothetical LOC418990	0.692607		2.298861
hypothetical LOC418990		0.881968	0.942141
similar to similar to RIKEN cDNA 4933405A16 /// sphingor	2.428624	0.822279	2.105324
fibrinogen alpha chain			
cytochrome P450, family 8, subfamily B	0.855562	1.004852	4.755777
chromodomain protein, Y-like 2		2.444428	
chromosome 2 open reading frame 18	0.7493	1.059132	1.958422
oncostatin M receptor	1.275975		3.309956
JMJD7-PLA2G4B readthrough transcript	6.425811	0.61179	0.156465
N-sulfoglucosamine sulfohydrolase (sulfamidase)	1.107683	1.364547	4.03433
similar to Rps15a protein	1.976773	0.975907	0.38719
GNAS complex locus	0.373411	0.927106	
Dual specificity phosphatase 13			11.50077
syntaxin binding protein 4	2.046823	1.166284	2.144421
Similar to RAB15	2.121759		
similar to Rho-GTPase-activating protein 6 (Rho-type GTPa	1.262441	1.269799	2.04411
developmentally regulated GTP binding protein 1	1.520143	0.820788	1.050772
oleoyl-ACP hydrolase	1.95355	1.261712	0.2474
phenazine biosynthesis-like protein domain containing	0.344112	0.713261	0.90173
retinoblastoma binding protein 4	1.001543	0.988707	0.616194
retinoblastoma binding protein 4	0.642103	1.093504	0.362978
similar to RIKEN cDNA 3110009E18	1.075559	1.809511	0.950064
similar to hypothetical protein MGC17337	0.701679	0.877999	0.627137
carnitine palmitoyltransferase 1A (liver)	0.792444	0.977201	4.520892
ER degradation enhancer, mannosidase alpha-like 3		0.144472	
myosin, heavy chain 7B, cardiac muscle, beta	0.71758	0.40588	2.972533
caveolin 2	2.034206	0.819936	1.93165
GTPase activating protein and VPS9 domains 1	1.252363	0.732274	0.807187
HCLS1 binding protein 3	0.932011	1.286462	5.019706
exportin 5	28.06266	1.271888	1.56787
RNA binding motif protein 14	1.417484	1.220524	1.059801
RNA binding motif protein 14		0.292185	

similar to ENSANGP00000018456	0.4421	1.761196	
Hypothetical LOC422765		0.955666	
abhydrolase domain containing 11			2.808249
RNA binding motif protein 26	0.685877	1.561155	0.380003
similar to lysophospholipase I	0.345993	0.682905	0.060888
transglutaminase 2 (C polypeptide, protein-glutamine-gamm	3.30078	2.031522	9.471435
chromosome 19 open reading frame 12 /// similar to RIKEN	3.488899	1.900745	4.414374
similar to RIKEN cDNA 1600014C10	6.144438	2.694762	4.363682
Katanin p60 (ATPase-containing) subunit A 1	0.517155	1.00116	0.355274
ADP-ribosylation factor-like 11		0.559978	2.024722
CDC14 cell division cycle 14 homolog C (S. cerevisiae)	0.603811	1.449701	0.492357
Small nuclear ribonucleoprotein polypeptide A'	1.012663	1.077094	0.758589
adenomatous polyposis coli	0.382682	0.768748	1.031083
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.240236	0.881992	2.217709
G protein-coupled receptor 123			0.058537
Translocase of inner mitochondrial membrane 10 homolog (c	0.800935	3.595135	1.843172
solute carrier family 30 (zinc transporter), member 9	0.627067	1.102155	0.484735
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polype	0.480795	1.268549	
sorting nexin 16	0.445954	0.74961	1.424609
cylindromatosis (turban tumor syndrome)	1.082668		
MAM domain containing glycosylphosphatidylinositol anchor 1		3.027958	
nucleolar protein 10	1.399362	0.983086	0.389327
Similar to Myelin protein zero-like 1	0.718896	1.115231	3.345933
growth hormone inducible transmembrane protein		0.161858	
CSRP2 binding protein	0.791153	1.133555	0.591028
Similar to golgi-associated microtubule-binding protein HOC	0.772811	1.056399	2.76269
visinin-like 1	0.173887		
nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.871566	1.124498	0.685061
Wolf-Hirschhorn syndrome candidate 1	0.96797	1.715829	0.481998
fibronectin 1			2.00342
atrophin 1		4.48422	
ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D			0.06829
ring finger protein 151	0.455594	2.428633	
peroxisome biogenesis factor 10	0.183242	1.102833	
similar to dedicator of cytokinesis 11	0.930751	0.800349	0.276784
sel-1 suppressor of lin-12-like (C. elegans)	1.541269	1.169201	0.457928
similar to Family with sequence similarity 35, member A	2.889126	0.623095	0.459683
ankyrin repeat and FYVE domain containing 1			
3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1			
solute carrier family 36 (proton/amino acid symporter), mem	0.92439	1.427773	2.762508

teashirt family zinc finger 1			0.050757
teashirt family zinc finger 1	0.624904	0.488342	0.555524
cadherin 17, LI cadherin (liver-intestine)	0.126613		
Hypothetical LOC419647	0.059198		
polymerase (RNA) I polypeptide A, 194kDa	0.399149	1.07155	1.259378
Ellis van Creveld syndrome	0.242806		
engulfment and cell motility 2	0.806867	0.551121	0.496274
family with sequence similarity 102, member A	1.100262		1.074438
family with sequence similarity 102, member A	0.592642		3.609779
choline dehydrogenase			
bone morphogenetic protein receptor, type II (serine/threonine kinase)		1.027208	0.135073
potassium channel tetramerisation domain containing 15	0.788166		2.31049
distal-less homeobox 1			0.126261
cAMP responsive element binding protein-like 2	0.524459	0.801134	0.420241
leucine rich repeat containing 41	0.062636		
Glycoprotein, synaptic 2			
GTPase activating Rap/RanGAP domain-like 1	0.684096	0.9054	0.400315
DAZ associated protein 1 /// interferon regulatory factor 4	1.600714	0.51735	1.942455
Prokineticin 2			
Similar to RNase H, putative	2.283373	0.476826	1.002583
poly(A) binding protein, cytoplasmic 4 (inducible form)	1.551575	0.778246	2.724811
CCR4-NOT transcription complex, subunit 1	0.427564	0.501091	1.239287
CCR4-NOT transcription complex, subunit 1	0.369381	1.5472	0.479893
family with sequence similarity 38, member B			
serum response factor binding protein 1	0.695573	1.188572	1.702659
similar to MGC82198 protein			0.297468
peroxisomal biogenesis factor 7	0.542503	2.018378	1.005069
similar to EM4b			0.057891
hexokinase 2	2.421134	0.954237	1.68021
DEAH (Asp-Glu-Ala-His) box polypeptide 36	1.455708	0.450966	1.955799
calmodulin regulated spectrin-associated protein 1-like 1			0.036719
Obg-like ATPase 1	0.881327	1.05332	0.428972
oxysterol binding protein-like 5	5.765184		
nuclear factor of kappa light polypeptide gene enhancer in B	2.910817	1.184179	1.815423
similar to RIKEN cDNA 2600010E01	0.573095	0.720583	0.324324
BCL2/adenovirus E1B 19kDa interacting protein 2		0.193677	
BCL2/adenovirus E1B 19kDa interacting protein 2	1.295433	1.526752	0.139742
neutral sphingomyelinase (N-SMase) activation associated f	0.81729	1.95716	0.525286
interleukin 17 receptor A			0.239262
MAX gene associated	0.212976		

even-skipped homeobox 2	4.226799	9.368829	1.271715
adenosine monophosphate deaminase (isoform E)	0.155066	1.001183	0.612891
ubiquitin specific peptidase 24	1.278773	0.726068	0.987591
LYR motif containing 1	2.829001	0.781727	
suppressor of cytokine signaling 1	4.417478	1.876167	3.83691
p53 and DNA damage regulated 1	0.784208	1.209775	2.474109
chromosome 7 open reading frame 25	1.887418	0.745609	0.572852
popeye domain containing 2	0.698677	1.128084	1.459254
myotubularin related protein 3			0.499892
Similar to amino acid feature: cytoplasmic domain, aa 1 .. 91	2.171558	0.492982	0.449592
cytidine and dCMP deaminase domain containing 1	0.74732	1.017219	0.392059
kinesin family member 15		2.172108	
signal transducing adaptor molecule (SH3 domain and ITAM	0.82995	1.421652	0.436242
Chromosome 21 open reading frame 7	0.831059	1.119911	1.848359
pygopus homolog 1 (Drosophila)	1.657131	1.91058	0.306523
hect domain and RLD 3	1.262101	0.26371	
cytoplasmic linker associated protein 2	0.940286	0.422369	0.902727
Notch homolog 2 (Drosophila)	0.435593	1.052914	1.301066
DEP domain containing 5	1.054501	1.036062	2.131107
tRNA splicing endonuclease 54 homolog (S. cerevisiae)	0.88361	0.903586	0.400234
leucine rich repeat containing 20	1.116712	2.214728	4.435243
pentatricopeptide repeat domain 2	0.427955	1.046528	1.732949
tumor protein p53 inducible protein 11	0.143405	1.257524	1.689193
Ribosomal protein L23	0.945513	0.765827	0.451326
Similar to OTTHUMP00000065631		7.110085	
Fas (TNF receptor superfamily, member 6)	1.299807	1.937592	3.942662
vacuolar protein sorting 13 homolog B (yeast)	1.213929	0.714361	1.239039
DnaJ (Hsp40) homolog, subfamily A, member 4	0.201379	0.040252	0.557546
similar to hypothetical protein FLJ40773	2.724932	1.909738	
chitinase domain containing 1	0.962475	1.51001	2.288303
similar to aldo-keto reductase	3.380276	1.777032	2.138914
3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.526286	2.002173	0.470421
angiogenic factor with G patch and FHA domains 1	0.629671	0.847576	0.835706
Similar to synaptojanin 2	1.028769		0.088601
GINS complex subunit 1 (Psf1 homolog)			
dedicator of cytokinesis 7		0.045754	
myotubularin related protein 15		0.619172	
galactose mutarotase (aldose 1-epimerase)	0.755256	2.194187	0.930469
cytochrome P450, family 4, subfamily V, polypeptide 2	5.992682	2.617084	2.134352
cytochrome P450, family 4, subfamily V, polypeptide 2	5.37551		

Hypothetical protein LOC769486	0.793975	0.185961	
Hypothetical protein LOC769486			
GTP-ase like	0.951738	0.836849	2.200885
Similar to Ints3 protein			0.223066
receptor accessory protein 3	0.606531	1.891127	5.065551
PPPDE peptidase domain containing 2	0.637869	1.155179	0.250735
RAD52 motif 1	0.651083	0.326328	1.282742
nucleolar protein 8	0.862053	0.18642	0.302484
FAT tumor suppressor homolog 2 (Drosophila)		1.360512	
similar to Ran-binding protein 2 /// similar to RanBP2 (Ran-l	0.23491	1.698091	1.64367
similar to Ran-binding protein 2	0.234588	1.736717	1.393341
Similar to Ran-binding protein 2	0.231373	1.53217	1.4762
NMDA receptor regulated 1-like	0.45596	1.108178	
piggyBac transposable element derived 3	1.373309	1.102498	0.574068
Similar to KIAA1617 protein	1.351559	1.194585	2.038439
basic leucine zipper transcription factor, ATF-like 3	0.940202	1.106509	1.53502
glucosidase, alpha; acid (Pompe disease, glycogen storage di	0.600175	0.237706	1.196836
collagen, type IV, alpha 3 (Goodpasture antigen) binding prc	0.661079	1.728501	2.025911
P450 (cytochrome) oxidoreductase		1.332964	0.415816
methylenetetrahydrofolate dehydrogenase (NADP+ depende	2.132916	0.655057	1.060168
TBC1 domain family, member 24	0.385659		
leucine rich repeat containing 6		2.037552	
ATPase family, AAA domain containing 1	1.368506	1.628513	3.510451
zinc finger and BTB domain containing 38	1.097551	1.051621	2.671594
growth arrest-specific 8	0.706242	1.311245	1.155903
F-box protein 30		1.70199	
F-box protein 30	0.354652	1.337791	1.405091
thyroid hormone receptor interactor 12	0.651631	1.626423	0.265221
coiled-coil domain containing 18	1.322806	0.711407	0.518332
endothelin receptor type B	1.28199	2.279385	1.275329
histamine N-methyltransferase	0.754554	2.907196	
guanine nucleotide binding protein (G protein), gamma 13	1.075775	0.990107	0.450184
Phosphoserine phosphatase	0.651048	1.419209	2.526461
non-SMC element 2, MMS21 homolog (S. cerevisiae)	0.646949	1.251025	0.301259
leucine rich repeat containing 8 family, member A			2.966912
mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	0.727668	1.190046	0.044616
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ai	2.707632	31.84077	
Peptidyl-tRNA hydrolase 2	2.915638	0.571634	
bone morphogenetic protein 4		2.15183	
similar to vitelliform macular dystrophy 2-like 2; bestrophin	0.919495		0.202802

actin, beta-like 2			2.058101
Actin binding LIM protein family, member 2			8.361544
interferon regulatory factor 7	3.762804	1.318138	2.368789
carosine dipeptidase 1 (metallopeptidase M20 family)			
homeodomain interacting protein kinase 2		1.57271	0.114472
TBC1 domain family, member 8 (with GRAM domain)	1.112279	0.944744	0.955662
protein inhibitor of activated STAT, 4	1.651496	0.732961	1.668354
GRB2-related adaptor protein	0.814418	1.044856	1.776706
p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	16.517	0.640527	
Similar to PTD015 protein		0.469295	1.324643
similar to Galanin receptor type 1 (GAL1-R) (GALR1)			
Carbonic anhydrase VB, mitochondrial	0.825641	0.408552	1.190468
Similar to RIKEN cDNA 2810039F03	0.69202	2.530139	1.377197
solute carrier family 22 (organic cation transporter), member	2.283888		
Chromosome 22 open reading frame 13	2.243055	0.887792	0.910143
syntaxin binding protein 6 (amisyn)	8.973401		0.067534
pericentriolar material 1		0.550775	0.243366
cathepsin D	1.32781	1.0965	4.153223
cathepsin D	1.450422	1.157143	1.729374
X-ray repair complementing defective repair in Chinese ham	0.990988	1.296305	0.816238
CUB and zona pellucida-like domains 1	0.41765	2.558599	
IQ motif containing GTPase activating protein 2	0.438658	0.422441	0.740537
adaptor-related protein complex 1, sigma 3 subunit	0.961809	1.232167	0.665302
ubiquitin-like, containing PHD and RING finger domains, 1	0.75315	0.849709	0.510965
fucosidase, alpha-L- 2, plasma	1.777634	0.489757	0.272923
myosin XVI	2.660861	3.402367	
glutathione S-transferase omega 1	0.461271	5.174922	0.745024
Xg blood group		11.61523	
islet cell autoantigen 1, 69kDa	0.958914	0.878078	3.677331
suppression of tumorigenicity 5	1.289976	0.997472	
Potassium voltage-gated channel, Isk-related family, membe	1.074011	0.811996	2.825788
Pregnancy-associated plasma protein A, pappalysin 1			0.363791
pregnancy-associated plasma protein A, pappalysin 1			
DnaJ (Hsp40) homolog, subfamily C, member 19	1.212787	0.354204	0.472033
hypothetical gene supported by BX931420	2.257625	0.721937	0.680016
chromosome 1 open reading frame 80	0.697749	0.913608	1.103371
transmembrane protein 45A			
EF-hand calcium binding domain 1	0.694183	1.517113	1.370928
EF-hand calcium binding domain 1			
chromosome 9 open reading frame 23	0.386	0.977439	0.614717

Chromosome 9 open reading frame 23	0.498402	0.752799	2.828818
UBX domain containing 7	0.530735		2.034973
UBX domain containing 7	1.829856	1.357207	0.69223
transmembrane protein 63A	1.257174	0.960899	
TIA1 cytotoxic granule-associated RNA binding protein-like	56.68898	1.89025	0.966014
piggyBac transposable element derived 5	2.380467		17.17781
Solute carrier family 6, member 15	0.411341	1.534722	1.056323
Glycolipid transfer protein	0.99982	1.172468	2.426773
Polycystic kidney and hepatic disease 1 (autosomal recessive)	0.920186		2.590658
methyltransferase like 8	0.843583	0.757472	2.125617
threonyl-tRNA synthetase-like 2	0.839906	0.671686	0.639197
threonyl-tRNA synthetase-like 2	1.659657	1.112641	1.345514
Similar to gag/env fusion protein			
zinc fingers and homeoboxes 1	2.392912		0.821236
roundabout, axon guidance receptor, homolog 1 (Drosophila)		0.435614	
BCL6 co-repressor			
glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	28.85533		
centrosomal protein 110kDa		0.985418	
coiled-coil domain containing 45	1.13222	1.241908	0.973611
EF-hand domain (C-terminal) containing 2			0.030468
importin 8	0.887117	0.890473	0.376729
protein tyrosine phosphatase, non-receptor type 2	1.17584	1.14052	0.650674
chromosome 20 open reading frame 23	2.586802	1.21169	1.134596
limb bud and heart development homolog (mouse)	0.79847	1.407153	1.385099
Kruppel-like factor 13	2.322257	0.768321	0.52666
Kruppel-like factor 13	1.432042	0.836346	0.722782
Dermatan sulfate epimerase	0.90719	1.06523	0.463008
chromosome 20 open reading frame 42	1.187414		
similar to mKIAA0746 protein	0.782533	1.099596	0.786078
PHD finger protein 6	0.765833	1.666643	0.027012
IQ motif and WD repeats 1 /// similar to MSTP055	2.401088	2.617749	0.377773
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen)	2.298912	1.959825	6.747102
Dephospho-CoA kinase domain containing			
inhibitor of growth family, member 2	0.77031	1.084354	0.456854
zinc finger protein 518B			2.356479
LSM14A, SCD6 homolog A (S. cerevisiae) /// synovial sarcoma	2.489842	0.84632	1.785931
ubiquitin specific peptidase 18	3.231343	2.892901	5.609861
structural maintenance of chromosomes 6	0.560755	1.032208	0.314237
structural maintenance of chromosomes 6	1.849095	1.293049	0.48367
chromosome 3 open reading frame 23	1.575704	1.150971	0.6179

unkempt homolog (Drosophila)-like	0.976385	0.491509	0.854189
Similar to hypothetical protein	2.73115		
isoleucyl-tRNA synthetase	1.060763	3.12943	0.857517
DCN1, defective in cullin neddylation 1, domain containing	1.800946	0.992982	0.215073
zinc finger CCCH-type containing 7A	1.032289		0.49971
cdk inhibitor CIP1 (p21)	1.504687	0.906061	2.778977
Hypothetical protein LOC771662	0.94124		15.21561
cortactin binding protein 2	1.952692	1.736845	
stromal antigen 2	0.797815	0.663209	0.819433
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfe	0.48432	1.19053	1.469865
dedicator of cytokinesis 5			0.239782
methionine adenosyltransferase II, beta	2.485789	0.518986	0.831961
coiled-coil domain containing 117	0.969973	0.849485	2.690901
Pyroglutamyl-peptidase I		0.886261	0.124902
MYST histone acetyltransferase (monocytic leukemia) 3	0.643033	1.518518	0.454417
BTB and CNC homology 1, basic leucine zipper transcriptio	1.372097	2.192202	
Tetraspanin 9		0.200433	
Solute carrier family 22 (organic cation transporter), member	0.398298	0.344872	
retinoic acid receptor, alpha	3.094512	0.846833	2.669592
breast cancer anti-estrogen resistance 3		1.905544	0.729551
exocyst complex component 4			0.419485
Ankyrin repeat domain 46	1.107992	0.87336	0.694668
ankyrin repeat domain 46	2.130319	0.948817	0.446037
acyl-CoA synthetase long-chain family member 4	1.755952	1.612949	0.252561
cingulin-like 1	0.536104	1.140272	3.378293
estrogen-related receptor gamma	0.841048	0.889749	2.116451
Similar to Rasl11c protein	0.248714		
similar to cAMP-specific phosphodiesterase variant PDE4D9			0.092557
similar to RIKEN cDNA 5830418K08 gene	1.005855	0.97056	0.506801
protein phosphatase 1, regulatory (inhibitor) subunit 3D	1.406508	1.275634	0.356127
similar to Ubiquitin specific peptidase 30 /// ubiquitin specifi	0.195174		0.932479
glycosyltransferase 8 domain containing 2	1.244417	0.965212	2.463608
sperm associated antigen 17	0.385227	1.040348	0.453269
sperm associated antigen 17	0.854821	1.65313	1.270091
chemokine (C-C motif) ligand 19	4.675524	3.185068	4.97414
Wolfram syndrome 1 (wolframin)	0.634124	1.287043	1.261303
solute carrier family 7 (cationic amino acid transporter, y+ system), member 7			2.17624
solute carrier family 35, member F3			
CKLF-like MARVEL transmembrane domain containing 6	1.01335	2.574094	2.179797
Peripheral myelin protein 22	1.591968	1.072025	3.022934

G protein-coupled receptor 160	0.900326	1.804136	0.433677
Similar to cystatin B			2.053084
phosphodiesterase 8A	0.138771	2.346446	1.122779
Hypothetical LOC427516		0.756214	1.127112
superoxide dismutase 3, extracellular	1.14335	1.437364	1.723197
Hypothetical protein LOC768709	0.345354	1.052207	2.740882
integrin beta 1 binding protein (melusin) 2	0.551442	1.102258	3.031354
coiled-coil domain containing 76		0.482204	
Coiled-coil domain containing 76		0.266448	0.081715
similar to ovary-specific acidic protein	0.703341	1.056699	0.698438
myotubularin related protein 7			13.7287
similar to 1-aminocyclopropane-1-carboxylate synthase	0.830032	1.07283	0.72613
integrin beta 3 binding protein (beta3-endonexin)	1.014234	1.091061	0.768998
integrin, alpha 9	6.193476		
fibroblast growth factor 7 (keratinocyte growth factor)	1.761233	1.733953	2.008361
fibroblast growth factor 7 (keratinocyte growth factor)	1.761342	2.326337	1.383996
S100 calcium binding protein A10	0.777883	1.230915	1.999046
syntaxin binding protein 1	6.749277	0.829803	
similar to Torsin B precursor (Torsin family 1 member B) (F	2.309454	2.210398	1.41677
vasoactive intestinal peptide receptor 2	1.692526		38.42274
guanine nucleotide binding protein (G protein), alpha inhibit	0.739826	0.961504	0.386268
galactose-3-O-sulfotransferase 2	1.107628	2.885361	1.871599
Cardiolipin synthase 1	0.977461	0.488344	0.47837
angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	1.380661	3.255103	3.320804
angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	1.352577	2.76886	2.232194
additional sex combs like 3 (Drosophila)	2.195827	0.382605	0.846824
chromosome 3 open reading frame 63			
claspin homolog (Xenopus laevis)	0.747702	0.834507	3.166304
tubulin tyrosine ligase-like family, member 7	0.619274		2.33912
uroplakin 3A	1.849836	0.358966	0.937383
peripheral myelin protein 2	0.868935	2.35623	1.977098
alanyl-tRNA synthetase	0.803713	0.995302	2.136248
FERM domain containing 3	0.847306	0.859254	1.665372
dual specificity phosphatase and pro isomerase domain conta	0.926084	1.316718	0.101666
small muscle protein, X-linked	2.000266		2.48489
asparagine-linked glycosylation 13 homolog (S. cerevisiae)	0.488552	1.100969	1.266449
Similar to GPBP-interacting protein 130b	0.548522		4.412458
filamin A interacting protein 1-like	1.650515	0.879852	3.500428
leiomodulin 3 (fetal)	1.893223	1.370134	3.678527
glutamate-rich 1	1.351585	0.976902	0.43026

Mitochondrial trans-2-enoyl-CoA reductase	2.188779	0.906604	2.450846
endoplasmic reticulum aminopeptidase 1	1.108834	0.819731	2.61657
Cyclin J	1.69714	1.138872	0.429718
similar to ADP-ribosylarginine hydrolase (ADP-ribose-L-arg	0.696756	0.896859	1.684988
family with sequence similarity 3, member B	1.839878		20.3824
SEC24 related gene family, member D (<i>S. cerevisiae</i>)	0.121846		
doublecortin-like kinase 1	0.676206	0.574019	0.214626
proenkephalin	0.848305	1.42579	2.131197
thioredoxin domain containing 15		0.200158	
STARD3 N-terminal like	2.32204	0.914079	0.513009
TGF beta-inducible nuclear protein 1	0.358738	0.984442	1.242239
chromosome 10 open reading frame 26	0.569822	1.666321	0.786453
chromosome 9 open reading frame 64	0.421878	0.892318	1.155992
serine/threonine/tyrosine kinase 1	1.801866	1.453226	2.314181
phospholipase A2, group X		2.363654	
Myeloid/lymphoid or mixed-lineage leukemia (trithorax hom	1.974274	0.771785	2.515419
ethanolamine kinase 1	1.380647	0.606694	0.437321
elongation protein 2 homolog (<i>S. cerevisiae</i>)	2.476795	0.594132	0.422045
oral-facial-digital syndrome 1	1.31202	1.15642	0.483404
tropomodulin 3 (ubiquitous)	1.045994	1.100279	0.3027
aldehyde dehydrogenase 7 family, member A1	0.493678	0.804475	1.248691
cystatin A (stefin A)	1.412848	1.144852	7.17522
Sjogren syndrome antigen B (autoantigen La)	1.179491	0.961214	0.540324
ectonucleotide pyrophosphatase/phosphodiesterase 2 (autota	1.020627	0.536668	0.545368
G protein-coupled receptor 23	0.748195	0.936333	0.070951
G protein-coupled receptor 23	1.192759	0.943255	0.036055
peptidylprolyl isomerase C (cyclophilin C)	0.428813	1.101878	0.803051
potassium channel tetramerisation domain containing 20	0.91704	0.585997	0.391605
potassium channel tetramerisation domain containing 20	0.465448	1.213263	0.348919
mitogen-activated protein kinase 8	0.925577	1.023532	0.398327
nucleoporin 153kDa	0.777899	0.679655	0.775039
testis expressed 2	0.235345	0.933276	0.539358
Rieske (Fe-S) domain containing		0.527083	3.345091
hypothetical LOC418095	3.410284	1.233128	1.157958
polymerase (DNA directed) sigma	0.718116	0.883794	
polymerase (DNA directed) sigma	0.657732	2.09696	
ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	0.69511	1.153887	1.98873
BRI3 binding protein	1.133469	1.040799	0.322659
coiled-coil domain containing 18 /// similar to Rab6-interacti	0.986787	0.73956	0.518767
similar to rat ribosomal protein L9 homologue /// ribosomal j	0.893163	0.623136	0.610626

sterile alpha motif and leucine zipper containing kinase AZK	0.764403	1.304013	4.023024
olfactomedin-like 3	2.399209		1.514498
Pyrimidinergic receptor P2Y, G-protein coupled, 6	2.252715	1.215516	1.505559
similar to immunoglobulin-like receptor CHIR-AB1 /// simil	1.266094	0.647181	7.995399
similar to immunoglobulin-like receptor CHIR-AB1 /// simil	1.427316	0.846471	6.26647
discs, large homolog 7 (Drosophila)	0.642726	1.241945	0.76547
adenylate cyclase 7 /// similar to Adenylate cyclase type 7 (A	2.111242	0.806819	2.960471
Similar to interferon, gamma-inducible protein 30	0.915132	1.093498	1.906608
DnaJ (Hsp40) homolog, subfamily C, member 19	1.286463	0.489505	1.453897
Abhydrolase domain containing 11	1.065923	1.062833	5.352221
GDP dissociation inhibitor 2	0.94948	1.394005	0.25381
similar to CG10964-PA	0.622199	1.2718	3.886206
HOP homeobox	1.785877	1.571629	2.330409
HOP homeobox	1.610653	1.686387	2.83929
serine/threonine kinase 16	0.893908	0.855417	2.524477
transmembrane protein 35			
similar to expressed sequence AI847670	1.362328	0.703015	2.1329
FYVE, RhoGEF and PH domain containing 3	1.343008	1.420805	0.282666
signal transducer and activator of transcription 1, 91kDa	3.209194	2.632239	3.095561
signal transducer and activator of transcription 1, 91kDa	2.736524	2.376794	2.129059
signal transducer and activator of transcription 1, 91kDa	5.503363	0.855613	2.019932
tripartite motif-containing 65	1.280014	0.903313	2.040087
hypothetical LOC428877	1.135172	0.806504	0.383288
succinate dehydrogenase complex, subunit D, integral memb	8.414972	2.551236	5.428047
WNT inhibitory factor 1	1.383592	1.662385	0.443686
POT1 protection of telomeres 1 homolog (S. pombe)	1.021889	1.03031	0.763953
Similar to LOC443703 protein	1.790158	2.205097	1.329081
similar to LOC443703 protein	0.618088	0.639909	2.561255
polymerase (DNA directed), beta	0.706845	1.242185	0.510166
cytochrome P450 A 37	2.139578	3.110683	7.007102
hypothetical LOC426615	96.61513		0.768893
Hypothetical LOC426615	332.3778	1.498287	0.106606
Hypothetical LOC426615	132.7918	0.704371	0.157599
PML-RARA regulated adaptor molecule 1	1.162101	0.491275	0.277791
Rac GTPase activating protein 1		12.07892	
succinate receptor 1	2.125628	1.837989	6.183434
dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-C	0.79383	1.315775	2.337673
chromosome 20 open reading frame 42	1.002824	1.478527	2.188559
family with sequence similarity 20, member A			
Phytoceramidase, alkaline	1.152711	0.45284	2.802056

fibrinogen gamma chain	2.603111	1.226294	1.094857
glucosaminyl (N-acetyl) transferase family member 7	1.554967	1.304799	2.359837
G protein-coupled receptor 56	2.113719	2.009747	1.550772
bactericidal/permeability-increasing protein	1.913009	1.438014	5.543205
TNF receptor-associated factor 2	1.121205	0.454942	1.752413
chromatin modifying protein 4C	0.864731	1.210355	0.272256
chromatin modifying protein 4C	1.054328	1.471027	0.533181
basic helix-loop-helix domain containing, class B, 2	1.549631	1.465579	3.38566
signal peptide peptidase-like 2A	1.275062	0.786098	0.653271
Tubulin tyrosine ligase-like family, member 11	0.894189	0.480842	2.402455
TOX high mobility group box family member 3	1.379617	0.504645	3.538494
TOX high mobility group box family member 3	8.933427		1.548462
spastic paraplegia 21, maspardin (autosomal recessive, Mast	0.742787	1.388867	0.344949
synovial sarcoma, X breakpoint 2 interacting protein	0.462734	0.503468	0.022785
DENN/MADD domain containing 4A			0.383412
synaptogyrin 1	1.599492	1.139078	1.056731
Arylacetamide deacetylase-like 2	1.198243	1.487433	2.377984
phosphatase, orphan 2	0.753261	0.56726	1.247263
similar to hypothetical protein MGC33926	0.37268	0.825298	0.424672
alanyl-tRNA synthetase domain containing 1	0.547815	1.059152	2.547482
carbohydrate kinase-like	1.231322	0.723083	2.304914
lymphocyte antigen 6 complex, locus E	2.578044	2.541309	3.04393
hypothetical protein LOC769608 /// hypothetical protein LO	1.265683	1.457452	2.963937
Hypothetical LOC426179	2.044227		4.605055
Hypothetical LOC426179	1.39193	1.193512	2.077976
homeobox B7	0.73515		1.100484
dishevelled associated activator of morphogenesis 2	1.618493		0.945309
trinucleotide repeat containing 6B	2.017981	0.792005	0.59485
Growth arrest and DNA-damage-inducible, gamma	1.602383	1.526743	4.461463
solute carrier family 2 (facilitated glucose transporter), meml	2.547	0.221059	1.4725
similar to chromosome 6 open reading frame 119	1.05882	0.940285	0.473297
tissue factor pathway inhibitor (lipoprotein-associated coagu	0.630673	0.553458	0.189326
tissue factor pathway inhibitor (lipoprotein-associated coagu	0.398972	0.831451	0.288395
Tissue factor pathway inhibitor (lipoprotein-associated coagi	0.266476	0.50301	0.493013
Tissue factor pathway inhibitor (lipoprotein-associated coagi	0.263826	0.537642	0.126641
CDC42 effector protein (Rho GTPase binding) 3	1.002387	0.851022	0.485902
wings apart-like homolog (Drosophila)	1.086159	0.085997	0.561403
telomerase reverse transcriptase	0.723309	0.443466	0.301493
ankyrin repeat domain 13A	0.730946	0.939516	0.3567
ring finger and WD repeat domain 2	0.964793	0.77745	0.798123

transmembrane protein 103	1.262438	1.269966	3.326249
PFTAIRE protein kinase 1			
similar to hairy and enhancer of split 5			
GTP cyclohydrolase I feedback regulator	2.216698	0.901115	0.764536
Norrie disease (pseudoglioma)	4.075041		0.83274
Rac GTPase activating protein 1	0.470101	1.052272	0.176254
transmembrane 6 superfamily member 1	1.104507	1.259889	1.99238
Calpastatin	1.06493	0.8708	3.382153
interleukin 28 receptor, alpha (interferon, lambda receptor)	1.242121	0.700286	0.249901
SH3 domain binding glutamic acid-rich protein	1.34343	0.470622	0.549432
odz, odd Oz/ten-m homolog 4 (Drosophila)	1.314333		0.806105
C1q and tumor necrosis factor related protein 7	1.606763	1.659078	1.158036
N-myristoyltransferase 1	0.980864	1.413441	2.739874
similar to C6orf37	2.44398	1.344919	1.048654
signal peptidase complex subunit 1 homolog (S. cerevisiae)	1.21613	0.311456	1.010943
vaccinia related kinase 1	0.991792	1.118932	0.415139
selenoprotein N, 1	0.417733		
selenoprotein N, 1	0.330003	0.725491	0.620061
jumonji domain containing 2C	0.661864	0.694731	2.351101
chromosome X open reading frame 41	0.847761	2.375506	1.880375
centromere protein Q	0.815466	1.038654	1.126682
Mov10, Moloney leukemia virus 10, homolog (mouse)	2.466371	1.679052	5.067787
protein phosphatase 1, regulatory (inhibitor) subunit 3B	1.418735	2.162528	
glycerol kinase		2.475567	
WW domain containing adaptor with coiled-coil	0.560771	0.412255	1.359185
similar to organic solute transporter beta	0.761985	1.680874	1.887979
ninjurin 1	0.772938	0.731369	0.335834
ninjurin 1	0.96824	0.891165	0.07561
deoxyribonuclease I-like 3	1.802928	2.041627	0.97108
egl nine homolog 3 (C. elegans)			
nicotinate phosphoribosyltransferase domain containing 1	1.484657	0.615951	0.389615
COBL-like 1	1.57251	3.028829	1.086232
Kruppel-like factor 6	1.070009	0.751197	1.535955
Synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	1.390503	1.387949	2.129678
transmembrane protein 16A	2.003951	1.084172	7.329655
biotinidase	0.518117	1.532793	0.256492
Similar to ARMET protein	1.733164	0.37511	0.896593
Similar to ARMET protein			
nth endonuclease III-like 1 (E. coli)			0.064052
Hypothetical protein LOC771706	1.345876	1.510268	1.161488

tetraspanin 6	1.851925	1.4535	2.83416
similar to egg envelope component ZPAX	6.909696		
Rho GTPase activating protein 1	1.082436	0.811377	2.880493
LIM and senescent cell antigen-like domains 1 /// hypothetical	0.61075	1.628876	1.610734
solute carrier family 7, member 6 opposite strand	1.008958	1.015106	0.371186
chromosome 9 open reading frame 19	0.922732	1.424231	0.474395
chromosome 9 open reading frame 19	0.936446	1.194802	0.910139
chromosome 9 open reading frame 19	0.923866	1.222144	0.578877
sideroflexin 5	0.803705	1.328655	1.536514
Similar to SLC12A8 cation-chloride cotransporter	2.12782		
cytosolic iron-sulfur protein assembly 1 homolog (S. cerevis	0.635858	1.181226	1.491951
aspartate beta-hydroxylase	4.515996		
aspartate beta-hydroxylase	1.120175	1.501187	2.066569
high-mobility group nucleosome binding domain 1	1.163027	1.004993	0.429621
Nuclear prelamin A recognition factor	0.913761	1.187176	7.895663
family with sequence similarity 129, member A	1.7077	1.231935	0.504189
solute carrier family 4, sodium bicarbonate cotransporter, member 7		2.948425	1.404548
transmembrane protein 57	0.907022	1.113314	0.945694
COX assembly mitochondrial protein homolog (S. cerevisiae	1.197265	1.737948	1.002842
COX assembly mitochondrial protein homolog (S. cerevisiae	0.964976	1.459786	0.604324
COX assembly mitochondrial protein homolog (S. cerevisiae	0.125114		
membrane protein, palmitoylated 7 (MAGUK p55 subfamily	0.265941	1.275202	0.91081
zinc finger, MYND domain containing 11	0.372195	1.146164	0.590524
wings apart-like homolog (Drosophila)	1.065379	0.830698	0.322225
CD99 molecule-like 2	0.641871	0.822951	1.258717
TROVE domain family, member 2	0.832636	0.973092	0.344733
NOL1/NOP2/Sun domain family, member 3	1.493851	0.994344	1.315819
RNA (guanine-9-) methyltransferase domain containing 2	0.774512	1.290228	0.5728
basic transcription factor 3	0.489273	1.10327	1.494191
carboxypeptidase M	1.079593	1.418109	2.192693
kelch domain containing 8A	1.303895	0.494833	0.030115
protein tyrosine phosphatase, receptor type, C	1.073326	0.81886	0.380654
protein tyrosine phosphatase, receptor type, C	0.946444	0.904971	0.60896
fibronectin leucine rich transmembrane protein 2		0.383628	
asteroid homolog 1 (Drosophila)	2.107695	0.629753	0.858826
adenylate kinase 5		0.446347	1.062582
cannabinoid receptor interacting protein 1	1.974451	2.237128	0.723428
iron-sulfur cluster assembly 2 homolog (S. cerevisiae)		0.307473	2.225401
kinesin light chain 1	1.796108	1.04949	3.736351
kinesin light chain 1	1.229961	0.712001	1.465807

potassium channel, subfamily K, member 5	3.686226	1.200703	3.100918
Immunoglobulin superfamily, member 6	1.811354	0.96036	0.314592
Wolf-Hirschhorn syndrome candidate 1-like 1	4.783567	0.865976	1.068602
chromosome 1 open reading frame 35	1.514675	1.069657	2.222043
Zinc finger, CCHC domain containing 4	2.23166	0.585356	1.420841
mitochondrial ribosomal protein L53	1.420882	1.028374	0.493672
basic leucine zipper nuclear factor 1 (JEM-1)	1.3916	0.750373	0.447362
Trafficking protein particle complex 2-like	1.112711	0.849238	2.367696
regulator of calcineurin 2	3.073297	0.784506	
Glypican 5			0.918724
glutaminyI-tRNA synthase (glutamine-hydrolyzing)-like 1	1.085595	0.757945	0.464306
IKAROS family zinc finger 5 (Pegasus)		3.900208	1.062139
ELMO/CED-12 domain containing 1		21.69209	2.53368
polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	0.506248	1.376098	2.42517
ring finger protein 11	1.052441	1.056272	1.541541
RASD family, member 2	1.407222	1.398491	3.933473
Hypothetical LOC419483	1.090456	1.324453	2.581435
Secretogranin II (chromogranin C)	0.410419		
Secretogranin II (chromogranin C)	2.599512	1.033215	3.295616
calcyphosine-like	0.759425	0.971242	1.106471
THO complex 2	0.970736	0.866007	0.750382
Dicer1, Dcr-1 homolog (Drosophila)	1.787081	0.94939	1.324093
adrenomedullin	3.02217	1.60195	3.61758
chromosome 3 open reading frame 34	1.097156	0.76026	0.830357
glycogenin 1	0.668648	1.152138	2.098987
centrosomal protein 290kDa	0.375942	1.2051	0.581421
family with sequence similarity 118, member B	0.91411	0.824441	0.98649
bystin-like	0.638901	1.090666	2.037614
biphenyl hydrolase-like (serine hydrolase; breast epithelial n	1.302968	1.203549	0.370884
Neuron derived neurotrophic factor	2.775887	1.318972	0.643703
hypothetical LOC416518	0.779183	1.367529	0.562251
mitochondrial ribosomal protein S27	0.586874	1.204902	2.125243
peroxisomal biogenesis factor 16	3.250936	0.716134	0.668757
peroxisomal biogenesis factor 16	0.937796	1.007911	1.904758
hypothetical protein LOC769277	0.398705		1.398883
oxidoreductase NAD-binding domain containing 1	0.952437	1.169917	0.380408
Similar to C/EBP-induced protein	0.952382	0.788222	0.416898
tetraspanin 8	2.032493	2.743929	1.363454
palmdelphin	1.68524	1.642595	1.241231
zinc finger, AN1-type domain 1	1.027745	0.957617	0.435618

homolog of rat pragma of Rnd2	1.552004	0.974617	2.356305
lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltrans		0.40153	
similar to cylindromatosis (turban tumor syndrome); cylindro	6.32585	0.694505	
hypothetical LOC426515	1.247381	0.867114	1.48583
mediator of RNA polymerase II transcription, subunit 31 hor	0.699846	1.074872	0.356985
ceruloplasmin (ferroxidase)		1.258119	0.626419
similar to GLP_608_34837_33056	1.643246	1.029263	0.400805
purinergic receptor P2X, ligand-gated ion channel, 5	3.597729	3.514521	6.54902
phosphatidic acid phosphatase type 2	1.100532	1.011611	0.486937
solute carrier family 25 (mitochondrial carrier; Graves disease autoantig		1.370543	0.410401
Ras-related associated with diabetes	1.05347	0.276072	0.20703
similar to antithrombin 1 B chain			2.067765
fibronectin leucine rich transmembrane protein 3			
similar to vesicle amine transport protein 1; membrane prote	1.027941	2.36398	2.362532
Chromosome 6 open reading frame 57	0.943498	0.809576	0.543123
polymerase (DNA directed), alpha 1	0.298269	0.831403	0.481373
hypothetical gene supported by BX933262; BX935476; CR4	3.193818	1.201504	3.103493
uncoupling protein 3 (mitochondrial, proton carrier)			
CCR4 carbon catabolite repression 4-like (S. cerevisiae)			0.463092
receptor (G protein-coupled) activity modifying protein 2	1.438558	1.425218	3.845367
chromosome 2 open reading frame 34	1.506244	1.900812	
LSM14A, SCD6 homolog A (S. cerevisiae)	0.841939	0.855406	0.727343
olfactomedin 3	1.083149	1.219177	0.487479
Apolipoprotein B mRNA editing enzyme, catalytic polypept	0.690126	2.542624	
SH3 domain binding glutamic acid-rich protein like 2	0.410897	0.499545	
zinc finger protein 207	0.884781	0.98481	0.275988
MYST histone acetyltransferase (monocytic leukemia) 4	1.208759	0.599251	0.488974
hypothetical gene supported by BX930628	0.344909	0.864704	1.078932
protein kinase C and casein kinase substrate in neurons 3	0.651034	0.948769	0.263261
sushi domain containing 3	0.674805	0.418402	1.089272
RNA binding motif protein 26	0.323824	1.495217	0.954667
steroid 5 alpha-reductase 2-like 2	1.340065	0.471023	
tetratricopeptide repeat domain 14	1.708553	0.710126	0.318743
coiled-coil-helix-coiled-coil-helix domain containing 1	0.933507	1.162425	0.46925
zinc finger protein 294	1.044576	0.829799	0.818364
EGF-like-domain, multiple 7	1.99337	1.398509	2.595527
EGF-like-domain, multiple 7	1.927446	1.575732	3.304797
Rap guanine nucleotide exchange factor (GEF) 1	1.94707	0.418939	0.902869
intestinal cell (MAK-like) kinase	1.155128	0.872682	0.093875
heterogeneous nuclear ribonucleoprotein L-like	1.075922	1.605355	0.230313

Heterogeneous nuclear ribonucleoprotein L-like	0.849399	2.113966	
chromosome 12 open reading frame 57	0.6241	0.950436	1.348844
UBX domain containing 1	0.997113	1.016787	0.391802
chromosome X open reading frame 36	0.827823	2.531739	0.930403
family with sequence similarity 62 (C2 domain containing) r	0.808918	0.835462	0.419577
zinc finger E-box binding homeobox 2	2.579612	1.792325	1.9938
chromosome 16 open reading frame 42	0.95873	0.965424	0.653715
DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	0.995621	0.987636	0.684023
dehydrogenase/reductase (SDR family) X-linked	0.844149	1.173592	1.650136
lymphatic vessel endothelial hyaluronan receptor 1	2.26923		5.169535
oncostatin M receptor	1.260106	0.927364	3.265471
oncostatin M receptor		0.084114	
chromosome 7 open reading frame 16	1.734778	2.565699	2.850346
A kinase (PRKA) anchor protein (gravin) 12	35.7444		
craniofacial development protein 1	0.678558	1.128996	1.517942
chromosome 7 open reading frame 36	1.035906	0.707978	0.2519
chromosome 7 open reading frame 36	0.938659	1.295665	2.349138
SPC25, NDC80 kinetochore complex component, homolog (0.84093	0.826001	0.328836
katanin p60 (ATPase-containing) subunit A 1	0.980712	0.817274	0.49873
chromosome 13 open reading frame 7	0.535511	0.341957	
rotatin	0.683666	0.751255	0.575593
GIN5 complex subunit 1 (Psf1 homolog)	1.207054	0.699302	2.485228
Chromosome 4 open reading frame 31			2.685587
Wolf-Hirschhorn syndrome candidate 1		2.003978	
Lysophosphatidic acid receptor 2			
centromere protein K	0.334623	1.165957	0.84629
zinc finger, matrin type 5	0.780745	0.724861	1.42346
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein re	2.335109	1.669074	1.464889
5'-nucleotidase domain containing 1	0.845255	1.188079	0.603709
splicing factor, arginine/serine-rich 17A	1.470466	0.748009	0.50501
calcium/calmodulin-dependent protein kinase IV	0.277881	1.466811	
Kruppel-like factor 3 (basic)	1.436576	0.996267	2.257398
N-acylsphingosine amidohydrolase (acid ceramidase)-like	2.148952	1.464351	0.489983
thymidylate synthetase	0.806934	0.988964	0.267957
syntaxin 18	1.137757	0.623807	1.111845
acyl-CoA synthetase bubblegum family member 1	0.752355	23.32252	1.465687
protein tyrosine phosphatase, receptor type, f polypeptide (P'	0.519619		
protein tyrosine phosphatase, receptor type, f polypeptide (P'	1.228513	0.474607	0.318441
nudix (nucleoside diphosphate linked moiety X)-type motif 7	1.441717	0.574259	0.414316
RWD domain containing 2B	0.794496	1.267196	0.580942

developing brain homeobox 2	0.634401	1.68437	
Wiskott-Aldrich syndrome-like	1.232835	0.718511	0.483937
Wiskott-Aldrich syndrome-like	1.588021	0.762859	0.422163
Hypothetical protein LOC771073	1.022017	2.402548	
KIAA1274	0.92541	0.878314	2.017385
KIAA1274	0.872888	1.698537	0.756512
interleukin-1 receptor-associated kinase 1 binding protein 1	1.041672	1.319461	1.454256
stannin	1.361587	1.242454	1.611609
chick olfactory receptor 4	0.702779	1.155557	1.097382
fatty acid binding protein 3, muscle and heart (mammary-der	1.069179	1.647716	4.615017
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, as	0.727102	0.91433	0.527971
chromosome 15 open reading frame 40	1.271434	1.133096	0.855972
adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. c	0.699953	0.923359	0.472565
suppressor of variegation 4-20 homolog 1 (Drosophila)	11.18386	1.407232	
suppressor of variegation 4-20 homolog 1 (Drosophila)	0.835386	0.830855	0.068355
cytochrome b, ascorbate dependent 3	0.999419	1.038856	2.105524
V-set and transmembrane domain containing 2A			
muscle, skeletal, receptor tyrosine kinase	1.629223		2.626553
pleckstrin homology, Sec7 and coiled-coil domains 3	0.844043	1.137739	0.374902
inositol monophosphatase domain containing 1	1.193752	0.864109	0.441282
chromosome 18 open reading frame 55	1.107197	1.110214	0.645775
hypothetical LOC423054	1.016278	0.806241	0.717075
sorbin and SH3 domain containing 2	5.695766		
apoptosis-inducing factor, mitochondrion-associated, 2	1.86374	1.238971	1.769603
butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma	1.54453	2.023136	5.51872
Toll-interleukin 1 receptor (TIR) domain containing adaptor	1.638514	0.747682	1.593015
cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.119184	1.064435	1.699546
calcitonin-related polypeptide alpha	0.9672	0.403276	1.113857
calcitonin-related polypeptide alpha	2.137164	0.898221	0.916616
MAX interactor 1	1.74052	1.118839	0.975002
adaptor-related protein complex 3, beta 1 subunit	0.49334	1.333628	0.877647
protein-L-isoaspartate (D-aspartate) O-methyltransferase dor	0.807213	0.645804	0.247109
golgi phosphoprotein 3 (coat-protein)	0.80711	1.043032	1.100112
ankyrin repeat domain 16	1.198189	0.591206	2.854092
cytohesin 4	1.343957	0.424009	0.421441
General transcription factor IIE, polypeptide 2, beta 34kDa	2.938989	1.329738	0.357437
Werner syndrome	1.014342	1.096624	0.319184
protein tyrosine phosphatase, receptor type, F	0.390887		
solute carrier family 13 (sodium-dependent citrate transporte	0.815306	1.248684	
Similar to photolyase	1.70636	1.077835	2.864636

chromosome 3 open reading frame 39	1.075519	1.256403	1.070288
adipocyte-specific adhesion molecule	0.48212		
potassium voltage-gated channel, shaker-related subfamily, β	1.214099	0.966875	2.296053
Twist3			2.5938
uveal autoantigen with coiled-coil domains and ankyrin repeat	0.289553		
transmembrane protein 213	2.038494	2.849042	1.751044
zinc finger protein 330	0.906485	0.95478	0.40843
Transcription factor B1, mitochondrial	1.169626	1.249943	0.844867
transcription factor B1, mitochondrial	1.017489	0.821485	0.414763
Transcription factor B1, mitochondrial	2.852271	2.187956	0.764258
similar to MRC OX-2 antigen homolog	1.147548		
adducin 1 (alpha)	1.227936	0.786424	0.513891
Similar to Disabled homolog 2, mitogen-responsive phosphoprotein (Dr	1.812865		2.064998
corticotropin releasing hormone binding protein	0.783587	1.602948	0.043268
Fanconi anemia, complementation group L	1.008239	1.027604	0.471068
similar to adrenodoxin homolog	0.318752		1.280667
carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	0.633686	0.971442	2.094256
transmembrane protein 164	0.905377	0.600291	0.614793
fructose-1,6-bisphosphatase 2			0.134802
proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane	1.497594	0.959616	0.499504
similar to K60 protein			0.491796
ataxin 3	1.730656	0.80354	0.442511
Integrin beta 1 binding protein 1	1.3981	0.574445	0.516783
UBX domain containing 7	1.156807	1.198562	1.29081
similar to germinal center kinase-like kinase	1.482918	1.025566	0.524794
EFR3 homolog A (S. cerevisiae)	1.610069	46.94421	0.352073
kinesin family member 21A	0.966903	2.039287	2.415267
ankyrin repeat domain 10	2.362886	0.887774	0.406612
chromosome 10 open reading frame 57	0.839103	1.139139	0.248544
mitogen-activated protein kinase kinase kinase 7	1.574031	1.014525	0.474084
Splicing factor, arginine/serine-rich 11	0.623956	1.21036	2.221844
chromogranin A (parathyroid secretory protein 1)	1.471461	2.307571	5.218212
exosome component 7	1.290159	1.111202	0.265772
UBX domain containing 2	0.416784	1.05829	1.360542
formin-like 1	1.973507	0.831062	1.790032
LYR motif containing 1	1.146742	1.089137	0.415372
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase			0.058226
relaxin 3	1.580533	0.944189	0.167535
sirtuin (silent mating type information regulation 2 homolog)	0.607337	1.109316	2.645358
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to,			

RNA binding motif protein 17	0.75651	1.132839	0.493035
chromosome 3 open reading frame 37	0.699243	0.963194	0.246082
small nuclear ribonucleoprotein 35kDa (U11/U12)	0.558464	13.79748	0.437157
protein phosphatase 2 (formerly 2A), regulatory subunit B", l	0.77282	1.038365	1.06375
Potassium voltage-gated channel, Isk-related family, membe	0.433489	1.591784	2.160245
sulfatase modifying factor 2	0.540125	0.973323	1.381486
B6.1	3.354931	1.785907	0.372141
B6.1	1.651439	1.050431	0.453222
similar to TSG118.1 protein	1.135431	1.339262	0.836225
vasohibin 2	0.750029	0.950091	0.250241
similar to hypothetical protein DKFZp434F117.1	0.854886	3.026327	1.349935
Tweety homolog 3 (Drosophila)	1.264709	0.764637	0.454742
similar to N-ethylmaleimide-sensitive factor attachment prot	1.299051	0.714413	0.045116
junctional sarcoplasmic reticulum protein 1	1.099513	0.57986	2.861717
tetraspanin 13	1.11957	1.321382	2.475922
GrpE-like 1, mitochondrial (E. coli)	1.571297	2.010144	0.358134
deoxynucleotidyltransferase, terminal, interacting protein 1	0.684916	0.985208	1.134702
chromosome 9 open reading frame 30	1.951672		0.49805
zinc finger protein 451	1.163402	0.883505	0.250526
Nuclear assembly factor 1 homolog (S. cerevisiae)			
Nucleoredoxin-like 2	0.817324		3.79685
COMM domain containing 4	0.554372	1.353517	1.512323
echinoderm microtubule associated protein like 4	1.558443	1.474846	3.691208
zinc finger, DHHC-type containing 20	1.235698	1.10135	1.693529
similar to keratin 10; cytokeratin 10	0.584383	0.985098	0.746786
Plexin domain containing 2	1.160875	2.141556	1.658954
LIM homeobox 8	2.638869	1.75568	1.980017
interleukin 20 receptor, alpha	1.913035	1.402946	0.382948
zinc finger, CCHC domain containing 2	1.984381	1.051753	0.566365
calcineurin-like phosphoesterase domain containing 1	0.969855	1.342966	0.544223
FRAS1 related extracellular matrix 1	0.981934	0.370697	2.183696
Similar to LOC445864 protein	1.566138	0.791444	4.300813
M-phase phosphoprotein 9	9.358178	1.297758	0.631399
Nuclear protein localization 4 homolog (S. cerevisiae)	1.374361	0.915445	1.150603
nudix (nucleoside diphosphate linked moiety X)-type motif 2	0.241894	0.836598	1.551666
vacuolar protein sorting 8 homolog (S. cerevisiae)	0.407027	1.150276	1.017128
inositol polyphosphate-4-phosphatase, type II, 105kDa	10.68108	0.265495	1.308266
transmembrane protein with EGF-like and two follistatin-like	0.619756	1.493172	0.312342
choroideremia-like (Rab escort protein 2)	1.098329	1.44048	0.515865
dermatan sulfate epimerase	1.088135	1.497555	0.299121

chromosome 14 open reading frame 153	1.573719	0.6647	0.198221
chromosome 14 open reading frame 153	0.857793	0.776948	1.30158
chromosome 14 open reading frame 153	1.291942	0.753146	0.689037
regulator of G-protein signalling 7		0.037625	
LATS, large tumor suppressor, homolog 1 (Drosophila)	1.417178	0.787526	0.764646
calcium channel, voltage-dependent, alpha 2/delta subunit 1	2.456872		
leucine rich repeat containing 42	0.772265	0.742343	0.122964
formin binding protein 1-like	1.009089	1.064399	0.700527
Glucocorticoid induced transcript 1	1.959342	1.830403	3.462423
similar to hypothetical protein FLJ23861	2.888128		
Similar to pyridoxal kinase			
par-6 partitioning defective 6 homolog beta (C. elegans)			
Calnexin	1.297868	0.913634	0.508945
Hypothetical LOC430620	0.499619	1.154139	1.378574
Hypothetical LOC415770	0.771206	0.817103	0.194316
chromosome 19 open reading frame 40	1.163569	0.825865	0.255927
programmed cell death 6	1.209588	1.33837	1.279743
similar to TGF-beta type II receptor	1.973105	0.80765	1.59039
serine/threonine kinase 11	1.009422	0.394359	2.737152
Hypothetical LOC419381	1.170812	0.806255	
ras homolog gene family, member J	1.367638	0.969829	2.562015
WD repeat domain 12	0.761027	1.187183	0.455714
transducin-like enhancer of split 4 (E(sp1) homolog, Drosopl	0.845413	1.085992	2.016206
complement component 7	1.337983		10.83317
tripartite motif-containing 23	1.051092	1.472261	1.790472
membrane-spanning 4-domains, subfamily A, member 15	4.308551	1.35516	6.19129
Retinoic acid induced 14	0.44276		
retinoic acid induced 14			0.098919
angiogenic factor with G patch and FHA domains 1	0.888748	0.759275	0.633501
similar to DNA segment, Chr 11, Wayne State University 99	2.145403	0.56681	0.672511
NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (0.332765	0.988404	0.5968
CD99 molecule	1.534288	1.383471	2.346803
host cell factor C2	0.142277		0.652121
host cell factor C2	1.492701	0.910458	0.505141
WD repeat domain 12	0.940247	1.082033	0.454102
Similar to MLL5	1.58367	0.658052	0.349097
solute carrier family 45, member 1		0.059687	1.196212
similar to ARPP-21 protein	1.223505	0.823039	0.046724
Similar to ARPP-21 protein	0.650096	0.768707	0.092582
nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.773789	0.476737	0.381954

UTP18, small subunit (SSU) processome component, homol	1.590462	1.042086	0.353779
WD repeat domain 33	0.800036	0.901879	0.280005
hypothetical LOC424434	0.738011	0.791528	1.481178
six transmembrane epithelial antigen of the prostate 1			
3-phosphoinositide dependent protein kinase-1	0.959452	0.93531	0.498614
taxilin alpha	1.263516	1.274802	2.269982
proprotein convertase subtilisin/kexin type 5		3.247437	
patatin-like phospholipase domain containing 8	0.836599	1.294803	0.999155
signal transducer and activator of transcription 1, 91kDa	8.107924	1.872007	4.426861
regulatory factor X domain containing 2	1.090391	1.59439	0.558426
filamin A interacting protein 1	0.812328		
suppressor of variegation 4-20 homolog 1 (Drosophila)	1.081373	1.402412	1.084479
RAD1 homolog (S. pombe)	0.460133	0.968446	0.948729
Transmembrane protein 131	0.895031	0.933893	0.395488
similar to Intraflagellar transport 74 homolog (Coiled-coil dc	0.637892	0.993561	5.245346
Chromosome 12 open reading frame 43	0.868232	0.383753	0.969817
ras homolog gene family, member G (rho G)	1.137426	0.979403	0.596529
cancer susceptibility candidate 5		1.418971	0.787912
similar to Serine/threonine kinase 3 (STE20 homolog, yeast)	1.353858	0.923187	0.778531
exosome component 2	0.511794	1.157109	0.332379
selenoprotein X, 1			0.137424
G protein-coupled receptor 143	7.84159		
Chromatin modifying protein 5	0.193161		
development and differentiation enhancing factor 1		0.475003	
jumonji domain containing 2B	1.148872	0.896169	0.336036
TNF receptor-associated factor 3 interacting protein 1 /// ubi	1.168122	0.937045	2.467394
similar to delangin isoform A; Nipped-B-like	10.66774	1.066183	0.447917
dynein, light chain, roadblock-type 2	0.780357	1.329462	0.711991
Sodium channel, voltage gated, type VIII, alpha subunit	1.217168	0.392266	0.728743
sodium channel, voltage gated, type VIII, alpha subunit		0.407274	0.416374
ets variant gene 7 (TEL2 oncogene)	1.942659	1.914965	5.422186
HEAT repeat containing 5B	0.725596	1.525536	
OTU domain containing 7A	2.209754		6.290063
copine VIII	1.068795	0.496999	1.354688
SLIT-ROBO Rho GTPase activating protein 1	1.040128	1.053945	3.318611
Opiate receptor-like 1	5.444093		0.965356
LSM11, U7 small nuclear RNA associated	1.871995	0.934301	0.682643
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2,	2.315731	0.372216	1.171619
hypothetical LOC422427		0.088712	
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid recept		1.295953	2.40549

matrix metalloproteinase 3 (stromelysin 1, progelatinase)	0.704262	1.333936	2.447788
kinesin family member 1B		0.98822	0.749117
NUAK family, SNF1-like kinase, 2	1.031147	1.045094	1.201581
protein tyrosine phosphatase, non-receptor type 13 (APO-1/C	3.677011	1.585799	2.996717
TBC1 domain family, member 14	0.445213	1.13362	5.772053
Hypothetical protein LOC769019	1.653587	0.912937	1.380049
chromosome 14 open reading frame 79			3.649565
hyaluronan binding protein 2		0.779541	0.475823
PTC7 protein phosphatase homolog (S. cerevisiae)		0.655496	4.446432
Smg-7 homolog, nonsense mediated mRNA decay factor (C.	10.20564		
PAS domain containing serine/threonine kinase	1.488485	2.163287	0.53295
SPARC related modular calcium binding 2	1.595081	0.889437	0.298009
IQ motif containing K	0.898408	0.795172	
GATS-like protein 1	0.72324	1.042785	0.763063
similar to Hypothetical protein CBG04537	1.669638	0.70766	0.157915
N-acetylglucosamine-1-phosphate transferase, alpha and beta	0.994025	0.691587	0.154677
tektin 1		0.598525	0.174513
tektin 1		0.496673	
UDP-glucose pyrophosphorylase 2	1.521596		
nuclear receptor subfamily 2, group C, member 1	0.63622	1.379235	1.23732
Kv channel interacting protein 1	1.175938	1.645818	0.043293
chromatin modifying protein 1A	0.752315	1.723534	1.620749
ATPase, class VI, type 11B	0.546697	0.467977	0.408932
phospholipase A2 receptor 1, 180kDa	1.82463	1.414062	2.392187
ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	0.442587	1.589023	1.199313
cyclin T2	1.163573	0.592979	0.366854
solute carrier family 35, member B3	0.534374		
NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (0.2049	1.360914	0.500224
rhophilin, Rho GTPase binding protein 2	1.319374	2.95592	1.360128
RAS-like, family 11, member B	0.437693	0.516985	0.307945
chromosome 12 open reading frame 11	2.047097	1.009003	1.158488
NMDA receptor regulated 1-like	1.159949	0.828233	0.519137
solute carrier family 35, member B3	0.417519	0.554164	1.192161
solute carrier family 12 (potassium/chloride transporters), me	2.429609	1.360715	1.346947
Sarcoglycan, epsilon	1.070009	0.739962	2.000086
structural maintenance of chromosomes flexible hinge doma	1.733968	1.15318	2.137888
vascular cell adhesion molecule 1	4.260043	2.514499	2.108773
similar to KIAA0896 protein /// similar to progesterin induced	1.042375	0.896965	0.699294
elongation factor RNA polymerase II	1.374175	0.870489	2.667586
Regulation of nuclear pre-mRNA domain containing 1A	0.482613	0.631684	0.645622

neuropeptides B/W receptor 1	1.385636	0.390353	0.290927
KIAA1826	0.942784	0.8968	0.498737
myosin IF	1.896979	1.35399	4.219529
serologically defined colon cancer antigen 10	0.302492	1.391145	2.190134
CD8a molecule	0.898291	0.706252	0.118094
regulator of G-protein signalling 19		1.223971	0.363047
glucokinase	1.220645	0.644178	9.906418
asparagine-linked glycosylation 10, alpha-1,2-glucosyltransf	0.805895	2.214168	1.241414
lon peptidase 2, peroxisomal	1.434247	1.126449	3.237126
sperm associated antigen 9	1.442008	1.141979	0.488084
ubiquitin-conjugating enzyme E2A (RAD6 homolog)	1.083568	1.10508	0.323463
ubiquitin-conjugating enzyme E2A (RAD6 homolog)	1.143317	1.010935	0.583474
inositol polyphosphate-5-phosphatase, 75kDa	1.745288	1.337924	2.536341
Ankyrin repeat and SOCS box-containing 2	1.452392	2.357091	1.940302
BCL2-antagonist/killer 1	1.283732	1.245776	2.601663
chromosome 14 open reading frame 129	0.753481	0.840223	0.32941
chromosome 21 open reading frame 45	0.785585	1.095946	0.537473
DBF4 homolog (S. cerevisiae)	0.539354	0.876633	0.422414
adaptor-related protein complex 4, epsilon 1 subunit	1.703335	0.986844	0.547021
natural killer-tumor recognition sequence	2.038667	1.11996	1.053719
Collagen, type XXIV, alpha 1		0.646963	0.427476
PTPRF interacting protein, binding protein 1 (liprin beta 1)	0.279328		
chloride intracellular channel 4	1.12708	0.581992	1.499582
Paired related homeobox 2	2.932353	2.210873	4.171929
transmembrane protein 214	0.67229	0.853608	1.8742
RAB2A, member RAS oncogene family	1.01813	0.92822	0.39125
Similar to MAP kinase kinase 6b	0.502881	0.95299	0.345711
leucine-rich PPR-motif containing	14.26784		
activating signal cointegrator 1 complex subunit 3	17.47002	0.490217	2.247327
similar to cisplatin resistance-associated overexpressed prote	0.99192	0.937358	0.230494
chromosome 1 open reading frame 77	0.6953	0.918923	1.572309
DnaJ (Hsp40) homolog, subfamily B, member 4		0.286581	
potassium voltage-gated channel, subfamily H (eag-related),	2.186887	3.527716	1.125297
E74-like factor 1 (ets domain transcription factor)	2.064499	1.084559	0.398835
family with sequence similarity 53, member A	0.998706	0.790061	0.091593
Sorbin and SH3 domain containing 2	1.620702		0.465158
cytochrome b5 reductase 4	0.529123	1.736441	0.429206
cytochrome b5 reductase 4	0.693242	1.343939	0.427283
KIAA1467		0.842083	0.266557
dipeptidyl-peptidase 9	0.656914	1.076533	0.549496

non-SMC condensin II complex, subunit G2	0.593064	2.060834	0.872925
Mevalonate kinase (mevalonic aciduria)	0.404415	0.527651	2.209155
sema domain, immunoglobulin domain (Ig), transmembrane	1.082482	1.407617	2.66782
OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>)	0.650367	0.974586	1.078668
pleckstrin homology-like domain, family B, member 2	2.191874	5.058651	
kinesin family member 20A /// kinesin family member 20A	0.483482	1.946585	1.548153
similar to cytochrome P450 2D20	1.894849	1.642419	2.361188
transmembrane protein 41B	1.319179	1.17972	2.03613
similar to DKFZP434F2021 protein	0.774055	1.655301	0.486915
myxovirus (influenza virus) resistance 1, interferon-inducibl	10.26924	2.391996	4.122604
D-2-hydroxyglutarate dehydrogenase	0.400077	3.567374	0.822915
Glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)		2.15137	
similar to T-cell receptor beta	0.74108	0.814277	0.303643
similar to T-cell receptor beta chain	2.147672	0.415346	0.282274
Transmembrane protein 62	1.328113	0.496443	1.085478
Similar to Bardet-Biedl syndrome 7	1.553497	0.881393	0.874148
Similar to junctophilin type 2	2.518762	1.202311	1.842831
spleen focus forming virus (SFFV) proviral integration onco	3.000375	1.72354	1.645156
Zinc finger CCHC-type and RNA binding motif 1	1.52602	0.625429	1.617464
influenza virus NS1A binding protein	0.698768	1.376949	0.429986
zinc finger protein 512B	0.398903	1.805596	1.000106
uridine-cytidine kinase 1-like 1 /// zinc finger protein 512B	2.396227	1.07751	1.007617
chromosome 14 open reading frame 32	1.107777	0.790973	2.635435
Epithelial stromal interaction 1 (breast)	4.930083	2.12912	2.899373
Similar to interleukin 17 receptor C			14.97826
Prickle homolog 2 (<i>Drosophila</i>)	4.512341	1.110778	2.922391
tectonin beta-propeller repeat containing 1	0.108657		
Mitogen-activated protein kinase kinase kinase 7	0.463683	1.017902	0.908878
similar to LOC402959 protein			2.628918
TIP41, TOR signalling pathway regulator-like (<i>S. cerevisiae</i>)	1.151407		0.109938
phosphotriesterase related	0.883034	1.018917	0.604493
Tubulin, delta 1	3.665586	1.26618	5.979248
splicing factor 3b, subunit 3, 130kDa	1.427488	1.498285	0.427086
Ankyrin 2, neuronal	0.97196	0.821166	2.104384
Hypothetical protein LOC768612	0.296315	0.706968	0.585829
Amyloid beta (A4) precursor protein-binding, family B, men	0.866665	0.723226	1.64194
Microtubule associated serine/threonine kinase 3	2.248463		
Microtubule associated serine/threonine kinase 3	1.834145	1.112211	2.143397
ribosomal protein S6 kinase-like 1	1.20837	0.840348	2.921988
dystrobrevin binding protein 1	1.153098	0.826309	

Regulatory factor X-associated protein	1.323045	1.254221	0.399604
nudix (nucleoside diphosphate linked moiety X)-type motif 4	0.744753	3.968769	1.262131
Cell division cycle 37 homolog (S. cerevisiae)-like 1			
Cell division cycle 37 homolog (S. cerevisiae)-like 1	1.818467	0.836608	
Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha	1.253335	1.206865	2.253898
Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha	1.157472	1.297632	1.771118
tetratricopeptide repeat domain 33	0.639301	1.433599	2.94635
transmembrane protein 63A	1.227748	0.903257	0.788042
Similar to putative RIN zinc finger protein	1.032698	0.544326	0.288224
exonuclease domain containing 1	0.880359	1.137066	0.562016
TatD DNase domain containing 1	0.523004	0.666467	0.45469
KIAA1841	2.35735	0.992008	1.105513
testis derived transcript (3 LIM domains)	1.224243	0.795042	0.294258
Hypothetical LOC421552	2.669884	1.005766	0.705318
target of myb1 (chicken)-like 1	2.321727	1.646101	2.29156
sphingosine-1-phosphate receptor 1	2.158198		
RAB guanine nucleotide exchange factor (GEF) 1	1.346313	0.367959	
sorting nexin 8		0.103466	
beta-2-microglobulin	0.947635	1.168715	1.571804
Beta-2-microglobulin	1.19371	1.844615	3.307076
hypothetical protein LOC768499	1.072801	1.284478	2.099978
thioredoxin domain containing 13	0.605812	0.82306	0.471722
additional sex combs like 3 (Drosophila)	1.042715	0.511571	0.313404
aryl hydrocarbon receptor nuclear translocator-like	1.966161	0.707752	0.955468
ring finger protein, transmembrane 1	1.267161	0.791023	0.733565
oncoprotein induced transcript 3	1.730795	1.225661	2.887144
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polyp	2.481262	1.029618	0.563525
outer dense fiber of sperm tails 2	1.682258	0.598933	0.364308
beta-1,4-N-acetyl-galactosaminyl transferase 3			1.9317
vacuolar protein sorting 26 homolog B (S. pombe)	1.607509	0.86861	2.912128
Integrin beta 1 binding protein 3	1.524414	0.853616	1.083287
chromosome 1 open reading frame 9	0.055253		
Prohibitin	0.995308	0.636994	1.500567
Insulin-like growth factor 2 mRNA binding protein 3	1.199314	1.024144	0.441275
Bardet-Biedl syndrome 12	1.278904	1.007052	0.203313
chromosome 4 open reading frame 18	1.898009		2.198163
hippocampus abundant transcript 1	1.167135	0.852975	0.300562
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6			0.327105
COMM domain containing 9		2.541128	
Similar to pleckstrin homology domain containing, family H	0.793133	3.043039	

Thiosulfate sulfurtransferase (rhodanese)	0.345977		
mesoderm development candidate 2	0.911804	1.327775	2.135895
solute carrier family 4, anion exchanger, member 2 (erythrocyte)	0.993679	0.747909	1.99738
zinc finger, CCHC domain containing 7	0.827618	0.926141	1.062303
GTPase activating Rap/RanGAP domain-like 3	0.965024	1.127903	1.478947
GTPase activating Rap/RanGAP domain-like 3	1.047098	0.636478	0.244717
chromosome 1 open reading frame 41	0.253868	1.276835	0.274495
interferon stimulated exonuclease gene 20kDa-like 2	0.939319	0.929647	1.917976
angiomin like 2	1.424139	1.19621	2.214417
smooth muscle protein phosphatase type 1-binding subunit	0.730528	0.889284	2.185852
smooth muscle protein phosphatase type 1-binding subunit	0.634693	0.851427	0.349434
chondroitin sulfate N-acetylgalactosaminyltransferase 1		0.469663	0.973716
inositol polyphosphate-5-phosphatase F	0.916208	0.955844	0.538775
Hypothetical LOC430303	1.916321		
similar to collagen, type XXVII, alpha 1	1.043312		
Similar to RIKEN cDNA 1110007C09	0.150966		
leucine-rich repeats and calponin homology (CH) domain containing 1	1.11697	0.841571	2.354608
nuclear factor (erythroid-derived 2)-like 1	2.429757	0.735943	0.827937
zinc finger, CCHC domain containing 11	2.088253	11.86587	
cleavage and polyadenylation specific factor 3-like	0.784857	0.76148	0.740895
Oxysterol binding protein-like 2	0.922981	0.940434	1.432034
adducin 3 (gamma)	1.788344	1.677665	2.630287
kinesin family member 5B	0.981042	0.557295	0.446781
sodium channel and clathrin linker 1	1.690716	0.84636	0.372255
R3H domain containing 1	0.832756	0.727919	0.481354
phosphomannomutase 2	0.998017	0.911276	0.948091
RNA binding motif protein 5	1.035439	0.768115	0.456691
ARV1 homolog (S. cerevisiae)	1.246262	0.764211	0.638895
regulator of G-protein signaling 9	0.446706		
radixin	0.861163	1.148506	1.463467
nexilin (F actin binding protein)	1.120787	1.197685	0.514803
nexilin (F actin binding protein)	1.591478	0.405692	0.608835
osteocrin	2.029107		
YTH domain containing 2	0.397379	0.707234	
YTH domain containing 2	0.485759	1.356214	0.468741
suppressor of variegation 3-9 homolog 2 (Drosophila)	1.126257	0.846704	0.445345
heterogeneous nuclear ribonucleoprotein H3 (2H9)	1.229547	0.888475	0.610868
hypothetical protein LOC771290		0.476903	
Rho GTPase activating protein 24	2.867775	1.533099	2.526354
F-box and leucine-rich repeat protein 22	1.0167	0.943899	0.080506

interleukin 15	2.043946	1.440734	1.393769
C2 calcium-dependent domain containing 2	1.313201	1.001526	0.612591
creatine kinase, mitochondrial 1A	1.059083	2.15299	20.39546
similar to ovary-specific acidic protein	0.339305	0.787932	0.085346
centrosomal protein 152kDa	1.34597	0.882212	0.130419
neuregulin 1	4.555925	1.038488	0.557911
Splicing factor, arginine/serine-rich 3	0.663083	1.253825	0.251072
PHD finger protein 11	2.956257	1.561289	1.627752
Hypothetical protein LOC768787	1.345691	1.393027	2.42269
RAB21, member RAS oncogene family	0.845464	1.382657	0.768621
RAB21, member RAS oncogene family	0.649007	0.785962	0.439527
lamin B receptor	1.160836	1.322778	2.119084
solute carrier family 7 (cationic amino acid transporter, y+ sy	0.615649	1.661412	2.058445
Solute carrier family 31 (copper transporters), member 1	1.161539	1.447238	1.839763
Rho-associated, coiled-coil containing protein kinase 1	1.455281	0.937299	0.768845
N-acetylneuraminic acid phosphatase	2.345052	1.268209	0.939959
coiled-coil domain containing 47	0.851656	0.871725	0.612404
aminopeptidase puromycin sensitive	0.868583	1.091792	2.196715
nuclear receptor coactivator 7	2.220336	0.512371	0.186463
fibronectin type III domain containing 3B	32.46056	0.835006	0.696436
RAD52 motif 1	1.679404	0.333531	0.982779
KIAA1946		0.71457	
similar to LOC495836 protein	0.897411	1.018504	0.654861
folliculin-like 4	1.033661	0.7803	0.391612
zinc finger protein 92 homolog (mouse)	1.089435	0.674918	0.249181
zinc finger protein 92 homolog (mouse)	0.931666	0.705785	0.266004
NIMA (never in mitosis gene a)-related kinase 1	1.026823	0.917177	3.189606
CD36 molecule (thrombospondin receptor)	1.463913	1.764458	3.202619
triple functional domain (PTPRF interacting)	1.994899	1.732823	2.484618
family with sequence similarity 20, member A	1.055413	1.00217	2.848433
family with sequence similarity 20, member A	0.893146	1.102081	3.083435
Nuclear protein localization 4 homolog (S. cerevisiae)	0.795652	1.38445	3.335456
similar to TB2 /// receptor accessory protein 5	0.329871	0.398446	3.842939
RAB31, member RAS oncogene family	0.75348	1.364228	1.398861
mucin protein			0.398349
Ribosomal protein L9	0.670387	0.975876	2.06751
poly (ADP-ribose) polymerase family, member 11	1.370352	1.003076	0.682155
Tva receptor	5.52031	1.208756	0.269263
zinc finger, MYND-type containing 8	1.458843	1.130137	0.536397
acyl-Coenzyme A binding domain containing 7	1.349808	1.062948	4.316983

CD38 molecule	2.29983	2.616639	7.514364
utrophin	0.716688	1.54997	0.338025
NKf3 kinase family member /// tetraspanin 3	1.362371	0.978923	0.474667
programmed cell death 6 interacting protein	1.056324	0.574188	0.452192
family with sequence similarity 40, member B	4.4402	0.1478	1.440497
similar to RIKEN cDNA C030048B08		1.090271	
Acyl-CoA synthetase medium-chain family member 5	13.44152		2.232328
Non-SMC element 1 homolog (S. cerevisiae)	2.196021	0.479731	0.432186
purinergic receptor P2X, ligand-gated ion channel, 4	3.0303	0.906655	2.063336
CKLF-like MARVEL transmembrane domain containing 4	0.519903	1.116047	0.297439
endothelin receptor type A	2.008922	1.968185	4.046221
protein tyrosine phosphatase, non-receptor type 3	1.105152	2.710811	2.556939
EF-hand domain family, member A2	0.604902	0.758577	1.67038
Matrix metalloproteinase 23B	0.952054	1.624427	5.303098
Transmembrane protein 14C	0.699833	1.09852	0.378691
glyceraldehyde-3-phosphate dehydrogenase	0.595423	1.1488	1.42226
GULP, engulfment adaptor PTB domain containing 1	1.003157		2.083728
HAUS augmin-like complex, subunit 8	0.435298		
signal recognition particle 54kDa	0.797765	2.925666	0.546634
histone deacetylase 9	1.219292	0.637549	0.230395
heterogeneous nuclear ribonucleoprotein L-like	1.413049	0.599017	0.342361
endothelin receptor B subtype 2		0.147691	
carboxypeptidase A6	2.015069		
glycerol-3-phosphate dehydrogenase 1-like	0.745332	1.073277	0.386972
similar to testis specific leucine rich repeat protein	0.214826	2.405203	
dynein, axonemal, heavy chain 10			1.538211
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosamine 4-epimerase	1.686555	0.86785	0.579985
exportin 4	1.426801	0.816761	0.462307
tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1			0.075616
deformed epidermal autoregulatory factor 1 (Drosophila)	5.328695		
deformed epidermal autoregulatory factor 1 (Drosophila)	1.555046		
family with sequence similarity 73, member B		2.640437	
family with sequence similarity 69, member B	0.893609	1.230211	2.079089
armadillo repeat containing 8		2.148518	0.713058
AT hook containing transcription factor 1 pseudogene	1.557076	0.587918	0.180543
Solute carrier organic anion transporter family, member 5A1	0.142846		
KIAA1841	0.486896	1.944882	0.761829
zinc finger protein 532		25.03421	
Bardet-Biedl syndrome 5	0.87221	0.292237	
Bardet-Biedl syndrome 5			0.39443

coiled-coil domain containing 111	1.179465	1.014419	0.432485
glycosyltransferase 1 domain containing 1	1.019943		4.581154
similar to CG30016-PA	0.381676	1.419822	0.985106
trafficking protein, kinesin binding 1	2.164206	1.40805	2.204471
Xeroderma pigmentosum, complementation group C		1.047445	
transcription factor 7 (T-cell specific, HMG-box)		0.67867	0.476565
PWWP domain containing 2A	1.154319	0.871018	0.531307
paired-like homeodomain 1	1.500834	2.656543	
Hypothetical protein LOC769056	2.103241	1.136378	
CD93 molecule	1.099821	0.888416	3.187136
TBC1 domain family, member 9 (with GRAM domain)			8.336872
cystathionine-beta-synthase	0.984206	0.433693	
similar to glycoprotein		3.936462	
Gal 8			
Gal 8	1.223037	1.271217	2.442679
chromosome 13 open reading frame 24	0.612256	1.565983	0.67804
RNA binding motif protein 46	1.165417	2.056679	0.097889
lipoma HMGIC fusion partner-like 5	0.37051	1.592436	4.412549
S phase cyclin A-associated protein in the ER			0.310225
similar to mitochondrial fission regulator 1 /// mitochondrial fission regu		2.104493	
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F			
transcription factor 7-like 1 (T-cell specific, HMG-box)			
spastin	1.292519	0.581217	0.370916
DENN/MADD domain containing 4C	1.580515	0.395959	0.33537
Latent transforming growth factor beta binding protein 3			
sodium channel, voltage gated, type VIII, alpha subunit			0.450978
SAP30-like	1.206379		5.523506
Solute carrier family 16, member 12 (monocarboxylic acid tr	1.086749	3.194597	0.977495
thyroid hormone responsive (SPOT14 homolog, rat)	1.367697	1.327044	3.99248
hypothetical gene supported by CR353428			
multiple coagulation factor deficiency 2	1.671427	1.502171	0.475495
lin-28 homolog B (C. elegans)	0.444985	0.786293	0.62715
similar to immune costimulatory protein B7-H4	0.633243	1.083491	0.08541
similar to FERM, RhoGEF, and pleckstrin domain protein 1	1.363062		0.28898
DEP domain containing 6	1.132565	0.943223	4.233838
myotubularin related protein 12	0.921807	0.783151	
CD72 molecule	2.037429	1.801361	1.045068
7-dehydrocholesterol reductase		0.59453	0.220421
AHNAK nucleoprotein 2		0.63889	2.095394
activating transcription factor 7 interacting protein	1.106547	1.037323	0.704677

similar to delangin isoform A; Nipped-B-like	1.70768	0.890919	0.68517
hypothetical protein LOC771290	0.117501		
Nucleolar protein with MIF4G domain 1	0.730133	1.056673	0.474387
Cdk5 and Abl enzyme substrate 2	0.569707	0.695455	
Nance-Horan syndrome (congenital cataracts and dental anomalies)	1.656165	0.816491	0.078706
Development and differentiation enhancing factor 1	1.214459	0.669182	0.334355
tensin 3			0.274867
tensin 3	0.639407	1.255818	0.508625
Hypothetical protein LOC769469	1.137697	1.60148	3.219409
contactin associated protein-like 5	0.324793	0.591942	0.630493
Ankyrin repeat domain 34A	0.147572		
protein tyrosine phosphatase, receptor type, O	5.857042	1.360406	
Hypothetical LOC425403	2.163285	1.144413	1.690212
MLF1 interacting protein	0.368738	1.135026	0.481878
MLF1 interacting protein	0.859336	0.969879	0.759156
Notch homolog 2 (Drosophila)			
Low density lipoprotein receptor class A domain containing	0.561763	0.376437	0.483026
Fanconi anemia, complementation group B	0.849062	1.718559	1.593857
microtubule-associated protein 1A	9.813943		
hypothetical gene supported by CR352862	1.683043	1.274781	1.535463
phosphodiesterase 5A, cGMP-specific	23.01367		0.345373
secretin	0.663747	3.022152	4.235093
dual specificity phosphatase 22		0.699716	4.068555
RAS p21 protein activator (GTPase activating protein) 1	0.759899	0.858867	3.177951
melanocortin 5 receptor		1.153757	3.426947
transforming growth factor, beta receptor I (activin A receptor)	1.242219	0.787823	0.359868
GRB2-associated binding protein 2	0.501674		
myotubularin related protein 6	0.627782	2.746619	0.876392
similar to KIAA0294		1.582721	
fibroblast growth factor receptor 2	1.432092		8.890774
chromosome 13 open reading frame 15	1.617617	1.730833	0.762319
golgin B1, golgi integral membrane protein	0.313328		
hypothetical protein LOC771050 /// hypothetical protein LOC771050	0.976061	1.428205	2.158596
renal tumor antigen	3.124738		
pyridine nucleotide-disulphide oxidoreductase domain 1	0.858573	1.308578	0.404756
Guanine nucleotide binding protein (G protein), alpha z polypeptide	0.866038	0.96254	0.391644
guanine nucleotide binding protein (G protein), alpha z polypeptide		0.44954	
urotensin 2	0.606565	0.800722	1.502815
adenylate cyclase 5		0.282361	1.440866
phosphodiesterase 7B	1.656824	1.746252	2.14529

cytochrome P450, family 2, subfamily R, polypeptide 1	0.779153	0.639295	0.812269
Sprouty-related, EVH1 domain containing 2 /// Trinucleotide	2.031867	1.336419	1.814876
General transcription factor IIIC, polypeptide 4, 90kDa		2.340397	
ectonucleoside triphosphate diphosphohydrolase 8	1.313183	0.877531	1.523924
intraflagellar transport 122 homolog (Chlamydomonas)	0.593269		0.287107
dual-specificity tyrosine-(Y)-phosphorylation regulated kina	1.299765	0.939399	0.238652
formin binding protein 4	0.65152	0.832773	0.923568
hypothetical LOC426829 /// hypothetical protein LOC76998	0.784489	0.483337	0.996314
RNA binding motif protein 12		2.006184	
Similar to Chromosome 4 open reading frame 32	0.945265	0.86597	0.216444
LTV1 homolog (S. cerevisiae)	0.708664	1.097843	0.697124
Phosphatase and tensin homolog	1.03952	1.154344	0.887758
Solute carrier family 41, member 1	1.168227	0.927398	0.493487
cysteine and histidine-rich domain (CHORD)-containing 1	1.083727	0.783643	0.378026
lipase A, lysosomal acid, cholesterol esterase (Wolman disea	1.793903	1.572003	2.665036
Hypothetical protein LOC772054		0.668391	
Hypothetical protein LOC776315	0.632062	0.775479	0.399288
mitogen-activated protein kinase kinase 1	1.596594	1.340869	0.214172
H6 family homeobox 1			2.084972
ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	2.139907	1.108842	0.405824
solute carrier family 1 (high affinity aspartate/glutamate tran	1.285212	1.235718	1.725092
Pleckstrin homology domain containing, family B (evectins)	0.360287	0.799473	0.865338
ADP-ribosylation factor-like 8B	0.754787	0.951447	1.098452
Chaperonin containing TCP1, subunit 8 (theta)	0.705797	0.654215	0.725721
hypothetical protein LOC407087	0.41859	0.86455	0.337027
GTP binding protein overexpressed in skeletal muscle	3.090469	1.383631	0.83375
GTP binding protein overexpressed in skeletal muscle	2.080132	1.262901	3.360798
C-type lectin domain family 2, member D	6.457761		
similar to butyrophilin, subfamily 2, member A1 isoform 1 p	3.829465	1.640773	2.231802
SET domain containing (lysine methyltransferase) 8	0.929708	0.114254	
Protocadherin 17	0.366829		4.578121
acyl-CoA synthetase short-chain family member 3			0.10461
similar to newborn ovary homeodomain protein		0.27733	
5'-nucleotidase, cytosolic IB	2.124669	1.739128	1.98524
nuclear receptor subfamily 2, group C, member 1	0.924096	2.715306	0.691864
Similar to alpha 1 type XXIV collagen	0.557758	1.790529	0.975237
Collagen, type XXIV, alpha 1 /// Similar to alpha 1 type XXI	2.564401	1.415988	0.616665
DnaJ (Hsp40) homolog, subfamily B, member 5	0.334235	1.040013	0.804601
hect domain and RLD 2		2.499635	
similar to KIAA2026 protein	1.680813	0.618569	0.067827

ubiquitin protein ligase E3 component n-recognin 4	1.432991	0.865237	0.275659
fucokinase	0.813999	1.049896	0.767844
LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.740826	0.860283	0.364974
protein kinase C, alpha	0.770897	1.070655	0.409289
HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	1.568919	0.673701	0.600861
Hermansky-Pudlak syndrome 5	3.257737	1.37113	2.02389
Protein phosphatase 1J (PP2C domain containing)	2.194863	1.449668	1.539543
cubilin (intrinsic factor-cobalamin receptor)	0.735531	1.409269	4.065567
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase	0.478875	11.54322	
FYVE, RhoGEF and PH domain containing 6	0.340488	0.630891	0.796735
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase	0.608166	1.330455	0.45139
hect domain and RLD 4	1.169585	169.3747	1.278899
deltex 3-like (Drosophila)	3.491229	0.951457	0.973898
DEAD (Asp-Glu-Ala-Asp) box polypeptide 51			0.476927
dpy-19-like 1 (C. elegans)	1.062426	0.145182	
ubiquitin specific peptidase 16	1.505769	0.869898	0.49917
pro-melanin-concentrating hormone	1.396008		
tectonin beta-propeller repeat containing 1			
ADAMTS-like 1	0.781019	1.053643	0.540813
tuftelin 1	1.143051	0.588149	
Actin, beta-like 2		0.128779	
Actin, beta-like 2		1.223647	2.352701
Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.954836	0.976459	3.469525
similar to armadillo repeat containing 2	1.718227	2.00705	0.286651
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide	0.892122	0.896282	0.242265
hypothetical gene supported by CR387047	0.51179	0.44431	2.442257
jun oncogene	1.578506	1.183791	1.980235
dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic	0.903954	1.002558	0.99465
hypothetical gene supported by CR386914	1.124929	1.919849	2.502574
1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophospholipase)	0.710417	1.144387	0.608012
pleiotrophin	0.721532	2.02204	1.372548
pleiotrophin			
bromodomain and WD repeat domain containing 2	5.468165		2.507758
Karyopherin alpha 3 (importin alpha 4)	0.921806	0.730017	0.371073
breast cancer 1, early onset	0.865944	1.007467	0.452007
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma subunit	1.005318	0.753495	1.116467
Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	1.632387	1.282555	2.214541
vacuolar protein sorting 13 homolog B (yeast)	1.143605	0.658902	0.367294
eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	1.690732	1.022322	0.848334
SMAD specific E3 ubiquitin protein ligase 2	1.413462	0.451435	0.505191

coiled-coil domain containing 88A	1.220616	1.076759	0.613231
coiled-coil domain containing 88A	1.217175	1.490894	0.444469
G protein-coupled receptor 1	1.251216	1.495294	3.88877
Similar to nucleophosmin/nucleoplasmin, 2	19.6195		
KH domain containing, RNA binding, signal transduction associated 2		14.04181	
ras responsive element binding protein 1	1.701412	0.878938	0.362979
Oxytocin receptor	0.48009		
kinesin family member 14		1.170713	0.964058
kinesin family member 14	0.665048	1.037118	0.747741
interleukin 23 receptor	1.532561	0.509287	0.611652
polycomb group ring finger 5	2.886586	1.119747	
sodium channel and clathrin linker 1	2.564267	1.227488	
N-acetylated alpha-linked acidic dipeptidase-like 2	0.839128	1.753275	1.479247
family with sequence similarity 123B		8.768123	21.39697
Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2			0.132041
Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	0.690702	1.182663	1.45915
leucine rich repeat containing 48	0.370937	1.158423	0.169817
Abhydrolase domain containing 7	0.773432	1.004211	0.418176
Abhydrolase domain containing 7	0.424888	0.602633	0.051162
chromosome 21 open reading frame 70	1.081082	1.048459	0.741231
Alanine-glyoxylate aminotransferase 2-like 1	0.623219	0.675048	0.259814
glutaredoxin 3	1.090504	1.146668	0.690497
KIAA1109		2.549077	
Glycerophosphodiester phosphodiesterase 1	0.819358	0.941329	0.453231
peroxidase homolog (Drosophila)	2.205363	1.232805	0.050704
fms-related tyrosine kinase 1 (vascular endothelial growth factor receptor)	2.77068	1.190479	1.649728
zinc finger protein 509	2.23656	0.997295	0.317293
KIAA1333	1.11345	0.861558	0.42287
Acid phosphatase-like 2	2.748384	1.297578	0.587148
Tuftelin 1	0.890557	1.075933	1.741183
interleukin 6 (interferon, beta 2)	2.642528		
Signaling lymphocytic activation molecule family member 1	1.344296	0.823403	0.40792
Similar to bactericidal permeability-increasing protein	1.132261		10.91105
LIM and senescent cell antigen-like domains 1 /// hypothetical	0.659844	2.180943	1.123489
MAS-related GPR, member H	3.064102	1.243178	5.518506
ISL LIM homeobox 1	1.203381	0.907499	1.946576
ISL LIM homeobox 1	0.875215	0.958787	1.09959
KIAA1109	0.40353		
hypothetical gene supported by CR385901			0.468239
Solute carrier family 23 (nucleobase transporters), member 3		0.432664	

teashirt family zinc finger 2	0.976184	0.783813	2.313563
phosphoserine aminotransferase 1	1.2772	0.606029	0.786783
spectrin repeat containing, nuclear envelope 2	1.155956	0.853273	1.278112
MYST histone acetyltransferase (monocytic leukemia) 3	0.550611	0.632759	1.527525
family with sequence similarity 38, member B	1.291982	1.591462	2.105157
Hypothetical protein LOC769469	1.558274	1.131413	5.434678
similar to hypothetical protein	0.743418		
prostaglandin-D synthase	1.171568	1.1269	1.327021
titin			
Myosin VI		2.550199	
chromosome 7 open reading frame 46	0.526361	1.259284	0.163599
Contactin 4	2.433532	1.868787	0.787147
Protein phosphatase 1, regulatory (inhibitor) subunit 10	1.867185		
Transcription factor 25 (basic helix-loop-helix)	0.94437	0.868352	2.078953
mitofusin 2	1.108513	2.554567	0.070135
chromosome 17 open reading frame 85	1.111707	0.937538	0.810457
Chromosome 16 open reading frame 14	0.20095	0.831841	3.417528
Chromosome 21 open reading frame 70	0.551242	1.054524	3.097688
intraflagellar transport 88 homolog (Chlamydomonas)	0.647312	0.89056	0.584087
PHD finger protein 15	0.799373	0.770781	0.194191
jumonji domain containing 1C	2.32071	1.158278	0.536784
T-complex 11 (mouse)-like 1	1.543442	0.84108	1.190803
Solute carrier family 6 (neurotransmitter transporter, taurine)	3.393465	1.224126	0.790594
polycystic kidney and hepatic disease 1 (autosomal recessive)	2.137149		
methyltransferase like 7A	1.12793	1.684714	4.18028
V-myc myelocytomatosis viral related oncogene, neuroblast	0.886188	0.937609	0.273417
ELKS/RAB6-interacting/CAST family member 1	1.362729	0.260872	0.432577
palladin, cytoskeletal associated protein			
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide			0.450195
ubiquitin associated protein 2	6.395588	1.521185	0.689363
splicing factor, arginine/serine-rich 4		0.165972	1.955665
family with sequence similarity 134, member C	0.379267	1.531828	0.061942
family with sequence similarity 134, member C	1.246092	0.899	0.38424
StAR-related lipid transfer (START) domain containing 4	0.202988	0.54664	1.062324
RAP2C, member of RAS oncogene family	0.869632	1.760451	0.648471
Ribosomal protein SA	1.768913	0.513179	2.218013
guanine nucleotide binding protein (G protein), gamma 11	0.888293	2.351505	2.156968
microtubule-associated protein tau	0.698028	0.864238	2.389835
spastic paraplegia 3A (autosomal dominant)			0.111961
Rac GTPase activating protein 1	0.79272	1.139375	0.485293

Collagen, type IV, alpha 3 (Goodpasture antigen) binding pr	0.172106		
Chromosome 14 open reading frame 121	1.216294	1.1158	1.967089
hypothetical LOC425659	0.477536	1.309358	0.738845
transmembrane protein 175	0.681338	0.962171	2.642578
Non-SMC condensin II complex, subunit H2	0.353152	1.397476	0.558247
centrosomal protein 55kDa	1.163593	0.809616	0.424202
UDP-glucose ceramide glucosyltransferase	0.792938	1.095929	2.702426
vacuolar protein sorting 54 homolog (S. cerevisiae)	0.964736	0.79067	0.727333
adaptor-related protein complex 2, mu 1 subunit	0.611611	1.210542	0.384645
hypothetical protein LOC768772	1.179599	1.215711	2.015903
solute carrier family 24 (sodium/potassium/calcium exchang	1.590332	0.867799	3.738529
Enah/Vasp-like	0.769331	1.091886	0.115893
Fas apoptotic inhibitory molecule 2	0.396253		
signal-induced proliferation-associated 1 like 2	2.815393	2.735905	4.466204
WD repeats and SOF1 domain containing	1.323567	2.343607	0.706621
hypothetical LOC420734	1.146543		
kinesin family member 27	2.443153		
paired related homeobox 1	1.923623	1.817585	3.767112
Paired related homeobox 1	2.87429	1.462008	6.449259
DPH3, KTI11 homolog (S. cerevisiae)	1.03027	0.670269	0.461013
hypothetical LOC416390			
lectin, galactoside-binding, soluble, 3	1.842208	1.263343	4.835852
baculoviral IAP repeat-containing 5 (survivin)	0.492669	1.409104	0.401077
t-complex 11 homolog (mouse)		0.195151	4.847409
kelch-like 10 (Drosophila)	1.774668	1.825995	1.515244
similar to hypothetical protein MGC33370	1.468382	0.698758	2.250039
transmembrane protease, serine 2	2.65343	1.945855	2.756421
forkhead box N4	0.339367		
solute carrier family 24 (sodium/potassium/calcium exchang	2.089893	1.589893	1.46815
similar to NAD(P) dependent steroid dehydrogenase-like	3.7629	0.757685	0.507824
hypothetical LOC426161		0.058169	
Hypothetical LOC426985	0.834875	0.225227	
hypothetical protein LOC772356	4.102151	1.233356	2.074012
apoptosis inhibitor 5 /// pyruvate dehydrogenase complex, cc	2.204434	1.288967	0.681147
runt-related transcription factor 2	1.695834	3.402427	17.47121
Basic helix-loop-helix domain containing, class B, 2	2.577177	1.48248	6.380785
nuclear receptor subfamily 2, group C, member 2		0.802784	2.143646
nuclear receptor subfamily 2, group C, member 2	1.001845	0.762079	0.559439
nuclear receptor subfamily 2, group C, member 2	1.659772	0.882073	0.399824
transmembrane protein 184B	0.797995	0.792995	2.129272

Serine/threonine kinase 24 (STE20 homolog, yeast)	0.812976	0.962302	1.944381
THAP domain containing 7	1.23222	0.869345	1.119424
RCSD domain containing 1	3.896322	1.550408	0.914042
4-hydroxyphenylpyruvate dioxygenase	0.891122		5.07013
sorting nexin 3	0.830399	1.019267	0.389943
polyribonucleotide nucleotidyltransferase 1	0.324265		0.89907
jumonji domain containing 1C	1.41415	0.662706	0.481674
adenosylmethionine decarboxylase 1	0.909804	0.885146	2.157773
hypothetical gene supported by CR385274	0.663498	0.88319	0.331548
kinesin family member 24	0.442717	1.213295	23.06225
chromosome 6 open reading frame 186	7.209417	8.15834	0.057341
LysM, putative peptidoglycan-binding, domain containing 2	0.890369	0.842563	0.381298
ubiquitin-conjugating enzyme E2 variant 2	1.068909	0.870592	0.393408
interferon regulatory factor 10	2.340875	1.078732	4.06463
denticleless homolog (Drosophila)			0.048039
thioredoxin domain containing 16	1.460827	1.599772	3.136327
fms-related tyrosine kinase 4	2.185971	2.318331	3.68605
cytokine-like nuclear factor n-pac	0.530231	0.98153	0.394865
cytokine-like nuclear factor n-pac	0.737357	1.35587	0.460642
TRAF interacting protein	0.384405	1.121656	2.669114
LIM and SH3 protein 1	0.761108	0.932408	2.090533
Zinc finger protein 318	0.860659	0.811911	0.272461
ring finger protein 149	0.942803	2.184556	1.014812
centrosomal protein 63kDa	1.005402	0.409179	
similar to USP6NL protein	1.668644	1.098212	0.771438
chromosome 6 open reading frame 98	10.99415		
essential meiotic endonuclease 1 homolog 1 (S. pombe)	0.618674	1.531635	0.256154
stathmin-like 2	0.751417	1.701439	3.881511
coiled-coil domain containing 117 /// hypothetical protein LOC769136		0.032203	
Hypothetical LOC416916			0.346126
transmembrane protein 37	0.422117	1.040409	1.44111
leucine zipper-EF-hand containing transmembrane protein 2	1.23067	0.040264	
Zinc finger, DHHC-type containing 14	1.109953	0.731142	0.586982
zinc finger protein 106 homolog (mouse)	2.194409	0.941494	1.28151
spastic ataxia of Charlevoix-Saguenay (sacsin)	1.142943	0.652708	0.520604
high-mobility group 20A			0.466499
midline 1	2.477146	1.313127	1.861037
HIV-1 Tat specific factor 1	1.142336		0.633961
activating signal cointegrator 1 complex subunit 3-like 1	0.933343	0.887352	0.498027
PDZ domain containing RING finger 3	2.001145	1.015492	1.505089

TBCC domain containing 1	1.345165	0.621095	
protein phosphatase 1, regulatory (inhibitor) subunit 14C	0.87826	0.801656	0.273163
Hypothetical LOC428586	1.21226	1.048614	1.574116
nucleoporin 153kDa	1.896769		0.643628
family with sequence similarity 46, member D	3.1395	0.038358	1.125903
POZ (BTB) and AT hook containing zinc finger 1	2.484058	1.1316	0.695147
GRB2-associated binding protein 1	2.751234	1.588709	1.336409
Similar to Chromosome 1 open reading frame 33	0.578998		2.614433
KIAA0664	0.586137	0.938157	1.436957
centrosomal protein 76kDa /// similar to Centrosomal protein	2.164902	0.745928	0.769964
dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0.94918	0.730184	3.276705
nicotinamide phosphoribosyltransferase	3.853836	1.001201	2.470277
mannosidase, beta A, lysosomal	0.772271	1.655637	1.430467
frataxin	0.710163	0.957807	2.288807
poly (ADP-ribose) polymerase family, member 6	1.251601	0.76915	2.31324
Similar to KIAA1217 protein	2.089722	1.186436	2.562873
hypothetical LOC431243 /// similar to APH1A protein	0.803332		0.375881
collectin sub-family member 12	2.143329	1.508072	3.672692
ghrelin/obestatin prohormone	1.483341	1.052456	1.089267
follicle stimulating hormone, beta polypeptide		0.063073	
ecto-NOX disulfide-thiol exchanger 1	0.573199	0.359987	
tyrosyl-DNA phosphodiesterase 1	0.847339	1.213943	0.607503
family with sequence similarity 76, member A	0.863951	0.808038	0.154352
Hypothetical LOC425209	0.897216	1.105307	2.131212
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide			
chromosome 3 open reading frame 14	2.068067	1.696893	0.870449
Transmembrane protein 220	0.774963	0.662698	0.393429
YTH domain containing 1	1.13879	0.721364	0.498654
chondroadherin	2.407173	0.446128	1.071198
uveal autoantigen with coiled-coil domains and ankyrin repeat	1.667864	1.18239	0.4477
adiponectin, C1Q and collagen domain containing	1.49253	1.729474	2.95101
triple functional domain (PTPRF interacting)	0.103822	1.378802	
chromosome 5 open reading frame 24	1.108591	0.902662	0.469583
similar to hypothetical protein			2.720952
R-spondin 3 homolog (Xenopus laevis)			5.352421
DnaJ (Hsp40) homolog, subfamily C, member 3	1.062144	0.94582	0.671011
REST corepressor 3	0.707743	0.761585	0.459634
E2F transcription factor 8	0.808603	0.84435	0.279972
ankyrin repeat and BTB (POZ) domain containing 1	0.89737	2.671686	0.739871
Solute carrier family 1 (glutamate/neutral amino acid transporter)	0.430575	1.183984	0.751897

CD55 molecule, decay accelerating factor for complement (Cromer bloc	4.920405		
ferredoxin reductase	0.783286	1.361713	2.277745
hypothetical protein LOC769756	2.188992		
excision repair cross-complementing rodent repair deficiency	1.265104	0.760936	1.358616
hypothetical LOC427191	0.568778	1.182174	2.90908
BTB (POZ) domain containing 12	1.172019	1.020824	0.514101
apolipoprotein H (beta-2-glycoprotein I)	0.854253		
SRY (sex determining region Y)-box 5	0.774721	0.774013	3.090755
Similar to importin beta subunit	0.853605	0.639084	1.425573
chromosome 3 open reading frame 59	0.369254	0.987925	3.495354
VMA21 vacuolar H ⁺ -ATPase homolog (S. cerevisiae)	0.732414	0.781256	0.266976
G protein-coupled receptor 153	0.779833	0.631576	0.22369
Ceruloplasmin (ferroxidase)	1.102557	0.426105	2.409398
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	0.409033	1.115144	0.907793
Ca ²⁺ -dependent secretion activator	3.127783	1.423167	
hypothetical gene supported by CR385186	0.648124	1.156281	0.706076
STT3, subunit of the oligosaccharyltransferase complex, hon	1.168174	0.916689	0.504402
PITPNM family member 3	1.808393	1.634342	6.559222
ankyrin repeat and MYND domain containing 1	1.109189	0.901367	1.400741
transmembrane and tetratricopeptide repeat containing 1	1.711484	1.127162	2.122607
RAB14, member RAS oncogene family	1.481897	0.899637	0.319794
KIAA1310	0.807996	1.210071	2.988101
KIAA1310	0.478412	1.410112	3.177434
transmembrane and coiled-coil domains 7	1.451599	1.340704	2.989071
Protein tyrosine phosphatase, receptor type, K	0.848512	1.08522	0.468436
keratin 14	0.696736	0.841745	0.278914
Fucosidase, alpha-L- 1, tissue	0.858564	0.955621	0.900674
Similar to mKIAA1930 protein	0.971802	0.746783	0.397814
protein phosphatase 2 (formerly 2A), regulatory subunit B", ;	1.279302	0.544237	0.380645
Ring finger protein 19B	4.012212	1.42892	4.64298
Mannosidase, endo-alpha	0.74504	2.145941	1.166532
family with sequence similarity 81, member A			2.233691
PDGFA associated protein 1		1.578398	0.056078
N-6 adenine-specific DNA methyltransferase 2 (putative)	0.633513	2.428591	2.001422
potassium channel tetramerisation domain containing 3	1.340757	0.859561	2.624281
myosin IXA	1.327151	0.926307	2.174635
cytoplasmic polyadenylation element binding protein 2	0.834152	0.956168	2.072549
short coiled-coil protein	1.184626	0.967496	0.46472
hypothetical LOC418218			2.509034
regulator of chromosome condensation (RCC1) and BTB (Pc	0.841809	0.859249	0.345663

cortactin	1.096025	1.040047	2.201152
similar to class I alpha chain	0.912703	0.570258	4.313083
similar to MHC Rfp-Y class I alpha chain /// similar to MHC	0.955128	0.489267	3.691034
Chromosome 6 open reading frame 62	1.23232	3.762167	0.895924
Vacuolar protein sorting 8 homolog (S. cerevisiae)	0.66878	1.129645	2.090257
similar to dysferlin			0.40527
PHD finger protein 14	0.794903	1.356948	0.224688
similar to KIAA2026 protein	1.338472	0.753689	0.514512
hypothetical gene supported by CR387037	0.810177	0.498584	0.434642
Sec61 alpha 2 subunit (S. cerevisiae)	1.361082	0.402151	0.773021
Sec61 alpha 2 subunit (S. cerevisiae)	1.997286	1.218461	0.400108
1-acylglycerol-3-phosphate O-acyltransferase 3 /// similar to	1.350587	1.24459	2.700016
SECIS binding protein 2	0.35441	11.68548	1.585608
mitogen-activated protein kinase 10	0.722449	1.081641	
hypothetical gene supported by CR386657	0.7251	0.86631	0.251029
serine/threonine kinase 10	0.849109	1.735611	2.58678
Myotubularin related protein 9	1.201817	0.863164	2.07149
DIP2 disco-interacting protein 2 homolog B (Drosophila)	0.618071	1.726436	0.138036
KIAA1913	0.824504	0.685124	0.356707
WD repeat and FYVE domain containing 1	1.366306	0.924497	0.348543
hypothetical LOC420382			2.234357
hypothetical LOC426128	0.942196	1.653375	0.330959
abhydrolase domain containing 13	1.096626	0.940241	0.401505
DENN/MADD domain containing 4C	0.338924	1.247111	
cell division cycle 2-like 2 (PITSLRE proteins)	1.011373	0.55501	0.392457
similar to putative 40-2-3 protein	1.029203	0.961584	1.970601
similar to hypothetical protein FLJ39743	1.005506	0.712343	0.698038
translocation protein 1	1.173969	0.332887	0.527711
Similar to choline transporter-like protein 1, splice	0.409077	1.910312	1.308361
ATG4 autophagy related 4 homolog B (S. cerevisiae)	0.373727	1.783472	0.97275
ATG4 autophagy related 4 homolog B (S. cerevisiae)	0.692723	0.587933	0.464803
Notch homolog 1, translocation-associated (Drosophila)	0.971722	0.947791	0.749876
protein phosphatase 6, catalytic subunit	0.830632	1.076346	1.44572
spire homolog 1 (Drosophila)	1.926435	2.755335	5.331232
amidohydrolase domain containing 2	1.00461	1.225778	2.725736
KIAA1109	1.216332	0.89056	0.725294
transmembrane protein 220	0.542549	0.614136	0.428037
STT3, subunit of the oligosaccharyltransferase complex, homolog A (S.	1.343863		0.021931
ankyrin repeat and SOCS box-containing 5	0.29341	1.108025	0.854994
KIAA0368			2.513332

complement C4 /// steroid 21-hydroxylase	0.864399	1.23451	1.338914
nuclear receptor subfamily 2, group C, member 2	0.683318	1.979926	0.49833
membrane bound O-acyltransferase domain containing 1	1.271072	1.559802	2.127716
ubiquitin specific peptidase 24	1.378598	2.315481	1.197842
Nedd4 binding protein 1			
Chromosome 10 open reading frame 72	1.379322	1.171781	2.686904
interferon regulatory factor 2 binding protein 2	1.083361	1.20316	2.166288
ubiquitin specific peptidase 14 (tRNA-guanine transglycosyl	0.85799	1.018968	2.739966
Tripartite motif-containing 35	0.82011	1.06921	4.036332
hypothetical LOC423474	1.618591	1.683534	1.337948
SPARC related modular calcium binding 1		1.278308	0.17395
Similar to Bardet-Biedl syndrome 7	1.097897	0.976027	0.165863
PR domain containing 11	1.096351	1.863735	3.622881
pyruvate dehydrogenase kinase, isozyme 4	0.790822	2.155557	4.998191
hypothetical protein LOC769733	0.942985	0.908188	0.45796
Na ⁺ /H ⁺ exchanger domain containing 2	0.892287	2.398379	4.698542
UBX domain protein 2B	1.18284	0.873132	0.480423
interferon induced with helicase C domain 1	2.37039	1.358636	2.653053
spermatogenesis associated 17		3.47133	
RNA binding motif protein 7	0.718973	1.057546	0.478634
dynein, light chain, Tctex-type 3	0.861538	1.43216	2.067637
CDGSH iron sulfur domain 2	1.623408	1.106466	2.796847
RAS p21 protein activator 3	2.002371	0.926609	0.498224
chromosome 5 open reading frame 30	0.677403	1.001478	0.725379
similar to 2C4D /// MOB1, Mps One Binder kinase activator-like 3 (yea		0.06059	0.195646
Hypothetical protein LOC768787	1.325832	1.59863	6.665435
Hypothetical protein LOC768787	1.93968	3.060607	1.136212
hypothetical gene supported by CR386744	0.525538	0.884328	0.304915
SRY (sex determining region Y)-box 1	0.103406		1.362076
similar to ARPP-21 protein	0.680577	0.971613	0.238909
deoxyribonuclease II beta		2.484549	
family with sequence similarity 65, member A	0.880187	0.884999	2.633047
sphingomyelin phosphodiesterase 3, neutral membrane (neut	0.702034	1.247197	0.208838
WD repeat domain 44	1.191501	0.841319	0.351554
ATPase, Ca ⁺⁺ transporting, ubiquitous	2.534743	0.795312	0.327546
metaxin 3	0.420815	0.665767	
drebrin-like	0.669264	0.969086	1.877201
Melanoma inhibitory activity family, member 3		0.070415	
Melanoma inhibitory activity family, member 3	1.522061	0.655381	0.464563
hypothetical gene supported by CR386144	1.056809	0.943879	0.942257

hypothetical gene supported by CR387685	2.076503	1.119499	1.14638
hypothetical gene supported by CR387685	2.651317	1.3609	1.073681
CD81 molecule	1.018783	1.326086	2.090125
lysosomal associated protein transmembrane 4 beta	0.941451	1.822479	0.473834
spermatogenesis associated 18 homolog (rat)		2.945248	0.44418
succinate-CoA ligase, GDP-forming, alpha subunit	0.962926	0.498276	1.053172
myeloid cell leukemia sequence 1 (BCL2-related)	1.098719	1.162589	0.527311
Alpha thalassemia/mental retardation syndrome X-linked	1.207143	1.003245	0.681504
similar to KIAA1271 protein	1.205317	1.221681	0.856281
hephaestin	1.491912	1.290992	4.116605
GRAM domain containing 3	0.680992	0.933961	2.102744
cullin 1	1.643087	0.776	0.351632
chromosome 15 open reading frame 41	1.462284	0.815449	0.442952
bile acid Coenzyme A: amino acid N-acyltransferase (glycin	1.627351		2.250511
phosphotyrosine interaction domain containing 1	0.812955	1.50842	1.854076
T-cell lymphoma breakpoint associated target 1	0.111409		
T-cell lymphoma breakpoint associated target 1	0.111409		
ADP-ribosylation factor-like 4C	1.117633	1.293177	2.185362
Engulfment and cell motility 1		0.233022	
outer dense fiber of sperm tails 1			
similar to FLJ46082 protein			
bromodomain containing 8	1.149703	0.495896	0.688461
tubulin polymerization-promoting protein family member 2	0.699891		0.335551
lipoma HMGIC fusion partner	1.800722	1.031491	1.415825
leucine rich repeat containing 67			3.146885
hypothetical LOC419830	1.89982	0.655438	1.21974
sperm associated antigen 4	0.312368		
Cytochrome b5 domain containing 2	0.960044	1.311616	1.812942
hypothetical gene supported by CR387546	0.586098	1.000894	0.29796
hypothetical gene supported by CR386965 /// hypothetical pi	1.041976	0.85374	0.640378
PHD finger protein 5A		0.095795	
PHD finger protein 5A	0.608884		
PHD finger protein 5A	0.646966	0.974428	0.414319
Complement C4	0.507561	1.337139	2.014253
complement C4	0.834649	1.095138	2.984961
endonuclease/exonuclease/phosphatase family domain conta	1.03633	2.396173	3.376522
deoxycytidine kinase	0.715907	1.006613	0.334637
similar to myosin IIIA; deafness, autosomal recessive 30	1.204242	0.936192	3.222477
DENN/MADD domain containing 5B	1.196118	0.765302	0.493394
Membrane associated guanylate kinase, WW and PDZ doma	2.238816	1.016158	6.669768

farnesyltransferase, CAAX box, alpha	0.730275	0.903199	0.867183
parvin, beta	0.445384		
claudin domain containing 1	1.213567	0.770018	0.175364
protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)		0.953382	2.039405
nucleolar protein 11	1.781365	0.86054	0.43507
ecotropic viral integration site 5	1.630799	0.590529	1.170329
Similar to Vasohibin	0.915519	0.954018	0.349473
SLIT-ROBO Rho GTPase activating protein 1	2.1022	0.886101	1.795242
similar to dysferlin	1.364585	0.934573	2.252202
Neuro-oncological ventral antigen 1	2.759865	1.148203	1.169158
glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzym	0.265569	0.875345	0.450591
multiple EGF-like-domains 9	2.227948		
tumor suppressor candidate 2	1.007602	1.252528	2.610312
TAR DNA binding protein	1.042248	0.820803	0.626618
hypothetical gene supported by CR387102			0.454127
similar to Atp5c1-prov protein /// TAF3 RNA polymerase II,	0.838963	0.666669	0.381966
Kruppel-like factor 6	1.008987	1.01311	1.878118
Hypothetical protein LOC769351	0.88884		0.157971
E74-like factor 1 (ets domain transcription factor)	0.993389	0.648627	0.438864
KIAA0082	2.615685	1.243825	1.928474
PDS5, regulator of cohesion maintenance, homolog A (S. ce	0.397016	1.370606	0.363902
nuclear receptor coactivator 7	0.459784	2.086202	0.251498
fibroblast growth factor receptor 2	0.750616		3.33722
Homer homolog 3 (Drosophila)	1.685686	0.813066	2.110309
Homer homolog 3 (Drosophila)	0.8029	1.266424	2.510093
cAMP responsive element binding protein 3-like 2	0.772037	0.811554	0.422813
cAMP responsive element binding protein 3-like 2	0.369027	1.118074	0.40374
hypothetical gene supported by CR387752	0.835326	1.61116	2.017327
Similar to Parp3 protein	1.07063	1.675963	4.090956
Mannan-binding lectin serine peptidase 2	0.600174		
Cadherin 8, type 2		2.027176	
Nipped-B homolog (Drosophila)	0.922656	1.098686	0.477324
signal peptidase complex subunit 2 homolog (S. cerevisiae)	0.806588	0.861484	0.162169
syntaxin 1A (brain)	0.09462		0.041195
chromosome 14 open reading frame 149	1.236753	1.140109	2.159416
myelin expression factor 2	1.800708	1.217975	0.362736
similar to selenium donor protein /// selenophosphate synthet	1.077534	1.000067	0.591316
collagen, type III, alpha 1		4.807562	0.105899
chromosome 20 open reading frame 194	1.19758	0.808674	0.422987
zinc binding alcohol dehydrogenase, domain containing 1	0.975811	1.134809	0.909295

hypothetical gene supported by CR391572	1.661774	1.751194	2.253166
Gal 10	0.706422	2.49008	
amyotrophic lateral sclerosis 2 (juvenile) chromosome region	0.902883	4.983303	0.856883
ATPase family, AAA domain containing 5	0.612923	0.692149	0.45893
bruno-like 6, RNA binding protein (Drosophila)	0.990934	2.208696	0.673031
glucosidase, alpha; neutral C	1.051562	0.835029	2.477508
glycosyltransferase 25 domain containing 2			
Sel-1 suppressor of lin-12-like (C. elegans)	1.646902	0.779757	1.033688
family with sequence similarity 122B	1.093748	1.111386	0.394445
chromodomain helicase DNA binding protein 9	1.099829	0.82794	0.859554
galactosidase, alpha	1.511735	0.77245	2.911584
galactosidase, alpha	1.525894	0.963141	1.758656
oligonucleotide/oligosaccharide-binding fold containing 2A	1.17205	0.743965	0.584005
EPS8-like 2	2.893804	1.082932	2.890734
janus kinase and microtubule interacting protein 1	2.797357		1.786635
tetratricopeptide repeat domain 9	0.76841	3.473909	0.60989
piwi-like 1 (Drosophila)	0.803166	1.899979	4.503171
Gen homolog 1, endonuclease (Drosophila)	1.094954	1.759486	0.459634
laminin, gamma 1 (formerly LAMB2)	0.66607	0.864917	0.503431
calcium binding protein 1		0.048649	0.42571
Kelch-like 29 (Drosophila)	2.30669	1.338692	0.646133
hypothetical gene supported by CR389297	0.145762	0.758555	
alcohol dehydrogenase, iron containing, 1	2.731699	1.092269	1.063157
structural maintenance of chromosomes 6	1.41254	0.746371	0.489025
hypothetical LOC424473	0.886866	0.471287	2.733701
Solute carrier family 24, member 5	1.429382	1.049148	0.96047
oxidation resistance 1	1.13742	0.98971	2.445937
hypothetical gene supported by CR390941	1.571556	37.05172	
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.71327	0.770657	0.146028
Rho guanine nucleotide exchange factor (GEF) 10			
Hippocampus abundant transcript 1	0.983092	1.401993	0.205477
hippocampus abundant transcript 1	0.897445	0.836609	0.33824
family with sequence similarity 136, member A /// hypothetical	0.635629	1.164704	1.997924
KIAA0753	1.654989	0.743993	0.52312
glycoprotein M6B	1.14859		2.160501
yippee-like 2 (Drosophila)	1.404017	0.617083	0.380699
fibroblast growth factor 2 (basic)	0.823499	0.922059	2.305392
LON peptidase N-terminal domain and ring finger 3	0.634922	0.545089	2.573035
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl transferase 2		3.984968	
similar to UDP-glucose:glycoprotein glucosyltransferase 2	1.51791	8.097808	

ATP-binding cassette, sub-family C (CFTR/MRP), member	2.312679	0.647703	1.205614
zinc finger protein 644	0.508694	1.121697	0.427194
transcription elongation factor B (SIII), polypeptide 3 (110kD)	0.643954	1.268369	2.377119
asparagine-linked glycosylation 9 homolog (S. cerevisiae, alj)	1.049281	1.14944	0.807828
calpain 1, (mu/I) large subunit	0.96596	0.863417	2.205091
solute carrier family 25, member 32	1.055752	0.947537	0.73143
spectrin repeat containing, nuclear envelope 2	1.015031	0.849125	1.53321
hypothetical protein LOC771537	2.068852	0.941141	2.00999
chromosome 8 open reading frame 41	1.530202	0.502381	1.547063
scinderin	1.235965	1.233624	0.613266
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid recept	0.026333		
BCL2-like 15	1.345979	4.893666	0.823287
Hepatic leukemia factor	0.539346	1.222661	0.47835
Protein arginine methyltransferase 8	1.13759	2.318639	0.923207
dedicator of cytokinesis 3			
mesoderm development candidate 2	0.865314	0.698315	0.709079
transmembrane emp24 domain trafficking protein 2	1.276976	1.104803	0.452281
coiled-coil domain containing 127	0.595063	0.4495	0.961171
asparagine-linked glycosylation 14 homolog (S. cerevisiae)	0.785462	1.210396	1.171353
TNF-related apoptosis inducing ligand-like			
interferon induced transmembrane protein 5			3.075853
Fructosamine 3 kinase	1.884481	1.123082	1.042573
similar to putative endoplasmic reticulum protein family mei	1.89163	0.837798	0.865943
pleckstrin homology domain containing, family K member 1	1.275188	0.637136	0.799837
EPH receptor A1	2.105513	1.094248	
breast cancer anti-estrogen resistance 1	1.169913	1.006402	3.420632
WW and C2 domain containing 1	1.414508	1.660037	3.454045
Ras-related GTP binding C	0.733538	0.839452	0.437983
EF-hand domain family, member A2	1.471079	1.529777	2.339141
transmembrane protein 49	2.495839	1.274998	3.17881
solute carrier family 25 (mitochondrial carrier; phosphate car	0.36285	0.96927	1.0014
NKF3 kinase family member		3.026458	
hypothetical gene supported by CR387606	0.765927	2.153174	0.497476
Lymphoid enhancer-binding factor 1	0.501172	1.731705	0.247917
Zinc finger protein 827	1.538833	0.975283	0.361333
Choline phosphotransferase 1	2.203878	1.414319	0.479775
hypothetical gene supported by CR386328	1.926242	1.171306	1.477538
ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-	0.472345	0.761755	0.58108
erbb2 interacting protein			3.469221
ADP-ribosylation factor GTPase activating protein 2	0.990867	0.861169	1.667519

BTB (POZ) domain containing 3	0.756792	0.749072	0.277147
chromosome 1 open reading frame 168	2.491035	0.854418	2.30723
Solute carrier family 26, member 11	1.094386	0.836883	2.4003
sphingomyelin phosphodiesterase, acid-like 3B	1.923004		1.094343
sphingomyelin synthase 1	1.224786	0.876814	2.185384
nuclear factor I/B	2.008753	1.251118	2.597852
dynein, light chain, LC8-type 2	0.56533	0.887147	0.46402
Cappuccino homolog (mouse)	1.166571	1.055639	0.5296
zinc finger protein 292	1.002555	0.817257	0.47364
fibronectin type III domain containing 3A	0.783124	2.771555	1.588459
Transient receptor potential cation channel, subfamily V, me	1.204768	0.913902	2.706939
torsin A interacting protein 1	0.286188	0.80356	2.144216
Dehydrogenase/reductase (SDR family) member 2	1.221761	0.887906	0.399025
Hypothetical LOC416414	0.844792	0.788017	0.330561
spen homolog, transcriptional regulator (Drosophila)	0.920403	0.736999	1.426574
Splicing factor, arginine/serine-rich 8 (suppressor-of-white-a	0.753771	0.878388	0.451442
solute carrier family 27 (fatty acid transporter), member 4	1.039432	0.96693	2.730835
DCN1, defective in cullin neddylation 1, domain containing	1.426928	2.143931	1.054406
mitogen-activated protein kinase kinase 3	2.927041	1.230482	3.27125
Transmembrane protein 215			0.774042
Hypothetical protein LOC770202	0.827841	0.951101	0.359464
similar to MGC53931 protein	0.818709	1.233321	2.288322
Glucocorticoid induced transcript 1	1.283412	1.309622	1.641558
Retinaldehyde binding protein 1-like 1			
POM121 membrane glycoprotein (rat)		8.63144	
TBC1 domain family, member 22B			
mitochondrial tumor suppressor 1	0.911998	0.726899	2.494517
family with sequence similarity 101, member A	1.300377	2.128226	0.446371
nuclear respiratory factor 1	1.273265	1.075139	3.458977
ubiquitin specific peptidase 30	0.607179		2.366918
similar to kinesin, putative	6.03135	3.856516	9.768168
titin	1.23016	0.799864	3.35668
KIAA0319-like			
Thioredoxin domain containing 10		0.298337	
thioredoxin domain containing 10	1.135058	0.806454	0.349975
ATPase type 13A3	1.173596	1.194495	0.64991
hypothetical gene supported by CR389067; CR406161	0.724944	2.797186	1.552501
Patatin-like phospholipase domain containing 2	1.311924	1.049837	2.576901
Cdk5 and Abl enzyme substrate 1	2.444449		0.941898
Ankyrin repeat domain 13C		0.66119	0.258701

Fibulin 2	1.277005	1.833475	0.907438
ADP-ribosylation factor-like 13B	1.459333	0.514162	0.338715
ring finger protein 14	1.294404	0.88445	0.984254
ADAM metallopeptidase with thrombospondin type 1 motif, 13		2.137171	1.710339
Solute carrier family 16, member 2 (monocarboxylic acid tra	1.731516	1.295608	2.837902
follistatin-like 1	2.784903	1.43928	1.212205
SET binding factor 2	3.81081		
pleckstrin homology domain containing, family C (with FER	2.11264	1.110432	3.066691
activity-dependent neuroprotector homeobox	2.06561	0.548647	0.413516
nudix (nucleoside diphosphate linked moiety X)-type motif 5	1.072229	0.631748	0.966379
natural killer-tumor recognition sequence	1.575499	1.028249	0.499835
ubiquitin protein ligase E3 component n-recognin 2			0.086354
uroplakin 1B			
ras homolog gene family, member C	1.763911	1.995438	2.23641
YY1 associated factor 2	1.338053	1.139073	0.412652
acyl-CoA thioesterase 9	1.25466	0.823767	1.642813
nebulin	1.019929	0.596831	3.133365
similar to nebulin /// nebulin	1.199804	0.657053	3.702963
family with sequence similarity 76, member B	1.280234	0.93073	0.703366
KTI12 homolog, chromatin associated (S. cerevisiae)		0.916837	1.519626
Arachidonate 5-lipoxygenase-activating protein	0.372977	1.122808	0.296386
SLAIN motif family, member 2	1.059699	0.906696	0.56981
Hepatoma-derived growth factor (high-mobility group protei	0.658301	1.126207	2.183566
chloride intracellular channel 2	1.86396	1.006384	0.840288
cell adhesion molecule 1	0.663195	2.038113	0.570898
gallinacin 1	0.588128	1.156406	2.643057
importin 5	0.740738	1.288682	0.45309
G protein-coupled receptor 116	1.244769	1.327062	2.455646
Calcium/calmodulin-dependent protein kinase (CaM kinase)	1.03328	1.126213	0.356881
retinitis pigmentosa 2 (X-linked recessive)	0.830033	1.17629	0.468027
WAP four-disulfide core domain 1	0.930793	1.346793	4.510736
Similar to immunoglobulin-like receptor CHIR-B2	1.719832		0.995798
activating transcription factor 3	3.14317	1.900758	2.548599
glutaminase	2.06591	1.244791	0.25232
ring finger protein 213	3.887599	1.723825	4.676801
polymerase (RNA) mitochondrial (DNA directed)	11.71342	2.041724	1.008639
thyroid hormone receptor interactor 12	1.057039	1.077634	0.580278
neutrophil cytosolic factor 2 (65kDa, chronic granulomatous	1.001768	1.995652	2.010956
neutrophil cytosolic factor 2 (65kDa, chronic granulomatous	1.631553	1.76693	2.864808
jumonji domain containing 1A	2.070877	1.095958	0.349475

solute carrier family 30 (zinc transporter), member 6	0.388821	1.206002	0.436273
hypothetical LOC420411	1.231645	1.191207	2.810469
solute carrier family 33 (acetyl-CoA transporter), member 1	1.72853	0.839973	0.260627
transmembrane protein 131	1.684886	1.828248	0.218667
leucine rich repeat containing 40		3.95425	
UDP-glucose ceramide glucosyltransferase	1.160386	1.069619	0.708871
KIAA1324-like	0.35351		3.400836
FERM domain containing 5			9.241431
chromosome 16 open reading frame 68	0.821128	1.161946	2.24968
Similar to immunoglobulin-like receptor CHIR-A	0.806106	0.487101	1.588208
immunoglobulin-like receptor CHIR-B5 /// immunoglobulin-	1.883037	1.005347	3.609002
mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosam	1.267975	1.15384	1.798601
GLIS family zinc finger 2	0.854945	0.721258	2.131778
WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain cont		14.01764	
similar to LOC387763 protein	1.796381	1.281349	5.523727
Spen homolog, transcriptional regulator (Drosophila)	1.001021	1.006395	1.493303
death inducer-obliterators 1	1.411643	0.518686	1.560305
sperm associated antigen 16		3.184159	
adenylate cyclase 9	0.949334	1.069902	1.616336
phosphoribosyl pyrophosphate amidotransferase	1.744738	1.466438	0.394926
chromosome 9 open reading frame 82	0.409847	1.080923	1.198921
TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	0.570165	0.856957	2.22642
Similar to chromosome 6 open reading frame 60	0.08413	0.46488	
hypothetical gene supported by CR388594	0.277383	0.958078	
chromosome 6 open reading frame 60	1.028479	0.61246	0.499005
kinesin family member 5C	0.266222	1.072567	
tumor necrosis factor receptor superfamily, member 13B			
Membrane associated guanylate kinase, WW and PDZ domain	1.470988	1.654779	2.027378
guanylate binding protein	5.197248	1.407721	13.67494
pumilio homolog 2 (Drosophila)	1.268037	1.183371	0.474422
heterogeneous nuclear ribonucleoprotein A3	1.007632	0.634696	0.247964
chromosome 10 open reading frame 47		0.776395	0.141641
Nedd4 family interacting protein 1	0.667755	0.943712	3.221432
KIAA1217			1.574721
solute carrier organic anion transporter family, member 2B1	1.065745	1.22886	2.405431
integrin, alpha 8		2.30072	
integrin, alpha 8	0.980763	1.488495	3.515881
similar to hypothetical protein FLJ32658			0.055509
similar to LOC129293 protein	1.310002	0.43417	1.065546
docking protein 7	1.648113	2.404147	

tetraspanin 12			0.242807
SH3 domain containing ring finger 1	0.388283	0.332933	
spectrin repeat containing, nuclear envelope 2			
avidin related protein 2 /// hypothetical LOC427416	0.286981	0.308797	1.625744
Fanconi anemia, complementation group A	0.484675	0.687464	
nuclear receptor binding SET domain protein 1			
Splicing factor, arginine/serine-rich 11	0.921455	1.125029	1.687542
coiled-coil domain containing 91	0.705118	0.762583	0.469946
Neural cell adhesion molecule 1	1.145693	1.155802	3.82426
anaphase promoting complex subunit 4	0.828836	1.138011	0.767306
pleckstrin homology domain containing, family B (evectins)	0.750086	1.084217	0.702508
sphingomyelin phosphodiesterase 4, neutral membrane (neut	0.79253		2.513927
hypothetical gene supported by CR389209			9.585346
TSC22 domain family, member 1	1.24648	0.693119	0.497655
TSC22 domain family, member 1	1.474437	0.753327	0.333331
similar to Auh protein	0.343635	0.747128	1.972718
similar to Auh protein	0.298987	0.899284	3.350374
FERM domain containing 4B	0.833797	0.677636	1.702327
janus kinase and microtubule interacting protein 2			2.334153
ribosomal protein L29	0.665167	1.075925	0.491537
zinc finger CCCH-type, antiviral 1	3.230821	1.499093	1.80952
ATP-binding cassette, sub-family B (MDR/TAP), member 10			0.351554
protein kinase, cAMP-dependent, catalytic, beta	1.114926	0.876749	0.229844
DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	3.723095		
similar to Protein C20orf129	0.68987	1.231663	2.013758
similar to Dual specificity protein phosphatase 13 (Testis- an	0.988075		2.908156
solute carrier family 35, member B4	6.152582		
solute carrier family 35, member B4		1.264526	
E4F transcription factor 1	1.386407	0.469723	0.657566
protein tyrosine phosphatase-like (proline instead of catalytic	0.667491	2.40114	0.720725
SOUL protein	1.528827	0.384904	1.94283
FERM domain containing 1	1.060861		
asp (abnormal spindle) homolog, microcephaly associated (Drosophila)			
FK506 binding protein 6, 36kDa	1.120877	1.649337	1.578851
heat shock 27kDa protein 1	1.727075	0.605875	2.05219
myotubularin related protein 8	0.419169	2.397535	0.720739
CCR4-NOT transcription complex, subunit 2	1.449189		21.70014
lactase		0.920452	2.915142
NMDA receptor regulated 2		5.027103	
plexin C1	0.7946	0.272725	0.915976

Hypothetical LOC429096	4.129702		0.767064
similar to hypothetical protein FLJ10081		0.88223	
Zinc finger, DHHC-type containing 21	0.885465	0.857087	0.490504
putative neuronal cell adhesion molecule	0.675646	0.637212	0.267715
tubulin, beta 2B	0.712304	1.094548	0.443824
Basonuclin 1		17.23839	
BCL6 co-repressor	1.221539		
transmembrane protein 59	0.550417	0.886112	0.348135
adaptor-related protein complex 3, delta 1 subunit	0.668807	0.86007	1.84392
Peroxisome biogenesis factor 1	0.826029	0.633597	0.727568
sal-like 1 (Drosophila)	2.970838	1.32998	0.902364
sal-like 1 (Drosophila)	2.247962		
deiodinase, iodothyronine, type II	2.333705	1.356145	2.269224
regulator of telomere elongation helicase 1	5.555022	0.833882	
chromosome 9 open reading frame 75	2.270344	1.115731	4.472449
Notch homolog 1, translocation-associated (Drosophila)	0.574769	0.374786	
nuclear receptor co-repressor 1	1.112994	0.870316	0.427353
Similar to Hypothetical protein BC001096	2.08551	1.045119	1.7969
PET112-like (yeast)	0.823506	0.927025	0.655306
hypothetical protein LOC768462	2.181506	1.670577	0.715585
Golgi associated, gamma adaptin ear containing, ARF binding protein 2			
Golgi associated, gamma adaptin ear containing, ARF bindir	0.77757	1.676627	25.96041
progesterone receptor membrane component 1	0.775342	1.057465	2.577742
KIAA2018	0.43919		
protein tyrosine phosphatase-like A domain containing 1			31.56909
mutS homolog 6 (E. coli)	0.66391	0.651465	0.468837
mutS homolog 6 (E. coli)	1.098121	1.144457	0.439005
ankyrin repeat domain 26	1.2199	0.796877	0.637942
Similar to DNA helicase HEL308	2.016216		
Similar to DNA helicase HEL308	1.720846	1.81701	2.695311
helicase, POLQ-like	1.161122	1.209872	2.627257
RAB11B, member RAS oncogene family		0.734902	0.345654
chromosome 14 open reading frame 135		0.688771	
UDP glycosyltransferase 8	2.013385	0.842684	0.713087
SLIT and NTRK-like family, member 2	0.863406	1.217512	0.130558
solute carrier family 16, member 10 (aromatic amino acid tra	0.852969	1.330009	2.456718
Hypothetical LOC422400		1.95689	
opioid growth factor receptor-like 1			
sulfatase 1	2.130678	2.700554	
Hypothetical protein LOC771883	0.076584		

SRY (sex determining region Y)-box 30		4.432604	
similar to Egfl3 protein	2.255776		0.518378
Ca ²⁺ -dependent secretion activator		3.6979	
signal peptide, CUB domain, EGF-like 2		0.311751	
chondroitin sulfate proteoglycan 5 (neuroglycan C)			
chromosome 16 open reading frame 62	0.409003		1.05826
sterile alpha motif domain containing 13	1.07312	1.264249	0.32561
ubiquitin associated and SH3 domain containing, B			2.077788
Chromosome 10 open reading frame 54	0.866054	0.728649	2.854793
Hypothetical LOC423545		14.14457	
spindlin 1	7.413218	1.969263	0.223725
ATP-binding cassette, sub-family D (ALD), member 3	1.22596	1.185006	0.385424
protein tyrosine phosphatase, receptor type, F	1.282605	0.600108	0.331037
Metaxin 3	0.790795	0.820154	0.656531
dedicator of cytokinesis 8	0.800805	0.956412	4.154333
Rab interacting lysosomal protein	0.795449	0.774151	1.502267
Hypothetical LOC429131			
XK, Kell blood group complex subunit-related family, meml	1.525307	0.948524	0.932378
protein tyrosine phosphatase, receptor type, S	2.018413	1.203966	1.658715
parvin, alpha	1.158769	0.883695	0.401977
similar to FNDC3 protein		2.709738	
AP2 associated kinase 1	1.483574	0.947629	2.01831
ankyrin repeat domain 50			0.75449
transcription elongation factor A (SII), 1	1.360349	1.46514	1.244028
leucyl-tRNA synthetase	0.943741		0.322221
phospholipase A2 receptor 1, 180kDa	2.679903	2.138547	6.068629
MutS homolog 3 (E. coli)	0.047366		
ADAM metallopeptidase with thrombospondin type 1 motif,	0.031412	37.78676	
chromosome 22 open reading frame 30	1.55802	0.722638	0.467472
serine palmitoyltransferase, long chain base subunit 3	2.812488	0.59456	1.470808
vacuolar protein sorting 53 homolog (S. cerevisiae)	0.898325	1.0778	2.21485
mitochondrial ribosomal protein L41	0.729319	0.771892	1.900821
coiled-coil domain containing 125		0.557707	0.441409
ligand dependent nuclear receptor corepressor-like	1.895867	0.491597	0.608985
hypothetical gene supported by CR391077		2.013996	1.362057
sirtuin (silent mating type information regulation 2 homolog)	0.732891	0.75718	1.405729
transmembrane and coiled-coil domain family 3			21.27035
similar to rapamycin insensitive companion of mTOR; rictor	0.472009	1.132377	1.938342
similar to hypothetical protein AN5649.2	0.446864		
sal-like 4 (Drosophila)	6.718767	1.525726	

Hypothetical protein LOC777388			
mucin 1, cell surface associated	1.452279	0.731963	0.502027
hypothetical gene supported by CR391215	1.835762	1.476587	2.102361
lung lectin	0.946002	2.412724	2.425365
family with sequence similarity 84, member A	0.902135	0.604377	0.3336
hypothetical protein LOC769331			
transmembrane and coiled-coil domains 3	9.757479	1.03822	0.148281
F-box and leucine-rich repeat protein 10		0.912601	
dihydrolipoamide branched chain transacylase E2	1.041967	0.77799	0.280921
Rho GTPase activating protein 5	1.721259	0.881208	0.380526
family with sequence similarity 96, member B	0.404715	1.0972	0.999562
alveolar soft part sarcoma chromosome region, candidate 1	0.964838	0.607965	0.339039
centrosomal protein 192kDa	1.559448	0.926823	0.41008
cyclin Y-like 1		1.013467	
echinoderm microtubule associated protein like 1	4.9084	0.929039	
fidgetin-like 1	0.890396	1.151518	0.848738
ELAV (embryonic lethal, abnormal vision, Drosophila)-like	1.525213	0.804659	0.359643
nei endonuclease VIII-like 3 (E. coli)	0.692948	0.699894	0.36437
ADAM metallopeptidase with thrombospondin type 1 motif,	0.106227		
similar to cDNA sequence BC016423		0.950731	4.941025
archain 1	1.253843	0.990392	0.74175
LanC lantibiotic synthetase component C-like 2 (bacterial)	0.782021	1.335547	3.028461
Hypothetical LOC418298	0.862283	1.216829	0.917992
solute carrier family 25, member 28	2.027351	0.58867	0.97069
structural maintenance of chromosomes 6	1.189416	1.070695	0.787902
ectonucleoside triphosphate diphosphohydrolase 1	0.779772	1.397078	1.084653
similar to KIAA1546 protein	1.24358	2.64625	1.279354
ATP citrate lyase			0.084866
similar to FLJ42526 protein	2.349956	1.641735	
hydroxysteroid (11-beta) dehydrogenase 1-like	3.594263	1.296746	1.20101
RAB39B, member RAS oncogene family	0.9615	0.846791	0.457266
programmed cell death 1	0.702331	1.261662	0.444481
small nuclear ribonucleoprotein D3 polypeptide 18kDa	0.877942	1.16463	0.604271
glucocorticoid induced transcript 1	1.251932	1.658271	1.953372
myosin, light chain 1, alkali; skeletal, fast	1.315895	1.4413	2.156397
v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.014355		0.897659
v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.34743	1.479084	1.431817
guanine nucleotide binding protein (G protein), alpha inhibit	1.139826	1.337544	0.449402
guanine nucleotide binding protein (G protein), alpha inhibit	1.168464	1.583013	0.867786
Notch homolog 2 (Drosophila)			2.407026

par-3 partitioning defective 3 homolog (C. elegans)	1.304371	1.430793	3.868698
protein tyrosine phosphatase type IVA, member 3	0.822699	0.617816	0.348874
trinucleotide repeat containing 15	1.101429	0.701803	0.640163
Protein tyrosine phosphatase type IVA, member 1	1.11993	0.909715	1.508766
Ras association (RalGDS/AF-6) domain family 5	0.908278	0.802495	0.77454
serine carboxypeptidase 1	1.517689	1.388808	2.179563
acyl-CoA synthetase long-chain family member 1	1.030276		
phosphatidylinositol-3,4,5-trisphosphate-dependent Rac excl	1.781078	1.558201	3.712039
ADNP homeobox 2	1.306025	0.825649	0.480706
transforming, acidic coiled-coil containing protein 1	1.248081	1.113974	2.076699
Ubiquitin specific peptidase 9, X-linked	6.177838		
gamma-aminobutyric acid (GABA) A receptor, gamma 2			
Vpr (HIV-1) binding protein	0.734655	1.341286	2.619565
polymerase (DNA directed), lambda	0.959569	1.17957	5.461015
antigen identified by monoclonal antibody Ki-67	0.784134	0.958176	0.700498
similar to RIKEN cDNA 1700047I17	1.054232	0.579815	0.232272
guanylate binding protein family, member 6		0.360642	2.80234
transmembrane BAX inhibitor motif containing 1	0.855775	0.972786	2.013626
RNA binding motif protein 16	1.225397	0.823215	0.308194
inositol 1,3,4-triphosphate 5/6 kinase		0.165253	
NUAK family, SNF1-like kinase, 1	1.308531	1.243099	2.09495
nestin	0.987374	1.509813	2.313301
diacylglycerol kinase, iota			40.35094
interleukin 1, beta	2.495466		1.770766
splicing factor, arginine/serine-rich 11	1.518729	0.954336	0.693352
Solute carrier family 29 (nucleoside transporters), member 3	0.992904	0.879775	0.496765
family with sequence similarity 134, member C	0.872207	0.86664	0.474808
zinc finger and BTB domain containing 1	1.615276	0.632589	0.385102
similar to similar to expressed sequence AI316785 /// USP6	0.637589	1.301813	0.17546
amylase, alpha 2A; pancreatic	2.114347	0.824184	1.821968
Dual specificity phosphatase 5	2.882029	0.969417	1.329652
zinc finger, DHHC-type containing 23	0.891793	0.408745	1.062019
kinesin family member 3B	1.076731	1.458928	1.516529
CDC5 cell division cycle 5-like (S. pombe)	0.445379	1.395525	1.804445
isocitrate dehydrogenase 3 (NAD+) alpha	0.320904	0.889522	1.183563
interleukin 18 (interferon-gamma-inducing factor)	5.627726	2.65775	14.82556
GTPase activating protein and VPS9 domains 1			0.058716
chromosome 11 open reading frame 46	1.222705	0.539579	0.400107
Secernin 1	2.590006		0.973834
cysteine-rich secretory protein LCCL domain containing 1	3.202246	2.470281	2.239454

Peroxidasin homolog (Drosophila)	1.458982	1.150971	0.599399
TEL2, telomere maintenance 2, homolog (S. cerevisiae)	0.862151	0.031883	0.046401
Vps20-associated 1 homolog (S. cerevisiae)	1.141636	1.096116	0.396733
v-ral simian leukemia viral oncogene homolog B (ras related chromodomain protein, Y-like	0.793073	0.941674	0.648438
			0.495669
solute carrier family 39 (zinc transporter), member 6	6.80279	4.047414	1.263753
ADP-ribosylation factor-like 2 binding protein	0.728664	1.374242	1.409538
growth hormone secretagogue receptor		0.47758	
chromosome 6 open reading frame 192	0.94664	1.484577	2.593807
Diacylglycerol kinase, delta 130kDa	1.47674	1.023151	2.828617
catenin (cadherin-associated protein), delta 1	1.256848	1.259861	2.787941
ankyrin repeat domain 28	1.576615	1.256014	2.19511
Ubiquinol-cytochrome c reductase complex chaperone, CBP	1.312979	1.028362	0.537328
methytransferase like 5	0.654211	0.874151	0.430862
replication factor C (activator 1) 1, 145kDa	1.147816	1.193731	0.74944
Muscle-restricted coiled-coil protein	0.766329	0.750381	0.239471
retinoblastoma binding protein 6	0.646574	1.248938	0.422108
sorting nexin family member 21	2.137133	0.621667	2.494916
Cyclin J	1.794307	1.231493	0.457487
Hypothetical LOC417822	0.967984	0.486381	0.179821
similar to similar to CDNA sequence BC043118	1.332586	2.020714	1.258031
Cache domain containing 1	1.106079	1.52933	0.834733
solute carrier family 10 (sodium/bile acid cotransporter family), member 7			0.881563
ret proto-oncogene	1.032179	1.951045	6.708891
cadherin 2, type 1, N-cadherin (neuronal)	2.399815	1.36145	1.216971
Myoneurin	1.074761	1.084118	0.489316
Similar to trans-Golgi protein GMx33	7.840203	0.896614	0.188312
limb region 1 homolog (mouse)	1.164768	0.990425	0.436476
MAX interactor 1	2.030275	1.435534	1.579676
similar to FKSG11	3.749151	0.619642	2.199139
ER lipid raft associated 1	1.110017	1.03417	0.401409
kelch repeat and BTB (POZ) domain containing 10	1.294059	0.999993	4.361946
Seizure related 6 homolog (mouse)-like	0.449949	1.157626	0.765888
hypothetical gene supported by CR406964	1.100029	0.904584	0.601316
Hypothetical LOC421229	0.470308	1.181485	0.024995
Similar to PIAS-like protein hZimp10	1.071358	0.737996	0.820697
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5			
GA binding protein transcription factor, beta subunit 2	1.008964	1.011387	0.893804
ZXD family zinc finger C	1.317222	1.054622	0.481367
RAB GTPase activating protein 1	1.341778	0.465086	

bromodomain and WD repeat domain containing 1		0.486544	1.468212
Paired related homeobox 2	1.434169	0.693626	3.31354
TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0.965588	0.90561	0.538572
RAN binding protein 1	0.861301	1.242891	0.805806
retinoblastoma binding protein 6		8.028213	0.050572
growth arrest and DNA-damage-inducible, alpha	0.517658	0.834384	0.478646
Similar to hypothetical protein MGC42105		0.242306	
similar to endoU protein	0.883651	5.731008	1.434289
hypothetical gene supported by CR406014	2.048923	0.458724	0.525292
aldehyde dehydrogenase 9 family, member A1		1.452486	0.3642
CLPTM1-like	2.694037	0.648775	1.361726
phosphoribosyl pyrophosphate synthetase 1	0.720832	1.396955	0.688674
transmembrane protein 57	6.30176		
solute carrier family 35, member E3	1.664004	0.695286	0.782906
Solute carrier family 16, member 2 (monocarboxylic acid tra	1.191067	0.866971	1.421298
R-spondin 3 homolog (Xenopus laevis)	2.16162	1.182292	4.625516
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3		1.682572	2.334378
hypothetical protein LOC772031	0.455777	1.606161	2.008477
Nasal embryonic LHRH factor		2.379555	0.137127
v-crk sarcoma virus CT10 oncogene	1.0862	1.369962	0.472484
hypothetical gene supported by CR406681		1.576401	
epoxide hydrolase 2, cytoplasmic	1.057181	1.231639	3.571159
Zinc finger protein 704	1.113342	0.785828	0.421716
Chromosome 10 open reading frame 38	0.649246	1.476538	0.209586
Mitochondrial ribosomal protein L20	1.37842	0.335882	1.273837
melanoma inhibitory activity family, member 3	1.137578	1.113342	5.79873
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalac		3.428819	
similar to RIKEN cDNA 2700049P18	0.721552	1.104771	0.419462
Fatty acid desaturase 2	0.598023	1.01016	0.551706
torsin A interacting protein 2		4.569411	
trinucleotide repeat containing 6C	2.968726	0.687509	0.929783
myb-like, SWIRM and MPN domains 1		0.324028	
BMP2 inducible kinase	0.657538	0.887331	0.582785
Ninein (GSK3B interacting protein)	1.347902	0.926345	0.380284
ataxin 7	1.226957	0.956155	0.776626
Epithelial membrane protein 1	1.547678	1.293933	5.386149
mediator complex subunit 13			
cytochrome P450, family 26, subfamily C, polypeptide 1	0.897096	0.383278	0.963505
RAB22A, member RAS oncogene family	1.600618	0.744252	0.452345
Nucleolar protein 12	0.499469	0.21595	2.082225

Cas-Br-M (murine) ecotropic retroviral transforming sequen	0.988685	1.134439	0.30594
Lysyl oxidase-like 3			3.57193
Similar to MEG3	1.423652	1.240147	3.469322
acyl-CoA thioesterase 9			2.05587
collagen, type IV, alpha 2	1.919938	1.034933	2.432577
frizzled homolog 4 (Drosophila)	1.890019	0.981431	4.70861
hypothetical protein LOC772356	2.587585	1.104711	4.485047
similar to UDP-glucose ceramide glucosyltransferase-like 1	2.01734	1.060828	0.565662
transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)		0.458136	0.715751
KIAA0368	0.514979	1.026476	5.928019
Similar to pol			1.33519
ADAM metallopeptidase domain 28	2.593618	1.668543	1.988658
CD44 molecule (Indian blood group)	0.937998	0.771527	0.394288
Hypothetical LOC417937	2.038274	1.285322	2.59169
carbohydrate sulfotransferase 10	1.452362	0.903871	0.675888
ankyrin repeat domain 32	0.656151	0.709872	0.940239
solute carrier family 25, member 39			0.348722
ring finger protein 34		0.753242	
ring finger protein 34	2.114659	0.926972	1.409267
coiled-coil domain containing 73	3.286166	0.658434	
MAP7 domain containing 3	2.622559	0.442457	1.120079
transmembrane protein 106C	1.203674	2.118425	3.418888
titin	0.754466	1.160512	5.148635
titin	0.800775	1.200612	2.6746
titin	1.348194	1.474374	3.319728
titin			10.14445
ERGIC and golgi 2	0.873561	0.903619	1.865305
nuclear transcription factor Y, alpha	1.188092	0.918717	0.654114
Similar to similar to CDNA sequence BC043118	1.096876	0.666962	2.16371
G protein-coupled receptor 149	13.09752	4.611315	3.663429
FAT tumor suppressor homolog 3 (Drosophila)		0.231337	0.702382
Hypothetical LOC419269			20.01099
GRB2-associated binding protein 1		2.071469	0.873502
chromosome 14 open reading frame 143	0.969251	1.705357	2.347784
chromosome 20 open reading frame 58	2.173892		
hypothetical gene supported by CR405884	0.410026	0.809373	0.132256
chromosome 15 open reading frame 23	0.814407	0.989911	0.598965
transmembrane and tetratricopeptide repeat containing 1			
transmembrane and tetratricopeptide repeat containing 1	0.746541	0.557353	
purinergic receptor P2Y, G-protein coupled, 8	2.032976	1.378374	1.085822

peroxisomal proliferator-activated receptor A interacting con	0.453645		1.173887
FERM and PDZ domain containing 2	0.365517		
Heterogeneous nuclear ribonucleoprotein K	18.81659	2.933654	0.344409
Heterogeneous nuclear ribonucleoprotein K	25.81952	1.735626	0.255857
CDC28 protein kinase regulatory subunit 2	0.368561	1.007839	0.94925
coiled-coil domain containing 103	1.442957	1.254054	0.976645
Influenza virus NS1A binding protein	1.614534		12.68456
ubiquinol-cytochrome c reductase binding protein	1.350747	0.974595	0.4752
myoglobin	0.715532	0.276972	0.348812
Similar to KIAA0644 protein	0.641621	0.83459	0.121106
hypothetical gene supported by CR406167	0.674513	0.655224	0.275772
PHD finger protein 2	1.064952	0.712597	0.310244
Transmembrane protein 179	0.430841		
Similar to coiled-coil domain protein D53			
myosin X	0.944193	0.788841	0.287282
myosin X	0.951682	0.673525	0.254473
iduronidase, alpha-L-			
protein kinase N2	0.892054	1.408024	0.23616
doublecortin-like kinase 1	1.608297	0.90594	0.178759
notum pectinacetylsterase homolog (Drosophila)	0.649534	0.905129	3.523738
Hypothetical LOC415615	0.484239	0.982552	0.816337
phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor		1.275772	
protein phosphatase 4, regulatory subunit 1	1.141502	0.361679	0.552428
Family with sequence similarity 107, member B	1.046052	0.901287	0.494392
DCN1, defective in cullin neddylation 1, domain containing	0.886709	0.896192	0.499425
Enah/Vasp-like	0.228024		0.667322
Hypothetical LOC427846	0.348692	0.977194	
Hypothetical LOC427846	0.860495	0.593206	3.096736
forkhead box O3	0.45475	0.473214	0.585106
ATG2 autophagy related 2 homolog B (S. cerevisiae)	1.692388	0.532868	1.223057
uridine phosphorylase 2		1.119216	
coagulation factor V (proaccelerin, labile factor)	2.389683		
diaphanous homolog 3 (Drosophila)	1.037609	1.29846	0.541768
molybdenum cofactor sulfurase	1.53643	4.626714	
similar to echinoderm microtubule associated protein like 5	0.388118	0.969873	
G protein-coupled receptor 97	1.236344	0.667047	0.754034
Vacuolar protein sorting 41 homolog (S. cerevisiae)	0.853149	1.11025	0.377409
Vacuolar protein sorting 41 homolog (S. cerevisiae)	3.150085	0.588575	0.367972
claudin 15	1.699181	2.888036	0.926927
low density lipoprotein-related protein 12	1.521938	0.915947	0.277381

Chromosome 14 open reading frame 32	1.747954	1.420496	0.808337
matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9	7.579496		4.315287
zinc finger, ZZ-type with EF-hand domain 1		1.240753	0.20542
DIP2 disco-interacting protein 2 homolog A (Drosophila)		0.487496	0.586937
MAD2 mitotic arrest deficient-like 1 (yeast)	0.668617	1.128313	0.472957
similar to Chromosome 2 open reading frame 3			0.698432
TOX high mobility group box family member 3	3.765452	1.647679	1.579909
target of EGR1, member 1 (nuclear)	0.783722	0.80337	1.471765
anaphase promoting complex subunit 2	0.424976	0.875053	0.447555
plexin A2	1.05798	0.834734	3.426852
Malate dehydrogenase 2, NAD (mitochondrial)	0.788041	0.707446	0.291428
AT rich interactive domain 1A (SWI-like)	2.327885	1.432004	1.522655
coiled-coil domain containing 112	0.719622	1.608045	3.593658
mitochondrial ribosomal protein L35	0.895657	1.106128	0.950191
Fas (TNFRSF6) associated factor 1	1.83719	0.978166	0.70097
phosphatidylinositol glycan anchor biosynthesis, class S	0.927353	1.093933	2.191981
similar to zinc finger RNA binding protein	2.656919		0.608851
chromosome 20 open reading frame 7	1.323096	0.94695	0.432947
snail homolog 2 (Drosophila)	1.711763	1.25592	2.425142
ring finger protein 207	2.132008		3.143831
mediator of RNA polymerase II transcription, subunit 31 hor	1.197297	0.875357	0.324494
trefoil factor 2	1.042537	1.135465	2.426958
hypothetical protein LOC769949		0.266662	
coiled-coil domain containing 60	3.014278		
Coagulation factor XIII, A1 polypeptide	0.947832	1.503367	10.37932
chromosome 10 open reading frame 63	0.584646	0.949758	3.400589
chromosome 10 open reading frame 63	0.91851	3.528046	1.27222
Zinc finger, DHHC-type containing 3	1.044215	1.328717	1.419172
chitinase, acidic /// similar to CBPch04	11.99135		0.756885
KIAA0430		19.83793	
dedicator of cytokinesis 9	1.330251	0.923027	0.217743
fibrillin 2			0.311979
coiled-coil domain containing 84	1.315009	0.480996	0.323948
ring finger protein 19A		1.393012	
delta/notch-like EGF repeat containing			
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.792541	0.631369	0.019252
tec protein tyrosine kinase	1.925379	0.580715	0.370992
thrombomucin	1.964773	1.284614	2.216014
Exocyst complex component 3-like	1.060258	1.506348	1.354346
Similar to nitric oxide synthase 1 (neuronal) adaptor protein	0.951938	1.254443	3.048297

proprotein convertase subtilisin/kexin type 6	1.455922	1.318062	2.80515
LATS, large tumor suppressor, homolog 1 (Drosophila)	0.912375	1.086928	0.711199
chromosome 20 open reading frame 11	0.829541	0.71058	0.591962
paralemmin 2	0.994744	1.290799	2.513742
4-aminobutyrate aminotransferase	0.781119	1.036374	1.136334
ninjurin 2	2.287693	0.531934	1.106555
signal-induced proliferation-associated 1 like 2	1.138613		4.475415
unc-119 homolog B (C. elegans)	1.078952	1.122279	0.216988
mannosidase, alpha, class 1A, member 1	0.447591	0.914724	0.551589
BCL2/adenovirus E1B 19kDa interacting protein 3	0.363362	1.084907	0.171553
topoisomerase (DNA) II alpha 170kDa	1.078949	1.058107	0.435321
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen)	1.850876	1.975765	5.611638
musashi homolog 1 (Drosophila)			2.386063
deoxynucleotidyltransferase, terminal, interacting protein 2	0.439373	0.569341	0.057704
pleckstrin homology domain containing, family M (with RUF1)	1.68279	1.123377	2.173593
chromosome 13 open reading frame 34	1.015541	1.254811	0.437024
cell division cycle associated 2		1.247295	0.236915
mab-21-like 2 (C. elegans)			6.246142
heme oxygenase (decycling) 1	1.679744	1.35757	4.09
tropomodulin 4 (muscle)	0.991436	1.251187	2.861436
Endoplasmic reticulum-golgi intermediate compartment (ER) protein 1	1.022466	1.001055	1.175609
pyruvate dehydrogenase (lipoamide) alpha 1	1.61044	0.898792	0.297608
chromosome 1 open reading frame 83	0.652562	0.784472	0.321388
chromosome 1 open reading frame 83	0.809599	0.960042	0.289605
glutaminase	2.468722	0.79645	0.510431
glutaminase	1.442418	0.886808	0.476164
GATA binding protein 6	1.869361	1.200601	9.57096
v-ets erythroblastosis virus E26 oncogene	2.218742	1.757985	1.46521
v-ets erythroblastosis virus E26 oncogene	1.093134	1.851706	2.258922
kinesin heavy chain member 2A	0.696131	1.324123	3.20175
inhibitor of DNA binding 4, dominant negative helix-loop-helix	1.469613	0.676197	0.469833
GATA binding protein 5	1.156287	1.634898	1.670464
thioredoxin-like 1	0.4504	1.34787	1.542838
ubiquitin specific peptidase 25	2.088339	1.329888	0.481609
casein kinase 1, epsilon	0.844898	0.784584	0.313549
casein kinase 1, epsilon	1.430296	0.52109	0.397668
DNA2 DNA replication helicase 2-like (yeast)	1.300029	2.036099	0.778465
myosin phosphatase Rho interacting protein	2.162187	0.531683	1.302205
WD repeat domain 5	0.873755	1.096057	0.734409
hypothetical LOC426015	0.648494	1.142164	2.439854

hypothetical LOC426015 /// hypothetical protein LOC76844	0.652819	0.870459	2.071008
neurexin 1	1.295564	1.815363	3.362807
suppression of tumorigenicity 14 (colon carcinoma)	1.248599	1.342074	2.26983
hypothetical protein LOC768920	0.780012	0.860071	0.505025
microtubule-associated protein 1B			
similar to GTP-binding protein SB128	1.605069	1.059006	2.380203
adenosine deaminase, RNA-specific, B1 (RED1 homolog rat	1.330327	0.82655	0.463102
chromosome 5 open reading frame 21	1.622533	1.132749	0.417163
heat shock transcription factor 2	1.261518	1.516319	0.266797
solute carrier family 31 (copper transporters), member 1	0.787799	0.601144	2.078568
KS5 protein	1.044651	0.843537	2.96073
Slit homolog 1 (Drosophila)	0.443684		
mitogen-activated protein kinase 1	1.181507	0.41049	0.578461
guanine nucleotide binding protein (G protein), alpha inhibit	1.039159	0.882425	0.435171
MHC class II antigen B-F minor heavy chain	291.5095	3.516264	0.032792
fer-1-like 3, myoferlin (C. elegans)	3.005156	1.176118	2.324343
protein phosphatase 1, regulatory (inhibitor) subunit 12B	0.458222	1.732789	1.126359
DOT1-like, histone H3 methyltransferase (S. cerevisiae)	0.603489	1.090834	2.406644
twist homolog 2 (Drosophila)	1.916296	1.957323	3.281041
Growth hormone regulated TBC protein 1	0.51109	1.361467	0.126295
chromosome 5 open reading frame 13	0.673331	1.095124	0.673354
GPN-loop GTPase 2	0.92601	0.908024	1.641004
suppressor of cytokine signaling 2	1.8109	1.316001	1.850915
cysteine-rich, angiogenic inducer, 61	3.441224	1.773256	1.581363
FK506 binding protein 1B, 12.6 kDa	0.601676	0.927576	2.198998
interleukin 6 signal transducer (gp130, oncostatin M receptor	2.185428	1.266791	1.172481
similar to alpha2,3-sialyltransferase	0.620685	0.809582	2.858311
zona pellucida glycoprotein 1 (sperm receptor)	3.709076		9.463066
frequenin homolog (Drosophila)	1.284148	0.564946	1.595566
HIR histone cell cycle regulation defective homolog A (S. ce	0.865149	0.911776	0.541184
transmembrane protein 163	2.05933	0.575698	
coagulation factor XIII, A1 polypeptide			3.2262
coagulation factor XIII, A1 polypeptide			
steroidogenic acute regulator		0.238611	
KIAA1529 /// similar to RP11-23J9.1		39.18995	
delta-like 1 (Drosophila)	3.339141		1.466343
histidine triad nucleotide binding protein 1	0.48173	1.152426	2.205078
Cell division cycle 37 homolog (S. cerevisiae)	0.474363	0.750063	0.490076
cone-type transducin alpha subunit		0.567439	1.007614
adenomatosis polyposis coli down-regulated 1	1.11689	2.145867	1.67764

nuclear VCP-like	5.294993		
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	0.693498	1.100329	0.543146
chemokine (C-X-C motif) receptor 4	0.933392	0.80233	0.194278
SET domain containing 3	2.330379	0.443231	
DnaJ (Hsp40) homolog, subfamily C, member 9	0.862939	1.032619	0.683208
DnaJ (Hsp40) homolog, subfamily C, member 9	0.435899	1.115596	0.770445
transmembrane and coiled-coil domains 1	0.254236	0.756299	4.679155
centromere protein C 1	1.132413	1.058833	0.538588
leucine aminopeptidase 3	2.256764	1.196802	0.961369
nucleoporin like 1	0.977821	1.014007	0.44088
eyes absent homolog 1 (Drosophila)	1.959687	1.074707	
similar to conserved hypothetical protein	1.414623	1.906346	2.736948
Sp3 transcription factor	0.966193	0.881197	0.550938
TP53 regulated inhibitor of apoptosis 1	1.00626	1.000046	0.589833
LIM homeobox 9	0.198121		
LIM homeobox 9	2.060383		
disabled homolog 1 (Drosophila)	2.136399	0.801248	0.781597
synaptobrevin-like 1	0.710952	0.9055	0.885223
Synaptobrevin-like 1			
resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	0.616508		0.244755
resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	1.243551	1.275786	0.452466
Smith-Magenis syndrome chromosome region, candidate 8	0.961019	0.805442	1.345829
similar to M-phase phosphoprotein 1	0.728847	1.301236	0.777588
similar to M-phase phosphoprotein 1	0.830475	0.767819	0.857993
cyclin E1 /// similar to cyclin E	1.543645	1.921463	0.953707
similar to KIAA0614 protein	2.061068	1.713095	1.908001
leucine rich repeat containing 17	2.40051	3.217743	3.10076
similar to Putative ubiquitin-conjugating enzyme E2 D3-like	0.862286	0.946729	0.451604
similar to Putative ubiquitin-conjugating enzyme E2 D3-like	16.68352	1.843322	0.414127
zinc finger protein, X-linked	0.860307	1.010994	0.275361
cryptochrome 2 (photolyase-like)	0.714145	0.71592	0.059008
cryptochrome 2 (photolyase-like)	1.265312	0.733393	0.512568
cryptochrome 2 (photolyase-like)	1.329228	0.752784	0.557431
dpy-19-like 1 (C. elegans)			
WD repeat domain 1	1.029914	1.317727	0.535551
similar to early response to neural induction ERNI		1.02237	0.391253
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide	1.064188	1.238905	2.875949
Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing	4.110894	1.027589	0.707524
neurotrimin	1.010342	1.005698	2.421729
chromosome 1 open reading frame 115	0.77911	0.825176	1.4063

glutathione S-transferase theta 1	0.76841	0.714248	0.082646
glutathione S-transferase theta 1	0.592636	0.750355	0.141111
MOB1, Mps One Binder kinase activator-like 1A (yeast)	1.442965	1.020993	
RAN binding protein 9	1.215127	0.881966	0.38592
fibroblast growth factor 18		0.368059	2.797958
Hypothetical LOC421802	0.451149	0.526578	
interferon-related developmental regulator 1	1.042056	1.079076	0.696812
tyrosine kinase with immunoglobulin-like and EGF-like dom	7.540117	0.871855	2.825521
glutamate-ammonia ligase (glutamine synthetase)	0.823584	0.956105	2.493061
glutamate-ammonia ligase (glutamine synthetase)	1.09839	1.18313	2.261168
immunoglobulin J polypeptide, linker protein for immunogl	2.369604	1.557781	0.180305
Solute carrier family 40 (iron-regulated transporter), member	0.79004	2.05465	0.902512
proprotein convertase subtilisin/kexin type 5	5.197226		
paraoxonase 2			2.734103
inhibitor of growth family, member 1	1.243819	0.940942	0.615099
primase, DNA, polypeptide 2 (58kDa)	1.500531	1.964139	0.482021
neurochondrin	0.205938	1.284513	
xanthine dehydrogenase	1.259173		2.762937
cysteine conjugate-beta lyase 2	1.005493	0.883303	2.685095
ubiquitin B	0.54743	1.266642	1.50724
ubiquitin B	0.584148	1.292028	1.382976
similar to hypothetical protein FLJ38973	0.726223	0.761541	0.488153
purinergic receptor P2Y, G-protein coupled, 1	1.451125		2.251043
complement component 3	0.916921	0.997212	2.57155
protein tyrosine phosphatase, receptor type, G	0.924832	1.141977	0.338949
CHK2 checkpoint homolog (S. pombe)	0.960462	1.294657	0.639669
heat shock factor binding protein 1	0.690263	1.054245	0.41171
forkhead box K1	0.813379	0.39503	0.611499
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)			4.601584
interleukin 1 receptor-like 1	1.608865	2.069449	4.038357
interleukin 1 receptor-like 1	0.935653	2.123495	8.117787
brain factor-2			
lipoma HMGIC fusion partner-like 2 /// osteoblast membran	2.517398	1.229699	2.255386
glutathione S-transferase alpha 3	1.27537	1.794011	2.115105
latent transforming growth factor beta binding protein 1	0.775202	1.835479	1.45346
neuropilin 2	1.1521	1.451014	
RALBP1 associated Eps domain containing 2	0.850653	1.145967	0.345898
Similar to MGC83953 protein	0.696796	0.82156	0.193713
similar to LOC283951 protein	0.911379	1.836156	0.498398
chemokine (C-C motif) ligand 4	82.85354		7.323856

lactotransferrin	2.413333	1.190915	0.866849
lactotransferrin	2.226141	1.444311	0.863581
succinate-CoA ligase, GDP-forming, beta subunit	1.682792	0.583006	0.949403
collagen, type XIV, alpha 1 (undulin)	0.777831	0.809527	0.543931
Tumor protein D52-like 1	1.622065		3.839991
UTP6, small subunit (SSU) processome component, homolo	1.194005	1.441442	0.448212
lysosomal-associated membrane protein 2	1.266496	2.252354	0.828265
Nuclear receptor interacting protein 3	1.973737	3.145179	3.320178
major facilitator superfamily domain containing 10	0.88348	0.93558	2.373513
similar to PLCG1 variant protein	0.758592	0.874109	1.641351
coiled-coil domain containing 86	0.60939	1.388669	1.976451
doublesex and mab-3 related transcription factor 1	0.72878	0.843954	1.570562
v-maf musculoaponeurotic fibrosarcoma oncogene homolog	3.640804	1.622886	7.674698
doublecortex	0.650197	3.304656	0.355275
three prime histone mRNA exonuclease 1	1.051361	1.088303	2.104003
keratin 19	1.033809	1.15189	0.299475
keratin 19	0.435386	0.951768	0.213901
keratin 19	0.773187	3.1071	0.128669
secreted protein, acidic, cysteine-rich (osteonectin)	1.185094	1.06365	0.416693
tropomodulin 1	0.47729	0.799	1.241924
4-aminobutyrate aminotransferase			
mucolipin 2	2.52591	1.789679	2.063888
cripto, FRL-1, cryptic family 1B			4.580862
similar to peripheral clock protein 2	0.957233	1.040286	2.365939
transforming growth factor, beta receptor II (70/80kDa)	1.619095	1.070943	0.408851
myotubularin related protein 2	0.963592	0.47275	1.104761
homeobox B3	2.907315	0.647538	1.237151
macrophage receptor with collagenous structure	2.917887	1.620523	0.822768
hypothetical gene supported by CR354225	0.846573	3.950516	
FK506 binding protein 9, 63 kDa	2.739212	1.483242	2.806661
sulfotransferase family, cytosolic, 1C, member 3	1.626838	1.29886	2.776973
retinoic acid receptor, beta	1.522001	1.526583	2.149719
methylenetetrahydrofolate dehydrogenase (NADP+ depende	1.384914	0.956298	0.215565
family with sequence similarity 69, member B	0.593038	1.36379	1.876765
family with sequence similarity 69, member B		2.168094	
fibulin 1	1.778176	1.831455	5.140056
aquaporin 1 (Colton blood group)	1.189872	1.466677	5.162772
fibroblast growth factor 13	1.074103	21.027	3.134738
runt-related transcription factor 1; translocated to, 1 (cyclin I	1.771061	1.447092	2.141031
frizzled homolog 6 (Drosophila)	2.587858	3.291985	0.455547

frizzled homolog 6 (Drosophila)	10.30159		
La ribonucleoprotein domain family, member 4	1.249517	2.009763	1.71858
lymphoid enhancer-binding factor 1	0.653143	1.07825	0.115798
lymphoid enhancer-binding factor 1	0.857836	0.987736	0.1661
RNA binding protein with multiple splicing 2	2.493628	1.11525	2.475775
retina and anterior neural fold homeobox	0.148075	1.199093	
nuclear receptor subfamily 6, group A, member 1	1.270319	1.693926	2.174767
clock homolog (mouse)	1.816299	0.597752	0.488849
calmegin	1.242554	4.405936	0.800895
bone morphogenetic protein 1	2.431551	0.969158	0.523179
bone morphogenetic protein 1	1.133396		5.849726
potassium voltage-gated channel, subfamily G, member 2		0.760245	2.79903
F-box protein 5	1.462125		0.469029
creatine kinase, brain	1.435054	1.480389	1.529247
synuclein, alpha (non A4 component of amyloid precursor)	1.390384	1.883743	1.091451
transcription factor 7-like 2 (T-cell specific, HMG-box)	1.463929	1.15698	0.578297
cannabinoid receptor 1 (brain)	2.04543		5.728003
activated leukocyte cell adhesion molecule	1.021554	0.838104	0.491304
integrator complex subunit 6		0.809704	0.089508
glutamate receptor, ionotropic, AMPA 4	0.427953	1.243006	0.822374
family with sequence similarity 96, member A	2.236385	0.234492	0.541317
Rho GTPase activating protein 21	1.930519	1.525496	2.634774
COX11 homolog, cytochrome c oxidase assembly protein (y	3.291381	0.905429	0.858629
zinc finger, CCHC domain containing 4	0.47658	0.35073	1.218222
microphthalmia-associated transcription factor			
Zwilch, kinetochore associated, homolog (Drosophila)	0.630862	1.231723	3.603106
leucine-rich, glioma inactivated 1	3.069115	1.433104	0.926185
seven in absentia homolog 1 (Drosophila)	0.485167	1.407251	0.739218
adducin 3 (gamma)	1.657321	1.608286	2.774761
early B-cell factor 1	2.197584	2.084862	2.944317
DEAH (Asp-Glu-Ala-His) box polypeptide 30	1.109636	0.804794	0.679759
splicing factor 3a, subunit 3, 60kDa	0.743623	1.268239	0.382477
solute carrier family 35, member F1	1.289568	1.406315	2.141486
interleukin 6 (interferon, beta 2)	3.619404		46.51493
v-src sarcoma viral oncogene	2.067374		2.274828
similar to Protein C18orf1	0.561634	3.900918	2.748873
similar to Protein C18orf1	1.293891	2.421524	5.804923
myosin IXA	2.565661	0.795472	2.302902
transmembrane protein 192	1.095764	1.002779	0.484116
v-maf musculoaponeurotic fibrosarcoma oncogene homolog	0.974243	0.891115	1.57505

chromosome 1 open reading frame 102	0.918903	0.866062	0.798133
v-maf musculoaponeurotic fibrosarcoma oncogene homolog	1.848327	0.885785	1.614651
phosphofructokinase, muscle	1.187788	0.436452	2.603456
phosphofructokinase, liver	0.877577	1.041297	2.168976
aryl hydrocarbon receptor nuclear translocator-like 2	1.374443	0.861638	1.579729
TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy	2.867467	1.845621	3.352392
cholinergic receptor, nicotinic, alpha 9	1.469286	0.3725	0.357894
hypothetical protein LOC776660	2.435552	1.490744	1.709908
ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	0.868685	0.885612	0.365533
similar to CASP gene product	0.818763	0.955371	0.468729
cut-like homeobox 1 /// similar to CASP gene product	0.55865	0.689931	0.252282
attachment region binding protein	0.947057	0.384105	3.206524
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polyp	1.008208	1.185596	4.571989
leucine rich repeat containing 8 family, member D	0.925917	0.979933	0.648935
stathmin 1	0.370442	1.132591	0.317107
activin A receptor, type IIA			
hyaluronan binding protein 4	1.053899	1.103619	2.612181
Phosphatase and tensin homolog	1.031028	1.390096	0.4724
solute carrier family 12 (sodium/chloride transporters), mem	0.987146	0.456817	5.310114
Transporter 2, ATP-binding cassette, sub-family B (MDR/T	1.683743	1.388565	3.689806
vav 3 oncogene	1.196671	0.711722	0.358815
vav 3 oncogene	1.066912	0.774264	0.612814
DnaJ (Hsp40) homolog, subfamily C, member 18	2.575387	0.596658	0.793793
DnaJ (Hsp40) homolog, subfamily C, member 18	3.071274	0.699591	0.831207
DnaJ (Hsp40) homolog, subfamily C, member 18	2.527498	1.130252	0.511367
dihydrofolate reductase	0.327056	1.302426	2.128062
fibrillin 1	0.590442	0.972466	3.615338
methyltransferase like 14	0.691136	0.954485	0.377787
c-mer proto-oncogene tyrosine kinase	1.668502	1.505839	4.743076
carbonyl reductase 1	0.967041	1.011214	1.45039
smoothelin		2.59691	0.798196
Rho GTPase activating protein 26		1.163176	2.744898
Rho GTPase activating protein 26	0.504055	3.253635	
hemoglobin, alpha 2	0.480146	1.921648	5.434627
hemoglobin, alpha 2	0.531891	1.671765	5.308849
similar to chromosome 2 open reading frame 24	0.840427	0.90905	2.029083
hemoglobin, alpha 1	0.587715	1.357911	4.477974
hemoglobin, alpha 1	0.471881	1.539881	4.347862
Glypican 4	2.041791	0.744664	1.018833
centromere protein F, 350/400ka (mitosin)	1.175441	1.106449	0.858912

Similar to stomatin related protein	1.130723	1.10316	2.67258
metal-regulatory transcription factor 1	1.069158	0.744785	0.309758
ribosome binding protein 1 homolog 180kDa (dog)	1.798158	1.208668	1.219651
paired-like homeobox 2b	9.87342		
lysosomal-associated membrane protein 2	0.403811	1.736651	0.658568
claudin 3	0.616332	0.747024	2.306872
interleukin 22 receptor, alpha 1	3.224229	3.241365	1.435847
chemokine (C-C motif) ligand 1	2.010654	1.885237	3.122369
caspase 6, apoptosis-related cysteine peptidase	1.509581	0.849378	0.423765
chaperonin containing TCP1, subunit 6A (zeta 1)	1.739382	0.872099	0.729275
TIMP metalloproteinase inhibitor 2	0.858679	1.155226	1.448877
chromosome 3 open reading frame 64	0.07127	0.569674	1.655023
Glycosyltransferase	2.078346	0.954314	0.30872
protein tyrosine phosphatase, receptor-type, Z polypeptide 1	2.343234	1.225848	0.70653
iroquois homeobox 2	1.330604		
odx, odd Oz/ten-m homolog 2 (Drosophila)	1.003777	0.619065	2.864115
retinoblastoma 1 (including osteosarcoma)	1.022376	1.113594	0.714985
chromosome 18 open reading frame 37	0.484773	1.419429	1.402869
aldehyde dehydrogenase 1 family, member A2	1.601611	1.416561	1.492856
aldehyde dehydrogenase 1 family, member A2	5.558109		0.648949
nischarin	1.200824	0.827431	0.539101
PRKR interacting protein 1 (IL11 inducible)	1.075789	0.793962	0.610804
SEC24 family, member B (S. cerevisiae)	1.258069	0.724045	0.391205
fibroblast growth factor 14			
ARP2 actin-related protein 2 homolog (yeast)	0.834768	1.264786	1.936654
cAMP responsive element binding protein 1	4.702666	1.061562	1.047918
Similar to Mediator of RNA polymerase II transcription subunit	0.883405	0.975339	0.784842
retinol saturase (all-trans-retinol 13,14-reductase)	0.785113	0.97235	2.140006
similar to Small inducible cytokine A13 precursor (CCL13) (11.73451		
chordin-like 1	1.130213	2.334973	1.722335
formin binding protein 1-like	1.628732	0.824116	0.417301
EPH receptor A5	1.137063	1.49064	1.899939
YTH domain family, member 1	1.300674	1.112561	0.70788
EPH receptor B3	1.183494		
BARX homeobox 2			
hypothetical LOC423006	0.427771	1.299982	1.001353
myosin binding protein C, slow type	1.374063	0.753797	2.123067
HCLS1 binding protein 3	1.797456	1.280808	3.21478
galectin CG-16	0.336295	0.794399	0.511667
Galectin CG-16	1.007054	0.992602	2.096253

ADAMTS-like 3		1.102122	13.27558
similar to general transcription factor	8.546334	1.471567	3.627541
golgi apparatus protein 1	0.733711	0.973323	1.72431
golgi apparatus protein 1	0.616633	0.887605	1.347206
phospholipase B domain containing 1	1.284474	1.106125	1.844216
collagen, type IV, alpha 2	1.184308	1.015152	2.35835
Frizzled-8	2.001433	5.913417	2.704442
collagen, type VI, alpha 1	1.788846	1.660956	2.238648
claudin 5		2.533384	1.759195
neurocalcin delta	1.667229	0.380319	0.117566
diazepam binding inhibitor (GABA receptor modulator, acyl	3.254142	0.197089	1.230238
proline rich 11	0.830487	1.034453	0.738421
inhibitor of DNA binding 2, dominant negative helix-loop-h	1.095056	0.897194	0.341034
CAP-GLY domain containing linker protein 1	0.749917	1.577115	1.752053
syndecan 3	0.950673	1.088615	2.873306
prostaglandin-D synthase	2.466216	1.844215	1.018712
thrombospondin, type I, domain containing 7A		0.458108	
cannabinoid receptor 1 (brain)	0.330466	0.809123	
family with sequence similarity 122A	0.802146	1.122108	0.443331
similar to Moesin (Membrane-organizing extension spike protein)		3.293328	
cyclin B2	0.718587	1.168158	0.835277
exocyst complex component 5	0.406848		
keratin	0.711906	0.737221	0.449429
MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	1.710588	0.563941	0.411712
ORM1-like 3 (S. cerevisiae)		0.822272	0.402585
quaking homolog, KH domain RNA binding (mouse)	1.132904	0.857971	0.43176
cell division cycle associated 3	0.621968	1.054264	0.477165
dachshund homolog 2 (Drosophila)	0.767929	1.112252	0.495442
potassium intermediate/small conductance calcium-activated channel, subfamily N,			0.116277
LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransfe	1.627337	1.379977	3.066934
mitochondrial ribosomal protein L21		0.45669	
homeobox D8	0.609528		8.297633
ubiquitin specific peptidase 10	0.966311	0.855667	1.06158
Tumor necrosis factor, alpha-induced protein 1 (endothelial)	0.549023	2.08712	2.300634
structural maintenance of chromosomes 4	0.900351	0.983508	0.445407
C-RF amide	1.643638	0.632375	
chromosome 7 open reading frame 23	1.931041	1.032758	1.605154
inositol polyphosphate multikinase	1.158135	1.384542	2.793183
Anillin, actin binding protein	0.756699	1.074437	0.304756
anillin, actin binding protein	0.114699		

X-ray repair complementing defective repair in Chinese ham	1.069045	1.200015	0.992513
required for meiotic nuclear division 1 homolog (S. cerevisia	1.3951	0.655644	0.457983
mannosidase, alpha, class 1B, member 1	1.581527	0.85939	0.428808
c-fos induced growth factor (vascular endothelial growth fac	1.677466	2.059323	5.195278
sprouty homolog 1, antagonist of FGF signaling (Drosophila	0.75787	0.491343	0.640463
HemK methyltransferase family member 1	0.999494	1.220804	0.783458
myosin, heavy chain 11, smooth muscle	1.538989	1.00877	4.458451
NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (0.331912	0.530579	1.111572
PHD finger protein 11	3.299323	1.144717	1.983491
neuronal growth regulator 1	1.302885	1.031516	2.895689
similar to Breast carcinoma amplified sequence 1 (Novel am	7.440256		
v-abl Abelson murine leukemia viral oncogene homolog 2 (a	0.314701	0.968089	
visinin-like 1	1.238583		0.029577
lecithin-cholesterol acyltransferase	2.078016	2.137977	10.80032
angiopoietin 2	2.374574	1.720765	1.829934
hypothetical LOC425605	0.503175	1.367474	2.185424
similar to MGC80370 protein		3.497344	1.913483
MHC B-G antigen	1.080911	0.696556	0.697069
MHC B-G antigen	5.606188		
cerebellin 1 precursor	1.189853	1.140943	1.254747
Mitochondrial ribosomal protein S16	0.967149	1.109711	0.254877
hyaluronan synthase 2	3.758232	1.676101	1.205537
ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	1.345253	1.426018	1.862079
hypothetical LOC425172 /// tRNA 5-methylaminomethyl-2-	1.498075	0.618136	0.562528
endothelin receptor type B	1.182092	1.032051	2.889225
ankyrin repeat domain 38	4.568518	0.792857	2.755526
cytochrome P450, family 26, subfamily A, polypeptide 1	1.697711	0.581587	0.037541
mitochondrial ribosomal protein L17	0.395974	1.171279	1.772798
mitochondrial ribosomal protein L17	0.327294	1.000777	1.529609
mitochondrial ribosomal protein L17	0.40899	1.057628	1.556768
hematopoietically expressed homeobox	1.262886	1.172605	1.874177
nuclear receptor coactivator 1	1.373789	0.833674	2.365558
fatty acid binding protein 5	1.190769	0.916251	2.668652
chromosome 18 open reading frame 21	1.640421	1.26988	0.391262
spondin 1, extracellular matrix protein	8.473291	1.663639	1.306609
matrix-remodelling associated 8	2.439311	2.099623	2.465011
mucin 5B, oligomeric mucus/gel-forming	1.191861	2.220426	
capping protein (actin filament) muscle Z-line, alpha 2	1.536225	1.011044	0.936945
arylsulfatase family, member H	2.286081	1.549821	1.299164
podocalyxin-like	1.936293	1.029361	3.080452

ATPase, Ca ⁺⁺ transporting, plasma membrane 1	1.732199	1.022497	0.68094
protocadherin 9	2.911247		45.7665
complement component 4 binding protein, alpha	1.08866	0.913083	0.724662
lysozyme G-like 2	3.486435		3.133091
Similar to MGC81154 protein	0.599669	1.046096	1.881224
interferon regulatory factor 2	1.037782	0.837072	0.490052
tumor necrosis factor receptor superfamily, member 1A	1.667186	1.099755	2.031239
popeye domain containing 3	0.87801	0.772626	0.416828
popeye domain containing 3	0.804508	0.367923	0.673515
popeye domain containing 3	1.187071	0.800157	0.632746
SH3-domain kinase binding protein 1	0.949856	1.875325	0.400756
SH3-domain kinase binding protein 1	12.03348		
SH3-domain kinase binding protein 1	0.893869	0.783824	0.320542
T cell receptor alpha locus	0.656161	1.105889	0.338924
lipopolysaccharide-induced TNF factor	1.517638	2.790421	9.931461
lipopolysaccharide-induced TNF factor	1.47572	2.259956	3.802655
adrenergic, alpha-1B-, receptor	0.684882	2.045896	
solute carrier family 34 (sodium phosphate), member 1	1.544036	1.154177	2.247447
paired-like homeodomain 2	2.520153	0.483826	1.400022
FCH and double SH3 domains 2	0.976859	0.921842	0.450012
calcium channel, voltage-dependent, gamma subunit 4		3.665758	2.643293
olfactomedin 1	1.017882	3.551179	
Growth differentiation factor 5		2.412833	
EPH receptor B2	0.818471	1.448828	1.834512
cholinergic receptor, nicotinic, beta 4		2.377781	2.397416
mitogen-activated protein kinase 6	5.38117		1.04364
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy	1.662742	1.502624	4.081304
HESX homeobox 1		0.93268	2.524873
neurexin 3	1.018801	1.187852	2.197221
zinc finger protein 609	9.279846	0.14608	0.836581
sterol carrier protein 2	1.354736	1.139334	0.517883
ELAV (embryonic lethal, abnormal vision, Drosophila)-like	2.573113	0.477971	2.67754
PDZ and LIM domain 3	0.293728	0.558648	0.250955
PDZ and LIM domain 3	0.384331	0.704071	0.458603
transmembrane protein 167	0.582391	1.096891	0.544983
transmembrane protein 167	0.22141		
frizzled homolog 9 (Drosophila)	1.285264	1.274311	1.320034
phospholipase C, delta 1	2.508857	2.505011	0.722469
collagen, type IX, alpha 3	19.93803		
collagen, type IX, alpha 3	4.762602	0.44007	4.770791

ets variant gene 6 (TEL oncogene)	1.170614	1.150881	2.500015
fibroblast growth factor receptor 2	1.582902	1.436074	4.699017
fibroblast growth factor receptor 2	1.811013	1.131411	3.053947
Rho-associated, coiled-coil containing protein kinase 2	0.683823	1.53871	1.75626
regulator of G-protein signaling 20	0.855868	1.307886	0.253367
mitochondrial ribosomal protein L27	0.892625	1.174653	0.778444
myosin VA (heavy chain 12, myoxin)	2.093092	0.874967	0.562272
similar to myosin VA (heavy polypeptide 12, myoxin) /// sin	2.121912	0.814256	0.396814
secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, s	1.608139	0.615076	0.934598
solute carrier family 16, member 3 (monocarboxylic acid tra	1.20651		1.002164
CD44 molecule (Indian blood group)	1.739684	0.568252	0.252589
CD44 molecule (Indian blood group)	1.041954	1.179708	0.45999
dickkopf homolog 3 (Xenopus laevis)	0.874442	2.023534	2.71742
similar to Gag-Pol polyprotein	0.586796	1.00436	0.165217
T-cell receptor V alpha	0.621523	1.427991	0.175918
insulin receptor		0.331488	
K(lysine) acetyltransferase 2A	1.366785	0.83435	2.030252
eukaryotic translation initiation factor 4E	1.002565	0.900759	0.437356
Sec23 homolog A (S. cerevisiae)	1.352374	0.89986	0.445392
Sec23 homolog A (S. cerevisiae)	1.594924	0.801797	0.430956
Sec23 homolog A (S. cerevisiae)	0.694135	2.248413	0.217101
Sec23 homolog A (S. cerevisiae)	0.506522	0.930787	0.398378
Sec23 homolog A (S. cerevisiae)	0.935633	1.197364	0.259177
hypothetical LOC426458 /// hypothetical protein LOC77085	0.426536	0.742762	0.641452
E2F transcription factor 4, p107/p130-binding	0.747459	0.98743	2.005825
folliculin		0.401806	4.035666
folliculin	0.798051	0.395195	
hypothetical LOC415913	0.677826	1.071594	0.24537
crystallin, zeta (quinone reductase)		1.974052	10.10022
cortactin	2.279575	1.175518	0.653661
kinectin 1 (kinesin receptor)	0.474973	1.203154	1.491742
C-type lectin domain family 3, member B	1.766189	2.027471	1.036807
nuclear factor (erythroid-derived 2)-like 2	1.642987	1.278397	1.815333
nuclear factor (erythroid-derived 2)-like 2	1.213014	1.320143	3.029044
Cadherin 20, type 2	1.0088	1.554542	1.43426
T cell receptor alpha locus	1.386206	0.289733	0.28656
glutamine rich protein	0.670772	0.898226	1.687142
Trinucleotide repeat containing 15	2.673298		0.111864
Rous sarcoma virus transcription enhancer factor II	0.699472	1.06472	2.035865
ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1.327486	1.177074	3.534508

calpain 2, (m/II) large subunit	1.788386	2.07343	2.774243
TATA box binding protein (TBP)-associated factor, RNA pc	0.609095	0.913541	0.341819
myosin, heavy chain 1, skeletal muscle, adult /// myosin, hea	1.465602	1.011775	0.524806
fatty acid binding protein 1, liver	0.905424	2.342217	15.0514
histone deacetylase 4	1.306755	1.230466	2.15569
Zinc finger protein 207	1.273643	0.791706	1.360336
zinc finger protein 207	1.010945	0.885658	0.88295
MHC B-G antigen /// hypothetical LOC425214 /// similar to	1.561027	1.514457	2.101648
Similar to ATP-binding cassette, sub-family C, member 9 isc	0.841322	0.943101	0.494651
hypothetical LOC416899		2.928216	
centromere protein F, 350/400ka (mitosin)	0.725012	1.007399	0.381014
muscleblind-like 2 (Drosophila)	1.855334	1.162553	2.280797
calcium/calmodulin-dependent protein kinase kinase 2, beta	2.945828	1.06519	1.211429
B-cell linker	5.881552	1.205445	0.583431
integrator complex subunit 6	0.809736	0.425054	0.325768
thyroid hormone receptor interactor 13	0.972449	1.232274	0.801412
carboxypeptidase Z	0.984183	0.961031	
T cell receptor alpha locus	0.944947	3.484862	0.17052
RYK receptor-like tyrosine kinase	1.021822	1.310377	0.822226
hairy and enhancer of split 1, (Drosophila)		0.095288	
potassium channel, subfamily T, member 1	1.3287	1.130473	3.350942
RCD1 required for cell differentiation1 homolog (S. pombe)	0.902336	0.958317	0.43411
interleukin 17 receptor D	1.235851	1.088526	0.235903
sterol carrier protein 2	1.084834	1.273968	2.021867
angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0.687023	1.975312	2.458406
target of myb1 (chicken)	0.873499	1.527231	4.272393
aldehyde dehydrogenase 1 family, member A3	0.916719	1.884792	3.845217
BCL2-related ovarian killer	0.764189	1.225307	1.038951
tenascin C	2.619977	1.173297	0.914815
nuclear autoantigenic sperm protein (histone-binding)	0.566178	1.198336	0.372458
period homolog 2 (Drosophila)	0.906235	0.426942	0.663466
period homolog 2 (Drosophila)			4.827294
Period homolog 2 (Drosophila)	0.701093	1.326725	5.638754
embigin homolog (mouse)	0.455852	1.230886	0.408237
protein phosphatase 3 (formerly 2B), regulatory subunit B, a	1.167108	1.128748	0.362541
Pleckstrin homology domain containing, family A (phosphoi	1.554864	1.465919	2.623678
frizzled homolog 3 (Drosophila)	0.494066	1.044248	0.39104
17-beta-hydroxysteroid dehydrogenase			1.835699
deoxythymidylate kinase (thymidylate kinase)	0.776397	1.031501	0.693902
ras homolog gene family, member B	1.718173	1.643899	2.61076

zinc finger protein 622	0.846631	0.986583	1.091355
cathepsin B	2.037703	1.383431	3.811512
peroxisome proliferator-activated receptor gamma	2.41938	0.920576	0.776053
peroxisome proliferator-activated receptor gamma			4.010248
regulator of G-protein signaling 17	0.901318	1.240407	0.165521
presenilin 1 (Alzheimer disease 3)	3.108389	0.664146	0.750107
Ras association (RalGDS/AF-6) domain family 8	1.235746	1.230062	2.936586
Carbohydrate sulfotransferase 10	1.104423	0.958267	0.885995
general transcription factor IIH, polypeptide 1, 62kDa	1.952818	4.194649	0.275181
v-akt murine thymoma viral oncogene homolog 1	1.216462	1.073662	0.316271
deltex 3-like (Drosophila)	2.251792	0.90276	2.08326
platelet-derived growth factor alpha polypeptide	1.920424	1.174885	1.220717
ADP-ribosyltransferase	1.083997	0.719464	0.41722
cadherin 13, H-cadherin (heart)	1.559026	1.371565	2.07307
cadherin 13, H-cadherin (heart)	3.960881	1.118563	1.65745
Epidermal retinal dehydrogenase 2		5.984656	
transgelin	1.309205	1.570406	3.115844
interleukin 10 receptor, beta	1.633849	1.342485	2.537236
pleckstrin	1.464136	1.500168	0.458783
pleckstrin	1.462806	0.73927	0.417604
eukaryotic translation initiation factor 5B	1.474267	0.372306	1.716067
hyaluronan and proteoglycan link protein 1	0.824373	0.79049	0.065298
v-erb-a erythroblastic leukemia viral oncogene homolog 4	1.145458	1.325212	0.488448
transmembrane and coiled-coil domains 3	2.256096	0.838649	1.332661
bone morphogenetic protein 2	1.744006	3.583792	4.069346
transcription factor Dp-1	1.130366	1.248298	0.87641
GC-rich promoter binding protein 1-like 1	0.837788	1.120186	0.449772
enabled homolog (Drosophila)	2.033372	0.648787	0.197046
tachykinin receptor 1			
survival motor neuron	0.522743	1.151596	0.440875
sema domain, immunoglobulin domain (Ig), short basic dom	1.655779	1.483807	
sema domain, immunoglobulin domain (Ig), short basic dom	0.480532	0.860233	0.895129
twist homolog 1 (Drosophila)			2.05778
multiple inositol polyphosphate histidine phosphatase, 1	0.341222	1.71654	1.135904
matrix metalloproteinase-13	0.102004	0.465095	0.429503
inhibin, beta A	2.454489	1.813505	3.286439
carbonic anhydrase II	0.551772	2.446552	1.041282
Fibronectin 1	2.821707	1.311211	2.40749
liver basic fatty acid binding protein			0.075157
ChaC, cation transport regulator homolog 1 (E. coli)	0.928786	0.539401	0.152737

peroxisome proliferator-activated receptor alpha	0.735794	0.533451	1.210725
transcription factor 12	2.260632	2.128454	0.417361
IKAROS family zinc finger 5 (Pegasus)		2.223042	0.676382
ezrin	1.443182	1.575085	3.83333
tumor protein p63	1.146249	1.277261	1.920407
pepsinogen 5, group I (pepsinogen A)	0.635799	1.043765	0.293249
mitogen-activated protein kinase-activated protein kinase 5	0.933143	1.201472	2.237224
zona pellucida glycoprotein 4			3.34976
K123 protein	3.40534	1.902315	2.500258
MHC class II antigen alpha	4.592145		0.076628
SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	0.498786	1.543504	1.064589
thioredoxin	0.689624	1.167329	2.181056
similar to DNA segment, Chr 10, Johns Hopkins University	0.592957	1.357981	0.561674
inhibitor of DNA binding 3, dominant negative helix-loop-helix	0.785186	0.681411	0.486432
inositol 1,4,5-trisphosphate 3-kinase A	0.484473		0.578843
connective tissue growth factor	1.345394	3.707102	6.006635
myosin, light chain 9, regulatory	0.935583	1.010761	3.145778
eukaryotic translation elongation factor 1 alpha 2	1.557678	1.237919	3.523644
single stranded DNA binding protein 3	0.742907	0.83286	0.555395
single stranded DNA binding protein 3	0.734363	0.923697	0.377603
high-mobility group box 2	0.62518	1.019842	0.411563
structural maintenance of chromosomes 2	0.35282	1.07394	1.598716
translin	0.857721	1.182723	0.427666
RAN, member RAS oncogene family pseudogene 1	0.924468	1.166298	0.711692
Colony stimulating factor 1 receptor, formerly McDonough 1	1.681139	1.856326	2.131509
KIAA1143	1.455395	1.343792	1.880992
lumican	1.042876	1.329704	0.492446
smoothened homolog (Drosophila)	1.047124	0.792557	1.00448
homeodomain protein	0.14785	0.490027	0.082055
frizzled homolog 1 (Drosophila)	1.350525	0.992693	2.085886
SLIT and NTRK-like family, member 4	1.044662	2.992773	
wingless-type MMTV integration site family, member 5A	1.135773	1.511159	1.087464
troponin T type 3 (skeletal, fast)	1.088549	1.236266	2.394997
myosin, light chain kinase	2.138912	2.255425	4.764131
myosin, light chain kinase	2.049479	1.675162	3.003498
epidermal growth factor receptor pathway substrate 15	0.188516		
epidermal growth factor receptor pathway substrate 15	0.451542		0.826646
Similar to surfeit 6			
Similar to surfeit 6	0.985861	0.566278	0.484216
parvalbumin		1.111544	1.749523

2',3'-cyclic nucleotide 3' phosphodiesterase	1.101307	1.324192	2.069201
similar to guanine nucleotide exchange factor Lbc	0.828839	0.082368	1.203497
beta-carotene 15,15'-monooxygenase 1	2.605689	1.706315	1.731462
transmembrane 9 superfamily member 3	0.342366		1.265467
solute carrier family 15 (oligopeptide transporter), member 1	0.99668		5.197547
tropomyosin 1 (alpha)	0.837434	1.238296	2.306769
tropomyosin 1 (alpha)	1.673097	1.27741	0.932867
ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.835299	1.120161	2.229946
ATP-binding cassette, sub-family B (MDR/TAP), member 1	2.150683	0.94219	1.982271
immunoglobulin lambda-like polypeptide 1	5.448275	1.050933	0.238897
immunoglobulin lambda-like polypeptide 1	5.161595	0.938063	0.443212
immunoglobulin lambda-like polypeptide 1	9.246994	1.096676	0.674674
immunoglobulin lambda-like polypeptide 1	11.01102	1.149009	0.29609
immunoglobulin lambda-like polypeptide 1	4.954589	0.917705	0.570688
apolipoprotein B (including Ag(x) antigen)	4.112413	3.871205	11.34393
plasminogen	0.892153	0.045099	
caspase 9, apoptosis-related cysteine peptidase	0.725201	0.783359	1.902132
aldehyde dehydrogenase 1 family, member A1		2.26718	
tensin 1	1.302631	1.10917	4.059835
tensin 1	0.958974	1.28006	4.31788
cyclin A2	0.982302	1.164301	0.660027
enolase 2 (gamma, neuronal)			56.07011
SMAD family member 5	1.939278	0.673686	0.475772
cholinergic receptor, nicotinic, alpha 1 (muscle)	1.40662		
Eukaryotic translation initiation factor 4 gamma, 2	0.069231		0.469529
matrilin 1, cartilage matrix protein			0.27936
COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)		0.877348	
COP9 constitutive photomorphogenic homolog subunit 5 (A	1.171588	1.01353	0.594752
serpin peptidase inhibitor, clade B (ovalbumin), member 10		2.439484	
basigin (Ok blood group)	0.980935	1.035434	2.03819
Similar to 5A11/Basigin-2	0.769055	1.055939	2.277059
Thy-1 cell surface antigen	2.439451		3.356593
high-mobility group nucleosomal binding domain 2	0.902671	1.053582	0.836595
exportin 7	3.194124	1.361176	1.042347
aldo-keto reductase family 1, member B10 (aldose reductase	1.52992	1.134194	1.728541
neurofilament, medium polypeptide 150kDa	1.876845		10.46685
major histocompatibility complex class I glycoprotein	51.12829	1.198863	0.151755
Interferon (alpha, beta and omega) receptor 1	1.144494	1.541976	3.082514
osteoglycin	0.96708	1.430202	0.461611
Chromosome 20 open reading frame 11	1.093944	0.837037	0.31915

actin binding LIM protein family, member 2	1.059682	0.835849	2.073928
actin binding LIM protein family, member 2	0.967739	1.056447	0.741894
actin binding LIM protein family, member 2	5.958656	0.965264	1.641827
reticulon 4	1.423933	0.750905	0.28446
thymidine kinase 1, soluble	0.666907	1.039912	0.706779
metallothionein 4	0.538529	1.234744	4.500221
cartilage associated protein	1.80795	1.041732	2.431079
myomesin (M-protein) 2, 165kDa	1.226233	1.17856	3.387962
myosin, heavy chain 1, skeletal muscle, adult /// myosin, hea	0.696685	1.805766	4.37316
myosin, heavy chain 6, cardiac muscle, alpha	1.354829	0.622946	0.705712
myosin, heavy chain 6, cardiac muscle, alpha	0.92749	0.634922	0.290472
myosin, heavy chain 2, skeletal muscle, adult	0.397025	1.152968	6.463645
myosin, heavy chain 2, skeletal muscle, adult	0.707415	1.560372	3.558466
myosin, heavy chain 2, skeletal muscle, adult	0.82104	1.687942	5.181946
myosin, heavy chain 3, skeletal muscle, embryonic	0.624262	1.288711	6.213583
leukocyte cell-derived chemotaxin 2	0.40806		
V-set and immunoglobulin domain containing 1	0.71702	0.853544	0.129565
homeobox A4	1.071721	0.436666	0.632379
collagen, type VI, alpha 2	1.686763	1.61513	2.207325
pterin-4 alpha-carbinolamine dehydratase/dimerization cofac	1.356997	1.667957	1.805767
similar to trypsinogen /// similar to trypsinogen /// protease, s	0.714499	1.898014	0.130515
similar to trypsinogen /// similar to trypsinogen /// protease, s	0.643639	2.704625	0.17036
similar to trypsinogen /// similar to trypsinogen /// protease, s	0.879288	1.479195	0.246228
CCAAT/enhancer binding protein (C/EBP), beta	3.183117	1.78913	3.9086
STT3, subunit of the oligosaccharyltransferase complex, homolog A (S.	1.390512		2.436182
tryptophan hydroxylase 1			
laminin, gamma 1 (formerly LAMB2)	1.286474	0.834486	8.491019
argininosuccinate lyase	1.066633	1.095988	1.924217
CDC-like kinase 3	0.611095	1.325898	0.193721
CDC-like kinase 3	2.021563	0.891833	0.270181
chromodomain helicase DNA binding protein 1	0.581669	1.065166	1.288266
desmuslin	1.334009	0.743913	1.598707
parvalbumin			2.642986
M-CK	1.436244	1.50211	4.369845
SRY (sex determining region Y)-box 8	0.476003	0.760164	0.918338
poly(A) polymerase alpha	0.929415	0.864458	0.409164
calcium channel, voltage-dependent, N type, alpha 1B subun	1.507307	1.167711	5.638233
Hypothetical protein LOC777119	1.963976	1.297868	3.338997
5'-nucleotidase, cytosolic III-like	1.565441	1.838761	2.333557
growth hormone receptor			

heat shock 90kDa protein 1, beta	0.695728	1.153081	3.261774
ubiquinol-cytochrome c reductase core protein I	0.646914	1.004183	0.245383
myb-like, SWIRM and MPN domains 1	2.723778	0.550297	0.698575
hypothetical LOC417822	1.269712	0.73116	0.498579
SWI/SNF related, matrix associated, actin dependent regulat	0.86944	1.132129	0.581305
SWI/SNF related, matrix associated, actin dependent regulat	0.581549	1.334235	0.449481
FYN oncogene related to SRC, FGR, YES	0.919448	0.956497	1.598859
tumor necrosis factor (ligand) superfamily, member 13b	4.18635		1.332464
tumor necrosis factor (ligand) superfamily, member 13b	4.344528	2.074895	2.807566
IKAROS family zinc finger 3 (Aiolos)		0.758688	0.473643
N-acetylgalactosaminidase, alpha-	1.007891	0.850476	2.152967
tyrosine kinase 2	0.908769	1.662795	2.64754
minichromosome maintenance complex component 6	0.68006	1.230358	0.445374
putative homeodomain transcription factor 2	2.194722	1.001889	2.960055
cytochrome b5 reductase 2	0.914772	1.468586	2.601367
interferon regulatory factor 4	1.210796	1.989222	4.052806
general transcription factor IIIC, polypeptide 3, 102kDa	0.907548	0.822798	0.295363
RAP1A, member of RAS oncogene family	1.038861	1.000436	0.605261
baculoviral IAP repeat-containing 2	1.736308	1.185983	2.008698
baculoviral IAP repeat-containing 2			
baculoviral IAP repeat-containing 2	2.011516	0.938414	0.904358
ferritin, heavy polypeptide 1	0.899764	1.231652	2.015345
ferritin, heavy polypeptide 1	0.898307	1.272444	1.70975
ferritin, heavy polypeptide 1	0.93148	1.3161	1.88392
B-cell CLL/lymphoma 2	1.135632	1.176446	0.578875
prosaposin	2.03521	1.171888	1.013222
prosaposin	1.202827	1.304221	1.77049
chemokine (C-C motif) ligand 4	44.24128	2.403212	4.186489
TAP binding protein (tapasin)	1.628076	1.502808	3.841823
CD74 molecule, major histocompatibility complex, class II i	0.785448	1.360365	0.475867
serpin peptidase inhibitor, clade I (neuroserpin), member 1	0.462794	0.330556	0.437571
AQ		2.598385	
reticulon 1	1.376145	1.325764	2.43302
Ubiquitin C	0.428866	1.243454	0.788383
SH3-domain GRB2-like 3	0.698229	0.719773	0.192579
similar to T cell receptor alpha /// similar to T cell receptor a	0.649243	0.819287	0.398818
solute carrier family 35 (CMP-sialic acid transporter), member A1		4.959918	1.612063
microtubule-associated protein 6	0.912957	2.572959	1.407207
similar to T cell receptor alpha /// similar to T cell receptor a	0.601656	1.622245	0.319731
similar to trypsinogen /// similar to trypsinogen /// similar to	2.297392	0.397978	0.723272

nuclear receptor subfamily 2, group F, member 2	2.403026	0.912786	2.707636
G protein-coupled receptor kinase interactor 2	0.493339	0.476068	2.083418
phosphoenolpyruvate carboxykinase 1 (soluble)	2.086015	8.059832	11.77938
similar to T cell receptor alpha	0.507806	2.11918	0.702073
Similar to T cell receptor alpha	1.111399	2.007769	0.324923
chromosome 11 open reading frame 61	0.915147	0.721963	1.506452
calmodulin 2 (phosphorylase kinase, delta)	0.502205	1.451901	0.427296
ribosomal protein L35a	0.823987	1.061612	0.295896
ets variant gene 4 (E1A enhancer binding protein, E1AF)	0.935596		
SET translocation (myeloid leukemia-associated)			0.245586
ets variant gene 5 (ets-related molecule)	1.68069	0.816462	1.997337
ubiquitin specific peptidase like 1	1.395991	0.688265	0.602715
RAD21 homolog (S. pombe)	0.935385	0.97097	0.644629
ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast	2.21311	1.06141	0.422673
tight junction protein 2 (zona occludens 2)	2.016054	1.333194	2.265444
ribophorin II	0.512491	0.532469	0.033608
ribophorin II	1.246151	2.383542	1.019391
noggin	1.205825	0.789899	0.194961
breast cancer 1, early onset	1.194908	0.853414	0.878823
breast cancer 1, early onset	1.178662	1.044036	0.573774
CD5 molecule	1.368071	0.651383	2.859641
Ribosomal protein S28	0.638363	1.433071	0.028867
T-cell, immune regulator 1, ATPase, H ⁺ transporting, lysoso	1.26645	0.782934	2.171738
Ribosomal protein S14	1.220692	0.433853	
ribonucleotide reductase M1 polypeptide	0.65476	1.22573	0.465238
ribonucleotide reductase M1 polypeptide	0.46559	1.400942	0.384154
Peroxiredoxin 3	0.785235	0.889637	0.662687
septin 11	0.914871	1.988639	4.187456
DEAH (Asp-Glu-Ala-His) box polypeptide 15	0.445588	0.929516	0.632981
Dynein, light chain, Tctex-type 1	0.445155	1.021196	1.171619
A kinase (PRKA) anchor protein (gravin) 12	0.860583	0.905817	0.217087
A kinase (PRKA) anchor protein (gravin) 12	1.051182	0.922757	0.166999
aldo-keto reductase family 1, member D1 (delta 4-3-ketoster	0.33322	1.637708	0.469655
BRG1 protein	1.07432	0.836249	2.276872
myosin, heavy chain 10, non-muscle	0.489855	0.90766	1.098919
fibrinogen beta chain	2.575877	2.517073	1.964265
MAX dimerization protein 4	0.962277	0.944927	0.27226
selenoprotein X, 1	0.911404	1.382293	3.532663
Gal 9	0.467984		1.927778
flavin containing monooxygenase 6 pseudogene	1.089438	1.292397	2.047914

testis expressed 264	0.665974	1.036112	1.563382
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, s	0.903838	0.50881	0.388963
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, s	1.501488	0.717417	1.124196
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, s	1.124611	1.135845	0.54758
Ras association (RalGDS/AF-6) domain family member 2	1.041237	0.97924	2.736708
tubulin, beta 2A	1.516339	0.913128	0.994758
cytidine deaminase			1.582584
Arginine and glutamate rich 1	1.177871	0.507693	0.578405
Ribosomal protein L24	3.16002	0.444623	1.551792
Ribosomal protein L24	1.454909	1.018058	1.663791
Rho-related BTB domain containing 2		2.401908	
hypothetical protein LOC422090	0.607094	0.648826	0.609992
ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	1.123436	1.161511	0.762482
parathymosin	0.895582	0.89686	0.558567
TAF13 RNA polymerase II, TATA box binding protein (TB	1.020068	0.779855	0.484434
Prefoldin subunit 1			2.405358
luteinizing hormone/choriogonadotropin receptor	5.698554		
Similar to ubiquinol-cytochrome c reductase complex (7.2 kI	1.028595	0.51714	
Chromosome 10 open reading frame 84	1.058287	1.389564	0.387154
Similar to RIKEN cDNA 2610205E22 gene	0.63223	0.950968	1.777977
phosphohistidine phosphatase 1	0.630645	1.01182	1.086264
Methyltransferase 10 domain containing			
apolipoprotein A-IV	1.407931	2.653104	16.56821
apolipoprotein A-IV	1.337143	6.651408	10.93978
TNF receptor-associated protein 1	0.979002	1.086292	2.133243
similar to forkhead box M1	1.000024	0.921071	0.302815
tyrosyl-tRNA synthetase	0.826262	0.872648	2.548166
Axin 1			9.006218
axin 1	0.330739		2.346021
chromosome 19 open reading frame 6	0.610014	1.285821	2.19593
proteasome (prosome, macropain) 26S subunit, ATPase, 3	0.974924	0.927891	0.333808
ribosomal protein L31	0.660996	1.23688	0.385137
chromosome 19 open reading frame 12	1.214999	1.115983	1.846911
Tubulin, alpha 1c	0.777867	1.06269	1.780986
tubulin, alpha 1c	0.700344	1.133486	1.989681
phosphoserine phosphatase	1.087507	1.132929	0.734171
Hypothetical protein LOC769329	2.79315	0.763363	0.992896
delta/notch-like EGF repeat containing	1.051727	0.61585	0.952448
delta/notch-like EGF repeat containing		0.036485	0.732137
T-box 19	16.58643		

ATPase, H ⁺ transporting, lysosomal V0 subunit a1	1.085255	1.132306	2.904278
syndecan 2	2.638214	1.698411	1.255259
syndecan 2	2.590996	1.094031	1.173189
uracil-DNA glycosylase	0.449031	1.357674	0.542444
uracil-DNA glycosylase	0.426424	1.203098	1.268414
acyl-CoA thioesterase 8	1.156234	0.789999	1.2594
forkhead box C2 (MFH-1, mesenchyme forkhead 1)	1.251924	3.995772	1.273668
MAX-like protein X	1.342559	0.72824	0.87619
hypothetical LOC415641 /// similar to rat GCP360	0.506749	0.66297	
Nedd4 family interacting protein 1	1.475397	0.911015	0.729199
dihydroorotate dehydrogenase	0.958958	1.050279	1.33249
calcium binding and coiled-coil domain 2	2.251957	1.337964	1.309682
RNA-binding region (RNP1, RRM) containing 3	0.595475	0.796002	0.296782
3-oxoacid CoA transferase 1	0.239166	0.77517	0.98029
Splicing factor, arginine/serine-rich 3	1.605942	0.608975	0.398448
apolipoprotein A-I	2.912112	2.35725	11.29423
apolipoprotein A-I	2.872472	3.289707	10.73986
leukocyte cell derived chemotaxin 1	2.362088	1.128756	
heat shock protein 90kDa beta (Grp94), member 1	0.983007	1.210481	0.517083
heat shock protein 90kDa beta (Grp94), member 1	1.118497	0.945232	0.422426
PTPRF interacting protein, binding protein 1 (liprin beta 1)	1.076719	0.955409	2.644161
chromosome 6 open reading frame 72	2.18079	1.706639	1.082319
Ribosomal protein L18a	1.770263	0.355497	1.134778
N-ethylmaleimide-sensitive factor attachment protein, beta	1.285607	0.812916	0.980583
syndecan binding protein (syntenin)	1.304637	0.51412	0.49627
low density lipoprotein receptor-related protein 11	0.998433	1.170849	0.280612
low density lipoprotein receptor-related protein 11	0.993847	1.00715	0.172741
low density lipoprotein receptor-related protein 11	0.911542	1.907555	0.099401
neogenin	0.713216	1.37037	2.074396
peptidase (mitochondrial processing) alpha	1.445104	0.928074	1.034978
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7	0.665008	1.386714	0.907804
solute carrier family 25 (mitochondrial carrier; phosphate car	0.860839	0.692986	0.795063
hydroxyacyl-Coenzyme A dehydrogenase	1.015249	1.145393	0.933849
follicle stimulating hormone receptor		2.165758	0.104784
FK506 binding protein 5	1.212912	1.405607	5.669345
heterochromatin protein 1, binding protein 3		20.17082	
heterochromatin protein 1, binding protein 3	1.179015	0.876601	0.435047
cold inducible RNA binding protein	0.809932	0.676785	0.288173
mitogen-activated protein kinase kinase kinase 4			0.023524
TEA domain family member 3	1.018862	1.075611	5.083906

ADP-ribosylation factor-like 1	1.902004	0.718319	2.337192
N-acetyltransferase 11	1.236814	0.804751	1.81395
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.674048	0.984679	0.99776
cullin 3	0.421565	1.401377	0.549407
YY1 transcription factor	1.105242	0.903242	0.337223
YY1 transcription factor	0.845005	1.10045	0.281634
nonhistone chromosomal protein HMG-14A	0.678061	1.303735	0.376384
similar to rat ribosomal protein L9 homologue /// ribosomal p	0.487172	0.688504	0.55611
heterogeneous nuclear ribonucleoprotein A/B	0.778653	0.96067	0.39242
heterogeneous nuclear ribonucleoprotein A/B	1.124266	0.524747	0.21477
nitrilase family, member 2	1.27417	1.13686	2.112856
short chain dehydrogenase/reductase family 16C, member 5			0.337055
Family with sequence similarity 70, member A	0.800244	0.371891	0.816598
interferon-induced protein 35	1.552919	1.661799	4.42231
NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	2.677341		0.378892
kelch domain containing 2	0.811959	0.951217	0.275237
glycoprotein M6A			2.280123
protein phosphatase 1M (PP2C domain containing)	1.111465	1.130212	2.140487
D4, zinc and double PHD fingers family 2		2.259666	
Eukaryotic translation initiation factor 3, subunit E	0.687992	0.407785	
Synaptosomal-associated protein, 25kDa		13.10662	0.178516
lysine (K)-specific demethylase 6A	1.108347	0.685729	0.881194
fibromodulin			
heterogeneous nuclear ribonucleoprotein K	1588.08	1.682791	0.121908
F-box protein 45	1.215812	0.788066	0.463071
solute carrier family 25 (mitochondrial carrier; adenine nucle	0.758837	1.039583	0.570798
cathepsin K	1.901841	0.978035	6.941406
secreted frizzled-related protein 1		1.366381	1.129531
secreted frizzled-related protein 1	1.436882	1.379674	2.073058
hypothetical protein LOC770612	1.275535	1.342615	2.741159
clathrin, light chain (Lca)	0.517436	1.016894	0.539242
transmembrane protein 141	0.508626	0.814085	2.22877
transmembrane protein 141	0.777029	1.049759	2.599233
keratocan	0.21066		
chromosome 19 open reading frame 10	0.911731	0.773404	0.467659
malate dehydrogenase 2, NAD (mitochondrial)	0.415464	1.221882	0.452101
solute carrier family 4, anion exchanger, member 1	0.919006	1.531883	6.659634
similar to Splicing factor, arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-in			
similar to Splicing factor, arginine/serine-rich 5 (Pre-mRNA	2.668459	0.862527	0.237566
similar to Splicing factor, arginine/serine-rich 5 (Pre-mRNA	2.037853	0.934468	0.247267

anti-apoptotic NR13	2.453153	1.766065	1.424677
anti-apoptotic NR13	2.158319	1.290584	2.82547
E74-like factor 1 (ets domain transcription factor)	2.675926	1.07645	0.623937
TEA domain family member 4	0.756701	0.910445	3.38156
TEA domain family member 4		0.434403	1.063371
glutamate receptor interacting protein 1	2.438266	0.844209	0.728762
Collagen, type III, alpha 1	1.424586	0.948552	0.456862
collagen, type III, alpha 1	1.164115	1.47033	0.442051
chromosome 20 open reading frame 149	0.966754	1.116317	1.498564
Hypothetical protein LOC769345	0.266146	1.280727	0.612983
peripheral myelin protein 22	1.633519	1.18964	3.235665
ring finger protein 185	1.009033		0.394611
Thioredoxin domain containing 17	0.700299	1.437902	1.548981
Thioredoxin domain containing 17	0.685325	1.12902	1.423831
pancreatic lipase		0.293705	
actin, alpha, cardiac muscle 1	2.070329	1.012052	0.796038
proteasome (prosome, macropain) 26S subunit, ATPase, 5	0.754621	1.098081	2.156943
heat shock 10kDa protein 1 (chaperonin 10)	0.67532	1.283343	0.735774
tubulin, beta 2C	0.718087	1.053637	0.552155
ribosomal protein L7	0.500601	1.692474	
heat shock protein 90kDa alpha (cytosolic), class A member	1.182123	1.067484	0.611024
ankyrin repeat and SOCS box-containing 7			0.785851
annexin A1	1.026395	1.606552	3.321433
protein tyrosine phosphatase type IVA, member 1	1.125818	0.91726	0.221047
neurofascin	1.172478	1.357663	4.278413
heterogeneous nuclear ribonucleoprotein A2/B1	1.000875	1.072747	0.434595
Similar to Glutathione peroxidase 3 precursor (GSHPx-3) (G	0.367002	1.571138	2.607494
chromobox homolog 4 (Pc class homolog, Drosophila)	2.06627	1.559492	2.221932
similar to C-type lectin-like receptor	0.751193	0.99028	2.032943
similar to amino acid feature: cytoplasmic domain, aa 1 .. 91	1.040759	0.537422	2.001983
Similar to amino acid feature: cytoplasmic domain, aa 1 .. 91	1.076662	0.613692	0.44729
POU class 2 associating factor 1			30.79568
GTPase activating protein (SH3 domain) binding protein 1	1.203321	1.723271	0.419683
GA binding protein transcription factor, beta subunit 2	1.328677	0.887625	0.572416
similar to KIAA0332	2.523221	0.890087	0.359522
PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	1.082018	0.746021	0.189908
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-h	1.4999	0.964642	1.79941
amylase, alpha 2A; pancreatic	3.582466	0.834391	0.86267
fatty acid binding protein 4, adipocyte	2.330237	2.642717	8.966799
ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	0.983813	1.046562	0.493064

heat shock protein 70	0.884643	0.713653	0.307583
FK506 binding protein 1A, 12kDa	0.486498	1.206847	0.659624
sterol regulatory element binding transcription factor 2	0.500291	1.009037	2.294434
gallinacin 2	0.333622	0.834702	
frizzled-related protein	2.160465	1.128953	2.198675
left-right determination factor 2	0.766613		1.200408
xin actin-binding repeat containing 2	2.440415	0.597299	1.297783
similar to T-cell receptor gamma Vg3-Jg3	0.543679	0.971814	0.280655
similar to T-cell receptor gamma Vg3-Jg3	0.844008	1.142423	0.232822
similar to T-cell receptor gamma V2.6a /// similar to T-cell r	0.554365	0.765848	0.304534
similar to T-cell receptor gamma V2.6a /// similar to T-cell r	0.653389	1.368582	0.200312
similar to T-cell receptor gamma Vg3-Jg3	0.724182	0.969471	0.156519
similar to T cell receptor gamma /// similar to T-cell receptor	0.885524	1.183984	0.192625
similar to T-cell receptor gamma Vg3-Jg3 /// similar to T-cel	0.578105	1.499778	0.4413
Similar to T-cell receptor gamma chain Vg1-Jg2	0.717015	1.118853	0.140873
similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to	0.803434	1.213619	0.492432
similar to T-cell receptor gamma Vg3-Jg3	0.951674	1.014395	0.228973
Similar to T-cell receptor gamma chain Vg3-Jg3	0.787407	0.918063	0.564299
similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to T-cell rece	0.275827		
similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to T-cell rece	37.9857		
similar to T cell receptor gamma /// similar to T-cell receptor	0.754327	4.102089	0.180623
similar to T cell receptor gamma /// similar to T-cell receptor	0.856413	1.034776	0.158959
similar to T-cell receptor gamma Vg3-Jg3 /// similar to T-cel	33.68452		
similar to T cell receptor gamma /// similar to T-cell receptor	0.931211	1.107974	0.17919
Similar to T-cell receptor gamma chain Vg3-Jg3	1.064038	0.780954	0.344593
similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to	0.553338	1.42418	0.418942
collagen, type XII, alpha 1	0.322542	1.149299	1.556154
protein tyrosine phosphatase, receptor type, A	0.633593	2.27682	0.565882
protein tyrosine phosphatase, receptor type, A	0.941653	0.892133	0.479513
major histocompatibility complex class I glycoprotein	2.650126	3.963451	2.292785
MHC class I antigen B-F minor heavy chain /// major histoc	1.529753	1.428223	3.495125
MHC class I antigen B-F minor heavy chain /// major histoc	2.922054	3.477581	2.752367
versican	1.271077	1.241033	11.40564
versican	1.305076	1.227105	8.109183
tropomyosin 3	0.710645	1.823288	3.573499
tropomyosin 3	0.718165	1.258401	3.330654
tropomyosin 3	0.529558	1.141268	2.584088
tropomyosin 3	1.12302	1.351888	2.593454
msh homeobox 2	0.576945		
calbindin 2, 29kDa (calretinin)	0.660327	1.04533	1.271115

transcription factor 3 (E2A immunoglobulin enhancer bindin	0.918753	0.595022	0.336324
adenosine A1 receptor			
hemoglobin, gamma A /// hemoglobin, gamma G	0.541377	1.500658	4.681903
hemoglobin, epsilon 1 /// hemoglobin, gamma G	0.359922	1.146098	
Aldolase A	1.235883	1.294688	3.016856
troponin T type 2 (cardiac)	0.923498	0.47623	2.799286
histone deacetylase 1	0.612679	1.12208	1.391247
myosin binding protein C, fast type	0.198327	1.900271	1.035484
caldesmon 1	3.172612	1.628333	2.685914
caldesmon 1	3.187307	1.908553	3.290035
Similar to T-cell receptor gamma chain Vg2-Jg3	1.330215	0.527027	0.714302
similar to T-cell receptor gamma chain Vg2-Jg3	1.85124	0.643863	0.158075
integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4	1.82431	0.943908	0.570116
integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4	0.229002	2.435542	1.831747
midkine (neurite growth-promoting factor 2)	0.424486	0.794086	1.725156
chitinase, acidic	0.565937		
chitinase, acidic		1.539676	2.644258
cyclin-dependent kinase inhibitor 2B (melanoma, p16, inhibi	1.373595	3.960395	8.144782
cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibi	0.967598	2.026598	9.333667
matrix metalloproteinase 27		2.751026	
zinc finger protein, X-linked	0.807273	0.845242	0.698979
high mobility group AT-hook 2			0.348919
Y-Lb III	0.492517		0.337535
5'-nucleotidase, cytosolic III	0.997652	1.26247	2.079237
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase	0.874925	1.030417	0.364429
similar to Trappin-6	1.987057	2.484322	7.304639
ovomucoid	0.782916	8.413291	
immunoglobulin, light chain, lambda, psi-V12 pseudogene	4.896084		
caveolin 1, caveolae protein, 22kDa	1.936309	1.338037	2.888219
Annexin A2	0.75832	0.986475	1.173838
cholinergic receptor, nicotinic, alpha 3	0.997979	2.555238	
zinc finger and BTB domain containing 16			
v-myc myelocytomatosis viral related oncogene, neuroblasto	0.828277	0.882906	0.450608
T-cell leukemia homeobox 1	0.493672	1.031957	
coiled-coil domain containing 80	1.053565	2.114327	2.363409
interleukin 8	2.140995	1.506982	0.827026
homeobox A7	0.470708	0.388534	0.141218
glutamate receptor, ionotropic, AMPA 2			0.664741
similar to T-cell receptor gamma V2.9 /// similar to T-cell re	1.389433	0.690251	0.48086
coagulation factor VIII, procoagulant component	0.946846		3.079478

coagulation factor VII (serum prothrombin conversion accel	1.248867	0.616666	2.708629
deleted in azoospermia-like			4.304927
MHC class II beta chain	1.236546	0.014338	0.157274
coagulation factor X	1.455787	1.021522	0.431387
Selenophosphate synthetase 1	0.630319	1.102054	0.435277
Selenophosphate synthetase 1	0.794505	1.079438	0.45019
damage-specific DNA binding protein 1, 127kDa			1.43955
MHC class II beta chain			0.328747
tumor necrosis factor receptor superfamily, member 1B	55.29062	60.74509	45.66635
tumor necrosis factor receptor superfamily, member 1B	0.859649	1.310199	2.996088
tumor necrosis factor receptor superfamily, member 1B	1.536882	1.326694	2.704626
periostin, osteoblast specific factor	2.087969	1.939728	3.153747
calcium channel, voltage-dependent, beta 4 subunit	0.684139	0.577157	0.609833
ankyrin 3	2.203751		
coagulation factor V (proaccelerin, labile factor)	2.809604	1.01958	1.665368
nerve growth factor, beta polypeptide	2.25937		
BCL2-related protein A1	1.445537	2.094443	1.022752
BCL2-related protein A1	2.546234	1.767735	1.832059
tetraspanin 32	0.255027	5.541969	
CD81 molecule	0.792722	1.353054	2.405307
Ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeas	0.891282	0.961749	0.471695
MHC class II antigen B-F minor heavy chain	82.2093	1.550271	20.57477
podocalyxin-like	1.959234	1.103526	2.596262
cadherin 5, type 2, VE-cadherin (vascular epithelium)	1.50848	1.352947	3.084893
PHD finger protein 20-like 1	1.077915	0.87604	0.577689
MICAL-like 1	2.08765	0.746858	1.362183
protein tyrosine phosphatase, receptor type, F	1.07654	0.743461	0.218023
MHC class II antigen B-F minor heavy chain	0.575303	0.327192	2.416155
tumor necrosis factor receptor superfamily, member 8	0.98776	2.48984	30.0138
sequestosome 1	0.813031	1.240324	1.109344
sequestosome 1	0.655103	1.719309	1.618457
extracellular leucine-rich repeat and fibronectin type III cont	0.076604		
Sin3A-associated protein, 30kDa	0.7138	1.19569	0.345998
abl-interactor 1	1.058468	1.151038	0.328345
benzodiazapine receptor (peripheral)-like 1	1.288463	1.705162	11.13672
ubiquilin 1	0.56816	0.842938	0.49913
G kinase anchoring protein 1	0.589809	0.767143	0.397323
nucleoporin 98kDa	0.845391	1.083331	1.470052
KIAA1609	5.698385		1.20708
chromosome 18 open reading frame 22	0.920163	1.554122	0.482689

protein phosphatase 4, regulatory subunit 2	0.739475	0.730172	0.53992
Protein phosphatase 4, regulatory subunit 2	0.944258	0.791495	0.643413
CWC15 homolog (S. cerevisiae)		0.642793	0.166878
importin 7			
hydroxysteroid (17-beta) dehydrogenase 11	1.407862	1.123146	2.038054
poly-U binding splicing factor 60KDa	1.021998	0.777697	0.493606
poly-U binding splicing factor 60KDa	1.00442	1.099292	0.393068
KIAA0317	1.114203	0.996004	0.554804
KIAA0317	0.593424	0.491691	0.693312
EGF-containing fibulin-like extracellular matrix protein 1	2.342815	1.626154	2.954254
REX1, RNA exonuclease 1 homolog (S. cerevisiae)	0.611735	1.067341	2.239926
acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A)	0.705832	1.424854	5.051304
Hypothetical LOC422270	0.238976	0.029613	
threonyl-tRNA synthetase-like 2	1.293524	1.046046	2.267955
acylphosphatase 2, muscle type	1.214207	1.082935	0.346811
scavenger receptor class B, member 2	1.14017	1.034861	0.327016
LanC lantibiotic synthetase component C-like 1 (bacterial)	1.449018	1.128645	2.184961
thyrotrophic embryonic factor	1.097947	0.673741	0.852546
Glycerol-3-phosphate dehydrogenase 1 (soluble)	1.581014	2.486872	5.387204
cell adhesion molecule 1	3.209706	1.62939	2.15969
hypothetical LOC424892	1.858654	1.140383	0.885211
calcium channel, voltage-dependent, L type, alpha 1D subunit	0.570428	1.218933	0.914784
phosphodiesterase 6D, cGMP-specific, rod, delta	0.803525	1.276408	0.653009
sprouty-related, EVH1 domain containing 1	2.319846	1.334798	1.401625
autocrine motility factor receptor	0.538469	1.100284	1.61409
autocrine motility factor receptor	0.575394	0.950025	1.371152
leucine rich repeat and fibronectin type III domain containing 1	1.052271	0.544292	
MADS box transcription enhancer factor 2, polypeptide C (nucleosome)	0.641595	1.105303	7.021376
B-cell CLL/lymphoma 7A	0.948284	0.948012	0.341429
similar to Phosphopantothienoylcysteine synthetase	2.546998	1.484635	1.212395
SH3 and multiple ankyrin repeat domains 2	0.925095	0.862211	0.427279
alkB, alkylation repair homolog 2 (E. coli)	0.806847	0.907613	0.465968
mitochondrial ribosomal protein S6	0.982418	1.001419	0.193359
O-sialoglycoprotein endopeptidase-like 1	1.00554	1.306376	0.645201
dipeptidyl-peptidase 7	1.496789	0.775026	1.562109
hypothetical LOC417676	10.98071	1.594213	0.665877
2'-5'-oligoadenylate synthetase-like	3.970471	2.15335	4.969732
TSC22 domain family, member 3	0.88558	1.15269	1.829182
alcohol dehydrogenase 5 (class III), chi polypeptide	1.236044	0.569743	0.253648
sodium channel, nonvoltage-gated 1, gamma	1.210607	0.648087	1.08509

vascular endothelial growth factor A	1.351935	0.852406	5.718562
transmembrane protein 45B			
heterogeneous nuclear ribonucleoprotein U (scaffold attachr	1.066663	0.999255	0.332355
programmed cell death 2-like /// programmed cell death 2-lik	1.120076	1.361906	0.598636
NIMA (never in mitosis gene a)-related kinase 4	0.494694	1.099811	2.455619
argininosuccinate synthetase 1	2.24455	1.560624	3.1731
tumor necrosis factor receptor superfamily, member 6b, decc	1.140377	1.285186	3.867566
CD247 molecule	0.767646	0.916114	0.523669
similar to serine protease	2.321678	1.642544	1.982518
serine/threonine kinase 40	0.974029	0.579766	1.62939
complement component 1, q subcomponent, B chain	1.808432	1.533044	5.473615
cytochrome P450, family 2, subfamily J, polypeptide 2	23.50637		1.072459
cytochrome P450, family 2, subfamily J, polypeptide 2		1.406416	0.374089
ArfGAP with GTPase domain, ankyrin repeat and PH domai	2.084784	0.813038	1.722864
matrix Gla protein	0.989151	1.7845	2.789399
dehydrogenase/reductase (SDR family) member 7	0.690867	1.123668	1.412047
transcription elongation factor A (SII), 2	1.186286	0.909473	1.858145
Lon peptidase 1, mitochondrial	0.494841	0.998595	1.226877
claudin 11 (oligodendrocyte transmembrane protein)	1.321864	0.883127	2.141491
lymphotactin	1.732345	1.424461	0.218577
EF-hand domain family, member A1	1.25336	0.613947	0.561221
Ras-related GTP binding B	0.892747	0.886014	2.443743
B-cell CLL/lymphoma 7A	1.42738	0.664805	0.322104
HIV-1 Tat interactive protein 2, 30kDa	1.250539	1.148859	2.215647
3-hydroxybutyrate dehydrogenase, type 1	0.36844		
3-hydroxybutyrate dehydrogenase, type 1			
adaptor-related protein complex 4, beta 1 subunit	1.437441	0.930288	1.637158
CDK5 regulatory subunit associated protein 1-like 1	1.507991	0.508701	0.452755
cytokine induced apoptosis inhibitor 1	0.576872	0.786839	0.255281
regulator of calcineurin 1	0.547729	0.724827	0.42571
dynein, cytoplasmic 2, light intermediate chain 1		1.033488	1.964672
polymerase (DNA directed), epsilon 3 (p17 subunit)	1.189306	0.974556	1.045701
mitochondrial ribosomal protein L42	0.463867		
SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	0.756103	1.049747	0.131062
muscle RAS oncogene homolog	1.207995	1.054107	0.80307
dihydrouridine synthase 1-like (S. cerevisiae)	0.725351	0.717935	2.504314
hypothetical LOC415950	0.511821	0.970807	1.129451
similar to nuclear DNA-binding protein; small unique nuclea	0.84506	0.933464	1.423822
deiodinase, iodothyronine, type III	0.313675	1.272375	2.599575
Solute carrier family 25 (mitochondrial carrier; citrate transp	0.65629	0.843	0.481905

tetraspanin 1	1.676545	2.283681	1.437146
Mitogen-activated protein kinase 14	0.829029	1.162616	2.008992
deiodinase, iodothyronine, type I	1.106436	2.278016	1.626527
smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	0.886914	3.014845	1.544358
LATS, large tumor suppressor, homolog 1 (Drosophila)	2.233899	0.829313	0.298898
FUN14 domain containing 1	1.258837	0.981398	0.763096
hepatocyte growth factor (hepapoietin A; scatter factor)		2.097648	
diacylglycerol lipase, beta	1.638612	0.898428	0.839749
platelet/endothelial cell adhesion molecule	1.613374	0.875054	0.682457
leptin receptor overlapping transcript-like 1	1.287832	1.03866	0.45323
SCY1-like 3 (S. cerevisiae)	0.946298	0.949781	1.776537
nucleophosmin/nucleoplasmin, 3	0.972176	1.788191	3.911316
G protein-coupled receptor 153	0.774318	0.477918	0.201795
G protein pathway suppressor 1	1.318893	0.961089	0.28678
cysteine and glycine-rich protein 3 (cardiac LIM protein)	1.435707	1.363803	2.609453
RWD domain containing 4A	0.956677	0.960118	0.768815
dynein, light chain, roadblock-type 1	0.56709	2.039509	1.33242
paired box gene 6	2.60204		6.653445
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4			
gem (nuclear organelle) associated protein 5	1.108967	0.793901	1.182294
elongation factor Tu GTP binding domain containing 1	0.788267	1.342833	0.271742
hypermethylated in cancer 2	3.311151	2.566508	5.629719
F-box and leucine-rich repeat protein 18	0.731308	0.662712	2.133136
PDZK1 interacting protein 1	1.111791	1.622978	1.317253
transient receptor potential cation channel, subfamily V, member 1	2.207263	3.175826	3.543737
signal recognition particle 14kDa (homologous Alu RNA binding protein)	1.083771	0.654237	0.572804
signal recognition particle 14kDa (homologous Alu RNA binding protein)	0.930063	0.989782	0.657254
voltage-gated sodium channel SNS	0.341007	0.944423	
Adenylate kinase 3-like 2	1.348581	1.359099	2.374921
BTG3 associated nuclear protein	1.447045	0.898363	0.452619
hypothetical protein LOC770126	2.139706	0.582517	1.677596
phosphoglycolate phosphatase	0.719492	1.011207	1.881206
Enah/Vasp-like	1.257517	0.946387	0.520715
Lipase, endothelial	0.991407	1.473522	4.59386
hypothetical LOC415671	0.654023	1.066335	0.574919
sodium channel, voltage-gated, type IX, alpha subunit	0.428806		
IKK interacting protein	3.270341	1.72444	0.919162
IKK interacting protein	0.8058	1.197976	0.457925
ATP-binding cassette, sub-family C (CFTR/MRP), member 1	4.93772	0.955391	
cell cycle associated protein 1	0.946531	0.599806	0.219392

interleukin 4	1.030405	0.76215	9.770724
DnaJ (Hsp40) homolog, subfamily A, member 1	1.289774	0.687084	0.532606
DnaJ (Hsp40) homolog, subfamily A, member 1	0.801016	0.742971	0.529844
Immunoglobulin superfamily containing leucine-rich repeat	5.021068	2.501117	4.611899
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.847934	1.198134	0.791008
syntxin1B		0.432149	
glutamate receptor, ionotropic, delta 2			0.764619
kinesin family member 2C	0.895358	1.065121	0.69155
kinesin family member 2C	0.686836	1.462237	
kinesin family member 2C	0.770931	1.066996	0.68135
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 1	0.742829	0.899853	0.313401
chromosome 7 open reading frame 26	0.819247	0.89384	0.446837
reticulon 4 interacting protein 1	1.079135	0.705883	0.393595
nuclear receptor subfamily 5, group A, member 2	1.422498	1.714791	2.59067
nuclear receptor subfamily 5, group A, member 2	7.60621		1.269722
CD8b molecule	0.621424	0.838618	0.106222
lymphocyte antigen 96	5.027757	2.496606	2.290418
HD domain containing 2	0.989534	1.477486	2.00371
Salvador homolog 1 (Drosophila)	0.841067	1.418801	0.411901
interleukin 13 receptor, alpha 2	1.237152	1.605677	4.104223
CD8a molecule	0.942014	0.665975	0.277972
ankyrin repeat domain 1 (cardiac muscle)	1.872628	1.013373	1.580372
ankyrin repeat domain 1 (cardiac muscle)	2.222048		0.978494
phosphofructokinase, platelet	1.673122	1.37703	2.262282
tetraspanin 4	2.088391	1.303636	0.562668
inducible T-cell co-stimulator ligand			2.281939
pumilio homolog 1 (Drosophila)	1.665837	0.646541	0.421427
CD34 molecule	0.927384	0.999229	1.937304
cAMP responsive element binding protein 3	0.787209	1.147043	3.038959
Hypothetical protein LOC769246	0.361508		0.912827
CutC copper transporter homolog (E. coli)	1.887548	0.610818	0.363229
Trinucleotide repeat containing 18	1.781829	0.772516	0.862979
transmembrane protein 121	0.253867		
similar to Brn1-prov protein	0.74285	1.189643	0.811979
prolyl 4-hydroxylase, alpha polypeptide II	1.529352	1.554021	1.091862
ubiquilin 4	1.074827	1.619126	0.357718
tripartite motif-containing 59	0.839477	1.035964	0.487059
Sjogren's syndrome nuclear autoantigen 1	0.772061	0.885644	0.42093
mediator of RNA polymerase II transcription, subunit 10 hor	0.629082	1.711977	1.09448
sucrase-isomaltase (alpha-glucosidase)	1.108998	8.96381	1.974183

RNA binding protein with multiple splicing	2.017465	2.384141	9.227642
RNA binding protein with multiple splicing	4.691075	1.261521	3.947085
hypothetical protein LOC770695	2.473269	1.91543	1.055174
microtubule-associated protein tau	1.491973	0.691166	2.64928
Down syndrome cell adhesion molecule			4.92615
sucrase-isomaltase			
RWD domain containing 2B			1.116259
Similar to immunoglobulin-like receptor CHIR-AB1	0.796022	1.276641	1.197926
immunoglobulin-like receptor CHIR-B3 /// similar to immun	2.053751	0.525251	3.101414
vitamin D (1,25- dihydroxyvitamin D3) receptor	2.548413	0.579776	1.638775
hypothetical protein LOC771291	1.447658	1.780642	2.366648
ProSAPiP1 protein	1.043828	0.884216	4.051028
claudin 10	2.234078	2.000184	1.759244
mediator complex subunit 21	0.943297	0.983589	0.349275
UDP glucuronosyltransferase 1 family, polypeptide A1	1.97926	3.513547	6.325312
peptidase D	1.277229	1.688402	2.790349
ectonucleotide pyrophosphatase/phosphodiesterase 7	1.600614	2.053466	8.652059
glycoprotein A33 (transmembrane)	1.33909	3.02657	3.240325
tubulin folding cofactor A	0.423252	0.798867	0.519743
Olfactomedin-like 2B	2.02086	1.580746	2.421966
DAZ associated protein 1	0.946931	0.239727	1.113814
mitochondrial ribosomal protein L1	0.830977	0.77733	2.151592
MICAL-like 2	1.125008	1.433787	3.407196
GDNF family receptor alpha 1	2.050159	1.630579	6.455085
myeloid/lymphoid or mixed-lineage leukemia 3	0.589556	0.936686	1.526527
WD repeat domain 77	1.319716	0.912309	1.362692
programmed cell death 6	1.042585	0.983076	0.421791
alkylglycerone phosphate synthase	1.318985	1.198629	0.153056
family with sequence similarity 125, member B	0.874596	0.938251	0.483826
cgABP260	1.342504	0.654447	2.297854
DnaJ (Hsp40) homolog, subfamily A, member 4	1.22059	0.774965	0.27879
DnaJ (Hsp40) homolog, subfamily A, member 4	1.029563	0.977949	0.148881
brain protein 44-like	2.07283	0.852976	0.407274
brain protein 44-like	0.90922	1.352318	0.449147
chromosome 1 open reading frame 123	0.053843	1.171074	
synaptogyrin 3	3.013721	0.991388	1.325399
cytochrome P450, family 11, subfamily A, polypeptide 1			
hypothetical protein LOC769799	0.544579	0.826347	0.285148
cytochrome c, somatic	1.164273	1.46083	2.002783
cytochrome c, somatic	0.845356	1.102902	0.441895

lysyl oxidase-like 1	1.247099	1.298048	2.965499
Hypothetical protein LOC769360		2.617747	
ADP-ribosyltransferase	5.701627		
ADP-ribosyltransferase /// ADP-ribosyltransferase	0.722729	0.746591	0.477797
chloride channel 7	1.124324	0.82964	2.041982
syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa	2.521844	1.828599	1.276717
carboxypeptidase A2 (pancreatic)			0.487731
NEL-like 2 (chicken)	1.031449	2.266772	1.346031
solute carrier family 43, member 3	1.23106	1.122002	2.857275
hypothetical gene supported by CR389157	1.745108	1.735995	2.418241
CAMP responsive element binding protein 3-like 2	0.903691	0.942505	0.385485
CAMP responsive element binding protein 3-like 2		1.913945	
nemo-like kinase	0.974676	1.167024	2.442956
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid d	1.841265	0.290981	
uroporphyrinogen III synthase (congenital erythropoietic por	0.885513	2.039388	2.23233
progesterone and adipoQ receptor family member VII		1.676504	0.128449
methyl-CpG binding domain protein 2	0.536885	0.968381	1.822586
STE20-related kinase adaptor alpha	1.441624	1.412064	0.104188
similar to phosphatidic acid phosphatase type 2 domain cont	0.923029	0.865468	0.559321
similar to FLJ46266 protein	0.739969	0.875815	1.490462
OAF homolog (Drosophila)		0.13653	
proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki	1.140769		1.478826
malic enzyme 3, NADP(+)-dependent, mitochondrial	0.757336	1.31336	0.424751
ring finger protein 128			0.601558
CDC45 cell division cycle 45-like (S. cerevisiae)	0.995283	0.965205	0.550221
ubiquitin-like, containing PHD and RING finger domains, 2	1.283183	1.255331	0.373755
hypothetical LOC418426	0.771814	0.90538	0.327981
proline-rich nuclear receptor coactivator 1	0.749284	1.057478	1.800942
cathepsin S	1.743456	1.290501	1.848857
succinate-CoA ligase, GDP-forming, alpha subunit		2.122162	
succinate-CoA ligase, GDP-forming, alpha subunit	1.466797	1.234462	0.579014
proteasome (prosome, macropain) 26S subunit, non-ATPase	0.621122	1.112742	1.858699
hepatitis A virus cellular receptor 1	0.889729	1.052453	0.254959
NIMA (never in mitosis gene a)-related kinase 6	1.399306	1.273825	2.234517
chromosome 20 open reading frame 54	0.805366	1.23618	1.845417
GTPase activating Rap/RanGAP domain-like 3	1.375882	1.03645	0.41501
Mitochondrial ribosomal protein S18C	1.528739	0.538563	0.264038
CDC-like kinase 4	1.182874	0.759886	0.558081
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, s	0.590199	1.533864	0.177367
stearoyl-CoA desaturase 5	0.887997	0.803726	1.598183

polycystic kidney disease 2 (autosomal dominant)	0.793601	2.096775	1.216196
polycystic kidney disease 2 (autosomal dominant)	2.741319	0.952043	0.768462
heterogeneous nuclear ribonucleoprotein A0	0.774554	1.015342	0.37376
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hon	0.424401	1.19865	0.593855
SEC11 homolog A (S. cerevisiae)	1.849508	0.837214	0.508822
transcription factor 7 (T-cell specific, HMG-box)	0.487783	0.954827	0.330012
dynein, axonemal, light intermediate chain 1	1.236646	0.68545	0.34218
bone morphogenetic protein receptor, type IB	0.457193	0.973453	1.440911
prostate stem cell antigen	2.175788	0.959722	1.676803
serglycin	0.999494	1.558973	3.38615
similar to Kunitz-like protease inhibitor			2.363156
transmembrane and immunoglobulin domain containing 1		9.208269	
hypothetical LOC419498	1.436278	5.753975	1.332766
solute carrier family 27 (fatty acid transporter), member 2	1.187867		35.56762
thyroid hormone receptor beta 2		0.548815	2.222149
5'-nucleotidase domain containing 2	0.53944	0.968389	1.64639
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, s	0.361662	1.107555	1.406008
chromosome 9 open reading frame 91	1.163005	0.900235	1.901438
Similar to contactin associated protein	8.848162		2.003163
similar to Acyl-CoA thioesterase 2	1.345762	1.191394	2.547388
H3 histone, family 3A /// similar to histone protein Hist2h3c	0.478297	1.519229	1.007802
H3 histone, family 3A /// similar to histone protein Hist2h3c	0.477543	1.103781	1.07579
chromosome 6 open reading frame 86	0.546993	1.069366	0.590693
chromosome 6 open reading frame 86	0.742181	0.900991	0.453883
retinoic acid receptor responder (tazarotene induced) 2	1.163963		3.501111
translocator protein (18kDa)	1.516035	1.646043	1.327816
UBX domain containing 2	0.482637	0.163866	0.961159
DnaJ (Hsp40) homolog, subfamily C, member 8	0.824069	1.01301	1.194696
lectin, galactoside-binding, soluble, 2	0.742325	2.199319	1.579038
actin binding LIM protein family, member 3	3.51299	0.752041	2.350946
acyl-Coenzyme A dehydrogenase, long chain	1.053921	1.155315	2.168559
similar to beta chain spectrin /// spectrin, beta, non-erythrocy	1.337837	0.979861	0.735429
kinesin family member 9	3.480453	1.039058	4.27512
LYR motif containing 2	0.800813	0.789648	0.406746
cytochrome P450, family 1, subfamily A, polypeptide 1	2.297443	1.204993	0.905689
Cytochrome c oxidase subunit VIIc	0.407055	1.102347	1.717645
chromosome 12 open reading frame 31	1.088641	2.00184	0.959717
SIL1 homolog, endoplasmic reticulum chaperone (S. cerevis	1.469266	1.050322	4.175556
cytochrome P450 1A4	0.971224	2.457564	
Hydroxysteroid (11-beta) dehydrogenase 1	1.488173		8.62113

Similar to phosphoseryl-tRNA kinase	0.655498	1.212201	2.382501
regenerating islet-derived family, member 4	0.638166	1.883396	2.153437
Hypothetical protein LOC770190	0.747867	1.060298	0.44143
ISG12-2 protein-like	2.56202	4.619786	4.073908
BTB (POZ) domain containing 11	1.076626	1.312419	3.089975
BTB (POZ) domain containing 11	1.479377	1.044556	5.758236
homeobox A2	6.353515	0.595724	2.06734
phospholipase A2, group IB (pancreas)	0.737749		1.641643
beaded filament structural protein 1, filensin	1.497098	2.522578	1.672022
ovalbumin	2.091467	1.570105	1.33812
switch-associated protein 70	0.877826	1.336837	0.448318
discoidin, CUB and LCCL domain containing 2	1.080597	0.943859	0.530217
selenium binding protein 1	1.244033	0.876255	0.48226
transmembrane protein 16A	3.024439	8.531697	4.021624
glycine N-methyltransferase	0.845446	0.828984	0.319717
Hypothetical protein LOC770490	0.592561	1.087057	2.014786
similar to methyltransferase 24 (37.8 kD) (3D495)	0.420933	1.532235	0.650104
glutathione S-transferase theta 1	0.707883	0.763022	0.336318
stomatin	2.256195	1.669738	2.046465
phenylalanyl-tRNA synthetase, beta subunit	0.914011	1.994033	0.480551
pescadillo homolog 1, containing BRCT domain (zebrafish)	0.78176	1.000253	2.906192
pescadillo homolog 1, containing BRCT domain (zebrafish)			
chromosome 16 open reading frame 57	0.666301	1.173203	0.66023
calcium binding protein 39-like	0.572917	1.907986	3.564753
calcium binding protein 39-like	0.533002	1.551144	2.060562
transmembrane 4 L six family member 4	0.725331	2.87711	4.354819
SH3 and PX domain containing 3	0.885491	0.47214	0.841576
phosphoribosyl pyrophosphate synthetase-associated protein	0.82605	0.935422	0.444114
hairly/enhancer-of-split related with YRPW motif 1	1.466795	1.359463	5.248457
similar to FNDC3 protein	2.200957	1.155505	2.96942
adrenergic, beta, receptor kinase 2	2.497142	0.865585	0.631445
angiotensin II receptor, type 1		9.660226	
retinol binding protein 2, cellular	1.745211	4.89546	20.43699
translocase of inner mitochondrial membrane 17 homolog A	0.660106	1.163047	0.670994
hypothetical LOC420860	0.539887	1.074037	1.177844
EPH receptor B6	0.934066	1.14465	0.45714
ring finger protein 7	0.935513	1.069395	0.428583
bromodomain containing 7	1.162519	1.086571	0.519903
troponin I type 1 (skeletal, slow)	0.503538		1.253782
deafness, autosomal dominant 5	0.451233	1.470179	5.431844

cyclin-dependent kinase inhibitor 3 (CDK2-associated dual s	0.568614	1.179841	0.498152
IWS1 homolog (S. cerevisiae)	0.910797	1.206598	3.313463
chromosome 7 open reading frame 30		1.228249	0.105868
glutaredoxin (thioltransferase)	0.217603	0.938272	1.105501
similar to nuclear cap binding protein subunit 2; nuclear cap	0.619479	1.045022	0.300029
integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II)		0.384127	
DEP domain containing 7	0.898552	0.86484	0.292092
dual specificity phosphatase 14	0.967001	1.234261	1.508354
ectonucleoside triphosphate diphosphohydrolase 8	1.432266	0.747928	2.195956
BTG family, member 2	1.093418	0.678699	0.374723
basic helix-loop-helix domain containing, class B, 8	0.505728	0.894119	0.458578
Protein phosphatase 2 (formerly 2A), regulatory subunit A, t	1.034079	0.823062	2.331153
S100 calcium binding protein A11	0.784489	1.103325	1.93273
cathepsin C	2.420805	1.847124	4.265418
receptor-associated protein of the synapse			1.975933
mal, T-cell differentiation protein-like	1.001279	2.530187	2.654953
similar to T-cell receptor gamma V2.9 /// similar to T-cell re	0.935237	1.060276	0.129074
chromosome 1 open reading frame 190	1.282669	1.639	2.292075
diacylglycerol kinase, epsilon 64kDa		0.658214	0.479833
ribosomal protein L38	0.477694		0.738334
SKI-like oncogene	0.686192	0.957669	2.12562
MTERF domain containing 1	0.909851	0.726567	0.909462
similar to Myo15b protein	2.579018	3.309265	3.623139
transmembrane protein 104		0.469594	
chromosome X open reading frame 39	2.051323	0.494944	0.060438
fibroblast growth factor 1 (acidic)	0.857972	2.590352	2.910217
calpain 8	0.736418	9.037849	1.522102
similar to chemokine CXCL13/BCA-1	7.620164	3.038143	6.837249
Gallicin 11		4.436104	
similar to inteferon-induced membrane protein Leu-13/9-27	1.830237	1.51397	6.568122
lysophospholipase II pseudogene 1	0.9425	1.059923	2.52849
fatty acid binding protein 2, intestinal	1.971333	1.84881	5.438075
Transmembrane protein 173	1.971216	1.071093	4.077681
Fc fragment of IgE, high affinity I, receptor for; gamma poly	1.928297	1.242552	3.838469
tenascin XB	1.655481	1.227155	5.341344
Kelch repeat and BTB (POZ) domain containing 8	1.294432	0.776152	0.40297
G protein-coupled receptor 87	0.296728	1.189473	0.567147
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G			
forkhead box G1	1.491877	1.335815	2.816959
ryanodine receptor 3	0.433566	1.127158	

ryanodine receptor 1 (skeletal)			
syndecan 1	2.674267	1.667569	1.336423
pyrimidinergic receptor P2Y, G-protein coupled, 6	0.80161	1.53887	0.306592
NK-lysin	0.626284	1.139161	
chromosome 1 open reading frame 66	1.003736	1.158976	2.12994
purinergic receptor P2Y, G-protein coupled, 5	1.304969	1.547856	2.008786
similar to LOC443683 protein	1.174939		1.11076
programmed cell death 1 ligand 2	0.797959	1.053157	0.438048
hepatic nuclear factor 4beta	1.47755	1.660189	2.977297
vasoactive intestinal peptide	0.429918	0.74241	0.599618
major intrinsic protein of lens fiber	0.651909	2.288939	0.735861
macrophage stimulating 1 (hepatocyte growth factor-like)	1.966666		8.629267
ATP-binding cassette, sub-family G (WHITE), member 1	0.571692	0.909834	0.886847
similar to feather keratin /// similar to feather keratin /// simil	0.771706	0.13043	0.887837
granzyme A (granzyme 1, cytotoxic T-lymphocyte-associate	3.863542	3.990535	47.08629
RAD9 homolog A (S. pombe)	1.476969	0.847856	2.237282
vacuolar protein sorting 16 homolog (S. cerevisiae)	0.611566	1.052029	2.572065
RAB40C, member RAS oncogene family	0.710684	0.4139	
DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 /// similar to DEAH		0.184769	0.467727
GTP cyclohydrolase 1 (dopa-responsive dystonia)	4.851989	2.297348	8.023099
Dolichyl-diphosphooligosaccharide-protein glycosyltransfer:	0.754362	1.161082	2.204233
KIAA1244	0.634892	0.711806	0.483228
regulator of G-protein signalling 12	1.655735	12.27865	0.977599
Gnot1 homeodomain protein	1.27111	0.480428	0.79397
solute carrier family 10 (sodium/bile acid cotransporter family), member 4			0.18996
similar to Scale keratin (S-ker) (sKer)		0.403197	2.08614
similar to Scale keratin (S-ker) (sKer)		0.107403	
similar to Scale keratin (S-ker) (sKer)		0.133067	
very low density lipoprotein receptor	2.1681	1.154113	2.006964
nuclear factor I/B	1.155676	0.973533	2.435608
nuclear factor I/B	5.892205	1.501609	1.466971
kelch-like 8 (Drosophila)			2.57554
Kinesin family member C1	0.347176	0.75834	0.726
hypothetical protein LOC768701	0.994054	1.271766	1.275035
neurotrophic tyrosine kinase, receptor, type 2	0.244877		
ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-	6.658791		
proteasome (prosome, macropain) 26S subunit, ATPase, 3	0.362616	1.519795	0.706768
hypothetical LOC419812	0.564241	1.45892	3.343568
chromosome 2 open reading frame 43	1.131381	1.829526	0.271887
CCR4-NOT transcription complex, subunit 4	2.223518	0.942439	1.805678

hypothetical LOC425364 /// hypothetical LOC425625 /// hy	1.676621	0.426332	1.013218
GLI pathogenesis-related 1	0.973138	1.480071	0.371493
v-raf-1 murine leukemia viral oncogene homolog 1	1.584557	0.883087	0.545803
solute carrier family 26, member 9	1.700548	0.35705	
hypothetical LOC425311	0.639967		
similar to cytidine deaminase			2.031299
F-box protein 39	1.061192	0.787438	0.486814
Hypothetical protein LOC776097	1.072608	1.119428	0.464871
roundabout, axon guidance receptor, homolog 2 (Drosophila	0.664869	3.244282	1.126118
adenylate cyclase 7	1.154205	0.618102	2.891701
metallo-beta-lactamase domain containing 2		0.311409	
ribonuclease H1			0.036875
CXXC finger 5	1.130013	0.104672	
GABA A receptor	2.117676	1.161929	0.573526
myb-like, SWIRM and MPN domains 1	1.419886	0.60124	0.380778
cysteine and glycine-rich protein 1	0.967514	1.323598	3.330671
Dynein, axonemal, heavy chain 9	1.154749		
EPH receptor B1	1.483891	1.019303	1.335927
Similar to guanine nucleotide exchange factor Lbc	1.07959	1.638027	0.497607
interleukin 4 receptor	1.182859	0.944551	2.077681
ABI gene family, member 3	3.401904	1.059217	
vinculin			1.614075
similar to Hypothetical protein FLJ11506	1.126367	0.976408	0.449214
similar to Hypothetical protein FLJ11506	0.378017	1.167195	0.976855
mahogunin, ring finger 1	0.550526	0.923872	2.262094
Hematological and neurological expressed 1	0.774494	1.083047	0.847421
hematological and neurological expressed 1	0.696358	0.874195	0.396018
Programmed cell death 5	9.425183		
thyroid hormone receptor beta		0.268763	
Similar to KIAA1990 protein	0.932845	0.891148	2.728878
NK3 homeobox 2	0.995612	0.437616	
troponin I type 2 (skeletal, fast)	0.959079	1.14305	2.051625
F-box and WD repeat domain containing 8	0.655861	1.303137	4.18072
similar to stem cell antigen 2	2.194541	1.396181	1.115839
guanine nucleotide binding protein (G protein), beta polypep	1.195413	1.625501	3.747133
leukocyte ribonuclease A-2	2.218934	2.271751	4.075813
leukocyte ribonuclease A-1 /// leukocyte ribonuclease A-2	2.419965	2.216785	2.907348
similar to cAMP-dependent protein kinase inhibitor gamma	2.482759	1.175117	0.910533
Chondroitin polymerizing factor	1.668638	1.045653	2.056805
guanine deaminase /// hypothetical protein LOC770483		0.477204	0.555967

FYVE, RhoGEF and PH domain containing 3	0.928877	0.932312	0.496198
v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	1.147275	0.925673	4.476453
sirtuin (silent mating type information regulation 2 homolog)	0.708479	1.088672	1.161063
leukocyte ribonuclease A-1	2.242966	1.507305	3.191123
Hypothetical protein LOC769722	0.878469	1.032027	0.516148
Hypothetical protein LOC769722	0.932205	0.980874	0.639264
Hypothetical protein LOC769722	0.931294	0.93656	0.647265
suppressor of Ty 5 homolog (S. cerevisiae)	1.018345	0.816793	2.135918
suppressor of Ty 5 homolog (S. cerevisiae)	0.673661	0.748917	2.54415
cathepsin H	1.18363	1.089878	1.567345
similar to LOC494798 protein		0.92661	1.628146
selenoprotein P, plasma, 1	0.543918	0.730681	0.622753
selenoprotein P, plasma, 1	0.734425	0.997346	2.074177
Deleted in malignant brain tumors 1	3.654652	2.405131	2.798229
MBD2-interacting zinc finger	0.616668	0.803629	1.302452
progesterone receptor	2.70368	3.317997	1.378654
hypothetical protein LOC776812	0.808692	1.183848	3.016047
tumor protein p53	3.685075		
SH3-domain GRB2-like endophilin B1	1.237564	1.066668	0.497068
immunoglobulin superfamily, member 1	3.650528	1.89107	1.861073
signal-induced proliferation-associated 1 like 1	0.660281	0.851405	0.357515
nuclear factor I-X protein	1.284601	1.184881	1.522645
peptidylprolyl isomerase H (cyclophilin H)	0.786296	1.203948	0.401664
Forkhead box K2	1.299264	0.957011	0.733132
nuclear factor I/C (CCAAT-binding transcription factor)	3.943064	0.97188	1.172236
nuclear factor I/C (CCAAT-binding transcription factor)	1.627059	1.428045	
son of sevenless homolog 2 (Drosophila)	1.694534	1.165493	0.82318
hypothetical LOC420010	1.676277	1.495601	2.480044
Cytoskeleton associated protein 5	1.068616	1.245763	0.680304
transmembrane protein 22	0.556833	1.582218	0.407855
nuclear factor I/B	0.879692	1.218346	1.885854
family with sequence similarity 120A	1.869381	0.90636	0.634384
platelet-derived growth factor beta polypeptide (simian sarcc	1.200055	0.990902	3.318239
nuclear factor I/A	2.582238	1.085413	1.404352
nuclear factor I/A	6.385803	1.576672	0.717784
similar to macrophage inflammatory protein-2	16.30568	3.510748	7.923984
U-box domain containing 5	0.442695	0.959451	
cysteine-rich PDZ-binding protein	1.338665	1.342217	0.40807
inositol polyphosphate-5-phosphatase K	0.91709	0.96947	0.711798
tenascin R (restrictin, janusin)			4.565133

angiotensin II receptor-associated protein	0.955149	1.120959	0.472563
ligatin	0.450995	1.222243	0.578304
methyltransferase like 9	0.66633	1.124697	0.44011
lysozyme (renal amyloidosis)	2.821059	1.468645	0.594182
oxysterol binding protein-like 10	0.827404	0.889076	0.451465
Chromosome 14 open reading frame 32	1.313665	0.876587	0.463499
formin 1	1.14551	1.220288	0.724203
FXD domain containing ion transport regulator 6	0.829382	0.695177	1.689172
chromosome 19 open reading frame 28	0.534447	0.843872	0.276137
intraflagellar transport 172 homolog (Chlamydomonas)	0.792931	1.21002	3.444523
phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.532492	1.149308	4.004355
leupaxin	0.868076	0.89494	0.306536
lamin A	1.419554	0.226281	2.497593
similar to DNA replication initiator protein	0.728482	1.193267	0.760726
mitochondrial trans-2-enoyl-CoA reductase	1.492623	0.98837	2.284103
dystrophin	1.369737	1.272879	0.776996
dystrophin	2.268413	1.028915	0.650953
dystrophin	2.818693		
BUB1 budding uninhibited by benzimidazoles 1 homolog (y	0.738454	1.073051	0.604683
3'(2'), 5'-bisphosphate nucleotidase 1	0.713827	0.922044	0.366361
3'(2'), 5'-bisphosphate nucleotidase 1	0.834927	1.07589	0.21738
spermatogenesis associated 13	0.8054	1.180534	
similar to Cytochrome P450 4A2 precursor (CYPIVA2) (Lau	1.501171	1.466588	3.214292
catechol-O-methyltransferase		0.716865	0.328197
calpain 3, (p94)	1.146174	1.480777	1.231303
peroxisomal membrane protein 4, 24kDa	0.91452	0.998828	0.420299
serine/threonine kinase 10	1.728407	1.577583	2.636814
hypothetical protein LOC769044	1.921456	2.479096	2.47362
v-myb myeloblastosis viral oncogene homolog (avian)	0.904834	0.869527	0.214672
zona pellucida glycoprotein 3 (sperm receptor)	1.886965		0.163413
transmembrane BAX inhibitor motif containing 1	1.175536	0.896554	2.097132
similar to Ephx1 protein	1.147565	1.374633	2.337817
CGI-146 protein	1.413643	1.414658	2.01549
cKrl protein	1.101516	1.035949	1.058749
adaptor-related protein complex 1, gamma 1 subunit		3.297553	
nuclear receptor binding protein 1	1.108491	0.840013	2.189018
hypothetical gene supported by CR387739	1.138032		2.532934
carboxymethylenebutenolidase homolog (Pseudomonas)	3.996085	1.922709	0.927757
CD28 molecule	0.721533	0.895602	0.245355
similar to ovary-specific acidic protein	0.362856	0.830516	0.170962

SRY (sex determining region Y)-box 17	1.717021	1.233974	3.931103
dehydrogenase/reductase (SDR family) member 3	1.093114	1.033405	3.739194
Hypothetical LOC425086	0.765491	1.26606	2.774106
homeobox D4			
phospholipid transfer protein	0.703707	1.395802	2.013381
hypothetical LOC428693	1.177922	0.748327	0.401382
Hypothetical LOC426184	5.115493		3.550704
cAMP responsive element binding protein 3-like 3		1.686905	2.464799
Mitochondrial ribosomal protein S12	0.662492	1.262708	1.614559
Similar to NAD(P)H dehydrogenase, quinone 1	0.487406	1.111028	0.617613
SEC14-like 2 (S. cerevisiae)	1.794037	2.035521	0.731356
hypothetical protein LOC769608	0.854451	0.992354	1.316807
cell division cycle 2, G1 to S and G2 to M	0.660164	1.229442	0.533325
Scavenger receptor class F, member 1	1.460893	1.312613	1.367167
mitochondrial ribosome recycling factor	1.174986	0.771171	2.760967
mitochondrial ribosome recycling factor	1.187908	1.21456	3.078192
chromosome 7 open reading frame 55	0.6001	1.132978	1.655921
WD repeat domain 13	2.208559	1.403431	1.065283
similar to isocitrate dehydrogenase 2 (NADP+), mitochondri	0.659481	1.117482	0.321627
membrane protein, palmitoylated 1, 55kDa	0.988226	0.944519	2.236164
motile sperm domain containing 1	2.337653	0.984021	0.398389
phosphatidylinositol glycan anchor biosynthesis, class C	0.504682	1.040008	2.83234
Solute carrier family 25, member 29	2.777598	1.031899	3.264323
F-box and leucine-rich repeat protein 21	2.723504	0.714582	0.578363
F-box and leucine-rich repeat protein 21	0.5818	1.241657	1.46756
chromosome 20 open reading frame 116	0.84315	1.25291	2.529242
similar to feather keratin		0.287045	
mature avidin	18.48336	20.68621	208.2145
interferon gamma receptor 2 (interferon gamma transducer 1	1.396179	1.411081	1.167912
complement component 1, q subcomponent, A chain	2.012853	1.739779	3.26899
similar to Potassium channel modulatory factor 1	9.747985	1.701651	0.229502
protein kinase, AMP-activated, beta 1 non-catalytic subunit			
glial fibrillary acidic protein	0.511355	1.452444	0.768652
hypothetical LOC426622	0.705199	1.256842	0.494509
hypothetical LOC426622	0.807541	0.890927	0.429664
thioredoxin reductase 3		1.452173	0.281942
thioredoxin reductase 3	0.460573	1.107562	0.46075
ADP-ribosylation factor GTPase activating protein 3	0.117766	3.978085	2.414196
retinoic acid induced 2	0.909039	1.586982	
Single-stranded DNA binding protein 2	1.082096	0.77189	0.234826

single-stranded DNA binding protein 2	0.734588	1.002451	0.102149
sarcalumenin	1.174736	0.815864	2.097891
chromosome 6 open reading frame 161	0.69848	1.129261	0.480642
IKAROS family zinc finger 2 (Helios)	1.113911	0.931283	0.358665
MIS12, MIND kinetochore complex component, homolog (y	0.749133	1.221603	0.548183
Pantothenate kinase 3	2.104469	0.997737	0.969652
hypothetical protein LOC769609	0.874166	0.876718	0.938514
nonhomologous end-joining factor 1	0.835822	2.351699	
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 1	0.995403	0.409754	0.376202
RNA binding motif protein 41	0.636871	0.893904	1.315504
ELOVL family member 6, elongation of long chain fatty aci	0.819118	1.079045	2.038777
goosecoid homeobox	2.842149	6.404926	2.701925
WDR45-like	1.061071	1.724927	0.273009
nucleolar protein with MIF4G domain 1	1.412353	1.259231	0.599014
torsin family 1, member A (torsin A)	1.070615	1.340105	0.467
quiescence-specific protein	1.759008	1.006658	1.383564
chromosome 11 open reading frame 77	0.816912	1.625036	2.061126
Chromosome 9 open reading frame 167	1.405248	1.081837	1.775432
LIM domain only 2 (rhombotin-like 1)	2.837635	1.454736	3.433939
S100 calcium binding protein A9			2.266534
similar to MGC69149 protein	2.207726	1.454884	2.260773
Tripeptidyl peptidase I	0.807341	0.956273	2.596825
somatostatin	1.756941	1.629714	6.367144
synaptojanin 2	1.201755	2.016149	1.870738
Annexin A8-like 1	0.724715	1.015198	0.425531
cardiomyopathy associated 5			2.848339
synaptotagmin XI	0.904727	1.249589	2.742459
oxysterol binding protein-like 1A	3.553625	2.789949	1.367228
teashirt family zinc finger 2	1.875565	2.344001	1.314704
prostaglandin E receptor 3 (subtype EP3)	0.727303	1.10234	1.514299
similar to type I hair keratin KA31	0.37826	0.757926	0.133058
similar to type I hair keratin KA31		0.326359	0.742412
similar to type I hair keratin KA31	0.440645	0.816089	0.069172
mediator complex subunit 24	0.717072	1.077573	1.763895
apical protein 2	0.491784	1.667699	0.683111
chromosome 9 open reading frame 151	0.579691	1.076592	1.891941
Chromosome 9 open reading frame 151	0.704111	0.552703	1.385983
family with sequence similarity 123A	0.627485	1.100167	2.4344
PDZ and LIM domain 4	0.8225	0.84588	0.657801
PERP, TP53 apoptosis effector	0.814698	1.361165	0.245098

heparan sulfate proteoglycan 2	1.069537	1.119972	3.025067
heparan sulfate proteoglycan 2	2.938134	0.74178	1.990742
transmembrane protein 108	0.952155	1.051237	0.592153
mutS homolog 6 (E. coli)	0.924627	1.128163	0.521432
SET domain containing 4	3.747595	1.036325	2.069154
plastin 1 (I isoform)	0.458284	0.95927	0.432703
RAS-like, family 11, member B	0.708522	0.595184	0.469977
general transcription factor IIH, polypeptide 4, 52kDa	1.126414	0.962586	2.162674
myogenic differentiation 1	1.784265	0.917001	4.131697
similar to p150 target of rapamycin (TOR)-scaffold protein c	2.218724	1.124424	1.100305
beta-1,4-galactosyltransferase			
carbamoyl-phosphate synthetase 2, aspartate transcarbamyla	0.827749	1.152407	3.323085
carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihy		1.053941	3.169876
FUS interacting protein (serine/arginine-rich) 1	1.005841	0.950471	0.624971
T-cell acute lymphocytic leukemia 1	0.565709	1.22606	1.755436
Kruppel-like factor 2 (lung)	2.009831	1.587864	1.398614
Nuclear protein, ataxia-telangiectasia locus	1.546977	0.930838	0.597262
nuclear receptor binding SET domain protein 1	1.020411	0.925941	1.696474
MORN repeat containing 2	1.074206	0.505473	26.26952
WNT1 inducible signaling pathway protein 1	1.010311	0.843258	1.478377
similar to Chymotrypsin inhibitor (DPCI)	1.044568		2.526408
ankyrin 2, neuronal			0.303178
Hypothetical protein LOC770202	0.646543	0.965774	0.707324
hypothetical LOC424918	1.466673	2.270203	
small nuclear ribonucleoprotein polypeptide A'	0.946991	0.690947	3.4436
kelch-like 18 (Drosophila)	1.788795	0.897842	2.062048
gamma-glutamyltransferase-like 3	1.131167	1.600253	1.165789
insulin-like growth factor binding protein 2, 36kDa	2.068699	1.17288	1.174934
similar to Maltase-glucoamylase (alpha-glucosidase)	0.613106	3.171021	5.427752
Similar to Im:7137941 protein	1.36318		0.75748
phospholipid scramblase 1	2.048191	1.472475	1.939562
phospholipid scramblase 1	2.698575	1.411904	2.022357
Pleckstrin homology, Sec7 and coiled-coil domains 3	1.202053	0.86872	0.465067
component of oligomeric golgi complex 7	1.447812	0.863799	0.768578
chromosome 11 open reading frame 54	0.764001	1.026988	0.383287
chromosome 6 open reading frame 129	0.628128	0.961253	0.591325
myosin IXA	2.872065	0.571735	3.637131
chromosome 8 open reading frame 80	3.502652	2.010985	3.970815
activin A receptor, type IIB		6.678993	
similar to 6.8 kDa mitochondrial proteolipid	0.829415	1.351337	0.096895

glycogen synthase kinase 3 beta	0.823267	0.971819	1.803991
proline rich 6	0.466329	1.790475	1.088838
adenylosuccinate synthase	1.120489	1.438943	0.488475
sema domain, immunoglobulin domain (Ig), transmembrane	0.822397	0.85316	1.236094
SAPS domain family, member 3	0.146629	4.417114	3.489949
chromosome 9 open reading frame 18		0.74816	
c-myc binding protein	0.888047	0.433137	0.471895
similar to RIKEN cDNA A930008G19 gene	1.279992	1.385632	2.146529
G-protein signaling modulator 2 (AGS3-like, C. elegans)	1.060519	0.967627	0.667974
anaphase promoting complex subunit 2	0.820521	0.926583	1.585251
chromosome 20 open reading frame 72	0.869171	1.043416	0.509698
calcium/calmodulin-dependent serine protein kinase (MAGU	1.19534	0.399463	
calcium/calmodulin-dependent serine protein kinase (MAGU	1.123126	0.624616	0.400302
transgelin 3	1.6693	0.975647	2.398129
hypothetical LOC423257	0.832696	1.240541	0.6768
monoamine oxidase A	2.830139	1.867308	4.435587
Hypothetical LOC415966	0.488527	1.099309	0.29663
villin-like	1.020888	1.400703	2.328156
similar to PINCH protein	2.486926	0.31645	0.755261
Arylsulfatase family, member I	0.47362	0.650051	0.990195
Ectonucleoside triphosphate diphosphohydrolase 7	1.322238	1.269949	2.179662
deoxynucleotidyltransferase, terminal	0.591973	0.471255	0.414993
pentatricopeptide repeat domain 1	0.99387	0.859447	0.793067
mitochondrial ribosomal protein L33	0.647654	0.436314	
oxysterol binding protein-like 10	0.905626	1.195923	2.117384
calcium-binding protein	1.03326	1.255504	0.937851
hypothetical LOC422459	0.820555	1.312259	2.042696
hypothetical protein LOC770248	0.76921	1.857063	0.373613
Unc-50 homolog (C. elegans)	1.049522	0.699442	0.773131
chaperonin containing TCP1, subunit 2 (beta)	0.98893	1.109494	0.477301
similar to human phosphotyrosine phosphatase kappa	0.787799	0.766365	2.017934
similar to LOC446287 protein	2.228105	0.863805	3.467716
TM2 domain containing 2	1.317103	0.550767	0.391058
hypothetical LOC396357	2.030411	0.518496	1.956335
chromosome 4 open reading frame 8			0.276118
ADAM metallopeptidase with thrombospondin type 1 motif,	0.894493	1.512392	0.95414
nuclear receptor subfamily 0, group B, member 2	1.794227	0.451673	1.384576
acyl-CoA synthetase bubbligum family member 2	0.738129	1.187244	1.757253
inhibitor of growth family, member 4	1.142649	0.780287	0.785281
islet amyloid polypeptide	0.805673	1.118638	0.905159

similar to very large inducible GTPase-1	8.38246	2.568482	9.438594
coiled-coil domain containing 28A	1.305947	0.877801	0.371846
coiled-coil domain containing 28A	1.088931	0.558834	0.331585
chromosome 6 open reading frame 89	0.644643	0.708506	0.498852
Milk fat globule-EGF factor 8 protein	1.549078	1.485449	7.578666
Hypothetical protein LOC771069	0.528656	1.836183	2.495391
non-metastatic cells 6, protein expressed in (nucleoside-diph	1.242551	1.044123	0.476242
origin recognition complex, subunit 6 like (yeast)	0.964913	1.053238	1.212944
origin recognition complex, subunit 6 like (yeast)	1.036149	1.219097	0.287077
similar to aldose reductase	1.135402	1.039201	1.623191
nasal embryonic LHRH factor	6.918679	0.605266	2.931586
intersectin 2	0.607217	0.849015	2.682951
similar to Ppp4r1-prov protein	1.399279	1.00564	0.658858
chromosome 15 open reading frame 48	2.116995	1.827715	3.289798
coiled-coil domain containing 12	0.927683	1.074585	0.478308
kelch-like 8 (Drosophila)	1.112766	1.114405	0.825233
colony stimulating factor 2 receptor, alpha, low-affinity (gra	1.395501	1.436475	3.843498
protein tyrosine phosphatase, receptor type, S	0.475913	0.747516	0.573781
mannan-binding lectin serine peptidase 1 (C4/C2 activating c	0.739628	2.566619	1.379272
Arrestin domain containing 2	1.38775	1.005761	3.16631
synaptophysin-like 1	1.17849	2.553278	8.636956
hypothetical protein LOC769446	1.239002	0.735362	0.24575
glyoxalase I	1.122938	1.331645	0.061529
BMP binding endothelial regulator		1.536643	2.107827
exportin 6	0.457362	0.754597	2.886944
interleukin-1 receptor-associated kinase 2	1.643329	0.995576	0.495766
cofilin 2 (muscle)	1.663128	0.776807	2.225127
phosphatidylinositol glycan anchor biosynthesis, class L	1.581072	1.452021	1.452423
peroxisome biogenesis factor 10	0.63521	1.053027	0.32897
peroxisome biogenesis factor 10	1.092803	0.762964	0.180708
glutathione transferase	0.981903	1.810814	2.229885
B-cell CLL/lymphoma 9	2.999128	1.168417	1.688996
polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	0.735534	0.958143	0.479843
mutS homolog 4 (E. coli)	1.689678	0.794936	0.442401
C1q and tumor necrosis factor related protein 2	1.025461	1.207458	1.058709
secreted frizzled-related protein 4	0.438373	0.090162	
similar to ribosomal protein L23A	0.40646	0.661902	0.456485
leucine rich repeat and sterile alpha motif containing 1	0.288187	0.391284	0.837263
domesticus (clone 1.6 kB) islet-2	2.100044	0.933841	1.561401
fin bud initiation factor homolog (zebrafish)	0.668877	2.152591	3.51669

Boc homolog (mouse)	0.496735	0.716746	0.384558
leucine rich repeat containing 16A	2.085301	1.111413	1.878364
Chromosome 16 open reading frame 61		2.929699	0.780767
Chromosome 16 open reading frame 61	0.962168	1.114137	0.489406
interferon regulatory factor 1	2.963294	1.547715	2.323075
GRAM domain containing 2	1.664309	1.059267	0.598267
Similar to 1600002O04Rik protein	2.454808	2.342421	1.799491
Similar to 1600002O04Rik protein	1.555553	1.604301	2.463152
chromosome 11 open reading frame 52	0.559145	1.117944	4.26904
cytoskeleton associated protein 5	0.604439	1.674178	2.545687
cytoskeleton associated protein 5	2.005532	1.16282	0.769541
family with sequence similarity 108, member C1	1.508804	1.149524	0.706554
ring finger protein 34	0.991691	0.951177	2.30052
acetylcholinesterase		0.275943	
ATG12 autophagy related 12 homolog (S. cerevisiae)	0.52648	1.133285	1.266849
WWC family member 3	1.810687	1.115991	2.511958
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	0.910549	1.165409	1.845618
Sterile alpha motif domain containing 4A	2.002891	0.840687	1.222648
GATA binding protein 4		0.375793	
Ribosomal protein L27a	1.070007	0.720434	0.233015
solute carrier family 14 (urea transporter), member 2	1.887711	1.443279	0.867014
wingless-type MMTV integration site family, member 5B	1.127389		2.117358
chromosome 1 open reading frame 128	0.657673	0.925457	1.401408
ring finger protein 4	1.5113	0.9234	0.205376
similar to Prt1 homolog	0.677828	1.103187	0.732204
chromosome 20 open reading frame 177	1.254268	0.912332	0.236743
chromosome 20 open reading frame 177	0.973135	0.934534	0.513751
ATP synthase mitochondrial F1 complex assembly factor 1	0.932238	0.919133	0.51177
ATP synthase mitochondrial F1 complex assembly factor 1	0.717049	0.896885	0.388332
ATP synthase mitochondrial F1 complex assembly factor 1	0.729519	2.746413	1.017528
chromosome 2 open reading frame 33	1.848456	0.775783	1.262409
chromosome 20 open reading frame 30	1.034282	1.157904	0.349839
phosphatidylethanolamine N-methyltransferase	0.473663	0.937581	1.568984
phosphatidylethanolamine N-methyltransferase	0.604205	1.002454	0.342236
interferon			
chromosome 5 open reading frame 32	1.301194	1.165219	1.564542
IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	1.104229	0.791751	0.897687
tissue factor pathway inhibitor 2	1.511668	1.56038	3.094491
chromosome 6 open reading frame 154	2.158325	1.716475	1.668007
replication factor C (activator 1) 4, 37kDa	0.975865	2.279025	1.235626

transforming growth factor, beta receptor III	0.886623	0.378096	
chromosome 6 open reading frame 32	2.255476	1.786693	3.058107
LYR motif containing 5	0.752536	1.181812	0.299642
EPH receptor A3	1.68457	1.25844	2.196478
HscB iron-sulfur cluster co-chaperone homolog (E. coli)	0.780248	1.470888	0.339839
ADP-ribosylation factor-like 6 interacting protein 1	1.037153	1.085819	
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosyl transferase	1.213221	1.577051	2.90423
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosyl transferase	1.698248	1.407419	2.197137
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide			0.016855
growth arrest-specific 6	0.836455	1.217912	2.693595
folliculin-like 4	0.759585	1.633026	0.322864
CASP8 associated protein 2	1.151866	1.001552	0.979484
Kruppel-like factor 1 (erythroid)	0.808072	1.069892	1.7353
TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor		0.475853	
Translocase of outer mitochondrial membrane 7 homolog (yeast)	0.746458		0.070764
hypothetical gene supported by CR389297	0.658575	0.997798	0.434612
ariadne homolog 2 (Drosophila)			
ariadne homolog 2 (Drosophila)	2.173856	0.513373	1.415016
hemopoietic cell kinase	3.867596	1.375688	4.429757
KIAA0020	0.62586	1.113216	2.104642
solute carrier family 46, member 3	1.016461	0.681755	0.126432
Heat shock transcription factor 1	0.831351	0.673371	1.86149
musculoskeletal, embryonic nuclear protein 1	1.304485	1.116151	2.771473
gap junction protein, beta 1, 32kDa	0.760122	0.67291	1.675682
pseudouridylate synthase 7 homolog (S. cerevisiae)	0.972347	1.089127	2.198935
similar to hypothetical protein 4933429F08	1.762754	6.835208	
hypothetical protein LOC770818	0.798392	2.300165	5.797689
intestinal zipper protein	5.452234	1.837004	0.239058
intestinal zipper protein	1.03864	3.707	0.544204
Chromosome 10 open reading frame 65		0.439724	
kelch domain containing 4	1.106083	1.053402	1.804721
coenzyme Q10 homolog B (S. cerevisiae)	0.85071	0.856906	1.633967
E74-like factor 3 (ets domain transcription factor, epithelial-specific)	1.245626	1.050282	1.558066
hypothetical gene supported by CR385622			
fibroblast growth factor binding protein 1	1.284189	2.857923	1.291526
envoplakin	0.541944	1.010993	0.411713
family with sequence similarity 70, member A	0.66563	0.463293	0.669575
integrin, alpha V (vitronectin receptor, alpha polypeptide, an	1.572453	0.846966	0.439646
RAB17, member RAS oncogene family	0.977831	4.792392	1.400736
androgen receptor			2.341787

similar to LOC495234 protein		0.939807	0.061199
villin 1	1.357554	0.826143	1.67895
aspartylglucosaminidase	1.276971	0.913226	0.421257
similar to Ras-related protein Rab-10	2.42179	1.931503	1.158965
similar to Ras-related protein Rab-10	4.010339	1.050137	0.41711
chromosome 11 open reading frame 34	1.268636	2.109211	1.728262
RAB20, member RAS oncogene family	2.419436	1.732896	4.73639
Chromosome 16 open reading frame 14	1.226879	1.881298	3.864426
influenza virus NS1A binding protein	1.475456	0.87154	0.502869
tubulin, beta 1	0.815373	1.434461	1.15372
RCC1 domain containing 1	1.136379	0.434448	
centrosomal protein 192kDa	0.959904	1.0817	0.841172
ladinin 1	0.791976	1.55458	2.212901
troponin I type 3 (cardiac)		0.424204	
similar to hypothetical protein	1.493218	0.406349	1.20364
Similar to KIAA1237 protein	4.449758	2.226501	3.715159
solute carrier family 7 (cationic amino acid transporter, y+ system), mer		0.136541	
NDUFA12-like	0.519083	1.339816	2.160735
elastin (supravalvular aortic stenosis, Williams-Beuren syndr	0.565795	0.661619	0.726381
Similar to Chromosome 4 open reading frame 32	0.694861	0.931408	0.390072
similar to Ran binding protein 11	0.557483	1.153965	2.446132
ISG12-1 protein-like	4.453338	2.662163	10.75652
troponin C type 2 (fast)	0.82471	1.055422	3.635145
F-box protein 31	1.208219	0.576299	2.439155
hypothetical protein LOC770630	112.8299	1.118901	0.397148
endothelin 2	1.242075	4.139586	1.259831
hypothetical LOC427229	1.407474	0.754078	0.437909
transcription factor 21	4.745378	1.072599	4.685581
peroxisomal biogenesis factor 12	1.036293	1.419055	2.533562
cytidine monophosphate (UMP-CMP) kinase 2, mitochondri	6.040607	2.562893	4.679065
ribosomal protein L7-like 1	1.09204	0.955646	0.594318
interleukin 8	5.052205	2.15385	1.466765
chromosome 8 open reading frame 80	2.301619	2.006848	2.574014
chromosome 13 open reading frame 18	1.269735	1.969471	2.098776
TIA1 cytotoxic granule-associated RNA binding protein-like	1.482059	0.794805	0.308033
Hypothetical LOC417387	1.309219	0.849695	0.412801
phosphoglycerate mutase family member 5	1.084488	1.459953	0.472504
TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	1.16844	1.336623	0.728557
ankyrin repeat domain 40	1.260711	1.208677	1.092409
calmodulin binding transcription activator 1	0.631143	0.795001	0.563994

similar to ST3A1	1.655054	4.437985	4.74288
hypothetical LOC424241	0.728586	0.896693	0.200207
chromosome 1 open reading frame 9	0.71921	0.842553	0.144444
similar to thioesterase B	1.279197	2.303794	5.339675
similar to LOC443703 protein	1.073517	1.155471	5.239765
carboxylesterase 1 (monocyte/macrophage serine esterase 1)	1.017549	2.062812	3.366569
Similar to thioesterase B	20.38913	0.800833	
similar to thioesterase B /// similar to thioesterase B	0.776777	1.763851	15.616
acylglycerol kinase	0.857693	1.376301	0.363837
acylglycerol kinase	0.578093	1.683883	0.365744
fragile X mental retardation, autosomal homolog 1	1.295897	0.899602	0.429168
protein kinase C, eta	1.398246	2.137347	2.47655
transmembrane protein 120A	0.397214	0.759878	0.287479
hypothetical protein LOC768701	1.258708	0.784615	1.973581
similar to similar to CDNA sequence BC043118	0.744405	1.585787	2.14163
laminin, alpha 2 (merosin, congenital muscular dystrophy)	0.779413	2.175772	8.986461
kinesin family member 13A	0.986279	0.779646	2.17386
glutathione S-transferase alpha 3	0.731397	1.355493	2.695437
Atonal homolog 8 (Drosophila)	1.352379	1.552728	1.050289
axin 2	1.056964	0.853605	3.20673
Axin 2	1.42943	0.843208	2.597852
glucuronidase, beta	1.350038	1.498378	2.307096
aldehyde dehydrogenase 2 family (mitochondrial)	1.28865	1.071996	2.379984
tandem C2 domains, nuclear	1.01785	1.162437	2.939153
neuropeptide Y	1.452234	0.980368	4.536183
Rap guanine nucleotide exchange factor (GEF) 3			84.72007
ring finger protein 122	0.46548	1.473551	1.44052
small nuclear ribonucleoprotein D3 polypeptide 18kDa	0.743728	1.104813	0.402511
FUS interacting protein (serine/arginine-rich) 1	1.099469	0.942148	0.523976
ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide	0.352292		
secretory carrier membrane protein 5	0.957437	0.913212	2.05026
LATS, large tumor suppressor, homolog 1 (Drosophila)	0.775845	2.398883	0.578112
similar to KIAA0592 protein	1.578172		0.372411
epithelial membrane protein 1			2.021258
centrosomal protein 57kDa	0.476257	1.129249	0.938405
FUN14 domain containing 2	0.545278	1.021101	2.446939
similar to C-type lectin	0.642936	0.36179	1.536572
cadherin	0.484985		
cadherin	0.793064	0.382255	1.510314
Ubiquitin-conjugating enzyme E2F (putative)		0.067361	

Jumping translocation breakpoint	0.670498	1.147595	1.200972
chromosome 20 open reading frame 42	1.704282	1.53372	2.083208
myosin, light chain 2, regulatory, cardiac, slow	0.243548	1.006451	0.380106
Der1-like domain family, member 3	1.372317	0.464165	0.479225
F-box and leucine-rich repeat protein 12		0.621793	
chromosome 18 open reading frame 45	1.238171	1.549081	0.984284
chromosome 9 open reading frame 21	2.381829	0.739918	2.427491
similar to tRNA selenocysteine associated protein	0.817184	1.112515	0.491233
chromosome 9 open reading frame 80	0.721127	0.143354	
phosphatase and actin regulator 1			
insulin-like growth factor binding protein 4	1.887495	0.551855	2.062228
Similar to Ecrg4-A protein	1.377714	0.497799	0.208165
Chromosome 4 open reading frame 33	1.422401	2.532237	0.645066
Chromosome 4 open reading frame 33	1.182726	2.467201	1.031335
dual specificity phosphatase 6	2.350251	0.97049	1.799413
Glutathione reductase	0.886533	1.111797	1.716178
fibroblast growth factor binding protein 2	0.877277	0.886027	0.776446
histidine ammonia-lyase			
similar to Scale keratin (S-ker) (sKer)	0.952769	0.473372	
telomeric repeat binding factor (NIMA-interacting) 1	0.445666	1.036543	0.795694
Similar to immunoglobulin-like receptor CHIR-AB1	1.364975		2.475017
interleukin 1 receptor, type I	1.737891	2.685704	4.920364
glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzym	0.320404	0.971591	0.167601
BUB1 budding uninhibited by benzimidazoles 1 homolog be	0.692599	1.128802	0.681406
chromodomain helicase DNA binding protein 1	316.2725	1.339711	0.197797
SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	0.8785	1.036399	0.494597
non-SMC condensin I complex, subunit G	0.598123	1.254538	0.735828
Peroxisome biogenesis factor 10	2.401127	0.990037	0.515777
far upstream element (FUSE) binding protein 1	0.732673	0.600573	0.355263
far upstream element (FUSE) binding protein 1	1.319722	0.878779	0.49138
signal recognition particle 72kDa	1.186863	1.079184	2.594105
signal recognition particle 72kDa	1.812699	0.26979	1.395344
NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	0.768359	1.061186	1.617273
fibroblast growth factor 9 (glia-activating factor)		0.158371	
ribosomal protein S13	6.458999	0.065755	1.251301
Ribosomal protein S13	9.002128	1.412891	
nipsnap homolog 3A (C. elegans)	0.708941	0.81101	2.259385
tribbles homolog 2 (Drosophila)	1.117219	0.951277	0.382237
tribbles homolog 2 (Drosophila)	1.16739	1.166007	0.4887
Src-like-adaptor	1.267968	0.665499	0.131049

Src-like-adaptor	0.686725	0.676497	0.309472
aspartyl aminopeptidase	0.695098	1.061413	2.072233
lipoma HMGIC fusion partner-like 5		10.28834	3.679422
low density lipoprotein receptor	3.029991	1.056424	0.633477
cAMP responsive element binding protein 1	0.638	0.481522	2.048235
cAMP responsive element binding protein 1	1.427968	2.630325	0.208984
unc-5 homolog C (C. elegans)	0.764515	0.319367	1.02454
tankyrase, TRF1-interacting ankyrin-related ADP-ribose pol	1.03541	1.167059	0.956118
lectin, galactoside-binding, soluble, 1	0.837567	1.56736	2.824501
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, c	1.727762	0.274073	1.037658
basic transcription factor 3-like 4	0.741413	1.246796	0.538362
interleukin 17F		2.323662	1.711169
similar to Transcriptional adaptor 1 (HFI1 homolog, yeast)-li	0.824672	0.900568	0.471943
Syndecan 1	1.141391	1.256288	3.30958
signal transducer and activator of transcription 3 (acute-phas	1.82104	1.021019	2.437026
similar to CG9147-PB	0.441398	1.274818	0.997773
Solute carrier family 5 (sodium/glucose cotransporter), mem	0.857598	1.708718	5.779653
gap junction protein, delta 3, 31.9kDa	2.105465	0.807608	0.764357
Similar to Williams Beuren syndrome chromosome region 2'	0.862338		
gap junction protein, alpha 5, 40kDa	1.564576		4.881511
solute carrier family 5 (sodium/glucose cotransporter), meml	1.456952	2.466588	1.646705
collagen, type XVII, alpha 1	0.65621	1.006708	0.723273
cytohesin 4	1.111161	0.582183	0.304619
chromosome 14 open reading frame 83	1.697812	0.689634	0.550319
fibroblast growth factor receptor 1	1.503856	1.092461	2.410799
dual specificity phosphatase 15	1.297641	1.331939	2.66725
solute carrier family 2 (facilitated glucose transporter), meml	0.937742	1.316617	3.516434
calponin alpha	1.650329	0.714749	1.234975
regulator of G-protein signalling 14	0.945118	0.608527	1.357659
polo-like kinase 3 (Drosophila)	1.407741	1.205476	2.546442
microtubule associated monooxygenase, calponin and LIM do	1.175839	0.705042	1.981197
mal, T-cell differentiation protein 2	1.191121	1.416167	3.544155
similar to Junction plakoglobin	0.767748	0.790592	0.540656
similar to Ig V-region-like B-G antigen 17	1.404408	1.36664	0.175753
YTH domain containing 1	1.388355	0.771614	0.318788
ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1	3.586559	1.280358	4.192113
fibroblast growth factor receptor-like 1	1.561324		
tumor necrosis factor (ligand) superfamily, member 10	1.939339	1.17937	1.969265
tumor necrosis factor (ligand) superfamily, member 10	1.324276	0.991359	3.929961
E4F transcription factor 1	2.359416	0.992104	0.617378

parvalbumin	0.561755	1.047877	0.10366
leucine-rich repeat-containing G protein-coupled receptor 4	1.66654	1.899686	1.867794
Transmembrane protein 34	1.058307	0.45872	0.568625
FCF1 small subunit (SSU) processome component homolog	0.482674	1.137849	1.609673
Ewing sarcoma breakpoint region 1	3.058683	0.580688	0.793586
zinc finger and BTB domain containing 17	1.08502	0.74736	1.547863
N-acetylneuraminic acid synthase (sialic acid synthase)	1.021216	1.460132	0.419934
farnesyl-diphosphate farnesyltransferase 1	0.478658	0.926035	0.990897
myosin binding protein H	0.734603	0.822844	0.293801
Wiskott-Aldrich syndrome-like	1.25058	0.929244	0.988843
family with sequence similarity 100, member A	0.627988	1.153417	2.261611
similar to MUC2	1.011593	3.126339	0.937004
Similar to keratin 18	1.06183	1.566923	1.619396
Tubulin, delta 1	2.040591	0.70006	1.598583
Tubulin, delta 1	0.796861	1.018158	2.193119
ATPase, H ⁺ /K ⁺ exchanging, beta polypeptide	1.346774	1.676555	1.1052
kelch repeat and BTB (POZ) domain containing 2	1.174989	0.865498	0.430129
isopentenyl-diphosphate delta isomerase 1	0.804519	1.078639	0.681181
sulfotransferase family, cytosolic, 1B, member 1	1.460023	0.941116	2.060114
zinc finger and BTB domain containing 43	0.986819	1.227848	0.238818
FK506 binding protein 7	2.031293	0.935552	1.475602
bromodomain containing 1	1.650849	0.89461	0.402507
mitogen-activated protein kinase kinase kinase 8	3.406311	2.003632	2.01142
adenosylmethionine decarboxylase 1	0.901628	2.564122	1.745425
glycerophosphodiester phosphodiesterase 1	0.38634	0.7668	0.906921
oncomodulin 2	0.181644	0.894084	0.010404
N-myc (and STAT) interactor	1.967915	1.784052	2.00821
aquaporin 11		9.957932	
Ataxin 7-like 1	1.228888	0.849157	1.05501
Diacylglycerol kinase, delta 130kDa	1.930394	1.012993	2.023154
collagen, type VI, alpha 3	1.681778	1.462163	2.61485
membrane metallo-endopeptidase	3.475706	1.380113	13.07196
membrane metallo-endopeptidase			
Dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein		22.92608	
integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3	1.141352	0.776711	1.328216
presenilin associated, rhomboid-like	0.91372	0.345006	1.285848
Cadherin 8, type 2	0.570512	1.763433	1.515332
protein phosphatase 2, regulatory subunit B', gamma isoform	1.36746	2.501677	0.425897
eukaryotic translation initiation factor 5	1.045507	1.107556	0.485509
meprin A, alpha (PABA peptide hydrolase)	1.495062	1.47809	4.132357

WD repeat and FYVE domain containing 3	0.366494		1.716018
protein phosphatase 1, regulatory (inhibitor) subunit 16B	2.075271	0.711475	2.701115
antizyme inhibitor 1 /// similar to ornithine decarboxylase an	0.898772	1.223386	1.175128
oxysterol binding protein-like 6	0.407329	0.67878	
perilipin	2.322896	1.186029	3.524034
corticotropin releasing hormone receptor 2		0.27519	
thioredoxin 2	0.793411	1.125994	0.429395
similar to HBxAg transactivated protein 2 /// similar to HBx.	0.689125	0.969217	2.860472
S100 calcium binding protein A6	1.435396	1.51135	3.72006
hypothetical protein LOC769755	0.673902	0.627029	1.787733
fatty acid binding protein 6, ileal (gastrotropin)	1.420443	1.345768	1.137572
similar to GTPase, IMAP family member 7	1.166176	1.281699	8.777992
chromosome 1 open reading frame 58	1.036568	3.451736	2.160775
acyl-Coenzyme A dehydrogenase family, member 11	0.823403	1.083361	2.093031
hypothetical LOC424832	0.978044	0.741822	0.323916
chemokine (C-C motif) receptor 8	1.877737	2.334662	3.904043
THO complex 7 homolog (Drosophila)	0.5768	0.766251	0.204298
nucleoporin like 2	0.460976	1.24866	0.352607
protocadherin 24	2.149657	3.262589	6.030731
A kinase (PRKA) anchor protein 13	1.345197	1.141566	2.675684
mesenchyme homeobox 2	3.696918	1.03825	2.086782
adenosine A3 receptor	0.826941	2.171077	0.92338
keratin associated protein 10-4	0.463102		
serine/threonine kinase 17b	0.93802	0.577873	0.411859
FK506 binding protein 4, 59kDa	0.770449	0.978137	0.590587
KIAA0494	0.912673	1.041586	2.30536
atrophin 1	2.160497	0.778244	1.375702
sorting nexin 4	1.188434	0.797901	0.422923
sorting nexin 4	0.59325	1.346906	0.235812
complement component 1, r subcomponent	3.037259	2.052326	3.531933
scavenger receptor class B, member 1	1.407828	1.008473	2.759235
syntaxin 2	0.385164	1.1483	1.387105
beclin 1, autophagy related	1.213798	0.905989	0.694912
NCK adaptor protein 2	1.172191	1.086055	0.592862
Ethylmalonic encephalopathy 1	0.859967	1.16985	1.330032
dedicator of cytokinesis 9	2.145856	0.845763	1.103954
Golgi membrane protein 1	1.39806	1.000338	0.555297
Wolf-Hirschhorn syndrome candidate 2	0.882996	1.044982	0.449585
similar to pim-3 protein	1.52788	1.30915	4.077858
similar to cytosolic nucleotidase I	0.874973	0.936441	0.945099

ectonucleotide pyrophosphatase/phosphodiesterase 3	2.896299	2.974906	3.319189
chromosome 12 open reading frame 10	0.892357	1.159249	1.508004
transcobalamin II; macrocytic anemia	1.444106	3.845743	1.871388
hydrogen voltage-gated channel 1	2.15275	0.534347	0.681513
abl interactor 2	0.692022	0.997079	0.468827
DnaJ (Hsp40) homolog, subfamily C, member 3	0.407527	0.950643	
potassium voltage-gated channel, shaker-related subfamily, r	1.612056	1.02999	0.809357
Rh-associated glycoprotein	0.678059	2.143402	3.076522
Rh-associated glycoprotein	0.903096	1.219892	3.381127
somatostatin II			
slit homolog 2 (Drosophila)	2.016965	1.43701	
lysozyme G-like 2	5.55333	2.880743	6.193183
immunoglobulin-like receptor CHIR-A2 /// similar to immu	1.734975	0.582035	2.769917
ATPase, class V, type 10D	0.820489	1.306111	
fizzy/cell division cycle 20 related 1 (Drosophila)		0.36488	
alanyl-tRNA synthetase			0.276429
Chemokine ah221	9.107544	2.561138	9.052442
tumor-associated calcium signal transducer 1	1.709032	2.185387	1.182811
tumor-associated calcium signal transducer 1	1.207523	1.369786	2.257456
tumor-associated calcium signal transducer 1	2.172786	3.632697	0.505414
GEM interacting protein	1.173481	1.027811	2.62586
fizzy-related protein homolog	0.452644	0.074535	
hypothetical LOC424588	1.219454	0.825974	2.573654
haloacid dehalogenase-like hydrolase domain containing 2		0.393402	1.917629
suppressor of cytokine signaling 3	1.016029	1.134717	2.87136
transmembrane protein 169	1.113749	0.716379	2.414502
phosphofurin acidic cluster sorting protein 2	0.341791	0.342558	1.042839
transmembrane protein 57	1.202401	1.031463	0.741089
COX19 cytochrome c oxidase assembly homolog (S. cerevis	0.901344	1.02152	0.475141
AHA1, activator of heat shock 90kDa protein ATPase homo	2.708017	0.680856	0.721467
interferon, gamma	3.606716	3.404986	4.745357
DnaJ (Hsp40) homolog, subfamily B, member 6	1.254165	1.29399	0.406413
DnaJ (Hsp40) homolog, subfamily B, member 6	1.079453	1.630744	0.387191
Pantothenate kinase 3	1.086128	1.101842	0.534679
chromosome 6 open reading frame 163		2.626562	
S100 calcium binding protein B			10.01721
potassium channel tetramerisation domain containing 10		1.334129	0.04632
potassium channel tetramerisation domain containing 10			0.074344
potassium channel tetramerisation domain containing 10	3.419786	1.83927	0.394651
potassium large conductance calcium-activated channel, sub	5.554926		7.753195

Ribosomal protein S25			
Similar to MGC83563 protein	1.004148	0.921939	0.957438
neuralized homolog (Drosophila)	1.584212	1.282628	3.8413
phosphoribosyl pyrophosphate synthetase-associated protein	0.573246	0.867198	0.866322
agmatine ureohydrolase (agmatinase) /// similar to putative a	1.263669	1.422745	2.93834
Sp1 transcription factor	7.836747	0.539776	0.734763
ectonucleoside triphosphate diphosphohydrolase 1	0.689813	0.864404	0.789359
placenta-specific 8	1.283966	2.30541	2.723897
similar to Pre-mRNA cleavage complex 2 protein Pcf11 (Pre	2.186431	1.048438	0.409257
nucleolar protein 14	1.036192	1.16906	1.03072
M-phase phosphoprotein 10 (U3 small nucleolar ribonucleop	0.957485	0.953063	0.431968
mitochondrial ribosomal protein S10	0.768242	1.044983	0.515471
alpha thalassemia/mental retardation syndrome X-linked	0.38105	0.873018	0.820984
ELMO/CED-12 domain containing 2	0.774829	0.989791	0.559511
leptin receptor	2.375417	0.810315	
HLA-G histocompatibility antigen, class I, G /// similar to M	0.755021	3.907836	33.51654
major histocompatibility complex class I glycoprotein	1.110531	1.611255	0.980386
tektin 4	2.002716		
similar to MHC Rfp-Y class I alpha chain /// similar to MHC	1.017612	0.383146	2.117626
high mobility group AT-hook 1	0.769999	1.285612	0.483886
jumonji domain containing 2C	1.097269	1.054941	2.10766
mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.755778	1.146401	0.803803
phospholipase A2, group VI (cytosolic, calcium-independent	2.414054	0.860137	2.029066
alanyl (membrane) aminopeptidase (aminopeptidase N, amin	0.857335	2.22266	6.681004
serine hydrolase-like 2	0.755581	0.513287	0.4276
Hypothetical protein LOC772074	1.074416	0.901628	2.642076
centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	0.362292	1.087952	0.584366
eukaryotic translation initiation factor 2 alpha kinase 4	1.194473	1.025579	0.09374
heparan sulfate 2-O-sulfotransferase 1	1.737299	1.021035	0.503822
heparan sulfate 2-O-sulfotransferase 1	0.564755	1.059376	0.650674
fibronectin 1	3.549117	1.226821	1.534356
IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	0.484922	1.284277	1.033453
carnitine palmitoyltransferase 1A (liver)	0.555198	0.696945	1.948982
v-akt murine thymoma viral oncogene homolog 2	0.710428	0.823961	1.155651
similar to RIKEN cDNA 5830415L20	0.838368	0.969321	0.718692
similar to MGC80162 protein	1.061129	1.124848	1.592897
neuronal pentraxin II	0.636269	0.417951	0.551969
plasminogen activator, tissue	0.756332	0.092561	0.152757
FAST kinase domains 2	0.548667	1.377803	2.039218
glycine/arginine rich protein 1	1.333972	0.887096	2.337495

SRY (sex determining region Y)-box 4	0.708699	0.562629	0.428962
Keratin 222 pseudogene	0.998671	0.593562	0.035429
ADP-ribosylhydrolase like 1	0.767515	0.33362	1.164533
WEE1 homolog (S. pombe)	0.826282	1.171021	0.564709
chromosome 4 open reading frame 34	0.892017	2.086032	0.90974
serum/glucocorticoid regulated kinase 1	2.053299	1.744389	4.035993
serum/glucocorticoid regulated kinase 1	1.404177	2.075523	2.453271
G1 to S phase transition 1	0.932982	1.09393	0.484333
Histidine triad nucleotide binding protein W	2.214362	4.190777	0.83144
ubiquitin specific peptidase 7 (herpes virus-associated)	1.125013	0.92529	0.520698
ubiquitin specific peptidase 7 (herpes virus-associated)	0.807311	1.131388	0.015375
apoptosis, caspase activation inhibitor	4.2528	0.543372	0.039731
vimentin	1.112027	1.210148	1.06926
nuclear factor related to kappaB binding protein	2.155732	0.921819	0.643015
nuclear factor related to kappaB binding protein	2.367941	1.130264	0.433766
surfactant, pulmonary-associated protein A1	1.15118	1.741931	3.256441
hypothetical LOC423783	2.015953	1.422106	0.488265
insulin-like growth factor binding protein 5		1.508486	11.50401
RIO kinase 1 (yeast)	0.353065	0.88015	0.851604
tudor domain containing 3	1.022965	0.927724	1.274341
superoxide dismutase 2, mitochondrial	0.895134	1.065026	0.491121
glycyl-tRNA synthetase	2.175394	1.435447	3.591631
acidic (leucine-rich) nuclear phosphoprotein 32 family, mem	0.441976	1.140832	0.570744
acidic (leucine-rich) nuclear phosphoprotein 32 family, mem	2.601655	0.595131	0.952056
IKAROS family zinc finger 2 (Helios)	0.745254	0.85885	0.29192
Gem (nuclear organelle) associated protein 4	0.723402	1.421307	3.005865
SIVA1, apoptosis-inducing factor	0.892677	0.905881	0.48985
retinol binding protein 7, cellular	2.878328	2.456374	6.285202
gamma-glutamyltransferase 1	0.703259	1.567971	2.159741
prominin-like protein	1.591382	0.553829	3.168032
Actin, beta	0.958873	0.925542	0.348695
KH-type splicing regulatory protein		2.400341	
coiled-coil domain containing 109B	0.976984	2.21351	0.845396
proprotein convertase subtilisin/kexin type 2	2.167185	1.627126	2.905537
family with sequence similarity 101, member B	1.195024	1.146022	3.837599
selenoprotein T	1.025355	1.183794	0.651125
glutamate receptor, ionotropic, AMPA 1		0.33325	
centromere protein H	0.539081	1.074351	1.087254
similar to orphan G-protein coupled receptor Dez	1.355615	1.280763	1.847911
chromosome 17 open reading frame 63		0.72877	2.410772

integral membrane protein 2B	0.740567	1.017735	0.488353
angiopoietin 1	4.466857		
lin-52 homolog (C. elegans)	0.956252	0.995958	0.385355
integrin, beta 5	1.837185	1.268536	2.022104
dystroglycan	0.435208		
dystroglycan	0.682004	0.937799	6.417893
dystroglycan	0.710161	0.910749	2.974739
receptor tyrosine kinase-like orphan receptor 1	1.684302	0.910212	0.492276
brain-specific homeobox	0.779808	0.068909	
cHz-cadherin			3.760671
receptor interacting protein kinase 5	1.157189	0.534537	0.29628
heparan sulfate 6-O-sulfotransferase 2	0.743117	0.821817	0.702553
heparanase	2.117394	1.120967	1.823275
basic helix-loop-helix domain containing, class B, 4	2.257845	7.902049	0.084033
protocadherin 17	0.894483	2.048339	0.914436
protocadherin gamma subfamily C, 5	0.467305	1.022571	
FAT tumor suppressor homolog 3 (Drosophila)			
bone morphogenetic protein 10	1.275666	7.545814	0.934796
tubby like protein 1			19.51533
protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform			0.057199
3-hydroxyisobutyryl-Coenzyme A hydrolase		1.24558	0.288498
chemokine (C-X-C motif) ligand 12 (stromal cell-derived fac	0.774954	0.894717	0.797204
Chemokine (C-X-C motif) ligand 12 (stromal cell-derived fa	0.938235	0.792307	0.356384
3-hydroxyanthranilate 3,4-dioxygenase	1.535529	1.17071	2.072118
DENN/MADD domain containing 4A		0.322471	
chromosome 6 open reading frame 117	0.377235	1.298564	1.148367
NK2 homeobox 1		13.7962	
KIAA1946	0.275367	0.810874	1.147337
EF-hand calcium binding protein 1	0.453017	1.263278	0.193664
chromosome 14 open reading frame 143	1.198458	2.72963	0.505933
cathelicidin antimicrobial peptide	0.28427		
zinc finger, DHHC-type containing 6	0.985311	1.054877	0.463851
coiled-coil domain containing 131	2.181873	0.731726	1.265437
motile sperm domain containing 2	0.668294	1.046915	0.416256
Solute carrier family 7 (cationic amino acid transporter, y+ s	3.190525		
Family with sequence similarity 120A	0.719167	0.693827	0.615031
zinc finger and BTB domain containing 34	1.728414	0.674229	0.500023
chemokine (C-C motif) ligand 4 /// chemokine (C-C motif) li	0.789418	1.577483	0.491768
chromosome 1 open reading frame 55	1.117967	0.761642	0.330261
Solute carrier family 25, member 37	19.7954	0.836707	

solute carrier family 25, member 37	0.211071	2.199596	3.234434
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfe	1.869807		11.81605
extracellular matrix protein 2, female organ and adipocyte sp	0.967286	0.553097	0.553004
similar to enhancer of split related protein-7	0.909872	0.821771	0.257231
Tubulin, gamma complex associated protein 4	0.838223	0.457329	0.66484
aldo-keto reductase family 1, member B1 (aldose reductase)	1.232925	1.655508	2.455979
RNA-binding region (RNP1, RRM) containing 3			
RNA-binding region (RNP1, RRM) containing 3	1.113491	0.765107	0.337207
coiled-coil domain containing 141		0.518431	
SRY (sex determining region Y)-box 18	1.318459	0.940059	3.482861
ArfGAP with GTPase domain, ankyrin repeat and PH domain 1			5.594456
docking protein 5	0.655493	0.826675	0.361261
epithelial membrane protein 2	1.16404	0.765222	0.335674
UBA domain containing 2	0.611137	1.214123	
gap junction protein, delta 2, 36kDa	1.733346	1.621671	1.115746
vasoactive intestinal peptide receptor 1			
dynactin 5 (p25)	1.027503	1.40891	4.591823
poly (ADP-ribose) polymerase family, member 4	0.582244	0.58032	0.934225
heat shock 70kDa protein 4	0.894796	0.880531	0.434673
T-box 5		0.113529	
BMS1 homolog, ribosome assembly protein (yeast)			
BMS1 homolog, ribosome assembly protein (yeast)	1.399223	0.819258	0.36336
synapsin II	0.067483		
DCN1, defective in cullin neddylation 1, domain containing	1.144103	0.830454	2.13619
proline rich 5 (renal)	1.408028	1.582271	5.027688
proline rich 5 (renal)	0.421343	0.886052	1.466968
Similar to platelet-activating factor acetylhydrolase 2	0.488012		2.082168
platelet-activating factor acetylhydrolase 2, 40kDa	1.139586	1.12247	1.063939
paired-like homeodomain 1	11.73831	1.159551	
calcium/calmodulin-dependent protein kinase II alpha	0.709837		2.109159
glycolipid transfer protein domain containing 1		0.437693	0.736769
chimerin (chimaerin) 1	1.429482	0.784493	0.441406
chimerin (chimaerin) 1	0.205904	1.354845	0.262125
RNA polymerase II associated protein 2		9.035877	
RNA polymerase II associated protein 2	1.496263	0.92203	0.45984
2,4-dienoyl CoA reductase 1, mitochondrial		0.481398	1.664122
similar to C-type lectin	0.50342	0.342786	1.583418
small nucleolar RNA, H/ACA box 32	0.884472	0.859409	0.947635
Spermidine/spermine N1-acetyltransferase 1	1.04076	0.589012	0.210241
hydroxyprostaglandin dehydrogenase 15-(NAD)	1.682427	1.323612	5.280044

cytochrome P450 3A80	1.084197	1.960855	1.577424
annexin A13	1.469368	2.396446	4.697372
Yip1 domain family, member 5		0.103704	0.412139
zinc finger and BTB domain containing 25	0.472351	1.194511	0.978202
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4			
Chromosome 9 open reading frame 100		2.013098	
meiotic nuclear divisions 1 homolog (S. cerevisiae) /// tripart	0.64409	1.402178	0.360537
spectrin, beta, non-erythrocytic 1		0.37187	1.561529
chromosome 15 open reading frame 42	1.045305	1.141466	0.62951
DALR anticodon binding domain containing 3	1.821165	1.026188	2.814817
DALR anticodon binding domain containing 3	1.642168	1.060442	2.820745
chondrolectin		0.793414	0.24439
alpha thalassemia/mental retardation syndrome X-linked	1.284771	0.848106	0.354804
fumarylacetoacetate hydrolase (fumarylacetoacetase)		0.674373	2.949318
tripartite motif-containing 55			2.204565
platelet derived growth factor D	2.054848	1.970185	3.936215
host cell factor C2		0.395319	
chromosome 17 open reading frame 39	2.038223	1.11406	1.258785
RAD51-like 3 (S. cerevisiae)	0.95434	1.058705	0.450542
family with sequence similarity 77, member D	3.278224	1.023097	0.023414
BCL2-associated transcription factor 1	0.893042	1.116359	0.527781
retinol dehydrogenase 10 (all-trans)		4.161876	
family with sequence similarity 149, member A	3.736622	1.354295	1.432431
monooxygenase, DBH-like 1	0.603432	1.736381	7.814603
hypothetical protein LOC770574	1.638391	0.962901	0.418004
HEAT repeat containing 2	1.245495	0.989995	0.521408
HEAT repeat containing 2	1.097241	0.811488	2.750116
pinin, desmosome associated protein	0.749158	0.573087	0.827677
JMJD7-PLA2G4B readthrough transcript	1.625356	3.007329	0.74404
photopigment melanopsin-like			1.214792
tetraspanin 7	1.468045	0.819671	3.044519
tetraspanin 7	0.807231		
dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglu	0.631607	1.077368	0.693338
dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminepl		0.830025	0.387812
eukaryotic translation initiation factor 1B	1.013838	0.986458	0.458204
phosphatidic acid phosphatase type 2A	1.589876	1.467832	3.373476
Phosphatidic acid phosphatase type 2A	1.468695	1.18965	2.035479
SH2 domain containing 4A	2.298601	1.304923	1.71377
Similar to hypothetical protein FLJ38663	0.742673	1.237603	0.818514
histidine triad nucleotide binding protein W	694.6108	1.523488	0.655596

similar to Cyclin F		0.759296	0.042482
Hypothetical protein LOC770050	0.063067	0.39531	0.679587
Hypothetical LOC422005	0.607068	1.023159	0.288799
Hypothetical LOC422005	0.91694	1.143379	0.582982
spondin 2, extracellular matrix protein	2.129862	1.187043	0.742587
phosphopantothenoylecysteine decarboxylase	0.846316	1.165303	0.21887
phosphopantothenoylecysteine decarboxylase	0.861715	1.086718	0.272423
splicing factor 3a, subunit 1, 120kDa	1.071918	0.946702	0.724604
similar to AP-2 repressor	1.174201	0.537322	0.47273
intraflagellar transport 80 homolog (Chlamydomonas)	1.004482	0.711076	0.493381
itchy homolog E3 ubiquitin protein ligase (mouse)	9.336546	2.811548	0.545588
regulator of G-protein signalling 5	0.447682	1.636654	0.583881
Cold inducible RNA binding protein		0.970214	0.053262
chromosome 12 open reading frame 5	1.536714	0.930413	0.45732
cytidine deaminase	0.846583	0.915353	2.223723
ankyrin repeat domain 9	2.058138	0.868449	1.836442
leucine proline-enriched proteoglycan (leprecan) 1	3.362189	1.388109	1.024756
myotubularin related protein 14	0.561051	1.391121	1.89686
pleckstrin homology, Sec7 and coiled-coil domains, binding	1.587236	0.981197	2.169735
polymerase I and transcript release factor	1.163641	1.352944	1.968804
polymerase I and transcript release factor	0.594413		2.710325
Chromosome 5 open reading frame 3	0.425362		
chromosome 5 open reading frame 3	0.962975	1.06118	0.611722
RNA binding motif protein 24	2.73165	1.241339	2.25463
immunoglobulin mu binding protein 2		0.459857	
premature ovarian failure, 1B	1.833401	2.021575	0.747191
Premature ovarian failure, 1B	17.47757	0.581142	0.117177
phosphoenolpyruvate carboxykinase	0.484048	1.679957	1.146816
hypothetical LOC427134	6.052747	2.354407	0.170408
RUN and FYVE domain containing 1	1.305327	1.090014	1.213825
chromobox homolog 7	0.582097	1.203454	1.861216
chromosome 4 open reading frame 20	0.512392	2.26629	0.601205
toll-like receptor 2	2.445508	0.910139	0.560168
cyclin H	0.563815	0.628043	2.689304
inositol(myo)-1(or 4)-monophosphatase 1	0.664884	1.028872	0.062924
AIG2-like domain 1	0.978079	2.123902	
bromodomain containing 3	0.468623	1.031456	0.585965
GDP-mannose pyrophosphorylase B	2.500627	0.909908	2.528963
peroxisome biogenesis factor 13	1.269341	1.114823	0.727118
chloride intracellular channel 2	1.677661	0.893851	2.145801

Hypothetical protein LOC777379	1.57219	0.593885	0.142453
tetratricopeptide repeat domain 14	1.301391	0.682318	0.383813
ribonuclease P/MRP 30kDa subunit		0.786433	0.322463
golgi integral membrane protein 4	0.663488	0.816947	0.941733
carbonic anhydrase VB, mitochondrial	0.065689	2.037372	0.325948
WD repeat domain 21A	3.268496	0.707586	0.52558
heat shock protein 25	2.198658	0.941761	0.511903
ADP-ribosylation factor-like 4A	1.159831	0.895577	2.622251
RAB3B, member RAS oncogene family	0.911357	1.375166	2.064321
transmembrane protein 39A	0.827074		0.295952
tumor necrosis factor receptor superfamily, member 18	0.948866	1.344155	0.472244
ubiquitin specific peptidase 38	0.998977	1.088045	0.965516
Hypothetical protein LOC768982	1.012206	0.870857	0.146542
v-ral simian leukemia viral oncogene homolog B (ras related	0.925436	1.198329	0.417807
solute carrier family 9 (sodium/hydrogen exchanger), memb	1.305642	1.12951	0.421935
zinc finger, CCHC domain containing 6	0.49451	1.427824	0.905254
homocysteine-inducible, endoplasmic reticulum stress-induc	2.031378	0.949012	0.100186
complement component 1, q subcomponent, C chain	2.572676	1.64369	3.288132
Purinergic receptor P2Y, G-protein coupled, 13	2.528181	1.49588	4.355588
colony stimulating factor 2 receptor, alpha, low-affinity (grai	1.047897	1.140078	0.32594
transforming, acidic coiled-coil containing protein 3	0.66849	1.268254	1.584634
oxidation resistance 1	1.634991	0.995192	1.363369
immunoresponsive 1 homolog (mouse)	1.69884	1.475367	126.2908
Solute carrier family 7 (cationic amino acid transporter, y+ system), mei		1.405314	0.78581
Solute carrier family 7 (cationic amino acid transporter, y+ s	0.936266	0.904363	2.155723
hypothetical protein LOC770777	1.806495	3.244188	7.096649
septin 10	1.922295	1.16775	2.108561
Anthrax toxin receptor 2	3.465678	0.722039	1.507927
meteorin, glial cell differentiation regulator-like	1.357666	1.395529	3.071322
mitochondrial ribosomal protein L50	0.456978	1.92448	3.884596
chromosome 10 open reading frame 118	0.537957	1.907792	3.413466
kelch-like 6 (Drosophila)	1.044607	0.698477	0.438088
platelet/endothelial cell adhesion molecule /// platelet/endoth	3.987391	0.803001	0.649885
Platelet/endothelial cell adhesion molecule	1.38855	1.231683	0.321404
NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	0.739144	0.944723	2.10102
hypothetical gene supported by BX933423			0.026324
chromosome 17 open reading frame 62	0.788789	1.300989	0.625281
similar to BC039210 protein	1.739222	0.968875	4.677564
deleted in malignant brain tumors 1	2.421762	1.621776	3.393142
thrombospondin, type I, domain containing 7A	0.776791	0.640997	3.695375

NAD(P) dependent steroid dehydrogenase-like	0.483783	1.120032	0.837787
PAN3 polyA specific ribonuclease subunit homolog (S. cere	1.453432	0.626318	0.351516
zinc finger protein 652	0.452649	1.115266	1.390479
ectonucleoside triphosphate diphosphohydrolase 1	1.017341	0.609888	26.90203
TBC1 domain family, member 13	0.840009	2.397165	
annexin A10	0.890271	1.163227	0.398628
RAS, dexamethasone-induced 1	1.203713	2.688214	4.303764
WD repeat domain 51A	0.855241	1.22342	52.06071
similar to HEXIM1 protein	0.802112	0.714348	1.199196
fascin homolog 1, actin-bundling protein (Strongylocentrotu	1.069747	2.583971	1.749559
ubiquinol-cytochrome c reductase binding protein	1.661525	1.053233	0.193494
Signal recognition particle 19kDa	0.450097	0.927396	0.94055
KIAA1712	0.623114	1.701489	1.14019
RAS p21 protein activator 3	0.785705	0.725985	0.359791
nuclear factor of kappa light polypeptide gene enhancer in B	1.165573	1.354698	2.384509
fructosamine 3 kinase related protein	0.804069	0.781145	0.3256
nuclear receptor interacting protein 1	0.780969	0.803678	0.414422
zinc finger, FYVE domain containing 28	12.27069		1.375076
chromosome 4 open reading frame 15	1.386362	1.323776	0.781411
polymerase (DNA directed) nu	8.284039	0.911197	2.648654
Wolf-Hirschhorn syndrome candidate 2			
coxsackie virus and adenovirus receptor	0.979765	0.977928	0.383237
leucine zipper-EF-hand containing transmembrane protein 1	0.702943	0.489345	1.50247
stem-loop (histone) binding protein	2.869438	1.252018	1.398714
MDN1, midasin homolog (yeast)	0.136221	0.671736	0.88287
zinc finger protein 704	0.766062	0.85927	0.213401
gamma-aminobutyric acid (GABA) receptor, rho 1		5.283282	
aminoacylase 1-like 2	1.487664		5.111879
ADAM metallopeptidase with thrombospondin type 1 motif, 1		1.596154	
ADAM metallopeptidase with thrombospondin type 1 motif,	1.219499		3.94464
chromosome 6 open reading frame 165	6.35545		
solute carrier family 7, (cationic amino acid transporter, y+ s	0.092189		
E2F transcription factor 5, p130-binding	3.380595	1.011269	0.794455
5'-nucleotidase, ecto (CD73)		3.013972	
protease, serine, 35			
chromosome 6 open reading frame 157	0.407832	1.577	0.244136
ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit D2		7.124945	4.631216
similar to RHACD8-4L			0.050338
TTK protein kinase	0.792489	0.808964	0.361587
Leber congenital amaurosis 5	0.397617	1.938997	0.655806

receptor-interacting serine-threonine kinase 2	2.177991	0.606618	0.41111
similar to CD8 alpha chain /// similar to RHACD8-4L	0.710464	1.072208	0.291059
similar to RHACD8-4L /// similar to CD8 alpha chain /// sim	0.398137	1.925524	
similar to CD8 alpha chain /// similar to RHACD8-4L /// sim	1.298912	0.770098	0.131416
similar to CD8 alpha chain /// similar to RHACD8-4L /// sim	1.028359	0.451516	0.186803
synaptojanin 1	0.5879		0.838231
transmembrane protein 64	1.684115	1.940633	6.561656
DEAD (Asp-Glu-Ala-Asp) box polypeptide 43		0.377858	
hypothetical LOC428371	0.779847	1.196812	0.468787
RNA binding motif protein 12B	1.070686	1.085836	0.252238
protein phosphatase 2C, magnesium-dependent, catalytic subunit		0.363142	
WD repeat domain 76	0.955633	1.146185	2.129359
regulating synaptic membrane exocytosis 1	0.848307	1.013548	4.286289
cadherin 17, LI cadherin (liver-intestine)	1.858774	1.359779	2.209592
dpy-19-like 4 (C. elegans)	1.830439	1.296996	0.542125
dpy-19-like 4 (C. elegans)	1.378234	0.834091	0.576699
potassium voltage-gated channel, Isk-related family, member 2		8.063368	
similar to Serine/threonine kinase 3 (STE20 homolog, yeast)	1.144326	0.462315	0.59108
vacuolar protein sorting 13 homolog B (yeast)	0.729379	1.068339	0.49527
regulator of G-protein signalling 22	0.237945		
F-box protein 43 /// similar to F-box only protein 43 (Endogenous meiotic inhibitor			0.179962
sperm associated antigen 1		0.797974	
sperm associated antigen 1	0.646026	1.287825	0.360812
ribonucleotide reductase M2 B (TP53 inducible)	0.524859	0.924886	0.104561
tetratricopeptide repeat domain 3	1.283068	0.442279	0.615559
potassium inwardly-rectifying channel, subfamily J, member 15		1.811375	2.210077
forkhead box K2	1.091875	0.924638	0.435481
brain and acute leukemia, cytoplasmic	0.448834		
regulating synaptic membrane exocytosis 2	0.389493	1.258233	
transmembrane 7 superfamily member 4	1.234933	0.930812	2.600998
zinc finger protein, multitype 2		39.99725	
oxidation resistance 1	0.926516	1.362334	0.430322
exocyst complex component 6B		9.824823	
Down syndrome cell adhesion molecule	0.397681	0.807536	
beta-site APP-cleaving enzyme 2	17.8287		
transmembrane protease, serine 2	0.352074		1.032046
C2 calcium-dependent domain containing 2			
G protein-coupled receptor 20			27.82794
inositol polyphosphate-5-phosphatase, 145kDa		0.439877	
ubiquitin associated and SH3 domain containing, A	2.237587	1.482746	1.330136

similar to fibropellin Ia			0.121962
myeloid/lymphoid or mixed-lineage leukemia (trithorax hom	0.387346	0.749594	0.947593
trafficking protein particle complex 9	0.812427	1.05366	0.288065
potassium channel, subfamily K, member 9	0.499184		
similar to Cystathionine-beta-synthase	1.024092	0.843555	2.948457
family with sequence similarity 135, member B	0.272124		
crystallin, alpha A			
ZFAT zinc finger 1	2.112331	1.771366	0.763916
monoamine oxidase B		2.561508	
monoamine oxidase B			
PHD finger protein 20-like 1	0.69967	1.087833	0.379406
potassium voltage-gated channel, KQT-like subfamily, member 3		0.061609	
otoconin 90			
X-linked Kx blood group	13.17846	4.252493	
hypothetical LOC428640		0.311972	
hypothetical LOC418592 /// hypothetical protein LOC76843	0.140375		
collagen, type XXI, alpha 1	0.158593		
hypocretin (orexin) receptor 2	0.175284	14.82916	1.01453
hypothetical LOC428238	14.66986		
adenylate cyclase 8 (brain)	0.415885	0.046587	
chromosome 6 open reading frame 142	0.449458		
kelch-like 31 (Drosophila)			2.596056
hypothetical protein LOC772218	2.469252		
kelch-like 15 (Drosophila)	1.0867	0.729395	0.342754
kelch-like 15 (Drosophila)	2.214064	0.316985	0.223077
family with sequence similarity 91, member A1		2.465004	1.325455
similar to Acp1 protein	1.292296		6.162565
chromosome 8 open reading frame 32	0.768005	1.083061	0.675466
ATPase family, AAA domain containing 2	0.859549	1.179567	0.531876
tumor suppressing subtransferable candidate 1	0.525447	1.613409	0.28718
tetratricopeptide repeat domain 15	1.133597	0.84746	0.602856
radical S-adenosyl methionine domain containing 2	5.18347	2.075869	5.57553
ring finger protein 144A		2.85858	
membrane bound O-acyltransferase domain containing 2	1.082862	0.474096	0.048742
defective in sister chromatid cohesion 1 homolog (S. cerevis	1.397348	1.396676	0.3399
TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa			
maternal embryonic leucine zipper kinase	0.593407	1.036222	1.161392
hypothetical LOC421935	1.831226	2.086577	0.857244
ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	0.525587		2.201175
ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	1.730823	2.207982	1.765376

potassium voltage-gated channel, subfamily F, member 1		7.435446	
Rho-associated, coiled-coil containing protein kinase 2	0.909271		0.337571
phosphatidylinositol-5-phosphate 4-kinase, type II, beta		0.370396	
similar to GREB1 protein			
similar to egg envelope component ZPAX			10.24064
potassium voltage-gated channel, delayed-rectifier, subfamily	1.190043	1.108241	0.043728
ATPase family, AAA domain containing 2B	1.460675	0.806848	0.468824
similar to A830093I24Rik protein			0.159641
intersectin 2	0.744599	0.487397	1.645093
zinc finger protein 512		0.694123	
nuclear receptor binding protein 1	0.654989	1.186185	1.126152
phosphorylase kinase, alpha 2 (liver)	0.694069	0.978115	0.793998
dystrobrevin, beta		0.409927	
cyclin-dependent kinase-like 5			3.121144
similar to KIAA1833 protein /// hypothetical protein LOC77	0.508999		1.470211
similar to chromosome X open reading frame 20	1.062283	1.772699	0.372566
Nance-Horan syndrome (congenital cataracts and dental anomalies)		2.011789	
RALBP1 associated Eps domain containing 2	0.427501		
selenoprotein I	3.088302		
motile sperm domain containing 2	0.707322	0.623881	0.398679
RAB9A, member RAS oncogene family	0.902419	1.191883	0.58986
scavenger receptor class A, member 5 (putative)	1.450361	0.820129	5.361535
toll-like receptor 7	2.070571	0.958591	1.110561
calcium/calmodulin-dependent protein kinase kinase 1, alpha		6.33802	
hypothetical protein LOC768434	0.435324		1.150065
adenylate cyclase 3		1.256348	
shroom family member 2	0.04929		
neurologin 4, X-linked	0.495492		0.039231
exostoses (multiple)-like 3	3.586706	1.255018	0.948784
integrator complex subunit 9	0.990224	0.512473	0.51677
hypothetical LOC427799	1.538529		0.18402
arylsulfatase D	0.935047	1.082381	0.052141
chromosome 8 open reading frame 13	0.774694	1.437743	0.961569
progesterone and adiponectin receptor family member VIII	0.726734	2.061566	
CD7 molecule	1.28263	1.591799	2.112591
methylmalonyl Coenzyme A mutase	0.831634	0.923387	0.400443
ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	0.436236	1.167462	0.279139
GTP binding protein 6 (putative)	1.057688	0.408941	1.349958
isochorismatase domain containing 1		2.514224	1.236208
transmembrane protein 166	0.5771	0.894058	0.717482

non imprinted in Prader-Willi/Angelman syndrome 1	1.056362	1.165623	0.505896
ATPase, class V, type 10A	2.888772	1.153486	3.572105
ATPase, class V, type 10A	7.35941		1.516842
ATPase, class V, type 10A	2.114125	2.438514	1.752747
hypothetical LOC418688			26.53126
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosyl transferase	1.150292	0.732272	0.357876
MIT, microtubule interacting and transport, domain containing	1.655257	1.076907	0.835112
interleukin 1 receptor, type II	0.521768	0.665372	0.392651
interleukin 1 receptor-like 2	1.503525	1.442069	2.514705
interleukin 18 receptor 1	3.086522	1.174967	0.879779
solute carrier family 9 (sodium/hydrogen exchanger), member 1	1.002615	1.57125	6.632906
major facilitator superfamily domain containing 9	1.039751	0.694876	0.646067
UDP-glucuronate decarboxylase 1	1.345996	1.150328	0.286713
mannosidase, endo-alpha-like	2.914145		
PCI domain containing 2	1.060056	0.938143	0.369924
similar to Guanine nucleotide exchange factor DBS (DBLs b	3.88562	1.539751	5.056529
similar to Guanine nucleotide exchange factor DBS (DBLs b	2.888861	1.840934	2.779066
MCF.2 cell line derived transforming sequence-like	1.005029		3.153575
Rho guanine nucleotide exchange factor (GEF) 7	0.871224	2.420838	0.925722
solute carrier family 10 (sodium/bile acid cotransporter family)	1.678345	2.446437	1.1284
sodium leak channel, non-selective	1.297083	0.789617	
Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	1.399294	0.843198	0.203008
Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	8.176481	2.888663	1.966572
serine/threonine kinase 24 (STE20 homolog, yeast)	0.766884	0.929881	1.874478
ATP-binding cassette, sub-family C (CFTR/MRP), member 1	6.763999	0.95841	
G protein-coupled receptor 180	1.842816	0.875783	0.52941
ceroid-lipofuscinosis, neuronal 5	0.457478	3.211181	
TBC1 domain family, member 4		0.402579	1.309821
protocadherin 20	0.466675		
diaphanous homolog 3 (Drosophila)	0.1058	0.735749	
NMDA receptor regulated 1-like	1.022558	0.813227	0.501916
NMDA receptor regulated 1-like	1.424652	1.250405	0.476698
hypothetical LOC428066	0.810877	1.477171	2.193841
diacylglycerol kinase, eta	0.395698		
diacylglycerol kinase, eta	6.472975	0.628613	2.065406
tumor necrosis factor (ligand) superfamily, member 11		3.660468	0.439595
solute carrier family 25, member 30	0.450943	0.839832	0.164403
lymphocyte cytosolic protein 1 (L-plastin)	0.746025	2.505786	1.589497
succinate-CoA ligase, ADP-forming, beta subunit	1.125398	1.141673	0.462342
SET domain, bifurcated 2			6.190028

SET domain, bifurcated 2	0.882977	1.130607	2.010918
karyopherin alpha 3 (importin alpha 4)	1.197573	0.639902	0.267005
dehydrogenase/reductase (SDR family) member 12 /// simila	0.670866	0.257293	0.916013
ATPase, Cu ⁺⁺ transporting, beta polypeptide	0.573228	0.656171	2.253117
component of oligomeric golgi complex 6	0.781218	0.886454	0.339308
component of oligomeric golgi complex 6	0.727253	1.201477	0.382649
chromosome 13 open reading frame 23	2.804658	0.688334	1.057733
stomatin (EPB72)-like 3	0.929899		3.927225
cyclin A1			0.363269
doublecortin-like kinase 1			
StAR-related lipid transfer (START) domain containing 13	1.688091	0.452289	
furry homolog (Drosophila)	2.174104		0.349164
heat shock 105kDa/110kDa protein 1	0.857908	0.666839	0.114921
heat shock 105kDa/110kDa protein 1	0.493807	0.330066	
solute carrier family 7 (cationic amino acid transporter, y ⁺ sy	0.680777	0.712221	2.099314
solute carrier family 46, member 3			0.153556
nucleoporin 88kDa			0.165181
ubiquitin specific peptidase 12	1.620873	1.435956	2.52447
ATPase, aminophospholipid transporter-like, class I, type 8A, member 2			4.466952
SET binding protein 1	2.978781		2.263374
mitochondrial intermediate peptidase	1.039503	1.226762	0.925113
mitochondrial intermediate peptidase	0.605766	1.158002	0.474014
protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.196601	0.772528	0.691333
zinc finger, MYM-type 2	1.229274	1.133903	0.446186
centromere protein J	1.095797	0.972077	0.52923
exophilin 5	27.00298		
exophilin 5 /// KDEL (Lys-Asp-Glu-Leu) containing 2	1.148153		0.196722
RAB39, member RAS oncogene family	0.552777		0.264109
RAB39, member RAS oncogene family	0.668231	0.983671	0.408299
guanylate cyclase 1, soluble, alpha 2	0.880948		2.047756
aminoadipate-semialdehyde dehydrogenase-phosphopantethe	0.742044	1.790937	0.065779
aminoadipate-semialdehyde dehydrogenase-phosphopantethe		1.388444	0.395719
dynein, cytoplasmic 2, heavy chain 1	0.697905	0.791139	0.90263
dynein, cytoplasmic 2, heavy chain 1	1.376576	0.581486	3.10668
matrix metalloproteinase 1 (interstitial collagenase)		0.506765	0.105065
hypothetical LOC418990			0.468979
family with sequence similarity 76, member B	1.221044	1.074679	0.374609
protein phosphatase 2A activator, regulatory subunit 4	1.249328	1.503877	1.48176
coiled-coil domain containing 67	0.040174		
solute carrier family 36 (proton/amino acid symporter), mem	0.273323	1.099263	0.946975

Rho guanine nucleotide exchange factor (GEF) 19	0.069286		
fibroblast growth factor 23			
male sterility domain containing 1			0.087176
similar to metalloprotease/disintegrin/cysteine-rich protein	1.428213		0.046351
polymerase (DNA-directed), delta 3, accessory subunit	0.457474	1.134071	0.61547
DnaJ (Hsp40) related, subfamily B, member 13		0.323927	
similar to olfactory receptor, family 52, subfamily R, member 2	0.588584	1.174994	1.161162
receptor accessory protein 2	2.427915		
cAMP-regulated phosphoprotein, 19kDa	0.51077	0.917089	0.369024
cAMP-regulated phosphoprotein, 19kDa	0.712252	0.916735	0.492577
similar to calcium-activated potassium channel SK3	1.071127	0.812547	
coiled-coil-helix-coiled-coil-helix domain containing 8	0.455534	0.974406	2.094057
hypothetical LOC429831	0.650028		
olfactory receptor, family 10, subfamily A, member 7	0.587777	0.996132	2.618546
chromosome 16 open reading frame 35		1.304853	0.310384
tudor and KH domain containing		0.87382	0.521542
development and differentiation enhancing factor-like 1			
toll-like receptor 6	4.984224	1.739063	0.476797
similar to toll-like receptor 1 /// toll-like receptor 16 /// toll-like receptor 1	2.072388	1.084468	0.763507
similar to toll-like receptor 1 /// toll-like receptor 16 /// toll-like receptor 1	3.382301	1.526372	2.247171
ligand dependent nuclear receptor corepressor-like	0.726253	0.634373	0.395133
hypothetical protein LOC776768	1.352689	3.723297	4.738505
hypothetical protein LOC776768	2.136649	3.541695	2.858468
similar to PINCH-1	0.158055		
WD repeats and SOF1 domain containing	0.567892	1.384912	0.291118
tuberous sclerosis 1	0.659105	0.200314	1.248081
hypothetical protein LOC772235	1.104472	0.774245	0.388468
coiled-coil domain containing 83	15.43621	2.062548	0.511305
THUMP domain containing 2	1.265702	0.812791	0.686089
attractin	0.743018	1.095256	0.328881
attractin	0.709294		
similar to WC1 tail	0.559883	0.59256	0.342603
CD5 molecule-like /// similar to scavenger receptor cysteine-rich type 1	0.449879		
fibrillin 2	0.453135		
similar to death receptor 3	2.294586	0.538375	1.120385
glutaminy-peptide cyclotransferase-like	0.945043	0.587119	2.221254
progressive external ophthalmoplegia 1	0.911662	3.311179	1.305331
similar to Rhomboid family 1 (Drosophila) /// rhomboid 5 homolog	0.923021	1.283397	0.247545
WWC family member 3	1.450674	1.121836	2.202414
similar to MOV10-like 1 /// similar to Zcwpw2 protein	2.127378		

similar to MOV10-like 1 /// similar to Zcwpw2 protein			5.616337
F-box protein 38 /// hypothetical LOC426479 /// similar to F.	2.862438	0.496993	1.076097
CDC42 small effector 2	0.324991	1.511563	0.62855
similar to KIAA0540 protein	0.717267	0.856824	3.675079
potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2			4.833761
KIAA1324-like	0.224764		1.669258
cylindromatosis (turban tumor syndrome)			0.146658
KIAA0802		0.448743	
hypothetical LOC430965	3.312936		
zinc finger CCCH-type, antiviral 1	0.848246	1.341443	1.707788
small G protein signaling modulator 1	0.345241	1.390506	
Mdm2, transformed 3T3 cell double minute 2, p53 binding p	1.49208	1.545481	1.007574
primase, polypeptide 1, 49kDa	0.485406	1.005724	0.68348
metastasis suppressor 1	2.638116	0.824034	0.590864
chromosome 20 open reading frame 59	1.69206	0.931617	
solute carrier family 27 (fatty acid transporter), member 6			
NIMA (never in mitosis gene a)-related kinase 2	0.841501	1.09847	0.425944
MAX interactor 1	1.337603	1.294147	3.986459
nuclear receptor coactivator 7	1.378457	0.992438	0.700244
eukaryotic translation initiation factor 2, subunit 3 gamma, 5	0.863942	1.149727	0.79803
TAF8 RNA polymerase II, TATA box binding protein (TBP	1.007684	1.069343	1.923988
kinesin family member 11	0.809584	1.102862	1.049469
exportin 4	0.823845	0.985323	0.443255
FUS interacting protein (serine/arginine-rich) 1	0.967061	0.893214	0.574336
uridine monophosphate synthetase (orotate phosphoribosyl t	0.683538	0.810555	0.333572
tumor necrosis factor receptor superfamily, member 18	0.933956	1.641738	0.429844
matrix metalloproteinase 7 (matrilysin, uterine)	1.491131	1.022488	1.51583
SH3-domain kinase binding protein 1	0.806748	1.006344	0.771867
sorting nexin 13	1.095695	2.107544	1.624944
dynein, cytoplasmic 1, light intermediate chain 2	0.759957	0.494012	0.779346
solute carrier organic anion transporter family, member 4A1	8.00668		119.3875
spermatogenesis associated 6	3.383733		
adaptor-related protein complex 3, mu 1 subunit	0.818112	1.029072	0.68683
splicing factor 3b, subunit 3, 130kDa			0.086587
galactokinase 2	0.439766	1.097955	2.124789
chromosome 10 open reading frame 46	0.966049	1.062202	0.616341
similar to Tcf-3 co-repressor CtBP	1.039293	0.904482	0.591965
zinc finger protein 706	1.19779	1.005685	0.610265
chromosome 14 open reading frame 169	1.156469	1.368605	0.691327
CDK2-associated protein 1	0.761819	0.902805	0.489271

lysosomal-associated protein transmembrane 4 alpha		1.068285	0.442124
lysosomal-associated protein transmembrane 4 alpha	1.286955	1.222428	0.310745
Ras association (RalGDS/AF-6) domain family member 2	1.834941	1.272227	1.036671
ubiquitin-fold modifier 1	0.940622	1.19986	0.344627
USP6 N-terminal like	1.137928	1.095801	0.75506
chromosome 9 open reading frame 41	1.089955	0.850364	0.961837
KIAA1524	0.678313	1.063922	0.77604
solute carrier family 25 (mitochondrial carrier; adenine nucle	1.077582	1.317621	2.07505
chromosome 20 open reading frame 24	0.692731	0.940848	0.377123
asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-m		0.481868	
asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-m		0.49003	0.662153
TRAF-type zinc finger domain containing 1	2.865745	1.310492	2.121759
cyclin E2	0.726332	1.306011	0.653343
cyclin E2	0.490288	1.002587	0.469388
ras homolog gene family, member G (rho G)	0.016771		33.2223
chaperonin containing TCP1, subunit 4 (delta)	0.765134	1.245421	0.332234
claudin 1	1.567063	1.38188	2.865758
D-dopachrome tautomerase	9.175349	0.31832	0.150312
D-dopachrome tautomerase	1.31076	0.513226	0.347755
coiled-coil domain containing 5 (spindle associated)	0.238548	1.583422	1.397302
epsin 2	1.028201	0.491039	0.614143
similar to Sphingomyelin phosphodiesterase, acid-like 3A	1.441893	1.939592	3.60698
H2A histone family, member V	0.83788	1.054592	0.567403
chromosome 5 open reading frame 41	0.811258	0.467556	0.483479
transducin (beta)-like 3	1.540576	2.705659	0.832211
nucleolar protein 5A (56kDa with KKE/D repeat)	0.965169	1.011679	2.27227
c-mer proto-oncogene tyrosine kinase		0.058709	1.415173
chromosome 14 open reading frame 129	0.785566	0.782987	0.608282
origin recognition complex, subunit 1-like (yeast)	1.796831	1.136744	2.48704
cyclin C	1.550469	0.995425	0.4208
WD repeat, sterile alpha motif and U-box domain containing	1.78621	0.784573	0.568403
myosin IG	1.04001	0.853361	2.365695
similar to RIKEN cDNA 4931428F04 gene	1.566134	0.779905	4.744235
proline-rich nuclear receptor coactivator 2	0.890492	0.997261	0.61079
heme binding protein 1	1.436182	1.476646	1.757391
karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.691063	1.233969	0.799614
synovial sarcoma translocation, chromosome 18	1.341894	0.880444	0.490372
RNA binding motif protein 24	2.448491	1.144278	2.534897
15 kDa selenoprotein	1.654364	1.067838	0.37666
chromosome 18 open reading frame 22	0.973767	0.771253	0.657454

Hypothetical protein LOC769469	1.135873	1.318124	3.017607
cytochrome b5 reductase 4	0.866768	0.882779	0.78364
clathrin interactor 1	1.453994	1.07652	2.010958
E2F transcription factor 6	1.512489	1.08197	0.694613
WD repeat domain 51B	1.073013	1.17862	0.294829
similar to Auh protein	0.805236	0.863712	3.790608
PCI domain containing 2	0.831297	1.147582	0.15392
zinc finger protein 384	0.790432	0.449188	1.529451
zinc finger protein 313	0.840616	0.740209	0.497486
integrin, alpha 9	0.67048	1.826207	2.190947
chromosome 16 open reading frame 75	1.711818	1.31997	2.925587
primase, DNA, polypeptide 2 (58kDa)	0.329548	2.397382	0.314654
splicing factor, arginine/serine-rich 18	2.096923	0.761736	0.482435
cAMP-regulated phosphoprotein, 19kDa	0.837709	1.013093	0.41128
pleckstrin homology domain containing, family F (with FYV	1.157599	2.600837	1.482169
pleckstrin homology domain containing, family F (with FYV	1.04064	0.956232	0.809015
RNA U, small nuclear RNA export adaptor (phosphorylation	0.706616	0.818885	0.845366
Rho guanine nucleotide exchange factor (GEF) 3	0.985539	0.952075	0.430854
progesterone receptor membrane component 2	0.980844	1.267447	0.385545
progesterone receptor membrane component 2	0.938122	1.572646	0.350083
dymeclin	0.47866	0.890661	1.789772
threonyl-tRNA synthetase	0.540249	1.128303	2.097912
lymphocyte cytosolic protein 1 (L-plastin)	1.068838	1.40648	2.241243
glycosyltransferase 1 domain containing 1	2.322277	1.621146	6.185924
early growth response 1	1.642747	0.718556	0.524935
inositol hexakisphosphate kinase 2	0.869538	0.925886	0.457201
stem-loop (histone) binding protein	2.944013	1.334555	2.250091
Nedd4 binding protein 3	0.80485	0.824296	2.031407
similar to cytochrome b-5 reductase	0.394973	1.511293	0.580487
ring finger protein 20	0.426343	0.748146	1.938436
IKAROS family zinc finger 5 (Pegasus)	1.116699	0.775805	0.497377
ADP-ribosylation factor-like 13B	2.126533	0.95715	0.393202
centrosomal protein 55kDa	0.329505	1.345253	0.881942
similar to SRF-related protein	0.926401	0.672479	1.78472
similar to SRF-related protein	1.082727	0.807785	1.376955
GUF1 GTPase homolog (S. cerevisiae)	1.63531	0.832552	0.604503
SAP domain containing ribonucleoprotein	0.744977		3.56887
capping protein (actin filament) muscle Z-line, alpha 1	1.197004	0.931101	0.269934
APAF1 interacting protein	0.882246	0.746627	0.218168
SWI/SNF related, matrix associated, actin dependent regulat	0.671231	1.018131	0.435915

similar to gamma filamin protein	35.32156		
twinfilin, actin-binding protein, homolog 1 (Drosophila)	3.453667	0.348873	3.517727
similar to chromosome 7 open reading frame 28B; CGI-43 li	1.141073	0.968044	0.526443
death inducer-obliterators 1	1.303073	0.892611	0.687866
YTH domain family, member 3	1.013571	0.886622	0.587138
solute carrier family 7 (cationic amino acid transporter, y+ sy	1.105917	1.548776	0.397124
coronin 7 /// mitochondria-associated protein involved in gra	1.068939	0.877749	3.416102
fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood		0.386193	
prolyl 4-hydroxylase, alpha polypeptide II	1.392244	1.032863	1.448208
globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	1.091026	0.811299	1.146331
intraflagellar transport 52 homolog (Chlamydomonas)	1.10363	0.40295	0.432648
transmembrane protein 59	0.630007	0.847266	0.281584
CD36 molecule (thrombospondin receptor)	1.692145	1.452296	3.215609
G protein-coupled receptor 158	0.763199		
potassium channel, subfamily K, member 1		3.128731	
synaptotagmin binding, cytoplasmic RNA interacting protein	1.30188	1.200073	0.762241
SLIT-ROBO Rho GTPase activating protein 3		1.014024	7.148929
ARP6 actin-related protein 6 homolog (yeast)	0.653196	1.247991	0.229873
chromosome 1 open reading frame 57	1.208184	1.169128	0.366206
chromosome 1 open reading frame 107	0.052778	0.776686	0.678035
splicing factor, arginine/serine-rich 5			0.027463
damage-specific DNA binding protein 1, 127kDa	0.907873	0.924251	1.883148
Bruton agammaglobulinemia tyrosine kinase	1.329407	1.262047	2.040343
G1 to S phase transition 1	0.550232	1.402784	0.446763
eukaryotic translation initiation factor 3, subunit H	0.644549	1.118692	0.526305
purinergic receptor P2Y, G-protein coupled, 10		0.657569	0.167416
dolichyl pyrophosphate phosphatase 1	2.05958		
F-box protein 22			1.264447
vacuolar protein sorting 53 homolog (S. cerevisiae)	1.325588	0.768755	0.706262
kelch-like 9 (Drosophila)	1.260296	1.342913	2.269216
fumarate hydratase	0.819307	1.490653	0.769277
ankyrin repeat domain 10	1.777589	0.714634	0.516058
oxysterol binding protein-like 2	0.780999	0.882178	0.378557
mitochondrial ribosomal protein L50	0.38617	0.968113	1.558272
guanine nucleotide binding protein (G protein), beta polypep	1.646444		0.388643
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	2.337174	1.126294	0.020416
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.722998	0.606878	0.111883
similar to Transcription factor 12 (Transcription factor HTF-	0.345609	0.173689	
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	0.840754	1.135984	1.339975
myosin IC	3.10553	1.922481	2.672028

dihydrofolate reductase	0.329476	1.275637	1.248272
neuralized homolog (Drosophila)	2.158626	1.937197	1.513631
phosducin-like 3			0.021362
G patch domain containing 1	0.51762	0.719081	0.376689
RAP1, GTP-GDP dissociation stimulator 1	1.277125	0.850264	0.728808
LIM and senescent cell antigen-like domains 1 /// hypothetical	0.393305	1.852131	2.051606
heterogeneous nuclear ribonucleoprotein M	0.773796	0.778584	0.373955
phosphoinositide-3-kinase, regulatory subunit 4, p150	0.174149	3.881553	
phosphoinositide-3-kinase, regulatory subunit 4, p150	0.847128	0.957598	0.704348
proteasome (prosome, macropain) activator subunit 4	0.653497	1.069417	1.386172
heat shock 60kDa protein 1 (chaperonin) /// similar to similar	0.895323	1.088285	0.587079
tripartite motif-containing 8	1.031258	0.884992	1.4598
family with sequence similarity 13, member C1	0.737674	2.082852	0.334494
Similar to pancreatic intrinsic factor	2.389428		
alpha-methylacyl-CoA racemase	0.821548	1.172795	2.504289
prosaposin	1.498536	1.154635	0.428273
acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	1.204788	0.861407	0.565306
vacuolar protein sorting 35 homolog (S. cerevisiae)	1.053368	1.054833	0.884871
staufen, RNA binding protein, homolog 2 (Drosophila)	1.546998	0.735946	0.685581
nuclear transcription factor Y, beta	0.751827	0.805864	0.384987
nephroblastoma overexpressed gene	0.044746		
phytanoyl-CoA 2-hydroxylase interacting protein-like	0.803131	1.263194	0.424488
succinate-CoA ligase, GDP-forming, beta subunit	0.290383	106.7644	809.5533
arginine and glutamate rich 1	1.578526	0.790851	0.383083
LSM14A, SCD6 homolog A (S. cerevisiae)	1.04957	0.828615	0.380369
catalase	0.271956	0.901679	2.534438
amyloid beta (A4) precursor protein-binding, family B, mem	0.801389	0.826642	0.515024
transcription factor 3 (E2A immunoglobulin enhancer bindin	1.141485	0.707839	0.246156
forkhead box M1	1.128062	0.997547	0.394988
tumor necrosis factor receptor superfamily, member 1B	1.250094	1.541355	3.218207
mitogen-activated protein kinase kinase 3	0.490751		0.455443
ORAI calcium release-activated calcium modulator 1	0.971726	1.029282	1.473459
transducin (beta)-like 1 X-linked receptor 1	1.034099	0.913675	2.211594
chromosome 1 open reading frame 69	1.003608	0.891264	1.27376
MANSC domain containing 1	1.362118	1.354964	1.572014
muscleblind-like (Drosophila)	0.822118	1.032378	2.514712
leucine zipper and CTNNBIP1 domain containing	1.033271	0.87501	0.581603
tRNA 5-methylaminomethyl-2-thiouridylate methyltransfera	0.867928	0.895718	1.913146
TEK tyrosine kinase, endothelial (venous malformations, mu	0.894523	1.526033	3.350663
deoxycytidine kinase	0.433017	0.906453	0.48853

arrestin domain containing 1	2.658875	2.09886	3.085698
arrestin domain containing 1	3.519953	1.311534	2.763842
FK506 binding protein 5	0.68643	1.498547	9.836465
centromere protein L	1.063629	1.059574	0.805528
YTH domain containing 2			0.477993
rogdi homolog (Drosophila)	2.290957	1.081149	0.746668
PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.747585	0.713091	0.32834
similar to Splicing factor, arginine/serine-rich 5 (Pre-mRNA	1.103132	0.958538	0.539004
DnaJ (Hsp40) homolog, subfamily B, member 14	0.792116	0.794697	2.004612
similar to MRC OX-2 antigen homolog	1.468487	0.75908	0.482826
HAUS augmin-like complex, subunit 6	0.470649	1.267564	1.355064
ras homolog gene family, member F (in filopodia)	2.392261	0.851747	1.670245
protein inhibitor of activated STAT, 2	0.406087	0.78706	
similar to nuclear cap binding protein subunit 2; nuclear cap	0.644101	0.991553	0.439108
chromosome 20 open reading frame 11	1.287166	0.970286	0.462473
quinoid dihydropteridine reductase	0.887475	0.829851	0.496067
trafficking protein particle complex 2	0.995728	1.837551	0.498659
trafficking protein particle complex 2	1.12133	2.213122	1.028027
family with sequence similarity 53, member A	0.781756	0.880541	0.277276
progesterone receptor membrane component 1	1.144731	1.353815	1.810696
cyclin-dependent kinase 9	0.697033	1.385293	0.76286
similar to immunoglobulin-like receptor CHIR-B2 precursor	0.718483		0.612128
zinc finger CCCH-type containing 15	1.360446	1.127166	0.339252
transient receptor potential cation channel, subfamily C, member 4 associated protein			
ligase IV, DNA, ATP-dependent	0.879278	0.671493	0.110501
FtsJ homolog 3 (E. coli)	0.908849	0.830688	2.847834
membrane bound O-acyltransferase domain containing 2	1.067029	0.088557	0.149757
CD200 molecule	0.91805	0.818142	0.662653
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase act	0.950522	0.849385	0.475171
CLPTM1-like	1.222271	1.490033	2.294933
round spermatid basic protein 1	2.076368	1.245502	0.387998
glycosyltransferase 8 domain containing 3	1.162553	0.910878	0.39752
syntaxin 17	0.968955	1.408864	0.732871
calcium/calmodulin-dependent protein kinase (CaM kinase)	1.72858	1.39937	0.348976
kinesin family member 20A	0.895088	0.959258	0.410628
DNA2 DNA replication helicase 2-like (yeast)	0.941914	1.64224	0.918593
mitochondrial ribosomal protein L51	0.984104	1.00583	0.551677
low density lipoprotein receptor-related protein 5	1.586788	0.589128	1.174819
5'-nucleotidase, cytosolic III-like	1.379364	1.258428	3.141409
high-mobility group 20A	0.841478	1.098354	0.474574

O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-1	2.334001	0.781576	0.270739
membrane bound O-acyltransferase domain containing 1		1.645811	2.402727
similar to ADP-ribosylation factor-like 10B /// sperm adhesio	0.571928	1.136951	0.414927
KRR1, small subunit (SSU) processome component, homolo	1.096642	0.822457	0.591751
ubiquitin specific peptidase 4 (proto-oncogene)	1.0536	1.099791	0.571324
leucine rich repeat and Ig domain containing 2			
ribosomal RNA processing 12 homolog (S. cerevisiae)	0.990461	1.096152	2.332565
N-acetylneuraminate pyruvate lyase (dihydrodipicolinate syr	0.948282	1.518264	2.463118
N-acetylneuraminate pyruvate lyase (dihydrodipicolinate syr	0.961903	1.121279	4.239685
lysophosphatidylglycerol acyltransferase 1	1.073283	1.292423	2.824029
nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.571378	1.138989	0.691551
ATPase, class II, type 9B	2.870602	0.768837	
ATPase type 13A4	2.152097		
cysteine-rich PDZ-binding protein	1.153541	1.06576	0.474516
proprotein convertase subtilisin/kexin type 7	0.841689	1.251695	2.996422
minichromosome maintenance complex component 6	1.655633	1.864724	2.540409
minichromosome maintenance complex component 6	0.784761	1.535603	0.821638
succinate-CoA ligase, ADP-forming, beta subunit	1.113092	1.076112	0.185043
KIAA1128			1.968674
Hypothetical LOC416414	0.934322	0.812017	0.425397
transglutaminase 4 (prostate)	4.723535		2.89923
family with sequence similarity 102, member A	0.531108	1.113458	1.789026
major vault protein	1.194885	0.983026	1.383682
coiled-coil domain containing 43	1.749523	0.281277	1.634417
spastin	1.421421	0.740301	0.345141
arylsulfatase family, member K	0.75586	0.953847	2.355924
chromosome 9 open reading frame 3	0.928561		
stromal cell derived factor 4	1.117654	1.264129	2.07673
alcohol dehydrogenase 5 (class III), chi polypeptide	0.595298	1.011935	0.448397
hypothetical protein LOC769855	2.108607	0.736153	5.328231
hypothetical protein LOC769855	1.228709	0.911003	0.417972
StAR-related lipid transfer (START) domain containing 4	0.510595	1.014206	0.886818
golgi reassembly stacking protein 1, 65kDa	0.987047	0.469256	1.466155
ecotropic viral integration site 2A	2.029688	1.033013	1.273314
golgi SNAP receptor complex member 1	1.214524	0.858824	0.64073
glutamate receptor, ionotropic, delta 1	0.378712	0.848411	1.794029
solute carrier family 47, member 1	0.874463	1.572557	6.04019
inhibitor of growth family, member 3	1.232253	0.801481	0.486132
exocyst complex component 2	5.37314	0.767716	0.701972
ras homolog gene family, member A	0.687542	1.302097	0.317286

protein-O-mannosyltransferase 1	0.822739	0.6553	0.261684
polymerase (DNA-directed), delta 3, accessory subunit	0.784898	1.737646	0.734459
matrix metalloproteinase 24 (membrane-inserted)	0.905979	1.045942	2.143128
chromosome 1 open reading frame 144	0.430487	1.05756	0.38657
protein disulfide isomerase family A, member 4	0.649843	114.564	0.996228
dynactin 3 (p22)	0.384862	1.10963	1.489825
glutamate receptor, ionotropic, delta 1	0.80888	0.772246	0.270819
toll interacting protein	0.851772	1.107109	0.460715
eukaryotic translation initiation factor 4A, isoform 2	1.034085	1.026891	0.384737
pelota homolog (Drosophila)	0.459239	1.097887	1.416338
l(3)mbt-like 3 (Drosophila)	0.62075		0.200378
3-hydroxybutyrate dehydrogenase, type 1	0.7704	1.167376	0.568555
transmembrane protein 194B	1.104417	0.834213	2.08634
PDZ and LIM domain 7 (enigma)	1.36529	1.100855	0.877287
GTPase activating Rap/RanGAP domain-like 3	0.832221	0.745597	0.304563
general transcription factor IIIC, polypeptide 6, alpha 35kDa	1.260442	1.238877	1.996912
solute carrier family 25 (mitochondrial carrier, brain), memb	1.105164	1.559116	0.670682
pantothenate kinase 3		0.806014	0.3723
family with sequence similarity 125, member A	1.128127	0.250585	1.079552
KIAA1609	1.692135	0.854103	2.640689
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.902223	1.597336	0.386496
PQ loop repeat containing 2	1.539906	1.246164	1.957145
pericentrin	0.661706	0.763285	1.551682
denticleless homolog (Drosophila)	1.688895	1.14419	0.779468
split hand/foot malformation (ectrodactyly) type 1	0.92457	1.252268	0.182566
split hand/foot malformation (ectrodactyly) type 1	0.93426	1.127206	0.373989
phospholipid scramblase 1	1.837283	1.660324	1.56436
cat eye syndrome chromosome region, candidate 1	2.507049	1.004904	
chromosome 10 open reading frame 119	1.069939	1.159656	0.565835
POU class 2 associating factor 1	4.187156	17.85227	47.70974
kelch-like 15 (Drosophila)	1.054562	0.623517	0.362948
transmembrane protein 208	0.494567	0.985999	2.465074
nucleolar complex associated 2 homolog (S. cerevisiae)	0.779659	1.244053	3.544006
receptor-interacting serine-threonine kinase 2	2.158036	1.428436	0.959755
lectin, galactoside-binding, soluble, 8 (galectin 8)	0.363695	0.94992	0.55335
casein kinase 1, gamma 1	0.630209	0.935114	0.463326
similar to Protein C18orf1	1.364084	2.661833	8.993832
zinc finger, AN1-type domain 5	0.549548	0.911307	2.616857
centrosomal protein 170kDa	2.2501	1.071012	0.350642
UBA domain containing 2	0.742631	1.082577	0.48673

serum/glucocorticoid regulated kinase family, member 3	0.78412	1.021876	0.438943
excision repair cross-complementing rodent repair deficiency	0.630394	1.034672	0.458723
potassium channel tetramerisation domain containing 7	0.681403	2.078952	1.472949
diaphanous homolog 1 (Drosophila)	1.853557	0.840155	0.462929
fibronectin type III domain containing 3A	1.439949	1.324479	1.836851
family with sequence similarity 96, member A	4.598352		
replication factor C (activator 1) 3, 38kDa	0.982211	1.137545	0.56642
similar to T cell receptor alpha	3.048135	0.690566	0.315266
calcium activated nucleotidase 1	0.744964	1.098484	1.559846
solute carrier family 25, member 32	0.797869	1.290831	2.002772
dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0.673929	1.242908	0.730659
dCMP deaminase	0.936159	0.929013	0.721086
neuroepithelial cell transforming gene 1	1.0651	1.166281	3.30603
origin recognition complex, subunit 2-like (yeast)	1.392779	1.251453	2.17778
centromere protein O	0.773545	0.811679	0.679436
NSFL1 (p97) cofactor (p47)	1.584932	1.333368	1.751095
ligand dependent nuclear receptor corepressor-like			
serine/threonine kinase 4	0.856781	1.054894	3.610053
tRNA methyltransferase 6 homolog (S. cerevisiae)	0.237708	0.096747	0.319162
claudin domain containing 1	0.928321	0.654864	0.280782
coiled-coil domain containing 13	0.926119	2.605864	2.250842
similar to transcript expressed during hematopoiesis 2	0.898817	0.689656	1.664877
sterile alpha motif domain containing 11	0.511067	0.947965	2.387522
tyrosylprotein sulfotransferase 2	0.986039	0.868141	0.654914
survival of motor neuron protein interacting protein 1	2.060169	0.785957	0.880056
coiled-coil domain containing 5 (spindle associated)	0.337295	1.295403	1.369077
hypothetical protein LOC422090	0.827898	0.785499	0.831194
aspartylglucosaminidase	1.13733	2.201377	1.70894
dual specificity phosphatase 10	2.1656	1.19898	6.043369
cytoskeleton associated protein 2	0.910106	1.458843	0.430433
similar to BC027088 protein	0.772772	1.019014	1.066397
SERTA domain containing 2	0.344798	0.939344	2.432853
transmembrane protein 68	1.418693	1.082979	0.456404
acidic (leucine-rich) nuclear phosphoprotein 32 family, mem	0.613652	1.152733	0.510086
Ran GTPase activating protein 1	0.812051	0.795253	1.362264
adrenergic, beta, receptor kinase 1	0.868918	1.045635	1.679466
loss of heterozygosity, 12, chromosomal region 1	1.003272	0.79914	2.101255
cerebellar degeneration-related protein 2, 62kDa	1.494798	0.86937	0.205467
spleen tyrosine kinase	1.980032	1.292847	0.463727
similar to immunoglobulin-like receptor CHIR-B2 precursor	1.634433	0.885104	3.640183

solute carrier family 12 (potassium/chloride transporters), member 12	0.817002	0.782743	0.757446
neutrophil cytosolic factor 4, 40kDa	2.172879	1.285741	0.927506
poly(A)-specific ribonuclease (deadenylation nuclease)	1.020763	1.102824	0.878487
AT rich interactive domain 5B (MRF1-like)	1.530687	1.437492	1.791521
nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.988785	0.979288	0.501101
glutamyl-tRNA synthetase 2, mitochondrial (putative)	0.767977	1.441495	1.745926
family with sequence similarity 76, member A	0.771718	0.835475	0.426698
splicing factor, arginine/serine-rich 6	1.181637	0.939689	0.799464
NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (similar to C6orf37)	0.520403	7.33346	14.84032
GA binding protein transcription factor, alpha subunit 60kDa (similar to GABP1)	2.829796	1.635109	2.106979
RIO kinase 2 (yeast)	2.726804	0.58036	0.212485
REST corepressor 3	0.472876	0.920992	1.040323
RAN binding protein 1	1.544747	0.939255	0.239454
polo-like kinase 1 (Drosophila)	0.645453	1.122167	0.482206
chromosome 9 open reading frame 80	0.812255	1.118553	0.909628
hypothetical protein LOC768701	0.466391	1.297522	1.085978
glia maturation factor, beta	1.071346	1.057542	2.02416
RAB GTPase activating protein 1-like	0.600854	1.015475	0.080415
liver glycogen phosphorylase	0.798769	1.402768	0.54787
magnesium transporter 1	0.871631	0.999316	1.803276
family with sequence similarity 108, member B1	0.900313	0.982069	0.618665
membrane protein, palmitoylated 1, 55kDa	0.473978	1.069241	1.530714
C-terminal binding protein 1	1.015666	2.095842	17.24312
5'-nucleotidase, cytosolic II	0.864265	0.944158	0.346211
SMYD family member 5	1.940442	1.091872	5.348654
protein phosphatase 1, regulatory (inhibitor) subunit 12A	0.726539	0.569742	1.252895
protein phosphatase 2, regulatory subunit B, delta isoform	1.498572	1.136279	0.441577
protein phosphatase 2, regulatory subunit B, delta isoform	0.991738	0.799926	0.419086
BCL2-associated athanogene 3	1.356325	0.82374	0.519521
ras guanine nucleotide dissociation stimulator-like 1	2.379676	0.6099	0.900721
DnaJ (Hsp40) homolog, subfamily B, member 9	1.785508	1.114846	1.936658
DnaJ (Hsp40) homolog, subfamily B, member 9	0.985254	0.9799	0.972411
cysteine-rich hydrophobic domain 1	1.251337	0.781524	0.447733
RWD domain containing 1	0.619765	1.003497	0.99935
phosphatidylinositol-specific phospholipase C, X domain containing 1-like	0.571102	0.643227	0.254536
similar to cisplatin resistance-associated overexpressed protein 1	2.28722	1.875979	6.460738
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1-like		0.433448	0.568012
tetratricopeptide repeat domain 7B	1.314964	0.658704	0.568468
	0.838585	0.713279	0.287079
	2.024492	0.799283	0.850645

La ribonucleoprotein domain family, member 7	1.054282	0.911359	0.475721
WD repeat domain 68	0.898756	0.95762	0.45992
SGT1, suppressor of G2 allele of SKP1 (<i>S. cerevisiae</i>)	0.88319	0.950003	0.494479
homeodomain interacting protein kinase 1	2.85598	0.701758	0.665452
similar to RIKEN cDNA 1810055E12	1.036961	1.216302	0.400359
HEAT repeat containing 3	0.873879	1.217866	2.304869
chromosome 20 open reading frame 108	1.909959	0.586072	0.309028
transmembrane protein 128	0.981399	1.195726	0.486462
brain protein 44-like	0.783385	0.980185	0.495002
KIAA1704	1.327019	0.85729	0.503615
enolase 1, (alpha)	0.332899	1.304413	0.307972
heterogeneous nuclear ribonucleoprotein K	85.26582	0.508156	0.286854
protein tyrosine phosphatase type IVA, member 1	0.816219	0.749261	0.479171
LAS1-like (<i>S. cerevisiae</i>)		1.836358	0.275863
similar to endoplasmic reticulum protein 29 /// endoplasmic r	1.199438	1.024238	0.27677
tripartite motif-containing 14	0.615602	0.812282	0.584467
immunoresponsive 1 homolog (mouse)	3.784739	2.68941	12.64198
torsin family 1, member A (torsin A)	0.349126	0.953912	1.960937
leucine-rich PPR-motif containing			0.468962
complement component 3a receptor 1	5.426692	1.521684	1.722459
tRNA splicing endonuclease 2 homolog (<i>S. cerevisiae</i>)	0.887207	1.069116	0.441866
RFT1 homolog (<i>S. cerevisiae</i>)	1.327522	0.832389	0.286627
pallidin homolog (mouse)	0.731502	1.359857	0.411352
abl-interactor 1	2.040894	0.565447	0.421084
tetratricopeptide repeat domain 7A	2.228993	3.680379	
transmembrane protein 41B	1.632458	1.261893	0.913686
spermatid perinuclear RNA binding protein	1.256716	1.027123	0.622485
mitogen-activated protein kinase 11	1.671232	1.188616	2.397165
R-spondin homolog (<i>Xenopus laevis</i>)			0.462179
ATPase, H ⁺ /K ⁺ transporting, nongastric, alpha polypeptide		1.113521	
mindbomb homolog 2 (<i>Drosophila</i>)	1.167882	1.000099	0.543002
tripartite motif-containing 39	2.095248	1.791471	3.344444
cathepsin A	1.229909	1.381704	3.354782
NFKB activating protein	1.416398	0.925255	0.576973
mitochondrial ribosomal protein S6	0.775153	1.216291	0.217851
BUD13 homolog (<i>S. cerevisiae</i>)	1.039533	1.018766	2.009652
solute carrier family 30 (zinc transporter), member 6	1.200058	0.620164	0.196368
acyl-CoA synthetase long-chain family member 5	0.962963	1.126764	0.806749
acyl-CoA synthetase long-chain family member 5	1.04222	1.22753	0.808701
similar to hypothetical protein FLJ22557	0.992414	0.822913	0.386062

zinc finger, matrin type 2	0.935511	1.009282	0.606539
tetraspanin 12	0.899537	1.000734	0.398689
chromosome 4 open reading frame 20	1.140552	0.835578	0.361268
24-dehydrocholesterol reductase	0.538285	1.224003	0.598632
highly divergent homeobox	0.92487	1.204954	0.601218
similar to FLJ20359 protein		0.425045	
ubinuclein 1		0.179851	
ankyrin repeat and SOCS box-containing 3	0.400382		
carbohydrate sulfotransferase 10	1.431013	0.777695	0.413315
RAS guanyl releasing protein 3 (calcium and DAG-regulated)	1.902481	1.180881	0.422046
itchy homolog E3 ubiquitin protein ligase (mouse)	2.329381	0.837951	
basic helix-loop-helix domain containing, class B, 4	0.933796	8.97005	0.368329
5'-nucleotidase, cytosolic III	1.759786	1.048266	1.552926
sirtuin (silent mating type information regulation 2 homolog)	0.608503	1.097221	1.633973
5-methyltetrahydrofolate-homocysteine methyltransferase	1.535046	0.675083	0.560132
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0.61747	0.854609	1.802124
heat shock protein 90kDa alpha (cytosolic), class A member	0.602597	0.766743	0.176347
phosphoinositide-3-kinase, regulatory subunit 5, p101	0.991931	0.481212	1.832772
chromosome 1 open reading frame 59	0.588737	1.171248	4.711847
zinc finger family member 767	1.058923	2.089888	1.248723
stromal cell-derived factor 2-like 1	0.958135	1.078258	0.355834
TAP binding protein-like	2.127038	1.250799	1.123174
glucuronidase, beta	1.427299	1.459139	2.506685
glucuronidase, beta	1.294777	1.183297	1.691741
sorting nexin 3	0.677559	0.997241	0.273721
tetratricopeptide repeat domain 14	0.824974	0.844309	1.162678
spermatogenesis associated 2	1.227351	0.890374	0.669909
tec protein tyrosine kinase	1.07105	0.979653	0.475619
nucleosome assembly protein 1-like 4	0.81034	0.968197	0.47138
purinergic receptor P2Y, G-protein coupled, 8	3.950109	1.273292	1.765441
Kruppel-like factor 6	1.019139	1.253894	2.036585
tumor necrosis factor, alpha-induced protein 8	0.812885	0.976929	1.567377
NUF2, NDC80 kinetochore complex component, homolog (f	0.052094	0.696026	12.86634
heterogeneous nuclear ribonucleoprotein D-like	1.364565	0.77286	0.615216
mitochondrial ribosomal protein L37	0.686953	1.067962	2.173221
synaptotagmin VI		0.265562	
similar to zinc finger and BTB domain containing 8; BTB/POZ	1.040993	0.982816	1.793686
kinesin family member 23	1.179	0.934244	0.649578
chromosome 22 open reading frame 25	1.020126	0.843813	0.447825
glycosyltransferase-like domain containing 1	1.491042	1.045801	1.097491

plastin 3 (T isoform)	1.537732	1.304352	2.046322
WD repeat and FYVE domain containing 1	1.425417	0.856627	0.44091
ubiquitin-conjugating enzyme E2O	0.790007	0.498587	2.06848
chromosome 10 open reading frame 58	1.625466	1.421366	4.006158
kelch-like 7 (Drosophila)	2.948998	0.455309	4.253596
F-box protein 8	1.288856	0.574739	0.298336
E2F transcription factor 5, p130-binding	2.155774	0.977178	1.143789
complement component (3d/Epstein Barr virus) receptor 2	4.21871	2.192497	2.522847
nucleoporin like 2	0.675391	1.000303	0.423516
solute carrier family 39 (zinc transporter), member 13	1.36517	1.226324	1.637768
proteasome (prosome, macropain) 26S subunit, non-ATPase	0.686324	1.1637	1.534264
similar to Heat shock protein 67B2	0.757733	1.106329	0.407834
tripartite motif-containing 33	1.421835	0.9886	0.490537
yippee-like 2 (Drosophila)	1.20696	0.567183	0.421524
small nuclear RNA activating complex, polypeptide 5, 19kD	0.86775	1.093752	0.753357
chemokine (C-C motif) receptor 8	1.309259	2.351821	7.621622
RNA binding motif protein 12B	0.833446	0.900786	0.522956
transmembrane protein 123	2.481066	1.019203	0.235957
FYN binding protein (FYB-120/130)	0.975756	0.809817	0.166905
STIP1 homology and U-box containing protein 1	0.800293	0.884833	2.043901
protein phosphatase 1, regulatory (inhibitor) subunit 16B	1.567008	0.732789	3.575388
myelin expression factor 2	1.968616	0.569224	0.531498
coiled-coil domain containing 34	2.2128	1.629215	0.548316
WD repeat domain 36	0.469837	0.872341	1.89745
leucine rich repeat containing 28	0.970223	0.945369	0.328631
ribosomal protein S14	0.372951	1.107036	0.395333
proteasome (prosome, macropain) subunit, alpha type, 2	0.912099	0.898048	
chromosome 15 open reading frame 23	0.721298	1.035131	0.927396
far upstream element (FUSE) binding protein 1	0.845075	0.886196	0.483102
RM11, RecQ mediated genome instability 1, homolog (S. cer	0.59039	0.929589	0.796976
chromosome 13 open reading frame 1	1.012401	0.816833	0.398217
GrpE-like 1, mitochondrial (E. coli)	0.86243	1.104174	0.487527
RAB33B, member RAS oncogene family	0.967621	0.881816	0.392489
tumor necrosis factor (ligand) superfamily, member 13b	5.573077	2.130432	5.529872
catenin, beta like 1	0.814521	0.943001	2.306259
Hypothetical LOC424678	0.417268	0.892891	0.736946
similar to DNA polymerase-transactivated protein 6	1.606364	1.20119	0.607887
fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	1.168116	0.866468	0.735243
crystallin, zeta (quinone reductase)	1.06653	0.935098	2.09775
sorting nexin 5	1.036151	1.422454	0.726841

clathrin, light chain (Lca)	0.372132	1.079296	1.122413
prune homolog (Drosophila)	0.48314	0.534194	
methylthioadenosine phosphorylase	0.627611	1.158884	3.610689
flotillin 2	1.331838	0.604316	3.236728
chromosome 6 open reading frame 130	1.270501	0.907478	0.493076
poly(A) polymerase alpha	1.328865	0.729218	0.327089
immunoglobulin mu binding protein 2	1.274991	1.294415	1.371328
Src-like-adaptor	0.951705	0.674017	0.163664
F-box protein 32	0.357631	1.16862	0.783107
vanin 1	0.68454	1.346787	1.895379
nuclear factor of kappa light polypeptide gene enhancer in B	2.156216	0.881063	2.404678
3-oxoacid CoA transferase 1	0.366413	1.054033	0.790248
myotrophin	0.906148	0.810141	0.434791
mitogen-activated protein kinase kinase 5	0.942651	1.093943	2.522275
ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit D2	1.519167	2.447396	8.959435
kelch domain containing 10			0.975331
glucocorticoid induced transcript 1	2.374527	1.77354	3.822957
solute carrier family 16, member 1 (monocarboxylic acid tra	0.854753	1.013193	2.300337
syntaxin binding protein 3	0.341914		
SUMO/sentrin specific peptidase family member 8	1.779545	0.882956	0.420446
protein kinase C, delta	1.157437	0.653106	0.43486
zinc finger CCCH-type containing 12A	1.460885	0.24337	0.642954
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4		0.925128	0.15668
similar to Hypothetical protein SB153, isoform 1	2.351444	0.691003	0.668854
RNA binding protein, autoantigenic (hnRNP-associated with lethal yellc		15.73246	0.303435
asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homok		0.487516	0.313075
adenosine monophosphate deaminase 1 (isoform M)	1.103058	2.404491	
dedicator of cytokinesis 2	1.01049	0.911036	0.444084
hypothetical LOC415325	2.203358	3.176225	5.582749
forkhead box I1	1.515471	1.81299	3.275486
chloride channel CLIC-like 1	0.895233	0.329376	
envoplakin		1.556648	
poly (ADP-ribose) glycohydrolase	0.946484	1.061632	0.439782
chromosome 16 open reading frame 62	0.373241	1.09667	0.214668
WD repeat domain 47	2.111318	0.784335	0.784971
KIAA0692	2.963765	0.84135	0.914007
calmodulin regulated spectrin-associated protein 1-like 1		0.935037	0.303567
gamma-aminobutyric acid (GABA) A receptor, pi	0.945104	0.954364	3.347601
similar to KIAA1032 protein	1.917577	0.468111	0.391275
similar to egg-specific protein	2.565518	0.856517	2.463409

tumor suppressor candidate 4		0.805734	0.227075
hypothetical LOC415671		0.101683	
galactose-1-phosphate uridylyltransferase	0.713925	0.445804	1.772905
formin homology 2 domain containing 1	1.330981	0.80026	4.019383
formin homology 2 domain containing 1	1.819659		3.475478
CD6 molecule	0.824579		1.102713
CD6 molecule	0.392746	0.498723	
ring finger and FYVE-like domain containing 1	1.312237	1.422735	0.793337
ubিনuclein 1		0.475094	1.018731
Dmx-like 1		5.047422	0.63381
unc-13 homolog D (C. elegans)	1.093643	0.777886	1.980235
hypothetical LOC415913	0.497859	1.181657	0.212095
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase	1.379886	1.41377	1.275585
CUB and zona pellucida-like domains 1	0.634619	8.516839	0.420342
eukaryotic translation initiation factor 2C, 1		0.304931	
oxoglutarate dehydrogenase-like	0.626804	0.551738	1.287261
oxoglutarate dehydrogenase-like	0.596528	1.082072	2.191678
unkempt homolog (Drosophila)	0.833689	0.539002	0.848266
casein kinase 1, gamma 1	0.819067	0.946596	0.218861
casein kinase 1, gamma 1 /// similar to KIAA0101	0.46055	1.059876	0.404773
solute carrier family 25, member 46	1.232918	0.647541	0.354804
COMM domain containing 10	0.541884	2.141534	0.690163
similar to laeverin	1.643036	1.393717	0.397752
neuregulin 3		1.064876	
dynein, axonemal, heavy chain 3	0.648722	1.009497	2.284607
coagulation factor XIII, B polypeptide	0.529265		2.030609
coagulation factor XIII, B polypeptide	0.281447		
KIAA0258	6.293525		1.32507
EGF-like-domain, multiple 7			2.921704
similar to KIAA1328 protein		1.048059	
complement factor H	0.897759	0.897088	0.067372
complement factor H			0.014543
WD repeat domain 24	0.857307	1.134861	2.776845
aquaporin 7			
aquaporin 7	0.43227	0.987834	
dual oxidase maturation factor 1	2.152313	1.503761	0.845181
Vac14 homolog (S. cerevisiae)		0.97208	1.558578
WD repeat domain 75	0.991937	0.866688	0.933488
ubiquinol-cytochrome c reductase core protein II	1.073894	1.459326	0.357768
zinc finger, MYM-type 4		0.07501	

regulator of G-protein signalling 13	1.1041	1.109351	0.492289
olfactory receptor, family 10, subfamily A, member 4		0.713825	2.086079
hypothetical protein LOC770019		2.35396	
hypothetical LOC427084	1.385846	1.032996	0.485164
CUB and Sushi multiple domains 2	0.354929		
geranylgeranyl diphosphate synthase 1	1.110323	1.050163	0.470075
adenylate cyclase 10 (soluble) /// hypothetical protein LOC7	1.819968	0.427671	
adenylate cyclase 10 (soluble)		0.345598	
retinoid X receptor, alpha		0.43671	
nicotinamide nucleotide adenylyltransferase 1		8.944266	1.445121
KIAA1946	0.510879	1.398858	0.35606
prenylcysteine oxidase 1 like	2.187726	1.898124	3.823356
dymeclin	0.653407	2.017987	1.277821
dymeclin	0.375742		1.665156
t-complex 11 homolog (mouse)	0.737171	0.627861	
t-complex 11 homolog (mouse)	0.851736	2.394296	
solute carrier family 15, member 4	0.816303	1.237889	0.509687
similar to retinoblastoma-binding protein 1-related protein	2.020257	0.890768	0.782661
UDP-N-acetylglucosamine pyrophosphorylase 1	1.78491	0.791772	2.108193
exportin 6	6.59355		
coiled-coil domain containing 57			
protocadherin 15	3.683202		
protocadherin 15	0.452645		
pecanex homolog (Drosophila)	1.128827	0.934785	0.7396
protocadherin 15	0.387185	0.922114	0.673312
transcription factor Dp-2 (E2F dimerization partner 2)	0.866795	0.910774	0.333078
transcription factor Dp-2 (E2F dimerization partner 2)	0.70013	0.81461	0.329008
protocadherin 15			18.75425
chromosome 2 open reading frame 21	1.333615	0.509435	0.414868
G protein-coupled receptor kinase 7	0.675845	2.215482	0.76297
protein kinase C and casein kinase substrate in neurons 1	0.33712		
similar to Acylamino-acid-releasing enzyme (AARE) (Acyl-	0.488405	0.790513	
zinc finger and BTB domain containing 38	3.810678	0.940858	1.312543
ectonucleotide pyrophosphatase/phosphodiesterase 1		3.867216	1.434892
acetoacetyl-CoA synthetase	0.552201	1.613555	0.343275
amine oxidase, copper containing 3 (vascular adhesion prote	0.342202		
macrophage stimulating 1 receptor (c-met-related tyrosine kinase)			
ADAMTS-like 2		2.537758	
WD repeat domain 69	11.64969		1.553516
hypothetical LOC420114			0.279659

Rho-related BTB domain containing 1	0.895442	2.177696	0.785742
exosome component 10	0.890187	1.03087	0.953665
core-binding factor, runt domain, alpha subunit 2; translocat	0.834009	1.234192	0.407074
ankyrin-repeat and fibronectin type III domain containing 1			7.611201
regulator of G-protein signalling 14	1.305792	0.979383	1.056125
ankyrin 3	3.169329	1.248818	0.52756
solute carrier family 9 (sodium/hydrogen exchanger), member 2		14.0154	
zinc finger CCCH-type containing 7A	1.279375	0.887165	0.858931
phosphatidylinositol glycan anchor biosynthesis, class V	0.808081	0.850662	2.087602
LAG1 homolog, ceramide synthase 1		1.135599	0.340627
hypothetical protein LOC768480 /// solute carrier family 16,	1.680332	1.16055	0.404954
homeobox A6	1.208462	0.51732	0.27103
SRY (sex determining region Y)-box 5	1.096621		117.9329
axin 1	0.669777	0.888175	0.989386
heat shock protein 25	2.516575	1.092583	0.456345
carnitine palmitoyltransferase 1A (liver)	1.303206	1.15344	2.247803
growth differentiation factor 9	0.457046	1.001028	0.329081
periostin, osteoblast specific factor	1.285458	1.083249	0.926536
transient receptor potential cation channel, subfamily C, member 1		1.438361	0.42225
protein kinase C, beta		0.897192	1.189878
protein kinase C, alpha	0.97671	1.228595	0.081328
signal transducer and activator of transcription 3 (acute-phas	1.514709	1.191119	1.558734
distal-less homeobox 6	2.340132		
orthodenticle homeobox 2			
protocadherin gamma subfamily A, 2	1.64362	1.160386	2.692418
Copine VIII	1.987325	1.330001	1.941036
Down syndrome critical region gene 3	1.134544	0.946452	0.489041
chromosome 16 open reading frame 70		1.212458	0.724542
leucine rich repeat containing 28	0.742906	1.061646	0.260352
similar to nucleophosmin/nucleoplasmin, 2		0.790678	0.600655
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla		0.796303	0.322619
dynein, cytoplasmic 2, light intermediate chain 1	0.441424	2.312286	0.734357
MAP-kinase activating death domain		0.278656	
dynammin binding protein	5.377087	1.971727	
RCD1 required for cell differentiation1 homolog (S. pombe)	0.451522	1.651079	0.485705
PAP associated domain containing 1	1.491748	0.891109	0.545221
Zinc and ring finger 2	0.961254	0.787865	0.392231
Hypothetical LOC418900	0.72114	1.133073	0.192198
Hypothetical LOC422903	1.019937	1.342205	2.23829
5-hydroxytryptamine (serotonin) receptor 2C		9.169883	

NHL repeat containing 2	0.976675	1.251183	0.445859
Excision repair cross-complementing rodent repair deficiency	0.981136	0.829522	0.256293
myc target 1		1.561901	1.363128
phosphoribosyl pyrophosphate synthetase-associated protein	0.941366	0.742526	1.2892
RNA binding motif protein 33	1.130226	1.102706	0.880572
FCH and double SH3 domains 2	0.843828	0.937646	0.428371
RAB4A, member RAS oncogene family	0.757719	1.005132	1.246964
Antagonist of mitotic exit network 1 homolog (S. cerevisiae)	2.093466	1.072278	1.173623
poly (ADP-ribose) polymerase family, member 4			
RNA binding motif protein 33	0.879913	1.018645	0.809191
activated leukocyte cell adhesion molecule	0.998854	0.879338	0.328497
LOC417551	1.097959	0.452254	1.685596
hypothetical gene supported by CR390948		0.615856	2.519035
N-acetylated alpha-linked acidic dipeptidase 2			
NUAK family, SNF1-like kinase, 1	1.43459	1.391298	2.191658
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-h	1.218679	1.030283	1.722237
Ribosomal protein S6 kinase, 52kDa, polypeptide 1	0.487415	0.812238	0.922274
Collagen, type IV, alpha 5 (Alport syndrome)	1.013721	0.820114	6.345138
hypothetical gene supported by CR353498	1.685264	0.76711	1.875608
zinc finger and BTB domain containing 25	0.669073	0.826435	0.469053
KIAA0802	2.764797	1.031569	2.864227
PDZ and LIM domain 5	2.585628	1.090669	1.079122
Immunoglobulin superfamily, member 10	1.98554	1.036437	2.72823
RAB11 family interacting protein 4 (class II)	0.059083		
chromosome 6 open reading frame 130			0.211145
1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid ε		0.18169	1.041127
collagen, type XVI, alpha 1	2.023953	0.959968	4.071076
protein tyrosine phosphatase, receptor type, S	1.33384	0.534338	3.381881
General transcription factor IIIC, polypeptide 2, beta 110kDa	0.572602	0.807027	1.636049
Similar to RIKEN cDNA 8030446C20	19.26087	1.057359	0.873056
Hypothetical protein LOC768386		1.629327	0.037017
FtsJ homolog 3 (E. coli)		0.94282	1.334631
Wolf-Hirschhorn syndrome candidate 1	0.40124	1.469457	3.420993
pyruvate dehydrogenase phosphatase isoenzyme 2	0.774595	0.904807	0.265585
NEDD4 binding protein 2-like 1	0.480203	0.885739	2.821896
RAD54-like 2 (S. cerevisiae)	9.2002	0.675047	1.072787
RAB27A, member RAS oncogene family	0.981513	0.931589	0.259664
membrane bound O-acyltransferase domain containing 2	0.877836	1.229051	0.962779
tetratricopeptide repeat domain 13	3.915017	0.858969	0.313527
chromosome 9 open reading frame 41	0.55264	0.948098	0.611194

membrane protein, palmitoylated 3 (MAGUK p55 subfamily KIAA0430	2.437604	0.681195	0.598868 0.026831
LOC420939	1.607527	1.497546	2.484914
Solute carrier family 30 (zinc transporter), member 1	1.467951	1.562153	2.474627
Hypothetical LOC423879	1.058225	0.96464	0.242216
exophilin 5	1.347009	2.259832	2.754441
zinc finger CCCH-type containing 6	2.126642	0.644967	0.599669
chromosome 12 open reading frame 10	0.532848	0.934754	2.884425
chromosome 12 open reading frame 10	0.646312	0.759544	2.859256
chromosome 14 open reading frame 43	1.519166	0.59892	2.164389
Hypothetical LOC417130	0.489764	0.814428	1.428166
Host cell factor C2	1.276877	0.605038	0.33822
protein S (alpha)	1.563748	1.371124	1.315197
replication factor C (activator 1) 1, 145kDa	0.948909	0.827479	2.336322
ATP binding domain 4	0.848519	1.096746	2.046452
Microtubule-associated protein 7	1.270468		2.621625
similar to RIKEN cDNA 2810451A06 gene	0.079315		1.248189
Chromodomain helicase DNA binding protein 1	56.38715	1.112245	0.207518
yippee-like 2 (Drosophila)	1.539645	0.57341	0.357503
WD repeat and FYVE domain containing 3			41.70946
microtubule-associated protein 7	1.009216	1.022284	1.084252
nucleolar protein 5A (56kDa with KKE/D repeat)	0.951492	0.989234	1.579202
zinc finger CCCH-type, antiviral 1	3.774448	1.5602	0.870237
transforming, acidic coiled-coil containing protein 2	19.90378	0.511254	
ATPase family, AAA domain containing 5	0.745701	1.235869	0.286409
similar to hypothetical protein FLJ38973	0.843435	0.844	0.345185
LSM8 homolog, U6 small nuclear RNA associated (S. cerev	2.873586	1.018684	0.343538
T-cell immunoglobulin and mucin domain containing 4	0.500555	2.415244	1.69128
hematological and neurological expressed 1	0.961122	1.058422	0.913496
Olfactomedin-like 2B	1.226582	0.945645	2.4739
Family with sequence similarity 107, member B	1.502271	1.203251	0.455283
nuclear prelamin A recognition factor	1.055565	0.926338	1.015924
ZFAT zinc finger 1	1.342628	1.346862	0.514342
phosphofurin acidic cluster sorting protein 2	1.409669	0.79412	1.365153
membrane-bound transcription factor peptidase, site 1	0.614321	1.231678	0.834639
Sodium channel, voltage-gated, type II, alpha subunit	7.042868	1.005598	
Similar to SSFA2 protein	1.341557	1.170413	0.427947
coiled-coil domain containing 52	0.76712	0.84122	0.534465
spleen focus forming virus (SFFV) proviral integration onco	3.417788	1.618024	1.879086
ORM1-like 1 (S. cerevisiae)	0.731691	0.860467	0.485073

doublecortex		8.253369	
mitofusin 1			0.659112
BTB (POZ) domain containing 1	0.931766	0.985907	0.458502
mitochondrial ribosome recycling factor	1.337491	0.767866	2.205522
myosin phosphatase Rho interacting protein	1.551458	0.77497	2.851405
similar to Myotubularin related protein 9	1.060607	0.838319	2.122418
Inhibitor of kappa light polypeptide gene enhancer in B-cells	0.409959	0.88902	1.211987
Triple functional domain (PTPRF interacting)	2.145023	1.118903	5.258018
Similar to trypsinogen	1.127867	0.301657	0.253473
centaurin, alpha 2	1.251512	1.417119	2.470093
zinc finger protein 706	1.066397	1.004257	0.455719
Similar to Poly [ADP-ribose] polymerase 14 (PARP-14) (B	4.165403	1.383867	2.075972
mitochondrial translation optimization 1 homolog (S. cerevis	0.44323	1.467963	0.559027
SET domain containing (lysine methyltransferase) 8	0.626213	1.493465	0.451311
transmembrane protein 119		0.364667	
tensin 1	1.595666	2.273633	
actin-like 6A	0.448183	2.921839	0.405595
Ch-runtB2	0.814502	0.879087	0.307598
Solute carrier family 45, member 4	0.458769	1.251358	0.860609
kelch-like 26 (Drosophila)		12.01196	
Zinc finger, RAN-binding domain containing 2	1.393874	0.95945	0.51714
WWC family member 3	1.660769	1.473075	2.386892
Ribosomal protein, large, P1	12.49346		
Ribosomal protein, large, P1	1.529404	0.405305	0.939354
chromosome 9 open reading frame 96	1.991931	0.874591	2.177922
HECT, C2 and WW domain containing E3 ubiquitin protein	0.818352	0.52462	0.120015
FK506 binding protein 12-rapamycin associated protein 1			0.394091
F-box and leucine-rich repeat protein 20	1.126569	0.737646	0.53098
Myotubularin related protein 7	1.702621	1.082425	6.82641
N-acylaminoacyl-peptide hydrolase	1.030522	0.714788	2.388217
ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.704364	1.368298	4.982566
CDC5 cell division cycle 5-like (S. pombe)	0.642089	0.793458	2.31445
activating transcription factor 7 interacting protein	0.643509	0.857325	2.380037
SRY (sex determining region Y)-box 7	2.892748	1.342849	3.490411
NOP16 nucleolar protein homolog (yeast)	0.834611	1.393462	1.122727
hypothetical LOC423478	2.018656		
protein phosphatase 1, regulatory (inhibitor) subunit 12B		1.268635	
protein phosphatase 1, regulatory (inhibitor) subunit 12B	1.017841	1.005056	2.995721
Thioredoxin domain containing 10	1.212257	0.95238	0.549276
Similar to KIAA0612 protein	1.606743	0.666239	1.809951

Solute carrier family 29 (nucleoside transporters), member 3	1.481216	1.114312	0.069469
Zinc binding alcohol dehydrogenase, domain containing 2	0.861609	0.767418	0.449589
Zinc finger protein 511		0.844689	
PDS5, regulator of cohesion maintenance, homolog B (<i>S. cerevisiae</i>)		0.037283	
diacylglycerol kinase, delta 130kDa	0.922939	1.487195	1.729346
NEDD4 binding protein 2	0.717721	0.898687	0.470411
NEDD4 binding protein 2	0.687844	1.030744	0.622899
Similar to KIAA1370 protein	0.808093	0.751984	1.296305
Similar to RanBP7/importin 7	0.999413	0.96818	0.941636
Tetratricopeptide repeat domain 39A	0.989994	1.889526	0.351774
microtubule-actin crosslinking factor 1		0.995571	
fibroblast growth factor receptor 2	0.927428		
Glutamate receptor, ionotropic, AMPA 3	0.259989	1.088304	
Brain protein 44-like	1.21321		
PAS domain containing serine/threonine kinase	0.543593	1.042902	0.283294
PAS domain containing serine/threonine kinase	0.880742	1.257876	0.671277
adenosine deaminase, tRNA-specific 1	1.438243	0.659091	0.926918
G protein-coupled receptor kinase 6	0.563372	0.802331	1.297305
POM121 membrane glycoprotein (rat)	0.813528	1.181384	2.424227
RELT-like 1	0.358273	0.907397	1.480123
caldesmon 1	1.659272	2.189153	5.282702
WD repeat domain 76	0.865213	1.130048	2.358092
bromodomain adjacent to zinc finger domain, 1B	1.839095	0.897007	0.677245
family with sequence similarity 44, member B	0.754402	1.230554	1.800887
B-cell CLL/lymphoma 9	1.460107	1.143977	2.73332
transducer of ERBB2, 2	1.161463	0.591445	0.28073
Dapper, antagonist of beta-catenin, homolog 2 (<i>Xenopus laevis</i>)	3.072675	1.877368	2.21419
Dapper, antagonist of beta-catenin, homolog 2 (<i>Xenopus laevis</i>)	2.108629	1.850548	1.371065
TSR1, 20S rRNA accumulation, homolog (<i>S. cerevisiae</i>)		0.653139	0.391988
development and differentiation enhancing factor 1	1.277924	0.664643	0.445509
hect (homologous to the E6-AP (UBE3A) carboxyl terminus	1.228392	0.876477	0.602014
porcupine	0.931372	1.382284	1.550229
porcupine	0.974355	1.554689	2.127761
BCL6 co-repressor	1.132971	0.971506	0.387346
Similar to Tcf-3 co-repressor CtBP	0.884656	1.166094	0.659831
Calcineurin binding protein 1	1.328841	0.895795	0.596744
nucleoporin 35kDa	0.698694	1.082901	0.624435
TBC1 domain family, member 23	1.692474	0.996082	0.413132
ADAM metallopeptidase domain 9 (meltrin gamma)	1.465924	1.154191	0.661401
aldolase B, fructose-bisphosphate	1.010749	1.423848	4.437392

oxidative stress induced growth inhibitor 1	1.320023	0.98094	2.34087
microtubule-associated protein 1A	0.784602	0.812755	0.521422
similar to long microtubule-associated protein 1A; long MAI	1.246917	0.534739	0.403238
cathepsin B	2.19162	1.441065	2.885587
CDK2-associated protein 1	0.677991	0.827376	0.293397
FYVE, RhoGEF and PH domain containing 3	0.82409	0.972817	0.747504
unc-93 homolog B1 (C. elegans)			0.052765
tubulin tyrosine ligase-like family, member 12	0.433491	1.899772	0.108589
tubulin tyrosine ligase-like family, member 12	0.503657	1.319459	0.361315
BTG family, member 2	0.91301	0.626426	0.413663
Similar to MCTP2	1.205581	1.836495	3.06681
Zinc finger protein 592	2.94933	0.798791	1.250723
Ribokinase	0.951275	0.474736	0.641483
WD repeat domain 73	0.852485	0.888456	0.805256
Acidic (leucine-rich) nuclear phosphoprotein 32 family, men	0.667915	1.274619	0.245703
vacuolar protein sorting 4 homolog B (S. cerevisiae)	0.54172	1.172786	0.711962
fukutin related protein	1.441151	0.682303	1.025016
M-phase phosphoprotein 9		2.659385	0.670252
Membrane-associated ring finger (C3HC4) 11			
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfar			0.174404
Galactose-3-O-sulfotransferase 1	0.979271	0.997461	0.175872
PH domain and leucine rich repeat protein phosphatase	0.342741	0.943118	1.301907
WD repeat domain 31			2.269904
Guanylate cyclase 1, soluble, alpha 2	2.107626	1.191096	1.897264
chromosome 9 open reading frame 58	1.220128	1.225866	1.017849
transient receptor potential cation channel, subfamily M, mei	1.299737	1.153998	
B-cell CLL/lymphoma 11A (zinc finger protein)	2.87882	0.651114	0.606216
Amyloid beta (A4) precursor protein-binding, family A, member 1 (X11)			
Phospholipase A2, group X	0.405037	1.42251	0.797133
Ankyrin repeat domain 13C	0.795152	0.995245	0.319101
copine IV	2.686111	0.735694	4.353081
hypothetical protein LOC772356	2.594922	1.304412	2.596886
Discoidin, CUB and LCCL domain containing 1	0.467579	0.689146	0.200245
Discoidin, CUB and LCCL domain containing 1	0.527865	0.7061	0.209325
Hypothetical protein LOC771033	4.997049	0.513238	1.811264
Hypothetical protein LOC771033	29.67889		
Rho GTPase activating protein 5	1.091204	0.979759	0.308294
KIAA1797	0.322644	0.906256	2.108681
coronin, actin binding protein, 2A	1.795962	1.125107	1.639826
LOC421235		0.445643	

Non imprinted in Prader-Willi/Angelman syndrome 1	1.82473	0.424755	0.652885
non imprinted in Prader-Willi/Angelman syndrome 1	2.095974	0.97538	0.431008
carbonic anhydrase IV	0.79855		2.975108
yippee-like 1 (Drosophila)	0.725376	0.7906	0.228322
SAM domain and HD domain 1	2.758332	1.508576	3.293049
WD repeat domain 34	1.040874		3.748781
abhydrolase domain containing 12		1.416698	0.224182
CCCTC-binding factor (zinc finger protein)	1.304042	1.002359	0.528441
Heterogeneous nuclear ribonucleoprotein D (AU-rich element)	1.033334	0.764441	0.414672
F-box protein 11	0.883728	1.615732	0.391098
Similar to Solute carrier family 30 (zinc transporter), member 1	1.226736	1.420109	0.455107
palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal)	1.593126	0.866643	0.317759
ATP-binding cassette, sub-family C (CFTR/MRP), member 6			
COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase			0.083674
caldesmon 1	2.712007	1.40405	1.279848
Hypothetical protein LOC769096	6.410654	1.229453	
solute carrier family 25, member 13 (citrin)	0.901436	1.120369	0.407772
chromosome 5 open reading frame 35	0.488735	0.861232	0.568708
lysocardiolipin acyltransferase	2.064216	2.468146	0.66875
ubiquitin protein ligase E3B	1.51625	0.850945	0.853953
hypothetical gene supported by CR406014	0.861245	0.555147	0.534767
Zinc finger CCCH-type containing 12D	1.289016	3.094465	2.570006
Potassium channel tetramerisation domain containing 9		2.37186	0.378989
ADAM metallopeptidase domain 8			
chromosome 4 open reading frame 29	2.020431	0.816758	0.60903
tectonin beta-propeller repeat containing 1	2.202789	0.944285	0.552047
Hypothetical LOC421802	0.516884	0.487095	0.53771
serine/threonine kinase 25 (STE20 homolog, yeast)	0.610779	1.344583	0.021895
mesoderm development candidate 1	1.644511	0.923695	0.610211
Nucleolar protein family A, member 1 (H/ACA small nucleolar RNA binding protein)	2.046313	9.206406	0.070311
Y box binding protein 1	1.662375	0.593853	0.666897
formin binding protein 1	0.75214	1.116047	0.381216
similar to MGC80370 protein		2.150274	
Hypothetical protein LOC777054	2.330263	1.263289	1.012839
fragile X mental retardation, autosomal homolog 1	1.22185	0.771558	0.435573
ADAM metallopeptidase domain 32	0.31602		1.464488
benzodiazapine receptor (peripheral) associated protein 1	0.973837	1.128692	0.664165
PHD finger protein 20-like 1	0.952439	1.036975	0.486855
KIAA0774			0.098993
fibroblast growth factor receptor substrate 3	1.61129	0.541619	

UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfe	0.838631	1.347979	0.474077
GC-rich promoter binding protein 1	0.46507	0.964759	1.339788
DD1 protein	1.006008		1.492585
human immunodeficiency virus type I enhancer binding prot	0.93781	0.739742	0.444537
Myeloma overexpressed 2	0.482718	1.102012	0.791363
Phospholipase A2, group XIIA	1.339767	1.013556	2.497732
RAS-like, family 10, member B	0.179721	1.61938	1.727508
protein tyrosine phosphatase, receptor type, T			
Hypothetical protein LOC770534			6.648183
protein phosphatase methylesterase 1	0.424281	1.789542	2.357965
FK506 binding protein 15, 133kDa	0.992003	0.892911	2.042445
nipsnap homolog 1 (C. elegans)	0.930039	1.287366	2.267678
hypothetical protein LOC768803		0.569987	0.627161
hypothetical protein LOC768803	0.43131	1.053238	0.921787
coiled-coil domain containing 92	0.821986	1.110565	0.442622
carbonic anhydrase XII			0.076937
Forkhead box K2	1.58397	1.010217	0.424778
chromogranin A (parathyroid secretory protein 1)	1.77722	1.946145	9.754737
LOC416951	1.309207	0.705277	0.454999
hypothetical protein LOC771106	1.755658	0.696648	0.435641
Cell division cycle associated 8	3.38928	0.87467	0.439289
Similar to trans-Golgi protein GMx33	9.36847	1.400062	0.106722
Similar to putative selenoprotein O	1.633753	0.689956	1.012845
oral cancer overexpressed 1	1.472665	0.819972	0.615998
Family with sequence similarity 91, member A1	1.879484	0.839826	0.198203
Hypothetical protein LOC771190	2.046511	1.386291	2.828574
Coiled-coil domain containing 72	1.149626	0.640856	0.118313
Hypothetical LOC427838	1.455157	7.983209	1.557882
chromosome 14 open reading frame 83	1.39272	0.818494	0.654547
WSC domain containing 2	0.487666	2.429091	1.646325
G protein-coupled receptor kinase interactor 1	2.361571		
Protein tyrosine phosphatase, receptor type, R	2.130346	1.184291	3.65227
Sodium channel, voltage gated, type VIII, alpha subunit	3.194932	0.681901	0.317834
bromodomain adjacent to zinc finger domain, 1A	0.468043	1.516349	1.446139
similar to RIKEN cDNA A830006F12 gene	0.491729	1.133414	0.951799
Similar to normal mucosa of esophagus specific 1	3.730888	1.341368	2.480521
Similar to MS1	0.578866	0.683162	4.85152
lemur tyrosine kinase 2	0.632167	0.197985	
coiled-coil domain containing 132	0.561011	3.059242	1.026586
interferon-related developmental regulator 1	0.92665	1.011424	0.281159

solute carrier family 16, member 1 (monocarboxylic acid tra	1.037094	1.057965	2.137142
BRCA1 associated RING domain 1	1.058925	1.298146	1.057887
protein tyrosine phosphatase, receptor type, T			
xylosyltransferase I	1.13942	1.832423	1.561847
interleukin 18 (interferon-gamma-inducing factor)	3.910009	1.389383	2.834343
calcium channel, voltage-dependent, beta 4 subunit	1.082685	0.701118	0.410842
gametogenetin binding protein 2	1.175113	0.89742	0.73984
t-complex 11 (mouse)-like 2	0.975935	0.976744	2.07422
stathmin 1	0.53652	1.060916	0.502847
anti-Mullerian hormone			1.82524
lipoprotein lipase	0.865271	2.332225	11.95701
slow muscle troponin T	1.021312	1.519328	2.889678
collagen, type VI, alpha 1	1.68955	1.682683	2.902373
interleukin 10 receptor, beta	1.632742	1.363772	1.017059
cytochrome P-450 2C45		1.287058	4.025112
intestinal zipper protein	2.280811		
glucagon	2.038884	1.325308	2.39405
glucagon	3.046135	1.381676	1.037291
NK2 transcription factor related, locus 6 (Drosophila)			0.171451
forkhead box A2	1.119822	1.756248	2.559201
bHLH transcription factor beta3	3.424382	1.302846	2.602551
thrombopoietin	0.950877		
homeobox A7	0.496709	0.679575	0.397105
zinc finger protein 313	0.839531	0.813916	0.367313
LIM and senescent cell antigen-like domains 1 /// hypothetical	0.365523	3.522506	0.941903
cadherin 13, H-cadherin (heart)	1.756945	2.880154	6.230001
aldehyde dehydrogenase 3 family, member B1 /// similar to 1	1.408528		0.335029
cytochrome P450 A 37	1.402543	1.566933	2.564651
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3			2.442629
iroquois homeobox 4	0.022386		0.966549
iroquois homeobox 4			
fibroblast growth factor 13			14.69022
cholecystokinin	2.116844	3.976333	1.826861
beta-defensin 12		0.148092	
Gal 5	0.394012	0.81218	0.309427
Gal 4	0.419988	1.628073	
Gal 7	0.326109		1.451431
cytochrome P450 2H1	1.472301	4.223658	3.410433
cytochrome P450, family 2, subfamily C, polypeptide 18	0.924355	5.67421	6.422395
cytochrome P450, family 2, subfamily C, polypeptide 18	2.030014	14.32135	4.453572

cadherin 2, type 1, N-cadherin (neuronal)	2.012161	1.301523	1.567573
cathelicidin antimicrobial peptide	0.230572		50.75547
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6			
piggyBac transposable element derived 3		2.515413	
galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndr	0.46016	0.788153	0.356416
ARP3 actin-related protein 3 homolog B (yeast)			0.488233
histone deacetylase 7A	0.78973	0.689794	0.462368
DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	1.223127	1.017289	0.844055
protein tyrosine phosphatase, non-receptor type 5 (striatum-e	12.8928		2.602392
interferon-induced protein with tetratricopeptide repeats 5	9.720315	3.856989	4.438786
WD repeat domain 53	1.107335	0.814694	0.444827
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.962617	0.911304	0.592012
1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosph	0.968495	1.110232	1.504696
solute carrier family 16, member 12 (monocarboxylic acid tr	0.713129	5.647218	
kelch-like 22 (Drosophila)	0.754034	1.0317	3.442358
angiomotin like 2		6.570074	
hemopoietic cell kinase	2.101895	0.85075	1.933918
hemopoietic cell kinase	4.957073	2.156935	3.471772
nucleolar complex associated 3 homolog (S. cerevisiae)	0.761511	1.081122	0.499112
perilipin	1.343015	2.040622	1.779939
additional sex combs like 1 (Drosophila)	1.702142	0.769719	2.472158
chromosome 15 open reading frame 42	0.405556	1.166877	0.612186
centrosomal protein 63kDa	16.7407	0.626097	
dual specificity phosphatase 8	0.965438		0.143531
mitogen-activated protein kinase kinase kinase 13	0.840139		0.607354
similar to ovary-specific MOB-like protein	0.880082	1.210395	0.22334
abhydrolase domain containing 2	0.651046	1.25158	1.129031
L-amino-acid oxidase precursor	3.313757		3.743162
ATP-binding cassette, sub-family C (CFTR/MRP), member 6		0.189426	
vacuolar protein sorting 8 homolog (S. cerevisiae)	1.013562	1.16561	2.277904
fer-1-like 3, myoferlin (C. elegans)		2.217816	1.688905
NADPH oxidase 1	0.768636	1.235352	2.037678
similar to glypican-5			
RAD50 homolog (S. cerevisiae)	2.226771	1.185131	1.584168
RAD50 homolog (S. cerevisiae)	1.037405	1.135153	2.200114
A kinase (PRKA) anchor protein 13	0.929762	1.154564	2.916284
spermatogenesis associated 20			
similar to MGC83953 protein	0.523478	1.294072	0.242162
lysophospholipase 3 (lysosomal phospholipase A2)	0.788247	1.259141	0.22716
phospholipid transfer protein	0.819698	1.349475	3.066793

eukaryotic translation initiation factor 4E nuclear import factor 1	1.059875	3.105782	
discs, large homolog 1 (Drosophila)	1.946899		0.022335
choline kinase alpha	2.655276	0.912897	0.509997
similar to MGC64341 protein	0.558117	0.820919	0.051395
similar to p150 target of rapamycin (TOR)-scaffold protein c	1.010753	1.035478	0.108588
ATP-binding cassette, sub-family A (ABC1), member 12	0.525393	0.787471	0.248611
CDK5 regulatory subunit associated protein 2	0.850047	2.123318	0.897448
sphingomyelin phosphodiesterase 3, neutral membrane (neut	1.21259	1.005512	0.40566
multiple EGF-like-domains 9	1.642493	1.977469	
copine VIII	1.324629		2.300081
copine VIII	1.484502	0.353027	1.873754
cell adhesion molecule 1	0.841293	1.376885	1.036308
pitrilysin metallopeptidase 1		2.042041	
hypothetical LOC425659	1.502566		
chromobox homolog 8 (Pc class homolog, Drosophila)	0.54792	0.649345	0.290415
DnaJ (Hsp40) homolog, subfamily C, member 8	0.696284	1.268318	0.556268
ankyrin repeat and SOCS box-containing 7		1.197043	0.303131
chromosome 5 open reading frame 33	1.209504	1.294067	3.011512
similar to BC033915 protein	3.10471		4.975729
similar to BC033915 protein	0.784694	1.18796	2.170712
chondroitin sulfate synthase 1			0.068816
mitochondrial ribosomal protein L12	0.495407	0.977157	0.97893
interleukin 1 receptor accessory protein	0.88922	0.882789	0.999808
peroxisomal biogenesis factor 11 gamma	0.842153	1.176272	4.081269
Ca ²⁺ -dependent secretion activator	0.816388	1.29441	1.518504
Ca ²⁺ -dependent secretion activator	0.51286	2.632511	1.19585
Ca ²⁺ -dependent secretion activator	0.377451		
hypothetical LOC428323	0.844936	5.780867	
heat shock 70kDa protein 4	1.084144	0.998311	0.455846
transmembrane protein 130	3.574982	0.789923	2.290257
KIAA0174	1.166952	1.143883	0.326665
tumor protein p63	0.714066	0.208648	0.719151
catenin (cadherin-associated protein), delta 1			2.397982
somatostatin	2.044411	1.257789	5.988626
zinc finger, DHHC-type containing 5	5.668034	0.653384	1.001414
WW domain containing adaptor with coiled-coil	2.154536		
acyltransferase like 1	1.054844	1.48781	0.9954
COX15 homolog, cytochrome c oxidase assembly protein (y	0.764426	1.107596	1.342998
phosphate cytidylyltransferase 1, choline, alpha	0.706785	0.730301	0.492194
DENN/MADD domain containing 4A	0.680953	2.067449	0.4509

hypothetical protein LOC770883	0.994176	0.061674	
leucine-rich repeats and calponin homology (CH) domain containing 3			
mahogunin, ring finger 1	0.757014	0.982952	1.563336
amine oxidase (flavin containing) domain 2	0.28929	0.984831	0.682405
ADAM metalloproteinase domain 28	1.182003	0.910188	2.228148
DOT1-like, histone H3 methyltransferase (<i>S. cerevisiae</i>)		0.508237	
BTB (POZ) domain containing 12	2.063733	0.756311	0.549335
myosin IIIA		1.627306	0.429044
signal transducer and activator of transcription 1, 91kDa	4.189686	1.839424	2.880142
RAE1 RNA export 1 homolog (<i>S. pombe</i>)	0.871341	1.017267	0.378273
B-cell CLL/lymphoma 9-like	2.722704	0.50894	1.027222
armadillo repeat containing 9	0.279516	0.853141	1.311913
myosin IB	3.689026	1.073914	0.644099
myosin IB	0.830227		0.129668
F-box and WD repeat domain containing 4	0.406155	1.344193	1.009051
Rho GTPase activating protein 21	2.450396	2.703679	1.236527
KIAA2022		6.013168	
KIAA1217			5.801391
Similar to KIAA1217 protein	1.988259	2.443818	2.457479
docking protein 5	1.298099	0.649654	0.164046
hypothetical LOC415641 /// similar to rat GCP360	3.402462	0.866237	0.613583
chromosome 17 open reading frame 28			
KIAA1841		0.334547	
Similar to tetratricopeptide repeat domain 12	1.393845	1.414842	
similar to pyruvate dehydrogenase complex, component X			0.431859
alpha thalassemia/mental retardation syndrome X-linked	0.867738	0.890166	0.430794
chromosome 11 open reading frame 57	0.343033	0.395867	1.134278
sperm associated antigen 6	0.467115		
sperm associated antigen 6	0.038904		
myeloid/lymphoid or mixed-lineage leukemia (trithorax hom	8.678377	0.645973	0.306455
mitogen-activated protein kinase kinase 5	8.578166	2.092991	1.835904
PH domain and leucine rich repeat protein phosphatase-like	1.023474	1.003138	2.064117
solute carrier family 16, member 5 (monocarboxylic acid tra	4.366852	2.083733	
ATPase, Ca ⁺⁺ transporting, plasma membrane 4		0.404397	1.655632
transmembrane protein 209			0.050876
transmembrane protein 209			0.230264
tRNA splicing endonuclease 54 homolog (<i>S. cerevisiae</i>)	1.864582	0.67941	0.241292
myotubularin related protein 3	0.540093	0.46253	1.719298
HMG-box transcription factor 1	0.992003	0.871104	0.373824
PR domain containing 11	1.033946	1.070326	4.277841

hypothetical protein LOC770890	1.077663	2.800731	2.986177
mesoderm specific transcript homolog (mouse)	1.922086	1.305161	0.085672
olfactory receptor OR35	0.832135		2.544768
chromosome 2 open reading frame 60	1.185989	0.727687	0.529025
similar to olfactory receptor 2	1.646778	1.256854	0.060262
SFRS protein kinase 2	1.357777	0.855333	0.28286
SFRS protein kinase 2	1.284456	0.909886	0.241777
spectrin, beta, non-erythrocytic 1	0.869142	1.098673	0.541276
ankyrin repeat domain 34A	1.222303	2.112959	
hypothetical LOC424944			
coiled-coil domain containing 146	0.387036		2.183199
arginine decarboxylase	1.122411	0.776704	2.283568
arginyl aminopeptidase (aminopeptidase B)-like 1			0.426432
arginyl aminopeptidase (aminopeptidase B)-like 1	2.059105	1.812453	0.761755
cytoskeleton associated protein 5	0.646496	1.062912	0.312321
cytoskeleton associated protein 5	1.267204	1.52671	0.258393
solute carrier family 24 (sodium/potassium/calcium exchanger), membe		0.488138	0.987739
GDNF-inducible zinc finger protein 1		1.510327	
GDNF-inducible zinc finger protein 1 /// zinc finger protein 1	4.715968		
GDNF-inducible zinc finger protein 1	0.963852	0.876408	1.124876
amyotrophic lateral sclerosis 2 (juvenile) chromosome region	1.060724	0.892403	0.479469
chromosome 20 open reading frame 19	0.455965	0.235454	0.502054
ankyrin repeat domain 12	0.94338	0.959904	0.480412
amyotrophic lateral sclerosis 2 (juvenile)	1.144555	0.736084	0.390281
zinc finger and BTB domain containing 34	2.04816	0.912552	0.368164
guanine nucleotide binding protein, alpha transducing 3	0.485066		0.013298
solute carrier family 35, member B4			0.41433
solute carrier family 35, member B4	0.426664	1.845008	1.059354
heterogeneous nuclear ribonucleoprotein L-like	1.158113	0.980404	0.499437
aspartyl-tRNA synthetase 2, mitochondrial			0.129636
delta-like 4 (Drosophila)		0.121923	0.187479
family with sequence similarity 125, member B	0.571533	0.265324	0.286939
nuclear receptor subfamily 2, group C, member 2	1.079419	1.174863	0.325005
bromodomain containing 1	1.111119	0.715575	0.282412
bromodomain containing 1	1.056923	0.857417	0.409575
asparagine-linked glycosylation 12 homolog (S. cerevisiae, a	2.33511	0.947389	0.340374
FYVE, RhoGEF and PH domain containing 5		0.026723	
zinc finger, BED-type containing 4		1.258977	
zinc finger, BED-type containing 4	1.430055	0.946285	0.511286
INO80 complex homolog 1 (S. cerevisiae)	0.728609	1.940629	0.664151

interleukin 17 receptor E-like	0.494758	0.868359	0.516639
FK506 binding protein 5	0.740458	1.571545	7.136981
IQ motif containing GTPase activating protein 1	1.478177	1.001455	0.425787
family with sequence similarity 125, member B	0.723514	0.169024	0.84633
mitogen-activated protein kinase 11			0.097831
mitogen-activated protein kinase 11	2.191586	0.936496	1.507974
leukocyte receptor tyrosine kinase	0.371352	0.557829	
general transcription factor IIH, polypeptide 4, 52kDa	1.760865	1.127858	4.355519
MAX gene associated	1.599822	0.931431	0.488286
activating transcription factor 2	1.560228	1.026145	0.338914
Ras association (RalGDS/AF-6) and pleckstrin homology do	1.126238	0.945869	0.382926
solute carrier family 25, member 43	0.183753	1.38337	
cubilin (intrinsic factor-cobalamin receptor)		3.081995	0.552477
chromosome 20 open reading frame 23	1.045163	1.836558	4.965624
chromosome 20 open reading frame 23	1.052751	1.08914	1.059106
WD repeat domain 85			0.118924
synovial sarcoma, X breakpoint 2 interacting protein		2.138176	
synovial sarcoma, X breakpoint 2 interacting protein	0.621129	0.683188	0.369001
chromosome 10 open reading frame 38	1.221428	1.543957	0.8402
spermatogenesis associated 1	1.714178		2.095721
leucine rich repeat and sterile alpha motif containing 1	0.68736	0.910979	2.034669
aftiphilin	0.864366	1.246432	0.467764
aftiphilin	1.573841	0.442113	0.655293
ATPase, class VI, type 11B	1.103858	2.167988	0.391465
ATPase, class VI, type 11B		1.351092	0.228583
thioredoxin domain containing 13	1.171747	0.759006	0.78624
WD repeat domain 31	2.306766		
phospholipase C, beta 1 (phosphoinositide-specific)			1.905853
EGF, latrophilin and seven transmembrane domain containin	2.166648	1.11428	2.830083
ring finger protein 208		0.381273	
EH domain binding protein 1	0.847566	1.715117	0.815523
F-box protein 11	1.795756	0.924146	0.584792
p21(CDKN1A)-activated kinase 7	0.291444		11.44774
mitogen-activated protein kinase kinase kinase kinase 4	0.705918	0.90275	0.773455
elongation factor Tu GTP binding domain containing 2	0.887108	0.977646	0.799302
transmembrane protein 16C			
chromosome X open reading frame 57	1.085136	0.557829	0.860143
McKusick-Kaufman syndrome	1.646257	0.786986	0.374922
transmembrane protein 87A	0.547948	1.28126	0.862042
lipocalin 15	5.26941	2.972869	1.620777

hypothetical LOC420542		0.503599	
hypothetical LOC420542	1.07388		0.079503
solute carrier family 13 (sodium-dependent dicarboxylate tra	0.099347	3.228088	
titin			
myotubularin 1	1.082492	0.634455	0.456504
forkhead box N1	1.920615	0.919203	0.340928
ankyrin repeat domain 26	24.51914	1.374497	0.617932
ankyrin repeat domain 26	0.439966	1.299602	0.636602
centrosomal protein 27kDa	0.784555	1.159868	0.464998
diacylglycerol O-acyltransferase homolog 2 (mouse)	1.581529	0.885141	0.495361
unc-119 homolog (C. elegans)			2.410209
attractin-like 1		2.859176	
epithelial cell transforming sequence 2 oncogene		1.16195	0.058513
CDC42 binding protein kinase alpha (DMPK-like)	1.008274	1.591994	2.001981
cyclin F	0.828956	1.363803	0.457119
hypothetical protein LOC770184	0.297978	0.850896	0.620433
TBC1 domain family, member 24	0.733461	1.010838	0.078244
ubiquitin protein ligase E3 component n-recognin 1	0.453282		0.298235
ubiquitin protein ligase E3 component n-recognin 1			2.390709
phospholipase D1, phosphatidylcholine-specific			0.26267
benzodiazapine receptor (peripheral) associated protein 1	1.117631	0.846668	0.826058
benzodiazapine receptor (peripheral) associated protein 1			
Fanconi anemia, complementation group F	0.763835	1.310036	0.444994
TRAF2 and NCK interacting kinase	2.495747	0.869665	1.132451
cornichon homolog 3 (Drosophila)			0.418676
Obg-like ATPase 1	0.60985	0.964472	0.458706
eukaryotic translation initiation factor 3, subunit A	0.471941	1.163594	0.676751
Crm, cramped-like (Drosophila)	1.363634	0.438073	0.50453
erythrocyte membrane protein band 4.1-like 1	0.72395	2.38728	1.729686
regulator of G-protein signaling 6			
suppression of tumorigenicity 7		1.576675	2.34513
ankyrin repeat and IBR domain containing 1		5.662854	0.435008
leucine rich repeat containing 34	2.472031	0.652737	1.112037
dispatched homolog 1 (Drosophila)		2.955098	
ecotropic viral integration site 1	4.393488	0.577306	1.24148
golgi integral membrane protein 4	0.471397	0.72394	0.713253
Rap guanine nucleotide exchange factor (GEF) 2	4.718527	1.359522	0.511572
folliculin interacting protein 2	2.039135	0.953539	0.689713
neuropeptide Y receptor Y5	0.392235	0.460544	0.799953
RAB3 GTPase activating protein subunit 2 (non-catalytic)	2.199235	0.869949	0.465017

sucrase-isomaltase (alpha-glucosidase)	0.913085	2.225877	1.026489
similar to mitochondrial methionine aminopeptidase 3	2.921544	1.328321	0.159472
transforming, acidic coiled-coil containing protein 2	1.006234	0.924919	1.554748
type XXIII collagen alpha 1 chain /// type XXIII collagen alpha 1	0.624065		1.207788
tousled-like kinase 1	1.583567	0.953095	0.48427
tousled-like kinase 1	1.07455	1.094343	0.43796
ubiquitin-like domain containing CTD phosphatase 1	0.823448	1.430448	0.23848
membrane protein, palmitoylated 5 (MAGUK p55 subfamily)	4.0621	1.128743	1.048411
thrombospondin 1			0.597214
hypothetical LOC422427	17.91866	2.73274	7.424909
cholinergic receptor, muscarinic 5	3.786818		
collagen, type I, alpha 2	0.832408	1.185218	0.416679
amiloride-sensitive cation channel 1, neuronal (degenerin)	0.268404	0.950963	0.600509
arginine/serine-rich coiled-coil 1	1.102942	0.168413	1.175278
sprouty-related, EVH1 domain containing 1	2.117909	1.510061	0.881266
hematopoietic cell-specific Lyn substrate 1	1.102911	1.006936	1.079452
similar to NADH dehydrogenase	0.95789	1.043368	0.313879
MON2 homolog (S. cerevisiae)	0.902613	0.942283	0.369021
zinc finger protein 770	1.819074	9.275853	0.041138
inositol polyphosphate-4-phosphatase, type II, 105kDa	0.969175	1.492094	1.711512
transcriptional regulating factor 1	1.637672	1.453556	2.331739
echinoderm microtubule associated protein like 4	5.350184	1.023253	3.381628
striatin, calmodulin binding protein 3	2.08958	1.43973	0.873514
pleckstrin homology domain containing, family H (with MyTH4 domain) member 1			0.950846
tyrosine kinase with immunoglobulin-like and EGF-like domains	0.58975	0.803537	5.50042
RAB3A interacting protein (rabin3)	0.733653	0.912799	0.514014
elongation of very long chain fatty acids (FEN1/Elo2, SUR4)	0.889824	1.427086	0.354545
bromodomain adjacent to zinc finger domain, 1A	1.690938	1.398072	0.452656
growth arrest-specific 7	0.878995	1.78502	3.305367
insulin receptor	0.362467		0.159698
dishevelled associated activator of morphogenesis 2	0.848081	1.188746	2.106295
jumonji domain containing 2A	1.041559	0.832474	0.441573
KIAA0082	2.821279		1.634926
steroid 21-hydroxylase	4.730613		
leucine-rich repeat-containing G protein-coupled receptor 5			
coiled-coil domain containing 131	1.173225	1.093257	0.392836
RAB21, member RAS oncogene family	0.914726	1.669721	0.373993
F-box protein 33	0.76568	1.444154	0.585623
vacuolar protein sorting 13 homolog C (S. cerevisiae)	2.699767		1.162717
chromosome 14 open reading frame 44	0.654208	0.894459	1.848635

major facilitator superfamily domain containing 8	3.432963	0.968163	1.433695
similar to KIAA1193 /// mesoderm induction early response	0.589916	1.028026	2.801037
similar to acetyl-CoA synthetase 2-like	1.050381	0.484096	0.972643
similar to acetyl-CoA synthetase 2-like	0.725009		
keratin 79		3.933899	
latent transforming growth factor beta binding protein 3	0.404138		0.521589
YLP motif containing 1	1.359442	0.76082	0.376548
nucleophosmin/nucleoplasmin, 3	0.927157	1.519906	3.567424
helicase with zinc finger	2.803421	0.903345	0.209293
ribosomal protein S6 kinase-like 1			11.49658
solute carrier family 33 (acetyl-CoA transporter), member 1			
similar to KIAA0612 protein	2.261571	0.700122	1.670662
ceruloplasmin (ferroxidase)	1.62411	1.361411	0.272324
Hermansky-Pudlak syndrome 3	0.810753	0.955954	0.733938
latent transforming growth factor beta binding protein 1	1.749308	9.744562	0.380304
early B-cell factor 3	2.348315	1.996922	3.074215
AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)			0.19854
SCL/TAL1 interrupting locus			0.393962
solute carrier family 5 (sodium/glucose cotransporter), meml	3.77562	0.528212	
chromosome 1 open reading frame 165	1.076948	0.98999	0.898224
Fc receptor family member	0.462865		
alanine-glyoxylate aminotransferase 2-like 1	2.887218	0.497938	0.224219
hairy and enhancer of split 5 (Drosophila)		2.807822	
3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.957415	1.142392	0.421815
family with sequence similarity 82, member A	0.375039		
family with sequence similarity 82, member A		1.566716	0.82024
similar to chromosome 14 open reading frame 145	2.933726	1.1692	0.720814
fibronectin leucine rich transmembrane protein 2			
fasciculation and elongation protein zeta 2 (zygin II)	0.422375		1.088575
similar to KIAA1546 protein	1.518472	0.962672	0.654257
G protein-coupled receptor 65	1.221752	0.269898	1.925611
G protein-coupled receptor 65	2.95183	1.336762	0.753795
sorting nexin 25	2.849456	0.882448	0.47264
coiled-coil and C2 domain containing 1B	0.032958	1.333011	
acyl-CoA synthetase long-chain family member 1	1.503163	1.270209	1.427212
zinc finger, CCHC domain containing 11	1.793649	1.211366	0.905722
coiled-coil domain containing 111	2.03921	1.278782	2.003169
transcription factor B2, mitochondrial	2.24831	0.64145	0.651805
sterol carrier protein 2	2.047528	1.378501	2.845885
echinoderm microtubule associated protein like 5	0.849348		0.304323

WW and C2 domain containing 2	2.098504	1.495209	1.529986
missing oocyte, meiosis regulator, homolog (Drosophila)	0.795746	0.844441	1.066703
coiled-coil domain containing 88C	1.706516	0.731277	0.489234
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosyl transferase	3.760844	0.609334	0.597196
similar to RIKEN cDNA 2810410C14 gene	0.447704	1.320897	0.133745
similar to RIKEN cDNA 2810410C14 gene	0.868069	0.719116	0.576283
formin 2		2.778297	
golgi autoantigen, golgin subfamily a, 5	1.302075	1.183061	0.444857
Fanconi anemia, complementation group D2	0.954537	1.30477	1.075294
phosphatidic acid phosphatase type 2B	0.428508	0.761382	
spermatogenesis associated 4	5.138623		1.115458
complement component (3d/Epstein Barr virus) receptor 2	2.101748	1.05364	1.260789
sorting nexin 13		2.228022	
myb-like, SWIRM and MPN domains 1	2.305855	1.777006	0.624591
similar to MGC83505 protein /// retinol dehydrogenase 5 (11-cis/9-cis)			0.136914
retinol dehydrogenase 5 (11-cis/9-cis)	0.733489	1.301131	0.072848
chromodomain helicase DNA binding protein 9	2.637667		
integrin, beta 8	3.707721		
anthrax toxin receptor 2	3.240504		
InaD-like (Drosophila)	1.346249	0.795584	0.173151
InaD-like (Drosophila)	7.187179		
ankyrin repeat domain 38	1.015388	0.536517	
nidogen 1	2.767054	5.981386	
dedicator of cytokinesis 7	0.896434	0.532091	0.440893
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4			7.025928
similar to PWP2 periodic tryptophan protein homolog (yeast) /// similar to PWP2H			0.39606
similar to PWP2 periodic tryptophan protein homolog (yeast) /// similar to PWP2H			0.393869
signal-induced proliferation-associated 1 like 2	30.1645	1.008864	
signal-induced proliferation-associated 1 like 2	0.723248	7.424616	1.280856
similar to C3 and PZP-like alpha-2-macroglobulin domain c	0.574627	0.908778	0.977046
homeobox A6	0.857769	0.7576	0.467682
homeobox A11	5.037512		
Homeobox A10			2.180918
protein tyrosine phosphatase, non-receptor type 13 (APO-1/C	0.440561	0.998685	0.682265
interferon induced with helicase C domain 1	3.67284	1.580525	1.775657
Rho GTPase activating protein 24	1.269804	1.550029	1.972131
lin-54 homolog (C. elegans)	2.619796	1.164898	2.049886
similar to rapamycin insensitive companion of mTOR; rictor	0.802627	0.654491	1.169053
ALX homeobox 1	1.303664	7.240795	
chimerin (chimaerin) 2	1.370207	4.618819	0.95483

chromosome 12 open reading frame 29	1.252374	1.839798	0.467863
centrosomal protein 290kDa	1.151054	0.855317	2.296871
centrosomal protein 290kDa	0.802301	1.323401	0.393011
family with sequence similarity 120B	2.734739	0.715348	1.058846
chromosome 6 open reading frame 70	1.555676	0.898454	1.138562
placenta-specific 8	2.556402	3.535342	7.316953
helicase, POLQ-like	1.355029	0.877662	0.709508
phospholipase C, eta 2			
SATB homeobox 1	1.389805	0.637786	0.117041
WD repeat and FYVE domain containing 3	0.496427		0.129829
ATPase, Ca ⁺⁺ transporting, plasma membrane 1	0.638688	2.436265	0.620639
RAR-related orphan receptor A	1.761705	2.185779	4.137951
RAR-related orphan receptor A	1.803001	1.322645	2.212553
DEP domain containing 1	0.689835	0.990376	0.74222
myeloid/lymphoid or mixed-lineage leukemia (trithorax hom	0.458249	0.718907	
homocysteine-inducible, endoplasmic reticulum stress-induc	1.203814	0.810331	0.403103
protein kinase, AMP-activated, gamma 3 non-catalytic subur	0.863777	1.023818	0.883382
chromosome 14 open reading frame 131	0.373985	0.974685	1.725096
Rab geranylgeranyltransferase, beta subunit	0.917403	0.997848	0.623136
ubiquitin specific peptidase 44	2.53378	0.508936	1.285444
chromosome 17 open reading frame 38	1.187107	1.047463	1.869407
ubiquitin specific peptidase 37	2.179729	1.234634	0.689176
CDC42 binding protein kinase beta (DMPK-like)	6.939865	0.614311	0.927606
septin 11	0.765876	1.193913	1.968638
nucleoporin 54kDa	0.859457	0.832168	0.479708
apoptotic peptidase activating factor 1	1.175984	1.300522	0.409119
UHRF1 binding protein 1-like		0.574994	0.469608
SIN3 homolog B, transcription regulator (yeast)	0.45012	0.871393	1.191544
RUN and FYVE domain containing 3	0.52924	1.306609	0.497895
RUN and FYVE domain containing 3		2.447241	0.806718
sirtuin (silent mating type information regulation 2 homolog)	0.640967	0.673043	0.362381
solute carrier family 22 (organic cation transporter), member 2		0.374336	0.688369
solute carrier family 22 (organic cation transporter), member	0.764115		
COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)		9.467094	
similar to Nel-like 1	0.970946	0.844315	1.352991
AHNAK nucleoprotein 2		0.020015	0.488998
AHNAK nucleoprotein 2	0.825363	0.437526	1.263817
protein disulfide isomerase family A, member 5	0.649152	0.742161	0.552812
ATP/GTP binding protein-like 3		0.686748	1.490736
ubiquitin-activating enzyme E1-like 2	0.86428	1.478843	1.824483

histone cluster 2, H2ac /// similar to histone 2, H2ac /// hypot	0.488018	1.177055	0.623876
leucine zipper transcription factor-like 1	1.194552	1.767189	0.33498
sulfotransferase family 1E, estrogen-preferring, member 1	1.127892	1.543838	1.584131
LIM domains containing 1	0.500473	0.981363	0.345514
FYN binding protein (FYB-120/130)	5.088722		
FYN binding protein (FYB-120/130)	0.661119	0.797831	0.276086
kinesin family member 15	0.725776	1.155041	0.416667
transmembrane protein 186			0.245083
F-box and leucine-rich repeat protein 2	26.80278	0.939385	
huntingtin interacting protein 1 related			0.067769
phosphodiesterase 5A, cGMP-specific	1.405021	0.5364	0.842603
SEC24 related gene family, member D (S. cerevisiae)	1.348237	0.972154	2.575632
SEC24 related gene family, member D (S. cerevisiae)		2.685948	1.298743
FYN binding protein (FYB-120/130)	0.626211	0.835575	0.211078
protease, serine, 12 (neurotrypsin, motopsin)	0.318319	0.990607	0.506654
solute carrier family 25 (mitochondrial carrier; peroxisomal)	0.592567	0.944186	0.45224
similar to alpha 7A integrin			
arylsulfatase family, member J	0.945837	1.168702	1.083867
solute carrier family 12 (potassium/chloride transporters), me	1.223279	1.02647	0.472894
lupus brain antigen 1	1.926805	1.486282	1.747854
interleukin 28B (interferon, lambda 3)	1.104551	2.197305	
Fas apoptotic inhibitory molecule	0.938411	0.9874	0.259636
N-acetyltransferase 12	1.404453	1.184958	0.506917
chromosome 14 open reading frame 108	1.263112	1.091035	0.589438
anillin, actin binding protein	0.853453	0.750201	0.682019
reticulocalbin 1, EF-hand calcium binding domain		0.041755	
chromosome 1 open reading frame 130	0.806697	0.897119	0.263584
solute carrier family 35, member F5	8.111066	1.228368	0.983832
hypothetical protein LOC769503 /// hypothetical protein LO	0.982271	0.930584	0.415087
Bardet-Biedl syndrome 9			
sterile alpha motif domain containing 4A	1.083199	1.458035	4.168526
KIAA0241	0.607443	0.948677	0.563496
KIAA0241		0.492778	0.66617
cell growth regulator with ring finger domain 1	1.335802	1.04227	0.16112
cyclin T2	2.146353	0.597278	1.162401
kelch domain containing 1	1.374371	0.770421	0.909136
R3H domain containing 1	1.679437	0.612182	0.516624
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	2.286445	0.966454	0.271417
alcohol dehydrogenase 1C (class I), gamma polypeptide	0.501764	0.662273	0.40893
utrophin			

microsomal triglyceride transfer protein	2.780808		
phospholipase A2, group VI (cytosolic, calcium-independent)	1.73534	0.831547	2.677398
similar to T-cell receptor gamma V2.9	1.067948	1.113404	0.262559
POU domain, class 6, transcription factor 2		0.838646	
chromosome 7 open reading frame 11	1.062371	1.153512	0.558373
Na ⁺ /H ⁺ exchanger domain containing 2	0.744149	1.177182	3.240933
salvador homolog 1 (Drosophila)	0.644924	0.856458	0.195399
mitogen-activated protein kinase kinase kinase 7 interacting	1.110644	0.899005	0.400311
mitogen-activated protein kinase kinase kinase 7 interacting protein 2		2.549271	
ninein (GSK3B interacting protein)	1.389326	1.052059	0.475935
chromosome 6 open reading frame 72	1.076895	1.380684	0.632649
speckle-type POZ protein-like	1.593086	1.327588	0.235428
protein phosphatase 1, regulatory (inhibitor) subunit 14C		0.86112	0.238284
thioredoxin domain containing 16	0.227811		
golgi associated, gamma adaptin ear containing, ARF bindin	0.566499	0.758338	0.490768
adenylate cyclase 1 (brain) /// similar to brain adenylate cycl	4.043867		0.278805
zinc finger E-box binding homeobox 2	1.457929		1.017787
HUS1 checkpoint homolog (S. pombe)	0.843059	0.844064	0.250003
kinesin family member 5C	1.156601	1.496805	2.231306
hypothetical LOC420793		2.001496	
retinoblastoma-like 1 (p107)	1.148823	0.519461	0.15569
nuclear transcription factor, X-box binding 1		0.285668	
solute carrier family 12 (potassium/chloride transporters), m	0.494032		
solute carrier family 12 (potassium/chloride transporters), m	0.25714		
FAD-dependent oxidoreductase domain containing 2	0.532595	3.23664	
myosin, heavy chain 9, non-muscle			0.428695
glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	2.284689	1.194182	2.500966
uridine phosphorylase 2	0.39345		0.966061
tetratricopeptide repeat, ankyrin repeat and coiled-coil contai	2.636489	0.817091	1.01545
zinc finger, CCHC domain containing 6	0.671233	0.751382	2.499522
PR domain containing 4	1.094649	0.773727	0.958528
CDC14 cell division cycle 14 homolog C (S. cerevisiae)	0.370285	0.305509	0.519432
NUAK family, SNF1-like kinase, 1	0.43405	1.246594	
glycosylphosphatidylinositol specific phospholipase D1			
KIAA1033	0.971184	1.187316	0.469714
CDK5 regulatory subunit associated protein 1-like 1	0.363099	2.272597	0.667229
CDK5 regulatory subunit associated protein 1-like 1	0.83574	1.116693	0.452139
membrane bound O-acyltransferase domain containing 1	0.390958	0.846294	0.729823
glucose-fructose oxidoreductase domain containing 1		0.63008	0.030657
N-acetylglucosamine-1-phosphate transferase, alpha and beta	0.80811	0.901184	0.211979

N-acetylglucosamine-1-phosphate transferase, alpha and beta	1.36523	0.948196	0.109769
lipic acid synthetase	0.943354	1.60556	0.492226
heterogeneous nuclear ribonucleoprotein M	1.02399	1.126911	0.214299
desmoplakin	1.226547	0.766503	0.216581
desmoplakin	0.687459	0.70949	0.418507
desmoplakin	0.800855	0.926888	0.337046
LYR motif containing 4	0.459245	1.050137	1.208493
chromodomain protein, Y-like		2.69185	0.746997
PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1.426277	0.908046	0.570332
chromosome 6 open reading frame 86	2.773239	0.761228	0.636588
solute carrier family 37 (glycerol-3-phosphate transporter), n	1.757524	2.280804	1.279674
DENN/MADD domain containing 2A	0.295713		0.173061
cAMP responsive element binding protein 3-like 2	0.720852	1.099971	0.404853
diacylglycerol kinase, iota	0.496079	0.768383	0.637651
diacylglycerol kinase, iota		1.584661	2.331013
tubulin tyrosine ligase-like family, member 11			1.028852
tyrosyl-tRNA synthetase 2, mitochondrial	2.400974	1.167434	0.658044
dynamitin 1-like			2.465023
DENN/MADD domain containing 5B	0.165535	1.11798	1.58435
myosin X	1.009763	0.687692	0.058464
myosin X	0.917152	0.612382	0.309183
tubulin tyrosine ligase-like family, member 11	0.560226	0.847442	2.203418
tubulin tyrosine ligase-like family, member 11	0.740499	1.210558	2.216875
chromosome 6 open reading frame 97	14.31288		
chromosome 6 open reading frame 98	1.530878	0.998363	0.357375
chromodomain protein, Y-like 2		0.32259	1.213503
triple functional domain (PTPRF interacting)	2.48908	1.253303	3.755219
triple functional domain (PTPRF interacting)		1.350017	
midline 2		0.392749	
ELKS/RAB6-interacting/CAST family member 1	0.643136		3.260563
F-box and leucine-rich repeat protein 14	0.956732	0.818461	0.432259
similar to olfactory receptor, family 5, subfamily U member	4.965479	3.681864	
microtubule associated monooxygenase, calponin and LIM domain conta		3.220408	
sema domain, seven thrombospondin repeats (type 1 and typ	0.125139	1.128828	0.289021
5-methyltetrahydrofolate-homocysteine methyltransferase re	0.533132	0.65647	0.352295
microsomal glutathione S-transferase 1	1.10786	1.454327	0.774568
similar to immunoglobulin-like receptor CHIR-B4 /// similar	1.893798	0.908033	1.289772
ADAM metalloproteinase with thrombospondin type 1 motif,	1.056478		
chromosome 9 open reading frame 4	2.004051	0.645636	0.976702
phosphodiesterase 3A, cGMP-inhibited		1.267382	0.458392

similar to olfactory receptor, family 5, subfamily U member	1.705424	5.732099	0.812492
semaphorin 7A, GPI membrane anchor (John Milton Hagen)	0.80195	0.446994	0.47161
KIAA0528	0.484884	0.574153	
KIAA0528	1.26171	1.102621	0.534167
KIAA0528		0.584633	0.312983
helicase with zinc finger	0.452865	1.517687	0.593844
protein arginine methyltransferase 8		0.111446	
protein arginine methyltransferase 8	4.580247		0.82478
KIAA1219	0.046868	1.313315	0.583644
KIAA1219	0.347838	1.112414	1.177805
KIAA1219	0.910377	0.795007	2.684147
interleukin 7 receptor		0.445284	0.846569
PWWP domain containing 2A	1.204293	1.406601	0.396321
similar to LOC402959 protein	4.821391		5.530249
RAN binding protein 10	3.848035	0.79554	1.373337
T-cell immunoglobulin and mucin domain containing 4	0.383527	0.683622	0.194419
hypothetical LOC415891	1.394244	0.784061	0.405704
leucine rich repeat containing 16A	1.403516	0.836937	3.090604
RNA binding motif protein 16	1.013841	0.709547	0.3528
transcription factor B1, mitochondrial	0.860829	1.543474	0.362083
zinc finger protein 236	2.168809	0.622162	0.603327
zinc finger protein 236	0.654768	0.884633	0.452667
teashirt family zinc finger 1	1.324865	0.876011	0.158145
chemokine (C-C motif) receptor 7	0.459021		
chromosome 10 open reading frame 137	0.840197	0.838502	0.497892
chromosome 10 open reading frame 137	1.042433	0.881404	0.47179
karyopherin (importin) beta 1	0.968968	1.398928	2.171163
aminoadipate-semialdehyde dehydrogenase	1.2171	0.71123	0.399696
similar to hypothetical protein DKFZp434F117.1			
fucosidase, alpha-L- 2, plasma	1.236796	0.852913	0.490867
centrosomal protein 135kDa	1.348541	1.279409	0.829116
exocyst complex component 1	1.848199	0.794962	0.501233
LSM domain containing 1	0.461458	0.121837	
human immunodeficiency virus type I enhancer binding prot	1.124198	0.81826	0.374711
steroid 5 alpha-reductase 3 /// transmembrane protein 165	0.882366	0.796662	0.220006
ubiquitin associated protein 2	0.509987		1.207573
promyelocytic leukemia	2.875375	1.36529	1.090287
synaptojanin 2 binding protein	0.872443	0.99216	0.452523
dual specificity phosphatase 16	3.021404		
AFG3 ATPase family gene 3-like 2 (yeast) /// hypothetical L	0.551751	1.020518	1.601047

dehydrodolichyl diphosphate synthase	1.309553	1.358882	0.483907
prenylcysteine oxidase 1	1.337691	0.947571	0.300009
centrosomal protein 192kDa	1.538862	0.711893	0.782219
mitogen-activated protein kinase kinase kinase 5	1.163844	0.529665	1.763089
F-box protein 40	0.093713		
heterogeneous nuclear ribonucleoprotein A3 pseudogene 2	0.762462	1.017658	0.456411
chromosome 1 open reading frame 77	0.688405	0.738882	2.14085
immunoglobulin-like receptor CHIR2D-956 /// similar to immunoglobulin-like receptor CHIR-nischarin	1.717781	0.712843	0.32589
nuclear receptor binding protein 2		0.596288	2.565632
solute carrier family 6 (neurotransmitter transporter, glycine), member 5			0.091729
solute carrier family 6 (neurotransmitter transporter, glycine), member 5			0.385706
phospholipase A2, group V	2.426593	1.140067	0.983316
parvin, beta			2.433476
Rho GTPase activating protein 8	2.135645	0.848276	0.967167
TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1		1.087213	0.125701
microfibrillar associated protein 5	0.832856	1.237421	2.832558
hypothetical protein LOC772329	1.177483	1.295632	2.001735
phosphatidylinositol glycan anchor biosynthesis, class T			0.093387
similar to mKIAA0746 protein	1.197082	0.887228	0.299807
cell division cycle 37 homolog (S. cerevisiae)-like 1	0.889025	0.924578	0.404642
stabilin 1	0.973043		0.592904
splicing factor, arginine/serine-rich 7, 35kDa	1.355952	0.746915	0.302631
hypothetical LOC426599	2.069514	1.693956	1.013025
vacuolar protein sorting 16 homolog (S. cerevisiae)	0.809289	1.108475	2.577333
cell division cycle associated 3	0.566753	1.213587	0.337014
cell division cycle associated 3	0.708622	1.077743	0.312273
coiled-coil and C2 domain containing 2A	1.537954	1.00641	0.448768
atrophin 1	1.383144	0.532776	0.234316
patatin-like phospholipase domain containing 2		2.18291	
membrane bound O-acyltransferase domain containing 5	0.496784	1.763747	0.360273
zinc finger, ZZ-type with EF-hand domain 1		0.19984	
leiomodrin 3 (fetal) /// similar to leiomodrin 3 (fetal)	21.17951		
complement component 1, r subcomponent	3.17746	1.410197	1.821374
endoplasmic reticulum aminopeptidase 1	0.598975	1.64392	2.332404
fibrillin 2		4.105241	
proline-rich coiled-coil 1	1.375754	0.705545	0.333672
mesoderm induction early response 1, family member 3	0.016585		
GABA(A) receptors associated protein like 3	0.666922	0.959144	0.652214
transient receptor potential cation channel, subfamily V, member 6			

erythrocyte membrane protein band 4.1-like 3			
erbb2 interacting protein	1.015228	0.75795	2.10178
erbb2 interacting protein	0.497318	1.138526	0.620117
amyloid beta (A4) precursor protein-binding, family A, member 2 (X11)	0.998639		0.063
splicing factor, arginine/serine-rich 12	0.614325	0.871582	1.942829
complement component 7		3.953335	23.11609
chromosome 6 open reading frame 60	0.698109	0.720602	1.165661
discoidin, CUB and LCCL domain containing 1	0.56229	0.571224	0.158581
ectodermal-neural cortex (with BTB-like domain)		1.369641	1.924742
establishment of cohesion 1 homolog 1 (S. cerevisiae)	2.048894	0.916956	1.212367
ankyrin repeat domain 31	0.820624		1.183888
dermatan sulfate epimerase	1.116869	1.370361	0.386724
collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia)			7.155311
lon peptidase 2, peroxisomal			
laminin, alpha 4	2.850268	1.756321	1.970232
CD274 molecule	2.323935	2.159913	1.348117
REV3-like, catalytic subunit of DNA polymerase zeta (yeast	1.069683	0.80565	0.284002
ankyrin repeat domain 29	0.049164	1.422014	
KIAA1919		0.95105	0.616282
hypothetical LOC418339			0.414057
hypothetical LOC427229	1.490443	0.798135	0.527637
hypothetical LOC418339	0.743617	0.779833	0.064162
ADAMTS-like 1			1.354781
similar to histamine H3 receptor H3S	1.097268	3.065474	3.825509
zinc finger protein 521		2.25287	
hypothetical LOC418360	0.678147	1.585655	0.312679
zinc finger, AN1-type domain 5	0.427293	1.336928	1.291882
similar to aminopeptidase P	2.092518		
syntrophin, gamma 1	1.535374	10.98682	0.639783
transcription termination factor, RNA polymerase II	0.652046	0.955397	0.386511
histidine acid phosphatase domain containing 1	0.318316	1.009164	0.630485
histidine acid phosphatase domain containing 1	0.716308	1.010837	1.839469
filamin A interacting protein 1-like	2.57741	0.959002	1.919134
sestrin 1	1.838307	1.16887	0.441341
forkhead box O3	0.653812	0.426605	0.573375
ring finger protein 38	0.867606	0.765896	1.108285
polycomb group ring finger 3	0.812655	0.987277	2.865435
ATG16 autophagy related 16-like 1 (S. cerevisiae)	2.18577	0.751789	0.393442
ADP-ribosylation factor-like 13B	1.085039	0.575063	0.452005
syntaxin 19		0.080002	

syntaxin 19	28.11374		
Eph receptor A6	0.988824		1.669959
neutral sphingomyelinase (N-SMase) activation associated f	1.110564	0.868345	0.483983
chromosome 1 open reading frame 32	0.63156	1.106081	2.64864
chromodomain helicase DNA binding protein 7	1.269377	2.712852	
chromosome 5 open reading frame 4	0.524574		0.261486
PDZ domain containing 1		1.665765	0.366173
glucan (1,4-alpha-), branching enzyme 1 (glycogen branchin	0.790068	0.982625	0.901024
ectonucleoside triphosphate diphosphohydrolase 4	1.199131	0.986459	0.462917
ectonucleoside triphosphate diphosphohydrolase 4	4.189041	0.903246	0.40931
janus kinase and microtubule interacting protein 1			3.573425
similar to brefeldin A-inhibited guanine nucleotide-exchange	1.434802	0.766547	0.433585
SH3 domain and tetratricopeptide repeats 1	0.109095	0.445746	
solute carrier organic anion transporter family, member 5A1	1.722563	0.328384	
hypothetical protein LOC768383	0.459533	0.849259	1.050152
mitogen-activated protein kinase kinase kinase 7	1.804715	0.97125	0.450633
nuclear receptor coactivator 2	1.441295	0.560649	2.601664
X-ray repair complementing defective repair in Chinese ham	0.250956	2.050443	0.525666
X-ray repair complementing defective repair in Chinese ham	0.46163	1.008042	0.780031
regulator of G-protein signalling 12	0.761021	1.689458	1.269794
hypothetical LOC420181	0.823453	0.221808	
BCL6 co-repressor-like 1		2.619896	
BCL6 co-repressor-like 1		0.455673	
KIAA0368	1.562468	1.262789	7.750818
Wolf-Hirschhorn syndrome candidate 1	0.753414	0.709665	1.578022
ankyrin repeat domain 6	2.669922		0.035247
Ras-related GTP binding D	1.309586	0.936746	0.736594
chromosome 17 open reading frame 59	1.01699	1.643371	1.628866
sorting nexin 16			0.311249
T-cell lymphoma invasion and metastasis 1		0.695575	0.600536
WW domain containing E3 ubiquitin protein ligase 1	2.695723	1.039411	0.73273
filamin A interacting protein 1	0.443317	2.72946	1.617307
solute carrier family 7 (cationic amino acid transporter, y+ system), mer		0.369469	0.662212
chromosome 21 open reading frame 66	1.393758	0.946762	0.413542
asparaginase like 1			30.50434
opioid growth factor receptor-like 1	0.812434	1.007426	1.542177
KIAA1429	0.595715	0.897336	0.587695
transmembrane protein 50B	0.810464	0.941674	0.174204
FAST kinase domains 5		2.477942	0.077077
Alstrom syndrome 1	0.920833	0.940017	0.544387

ring finger protein 19A	0.478321	1.728999	0.929085
holocarboxylase synthetase (biotin-(propionyl-Coenzyme A	7.389826	0.302733	
Kruppel-like factor 10	0.764678	0.786176	2.189841
bromodomain and WD repeat domain containing 1	2.025298	1.304317	1.099576
regulating synaptic membrane exocytosis 2			47.35082
Alstrom syndrome 1	0.738645	1.070791	0.592771
similar to chronic myelogenous leukemia tumor antigen 66 /	1.051903	2.096232	0.390944
phosphorylase kinase, beta	17.28131		
phosphorylase kinase, beta	2.034308	0.706487	0.487006
CUB and Sushi multiple domains 3	2.256824	0.874415	
SAP30-like	0.808843	0.898454	0.741383
PR domain containing 15	1.329323	0.924395	0.563169
PR domain containing 15		1.934538	0.104737
protein tyrosine phosphatase type IVA, member 3	0.749514	0.564944	0.270583
protein tyrosine phosphatase type IVA, member 3	0.639463	0.662869	0.214452
chromosome X open reading frame 36	1.714008	0.884569	0.434401
lysine (K)-specific demethylase 6A	0.826498	0.86615	0.876113
FUN14 domain containing 1	0.74314	1.27334	0.452762
EF-hand domain (C-terminal) containing 2	1.040499	36.30155	0.570117
monoamine oxidase A	0.968826	2.348321	1.146005
monoamine oxidase A	3.072835		2.137364
BCL6 co-repressor	1.577462	1.036231	0.374004
EFR3 homolog A (S. cerevisiae)	1.467562	0.82517	0.298799
mitogen-activated protein kinase kinase kinase 7 interacting	1.731785	0.982002	0.805798
polymerase (DNA directed), alpha 1	0.912479	0.655497	0.372653
glutamate-cysteine ligase, catalytic subunit			0.431533
ELOVL family member 5, elongation of long chain fatty ac	1.809553	1.473425	0.277306
phosphate cytidylyltransferase 1, choline, beta			0.997371
microcephaly, primary autosomal recessive 1	1.314652	0.826982	0.465608
zinc fingers and homeoboxes 1		0.161116	
kinase D-interacting substrate, 220kDa	0.874322		
MAP7 domain containing 2			0.075833
MAP7 domain containing 2			0.246573
structural maintenance of chromosomes 6	1.134177		
apolipoprotein B (including Ag(x) antigen)		2.463934	
PHD finger protein 12	1.028905	1.098355	0.752479
dystrobrevin, beta	0.664105	0.936807	1.001451
epoxide hydrolase 2, cytoplasmic	0.388032	1.177697	4.052452
similar to ADAMTS-like 2			23.07459
frizzled homolog 3 (Drosophila)	0.498733	0.87847	1.083657

kinesin family member 13B	0.547713	0.519378	1.402846
methionine sulfoxide reductase A	0.691262	1.191697	0.449097
XK, Kell blood group complex subunit-related family, meml	2.141621	0.944655	1.573263
PHD finger protein 16	0.918316	0.875039	1.229361
cytoplasmic FMR1 interacting protein 1	0.954166	0.80917	1.388164
hect domain and RLD 2	0.211527		0.718031
lysozyme G-like 2	5.198005	3.637154	7.371249
eukaryotic translation initiation factor 5B	0.97421	1.13983	0.410706
mitogen-activated protein kinase kinase kinase 4	1.551382	2.039041	0.968235
septin 10	1.750314	0.681992	0.676439
regulator of G-protein signaling 9	0.692017	3.250614	2.557593
RAS p21 protein activator 3	1.317149	0.949407	0.241681
myosin XVI	0.817597	0.040545	0.819127
myosin XVI	0.547994	0.464689	
transmembrane and tetratricopeptide repeat containing 4	0.796835	1.214753	0.308389
dedicator of cytokinesis 9	4.102089	0.894805	0.716454
MICAL-like 2	3.080575	2.871413	
muscleblind-like 2 (Drosophila)		1.136215	2.119984
DAZ interacting protein 1	3.768897	1.053578	0.915942
SLIT and NTRK-like family, member 1	2.514289		1.698164
RNA binding motif protein 26	0.507437	1.151233	0.508767
RNA binding motif protein 26	1.79684	0.89785	0.468338
RNA binding motif protein 26	1.718151	0.912192	0.552638
chromosome 13 open reading frame 7	1.609678	0.819185	0.494481
COMM domain containing 6	0.248619	1.183562	0.685967
tet oncogene 1	0.962783	0.749931	0.324165
DIS3 mitotic control homolog (S. cerevisiae)	1.21849	1.11566	0.782579
olfactomedin 4		5.708705	
component of oligomeric golgi complex 3	1.562717	0.653097	1.166136
zinc finger CCCH-type containing 13	1.257457	0.947517	0.493107
leucine-rich repeats and calponin homology (CH) domain containing 1			
leucine-rich repeats and calponin homology (CH) domain co	0.687347		0.905026
leucine-rich repeats and calponin homology (CH) domain co	0.889453	1.103481	2.020322
potassium channel regulator	1.34596	0.228563	
dehydrogenase/reductase (SDR family) member 12		23.42153	1.452012
doublecortin-like kinase 1	2.544515	0.863591	0.058139
PAN3 polyA specific ribonuclease subunit homolog (S. cere	0.963242	1.40661	0.193036
similar to CG10964-PA /// hypothetical LOC427532	0.296509	1.032701	0.620596
tumor necrosis factor receptor superfamily, member 19			2.025633
thrombospondin, type I, domain containing 4	1.156898		

hypothetical protein LOC771527	1.665941	0.689911	0.398259
hypothetical LOC418990	0.186264		
family with sequence similarity 76, member B		1.4159	
dihydrouridine synthase 3-like (<i>S. cerevisiae</i>)	1.225303	0.452164	2.100358
pannexin 1	1.764158	1.710728	2.202463
RAB30, member RAS oncogene family	0.77441	2.415492	0.541009
PCF11, cleavage and polyadenylation factor subunit, homolog	2.044409	0.774751	0.823399
transmembrane and coiled-coil domains 4	0.940288	2.292353	
transmembrane and coiled-coil domains 4	10.72226		0.123446
asparaginyl-tRNA synthetase 2, mitochondrial (putative)			0.461284
von Willebrand factor	1.818873	1.245266	2.662308
growth arrest and DNA-damage-inducible, beta	1.252198	1.82627	3.391804
cut-like homeobox 1	1.342458	0.716051	0.368946
solute carrier organic anion transporter family, member 2B1	0.03117	0.74827	1.143587
KIAA0280	0.466438	1.066083	2.767708
speedy homolog A (<i>Xenopus laevis</i>)	0.05096		
thioredoxin-like 4A		1.276052	
TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0.396254	2.021899	
hypothetical LOC426599	0.4524	1.115844	3.188509
zinc finger, DHHC-type containing 13		0.555839	1.628956
deoxyribonuclease I /// similar to deoxyribonuclease I	0.171773		
hypothetical LOC426179	0.868294	1.117915	0.226433
coactosin-like 1 (<i>Dictyostelium</i>)	0.681066	1.160226	0.414238
PRP3 pre-mRNA processing factor 3 homolog (<i>S. cerevisiae</i>)	0.635265	3.24079	
hypothetical LOC426125	0.628303	0.822672	0.494741
VAMP (vesicle-associated membrane protein)-associated protein	0.591264	1.395783	0.162554
scribbled homolog (<i>Drosophila</i>)			0.053426
phosphoribosyl pyrophosphate synthetase-associated protein	0.473851	2.292296	
vitellogenin 2		0.08644	
chromosome 9 open reading frame 72	0.711037		
hypothetical LOC419425	1.173674	2.778845	0.412258
netrin G1	0.279223	3.609023	1.476822
scaffold attachment factor B2	2.762105	0.780162	1.355692
ATP-binding cassette, sub-family A (ABC1), member 3	1.120762	1.231047	2.077833
similar to HBV pX associated protein 8 large /// remodeling	1.136068	0.712145	0.446355
similar to HBV pX associated protein 8 large /// remodeling	0.865795	0.912462	1.413811
chromosome 19 open reading frame 22	1.237631	0.79577	6.661934
LIM and senescent cell antigen-like domains 2	0.407649	0.482255	1.354831
G protein-coupled receptor 17	0.177394		
catechol-O-methyltransferase	0.67836	0.915566	0.26802

S-adenosylhomocysteine hydrolase	0.3972	1.222478	0.340601
slingshot homolog 2 (Drosophila)	0.743101		1.1502
similar to Family with sequence similarity 35, member A	2.342474	0.815233	0.453787
DENN/MADD domain containing 2C	0.911147	1.514666	2.226945
WD repeat domain 33	0.806566	0.783796	0.34477
calcium/calmodulin-dependent protein kinase IV	0.099767		
DiGeorge syndrome critical region gene 8	1.258014	1.012632	0.461448
dedicator of cytokinesis 2	0.825559	1.148011	1.364336
N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		0.99262	1.12236
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0.664633	1.498141	2.94574
kinesin family member 14	0.975883	0.827199	0.536883
kelch-like 6 (Drosophila)		0.346899	
kelch-like 6 (Drosophila)	0.949191	0.712911	0.29111
DnaJ (Hsp40) homolog, subfamily A, member 2	1.629151	0.290136	
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin			0.331093
CCR4-NOT transcription complex, subunit 1	0.832788	1.168118	0.309695
YEATS domain containing 2		0.531454	
claspin homolog (Xenopus laevis)	0.035405	0.966871	1.521945
ORM1-like 1 (S. cerevisiae) /// solute carrier family 40 (iron	0.709238	2.807224	0.875352
avidin related protein 2 /// hypothetical LOC427416	0.625272	1.334802	5.613064
SIL1 homolog, endoplasmic reticulum chaperone (S. cerevis	1.287035	1.155876	2.028104
solute carrier family 2 (facilitated glucose/fructose transporter), member		1.881368	0.987274
glutaredoxin 2	0.77009	0.832629	0.291003
splicing factor, arginine/serine-rich 8 (suppressor-of-white-a	1.016009	0.67257	0.218809
splicing factor, arginine/serine-rich 8 (suppressor-of-white-a	1.081212	0.33959	0.233419
collagen, type V, alpha 2	0.73589	1.155726	0.476643
collagen, type III, alpha 1	0.936449	1.398521	0.409584
GULP, engulfment adaptor PTB domain containing 1	1.791021	1.229053	2.498
RAB guanine nucleotide exchange factor (GEF) 1	1.382625	0.576646	0.663062
similar to LOC495387 protein	2.455431		0.393332
hypothetical LOC419703 /// salt-inducible kinase 2	1.651806	0.487836	
piwi-like 1 (Drosophila)		1.888635	4.824338
ubiquitination factor E4B (UFD2 homolog, yeast)	1.415959	0.723984	0.881001
neurofilament, light polypeptide 68kDa	0.814142	0.819664	0.150958
strawberry notch homolog 2 (Drosophila)	0.585999	2.941242	1.180638
strawberry notch homolog 2 (Drosophila)	0.865324	1.792471	1.673844
strawberry notch homolog 2 (Drosophila)			
similar to KIAA1990 protein	0.559797	1.326963	2.260733
hypothetical LOC415345	2.62855	0.681323	1.242329
casein kinase 1, delta	0.694909	0.988909	0.995319

aquaporin 5	0.448124	2.130307	
A kinase (PRKA) anchor protein 7 /// hypothetical protein LOC768867			
cysteinyl leukotriene receptor 1			0.437881
neighbor of BRCA1 gene 1			
small nuclear ribonucleoprotein polypeptide C	0.56964	1.377206	0.464539
fatty acid 2-hydroxylase	0.981841	4.181992	
ubiquitin specific peptidase 52			
mediator complex subunit 23	1.768206	0.992693	0.695213
microtubule-associated protein 2	3.096533		
Rho family GTPase 2	0.824959	0.363383	
serine/threonine kinase 10		4.214102	1.106984
vesicle amine transport protein 1 homolog (T. californica)	0.42423	1.477138	0.600002
peroxisomal biogenesis factor 14	0.204878	0.65043	1.100499
similar to KIAA1629 protein	0.397334	1.317849	
zinc finger protein 532			12.72172
alveolar soft part sarcoma chromosome region, candidate 1	0.881613	1.098714	0.363179
C-type lectin domain family 2, member B /// C-type lectin domain famil		0.308804	
C-type lectin domain family 2, member B /// C-type lectin domain famil		0.380999	
hypothetical LOC426235 /// hypothetical protein LOC77200	3.222875	1.16316	0.779085
hypothetical LOC426235	4.152623		
DEAH (Asp-Glu-Ala-His) box polypeptide 37	1.079295	1.292535	2.098144
serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithel		1.546492	0.182692
potassium channel, subfamily K, member 15			0.247248
carbonic anhydrase X	0.934185	0.746358	0.382397
WD repeat domain 7	0.23855		
solute carrier family 19, member 3	4.045511		
myosin IE			2.620047
DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	0.828303	1.240058	0.371304
solute carrier family 37 (glycerol-3-phosphate transporter), member 2		0.490476	0.552327
exosome component 10	1.124612	1.175885	3.055175
nuclear receptor co-repressor 2		0.754876	0.426944
nuclear receptor co-repressor 2	14.05246		
tripartite motif-containing 25	2.040152		
tripartite motif-containing 25	3.726135	2.202701	0.393964
tripartite motif-containing 25	1.209337		0.386306
BCL2-antagonist/killer 1	1.135433	1.459798	1.704098
nuclear transcription factor Y, gamma		0.529267	0.788667
similar to zinc finger RNA binding protein	11.65475	1.125213	0.073618
zinc finger RNA binding protein	3.005828	2.498426	0.302883
similar to zinc finger RNA binding protein	64.22788	2.938374	0.012159

protocadherin 24	0.956678		2.807768
similar to HBxAg transactivated protein 2	1.280133	1.320289	0.264073
similar to HBxAg transactivated protein 2 /// similar to HBxAg transacti		1.28683	0.468472
CREB regulated transcription coactivator 1	2.910193	1.427861	2.266803
CREB regulated transcription coactivator 1			22.41623
CREB regulated transcription coactivator 1	1.310297	1.11887	6.223299
leucine-zipper-like transcription regulator 1	2.288777	0.666724	0.714343
ER lipid raft associated 1	1.035148	1.243195	0.938707
ATX1 antioxidant protein 1 homolog (yeast)	0.38563	0.938259	0.600397
K(lysine) acetyltransferase 2A	2.877101	1.26997	2.519675
DnaJ (Hsp40) homolog, subfamily C, member 21			3.054953
strawberry notch homolog 1 (Drosophila)	1.811459	1.492247	0.483741
DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 /// simila	0.483952	1.059081	1.211365
importin 9	1.528099	1.363156	0.355243
similar to pepsinogen C	0.531691	0.907055	0.463452
minichromosome maintenance complex component 10	1.166104	1.589401	1.214784
lysyl oxidase-like 2	0.706533	0.867748	0.543794
kelch-like 5 (Drosophila)			0.079996
aldehyde dehydrogenase 9 family, member A1	2.083396	1.368846	0.881964
microtubule associated serine/threonine kinase 3	3.174249	1.061686	3.081102
platelet/endothelial cell adhesion molecule (CD31 antigen)	0.951504	1.016506	0.312972
platelet/endothelial cell adhesion molecule /// platelet/endoth	2.269534	0.879135	0.674462
arrestin domain containing 2			2.648997
solute carrier family 12 (potassium/chloride transporters), m	1.249344	0.837139	0.204182
solute carrier family 12 (potassium/chloride transporters), m	0.898615	1.104192	0.301534
solute carrier family 1 (glial high affinity glutamate transport	1.148581	0.941316	
transformation/transcription domain-associated protein	0.989064	0.902508	0.703738
RPGRIP1-like	2.199993	0.948963	0.857593
transcription termination factor, RNA polymerase I	0.620192	1.405735	0.472363
MYST histone acetyltransferase (monocytic leukemia) 3	1.568154	0.978983	0.556514
retinoblastoma-like 2 (p130)	1.163967	1.333474	0.250831
phosphatidylinositol transfer protein, cytoplasmic 1	0.717693	0.679026	0.836957
lysine (K)-specific demethylase 5B			0.368447
ring finger protein 145	1.169178	1.097415	0.446723
microtubule-actin crosslinking factor 1	1.526637	0.35056	
helicase with zinc finger	2.15803	0.87148	0.453628
SRY (sex determining region Y)-box 30			
F-box protein 42	0.483755		
TOX high mobility group box family member 3	3.737701	0.710058	1.187544
melanoregulin		2.344863	

BCL2/adenovirus E1B 19kDa interacting protein 2	1.667193	0.808211	0.497466
OTU domain containing 7A	1.476669	1.102135	2.154037
keratin 15	0.524797	1.413714	0.462878
tRNA isopentenyltransferase 1	1.07282	0.779693	0.542432
intraflagellar transport 81 homolog (Chlamydomonas)	0.523369	5.413198	
purinergic receptor P2X, ligand-gated ion channel, 7	7.019653	0.880146	1.557137
serine incorporator 3	1.212774	1.328492	0.257288
zinc finger protein 423			2.310378
xenotropic and polytropic retrovirus receptor	0.591733	1.18491	0.900499
PR domain containing 12			
oculocerebrorenal syndrome of Lowe	0.793065	0.536244	0.799918
immunoglobulin-like receptor CHIR-B3 /// similar to immun	1.934899		0.705281
myopalladin	1.418522		1.219425
heterogeneous nuclear ribonucleoprotein H3 (2H9)	0.976267	0.963338	0.322106
tight junction protein 1 (zona occludens 1)	1.177297	1.225622	0.499557
coiled-coil domain containing 46	6.480273		
twinfilin, actin-binding protein, homolog 2 (Drosophila) /// V	0.784195	0.995184	0.926024
NIMA (never in mitosis gene a)- related kinase 8	0.404657		
MAD1 mitotic arrest deficient-like 1 (yeast)		0.941353	0.287938
RUN and FYVE domain containing 2	0.61285	0.790821	0.048147
RUN and FYVE domain containing 2	0.496596	1.402756	0.036056
lysophospholipase II pseudogene 1		0.512923	0.691357
jumonji domain containing 2B	1.446348	0.742905	0.736567
family with sequence similarity 81, member A		0.761138	2.13168
F-box and leucine-rich repeat protein 10	1.364472	0.806641	0.437598
F-box and leucine-rich repeat protein 10	1.40722	0.755803	0.239499
cell division cycle and apoptosis regulator 1	1.361873	0.829767	0.442656
glucosidase, alpha; acid (Pompe disease, glycogen storage di	1.042158	0.991136	2.163836
family with sequence similarity 20, member A		0.690598	2.913172
UDP glucuronosyltransferase 1 family, polypeptide A1 /// U	1.531946	2.431532	2.853778
similar to 26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subu			
hexokinase domain containing 1	0.743858	1.384666	2.081896
vacuolar protein sorting 13 homolog D (S. cerevisiae)	0.930839	0.787952	0.497717
similar to LOC495387 protein	3.103987		
cingulin-like 1	40.47752		
ATP-binding cassette, sub-family A (ABC1), member 5	0.779599	0.409309	
chromosome 7 open reading frame 27	1.095623	0.737469	0.638318
WD repeat domain 66	0.429793	0.44163	1.674221
similar to MAP kinase kinase 6b	0.382233	0.828844	0.533587
exportin 1 (CRM1 homolog, yeast)	1.491333	0.955325	0.432754

DnaJ (Hsp40) homolog, subfamily B, member 12	1.266818	0.93862	1.191164
sperm antigen with calponin homology and coiled-coil domain	0.965868	1.060505	2.237453
solute carrier family 39 (metal ion transporter), member 11	0.095992	1.746634	1.422363
Similar to olfactory receptor MOR172-4		7.037157	
SHC SH2-domain binding protein 1	0.528294	1.165696	0.405451
sema domain, immunoglobulin domain (Ig), short basic domain	0.460989		
sema domain, immunoglobulin domain (Ig), short basic domain	1.085706	3.92701	
ephrin-B1	0.994112	1.146385	0.14828
kinetochore associated 1	1.123528	0.830785	0.855886
serine/threonine kinase 38	0.938911	2.676246	0.6701
protein tyrosine phosphatase, receptor type, f polypeptide (P ^r)	0.991779	0.830969	0.415012
selenophosphate synthetase 1		1.340534	
leucine rich repeat containing 8 family, member A			
FancA associated protein of 100 kDa /// nuclear protein local	1.728635	0.689342	
RNA binding motif protein 5	1.77563	0.704587	0.369261
solute carrier family 45, member 1	0.83725	0.707666	1.616656
hypothetical LOC423006		0.537776	0.425801
ataxin 2	1.87584	0.56586	0.545965
ataxin 2	0.781381	0.840196	0.458007
ataxin 2		0.921375	0.456183
RNA binding motif protein 5	1.129409	0.780696	0.484258
ring finger protein 216	4.557001		
patched domain containing 2	0.560662	0.979696	0.526276
ADP-ribosylation factor guanine nucleotide-exchange factor	0.628503	0.81815	
ADP-ribosylation factor guanine nucleotide-exchange factor	2.071493		0.710236
zinc finger, DHHC-type containing 12	1.068857	0.82713	0.393051
A kinase (PRKA) anchor protein 10	0.734665	1.511317	0.448407
coiled-coil domain containing 21			
solute carrier family 7 (cationic amino acid transporter, y ⁺ symporter)	1.27941	2.638824	
obscurin, cytoskeletal calmodulin and titin-interacting RhoGAP	0.51961	1.082101	2.079206
immunoglobulin-like receptor CHIR-AB3 /// similar to immunoglobulin-like receptor	2.294402		4.091546
zinc finger, NFX1-type containing 1	2.314154	2.536104	4.645526
RAS, dexamethasone-induced 1	2.156833	1.6907	2.525768
solute carrier family 10 (sodium/bile acid cotransporter family)	2.142312		
solute carrier family 6 (neurotransmitter transporter, GABA)	0.531315	3.640933	0.589774
solute carrier family 6 (neurotransmitter transporter, GABA)	1.4956	0.549302	2.299498
glycine receptor, alpha 4	0.507055	1.240429	0.375153
vestigial like 4 (Drosophila)	4.151865		
chromosome 3 open reading frame 31	1.459293	1.191536	0.486168
KIAA0355	1.446825	1.022935	0.353583

TIMP metalloproteinase inhibitor 4		0.872609	
discs, large homolog 5 (Drosophila)	1.379734	1.598745	1.111987
similar to Cat eye syndrome chromosome region, candidate 5	2.293934	0.859164	1.219068
dedicator of cytokinesis 10	0.374599	0.776845	0.558066
deformed epidermal autoregulatory factor 1 (Drosophila)	1.382059	0.75828	0.407183
NIPA-like domain containing 3		1.209885	0.0696
centrosomal protein 152kDa	1.094384	1.018369	0.346387
translocated promoter region (to activated MET oncogene)	0.903961	0.87349	0.496511
carboxylesterase 1 (monocyte/macrophage serine esterase 1)	1.691767	2.748619	3.72252
hypothetical LOC416899	1.207543	1.224158	2.012114
carbohydrate (chondroitin 4) sulfotransferase 12	0.489336	0.854926	1.009672
carbohydrate (chondroitin 4) sulfotransferase 12	0.603926	0.773853	0.181249
secretogranin II (chromogranin C)	1.486373	0.822186	2.080172
collagen, type XI, alpha 1	1.071807	0.788681	1.948672
CD72 molecule		0.722647	1.368364
glutathione S-transferase theta 1	0.644786	0.896137	0.184641
ubiquitin specific peptidase 54	4.420108	1.360803	0.435195
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.346209	1.006494	0.744334
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	1.537063	0.40878	
G protein-coupled receptor 88	0.311174		2.051942
acid phosphatase-like 2	1.388741	0.643741	0.45848
BRCA1 interacting protein C-terminal helicase 1		0.403952	0.684498
DCP1 decapping enzyme homolog A (S. cerevisiae)	0.710791	0.950439	0.586695
zinc finger protein 232	0.762222	0.875492	0.631722
polymerase (RNA) I polypeptide E, 53kDa	0.509084	0.928932	2.146062
amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen)	1.082581	0.686091	0.717579
PDZ and LIM domain 1 (elfin)	1.153564	1.240442	1.437924
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine 4-epimerase)	2.268137	0.724639	0.655816
FRAS1 related extracellular matrix 1	0.998789	0.544462	2.566707
chromosome 3 open reading frame 63	1.369163	0.74474	0.646426
TAF1 RNA polymerase II, TATA box binding protein (TBP)	0.971606	0.768591	0.583269
TAF1 RNA polymerase II, TATA box binding protein (TBP)	1.829472	0.694968	0.615995
similar to Malonyl-CoA decarboxylase, mitochondrial precursor (MCD)		2.747203	
similar to Malonyl-CoA decarboxylase, mitochondrial precursor	1.229979	1.337241	0.666085
myelin protein zero-like 1	1.078372	2.237754	1.614962
kinesin family member 9	8.711238		
kinesin family member 9	30.80197		3.677739
Treacher Collins-Franceschetti syndrome 1	0.63313	0.964576	1.83454
hypothetical LOC424832	0.719068	1.051102	0.070104
hypothetical LOC424832	1.633122	0.506088	0.171958

similar to KIAA0703 protein	0.316354		
growth factor, augments liver regeneration (ERV1 homolog)	0.77061	0.644288	0.568423
collagen, type XIII, alpha 1	0.946717		6.966872
collagen, type XIII, alpha 1	13.18968		
Rho GTPase activating protein 29	2.510908	0.911763	0.709019
kinase suppressor of ras 1	1.999819	2.130266	5.110702
kinase suppressor of ras 1	1.22479	2.335093	6.882602
kinase suppressor of ras 1		1.654535	1.972192
zinc finger, DHHC-type containing 7	1.070065	0.872786	0.491597
colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms)			0.062978
solute carrier family 7 (cationic amino acid transporter, y+ system)	5.050246	1.397771	0.73221
switch-associated protein 70			
hypothetical LOC416916	0.977687	0.658022	0.277857
ADP-ribosylation factor GTPase activating protein 1	0.716275	0.649354	0.273721
zinc finger protein 143	1.503331	1.190936	0.480584
discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	0.898509	1.526402	0.431066
transient receptor potential cation channel, subfamily M, member 1	1.352135	0.930989	0.400877
KIAA0664	0.515213	1.41369	2.12213
TBC1 domain family, member 9B (with GRAM domain)	1.411202	1.039906	0.062421
Ets2 repressor factor	1.670693	0.981644	
leucine-rich repeats and calponin homology (CH) domain containing 1	1.178356	0.644905	4.133235
leucine-rich repeats and calponin homology (CH) domain containing 1	1.387634	0.408623	0.55743
leucine-rich repeats and calponin homology (CH) domain containing 1	0.439014	0.836166	4.167286
leucine-rich repeats and calponin homology (CH) domain containing 1	0.878165	0.286686	0.815398
leucine-rich repeats and calponin homology (CH) domain containing 2		0.255363	
WSC domain containing 1	0.404992	1.246007	0.259514
signal peptide, CUB domain, EGF-like 2			
signal peptide, CUB domain, EGF-like 2		3.151799	
AN1, ubiquitin-like, homolog (Xenopus laevis)	1.685441	0.852463	0.534831
sequestosome 1	0.832817	0.655242	2.059346
sequestosome 1	1.990658	2.550945	
myosin ID	1.076562	0.998236	0.782567
suppression of tumorigenicity 5	2.020142	0.886072	0.405164
mastermind-like 1 (Drosophila)	1.288118	1.490884	0.31392
solute carrier family 5 (sodium/glucose cotransporter), member 1	0.769317	0.861746	3.158948
ecotropic viral integration site 5	1.676276	0.552476	1.069981
ecotropic viral integration site 5	1.686539		0.294817
similar to tumor endothelial marker 8	1.594926	4.531445	4.533059
phosphatidylserine synthase 2	0.280775	1.665454	0.264696
similar to RUFY1 /// RUN and FYVE domain containing 1	0.976785	1.099054	0.76991

solute carrier family 13 (sodium-dependent citrate transporte	14.42176	5.702733	
ADAM metallopeptidase with thrombospondin type 1 motif,	0.491477		
PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae	0.609364	0.896475	0.084129
similar to dedicator of cytokinesis 11	0.934128	0.588145	0.133827
abhydrolase domain containing 7	0.628816	0.907131	0.02191
abhydrolase domain containing 7	0.558886	0.63198	0.028842
retinoblastoma binding protein 6	0.750652	0.868251	1.93736
zinc finger and BTB domain containing 46	1.506403	0.650917	0.400263
trinucleotide repeat containing 6A	2.170084	1.026445	1.336412
pleckstrin homology domain containing, family A member 7		3.422979	
zinc finger protein 644	0.877047	1.091881	0.406237
similar to Aryl Hydrocarbon Receptor 2			3.253082
phosphoinositide-3-kinase, class 2, alpha polypeptide	0.846768	1.029795	0.634035
transmembrane protein 32	0.978134	2.025438	1.261793
myosin light chain kinase 3			
LIM domain and actin binding 1	1.464544	1.779081	1.066805
leucine rich repeat containing 8 family, member C	1.184067	1.136727	2.444317
solute carrier family 9 (sodium/hydrogen exchanger), member 6			0.410167
thioredoxin reductase 3	0.926677	1.069709	0.759546
FAT tumor suppressor homolog 2 (Drosophila)	0.338579		
kelch-like 12 (Drosophila)	0.440318	0.510105	0.92047
RAS protein activator like 2		1.419707	
RAS protein activator like 2	0.801862	0.17792	1.393308
ATP-binding cassette, sub-family A (ABC1), member 8	0.257912	1.009355	
ATP-binding cassette, sub-family A (ABC1), member 5	0.451004	0.698234	12.73428
endoplasmic reticulum metallopeptidase 1	1.023584	0.421213	1.538053
myosin light chain kinase 3	0.862084	0.304355	0.767186
inositol polyphosphate phosphatase-like 1		1.210354	2.247599
WD repeat domain 41	0.489757	1.099307	0.872541
coiled-coil domain containing 109A	3.18772	0.954472	0.269615
hypothetical LOC428824	1.089503	0.432784	1.219423
cell cycle progression 1	1.205061	1.321346	0.381598
wingless-type MMTV integration site family, member 11b			0.511376
leucine zipper protein 2			
chick olfactory receptor 4			1.420057
RAB27A, member RAS oncogene family	0.920292	0.858047	0.072814
arylsulfatase B	0.677596	1.593679	2.003995
astrotactin 1	0.269413		
pleckstrin homology domain containing, family F (with FYV	0.069237		
zinc finger, CCHC domain containing 8	2.292345	0.744777	0.468926

coiled-coil domain containing 137	1.299937	1.304429	1.251459
betaine-homocysteine methyltransferase	0.923747	0.760119	2.570336
RNA binding motif protein 22	0.961112	0.822164	1.011315
tectonic family member 1	1.219887	0.689208	0.708984
trinucleotide repeat containing 18	0.480007	0.488276	
KIAA1370	1.020662	0.854608	0.286663
KIAA1370	1.257748	0.724402	0.352508
phytanoyl-CoA dioxygenase domain containing 1	0.375202	1.460145	
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1		0.501025	0.061649
nuclear protein localization 4 homolog (S. cerevisiae)		0.840418	0.349402
trinucleotide repeat containing 18	0.352936	0.574069	
5,10-methylenetetrahydrofolate reductase (NADPH)	0.742386	1.63655	0.416124
5,10-methylenetetrahydrofolate reductase (NADPH)			0.19491
hypothetical LOC428696	1.197177	0.764465	1.081467
similar to cHz-cadherin	0.146191		
similar to cHz-cadherin		3.103778	
similar to myosin 5c; myosin Vc /// myosin VC	1.511029	1.017232	
nicotinamide nucleotide adenyltransferase 2	0.580448		2.71746
DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	1.093023	0.497084	1.107581
F-box protein 2		1.041567	0.058741
transient receptor potential cation channel, subfamily V, member 3			
similar to LOC398026 protein	2.662359		
aspartoacylase (Canavan disease)			1.861193
glycerophosphodiester phosphodiesterase domain containing	0.436723		
isovaleryl Coenzyme A dehydrogenase	1.152407	1.30928	0.752709
notchless homolog 1 (Drosophila)	1.695929		2.137698
WD repeat domain 34	1.250645	1.048764	2.385634
potassium inwardly-rectifying channel, subfamily J, member	0.459673	0.641895	0.551123
solute carrier family 7, (neutral amino acid transporter, y+ sy	0.143934	0.639454	0.033747
secretogranin III	0.520852	1.584562	0.476514
similar to voltage-gated potassium channel KV11.1 transcrip	0.379151	0.611245	0.964875
complement component 1, q subcomponent, B chain	3.248248	1.788189	4.307354
solute carrier family 47, member 1	0.297308		2.091339
solute carrier family 47, member 2		2.088053	
Dmx-like 2 /// similar to rabconnectin		1.517126	
phospholipase C, beta 2	1.442967	1.00015	
phospholipase C, beta 2	1.405872	0.975352	0.86845
phospholipase C, beta 2	1.651773	1.91098	2.122703
chromosome 12 open reading frame 51		0.309034	
phosphorylase kinase, alpha 1 (muscle)	2.05403	0.788573	1.025996

TRAF-type zinc finger domain containing 1	3.368181	1.023592	
chromosome 10 open reading frame 56	0.863307	0.807038	0.456155
erythrocyte membrane protein band 4.2			13.99565
hypothetical protein LOC771136 /// transglutaminase 3 (E polypeptide, .	0.114799		0.078063
hypothetical protein LOC771136			15.49335
ATPase, Ca ⁺⁺ transporting, plasma membrane 2	0.358627		0.757128
Sema domain, transmembrane domain (TM), and cytoplasmic	1.366447	0.898273	2.291115
phosphatase and actin regulator 3	1.187831	3.003984	1.956656
solute carrier family 6 (neurotransmitter transporter, GABA), member 11			
synaptonemal complex protein 2	0.517917		0.19858
G-2 and S-phase expressed 1	0.542908	1.529715	0.499491
similar to TBP-associated factor	1.215856	0.709356	0.316237
similar to TBP-associated factor	0.747776	1.230594	0.777943
ATG7 autophagy related 7 homolog (S. cerevisiae)		0.427927	
ATG7 autophagy related 7 homolog (S. cerevisiae)	2.330303	2.981335	0.465371
LSM14A, SCD6 homolog A (S. cerevisiae)	4.415528	0.56683	0.828828
LSM14A, SCD6 homolog A (S. cerevisiae)	1.588275	0.681247	0.43083
insulin receptor substrate 1	1.029494		
similar to KIAA1486 protein			0.33963
tRNA splicing endonuclease 2 homolog (S. cerevisiae)	0.784812	1.279537	0.590142
chromosome 10 open reading frame 11	2.073068	1.25986	1.085767
peptidyl arginine deiminase, type II	1.003429		1.254066
catechol-O-methyltransferase domain containing 1	0.809359	0.846638	2.338606
SHC (Src homology 2 domain containing) family, member 4	2.549623	0.81536	0.177102
SHC (Src homology 2 domain containing) family, member 4	1.492184	0.448509	0.256052
SHC (Src homology 2 domain containing) family, member 4	1.416286	0.42691	0.283754
hypothetical LOC415973			2.631491
DEAH (Asp-Glu-Ala-His) box polypeptide 30	0.883065	1.038272	1.687012
similar to UPF0101 protein CGI-137 (Protein AD-004)	0.742425	0.781054	0.836539
MYST histone acetyltransferase (monocytic leukemia) 4	3.652427	1.343345	0.37634
testis expressed 14		0.444608	0.064466
Fanconi anemia, complementation group A		2.352982	
chromosome 1 open reading frame 27	1.441255	0.995216	1.063826
chromosome 1 open reading frame 27	1.614273	0.937318	0.59138
dopamine receptor D4	0.562384		
chromosome 1 open reading frame 26	0.42753	1.118611	0.649402
family with sequence similarity 124B		2.215129	0.861479
fibulin 2	0.720933	1.584875	0.274876
TAF4 RNA polymerase II, TATA box binding protein (TBP	1.40525	0.952166	0.419265
hypothetical LOC416899 /// hypothetical protein LOC768372		0.838063	

KIAA0913		0.337069	1.34659
similar to KIAA0595 protein		0.104648	
PHD finger protein 2	1.178356	0.707161	0.216382
PHD finger protein 2	1.006048	0.584759	0.321744
GTP binding protein 5 (putative)	0.660087	0.861509	0.641418
similar to GTPase, IMAP family member 7	0.320247	0.893034	1.733279
similar to GTPase, IMAP family member 7	0.363129	0.939182	1.323637
KIAA0423	0.596317	0.95748	
kelch-like 12 (Drosophila)		16.17075	0.683587
similar to mKIAA0746 protein	0.946695	0.926615	0.363918
synaptopodin 2-like	0.491422		
WNK lysine deficient protein kinase 2	3.194813	0.51636	0.277924
WNK lysine deficient protein kinase 2	1.994309	0.353096	0.454963
WNK lysine deficient protein kinase 2	1.723105	0.341989	0.123407
monoacylglycerol O-acyltransferase 1		0.778977	5.902982
adenylate cyclase activating polypeptide 1 (pituitary) receptc	0.871145	4.519436	1.466497
UBX domain containing 5	0.66185	0.755876	0.245637
adenylate cyclase activating polypeptide 1 (pituitary) receptc	0.564721	1.098815	4.307844
ubiquitin specific peptidase 54		2.835677	0.596534
exostoses (multiple)-like 2		0.1682	
growth-hormone releasing hormone-like peptide receptor	0.73278	0.141609	
growth-hormone releasing hormone-like peptide receptor	0.253853		0.200276
bicaudal D homolog 2 (Drosophila)	0.816405	1.021083	0.027713
spermatogenesis associated 2-like			0.051047
similar to SYT9 protein		6.257423	17.44529
hypothetical LOC424816	0.970936	0.998968	0.64056
olfactomedin-like 1			3.587683
lipase maturation factor 1	0.480774	1.170322	0.684292
solute carrier family 25, member 36	0.822537	1.407417	0.187273
T-box 2 /// T-box 4	0.304265	8.224118	0.529658
zinc finger and BTB domain containing 47		0.363385	
kelch repeat and BTB (POZ) domain containing 5		3.15968	
kelch repeat and BTB (POZ) domain containing 5	1.013975	0.827959	0.27564
kelch repeat and BTB (POZ) domain containing 5			0.244574
PTPRF interacting protein, binding protein 2 (liprin beta 2)	2.529941	1.020555	0.797406
spire homolog 2 (Drosophila)			2.090484
carbonic anhydrase VII		3.656593	
ovochoyase 2		0.187234	1.000851
chromosome 20 open reading frame 151		30.92738	
seryl-tRNA synthetase	0.679793	1.070692	1.928373

ubiquitin specific peptidase 32	1.074009	0.756232	1.286817
fatty acyl CoA reductase 1	0.488239		0.559935
sorbin and SH3 domain containing 1		3.547469	
sorbin and SH3 domain containing 1			1.910623
similar to lysophosphatidic acid receptor		2.208671	0.073605
tumor necrosis factor receptor superfamily, member 9	1.158833	0.628921	0.660543
tumor necrosis factor receptor superfamily, member 9	1.274562	1.018753	0.275995
similar to Ran-binding protein 2 /// similar to RanBP2 (Ran-binding pro		3.235959	1.181565
mitochondrial rRNA methyltransferase 1 homolog (S. cerevi	0.934082	0.920442	2.223109
COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)		17.03376	
apoptosis antagonizing transcription factor		5.200778	0.132729
FRAS1 related extracellular matrix 1	0.391172	1.102593	
FRAS1 related extracellular matrix 1		1.30925	
zinc finger, DHHC-type containing 21	0.360735	0.903699	1.779497
coiled-coil domain containing 66	0.914749	1.229934	1.666079
hydroxysteroid (17-beta) dehydrogenase 2		0.303199	
AP1 gamma subunit binding protein 1	0.469704	1.130953	1.674988
parathyroid hormone 1 receptor	5.803699	2.108162	2.740852
Rho guanine nucleotide exchange factor (GEF) 3	1.574268	1.038185	0.59826
hypothetical protein LOC769642			
similar to voltage-gated sodium channel type IV alpha subun	0.7984		
phosphoinositide-3-kinase, catalytic, beta polypeptide	0.759308	2.837742	0.10115
adaptor protein, phosphotyrosine interaction, PH domain and	0.972627	1.136511	1.958349
myosin XVIIIIB	1.27149		2.332171
integral membrane protein 2C	1.055594	0.699402	0.173773
G protein-coupled receptor 55	0.782383	1.227056	0.223288
G protein-coupled receptor 35		0.102406	
G protein-coupled receptor 35	3.736485	0.608998	0.15329
period homolog 3 (Drosophila)			4.534376
period homolog 3 (Drosophila)	3.120841	0.887343	0.679697
transducin (beta)-like 3	0.9689	1.460325	2.130645
neurofibromin 1	2.016468	0.732175	1.559857
Hermansky-Pudlak syndrome 4		1.508938	2.644766
dynein heavy chain domain 2	2.412892	0.991291	0.669595
opioid growth factor receptor	2.074239	1.573638	2.946644
solute carrier family 44, member 3	1.372199		2.050556
coagulation factor III (thromboplastin, tissue factor)	4.311979	2.162928	3.530741
transient receptor potential cation channel, subfamily M, mei	1.062806		0.744443
myosin IG			
tuberous sclerosis 2			

hypothetical LOC422211			2.257869
hypothetical LOC428402		1.616475	0.58856
hypothetical LOC428402	1.388583	7.354839	0.183501
similar to OTTHUMP00000028696		4.736291	
cysteine-rich secretory protein LCCL domain containing 2	0.497709	0.866515	0.67681
tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.46528	1.676027	1.520223
sulfide quinone reductase-like (yeast)	0.92841	1.237857	0.386872
sulfide quinone reductase-like (yeast)	1.062379	1.070722	0.593764
cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo)	2.320024	0.852635	1.51372
small G protein signaling modulator 2	0.743262	2.596652	
hypothetical LOC428705	0.587144		
similar to MGC82394 protein	0.579852	2.078597	2.442371
baculoviral IAP repeat-containing 7 (livin)			2.968814
polycystic kidney disease 2-like 1		7.162791	
HMG box domain containing 3	3.113907	0.508235	1.295402
junctophilin 3	1.051993	0.985722	2.477543
ATP-binding cassette, sub-family G (WHITE), member 2	0.672483	2.158604	2.165752
ATP-binding cassette, sub-family G (WHITE), member 2	0.825761	2.172598	0.825648
arachidonate 5-lipoxygenase	3.479931		
WD repeat domain 40A	0.354315	1.49284	0.629152
hypothetical LOC427400	0.350133	0.690808	0.374006
hypothetical protein LOC772338	0.804785	2.0651	
potassium voltage-gated channel, KQT-like subfamily, member 2			
SRY (sex determining region Y)-box 13	0.549207	2.390148	
src-related kinase lacking C-terminal regulatory tyrosine and	0.220183	0.520591	
src-related kinase lacking C-terminal regulatory tyrosine and N-terminal		1.080357	0.422047
hexosaminidase (glycosyl hydrolase family 20, catalytic dom	0.658884	1.363664	1.243245
eukaryotic elongation factor, selenocysteine-tRNA-specific	0.776191		0.256749
family with sequence similarity 69, member A	1.229971	1.09396	0.475731
pancreatic polypeptide receptor 1	2.770532		6.010033
histidine decarboxylase			0.157809
dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0.566306	1.303589	0.461771
Sec61 alpha 1 subunit (S. cerevisiae)	0.785722	0.876866	1.073946
leucine carboxyl methyltransferase 1	1.268545	1.174731	0.672137
BTB (POZ) domain containing 8	0.751661	1.140684	0.723674
BTB (POZ) domain containing 8	1.665939	0.838762	0.48085
protein tyrosine phosphatase, non-receptor type 7	1.558877		1.369613
growth differentiation factor 10	2.225514	0.814751	0.720008
ankyrin repeat and BTB (POZ) domain containing 1	0.76202	0.978186	0.376163
WAS protein homology region 2 domain containing 1	2.158546	1.042495	1.654504

pecanex homolog (Drosophila)	1.647088	1.013789	0.204172
BTB (POZ) domain containing 8	1.235596	0.91704	0.706405
sterile alpha motif domain containing 10	3.149559		
homer homolog 2 (Drosophila)	0.4422	0.752203	
similar to dedicator of cytokinesis 11	0.824334	0.083135	0.339014
AXIN1 up-regulated 1	1.050261	0.849793	0.154558
PITPNM family member 3	1.886679	2.231915	4.988335
cell division cycle 7 homolog (S. cerevisiae)	1.663817	1.034652	0.56149
membrane-associated ring finger (C3HC4) 2	0.871597	1.03745	0.429077
zinc finger and BTB domain containing 46		0.492252	0.624113
tektin 1	0.496419	0.868348	0.770891
partner and localizer of BRCA2	0.838096	1.457673	2.250845
glypican 3	1.204681	3.454945	13.06277
zinc finger CCCH-type containing 18	0.369156	1.227521	0.426066
plexin A1	1.113092	0.490658	0.758519
endonuclease G-like 1	0.695492	1.307515	0.425453
heterogeneous nuclear ribonucleoprotein A0	1.327114	1.177259	0.151231
Ras homolog enriched in brain	1.349394	1.108832	0.305559
otogelin	0.851776		
acyl-CoA synthetase family member 3			2.026536
MAP7 domain containing 3	2.238932	0.634927	0.765114
Kruppel-like factor 15	4.79698		1.628987
piggyBac transposable element derived 3	0.696053		
MAP7 domain containing 3	0.793791	0.746506	1.346819
espin-like	1.920573	0.828404	2.04396
galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, muco		1.062922	0.659622
jumonji domain containing 5		1.100771	0.705919
similar to Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)			0.174678
G protein-coupled receptor 112		4.137325	
interleukin 4 receptor		5.526638	0.155915
dipeptidyl-peptidase 6			11.70656
interleukin 21 receptor	3.161778	1.613979	4.573983
chloride channel, calcium activated, family member 2	1.722984	1.978831	0.203845
similar to calcium-activated chloride channel		4.334696	14.41544
family with sequence similarity 38, member A	0.468659		
PAX interacting (with transcription-activation domain) prote	1.02969	0.948076	0.470877
ankyrin repeat domain 47	0.785293	0.796979	1.290036
potassium channel tetramerisation domain containing 5	0.889388	1.108492	0.362196
solute carrier family 6 (neurotransmitter transporter, taurine)	2.03066	0.834641	0.463438
p21 (CDKN1A)-activated kinase 2		0.66846	0.351341

ADP-ribosyltransferase 1 /// GPI-anchored ADP-ribosyltrans	17.8758	9.941776	3.950572
ADP-ribosyltransferase 1			16.78286
ADP-ribosyltransferase 1	10.00701	4.741426	2.10108
aryl-hydrocarbon receptor nuclear translocator 2	2.281846	1.018512	0.413108
chromosome 16 open reading frame 45	0.233723	1.142596	
chromosome 16 open reading frame 45		2.58814	0.681618
potassium voltage-gated channel, KQT-like subfamily, mem	0.107006		
PHD finger protein 13	2.004295	0.905406	1.118107
tubulin tyrosine ligase-like family, member 9	1.755735	0.805504	5.166606
tubulin tyrosine ligase-like family, member 9	1.678435	0.46072	2.968992
XK, Kell blood group complex subunit-related family, meml	0.687616	0.853244	0.868451
plexin A4, B	0.620999	1.009876	2.117933
KIAA0430	0.020243		
5-hydroxytryptamine (serotonin) receptor 7 (adenylate cycla	1.081477	2.438446	0.201427
similar to Transmembrane 9 superfamily protein member 2 p	0.607853	1.208351	0.486078
protein tyrosine phosphatase, receptor type, N polypeptide 2		2.012525	
zinc finger, AN1-type domain 6		0.214963	
human immunodeficiency virus type I enhancer binding prot	4.919955	0.860681	0.819968
family with sequence similarity 62 (C2 domain containing) r	0.834199	0.256132	0.604947
cirrhosis, autosomal recessive 1A (cirhin)	1.622807	0.995908	3.021261
ubiquitin associated and SH3 domain containing, B	0.758669		1.002029
kinesin family member 3B		0.437654	0.894086
similar to cytosolic nucleotidase I	1.436029	1.023235	0.400039
component of oligomeric golgi complex 8	0.925364	0.969521	1.614987
ATPase, class VI, type 11C		0.223905	
XK, Kell blood group complex subunit-related, X-linked	1.120498	1.404298	1.080891
glutamate receptor, ionotropic, kainate 4	0.389623		
adenosine A2a receptor	1.031867	1.059079	0.800232
lipase, member H	2.357244		1.067366
ATP-binding cassette, sub-family C (CFTR/MRP), member	1.781061	0.782204	0.424632
Rho guanine nucleotide exchange factor (GEF) 12	0.940137	1.141981	0.769982
BR serine/threonine kinase 2		0.487243	
transcriptional adaptor 3 (NGG1 homolog, yeast)-like	0.771379	0.723728	1.348914
RAB36, member RAS oncogene family	0.79754	0.602469	1.779679
POU class 2 homeobox 3			0.071599
tripartite motif-containing 29		1.464189	1.744179
outer mitochondrial membrane cytochrome b5			
xylosyltransferase I	1.888335	0.851315	3.143647
xylosyltransferase I	1.12803	0.691334	0.372006
exocyst complex component 6	0.471177	1.496354	0.94706

melanoma cell adhesion molecule	1.75502	1.32847	
KIN, antigenic determinant of recA protein homolog (mouse	0.587415	0.50099	2.445843
PDZ domain containing 3	0.677536		
Regulation of nuclear pre-mRNA domain containing 1B	0.946627	0.960058	0.27209
ATP-binding cassette, sub-family G (WHITE), member 4	0.90021		1.26453
sushi-repeat-containing protein, X-linked 2			0.36005
kelch-like 25 (Drosophila)	0.884138	2.374445	0.085682
similar to iron binding protein	0.886485		0.484698
hypothetical protein LOC771371	1.286704		
solute carrier organic anion transporter family, member 3A1	1.15988	0.77735	0.432548
hypothetical LOC415505	0.863162	1.136713	1.240254
transmembrane channel-like 7	0.884968	1.7173	0.354579
similar to GalNAc alpha 2,6-sialyltransferase	1.582519		4.114184
BAI1-associated protein 2	0.624238	0.899938	1.101935
minichromosome maintenance complex component 10	0.755959	2.416636	0.543545
similar to KIAA0419	0.399602	0.973973	0.535911
claudin 22	0.763632	0.539937	2.029738
phosphofructokinase, platelet	1.446906	0.827294	0.112094
dual specificity phosphatase 11 (RNA/RNP complex 1-intera	2.385062	0.829228	0.987465
dual specificity phosphatase 11 (RNA/RNP complex 1-intera	0.770511	1.934286	0.346945
hypothetical LOC423820	1.035601	0.974207	3.053236
von Willebrand factor A domain containing 3A			
similar to furosemide-sensitive K-Cl cotransporter	0.378672		1.132515
similar to NAD(P) dependent steroid dehydrogenase-like			0.131352
ubiquitin specific peptidase 28	1.403772	1.131891	0.374305
multiple C2 domains, transmembrane 2	1.067496	1.195567	5.10507
toll-like receptor 4	2.052783		
ring finger protein 213	3.614724		13.83462
arrestin domain containing 4	0.455114	0.451113	1.169442
hypothetical LOC427509	0.680049	0.241363	0.520826
hypothetical protein LOC771298	1.630094	0.952089	0.375824
similar to putative endoplasmic reticulum protein family member, with ε		0.492995	
similar to acid alpha glucosidase	1.043792	1.630571	1.269435
similar to gamma-aminobutyric acid (GABA) A receptor, pi			0.184721
leucine rich repeat containing 28	0.955635	1.022688	0.20038
ATPase type 13A3	1.40738	1.256579	0.406349
ATPase type 13A3	1.460869	0.652029	0.474748
KIAA0152	0.874009	1.099599	0.514521
lines homolog 1 (Drosophila)	2.232427	0.881489	0.745654
ring finger protein 207		0.661618	2.790097

par-3 partitioning defective 3 homolog (C. elegans)		1.161194	1.373203
AF4/FMR2 family, member 4	0.904325	1.144814	0.479259
AF4/FMR2 family, member 4	0.921841	1.289449	0.507474
acyl-Coenzyme A oxidase 2, branched chain	0.950972	0.428036	0.22082
acyl-Coenzyme A oxidase 2, branched chain	0.775366	0.546913	0.474895
C-type lectin domain family 16, member A	0.780099	0.738034	0.490892
similar to leucine-rich repeat kinase 2	0.706493	0.812805	0.465318
phosphatidylglycerophosphate synthase 1	1.189812	0.908467	0.682234
phosphatidylglycerophosphate synthase 1	1.016459	0.275077	
enhancer of polycomb homolog 1 (Drosophila)	2.805057	1.412268	0.737913
ATPase type 13A4	0.164345		
RAB3A interacting protein (rabin3)-like 1	1.231288	0.468489	0.43565
kinesin family member 5B	2.03773	1.134622	0.504694
musashi homolog 1 (Drosophila)			1.3813
proprotein convertase subtilisin/kexin type 6	0.55121		0.42437
similar to PH domain containing protein	1.364891	1.3309	1.429738
Rho GTPase activating protein 12	1.452696	1.266158	1.057898
zinc finger protein 438	1.67471	0.779826	0.379985
hypothetical LOC416638	0.490036	3.041626	
similar to Down syndrome cell adhesion molecule DSCAML1			
hypothetical protein LOC771141	0.055017		
LIM domain containing preferred translocation partner in lip	0.474441	1.075855	1.534348
hypothetical LOC427511			
LIM domain containing preferred translocation partner in lipoma		1.092341	3.493564
mediator of RNA polymerase II transcription, subunit 19 hor	0.673663	1.344051	1.131245
similar to alpha 1 type XXIV collagen	0.373656	0.037734	
RAS-like, family 12		34.07162	0.093831
hypothetical LOC422293	0.795176	1.143964	0.401188
similar to S6 kinase 2	0.713206	0.254912	
syntaxin 12	1.71007	0.705377	0.360597
suppressor of defective silencing 3 homolog (S. cerevisiae)	1.287741		
ATP-binding cassette, sub-family C (CFTR/MRP), member 2		11.80554	
chromosome 20 open reading frame 174	1.346799	1.681456	1.02464
membrane associated guanylate kinase, WW and PDZ doma	0.334946	2.107364	0.372088
hypothetical protein LOC771647		7.439543	0.604442
slingshot homolog 1 (Drosophila)		1.513673	2.783848
slingshot homolog 1 (Drosophila)			2.34166
selectin E (endothelial adhesion molecule 1)	24.7431		
hypothetical LOC420485		2.464282	
similar to neuropeptide /// similar to TAF4 RNA polymerase II, TATA b		0.078116	

transmembrane protein 8 (five membrane-spanning domains)	0.331577	0.875814	1.002954
similar to P1-A			0.198963
similar to P1-A	0.756874	2.47981	0.035908
cyclin M1		0.384573	
leucyl-tRNA synthetase	2.554748	0.976479	1.954327
leucyl-tRNA synthetase	1.301622	1.197572	0.499442
microtubule associated serine/threonine kinase-like		4.443906	0.568541
integrin alpha FG-GAP repeat containing 3	0.831791	1.032653	0.070384
DENN/MADD domain containing 4A	0.61307	4.587178	1.306325
zinc finger, FYVE domain containing 27	1.120344	0.74929	0.70433
ankyrin repeat domain 2 (stretch responsive muscle)	1.985623	0.756652	0.127838
similar to RIKEN cDNA 4931428F04 gene /// hypothetical I	0.65131	0.696915	1.484162
similar to BTB/POZ domain-containing protein KCTD16	0.625542	0.751916	0.378393
similar to putative selenoprotein O	0.292818		
kelch repeat and BTB (POZ) domain containing 8	1.294172	1.020468	2.295124
myotubularin related protein 8	1.677279	0.181126	
N-acetyltransferase 15 (GCN5-related, putative)	1.516157	0.969984	1.49429
Cdc42 guanine nucleotide exchange factor (GEF) 9	1.293725	1.001097	1.748209
slit homolog 1 (Drosophila)	0.723654	0.41826	1.615999
calcium channel, voltage-dependent, T type, alpha 1G subun	0.839239	5.496658	
chromosome 20 open reading frame 86		0.270838	
multiple EGF-like-domains 11			
myosin IIIA	0.515129	1.234243	0.067655
TIMELESS interacting protein	1.000646	0.92218	0.39059
chromosome 10 open reading frame 63	0.593494	0.366971	2.77898
myosin IB	0.64086	1.237707	
neuromedin U receptor 1	1.339427	1.009871	
hypothetical LOC427595	0.755483		2.753497
proline dehydrogenase (oxidase) 1	1.038342	0.662098	1.75956
similar to WAS protein family, member 3			1.078555
hypothetical LOC416090			0.407374
transmembrane protein 104	0.021094	0.786153	0.843929
pleckstrin homology-like domain, family B, member 1	1.622107	0.708785	3.307913
F-box protein 3	0.830795	0.970791	0.372215
KIAA1217			15.13056
DIS3 mitotic control homolog (S. cerevisiae)-like 2		0.847307	0.847326
forkhead box P1	0.961387	1.568929	1.390369
fatty acid desaturase domain family, member 6		1.772806	0.497587
cerebellin 4 precursor			
eukaryotic translation initiation factor 4E family member 3	3.257957	0.962597	0.384112

SHQ1 homolog (<i>S. cerevisiae</i>)	1.411938	0.946085	0.396719
zinc finger, DHHC-type containing 15		0.434591	1.204516
hypothetical LOC415641 /// similar to rat GCP360	1.088557	2.029891	0.531882
hypothetical LOC415641 /// similar to rat GCP360	0.871766	3.777949	0.259291
Potassium voltage-gated channel, shaker-related subfamily, 1	1.958998	0.378442	1.075111
alkaline phosphatase, intestinal	1.165521	0.842614	0.653539
beta-transducin repeat containing	0.724555	2.097548	
hypothetical LOC417007	0.967245	1.16371	2.684795
beta-carotene dioxygenase 2			6.77709
Similar to TJP3 protein	1.580191	1.179218	2.689491
endothelin converting enzyme-like 1			18.57505
similar to neuropathy target esterase	0.974368	0.439423	1.316674
peptidase domain containing associated with muscle regeneration 1		1.981509	0.159373
low density lipoprotein receptor class A domain containing 3	0.922055	1.361773	0.140671
low density lipoprotein receptor class A domain containing 3	1.070401	1.347149	0.017049
cholinergic receptor, nicotinic, delta	1.64306	0.421297	1.117304
laminin, beta 1	1.283943	0.906465	0.538029
cholinergic receptor, nicotinic, gamma		2.096359	50.50664
calpain 5	1.377127	0.819787	
IQ motif containing H	1.301031	1.448897	2.48175
TNF receptor-associated factor 6	1.031612	0.958964	0.508177
TNF receptor-associated factor 6	1.843053	1.021498	0.59656
recombination activating gene 1	0.602948	0.738621	0.069896
recombination activating gene 1	0.969228	0.806269	0.092181
recombination activating gene 2	0.895548	0.909411	0.006622
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2			
solute carrier family 26, member 3	0.476905		
chromosome 10 open reading frame 112	2.232567	1.541726	
similar to GPI inositol-deacylase PGAP1		8.350884	
exostoses (multiple) 2	0.545729	1.510905	0.719424
chromosome 20 open reading frame 175	2.100797	0.609924	0.827654
leukemia inhibitory factor (cholinergic differentiation factor)	1.050454	0.646443	1.465215
component of oligomeric golgi complex 5	0.952935	0.888363	0.358795
cellular repressor of E1A-stimulated genes 2	5.134453	3.9804	
component of oligomeric golgi complex 5	12.92375		0.69581
coronin, actin binding protein, 2B	1.300336	0.462543	
p21 (CDKN1A)-activated kinase 3		1.960615	2.646444
astacin-like metallo-endopeptidase (M12 family)	0.475638		3.516369
kinesin family member 23	1.325923	1.034293	0.759287
eyes absent homolog 3 (<i>Drosophila</i>)	1.503456	1.287988	0.353917

coiled-coil domain containing 88A	0.969248	1.346105	0.393382
coiled-coil domain containing 88A	0.796397	0.68547	0.319095
coiled-coil domain containing 88A	1.264557	0.93028	0.492763
ataxin 7-like 1	2.247859	0.55566	0.310486
myosin, heavy chain 13, skeletal muscle			20.5194
chromosome 10 open reading frame 112	0.181433		
shugoshin-like 2 (S. pombe)	0.822571	0.377103	0.943967
F-box protein, helicase, 18	0.966636	0.869771	0.698627
toll-like receptor 15	2.875911	0.710201	1.797109
hypothetical LOC424943			
5'-nucleotidase, cytosolic II	1.939611	1.758948	0.351961
phosphatidylinositol-4-phosphate 5-kinase, type I, gamma		1.227377	0.196506
hyaluronoglucosaminidase 1			3.720752
acid phosphatase 2, lysosomal	0.876126	0.872588	0.415693
CASP8 and FADD-like apoptosis regulator	2.947637	2.031154	0.875779
CASP8 and FADD-like apoptosis regulator	0.224891	0.968012	1.133869
Cell division cycle associated 8	3.801046	0.755747	0.468205
interleukin 5 receptor, alpha	0.420944	0.809388	0.952656
family with sequence similarity 26, member B	1.115389	1.670965	0.20965
family with sequence similarity 26, member A		0.452969	
hypothetical LOC416107		0.910388	
leucine-rich repeats and calponin homology (CH) domain co	0.46181	0.885962	0.275361
inositol 1,4,5-triphosphate receptor, type 1	1.031251	3.087388	1.170763
oligonucleotide/oligosaccharide-binding fold containing 1	2.273579	0.734546	0.539758
oligonucleotide/oligosaccharide-binding fold containing 1	2.780617	1.34572	0.423051
caspase 10, apoptosis-related cysteine peptidase	4.192648		0.960417
fibrinogen-like 2	0.896211	0.570078	0.467524
calpain 10	0.894323	0.664516	0.489331
calpain 10	0.808647	0.774905	0.317697
pigeon homolog (Drosophila)	2.425124	1.265917	0.571368
similar to synaptotagmin-like protein 2-a delta 2S-II	1.234755		0.062361
round spermatid basic protein 1-like	1.415225	0.70367	0.202445
feline sarcoma oncogene	0.879083		5.261864
initiator caspase	0.657823		0.180515
LIM and cysteine-rich domains 1	0.747955		2.034514
similar to synaptotagmin-like protein 2-a delta 2S-II	0.774976	0.61684	0.228407
chromosome 10 open reading frame 78	1.187232	0.823738	0.388452
histidine acid phosphatase domain containing 2A		1.300125	
chromosome 20 open reading frame 74	0.595565	0.958195	
von Hippel-Lindau tumor suppressor	0.885355	0.830802	0.024181

hypothetical protein	3.498598	1.283561	0.56626
interleukin-1 receptor-associated kinase 2	1.49213	0.747617	0.718374
KIAA1754	1.333481	6.525229	0.645745
dishevelled, dsh homolog 3 (Drosophila)		0.182805	
PFTAIRE protein kinase 2	0.643691	1.110775	0.492253
carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0.865758	0.51431	0.149039
DEAH (Asp-Glu-Ala-His) box polypeptide 8	0.391635	1.107893	0.568215
DEAH (Asp-Glu-Ala-His) box polypeptide 8		0.26092	
cyclin-dependent kinase 3		13.94269	
plexin D1		0.146473	
amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8			31.68498
guanylate cyclase 2F, retinal	0.162312		
pleckstrin homology domain containing, family M, member	0.843633	0.392588	
vacuolar protein sorting 18 homolog (S. cerevisiae)	1.223199	0.888321	0.186515
Kruppel-like factor 7 (ubiquitous)	1.103531	0.714896	0.066724
asparagine-linked glycosylation 3 homolog (S. cerevisiae, alj	0.936529	0.51129	4.26359
carboxypeptidase O	2.14912	1.677715	0.952311
similar to glutamine synthetase	1.686009	1.307426	2.220846
eukaryotic translation initiation factor 4 gamma, 1		1.237486	2.266787
bromodomain containing 1		0.621242	0.043703
bromodomain containing 1	1.067954	1.167239	0.469642
leucine rich repeat containing 32	0.398877		
protein phosphatase 2, regulatory subunit B', delta isoform	0.849919	2.156767	0.578063
malate dehydrogenase 1B, NAD (soluble)	0.65846	0.55937	0.367318
malate dehydrogenase 1B, NAD (soluble)		0.418671	
mal, T-cell differentiation protein	0.854236	1.756508	0.814708
INO80 complex homolog 1 (S. cerevisiae)	1.259696	2.084262	0.83141
survival motor neuron domain containing 1	0.510096	0.831921	1.62319
NOL1/NOP2/Sun domain family, member 6	1.501523	0.755063	0.207529
Opa interacting protein 5	0.846193	1.243581	0.252782
kelch-like 5 (Drosophila)		0.938668	0.408559
ADAM metallopeptidase domain 23	0.465163	0.496048	0.59866
nucleolar and spindle associated protein 1	0.79943	0.952538	0.696911
G protein-coupled receptor 1	0.368926		
similar to glutaryl-Coenzyme A dehydrogenase	0.90741	0.749663	2.456779
similar to glutaryl-Coenzyme A dehydrogenase	1.090222	0.820954	2.293687
Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevi	1.166647		0.241629
hypothetical protein LOC771349			
hypothetical protein LOC771361		7.402308	
zinc finger and BTB domain containing 33	0.796796	1.941842	0.367364

cullin 9		2.283765	
hypothetical protein LOC771422			
MAX gene associated	0.779138	0.484354	2.19974
cytotoxic T-lymphocyte-associated protein 4	4.87602	4.993838	5.654279
RNA binding motif protein 20		4.572618	
selenoprotein O			0.132083
Ras association (RalGDS/AF-6) and pleckstrin homology do	2.050218	0.284736	0.158357
WD repeat domain 63			
TraB domain containing	1.134333	1.761518	3.122713
zinc finger protein 800	0.78365	0.929476	1.139364
mitogen-activated protein kinase 14			0.152871
complement component 1, q subcomponent-like 3			0.403682
JMJD7-PLA2G4B readthrough transcript	3.242935		
patatin-like phospholipase domain containing 7		0.062391	
hypothetical LOC420526	2.3417	1.828238	0.942915
chromosome 2 open reading frame 13	1.257446	0.902029	0.417342
MCF.2 cell line derived transforming sequence-like 2		1.342187	0.731732
lysosomal-associated membrane protein 3	0.620446		0.467322
hypothetical LOC421270			3.048914
glycerol-3-phosphate acyltransferase, mitochondrial	0.471029	2.130521	
Ras association (RalGDS/AF-6) domain family 5	0.488663	0.777683	0.467931
solute carrier family 1 (glutamate/neutral amino acid transpo	0.574523	0.885428	0.49442
isocitrate dehydrogenase 1 (NADP+), soluble	0.593837	1.195998	0.389042
IQ motif and ubiquitin domain containing	0.893529	1.360508	0.806879
similar to urate oxidase (EC 1.7.3.3)		0.051303	
sterile alpha motif domain containing 13	0.617263	0.676958	0.768906
ATPase, H ⁺ transporting, lysosomal accessory protein 1	1.178837	0.92551	0.401496
protein-kinase, interferon-inducible double stranded RNA de	2.03439	0.833698	0.518581
hydroxyacid oxidase (glycolate oxidase) 1			
DnaJ (Hsp40) homolog, subfamily C, member 10	0.79724	1.027693	0.489179
phospholipase C, beta 1 (phosphoinositide-specific)	2.620179	1.41601	1.101031
phospholipase C, beta 1 (phosphoinositide-specific)	0.475257	2.807717	1.403146
vesicle transport through interaction with t-SNAREs homolo	0.95349	0.891818	0.312008
solute carrier family 26, member 8	3.097602	0.83918	0.217714
interleukin 1 receptor accessory protein-like 2	0.268851	0.116031	
interleukin 1 receptor accessory protein-like 2	0.09428	0.164314	0.25655
hypothetical LOC427775			0.348963
synaptotagmin IV	2.828292	1.560037	
leucine rich repeat containing 26	2.334522		
EH domain binding protein 1	0.712177	0.975269	0.283523

phospholipase C, beta 4	0.096868		
GTPase, IMAP family member 1	1.212246	2.519188	0.900758
transmembrane protein 17	1.35052	0.899571	0.228112
peroxisomal biogenesis factor 5-like	0.792223	0.843021	0.401229
rearranged L-myc fusion	0.91612	0.70424	0.447063
spectrin, beta, non-erythrocytic 5		0.096282	
spectrin, beta, non-erythrocytic 5		2.032557	
forkhead box N2	0.442835	0.902156	1.518423
family with sequence similarity 73, member A	0.892731	1.238373	1.112678
exonuclease 3'-5' domain containing 3	0.378872	0.549783	0.549994
similar to tandem pore domain potassium channel THIK-2	0.577058	2.869624	0.368074
phospholipase A2, group IVF	0.80468	0.915878	0.257706
SMAD family member 7	0.481187	0.560959	1.457162
hypothetical protein LOC768788		1.022394	0.024191
guanine nucleotide binding protein (G protein), beta polypep	0.856738	2.058764	1.444972
wingless-type MMTV integration site family, member 16		0.158175	
zinc finger, ZZ-type containing 3	1.559981	1.055516	0.474757
STEAP family member 4	0.680303		
CWC22 spliceosome-associated protein homolog (S. cerevis	0.661838	1.037158	0.318447
phosphatidylinositol glycan anchor biosynthesis, class K	1.05022	1.103935	0.499467
similar to olfactory receptor MOR260-5		7.154695	
TBC1 domain family, member 8B (with GRAM domain)	1.637278	1.392449	0.40235
ankyrin repeat domain 9	1.710065	0.39417	
fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	2.159017		1.335402
lysocardiolipin acyltransferase	0.46633	1.164352	0.647041
actin-like 6A			
calpain 13	3.708238	1.819757	1.549725
calpain 13			2.554661
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosami	1.071521		0.030526
general transcription factor IIA, 1-like	1.283356	0.487832	0.560486
general transcription factor IIA, 1-like	0.851215	0.825936	0.498066
titin			
MARVEL domain containing 3	1.308466	1.069437	0.452337
titin			2.623321
congenital dyserythropoietic anemia, type I	1.619838	0.592941	1.407086
CDC42 binding protein kinase alpha (DMPK-like)	0.252348	0.643558	1.301113
SFRS protein kinase 1	0.86051	0.842167	2.263649
similar to fragile X mental retardation 2	1.182246	0.758181	0.139066
tRNA methyltransferase 6 homolog (S. cerevisiae)	1.564609	0.924249	0.479558
chromosome 10 open reading frame 96			0.119603

similar to Scale keratin (S-ker) (sKer)			2.045472
similar to ankyrin-repeat and fibronectin type III domain con	7.122795		
hypothetical protein LOC770919	0.412456		0.565246
hypothetical LOC426835 /// hypothetical protein LOC77010	0.92035		2.151048
amidohydrolase domain containing 2	3.571161	1.495254	1.684756
pancreatic lipase-related protein 3			0.243127
phospholipase D1, phosphatidylcholine-specific	0.438534		1.065441
similar to RIKEN cDNA 6430537H07 gene	1.397585	1.036773	0.244776
transmembrane protein 62	1.103394	0.734174	0.831952
RNA binding motif protein 46	19.44258	0.868284	
similar to KIAA1617 protein /// Scm-like with four mbt dom	1.873488	0.93578	4.801363
neuropeptide Y receptor Y2			
dynein, axonemal, light chain 1	19.23288		
RNA binding protein S1, serine-rich domain	0.856552	0.916324	0.491816
solute carrier family 18 (vesicular monoamine), member 2	0.828521	0.836234	10.93071
PDZ domain containing 8	2.25552		
numb homolog (Drosophila)			2.178281
nuclear VCP-like		1.905424	0.533683
RNA binding motif protein 25	1.741116	2.182773	0.815799
RNA binding motif protein 25	0.931001	1.210117	2.130058
zinc finger, FYVE domain containing 1	0.890286	0.642951	1.80823
hematological and neurological expressed 1-like			0.159333
hematological and neurological expressed 1-like	0.823365	0.852759	0.314488
wingless-type MMTV integration site family member 2		0.100979	
polyhomeotic homolog 3 (Drosophila)	1.126184	1.170899	1.096444
polyhomeotic homolog 3 (Drosophila)	0.735433	1.306079	1.269841
leucine rich repeat containing 31	1.021907	0.935153	3.011339
G protein-coupled receptor kinase 5			0.10613
SPARC related modular calcium binding 1	0.297978	1.458857	0.198023
BCL2-associated athanogene 3	2.411889	0.636526	0.64775
protein phosphatase 1, regulatory (inhibitor) subunit 3A (gly	0.063926	4.749772	
KIAA1822-like	1.178651	0.620517	0.297005
profilin 3	0.316572	0.998743	
similar to Egfl3 protein			2.082774
similar to RIKEN cDNA C030048B08	1.521345	0.77588	0.560457
phosphatidic acid phosphatase type 2 domain containing 1A	5.953728	0.85301	
cyclin-dependent kinase 6	0.768301	1.712233	0.283348
sterile alpha motif domain containing 9-like	8.571686	2.336709	2.786612
dedicator of cytokinesis 4			
HEPACAM family member 2	1.281053	1.703025	2.020556

chromosome 14 open reading frame 83		0.977544	
arginyltransferase 1	0.972966	0.571527	0.572053
phosphatidylinositol glycan anchor biosynthesis, class H	1.255347	1.118257	0.333821
similar to protein kinase C-theta	1.239455	0.801938	0.597639
dynein, cytoplasmic 1, intermediate chain 2	1.231337	0.83942	0.317923
prickle homolog 1 (Drosophila)		7.26675	0.789133
sparc/osteonectin, cwcv and kazal-like domains proteoglycan	0.559566		0.114415
ADAM metalloproteinase with thrombospondin type 1 motif, 20			0.043312
transmembrane protein 117			
phosphoenolpyruvate carboxykinase	0.817422	1.8535	
myosin IIIB			2.308375
G patch domain containing 2			0.110808
neuregulin 2	2.53598		
hypothetical LOC422427	9.059916	2.891828	10.05838
collagen, type I, alpha 2	0.437284	0.928533	0.831367
CAS1 domain containing 1	0.365142		0.881012
Usher syndrome 2A (autosomal recessive, mild)	0.973189		
Usher syndrome 2A (autosomal recessive, mild)		0.05483	
Usher syndrome 2A (autosomal recessive, mild)	0.941092		3.94172
hypothetical protein LOC771944	1.199035	1.278726	2.133735
AT rich interactive domain 2 (ARID, RFX-like)	1.806672	1.05295	0.37305
squamous cell carcinoma antigen recognized by T cells 3	0.699713	1.000726	0.845179
KIAA0157	1.347019	0.988031	2.210808
Rho GTPase activating protein 11A	1.684027	1.131256	0.5056
RAS guanyl releasing protein 1 (calcium and DAG-regulated)	1.489796	0.937198	2.818056
centromere protein F, 350/400ka (mitotin)	1.222795	0.882434	2.713194
solute carrier family 7, (cationic amino acid transporter, y+ system) member 14		14.90977	
solute carrier family 7, (cationic amino acid transporter, y+ system) member 11			
E74-like factor 2 (ets domain transcription factor)	1.307616	0.745428	0.447475
centromere protein F, 350/400ka (mitotin)	0.402895	0.975559	1.130954
ribosomal protein S6 kinase, 52kDa, polypeptide 1	0.959234	1.590668	0.881609
feline leukemia virus subgroup C cellular receptor 1	0.896835	1.568251	0.366617
NSL1, MIND kinetochore complex component, homolog (S. pombe)	0.847737	1.127998	0.391037
similar to LOC129881 protein	0.67382		
calmegin	0.751821	1.39558	0.250606
similar to UDP-GlcNAc:alpha-1,3-D -mannoside b-1,4-N-Acetylglucosaminyl transferase	1.994322		
TANK-binding kinase 1	0.884848	1.392686	1.326156
FAST kinase domains 1		0.520575	0.638919
glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)			6.059769
hypothetical gene supported by CR406281	0.39397	0.793856	1.759817

similar to Calcium/calmodulin-dependent protein kinase ID /	0.894784	1.217145	0.140703
coiled-coil domain containing 3			0.37581
LEM domain containing 3	1.412217	0.859176	0.678397
SERTA domain containing 4	1.758273	2.167024	2.027157
synaptotagmin XIV	0.472255	1.149337	0.48812
chromosome 1 open reading frame 107	4.687359	1.576415	97.20112
chromosome 1 open reading frame 107	0.714785	0.80981	0.717561
chromosome 1 open reading frame 160	0.467288	0.615555	0.679101
endothelial cell adhesion molecule	0.445846		6.215136
KIAA1333	1.098698	0.74794	0.278398
cylindromatosis (turban tumor syndrome)	0.085996	1.33062	
potassium voltage-gated channel, subfamily G, member 3	0.439772		
hypothetical LOC421394	0.496899	2.055408	
thyroid adenoma associated	1.515878	0.823865	1.489185
thyroid adenoma associated	1.233437	1.454074	0.520897
hypothetical protein LOC772366	0.036775		
ATP-binding cassette, sub-family G (WHITE), member 5 (st	2.227909		0.573996
ATP-binding cassette, sub-family G (WHITE), member 8 (sterolin 2)			2.125992
pannexin 3		0.491634	
nephronophthisis 4	0.894434	1.134559	0.700488
zinc finger protein 827	0.76685	1.264728	0.402396
S1 RNA binding domain 1	1.101785	1.044471	0.24406
S1 RNA binding domain 1	0.511593	2.127723	0.761221
Rho GTPase activating protein 5	1.691117	0.712776	0.434826
KIAA0467		2.005344	
protein kinase C, epsilon	0.882251	0.738897	2.116842
protein kinase C, epsilon	1.032633	0.581204	1.283613
hypothetical LOC423317		0.27759	1.749246
KIAA0467	0.824282	1.454197	0.994937
suppressor of cytokine signaling 5			0.413505
transmembrane protein 34	1.607008	1.532645	0.313806
tetratricopeptide repeat domain 7A	0.648506	1.677099	2.048415
chromosome 1 open reading frame 174	0.827449	0.947378	0.409617
phospholipase B1	0.406728		2.263351
suppressor of Ty 7 (S. cerevisiae)-like	0.322508	0.697882	
DDI1, DNA-damage inducible 1, homolog 2 (S. cerevisiae)		0.17916	
lactoperoxidase	0.471667		
polo-like kinase 3 (Drosophila)	1.057944	1.958454	2.729972
COBW domain containing 1	0.580701	0.961052	0.453084
ring finger protein 8	1.59178	0.949217	0.348642

ankyrin repeat domain 15	0.442986	1.34103	0.933693
doublesex and mab-3 related transcription factor 3			0.044639
inturned planar cell polarity effector homolog (Drosophila)	0.756712	1.006395	0.356511
similar to LOC506727 protein	2.052315	0.891589	3.019366
tudor and KH domain containing	0.790321	0.567234	0.155716
solute carrier family 29 (nucleoside transporters), member 1	1.498772	0.911558	
heat shock 70kDa protein 4-like	1.279482	0.862354	0.497814
heat shock 70kDa protein 4-like	1.085861	1.157604	0.309065
adaptor-related protein complex 3, delta 1 subunit	0.983059	0.450072	0.992011
zinc finger protein 410	1.114261	1.109374	0.57412
similar to Polo-like kinase 4 (Drosophila)	0.770947	0.999859	0.637993
thyrotropin-releasing hormone degrading enzyme	0.043228		0.036006
thyrotropin-releasing hormone degrading enzyme		13.27487	0.092019
chromosome 4 open reading frame 29	5.3817	0.966774	0.826331
La ribonucleoprotein domain family, member 2			
uroporphyrinogen decarboxylase	0.690982	1.079317	1.02152
GLI pathogenesis-related 1 like 2	6.93792		
mitogen-activated protein kinase kinase 4	1.221548	1.313792	0.435933
ATP-binding cassette, sub-family D (ALD), member 4	0.979572	1.288287	0.854247
myeloperoxidase		0.643406	3.125424
zinc finger, DHHC-type containing 17	1.189903	0.927547	0.483136
collagen, type XXVIII, alpha 1		0.772084	0.487294
E2F transcription factor 7	0.336304	1.351291	0.157106
KIAA0317			0.192321
fer-1-like 5 (C. elegans)	0.236448		
CCR4-NOT transcription complex, subunit 6-like	0.675835	0.789919	0.400884
CCR4-NOT transcription complex, subunit 6-like		0.470475	
taste receptor, type 2, member 7	0.723066	1.151206	0.279002
phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	0.814746	1.153885	0.63391
phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	1.201417	1.363848	0.480728
hypothetical protein LOC772154	0.749406		2.827537
DBF4 homolog B (S. cerevisiae)	0.701376	0.252241	0.800556
protein O-linked mannose beta1,2-N-acetylglucosaminyltran	0.338468	1.777598	
muscleblind-like (Drosophila)		0.7636	0.607499
estrogen-related receptor beta	1.011774		
G protein-coupled receptor 171	2.131234	1.480621	0.860589
multimerin 1		0.092052	
KIAA1737			0.145633
ATP-binding cassette, sub-family C (CFTR/MRP), member	1.514411	0.71649	2.734328
golgi autoantigen, golgin subfamily a, 1	1.198821	0.851324	1.486251

hypothetical protein LOC771115	0.26991	0.924175	
protein phosphatase 2, regulatory subunit B, delta isoform	2.438037	0.926624	0.270895
alkB, alkylation repair homolog 1 (E. coli)	2.215878	1.44335	0.644464
PWWP domain containing 2	1.793377	0.347933	
hypothetical protein LOC772154			2.509254
collagen, type XXV, alpha 1		9.650008	
latent transforming growth factor beta binding protein 1	0.623104	0.446656	1.536998
epidermal growth factor receptor pathway substrate 15	0.74291	0.778089	2.622155
Yip1 domain family, member 4	0.691855	1.198281	0.445622
arachidonate lipoxygenase 3 /// similar to Arachidonate lipox	2.424824		
TBC domain-containing protein kinase-like	1.166093	1.296572	0.780269
glutathione S-transferase, C-terminal domain containing	2.677582	2.59758	0.630356
general transcription factor IIA, 1, 19/37kDa		0.665053	1.210594
stonin 2	0.847028	1.809605	2.552223
vitrin		35.42203	
sulfotransferase family, cytosolic, 6B, member 1			2.120866
LRP2 binding protein	2.037525	1.113643	1.192685
protein kinase D3	1.052405	0.912713	0.318422
protein kinase D3	1.804023	1.137152	0.612891
protein tyrosine phosphatase, non-receptor type 21	0.946952	8.095678	0.330316
zinc finger CCCH-type containing 14	1.056445	1.39894	0.489976
zinc finger CCCH-type containing 14	1.258692	1.090469	0.591058
echinoderm microtubule associated protein like 5			
storkhead box 2	1.062228	0.661485	2.165301
mannosidase, alpha, class 1C, member 1	0.942107	0.739511	0.418462
CDKN2A interacting protein /// similar to MGC68690 protei	1.618183	0.785742	0.383028
tetratricopeptide repeat domain 8	1.039365	2.338129	1.41831
forkhead box N3	0.84075	0.787568	
similar to hypothetical protein MGC33370			0.032866
zinc finger protein 238	2.27784	1.093391	0.718587
transmembrane protein 106B	1.145775	1.116155	0.423515
transmembrane protein 16H	0.27134	0.048977	1.781115
centrosomal protein 170kDa	0.610408	1.074896	0.691829
SMEK homolog 1, suppressor of mek1 (Dictyostelium)	0.810669	1.012574	1.207431
exonuclease 1	1.005624	1.681026	1.201649
WD repeat domain 64	2.583916		
WD repeat domain 64	0.507819	8.118555	0.721954
thyroid hormone receptor interactor 11	1.429357	0.790374	0.488423
F-box protein 8	0.920464	0.86618	0.472753
phosphatidylinositol glycan anchor biosynthesis, class M	2.573132	0.82633	1.368101

myotubularin related protein 4	0.30935		
cleavage and polyadenylation specific factor 2, 100kDa	1.308624	1.088122	0.429924
acyl-CoA thioesterase 11			0.037589
diacylglycerol kinase, beta 90kDa			
solute carrier family 24 (sodium/potassium/calcium exchang	1.993903	1.440472	0.822094
transmembrane protein 61			
ryanodine receptor 2 (cardiac)	1.470133	0.473274	
ubiquitin specific peptidase 24	2.687228	0.865968	
WD repeat domain 17	0.227204		
ubiquitin specific peptidase 24	0.978758	0.443225	1.551034
anterior gradient homolog 3 (<i>Xenopus laevis</i>)	1.328874		0.368271
similar to LOC495387 protein		10.20176	
5-methyltetrahydrofolate-homocysteine methyltransferase	1.424658	0.907031	0.395288
ERO1-like beta (<i>S. cerevisiae</i>)		0.649218	0.137417
ERO1-like beta (<i>S. cerevisiae</i>)	0.652168	1.171313	0.186647
KIAA1409	0.320118		
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like		0.187464	2.446379
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like		0.890295	0.40272
tumor-associated calcium signal transducer 2		0.98398	0.48152
USO1 homolog, vesicle docking protein (yeast)	5.284113		4.004469
anthrax toxin receptor 2		1.631272	0.371784
anthrax toxin receptor 2			1.071055
fibroblast growth factor 5			1.253471
transmembrane protein 161B			0.063136
similar to RASGEF1B protein			2.266707
Sp4 transcription factor	0.631043	1.075724	0.411951
Sp4 transcription factor	1.060007	0.548524	0.43171
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polype	0.033446		
glycoprotein (transmembrane) nmb		0.425165	
chromosome 7 open reading frame 30	0.756544	1.070193	0.415783
tetratricopeptide repeat domain 21B	1.984615	0.905872	0.29711
ubiquitin specific peptidase 1	1.306037	1.208715	0.519042
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5			
transmembrane and tetratricopeptide repeat containing 2	1.72709	1.637314	2.961186
transmembrane and tetratricopeptide repeat containing 2	0.904562	1.300664	1.763943
membrane protein, palmitoylated 6 (MAGUK p55 subfamily	0.750688	1.110254	1.073685
oxysterol binding protein-like 3	2.493775	0.53734	3.466094
similar to mixed lineage kinase 4 (KIAA1804)	1.053632	0.888494	0.920517
similar to FLJ00149 protein /// pecanex-like 2 (<i>Drosophila</i>)	1.068754	2.310109	

kelch-like 8 (Drosophila)	4.38114	0.689246	0.476641
prolylcarboxypeptidase (angiotensinase C)			0.009893
similar to voltage-gated sodium channel type II alpha subuni	0.623476	1.130364	3.919329
sodium channel, voltage-gated, type I, alpha subunit			9.8943
actin-related protein T2	0.383965	0.714788	0.119486
fidgetin	6.048101	1.712199	0.35915
chromosome 14 open reading frame 49	0.208819	2.175188	
chromosome 1 open reading frame 96	0.772302	0.983485	0.314205
TAF5-like RNA polymerase II, p300/CBP-associated factor	1.571803	1.152185	0.291417
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgl	0.618448	1.125171	1.024332
component of oligomeric golgi complex 2	1.925876	0.789829	0.490322
WD repeat domain 78		3.012891	
B-cell CLL/lymphoma 11B (zinc finger protein)	1.048218	0.952952	0.407364
B-cell CLL/lymphoma 11B (zinc finger protein)	2.050459	0.931465	0.317855
THAP domain containing 9	2.137781	0.536854	1.010004
chromosome 12 open reading frame 50			
programmed cell death 2	0.995454	1.285176	0.320915
hypothetical LOC422599	0.157894		
centrosomal protein 290kDa	2.170375	1.395237	0.887531
centrosomal protein 290kDa	2.707052		0.574108
echinoderm microtubule associated protein like 1			
ST3 beta-galactoside alpha-2,3-sialyltransferase 4			4.749721
collagen-like tail subunit (single strand of homotrimer) of as	0.582713	3.621925	0.762398
collagen-like tail subunit (single strand of homotrimer) of as	0.463961	0.947037	1.199839
2-hydroxyacyl-CoA lyase 1	1.218816		0.081068
WD repeat domain 25	0.986114	0.908363	0.41301
phospholipase C-like 2	2.83347	1.072375	0.327775
similar to methylcrotonoyl-Coenzyme A carboxylase 2 (beta	1.560198	1.277796	0.641088
WD repeat and FYVE domain containing 3	25.40557		
protein phosphatase 1K (PP2C domain containing)		0.594392	0.038569
shugoshin-like 1 (S. pombe)	0.951675	0.987523	0.40762
kinesin family member 25	0.619628	0.184753	
N-glycanase 1	1.133278	0.900051	0.548386
N-glycanase 1	1.316661	1.028817	0.408934
N-glycanase 1	0.457126	1.059222	1.267865
plexin C1	1.526837	1.350937	0.321689
coiled-coil domain containing 41	1.254181	0.442393	0.907952
cysteine-rich with EGF-like domains 2	1.2473	0.919248	0.506932
similar to CENPJ		0.255214	
chromosome 1 open reading frame 173		1.002016	10.3683

WD repeat domain 20		0.807737	0.430331
chromosome 14 open reading frame 131	1.231488	1.254235	
ring finger protein 25			0.41002
zinc finger protein 142	2.036478	0.959398	1.244138
similar to CENPJ		0.090771	
chemokine (C-C motif) receptor 6	1.021836	1.426676	0.0827
RNA binding motif, single stranded interacting protein			
malignant fibrous histiocytoma amplified sequence 1		0.818135	0.252129
hypothetical LOC417921	0.358769		
ribosomal protein S6 kinase, 90kDa, polypeptide 2	2.3567	1.810506	1.315547
SWI/SNF related, matrix associated, actin dependent regulat	0.752001	1.028405	0.372368
SWI/SNF related, matrix associated, actin dependent regulat	0.519905	0.927418	0.074003
SWI/SNF related, matrix associated, actin dependent regulat	0.646145	1.11964	0.427794
glycerol-3-phosphate dehydrogenase 1-like	0.242705	0.965005	0.433242
peroxisomal trans-2-enoyl-CoA reductase	0.907691	1.059351	0.934127
cytochrome P450, family 27, subfamily C, polypeptide 1	0.349719		
nucleotide-binding oligomerization domain containing 1	0.628387	0.601905	0.409128
hypothetical LOC419095	0.318708	0.791411	2.204177
mex-3 homolog D (C. elegans)			0.183831
calpain 7			
SCY1-like 2 (S. cerevisiae)		45.29516	
phosphoinositide-3-kinase, regulatory subunit 4, p150	1.046398	0.96654	0.569377
ATPase, Ca ⁺⁺ transporting, type 2C, member 1	0.413685		
ATPase, Ca ⁺⁺ transporting, type 2C, member 1	1.078394	1.127164	0.4242
solute carrier family 17 (sodium-dependent inorganic phosph	0.062647		
solute carrier family 17 (sodium-dependent inorganic phosph	0.05155		
speckle-type POZ protein	1.151151	0.997571	0.309213
tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)			0.142107
solute carrier family 4, sodium bicarbonate cotransporter, member 4			
copine IV	2.034404		
neuropeptide FF receptor 2	0.20816		
ADAM metalloproteinase with thrombospondin type 1 motif, 3		0.374877	
poly(A)-specific ribonuclease (PARN)-like domain containin	2.607674	1.005614	
solute carrier family 5 (iodide transporter), member 8	3.717536	0.432715	
solute carrier family 5 (iodide transporter), member 8		2.298093	
transcription factor CP2-like 1	0.049514		
UTP20, small subunit (SSU) processome component, homol	0.285849		
KIAA0284			0.24432
phospholipase D family, member 4	1.582257	0.612502	0.135982
phospholipase D family, member 4	1.726942	0.72728	0.088293

ATG9 autophagy related 9 homolog A (S. cerevisiae)	1.097517	0.828683	2.107453
acid phosphatase, prostate	0.635209	0.46304	
nucleoporin 205kDa	0.711597	1.013866	0.500634
syntaxin 11		10.04504	
syntaxin 11	1.415927	0.911045	
cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	1.45375	1.079088	0.676945
coiled-coil domain containing 14	1.61744	1.314299	0.4974
dynein, axonemal, heavy chain 9		1.275564	0.269669
chemokine (C-C motif) receptor 2	0.048539		
chemokine (C motif) receptor 1			0.051902
chemokine (C motif) receptor 1	1.142893		0.022021
FYVE and coiled-coil domain containing 1		1.433201	
FYVE and coiled-coil domain containing 1		0.711669	
hypothetical protein LOC769813	1.700288	1.452814	
UDP glucuronosyltransferase 2 family, polypeptide A3			5.450598
sphingosine-1-phosphate phosphatase 1	0.279185	0.930355	0.898702
spermatogenesis associated 5	1.208296	1.082718	0.491439
guanylate cyclase 2C (heat stable enterotoxin receptor)	5.905048		1.65134
guanylate cyclase 2C (heat stable enterotoxin receptor)	0.568264	0.820437	1.586054
KIAA1109	1.172593		
KIAA1109	0.448966	0.939465	2.922113
KIAA1109	0.696836	0.907448	2.848758
CUB domain containing protein 1	1.453922	0.637997	1.968666
protein kinase C, eta			0.452855
solute carrier family 38, member 6	0.744301	1.688969	3.078948
unc-51-like kinase 4 (C. elegans)		1.220373	0.460233
septin 3	0.535515	0.429725	0.464039
meiosis inhibitor 1	0.587699		0.477197
similar to Alpha-2-macroglobulin precursor (Alpha-2-M)	0.156965		
solute carrier family 25, member 38			
chemokine (C-X3-C motif) receptor 1			2.38812
chemokine (C-X3-C motif) receptor 1	2.318821	1.577389	2.590771
TNFAIP3 interacting protein 3	0.065927		
transducer of ERBB2, 2		0.699879	0.288081
chemokine (C-C motif) receptor 4	0.267721	1.107388	0.275887
TNFAIP3 interacting protein 3	2.005986		1.100788
similar to protocadherin beta 20 /// hypothetical protein LOC776078 /// protocadher			0.209761
G protein-coupled receptor 114	1.058466	0.761225	2.131852
cytoplasmic linker associated protein 2	0.225047	0.411483	0.591387
megakaryoblastic leukemia (translocation) 1	0.766569	1.049827	2.307085

glutamine and serine rich 1		1.178493	0.717616
AT rich interactive domain 4A (RBP1-like)	1.283578	0.982539	0.448719
La ribonucleoprotein domain family, member 7	0.906302	0.959702	0.430187
doublecortin-like kinase 3			0.292421
GRB2-related adaptor protein 2	1.219156	0.696201	0.130009
lupus brain antigen 1	1.484446		6.074037
Similar to Poly [ADP-ribose] polymerase 14 (PARP-14) (B	2.337955	1.740638	1.621042
poly (ADP-ribose) polymerase family, member 14	3.773962	1.786804	1.960749
TRAF-interacting protein with forkhead-associated domain		0.759803	0.103311
TRAF-interacting protein with forkhead-associated domain	1.539305	0.699176	1.483588
poly (ADP-ribose) polymerase family, member 9	2.89319	2.145787	1.903398
chromosome 4 open reading frame 16	0.730861	1.310632	2.007931
chromosome 4 open reading frame 16	0.620113	0.836221	0.353121
G protein-coupled receptor 141		1.119012	
similar to Chromosome 4 open reading frame 32	0.661719	0.909053	0.402129
family with sequence similarity 62 (C2 domain containing), 1	0.481641		
family with sequence similarity 62 (C2 domain containing), member C			
coiled-coil domain containing 73	0.963028	2.391485	1.544269
acyloxyacyl hydrolase (neutrophil)	2.055507	2.440246	3.553998
engrailed homeobox 1	1.684434		1.541508
elongation protein 4 homolog (S. cerevisiae)	2.01355	1.326903	0.259751
HERPUD family member 2	0.962739	1.098091	0.41821
lin-7 homolog C (C. elegans)	0.517065	0.974357	0.348552
Bardet-Biedl syndrome 9	0.717179	0.674733	1.00728
aminocarboxymuconate semialdehyde decarboxylase		0.427966	
zinc finger, RAN-binding domain containing 3	0.549909	1.015717	0.508504
phosphodiesterase 1C, calmodulin-dependent 70kDa	1.984142	1.294526	1.962064
chromosome 14 open reading frame 104	0.662287	0.812515	4.170044
utrophin	1.032103		0.41685
Williams-Beuren syndrome chromosome region 16	1.626146	0.963817	0.345916
similar to serologically defined colon cancer antigen 3	0.321832		
golgi autoantigen, golgin subfamily a, 4	1.291145	0.637057	0.57978
transmembrane protein 184B	0.343079		
L-2-hydroxyglutarate dehydrogenase		0.332327	
SNF2 histone linker PHD RING helicase	2.002954	0.798845	0.655533
cyclin-dependent kinase-like 1 (CDC2-related kinase)	2.534554	1.540618	0.392216
solute carrier family 39 (zinc transporter), member 8		1.535983	2.177044
chromosome 6 open reading frame 103	4.248219		
chromosome 6 open reading frame 103	0.959562		2.137985
mitogen-activated protein kinase kinase kinase 5	1.29734	0.45508	1.627675

chromosome 7 open reading frame 10		0.659601	0.925123
uronyl-2-sulfotransferase	5.189391		
HECT, C2 and WW domain containing E3 ubiquitin protein	1.160023	0.498701	0.092919
HECT, C2 and WW domain containing E3 ubiquitin protein	1.039265	0.597668	0.086605
tudor domain containing 7	0.992685	1.328651	2.535779
serine/threonine kinase 17a	1.089512	0.853253	0.329858
FERM domain containing 6			2.782772
neurexophilin 2	0.297058		2.024195
hypothetical LOC424300	0.4927		
nidogen 2 (osteonidogen)	14.46408	1.511729	1.901892
G protein-coupled receptor 137C	0.622711	1.52792	0.150862
low density lipoprotein-related protein 1B (deleted in tumors)			2.012867
debranching enzyme homolog 1 (S. cerevisiae)	1.466779	0.994818	0.426642
methylenetetrahydrofolate dehydrogenase (NADP+ depende	0.03041		
similar to IP4/PIP3 binding protein-like protein	18.49684		
DDHD domain containing 1	0.25169	0.815383	
extracellular leucine-rich repeat and fibronectin type III cont	1.677686	0.379556	
chromosome 14 open reading frame 106	1.314685	0.795945	0.751762
enhancer of polycomb homolog 2 (Drosophila)	1.546413	1.09492	0.396168
eukaryotic translation initiation factor 2B, subunit 4 delta, 67	1.120255	1.122902	2.590456
transmembrane protease, serine 6	12.8486		1.569928
RNA binding motif protein 43	3.755623		0.897449
transmembrane protease, serine 6	2.502885	0.873517	
solute carrier family 12 (potassium/chloride transporters), me	1.297415	0.71559	0.337945
CD1c molecule	0.90184		0.118933
bromodomain containing 9	1.386546	1.29485	0.179425
solute carrier family 9 (sodium/hydrogen exchanger), member 3			
formin-like 2			2.700148
collagen, type XV, alpha 1		0.371933	
nuclear receptor subfamily 4, group A, member 2	25.56608		0.31455
chromosome 16 open reading frame 48		1.100106	3.176136
transducin-like enhancer of split 1 (E(sp1) homolog, Drosopl	0.382819	1.109089	1.394595
membrane-associated ring finger (C3HC4) 7	0.93772	1.063359	0.407316
solute carrier family 28 (sodium-coupled nucleoside transporter), member 3			0.187884
ATP/GTP binding protein 1	0.619506	0.606948	3.066929
phospholipase C, eta 2	2.182313		1.528661
chromosome 22 open reading frame 28	1.050999	0.897552	0.481056
Fanconi anemia, complementation group C	0.975595	0.934527	0.708701
reversion-inducing-cysteine-rich protein with kazal motifs	1.488002	1.364206	0.194034
tumor protein p53 inducible nuclear protein 2	0.379849	1.224447	1.44463

resistance to inhibitors of cholinesterase 8 homolog B (C. ele	1.644638	1.110206	0.313446
ATPase, class II, type 9B	0.6483	2.508116	1.102591
aldehyde dehydrogenase 5 family, member A1 (succinate-se	1.636677	0.212313	
aldehyde dehydrogenase 5 family, member A1 (succinate-se	2.958103	0.469039	
hypothetical protein LOC771624	1.143753	1.484768	3.320515
similar to Doublecortin domain containing 2a	0.717085	0.364109	0.716584
kinesin family member 13A			
aldehyde dehydrogenase 1 family, member L2	19.47454		
chromosome 12 open reading frame 45		1.026245	0.394296
RAN binding protein 9			
RAN binding protein 9	1.797513	0.733294	0.711518
coiled-coil domain containing 90A	0.934457	1.187532	0.393414
guanosine monophosphate reductase	2.11412	0.882639	0.796636
5'-nucleotidase domain containing 3	1.046387		3.002535
human immunodeficiency virus type I enhancer binding prot	0.993123	1.204321	0.362367
ADAM metalloproteinase domain 12 (meltrin alpha)			
chromosome 12 open reading frame 48	1.248086	1.038285	0.264114
N-acetylglucosamine-1-phosphate transferase, alpha and bet	0.92228	0.683517	0.236505
synaptonemal complex protein 3	0.757276	1.458124	0.109452
similar to MGC82474 protein	1.614284	2.787877	2.939536
ubiquitin protein ligase E3 component n-recognin 4	3.732041	2.12546	
poly (ADP-ribose) polymerase family, member 12	0.066562		
thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)			
ATPase, H ⁺ transporting, lysosomal V0 subunit a4	0.042424		
SVOP-like		0.044321	
chromosome 6 open reading frame 85	1.474291	2.073932	0.892614
exocyst complex component 2	1.118282	0.933522	0.414721
hypothetical LOC418108	1.87923	2.316677	2.601978
aarF domain containing kinase 2	1.956075	0.709346	0.788714
serpin peptidase inhibitor, clade B (ovalbumin), member 1	1.313694	2.232017	0.862637
serpin peptidase inhibitor, clade B (ovalbumin), member 5	1.636632	1.039036	0.421586
hypothetical LOC429942			
FYVE, RhoGEF and PH domain containing 4	0.997174	2.045763	1.666292
membrane-associated ring finger (C3HC4) 11	3.483815		
hypothetical protein LOC769855	0.621012	0.667729	0.337392
WAS protein family homolog 2 pseudogene		1.258643	0.027336
chromosome 6 open reading frame 98	1.034662	0.957814	1.078551
solute carrier family 6 (neurotransmitter transporter, GABA), member 13			0.105631
WNK lysine deficient protein kinase 1	0.793054	4.562095	
ankyrin repeat domain 33B	1.051793	0.381679	0.263448

interleukin 17 receptor A	1.249967	1.373071	0.06856
SH3-binding domain kinase family, member 2	0.473653		
chaperonin containing TCP1, subunit 5 (epsilon)	0.892716	1.427957	0.68396
hypothetical LOC425916	0.816059	1.176248	0.445938
hypothetical LOC425916	0.83464	1.372343	0.431699
hypothetical LOC426958	0.975349	0.530913	2.150025
similar to ABC A13			
fidgetin-like 1		0.473764	
epidermal growth factor receptor pathway substrate 8	8.789858		
dopa decarboxylase (aromatic L-amino acid decarboxylase)	0.391151	1.341488	
chromodomain helicase DNA binding protein 2			2.140184
growth factor receptor-bound protein 10	2.193025		3.205449
growth factor receptor-bound protein 10	2.996455		3.957242
hypothetical LOC430359			2.227238
phosphoinositide-3-kinase, class 2, gamma polypeptide	2.314563		
phospholipase C, zeta 1	0.253456		0.17558
capping protein (actin filament) muscle Z-line, alpha 3		2.042528	
chromosome 18 open reading frame 37	0.938678	0.838968	0.643281
chromosome 9 open reading frame 5	1.645769	0.533627	0.717028
molybdenum cofactor sulfurase			
tubulin, gamma complex associated protein 6	0.821077	0.907487	0.471745
solute carrier organic anion transporter family, member 1A2	0.45725		1.286326
solute carrier family 6 (neutral amino acid transporter), mem	1.385082	3.172152	1.968958
solute carrier family 6 (neutral amino acid transporter), mem	0.934118		0.475455
GRAM domain containing 4 /// similar to KIAA0767 protein			19.18834
GRAM domain containing 4 /// similar to KIAA0767 protein	1.230088	1.19609	2.1765
gamma-aminobutyric acid (GABA) B receptor, 2	0.367487	4.754447	1.328587
centromere protein E, 312kDa	0.937739	0.839802	0.475832
complement component 3a receptor 1	2.817015	1.080969	0.708502
similar to alternate SOS1	2.663939	0.663367	1.509091
hypothetical LOC427933	1.566462	10.38806	1.204568
pyruvate dehydrogenase kinase, isozyme 1	1.143462	0.750884	0.315569
hypothetical LOC425987	1.067794	2.107066	4.488675
mitogen-activated protein kinase kinase 2	0.734394	1.106814	2.544209
centrosomal protein 152kDa	1.14726	0.781151	0.383017
Dmx-like 2 /// similar to rabconnectin	2.676605	0.812738	0.629788
solute carrier family 5 (sodium/glucose cotransporter), mem1	5.351162		
GEM interacting protein	1.207283	1.587794	0.238846
GEM interacting protein		9.016928	
SECIS binding protein 2-like	1.038638	0.895407	0.294697

SECIS binding protein 2-like	1.548342	0.811658	0.219009
similar to T-cell receptor alpha chain V domain 1 /// similar to	0.672911	0.913367	0.405611
OTU domain containing 7B	0.480918		
phosducin-like	0.737893	0.933072	0.468121
LMBR1 domain containing 2	0.459751	0.794096	0.695676
similar to ligase I	1.403854	1.429361	1.410012
insulin-degrading enzyme		0.958131	0.151841
insulin-degrading enzyme	0.937853	1.270716	0.711755
hypothetical protein LOC772153		2.650599	
chromosome 9 open reading frame 98		9.561112	
similar to immunoglobulin-like receptor CHIR-B3 /// similar to immunoglobulin-like receptor			
stromal antigen 1	2.675778	0.742173	0.355722
pre-B-cell leukemia homeobox 4	1.690285	0.816367	2.044077
proteasome C1 subunit	0.32224	1.076375	0.501638
sorbin and SH3 domain containing 2	0.900148	1.032018	0.739349
similar to zinc finger protein	1.165309	0.695017	0.252955
par-3 partitioning defective 3 homolog B (C. elegans)			0.3044
par-3 partitioning defective 3 homolog B (C. elegans)	1.608304	1.169635	2.983514
thioredoxin domain containing 4 (endoplasmic reticulum)	1.088839	1.173438	0.478072
pleckstrin homology domain containing, family O member 1		1.098791	1.020182
toll-like receptor 3	3.807834	1.09327	
similar to PDZ domain-containing guanine nucleotide exch	1.572948	0.830548	0.42538
similar to PDZ domain-containing guanine nucleotide exch	1.645539	0.847133	0.729131
S100 calcium binding protein A13	0.802031	1.332536	2.193181
CAP-GLY domain containing linker protein 2			3.092932
coiled-coil domain containing 82	1.771606	0.866636	0.38227
centromere protein N	0.800206	2.029366	0.580691
cancer susceptibility candidate 3		1.500853	0.422921
hypothetical LOC429920 /// hypothetical LOC429942 /// hypothetical LOC430285 /// hypothet			
granzyme K (granzyme 3; tryptase II)	3.202441	3.18188	8.21312
cell division cycle 20 homolog B (S. cerevisiae)			6.065487
similar to Chromosome 5 open reading frame 5	2.025507		
coagulation factor XI	7.763533		
FAT tumor suppressor homolog 1 (Drosophila)	0.832698	0.724256	0.390127
CAP-GLY domain containing linker protein 2	2.153958		
FSHD region gene 1	1.002181	1.026634	0.448322
chromosome 6 open reading frame 98	1.196846		0.288558
myc target 1	3.244276		2.519544
similar to opioid receptor B	0.42431	0.835422	0.028309
CNKSR family member 3	1.3223	3.080189	1.556532

chromosome 6 open reading frame 62	1.305496	0.558584	0.487902
paroxysmal nonkinesigenic dyskinesia			
claudin 20		1.520543	0.080055
zinc finger protein 236	0.366898	0.474698	0.098059
zinc finger protein 236	1.281306	0.151092	0.26042
zinc finger protein 236		0.347204	0.34825
C-type lectin domain family 2, member B /// C-type lectin dc	0.425516	0.64762	
similar to Autoimmune regulator (Autoimmune polyendocrii	1.142853	1.02402	0.404723
NADPH oxidase 3	0.743153	2.284312	
chromosome 10 open reading frame 137	0.926	0.451514	0.398258
chromosome 10 open reading frame 137	0.631621	1.979277	0.489395
deleted in liver cancer 1	0.643901	0.840039	3.438225
hypothetical protein LOC771735			2.012716
zinc finger, DHHC-type containing 14	0.91913	0.457367	
zinc finger, DHHC-type containing 14	1.40223	0.864718	0.938338
CNDP dipeptidase 2 (metallopeptidase M20 family)	0.935858	1.096801	0.440687
chromosome 18 open reading frame 51	0.332532	1.135295	0.297742
pecanex homolog (Drosophila)	0.60674	0.557342	0.275558
hypothetical protein LOC770831	1.297212	3.085285	1.364458
deleted in liver cancer 1	1.464682	0.946695	4.468535
PR domain containing 2, with ZNF domain		1.083268	2.043558
tRNA selenocysteine associated protein 1	0.875513	1.022418	0.432151
LON peptidase N-terminal domain and ring finger 1	0.403703	0.926898	0.753542
cerebellin 2 precursor	0.456503	1.174872	5.670957
ectonucleotide pyrophosphatase/phosphodiesterase 7		2.810009	
similar to FKSG15	2.014437	1.222474	0.861378
CD226 molecule	1.593905	0.812078	0.175529
synaptosomal-associated protein, 29kDa	1.232229	0.91972	0.394608
similar to PRDM15 protein		2.518736	0.051412
docking protein 6	0.778073	0.440063	0.48115
glutamine-fructose-6-phosphate transaminase 2 /// hypothetic	1.458452		3.53995
galactokinase 2	1.214324	2.242266	0.607971
similar to olfactory receptor MOR146-3		0.391884	
human immunodeficiency virus type I enhancer binding prot	0.653162	0.76739	
hypothetical protein LOC768893	1.884756	0.527508	0.626885
inositol(myo)-1(or 4)-monophosphatase 2	2.815686	1.070432	0.999596
transportin 3	0.711995	2.000241	0.65267
prostaglandin-endoperoxide synthase 1 (prostaglandin G/H s	9.192511	2.267725	1.195562
solute carrier family 35, member D3			
COX10 homolog, cytochrome c oxidase assembly protein, h	0.059708	0.836288	

RNA (guanine-7-) methyltransferase	0.824449	0.935526	0.70708
melanocortin 2 receptor (adrenocorticotrophic hormone)			0.242588
similar to Meiosis-specific nuclear structural 1 /// similar to 1	1.296098	1.260636	2.509787
vacuolar protein sorting 45 homolog (S. cerevisiae)	1.113726	0.813098	2.113655
GTPase, IMAP family member 1		0.867671	2.187414
hypothetical LOC421690	0.483149		0.424905
similar to protein tyrosine phosphatase, receptor type, M		2.128796	1.05688
similar to protein tyrosine phosphatase, receptor type, M /// similar to Ptpm protein			
suppressor of variegation 3-9 homolog 2 (Drosophila)	0.644822	1.055157	0.419642
sec1 family domain containing 2			0.346976
family with sequence similarity 38, member B			
guanine nucleotide binding protein (G protein), gamma 4	3.072972	2.370613	0.858113
quinoid dihydropteridine reductase	0.677017	0.900392	0.33748
vanin 1 /// vanin 1	4.351387	1.231482	1.918582
trace amine associated receptor 1	0.541707		2.277226
zinc finger and BTB domain containing 44	0.553803	1.010384	0.350355
similar to immunoglobulin-like receptor CHIR-A2		0.49112	1.901159
similar to immunoglobulin-like receptor CHIR-A2			
erythrocyte membrane protein band 4.1-like 2	0.808739	0.756399	1.059688
l(3)mbt-like 3 (Drosophila)		0.75424	2.262695
lymphoid-restricted membrane protein	1.260147	1.002641	0.303337
Rho GTPase activating protein 18			
DnaJ (Hsp40) homolog, subfamily B, member 14		0.0511	
DnaJ (Hsp40) homolog, subfamily B, member 14	1.432147	0.874252	0.496691
cancer susceptibility candidate 1	1.100263	1.429018	1.166815
similar to Serine/threonine kinase 3 (STE20 homolog, yeast)	1.255196	0.6765	0.285897
KIAA0802		0.046945	
hypothetical LOC422763	2.502126	0.787426	1.685571
similar to KIAA0896 protein	1.199537	1.492465	2.862567
hypothetical LOC419599	5.060207	2.179323	2.277715
TXK tyrosine kinase	2.057835	0.530073	1.672819
similar to RanBP2 (Ran-binding protein 2) /// similar to Ranl	0.684632	1.573745	0.974141
similar to Ran-binding protein 2 /// similar to RanBP2 (Ran-l	0.409084		
NIPA-like domain containing 1	2.631095	1.393734	0.142605
hypothetical protein LOC769475	0.85204	3.730691	
hypothetical protein LOC776064		9.74717	
MANSC domain containing 1	0.635309	2.453348	1.630869
tubulin tyrosine ligase-like family, member 1	0.848623	1.066725	1.430065
cell cycle associated protein 1	0.481965	1.10907	1.036694
ATPase, class V, type 10D	3.303807	3.6044	0.222837

ATPase, class V, type 10D		0.09646	0.663584
parvin, gamma	0.314249	0.668817	0.116197
parvin, gamma	1.086508	1.224227	0.247153
glucosamine-6-phosphate deaminase 2	1.088711	1.28084	0.34937
EF-hand calcium binding domain 4B	11.42166		
zinc finger protein 250	0.70662	1.111441	0.302543
ataxin 10	0.646523	1.324643	0.400099
ATPase, aminophospholipid transporter (APLT), class I, type 1	11.93369		
ATPase, aminophospholipid transporter (APLT), class I, type 1	11.16751	0.988005	2.590365
similar to LOC150383 protein	1.105576	1.699668	1.478162
coiled-coil domain containing 4	0.847995	1.30057	0.288066
alpha-2-macroglobulin			3.059321
amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65)	26.82589		
RNA binding motif protein 47	1.628494	0.814373	0.480485
ras homolog gene family, member H		1.04908	0.261304
NAD kinase	2.869074	0.336029	0.176406
NmrA-like family domain containing 1	1.573515		0.051589
UDP-glucose dehydrogenase	0.722564	1.566941	0.268344
ADP-ribosylation factor-like 2 binding protein	0.67417	0.356066	0.7164
integrin alpha FG-GAP repeat containing 2	0.998008	0.71821	0.392338
RELT-like 1	1.60103	1.366531	0.395859
centaurin, delta 1	1.263692	0.792452	0.212823
hypothetical LOC426508 /// hypothetical protein LOC77672	3.546787		
stromal interaction molecule 2	1.649585	1.14822	1.063734
R3H domain containing 2			
MYB binding protein (P160) 1a	0.87136	1.209386	1.541154
mannosidase, alpha, class 1A, member 2	1.104911	0.985958	0.328732
mannosidase, alpha, class 1A, member 2		2.342056	
cholecystokinin A receptor	0.692175		
cholecystokinin A receptor	0.127342		
apolipoprotein A-V	0.451377		
lectin, galactoside-binding, soluble, 8 (galectin 8)		0.279785	
lectin, galactoside-binding, soluble, 8 (galectin 8)	1.822148	0.757959	0.191412
lectin, galactoside-binding, soluble, 8 (galectin 8)	1.72543	0.100605	0.33686
lectin, galactoside-binding, soluble, 8 (galectin 8)	2.889066	1.356706	0.347724
Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthetase	0.63723	1.492113	1.501702
peroxisome proliferator-activated receptor gamma, coactivator 1 alpha			0.110387
similar to GT334 protein	1.397173	0.452217	0.905814
calcium-sensing receptor			0.046864
heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 /// s	0.69908	3.060199	4.348557

non-SMC condensin I complex, subunit G	0.681481	1.421236	0.14848
DEAH (Asp-Glu-Ala-His) box polypeptide 32		4.62016	
family with sequence similarity 46, member C	1.418064		1.496357
chromodomain helicase DNA binding protein 4 /// hypothetical	0.96746	1.302756	0.699316
chromodomain helicase DNA binding protein 4 /// hypothetical	0.622018		0.742733
G protein-coupled receptor 92		13.06592	
G protein-coupled receptor 92	0.83139	0.915918	0.331149
chromosome 12 open reading frame 53	0.969937		
lymphocyte-activation gene 3		2.688206	2.434324
similar to DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	0.934914	0.931004	1.228739
poly(A) binding protein, cytoplasmic 1	1.682904	0.457836	0.642418
prominin 1			17.33584
centrosome and spindle pole associated protein 1	1.218399	0.730642	0.215763
centrosome and spindle pole associated protein 1	2.18851	0.664353	0.119269
similar to OTTHUMP00000016587		2.196907	1.3031
SH3 domain and tetratricopeptide repeats 2			
CCR4-NOT transcription complex, subunit 6 /// similar to C	2.571789	0.876618	0.196915
CCR4-NOT transcription complex, subunit 6	0.922693	1.061717	0.308236
complement component 1, s subcomponent	3.379458	1.597147	1.331501
ATP/GTP binding protein-like 2	0.125066		3.909345
metallothionein 3	0.731421	1.187904	3.712142
suppressor of Ty 5 homolog (S. cerevisiae)		0.930338	2.302522
LAG1 homolog, ceramide synthase 3	1.750323	0.571186	0.316069
LAG1 homolog, ceramide synthase 3		1.91273	0.418469
spinster homolog 2 (Drosophila)			
chromodomain helicase DNA binding protein 1		1.381052	0.399296
hypothetical LOC427110		0.462234	0.093867
hypothetical LOC427110	0.360558	1.013726	0.578694
multiple C2 domains, transmembrane 1	1.352732	1.45875	2.457731
calsyntenin 3	1.022353		0.358008
elongation factor, RNA polymerase II, 2		1.141886	2.349776
similar to PC1 /// prohormone convertase1	0.275137		0.552948
calpastatin	0.980352		3.695224
membrane-associated ring finger (C3HC4) 3		0.86132	0.662093
multiple EGF-like-domains 10			23.53209
interleukin 31 receptor A	0.735741		2.336389
C-type lectin-like receptor variant	0.825598	2.344211	1.505107
similar to RAB3C, member RAS oncogene family	0.31621	0.804972	1.048325
DEP domain containing 1B	0.708636	1.259949	0.52409
ELOVL family member 7, elongation of long chain fatty acid	1.442649	1.14948	1.473256

hypothetical protein LOC770670	1.758665	0.610442	0.479026
similar to KIAA1577 protein	2.773452	0.59236	0.765042
ring finger protein 180	0.584104	1.539075	0.272279
SFRS12-interacting protein 1	0.376784	1.165296	2.061121
ADAM metallopeptidase with thrombospondin type 1 motif, 6			0.038437
ADAM metallopeptidase with thrombospondin type 1 motif, 6		1.061955	14.48766
similar to Microtubule-associated serine/threonine-protein ki	0.964415	0.819724	0.286607
hypothetical protein LOC770116	2.154618	1.317318	2.228347
KIAA2018	2.195482		
homer homolog 1 (Drosophila)	2.021694	1.008223	0.333773
similar to Junction-mediating and regulatory protein	0.587402	4.960792	1.592842
elastin microfibril interfacier 2	1.289145	0.953063	2.302324
protein tyrosine phosphatase, receptor type, K			0.037237
tripartite motif-containing 45	0.722721	0.960209	2.204655
chromosome 6 open reading frame 190	0.905373	1.084112	0.198821
prostaglandin E receptor 4 (subtype EP4)	1.004303	1.359052	10.29238
prostaglandin E receptor 4 (subtype EP4)	1.886731	1.638295	2.566164
chromosome 6 open reading frame 174	0.819037	1.050831	0.158161
protein kinase, AMP-activated, alpha 1 catalytic subunit	0.32693	0.90092	1.802872
lipin 2	0.742116		3.34463
F-box protein 4			
Similar to Sphingomyelin phosphodiesterase, acid-like 3A	2.839447	1.091758	0.986116
autoimmune regulator	0.794281	0.796757	1.594147
discoidin, CUB and LCCL domain containing 1	0.522665	1.445229	0.016021
similar to Rho-guanine nucleotide exchange factor	0.19073	0.610983	5.484241
polymerase (DNA directed), theta		7.077557	0.926786
similar to Rho-guanine nucleotide exchange factor	1.045766	0.536981	0.068368
karyopherin alpha 5 (importin alpha 6)		0.79191	0.428881
karyopherin alpha 5 (importin alpha 6)	0.472768	1.357825	0.954627
syntaxin binding protein 5-like		0.411554	2.797972
similar to KIAA0888 protein	1.114314	0.752322	1.516006
general transcription factor IIE, polypeptide 1, alpha 56kDa		0.318876	
chromosome 5 open reading frame 37	0.479649	0.887771	0.56936
synaptic vesicle glycoprotein 2C	0.972368	0.875858	
mindbomb homolog 1 (Drosophila)	0.825942	0.292122	0.938917
mindbomb homolog 1 (Drosophila)	0.906098	0.707601	1.39269
coagulation factor II (thrombin) receptor	1.075999	1.345239	0.664654
transmembrane protein 128		1.047837	0.213533
transmembrane protein 128	0.702734	1.511973	0.353114
Ly1 antibody reactive homolog (mouse)	1.181181	2.13626	1.084203

solute carrier family 22 (organic cation transporter), member	0.487418	0.339538	
Ellis van Creveld syndrome			0.210717
cell division cycle 2-like 6 (CDK8-like)	0.799628	1.085149	0.352884
laminin, alpha 3	2.338572	1.40452	1.385732
protein tyrosine phosphatase, receptor type, D	1.169136		
cell division cycle 40 homolog (S. cerevisiae)	1.118029	0.951555	0.439725
similar to Cdc42 GTPase-activating protein	0.278054		
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Dros		7.360351	1.339029
myeloid/lymphoid or mixed-lineage leukemia (trithorax hom	1.550006	0.431562	1.180136
N-acylsphingosine amidohydrolase 3-like		0.859271	
DENN/MADD domain containing 4C	2.346525	0.75149	1.05696
oxysterol binding protein-like 1A	1.850278	1.171622	2.46983
hypothetical LOC427239 /// HAUS augmin-like complex, su	0.348303	0.681792	0.976972
chromosome 9 open reading frame 39	0.271217	1.082741	13.05556
similar to basonuclin 2	1.866505		2.274749
hypothetical LOC421081			
amyloid beta (A4) precursor protein-binding, family A, member 1 (X11		0.377998	
TAF4b RNA polymerase II, TATA box binding protein (TB	1.592386	1.004005	0.893138
TAF4b RNA polymerase II, TATA box binding protein (TB	1.357345	3.859926	2.395851
G protein-coupled receptor 15			0.085334
G protein-coupled receptor 15	1.005693	1.937794	0.344903
immunoglobulin-like domain containing receptor 1	0.876857	0.973773	0.125255
WD repeat domain 52		0.652809	1.216018
guanine deaminase	2.458185		1.251433
desmoglein 2		0.371537	0.673095
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polyp	1.195961	0.778578	0.150709
hypothetical LOC421093		2.67653	0.349159
hypothetical LOC431610		1.665317	0.457884
hypothetical LOC431610	0.135972		
guanine nucleotide binding protein (G protein), alpha 14		0.142956	2.572171
guanine nucleotide binding protein (G protein), q polypeptid	1.11727	0.585206	1.026667
guanine nucleotide binding protein (G protein), q polypeptid	0.174465	0.476249	
dystrobrevin, alpha			
zeta-chain (TCR) associated protein kinase 70kDa	0.845959	1.214884	0.441376
similar to Protein KIAA0146	0.984651	1.09174	1.422007
transmembrane protein 157	0.47824	0.858208	1.43921
similar to organic anion transporter OATP-M1		3.095462	1.618864
gypsy retrotransposon integrase 1	0.973559	1.264991	0.365476
non-SMC condensin II complex, subunit D3	1.257008	1.897557	0.379924
RB1-inducible coiled-coil 1	1.252724	2.222851	2.073548

protein phosphatase 1F (PP2C domain containing)	1.164801	2.363902	5.762789
TBC1 domain family, member 23	1.117707	1.507854	0.339449
TBC1 domain family, member 23		0.798382	0.405913
armadillo repeat containing 2	1.210813	1.787496	0.489679
G protein-coupled receptor 128		0.132683	
leucyl/cystinyl aminopeptidase	0.326316	0.576718	0.8292
lactation elevated 1	1.624604	1.099258	1.481843
lactation elevated 1	1.753903	1.007395	1.19744
ABI gene family, member 3 (NESH) binding protein			5.683592
sex comb on midleg-like 4 (Drosophila)	0.064469		
tripartite motif-containing 14	0.698193	0.818039	0.565741
tripartite motif-containing 14	0.448283	1.272914	0.486108
similar to KIAA1889 protein	1.526692	0.559551	2.137649
interphotoreceptor matrix proteoglycan 2	1.647787	0.782835	
SUMO1/sentrin specific peptidase 7	0.92022	0.357613	0.590641
hypothetical LOC421125	1.200608	0.577601	0.221147
absent in melanoma 1	1.336151	0.473025	0.551765
Cas-Br-M (murine) ecotropic retroviral transforming sequen	0.816124		2.761425
SH2 domain containing 1B	1.202038	0.429128	0.446528
T cell receptor associated transmembrane adaptor 1	0.838138	0.877029	0.13859
THAP domain containing, apoptosis associated protein 1	0.978761	0.948752	0.753756
PR domain containing 1, with ZNF domain	9.61953	1.37781	3.382596
transmembrane protease, serine 7	12.00788		
hook homolog 3 (Drosophila)	0.610842	1.524311	3.123709
CGG triplet repeat binding protein 1	0.504066	0.504258	0.062289
hypothetical LOC430761 /// hypothetical protein LOC77646	1.621633	2.168481	0.578762
prolyl endopeptidase		1.392483	0.055183
HECT domain and ankyrin repeat containing, E3 ubiquitin p	1.376369	1.119285	0.480738
HECT domain and ankyrin repeat containing, E3 ubiquitin p	12.7601		8.04084
MYC induced nuclear antigen /// MYC induced nuclear anti	1.121885	1.32729	0.387449
pleckstrin and Sec7 domain containing 3	0.84689	0.102772	1.904926
solute carrier family 12 (sodium/potassium/chloride transporters), member 1			19.50923
fibronectin type III and SPRY domain containing 1-like	0.867661	0.746733	0.306563
CD2 molecule	0.680241	0.672787	0.095417
immunoglobulin superfamily, member 3		7.951039	1.065421
chromodomain helicase DNA binding protein 7	1.23289	0.772727	0.370812
KTEL (Lys-Tyr-Glu-Leu) containing 1			0.605177
gamma-glutamyl hydrolase (conjugase, folylpolygammaglut	1.538507	1.169171	0.229331
armadillo repeat containing 1	1.775457	1.275913	0.563689
kelch-like 32 (Drosophila)	1.97461	2.277745	

kelch-like 32 (Drosophila)	0.551035	0.933402	0.705987
centrosomal protein 110kDa	1.008104	0.438857	0.512251
roundabout, axon guidance receptor, homolog 2 (Drosophila)	3.590213	0.733791	
serum/glucocorticoid regulated kinase family, member 3	1.031138	0.802988	0.346953
glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	0.391554	0.703733	0.231592
glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	0.543554	0.471866	0.235535
similar to AASA9217		2.138558	
ankyrin repeat domain 34B	0.82368	0.187159	
KIAA0776	1.420732	0.95108	0.637505
solute carrier organic anion transporter family, member 5A1		0.811411	
hypothetical LOC427318	0.626766	1.049519	0.699881
HGF activator	17.99127	1.164233	
lactamase, beta 2		0.091987	
lactamase, beta 2	0.828239	1.408095	0.313645
huntingtin	1.066854	0.938988	0.753199
von Willebrand factor A domain containing 1		0.858534	0.165755
ROD1 regulator of differentiation 1 (S. pombe)	7.065658		0.163011
sushi domain containing 1		3.754582	

ifference for the comparison of uninfected and infected transcripts. (*) indicates $p < 0.05$ and (**

	Significant Level				7DPI_inf	14DPI_m	21DPI_m	28DPI_m
28dpi	7dpi	14dpi	21dpi	28dpi	ected_call	ected_ca	ected_ca	ected_ca
0.363716				**	P	P	P	P
13.96645			*	**			P	P
2.121137	*	*	*	*	P	P	P	P
0.926058	*				P	P	P	P
		*			P	P		
3.276955				*	P	P	P	P
2.11441				*	P	P	P	P
2.13054				*	P	P	P	P
0.762227					P	P	P	P
1.480932			*		P	P	P	P
0.464085					P			A
2.229571				*				P
		**				P		
0.542844					P	P	P	P
0.502223					P	P	P	P
	*		*		P	P	P	
4.011218		*		*	P	P	P	P
	**	*			P	P	P	
2.007602		*		*	P	P	A	M
0.391681					P	P	P	P
							A	
8.760839	*		**	**	P	P	P	P
1.260786	**				P		A	A
0.925184					P	P	P	P
0.257523					P	P	M	A
2.304867				*				P
0.461588					P	P	P	P
0.525039					P	P	P	A
1.49441					P	P		A
0.277195					M	A	A	A
							A	
51.04888				**				P
1.798106			*		P	P	P	P
1.751985			*		P	P	P	P

1.076321				A	P	A	A
						A	
1.04054	*	*		A	P	P	A
	*				P		
0.48258				P	A	A	A
		*		P	P	P	
2.243043			*			A	P
0.347495				P	P	P	P
1.311711				P	P	A	P
	*			P	P	A	
				A	P	A	
0.924559				P	A	A	P
1.305182		*		P	P	P	P
		**				P	
2.060813			*		A		P
0.228346				P	P	P	P
0.468414							A
						A	
0.419118				P	P	P	P
1.72937				P	M	A	P
2.064552			*	P	P	P	P
2.284964			*	P	P	P	P
0.585887	*			P	P	P	A
					P	A	
	**			P	A		
		**			P		
1.721305		**		P	P	P	P
2.03357	**	**	*	P	P	P	A
	**			P			
17.03985		**	**			P	P
0.885255				P	P	P	A
0.789722				P	P	P	P
1.227606				P	P	A	A
					A		
	*				P	A	
				M		A	
				A			
0.478805				P	P	P	P
0.199077				P	P	P	P
2.007971			*				M

9.235327			**	**	P	P	P	P
		**				P		
6.609344	**			**	P	P	P	P
2.639131	*			*	P	P	P	P
1.529801			**		P		P	P
2.166892				*	P	P	P	P
0.793024						M	A	P
2.577168				*	P	P	P	P
6.873447			*	**	P		P	P
2.992053				**		A	A	M
21.2442	*		*	**	P	M	P	P
3.045599				**				P
2.542212			**	*	P	P	P	P
2.777203		*		*		P		P
2.633987				*	P	P	P	P
3.346363			*	*	P		P	M
	**				P	A	A	
4.920852			*	*	P	P	P	P
0.897622					P	P	P	P
1.395677					A	A		A
			**				M	
1.047658	*		*		P	P	M	A
	*				P			
1.93402			*		P	P	P	P
0.3904					P	P	P	P
3.743722				*	P	P	A	P
1.378504					P	P	P	P
0.261587					P	P	P	P
2.389896				*	P	P	P	P
0.361547					P	P	P	A
0.288118					P	A	P	A
1.296007			**		P	P	P	P
						A		
1.586824			*		P	A	P	P
1.445802	*				P	P	P	P
2.808742				*	P	P	P	A
2.908747			**	**	P	P	P	P
	**				P	A	P	
13.53496				**	P	P	P	M
						A		

0.186923					M	P		A
			*			P		
1.624577					P	P	M	A
0.746307					P	P	A	A
4.759889	**	*	**	*	P	P	P	P
5.049894	*		**	*	P	P	P	P
7.868758	**	*	*	**	P	P	P	P
0.361564					P	P	P	A
			*			A	P	
					A	M	A	
0.458264					P	P	P	A
1.356079					P	P	P	P
1.236178			*		P	P	P	P
							A	
0.483313		*			A	P	P	A
1.369649					P	P	A	P
3.173813				**	P	M		P
					A	P	P	
0.452937					A			A
		*				P		
0.731145					P	P	P	P
1.723337			*		P	P	P	P
						A		
4.044955				*	M	P	P	P
1.573838			**		P	P	P	P
					A			
0.443436					P	P	P	P
0.982086					P	P	P	A
			*				P	
		**				P		
							A	
0.783114		*			A	P		P
					A	A		
0.528131					P	P	P	P
1.483017					P	P	A	A
0.570978	*				P	P	P	A
12.35487				**				P
5.336641				*				P
1.242246			**		P	M	P	A

						A	
				A	A	A	
2.502155			*	A			A
				A			
2.699011			*	M	P	P	P
				A			
0.654999				P	P	P	A
2.109851			*	M		P	A
1.198348		*		A		P	M
54.24393			**				P
					P	A	
		*		A		A	
						A	
0.73467				P	P	P	P
				A			
2.309592			*				M
0.438076				P	P	P	P
5.388739			*	P	A	P	P
2.167751			*				P
0.803491	**			P	A	A	A
1.07768		**		P	P	P	P
				A	A	P	
3.046458			**	A	A	A	P
6.431019			*				P
0.482606				P	P	P	P
						A	
0.993333		*		P	P	P	P
						A	
1.033961	*			P	P	P	A
0.809696				P	P	P	A
						A	
				P	P	P	
	**			M			
3.355837	*		*	P	P	M	P
0.341383				P	P	P	P
					A		
0.652055				P	P	P	A
2.633869			*	P	P	P	P
						A	
				A			

	**	**			P	P	A	
					A	A	A	
2.289936				*	A	A	A	P
0.834367	*				M	A		A
2.587289	**		*	*	P	P	P	P
2.406765			**	*	P	P	P	P
0.434477					P	P	P	P
2.770905				*	P	P	P	P
							A	
1.304912	*				P	P	A	A
1.526519					P	P	P	P
0.428654		*				P		A
					P	P	A	
0.158108					P	P	P	A
0.19664					P	M	A	A
					M	A		
0.847624					P	P	P	A
0.802988					P	P	P	P
0.54624			*		P	P	P	P
1.458595					P	M	A	P
6.504479		*	**	**	P	P	P	P
1.147503					P	P	P	P
0.434793					A	P	P	A
0.614971					P	P	P	P
		**				P		
2.316484			*	*	P	P	P	P
3.20737				**	P	P	P	P
3.096613				**	A	A	A	P
	*				P	A		
1.19673			*		P	P	P	P
1.868071	**		*		P	P	P	P
1.232252		*			A	P	P	P
0.3609					P	P	P	P
					A		A	
2.10543				*				P
						A		
0.119821						P		A
1.849683		*			P	P	P	A
1.417516	**	*	*		P	P	P	P
	**				P			

				A	A		
3.032396			**				M
2.105586		*	*	P	P	P	P
						A	
0.389312		**		P	P	P	A
0.579188				P	P	P	P
0.858342				P	P	P	P
0.356737				P	A	A	A
0.128305					P		A
5.01248			*	P	P	P	P
5.383987			*	P	P	P	P
11.55273			**	P	P	P	P
				P	P		
0.230706				P	P	P	A
3.103345		*	**	P	P	P	P
2.353079			*	P	P	P	P
3.013534			**	A	A	P	P
2.815635		*	*	P	P	P	P
1.454008					P	A	P
	*			P	P	P	
0.284409				P			A
0.099034		*			P		A
1.896013		*		P	P	P	P
2.112109		**	*	P	P	P	P
2.910214			**	P	P	P	P
0.366665					P		A
1.402815				P	P	P	P
				P	P	A	
0.422734				P	P	P	P
3.796117		*	*	P	M	P	P
2.003056		*	*	P	P		P
0.556043				P	M	M	A
			**	M	A	P	
0.492902				P	P	P	P
		*				P	
				A	P	A	
	*	**		M	P		
	*			P	A		
0.270503		*			P		A
0.841607				P		A	A

			*				M	
			**				P	
2.752926	*		*	*	P	P	P	P
24.42688				**				P
						P	A	
0.336018					P	P	A	A
4.654975				*	P	P	P	P
2.098648				*	P	P	P	P
0.716938	**				P	A		A
0.631921						A	P	A
0.15968								A
					P	M	A	
		**			P	P	P	
	*				P			
2.414482	*			*	P	P	P	P
0.853157	*				P		A	A
						A	A	
6.70071			*	**	P	P	P	P
2.18329				*	P	P	P	P
0.25411					M	P	P	A
		**			A	P		
0.96119					P	A	P	P
2.919163				**	P	P	P	P
0.39324					P	P	P	P
					P	A	A	
0.578625	*	*			P	P		A
1.622683		**			P	P	P	A
0.134465		**				P		A
5.184461			*	*	P	P	P	P
4.076199				*	P	A		P
8.122546			*	**	P	P	P	M
							A	
28.79579				**				P
0.358195					P	A	A	A
1.099669	*				P	P	M	A
0.325077					P	P	P	P
6.801782				**				P
3.367453				*	M	M	A	P
6.148662				*				P
0.968629					P	P	P	P

0.766914			*		P	P	P	P
			*		M		P	
0.420147					P	P	P	M
2.065095				*	A	P		P
	**				P	P	P	
	*		**		P		M	
					P	P	A	
3.445492			*	*	P	P	P	P
3.077197			**	**	A		M	P
1.328019			*		P	A	P	P
2.173396				*	P	M	A	P
0.045824					P	P	M	A
10.93148				**				P
0.133064	*				P		A	A
						A		
9.669394				**				P
	**				P			
11.37927				**		A		P
0.374658					P	P	P	A
							A	
0.560519					P	P	A	A
2.032083				*	P	P	P	P
0.763641	**				P	P	P	P
2.566432				*	P	P	P	P
0.575937	*				P	P	P	P
0.492005					P	P	P	P
1.942457					P	P	P	P
10.53901				**	A			P
0.455062					P	P	P	A
					A	P	A	
0.902199	*	*			P	P	P	P
5.109856	*		**	*	P	P	P	P
2.714198				*				P
0.620174					P	P	P	P
			*				P	
0.416241	*				P	P	P	P
5.12397	**	*	**	*	P	P	P	P
1.146582					P	P	A	P
0.460772					P	P	P	A
0.451599					P	P	A	A

0.91677					P	P	P	P
	*				P			
0.22964		**			A	P	A	A
					P	P	A	
0.927137					P		A	P
2.572853			**	*	P	P	P	P
			**		P		P	
3.159621				**	P	P		P
2.277462				*	P	P	P	P
0.685764					P	P	P	P
							A	
0.523654	*				P	P	P	A
1.506186			**		P	P	P	P
0.121183						P	A	A
					P	A	A	
		*			P	P		
1.792111						A		A
0.159312					A	A		A
2.022649	*		**	*	P	P	P	P
2.874332				**		P	A	P
							A	
0.45999					P	P	P	P
	*				M	M	A	
1.190474					P	P	A	A
3.136412			*	**	P	P	P	P
1.694376			*		P	P	P	P
					A			
							A	
0.499903					P	P	P	P
					A	P	A	
36.0344				**	A		P	P
			**		P	A	M	
					A	P	A	
3.180223				**	A	P	P	P
6.048607	*	**	**	*	P	P	P	P
3.40625				*	P	P	A	P
			*				P	
2.975532				**				P
		*	*		P	P	P	
1.415941			*		P	P	P	P

0.416139				P	P	P	P
		*				M	
	*			A	P	A	
11.03451			**		P	A	P
2.741484			*	P	P	P	P
2.641638		**	*	P	P	P	P
2.683852		*	*	P	P	P	P
0.182584					A		A
2.419045			*		A	A	M
0.268281				M	P	A	A
		**				P	
0.192644				P	P	P	A
0.426663				P	P	P	P
	**			M			
1.874573		*		P	P	P	P
1.342618		*		P	P	P	P
2.648315			*	P	P	P	P
2.598873	**		*	P	P		P
1.954446	*	*		P	P	P	P
3.546456		**	*	P		P	P
0.6804				P	P	P	P
2.328668		*	*	P	P	P	P
0.284559				P	P	P	A
2.657552		*	*	P	P	P	P
1.414627		*	*	P	P	P	A
	*			P	A	A	
0.286386							A
2.879842		*	**	P	P	P	P
1.817474		*		P		P	P
				P	A	A	
20.51612		*	**	P	P	P	P
1.949054		*		P	P	P	P
23.46936			**	P	P	P	P
1.086028				P	P	A	A
	*	**		P		M	
1.353216				P	P	P	P
		**		P		P	
3.151759		*	**	P	P	P	P
1.837548		*		P	P	P	P
0.363327				P	P	A	A

1.571891	*		*		P	P	P	P
0.815357			**		P	P	P	P
0.569305					P	P	P	P
2.394245				*	P	P	P	P
			**		P		P	
					A			
0.419049					P	P	A	A
1.309093			*		P	P	P	P
						A		
0.547719	*				P	P	P	P
0.786723					P	P	P	P
0.141705					P	P	P	A
0.521983					P	P	P	P
1.573484			*		P	P	P	P
		*				M		
3.138345			**	**	P	P	P	P
0.077624					P	P	P	A
0.450276	*				P	P	P	A
0.634183					P	P	P	P
0.663125					P	P	P	P
0.935021					P	P	P	P
10.06624			**	**	P	P	P	P
0.404449					P	P	P	P
2.833315				*	P	A	A	P
0.188208					P	P	P	P
0.197111					P	P	P	P
0.501725					P	P	P	P
					M	P	A	
1.122863					P	P	P	A
1.055673					P	P	P	A
2.086544				*	P	P	M	P
2.148204				*	A	P	A	P
1.77158			*			A	P	P
1.8512	**				P	P	P	P
5.701534				*	P	A		P
		*			A	P		
2.163173				*	P	P	P	P
0.332946					P	P	P	P
0.371158					P	P	A	A
0.305137					P	P	P	A

1.501309			*		P	P	P	P
	*				P		P	
1.587057	*				P	P	P	P
4.774251			**	*	P	P	P	P
4.881579			**	*	P	P	P	P
0.282214					P	P	P	P
2.787846	*		*	*	P	P	P	P
3.37145				*	P	P	P	P
2.046837				*	P	P	P	P
2.922958			**	**	P	P	P	P
0.564095					P	P	P	P
2.217163			*	*	P	P	P	P
2.953069			*	**	P	P	P	P
3.464259			*	*	P	P	P	P
3.955939			**	*	P	P	P	P
0.201042								A
2.359088			*	*	P	P	P	P
					P	P	A	
7.05353	**	*	*	**	P	P	P	P
4.467553	*	*	*	*	P	P	P	P
2.356405	**		*	*	P	P	P	P
1.900422			*		P	P	P	P
0.617188					P	P	P	P
8.397253	*	**	**	**	P	P	P	P
0.430284					P	P	A	A
0.455211					P	P	P	P
0.410315		*			P	P	P	A
1.398984			**		P	P	P	P
2.141617				*	P	P	P	P
3.57762	*	**	**	*	P	P	P	P
	**				P		A	
0.471716	**				P	P	P	A
0.391713	**				P	P	P	M
0.600492					P	P	P	P
		**				P		
6.484647	*		**	**	P	P	P	P
2.613985			*	*	P	P	P	P
6.083329			*	*	P	P	P	P
4.341564				*				M
0.885382			*		P	P	P	P

3.599023	*			*	P	P	P	P
2.231513			*	*	P	P	P	P
7.50918	*	*		**	P	P	P	P
5.514156			**	*	P	P	P	P
1.490012					P	P	P	P
0.133731					P	P	A	A
0.088751					P	A	A	A
2.420158			*	*	P	A	P	M
0.45857					P	P	P	A
2.146188			*	*	P	A	P	P
2.337335			*	*	P	A	P	P
	*				P		P	
1.139703					P	P	P	P
0.715627					A	A	A	A
2.225084				*			A	P
2.296246				*	P	P	A	P
2.45055			*	*	P	P	P	P
0.244512					P	A	P	A
					A	P	A	
2.466413			**	*	P	P	P	P
1.681676			*		P	P	P	P
2.651695	*	**	*	*	P	P	P	P
1.277223			*		P	P	P	A
7.519582	*		**	**	P		P	P
2.394199			*	*	P	M	P	P
2.794786				*	A		P	P
2.120179				*	P		P	A
	*				P	P	M	
5.076858			**	*	P	P	P	P
	*				P	A	P	
0.411906					P	P	P	P
0.188084					P	P	P	P
0.617723					P	P	P	P
0.201681					A	P	A	A
0.071897					P	P	P	P
0.749981					P	P	P	P
1.000007					P	A	P	A
1.042682					A	A	A	A
					M	P	A	
0.443726					P	P	P	P

1.604101			*	P	P	P	P
2.591699				*			P
3.090979				**			P
	*			P	P	A	
0.470681	**			P		A	A
1.928375				P	P	A	A
2.48387			*	P	P	P	P
2.29687		*	*	P	P	P	P
1.378744				P	P	A	P
2.34519			*	P	A	A	P
0.285934				P		A	A
2.093576			*	P	P	P	M
2.053447		**	*	P	P	P	P
1.1145	*			P	P	P	P
0.841201				P	P	P	P
0.772767				P	P	P	P
				A			
2.023631			*	P	P	P	P
7.083459		*	**	P	M	P	P
0.661919		*		P	P	P	A
0.496373				P	P	P	P
3.5529	*	**	*	P	P	P	P
0.914572		*		M	P		A
		*			P		
1.066205				A	P	A	P
4.404313			*	P	P	P	P
0.413727				P	P	P	P
0.37561				P	P	A	P
1.276806		*		P	P	P	P
0.359563							A
0.731977				A	A	A	A
1.002812		*		P	P	P	A
2.591399			*	P	P	P	P
2.043634		*	*	P	P	P	P
3.341977	*	**	*	P	A	P	P
0.96957				P	P	A	A
0.463511				P	P	P	P
3.941812			*				P
						A	
3.361736			*	P	P	P	P

1.823759		*		P	P	P	P
	**			P			
		*		M	A	P	
3.904173			*	P	P	P	P
0.647936				P	P	P	P
0.684123				P	P	P	P
0.384961				P	P	P	P
0.499132				P	P	P	P
2.662343			*	P	P	P	P
	*			P			
2.200445			*	P	P	P	P
	*			M			
2.905566		*	**	P	P	P	P
0.399817				P	P	P	P
0.943049		**		P	P	P	A
0.385293				P	P	P	A
0.087917		*			P	P	A
2.778478			*	P	A	P	P
0.423988				P	P	P	P
0.41156				P	P	P	P
				A			
2.158115			*	P	P	P	P
1.507326				P	P	P	P
1.386983				P	P	P	P
4.198215			*	P	P	P	P
0.217248				P	P	P	A
3.213267			**	P	P	P	P
0.47737				P	P	P	P
0.858349				P	P	P	P
2.694341		*	*	P	P	P	P
0.091322				P	P	A	A
0.393604				P	P	P	P
0.378256				P	P	P	P
					A		
0.501495	*			P	P	P	P
0.621869					A	A	A
0.642075		*		P	P	P	P
		*			A	P	
1.920983		*		P	P	P	P
2.070137			**	P	P	P	P

	*		*	P	P	P	
0.966559				P	P	P	P
	*			P	A	A	
1.499909			*	P	P	P	P
2.375526	*		*	P	A	P	P
0.647594				P	P	P	M
0.391197				P	P	P	P
1.615798			*	P	P	P	P
	*			P	A		
0.393398						A	A
0.420111				P	P	P	P
0.958378		**			P	A	A
		**	**		P	P	
1.375189			*	P	P	P	P
2.064512			*	P	P	P	P
			*	A	A	P	
1.891481			**	P	P	P	P
				A			
1.246809	*		*	P	P	P	P
2.33122			*	P	P	P	P
2.340205			*	P	P	P	P
0.12785				M	P	M	A
3.056564	*		*	**	P	P	P
0.367229				P	P	A	A
3.135505			*	**	P	P	P
0.51082				P	P	A	P
2.15152			*	P	P	P	P
2.535913			*	*	P	P	P
0.37214				P	P	P	A
1.656	*			P	P	P	M
0.36706				P	P	P	P
0.716506			*	P	P	P	P
1.049411	**			P	A	A	A
2.193253			*	P	P	P	P
2.543941			*	A		M	P
0.656094				P	P	P	P
0.511881				P	P	P	P
1.4301	*	*		P	P	P	P
2.751152			*	P	P	P	P
0.460361				P	P	P	P

2.583272			*	*	P	M	P	M
	**				P	A		
2.466672				*	P	P	P	P
0.654098					P	P	P	P
0.249485						P	A	A
0.773641					P	P	P	A
2.94504	*	*	**	**	P	P	P	P
0.519813					P	P	P	P
						P	A	
4.106575				*	M	A	A	P
2.125136			*	*			P	P
0.057788								A
1.695217		*	*		P	P	P	P
0.436246					P	P	P	P
0.03584					A	P	A	A
3.732541	*		*	*	P	P	P	P
2.580464				*				P
0.424478							A	A
4.625257			*	*	P	P	P	P
3.222111				**	P	P		P
0.426281					P	P	P	P
1.030552					P	P	P	A
		**			P	P		
0.083579					A	M		A
					P	P	P	
					P	M	A	
					P	P	P	
0.359269					P	P	P	P
0.799087					P	P	P	P
3.528763				*	P	P	P	P
					P	A		
0.415253					P	P	P	M
0.589279					P	P	P	P
0.428859					P	P	P	P
4.46117			**	*	P	P	P	P
3.225757			*	**	P	P	P	P
					P	A	A	
1.338479					P	P	A	P
					P	P	P	

0.100719		*			P	P		A
3.057358				**	P	P	P	P
					M	P	A	
1.431378		**			P	P	P	P
1.19512					P	P	P	A
3.815817	*			*	P	P	P	P
0.457542					P	P	P	P
0.456585					P	P	P	P
2.062044				*	P	P	P	P
2.56741	**		**	*	P		P	P
1.305285			*		P	P	P	P
						A		
3.313437		*	*	*	P	P	P	P
	**				P			
2.771259				*	P	P	P	P
0.343248					P	P	P	P
2.385182			*	*	P	P	P	P
0.620765					P	P	P	P
0.375971					P	P	P	P
					A	A		
0.424777					P	P	P	P
			**		P	A	P	
			**				P	
1.003874		*				A		A
9.222591				**				P
0.195477					P	P	P	P
2.280893				*	P	P	P	P
0.284759	**				P	P	P	A
0.297277					P	P	P	P
0.461708					P	P	P	P
					A	P		
1.789713			*		P	P	P	P
0.777952	*				P	P	P	P
0.153454					P	P	P	P
0.055147					P	P	P	A
		**			P	P	P	
4.087299				*	M			P
2.941821				**	P	P	P	P
0.968667					P	P	P	P
0.398446					P	P	P	P

3.333798			*	M	M		P
0.687519				P	P	P	P
0.612739				P	P	P	P
		*		P	M		
1.773996			*	P	P	P	P
0.175917				P	P	P	A
2.087897				*	P	P	P
2.293184				*	P	P	P
2.617751				*	P	P	P
4.733684		**		*	P	P	P
0.471548					P	P	P
0.423451					P	P	P
0.407454					P	P	P
2.2951	**			*	P	P	P
0.141232					P	P	A
3.374297			*	*	P	P	P
0.282278							A
		**			P		M
2.553623				*	M	P	A
0.800629					P	P	P
0.46246					P	P	P
0.414753					P	P	P
51.76439	**			**	P		P
3.431669				*	P	P	P
4.710387		*	**	*	P	P	P
2.754165				*	P	P	P
3.03161				**	P	P	P
3.63681				*	P	M	P
0.645506	*				P	P	P
2.210855				*	P	P	P
0.87285					P	P	P
					P	P	A
0.284329					P	P	P
0.865195			*		P	P	P
0.50473					P	P	P
	*				P	A	P
0.610054					A	P	A
					A		
0.427115					A	A	
1.738308			*		P	P	P

0.251397					P	P	A	A
					A			
1.522174			*		P	P	P	P
			**				P	
					A			
1.146189	*	*			P	P	P	P
0.337183					P	P	P	P
0.461752					P	P	P	P
0.058536					P	P	P	A
0.942944	*	*			P	P	P	P
0.129005					P			P
0.406553					P	P	P	P
			*			P	P	
1.474609					P	A	A	A
0.325359					P	P	P	P
					A		M	
2.836359			*	*	P	P	P	P
17.16753				**	P	A	A	P
							A	
0.505219					P	P	P	A
							A	
1.470037					P	P	P	P
0.396298					P	P	P	P
0.41995					P	P	P	P
0.383184					P	P	P	P
		**			P	P	A	
2.019771		*	*	*	P	P	P	P
0.326021	**				P	P	M	A
2.219054				*	P	P	P	P
0.503429					P	P	P	P
1.009108			*		P	P	P	M
2.054908		*	**	*	P	P	P	P
0.575683					P	P	P	P
2.733166				*	P	P	P	P
2.11203				*	P	P	P	P
0.859136					P	P	P	P
							A	
0.759627					P	P	P	P
4.30689			**	*	P	P	P	P
34.59472				**				P

0.671047				P	P	P	P
0.338208				P	P	P	P
		**		A	P	P	
0.48929				P	P	P	A
3.547934			*	*	P	P	P
2.211904				*	P	P	P
0.675856	**				P	P	P
					P	P	A
2.094493				*	P	P	P
0.510956					P	P	P
		*			P	P	A
0.806288					P	P	P
0.810815					P	A	A
6.019977			*	*	P	A	P
1.890454			**		P	P	P
0.598818		*			P	P	A
2.083157				*	P	P	P
1.480266					P		A
0.907403					P	P	P
5.907765				*			P
0.971447			*		A		P
2.114414				*	P	P	P
3.687262			*	*	P	P	P
2.726502				*	P	P	P
2.262731				*	P	P	P
1.697295		*			M	P	P
1.430952	*				P	P	P
1.268696					P	P	P
0.465208					P	P	P
0.209477					P	P	P
0.292186			*		P	A	P
1.811644			*		P	P	P
0.835381	**				P	A	A
0.49933					P	P	P
1.692592					P	P	P
1.620454					P	P	A
1.810833	**				P	A	P
0.733549					P	P	A
0.30485					P	P	P
0.285956					P	P	P

0.52516				P	P	P	P
0.468164				P	P	P	P
0.47233				P	P	P	P
					A		
0.169877				P	P	A	A
3.514476	*		*	P			P
0.276443				P	P	P	P
0.015748				P	P	A	A
3.444684		*	*	P	P	P	P
	*			P			
3.062752			**				M
3.543962			*				A
0.408982				P	P	P	P
2.519892			*	P	P	P	P
0.210126				P	P	P	P
1.022584				A	P	A	A
0.424856				P	P	A	A
3.113497			**	P	P	P	P
0.405744		**		P	P	P	A
2.403959			*	P	P		P
3.833925		**	*	P	P	P	P
1.479426				P	P	P	P
0.736807		*		P	P	P	P
2.65112		**	*	M		P	P
2.388086			*	P	P	P	P
6.238506	**	**	*	P	P	P	P
				A			
0.154269						A	A
0.442536				P	P	P	A
0.577791	*			P	P	P	P
0.490882				A	P	A	A
3.262031		*	*	P	P	P	P
1.175018				A		A	A
0.338842				P	P	P	P
0.648247				P	P	P	P
0.701882				P	P	P	P
					A	P	
				M	A	A	
0.205149				P	P	P	P
2.71906			*	P	P	M	M

0.45106				P	P	P	P
0.296505				P	P	P	P
4.018166			*	P	P	P	P
0.239609							A
				P	P	A	
1.466337		*		P	P	P	P
	*				M		
2.089587			*	P	P	P	P
2.142422	*	**	*	P	P	P	P
16.3291			**	P	P	A	M
0.073693				P			A
0.19716				P	P	P	A
0.595952				P	P	P	P
0.972456				P	P	P	P
1.351257		**		P	P	P	P
1.256758				P	P	P	P
0.449402				P	P	P	P
2.980785			**		P	A	P
0.492611				P	P	P	P
0.345474				P	P	P	A
	*			P		A	
				A			
					A		
0.662599				P	P	P	P
1.936562		**		P	P	P	P
1.46699	**			P	P	P	P
0.40899				P	P	P	P
0.74586				P	P	P	P
0.100618					M	P	A
9.342858		**	**	P	P	P	P
0.31018				P	A		A
	*	**		P		P	
4.221434			*	P	P	P	P
3.8217		*	*	P	P	M	P
	**			P		M	
0.422183				P	P	P	A
1.046829	*			P	P	P	M
2.107756			*		A		A
0.81398		*			P	P	A

1.991492			*		P	P	P	P
81.13336				**		A	P	P
0.403255					P	P	P	P
	*		*		P	P	M	
0.290985			**		P	P	P	M
2.225469				*	P	P	P	P
1.291786			*				P	P
						M	P	
2.591845			**	*		P	P	M
	**				P			
0.136313		*			P	P	A	A
					P	A	A	
2.134389				*	P	P		M
0.334548					P	P	P	M
1.708704					P	A	A	P
0.25183					P	P	P	P
						A	A	
						A		
0.458194					P			A
0.461565					P	P	P	P
0.626456					P	P	A	P
2.005996				*	P	P	P	P
0.528781					P	P	P	P
2.4634			*	*	P	P	P	P
2.597449				*	A	P	P	P
0.862686					P	P	P	A
2.296872				*	A			P
0.495898					P	P	P	P
		*			P	P	M	
0.340778					P	P	P	A
1.390444	*				P	P	P	P
0.389271					P	P	P	P
1.056765					P	P	P	P
0.958821	*				P	P	P	P
1.779499			*		P	P	P	P
1.56846			*		P	P	P	P
3.861555	**	*	*	*	P	P	P	P
0.411185					P	P	P	P
2.494501			**	*	P	P	P	P
0.707453					P	P	P	P

0.259255				P	P	P	A
0.639187				P	P	P	P
5.077252		*	*	P	P	P	P
1.543787		*		P	P	P	P
0.281321				P	P	P	P
					A	A	
5.793366		**	*	P	M	P	P
1.227749		*		P	P	P	M
		*		P	A	P	
0.730522				P	P	P	P
0.620312				P	P	P	P
0.466002				P	P	P	P
1.737787		**		P	P	P	P
0.888503		*		P	P	P	P
1.607075		**		P	P	P	P
0.389549				P	P	P	P
0.419654				P	P	P	P
1.191404				P	P	P	P
0.417831				P	P	P	P
0.711301	*			P	P	P	P
0.516452					M	A	A
				M			
3.689376			*	P	P	P	P
	*	*	*	P	P	P	
3.257579			*	P	P	P	P
0.717136				P	P	P	P
1.796338				P	P	A	P
	**			P			
	**		*	P	A	M	
0.30196				P	P	P	P
4.309831			*	P	P	P	P
					A		
	*	*		P	P	M	
1.086113	*			P	P	P	P
0.210487				P	P	P	P
2.557143			*	A		A	M
1.374017				P	P	P	P
0.436812				P	P	P	A
					A	A	
2.096396			*	A	P	A	M

		*			A	P	P	
1.330838			*		P	A	A	P
5.562644			**	*	P	P	P	P
2.066794				*	P	P	P	P
2.715321	*	**		*	P	M		P
1.041529					P	P	P	A
2.027522			*	*	P	P	P	P
1.38766			*		P	P	P	P
0.945588					P	P	P	P
2.721187	**	*	*	*	P	P	P	P
		*			P	P	P	
0.093966		*				P		A
0.404174					P	P	P	P
0.22555	*				P	P	M	P
0.445824					P	P	P	P
0.453123					P	P	P	P
2.371835	*			*	P	P	P	P
2.393824	*			*	P	P	P	P
2.98773				**	P	P	P	P
					P	P	A	
					A	P	A	
1.283984	*				P	P	P	P
2.971282			**	**	P	P	P	P
6.680314	*	*	*	**	P	P	P	P
32.17386			**	**			P	P
2.81755	*		*	*	P	P	P	P
					A			
0.776113					P	P	P	P
			**				P	
0.112482					P		A	A
0.244277					P	P	P	P
2.587188	*		**	*	P	P	P	P
1.099256					P	P	P	A
0.673435			*		P	P	P	P
					A	P	A	
2.183767				*	P	P	P	M
	*				P			
3.013552			*	**	P	P	P	P
4.307387			*	*	P	M	P	P
0.181603					M	A		A

0.497994				P	P	P	P
62.0682		*		**	P	P	A
24.67871				**			P
5.729495				*	A	P	M
2.808327			*	*	P	P	P
2.723051				*	P	P	P
4.152802			*	*	P	P	P
0.455885					P	P	P
0.43688					P	P	P
0.192164					P	P	P
0.465269					P	A	A
1.543646	**				P	P	P
0.61954					P	P	M
0.734389	*				P	P	P
1.353391	*		*		P	P	P
0.743791	*				P		A
0.990331					P	A	P
						A	
2.091926				*	P	P	P
3.085645			*	**	P	P	P
1.769403			*		P	P	P
0.377319					P	P	P
0.209064					P	P	P
0.491095					P	P	P
0.480363					P	P	P
6.167373			*	*	P	P	P
0.78435	*				P	P	A
0.686239					P	A	A
7.244535				**			P
1.626808			*		P	P	P
0.438823					P	P	P
					A		
2.280961				*	P	P	P
1.055232					P	P	P
0.249826					P	P	P
2.690597			*	*	P		P
0.384421					P	P	P
							A
		**				M	
		*			P	P	

				A			
1.967263		*		P	P	P	P
2.620431			*	P	P	P	P
0.400449				P	P	P	P
0.482091				P	P	P	A
0.42191				P	P	A	A
0.442541				P	P	P	P
2.149485			*	P	P	P	P
2.938818		*	**	P	P	P	P
1.731606		*		P	P	P	P
2.855637			**	P	P	P	A
					A	P	
2.47747			*	P	P	P	P
21.66716			**	P			P
13.54246			**	P			P
				A			
1.514605		*		P	P	P	P
1.229023	*			P	P	P	P
	*	**		P	P		
0.413308				P	P	P	A
2.115109			*	P	P	P	P
1.415489		**		P	P	P	P
0.536587				P	P	P	P
0.442316				P	P	P	P
0.43482				P	P	P	P
0.335771				P	P	P	P
0.668494				P	P	P	P
0.440807				P	P	P	P
9.457492			**	A			P
2.045404			*	P	P	P	P
0.171616				P	P	M	A
1.06236				P	P	P	P
	*			P			
2.008225			*	P	P		P
				P	P	A	
0.470543				P	P	P	P
0.486278				P	P	P	P
					A		
1.274721	*	**		P	P	P	P
				P	P	A	

2.097602	*			*	P	P	P	P
0.486678					P	P	P	A
2.115697		*	**	*	P	P	P	P
0.492385					P	P	A	A
0.548583					A	P	A	M
0.882121	*				P	P	P	A
0.677971					P	P	P	P
2.620785	*			*	P	P	P	P
3.165117			*	**	P	P	P	P
0.096783					P	P	P	A
0.523042					P	P	P	P
1.627479			*		P	P	P	P
1.960559			*		P	P	P	P
2.537393				*	P	P	P	P
0.463819					P	P	P	P
0.699572	**				P	P	P	P
3.097738				**	P	P	P	P
1.973045			*		P	P	P	P
0.085996	*				P	P	A	A
	**				P	P	A	
0.945796					P	P	P	P
0.330533						A		A
0.455682					P	P	P	P
0.35315					P	P	P	A
0.273777					P	P	P	P
0.256782					P	P	P	P
3.23815			*	*	P	P	P	P
5.012141			*	*	P	P	P	P
1.888108			**		P	P	P	P
5.650423			*	*	P	P	P	P
2.697089			*	*	P	P	P	P
2.839606			*	*	P	P	P	P
3.302813			*	*	A	A	P	P
0.485696					P	P	P	M
0.513269							A	A
1.966149			*		P	P	P	P
0.488298					P	P	P	P
0.852752	**				P	P	P	A
0.443332					P	P	P	P
4.914649			*	*	P	P	P	P

4.2496	*	*	**	*	P	P	P	P
					A	A	A	
0.527899					P	P	P	P
0.659311					P	P	P	P
	**				P	A	P	
0.116661						A		A
24.75504	**		*	**	P		P	P
1.052335	*				P	A	A	A
2.07041	*		*	**	P	P	P	P
0.382759					P	P	P	P
2.635649	*		*	*	P	P	P	P
		*	**		P	P	P	
5.605566				*	A	A	P	P
119.0426			**	**	P	P	P	P
0.519216					P	P	A	A
2.036603				*	P	P	P	P
4.059942			*	*	P		P	P
					A			
0.082472		*			P	P	P	A
0.26852					P	P	P	P
0.339494					P	P	P	P
						A		
	*				P			
0.295513					P	P	P	A
1.320422		*			A	P		A
2.342817				*			P	A
0.451359					P	P	P	P
0.454525					P	P	A	A
							A	
	*				P			
0.093448					P			A
		*				P		
1.926134			*		P	P	P	M
		*				P	P	
0.876072					P	P	A	A
					A			
1.331509					P	P	P	P
		**				P		
0.955744					A	A		A
							A	

1.100227				P	P	A	A
		**		P		P	
1.400403				P	P	P	P
3.700459	**	*	*	P	P	P	P
7.572843			**		A		M
0.864641					A	P	P
16.34281			**	P	P	A	P
		*		P	P		
	*			P	P		
2.333492		*	*	P	P	P	P
		**				P	
10.34904			**	P	A		P
1.29665		*			P		A
0.324827							A
2.748778		*	*	P	P	P	P
2.092069			*	P	P	A	A
		*		P	P	A	
8.991676		**	**	A	P	P	P
						A	
		*			M		
48.80223			**				P
7.051243			**				M
0.686511				P	P	P	P
0.36002				P	P	P	A
2.026059			*				P
0.397302						A	A
		**		A		M	
0.369523	**			P	P	P	P
		*		M	M	P	
20.59094			**				P
0.495792				P	P	A	A
1.950034				P	P	A	A
0.826997				P	P	P	P
				P		A	
2.001909		*	*	P	P	P	P
0.42728				P	P		A
1.126193	*			P	P	P	P
					M	A	
		*			A	A	
0.450274				P	P	P	P

2.443385			*	P	P	P	P
0.821681				A			A
1.451001				P	A	A	A
0.17309				P	A		A
1.059547				P	P	A	P
0.428453				P	P	P	P
						A	
0.110012				P	P	A	A
2.906325		*	**	P	P	P	P
0.254484				P	P	A	A
				A			
	**			M	A		
1.480758	*			P	P	P	P
0.887932				P	P	P	A
0.40531				P	P	P	P
9.311782			**				P
0.702717				P	P	P	P
2.614604			*	P	P	P	P
0.692778	**			P			A
3.120875			**	P	P	P	P
	**			M		A	
1.405766		*	*	P	P	P	P
			*		A	P	
1.479563			*	P	P	P	M
1.541468			*		P	P	P
0.691641				P	P	P	P
2.795605			*	A			P
3.328558		*	*	A	P	A	P
0.184328					P		A
1.104323		**		M		P	M
2.074696			*	P	P	A	P
				A			
2.055391		*	*	P	P	P	P
0.272023	*			M			A
0.888471				P	P	P	A
0.185838				P	P	P	A
					A		
6.740546			**	A	A	A	M
					A	A	
1.509384		*		P	P	P	P

0.333291				P	P	P	P
1.423753	*			P	P	P	P
3.797358		*		*	P		P
2.005035				*	P	A	M
					P	A	
1.166984				M	P	A	P
2.431755				*	P	P	P
0.816285					P	P	P
		*				P	
0.26162				P	P	P	P
0.419411				P	P	P	P
0.346287				P	P	P	P
1.452368				P	P	P	P
0.126792				P	P	P	P
2.322979			**	*	P	P	P
5.548574				*		P	M
0.43391				P	P	A	A
0.894598				P	P	P	A
1.03879			*			P	M
0.326929	*			P	P	P	A
4.913055				*	P	M	P
					P	A	A
2.252468				*	P	P	P
0.312859					P	P	P
0.279229					P	P	P
0.792441	*				P	P	P
1.338641	*		*		P	P	P
	**				P		
0.046318	**		*		P	P	P
					A	A	
			**		A		M
						A	
						A	
1.759973	*			P	P	P	P
0.585517		*		P	P	P	P
2.751927				*	A	P	M
	*				P	P	A
0.831218					A	A	A
		*				P	
					P	P	A

1.333233				P	P	A	A
3.925888			*	P	A	P	P
0.651263				P	P	P	M
0.505193				P	P	P	P
0.243065				P	P	P	A
3.274358	**		*	*	P	P	P
1.865982	*				P	P	P
1.448811			*		P	P	P
		**			A	P	
0.836545					A	A	A
0.820873					P	P	P
0.684751		**			P	P	A
2.27395	*			*	P	A	A
						A	
				P	A		
0.963212				P	P	P	P
0.026865				P			A
8.53281				**			P
0.174496					P	A	A
2.405312				*	P	M	P
					A		
		*			A	P	
3.934269		*	*	*	P	P	P
0.63031		*			P	P	A
0.143026					P	P	P
2.388556		*	*	*	P	P	P
1.996171					P	P	P
0.455467					P	P	P
2.065987		**	*	*	P	P	P
0.069601					P	P	A
1.843396		*			P	P	P
106.9012			**	**			P
	**		**		P	M	
0.264015					P	P	P
0.675731					P	P	P
0.474376					P	P	P
2.076942		*	*	*	P	P	P
1.200195					P	P	A
0.374389					P	P	P
0.144796					P	P	A

0.304587					P	P	P	A
0.788802					P	P	P	P
2.960145			*	**	P	P	P	P
0.576322	**				P			A
0.326053		**				P		A
0.26031					P	P	P	A
3.675989				*	A			P
0.055438						P	A	A
2.472996				*	P	P	A	P
0.359435					P	P	P	A
	*				M	P		
0.563929	*				P	P		A
2.593771				*	P	P	P	P
		*	**			M	M	
							A	
2.522101				*	P	P	P	P
0.14937					P	P	P	P
0.258347					P	P	A	A
0.17672					P	P	P	P
0.492801					P	P	P	P
0.661314					P	P	P	P
0.115482					P	P	P	P
		**				P		
0.338186					P	P	P	P
	*				P	P	A	
	*				P	A	M	
0.023	*				P	P	P	A
0.26516					P	P	P	P
0.891718	*				P	P	P	M
3.228465				**	P	P	P	P
0.274987	*				P			A
0.672134					P	P	P	P
1.747955			**		P		P	M
4.70788		*		*	P	P	P	P
6.838148	*		**	**	P	A	P	P
0.449166					P	P	P	P
3.084495				**	P	P	P	P
					A			
							A	
2.511243				*		A		P

2.238946		*	*	P	P	P	P
0.394751				P	P	A	A
2.099356			*	P	P	P	P
2.266452			*	P	P	P	P
5.263128		*	*	P	P	P	P
2.399455		**	*	P	P	P	P
2.423889			*	M			P
2.849283			**	P	P	P	P
2.679809			*				M
		**			M		
				A	A	A	
1.368219	*			P	P	P	P
3.127637			**	A			P
1.091486		*		P	P	P	P
0.409464		**		P	P	A	A
0.494267				P	P	P	P
2.255021		*	*	A	P	P	P
4.5735		*	*	P	P	P	P
2.03905			*	P	P	A	P
0.315365				P	P	P	P
1.674713	*			P	P	M	A
2.213382			*	P	P	P	P
1.0759	**			P	P	A	P
	*			M			
2.66712		*	*	P	P	P	P
0.142742				P	P	P	A
				P	A	A	
11.83033			**				P
4.468908			*			A	P
1.842747	**			P	P	P	P
3.626986			*		A	P	P
				A	P	A	
0.940197				P	P	A	P
0.669331				P	P	P	P
0.332744				P	P	M	A
1.776761		*		P	P	P	P
6.14471		*	*	P	P	P	P
1.756459		*		P	P	P	P
						A	
0.464758				P	P	P	P

29.64944				**	A			P
3.330715				*	P	P	P	P
1.703423					P	P	P	P
0.926969			**		P	P	P	P
0.847515					A	P	A	A
0.331812					P	P	P	P
2.788418			**	*	P	P	P	P
0.455249					P	P	P	P
1.265638					P	P	P	P
2.588895			*	*	P	P	P	P
1.581129			*		P	P	P	P
0.481856					P	P	P	A
					A			
5.263544	*	*	**	*	P	M	P	P
0.818716		*			P	P	P	A
2.388091				*	M			M
0.080366	*				P			A
3.973397			*	*	P	P	P	P
5.525441	*		**	*	P	P	P	P
0.667884					P	P	P	P
0.181926								A
5.052963			**	*	P	P	P	P
0.461003					P	P	P	P
3.04166			**	**		A	P	P
3.555426				*	P	P	P	P
0.963062			*		P	P	P	A
1.917189	*		**		P	P	P	M
					A			
	*				P	P	P	
1.019596	*				P	P	A	P
						A		
					A	A		
2.628886	**		*	*	P	P	P	P
1.197867	*				P	P	P	P
12.54594		*	**	**	P	P	P	P
4.568783	*		**	*	P	P	P	P
			*			A	P	
0.396371					P	P	P	A
0.470749					P	P	P	P
1.56195			*		P	P	P	P

2.337025				*	P	P	P	P
2.357969				*	P	P	P	P
1.23036	**				P	P	P	P
2.062307			**	*	P		P	M
0.363719					P	P	P	P
1.756252					A		P	P
0.562277					P	P	P	P
1.274168			*		P	P	P	A
0.60696					P	P	P	P
0.641827			**		A	P	P	A
	*	*			P	P	A	
0.91243					P	P	P	P
0.441261					P	P	P	P
3.990568	**		*	*	P	P	P	P
							A	
1.470691			*		P	P	P	P
1.945317	*	*	*		P	P	P	P
0.411787					P	P	P	P
0.411416					P	P	P	P
			**		P	M	A	
0.942167			*		P	P	P	P
0.423568					P	P	P	P
		*			A	P	A	
0.375787					P	P		A
0.446678					P	P	P	P
1.131522	**				P			A
0.130453					P	P	A	A
0.733232			*		P	P	P	P
						A		
1.130803							A	A
					A	P	P	
					P	A		
0.41364					P	P	P	P
0.344712	*				P	P	P	A
0.472874					P	P	P	P
1.708169							A	A
0.936904	*				P	P	P	P
4.444434				*	P		A	P
1.465101					P	P	P	P
	*				P	A	A	

0.186757				M	A		A
0.540857				P	P	P	P
2.704736			*	P	P	P	P
3.569117			*	M		A	M
0.700317	*			P	A	P	A
0.059553	*			P	P	P	A
2.710744	*		*	P	P	P	P
		**		A		P	
2.202329			*	P	P	P	P
0.763233	**			P	P	P	P
2.483648		*	*	P	P	P	P
3.211199	**	**	**	P	P	P	P
2.738174			*	P	P	P	P
1.368229		*		P	P	P	P
1.951498		*		P	P	P	P
2.59423	*	**	*	P	P	P	P
				A		A	
3.170908	*	*	**	P	P	P	P
3.607244			*	P	P	P	P
					A		
				P	A		
0.424661				P	P	P	P
				P	P	A	
3.151049		*	**	P	P	P	P
0.486566							A
	*			P	P	A	
0.370756				P	P	P	P
1.303236				P	P	P	P
0.575939	*			P	P	P	P
				P	P	A	
1.56961		*		P	P	P	P
5.362843			*	A	A		P
0.512065				P	P	P	P
		**				P	
2.446541		**	*			M	P
0.413417				P	P	P	P
0.592656				P	P	P	P
0.299149				P	P	P	P
0.911056		*		P	P	P	P
0.803918				P	P	P	P

		**			P			
2.608542			*	*	P	P	P	P
	*				M			
2.062298				*	P	P	P	P
1.703079			*		P	P	P	P
0.426411					P	P	P	P
0.24068					P			A
0.536072			*		P	P	P	A
2.135061				*	P	P	P	P
			*		P	M	P	
0.339013					P	P	P	P
0.534801					P	P	P	A
1.928296			*		P	M	P	P
0.354171					P	P	P	P
	*				P	A		
0.481865					P	P	P	P
0.33747					P	P	P	P
2.992043			**	**	P	P	P	P
2.646375				*	P	P	P	M
1.877736			*		P	P	P	P
1.555311					P	P	P	P
3.187658			*	**	P	P	P	P
3.439574			*	*	P	P	P	P
1.943977			*		P	P	P	P
0.544777					P	P	P	P
0.555635					P	P	P	P
2.236188				*	P	P	P	P
0.30128					P	P	P	P
1.021038					P	P	P	P
6.119272	**		**	*	P	P	P	P
0.488651		*			P	P	P	P
9.214926			*	**			P	M
						P	A	
0.81068		*	*		P	P	P	P
1.495616			**		P	P	P	P
1.707781			*		P	P	P	P
2.307863			*	*	P	P	P	P
0.388727					P	P	P	P
			**				M	
0.383457					P	P	P	P

0.729584		*		P	P	P	P
0.527227		*		P	P	P	P
0.445251		*		P	P	P	P
0.635419	**			P	P	P	A
4.037049		*	*	P	P	P	P
						A	
0.451867				P	P	M	A
0.402571				P	P	P	P
0.493338				P	P	P	P
1.040458				P	P	P	P
				P	A	A	
4.180674		**	*	P	P	P	P
5.145768	**		*	M	P	P	P
2.700542			*	P	P		P
0.575499				P	P	P	A
2.883434		**	**	P	P	P	P
1.591609		*		P	P	P	P
				A	P	A	
				M	M	A	
0.665371				P	P	P	A
0.697693		*				M	A
				P	P	A	
0.52761				P	P	P	P
1.063102				M	P		A
0.948728				P	P	A	P
2.056225			*	P	P	P	P
0.369342				P	P	P	P
0.557726				P	P	A	P
0.817928				P	P	P	P
1.430604				P	P	P	P
1.300942				P	P	A	P
0.488072				P	P	P	P
2.229116			*	P	P	P	P
5.468465	*	**	*	M	P	P	P
2.55842		**	*	P	P	P	P
0.432936				P	P	P	P
0.771043				P	P	P	P
					P	A	
0.805613				P	A	P	P
		**				P	

2.450673			*	P	P	P	P
0.760602				P	P	A	A
1.61096		*		P	P	P	P
	*			P	P	P	
0.348413							A
1.028005		**		P	P	P	P
2.4123		*	*	P	P	P	P
2.051069		**	*	P	P	P	P
2.49047		*	*	P	P	P	P
2.861678			**	P	P	P	P
					P	A	
0.61636				P	P	A	A
		*		P	P	P	
4.47146	*	**	*	P	P	P	P
0.53789				P	P	P	P
1.420942	*	**		P	P	P	P
0.488088				P	P	P	P
2.007202	**	**	*	P	P	P	P
		*			P		
1.174687				P	P	P	A
1.215002		*		P	P	P	P
1.143052		**		P	P	P	P
	*			P	A	A	
0.475539				P	P	P	P
					A	A	
4.03261		**	*	P	P	P	P
	*			P	P	P	
				P	A	A	
				A		A	
0.376696				P	P	P	P
0.617157		*			P		A
2.074777		**	*	P	P	P	P
0.231585				P	P	P	P
				P	P	A	
	*			P	P	M	
				P	A		
2.859824			**	P	P	P	P
					A		
				P	P	A	
0.41786				P	P	P	A

1.361917	*			P	P	P	P
1.677858	*			P	P	P	P
2.672002		*	*	P	P	P	P
				M	P	A	
		*			P	A	
				P	A	A	
2.891528			**	P	P	P	P
0.443341				P	P	P	P
0.411544				P	P	P	A
4.563928		*	*	P	P	P	P
0.919973		*		P	P	P	P
0.42479				P	P	P	P
0.575381				P	P	P	P
3.488557		*	*	P		P	M
2.190049			*	P	P	P	P
				A			
				A			
2.301948		*	*	P	P	P	P
					A		
2.800246			*				P
2.951613			**				M
0.420413				P	P	P	P
				P		A	
2.777867			*	P	P	P	P
		*				P	
0.390954				P	P	A	A
4.079159			*	A			P
2.686973			*	P	P	P	P
0.57547				P	P	P	P
0.390513				P	P	P	P
					A		
0.384839				A			A
0.376431				P	P	P	P
2.892176		*	**	P	P	P	P
3.362814		*	*	P	P	P	P
1.982291		*	*	P	P	P	P
1.069392				P	P	P	P
2.894253		*	**	P	P	P	P
1.116514				P	P	A	M
1.787631	*	**		P	P	P	P

0.395101				P	P	P	P
				A			
0.362567				P	P	P	P
		*			P	M	
0.429659				P	P	P	A
2.73787			*	P	P	P	P
0.330099				P	P	A	A
2.67946	*		*	P	P	P	P
0.781206		*		P	P	P	P
1.132825	*			P	P	P	M
0.878757				P	P	P	P
	*			P			
2.034246		**	*	P	P	P	P
0.457555				P	P	P	P
						A	
0.575311				P	P	P	P
2.776055			*	P	P	P	P
0.462694				A		A	A
0.673884				P	P	M	A
1.869914	*			P	P	P	P
0.92392				A	P	A	P
0.264363		*		P	P	A	A
1.267096		*		P		P	A
2.273172		*	*	P	P	P	P
1.617927		**		P	P	P	P
0.856868				P	P	A	P
1.143596				P	P	A	P
0.93034		*		P	P	P	P
10.08431		*	**	P	P	P	P
0.354786				A			A
	*				M		
1.34432				P	P	P	P
0.214402				P	P	P	P
				A		A	
3.014707		*	**	P	P	P	P
0.582817				P	P	P	A
0.421979				P	P	P	P
	**				P	A	
0.786134				P	P	M	A
0.250082				P	P	P	P

5.196233		*	*	P	P	P	P
	*			P	P		
1.866489	**			P	P	P	P
0.324003				P	P	P	P
	*			A	P	A	
0.942662		**		P	P	A	A
2.079055			*				P
0.426181				P	P	P	P
0.533881				P	P	P	P
0.482781				P	P	P	P
		*		P	P	P	
2.101778			*	P	P	P	P
0.380104				P	P	P	P
1.881814	*	*		P	P	P	P
2.483475	*		*	P		P	P
		*		P	P	P	
1.809216		**		P	P	P	A
0.486581				P	P	P	A
0.254185				P	P	P	A
0.460804					A	A	P
1.279183	*			P	P	A	P
				A	P		
0.789477	*			P	P	M	P
0.688399				P	P	P	P
1.403299		**		P	A	P	M
0.482046				P	P	P	M
1.117984		*		P	P	P	P
	**			P	M		
0.252362				P	P	P	P
0.02319							A
0.67082				P	P	P	P
0.530198				P	P	P	P
2.570001			*	P	P	P	P
0.355184				P	P	P	P
1.623075		*		P		P	P
0.397907				P	P	P	P
1.077786		*		P	A	P	A
1.3948		**		P	P	P	P
	*				P		
0.118594	*			P	M		A

2.671406	*		*	P	P	P	A
1.418581				P	P	M	P
1.295834		*		P	P	P	P
2.032478			*	P	P	P	P
2.67726		*	*	P	P	P	P
0.412454				P	P	P	A
4.014972			*	P	P	P	P
0.794712	*	*		P	P	P	M
2.422697			*	P	P	P	P
0.373655				P	P	P	P
					A		
2.030175		**	*	P	P	P	P
0.483968				P	P	M	P
		*		P	P	A	
0.37537							A
2.170109			*	P	P	P	P
0.45299				P	P	P	P
0.835137				M	P	P	P
0.377955				P	P	P	A
0.28144							A
		*				P	
3.145878			**	P	P	P	P
0.373356				P	P	P	P
0.341913				P	A	A	A
3.035697	*		**	P	A		P
2.814062		*	*	P	P	P	P
2.945764		*	**	P	P	P	M
0.387237				P	P	P	P
1.337918		*		P	P	P	P
1.964093	*	*		P	P	P	P
1.458077				P	P	P	P
		*			P		
0.256539		*		P	P	P	P
0.435497				P	P	P	P
0.440733				P	P	P	P
0.700117	*			P	P	P	P
2.157822			*	P	P	P	P
0.869158				P	P	P	P
		*				P	
2.389529			*	P	P	P	P

0.276936					P	P	P	P
1.605143	*		*		P	P	P	P
3.234741			*	**	P	P	P	P
3.726866				*	P		P	P
1.663905			*		P	P	P	P
2.206727	*		**	*	P	P	P	P
0.435608					P	P	P	P
0.395681					P	P	A	A
0.344831					P	P	P	P
		*			A	P	P	
1.288476			**		P	P	P	P
1.63396			*		P	P	P	P
0.943196					P	P	P	P
0.351399					P	P	P	A
2.128109				*	P	P	P	P
1.213335					P	P	P	P
2.808228			**	*	P	P	P	P
2.619898		*		*	P	P	P	P
1.713519	*		*		P	P	P	P
0.418498							A	A
0.350169					P	P	P	P
4.355629			*	*	P	P	P	P
2.915132				**	P	P	P	P
2.908219				**				P
16.00428		*		**		M		P
2.544542				*				M
3.142255			**	**	P	P	P	P
0.666579		*			P	P	P	P
2.155299			*	*	P	P	P	P
1.262812			*		M		P	P
18.09788	**	**	**	**	P	P	P	P
3.04927			*	**	P	P	P	P
2.166051				*				P
						A		
0.668725					P	P	P	P
0.330132					P	P	P	A
3.72686		*		*	P	P	P	P
2.170337			**	*	P	P	P	P
	*				P		A	
						A	A	

2.196422			*	P	P	P	P
1.583465				P	P	P	P
2.395252			*	P	P	P	P
		*			A	P	
1.058236		*		P	P	P	P
	*			M	P	P	
	**			P			
2.173446	*	*	*	P	P	P	P
0.230957	*			P	P	P	P
2.588975			*	P	P	P	P
0.970791				P	P	P	P
						A	
0.34107							A
4.321949		*	*	P	P	P	P
0.276359				P	P	P	P
3.932272			*	P	P	P	P
1.139435		*		A	M	P	P
2.317005		*	*	P	P	P	P
0.4334				P	P	P	P
2.195574			*		A	A	P
0.779004				P	P	P	P
0.469315				P	P	P	P
2.007085		*	*	P	P	P	P
2.422705			*	P	P	P	P
1.909753		*		A	P	A	M
2.320977		**	*	P	P	P	P
				A	P	P	
3.905628		**	*	P	P	P	P
0.38429				P	P	P	P
0.455299				P	P	P	P
3.702616		**	*	P	P	P	P
46.1159			**	P		P	P
1.468912	*	**		P	P	P	A
1.086983	*			P	P	P	P
5.82485	**	**	*	P	P	P	P
0.809644	**	*		M	P	P	A
0.431833				P	P	P	P
1.341213		*		P	P	P	P
1.433817		*		P	P	P	P
0.667999	*			P	P	P	P

				P	P	P	
1.717112		*		P	P	P	P
0.456112				P	P	P	P
				P	P	P	
0.615632	*				P		A
3.345505			*	P	P	P	P
		*		A		P	
		**				P	
1.095862		*		P	P	P	P
2.815059			*	P	A	P	P
9.062939		*	**	P	P	P	P
2.438579			*	P	P	P	P
		*		P	M	P	
	**				P		
3.458705		**	*	P	P	P	P
2.294895			*	P	P	P	P
0.453086				P	P	P	A
0.418956	**				P		A
3.491592			*	P	P	P	P
1.491374				P	P	P	P
0.677936				P	P	P	P
1.672078		*		P	P	P	P
				A	A		
				A	A		
				P	A	A	
				A	P		
172.5193			**				P
		*		P	P	M	
57.44754	*	**	**	P	P	P	P
0.806423				P	P	P	P
0.972944				P	P	P	P
					A	A	
3.273672		*	*	P	P	P	P
2.193341			*			A	M
2.948792		*	**	P	P	P	P
	*				M		
3.806371		*	*	P	A	P	A
2.208938			*			A	M
				P	P	P	
	*			P	P		

					A	
2.337708		*	A	A		P
7.07827		**				P
1.726397			P	P	P	P
4.526751		*	P	A		P
0.061064						A
2.241016		*	P	P	P	A
1.062575			P	P	P	P
1.312123		*	P	P	P	P
0.386673			P	P	P	P
2.007806		*	P	P	P	P
0.318482		**	A		P	A
		**			P	
0.312572			P	P	P	P
0.491079			P	P	P	P
23.9071		**	A	P	M	P
1.571908		*	P	P	P	P
2.775795		*	P	M	A	P
		*			P	
0.437667			P	P	P	P
1.420433	**		P	P	P	P
					A	
0.123186			P	P	A	A
4.343555	*	*	P			P
0.684254		*	P	P	P	A
		*	P		P	
	**		P			
2.525125		*		P		M
			P	M	A	
0.942958	*		P	P	P	P
3.105136		**	P	A	P	M
5.817652		*	M			M
2.449562		*				P
3.103258		**	P	P	P	P
1.754588		*	P	P	P	P
0.476657	*		P	P	P	P
		**	P		P	
		*		A	M	
	**			P		
0.593211			P	A	P	A

0.870513	**			P		P	A
0.492577					P		A
0.521867				P	P	P	P
0.527912				P	A	A	A
0.551441				P	P	P	P
		**			P		
2.289407			*	A			P
0.396743				P	P	P	P
2.15825			*	P	P	P	P
0.484323				P	P	P	P
0.757639	*			P	P	P	P
2.358958	*		*	P			P
1.831352	**	*		P	P	P	P
	**			P	A		
2.399662	**	**	*	P	P	P	P
0.660238				A	A		A
2.134622			*	P	P	P	P
1.593397	*			P	P	P	P
0.456124				P	P	P	P
1.292518	*			P	P	A	P
0.131307							A
1.521337		**		P	P	P	P
2.068466		**	**	P	P	P	P
1.600565				A			A
5.619389		**	*			P	P
				A	A	P	
0.848887				P	P	P	P
0.319592				P	P	P	P
	*			P			
2.807084		**	*	P	P	P	P
3.224787		**	**	P	P	P	P
					P	A	
3.514319			*		A		P
0.807328	*			P	P	P	P
0.060881				P	P	A	A
1.754745		**		P	P	P	P
3.302764			*		A		P
0.076664							A
	*	*		P	P		
				A			

		**				M		
	*				P		A	
		**				P		
						A		
2.156087				*				P
					A		P	
0.393378					P	P	P	P
			*				P	
2.099755			*	*	P	A	P	P
		**				P		
0.826988	*				P	P	A	P
0.630336					P	P	P	A
0.088219					P	P	P	A
0.349954					P	P	P	P
0.786288			*		P	M	P	P
2.657088				*	P	P	P	P
2.363207				*				P
3.534181				*	P	P	A	P
1.227178	*				P	P	P	P
0.940126					P	P	A	A
		*				P		
1.156602			*		P	P	P	P
0.077845							A	A
0.217426					P	P	P	A
					P		A	
8.769746	*	*	**	**	P	P	P	P
					A			
		**			A	M		
0.390867					P	P	P	A
0.784446	*				P	P	P	A
1.769833			*		P	P	P	P
2.857103				**	P	P	P	P
						A	A	
					P	A	A	
		*				P	P	
3.092144				**	P	P	P	P
			**				M	
1.224964					P	P	P	P
					A			
	**				M	A		

0.042915							A
0.209215				P	P	P	A
1.108132			*	P	P	P	P
1.238569		*	*	P	P	P	P
0.448177				P	P	A	P
2.933508							P
	**			P	P	A	
0.175291					A		A
0.551138				P	P	P	P
0.331704				P	P	P	P
0.560541				A	P	A	A
0.498176				P	P	P	P
0.849798				P	P	A	A
0.460769					P		A
	*			P	A		
0.327072				P	P	P	P
0.54258				P	P	P	P
0.072593				P	P	P	A
				A			
			**		P	P	
0.40887				P	P	P	P
2.655364			*	P	P	P	P
0.480247				P	P	P	P
1.034225	*			P	P	P	P
0.42844				P	P	P	A
2.090082				*	M	P	P
0.790347		*		P	P	M	M
						A	
0.810065	**			P	P		A
	*			P	A	A	
0.295146				P	P	P	P
0.761846				P	P	P	P
0.461811				P	P	P	P
4.874891				*	P	P	P
1.162017		*		P	P	P	P
0.091405				A		A	A
				A	P	P	
1.931361				P	P	P	P
2.1969				*	P	P	P
		*				P	

5.606949			*	*	P	P	P	P
0.373943					P	P	P	P
0.262904					P	P	P	A
0.341069					P	P	P	P
0.455476					P	P	P	P
2.396058			*	*	P	P	P	P
0.25561					M			A
2.87445			*	**	P	P	P	P
0.362082					P	P	P	P
1.269088			*		P	P	P	P
	**				P			
17.1713				**				M
0.922728			**		A	P	P	A
4.072673			**	*	P	P	P	P
0.328486					P	P	P	P
					P	P	A	
			*			A	P	
2.730984			*	*	P	P	P	P
0.469461					P	P	P	A
						A		
3.20146			*	**	P	P	P	P
1.591543			*		P	P	P	P
			**				P	
	*				P		P	
0.48102					P	P	P	P
0.499515					P	P	P	P
0.448983					P	P	P	M
0.310256					P	P	P	P
0.472904					P	P	A	A
0.872888	*				P	P	P	P
0.740392	*				P	P	P	P
0.850288					P	P	P	P
0.226415					P	P	P	A
2.611939				*	P	P	P	P
					A	A	P	
10.03388	**	*	**	**	P	P	P	P
							A	
1.167542					P	P	P	P
	**				A		A	
1.168258	*	*	*		P	P	P	P

0.267603					P	P	P	A
1.537304					A	A	A	A
0.373876					P	P	P	P
0.473422					P	P	P	P
							A	
1.552633	**	*			P	P	P	A
0.305097					P	P	P	A
						A		
3.100627			**	**	P	P	P	P
2.042731			*	*	P	P	P	P
2.788068			**	*	P	P	P	P
2.708902			*	*	M	P	P	P
0.307226					P	P	A	A
0.553567					P	P	P	P
0.35499					P	P	P	P
2.895102				**	M	A	A	P
0.717254					P	P	P	A
1.974954	*		**		P	P	P	P
0.54508					P	P	P	P
0.08074					P	P	A	A
1.326225		*			P	P	P	A
0.42155					P	P	P	A
0.152776							A	A
1.747526			**		P	P	P	P
2.373026	*			*	P	P	P	P
1.563483					P	P	P	P
0.699394	*				P	P	A	P
0.42514					P	P	P	P
1.69553	*				P	P	P	P
2.243094	*		*	*	P	P	P	P
0.839668					P	P	M	P
1.356015			*		P	P	P	P
1.43881					A	M	A	A
0.490337					P	P	P	P
0.083768					A	P	A	A
0.35882					P	P	P	P
0.491417								A
0.47914					P	P	P	P
0.534141					P	P	A	A
2.642947			*		P	A		P

0.845725					P	P	P
3.293125		*	*	P	P	P	P
0.409963				P	P	P	P
0.38396				P	P	P	P
		**			P	A	
0.718504				P	P	P	P
					A		
		**		P	P	P	
0.596644	*			P	P	P	P
					P	P	
1.072021	*			P	P	P	P
2.006881			*	P	P	P	M
0.557709	**			M			A
2.443927			*	P	A	P	P
2.599923			*	P	P	P	A
3.788439	*	**	*	P	P	P	P
		*			M	M	
1.186553		*		P	P	P	P
		*			P	A	
1.052771				P	P	P	A
5.767048			*		P		P
2.125763		*	*	P	M	P	P
0.456539				P	P	P	P
0.573923				P	P	A	A
0.895849				P	P	P	P
1.95339		**		P	P	P	P
		*			P		
0.257241				P	P	P	P
0.430597				P	P	P	A
		**			P		
0.925222	*			P	P	P	P
					A		
0.427208				P	P	P	P
				P	A	A	
0.484803				P	P	P	P
3.812653		**	*	P	P	P	P
16.30692			**				P
				P	A	P	
0.094035				P	P	P	A
2.595641		*	*	A	A	P	P

0.72099					P	P	P	P
			*				P	
5.006808			*	*	P	P	P	P
1.931649			*				P	A
1.413773			*		P	P	P	P
2.770263			**	*	P	P	P	P
4.023804	**		**	*	P	P	P	P
0.503583	*				P	P	P	A
2.126088				*		A	A	A
4.924984			**	*	P	P	P	P
2.04925				*			P	P
1.409673	**				P	P	P	P
0.372063					P	P	P	P
1.567477	*		**		P	P	P	P
0.415254					P	P	P	P
0.26146					P	P	P	P
							A	
0.240939						A		A
1.175393	*				P	P	P	P
	**				P	A		
0.910451	*				P	P	P	P
3.912301		*	*	*	P	P	P	P
2.020697			**	*	P	P	P	P
5.383709			**	*	P	A	P	P
3.414844			*	*	P	P	P	P
9.83859			**	**			P	P
2.470185				*	P	P	P	P
0.426294					P	P	P	P
			*		P	A	P	
2.176459	**	**	*	*	P	M	P	P
16.52779				**		A	A	P
			**				M	
		*				M	A	
			*		P	P	P	
3.972575	*			*	P			P
0.201154					P	P	P	P
0.327915					P	P	P	P
21.05945				**				P
2.004576				*	A	P		P
	*				P	P	P	

3.618634			*	A		A	P
				A			
1.702111	**	*		P	P	P	P
0.542472	**			P	P	P	P
0.481548				P	P	P	P
2.050621			*	P	P	A	P
		**		P		P	
0.468341				P	P	P	P
1.962223				P	M	P	A
				P	P	A	
0.421601				P	P	A	P
0.235956				P	P	P	P
				P			
10.16767			**				P
0.244803				P	P	P	P
0.258094				P	P	P	P
0.068121							A
				P	P	A	
0.489037				P	P	A	A
2.524536		*	*	P	P	P	P
0.719841				P	P	P	P
4.174588			*		A		P
0.985725				P	P	P	P
0.475764				P	P	P	P
0.288233				P	P	P	P
0.057321				A		P	A
1.143444				A	A		P
1.819033		*		P	P	P	P
				A	P	A	
0.493753				P	P	P	P
2.593			*		P		M
	*			P			
0.388832				P	P	P	P
		**		P	P		
				A	A		
0.384384				P	P	A	A
0.038371				P	P	A	A
0.319606	*			P	P	A	A
1.283424		*		P	P	P	P
0.102982				P	A	A	A

0.467785				P	P	A	A
8.572381	*		*	**	P	P	P
2.187166				*		P	A
					A	P	
0.437658				P	P	P	P
0.366173						P	A
1.771503	*			P	P	P	P
2.233428				*	P	P	P
				A	P	A	
1.508503			*	P	P	P	P
0.834867				P	P	P	P
0.770232	**			P	P	P	A
3.506357			*	*	P	P	P
0.32662				P	P	P	P
0.484402				P	P	P	P
2.431302			*	*	P	P	P
2.366584	*			*	P		A
				P	A	A	
2.524789			*	*	P	P	P
	*		*	P		P	
0.341047				P	P	P	A
1.546228			*	P	M	P	P
					A		
	*			P			
14.53431			**	**	P	P	P
1.750145			*		P	P	P
1.082879		*			P	P	A
2.443185				*	P	P	A
	**			M		A	
		**			P		
1.36915				P	P	P	A
						A	
0.787719				P	P	P	P
5.311891				*		M	P
0.191823							A
0.270508				P	P	A	P
0.349849				P	P	A	A
2.574848		*	*	P	P	P	P
2.782776			*	P	P	P	P
3.211476		*	**	P	P	P	P

1.289082		*		P	P	P	P
0.449689				P	P	A	A
0.474927				P	P	P	P
2.737584		**	*	P	P	P	P
0.499891				P	P	P	A
4.305477	*		*	P	A	P	P
		**		P		P	
0.236185				P	P	P	P
0.304656				P	P	A	A
2.027922			*	P	P	P	P
0.268694				P	P	P	P
5.723521		**	*	P	P	P	P
3.021203		*	**			P	P
0.022733				P	P	A	A
1.356736		*		P	P	P	P
0.408238				P	P	P	P
0.423584					P	A	A
		**				P	
3.217466		*	**	P	P	P	P
		*		P	P	M	
2.31431			*	P	P	P	P
0.471236				P	P	A	A
0.465796				P	P	P	P
0.820081				P	P	P	P
0.27019	*			P	P	P	P
0.395593				P	P	P	P
7.400183		**	**	P	P	P	P
	*			P	P	A	
1.400652		*		M	P	P	P
0.942524		*		P	P	P	P
0.937385				P	P	A	P
2.275772			*	P	P	P	P
0.939021				P	P	P	P
0.600513	*			P	P	P	P
1.925607				P	P	P	P
3.183125			**	P	P	P	P
1.002733		*		P	P	P	P
	*			P	P	P	
0.467333				P	P	P	P
1.930597		*		P	P	P	P

1.61331			*		P	P	P	P
3.992997			*	*	P	P	P	P
2.111895			*	*	P	P	P	P
0.336991					P	P	P	P
0.076963								A
0.485296			*		P	P	P	A
0.428127					P	P	P	P
2.314094				*	P	A	A	P
					P	P	P	
2.406054			*	*	P	P	P	P
3.200841			*	**	P	P	P	P
					A			
					P	P	A	
0.620226					P	P	P	P
20.14725	**	*		**	P	P	P	P
1.733731	*		*		P	P	P	P
0.596918					P	P	P	A
2.247039			*	*	P	P	P	P
1.724726			*		P	P	P	P
0.179202					P	P	P	P
0.36404					P	P	P	P
2.261577				*	P	P	P	P
2.422862				*	P	P	P	P
0.878018	*				P	P	P	P
1.06112			*		P	P	P	P
0.206786	*				P	A	P	A
1.360595			*		P	P	P	P
7.697361	*		**	**	P		P	P
2.84985				**	P	P	P	P
0.429578					P	P	P	A
	*				P	P		
			*				A	
27.08379				**				P
		**				A		
						M		
11.55026	**			**	P		P	P
1.433151			*		P	P	P	P
0.469305					P	P	P	P
2.523872				*		A	A	P
1.374329		*			P	P	P	M

2.872718	*			**	P			P
0.425383					P	P	P	P
0.311571					P	P	P	P
	**				P	A		
0.314401					P	P	P	P
1.216526					P	P	P	P
1.561142			**		P	P	P	P
0.350998					P	P	P	P
0.565552	*				P	A	A	A
0.236389					P	P	P	P
5.107232				*	M	P		M
2.325163			**	*	P	P	P	P
0.476646					P	P	P	P
0.421591					P	P	P	P
					A			
1.103264	*				P			A
0.604546	*				P	P	P	P
2.003693				*	P	P	P	M
0.166468								A
					A		A	
0.941513					P	P	A	P
2.277906				*	P	P	P	P
0.397324					P	P	P	P
0.489401					P	P	P	P
0.119073					P	P	P	A
1.852347	*				P	P	P	P
2.581376	*	*	*	*	P	P	P	P
0.462506					P	P	P	P
	**				P	P	A	
0.41236					P	P	P	P
0.086552					P	P	A	A
0.28556					P	P	P	P
0.254907					P	P	P	P
17.50767				**				P
0.487467					P	P	P	P
						A	A	
2.32057			*	*	P	P	P	P
0.600627	**				P	P	P	P
2.242942			*	*	P	P	P	P
3.856131				*	P	P	P	P

0.29126				P	P	P	P
0.359751				P	P	P	P
0.243796				P	P		A
0.035482				P	P	P	A
			**		A	P	
1.137914				P	A		A
0.389445				P	P	P	P
7.931007	*		*	**	P	M	P
5.954172			**	*	P	P	P
2.655576			*	*	P	P	P
0.635792	**				P	P	P
2.192365		*		*	A	P	A
0.612849	*				P		A
7.479081			**	**			P
0.441742					P	P	P
0.587187					P	P	P
					A	A	
			**		P		P
0.747247			**		P	P	P
2.311405				*	P	P	P
2.252729				*	P	P	P
0.304053					P	P	P
			*		P		M
3.02404			**	**	P	P	P
0.599281					P	P	P
0.366115					P	P	A
0.540533					P	P	P
					P	A	A
46.34201			**	**			P
2.879032		*	*	**	P	P	P
9.424267		*	**	**	P	P	P
3.672411				*			P
0.883642	*		*		P	P	P
7.427579			*	**	P	P	P
2.485665				*	P	M	P
0.084498					P	P	A
0.83516					P	P	P
0.39177					P	P	P
1.336534					M	M	A
6.488552	**		**	**	P		P

2.168812	*			*	P	P	P	P
2.631808	*			*	P	P	P	P
2.179159				*	P	A	A	A
0.398318					P	P	P	A
3.001129			*	**	P		P	M
0.853325					P	P	P	P
		*			P	P	M	
		**	*		P	P	P	
1.541378			*		P	P	P	P
2.030015				*	P	P	P	P
2.88947				**	P	P	P	P
2.311383				*	P	P	P	P
7.057978	*		**	**	P	P	P	P
0.970546		*			P	P	A	P
1.445549			*		P	P	P	P
0.449477					P	P	P	P
0.848852					P	P	P	P
		**			P	P	A	
1.037032					P	P	P	A
0.622123					P	P	P	P
0.193774								A
1.229418	*		*		P	P	P	P
			**				P	
1.957118			*		P	P	P	P
0.458441					P	P	A	A
1.395714					P	P	P	P
0.661388	*				P	P	P	A
1.142355	*				P	P	P	P
		*			A	P		
2.246473	*		*	*	P	P	P	P
0.987938			**		P	P	P	A
1.044356			*		P	P	P	M
0.624941					P	P	P	P
2.733746				*	P	P	P	P
		*				P		
3.67541			**	*	P	P	P	P
3.51834			**	*	P	P	P	P
		**	*		P	M	P	
1.993237			*		P	P	P	P
0.334293	**	*			P	P	A	A

	**				P			
1.850414		*			P	P	P	P
0.178162					P	P	P	P
0.155147					P	P	P	P
4.250461	*		**	*	P	P	P	P
					A	M		
2.090413			*	*	P	P	P	P
0.312084					P	P	P	A
0.496563		*			P	P	P	P
	*				P	P	A	
1.52575			**		P		P	P
			*			M	P	
					A		A	
2.534082				*	P	P	P	P
2.038918				*	P	P	P	P
0.116848					P	P	A	A
0.945135	*		**		P		P	A
0.496732					P	P	P	P
						P	A	
0.592085					A	A	A	A
	*				P	A	A	
0.88028			**		P	P	P	P
0.397389	**				P	P	P	P
0.776091					P	P	P	P
2.496482				*				P
0.482879			*		P	M	P	A
0.923082	*				P	P	P	A
					A	P	A	
2.15492			**	*	P	P	P	P
2.216625	*	*	*	*	P	P	P	P
0.487132					P	P	P	P
0.750935					P	P	P	P
1.186452			*		P	P	P	P
3.138103	*		**	**	P		P	A
	*		*		P		P	
1.35846		**	**		P	P	M	P
5.680441		*	**	*	P	P	P	P
0.736758	*		*		P	P	P	P
0.629504					P	P	P	P
2.229344				*	P	P	P	P

2.342247			*	P	P	P	P
3.568702			*	P	P	P	P
1.577588		**		P	P	P	P
1.031512		*		P	P	P	P
2.539423			*	P	P	P	P
2.409966	*	*	*	P	P	P	P
				P	A	A	
1.800816	*			P	P	P	P
0.320022				P	P	P	P
0.563652				P	P	P	P
0.722				P	P	A	P
1.562919		*		A	A	P	P
1.476884		**		P	P	P	P
0.138648				P	P	P	A
0.297367				P	P	P	P
2.52521			*				P
2.928354		**	**	P	P	P	P
0.454618				P	P	P	P
1.520215		**		P	A	P	P
3.58574		*	*	P	P	P	P
0.683339				P	P	P	P
0.367611				P	P	P	P
0.62427	*			P	P	P	P
0.380603	*			P	P	P	P
0.625847	*			P	P	P	P
0.330427		*		P	P	P	P
1.404094		*		M	P	P	P
0.310751				P	P	P	P
7.536146		**	**	P	P	P	P
2.97511			**	P	P	P	P
		*			M	A	
		**			P	P	
1.485342		*		M	P		A
9.726717		**	**	P	P	P	P
8.01593		**	**	P	P	P	P
1.732473		*		P	P	P	P
6.528448		**	**	P	P	P	P
7.835237		*	**	P	P	P	P
	*			P	A	P	
0.250466				P	P	P	A

2.930547			**	**	P	P	P	P
1.508029					P	P	P	M
3.128389				**	P	P	P	P
	**				M			
0.399118					P	P	P	A
2.029621			*	*	P	A	M	P
1.015401	**	*			P	M	P	M
2.550427	*		*	*	P	P	P	P
0.400536					P	P	P	P
0.327809					P	P	P	A
2.447415				*	P	P	P	P
0.201596					A	P	P	P
0.496574	*				P	P	P	P
1.366588	**				P	P	P	P
0.2521					A			A
2.233115			*	*	P	P	P	P
0.444409					P	P	P	P
0.772373					P	P	P	P
2.21535				*	P	P	P	P
	**				P		P	
0.345033					P	P	P	P
0.361188					P	P	P	A
0.890433					P	P	P	P
9.34012				**				P
2.858957				**	P	P	P	P
1.007492	*				P	P	P	P
0.360363					P	P	P	P
1.870547			*		P	P	P	P
	**				P			
2.078897		*		*	P	P	P	M
0.41666					P	P	P	P
2.739769				*	P	P	P	A
0.467429					P	P	P	P
5.075405				*	P			P
2.009981				*				P
0.477447					P	P	P	P
2.306771			*	*	P	P	P	P
1.950232			*		P	P	P	P
2.078876				*	P	P	P	P
2.265229			*	*	P	P	M	P

3.481904			**	*		P	P	P
14.28183	*		*	**	P	P	P	P
2.380593				*	P	P	P	P
2.57976				*	P	P	P	P
4.045724				*	P	P	P	P
1.815887			*		P	P	P	P
1.425868	*	**	**		P	P	P	P
2.198741			*	*	P	P	P	P
		**				P	P	
0.288781					P	P	P	A
0.535898	**				P	P	P	P
0.32991					P	P	P	P
0.617724					P	P	P	P
2.602552				*	P	P	P	P
2.239764			*	*	P	P	P	P
1.491705	*				P	P	P	P
						A		
					A	A		
0.538067					P	P	P	P
		*				P		
0.486559					P	P	P	P
					A			
					P	P	A	
1.088604					P	P	P	P
0.928388						A	A	P
0.447215					P	P	P	P
0.385817					P	P	P	P
0.483226					M	P	M	P
							A	
3.181277			*	**	P	P	P	P
						A		
2.322931			**	*	P		P	P
0.186242					P	P	P	P
0.622701		**	*		A	P	P	A
0.324414					P	P	P	P
2.28394				*	M	A		M
2.304917				*	P	P	P	P
2.448551			**	*	P	P	P	P
0.570318					P	P	P	A
7.04418				**	A			P

0.475217					P	P	P	P
0.363579					P	P	P	P
1.275382					P	P	P	P
		*	**		P	P	P	
0.43554					P	P	P	P
0.257968					P	P	P	P
1.734868			**		P	P	P	P
0.517258					P	P	P	A
1.713782	**				P	P	P	P
2.22425			*	*	P	P	P	P
	*				P			
1.450377					A	P		P
					P		A	
5.691897	*	*	**	*	P	P	P	P
1.070036	*				P	P	P	P
2.625043			*	*	P	P	P	P
		*				P	P	
13.68817				**	P	P	M	P
	**				P			
2.866044				**	P	P	P	P
0.94367					P	P	P	P
1.25789	*				P	P	P	M
2.250072				*	P	P	P	P
2.483699				*	P	P	P	P
2.017987			*	*	P	A	P	M
0.892441	*		**		P	A	M	A
0.599912					P	P	A	A
0.917875					P	P	P	P
0.823687					P	P	P	P
0.787892					P	P	P	P
4.690533				*	P	P	P	P
2.793841			*	*	P	P	P	P
1.838544			**		P	P	P	P
1.122939					P	P	P	P
0.69219	*				P	P	A	A
0.853074	*	*	**		P	P	P	P
		*			M	P		
0.460294					P	P	P	P
	*				P	M	P	
7.396891			*	**	P	P	P	P

0.492861				P	P	P	P
3.876217	*		**	*	M		P
0.446135					P	P	P
5.175397	*		*	*	P		P
2.491104				*	P	P	P
0.709464					P	P	P
1.576338			*		P	P	P
0.17767					P	P	P
0.517963					P	P	P
2.175035				*	P	P	P
0.828731					P	P	P
	**				P		
0.766434					P	P	P
0.239204					P	P	P
10.95137		*	**	**	P	P	P
4.842366		*	*	*	P	P	P
		*			P	P	
0.565996			*		P	P	M
2.329501	*			*	P	P	P
0.27941					P	P	P
		**	**			P	P
1.526043		*			A	P	
		*				P	
2.254621				*	A	P	M
		*	*			P	M
0.444871	**				A		A
2.553926			*	*	P	P	P
			**			M	P
2.583761			*	*	P	P	P
	**				M	A	P
0.457538					P	P	P
1.935882	*		**		P	A	P
0.201677					P	P	P
0.339411					P	P	P
0.497231					P	P	P
					A		
2.61073				*	P	P	P
0.843683	*	*			P	P	P
	**				P		
2.594974	*		**	*	P	P	P

2.192683		**	*	P	P	P	P
3.123386		**	**	P	P	P	P
2.057083		*	*	P	P	P	P
3.185816			**	P	P	A	P
0.184889				P	P	P	A
0.43491				P	P	P	P
1.181307	*			P	P	P	A
1.02715	*			P	P	P	A
2.369274			*	P	P	P	P
4.33949			*	P		P	P
0.533063				P	P	P	P
0.649942				P	P	P	P
3.360739		*	**	P	P	P	P
0.401147				P	P	P	P
0.852162				P	P	P	A
					A		
1.972215		*		P	P	P	P
0.740321				P	P	P	P
0.596532				P	P	P	P
1.306841				P	P	P	P
0.48589		*		P	P	A	A
0.959979				P	P	M	A
2.90481			**	P	A	A	P
0.972662				P	P	P	P
1.947437		*		P	P	P	P
10.93929		*	**		M	P	P
0.436341				P	A		A
0.222948				P	P	P	P
0.928174		**			P	P	P
2.058203	**		*	P	P	P	P
2.1473			*	P	P	P	P
1.213076		*		P	P	P	P
2.577687			*	P	P	P	P
3.119286		*	**	P	P	P	P
0.310406				P	P	P	A
				P	A	A	
3.831284			*	P	P	P	P
1.522985	*			M		A	A
2.260878		*	*	P	P	P	P
4.457136		*	*	P	P	P	P

2.746718	*	**	*	P	P	P	P
0.681892				P	P	P	A
0.220639				P	P	P	A
1.509752	*	**		P	P	P	P
1.493613		*		P	P	P	P
0.434351				P	P	P	P
0.477477				P	P	P	P
1.355675		*		A	P	P	P
0.791389				P	P	P	P
	*				P		
0.397879				P	P	P	P
2.086814		*	*	P	P	P	P
1.552009	*			P	P	P	P
0.568406	**			P	P	P	P
0.811885				P	P	P	P
0.30038				P	P	P	P
2.510772			*	P	P		P
	*			A	P	A	
0.340281				P	P	P	A
					A		
		*		P	A	P	
0.531729				P	P	P	P
0.84011				P	P	A	A
2.202294		*	*	P	P	P	P
		**		P	P	P	
6.390789		*	*	P	P	P	P
2.496467		*	*	P	P	P	P
2.086602			*	P	P	P	P
2.207461	*		*	P	P	P	P
0.744433				P	P	P	P
2.122418			*	P	A	A	M
8.352034		**	**			P	P
4.290926		**	*	P	P	P	P
0.256399				P	P	P	P
0.28828				P	P	P	A
2.912336		**	**	P	P	P	P
1.188728				P	P	A	A
4.194483			*			P	P
0.409184				P	P	P	P
3.089943		**	**	P	P	P	P

0.496487				P	P	P	P
3.714698	*		*	*	P	P	P
1.639737	*			P	A	A	A
			*			M	
0.346216				P	P	A	A
0.676157	*			P	P	P	A
3.285865			*	*	P	P	P
0.348943				P	P	P	P
0.323211		*		P	P	A	P
0.601133				P	P	P	A
1.185572	*		*	P	P	P	P
0.449189				P	P	P	P
0.2808				P	P	P	A
2.934028			*	**	P	P	P
	**			P	P	P	
		**			P		
3.035929			*	**	P	P	P
1.737079			**		P	P	P
0.868315				P	P	P	P
				P	P	A	
1.018807				P	P	P	P
0.362579				P	P	A	P
0.613731				P	P	A	A
1.263119	*			P	P	P	P
5.537836		*	*	*	P	P	P
0.434858				P	P	P	P
0.637017				P	P	P	P
0.475936	*			P	P	P	P
6.60253				**			P
0.992543				P	P	P	P
3.377314				*	P	P	P
1.377954				P	P	P	P
			*			P	
1.272499				P	M	M	A
0.437743				A	P	P	A
0.046591	*		*	P	P	P	A
4.20204		*		*	P	P	P
1.737918	*		*	P	P	P	P
						A	
0.43547				P	P	P	P

0.167207					P	P	P	A
1.09716	*	*			P	P	A	P
3.245186		*		*		P	A	P
2.221287			*	*	P	P	P	P
2.15284				*	P	P	P	P
2.620291				*	A	P	A	P
0.587714			*		M	A	P	P
5.218145			*	*			P	P
2.49081	**		**	*	P	P	P	P
	*				P		A	
1.610967					P	M	A	P
1.266343			*		P	P	P	P
0.447996					P	P	P	P
0.669025					P	P	P	P
					A		A	
8.55589		**	**	**	P	P	P	P
1.598286			*		P	P	P	P
1.963405			*		P	P	P	P
0.483383					P	P	P	P
0.511235					P	P	P	P
0.448666					P	P	P	P
0.630822					P	P	P	P
0.6753					P	P	P	P
0.471184					P	P	P	P
3.386136			*	*	P	P	P	P
2.506613				*	P	P	P	P
0.519866					P	P	P	P
3.455239				*	P	P	P	P
0.232864					P	P	P	A
1.565466			*		P	P	P	P
		*			P	P		
3.700287				*	P	P	P	P
1.162696			*		P	P	P	P
2.046051	*	*	**	*	P	P	P	P
2.998542	*		*	**	P	P	P	P
					A			
					A		A	
2.035766				*				M
0.958233					P	A	M	A
3.151122				**		P	P	P

1.309714			*		P	P	P	P
					P	A	P	
0.839797	*				P	P	P	P
2.361213				*	A		P	P
			**		P		P	
1.653852			*		P	P	P	P
2.306383				*	P	P	P	M
1.477815			*		P	P	P	P
0.941126	*				P	P	P	P
0.56303	**				P	P	P	A
0.69653	*				P	P	P	P
1.45661	**				P	P	M	M
0.724342	**				P	P	A	P
0.739848	*				P	P	A	P
4.121557	**	**	**	*	P	P	P	P
					A	A		
2.294464				*	P	P	P	P
0.61013		*				P		A
4.960409			*	*	P	P	P	P
6.417916			*	*	P	P	P	P
0.351222					P	P	P	P
26.62335			**	**			P	P
0.488117					P	P	P	P
2.376893				*	P			A
0.090195					A		A	A
							A	
0.264862						P		A
0.491217					P	P	P	P
1.702681		*				P		P
2.661726			*	*	P	P	P	P
2.889106			*	**	P	P	P	P
28.91675	*		*	**	P		P	P
0.435827					P	P	P	P
1.138634	*				P	P	P	P
2.046266				*	P	P	P	P
2.240399			**	*	P		P	P
93.25599	**			**	P	P	P	P
1.308986			*		P	P	P	P
0.134822					P	P	P	A
0.558314					P	P	P	P

1.348557		*		P	P	P	P
2.167814			*	P	P	P	P
1.663295	**			P	P	P	P
0.320755				P	P	P	P
0.416726				P	P	P	P
9.376152		**	**	P	P	P	P
1.897984		*		P	P	P	P
		*		P	A	P	
1.499337		**		P	P	P	P
0.035113				P	P	P	A
0.358288				P	P	A	A
1.467744		**		P	P	P	P
2.105385		*	*	P	P	P	P
1.696797		**		P	P	P	P
1.676674		**		P	P	P	P
17.44384			**	A			M
0.269548				P	P	P	P
0.750687				P	P	P	P
1.653441		*		P	P	P	P
2.153659			*	P	P	P	P
0.197736				P	P	A	A
0.058052		*		P	P	A	A
0.306471				P	P	P	P
5.119394	*	*	*	P	P	P	P
1.62068		*			P	P	P
26.10055			**				M
3.575951		**	*	P	A	P	P
4.106049			*	P	P	M	P
1.119926				A	P	A	A
0.201366	*			P	P	P	A
0.487976				P	P	P	P
3.269936			*	P	P	P	P
		**				P	
2.479496		*	*	P	P	P	P
1.45387				P	P	A	P
0.472696				P	P	P	P
2.823604		**	*	P	A	P	P
1.712619		*		P	P	P	P
3.700928		*	*	P	P	P	P
2.629379			*				P

1.386677			*		P	P	P	P
					P	P	P	
0.253655	*				P	A	A	A
0.562093					P	P	P	P
0.385639					P	P	P	P
0.907349					P	P	P	P
2.243344				*	P	P	P	P
	**				P		P	
3.657324	**	*	*	*	P	P	P	P
						A	A	
2.621855			*	*	P	P	P	P
1.770558			**		A	A	P	M
0.439651					P	P	P	P
1.821035	*		*		P	P	P	P
2.348908			**	*	P	P	P	P
5.012683			*	*	P	P	P	P
0.34516					P	P	A	A
0.483434					P	P	P	P
1.432845			*		P	P	P	P
0.036248								A
1.524708	*				P	P	P	P
3.183386			*	**	P	P	P	P
3.47104				*	P	P	P	P
2.091639				*	P	P	P	P
0.433746					P	P	P	P
1.897578	*				P	P	P	P
2.07416				**	P	P	P	P
36.23647	**	*	*	**	P	P	P	P
4.130565			*	*	P	P	P	P
2.088213				*	P	P	P	P
0.651662					P	P	P	P
		*				P		
0.925104			*		P	P	P	P
1.290045					P	A	P	M
0.518372					P	P	P	A
0.276817					P	P	P	A
		**				P	P	
1.42919		*			P	P	P	P
0.177416					P	P	P	A
0.741235	*				P	P	P	P

1.774311	*		**	P	P	P	P
0.576494			*	P	P	P	P
	*	**	**	P	P	P	
0.418506		*		P	P	P	P
0.738857		*		P	P	A	A
3.006098				**	P	P	P
1.913451					P	P	P
0.177101					P	P	P
3.827452				*	P		P
						A	
2.006481				*	P	P	P
0.428992					P	P	P
0.477829					P	P	P
0.885081	*				P	P	P
1.338999	*		*		P	P	P
0.567224					A	P	A
1.641402		*			P	P	P
					P	P	A
0.486818					P	P	P
0.351891					P	P	P
1.677829			*		P	P	P
					P	P	A
2.588984			*	*	P	P	P
1.666384					P	P	P
0.4433					P	P	P
1.330544					P	P	P
0.25568					P	P	P
2.872869			*	**	P	P	P
1.216023					P	P	P
0.831569					P	P	P
0.261363					P	P	P
0.230241					P	P	P
1.38266					P	P	P
3.447224			*	*	P	P	P
1.540784					P	P	P
2.056406	*	*		*	P	P	P
1.088188					P	P	P
3.017573			*	**	P	P	P
					A		P
1.818531			*		P	P	P

3.009356			**	P	P	P	P
0.63371				P	P	A	A
2.250231			*	P	P	P	P
0.117229				P	P	P	A
0.878662		**		P	P	P	P
2.173814			*	P	P	P	P
2.549513			*			P	P
0.228422				P	P	P	A
0.65645	*			P	P	P	P
2.800996			*	P	P	P	P
22.91228		*	**		P		M
5.741044			*	P	P	P	P
0.498498				P	P	P	P
0.325763				P	P	P	P
0.532648				P	P	P	P
		*				P	
	**			P			
2.085719			*	P	P		P
0.478958				P	P	A	A
2.860765			**	P	P	P	P
2.156641			*	P	P	P	P
2.314365			*				A
5.461037		*	**	*	P	P	P
13.09777		**	**	**	P	P	P
1.207944			*		P	P	P
0.241095					P	P	P
2.614112			**	*	P	P	P
			**			M	
			*		A	M	
4.990056			*	*	P	P	P
0.304726					P	P	P
0.333585					P	P	P
2.049242			*		P	P	P
2.138836			*		P	P	P
2.452033			*		P	P	P
0.280311					P	P	A
0.713003	*				P	P	P
0.415872					P	P	P
						A	
	**			P			

2.28984			*	*	P	P	P	P
	*				P	M	A	
0.94861	**				P	P	P	P
0.750671					P	P	P	M
0.499537					P	P	P	P
2.011442				*	P	P	P	P
		*			P	P	A	
0.490891					P	P	P	P
2.201374				*	A	A		P
0.469445					P	P	P	P
0.490945					P	P	P	P
1.022643	*				P	P	P	P
0.318296					P	P	P	P
0.78604					P	P	P	P
0.496543					P	P	P	A
13.18439	*	*	**	**	P	P	P	P
15.31266	*	*	**	**	P	P	P	P
	**				P	A		
0.490713					P	P	P	P
0.244958					P	P	P	P
2.491556			**	*	P	P	P	P
1.996271	*				P	P	P	P
1.030884					P	P	P	P
0.365672					P	P	P	P
1.956381					P	P	P	M
0.212213					P	P	P	P
0.359232					P	P	P	P
0.11089					M	P	A	A
1.657716			*		P	P	P	P
0.492595					P	P	P	P
0.476545					P	P	P	P
0.404743					P	A	A	A
0.418503					P	P	P	P
		*				M	A	
7.412905			**	**	P	P	P	P
		**				P		
0.662681					P	P	P	P
0.490423					P	P	P	P
							A	
4.857563			**	*	P	P	P	P

0.56667		*		P	P	A	A
2.080885			*	P	P	P	P
2.557097			*	P	P	P	P
				P	P	A	
0.32875				P	P	P	P
0.478962				P	P	P	M
0.551426				P	P	P	P
0.940609				P	P	P	P
0.238338				P	P	P	P
0.294321				P	P	A	A
0.958222		*		P	P	P	P
0.445466						A	A
0.965788				P	P	P	P
3.906417		**	*	P	P	P	P
12.31827	*		**	M		A	P
0.730377				P	P	P	A
		*				P	
1.300913		*		P	P	P	P
		*			M		
				A	A		
6.848544		**	**		P	A	P
0.42495				P	P	P	P
0.164151							A
0.648299	**			P	P	P	P
1.027196				P	P	P	P
0.217536				P	P	P	P
5.213965		**	*	P	P	P	P
3.812154			*		P	P	P
1.935586		*		P	P	P	P
6.147658		**	*	P	P	P	P
0.446721				A	P	A	A
2.174109		*	*	P	P	P	P
		**		M	M	M	
				A			
0.572973				P	P	P	P
0.868112				P	P	P	P
6.099035		**	*	P	P	P	P
0.348176							A
0.174272	*			P	P	P	A
0.495264	*			P	P	P	P

2.043765	*		*	P	P	P	P
2.581531	*	*	*	P	P	P	P
0.316213	*			P	P	P	P
1.969484		*		P	P	P	P
1.831189					A	P	A
1.186473	*			P	P	A	P
1.986945				P	P	P	M
0.326129				P	P	P	P
2.039396			*	P	P	P	P
4.057175			*	A	P	M	M
3.074019		*	**	P	P	P	P
0.475401				P		A	A
2.057367			*	P	P	P	P
2.017164			*	P	P	M	P
					A		
0.993707	*			P	P	P	P
2.722599		*	*	P	P	P	P
0.462731				P	P	P	P
0.49978				P	P	P	P
0.096254				A	P		A
0.183788				P	P	P	P
3.323501			*			A	P
4.752247		*	*	P	P	P	P
0.47661				P	P	P	A
2.023007		*	*	P	P	P	P
0.422634				P	P	P	P
2.142985		**	*	P	P	P	P
1.148799	*	*		P	P	P	P
1.220271		*		P	P	P	P
0.722312		*		P	P	P	P
1.624301				P	P	A	P
63.90585		**	**			P	P
1.256273				P	P	P	P
0.497406				P	P	P	P
0.488265	*			P	P	P	P
0.254084				P	P	A	A
2.041557			*	P	P	P	P
0.762106	*			P	P	A	A
5.440571	**	*	**	*	P	P	P
0.600332					P	P	P

0.320891				P	P	P	P
1.021851				P	P	P	P
2.819635		*	*	P	P	P	P
1.764731				P	P		M
	*	*		P	P	P	
5.468361			*	M		A	P
	*			P	A	A	
0.638175				P	P	P	P
0.704436				P	P	P	P
0.492787				P	P	P	P
0.656707				P	P	P	P
0.31932				P	P	P	P
0.380608				P	P	P	P
0.381535				P	P	P	P
0.280162				P	P	P	P
0.511428				P	P	P	P
0.314641				P	P	P	P
0.115267				M	P	M	A
					A		
0.166604		**			M		A
0.463897		*		P	P	P	P
0.186046				P	P	P	A
	**			P			
0.310517				P	P	P	P
0.591142				P	P	P	A
0.164543				P	P	P	P
2.018229			*	P	P	P	P
0.948013		*		P	P	P	P
0.661098				P	P	P	P
9.790428	*	*	*	**	P	P	P
7.059926			*	**	P	P	P
11.4648	*	*	**	**	P	P	P
4.931367			**	*	P	P	P
65.19303			**	**	P	P	P
2.161343			*	*	P	P	P
2.126618			*	*	P	P	P
1.372206			**		P	P	P
4.112507			**	*	P	P	P
0.063196					A		A
2.125548				*	P	P	P

0.503695				P	P	P	P
2.611575			*				P
9.472492		**	**	P	P	P	P
5.11793			*	P	P		M
2.820387		*	*	P	P	P	P
2.774681		*	*	P	P	P	P
2.219339			*	P	P	P	P
1.831373				A	P	P	M
3.124086	*	**	**	P	P	P	P
3.4893	*	*	*	P	P	P	P
0.402692				P	P	P	P
0.437408				P	P	P	P
2.203443			*	P	P	A	A
7.321194		*	**	P	P	P	P
1.530919				P	P	P	P
2.564463			*	P			P
		**			A	P	
4.143288		*	**	*	P	P	P
3.891492		*	**	*	P	P	P
		*			P		
0.473793				P	P	P	P
						A	
0.812421				A		A	P
1.758924		*		P	P	P	P
0.943905				P	P	P	A
29.98113		*	**	**	P	P	P
		*			P	P	
	*			P			
		*		P	P	P	
0.403411				P	M	P	A
		**		P	P		
10.3802			**				M
0.355494				P	P	P	A
3.029491			**	A	P		P
2.169219		*	*	*	P	P	P
1.87331	*				P	P	P
0.394097					P	P	P
2.58243			*			A	P
0.456476				P	P	P	A
1.100036		*		P		P	P

1.954719			**		P	P	P	P
7.33583			*	**			M	M
					P	A	P	
1.199486					P	P	P	P
0.913477					P	P	P	P
0.824561					P	P	P	P
2.786072				*			P	P
							A	
6.218312	**	**	**	*	P	P	P	P
2.462244			*	*	P	P	P	P
1.60972			**		P	P	P	P
3.971172	*		*	*	P	P	P	P
0.363547					P	P	P	P
	*				P			
0.917185	*				P	P	P	P
	*				P			
0.73484		**			P	P	P	M
1.634362	*				P	P	P	P
		**			A	M		
5.622801			*	*	P	P	P	P
0.64377					P	P	P	P
2.273073	**		**	*	P	P	P	P
1.950779			**		P	P	P	P
2.147552			*	*	P	P	P	P
0.368481					P	P	P	P
2.079632	*			*	P	P	P	P
0.131996					P	P	P	P
0.954039			*		P	A	P	P
27.25519		*	**	**	P	P	P	P
2.445743				*	P	P	P	P
2.783627				*	P	P	P	P
					A			
0.744584					P	P	P	P
					P	P	P	
12.04317			**	**	P	P	P	P
0.288149					P	P	P	M
0.678323					P	P	P	P
2.146928				*	P	P	P	P
11.32108	**			**	P		P	P
0.657146					P	P	P	P

0.471566				P	P	P	P
0.493335				P	P	P	A
0.898447					P	A	A
0.209886							A
1.357679		*		P	P	P	P
0.492049				P	P	P	P
1.124756				P	P	P	P
0.43349				P	P	P	P
				P	A	M	
1.291917	**		*	P	P	P	P
2.025211			*	*	P	P	P
5.407212			**	*	P	P	P
					P	A	
0.832864			*		P	P	P
0.713408					P	P	P
1.089419					P	P	P
1.816249			*		P	P	A
2.172297				*	P	P	P
5.653346		*	**	*	P	P	P
1.828092	**		*		P	P	P
0.286538					P	P	P
0.136059					P	P	A
0.475643					P	P	P
1.739726	*				P	P	P
2.326793				*	P	P	P
2.148908				*	P	P	P
0.133879					P	P	A
			**		A	P	P
0.769132					P	P	P
2.961676	*			**	P	P	P
0.612211					P	P	P
0.537541					P	P	P
0.519469					P	P	P
0.486439					P	P	P
2.289671				*	P	P	P
	**				P	P	P
5.136583	**	*	**	*	P	P	P
2.287388				*	P	P	P
0.350372					P	P	P
2.263951				*	P	A	P

4.817841		**	*	P	P	P	P
2.436263			*				P
0.336886				P	P	P	P
0.233843				P	P	P	A
2.414947		**	*	P	P	P	P
5.865502	*	*	*	P	P	P	P
7.268754		*	**	P	P	P	P
0.448843				P	P	P	P
3.011712	*		**	P	P	P	P
2.33816			*	P	P	P	P
9.952597		**	**	P	P	P	P
	**			P		A	
0.562177					P	A	A
0.938652	*			P	P	P	P
2.166159		**	*	P	P	P	P
2.770874			*	P	P	P	P
2.0872			*	P	P	P	P
1.112526				P	P	P	P
		*		P	P	P	
0.651907				P	P	P	P
0.418938				P	P	P	P
4.073749		*	*	P	P	P	P
0.247814				P	P	P	P
2.698156		*	*	P	P	P	P
1.232348				A			P
0.465228							A
2.31816			*	P	P	P	P
				P	P	P	
0.142609				P	P	P	A
0.744488				P	P	P	P
2.032028			*		M	P	A
0.252349				P	P	P	P
				A			
0.249289				P	P	P	P
3.122352			**	P	P	P	P
1.04413		**		P	M	P	A
2.255569			*	P	P	P	P
2.109516			*	P	P	P	P
2.526515		**	*	A	P	P	M
0.934058				P	P	P	P

1.927424		*			P	P	P	P
0.993886			*		P	P	P	P
1.105246		*			P	P	P	A
2.447169		*		*	P	P	P	P
0.236673	*				P	P	P	A
0.270609					P	P	P	A
1.274936		*				P		A
0.426263					P	P	P	P
0.497369					P	P	P	P
0.747086					P	P	P	P
2.040765				*	P	P	P	P
3.512687			*	*	P	P	P	P
0.227601					P	P	P	P
1.890893					P	P	M	A
3.302209			**	*	P	P	P	P
0.451755					P	P	P	P
1.867494		*			P	P	P	A
	*		**		P		P	
0.208849								A
2.022219				*	P	P	A	P
0.285214					P	P	P	P
6.472585	**	*	**	**	P	P	P	P
1.035448			*		P	P	P	P
3.087601				**	P	P	P	P
2.353887	*	**	*	*	P	P	P	P
0.488417					P	P	P	P
0.432977					P	P	P	P
					P	A		
2.131354			*	*	P	P	P	P
0.362021					P	P	P	P
1.393518	*				P	P	P	P
2.183643				*	P	P	P	P
0.389037					P	P	P	P
5.846126			**	*	P	P	P	P
0.387258					P	P	P	P
					A			
0.725638	**				P	P	P	A
					P	P	A	
	*				M	P		
0.381201					P	P	P	P

2.055734			**	*	P	P	M	P
0.340423					P	P	P	P
0.309117					P	P	P	P
4.322422	*	*	**	*	P	P	P	P
2.582135				*	P	P	P	P
						A		
2.322713				*			A	P
0.434797					P	P	P	P
0.044779					A	P		A
0.362664					P	P	P	M
0.558332					P	P	P	A
1.258616					M	P	P	A
0.812099					P	P	P	P
2.575205			**	*	P	P	P	P
	*				P		P	
0.254572					P	P	P	P
2.316627	*	*	*	*	P	P	P	P
0.729247			*		P	P	P	P
1.046982					P	P	P	P
3.092936			*	**	P	P	P	P
0.440386					P	P	P	P
2.508557				*	P	P	P	P
0.799067	*				P		A	A
2.274206			*	*	P	P	P	P
1.7424	*				P	P	A	P
			*				P	
					P	P	P	
2.248604				*	P	P	P	P
1.908016			*		P	P	P	P
					A		A	
0.318523					P	P	P	P
0.40511					P	P	P	P
					A			
0.416575					P	P	P	P
2.313827				*	P	P	P	P
					P	P	A	
0.294288					P	P	P	P
0.78731					P	P	P	P
0.409235					P	P	P	P
0.688875		*			P	P	P	P

8.588906	*	*	**	**	P	P	P	P
2.828006	*		*	*	P	P	P	P
0.740585	*				P	P	P	P
5.4265			**	*	P	P	P	P
			**				P	
0.06842								A
2.434155				*			A	P
2.604283				*	P	P	A	P
6.243366	*		*	*	P	A	P	P
4.504242	*			*	P	P	P	P
3.260728			*	*	P	P	P	P
2.206162			*	*	P	P	P	P
1.21529	*	*			P	P	P	P
0.367351					P	P	P	P
1.333508		*	**		P	P	P	P
1.566588			**		P	P	P	P
2.495909		*	**	*	P	P	P	P
1.117213		*	*		P	P	P	P
0.468626					P	P	P	P
1.22025	*		*		P	P	P	P
					P	A	A	
1.873819			*		P	P	P	P
1.423772			*		P	P	P	P
1.347388	*		**		P	M	P	P
2.612915				*	P	P	P	P
2.414121				*	P	P	P	P
0.553152					P	P	P	P
0.410045					P	P	A	P
0.836081					P	P	P	P
2.336121			*	*	P	P	P	P
0.214263					P	P	P	P
0.367241					P	P	P	P
0.290696	*				P	P	P	P
0.579958					P	P	P	P
0.460576					A	P		A
0.582569	*				P	P	P	P
5.65342				*				P
0.30571					P	P	A	A
1.008732			*		P	P	P	P
0.464459					P	P	P	P

1.900381			*	P	P	P	P
1.432844		*			P		A
	**			P			
0.760411				P	P	A	P
2.324117			*	*	P	P	P
1.283669	*			P	P	P	P
						A	
1.171564		*		P	P	P	A
2.705351			*	*	P	P	P
1.829631			*		P	P	P
0.398975					P	P	P
0.114612						P	A
1.794319			*		P	P	P
					P	A	
1.273444		*	*		P	P	P
						P	
3.91367				*	P	P	P
0.094644					P	P	A
0.212704					P	P	P
2.116436				*	P	P	P
2.325428				*		A	M
2.923432				**		A	P
0.456032					P	P	P
0.130464							A
0.229581					P	P	P
0.852904					P	P	P
0.395046					P	P	P
2.035474				*	P	P	P
2.37371				*	P	P	P
		*				P	
0.390615					P	P	P
3.531745				*	P	P	P
0.36766					P	P	P
1.341848			*		P	P	P
2.189757				*	M	P	P
0.307096					P	P	P
0.503153					P	P	M
0.476449					P	P	P
0.744767					P	P	A
2.122696				*	P	A	P

0.838955		*			P	P	A	A
0.899624	*				P	P	A	A
0.300957					P	P	P	P
0.408665					P	P	P	A
0.087194					P	A	A	A
0.265449					P	P	P	P
					M	A	A	
1.674348					P	M	A	M
1.903568	*				P	P	P	P
4.259045			*	*	P	P	P	P
			*				A	
		**				P		
1.208658		**			P	P	P	P
20.4183			**	**	A		P	P
			*			A	A	
2.200393				*	P	P	P	P
0.828312					P	P	P	P
2.115103				*	P	P	P	P
1.883535	*		*		P		P	P
1.218139			**		P	P	P	P
1.075846					P	P	P	P
0.915693					P	P	P	P
0.488068					P	P	P	P
0.458762					P	P	P	P
3.0059			*	**	M		P	P
2.112765				*	P	P	P	P
					A	A	A	
2.878701				**	P	P	P	P
1.660904		*			P	P	P	P
2.6813	*		*	*	P	A	P	P
1.872288			*		P	P	P	P
0.405512					P	P	P	P
6.437839	*		*	*	P	P	P	P
0.123247					P	A	A	A
0.766379	*				P	P	P	P
0.972075					P	P	P	P
0.846921		*			P	P	P	P
			*		P	P	M	
		*			P	P		
			**		P		P	

2.472096			*	*	P	P	P	P
3.709255			*	*	P	P	P	P
0.461123					P	P	P	P
3.614482	*	**	*	*	P	P	P	P
2.059267			*	*	P	P	P	P
10.14287			**	**	P	P	P	P
22.82157	**		*	**	P	M	P	P
0.450134					M		P	A
0.588507		**			P	P	P	A
1.643	*				P	P	P	P
0.591336					P	P	P	P
0.334021					P	P	P	P
0.330861					P	P	P	A
6.35781	*	*	*	*	P	P	P	P
0.451108					P	P	A	P
2.042106			*	*	P	P	P	P
0.424162					P	P	P	P
0.781438					P	P	P	P
1.173464	*		*		P	P	P	P
					P	P	P	
1.881724			*		P	P	P	P
5.571632				*				M
2.494865				*	P	P	P	P
			*		M	P	M	
2.010923			*	*	P	P	P	P
1.473469		*	*		P	P	P	P
1.562729					A	A	A	P
0.531095					P	P	P	P
12.02678			**	**	P	P	P	P
1.51963	*		*		P	P	P	P
0.462105	*				P	P	P	A
		**				P		
2.151836		**	**	*	P	P	P	P
0.34944					P	P	P	A
0.011805					P	P	P	A
0.358494					P	P	P	P
0.374842					P	P	P	P
0.463198					P	P	P	P
5.784284				*	A		P	P
4.90015			**	*	P	P	P	P

0.551223				P	P	P	P
6.323284		*	*	M	P	P	P
0.087612					P	A	A
3.256323			*	P	P	P	P
0.460301				P	P	P	P
					A		
0.854429				P	P	A	P
2.146794			*	P	P	P	P
2.527551		*	*	P	P	P	P
0.697203				P	P	P	P
0.267047				P	P	P	A
1.747368		*		A	P	P	P
2.561632			*	P	P	P	P
2.970179	*	*	**	P	P	P	P
7.118964			**			P	P
		**	**	P	M	P	
0.362421				P	P	P	P
2.384509		*	*	P	P	P	P
					A	A	
1.710843				A		A	A
1.424454		*		P	P	P	P
0.489974				P	P	A	A
	*	*	*	A	P	P	
					A		
0.667261	*			P	A	A	P
0.659508		*	*	P	P	P	A
1.284526		**		P	P	P	A
10.97727	*	*	**	P	P	P	P
		**			M		
6.433516		**	*	P	P	P	P
2.506548		**	*	P	P	P	P
1.96132		**		P	P	P	P
2.317748		*	*	P	P	P	P
4.174403		*	*	P	P	P	P
3.876264		**	*	P	M	P	P
0.312645				P	P	P	P
1.438887				A	P	A	P
17.71348			**				P
1.289096		*		P	P	P	P
1.179275				A	M		A

7.827719				**				P
1.565468	*				P	P	P	P
					P	P	A	
2.886453				**	P	P		P
2.307621		*		*	P	P	P	P
1.224845		*			P	P	P	P
3.092199				**	P		P	A
1.702474					P	P	P	P
3.124367		*		**	P	P	P	P
1.19149					P	P	P	P
		*			A	A	A	
8.35336			**	**	P		P	P
2.482116				*	P	A	P	P
0.73448					P	A	P	A
59.42147	**	*	**	**	P	P	P	P
1.006129			*		P	P	P	P
2.732016			**	*	P	P	P	P
					A	P		
						A	A	
22.11307	*	*	**	**	P	P	P	P
2.435711			*	*	P	P	P	P
0.574449					P	P	P	P
1.540841		**			P	P	P	A
1.722527					P	P	A	A
							A	
			*			A	M	
						A		
0.714141						A		A
1.510279	*		*		P	P	P	P
1.184726			*		P	P	P	P
3.24799	**			*	P	M	P	M
			**				P	
1.448113					P	P	P	P
2.601854				*	P	P	P	P
					A			
5.199203	**			*	M			P
1.75562					P	P	P	P
1.3942			*		P	P	P	P
					P	P	A	
2.318391	*			*	P	P	A	M

					P	A	A	
1.468842					P	P	P	P
0.366021					P	P	P	P
0.672368					P	P		A
2.409232				*	A			P
2.353374		*		*			A	M
0.476039					P	P	P	P
0.446945					P	P	P	A
1.393504		*			P	P	M	P
0.266607			*		P	A	M	A
						A		
					P	A		
2.564847	*			*	P	P	A	A
0.829239					P	P	P	P
4.553393		*		*	P	P	P	P
0.433098					P			A
2.030031				*	P	P	P	P
0.680272					P	P	P	P
1.443911			*		P	P	P	P
	**				M	A		
2.376558				*			P	P
1.42415					P	P	P	P
0.795492					P	P	P	P
3.751712		*		*	P	P	P	P
0.381606					P	P	P	A
0.618957					P	P	P	P
	**				M			
1.015388						A		A
2.095604		**		*	P	P	P	P
1.351926					P	A		A
2.730613		*		*	P	P	P	P
2.342266		*		*	P	P	P	P
1.440726	*				P	P	P	P
2.631819		*		*	P	P	P	P
9.734703	*	*	*	**	P	P	P	P
11.38283	*	*	*	**	P	P	P	P
1.245637	*				P	P	P	P
0.501775		*			P	P	P	P
						A	A	

0.597438				P	P	P	P
1.077036			**	A	P	P	A
2.247996				*	P	P	P
4.23932	*		*	*	P	P	P
0.354101				P	P	P	P
0.468026				P	P	P	P
0.454807				P	P	P	P
3.175507			*	**	P	P	P
3.115816			**	**	P	P	P
2.436061				*	P	P	P
0.246161						A	P
3.535075				*	P	P	P
2.306333			*	*	P	P	P
3.460183	*	*	*	*	P	P	P
2.649191				*	P	P	P
1.43685	**	*			P	P	P
3.383354			*	*	P	P	P
	*				P		
0.799027					P	P	P
4.150128	*			*	P	P	P
0.268531					P	P	P
3.084792				**	P	P	P
0.51687					P	P	P
0.478368					P	P	P
2.177846	**			*	P	M	P
3.839393				*	M	P	
0.467031					P	P	P
1.39616			**		P	P	P
0.358674					P	P	P
1.005213					P	P	A
2.396151				*	P	P	P
0.386949					P	P	P
4.323018			*	*	P	P	P
1.48334	*				P	P	P
	**				P	P	A
19.20338	**	*	**	**	P	P	P
					M	M	
1.001552					P	P	P
0.415774					P	P	P
			**			P	

0.635821				P	P	P	P
0.441481				P	M	A	A
1.25026				P	P	P	P
2.986605	*		**	P	P	P	M
0.349797				P	P	P	P
0.46543				P	P	P	P
0.461819				P	P	P	A
2.433347			*	P	P	P	P
0.498137				P	P	P	P
2.4217		*	*	P	P	P	P
1.357569		*		P	P	P	P
0.516983				P	P	P	A
		**		P	A	P	
0.405709				P	P	P	P
3.088703		*	**	P	P	P	P
0.498349				P	P	P	A
0.708452	*			P	P	P	P
	*			M			
0.429014				P	P	P	P
0.424615				P	P	P	P
0.632995				P	P	P	P
0.313843				A	P		A
		*		P	A	P	
					P	A	
2.003994			*	P	P	P	P
0.446447				P	P	P	P
4.859605		**	*	P	P	P	P
0.646214	*	**		P	P	P	P
0.026399				P	P	A	A
0.520031				P		A	A
1.873784		**		P	P	P	P
1.721383		*		P	P	P	P
1.249023		*		P	P	P	P
2.576502			*	P	P	P	P
	*				P		
3.638485		*	*	P	P	P	P
		**		P		P	
8.990442	**		**	P	A	P	P
0.267829				P	P	P	P
1.319654				A	P	A	A

2.73439			*	*	P	P	P	P
1.852571			*		P	P	P	P
1.866146			**		P	P	P	P
5.703775				*				P
3.847492			*	*	M	P	P	P
1.486361					P	P	P	P
	*		*		P		P	
			**			P	P	
2.258718				*	P	P	P	P
0.519484					P	P	P	A
2.397136		*		*	P	P	P	P
2.290618				*	A	P	P	P
0.486821					P	P	P	P
2.231683				*	P	P	P	P
2.356502			**	*	P	P	P	P
1.179592			*		P	P	P	P
2.687623				*	A	P	P	P
	*				P	P	A	
0.441611					P	P	P	A
1.795797			*		P	P	P	P
0.699078	**				P	P	A	A
			*		M	P	P	
2.644793	*		*	*	P	P	P	P
0.851792	*				P	P	P	A
2.991972				**	P	P	P	P
2.039484			**	*	P	P	P	P
						A		
285.1229	**	**	**	**	P	P	P	P
2.113661				*	P	P	P	P
6.305899	*		*	*	P	P	P	P
0.684481	**				P	P	A	P
2.093664				*				P
0.274669					P	A	A	A
0.622079					P	P	P	P
0.646866					P	P	P	P
						P	A	
					M	P	A	
1.694634		*	*		P	P	P	P
2.34331				*	P	P		M
0.254857					P	P	P	P

0.325256					P	P	P	P
16.07059			**	**	P	A	P	M
0.641962					P	P	P	P
0.313611					P	P	P	P
0.189382					P	P	P	P
0.706539	*				P	P	P	P
0.457622					P	P	P	A
		*			A	M		
0.706606					P	P	P	P
2.107444				*	P	P	P	P
2.429877			*	*	P	P	P	P
0.920028	*	**	**		P	P	M	A
0.896328					P	P	P	P
0.285286					P	P	P	P
1.55479					P	P	P	M
2.84218				**	P	P	P	P
1.500079			*		P	P	P	P
2.594648				*	P	P	P	P
1.835659	*		*		P	P	P	P
19.76108			*	**			M	P
4.716631	*		*	*	P	P	P	P
2.868372			**	**	P	P	P	P
2.549211			**	*	P	P	P	P
5.455999		*		*	P	P	P	P
0.784686					P	P	P	P
			*				P	
2.719335			**	*	P	P	P	P
2.971283	*	*		**	P	P	P	P
1.096743		*			P	P	P	M
2.123547				*	P	P	P	P
0.238717					P	P	P	P
						M	A	
0.253957					P	P	P	P
2.876619				**	P	P	P	P
0.768064					P	P	A	P
2.809971				*	P	P	P	P
2.491679				*	P	P	P	P
			*		P	A	P	
2.269978				*	P	P	P	P
0.510112					P	P	P	P

2.27502			*	*	P	P	P	P
3.173528	*			**	P	A	P	P
0.481314					P	P	A	A
0.428243					P	P	P	P
1.033852	*		*		P	P	P	P
0.366964					P	P	P	P
0.260103					P	P	A	A
2.751192			*	*	P	P	P	P
0.961903			*		P	P	P	P
0.528875	*				P	P	A	A
0.120812								A
2.692791			*	*	P	P	P	P
2.73841			*	*		P	P	P
0.419678					P	P	P	P
3.164122				**	P	P	P	P
1.111628	*				P	P	P	P
0.317517					P	P	P	P
2.866915				**	P	P	P	P
1.203387			**		P	A	P	A
2.045456				*	P	P	P	P
1.009653			**		A		P	A
							A	
0.281249					P	P	P	P
2.068281		*		*	P	M		M
1.720063			*		P	P	P	P
1.851123			*		P	P	P	P
2.504985				*	P	P	P	P
1.065139	*				P	P	P	P
1.134514		**	**		P	P	P	A
0.447046					P		P	A
3.868405	*			*	P	P	P	P
2.760531	**		*	*	P	P	P	P
0.668513					P	P	P	P
0.371143					P	P	P	P
1.6193					P	P	P	P
0.304481					P	P	P	P
4.566288	*		*	*	P	P	P	P
2.515447	*	*	*	*	P	P	P	P
		**				P		
0.916544					M	P	A	P

3.353252			*	P	P	P	P
0.993395				P	P	P	P
1.942525				P	P	P	P
2.158071			*	P	P	P	P
0.461043	**	*		P	P	P	P
2.803553			*		M		P
0.418883				P	M	P	P
1.177273		*		P	P	P	P
0.411897				P	P	P	P
2.072667			**	P	P	P	P
0.404208				P	P	P	P
				A	A		
0.560854				A	P	P	A
1.338461		*		P	P	P	P
0.466567				P	P	P	P
2.765494	*	**	*	P	P	P	P
				P	P	A	
2.062472		*	*	P	P	P	M
1.110034	*			P	P	P	P
1.221283				P	A	A	P
0.919143		*		P	P	P	P
0.680461				P	P	A	A
0.453351				P	P	P	P
				P	A		
0.896828		*		A	M	P	A
4.159748			*	P	P	P	P
1.190571		*		P	P	P	P
1.066799				P	P	A	M
0.468873				P	P	P	P
0.270997				P	P	P	P
1.619254		*		P	P	P	P
	*	*		P	P	P	
1.027768				P	P	P	P
1.971297	*			P	A	P	P
0.148995						A	A
2.077138			*	P	P	A	P
1.487398				P	A	P	P
2.520709			*	P	P	P	P
2.553301			*	P	P	M	P
3.461235			*	P	P	P	P

7.938298	*	*	**	**	P	P	P	P
1.131001					M	A	A	M
1.000504					P	P	A	P
0.44416					P	P	P	P
5.636228			**	*	P	P	P	P
6.548929			**	**	P	P	P	P
0.721559					P	P	P	A
0.45872					P	P	P	P
1.013603					P	P	P	A
2.29819				*	P	P	P	P
1.558517	**		*		P	P	P	P
3.769421			**	*	P	P	P	P
0.472557					P	P	P	P
6.055239	*		*	*	P	P	P	P
					A	P	A	
0.442156					P	P	P	P
3.913626			*	*	P	P	P	P
					P	P	A	
		*			P	P	P	
3.042263			*	**	P	P	P	P
85.64077		**	**	**	P	P	P	P
0.186042					P	P	P	A
0.595685					P	P	A	P
			*			P	P	
3.571449			*	*	P	P	P	P
0.57532					P	P	P	P
0.815984			*		P	P	P	P
2.835863				*	P	P	P	P
0.349478					P	P	P	P
0.74708					P	P	P	M
2.804147			*	*	P	P	P	P
0.863168	*				P	P	P	M
0.546385					P	P	P	P
0.511726					P	P	P	P
0.111141					P	P	P	A
					P	A		
0.565195					P	P	P	P
3.689746				*	A	P	P	P
2.245828	*			*	P	P	P	P
1.782377		*	*		P	P	P	P

					P	P	A	
	*				P	P	P	
		*				P	A	
0.324741					P	P	P	P
2.157158	*		*	*	P	P	P	P
0.384239					P	P	P	A
1.222599	*	*			P	P	P	P
3.994254			**	*	P	P	P	P
5.080347			*	*	A	P	P	P
0.373003			**		A	A	P	A
0.665744	*				P	P	P	P
0.376213					P	P	P	P
3.934319			*	*	P	P	P	P
						A		
2.010741				*	P	P	P	P
1.583033			**		P	P	P	P
2.39404				*	P	P	P	P
0.920812	*				P	P	P	P
						A		
0.540129					P	P	P	P
2.018959				*	P	P	P	P
			*		P		P	
3.308762				*	P	P	P	P
					P	P	A	
0.426992					P	P	P	P
0.122606					P	P	A	A
0.445548					P	P	P	P
0.426158					P	P	P	P
0.864993					P	P	P	P
1.576027		*			P	P	A	P
0.247139					P	P	P	A
0.596516					P	P	P	P
1.440687					P	P	P	P
0.72072					P	P	P	P
30.51464				**				P
2.095345				*	P	P	P	P
0.461138					P	P	P	P
2.302434			*	*	P	P	P	P
3.163953	*			**	P	P	P	P
		*			P	P	P	

				P	A		
1.03969	*		*	P	P	P	P
0.226185				P	P	P	P
2.673043			*	*	P	P	P
0.451667					P	P	P
15.42815				**	P	A	P
2.057611			*	*	P	P	P
1.847976			*		P	P	P
						A	
1.676808			**		P	P	P
0.429348					P	P	A
0.463807					P	P	P
2.724597				*	P	P	P
					P		
					P	A	
0.784364					P	P	A
7.960342				**			P
1.124229	*				P	P	P
4.507622	**		**	*	P	P	P
1.437651			*		P	P	P
0.355248					P	P	P
2.268408				*	P	A	P
			**		P	P	P
2.253842				*	P	P	P
1.754251			*		P	P	P
		**			P	P	
2.963112		*	**	**	P	P	P
1.236898	**				P	P	P
1.932217		**			P	P	A
						A	
2.125953				*	P	P	P
2.301995				*	P	P	P
2.658715				*	P	P	P
4.740365				*			P
1.730481		*			P	P	P
0.775411					P	P	P
0.344847					P	P	A
1.45416					P	P	P
2.977843		**		**	P	P	M
7.825981			*	**		P	P

2.087028				*	P	A	A	P
					P	P	P	
0.883798	*				P	P	P	P
0.635429	**				P	P	A	A
1.665601		*			P	M	P	P
5.826672	*		**	*	P	P	P	P
3.947858			*	*	P	P	P	P
0.474586					P	P	P	P
2.252544				*	P	P	P	P
0.851938					P	A		P
0.486382					P	P	P	P
2.69948			*	*	P	P	P	P
0.124518						A		A
0.509859					P	P	P	P
2.027245	**	*	*	*	P	P	P	P
						A		
1.185368			*		P	P	P	P
2.244637				*	P	P	A	P
0.519006					P	P	P	P
1.244181			*		P	P	P	P
14.92523	**	*	**	**	P	P	P	P
3.122494			*	**	P	P	P	P
2.39285			*	*	P	P	P	P
0.918473	**				P	P	P	P
1.880688		*			P	P	P	P
0.417578					P	P	P	P
4.192529	*		**	*	P	P	P	P
1.388603			**		P	P	P	P
4.171489	**	**	**	*	P	P	P	P
0.408504					P	P	P	A
	*	*			P	P	P	
7.187136	*	*	**	**	P	P	P	P
3.463314			**	*	P	P	P	P
0.276642					P	P	P	P
0.568297					P	P	P	P
0.931694					P	P	P	P
0.454916					P	P	P	P
0.117791					P	P	A	A
0.378166					P	P	P	A

2.318672		**	**	*	P	P	P	P
0.383445					P	P	P	A
					P	P	A	
3.116161		*	**	**	P	P	P	P
1.600987			**		P	P	P	P
		*	*		P	P	P	
3.092816	**			**	M	A		M
1.744317			**		A	P	P	A
0.330459					P	P	P	M
0.980659					P	P	P	A
0.30376					P	P	P	P
1.591929		*	**		P	P	P	P
1.016979					P	P	P	P
2.018605				*	P	P	P	P
0.810987			*		P	P	P	P
7.034816		*	**	**	P	P	P	P
1.945648			*		P	P	P	P
2.176422			**	*	P	P	P	P
2.583747				*	P	P	A	A
3.903323			*	*	P	P	P	P
1.530755			**		P	P	P	P
1.620733			*		P	P	P	P
1.946137			*		P	P	P	P
6.764693			*	**	P	A	P	P
7.994959			**	**	P	P	P	P
2.807187			**	*			P	P
1.275599					P	P	P	P
0.562044					P	P	P	P
0.410615					P	P	P	P
					A			
1.765242			*		P	P	P	P
	*				P	P	P	
					P		A	
			*				A	
2.585879				*	P	P	A	P
1.294103			*		P	P	P	P
1.119118					P	P	P	P
					A			
0.868009					P	P	P	A
						A		

2.106084			*	P	P	P	P
1.458593		*		P	P	P	P
				A	A	A	
0.782438				P	P	A	P
2.361405			*		A		P
2.62555			*	P	P	P	P
0.890584	*	*		P	P	P	P
0.740307				P	P	P	P
				A	A		
2.381559			*				P
1.687504		*		P	P	A	P
0.595064				P	A	A	A
1.241447		**		P	P	A	A
0.961359		*		P	P	P	P
1.39965	**			P	P	P	P
2.223146			*	P	P	P	P
0.462808				P	P	A	A
0.093491							A
				A	A		
0.734759				P	P	P	M
2.982525		**	**	P		P	P
6.125956		*	**	P	P	P	P
0.513518				P	P	P	A
0.308779				P	P	P	P
0.567771	**			P	P	P	P
0.698353				P	P	P	P
0.343034				P	P	P	P
0.558181	*			P	P	P	P
0.538288				P	P	P	P
0.403108				P	P	P	P
1.362814		**		P	P	P	P
1.969085				P	P	P	P
2.317283			*	P	P	P	P
					A		
2.208519	**		*	P	A	P	P
	**			P	P		
0.923499		*		P	P	P	P
0.590789				P	P	P	A
0.505723				P	P	P	P
0.236422				P	P	P	P

0.207362					P	P	P	P
2.340105			*	*	P	P	P	P
24.80621		**	*	**		P	P	P
	*				P	P	P	
			*		A	A	P	
0.424032		*			P	P	A	A
1.119041					P	M	P	P
2.125545				*	P	P	P	A
5.63506			*	*	P	P	P	P
0.809878					P	P	P	A
0.487929					P	P	P	P
1.854277		*				P	P	P
1.356162					P	P	P	P
			*		A	P	M	
2.593708			*	*	P	P	P	P
0.68584					P	P	P	P
0.775079			**		P	P	P	P
1.022162	*				P	P	P	A
3.323741				*	P			P
5.657239			**	*	P		P	M
0.309017		*			P	P	P	A
0.467832					P	P	P	P
0.339279					P	P	P	P
0.460261					P	P	P	P
1.91238			*		P	P	P	P
1.285361			**		P	P	P	P
3.538998			*	*	P	P	P	P
4.514599				*	P	P	P	P
2.107838				*	P	P	P	P
3.020982			**	**	P	P	P	P
2.620413				*	P	P	P	P
1.847373			*		P	A	P	P
0.476977					P	P	P	P
5.637981				*	P	P	P	P
0.568119					P	P	P	P
	*		*		P	M	P	
2.873809				**	P			P
3.03915				**	P	P	P	P
2.768451			*	*	P	P	P	P
0.786161	**				P	P	P	P

0.244747					P	P	P	P
2.479005				*	P	P	P	P
0.159436					P	P	P	A
0.998429					P	P	P	P
0.613033	*				P	P	P	P
2.079755				*	P	P	P	P
1.026863					P	P	A	A
1.051558					P	P	P	P
1.40432					P	P	A	P
0.44158					P	P	P	P
3.623189			*	*	P	P	P	P
		**			A	M	A	
2.856679				**	P	P	P	P
1.161159	*				P	P	P	P
2.068545			*	**	P	P	P	P
0.026406					P	P	P	A
0.324932					P	P	P	P
0.3121					P	P	P	P
2.002504			*	*	P	P	P	P
0.53648					P	P	A	P
0.615608	*				P	P	P	P
0.467085					P	P	P	P
0.814056	**	*	*		P	P	P	P
1.160271		**			P	P	P	P
6.699477				**	A	P	P	M
0.087957					P	P	P	P
1.887703			*		P	P	P	P
		**				M		
0.476925					P	P	P	P
			*		P	P	P	
2.018536			**	*	P	P	P	P
1.510203	*		**		P	M	P	M
0.398768								A
		**				M		
3.220911				**	P	P	P	P
0.308027					P	P	P	A
2.028215				*	P	P	P	M
0.554638		*			P	P	M	A
0.777266					P	P	P	P
1.998724			*		P	P	P	P

0.858758					P		P	P
1.768557	*		**		P	P	P	P
0.186959					P	P	M	A
1.01177					P	P		M
3.818489	**		*	*	P	P	P	P
						P		
1.060452					P	P	P	A
2.124427			*	*	P	P	P	P
3.407102			*	*	P	P	P	P
3.465755				*	P	M	P	P
3.347384				*	P	P	P	P
0.775604			**		P	P	P	P
0.582324		*	*		P	P	P	P
1.361113			*		P	P	P	P
0.455417					P	P	P	P
3.266535		*	*	*	P	P	P	P
0.132952					P	P	A	A
0.661419					P	P	P	A
2.545368	*	*	**	*	P	P	P	P
1.136973			**		P	P	P	P
1.608193	*		*		P	P	P	P
0.834032		*			P	P	P	P
					A			
0.501999					P	P	P	P
0.383022					P	P	P	P
2.084985			*	*	P	P	P	P
0.946514	*				P	P	P	P
0.764849					P	P	P	P
0.892081					P	P	P	P
2.307505	*	*	*	*	P	P	P	P
2.294241			**	*	P	A	P	P
0.630386					P	P	P	A
0.393817					P	P	P	P
0.451209					P	P	P	P
2.040625				*	P	P	P	P
0.694858	*				P	P	P	P
0.405344					P	P	P	P
0.868545					P	P	P	A
4.079346			*	*	P	P	P	P
2.036809				*	P	P	P	P

1.849606	*	*	*		P	P	P	P
2.014641				*	P	P	A	P
4.392857		**		*	P	P	P	P
0.252732	*				P	P	P	P
0.46072					P	P	P	P
0.201604					A	A		A
0.209919					P	A	P	A
4.162782		*	*	*	A	P	P	M
4.398699			*	*	P	P	M	P
4.118503				*				P
0.687412	*				P	P		A
3.528062	**	*	**	*	P	P	P	P
4.08222			**	*	P	A	P	P
3.156698				**	P	P		P
						A		
8.646903	**	**	**	**	P	P	P	P
1.182855		*			P	P	P	P
1.477875			*		P	P	P	P
1.439467	*	**			P	P	P	P
2.00403			**	*	P	P	P	P
1.377711					A	A		A
3.706979			**	*	P	P	P	P
3.597495				*		A	P	P
2.273676			*	*	P	P	P	P
2.189633			*	*	P	P	P	P
0.773648					P	P	P	A
0.39457					P	P	P	P
0.847209					P	P	P	P
0.812335	*				P	P	P	P
4.887964	*	*	**	*	P	P	P	P
0.904418					P	P	P	P
0.415067					P	P	P	P
0.406878					P	P	P	P
		*				P		
			**				M	
						P	A	
	**				P		A	
11.70856	**		**	**	P		P	P

3.047814				**				A
0.406908					P	P	P	P
7.590356		*		**	P	P	P	P
2.261627				*	P	P	P	P
0.975909		*			P	P	P	P
	*				P	A	A	
0.377005					P	P	P	P
2.166594		*	**	*	P	P	P	P
0.900583	*				P	P	P	P
2.034926				*	P	P	P	P
0.792619					P	P	P	P
0.425109					P	P	P	P
1.563405					P	P	P	P
0.440393					P	P	P	P
0.472069	*				P	P		A
7.497996		**	**	**	P	P	P	P
8.428905				**	P	P	P	P
	*				P			
0.549245			*		P	P	P	P
0.482327					P	P	P	A
1.520834			*		P	P	P	P
0.397635					P	P	P	P
1.038392	*		*		P	P	P	P
5.935432		*	**	*	P	P	P	P
					A	M	A	
1.359206			**		P	P	P	P
0.522462					P	P	P	P
0.286885					P	P	A	P
0.133597					P	P	M	A
0.353495					M	P	A	A
1.375766	*				P	P	P	P
1.409303					P	P	P	P
2.123506				*	P	P	P	P
0.163111					P	P	P	A
0.378348					P	P	P	P
2.528536				*	P	P	P	P
1.597976					P	P	P	P
0.60978					P	A	A	A
1.155867			*		P	P	P	P
1.691082			*		P	P	P	P

0.601866					P	P	P	P
1.954868					P	P	A	P
1.856278					P	A	A	P
0.421127					P	P	P	P
0.989918		*			P	P	P	P
2.867328	*		*	**	P	P	P	P
		*	**		P	P	P	
0.457247					P	P	P	P
4.502002	*	*		*	P	P	A	P
0.413492					P	P	P	P
					P	P	A	
0.083086	**				P	P	A	A
2.086257				*	P	P	P	P
0.715502	*				P	P	P	P
	**				P	P	P	
1.673153			*		P	P	P	P
0.402132	*				P	P	P	P
5.920248			**	*		P	P	P
1.475901					P	P	P	P
0.478924					P	P	P	P
0.544598					P	P	P	P
	*		*		P	P	P	
0.762714					P	P	P	P
0.215364	*				M	P	A	A
0.486891					P	P	P	P
1.16299			*		M	P	P	A
0.621225					P	P	P	P
4.830242	*	*	**	*	P	P	P	P
0.796067			*		P	P	P	P
2.066411			*	*	P	P	P	P
0.32074					P	P	P	P
		*				M		
0.637052		*			P	P	P	P
1.316958	*		*		P	P	P	P
3.122391			*	**	P	P	P	P
0.411541					P	P	P	P
0.510562						A		A
0.478903					P	P	P	P
2.102013				*	P	P	P	P
1.721689			*			M	P	P

0.960019				P	P	P	P
	*			P			
0.437746				P	P	P	P
3.123462		*	**	P	P	P	P
1.845504				A			P
4.77997		**	*	P	P	P	P
2.866117		*	**	P	P	P	P
0.521174				P	P	P	P
0.033242				M	A		A
		*				M	
1.266066				P	A	A	A
2.551552			*	P	P	P	A
1.051363	*			P	P	P	P
0.582758	*	**		P	P	A	A
0.780656		*		P	P	P	P
				A	A		
7.789748			**				M
2.522769		**	*	P	P	P	P
55.92291		**	**			P	P
						A	
					M	A	
2.313803			*	P	P	P	P
0.264686				P	P	P	P
1.786942		*		P	P	P	P
					A		
0.918573				P	P	P	P
		**			M		
0.699064				P	P	P	P
0.550806				P	P	P	P
		*		P	M	A	
0.905494				A			A
0.478484				P	P	P	P
0.373599	*			P	M	A	A
1.946864				P	P	P	P
	*			P			
0.41557				P	P	A	A
0.39376				P	P	P	P
1.253153				A	M	P	P
0.507564				P	P	P	P
1.739496	**			P	P		P

4.681576	*	*	*	A	P	P	P
		**		P		P	
0.27513				P	P	A	A
0.396941				P	P	P	A
0.990073				P	P	P	P
1.618117		**		P	P	P	P
12.47874			**				M
0.698774				P	P	P	P
25.44585			**		A		P
3.607914		*	*	P	P	P	P
		**				P	
1.026132				P	P	P	P
0.679772				P	M	A	A
2.048848			*	A	A		M
2.285054			*	P	P	P	P
3.345987			*				P
2.228071		**	*	P	P	P	P
2.216909			*	P	P	P	P
0.514301				P	P	P	P
0.367191					A		A
2.391789			*				P
0.578643				P	P	A	P
				A			
1.440256		*		P	P	P	P
3.820096		**	*	P	P	P	P
0.301608				A	P	P	A
1.729893		*		P		P	P
2.135176			*	P	P	P	P
	**			P	P		
		*		P		M	
					A	A	
0.411682				P	P	P	P
0.046289				A	P	A	A
	**				P		
0.794881				P	P	M	P
1.697832					A	A	P
0.522749				P	P	P	P
2.516293			*	P	P	P	P
0.298958				P	P	P	P
5.374721		**	*	P	P	P	P

3.157047			**	P	P	P	P
1.474526	*	**		P	P	P	P
					A	A	
1.069637				P	P	P	P
3.341875			*				P
	*				M		
0.410041				P	P	P	P
					P	P	
0.427371				P	P	P	P
1.802342		*		P	P	P	P
2.465481		*	*	P	P	P	P
					A	A	
0.21902				P	P	P	P
1.601056		*			A	P	A
		*				M	
4.647523	*	*	*	P	P	P	P
					P		
0.700439	*			P	P	P	P
1.186151				P	P	P	P
	**			P	A	A	
0.490739				P	P	P	P
	*				P		
	*			P	P	A	
7.403554		**	**	P	P	P	P
0.295599				P	P	P	P
0.235658				P	P	P	P
2.365908		**	*	P	P	P	P
2.843352			**	P	P	P	P
0.997045	*			P	P	P	A
2.356087			*			P	P
1.341323		*		P	P	P	P
0.324474				P			A
0.417255				P	M	A	A
					P	A	
0.978109				P	P	P	P
3.341676		*	*	P	P	P	P
1.280972		*		P	P	P	P
0.770647	*			P	P	P	P
0.482826				P	P	P	P
2.405541	**		*	P	P	P	P

					P	A	
				A	A	A	
0.636964				P	P	P	P
0.457835				P	P	P	P
0.555519	*			P	P	P	P
0.218731				P	P	P	P
0.396679				P	P	P	P
0.476685				P	P	P	P
0.354069				P	P	P	P
0.270098				P	P	P	A
0.160455	**	*		P	P	A	A
0.669558				A	P	A	A
					M	A	
0.799189				P	P	P	P
3.58111		*	*	P	M	P	P
2.416748	*		*	P	P	P	P
1.241154	**			P	P	P	P
3.760248			*	P	P	P	P
1.759346		*		P	P	P	P
2.929272			**	P	P	P	P
4.848114		**	*	P		M	P
3.691946			*	A			P
2.505265			*	P	P	P	P
1.868222	*	*		P	P	P	P
					A		
1.044342		*		P	P	P	P
2.468035	**		*	P	A	A	P
				P	P	P	
1.352624	**	*		P	P	A	P
0.461137				P	P	A	A
0.233425				A	P	A	A
2.023479		*	*	P	P	P	P
0.519221	*			P	P	P	P
0.87855		**		P	P	P	P
0.195369				P	P	P	P
0.669445		*		A	A		A
0.88306				P	P	A	A
3.859013	*	**	*	P	P	P	P
0.367396				P	P	M	A
2.412594		*	*	P	P	P	P

0.129091				P	P	P	P
0.362861				P	P	P	P
					P	M	
2.325315			*	P	P	P	P
1.968621		*		A	P	P	P
1.047754	**			P	P	P	P
0.764146	*			P	P	P	P
5.056584		**	*	P	P	P	P
0.495008		*		P	P	P	P
				M		A	
0.219255				P	P	P	P
2.135158			*	P	P	A	P
0.139278				P	P	A	A
0.714969				P	P	P	P
0.461416				P	P	P	P
3.030926			**	P	P	A	P
	*			P	P	A	
11.78424	*	*	**	P	P	P	P
4.531073	*	*	*	P	P	P	P
0.955958				P	P	P	P
2.189153			*	P	P	P	P
2.188158			*	P	P	P	P
5.847838		**	*	P	P	P	P
3.53894			*		P	P	P
1.641235		*		P	P	P	P
6.684909		*	**	**	P	P	P
1.681039		*			P	P	P
2.503253	*		*		P	P	A
2.394685		*	*		P	P	P
0.227702		*			P	P	A
3.320927		*	*		P	P	P
0.408442					P	P	P
0.707419	**				P	P	P
0.455772					P	P	P
2.646196		*	*		P	P	P
						A	
0.112015					P	P	A
7.485089		**	**		P	A	P
3.937083	*	*	*		P	P	P
1.574576		*			A	A	M

0.535275				P	P	P	P
0.525128				P	P	P	P
0.760668				P	P	P	A
		**		M	A	P	
1.668973	*			A	P		P
0.706721				P	P	P	P
7.482135	*	*	**	P	P	P	P
1.409796		**		M	M	P	A
2.637445			*	P	P	P	P
	*			P	P	M	
0.492171				P	P	A	A
0.542572				P	P	P	P
0.391276				P	P	P	A
0.359779				P	P	P	P
2.708605		*	*	P	P	P	P
3.368413			*	P	P	A	P
0.321954				P	P	P	P
	**			P		P	
0.478537				P	P	P	P
2.036666	*	**	*	P	P	P	P
21.62703			**				P
0.946224				P	P	P	P
1.186821				P	P	P	P
1.720748	*			P	P	P	P
14.30696			**	A	A	A	P
0.671579				P	P	P	P
	**				P		
1.764743		**		P		P	P
2.284557			*		A		P
		*		P		P	
	**			M			
	**			A			
	**			P	P	P	
		*			P		
0.047531							A
0.498829				P	P	A	A
21.18084	**	**	**		P	P	P
						A	
0.573199				P	P	P	P
0.950567				P	P	P	P

0.986067	*			P	P	P	P
0.676812				P	P	A	A
				P	A		
0.886331				P	M	A	P
1.005166				P	P	A	A
3.324863			*	A		M	P
4.623348		**	*	P	P	P	P
					A		
0.608412				P	P	P	P
0.510255				P	P	P	A
1.739425					A		P
1.720579		*		P	P	P	P
1.0728		*		P	P	P	P
1.218894		*		P	M	P	M
2.187599			*	P	P	P	P
0.391619				P	P	A	P
	*				P		
				P	P	A	
1.157007				M	A	A	P
				A			
						A	
5.589619			*		A		P
				P	P	A	
0.313755				P	P	P	P
0.611677				P	P	P	A
		*			P	P	
0.53276				P	P	P	P
				M			
2.32488			*	A	P		P
7.485289		**	**	P	A	P	P
	**				P		
1.535796				P	P	P	A
	**				P		
2.027596			*	A	A		A
	**			P			
				A		A	
4.532129			*				P
		**				P	
					A		
1.483944	*			P	P	P	P

1.043505					P	P	A	P
0.584546					P	P	P	A
					A			
			*		P	P	P	
					A			
6.545789				**				M
1.10845	*				P	P	P	P
		**				P		
2.398103				*				P
					P	P	A	
						A		
0.449838								A
1.429775	**	*			P	P		P
						A		
					A			
		**			A	P	A	
	**				M			
					M	A		
					A			
			**				P	
	*				P			
0.528545					P	P	A	M
1.152081	*				P	P	A	P
		*				P	P	
27.69871			**	**	P		P	P
0.415748					P	P	P	P
0.297883					P	P	P	P
0.376831					P	P	A	A
0.48058					P	P	P	P
11.6416	*	*	**	**	P	P	P	P
		*				P		
0.544753					P	A	A	P
0.439462					P	P	P	P
3.32032				*				P
0.476469					P	P	P	P
		**			M	A	P	
8.349726			*	**	P		P	P
4.857662		*		*	P	P	P	P

		**			P		
1.03838				P		M	P
					A		
5.354684			*				P
		**				P	
				P	A	A	
				P	P	A	
						A	
0.739275				P	A	A	A
2.068099			*		P		M
2.862629			**	P	P	P	P
0.413329				P	P	P	P
					A		
0.843007		*				P	A
2.292807			*	A		P	P
20.93817			**	P	P	A	P
		*			P		
0.547964				A			A
	*			P			
0.16837				P	P	A	A
0.449657				P	P	P	A
2.617764		**	*	P	A	P	P
0.459573	*			P	P	P	P
		**			P		
				P		P	
7.337218			**		P		P
				A			
				A		A	
	*			P	M	P	
0.36032				P	P	A	A
				P		A	
				P	P	A	
2.474514			*	P	P	P	M
	*			P	P		
4.084176		*	*	P	P	P	P
0.492426				P	P	P	P
1.470519				P	P	P	P
				P	A	P	
1.332811		*			P	P	M
0.182865				P	P	P	A

0.372923					P	P	P	P
3.20107	*		*	**	P	P	P	P
	*				M		P	
0.898426	*	*			P	P	P	P
			**				P	
0.852684					P	P	P	P
2.184439				*	P	P	P	P
1.548453					A	A	A	M
4.518439			**	*	P	P	P	P
0.869115	*				P	P	P	M
2.529404			**	*	P	A	P	P
0.369731					P	P	P	A
0.883013					P	P	P	P
	*				P			
0.494391					P	P	P	P
2.909775	**		**	**	P	P	P	P
4.384937	*		**	*	P	P	P	P
17.39327			*	**	P		P	P
2.427881		*		*	P	P	P	P
		*			P	P	P	
5.244718				*	P	A		P
1.830044					P	P	A	M
1.710536	*	*			P	P	P	P
2.775268				*	P	P	P	P
	**				P	P		
0.234097					P	P	P	A
		**			A	P		
						A	P	
					A			
0.303664					A	P		A
0.405398					P	P	P	P
0.802122					P	P	P	A
1.29134			*		P	P	P	A
					A			
2.631362	**		*	*	P	A	P	P
0.215667		**				P	A	A
1.19528					P	P	A	P
2.534976		*		*	P	P	P	P
0.296472					P	P	P	P
			**				P	

1.638756		*		P	P	P	P
0.306368				P	P	P	P
				P	A	P	
0.958544		*		A	A	P	P
0.31134				P	P	P	A
				P	P	P	
	*			P	M	P	
1.647121		*		P		P	P
						A	
11.79117			**				P
				P	A		
1.782966	*			P		A	P
0.162031				P	P	P	A
0.938336				P	A		A
1.385539		*		P	P	P	P
						A	
						A	
		**		P	P	P	
		**				M	
	*	*		P		P	
0.450097				P	P	P	P
0.955169				P	P	P	M
1.624974				A	P	P	P
0.477792				P	P	P	A
0.403081				P	P	P	P
	**			M			
				P		A	
				A		A	
0.641606				P	P	P	P
2.974203		*	**	P		P	P
0.566229				P	P	A	A
					P	A	
0.123301				P	P	P	A
1.826497		*		P	P	P	P
5.412825			*		P	A	P
						A	
				P	A	A	
2.642819			*	P	P	P	P
				A			
				A	P	A	

					A		
23.00143			**				M
						A	
				M		A	
1.066862				P	P	P	P
					A		
0.248105				M	P	P	A
	*			P			
0.733014				P	P	P	M
0.579718				P	P	P	P
2.117606			*	P	P		P
1.94173		*		A	M	P	M
17.05169			**	A			P
1.067896		**		P	P	P	P
0.625171					A	A	A
3.635201			*		P	A	P
4.463093			*				M
1.901631	*			P	P	P	P
1.816676	*			P	M	P	P
2.531847	**	*	*	P	P	P	P
0.627706				P	P	P	P
3.367818		**	**	P	P	P	A
	*	*	*	P	P	P	
				A			
1.431738				P	P	P	P
				P	A	M	
0.266568				P	P	P	P
	**	*		P	M	A	
0.441043				P	P	P	P
				P	P	A	
0.289939				A			A
0.38838				P	P	P	A
					A		
				A			
1.002368	*			P	A	A	A
3.3799		*	*	P	P	P	P
		*		P	P	P	
0.865768				P	P	A	A
2.448569		*	*	P	P	P	P
	*			P			

			**			P	
	*				P	P	
0.795513					P	P	A
		*			A	A	
0.969933		**				P	P
0.686297					A	M	A
						A	
					A		
0.612748	**				P		A
12.46333			**		P	A	P
0.787849					A	M	A
3.519059			*		P	A	P
1.109374					P	P	P
0.585495	*				P	P	P
2.144553			*		P	A	M
4.238418			*				P
0.320581					P	P	P
5.033448		*	*		P	P	P
0.394013					P	P	P
0.418787					P	P	P
2.398981			*		P	P	P
0.431827					P	P	P
0.509633					P	P	P
0.486671					P	P	P
1.004373					P	P	P
0.335025					P	P	P
2.162767			*		P	P	P
0.436187					P	P	P
0.205428		*			P	P	A
1.210566					P	P	P
33.84251	*	**	**		P		P
	**				M		
0.446143					P	P	P
						A	
		*			A	P	
0.469769					P	P	P
0.435614					P	P	P
0.434319					P	P	P
0.460954					P	P	P
0.833432					P	P	P

					M	A	
1.320225				P	P	P	P
0.264703				P	P	P	P
1.100298				P	P	P	P
2.03801			*	P	A	A	P
0.440576				P	P	P	P
0.4704				P	P	P	P
2.080381		*	*	P	P	P	P
0.536036				P	P	P	P
					A		
					A	A	
1.339279	*		*	P	P	P	P
0.270681				P	P	P	P
0.278338				P	P	P	P
47.32875		**	**	P		P	P
0.499646				P	P	P	P
3.252784		*	*	P	P	P	P
0.964159	**			P	P	P	P
0.82663				P	P	P	P
0.975149				P	P	P	P
1.153754				P	P	P	P
3.222294		*	**	P	P	P	P
0.475058				P	P	P	P
0.811483				P	P	A	A
0.923134		*		P	P	P	P
2.493227		*	*	P	P	P	P
					A	P	
0.244227				P	P	P	P
1.509613		**		P	P	P	P
0.739927				P	P	P	A
0.403379				P	P	P	P
3.831101		*	*	P	P	P	P
1.22846		**		P	P	P	P
0.38237				P	P	P	P
3.448653			*	P	P	P	P
0.390293				P	P	P	P
0.571334				P	P	P	P
1.402048	*	**		P	P	P	P
				A	P	A	
0.295705				P	P	P	A

1.403135			*	P	P	P	P
0.474225				P	P	P	P
1.175323			*	P	P	P	P
0.454523				P	P	P	P
0.333799				P	P	P	P
1.136857			*	P	P	P	P
				P	P	A	
1.495897				P	P	P	P
0.524179				P	P	P	P
			*	A	P	P	
1.327183			*	P	P	P	P
0.408013		*		P	P	P	P
0.503485	*			P	P	P	P
0.498684				P	P	P	P
1.318893		*		P	P	P	P
0.426641				P	P	P	P
0.458764				P	P	P	P
0.552537				P	P	P	P
0.514931				P	P	P	P
0.531319				P	P	P	P
1.25476				P	P	P	P
0.671536			**	P	P	P	P
1.873201			*	P	P	P	P
4.188491	**		**	*	P	P	P
0.413762				P	P	P	P
0.78471				P	P	P	P
1.481195	*		*	P	P	P	P
1.169884			*	M	A	P	P
0.298196				A	P	P	A
0.989271				P	P	P	P
0.820906				P	P	P	P
0.857796	*			P	P	P	A
0.633657				P	P	P	P
2.610185				*	P	P	P
3.092439			**	P	P	P	P
0.32581				P	P	P	P
3.874582		*	*	M		P	P
0.760118				P	P	P	P
0.387209				P	P	A	P
0.633011				P	P	P	P

	**			P			
	*		*	M	A	P	
0.497818				P	P	P	P
0.499199				P	P	P	P
0.493718				P	P	P	P
0.870839				P	P	P	P
2.693544		*	*	P	P	P	P
0.374833					A		A
3.292243			*	P	P	P	P
0.493529				P	P	P	P
0.794402				P	A	A	A
0.335637				P	P	P	P
4.649367		*	*	P	P	P	P
0.070822				P			A
	**				M		
2.083679			*	P	P	P	P
3.720033		**	*		P	P	P
0.454349				P	P	P	P
1.396586				P	P	P	P
0.414726				P	P	P	P
						A	
3.064507			**	P	P	P	P
1.891718		*		P	P	P	P
				A	P	A	
0.45362				P	P	P	P
					P	A	
	*			P			
0.469419						P	P
0.31959				P	P	P	P
2.838548		*	*	P	P	P	P
0.499223				P	P	P	P
0.328296				P	P	P	P
1.278144				P	P	P	P
0.950081				P	P	P	P
3.416231			*	P		A	P
0.031032	**			P	P	A	A
1.30981				P	P	A	A
				A	A		
0.485966				P	P	P	P
1.402834	*	**		P	P	P	P

1.274329				P	P	P	P
2.914243	*		**	P	P	P	P
1.123913						A	A
0.878147				P	P	P	P
0.474645				P	P	P	P
6.001936		*	*	P	P	P	P
0.862034				P	P	P	P
		**		A	P		
0.489237				P	P	P	P
3.147051			**	P	P	P	P
0.347779				P	P	P	P
2.428784			*	P	P	P	P
1.529359		*		P	P	A	P
3.316644	*		*	P			P
0.90081		**		P	P	P	P
3.21064			**	P	P	P	P
0.433592				P	P	P	P
0.495984				P	P	P	P
0.222443				P	P	A	A
0.388334				P	P	P	P
				A			
0.698416				P	P	P	A
1.797655		**	**	P	P	P	P
0.465565				P	P	P	P
0.483639				P	P	P	P
1.490526			**	P	P	P	P
0.460977				P	P	P	P
0.36546				P	P	P	P
0.226843				P	P	P	P
2.647383		*	*	P	P	P	P
				P		A	
2.302904			*	P	P	P	P
1.327679		*		P	P	P	P
0.498788				P	P	P	P
2.379077			*	P	P	P	P
1.986475		**		P	P	P	P
0.432865				P	P	P	P
2.650804			*	P	P	P	P
3.332638		*	*	P	P	P	P
0.331842				P	P	P	P

2.915932	*	*	*	**	P	P	P	P
3.028623	*		**	**	P	P	P	P
11.36112			**	**	P	P	P	P
0.356955					P	P	P	P
							A	
	*				P	P	P	
0.680355					P	P	P	P
0.473695					P	P	P	P
0.82008			*		P	P	P	P
0.133794					P	P	A	A
0.599206					P	P	P	P
0.814595	*				P	P	P	P
1.006506					A	P		A
0.611948					P	P	P	P
0.475786					P	P	P	P
0.700913					P	P	P	P
0.53301					P	P	P	P
0.440476		*			P	P	P	P
0.339035					P	P	P	P
2.095332				*	P	P	P	P
0.458972					M	P	A	A
0.389332					A		A	A
0.24093					P	P	P	P
2.148952				*				A
0.180458					P	P	P	P
3.330812			*	*	P	P	P	P
0.887536					P	A	A	P
0.430665					P	P	P	P
0.329473					P	P	P	P
0.788812			*		P	P	P	P
0.834135	*				P	P	P	P
0.674828					P	P	P	P
0.427033					P	P	P	M
0.305085					P	P	P	P
0.307239					P	P	P	P
0.366099					P	P	P	P
0.320422					P	P	P	P
3.089296				**	P	P	P	P
2.193219			*	*	P	P	P	P
0.568282					P	P	P	P

1.10444	**			P	P	P	M
		*			A	P	
0.470631				P	P	P	P
0.460049				P	P	P	P
0.490548				P	P	P	P
4.034428			*				P
1.54004		*		P	P	P	P
4.996334		**	*	P	P	P	P
3.785431		*	*	P	P	P	P
1.035719		*		P	P	P	P
0.498551				P	P	P	P
3.068645	*		**	P	P		P
	*			P			
0.578279				P	P	P	P
2.086568		*	*	P	P	P	P
0.444963		**		P	P	P	P
0.405088				P	P	P	P
1.05974				P	P	P	P
4.187024			*			P	P
0.302597				P	P	P	P
22.77102	*	*	**	P		P	P
2.597852			*	P	P	P	P
2.214388			*	P	P	P	P
1.985129				P	P	P	P
0.628402				P	P	P	P
1.605806		*		P	P	P	P
0.103764				P			A
1.57714		*		P	P	P	P
0.433577				P	P	P	P
0.666879	*	**		P	P	P	A
0.413574				P	P	P	P
0.421033				P	P	P	P
0.863924				P	P	P	P
1.277581	*			P	P	P	P
0.459562				P	P	P	P
1.44656				A	P	P	A
3.087264		**	**	P	P	P	P
0.851218				P	P	P	P
	*			P	M	P	
0.603291				P	P	P	P

					P	P	A	
0.298566					P	P	P	A
1.838922			*		P	P	P	P
1.028593					P	P	P	P
0.166338		**			P	P	A	P
0.86326					P	P	P	P
					M	P	A	
0.930833					P	P	P	P
0.3273					P	P	P	P
0.732824					P	P	P	P
					P		A	
0.373607					P	P	P	P
1.130977			*		P	P	P	P
2.020836				*	P	P	P	P
0.331595					P	P	P	P
2.193903				*	P	P	P	P
0.416067					P	P	P	P
						P	A	
1.074501					P	P	P	P
1.736531			**		P	A	P	P
					P	P	A	
3.411972				*	P	P	P	P
2.245365				*	P	P	P	P
0.433838					P	P	P	P
0.361522					P	P	P	P
0.273227					P	P	P	A
3.177057				**	P	P	P	P
	*				M	M		
0.482548					P	P	P	P
40.89316	**	**	**	**	P	P	P	P
0.711084					P	P	P	P
1.739881			**		P	P	P	P
2.311926			*	*	P	P	P	P
0.526333	*				P	P	P	P
0.508081					P	P	P	P
0.660778					P	P	P	P
12.57614		*	**	**	P	P	P	P
1.46044			**		P	P	P	P
0.664236	*				P	P	P	P
0.368856					P	P	P	P

0.60359				P	P	P	P
1.784584				P	P	A	A
		*		P	P	M	
0.752546				P	P	P	P
2.524726			*	P	P	P	P
	*			P			
0.276516				P	P	P	P
0.172997	*			P	P	P	P
2.937645			**	P	P	P	P
0.552341		*		P	P	P	P
0.372909				P	P	P	P
0.459083				P	P	P	P
4.866977		*	*	P	P	P	P
1.013804		*		P	P	P	P
0.406496				P	P	P	P
3.690839			*	P	P	M	P
0.119857							A
0.50832		*		P	P	P	P
0.066263				P	P	P	A
0.369305				P	P	P	P
2.719122		*	*	P	P	P	P
2.843642			**	P	P	P	P
1.458712		*		M	A	P	P
0.489466				P	P	P	P
	*			P	P	P	
0.587054				P	P	P	P
4.107063			*	P	P	P	P
0.458695		*		P	P	P	P
2.103191	**		**	P	P	P	P
0.350277				P	P	P	P
0.436128				P	P	P	P
0.647971		*		P	P	P	P
0.396885				P	P	P	P
0.393356				P	P	P	A
2.379471			*	P	P	P	P
2.008846			*	P	P	P	P
1.003676		*		P	P	P	P
0.213357				P	P	P	P
0.877329				P	P	P	P
3.199758		*	**	P	P	P	P

0.481237					P	P	P	P
0.904218	*				P	P	P	P
0.479978					P	P	P	P
2.374054				*	P	P	P	P
0.406111					P	P	P	P
2.862342				**	P	P	P	P
0.51482					P	P	P	P
0.418249					P	P	P	P
1.187309		**	**		P	P	P	P
2.178708	*		*	*	P	P	P	P
0.814986	*				P	P	P	P
1.189543					P	P	P	P
0.08563					P	P	M	A
0.678368					P	P	P	P
0.499463					P	P	P	P
0.553506					P	P	P	P
2.4034			*	*	P	P	P	P
0.84107					P	P	A	P
0.291007					P	P	P	P
2.012924				*	P	P	P	P
0.418619					P	P	P	P
1.210062					P	P	P	P
5.007693		**	**	*	P	P	P	P
0.491362					P	P	P	P
1.201116			**		P	P	P	P
2.361773				*	P	P	P	P
0.486454					P	P	P	A
0.608442					P	P	P	P
0.32421					P	P	P	P
0.925226	*				P	P	P	P
2.095932				*	P	P	P	P
0.364842					P	P	P	P
0.549408					P	P	P	P
0.062079					A	P	P	A
0.207356					P	P	A	A
3.028881	*		**	**	P	P	P	P
						A	P	
0.416922					P	P	P	P
0.185344					P	P	P	P
0.519511	*				P	P	P	P

0.605532					P	P	P	P
0.462277					P	P	P	P
0.344597					P	P	P	P
	*				P	P	P	
0.754021					P	P	P	A
1.032475			*		P	P	P	P
1.40905					P	P	P	P
0.831766					P	P	P	P
0.285987					P	P	A	A
0.345822					P	P	P	P
1.180741					P	P	P	P
1.231175	**				P	P	P	P
0.710065					P	P	P	P
						P	A	
					P	P	P	
0.38245					P	P	P	P
10.71477	*	*	**	**	P	P	P	P
1.306254					P	P	P	P
							A	
2.03663	**			*	P	P	P	P
0.420647					P	P	P	P
0.401075					P	P	A	A
0.714984					P	P	P	P
0.293131	*				P	P	P	P
	*	**			P	P		
2.269404				*	P	P	P	P
0.421373					P	P	P	P
2.072029			*	**	P	P	P	P
							A	
2.32325				*		M		A
0.469999					P	P	P	P
2.282464	*		*	*	P	P	P	P
2.699956			*	*	P	P	P	P
0.498193					P	P	P	P
0.76287					P	P	P	P
1.345989			*		P	P	P	P
0.187025					P	P	P	P
0.470861					P	P	P	P
0.497597					P	P	P	P
0.458859					P	P	P	P

0.467016				P	P	P	P
0.432108				P	P	P	P
1.141358				P	P	P	P
0.408323				P	P	P	P
0.470374				P	P	P	P
1.25021					A		A
					A		
				A			
0.479672				P	P	P	P
0.580161				P	P	P	P
	**			P	A		
0.247273		*		P	P	A	A
2.092568			*	P	P	P	P
3.067854			**	P	P	P	P
0.221682				P	P	P	P
2.692897			*	P	P	P	P
0.24708				P	P	P	P
0.984779				P	P	P	P
			**	P	M	M	
1.299475		**		P	P	P	P
0.442635				P	P	P	P
0.549698	*			P	P	P	P
3.04512			**	**	P	P	P
2.473626			*	*	P	P	P
0.355537					P	P	P
0.307385					P	P	P
0.406073					P	P	P
0.349979					P	P	P
0.879442					P	P	P
4.559577	**		*	*	P	P	P
2.959815		*	**	**	P	P	P
2.193976			*	*	P	P	P
0.451458		**			P	P	P
0.44281					P	P	P
1.766071		*			P	P	P
					A		
2.06544			*	*	P	P	P
0.339509					P	P	P
1.0921					P	P	A
0.466003					P	P	P

2.174189			*	*	P	P	P	P
0.488324					P	P	P	P
2.931939			*	**	P	P	P	P
2.63724			*	*	P	P	P	P
0.238708	*		*		P	P	P	A
0.284493					P	P	P	P
0.927557	*				P	P	P	P
1.626044	**	*	**		P	P	P	P
0.427733					P	P	P	P
2.425821				*	P	P	P	P
2.521692				*	P	P	P	P
0.412447					P	P	P	P
0.503777					P	P	P	P
0.393969					P	P	P	P
0.47758					P	P	P	P
1.985577		*	**		P	P	P	P
0.397058					P	P	P	P
0.48136	*				P	P	P	P
0.175114					P	P	P	P
3.184136			*	**	P	P	P	P
2.271095			*	*	P	P	P	P
0.464933					P	P	P	P
0.049402	*				P	P	A	A
0.743893					P	P	P	P
0.483382					P	P	P	A
0.575566					P	P	P	P
0.154967					P	A		A
0.488636					P	P	P	P
0.335315					P	P	P	P
0.262144					P	P	P	P
0.604512					P	P	P	P
0.658551					P	P	P	P
0.511315					P	P	P	P
4.184038	**	*	**	*	P	P	P	P
1.729383			*		P	P	P	P
0.814685					P	P	P	P
0.471843					P	P	P	P
0.42489					P	P	P	P
0.577974			**		P	P	P	P
0.465396					P	P	P	P

0.706258				P	P	P	P
1.461501				A	A		P
1.8602		*		P	P	P	P
2.382952		*	*	P	P	P	P
0.486516				P	P	P	P
0.464771				P	P	P	P
2.123881			*	P	P	P	P
0.227069				P	P	P	P
1.093182				P	P	P	P
2.168375			*	P	P	P	P
1.111336	*		*	P	P	P	P
				P	P	P	
0.701757				P	P	P	A
1.597092		**		P	P	P	P
12.61176		*	**	P	P	P	P
7.79093			**			A	P
2.399741	*		*	P	P	P	P
2.228687			*	P	P	P	P
				A			
0.858235				P	P	P	P
0.391454				P	P	P	P
				P	A	A	
					P	A	
1.016656	**			P	P	P	P
		**			P	A	
0.310442					P	A	A
		*		P	A		
0.696908				P	P	P	A
1.472572	*	**	**	P	P	P	P
1.40056			*	P	P	P	P
				P	A		
0.061917					P		A
0.65196				P	P	P	A
				P	P	A	
0.652262	*			P	P	P	P
1.132844	*			P	P	M	P
					A	A	
			*	A	P	M	
0.665053				P	P	A	A
2.195877	*	**	*	P	P	P	P

					P	A	
					A		
1.803334				P	P	P	P
3.471281		*	*	P	P	P	P
1.820748		*		P		P	P
0.104067				A		A	A
				A	A		
0.448136				P	P	P	P
0.276472					A	A	A
	**				P	A	
2.318808			*	P	P	P	P
0.159015				P	P	A	A
0.423648				P	P	P	P
0.824311		*		P	P	A	A
					A		
0.331746				P	A	P	A
1.755903		*		P	P	P	P
0.264565				P	P	P	A
0.437527				P	P	P	P
0.346483				P	P	P	P
0.356103				P	P	A	A
1.324949		*		P	P	P	A
0.498667				P	P	P	A
0.342629					A		A
3.318442		*	*	P	P	P	P
		*		A		A	
0.740035				A			A
**				P		A	
		*				P	
0.087564					P		A
0.576549				P	A	A	M
						A	
2.099288		**	*	P	P	P	P
4.738187			*				P
1.889501				A	P		P
*				P	P	P	
0.028978					P	A	A
0.427596				P	P	P	P
1.212179				P	P	P	P
					A		

0.801611				P	P	P	P
		*			A	M	
1.538452		*			M		P
0.314598				P	P	P	P
				P			
0.593185				P	P	P	P
				P	A		
					A		
1.253799					A		A
0.20959		*			P	A	A
0.189434				P	P	A	A
13.67217	*		*	**	P	M	P
		*			A	P	
0.867878					A		M
0.058225					P	M	A
		*			M	P	
14.423				**	P	P	M
1.440976	*				P	P	P
			*		P	M	
1.559993	**				P		P
22.95684				**			M
	*				M		
0.180621					A		A
0.497147					P	P	P
2.210147				*	A	P	M
0.466172					P	P	P
0.518785					P	P	P
			**				
					P	A	
		*			P	P	
					A		
2.839925				**	A	A	P
0.574303	**				P	P	A
		**				P	
					M	P	
					A		
3.61357				*			P
		**				A	
1.802571	**				P		P
						A	
						A	

1.400224		*		P	P	P	A
0.034789				P	P	P	A
0.761564				P	P	A	A
			**			P	
0.474305				P	P	P	A
0.671998	*			P	P	A	A
		**			P		
0.451277				P	P	P	P
1.957373			*	A	P	P	P
					P	A	
				P	P	A	
0.611389				P	P	P	P
			**	P		P	
0.458434				A	P	P	P
0.679666	*			P	P	P	P
3.848206			*	*	P	P	P
0.662302				P	P	P	P
2.890767				**	P	P	P
					P	A	
2.018234				*		P	A
0.596543				M	P	A	P
2.929083				**	P	P	P
	**			M			
0.092475							A
1.660386			**	P	P	P	P
2.07529				*	P	P	P
0.267939				P	P	P	P
6.171332				*		P	P
0.27296				P	P	P	P
2.292836				*		A	A
					P	A	
1.834388		*		M	P	P	P
2.232274				*		A	P
0.739879	**			M	M		A
1.958573				P	P	P	P
4.495818				*	P	P	P
0.686399				P	P	P	P
0.074048				P	P	A	A
2.927237			*	**	P	P	P
		**			P		

0.96005				P	P	A	P
0.167063				P	P	P	A
2.756925			*		P	P	P
5.293475			*	P	P	P	P
0.492885				P	P	P	P
0.28379				P	P	P	P
2.809323			*	A	P	P	P
0.366294	*			P	A	A	A
2.741112			*				P
0.441494				P	P	P	P
0.400492				P	P	P	P
3.061828			**	P	P	P	P
0.747688		**			A	P	A
21.74929			**				P
1.61963		*		P	P	P	P
2.031137			*	P	P	P	P
0.950809				P	P	P	A
2.070221		**	**	P	P	P	P
2.078572			*	P	P	P	P
0.364587				P	P	P	P
2.075953	*	*	*	P	P	P	M
0.94414	**			P	P	P	P
		**		P	P	M	
2.69929			*	A			P
						A	
					A	A	
8.885694	*	*	**	P	P	P	P
1.534949		*		P	A	P	P
2.35569			*	P	P	P	P
0.338218	**			P	P	A	A
0.432001					P	A	A
2.654649			*		M	M	P
3.162607		*	**	P	P	P	P
1.763886				P	P	A	A
1.434963		*		P	P	P	P
	**			P	A	P	
0.378414				P	P	P	P
0.203522				P	P	P	A
	**			P	A	A	
0.398222				P	P	P	P

0.351739	*			P	P	P	A
						A	
2.557746		**	*	P	P	P	P
2.872359		**	**	P	P	P	P
0.161939				P	P	P	A
2.79698		*	**	P	P	P	P
0.625501	*			P	P	M	A
2.381905		*	*	P	P	P	P
2.011169		*	*	P	P	P	P
1.567097		*		P	P	M	P
0.676808				P	P	M	A
0.565019				P	P	P	P
2.8381			*	P	P	P	P
1.791093		*		P	P	P	P
0.949377		*		P	P	P	P
		**		P		P	
				A		A	
0.307899	**			P	P	P	P
0.40339				P	P	P	P
		**				P	
2.165735			*	P	P	P	P
2.018685			*	P	P	P	P
2.646172	*		*	P	P	P	P
	**			M	A		
0.827341				P	P	P	P
0.270898				P	P	P	P
0.086806	*			P	P	A	A
		*		P	P	A	
0.490787				P	P	P	P
1.567919		**		P	P	P	P
0.337231				P	P	P	P
0.195612				P	A	M	A
0.485741				P	P	P	P
2.14399			*	P	P	P	P
2.224624			*	A	P	P	P
1.248574	*			P	A		P
0.396583				P	P	P	P
0.48822				P	P	P	P
2.981712	**		**	P	P	P	P
0.928433				P	P	P	P

		*			P		
6.021183				*		A	P
0.335703					P	P	P
1.711888			*		P	P	P
3.519348			*	*	M	A	P
1.608438			*		P	P	P
1.016065					P	P	P
4.611306	*		**	*	P	P	P
0.540954					P	P	A
2.759374			**	*	P	P	P
0.369233					P	P	P
1.655744	**		*		P	P	P
2.001651				*	P	P	P
0.73953					P	P	A
					A		
		*			A	P	
		*			P	P	A
1.056493					P	P	A
0.71671					P	P	P
		**				P	
0.430691					P	P	P
2.638595			*	*	P	P	P
	**				P		
2.118101				*	P	P	P
1.850237			*		P	P	P
0.156036					P	P	P
2.688638				*		A	A
0.451721					P	P	P
2.763522			**	*	P	P	P
2.996107			*	**	P	P	P
2.411485			**	*	P	P	P
0.895559			*		P	P	P
3.500267			*	*	P	P	P
4.11297	*		*	*	P	P	P
3.199705				**	P	P	P
	*				M		
3.431977				*		P	P
1.763406			*		M	P	M
0.464005					P	P	P
2.31811				*	P	P	P

0.682447				P	P	A	A
0.325626				P	P	P	P
0.102126					A		A
1.66183					A		P
3.047464			**	P	P	P	P
1.059428				P	P	P	P
0.438396				P	P	P	P
2.384662			*	P	P	P	P
0.349219				P	P	P	P
1.099022				P	P	A	A
9.779569			**		A		P
14.60371			**	P			P
				A	A		
0.328551				P			A
0.51635				P	P	M	A
0.273339				P	P	P	P
0.367302				P	P	P	P
2.374821			*	P	P	P	P
1.433981		*		P	P	P	P
1.695408				P	P	P	P
5.65143	*	**	*	P	P	P	P
1.624832		*		P	P	P	P
0.453022				P	P	P	P
2.025545			*	P	P	P	P
3.585696		**	*	P	P	P	P
0.248384				P	P	P	P
1.117018	*	*		P	P	P	P
	*			P	P	P	
					A	A	
0.423221				P	P	P	P
0.488934				P	P	P	P
3.323886			*	P	P	P	P
4.335556		*	*	P	P	P	P
0.456932				P	P	P	P
0.455604				P	P	P	P
0.482308				P	P	P	P
0.444803				P	P	P	P
0.304867				P	P	P	P
0.208084				P	P	P	A
2.573056		**	*	P	P	P	P

1.212795		*		P	P	P	P
0.298598				P	P	P	P
0.283925				P	P	P	P
3.776273	*	*	*	P	P	P	P
1.000682				P	P	P	P
2.011353			*	P	P	P	P
						A	
1.338705				P	P	P	M
				P	P	P	
0.344576				P	P	P	P
2.326543		*	*	P	P	P	P
0.633208	*			P	A	P	A
0.83994				P	P	P	P
2.21568			*	P	P	P	P
0.122317				P	P	P	P
0.175327				M	P	P	A
2.101089			*	P	P	P	P
3.088394		*	**		P	A	P
2.964151			**				P
						A	
				M	A	A	
1.444201				A	P	P	P
		*				P	
1.667969	*			P	P	P	A
2.188942			*	P	P	P	P
3.326245			*	P	P		P
0.473225	*			P	P	P	P
3.910002			*				P
1.880441				P	P	A	P
0.268848				P	P	P	P
2.198002	*	*	*	P	A	P	P
2.892972	**	**	**	M	P	P	M
0.328651				P	P	P	P
0.202131				P	P	P	P
0.830385	*			P	P	P	A
	**			P			
0.477192				P	P	P	P
2.278961		*	*	P	P	P	P
3.093597			**	P	P	P	P
2.697834			*		A		P

				P	P	P	
0.503775	*			P	P	A	A
3.381105		*	*	A		P	P
0.963259				P	P	P	P
2.864198	*	*	**	P	P	P	P
5.27936		*	*	P		P	P
					P	A	
0.430463				P	P	P	P
0.74961				P	P	P	P
0.095295				P	P	A	A
				P	P	A	
1.059452				P	P	P	P
2.107891			*				P
						A	
1.630042	*			P	P	P	P
1.182509	**			P	A		A
				P	P	A	
0.252235				P	P	P	P
0.81788	*	*		P	P	P	A
0.422671				P	P	P	P
0.478744				P	P	P	P
1.137289		*	**	P	P	P	P
		*			P	A	
0.438504							A
0.669687	*			P	P	P	P
1.901776	*			P	P	A	A
1.104018				M	A	P	A
0.035019				A	P	A	A
0.346996				P	P	P	P
1.437061	*	**		P	P	P	P
0.337678				P	P	P	P
0.774995				P	P	P	P
		*			M		
2.787576	**		*	P	P	P	P
0.467001				P	P	P	P
0.926414				A		A	A
0.153314				P	P	A	A
0.494412				P	P	P	P
						A	
0.306062				P	P		A

1.355647				P	P	P	P
0.838896				P	P	P	P
3.330414			*	P		P	P
0.353761				P	P	P	P
0.798642				P	P	P	P
0.947562		**		P	P	P	P
				A	P	A	
5.263842			*				P
		**				P	
3.851873		*	*	P	P	P	P
2.404245		*	*	P	P	P	P
1.573752		*		P	P	P	P
2.070314			**		P	A	P
0.981046				A	A	A	P
0.464223				P	P	P	P
0.151794						A	A
0.403276				P	P	P	P
1.227142		**		P	P	P	P
2.437647			*	P	P	P	P
0.270206				P	P	P	P
0.589574	**			P	P	A	A
0.48922	**			P	P	P	P
0.368756				P	P	P	P
0.463076				P	P	P	P
0.862614				P	P	A	P
	*		*	M	A	P	
0.085076				P	P	P	A
0.884046		**		P	P	P	A
0.38232				P	P	P	P
1.803307		*		A	P	A	A
	**			M			
2.602893	*		*	P	P	P	P
0.264899	*			P	P	P	A
1.680961				P	P	A	P
0.674017				P	A	P	A
3.043835	*	**	**	P	P	P	P
1.527568		**		P	A	P	A
				P	A		
1.047088		*		P	P	A	A
1.399718				P	P	P	P

1.286632			*		P	P	P	P
0.443376					P	P	P	P
50.1901				**				P
2.777408				*	P	P	P	P
	**		*		P	P	P	
0.367807					P	P	P	P
0.479388					P	P	P	P
1.625506			*		P	P	P	P
0.409183					P	P	P	P
0.493911							A	A
5.701462		*	**	*	P	P	P	P
6.184587			*	*	P	P	P	P
2.540666			*	*	P	P	P	P
2.321754				*	P	P	P	P
			*			M	P	
	**				P			
2.139122	*		*	*	P	P	P	P
0.951806	*				P	P	P	P
							A	
6.128024			**	*	P	P	P	P
5.787027	**		**	*	P	P	P	P
2.295552				*	M			P
0.302187					P	P	P	P
0.875545					P	P	P	P
3.987949		*		*	P	P	P	P
		*	**		P	P	P	
			**		P		A	
			*		P	M	P	
							P	
1.479319					A		A	A
2.359685				*				P
			**				P	
0.179418	*	*			P	P	P	M
						A		
0.65451					P	P	P	P
0.05866					P	P		A
4.066861				*	A		P	P
1.128414		*	*		P	P	P	P
1.531746		**	**		P	P	P	P
1.006457	*	**	**		P	P	P	P

2.145661	*			*	P	P	P	P
1.047938			**		A		P	A
2.609002				*				P
0.884444		*				P		P
					P	P	A	
							A	
1.467294					P	P	A	P
0.376406					P	P	P	P
	**		**		P		P	
7.476961	**	**	**	**	P	P	P	P
0.433584					P	P	P	P
0.491468					P	P	P	P
2.281262				*	P	P	P	P
		**			P	P		
0.765569			*		P	P	P	P
		**				M		
1.365685	*				P	P	P	P
4.850369	*	*	*	*	P	P	P	P
0.312931					P	P	P	A
		*			P	P	P	
1.689335			**		P	P	P	P
1.790933					P	P	P	P
	**				P	A		
					P		A	
0.33387					P		M	A
					P	P	P	
2.100534				*	P	P	P	P
8.517386	**		*	**	P		P	P
						A		
2.600835			*	*	P	P	P	P
0.243479		*				P	A	A
2.248748			*	*	P	P	P	P
2.350991				*				M
0.785184	*				P	P	P	P
2.941074			*	**	P	P	P	P
4.776593			*	*	P	P	P	P
3.332789				*				M
1.700778					P	P	A	P
1.013441					P	P	P	P
2.212719			*	*	P	P	P	P

0.618797		*			P	P	A
				P		A	
0.388065	*			P	P	P	P
				P	A	A	
3.797335			*	P	P	A	P
0.271351				P	P	P	P
1.706139		*		P	P	P	P
1.078635				P	P	M	A
0.078451				P	M		A
1.928611		*		P		P	P
2.060021			*	P	A	P	P
2.373566			*	P	P	P	P
		*			P		
2.291008			*	P			P
1.156381				P	P	A	P
2.348193			*	P	P	P	P
					P	A	
		*		P	P	P	
	*	**		P		M	
0.813122		*		P	A	P	P
						A	
1.768852				P	P	P	P
0.460013				P	P	P	A
3.404033		*	*	P	P	P	P
2.710104			*	P	P	A	P
0.356354		*		A	M	M	A
				A			
0.518546		**		M	P		A
0.484144				P	P	P	P
0.870878	*	*		P	P	P	P
1.004217				P	P	P	M
				P	A	A	
		*				P	
4.386682	*	**	*	P	P	P	P
	**			P	P	P	
2.271904	*		*	P			P
0.486109				P	P	P	A
2.494279			*	P	P	P	P
0.634664				P	P	P	A
		*		P	P	A	

					M	A		
0.106408								A
2.312301				*	P	P	P	P
					P	A	P	
0.537068			*		P	M	P	A
2.521977				*		P		P
	*				P	A	A	
0.297713						P	A	A
2.49969	**		*	*	P	P	P	P
1.013592					P	P	P	P
1.801062	*				P	P	M	P
2.163396				*	M	P	P	A
0.491079	*				P	P	P	M
					A		A	
2.388132				*	P	P	P	P
	*				P	P	P	
		*						
		**				P		
8.314333			**	**			P	P
		*	**		P	P	A	
0.581433					P	P	P	P
0.518533	**				P	P	P	P
0.273295								A
						A		
0.165327					P	P		A
							A	
1.06549					P	P	P	P
1.587789					P	P	P	P
					P			
					A			
0.562849	*				P	P	A	A
	*	**			P	P	A	
1.150294			*		P	P	P	P
	**	*			P	P		
1.201697						P	P	M
							A	
							A	
2.581007				*	P	P	A	P
0.311349					M	P	P	A
1.788862					P	P	P	P
6.745681			*	**	P	P	P	P

0.131222		*	*	P	P	P	A
				P	P	A	
0.315016			**	P		A	A
0.406419				P	P	P	M
2.165757			*	P	P	A	P
0.363543				P	P	P	A
0.028863				P	P	P	A
0.472586				P	P	P	P
1.78722		*		P	P		P
0.094777							A
			*	A		P	
1.734945			*	P	P	P	P
						A	
1.519733	*			P	P	P	P
0.445875				P	P	P	P
				P	P	A	
					A	A	
0.070312					P		A
	*			P			
0.155515				P	P	A	A
0.758586				P	P	P	P
0.55729				P	A	M	A
0.871945				P	P	P	A
0.383927				P	P	P	P
0.497461	*			P	P	P	A
				A		A	
						A	
4.141881			*	A	P	P	P
0.509046				P	P	P	P
						A	
					A	A	
0.654256				P	A	A	A
0.541318				P	P	M	A
0.200385				P	P	P	P
0.415163				P	P	P	P
0.961812	**			P	P	P	A
					A		
0.251573					A		A
0.424308				P	P	P	P
0.259376				P	P	P	A

				M	P	A	
8.376514		**	**	P	P	P	P
0.392914				P	P	P	P
0.951863				P	A	A	A
						A	
2.993735	*		**	P	P	P	P
1.476327				A	A		P
7.519135		*	**	A	A	M	P
1.322978				P	P	A	A
0.79307				P	P	P	P
0.356262				P	P	P	A
30.24619			**	A	P		M
		*			P	A	
1.525216			**	P	P	P	P
0.441529				P	P	P	A
						A	
		*			P		
0.735627				P	P	P	P
0.107013				P	P	P	A
0.763923		*		P		A	A
3.618972		*	*	P	P	P	P
1.396599				P	P	P	P
0.923743				P	P	P	P
0.458578		*		P	P	P	P
0.081443					P	P	A
2.613925			*	P	P	A	P
	*			P			
17.61319			**			P	P
	**	*		P	P	P	
					A		
0.057652				M	P	P	A
0.394362				P	P	P	A
		**		A		P	
0.450681				P	P	P	P
0.494026				P	P	P	P
2.725197			*				P
2.025553			*	P	P	M	A
0.646409				P	P	P	P
11.85555			**	A	P	P	P
12.06994	*	*	**	P	P	P	P

4.678745			*		A		P
				P		A	
		*		A	P		
3.904942			*				M
0.796495				P	P	P	P
1.116493				P	P	P	M
0.090868	**			P	P	A	A
				P	P	A	
0.702874				P	P	P	P
				P	P	A	
51.09869		*	**			P	P
		*			P		
					M	A	
0.134506		*		P	P	P	A
0.572578				P	P	P	P
				A	A	A	
				A	P	A	
				A		A	
		*				M	
						A	
0.449214				P	P	P	P
3.029035			**				P
0.315606				P	P	P	A
0.560359	*			P	P	P	P
						A	
0.472616				P	P	P	P
0.8366				P	P	P	P
0.610227				P	P	P	A
0.752331		*		M	A	A	M
0.131227							A
2.866119		*	**		P	P	P
0.534113		**			P	A	A
0.911833	*			P	P	P	P
		*			M		
1.277411	**			P	P	P	A
1.713092				P	P	P	P
0.889471	*			P	P	A	A
0.968513	*			P	P	P	P
				A	A	A	
0.917739	*			P	P	P	M

1.447334		*			P	P	P	P
	*				P	P	A	
3.075658				**	P	P	P	P
2.679133				*	P		M	P
					P	P	A	
					P	P	P	
0.802606					P	P	P	A
1.388028	**				P	P	P	A
2.147082				*			A	A
4.155042	**	*	**	*	P	P	P	P
	*				P			
0.541444					P	P	P	P
0.250601					A	A	A	A
0.608212					P	A	A	M
2.786551	*			*	P	P	A	P
2.668538				*	A	P	A	A
1.41068					P	P	P	P
0.379404					P	P	P	A
		**			P	P	A	
2.15705				*	P	P	P	P
0.570372			*		P	P	P	P
6.581076	*		*	**	P	P	P	P
1.024905	*				P	P	P	P
3.212348				**			A	P
			**		P	P	P	
0.216169					P	P	P	A
0.371958					A	P	P	A
0.769965					P	P	P	P
2.757034			*	*	P	P	P	P
					A		A	
1.63612			*		P	P	P	P
0.444121					P	P	P	P
	*				P		P	
	*				M			
3.603355				*				P
0.969696					P	P	P	P
0.657081					P	P	P	P
0.141131					P	P	A	A
0.249998	**				P		P	A
2.237129				*	P	P	P	P

0.854103	**			P	P	P	A
1.819255		*		P	P	P	P
				P	A	A	
0.198836				P			A
0.297505		**			P		A
2.575413			*	A		A	P
0.546095				P	P	P	A
2.618063		*	*	P	P	P	P
0.818896	*			P	P	A	A
		**				P	
0.130713							A
1.931653	*			P	P	P	P
2.006343			*	P	P	P	A
0.473532				P	P	P	P
2.834701		**	*	P	P	M	P
1.763943	**	*		P	P	P	P
						A	
	*			M	A		
2.045447			*	P	P	P	P
2.915115			**	P			P
1.587566	*			P	M	A	P
		*			M		
0.291442				P	P	P	A
				A			
2.632635			*		P	P	M
0.92473	*			P	P	P	M
0.331127							A
1.734289				P		A	P
0.417759				P	P	P	P
1.345744				P	A	P	P
1.188279	*			P	P	P	P
0.843519	*			P	P	P	P
				A	P		
4.53354			*	P	P	P	P
2.275947			*	P	P	P	A
0.610085	*	*		P	P	P	P
2.092013	*		*	P	P	P	P
1.795475	*	*		P	P	P	P
				P		A	

	*			M	P	A	
2.222507			*	P	P	P	P
0.495518				P	P	A	A
0.423646	*			P	P	P	P
				A	P	A	
0.09545				P	P	P	A
		*			M		
0.474874				P	P	P	P
2.111749			*	P	P	P	P
				A	P		
1.763325	*			P		P	M
	*			P	P	P	
		*			P		
0.041195	*			P	P	A	A
						A	
				P	P	A	
	*			P			
	*			M			
	**			P			
1.615793				P	P	A	A
	*			P			
2.095399			*	P	A		P
	*	**		P	P		
1.362564				P	P	P	P
			**			M	
1.319642						A	A
						A	
	**			P	A		
		**		P	P	A	
4.244169			*	P	A	P	P
0.934493				M	P	P	P
	*			P			
			*			M	
0.724531				P	P	P	P
1.473761	*			P	P	P	P
2.096437			*	P	P	P	P
0.383049	*		*	P	P	P	A
0.435607				P	P	P	P
		**		P	P		
1.724145		**		P	P	P	A

					P	P	P	
1.912916			*		P	M	P	P
					P	A	A	
1.004832	*				P	P	P	A
0.493791					P	P	P	P
3.129172	*	*	**	**	P	P	P	P
0.480822					P	P	P	P
0.124731								A
0.193137					P	P	P	P
					P		A	
1.970427		*			P	P	P	P
3.342818		*	*	*	P	P	P	P
2.626971			*	*	P	P	P	P
0.462691					P	P	P	P
					A	A		
0.717592					P	P	P	P
2.846825				**	P	P	P	P
2.979842				**	P	P	P	P
0.439458					P	P	P	P
0.260598	*				P	P	P	A
3.085093				**	P	P	P	P
0.570039	*				P	P	P	A
	**				P	M	P	
2.556439				*	P	P	P	P
0.912657					P	P	P	P
2.85374				**	P	P	A	M
0.076373						A	A	A
2.953718				**	P	M	P	P
					A	M	A	
0.103338		*				P	M	A
1.094211					P	P	A	P
						A	M	
2.675631				*	A			P
		**				P		
3.345431				*	P	P	P	P
						A	A	
0.615586					P	P	P	P
0.436485					P	P	P	P
0.303723						A	P	A
2.181094				*	P	P	P	P

0.830304				P	P	P	P
0.773947				P	P	A	A
2.962468			**	P	P	P	P
0.638284				P	P	P	P
	*			M			
0.519624				P	P	P	P
0.272123				P	P	P	A
	**					A	
				P	A		
						A	
31.43482			**	P	A	P	P
2.374323		**	*	P	P	P	P
		*			P	P	
0.436063				P	P	P	P
0.286555				M	P	A	A
1.245882				P	P	P	P
2.520805			*				A
2.144212			*	P	P	A	A
0.723374				P	P	P	P
2.622793			*	P	P	P	P
1.644696		*		P	P		A
0.256878				P	P	P	A
0.265121				P	P	P	P
0.487256				P	P	P	P
0.302207				P	P	P	A
					A		
1.181026				P	P	A	A
3.804396	*		*	P	P	P	P
1.13561				P	P	P	P
2.801763			*				P
2.921458		*	**	P	P	P	P
0.244086				P	P	P	A
					A	A	
				M	P	A	
0.561755	*			P	P	P	P
0.41273				P	P	P	P
0.480997				P	P	P	P
0.791288	*			P	P	P	P
1.252149				P	P	P	P
0.068796							A

	*			P			
0.383146		**		P	P	P	A
0.397161				P	P	P	M
2.425592			*		A		P
0.326005				P	P	P	A
2.596698		*	*	P	P	P	P
0.92101				P	P	A	P
3.111895			**	P	P	P	P
	**				P		
0.102395				P	P	A	A
2.869543			**	P	P	P	P
				P	A	A	
					P	A	
				A			
2.788828			*	P	P	P	P
	**			P		A	
4.228182			*	P		P	P
0.446734				P	P	P	A
1.159345		*		P	P	P	A
	*				P		
0.258743				P	P	A	A
					A		
				P			
		*		A			
				M	P		
						A	
3.634792	*	**	*	P	P	P	P
1.730023				A		P	P
0.500582	*			P	P	P	P
1.005809		**		P	P	P	P
0.236968				P	P	P	P
1.157643				P	A	A	A
				P	P		
8.591514			**				P
1.111792				P	P	P	P
	*			A	P	P	
1.192207				P	P	P	P
				A	P	A	
					A	A	
0.25231				P	P	P	P

0.180049				P	P	P	P
				P	P	A	
0.767648				P	P	P	P
0.175174				P	P	P	A
0.697531				P	P	P	P
0.481464				P	P	P	P
1.019197				P	P	P	P
0.231937		*			P	A	A
0.470219				P	P	P	P
0.594935	*			P	P	P	P
1.540974		*		P	P	A	P
				A		A	
1.047574				P	P	A	A
0.808364				P	P	P	P
			*		P	P	
3.359888				*		A	P
0.656056	*			P	P	P	P
			**			P	
0.586527				A	A	A	A
0.307515				P	P	A	A
0.45086				P	P	P	P
4.782934			*	*	P	P	P
2.760799			*	*	P	P	P
0.152403	**			P			A
0.716904				P	P	A	P
2.271482				*	A	M	M
4.465485	*		*	*	P	P	P
4.948239				*		P	P
					A		
4.566197			*	*	P	P	P
0.574696				P	P	A	A
	*	**		P	M		
		*			P		
				A	P	A	
0.75808				P	P	A	A
2.193514				*	P	P	P
2.757955				*	P	P	P
3.810111				*	M		P
0.677742	*			P	A	M	A
					A	A	

1.389457		**		P	P	A	P
0.459937				P	P	A	A
				A	A		
0.338372				P	P	P	A
					A	A	
1.797669				P	P	A	P
					A		
7.078972	*		**	P		A	M
1.022479				A	A	A	A
				P	P	A	
0.871924		**		P	P	P	P
					A	P	
2.461478			*	P	P	P	P
	*	**		P		P	
	**			P	P	P	
0.175347				P	P	P	M
2.400785			*	P	P	P	P
0.693605		*		P	P	P	P
1.074879				P	P	P	P
0.496311				P	P	P	A
1.832147	*			P	P	P	P
0.303343				A	P	P	A
0.501322				P	P	P	A
				A			
0.757017				P	P	P	P
0.686889				P	P	P	P
1.212329		*		P	P	P	P
1.782407				P	A	A	P
0.088922							A
1.21567				P	P	P	A
0.448993				P	P	P	A
0.429985				P	P	P	P
7.767401			**	A	A		P
0.221194				P	P	P	A
0.35137				P	P	P	P
2.759747			*	P		A	P
1.578021	*			P	P	P	P
0.543156				P	P	P	A
	*			P			
3.018084			**	P	P	P	P

0.120009				P	P	P	A
				P	P	P	
0.439413				P	P	P	P
0.145022				P	P	P	A
				A			
0.688028				P	P	P	P
1.848504		*		P	P	P	P
10.95108			**				P
0.292027				P	P	P	P
		**			A	P	
						A	
						A	
2.264895	*		*	P	P	P	P
		*				P	
0.072499	*			P	P	A	A
0.124017					P	A	A
3.101504		*	**	P	P	P	P
1.58736		*		P	P	P	P
						A	
0.33206				P	P	P	P
1.189322				P	P	P	P
3.316575			*	P		A	P
0.460441				P	P	P	P
1.440436	*			P	P	P	P
2.841964		**	**	P	P	P	P
0.098402				P	P	A	A
0.272809				P	P	P	P
0.435495				P	P	P	P
				P	A	A	
		*			M		
0.776185				P	P	P	A
					A		
	**			P			
1.973135	*			P	P	P	P
1.535231		*		P	P	P	P
		*			M		
0.348367				P	P	P	P
				A			
0.458123				A	P	A	A
10.396			**				P

28.87352				**				P
0.515205			*		P	P	P	P
0.525254					P	P	P	P
						A	A	
2.386738				*	P	P	P	P
		*	**			M	P	
2.736117				*	M	A	P	P
0.258337					P	P	P	A
0.35204						P	P	A
0.484553	*				P	P	P	P
2.339197				*	P		P	P
0.555366					P	P	P	M
			**				M	
0.075415								A
1.147632	*				P	P	P	P
1.779161	**	*			P	P	P	P
0.376029					P	P	P	A
					A	P		
0.231254						M	A	A
							A	
0.201437					P	P	P	P
0.337992					P	P	A	A
0.043185							M	A
2.492333		*	*	*	P	P	P	P
		*				M		
					P	P	A	
3.334073				*	P	P	P	P
	*				M			
		**			A	P	A	
0.341733					P	P	P	P
					A	A	A	
2.105255				*	P	P	P	P
1.182291	*				P	P	P	P
0.591515					P	P	P	P
					A	A	A	
0.482704					P	P	P	P
1.407307			*		P	P	P	P
0.276056	*				P	P	M	A
0.955333					P	M	A	A
						A		

	**			P			
3.621759			*	A		P	P
0.303263				P	P	P	P
		**		P	P	P	
0.713776		*		P	P		A
				P		A	
8.672032			**		P	A	M
0.251652				P	P	P	A
				P	P	A	
0.035339	**			P	A	A	A
		*				P	
0.391683				P	P	P	A
2.034278			*	A	A		P
				P	A		
0.465077				P	P	P	P
0.550503				P	P	P	A
0.664406		**		P	P	P	P
1.647072		*		P	P	P	P
1.007075				P	P	P	A
3.429891			*	P	P	A	P
				P	A		
		*			P		
2.605749			*		A		P
3.4859		**	*	P	P	P	P
2.147749			*	P	P	P	P
0.163462	*			M		A	A
0.388464				P	P	P	A
2.144636			*	P	P	P	P
						A	
					M	A	
	*			P	P	P	
3.209179		*	**	P	P	P	P
0.186959					A	M	A
0.391707				P	P	P	P
2.094227		**	*			P	P
2.083795			*	P	P	P	P
0.446624				P	P	P	P
0.018457				P	P	P	A
		*			P	A	
0.382594				P	P	P	P

1.598539				P	P	P	P
	*			P	A		
2.376527			*	*	P	P	P
	*				P	P	M
32.83286			**	**		P	P
0.109065					P	P	A
0.908534		**			P	P	A
1.2696	**				P		A
0.437745	*				P	P	P
	*				P	P	
0.43939					P	P	P
0.371715					P	P	P
						P	A
0.139185					P	P	P
0.435494					P	P	P
					P	P	P
2.143015				*	P	P	P
0.866172					P	P	P
		**			P	P	A
1.531328		*			P	M	P
	*		*		P		P
0.467055					P	P	P
1.839898					P	P	A
0.332332					P	P	P
0.669644					P	P	P
							A
1.123398					P	P	A
0.414667							A
0.963448					P	P	P
						A	
0.069764					P		
							A
						A	
14.01019				**	P		M
		*				M	
0.421162					P	P	P
3.090319				**	P	P	A
2.875994		*		**	A	P	P
5.431061		**		*			P
					A	P	M

3.831803				*	P	P	P	P
0.66699					P	P	P	P
0.837418	*				P	P	P	P
0.362124					P	P	P	M
2.701454				*	P	P	P	P
					A		A	
5.659215	*	**	**	*	P	P	P	P
1.899579					P	P	P	P
1.388884		*			P	P	P	P
4.360007				*	P	P	P	P
1.216629		*	**		P	P	P	P
					P	P	M	
1.861319					A	A	A	P
					A	A		
					A	P	A	
	**				P	P	A	
	*	*			P	M		
			*			P	P	
0.664511	*				P	P	P	P
	*				P		P	
2.03076				*	P	P	P	P
0.318482					P	P	P	P
0.491417					P	P	P	P
0.598412					P	P	P	P
					A	P	A	
0.509007					P	P	A	A
0.444131					P	P	P	P
		**				M		
14.23309				**	P	P	P	P
0.763808					P	P	P	P
28.63172				**				P
2.307094				*	M		A	P
1.970672			*		P	P	P	P
					P	A		
		**				P	M	
0.037292	*				P	A	A	A
0.740257					P	P	P	P
0.805718					P	P	P	P
			*				M	
2.274477				*	A			P

0.555265				P	P	P	P
				A			
3.219929			**		P		P
2.435612		*	*	P	A	P	M
1.700413		*		P	P	P	P
		*		M	A	A	
0.572555	*			P	P	P	P
		*		A	P		
0.090563	**			P		A	A
						A	
3.256234		**	*	P	P	P	P
2.79848		*	*	P	P	P	P
0.42214				P	P	P	P
				A	A	A	
0.973224		**		P	P	P	P
				A			
71.42501			**		P		P
1.60159		*		A	P		P
2.379396		*	*	A	P	P	P
3.44016			*		A	P	P
				A			
				P	P	A	
0.639232				P	P	P	P
		*		A	P		
1.16045				P	P	P	P
0.724686				P	P	P	P
						A	
0.8761		*		A	P		A
					A		
3.483341			*	A			P
0.714411		*		P	P	P	A
		*		A	P	A	
0.851578	*			P	P	P	P
1.76068		*		P	P	P	P
0.476334				P	P	P	A
2.145841			*	P	P	P	P
1.199909		**		A	A	P	A
2.940568			**	P	P	P	P
				A			
0.800184				P	P	P	P

1.379515				P	P	P	A
4.085739			*	P		P	P
0.439299	**			P	P	P	P
2.547048		*	*	P	P	P	P
0.390088				P	P	P	P
				A			
0.844997				P	P	P	A
2.160994			*	P	P	P	P
2.044909			*		P	P	P
9.408117		*	**	P	M	P	P
0.302122				P	P	P	P
0.422007					A		A
0.327406				P	P	P	A
				P	A		
2.682957			*			A	M
1.211144				P	P	P	P
2.123868			*		A		P
				A	P	P	
		*		P	P	A	
11.4451		**	**	P	P	P	P
1.864273		*		P	P	P	P
11.53542			**		M	P	P
0.836324				P	P	P	P
0.365939				P	P	P	P
0.499229				P	P	P	P
				P	P	A	
0.556235				P	P	P	P
2.42938		**	*	P	P	P	P
0.480762				P	P	P	P
1.845615	*			P		A	A
				P	A		
		**			M	P	
2.113617			*	P	P	P	M
				P	P	A	
3.686825		*	*	P	P	P	P
3.351732			*	P	P	P	P
41.46007			**				P
4.580424		*	*	A	P	P	P
2.02199	*		*	P	P	P	P
2.204463			*	P	P	P	P

		*		A	M		
36.64858			**				P
						A	
0.112514							A
0.709419				P	P	P	P
		*		M	P		
2.675026			*				M
0.444856				P	P	P	P
	*			P			
0.547849				P	A		A
1.295354		*			P	P	P
				A	P	A	
0.984924				A	M	P	A
				A	M		
			**			M	
				M	P	A	
					A		
0.380534					A		A
	**			P	P	A	
	**			P			
1.109783			**	P	P	P	P
					P	A	
						A	
				P	A	A	
				A			
	**			M			
3.711076			**	*		P	P
0.633192				P	P	P	A
0.437107					A	A	A
2.192862			*	*	P	P	P
0.583981					P	P	P
0.174378	**			P			A
	*			P			
2.311606	*	*		*	P	P	P
35.5105			**	*	P		P
2.641034			*	*	P	P	P
5.603309			*	*		P	P
0.626618	**			P	P	A	P
1.093116	*	*		P	P	A	P
0.854942	**	*		P	P	A	A

			*		A		M	
					P	P	A	
						P	A	
13.29271	*		*	**	P	P	P	P
			**				P	
9.282708			**	**	P	P	P	P
0.512005	*				P	P	P	A
2.66227				*	P	P	P	P
0.437537					P	P	P	P
3.108232	*		**	**	P	P	P	P
			*				P	
0.881017					P	P	P	P
1.049303					P	P	P	A
0.858625					P	P	P	P
0.722091					P	P	P	A
0.456271					P	P	P	A
2.111519				*	P	P	P	A
							A	
1.298763	*				P	P	P	P
	*		*		P	A	P	
0.49404					P	P	P	P
0.359811	**				P	P	P	P
			**				P	
0.564456					P	P	P	P
1.059506					P	P	P	P
0.30991					P	P		A
0.456403					P	P	P	P
0.728815	*				P	P	P	P
					P	P	A	
0.449762					P	P	P	P
0.495844					P	P	P	A
0.458698					P	P	P	P
							A	
					P	P	A	
					M	A		
0.456115	*				P	P	P	P
3.232095				**				P
1.890319					A			A
2.285091	*			*	P	P	P	P
		*				M		

0.849008				P	P	P	A
4.673796		*	*	P	P	P	P
1.647403				P	P	P	P
0.289931				P	P	P	A
		**		A	M		
2.342299	*		*	P	P	P	P
0.53794				P	P	P	P
		*				M	
0.381585				P	P	P	A
0.130541							A
6.531853			**	P	P	P	P
2.130212			*	P		P	P
3.069			**	M		P	P
0.495159				P	P	P	P
				P	P	A	
	**			M			
0.3274				P	P	P	A
0.199527				A			A
					P	A	
				P	A	A	
0.124986				P	P	A	A
2.020807			*		P	P	P
0.369225				P	P	P	A
40.65019		*	**		A	P	P
0.655573				P	P	P	P
0.548279				P	P	P	P
0.488162				P	P	P	P
3.748813		*	*	P	P	P	P
2.726235		*	*		A	P	M
2.095454		*	*	P	P	P	P
0.140232							A
1.743269		*		P	P	P	P
0.691809				P	P	P	P
	*			P			
	**			M			
				P	A		
0.429743				P	P	P	P
1.232223				P	A	P	A
1.555694				P	P	P	P
0.430097				P	P	P	P

2.332273			*	P	P	P	P
0.957517		*		P	P	P	P
				A	A	A	
		**			P		
0.953032				P	P	A	A
				A			
5.304863		**	*	A	P		P
2.087563			*	P	P	A	P
0.432766				P	P	P	P
		*		P	P	A	
1.337675				P	P	P	P
10.85168			**		A		P
2.074431			*				P
2.362838			*	P	A		P
0.548124				P	P	P	P
2.286867			*	P	P	P	P
0.683824					P	A	A
3.632105			*	M	M	P	P
0.737607				P	P	P	M
					P	A	
0.599804				P	P	P	P
1.828937	*			P			P
0.484818				P	P	P	P
0.377872				P	A		A
0.26983	*			P		A	A
0.105271				P	P	P	A
0.539916				P	P	A	A
0.271098							A
0.064608		*		P	P		A
			*	M	A	P	
5.024321	*		*	P		P	P
7.234614	*	**	**	P	P	P	P
3.024102	*		**	P	P	P	M
1.729441	*			P			A
1.15727		**		A	P	A	P
			*	P	A	A	
1.465604				A	P	A	A
	**			P			
0.992724				P	P	P	P
0.443632				P	P	A	A

2.05707				*		A		A
5.487836				*	A	P	A	P
1.02838	*				P	P	P	P
0.546386					P	P	P	P
0.556298					P	P	P	A
0.788511						P	A	A
0.741794					P	P	A	P
0.369679					P	P	P	P
0.980886		*	*		P	P	P	A
1.405646			*		P	P	P	A
0.648711					P	A	P	A
0.217235					P	P	P	P
0.86611			*		P	P	P	P
2.39405				*	P	P	P	P
0.171135						A	A	A
0.607896					P	P	P	P
0.38285	**				P	P	A	A
1.213762					P	P	P	P
0.934701					P	P		A
			*		A		A	
0.060381					P	P	P	A
						A	A	
0.13076					P	P	P	A
2.232883				*	P	P	A	P
1.422646			*		P	P	P	P
0.498555					P	P	P	P
2.157255				*	P	P	P	P
0.481308	*				P	P	P	P
0.360262			**		P	P	P	A
0.49866					P	P	P	P
0.282526					P	P	P	A
0.418494					P	P	A	A
1.480304		*				P		M
0.461798					P	P	P	P
		*			P	P	P	
	*				P			
12.68689	**		*	**	P		P	M
2.972872				**	P	P	P	P
0.176771					P	P	A	A
0.309051					P	P	P	P

0.452853					A			
1.31851			**		P	P	A	A
	**				P		P	P
0.772471	*				M			
6.443873		*	**	*	P	P	P	P
16.75187		*	**	**	P	P	P	P
2.922595				**		P	P	P
0.463639					P	P	P	P
							A	
	*				P	P	A	
4.622951				*				M
0.191552					P	P	P	P
0.17952					P	P	A	A
0.280594					P	P	P	A
1.214051					P	P	P	P
2.674374				*	P	P	A	A
1.786527		*			P	P	P	P
					P	A	A	
2.522382				*	P	P		P
2.355465		*		*	P	P	P	P
					P	A	P	
2.511212		*		*	P	P	P	P
0.5953					P	A	A	A
3.875563				*		A		P
0.612504					P	P	A	P
22.54872				**				P
		**				P		
0.476476					P	P	P	P
4.931102		*		*	P	P	P	P
1.071995		**			P	P		A
0.490601					P	A	A	A
1.291004	*				P	P	P	P
4.295676				*	P	P	M	P
4.532082		*		*	P	P	P	P
2.002986				*	P	P	P	P
					P		A	
		**	**		P	P	P	
					A	P	A	
2.090432				*	P	P	P	P

	**	**		P	P		
2.975545			**	A			P
				M	P	A	
0.233858				P	P	P	P
0.424213				P	P	A	A
0.053456				P	P	A	A
2.115314			*	P	P	P	P
0.410466				P	P	A	A
0.707526	*			P	P	P	A
1.448221		*			P		M
0.993832				P	P	P	P
0.89285			*			P	M
0.399764				P	P	P	A
0.602259		*		P	P	P	A
2.46657			*				P
2.053713			*	P	P	P	P
2.074665			*	P	P	P	P
						A	
0.410505				P	P	P	P
				A			
0.838103				A	M	P	A
0.368087					M		A
1.278721				A	A	P	A
				A	P		
0.816904		**		P	A	P	A
2.171508			*	P	A	P	P
1.366558				P	A	A	A
16.3417		*	**		P	P	P
0.598175				P	P	P	A
	*			M	P	A	
2.114418			*	A	A	A	P
0.740489				P	P	P	P
0.090475						A	A
3.840321			*				P
5.371536			*			A	P
0.11726				P	P	A	A
1.547517		*		P	P	P	P
				A			
				A			
0.436175	*			P	P	P	P

2.127047			*	P	P	P	M
1.092243		**		P	P	P	P
0.367795				P	P	P	A
0.425653				P	P	P	A
				A	A		
0.297462				P	P	P	P
0.207149				P	P	P	P
				A	P		
0.164849					A	A	A
					P	P	
				A	A		
0.892487				P	P	P	P
						A	
2.435329			*	P	P	P	P
				A			
	*				M		
0.109586				P	A		A
		**		A		P	
0.625225				P	P	A	A
					P	A	
3.885413			*				P
	*			M			
58.09682			**			P	P
				A			
0.036287				P	P	A	A
		*		P		P	
1.937454		*		P	P	P	P
0.961795				P	P	P	P
0.658342				A	P	A	A
0.604577				P	P	P	P
1.387194				P	A	M	P
10.42729	**	*	**	P	P	P	P
1.998194		*		P		P	P
1.66614		**			P		M
17.497			**		A		P
0.110696				P	P		A
0.389729				P	P	P	P
3.135854		*	**	P	P	A	P
					A		
0.707027	*			P	P	P	P

	**			P	P		
0.397506				P	P	P	P
1.449605			**			M	P
					A	A	
			**			P	
				A		P	
1.268378			*	P	P	P	P
1.912921		*		P	P	P	M
0.098285							A
				P		A	
1.129884				P	P	P	P
0.925023				P	P	A	A
2.0429				*	P	M	P
					A		
	**	*		P	P	A	
1.045921	**			P	P	A	A
0.420335				P	P	P	P
2.841351			**	M			M
						A	
0.454416				P	P	P	A
1.260035	*			P	P	P	P
2.31039			*	P		P	M
0.963113			*	P	P	P	A
0.785586	*			P	P	A	A
				P	A	A	
0.27075				P	P	P	P
1.909382			**			P	A
2.267644			*	P	P	P	P
0.039353				P	P	P	A
	*			P	P	P	
0.413785					A	A	A
		*			P		
0.496401				P	P	P	P
0.466684				P	P	P	A
2.838506			*	P			P
0.021866				P	M	A	A
		*			P	P	
				A	P	A	
0.264783				P	P	P	A
0.292948					P		A

					A	P	
					A		
0.330798				P	P	P	P
0.424681				P	P	P	P
0.310346				P	P	P	P
2.019948			*	P	P	P	P
1.886606				P	P	P	P
5.195815			*	A	P		M
18.50812	**		**		P	A	P
0.664782				P	P	A	A
1.268407				A			P
1.615947	*			P	P	A	A
0.854592				P	P	P	A
				P	A	A	
0.296282		**			P	P	A
3.040294	**		**	P	P	P	P
0.642412				P	P	P	P
11.15109		*	**	A	P	M	P
	*				M	A	
					A		
				A	A		
				A		A	
				P	M	A	
	**	**			M	P	
0.137954				P	P	P	A
		*				M	
0.140518				P	P	P	A
0.742064				P	P	A	M
2.908665	*		**	A	P	A	P
					A		
	**				P		
				P	P	A	
						A	
	*			P	P	A	
		*				M	
	**				P		
1.722166					A	A	P
	**				M		
2.043739			*	P	P	P	P

0.339989					P	P	P	A
					A		A	
		*				P		
3.590931				*			M	P
		*				P	A	
0.465379					P	P	P	A
4.491137				*	P	P	P	P
		*				P	P	
			*		A	A	A	
		**				M		
		**				P	A	
0.255842					A	A		A
0.102492						A		A
1.846826					P	P	P	P
2.217769				*	P	P	P	P
						A		
2.280506				*	P	P	P	P
3.270337	**	*	**	*	P	P	P	P
0.456091					P	P	P	P
4.370171				*				P
0.446246					P			A
		*			P	M	A	
2.416904				*	P	P	P	P
			*		A		P	
0.078493					P	P	A	A
0.642929					P	P	P	P
						A		
0.523592	*				P	P	P	P
			**				M	
	*				P	P	A	
3.136431			*	**	P	P	P	A
0.215913	*				P	P	P	A
1.586952			**			P	A	M
2.12126	*			*	P	P	A	A
1.766042	*		*		P	P	P	P
			*		P		P	
2.571955	**	*	*	*	P	P	P	P
7.570332				**	A		A	P
10.28292				**				M
0.244513								A

3.567362			*	*		P	P
0.049576					A	A	A
	**			M	P	A	
	**				P		
0.918644				P	P	P	P
2.112772				*	P	P	P
0.6051				P	P	P	P
0.060047				P	P	P	A
0.702079	*			P	A	P	A
		*		P	A		
3.66123				*	A		P
4.396049		*	*	*	A	P	P
		*				P	
	**				P		
	*			P	P	P	
3.040101		**	**	P	P	P	P
1.490684		*	*	P	P	P	P
		*		P	P	P	
	*			P			
0.341957				P	P	P	P
0.54632				P	P	P	M
		*		A	P		
5.642304			*				P
	*			A	P		
				A	A		
					A	A	
2.001989			*	P	P	M	P
				A		A	
0.388818				P	P	P	P
0.849573	*	**		P		P	A
						A	
0.41227				P	P	P	P
0.061566				P	A	P	A
0.397221				P	P	P	P
0.224626				P	P	P	A
0.727008				P	P	P	P
6.05492			*	P		P	P
1.530679	*			P	P	P	P
				P	P	A	
0.9267	*			P	P	P	P

0.584909				P	P	A	A
0.470503				P	P	P	P
	*			P			
0.584				A	M		A
				P	A	A	
0.488179				P	P	P	P
3.25323		*	**	*	A	P	P
0.141811				P	P	P	A
0.637479				P	A	A	A
					A	A	
1.002177				P	P	P	P
1.528475			*	P	P	P	P
5.816874		*	**	*	P	P	P
				A	P	A	
0.217173				P	A	P	A
0.700602				P	P	P	P
1.708234				P	P	A	P
0.409888				P	P	P	P
3.97894				*	P		M
			*			P	
0.464069	*			P	P	P	P
3.30122	*			*	P	P	P
2.222758				*	P		P
2.029075				*	P	P	P
1.228753			*	P	M	P	P
0.024043					P	P	A
2.027353				*	P	A	P
						A	
0.262012		*			P		A
		**			M	A	
			**			P	
1.33864	*		**	P	P	P	P
0.236683				P	P	A	A
36.67758		*	**	**	P	P	P
				A			
0.657993				P	P	P	P
2.275734				*	P	P	P
0.961118				P	P	P	P
0.679886	*			P	P	P	P
					A	A	

38.86379	**	**	*	**	P	P	P	P
1.530844			**				P	A
	**	**	*		M	P	P	
1.637188	**				P	P	A	P
2.198104				*	P	P		P
2.283056		*		*		P	A	P
0.697097					A			A
	*				P	A	A	
4.582064			**	*	P	P	P	P
3.520742			*	*	P	A	P	P
2.992688				**	P	P	P	A
			*		A	P	P	
					A			
0.020754		*			M	M	A	A
1.191999					P	P	P	P
		*				P		
	*					A		
					P	P	P	
					P	A	M	
2.122692			*	*	P	P	P	P
2.924599				**	P		P	A
0.712335						A	A	A
0.912791					P	P	P	P
3.133708				**	M	M	M	P
						A		
2.577768				*	P	P	P	P
2.787527				*	A			P
2.481725				*	P	P	P	P
	**				P		A	
0.376746					P	P	P	A
0.470249					P	P	P	P
						A		
2.027036				*	P	P	P	P
2.512379				*	P	A	P	M
							A	
3.442762				*		P	A	P
23.84411				**				P
			*		P	P	P	
					P	A	A	
					P	P	A	

2.824382			*	P	P		A
1.136775		*		P	P	P	P
0.117093				P			A
0.958074				P	P	P	P
2.65474			*	P		P	P
0.045225						A	A
	*			A	P	A	
				P		A	
0.341118				P			A
0.424671				P	P	A	A
2.347832			*	P	P	P	P
				P	P	A	
2.676452		*	*	P		P	P
2.113726			*	A	P	P	P
	*			A	A	A	
0.795236				P	P	A	P
1.953323		*		P	P	P	P
1.244341				P	P	A	P
0.861135	*			P	P	P	P
1.294202				P	P	A	A
1.819186		*		P	P	P	P
2.862202			**				P
				A		M	
						A	
1.160776				P	P	A	A
1.914514		**		P	P	P	M
	*			P			
	*	**		P		P	
2.481155			*	P	P	P	P
1.284275				P	A	A	P
0.380193				P	P	P	M
					A		
2.247068			*	P	P	P	P
						A	
0.302562				P	P	A	A
0.144375				P	P	P	A
0.0606				P	P	M	A
0.46452				P	P	P	P
0.35587	*			P	P	A	A
2.19634		**	*		A	M	P

3.721917			*		A	M	P
0.579721				P	P	A	A
0.495074				P	P	A	A
				P	A	A	
1.364103				P	P	P	A
				A	A	A	
				P	P	P	
0.41295				P	P	P	P
				P	A		
0.8215	*			P	P	P	P
3.206512			**	A			P
				P	A	A	
0.805261	*			P	P	A	A
0.186775						P	A
1.543987				P		A	A
2.639832			*	P	P	P	P
2.348887			*	P	P	P	P
0.357598				P	P	P	P
1.307159		*		M	P		A
6.291786			*				P
				A			
1.422568				P	P	P	P
3.118896			**				A
		*			P	P	
3.742894			*	P	P	P	P
				A	A		
0.512919		**			P	A	A
0.819761				P	P	P	P
0.444348				P	A		A
				P	P	P	
3.51387			*	P			P
		**			P		
2.468521			*	P	P	P	P
0.059403		*		A	M	A	A
		**			P	A	
2.786481			**	*	P	P	P
		*				P	
	**			M			
		*			P		
					A		

				A	P	A	
						A	
1.468659		*		P	P	A	A
					A		
0.854648	*			P	P	P	P
0.958591				P	P	P	P
1.176324		**			P	M	A
1.263923				P	P	A	A
		**		P	P	A	
0.479831				P	P	P	M
1.204561				P	M	A	A
2.124666			*	P	A	P	P
0.406561				P	P	A	M
				A			
1.997862			*	P	P	P	P
				P	A		
0.076783				P	P	A	A
2.695899			*	A	M	P	M
0.878441				A	A	P	P
		**		A	P		
					A		
5.120231			*				P
0.698293				A	P	A	A
0.645813				P	P	P	P
0.453481		**		P	A	P	A
2.922043			**	P	P		P
0.204716				P	P		A
1.511974		**		P		P	P
2.316571			*	P	P	P	P
2.126987			*			A	A
						A	
				A	P	A	
4.398961		*	*	P	P	P	P
				M	P	A	
3.337137		**	*			M	P
0.384154					A	P	A
2.819083			*	P	P	P	P
1.469218					P	A	A
0.079977							A
2.207294	**		*	P	P	A	P

0.484925				P	P	P	A
					A	A	
1.481932	*			P	P	A	A
1.005107	**			P	P	A	P
0.890178				P	P	P	A
2.208658			*	P	P	A	P
	*			A	P		
1.550554		**		P	P	P	P
		**				P	
0.702044		**		P	A	P	A
		**				M	
				A	P	P	
					P	A	
0.600671				A	P	A	A
0.284475				P	P	A	M
32.88776			**	P	P	P	M
0.482053				P	P	P	P
2.31167	*	**	*		P	P	P
7.479241			**	P	A		P
		**		P	P	M	
0.342804				P	P	P	P
0.456067				P	P	P	P
0.340297				P	P	A	P
0.551102				P	P	A	A
0.052382				P	P	A	A
10.44996			**				P
				P			
	*			M	P		
		*			P		
3.158725			**	P	P	P	P
0.265504	*			P	P	P	A
2.578792			*	P	P	P	P
				P	P	P	
1.193288	*	*		P	P		A
	**			P		A	
				P	A		
2.380786		**	*		P	P	P
		*		A		P	
0.241416				P	P	P	A
0.429443				P	P	P	A

0.469113				P	P	M	P
0.698112				P	A	A	A
0.279725				P	P	P	A
1.006084	*			P	A	A	A
		**				P	
				A			
2.318931			*	P	A	P	P
0.497153				P	P	P	P
1.23492	*			P	P	P	A
2.307056			*				A
0.263139				P	P	P	A
					P	A	
1.316458		*				P	P
				A	P	A	
1.187405	*	*		P	P	P	P
0.254863				A	P	P	A
1.10836	*			P	P	A	A
2.885585			**	A	M	P	P
1.043053				P	P	A	A
					A		
2.119707			*		A		P
0.428198				P	P	P	P
0.037607		*		P	M	A	A
0.490845	**			P	P	P	A
0.772047	*			P	P	P	A
	**			P		P	
				P	A	P	
0.71363				P	P	P	P
0.249891				P	P	A	A
	*			P	P	P	
2.397732			*	P		A	A
0.255612				P	P	A	A
4.759576		**	*	P		P	P
				P		A	
		*		P		P	
0.603882				P	P	P	P
0.680323				P	P	P	A
0.415043					P		A
3.204411			**	P	P		M
				P	P	A	

0.673472	*			P	P	P	A
0.443837				P	P	P	P
0.88918		**		P	M	A	A
					A		
				P	P	M	
0.294739				P	P	P	P
0.627457				P	P	P	P
1.279318					A		A
		**			M		
2.652947			*		A		P
		**				P	
				A			
1.728995				P	A		A
1.066284				P	P	A	P
				P	A	A	
2.0641		*	*	P	P	P	P
3.943088	*		*	P	P	P	P
18.27062		*	**	P	P	P	P
		*			P	P	
					A	A	
0.945939				P	P	P	P
				A			
		*		M	M	A	
0.459471				P	M	A	A
					A		
2.241518			*	M	P	A	P
		*		P	P	M	
2.661143			*	P	P	P	P
0.957603				P	P	A	A
0.603143				P	P	P	A
1.000893					P	A	A
				A	P	A	
0.391184				P	P	P	P
				A			
3.23256		**	**	P	P	P	P
3.088334		*	**	P	P	P	P
					P	P	
2.057901			*				P
		**			P		
0.097201				P	P	A	A

		*				M		
9.202382				**				P
			*		P	A	P	
8.215985	*	**	**	**	P	P	P	P
		**				M		
1.805111							A	M
0.976152	*				P	A	A	A
2.835446				*				M
2.393526			*	*	P	P	P	P
3.67166				*	P	P	M	P
							A	
1.173767							A	P
0.123051	**				P			A
						A		
0.904673	**				P	P	P	P
0.593692					P	P	P	P
2.862088				**		A	A	M
0.993028					P		A	A
1.382293			*				P	A
		*			A	P		
					P	P	A	
1.220952					P	P	P	P
1.32353					P	P	P	P
0.058674					A	P	A	A
						A		
0.399235					P	P	P	A
0.708726					P	P	P	P
0.715047	*				P	P	P	P
3.588991				*				P
0.769834					P	P	P	P
1.824677	*				P	P	P	P
1.954234		*			P	P	P	P
0.453222					P	P	P	P
0.313309	*				P	P	A	A
					A	A		
					A	P	P	
							A	
	*				P	P		
	**				P			
0.567596					P	P	P	P

				A			
9.466942	**	**		P	P	P	P
0.308378				P	P	A	A
				P	P	A	
0.693884				P	P	P	P
					A		
	*				P		
3.131142		**		P	P	P	P
2.991068		**		P	P	P	P
				A	A	P	
1.245107	*			A	P	A	P
1.846852				P	A	A	P
2.286126		*		P	P	P	P
					P	A	
	*			P	P	P	
					A		
0.894086				P	P	P	P
3.941748		*		A			P
1.193174				P	P	P	P
				P	P	M	
	**				P		
0.694491				P	P	A	A
1.899619				P	A		P
	*			M		A	
0.552237				A	P	P	A
23.42853		**					P
1.266586	*			P	P	A	A
		**				P	
					P	A	
1.440101				P	P	A	P
1.553032				P	A	A	P
3.483636		*					P
				P	P	P	
1.688727		**				P	A
0.392683				P	P	P	P
0.737094				P	P	P	A
1.441026		*		P	P	P	P
0.442404				P	P	A	A
0.63221				P	P	P	P
27.55266		**				A	P

			*				P	
	*				P			
0.717836					A		A	A
2.052967			*	*	M		P	P
1.274858	*				P	P	P	P
							A	
					P		A	
0.024509					A	P	A	A
0.474499					P	P	P	P
	**				M	M		
9.988901			**	**	P	P	P	P
26.68127				**				P
	**				P			
0.800254					P	P	P	P
9.144739			**	**	P	P	P	P
	*				M			
			*				P	
2.142524				*		P	A	P
0.690008		*			P	P	P	P
2.091132			*	*	P	P	P	P
2.279173				*	P	P	P	P
							A	
					P	P	A	
						A		
2.204719				*	P	P	P	P
2.847328				**	P	P	P	P
1.219992			*		P	P	P	P
							A	
					A	M	A	
0.659311	*				P	P	P	P
		**			A	P		
1.952249					P	P	M	A
1.518633					P	A		P
			*				M	
0.494139					P	P	P	P
	**				P	P		
0.929472					P	P	P	P
8.140944	*	*	**	**	P	P	P	P
2.856428				**				P
15.57817			*	**	P	A	P	P

2.10804				*		P		M
0.229709					P	P	P	P
0.751671					P	P	M	A
0.332534					P	P	P	A
1.055202					P	P	P	A
		**				P	P	
					P		A	
							A	
2.140836				*				P
0.464265					P	M		A
0.091791			*				A	A
1.100455							A	A
	*				P			
9.367625	**	*	**	**	P	P	P	P
					A	A	A	
					P		P	
2.816813				*	A			M
						A		
0.151522			*		P		P	A
1.302949			*		P	P	P	A
0.955783					P	P	P	A
2.149027				*	P	P	P	M
2.020394			*	*	P	P	P	P
0.284064					P	P	P	A
1.346408			*		P	P	P	P
0.316722			**		P	P	P	P
		**				P		
22.36011				**				P
0.876714					P	P	P	P
1.037723					P	P	P	P
0.452334					P	P	P	A
1.030099					P	P	P	P
0.874381					P	P	P	P
38.68812				**	P			P
0.386925					P	P	A	A
0.080641					P			A
2.296701				*	P	P	P	P
0.089544						M	A	A
			**				P	
1.151227					P	P	P	A

0.371305				P	P	P	P
						A	
0.376443				P	P	P	P
		*	*	P	P	M	
1.927562				A	P	A	A
3.035428	*		**	**	P	P	P
0.478753				P	P	P	P
1.365093				P	P	P	P
			**	A		P	
0.791484				P	P	P	P
				A	A		
				A			
3.020328		*		**	A	P	P
2.001371				*	P	P	A
2.025611				*	P	P	P
				A			
	*			P		A	
			*			P	
					A		
2.343599				*	P	P	P
0.37567					P	P	A
0.917792					P	P	P
0.778777		*			P	P	P
0.164273					P	P	A
		*				P	
1.06263			*		P	P	P
0.116466					A	A	A
4.752384				*		A	P
0.465976					P	P	P
						A	
				P	A	A	
1.861491			*	A	P	P	P
0.872945				P	P	P	A
			*	M		A	
				P	A		
					A		
			**	A			
				P	P	P	
0.483135				P	P	P	P
0.149043				P	P	A	A

0.893539				M	P	P	A
						A	
0.344752				P	P	P	P
1.529271	*		*	P	P	P	A
0.681608				P	P	P	P
0.420118				P	A		A
0.713087				P	P	P	P
0.626827				P	P	P	P
0.996636				P	P	P	P
0.48118				P	P	P	A
0.387454				P	P	P	P
				A		A	
		**			P	A	
0.291252	**			P	P	P	P
0.159475							A
2.023647			*	P	P	P	P
0.572914	**			M			A
0.602877				P	P	P	A
2.066475			*	P	P	P	P
3.984178			*	*	A	P	P
				P	P	P	
					A	A	
				A	P	A	
						A	
0.36972				A			A
				A	P	P	
					P		
1.090908				P	P	A	P
2.023942			*	P	P	P	P
				P	P	M	
1.720824			*	M		P	A
				P	A	P	
0.895209				A	P		P
0.357806					P	A	A
12.50189			**	A			P
2.067476	*		*	P	P	P	P
					A		
						A	
1.856237		**		P	P	P	P
2.035806			*	P	P	P	P

				A	P		
0.662857	*			P	P	P	P
0.079613	*			P	P	P	A
1.271165				A	A		A
			**			P	
		**			M		
				P	A	P	
0.854962			**	P	P	P	M
0.859363				P	P	P	P
4.128606	*			*	P		P
2.021147				*	P	P	P
0.489948	*	*		P	P	A	A
0.352081					A	A	A
			**	P	P	P	
		**			P		
			*			A	
0.968078	*			P	P	P	P
0.61912				P	P	P	P
0.407663				P	P	P	P
0.474674		*		A	P	A	A
0.788354				P	P	P	A
0.495038				P	P	P	P
3.294006				*			P
1.355173			*	P	A	P	P
0.821884				P	P	P	P
0.309977				P	P	P	P
0.985347		*		P	P	P	A
0.346233				M	P		A
						A	
1.041068	**			P	P	P	P
1.479392				P	P	P	A
1.930566				A	A	P	M
0.061758				P	A	A	A
0.33267				P	P	P	A
0.481079				P	P	P	M
	*			M			
		*		A	P	A	
				P	P	A	
1.719892				P	P	P	M
1.573234	*			P	P	P	P

0.550038				A P	P	P A	A
2.412229			*				A
3.665973			*	P	P	A	M
24.11799			**				P
				A M A	A A		
	*						
1.565984				P	A	A	P
0.514074				P		A	A
		**			M		
0.540802				P	P P	P A	P
0.83201				P A	P	P	M
			*		A P M	P A A	
1.251304							A
1.095198	*		*	M		P	A
0.711611					P	A	M
2.451405			*			P	P
17.18894			**			M	P
						A P A	
		*					
0.89375				P P A	P P	P	P
					A		
0.543074				P	P	P	P
0.24128				P	P	P	A
0.313498				P	P	P	P
2.82478			*				P
0.497441							A
2.293146		*	*	P	P	P	P
2.849304			**	P	P	P	P
0.069655				P	P	P	A
3.006707	*	*	**	P	A	P	P
0.468042				P	P	P	A
3.496117		*	*	A	P		P

	**			P	P	A	
						A	
6.52928		*	**	A	P	M	P
		**				M	
				P	P	A	
	**			P	P	A	
3.820678		*	*	A	P		P
0.429911				P	P	A	A
0.84134				P	P	A	A
0.223214				A	P	A	A
0.587492				P	P	P	P
		*			M		
				P	P	P	
	*			P	P	A	
0.547989	*			P	P	P	P
2.023379			*				P
0.31708				P	P	A	A
				A			
0.829444	*			P	P	P	A
	**			P		A	
2.265713			*				P
			**			P	
0.66359		*		P	P	A	A
1.561708				M	P	P	P
0.660368				P		A	A
1.501573				P	P	M	P
0.121118	*			P	P	A	A
0.444597				P	P	P	P
	**			M			
0.808817					P	A	A
0.286069				P	P	P	P
				P	A		
0.441493				P	P	P	P
0.665771				P	P	P	P
1.155562				P	P	P	P
0.77207				P	P	A	P
0.241949				P	A	P	A
0.476514				P	P	P	P
					A		
2.047506		**	*		A	P	A

0.131722			A	P	A	
				P		A
0.930559	*		P	P	A	A
				A		
0.108704			P	P	P	A
14.31433		**				P
1.855605				P	A	A
			A			
1.071787	**		P	P	M	A
0.473684			P	P	P	P
			M	P	A	
0.639658			P	P	P	P
1.366813			A	P	A	A
0.470205			P	P	P	P
			A			
1.280288			P	P	P	A
0.203934		*	A	A	A	A
					A	
0.052338						A
		**		M		
0.486893			P	P	P	P
			A			
0.616028			P	P	P	P
			A			
			A			
0.707105			P	P	P	P
					A	
3.237351		**				M
	*		P			
			A			
0.51187				A		A
	*		M	P		
	*		M	A		
		*		P		
			A			
			A			
					A	
			P	P	A	
0.203797			P	P	A	A

2.264946		*	*	P	P	P	P
2.007906			*	A	A		A
0.436707				P	P	P	P
	**				P		
2.523992			*	P	A		P
0.469228				P	P	P	P
0.786472				P	P	P	P
0.629249					P	A	A
96.11702			**	A			M
						A	
1.155275				A		A	A
2.611942			*		P		P
4.140365			*		M		M
0.241383				P	A		A
		**				P	
				M	P	A	
1.121334				P	P	P	A
	**			P		P	
2.0101			*	A	A	P	P
2.262822			*	P			P
2.475434		*	*	P	P	P	P
1.149136		*		P	P	P	P
3.497141			*	P	A	A	P
						A	
5.242837		*	*	P	P	P	P
					A	A	
1.370378				A	A	P	P
				A		A	
				A			
0.117721							A
		*				P	
1.472348	*	**		P	P	P	P
				A			
0.111903					P	A	A
1.115422				P	P	A	A
	*			P		A	
						A	
2.115216		*	*	P	P	P	P
2.837102			*	P	P	P	P
3.200384		*	**	P	P	P	P

0.478562					P	M	A
1.010587				P	P	P	P
0.271416				P	P	P	A
						A	
0.332349				P	P	P	P
2.205821		**	*	M		M	P
1.236377	**			P	P	P	P
1.274476	*			P	P	P	P
					A	A	
3.396276			*	P	P	P	M
1.523642	*	*		P	P	P	P
			*	A	P	A	
				M	A	A	
0.139933					A		A
0.490641				P	P	P	P
				A			
4.632043			*				P
		*		P	P	P	
3.629968	*	*	*	P	P	P	P
2.802015			*	P		P	P
0.04433	*			P	P	A	A
0.596306				P	P	P	P
1.11289				P	P	A	A
0.051204				P	A	P	A
					A		
0.080834				P	P	A	A
16.66846			**	P	M	P	P
		*		P	P	M	
				P		A	
				P	P	P	
				A			
2.962726			**	P	P	P	P
				A			
					P		
0.450528	*			P	P	P	P
0.915597	*			P	P	A	A
0.999133		*			A	P	A
	**			P			
		*		M		A	
2.320445			*	P	A	P	A

5.634704			*		A	P	P
	*			P			
0.109115				P	P	P	P
0.081307				P	P	A	A
1.522884		**		P	P	P	P
1.212315				P	P	P	P
		**				M	
		*		A		P	
				A			
	**			P	P	P	
0.904611				P	P	A	M
		*				M	
0.293101				P	P	P	P
				A			
	**			M			
3.473995			*	A	A		M
2.604671			*	P	M		P
0.495904				P	P	P	P
0.77431				P	P	P	P
1.637372		**		P	P	P	P
	**			P		P	
0.346778	*			P		A	A
	*			P	A		
0.869033				P	P	A	A
1.563351				P		A	A
0.470865				P	P	P	A
0.215647							A
9.454566		**	**			P	P
					A		
1.557318	**			M		A	A
1.959018		*			A	P	P
0.645666				A	P	P	A
0.74924				P	P	P	P
0.677245						A	A
0.702895		*		P	P	P	P
	*			P		P	
0.377779				P	P	P	P
0.235005				P	P	P	M
0.08696				P	P	A	A
2.304642			*	A	P	A	P

0.702837				P	P	A	P
1.450524		*		P	P	P	P
0.963466				P	A		A
0.2101	*			P	A		A
3.3324			*	*	P	P	P
0.962822				M	A	A	M
0.405663							A
	**			P			
0.873717					P	A	A
0.124156							A
0.377636				P	P	P	P
0.678608				P	P	P	P
0.870935	*			P	P	P	P
2.333527			*	*	P	P	P
1.780205				P	P	M	P
2.885708				**			P
0.310102				P	P	P	P
0.178137				P	P	P	P
0.191498				P	P	P	P
1.717535		*	*	P	P	P	P
	*	*		P	P		
				A			
2.611908				*			P
3.244955				*	A		P
					A		
		*		P	P	M	
0.335162				P	P	P	A
2.720157		*	**	*	P	P	P
0.326591				A	P	P	A
0.892657		*		P	P	P	P
0.669069				P	P	P	A
2.551387				*			A
1.033455		*		P	P	P	P
	*			P			
0.288652				P	P	P	P
					M	A	
0.486214				P	P	P	P
						A	
		**		P	P		
				P	A	A	

0.685928				P	P	A	P
				A			
0.445233				P	P	P	P
1.420102				P	P	P	P
				M	P	A	
3.390272		*	*	P	P	P	P
4.604558			*				P
					A		
	*			P			
				A	P		
		*				A	
5.370099	*	*	*	P		M	P
5.56563	*	*	*	P		P	P
7.64581		*	**			P	P
	*			M			
				A		A	
		*			P		
0.270492				P	P	P	A
0.371465				P	P	P	P
2.055916			*				P
0.333677				P	P	P	P
0.37698				P		A	A
1.488147		**		P	P	P	P
0.09927				A		A	A
1.659182			**			P	A
1.361953			*	P	P	P	P
		**		A	P	A	
0.435171				P	P	P	P
	*			P	P	P	
	*			M	A	P	
1.227613		**		P	P	P	P
0.581405				P	P	P	A
		*	**	P	P	P	
3.628182			**	P	P	P	P
0.604815				P	P	P	P
1.240658	*			P	P	P	A
	*			P			
				P	A	A	
1.014348		*			M		M
0.500931				P	P	P	P

0.769716					P	P	P	P
1.013399					P	P	P	P
2.523243				*	P			P
1.033283					P	P	A	A
0.515757					P	P	P	P
0.281786					P	P	P	A
						P	A	
0.294023					P	P	P	A
		*				P		
0.554682		**				P		A
2.411466				*				M
0.700885	*				P	P	P	A
0.59182			*		P	P	P	P
0.789064					A	P	A	A
10.01803				**	P	P	M	P
0.72582					P	P	P	P
							A	
2.972			*	**	P	P	P	P
0.582625					P	P	P	P
3.17267				**		A	P	P
	*				P	M		
0.569222					P	P	P	A
0.455203					P	P	P	P
2.885737			*	**	P	P	P	P
			*				P	
0.441397					P	P	P	P
1.116557		*			P	P	P	M
						P	A	
0.428489								A
5.851137	**	**	**	*	P	M	P	P
			**				P	
	*				P			
	*				P			
					P	P	P	
	*				P			
0.636145					P	P	P	P
					P		A	
	**		**		P		P	
					A	P	A	
2.394374		*		*	P	P	P	M

0.356659				P	P	P	P
2.023816			*				P
2.081218			*		P	A	A
0.781923				A	P	A	A
				A	P	A	
					M	A	
0.628328				A	P		P
2.279719			*	P	P	M	A
		*		A	P		
0.561567				P	P	P	A
1.144902				A	P	A	A
2.399022		*	*	P	P	P	P
1.415264		*				P	P
				P	P		
0.046691				P	P	P	A
1.900111				P	P	P	P
0.651643				P	P	A	A
				P	P	A	
2.248971		*	*	P	P	P	A
2.098736		**	*	P	P	P	P
1.023687		*			A	P	P
				M	P	A	
				M	M	M	
		**		P	P	P	
		*			P		
0.694801	*			P	P	P	A
0.169802				P	P	P	P
0.268161				P	P	P	P
		**			P	A	
0.191544				P	P	A	A
		*		P		P	
		*		M	P	A	
					A		
0.281469				P	P		A
0.424941				P	A	A	A
	*			P	P	M	
0.99245		*		P	P	A	P
1.783613	**	*		M	P	P	P
0.129777							A
				A	A		

0.497623				P	P	P	P
						A	
3.244675			**	*	P	P	P
0.963138			*		P	P	P
1.91324			*			A	P
					A		
3.475717		*		*		P	A
12.05775				**			P
					A	A	
						A	
2.873179							
0.773143	*	*			P	P	P
0.467368					P	P	P
	**				P	P	P
1.165606			*		P		P
0.041458					A	P	A
						A	
3.304767				*			P
2.788776				*	P	P	P
2.479776			*	*		A	P
0.496971					P	P	P
3.521131				*			P
2.232608				*		A	M
0.440546					P	P	P
3.061016				**	A	P	A
1.10529					A	P	A
						A	
	*				P	M	P
1.132263			*		P	P	P
	*	*	*		P	P	P
0.67771	*				P	P	P
3.431201				*	P	P	A
					A		
1.170773	*				P	A	A
		**			A	P	
		**				P	
1.693488		*			A	P	P
2.453072				*	A	A	P
0.817643					P	P	P
1.272193	**	*			P	P	A

1.404051					A	A	A
				A	A	A	
0.836116				P	P	P	A
0.533773				P	P	P	P
	**			P			
0.632527				P	P	P	A
0.422542				P	P	P	P
	**			M			
	**		**	P	P	P	
2.273686			*	P	P	P	P
0.773455				P	P	P	A
			*			P	
		**			P		
				P	P	A	
					P	A	
2.1882	*		*	P	A	A	P
				P		A	
0.695531				P	P	P	P
				A	A	P	
0.237516				P	P	P	A
1.212179				P	P	A	A
0.382035				P	P	P	P
	*			P			
0.486046				P	P	P	P
5.07491			*				M
2.624662			*	P	P	P	P
1.781343				P	P	P	M
		*			M		
13.26123			**	A			M
				A			
1.744061				A			P
					A		
				P	P	P	
				P	A	A	
1.021574	*			P	P	A	A
0.042044				A	P	P	A
						A	
				P	A	A	
						A	
1.106384		*	*	P	P	P	P

				A	P	A	
		**			M		
2.857155			**	P		P	P
2.201866			*	P	P	A	P
2.476494			*	A		A	P
		**			P		
0.695646				P	P	P	P
2.866015			**	P			P
		*	*		P	P	
0.131271				P	P	M	A
0.899348				P	A	A	A
			**			P	
				P	P	A	
0.769457	*			P	P	A	P
3.431852		*	*		P	P	P
6.467054			*				P
0.956526	*			P	P	P	P
1.229326				P	P	P	P
0.733938	**			P	P	P	P
			*	A		P	
8.015425			*	P	P	P	P
			*		A	P	
0.744386				P	P	P	A
0.782304					P	A	A
6.270834			*				P
1.161537					P	M	P
					A	A	
0.451649				P	P	A	A
		**		P	P	P	
1.008813				M		A	A
		*			P	P	
0.737957				A		A	A
2.328142		*	*	P		P	P
2.146106			*		A	M	P
2.127794		**	*			P	P
1.293029		*		A		P	A
1.068362	*			P	P	P	A
3.104065			**	P	P	A	P
0.457447				P	P	P	P
3.88915			*	P	P	P	P

1.212663				P	A	A	P
2.34965	*		*	P	P	P	P
0.352973				P	A	A	A
1.15261			*	P	P	P	P
			**		A	A	
0.277681				P	P	P	A
1.788768	*		*	P	P	P	P
	*			M			
1.405739	*			P	P	A	P
0.789434		**		A	P	A	A
2.262303			*	P	P	P	M
						A	
2.916691			*	**	A	P	P
0.122302					P	P	A
3.705871			**	*	P	P	P
5.334021			**	*	M	M	P
0.198494					P	P	A
1.964581					P	P	P
			*		A		
4.504955				*			P
1.65278	*				P	P	P
3.944318				*	P	A	P
					A	A	
20.6789			**	**	A	A	P
1.967601		**				P	P
					P	A	
1.130339						P	A
1.337473					A	P	P
			**			P	
2.265301				*	P	P	P
						A	
0.439334					P	P	P
2.282888				*	P	P	P
0.838976					P	A	M
4.14294				*	P	P	P
2.440781				*	P	P	P
						P	
					P	P	
2.480106		*	*	*	P	P	P

				A	A		
						A	
0.661721				P	P	P	P
1.304874	**			P	P	P	P
0.472844				P			A
0.390137				P	P	P	P
				A			
1.033319		**			P	P	A
0.853315				P	P	A	P
0.212467					P		A
0.668021	**			P	A	A	A
2.958583		**	**	P	P	P	P
0.672245				P	P	P	P
1.443927		**		A	P	P	A
2.821716		*	*	P		P	M
5.751699			*				P
					A		
5.693438			*	P	P	A	M
1.068542	**	*		P	P	P	A
						A	
1.432715				P	P	P	A
0.257147				P	P	A	A
0.297814					P	P	A
	*			P		A	
					A	A	
0.573793				P	P	A	P
	*				P	A	
					P	A	
0.28679				A			A
		**			A	P	
2.000649			*	P	P	M	M
0.598706				A	P		A
48.75513			**				P
0.403211				P	P	P	P
2.160894			*	P	P	P	P
0.61537				P	P	P	P
1.443135	*				P	A	M
0.175906				P	P	A	A
1.634175				P	P	A	A
0.129687	*	*		P	P	P	A

6.988173	*	**	**	P	P	P	P
0.508574				A	P	A	A
1.461176					P	A	P
0.715864				P	P	A	M
					A		
0.043652				A	P	A	A
0.475776				P	P	P	A
0.170869				P	P	P	A
		**				P	
				A			
0.304252				P	P	P	P
				P	P	P	
1.900465		*		P	P	P	P
0.453287				P	A		M
1.621503				P	P	P	P
0.519235				P	P	P	A
0.207972				P	P	A	A
1.527274		**		A		P	A
0.415599				P	P	P	P
0.198517				P	P	P	P
0.403189				A	P	P	A
6.170281	**	*	*	P	P	P	P
	**			P			
2.058799		*	*	P	P	P	P
0.260581				P	P	A	A
0.862184		*		P	P	A	M
					P	A	
1.127554				P	P	M	P
	**		**	M		P	
1.434252				P	P	P	P
				P	A	P	
3.592017		**	*			P	P
0.624575				P	P	P	P
0.343408				P	P	A	P
	**				P	A	
0.065029				P	P	P	A
3.235976			**			A	P
				M	P	A	
0.389347				P	P	P	A
	*			A	P		

2.04837			*	M	P	P	A
1.484922				P	P	P	P
	*			P	A		
0.561928				P	P	P	P
0.177321				P	P	P	P
0.288339				P	P	A	P
		*			P		
				P	A		
2.516551			*	P	P	P	P
0.030488					M		A
0.371647				P	P	P	M
	**			P	P		
					A		
1.03612				P	P	P	A
0.432834				P	P	P	A
					P	A	
8.566382	*		**	P		A	P
		**			P		

) indicates $p < 0.01$

7DPI_infected_NS	14DPI_infected_NS	21DPI_infected_NS	28DPI_infected_NS	7DPI_control_call	14DPI_control_call	21DPI_control_call	28DPI_control_call	7DPI_control_NS
10.19552	10.44202	10.15067	9.203243	P	P	P	P	10.17334
		5.87543	6.89289			A	A	
10.18994	9.491895	11.08423	10.38642	P	P	P	P	9.123819
7.869158	7.183572	7.311364	7.144451	P	P	P	P	6.552074
5.340441	5.820564			A	A			5.567853
9.058316	8.328654	9.277551	10.37327	P	P	P	P	8.808737
7.945015	7.533454	8.302444	8.590382	P	P	P	P	7.871104
7.180375	7.015988	7.185454	8.453822	P	P	P	P	7.449307
7.77819	7.870155	7.178321	8.152087	P	P	P	P	8.413168
6.432982	6.628202	7.556384	7.255614	P	P	A	P	6.665473
5.050903			5.358536	A			P	4.67063
			6.468948				A	
	5.2754				A			
9.140626	8.374593	7.719557	7.396269	P	P	P	P	8.361067
9.629493	10.38474	7.871738	8.283577	P	P	P	P	9.696231
7.548789	6.550621	7.751795		P	P	A		5.681376
7.386525	7.875166	7.544212	7.513964	P	P	P	A	6.584799
7.56174	5.623045	6.710955		P	A	P		5.588543
7.298696	6.68151	6.999373	7.408869	P	A	P	M	6.384976
9.347846	10.17532	9.309629	8.234849	P	P	P	P	9.864399
		0.974133				M		
8.995587	7.876212	10.71628	10.57613	P	P	P	P	7.846148
6.812044		4.97065	6.75226	A		P	P	5.62951
7.627664	9.09724	7.687954	7.344914	P	P	P	P	8.943914
6.782747	6.841561	6.672761	5.220653	P	P	P	P	6.575118
			6.191106				A	
10.88641	10.96394	10.79022	9.786455	P	P	P	P	10.74468
7.592851	8.176988	7.62833	6.589697	P	P	P	P	7.473492
4.836482	5.061822		5.998832	A	P		P	5.751135
5.630283	5.101179	3.290595	4.914375	A	P	P	P	5.8502
		2.923512				P		
			6.953981				A	
7.749697	7.160522	8.485636	8.151689	P	P	P	P	7.25697
8.24639	7.30022	8.596507	8.259504	P	P	P	P	7.426035

5.221299	5.855993	5.595351	6.183768	P	P	P	6.536495
		5.442345			M		
4.588681	5.463547	5.596523	5.646377	P	A	P	6.255781
	5.553836			A			
5.656951	4.389317	5.223449	4.986383	A	P	P	6.20431
7.103898	6.430776	6.900175		A	A		6.37335
		5.110023	6.07276		P	A	
12.15432	12.04144	10.8329	11.148	P	P	P	12.23087
5.860395	5.370818	4.74336	6.322329	A	P	P	6.008336
5.851858	5.388761	5.5044		P	A		6.501575
5.942143	6.994704	5.565408		P	P		7.197939
6.536578	4.348002	6.319188	7.205226	A	P	M	6.387747
6.496949	6.723972	6.592407	7.539631	P	P	P	7.218712
		6.291156			A		
	5.161308		7.634851	P		A	
10.22438	10.24927	9.202819	8.297502	P	P	P	10.09152
			4.64862			P	
		2.201722			P		
8.203019	8.082799	7.361718	7.06379	P	P	P	7.561062
5.712471	6.007329	5.965035	7.618601	P	P	P	6.919668
10.92767	10.86923	11.55864	12.72397	P	P	P	11.76264
8.118186	8.226439	8.778431	8.820941	P	P	P	8.1298
7.466178	7.468671	5.709704	6.327739	P	P	P	6.486038
	6.452875	2.278011		P	P		
6.811854	5.29429		A	P			5.434175
	7.315909			A			
9.892212	10.1959	10.85409	11.24344	P	P	P	10.36713
8.104098	6.74503	7.81375	7.751305	A	A	P	5.433383
6.41662			A				3.737211
		6.848228	6.605898		A	A	
6.991458	6.906173	6.573959	6.383831	P	P	P	6.536452
8.247705	8.446955	7.885915	7.629051	P	P	P	7.688804
6.154773	7.268832	5.710077	6.597411	P	P	P	7.124134
	4.539296			P			
	6.274386	2.089324		A	P		
5.406928		4.281526	A		P		4.511457
4.672141			P				5.83819
8.534125	7.388354	8.439219	7.541097	P	P	P	8.523251
8.516584	8.921233	6.986962	7.69666	P	P	P	9.112239
		6.860167				A	

9.853878	10.08499	13.44281	13.27418 P	P	P	P	10.73818
	6.342151			A			
7.466798	6.964422	6.454434	7.258049 A	P	P	A	4.076213
6.590661	5.942315	6.400131	6.597618 P	P	P	A	4.964596
5.905698		6.396262	7.748756 P		A	P	6.431142
9.24182	9.208154	9.510045	10.45184 P	P	P	P	9.473198
	5.746144		5.473174	P	P	P	
9.993662	10.20581	10.63791	11.98132 P	P	P	P	10.51232
5.199297		5.975376	7.878969 P		A	A	5.729189
	5.174463	5.733468	7.133697	P	P	A	
6.123968	5.250085	6.721136	7.877607 A	A	P	A	4.843829
			7.212179			A	
7.451132	6.37497	8.619824	8.354482 P	P	P	P	7.676189
	5.10507		6.97426	A		A	
9.322163	9.424512	10.46248	10.8156 P	P	P	P	9.738547
5.78228		6.201715	6.905055 P		A	A	5.430679
5.451757	4.869734	3.283114	A	P	P		2.767879
8.764896	8.679855	10.34506	10.78149 P	P	P	P	8.617351
8.339369	8.254387	7.289122	7.409915 P	P	P	P	7.356222
5.167586	5.865573		6.663303 P	M		M	6.58875
		6.027762			A		
6.145665	5.966895	6.326151	5.635666 A	P	A	P	5.112278
6.829692			A				5.744432
10.95596	10.3138	11.01911	10.93816 P	P	P	P	10.61974
8.306446	8.142502	8.36478	7.377304 P	P	P	P	7.702239
7.697441	6.619581	5.550181	6.585313 P	P	P	A	6.731342
8.169925	9.068368	8.649623	9.21398 P	P	P	P	9.708975
12.35301	12.80418	11.84354	10.49829 P	P	P	P	12.35079
8.077975	8.666151	8.412108	9.813703 P	P	P	P	8.717099
8.282548	8.670761	7.768466	6.462511 P	P	P	P	8.177462
6.401093	6.405356	6.074625	4.580219 P	P	P	P	6.91221
6.226595	6.354614	7.919	7.264885 P	P	P	P	6.562213
	2.136063			M			
7.516038	6.466514	9.03768	8.642921 P	P	P	P	7.994825
9.982952	9.070684	9.9287	9.607872 P	P	P	P	8.958486
7.527276	7.19723	6.814374	8.279195 P	P	P	P	7.202623
6.783157	5.523508	6.863627	8.343666 P	P	A	P	6.884738
6.527641	5.48838	6.604015	A	P	A		1.717061
6.154102	5.935264	5.665946	6.355922 P	M	M	A	5.65077
	3.907815			P			

6.963479	7.92844		M	A			8.141035
	4.894723		2.916733	P		P	
		7.607892			A		
5.02355	5.997695	5.036035	6.326386 P	P	P	P	5.567527
5.487656	6.162546	2.444228	6.668099 P	P	P	P	7.01884
11.7347	10.84651	12.87935	12.21868 P	P	P	P	10.01189
11.32145	10.09722	11.85798	11.22119 P	P	P	P	9.518676
12.35814	10.54862	12.18766	12.4887 P	P	P	P	9.73886
5.968882	6.704934	6.596448	5.16718 P	P	P	P	6.920212
	5.134634	6.055885		P	A		
6.024968	5.827	5.930145	P	A	P		6.7528
7.0471	7.232215	7.293792	6.160204 P	P	P	P	7.028945
6.152758	6.740793	6.644293	7.789558 P	P	P	P	7.538539
8.661873	7.710557	8.757257	8.937649 P	P	P	P	8.351258
		1.717393			P		
5.990211	7.360409	7.003361	6.073711 M	P	A	P	6.310453
5.931435	6.615542	6.26336	7.635505 P	P	P	P	6.604744
5.049074	5.268912		7.044928 A	A		A	6.105579
4.260842	5.015634	5.254735	P	P	A		5.425874
5.119562			4.821864 M			P	5.004971
	6.780409			A			
7.953152	8.258173	7.713885	7.168808 P	P	P	P	7.468382
7.674783	7.802867	8.822968	8.417908 P	P	P	P	8.150927
	2.933254			P			
6.522948	7.432809	7.21114	7.047172 P	P	P	A	6.86092
8.867084	8.547066	9.665875	10.10673 P	P	P	P	9.238896
2.061417			P				4.585197
7.797827	7.925959	7.563447	6.74099 P	P	P	P	7.996146
6.948925	7.394367	6.61592	6.712123 P	P	P	P	6.995891
		6.264974			A		
	4.7376			A			
		2.476115			M		
4.76402	6.445652		5.775965 P	P		P	5.898199
3.78484	5.102393		P	M			6.233017
9.495484	10.33006	8.719105	9.000872 P	P	P	P	9.599017
6.697106	6.845548	5.76543	6.671606 A	P	P	P	6.072988
7.694259	6.550422	6.573374	6.294148 P	P	P	P	6.163626
			6.103604			A	
			6.26464			A	
6.446546	6.90976	7.461266	6.632216 M	P	A	P	6.559971

		1.22149			P		
5.435325	5.155597	4.853	P	P	P		6.113618
2.089049		6.202733	P			M	5.070547
2.223744			P				6.302059
6.392759	6.933596	7.388696	8.596776	P	P	P	7.717759
3.440191			P				5.482317
6.4529	6.380021	6.653887	6.558361	P	P	P	6.762498
5.75999		5.611066	6.586301		A	P	5.622142
6.216097		7.278794	6.513004		M	A	6.970865
			7.156475			A	
	7.236851	4.784671		P	P		
5.318459		6.693955	P		P		5.661888
		2.900639			P		
8.434054	9.164177	8.721424	8.652944	P	P	P	9.365153
2.412044			P				6.408917
			6.377364			A	
7.151233	7.407493	6.121975	6.808879	P	P	P	7.698962
6.449732	6.151517	6.905981	7.463621	P	A	A	5.771017
			6.442003			A	
6.1337	5.39204	6.152886	5.879417	M	M	P	4.942534
10.12836	9.530589	10.80163	10.25124	P	P	P	9.494625
4.752561	5.214846	5.675242		P	A		5.978349
4.355779	5.957533	5.213491	6.619472	P	P	A	5.792598
			7.777931			A	
10.2164	10.69647	10.69671	9.329535	P	P	P	10.74012
		4.709342			P		
6.634409	7.771317	7.299015	7.434187	M	P	P	7.516706
		0.693225			M		
7.962647	7.57548	8.039053	7.583454	P	P	P	6.686965
7.516577	6.510406	6.999213	6.31978	P	M	P	6.974856
		1.641052			P		
7.960582	8.826316	8.423087		P	P		8.142833
6.048516			A				3.521149
8.267514	7.466241	8.111597	8.066409	P	P	A	6.72609
8.592906	9.645218	7.288332	8.111849	P	P	P	9.39606
	2.835962			M			
7.69412	8.351718	6.073227	6.197248	P	P	P	7.320686
5.754233	6.567256	5.842991	7.102788	P	P	P	6.045313
		4.731326			P		
3.689136			M				5.920373

6.084058	6.370958	6.182412		A	A	P		4.004493
4.248593	5.966365	6.143773		P	P	P		6.937639
5.54959	5.16617	5.880364	6.836155	P	P	P	A	5.19483
5.170098	5.757313		5.375532	A	P		P	3.669806
12.05602	10.72822	11.68353	10.98604	P	P	P	P	9.912792
11.14274	11.45008	12.21705	12.64446	P	P	P	P	11.49343
8.439894	7.950279	8.122702	6.483186	P	P	P	P	7.52348
6.968368	7.032764	6.450823	7.611822	P	P	A	A	7.48567
		5.693169				P		
7.647809	6.276005	6.448779	7.211878	A	P	P	P	6.529079
7.118356	7.383309	5.220309	7.469307	P	P	P	P	7.538558
	7.051194		5.363249		A		P	
5.716615	6.019434	5.231947		A	P	P		5.985519
7.33878	6.866508	7.563283	4.276892	P	P	P	P	7.605757
5.843411	5.800316	4.273842	3.898989	A	A	P	P	5.114724
5.543703	4.843362			A	P			5.207876
6.300794	5.372182	6.051527	6.264265	P	P	P	P	6.389622
5.849332	6.109345	7.031479	6.055831	P	P	P	A	7.048279
9.005889	8.177651	8.653124	8.403584	P	P	P	P	8.929328
7.370705	6.864622	6.518011	7.338022	A	P	P	M	7.549224
7.35135	7.711071	9.215995	9.451736	M	P	P	P	7.192093
9.037547	10.11599	10.35411	9.63136	P	P	P	P	10.26202
6.286078	8.355001	7.727142	6.746294	P	P	A	P	9.087907
13.31986	13.47182	12.98895	12.53889	P	P	P	P	13.40069
	5.66703				A			
8.883907	8.529493	10.23036	9.645453	P	P	P	P	8.50561
6.171732	5.678871	6.570808	7.417784	P	P	P	P	5.892048
3.502266	1.130793	5.109034	6.993838	P	P	P	A	5.814282
5.416606	6.200632			A	P			3.970386
9.908573	9.925227	10.58607	10.23566	P	P	P	P	9.963752
8.688234	6.772537	7.698347	8.04709	P	P	P	P	6.931093
5.718673	7.398443	6.300371	6.975147	P	P	P	P	6.644754
10.20769	10.55043	10.14097	9.362302	P	P	P	P	10.87502
5.195469		2.1719		M		P		5.154551
			6.231991				A	
	0.447682				P			
	5.503285		3.457004		A		P	
7.398865	7.724563	7.745752	6.869695	P	P	P	P	7.803828
8.907894	7.136502	8.007368	7.743215	P	P	P	P	6.324692
4.469041				A				2.042639

5.242381	3.943102		P	P			5.575216
			7.091685			A	
11.4249	11.11993	11.88006	12.77533 P	P	P	P	11.49627
		3.88088			P		
5.59084	5.525632	6.268907	5.590643 P	P	A	P	6.312186
8.180417	9.321405	7.562434	7.931281 P	P	P	P	8.829086
9.418139	8.343335	9.358934	9.497806 P	P	P	P	10.03723
6.30432	4.203345	4.971504	4.974643 A	P	P	M	6.518472
	6.244909		3.811582	A		P	
7.829891	9.001061	9.55802	10.46106 P	P	P	P	9.919712
8.593522	9.522251	9.910079	11.11587 P	P	P	P	10.68532
7.249528	8.063613	8.464512	10.28425 P	P	P	P	9.361233
4.715025	5.504808		P	A			5.848046
8.151629	7.561651	7.94801	5.711833 P	P	P	P	7.693973
7.209423	7.172917	8.012745	8.688533 P	P	P	P	6.774798
10.65063	10.33593	11.15221	11.07505 P	P	P	P	10.73959
5.998353	4.391201	6.828497	7.456349 P	M	P	P	6.734899
6.414286	6.885235	7.4624	7.553618 P	P	P	A	7.011392
	6.286989	5.749656	7.211048	A	P	A	
6.92069	6.949799	7.986658	A	P	P		5.827863
5.575677			4.569265 P			P	6.950281
	5.787681		2.907382	A		P	
8.787448	8.849051	9.749845	9.491881 P	P	P	P	8.334847
10.11608	9.610468	10.61997	11.04099 P	P	P	P	9.98179
8.226836	9.12602	8.588738	10.45575 P	P	P	P	8.728602
	6.72605		5.631059	A		P	
5.544718	6.482714	6.556786	7.208283 P	P	P	P	7.040241
4.419368	5.734278	3.791675	A	P	P		5.037242
9.349168	8.442202	8.194585	7.980591 P	P	P	P	8.945566
6.352335	5.514657	5.360622	7.275647 P	A	A	A	5.993949
5.687704	6.25557		6.693228 P	P		A	6.094008
7.371164	7.54639	6.546873	6.787643 P	A	P	P	7.265788
6.445435	7.097113	7.830333	A	P	A		7.0646
11.2245	11.74485	10.13935	10.33195 P	P	P	P	11.85278
		6.136512			A		
5.665358	5.960337	1.931311	P	P	P		6.124005
4.53558	5.313524		A	A			3.098548
5.944202	5.107907		A	M			4.400391
	5.833432		3.758412	A		M	
6.403868		4.092956	6.753793 P		P	M	6.524954

		5.65913			A		
		5.18363			A		
11.80145	10.41708	11.2111	11.27247 P	P	P	P	9.889642
			6.161259			A	
	6.366881	3.610093		P	P		
7.228903	7.030108	6.900016	5.152928 P	P	P	P	7.075385
7.628032	7.509823	8.526021	9.488286 P	P	P	P	6.904258
11.89572	11.7446	12.47016	13.27825 P	P	P	P	12.19188
6.409072	5.742075		6.403368 A	P		P	2.363192
	5.468703	5.649668	5.981179	P	P	P	
			3.418877			M	
6.64205	6.130558	6.213054	A	P	P		6.918463
6.440528	6.984342	6.647697	A	A	P		6.971642
5.6847			A				4.493208
7.722472	6.879088	6.943975	8.684674 P	P	P	P	6.557006
6.07668		1.752079	4.908649 A		P	P	2.911025
	5.712858	3.534807		P	M		
7.321257	6.712443	7.891542	9.130097 P	P	A	M	6.912208
11.62529	11.32883	11.96337	11.92445 P	P	P	P	11.08882
6.466658	6.479715	6.165949	5.228648 P	P	P	P	6.479719
5.746062	5.30662		P	A			7.005695
6.231037	6.248829	6.648698	7.316859 P	P	P	P	7.419868
9.517656	10.20542	9.398709	9.793812 P	P	P	P	9.573833
10.94039	11.63322	10.88239	10.24414 P	P	P	P	11.34938
6.337191	4.791228	4.442082	A	P	P		5.507232
6.102066	6.524292		5.421204 P	A		P	4.690173
6.093342	7.929726	6.744377	6.824848 P	P	P	P	7.209654
	5.555366		2.874012	A		M	
8.402868	8.210231	10.21102	10.60853 P	P	P	P	8.463395
7.056506	6.635574		7.653964 A	P		A	6.689162
6.674583	6.159718	8.047718	7.180329 P	P	P	A	6.571575
		4.626692			P		
			6.649663			A	
7.586669	6.238334	5.400101	6.297284 P	P	P	P	7.308343
7.21644	6.951771	7.161758	7.288119 A	P	P	P	6.041634
8.991995	9.692628	9.709286	8.220081 P	P	P	P	9.511215
			6.591949			A	
5.329679	6.499101	7.220989	7.838605 A	P	P	A	5.856291
			7.940187			A	
6.533763	8.693751	8.192336	7.308607 P	P	P	P	7.90709

9.914557	10.53429	11.16535	10.37811	P	P	P	10.91918
5.923435		6.918151	P		A		6.83737
9.090892	9.091206	8.461024	6.94924	P	P	P	8.219162
6.574399	6.326169		7.541215	A		A	6.244214
6.098426	5.800787	6.41153	A	A	P		0.27343
4.893044		6.337366	A		A		3.641799
6.123597	6.707409	6.389357	P	P	P		7.405189
8.979094	8.717618	9.442549	10.03995	P	P	A	8.979353
5.219058		6.559165	7.595762		A	A	5.339061
6.409057	5.773882	7.663843	7.742651	P	P	P	6.654456
5.538338	5.10479	5.755496	6.112375	P	P	A	5.790039
5.846028	5.143311	5.788141	1.826749	M	P	P	5.115143
			6.758716			A	
5.929328		5.761282	3.397422		P	P	4.67056
	4.212531			P			
			6.046415			A	
6.471489			A				1.620722
	5.550486		6.127326	P		A	
6.636792	6.666526	7.135706	5.012856	A	P	P	6.457637
					P		
7.31267	7.299024	5.722937	6.844235	P	P	P	7.485473
8.950353	9.354768	9.481104	8.986341	P	P	P	8.716661
8.446416	7.818905	7.824672	7.671041	P	P	P	7.075246
12.07995	12.2638	12.92496	12.78254	P	P	P	12.40464
9.169569	8.268591	8.444799	7.705104	P	P	P	7.954042
11.96947	11.53466	11.23862	10.63917	P	P	P	11.45139
6.69126	6.709709	6.192618	7.248542	P	P	P	6.831784
5.236257			6.926269			A	4.988434
6.808619	7.429825	7.000296	6.629626	P	P	P	7.162395
5.041979	5.007744	0.613439	M	A	P		5.426878
9.210625	9.22556	8.357532	8.458833	P	P	P	7.946937
11.42138	11.76214	13.33437	12.48747	P	P	P	10.22042
			8.94941			A	
9.140346	9.651889	8.33488	8.928095	P	P	P	9.516835
		5.761352			A		
8.272027	7.793399	7.625096	6.890878	P	P	P	6.955973
13.58533	12.3948	13.69667	14.07786	P	P	P	11.89319
6.687202	6.666305	6.001247	7.311815	P	P	P	7.521759
7.261016	6.681977	6.86021	5.832937	P	P	P	6.374197
6.847146	6.784895	6.559155	6.219825	M	P	P	6.191149

7.616837	6.628074	7.504902	7.715877	P	P	P	7.651315
5.5888			A				4.139291
5.643623	5.481796	5.618067	4.214555	P	A	P	5.558521
7.178925	7.46165	6.042458	P	P	P		6.33017
5.415624		5.425572	5.666992	A	P	P	5.369777
9.419651	8.258732	10.06096	10.19951	P	P	P	8.830188
6.661175		6.915637	P		A		6.74854
6.196812	6.346943		7.273496	A	P	A	5.231348
6.005891	5.917171	6.478329	6.873077	P	P	P	6.331766
5.917469	6.732068	6.043148	6.769003	P	P	P	6.963438
		2.968476			P		
6.929052	6.520635	7.624891	6.335977	P	P	P	5.615348
6.626017	6.301109	7.457314	7.108271	P	P	P	6.67
	8.094563	5.663914	4.832012	P	P	P	
5.956003	6.301715	5.575096	A	M	P		6.593038
6.037275	5.979606		A	A			5.580893
	3.705971		5.806822	P		P	
5.233456	4.393003		3.810835	P		P	6.561534
7.641659	6.177872	7.252044	7.291448	A	P	P	6.011947
	6.735206	6.056801	7.386857	P	P	M	
		4.901935			M		
10.65247	10.71738	10.16532	9.548753	P	P	P	10.50452
6.66918	6.358814	5.317378	A	P	P		5.578111
7.156756	7.504629	6.278886	6.865437	P	P	P	6.344502
5.865552	5.731733	6.658803	8.106676	P	A	P	6.764967
8.292181	8.198064	8.848559	8.940103	P	P	P	8.541921
3.317006			M				5.324449
		2.004019			P		
7.904194	8.645357	7.337902	7.564246	P	P	P	7.895771
7.02973	6.90474	5.783177	P	A	P		6.537613
3.963008		5.757019	6.458566	P	P	A	6.320172
5.847794	5.491915	6.461749	A	P	A		5.532324
4.396702	5.883374	4.619321	P	A	P		5.77292
6.055345	6.474405	6.585105	7.326961	P	P	P	6.281651
13.84731	12.0281	13.37022	13.68757	P	P	P	11.62218
5.868878	6.138454	5.968836	7.415858	P	P	A	6.526041
		6.497965			A		
			6.88302			A	
5.88721	5.850379	6.300551	P	A	A		5.868078
9.054264	7.889476	8.4739	7.865559	P	P	P	8.383453

8.044243	9.390333	7.124292	7.227927	P	P	P	8.195724
		7.16913			A		
3.202198	5.371583	6.165858	P	A	P		6.051423
	6.08375	6.727676	7.563032	A	P	A	
10.26036	9.946313	11.10204	10.72209	P	P	P	10.06709
8.535996	9.504983	10.17225	10.36805	P	P	P	10.06985
7.197844	7.678616	7.975863	8.317156	P	P	M	8.056562
	3.622553		2.754697	P		P	
	2.902167	1.365055	5.6876	P	M	A	
5.967985	6.028215	5.757724	4.026344	P	P	P	6.475689
		5.506033			A		
6.884345	5.866072	6.256548	4.834218	P	P	P	7.153105
10.55117	10.59526	10.00456	9.19905	P	P	P	10.53078
5.524159			A				2.89341
7.913583	6.725061	7.523604	7.477042	P	P	P	7.096997
7.214019	6.537294	7.612658	6.782726	P	P	P	6.397345
13.02234	13.16868	13.59901	14.41521	P	P	P	13.38471
5.749712	5.343021		7.468749	A		A	2.994979
9.995097	8.939212	9.279233	8.791585	P	P	P	8.787545
6.503769		8.268364	7.749143		A	A	5.744591
10.4749	11.38063	10.46624	9.798432	P	P	P	10.90965
7.07999	7.426467	7.121543	7.826413	P	P	M	6.932516
8.123837	7.788732	7.566188	6.893521	P	P	P	8.156725
8.300953	7.710596	7.906061	8.184534	P	P	P	7.835594
7.641114	7.474031	7.712669	6.757253	A	M	P	7.205403
5.941019	4.514678	5.284392	A	P	P		4.806254
			4.245997			M	
7.533266	7.525061	8.026473	8.657248	P	P	P	7.95273
6.045629		6.298545	6.261904		A	A	6.736979
5.139473	3.641232	5.664194	A	P	P		4.252075
6.830294	7.436408	7.814993	8.081591	P	P	A	7.032973
10.18165	10.38892	11.07418	11.51592	P	P	P	10.4969
6.192996	5.681642	6.706765	10.56724	P	P	P	6.43204
6.625043	6.240646	2.674496	6.602724	P	P	P	6.735828
6.620715		7.327522	A		A		5.620523
8.624628	9.018524	9.540962	9.478622	P	P	P	9.658045
5.846728		6.769555	M		A		6.713106
8.312557	6.793429	8.321827	9.336741	P	P	P	7.589641
6.940513	6.011355	6.40049	6.753511	P	P	P	6.019668
7.501759	7.028533	6.57472	4.707073	P	P	P	7.067106

8.000759	6.669641	7.289714	7.433852	P	M	P	6.870633
11.52496	10.95427	11.45641	10.84872	P	P	P	11.37592
9.963205	9.019562	8.506312	8.600421	P	P	P	9.200099
7.200759	7.531766	8.748276	9.198609	P	P	P	7.722035
6.010331		6.063838	P		A		5.130721
2.861096			P				5.897964
6.686002	6.088226	4.702746	6.359865	P	P	P	7.250467
10.29443	9.994052	10.66035	9.826086	P	P	P	10.53177
	3.596494			P			
11.36167	10.84694	10.46757	10.04595	P	P	P	10.14628
13.05462	14.0466	14.04826	13.75641	P	P	P	14.53362
7.27393	7.736049	7.32064	4.789722	P	P	P	8.085347
7.756	8.724668	8.539115	7.548965	P	P	P	9.001102
8.27289	7.931452	8.346421	8.308789	P	P	P	7.423398
	5.760134			A			
12.15901	11.16714	13.10353	13.40744	P	P	P	11.17769
8.059449	6.860434	6.150189	4.279927	P	P	P	7.594104
7.310738	5.713304	6.1454	5.23225	P	P	P	6.002263
7.581719	7.372334	6.637153	7.028576	P	P	P	7.18993
7.366225	7.629789	6.955311	6.965277	P	P	P	7.30135
10.61529	11.35605	11.55055	11.30101	P	P	P	11.63365
10.88243	10.02883	12.14799	12.94745	P	P	P	10.38382
11.55735	11.28889	10.33807	10.0946	P	P	P	11.31918
5.803676	4.649035	5.527059	7.027145	P	P	A	5.77422
13.4121	13.89265	9.793674	11.371	P	P	P	13.83062
11.81002	12.49571	7.973481	9.063156	P	P	P	11.55572
9.97647	11.312	10.38922	9.605777	P	P	P	11.19805
7.06924	6.422321	5.700354	P	P	P		7.194183
7.441012	8.414093	7.865471	7.739314	P	P	P	8.544322
6.140588	6.748228	6.310883	6.296283	P	P	P	6.252164
7.12773	6.26892	5.420044	8.250765	P	P	P	7.490075
3.550044	5.582895	5.727534	6.084127	P	P	A	5.637192
	6.942998	8.220986	8.219666	P	A	A	
10.0478	8.123398	9.000769	8.54254	P	P	P	8.277911
5.898353	5.519217		7.44307	P		A	6.376064
5.089698	5.417732		M	A			5.694126
12.55862	13.03004	13.49781	13.34288	P	P	P	13.08331
9.531095	9.866449	7.97117	8.428164	P	P	P	9.35035
7.521486	6.820001	6.316276	5.753938	P	P	P	7.540676
9.109683	9.019892	9.010259	7.880228	P	P	P	9.272687

7.340313	7.088058	7.928536	8.397651	P	P	P	7.727907
7.627918		7.539885	A		P		6.365359
9.460483	8.321991	8.762734	8.765642	P	P	P	8.288818
9.532741	7.639241	11.93197	11.0204	P	P	P	9.192357
9.972405	8.86305	12.23922	11.63647	P	P	P	9.4591
10.81794	11.58087	10.51436	9.447087	P	P	P	11.45567
7.891865	6.833173	8.209592	8.891302	P	P	P	6.813773
13.13683	12.95414	14.01855	14.39751	P	P	P	13.26478
7.037609	6.483871	7.053372	7.592912	P	P	P	6.674199
8.141874	7.89422	9.021138	9.612237	P	P	P	8.049771
7.738267	9.129523	8.523797	6.543715	P	P	P	7.813057
8.663759	9.047932	10.27554	10.12709	P	P	P	9.348311
10.59628	10.28526	11.40358	11.13492	P	P	P	9.75965
10.72701	10.56576	11.86065	11.57909	P	P	P	10.03936
9.307277	9.512268	10.10261	11.30503	P	P	P	9.469079
			3.640431			P	
8.884265	8.095957	9.068779	9.407208	P	P	P	8.438191
5.981386	5.480785	4.728077	A	P	P		5.555918
7.530362	6.574942	7.292687	7.506896	P	A	A	5.848151
7.95888	6.27487	6.988797	8.482889	P	A	P	6.506535
8.090339	6.46599	7.79222	8.080254	P	P	P	5.630025
8.419094	7.772646	8.521072	9.275885	P	P	P	8.062934
10.81821	10.10116	9.657537	10.07587	P	P	P	10.6353
8.132742	6.643009	8.450155	8.998193	P	A	A	5.059784
6.616077	6.00423	5.644523	5.169386	P	P	P	6.147658
9.832833	9.691155	9.440489	8.781134	P	P	P	9.801595
6.13574	6.38434	5.629211	5.295743	P	P	P	5.295653
7.528979	6.880386	7.682447	8.559898	P	P	P	8.223095
7.571261	8.478136	8.678609	8.166554	P	P	P	8.071795
9.449013	9.269117	10.57534	9.991172	P	P	P	8.351687
6.594177		6.072004	A		P		
8.37668	6.340991	5.705839	5.376461	P	P	P	
8.090833	7.021306	6.597532	6.539872	P	P	P	1.03781
11.74372	10.68612	9.560735	10.97569	P	P	P	11.52699
	5.999424			A			
8.125271	6.936591	8.087129	8.989718	A	A	A	7.037382
10.01114	10.43729	11.15548	11.48486	P	P	P	10.34423
7.756435	7.361197	8.246055	9.511369	P	P	P	7.752367
			8.938434			A	
9.772247	8.551149	9.884872	9.443244	P	P	P	9.567216

9.149581	7.730224	9.331927	9.573858	P	P	P	7.769344
8.203716	8.017983	8.559092	8.473113	P	P	P	7.566832
6.249629	6.460559	6.063707	7.081392	A	M	A	5.169845
9.327564	8.209679	10.18414	10.85414	P	P	P	8.39172
6.274778	4.764128	6.886758	7.192489	P	A	M	6.109728
6.993893	7.219666	5.572312	4.651024	P	P	P	7.20357
6.233204	7.193426	6.395332	4.047776	A	M	P	6.15688
7.086343	6.883316	7.982929	8.406349	A	P	P	6.454418
7.590002	6.916123	7.265519	6.45788	P	P	P	7.239435
5.925948	4.766764	6.972986	7.944673	A	P	P	6.087296
7.315931	4.802887	7.362452	8.050351	P	P	P	6.851664
6.076582		5.822474	A		A		2.917368
8.946508	10.13753	9.510214	8.813646	P	P	P	9.375487
5.112701	4.806307	1.040052	5.85955	P	P	P	6.224446
		4.124352	6.310636		M	A	
7.220972	6.281725	6.909481	7.743488	P	P	A	6.543358
8.361678	7.931181	8.780939	8.929953	P	M	A	8.100757
6.158627	5.499335	7.121076	5.019119	P	P	P	6.567405
4.891322	6.124452	4.912622	M	P	P		6.315314
9.949653	10.45283	10.83722	11.77008	P	P	P	10.81789
11.16888	10.26514	11.5763	12.16407	P	P	P	10.86867
14.51844	13.79083	14.66882	13.99908	P	P	P	13.15216
6.816362	5.397913	7.16688	6.864108	P	A	M	6.476446
7.013307		7.398448	7.19356	A	A	A	5.981751
8.11915	7.351144	8.310452	8.574815	A	P	A	7.642064
6.746868		7.155915	8.11291	P	A	A	7.190758
5.858718		6.071426	6.560911	P	A	P	5.164067
7.620916	7.226274	6.854708	A	P	P		6.608004
9.647099	9.374885	10.55727	10.4702	P	P	P	8.96688
6.889204	4.213673	6.397831	A	P	A		5.540405
12.51652	12.20882	11.38476	11.34664	P	P	P	12.43406
8.698037	8.518419	7.219793	7.750583	P	P	P	9.363074
7.537002	8.060748	6.893488	8.063405	P	P	P	8.862643
5.699361	6.092264	5.788034	5.779637	P	P	P	7.607286
9.026691	9.667067	7.63534	7.736895	P	P	P	10.94903
8.623023	8.772583	7.970897	7.984779	P	P	P	8.619584
5.842121	2.870788	5.496707	6.360651	A	P	P	5.722886
5.652535	4.8834	4.411731	5.630566	P	M	P	6.119851
6.098099	6.686322	5.948011	P	P	M		6.550263
8.540732	8.662724	8.525478	8.03229	P	P	P	8.59244

9.460407	9.137981	10.43741	9.925746 P	P	P	P	9.124195
			6.244452			A	
			7.558583			A	
6.606003	5.398741	5.565405	M	A	P		5.457591
6.227413		6.444224	5.790799 A		P	P	4.200598
6.686534	7.863066	6.934205	7.371919 P	P	P	P	7.775491
8.474187	8.093154	8.912663	9.218852 P	P	P	P	8.330784
7.396947	6.413925	8.374804	8.45158 P	P	P	P	7.306189
6.973564	6.37278	5.537439	7.122623 P	P	P	P	6.660758
7.100001	5.033972	4.763007	6.745182 P	P	P	P	6.67408
6.053714		5.259124	4.677149 P		P	P	5.659384
6.574799	6.352544	6.890356	7.117108 A	P	P	A	5.890642
8.361245	8.370831	8.762384	8.833883 P	P	P	P	8.38912
10.96503	10.1872	10.34862	10.53115 P	P	P	P	9.675797
8.35673	7.035195	8.204971	8.391049 P	P	P	P	8.074432
10.13272	10.28606	9.822376	9.468472 P	P	P	P	10.14461
5.651374			M				6.91072
5.256015	5.719774	5.932461	7.190062 P	P	P	P	6.855466
7.185614	6.260855	7.62892	9.461724 P	P	P	P	7.781008
6.703386	7.658466	6.871777	6.647544 P	A	P	P	6.941656
9.716691	10.01852	9.848134	9.109195 P	P	P	P	10.01099
11.46749	10.47329	11.91995	11.86059 P	P	P	P	10.1651
6.821675	6.518387		6.686936 A	A		P	6.31707
	4.754577			A			
6.440381	6.887237	6.459977	7.809174 P	P	P	P	7.274897
6.568165	6.391367	6.879694	7.43119 P	P	P	M	6.960331
12.48822	12.41138	10.94619	11.82722 P	P	P	P	12.8598
8.374821	8.891598	6.208585	6.805836 P	P	P	P	8.421384
9.929752	9.617951	9.731447	9.457989 P	P	P	P	9.07941
			4.064652			P	
7.019069	6.507698	5.789958	7.057736 P	P	P	P	6.448939
6.946723	6.871162	6.898511	6.441216 M	A	P	P	6.293653
8.766308	7.78173	9.21102	9.368691 P	P	P	P	8.668685
9.009763	9.227355	9.600019	9.700359 P	P	P	P	8.534156
6.558366	5.305302	7.248305	7.072331 A	P	A	A	5.555519
5.41025	5.916174	4.730305	5.768682 A	A	P	P	6.3589
8.095388	6.887295	6.993189	7.10805 P	P	P	P	7.30198
			6.803103			A	
		1.947964			M		
7.036233	6.8135	6.751545	7.932839 P	A	P	P	6.607688

9.121662	8.839981	10.23991	9.987662	P	P	P	8.232636
4.302645			A				1.514023
6.976066	6.488707	7.289577	M	M	P		6.861785
10.69195	11.25012	11.97548	12.18377	P	P	P	11.40329
9.521235	10.21826	9.477169	8.924929	P	P	P	9.508369
8.266925	8.053099	7.211387	7.117589	P	P	P	8.382942
9.783069	9.847035	9.123443	8.317872	P	P	P	9.877801
10.44533	10.32538	8.847891	8.983654	P	P	P	10.55957
6.76613	6.996631	7.710754	7.605254	P	P	M	7.081391
5.729986			A				4.64061
10.41165	11.01258	11.51801	11.63846	P	P	P	11.06487
4.541201			A				2.366156
7.821005	7.230492	7.926333	9.145679	P	P	M	7.657281
12.833	12.61037	11.41988	11.3922	P	P	P	12.61512
6.19319	5.879483	7.064424	5.946477	P	A	P	6.3233
8.160428	8.082962	7.79591	7.00398	P	P	P	7.388373
	5.829422	5.432256	2.128186	M	A	P	
6.348734	5.710924	6.404054	7.111856	P	P	A	6.489525
10.36876	10.90085	10.37559	9.118142	P	P	P	10.10902
7.912167	7.299977	7.075832	6.336453	P	P	P	7.963601
2.048472			P				5.047162
5.981189	5.842564	6.46904	8.18295	P	P	P	7.892012
6.281911	6.690768	6.912021	7.855622	P	P	P	7.707781
8.154573	8.409574	7.759525	8.296084	P	P	P	8.063206
5.945572	6.179339	7.186519	7.900839	P	P	M	6.585217
6.538258	6.857741	5.870261	5.616544	P	P	P	6.802499
8.99388	8.919734	9.617816	9.677802	P	P	P	8.414844
10.07392	10.73262	9.675499	9.442535	P	P	P	10.44256
11.80645	12.66026	12.73743	12.27785	P	P	P	12.83774
8.868551	8.895188	9.975654	9.308882	P	P	P	8.758063
8.526512	7.516416	3.298053	5.318708	P	P	P	8.143684
10.97894	11.19155	10.52222	8.988907	P	P	P	10.87685
13.78323	13.81086	13.38027	12.55738	P	P	P	13.86264
	4.175037			P			
9.295378	8.053552	8.401022	7.822308	P	P	P	8.219712
	4.976732	6.041423	4.939924	P	M	P	
8.918082	8.315061	7.550657	7.407221	P	P	P	7.936631
	4.854811	6.934467		M	A		
7.472012	7.103635	7.602093	7.732332	P	A	P	6.627138
9.719158	8.767887	9.397632	10.23391	P	P	P	9.420545

6.82825	6.186446	6.820698	A	P	A		4.946106
8.508949	7.31995	6.546904	7.762307 P	P	P	P	7.651881
5.157125	4.938192	5.570974	A	P	P		2.899038
9.550512	9.27212	10.22199	10.29501 P	P	P	P	8.951504
6.193791	5.317045	6.332122	6.492174 A	P	A	A	5.035674
8.156929	8.205075	7.336679	7.62534 P	P	P	P	7.650143
10.57319	10.22006	9.404441	9.382604 P	P	P	P	10.09645
9.539136	9.383481	9.865198	10.01851 P	P	P	P	9.385057
5.469609	5.263966		A	P			3.849822
		5.084003	3.83446		M	P	
10.69362	10.64765	10.05402	9.729245 P	P	P	P	10.57513
	5.048618	5.386424	6.096686	A	P	P	
	4.870943	4.751654		A	A		
10.65259	11.69773	12.2958	12.09568 P	P	P	P	11.63467
11.44898	11.39012	11.96495	12.57252 P	P	P	P	11.37524
7.097106	5.69337	7.323175	P	P	A		6.604256
8.780524	8.766027	9.490376	9.852469 P	P	P	P	8.655592
4.862117			P				6.146947
9.127024	8.767592	10.00427	9.079284 P	P	P	P	7.748783
6.876617	6.981832	7.436559	8.261353 P	P	P	P	7.273637
8.661469	8.092922	8.159731	9.959456 P	P	P	P	8.704318
6.664631	6.091249	6.3266	2.825193 P	P	P	P	5.827026
12.51907	11.41074	12.3448	12.51669 P	P	P	P	10.92349
6.215176	6.086248	5.666552	4.874054 P	P	P	P	6.081407
12.01423	12.18842	12.87974	14.28544 P	P	P	P	12.59491
6.418113	6.843169	5.76428	6.345015 M	P	M	P	7.829532
8.712265	8.762219	8.863409	9.606602 A	P	P	P	8.841826
9.877311	10.5287	10.85154	11.46208 P	P	P	P	10.52365
7.651856	7.846138	6.455487	5.749539 P	P	P	P	7.270053
6.709602	6.011074	6.606996	7.348214 A	A	P	P	5.236653
8.11722	8.712732	7.510955	7.715698 P	P	P	P	8.477186
9.812984	10.58276	10.76221	9.702823 P	P	P	P	10.58186
7.381895	5.930477	5.458929	6.047154 P	P	P	P	5.681039
10.16034	10.28304	10.50445	11.58368 P	P	P	P	10.25299
6.699047		7.922801	8.677181 P		A	A	8.025653
7.7021	7.943874	7.551816	7.199928 P	P	P	P	7.772404
11.90455	11.78909	10.65768	11.28517 P	P	P	P	11.97493
8.662799	7.921178	8.412601	7.236488 P	P	P	P	7.639548
6.984759	6.549611	6.48427	7.26123 M	A	P	A	6.231805
9.777893	9.649126	9.16512	8.940195 P	P	P	P	9.738411

8.695779	7.919593	9.080308	8.987463	P	P	A	8.061647
	4.595207			P			
5.891733	5.977347		A	P			3.230473
8.074298	8.389643	8.759541	9.334391	A	P	P	7.755395
9.325038	10.18967	9.332314	9.339325	P	P	P	9.839929
	5.54674	5.702691	4.15443	P	P	P	
7.909849	6.612321	6.372385	6.520537	P	P	P	7.1933
10.51949	10.4866	11.70298	10.16927	P	P	P	8.6724
7.660413	7.623244	6.841375	6.861455	P	P	P	7.522212
	7.04879	6.977706		P	P		
5.573718	4.130287	3.027039	6.850588	A	P	A	5.498569
		7.741566	7.169392		A	A	
			1.761544			P	
7.680778	7.95953	8.247373	8.067434	P	P	P	7.641021
7.494876	7.48864	6.687593	6.550003	P	P	M	7.578784
4.883572	5.362058	4.693761	0.998329	P	A	P	6.628884
11.70689	10.14676	11.82733	12.00949	P	P	P	10.03161
			6.550366			A	
		5.522286	4.995091		P	P	
8.551845	8.163781	9.68062	9.364535	M	P	A	8.027222
7.171652	6.95241		7.984799	P	A	P	6.580697
10.4296	10.49433	10.21878	9.85397	P	P	P	10.67781
6.313389	6.34219	5.912403	6.299324	P	M	P	6.198157
6.568834	6.354911		P	A			7.103903
4.897277	5.047008		2.821724	P		P	6.180429
9.076047	10.14331	9.334334	P	P	P		9.252654
7.000905	5.620381	5.553929	P	P	P		6.727378
5.038096	5.287437	6.410339	P	M	P		6.57381
10.47042	11.39828	9.634893	9.567746	P	P	P	11.08961
5.999422	6.003555	6.911938	5.933783	P	P	A	6.56688
7.063088	7.693001	7.045432	8.943762	P	P	A	8.689806
6.380159	4.940166		A	P			5.957856
8.497741	7.211863	6.729868	6.644194	P	P	P	7.724966
8.735072	8.55833	7.564515	7.484933	P	P	P	8.834339
11.91143	11.59829	11.6922	11.08533	P	P	P	11.84851
7.93748	6.658654	8.103669	8.43002	P	P	P	6.942271
7.844398	7.754463	8.649569	8.675795	P	P	A	6.897707
7.334252	5.223108	5.977517	A	P	P		6.372948
6.74432	6.130816	3.645992	6.492657	A	P	A	6.536268
7.232183	8.086113	6.690464	P	P	P		7.126609

5.973868	5.900331		2.369188	P	A		P	6.209354
11.54835	11.94701	12.42515	13.24748	P	P		P	12.2285
7.843987	7.928567	7.359351		A	P	P		7.848158
7.011233	7.092314	6.811233	6.852255	P	P		P	7.28384
7.193302	6.797865	6.903799	7.814846	P	P		P	7.499238
10.51394	9.657019	10.57064	10.63263	P	P		P	9.146782
10.70636	11.02371	10.20359	10.0518	P	P		P	10.76716
7.851939	7.875517	7.597087	6.800568	P	P		P	7.85827
8.810234	8.858954	9.961733	9.458633	P	P		P	9.054665
7.744551		8.275108	7.736823	P		A	A	6.562348
6.698302	6.51395	7.411856	6.749067	P	P		P	6.364757
	1.143412				M			
8.571404	7.71947	8.543265	8.581683	P	A	A	P	7.776652
6.015016				A				0.85537
9.514289	9.923266	9.991554	10.62213	P	P		P	10.07375
8.676287	8.550262	7.125754	7.705338	P	P		P	8.625394
7.619559	8.087068	8.77564	9.034893	P	P		P	7.710887
8.642564	8.108248	7.238259	8.335169	P	P		P	8.892506
10.21443	10.31985	9.598045	8.931083	P	P		P	10.24253
4.73948	2.777395			P	M			5.640492
10.55591	10.28001	9.752352	9.874832	P	P		P	11.10454
5.418372	5.167295	5.359204		A	P	A		5.146881
		6.943728				P		
	6.40051		6.441939		P		M	
			6.836366				A	
10.43583	11.88625	10.95591	8.918056	P	P		P	12.01522
10.19699	10.22367	10.7283	11.4155	P	P		P	10.55406
7.417923	6.899538	6.901145	5.600668	A	P	P	P	6.194433
9.7152	10.20103	9.740273	8.048286	P	P		P	9.957741
10.72364	10.14215	9.120203	9.700074	P	P		P	10.16737
4.649797	5.943713			P	P			6.497258
7.731404	7.028039	7.733504	7.242279	P	P		M	7.20877
10.79042	10.04726	9.483662	9.529474	P	P		P	9.686791
12.28737	12.31878	10.52263	9.78618	P	P		P	12.59685
7.143903	6.146453	6.982343	3.199671	P	P		P	6.957711
6.256991	5.115058	6.464126		P	A	P		6.667505
5.064548			6.981971	A			A	6.009022
6.96835	6.121891	5.742917	7.738893	P	P		P	6.671436
8.158687	7.855387	7.367944	8.701495	P	P		P	7.630899
9.018104	9.568329	8.889639	8.091496	P	P		P	9.349992

5.129128	5.188546		6.782582	P	A		A	5.78566
8.254512	8.259608	7.785377	7.765096	P		P	P	7.952532
9.025458	8.249424	7.929851	7.94265	P		P	P	8.358228
5.840369	5.579845			P	A			5.80895
9.720879	9.669118	9.974618	10.48	P		P	P	9.832714
6.673335	7.586949	7.129046	4.77945	P	M		P	6.869466
7.284254	7.041807	7.229171	7.448423	P		P	P	7.225353
7.987981	8.356935	9.041886	9.007811	P		P	P	7.542692
10.12455	10.55942	10.69814	11.62422	P		P	P	10.63341
9.887911	9.423602	11.2476	11.02469	P		P	P	9.791407
11.81416	12.26497	11.43185	11.12944	P		P	P	12.27393
12.17804	11.91657	11.23391	10.67142	P		P	P	11.83159
9.801403	10.49853	9.801434	8.942771	P		P	P	10.31607
9.000318	6.672181		8.192957	A	P		P	5.516972
7.097842	6.678739	4.263094	4.296716	P		P	P	7.357328
11.31851	10.9265	11.92633	12.99555	P		P	P	11.31935
			3.414778				P	
7.105687		7.445796		A		A		6.401503
5.81277	5.848095	4.540421	6.943446	M	P	P	A	6.057382
8.699986	9.003211	8.433866	8.220655	P		P	P	8.444482
10.56593	10.6961	9.807086	9.315002	P		P	P	10.41902
10.70723	10.27897	9.416476	9.518015	P		P	P	10.68394
4.993986			5.693888	A			A	2.484096
7.367655	6.40764	7.427632	7.786048	P		P	P	6.469454
7.485413	7.086117	8.396197	8.530582	P		P	P	6.858244
9.598956	8.868694	9.997152	10.22451	A	P	P	A	8.886568
8.72928	8.077066	8.768356	9.714762	P		P	P	8.566833
8.028295	7.057648	7.595032	8.235915	P		P	P	8.076409
10.00313	9.15471	9.272542	8.782319	P		P	P	8.907434
7.536015	7.552875	7.843104	7.713742	A	P	P	P	6.736496
7.694741	9.1918	8.803309	7.789908	P		P	P	8.714087
5.6909	5.297907	4.822704		P		P		5.999878
11.70308	11.5734	11.59058	10.14968	P		P	P	12.01224
7.515907	6.791617	8.160345	7.067416	P		P	P	7.255052
10.54737	9.227331	9.456927	9.120767	P		P	P	10.12088
7.118201	5.687946	5.674714		A	P	P		5.562881
6.396246	7.919675	6.86875	6.49611	P		P	P	6.375702
4.342032				P				5.697207
5.891	6.009844		5.497346	P			P	6.185587
9.165376	8.564607	9.533094	9.488637	P		P	P	8.394454

7.454879	7.650864	7.106835	5.595783	P	M	P	P	7.349846
4.469949				P				5.522484
10.35656	10.08184	10.26316	10.77948	P	P	P	P	10.07667
		7.221514				M		
4.119129				P				5.907228
8.12381	7.065554	7.505281	7.693601	P	A	P	A	7.096306
11.95264	12.01414	10.72779	10.82663	P	P	P	P	12.09429
10.74399	10.56228	10.37552	9.486131	P	P	P	P	10.51795
6.214273	6.670791	6.096314	2.543044	P	P	P	P	6.18926
8.423739	7.528478	7.575567	7.7644	P	P	P	P	6.911628
8.834833			6.610907	P			P	8.636279
12.19236	12.05698	11.33087	10.71844	P	P	P	P	11.89612
	5.761491	6.947206		A	A			
5.493604	5.215141	0.738247	5.838127	P	M	M	M	5.845439
10.45642	10.26685	9.538695	8.917414	P	P	P	P	10.44458
4.708684		6.42155		P		P		6.358177
9.502017	9.605913	10.32139	11.62303	P	P	P	P	10.16018
6.155648	4.330082	2.788306	6.503349	A	P	P	A	6.299057
		3.84448				P		
7.530886	7.656267	7.455181	6.457831	P	P	P	P	6.948239
		5.438651				P		
6.625798	6.214763	6.337714	6.740879	A	P	P	P	5.834479
9.88065	9.433062	9.158983	8.754618	P	P	P	P	9.397182
10.08133	10.07162	9.745717	8.70342	P	P	P	P	9.871178
9.53575	9.264084	8.684445	8.320964	P	P	P	P	8.967311
6.210448	5.60283	4.840652		A	A	P		5.523325
6.327228	5.959851	6.51831	6.777074	P	P	P	P	6.375785
9.100725	9.024718	7.994977	7.773493	P	P	P	P	7.860175
7.626808	8.121026	7.603322	7.772413	P	P	P	M	7.879889
9.240335	8.97639	8.115155	7.916594	P	P	P	P	8.585871
7.645096	7.590225	8.636096	8.004404	P	P	P	P	8.325579
9.258302	9.735766	11.19198	10.54891	P	P	P	P	8.701053
9.135029	9.370323	7.653172	8.019819	P	P	P	P	8.76748
11.53153	11.75615	12.04902	13.67436	P	P	P	P	12.79416
11.10852	9.821805	10.66962	11.46735	P	P	P	P	10.12776
9.332628	9.208751	7.913736	8.900636	P	P	P	P	9.135087
		3.113491				M		
8.96835	7.628638	7.136416	8.198144	P	P	P	P	8.307939
9.177814	9.56415	10.54964	10.88085	P	P	P	P	9.897246
			5.849752				A	

10.10704	10.37662	9.808999	9.369209	P	P	P	10.50961
9.323524	9.541092	7.68015	8.187663	P	P	P	9.839657
4.504325	5.674179	4.689235	P	A	A		5.34479
7.951532	8.439013	8.190063	6.582219	P	P	P	8.323327
7.222546	8.287742	9.27094	10.05282	P	P	P	8.428477
9.62517	9.735978	10.48562	10.58572	P	P	P	10.5138
9.311542	7.985792	7.05731	7.879261	P	P	P	7.565259
10.1114	9.030614	8.184656	P	P	P		9.38768
7.906241	7.395937	7.322147	8.248185	P	P	P	7.723
9.422369	9.23883	7.187268	8.861765	P	P	P	9.837351
6.340421	6.381728	5.581615	A	A	P		6.566618
10.59646	10.31935	10.1044	9.875439	P	P	P	10.25766
6.362268	5.151765	1.637668	6.401554	P	P	P	5.984809
8.17411	6.897434	9.039166	10.26337	P	A	A	8.037245
10.27631	9.568704	10.64436	10.56576	P	P	P	10.11337
7.247036	7.143003	6.097701	6.141586	P	P	P	6.59508
9.331993	9.69616	9.875331	10.26969	P	P	P	9.877995
6.322208		6.017107	6.212074		P	A	5.357498
6.803793	6.827025	6.074951	6.744452	P	P	P	6.585444
			7.000341			A	
4.871693		7.112659	5.838059		A	P	5.162713
10.07747	10.84979	10.83953	11.489	P	P	P	10.92855
10.62648	10.808	12.30984	11.99019	P	P	P	9.986378
9.596812	9.141686	9.900731	10.25751	P	P	P	9.291486
7.30239	7.295898	7.234375	7.774455	M	P	P	8.077405
6.565674	7.091035	7.620636	7.646459	A	P	P	6.350462
7.081981	5.89156	6.376855	6.098706	P	A	P	5.682061
8.342241	8.349322	8.217885	7.62309	P	P	P	7.406378
10.75624	10.26161	9.194405	9.211138	P	P	P	9.767553
9.019112	9.577409	8.4353	7.198849	P	P	P	9.063271
7.143766	5.496686	7.20803	5.829096	P	P	P	7.170068
7.320248	5.78489	7.674666	7.559323	A	A	A	6.673036
6.246639	5.401582	5.852032	6.451592	P	M	P	3.020411
6.986396	6.580329	6.958799	6.248832	P	P	P	6.527635
8.123574	9.290318	9.55649	9.581592	P	P	P	10.17113
6.262069	6.023517	6.402748	7.523946	P	P	P	7.558874
5.961907	4.153503	5.82113	6.47715	P	M	P	2.544922
6.895294	7.537845	6.019089	7.10844	P	P	P	7.585522
7.53713	8.120502	7.282396	6.168696	P	P	P	7.40182
8.373525	8.363424	6.754251	6.130824	P	P	P	8.251668

8.980245	8.841066	7.42903	8.152701	P	P	P	8.326067
9.558477	9.603815	9.285961	9.432081	P	P	P	9.779775
9.548114	9.472249	8.510304	8.731344	P	P	P	9.178573
				P			
6.755255	5.136737	6.077863	3.664446	P	P	P	6.252234
6.014304			6.908542			A	4.717481
13.14264	13.16388	10.98698	11.81011	P	P	P	13.51547
5.450337	5.792347	6.003213	0.373063	P	P	P	5.437284
9.9016	9.973848	11.211	11.07956	P	P	P	8.931231
5.739583			A				4.209448
			8.18438			A	
			6.4954			M	
12.0166	12.02597	10.94325	10.7833	P	P	P	11.64046
10.38365	11.19372	11.16254	12.41717	P	P	P	11.38475
8.335809	8.547943	6.675527	6.861115	P	P	P	8.710621
6.483126	7.139949	5.189524	6.39617	P	P	P	6.264569
6.572609	6.570375	5.978855	5.396666	P	P	M	6.298093
7.510209	6.871688	8.225137	8.134829	P	P	A	6.529741
8.014519	7.259418	8.4846	6.815246	P	P	P	8.000989
6.763683	5.955804		7.727877	M		P	6.536174
9.125963	8.014061	9.601462	10.34149	P	P	P	8.674277
8.024647	8.79635	8.466778	8.580296	P	P	P	8.418627
10.42082	10.2348	10.65632	10.15736	P	P	P	10.66309
6.199748		8.166105	7.74342		A	A	5.779688
6.225717	5.798697	6.536857	6.268105	M	P	A	6.153829
9.328355	7.930266	9.976393	10.04395	P	P	P	7.221152
4.564543			M				5.739947
		2.183894	3.231218		P	P	
7.324619	7.14957	6.28287	6.554558	P	P	P	7.494773
8.964328	8.525206	8.06569	8.451189	P	P	P	7.863079
5.898001	6.689534	6.205533	6.003581	A	M	P	7.485423
10.9984	10.46954	11.52826	11.54112	P	P	P	10.38083
3.132838		4.482708	5.72713		M	M	5.946068
10.77179	10.60509	9.527429	9.286063	P	P	P	10.19387
8.49015	9.059962	8.811941	8.119648	P	P	P	8.579038
10.11337	9.637218	8.402782	9.483156	P	P	P	9.450094
	0.736435	4.690733		P	A		
5.998148	6.213603	1.821981	A	P	P		5.707128
12.85093	12.62375	9.276541	11.49007	P	P	P	13.4722
5.626761	4.366498	4.592371	6.810622	P	P	M	5.996748

8.888082	9.104004	8.362633	7.553966	P	P	P	8.218636
7.6325	7.926115	7.162715	6.490158	P	P	P	7.954363
9.569157	9.552166	10.33048	11.97786	P	P	P	10.00744
			2.751249			P	
6.612127	6.141929	5.781689	P	P	P		6.671845
10.67875	10.87926	11.51965	11.09368	P	P	P	10.34131
	5.301732			A			
6.773381	7.447466	7.507402	7.238545	P	P	A	7.030773
12.29827	10.51862	11.56499	10.95975	P	P	P	9.278935
5.634034	6.035709	5.568456	6.390614	P	P	A	5.509189
6.042024			2.540135			P	6.34189
5.734704	6.593151	6.421829	5.425315	P	P	P	5.62184
8.936186	9.730028	9.473004	8.473181	P	P	P	10.05606
8.046349	8.18057	6.984229	8.214497	P	P	P	8.20634
8.729588	9.172923	10.45763	9.610799	P	P	P	9.378204
7.582335	6.489205	7.641037	8.468812	P	P	P	7.786182
12.63878	12.79763	11.96879	11.54125	P	P	P	12.45301
	6.794583	5.540544	7.094122	A	P	A	
9.873467	9.461531	8.979837	8.739657	P	P	P	9.43639
7.091418	8.430435	7.845799	6.08645	P	P	P	8.057784
		4.390588			P		
6.36028			A				3.389134
3.467246			P				5.83937
	6.096471			P			
8.463906	9.044257	8.36714	7.617561	P	P	P	8.263688
9.441935	8.723928	9.984768	10.31083	P	P	P	9.217744
10.28937	9.287312	8.956484	10.72659	P	P	P	6.874187
8.698851	9.487039	8.513907	7.45169	P	P	P	9.056644
7.269384	6.142646	6.56424	7.446361	P	P	P	6.985856
	4.826021	5.136157	2.511604	P	P	P	
9.354938	8.017124	9.969551	10.71827	P	P	P	8.396905
5.87806	6.321086		5.230315	P		P	6.340823
6.689359		7.620616	A		A		5.545473
6.215167	4.751513	6.737439	6.827513	P	P	A	6.119181
6.797752	6.121678	6.20599	7.335959	P	A	A	6.740992
5.377425		5.920692	A		A		2.932733
7.205686	6.801135	7.126685	6.025719	P	P	P	6.301109
7.584002	6.575798	6.879497	7.390112	P	P	P	6.372534
	1.734684		6.570766	P		P	
	5.603074	6.345396	5.82527	M	A	P	

5.496918	5.642245	6.913362	7.165358 P	A	P	A	6.002733
	5.959142	6.129133	7.994979	P	P	A	
7.491907	7.229507	7.627398	6.547646 P	P	P	P	7.447657
7.566329	6.928648	6.616452	P	P	A		5.687795
5.70991	7.82137	7.265373	6.601939 P	P	A	P	6.877341
8.517378	7.657804	8.335796	8.741529 P	P	P	P	7.791779
		6.525245	6.445879		A	P	
	4.741187	5.332085		A	P		
	5.979312	6.717493	6.520533	P	A	A	
6.453135			A				3.10184
6.248113	5.689618	5.306347	3.234881 P	A	P	P	5.674268
6.05065	6.233588	5.217564	A	P	P		5.37702
5.714016	5.653722		6.434595 M	P		A	5.868574
8.428676	9.083529	8.725253	7.593675 P	P	P	P	8.896129
6.351059	5.190044	3.199744	7.449909 A	P	M	P	5.611523
11.80098	11.96919	9.735192	10.06195 P	P	P	P	11.80962
	4.44143	3.557375		P	P		
	4.475857			P			
6.637385			6.038908 A			P	6.0318
8.354093	9.201172	8.904037	7.285046 P	P	P	P	9.006495
7.366951	7.368755	3.316999	6.725002 M	P	P	P	7.133139
8.538441	9.31187	9.399174	9.203419 P	P	P	P	8.949032
5.920514	6.943963	6.479453	7.429493 P	P	P	P	6.791699
10.15501	9.373442	10.58464	10.22365 P	P	P	P	9.287404
5.960149	6.346897	6.732115	7.041006 P	M	A	P	7.136115
7.630995	6.963774	6.410936	7.528918 P	P	P	P	7.412434
3.886125			6.731374 P			P	4.790203
7.242644	10.06433	8.819517	8.007405 P	P	P	P	9.529649
6.442627	6.491429	5.784719	M	A	M		6.042774
7.517457	7.389166	6.836421	6.31424 P	P	P	P	8.709466
8.309098	7.750451	7.904575	7.728218 P	P	P	P	7.275518
11.52284	11.61183	10.53954	10.32 P	P	P	P	11.30878
8.396646	8.333047	8.067001	10.70274 P	P	P	P	9.656732
8.905833	8.263472	8.277333	7.937264 P	P	P	P	7.625109
8.709311	8.410164	9.387802	9.301199 P	P	P	P	8.611688
12.60693	11.93761	12.68936	12.4762 P	P	P	P	11.81285
11.62849	9.963437	10.75385	11.12998 P	P	P	P	9.537622
10.63961	10.67092	10.13275	9.624755 P	P	P	P	10.57973
10.45535	10.16279	11.15372	11.61389 P	P	P	P	9.996779
6.141954	7.05626	6.738072	7.518163 P	P	P	P	7.193014

6.881082	8.081922	6.509619	6.143219	A	P	P	P	6.410533
9.656095	9.586652	8.932316	9.321732	P	P	P	P	9.741096
12.00446	11.06847	12.73192	13.50893	P	P	P	P	11.08076
9.197412	10.1437	10.29985	10.83714	P	P	P	P	10.92244
11.38506	11.57327	9.584405	9.683965	P	P	P	P	11.5398
	7.399607	5.056213		P	M			
6.613681	5.039595	7.320643	8.631851	A	A	A	A	6.326037
7.176758	7.538325	7.027445	7.190259	P	P	P	P	7.488094
6.000176	5.05974	5.907449	P	P	A			5.479883
8.491429	8.409792	7.734099	7.825762	P	P	P	P	7.96335
10.30512	10.72099	9.978223	9.056793	P	P	P	P	10.18933
12.65176	12.81554	12.28585	11.99359	P	P	P	P	12.45854
11.45788	10.99816	12.1597	11.60199	P	P	P	P	10.65441
8.581298	7.720548	8.481867	7.876897	P	P	P	P	8.042867
10.12406	10.28401	11.0509	10.5286	P	P	P	P	9.763716
8.936801	9.085567	8.021129	7.430854	P	P	P	P	9.345158
10.63569	11.0621	10.19834	9.517036	P	P	P	P	10.98385
8.228524	8.656572	7.666613	8.918842	P	P	P	P	9.119219
9.80043	9.212757	8.854485	8.371235	P	P	P	P	9.032068
12.4464	12.07024	11.9195	11.45583	P	P	P	P	11.41878
	5.088614	4.693155	5.754935	A	P	P	P	
4.562733			M					6.4027
8.031229	7.07698	7.739085	8.728511	P	P	P	P	7.85864
7.155185	6.00375	7.593483	A	A	A			5.603126
10.36728	10.2875	11.00377	12.69619	P	P	P	P	10.94012
8.422009	8.794917	8.335405	7.770906	P	P	P	P	8.396087
6.812398	7.638996	6.159323	7.67557	P	P	P	P	7.804109
4.922676			A					1.087981
5.82533	4.211367	5.568664	A	M	M			1.698521
9.324534	9.848267	8.47171	7.893838	P	P	P	P	9.336239
6.191145	6.525004	7.528472	8.449403	P	P	P	P	6.715437
	4.404666			P				
5.498442	4.976776	5.525625	M	A	A			4.369563
9.361752	8.436252	6.904268	9.164222	P	P	P	P	8.31596
12.00724	12.41742	9.701721	9.751199	P	P	P	P	12.00911
5.796282		4.81903	5.673432		P	A		5.099663
6.248068	7.158324	5.960719	7.290105	P	P	P	P	7.166393
6.714213	7.208769	6.459135	5.66216	P	P	P	P	7.242782
	4.711903	4.163528		P	P			
5.674641	6.85907	6.184815	7.165016	P	P	P	P	6.280864

5.838416	6.426706	6.852796		P	A	P		6.592157
6.008057	6.201314	8.110627	7.626412	P	P	P	P	7.314148
8.737492	7.866908	8.943626	10.47401	P	A	P	P	8.623149
6.532439	6.154989	6.848016	7.574035	P	P	P	P	7.153113
5.575948	4.989708		6.406492	A	A		A	4.443783
6.512482	6.930922	7.219053	6.979327	P	P	P	P	7.560949
9.090633	8.578188	9.557128	8.742196	P	P	P	P	8.16855
10.71582	10.49017	10.99858	10.69887	P	P	P	P	10.31618
9.127757	9.031426	8.072574	8.746708	P	P	P	P	9.497249
13.1044	10.63762	11.97241	11.51726	P	P	P	P	9.744139
5.650012	6.101098	6.562769		P	A	P		6.971661
	7.270016		3.598289		P		P	
10.50721	10.28887	9.521668	9.254393	P	P	P	P	10.93951
9.888081	8.616917	8.036353	8.553496	P	P	P	P	8.785307
8.61086	8.24008	8.509384	7.691743	P	P	P	P	8.201482
9.816607	9.403125	8.866624	8.718832	P	P	P	P	9.181088
9.395393	8.714956	8.280422	8.873914	P	P	P	P	8.062678
11.47032	10.2493	11.27737	11.28097	P	P	P	P	9.885176
6.773412	5.962555	7.227061	7.715104	P	P	P	A	6.163639
6.924438	7.852253	6.891436		P	P	P		7.441552
6.218838	7.150706	6.564714		P	P	P		7.544727
8.639918	8.183214	8.557323	8.588323	P	P	P	P	7.379154
10.87438	10.35152	11.65336	11.64494	P	P	P	P	10.72672
11.97286	10.43662	11.81088	11.39337	P	P	P	P	9.67125
		8.968898	9.139833			A	A	
7.417308	7.128405	7.924893	7.982641	A	P	A	P	5.243432
2.559746				P				5.76189
7.938507	8.904895	8.231607	9.136645	P	P	P	P	9.047295
		6.990499				A		
5.183767		2.320898	2.516254	A		P	M	4.98037
10.51485	10.91686	9.953819	9.207258	P	P	P	P	10.69431
11.85471	10.52243	12.02922	12.02236	P	P	P	P	9.980663
7.655495	7.847194	7.197018	6.815422	P	P	P	P	7.142016
8.745923	8.470465	9.46549	8.286495	P	P	P	P	8.786954
5.458442	6.61007	5.314145		P	P	M		7.213241
6.861506	6.049304	6.980433	7.559516	P	P	P	P	7.067959
6.937135				A				5.768196
10.1829	9.37681	10.70089	10.94633	P	P	P	P	9.307793
9.286533	8.951759	10.32597	11.01836	A	M	A	A	9.013471
6.261762	5.645279		4.118608	A	P		P	6.056247

9.166197	9.358362	8.288974	8.146733	P	P	P	8.762335
4.850099	5.433728	5.66042	5.955782	A	M	A	5.275266
			5.794065			A	
5.893786	5.650743		6.204836	P		A	5.031063
10.57099	10.17417	11.36606	11.73432	P	P	P	10.24522
9.270978	8.635036	9.815162	10.62961	P	P	P	9.060001
7.641549	8.190739	9.364163	8.886885	P	P	P	8.286982
10.06302	9.992116	9.255973	9.018702	P	P	P	9.767008
8.169471	7.604683	6.919681	7.295788	P	P	P	8.123052
10.89282	10.98435	10.27163	9.357182	P	P	P	11.07666
5.117906	5.033607	4.791695	5.236198	P	P	P	6.053011
8.560045	7.487158	7.8519	7.924336	P	P	P	7.322879
7.596594	7.789341	6.771884	6.673196	P	P	M	7.304704
8.63633	7.902231	6.530211	7.463901	P	P	P	7.219553
7.23835	6.79888	7.456067	6.684037	P	P	P	6.023151
6.994696			5.441519			P	5.884869
5.737851	4.153439		5.992639	P		P	5.308837
	3.162226			P			
15.18819	15.31292	15.62297	16.52589	P	P	P	15.26579
10.13105	9.787192	10.3504	11.51047	P	P	P	9.875596
9.066611	9.249251	10.09397	9.511576	P	P	P	8.965228
8.68954	9.242041	8.067123	7.969149	P	P	P	9.412598
8.96949	8.509573	6.985276	7.208246	P	P	P	8.909145
7.766573	7.839068	7.223405	7.70113	P	P	P	6.791192
11.35322	11.07599	10.73829	10.38878	P	P	P	11.01162
8.66058	8.573683	9.928171	10.91671	P	P	P	7.869145
6.681507	7.187538	6.099779	6.882613	P	M	P	5.370432
6.324038	5.284616	4.685866	5.955596	P	P	P	5.573639
		6.534488	8.041227		A	A	
10.11324	9.956927	9.775932	10.57432	P	P	P	9.428415
8.38436	7.542837	7.064089	7.551757	P	P	P	7.776105
1.606822			M				5.784623
7.743586	6.70165	7.702848	7.926597	P	P	P	7.750371
8.343134	8.31864	7.624775	7.648096	P	P	P	8.080924
7.722518	7.698733	5.85144	5.831766	P	P	P	7.367609
6.507347		6.278594	6.262518		A	A	5.58286
9.264724	9.469208	8.162646	6.999139	P	P	P	9.041753
		3.949746			P		
	7.949708			A			
5.656856	5.81599		P	M			5.99122

5.568029				P				7.099282
9.593282	9.275576	10.15633	10.23816	P	P	P	P	9.726486
8.52544	8.428445	9.256114	10.07572	A	P	P	P	8.534588
9.819136	10.18517	10.0555	9.070833	P	P	P	P	10.0921
7.462694	7.872738	7.807942	6.713329	P	P	P	P	7.514058
7.010387	7.052395	5.379536	5.854475	P	P	P	P	6.94399
7.621988	9.654402	7.770023	8.454245	P	P	P	P	9.599838
9.115201	9.333866	9.762228	10.38945	P	P	P	P	9.205514
8.509784	8.203002	9.155886	9.316809	P	P	P	P	7.999694
10.94968	11.03147	11.70807	11.91343	P	P	P	P	11.40267
7.65046	8.102133	7.77206	8.007089	P	P	P	P	8.30633
	4.116308	5.918614		P	P			
6.95245	7.094142	6.295612	8.426356	P	P	P	P	7.078703
6.390658			8.134098	A			A	5.452319
5.427018			6.081443	A			A	5.365847
2.532194				M				5.259902
9.23806	8.66975	9.650198	9.979964	P	P	P	P	9.078469
7.022048	7.214489	7.089533	7.317432	A	P	P	P	5.741236
5.339495	4.67596			A				4.277198
7.113383	6.835427	6.491725	6.184423	P	P	P	P	7.462881
9.54655	9.531792	10.15372	10.76519	P	P	P	P	9.662177
12.46773	12.51144	13.261	12.23865	P	P	P	P	11.62911
8.11797	7.096973	7.395489	7.07312	P	P	P	P	8.145582
11.56197	11.02348	10.18999	9.844132	P	P	P	P	10.80434
8.396102	8.492897	7.849053	7.722736	P	P	P	P	8.660137
10.78954	10.96032	10.33553	10.00933	P	P	P	P	10.7924
10.88993	10.58169	9.97614	10.51381	P	P	P	P	10.83969
9.649125	9.303463	8.874723	8.674815	P	P	P	P	9.331518
4.777068			6.865001	M			A	5.939672
9.808926	10.25283	10.75426	10.74723	P	P	P	P	10.02457
7.413845	6.669158	6.514061	4.883755	P	P	P	P	7.249333
8.039824	5.455698	6.88412	7.465419	P	P	P	P	7.369457
6.186628				A				5.165783
4.920828	5.312858		6.120837	P			A	6.25224
5.67049	6.384111	5.629828		P	P			6.712179
9.933574	10.00125	9.326104	9.019098	P	P	P	P	9.762038
12.63468	12.52953	11.92403	11.60044	P	P	P	P	12.33656
	5.771688			P				
9.689804	8.896771	9.738318	9.100992	P	P	P	P	8.169872
5.960663	4.943986	2.523291		A	P			5.936769

10.42549	9.817069	10.36798	10.19818	P	P	P	9.394129
8.080676	7.54816	7.203933	6.524699	P	P	P	7.687588
7.401924	6.813225	7.80359	7.837531	P	A	P	7.319109
7.085277	7.336283	4.575162	6.626374	P	P	P	8.644624
5.942135	5.835702	3.609342	5.555824	P	P	P	5.513489
8.848132	7.179928	6.254825	7.209671	P	P	P	6.660388
10.55932	10.9617	9.611055	9.9985	P	P	P	11.15206
8.721935	8.70201	8.554338	8.599176	P	P	P	7.158164
9.541571	9.140938	9.818364	9.79859	P	P	P	9.113224
6.973139	6.866931	6.541048	3.138233	P	P	M	7.215324
9.915574	9.907721	9.412456	9.885541	P	P	P	10.53927
11.63124	11.92171	12.54306	11.69282	P	P	P	11.41608
7.588923	8.38118	8.841283	9.278267	P	P	P	8.288742
9.109699	9.301991	9.612398	9.349012	P	P	P	8.893661
13.20751	12.77293	12.50155	12.19146	P	P	P	12.66621
10.83409	9.990538	10.15272	9.529141	P	P	P	9.604468
7.07854	6.909098	7.309294	7.483123	P	P	P	7.310197
11.75604	12.16778	12.76923	12.96741	P	P	P	11.95931
7.767481	6.543339	5.625033	3.129037	P	P	P	6.616703
5.909396	6.039252	5.342105	A	P	P		0.88878
11.47716	9.747485	10.45223	10.99708	P	P	P	10.72921
	7.391215		6.783357	P		P	
10.12748	10.6077	10.3576	9.218589	P	P	P	10.28364
8.406716	8.20818	6.517849	7.171796	P	P	P	8.358953
10.5501	10.58426	8.918719	8.90447	P	P	P	10.42652
10.24874	10.33808	8.814047	8.839346	P	P	P	10.35086
9.186505	8.59463	10.22077	10.36724	P	P	P	9.148317
9.229771	8.882893	10.04566	9.852181	P	P	P	8.679941
9.931591	9.691075	10.72765	10.03505	P	P	P	8.935275
7.540533	6.926961	8.014696	9.225191	P	P	A	7.462726
7.956812	7.833594	8.918363	9.536437	P	P	P	8.119844
9.753715	9.888202	10.75586	11.48274	P	P	P	10.08351
5.702292	5.19078	7.448492	8.806781	P	M	P	7.302317
7.124174	7.339624	7.299541	6.899079	P	P	P	7.532533
		3.93745	4.830126		P	M	
13.2776	13.09326	13.73977	15.04949	P	P	P	13.85453
11.62663	11.26255	10.76245	10.31618	P	P	P	11.17208
6.849984	7.516666	6.688583	6.790923	P	P	P	4.385234
9.573172	9.503896	9.707462	8.030303	P	P	P	9.028347
8.186328	8.077655	9.33497	9.486086	P	P	P	7.753573

10.74019	11.00101	12.7373	11.74939	P	P	P	9.538658
5.22438	4.909497	4.762591	M	M	P		5.704962
10.75686	10.85911	10.25716	9.393213	P	P	P	10.31074
9.918171	9.270083	8.991701	9.485889	P	P	P	9.839118
5.355218	2.632411	5.557585	A	P	A		3.204593
	5.711751		2.95149	P		P	
5.445687		5.647913	6.734998		A	A	1.697063
5.892387	4.840646	4.640689	6.17381	P	P	P	4.757495
8.727188	7.220813	9.248241	8.366618	P	P	P	7.127728
6.621174	6.681244	6.148431	5.755625	P	P	P	7.564859
9.958529	9.071701	10.29813	10.03687	P	P	P	8.952107
5.663609	5.653388	6.82395	A	A	A		5.519364
4.816396	4.6874	6.030246	6.71512	P	P	A	5.541623
6.126159	6.125453	7.034345	7.594019	M	A	A	6.197043
6.823907	6.61863	5.848562	6.015792	P	P	P	7.338825
14.30416	15.01497	15.28624	15.44241	P	P	P	15.05217
6.13417		6.206927	6.224123		A	A	6.129622
4.953288			P				6.153213
5.926998	7.259457	7.304844	2.610114	P	P	P	6.252963
9.780248	9.393779	8.068875	8.233332	P	P	P	9.494204
11.24952	10.2138	9.195387	8.968582	P	P	P	10.75071
	3.055528			P			
6.007908			A				4.997079
7.342653	8.270295	6.716158	5.779584	P	P	P	7.766697
4.086334	6.163643		6.800455	A		P	6.305092
		6.165756	6.793771		A	P	
11.87332	11.21312	11.13613	10.55205	P	P	P	11.11924
7.393542	7.071229	6.446806	6.75103	P	M	P	6.880758
		1.823623			P		
5.661805			A				3.248023
5.649467			2.088792	A		P	5.01251
	6.014797			A			
6.643697	6.413855	6.78845	6.94303	P	P	P	6.805982
	6.616136	6.658114		A	P		
6.55574	5.716661	4.629309	5.951158	P	P	P	5.916901
3.232413			P				6.039876
6.268986	6.796126	5.938895	6.740347	P	P	A	7.307302
	4.645829			A			
6.529045	4.611789		5.991204	M		P	6.726296
		4.152615			P		

5.417751	4.79149	4.689364	5.720665	P	A	P	P	5.179619
6.729023		7.926804		A		A		6.700535
8.474644	9.453922	8.632521	9.759965	P	P	P	P	9.864224
6.827581	6.841278	7.66679	7.275116	A	P	P	A	5.713743
	5.920003		8.055204		P		A	
	9.530981	8.71632	9.50392		P	P	P	
6.169344	5.755562	5.28718	6.884724	P	P	P	A	5.962303
5.149436	4.894362			A	A			4.563672
5.862924	5.604473			A	P			4.790309
6.492071	6.377031	7.975051	7.620936	A	P	A	A	6.354802
		6.080405				A		
5.578944	5.187572		6.809769	A	P		A	5.601911
	6.379597		6.810643		A		P	
			5.200187				P	
6.73549	6.185813	7.127312	7.563025	P	A	P	P	6.445022
5.704207	5.248396	5.185702	7.050754	P	M	P	P	6.412
5.522934	5.938781	2.510568		A	A	M		5.302088
5.720243	6.566507	8.474982	9.136325	P	A	M	A	7.152657
		3.248873				P		
	7.327178				A			
			7.77318				A	
			7.840415				A	
7.74015	6.474672	6.140893	6.729576	P	P	P	P	7.369964
8.488333	7.697334	6.889835	5.948989	P	P	P	P	7.827938
			9.173129				A	
		5.082978	5.41911			P	P	
5.744455		6.026516		P		A		5.473772
9.785788	9.727296	7.833263	8.119387	P	P	P	P	9.665769
8.025565	7.615086	8.932752		A	A	A		7.573816
			7.372627				A	
7.457169	7.300253	6.220872	6.302686	P	P	P	P	6.716088
6.346192	6.588985	5.170877	6.590726	P	P	P	P	7.514364
7.284082	8.31265	5.691992	6.889285	P	P	P	P	7.943251
6.089727		3.314874		A		M		5.642876
6.971679	6.428007	7.082002	7.729603	P	P	A	P	6.792085
6.324958	5.764978		5.190458	P	P		P	6.442422
8.368195	7.282421	7.316167	8.322186	P	P	P	P	7.341445
	4.537166	3.611072		A	A	P		
	5.805409	7.119496		P	P	M		
10.26158	9.957811	9.627421	9.586502	P	P	P	P	10.11551

10.11673	9.11818	9.362668	11.25337 P	P	P	P	9.344688
2.512499			5.749476 P			M	5.60176
5.135644	5.729275	5.039689	6.186057 P	M	P	P	5.589414
5.963558	5.821598		3.709652 P	P		P	6.775267
5.95497	5.831346	2.880931	6.549833 A	P	P	P	5.227124
9.165283	8.694881	7.634448	7.886825 P	P	P	P	8.884969
		3.231353			P		
5.515453	5.040763	4.966012	2.51157 P	M	P	P	6.160646
9.828464	9.758635	11.50383	10.8567 P	P	P	P	9.642347
5.607491	6.155309	5.560008	5.646293 P	P	P	P	7.2299
4.409322			M				7.169829
6.468691	6.538644		A	P			3.918519
8.37641	8.27256	9.09164	9.093431 P	P	P	P	7.263187
6.916057	8.026467	7.1835	7.699989 P	P	P	P	8.355389
8.570751	8.665395	7.823194	6.931619 P	P	P	P	8.789456
			7.322695			A	
9.771084	9.668432	8.947831	10.10133 P	P	P	P	10.60305
7.405805	8.146276	7.87605	8.051816 P	P	P	A	7.641863
5.642397			5.636545 A			P	2.347565
8.651449	7.748024	8.429399	8.92006 P	P	P	P	7.900377
5.794854		4.589891	A		P		1.270435
7.263304	8.582842	10.42036	9.583367 P	P	P	P	7.8546
	5.341707	5.390743		P	A		
6.635368	6.062523	7.347329	7.385873 P	P	P	P	7.031489
	5.885934	6.582676	6.20486	A	A	A	
9.36821	8.946334	8.550242	8.474278 P	P	P	P	9.055291
5.554802			7.595581 P			A	6.549978
5.3241	5.780007	5.68132	7.263342 P	P	P	A	5.995764
	5.668959		3.322339	A		P	
6.306355		6.466287	6.383542 A		A	A	5.78823
7.869556	7.175478	5.94382	7.265028 P	P	P	A	7.175685
4.556906			P				6.231162
6.869619	7.504577	8.297424	7.598749 P	P	P	A	6.904576
5.035555			3.972643 A			P	3.39182
7.45495	7.979676	7.059114	6.542842 P	P	P	P	7.674938
7.513819	7.398027	6.17288	6.081176 P	P	P	P	7.721316
	4.364809			P			
5.579117	5.647005	6.031168	7.275022 P	P	P	A	6.300384
	3.344117	6.569073		P	M		
7.537805	7.540201	8.161477	7.943234 M	P	P	P	6.809385

9.536972	9.066717	9.277355	8.508276	P	P	P	9.896994
9.900092	9.421916	10.1456	9.341462	P	P	P	8.877286
	6.129568		6.345371	A		A	
7.103384	5.962729	6.731317	7.236369	P	P	A	6.710315
5.79633		4.233565	M		P		6.549571
6.355471	6.373001	5.099785	5.83489	A	P	P	5.97722
8.403827	8.430336	8.937013	10.28736	P	P	P	9.021946
9.098247	9.017442	8.83345	9.724063	P	P	P	9.448422
	5.662178			A			
11.71225	12.34652	10.35358	10.35199	P	P	P	11.79346
7.721367	7.887205	7.208613	6.650837	P	P	P	8.218194
13.92199	14.17276	13.19713	12.81649	P	P	P	13.86608
8.652385	8.779329	7.709237	8.823017	P	P	P	8.428064
10.51156	10.70415	9.099628	8.286204	P	P	P	10.39556
12.28808	11.81593	12.41618	12.15947	P	P	P	11.44498
	5.786679		6.683227	P		A	
8.404175	9.106959	8.097922	7.45134	P	P	P	9.066036
7.085095	8.02047	6.898071	6.770004	P	P	P	6.410098
		7.512248	7.698579		A	P	
8.179666	8.051604	7.244629	6.145064	P	P	P	7.082118
7.6611	7.013905	7.817182	8.597118	P	P	P	7.299094
5.178006	5.478378	5.995408	P	P	P		6.650788
7.698655	7.863444	8.088449	8.964257	P	P	P	8.104513
6.733694	6.846074	7.171013	6.330952	P	P	P	7.236368
8.4489	7.602635	7.529223	7.209278	P	P	P	9.705289
7.217543	6.304739	7.410434	5.363334	A	M	P	5.589717
8.445084	7.492709	8.484393	7.817471	P	P	P	7.388409
6.06633			A				3.375296
7.696575	6.804767	6.923623	3.534674	A	P	A	5.759432
4.931535	1.557108		P	P			5.036686
4.744752		5.826716	P		A		6.191571
		2.526948			M		
	2.85771			P			
11.07015	10.44023	11.03698	10.66961	P	P	P	9.982916
9.638119	9.251511	10.02388	9.201205	P	P	P	9.752005
5.226117	6.547252	5.159399	7.152343	P	A	P	6.068405
7.683552	5.919436	5.815731	P	P	M		6.32493
5.53086	6.936844	6.161542	6.42809	P	M	P	7.111924
	5.668943			P			
6.968349	6.437645	3.521975	P	P	P		6.21919

7.03725	7.236824	6.510665	7.20492	A	P	P	P	6.51822
7.444057	7.097158	7.104125	8.429948	P	P	A	A	7.740958
8.333662	8.799665	7.639524	7.779443	P	P	P	P	8.766455
11.73985	12.44771	10.82963	11.31789	P	P	P	P	12.11524
8.232035	7.422588	6.851179	6.315804	P	P	P	P	7.582264
11.93227	10.17351	11.81225	11.94128	P	P	P	P	10.2284
9.810359	9.16124	9.467962	9.631171	P	P	P	P	8.676228
6.467312	6.634421	7.998478	7.1391	P	P	P	P	6.910453
4.928838	5.543932		P	A				5.991117
5.098096	4.96542	5.758724	6.042416	P	P	P	P	6.652422
6.575158	6.764114	5.211852	6.128407	P	P	P	P	7.292622
7.030201	7.678807	7.226172	6.375907	P	A	P	P	6.804204
6.364676	4.863883	5.874852	6.413286	A	M	P	M	4.560941
		5.091562				M		
5.885725	2.579942		P	P				5.798362
9.017461	8.355757	8.114316	8.57517	P	P	P	P	8.426961
6.272175			0.886803	A			P	5.790868
			6.387934				A	
5.566187	4.471471	4.709174	3.487144	A	A	P	P	5.922758
8.008116	7.397804		9.412153	A			A	7.815226
	3.006667			P				
	5.16372	6.655304		P	A			
10.94859	9.924471	11.828	12.7139	P	P	P	P	9.981545
7.45559	7.046996	5.964946	5.742885	P	A	P	P	6.674669
9.380682	9.942947	7.97572	7.079768	P	P	P	P	9.545369
8.048399	7.557965	8.943197	8.810365	P	P	P	P	9.014774
11.78849	11.3619	12.1686	12.45498	P	P	P	P	11.12993
10.57261	10.75744	10.47848	9.36119	P	P	P	P	10.71829
8.81401	9.477856	10.07584	9.751343	P	P	P	P	8.644176
7.538369	7.794566	7.182919	4.86519	P	P	P	P	8.031631
7.185173	7.227862	7.379487	8.293852	P	P	P	P	7.656037
			6.740134				A	
5.359811		6.091749	A		A			2.908754
12.19194	11.92491	11.05906	10.82649	P	P	P	P	12.3094
8.646703	8.852384	8.02992	7.983489	P	P	P	P	8.854357
9.373921	9.789414	9.774933	8.661629	P	P	P	P	9.366269
12.8098	12.13898	13.36198	13.19665	P	P	P	P	12.10282
7.210589	6.697578	5.926994	6.939694	P	P	P	P	7.017
9.135924	9.333094	8.818714	7.119108	P	P	P	P	8.378276
6.930647	6.141154	6.454221	4.952749	A	P	P	P	6.431414

7.268067	7.296756	6.346505	6.176333	P	P	P	6.980458
7.07144	7.6104	6.076305	6.77867	P	P	P	6.787903
8.652092	9.059339	10.21125	9.686268	P	P	P	8.328761
5.861912			5.984865			P	1.567696
	5.258424		3.594987	A		P	
8.560152	7.873891	7.205214	5.458165	P	P	P	7.793419
4.639162			7.131311			A	5.697784
	5.526503	5.298803	1.356435	P	P	P	
5.888	6.551302	5.759684	6.233738	P	P	A	6.476469
8.499756	7.550023	6.865621	5.961218	P	P	P	7.883812
8.101851	7.54812			P			6.572487
7.090451	6.673304		6.20525	P		P	5.731905
6.006836	6.544421	6.491703	6.844944	P	P	A	6.259872
	6.620638	7.46099		A	A		
		3.518965			P		
7.978233	8.315175	8.627863	9.255778	P	P	P	8.512099
8.32529	9.166478	6.582193	6.473968	P	P	P	9.756043
6.702379	6.844549	5.742613	4.557718	P	P	P	7.073033
9.544204	10.44319	6.888612	8.670574	P	P	P	10.77905
11.70249	11.89164	11.56988	10.6789	P	P	P	11.59002
10.22569	10.35178	9.589031	9.823755	P	P	P	10.90788
9.159999	9.321986	8.979052	6.793912	P	P	P	9.035004
	4.540313			A			
7.384194	7.400974	6.422733	6.498238	P	P	P	7.671628
6.999366	7.010222	2.555513		P	P		5.85835
6.896516	5.496621	6.746338		P	P		5.426276
8.703682	8.188571	7.266398	2.509457	P	P	P	7.5424
10.21452	10.28962	9.237322	8.680055	P	P	P	10.05948
7.676635	7.053816	7.003248	7.698141	P	P	P	6.218051
6.300912	5.963236	7.376952	7.711031	M	A	A	6.468132
5.454041			3.672504			P	4.052122
10.49159	10.47051	10.1944	9.732548	P	P	P	10.06473
6.176571		6.531038	6.740566		A	A	5.997365
8.111637	9.370868	9.636195	9.369133	P	P	P	8.711441
7.648825	5.958466	7.880621	8.479236	P	A	A	6.033361
7.975202	7.890382	8.340522	7.02921	P	P	P	7.708108
8.1217	8.404304	7.661288	8.286852	P	P	P	8.31399
5.208471							6.517724
			M				
		4.713612			M		
	4.851991		7.052353	P		A	

8.73479	7.807203	9.020564	9.791036	P	P	P	8.769565
8.709659	8.248632	7.514575	7.070709	P	P	P	8.356675
8.141445	7.211111	8.23206	9.072916	P	P	P	7.932359
9.557833	8.888672	9.328248	11.44661	P	P	P	10.41873
7.436033	6.927732	8.272737	8.328241	P	P	P	7.066447
9.891795	9.329145	11.07844	10.83676	P	P	P	9.251846
5.048908			6.208989			A	5.476662
8.757783	8.127098	8.901427	8.829525	P	P	P	8.529342
			7.572984			A	
	5.708036			A			
5.029578	5.617352	3.338303	P	P	M		5.955453
7.273714	6.405038	5.699	7.011175	P	P	P	5.990662
6.285519			8.446225			P	5.384654
8.830732	8.541995	9.400625	9.296388	P	P	P	8.913308
5.819054	6.234883	2.756984	4.652527	A	P	P	5.670427
9.320114	8.951872	8.698598	8.223358	P	P	P	9.167337
4.951131	6.179583	7.889207	8.082891	P	A	P	7.266221
9.106715	9.730518	10.82356	11.91657	P	P	P	9.965956
6.171057	5.845258	5.328267	6.946138	P	P	P	6.798523
11.78808	12.15346	10.34474	10.64154	P	P	P	12.11114
7.033993	5.820695	5.411344	6.0797	P	P	P	5.819427
8.819682	8.0266	8.393003	8.935593	P	P	P	8.193531
8.504847	8.909745	8.448085	8.25001	P	P	P	6.742088
5.196777			A				4.10109
7.552463	6.869312	8.537015	8.678533	P	P	P	7.378785
9.315216	9.564548	7.533872	6.288757	P	P	P	9.489531
6.767465	3.95065	4.996471	M	P	P		6.320966
			6.357371			A	
		4.769455	6.774981		M	A	
9.241632	7.986881	7.63773	9.159261	P	P	P	6.564555
	3.437484	6.077908	6.508224	P	A	A	
5.174305	6.437014	3.277191	P	A	P		6.573019
7.729886	7.516238	7.0453	7.113632	P	P	P	7.412475
6.520712	7.971754	7.989497	7.969664	P	P	P	8.821244
6.750445	7.185221	6.156788	4.950351	P	P	P	6.951969
9.418424	8.790782	10.14737	10.09482	P	P	P	8.595561
9.702209	8.439627	9.681722	11.27635	P	P	P	9.873101
8.292488	8.360321	9.163885	9.734143	P	P	P	8.811132
		3.103675			M		
10.21395	10.89741	9.838138	9.409532	P	P	P	10.54907

3.377056			6.486097 M			A	5.915685
8.500969	8.207787	9.217963	10.77855 P	P	P	P	8.218477
8.03604	9.137463	8.804667	9.141789 P	P	P	P	9.102358
9.953942	10.2413	10.9486	10.22101 P	P	P	P	10.5075
6.873722	8.053238	7.156179	7.633317 P	P	P	P	8.375362
8.903656	9.350726	8.206858	7.54546 P	P	P	P	8.68507
9.683337	9.106023	10.40591	10.71796 P	P	P	P	10.01806
7.942772	8.035771	7.833613	7.531838 P	P	P	P	7.994566
7.312435	8.76107	8.68741	7.085317 P	P	P	P	8.021749
8.332494	7.734422	8.9565	8.845936 P	P	P	P	8.094198
9.110214	8.230791	9.87102	9.983904 P	P	P	P	8.440886
7.801774	8.501517	7.329365	7.017761 P	P	P	P	8.180098
5.106905			M				6.442411
7.23633	5.751413	7.799547	8.265823 A	A	A	A	5.742993
5.805249	7.354778	5.912921	7.241644 A	P	P	P	5.400817
5.915125			7.297815 A			A	5.717835
5.858662			2.452882 A			P	4.569918
8.440828	7.844817	9.420224	9.009205 P	P	P	P	7.497002
9.312013	8.511567	10.33196	10.0731 P	P	P	P	7.788807
7.729652	7.795545	8.174178	7.593877 P	P	P	P	7.68663
			4.479967			P	
10.42532	9.632992	11.57406	11.67312 P	P	P	P	9.543887
9.613399	11.2313	10.07847	8.937123 P	P	P	P	10.63471
	2.699507	5.820518	6.383247	M	A	A	
8.186183	7.395328	7.516813	8.003866 P	A	P	A	7.358634
6.639124	5.835658	6.715092	6.344339 P	P	M	P	6.084897
7.968026	6.500128	7.296816	7.346077 P	P	M	P	6.560167
4.104615			M				5.663698
6.380725	4.83585	5.620563	P	A	A		5.317296
6.588131	6.939675	5.656671	7.219244 P	P	P	P	4.676286
	2.281026			M			
7.025482	5.40269		P	P			7.285849
8.920461	7.562884	9.423386	8.737788 P	P	P	P	6.88408
8.631924	8.262389	7.575418	7.593394 P	P	P	P	7.491516
8.781131	9.276867	11.46583	11.3928 P	P	P	P	8.019136
9.821994	8.861564	11.22349	10.9491 P	P	P	P	8.456203
	3.915146	5.350524		P	A		
7.000822	6.632829	6.41612	5.936595 P	P	P	P	6.998163
8.728317	8.771494	7.971129	7.400123 P	P	P	P	7.997332
10.22315	10.15512	11.01355	10.96063 P	P	P	P	10.54869

11.62598	11.55262	12.35532	13.0489 P	P	P	P	11.92469
7.878732	7.917378	8.391982	9.096252 P	P	P	P	7.577472
11.91434	11.878	10.88747	10.23802 P	P	P	P	9.95223
7.135459		7.29159	8.405033 P		A	P	7.301763
12.2375	12.52653	11.28015	11.0986 P	P	P	P	12.50562
5.863174		6.802638	7.054831 P		P	A	7.487928
10.21605	9.128409	9.265262	9.304778 P	P	P	P	9.716118
8.238498	7.223306	8.035466	8.441387 P	P	M	P	8.374871
7.82869	8.372196	7.389769	7.644104 P	P	P	P	8.420526
5.856484	7.053001	7.034214	6.469587 M	P	A	P	7.032027
6.997122	6.909962	1.699244	A	A	P		4.14724
11.17929	11.63072	10.71772	11.12358 P	P	P	P	11.34681
9.22103	9.666023	8.57871	8.466845 P	P	P	P	9.124891
9.047252	8.008373	9.459909	9.060888 P	P	P	P	7.820204
		1.142561			P		
9.302004	8.770363	9.865872	9.560788 P	P	P	P	8.755219
7.54863	7.420829	7.924557	8.066957 A	P	A	P	6.420356
9.636601	10.48833	9.420932	9.171599 P	P	P	P	10.55191
10.20919	10.92053	9.920993	9.390911 P	P	P	P	10.64875
6.551312	6.981823	7.354137	P	P	P		7.930611
8.570548	8.569229	9.287	9.069974 P	P	P	P	8.964375
9.872992	10.33387	8.706732	9.221548 P	P	P	P	10.08948
6.992524	7.045343	7.078754	P	A	P		7.077496
7.64494	5.676019		6.862958 P	P		P	7.637168
10.10498	9.770375	9.195967	8.496971 P	P	P	P	9.3663
5.081451			5.764175 A			P	1.622786
7.022335	7.865595	5.693601	4.909275 P	P	P	P	7.715083
6.630824	7.37207	8.462411	7.866961 P	P	P	P	7.043138
	0.59375			M			
		3.874551	6.587845		P	M	
6.276337	8.130325	7.975612	P	P	P		7.520623
5.609183	1.207467		A	M			5.30974
8.85717	8.469085	7.926704	7.665411 P	P	P	P	8.706671
7.210902	7.694511	7.731939	6.391905 P	P	P	P	6.07707
10.57177	9.613783	9.408957	8.915535 P	P	P	P	10.37901
		5.33109	6.558969		M	P	
8.644208	7.619957	8.234548	7.514115 P	P	P	P	7.335529
5.442032		5.316883	5.529292 P		P	A	5.250045
7.752519	8.621326	8.378044	7.929085 P	P	P	P	7.852039
6.617987	6.691851	6.975924	A	P	P		5.617161

6.516401	5.987256		4.079792	A		M		6.088618
7.353481	8.221787	7.04056	7.379702	P		P	P	7.540762
8.669107	8.026177	8.781539	9.119774	P		P	P	8.391408
4.973079		5.263162	5.845537	A		P	A	4.049535
6.472642	1.067031	5.666996	4.878019	M	P	A	M	4.822107
7.014701	6.591976	6.705158	3.113385	P	P	P	P	5.702002
7.983094	7.328987	7.743138	7.987195	P	P	P	P	6.523015
5.879194		6.734619		P		A		6.667564
9.659122	9.635178	10.37226	10.89103	P	P	P	P	10.42981
9.674454	8.920011	8.699151	9.296992	P	P	P	P	8.560152
8.361535	8.076368	8.930349	9.90579	P	P	P	P	8.436781
10.42939	9.260927	10.35651	9.947981	P	P	P	P	8.483096
7.034422	8.112721	8.236783	7.780284	P	P	P	A	7.407242
8.657049	8.816441	9.646714	8.994709	P	P	P	P	9.150826
9.313254	8.723429	9.179937	10.28193	P	P	P	P	8.989479
9.422565	8.403286	9.594574	9.660396	P	P	P	P	8.359254
5.821372		4.026559		P		P		6.137304
9.316682	8.392072	9.86893	9.629739	P	P	P	P	8.216829
6.881598	6.506571	7.30879	7.625705	A	P	P	P	6.312747
	1.35971				P			
6.058581	4.522983			P	P			6.861472
9.377252	9.923177	9.361214	8.614778	P	P	P	P	9.61624
7.029961	7.907535	5.997916		P	P	P		7.240939
6.722409	6.749369	6.93367	8.440467	P	P	P	P	6.878881
			6.674761				M	
5.3337	5.578294	4.976574		A	P	P		4.285417
7.771595	7.792136	8.839632	7.432474	P	P	P	P	8.139396
8.417125	8.210126	8.021685	8.610884	P	P	P	P	8.229623
10.09228	8.410208	9.189816	8.346711	P	P	P	P	8.824938
6.644135	7.059614	5.338115		A	P	P		5.906133
9.226257	9.092965	10.01651	9.033411	P	P	P	P	8.648497
3.263424	5.149558		9.188095	P	P		P	6.531234
12.2586	12.36038	11.76888	11.39633	P	P	P	P	12.10987
		7.187773				A		
		7.885969	7.341598			A	A	
11.24458	11.28753	10.65621	10.33627	P	P	P	P	11.1576
10.96037	10.97187	10.48695	10.71805	P	P	P	P	11.45907
10.34787	10.93673	9.570933	8.934178	P	P	P	P	10.65437
7.195437	7.915625	7.766231	7.452554	P	P	P	P	7.351661
9.235971	10.61218	10.03762	10.36248	P	P	P	P	10.45163

	6.14789			A			
7.320309	6.943233	7.961396	8.193971 P	P	P	A	7.672698
6.859755			A				5.729488
10.18735	9.527329	10.19541	10.84903 P	P	P	P	9.848098
9.53225	9.881869	10.72104	10.24646 P	P	P	P	10.34631
10.61114	10.37954	9.571307	9.560657 P	P	P	P	10.38214
5.42372			3.526085 A			M	5.650984
5.527279	5.814507	7.162977	5.223562 P	P	P	M	5.895531
8.30286	7.773092	8.668989	9.933657 P	P	P	P	8.53122
5.742897	5.643242	6.747071	A	A	A		7.180212
9.693888	9.988011	8.427652	8.798503 P	P	P	P	10.14316
8.927462	9.034586	7.291337	8.337194 P	P	P	P	9.286225
6.943403	5.578949	6.994122	8.041282 P	P	P	P	6.802549
8.20093	9.892349	9.080041	7.328967 P	P	P	P	9.49064
6.88862	5.816013		A	P			5.24348
10.32018	11.18762	10.57036	9.674303 P	P	P	P	10.94584
10.33835	10.63628	9.967327	8.750978 P	P	P	P	10.1141
8.685673	8.52175	10.68585	10.35817 P	P	P	P	7.830965
7.597792	7.02629	7.424808	8.408915 P	P	P	P	7.448287
8.101797	7.564523	8.520342	8.197172 P	A	P	P	7.326549
9.638051	9.021035	8.504597	9.034878 P	P	P	P	9.070606
10.13334	10.25589	11.51222	11.97555 P	P	P	P	10.44092
8.655942	9.168824	10.42536	10.31389 P	P	P	P	9.719617
8.289371	8.513253	8.927163	9.561218 P	P	P	P	7.751729
8.910992	9.552398	8.779228	8.295109 P	P	P	P	9.147985
10.46223	10.39359	8.819521	9.789113 P	P	P	P	10.98354
6.555944	6.553113	6.968885	7.003784 P	P	P	P	6.775947
9.142475	9.224423	8.346851	8.004367 P	P	P	P	9.18374
8.400195	7.424265	7.172082	7.774544 P	P	P	P	8.044838
10.69466	9.172606	11.06744	11.44434 P	P	P	P	8.690261
7.430265	8.421266	8.210775	7.447375 P	P	P	P	7.854876
		7.280098	6.262533		M	A	
	6.777597	2.550707		A	P		
6.562054	6.304519	6.720258	6.480895 P	P	M	P	7.220608
8.166172	7.466133	9.039664	8.66956 P	P	P	A	7.743124
9.366865	8.950475	9.338636	9.795601 P	P	P	P	8.958532
6.385787	5.785218	7.423693	7.421672 P	P	P	M	6.647405
11.41036	11.59149	10.35101	10.14048 P	P	P	P	11.16593
		6.187566			A		
12.13125	12.21461	10.88862	11.23762 P	P	P	P	12.37968

6.537153	6.920673	6.648586	6.141509	P	P	P	6.404872
12.3802	12.84496	12.40906	12.98025	P	P	P	12.51198
10.94791	11.489	10.99434	11.16872	P	P	P	11.01414
9.469386	9.188097	8.812473	7.70615	A	P	P	9.168009
10.86124	11.1872	11.94342	12.92331	P	P	P	11.44164
		4.078183			M		
6.856243	7.160534	5.580654	5.428643	P	P	P	7.187392
10.29997	9.451167	9.005659	9.116679	P	P	P	9.879378
7.059263	6.604294	6.640408	6.409896	P	P	P	7.362954
6.580105	6.761554	6.719923	6.532514	P	P	P	6.135351
6.31606	5.346791	3.777139		P	P		5.318019
8.779059	8.19951	9.836969	9.853426	P	P	P	8.345472
5.974156	6.317309	6.712349	8.263157	A	M	A	7.470665
5.60819	5.377613		6.955173	P		M	6.077222
8.788657	8.627509	6.742799	8.038226	P	P	P	9.252406
6.521372	7.185916	8.54938	8.572017	P	P	P	6.757351
10.80064	10.47273	11.33856	11.52013	P	P	P	10.53542
5.562585	5.914459	3.535191		P	P		6.256742
6.687075	6.853637	6.434183		P	P		6.965477
8.140402	7.89004	6.879446	7.114516	P	P	P	7.690122
		5.884397	6.075672		P	P	
7.131903	7.73146	5.659275		P	P		7.217804
10.24822	10.35029	9.837036	9.210324	P	P	P	10.11514
4.434481	5.828623		6.467505	P		P	5.995448
6.476646	6.164619	5.719298	6.717336	P	P	P	6.460331
8.865145	8.430586	9.173399	9.190218	P	P	P	8.823617
8.926469	9.080431	8.539342	7.410571	P	P	P	8.918547
7.316295	5.999775	6.493582	6.619954	P	P	P	7.084901
9.892289	10.73258	11.31144	10.42205	P	P	P	11.18184
5.336163	6.743226	6.583621	6.845439	P	P	P	6.756104
6.662918	6.804839	6.761607	7.401216	P	P	M	7.192568
11.21804	11.31128	10.96685	10.43029	P	P	P	11.25943
11.26162	11.72018	11.65666	12.39223	P	P	P	11.52934
6.189514	6.627139	7.733579	8.051774	A	A	M	5.24358
9.183144	9.206357	10.17062	10.81759	P	P	P	9.176509
11.33266	11.24295	11.03942	10.28783	P	P	P	11.05013
7.661171	7.668512	8.600536	8.419544	P	P	P	8.543346
	6.137937	1.270045		P	P		
6.019399	6.638026	6.386447	6.664493	P	P	P	7.788411
		7.078879			A		

10.17847	10.67884	10.85701	11.16498	P	P	P	10.3887
6.241915	6.760149	5.874925	6.681999	P	P	P	6.791286
8.335919	7.890793	8.405103	8.782948	P	P	P	7.989873
8.339002	7.064529	7.340403	P	A	P		7.8758
			4.026521			P	
7.997521	8.335167	9.044659	7.733616	P	P	P	7.533562
11.22804	11.38541	12.09276	12.38926	P	P	P	11.11252
9.984289	10.13339	11.16228	10.85354	P	P	P	10.20526
9.798199	9.364912	10.36723	11.39663	P	P	P	10.08431
7.489158	7.177129	6.999819	7.413795	P	P	A	6.794419
	6.523737	3.925347		A	M		
7.662212	6.851702	4.742803	6.326037	P	P	P	7.52747
7.322385	7.827522	8.510212	A	P	P		7.189675
8.589031	9.767872	11.27332	10.89386	P	P	P	8.927607
8.808745	8.951728	8.122149	8.316651	P	P	P	8.893439
7.516736	7.831614	8.450514	8.020887	P	P	P	7.681157
10.28447	10.35349	9.608439	9.390222	P	P	P	10.04222
8.133418	6.301311	7.265717	7.747461	M	A	M	6.888294
	4.945639			A			
8.374996	9.333809	9.083313	8.035792	P	P	P	8.850987
7.412584	7.675624	7.460288	7.287089	P	A	A	7.627598
7.343641	7.097292	8.032082	6.797875	P	P	P	6.644616
6.041199	5.786127	5.290621	A	P	P		5.03949
9.064895	9.51822	8.690128	8.207772	P	P	P	9.626808
	0.877184	3.113165		M	P		
10.37084	9.866805	11.23002	11.2714	P	P	P	9.963944
5.589927	6.391991	6.120957	A	A	P		4.634108
6.238293	6.637413	5.367833	P	P	P		7.166425
2.720108		5.407671	P		P		5.993722
9.847715	9.67267	8.271079	9.192057	P	P	P	10.40288
	5.741963		5.295138	A		P	
8.138264	7.940608	9.311059	9.339663	P	P	P	8.322382
9.517102	10.26474	8.075332	8.083528	P	P	P	10.02749
6.483925	6.427563	5.854831	P	P	P		6.231145
7.550948	8.15936	7.433504	A	P	P		6.209108
5.772732	5.441289		P	P			7.021475
8.774324	8.943873	9.769736	10.24163	P	P	P	9.353677
	2.822268			P			
6.882045	6.39443	5.483242	P	P	P		6.276019
7.895006	6.857142	7.012755	6.763732	P	P	P	7.815292

10.66901	9.203172	9.556256	9.375296	P	P	P	9.614849
9.473672	8.11229	8.560675	8.359703	P	P	P	8.066963
10.12473	10.26354	10.95413	11.1571	P	P	P	10.09788
6.265185	5.943101	5.228223	P	A	P		6.352227
	5.632563	4.877085		A	P		
6.184365	4.759806	5.444109	P	P	P		6.238869
8.358674	8.599348	8.659935	9.37652	P	P	P	8.222852
12.47361	12.55947	12.00618	11.3694	P	P	P	12.20201
7.188731	7.253361	7.069952	5.987453	P	P	P	6.919318
8.96557	8.602898	9.998304	10.85362	P	P	P	8.388407
8.176936	8.603372	9.205524	8.270906	P	P	P	8.731227
8.281275	7.862032	6.833012	6.803698	P	P	P	7.564866
8.21119	8.09289	7.71999	6.913005	P	P	P	7.662966
7.717854		8.238165	8.769683		P	A	7.015328
8.781496	8.878929	9.765282	9.650182	P	P	P	9.080248
2.397584			P				5.563645
2.397584			P				5.563645
11.29678	11.25304	11.72314	12.43581	P	P	P	11.13633
	3.685363			P			
		6.525353				A	
		6.93973				A	
8.740441	7.885965	7.86557	7.698516	P	P	P	8.53918
5.782419		5.05138	A		P		6.297216
7.705714	6.445895	7.73979	6.84666	P	P	A	6.857138
		5.740527			A		
7.871563	7.227919	7.388695	6.417254	P	P	P	6.945701
5.422135			6.566318			A	7.100818
9.293109	9.727397	10.35137	10.64422	P	P	P	9.351937
9.675942	10.58121	9.176944	9.016877	P	P	P	10.44673
9.837684	10.02804	9.089581	8.588866	P	P	P	9.778362
	2.512212			M			
7.719324			8.48198			P	8.435085
12.46937	13.17346	11.91057	11.46119	P	P	P	13.09761
9.592794	10.45585	11.21156	10.83942	P	P	P	10.57114
10.38622	10.64672	11.37724	12.03252	P	P	P	10.64698
8.079677	8.325048	9.99636	9.029617	P	P	P	8.028194
8.02366	8.701642	7.933686	8.132827	P	P	P	8.505816
9.687655	8.81507	10.63776	9.764458	P	P	P	9.41953
6.110539	4.991026	5.438342	6.577844	P	P	P	5.85218
6.851608	5.597177	7.835091	7.906951	P	P	P	5.688872

10.73814	11.30642	10.61854	10.04596	P	P	P	11.19163
4.973753			P				6.140632
9.765859	9.722723	8.157533	7.636704	P	P	P	9.486605
	5.676624	5.968788		A	P		
7.718829	7.558395	6.723048	6.577792	P	P	P	6.885846
7.144846	6.400406	7.207898	7.594039	P	P	A	6.439267
7.553862	7.504627	6.670776	5.907027	P	P	P	7.6812
8.778781	8.222461	8.338306	8.699329	P	P	P	7.706881
7.884682	7.800287	8.16671	7.61521	P	P	P	7.43622
8.020376	7.678745	8.263523	7.918189	P	P	P	6.555779
9.165547	10.44122	8.748261	10.1973	P	P	P	11.07839
6.52894			A				5.373225
7.757469	7.829569	8.294405	8.825487	P	P	P	7.746543
12.73317	12.79659	12.0385	11.8495	P	P	P	12.67347
		5.434396			M		
10.79924	10.6359	10.19052	10.46364	P	P	P	11.05256
8.697233	8.489528	9.022167	9.76973	P	P	P	8.684325
5.083292		2.962969	4.446686		P	P	5.253296
8.450759	8.47408	7.656402	8.450627	P	P	P	8.460329
10.15387	8.737577	9.71944	9.50489	P	P	P	8.766682
6.558455	8.306327	6.647049	7.797319	P	P	P	7.891185
6.328029	6.850217	5.078376	5.66834	P	P	P	7.448999
5.93074		6.839316	6.481412		A	P	6.344593
7.156815	5.942704	7.072643	7.589676	P	P	A	6.40348
7.364666	6.529233	7.88035	7.959087	M	A	P	7.681374
7.51758	7.743258	6.417905	7.469445	P	P	P	7.890837
7.039724	8.232574	6.2065	8.078081	P	P	P	8.477924
7.497892	7.403726	7.516631	7.440907	P	P	P	7.757482
8.128252	7.894015	9.507126	10.36328	P	P	P	8.029792
5.59245			6.048287			P	6.328997
	5.210655			A			
9.664948	8.846456	8.546643	9.891405	P	P	P	9.781082
9.201411	9.142032	7.782793	7.190469	P	P	P	9.511507
2.993824		1.711567	P		P		6.395536
7.080517	7.29654	8.237502	7.830483	P	P	M	6.77396
7.749782	8.162332	6.718575	7.252554	P	P	P	6.901218
10.67356	11.15893	10.30159	9.223445	P	P	P	10.56583
	6.958431	3.947574		A	P		
6.929182	5.973583	6.41959	6.144353	P	P	P	6.66906
9.168567	9.537348	8.794794	7.191592	P	P	P	9.203894

7.843266	7.508465	8.358237	8.578261	A	A	P	A	7.110541
8.296838	8.312015		M	A				8.798236
7.366424	6.600435	6.486871	6.529146	P	A	P	A	7.513812
9.879296	10.1571	8.965301	8.708525	P	P	P	P	10.58552
5.778721	6.30297	5.339976	P	A	P			5.791861
6.974024	6.455873	7.571841	7.350373	P	P	M	M	6.90149
			6.111183				A	
11.21257	10.74997	10.51964	10.28002	P	P	P	P	10.49282
8.830683	8.870037	7.872848	7.990957	P	P	P	P	8.701402
10.29426	10.03034	9.863049	9.595957	P	P	P	P	10.15698
7.494918	7.162895	8.301898	P	P	P			6.898713
8.859631	8.578371	9.306197	9.705271	P	P	P	P	8.249976
9.178556	8.953095	8.395622	7.197732	P	P	P	P	8.949522
9.295827	8.330573	9.047251	8.977086	P	P	P	P	7.76286
6.675615		6.657814	6.820013	A		A	A	5.191551
6.40079	6.561801	6.242273	A	A	A			6.780842
6.346019	6.20256	8.601203	7.191284	P	P	P	M	6.66225
7.489457	7.847462	6.88195	6.57888	P	P	P	P	7.358587
5.446574	6.142329	5.481808	3.642271	M	P	A	P	6.032829
	1.159115	5.174575	5.159934	M	P	P	A	
6.680152	5.835842	5.584426	6.459265	A	M	P	A	5.474328
5.67185	7.529243	P		P				8.450165
8.874438	7.183747	7.645328	7.236603	P	P	P	P	7.42464
10.65019	9.802003	9.745132	9.810354	P	P	P	P	10.1519
7.185158	5.787523	7.814434	7.427737	P	P	P	P	7.358369
7.892931	7.416117	7.55591	6.367113	P	P	P	P	7.37754
7.351857	7.687189	7.85299	7.36977	P	P	P	P	7.166092
5.997444	5.866153	P		A				5.34525
13.92466	13.81618	11.14234	12.46474	P	P	P	P	14.41214
			1.115089				P	
7.570177	8.146398	5.859974	6.198877	P	P	P	P	7.594779
11.32069	11.01478	9.98432	9.789488	P	P	P	P	11.4768
10.09403	10.53996	11.00853	11.71068	P	P	P	P	10.74777
11.25587	10.65405	9.930192	9.574183	P	P	P	P	10.52905
6.983589		7.23852	7.8436	P	P	P	P	6.783724
10.61556	10.062	9.676102	9.425219	P	P	P	P	10.126
5.039048	4.796355	6.898775	5.681379	A	M	P	P	5.319209
7.785187	6.854737	7.547772	8.08248	P	P	P	P	8.440537
	5.143532			A				
6.297714	5.637373		2.403316	A			M	5.695628

7.415117	6.034961	6.900406	7.663605	A	P	P	P	6.205552
6.751055	7.524672	6.442299	7.774289	P	P	P	P	7.726186
8.677175	9.286594	9.526412	9.515751	P	P	P	P	9.312145
7.896494	8.21687	8.507708	8.589787	P	P	P	P	7.827093
9.867099	9.663028	10.55616	11.25051	P	P	P	P	9.917063
8.244885	8.537034	8.267343	6.658608	P	P	P	P	8.166614
7.478155	6.488703	7.73966	9.194675	P	P	P	P	7.456632
7.174216	6.337353	6.930062	7.238009	A	P	P	P	6.125386
8.036673	7.027182	7.912059	9.357238	P	P	P	P	7.422951
10.1421	9.000515	8.529554	8.346242	P	P	P	P	9.836466
	0.59728			P				
8.190586	8.252216	7.786695	7.654598	P	P	P	P	7.76193
6.728798	7.588477	6.679819	5.854795	P	P	P	P	7.619516
7.131348	7.291629	6.790535		P	M			6.945367
			4.259295				P	
8.523397	8.766134	8.908614	9.551559	P	P	P	P	8.732101
11.87526	12.12198	11.48159	10.49546	P	P	P	P	11.52253
7.620125	7.51711	8.050398	8.318714	P	P	P	P	8.369012
7.945916	8.473589	8.406337	6.553457	P	P	P	P	8.294302
			4.277696				P	
		7.391617			M			
7.897069	7.328155	7.473949	7.692389	P	P	P	P	6.982902
8.728659	7.776884	7.480108	6.84142	P	P	P	P	7.809029
6.069925	5.78694	5.685428	4.684586	A	P	P	P	5.719215
6.994913	6.470935		7.377559	A	M		P	5.920741
9.597272	9.272762	10.44308	10.99979	P	P	P	P	9.370871
8.17698	7.512816	8.597462	8.960058	A	A	P	P	7.67668
13.44846	13.56803	11.99875	12.71111	P	P	P	P	13.89552
8.411774	8.031774	9.066674	8.718247	P	P	P	P	7.854899
12.79113	11.98366	13.31946	12.88664	P	P	P	P	11.47161
7.736475	7.757576	9.01228	9.942349	P	P	P	P	9.199028
	5.342318			A				
8.621364	8.172419	7.190249	6.804716	P	P	P	P	9.006086
7.510332	7.386075	5.92881	7.537509	P	P	P	P	8.506954
10.55899	10.23995	8.627846	8.539931	P	P	P	P	9.937154
9.49929	8.676522	7.679202	8.196336	P	P	P	P	8.359245
8.783087	8.307532	8.496453	10.17878	P	P	P	P	7.837298
7.38125	7.477582	6.524998	7.614978	P	P	P	P	8.463337
		6.341198			A			
8.23208	8.295112	9.127536	9.376784	P	P	P	P	8.245317

10.90277	11.06343	9.733191	9.710329	P	P	P	11.30481
7.664404	6.583292	7.584673	7.775506	P	P	P	6.347659
10.82027	10.73902	11.44165	12.53659	P	P	P	10.69015
7.603235		7.031666	8.345774		P	A	6.659874
9.961553	9.388309	10.57723	10.02022	P	P	P	9.669024
10.3877	9.625464	10.37022	10.26102	P	P	P	9.381402
10.60278	11.46555	10.48421	9.811269	P	P	P	11.42562
6.864961	6.627868	5.662156	5.464143	P	P	P	6.642687
10.08411	10.00164	9.422972	8.801104	P	P	P	10.08043
5.535613	6.059209	6.261645	P	A	A		5.8883
8.561949	8.351303	8.902793	8.711073	P	P	P	8.293194
8.295423	8.49718	9.390552	9.422863	P	P	P	10.10039
9.942562	10.0434	8.869651	10.12301	P	P	P	9.6536
7.535554	7.957013	6.618	6.045068	P	P	P	7.778885
8.55693	8.061821	8.557863	9.201478	P	P	P	8.676592
8.15308	8.632921	7.722318	8.565594	P	P	P	8.560882
8.985892	9.081812	10.13205	9.891904	P	P	P	8.930097
6.6423	7.313541	6.684574	7.469984	P	P	P	6.129387
9.590673	9.050453	9.936826	10.20937	P	P	P	8.04123
		5.675241	5.929092		P	P	
7.997489	7.810813	7.079221	6.129849	P	P	P	8.270064
8.624127	8.727124	10.0993	10.72915	P	P	P	8.912704
9.432525	9.355021	10.27275	10.34566	P	P	P	9.072541
			6.611852			A	
	6.097977		6.645708	A		A	
			6.306155			A	
7.503488	6.787983	7.830486	7.983779	P	P	P	7.636385
7.841517	8.449012	7.526535	6.90479	P	P	P	7.462588
7.674292	7.789242	8.549849	9.284478	P	P	P	7.325759
7.165807		9.020039	8.428269		A	A	7.885614
13.12081	11.46373	13.63561	14.28667	P	P	P	10.52833
9.025666	8.211937	10.00765	9.918318	P	P	P	8.72682
			8.430234			A	
	3.314903			P			
7.470313	7.12498	7.054461	6.692341	P	P	P	7.287547
8.270086	7.981624	7.285048	6.745995	P	P	P	8.03915
6.807646	7.006607	7.069193	7.946132	A	P	A	7.271704
10.52321	10.24707	11.28211	11.16269	P	P	P	10.13153
6.293685		6.743668	A		P		5.004176
	6.541567	5.597979		M	P		

6.461769	7.039794	6.644945	7.440254	P	P	P	6.109004
7.179567	5.679792	6.333592	6.650687	P	P	P	6.634258
9.416312	8.895072	9.215816	9.764737	P	P	P	9.044024
	6.368375	6.536061		M	P		
8.668227	8.480499	9.098598	8.415099	P	P	P	7.876191
5.959165	7.085555	6.620028	A	P	A		4.481537
5.342684			A				3.412587
10.41934	9.362397	10.26336	10.14199	P	P	P	9.34029
9.270306	8.686696	8.418321	7.013603	P	P	P	8.223738
9.307862	8.773952	9.259074	9.238504	P	P	P	9.207249
10.51174	10.00067	9.301648	9.968921	P	P	P	9.855928
		3.203446			P		
			3.906163			P	
7.134449	7.437162	8.560764	8.432836	P	P	A	6.315671
10.05227	9.702852	8.787447	8.008145	P	P	P	9.632134
9.108763	9.011574	9.610834	9.363699	P	P	P	8.781466
8.020237	7.510314	9.025805	7.880117	A	A	P	7.991768
8.206307	7.631327	9.522256	9.300068	P	P	P	7.943509
9.416837	9.277255	8.798359	8.213305	P	P	P	9.06043
	5.485292	5.696586	6.355386	P	P	P	
10.77697	11.48284	9.864147	10.70598	P	P	P	12.19981
9.954654	9.57006	9.199954	8.309993	P	P	P	9.871
12.55729	12.82624	13.12993	14.14928	P	P	P	13.16047
10.44192	10.20412	10.79213	10.18717	P	P	P	9.543549
6.48158	7.465409	6.268477	8.066978	M	P	P	7.074074
7.278909	6.501186	7.516194	8.772032	P	M	P	8.044706
5.61729	6.779179	6.507238	P	P	P		6.050255
6.795954	6.32514	7.154868	8.237555	P	A	A	6.480076
10.76872	10.78082	9.604264	9.569938	P	P	P	10.72149
11.12692	10.87782	10.32031	9.872557	P	P	P	11.39568
8.359942	8.368293	9.911861	9.715398	P	P	P	8.463409
6.177295		6.575879	7.007633		P	A	5.395027
7.175545	6.597209	6.87604	6.683582	P	P	M	5.523325
7.143701	7.653481	6.775763	6.993122	P	P	P	6.096923
9.74677	8.08626	10.34533	9.913333	P	P	P	7.78789
4.878707	4.877493	5.819958	4.981682	A	P	P	1.328616
10.15867	10.42445	9.914742	9.147741	P	P	P	10.07864
8.756067	7.858578	8.819944	9.018384	P	P	P	8.753518
7.91918	7.61275	9.127579	7.990599	P	P	P	7.212935
9.200505	9.347474	8.25577	8.498947	P	P	P	8.150263

5.18909	7.30297	7.287954	P	P	P		6.551914
10.38378	10.37214	11.12132	10.89421 P	P	P	P	10.08319
8.862487	8.377887	7.131014	6.95688 P	P	P	P	8.072941
5.863174	6.430842	4.884632	A	P	P		5.110523
	6.748588		6.137581	A		P	
6.482169	6.000013	6.140191	6.837679 P	P	P	A	6.267564
5.303323		6.93681	P		A		6.8035
		6.978841			A		
8.450208	7.800365	7.907608	7.603059 P	P	P	P	8.734529
6.545521	5.015319	7.439499	7.978933 P	P	P	M	6.856481
11.4736	9.622763	12.99759	13.14534 P	P	P	P	10.56053
12.13391	11.7426	12.63958	12.72498 P	P	P	P	11.79138
5.893291	5.543881	6.057696	P	P	A		6.119388
	5.626555			A			
12.53684	11.51417	13.84308	13.86484 P	P	P	P	11.69175
7.886099	7.804215	7.903876	9.172426 P	P	P	P	7.884626
7.134705	6.465394	7.485719	6.633137 P	P	P	P	6.63733
	6.321722		5.777472	A		P	
8.622902	8.767738	9.45439	10.18871 P	P	P	P	8.697914
7.654578	8.010023	7.109576	7.553373 M	P	P	P	6.851567
7.857621	8.567643	8.318517	8.153167 P	P	P	P	9.144463
8.332999	8.622447	9.367867	9.692424 P	P	P	P	9.143548
1.538853	4.672904		P	P			5.110081
4.481123	5.471584		P	P			6.331172
7.325913	6.866762	6.996112	A	M	P		7.2854
4.271589	5.95748		M	P			6.180886
		9.79115				A	
5.712415	5.796804	6.209797	A	P	P		5.15563
10.73566	7.885145	11.85406	12.88783 P	P	P	P	8.357907
11.23622	10.62178	10.45681	11.06357 P	P	P	P	10.89363
8.021687	8.462216	8.033616	7.590123 P	P	P	P	8.010718
	4.924745	3.200086		P	P		
7.461963	6.577962	7.763663	8.505414 P	M	P	P	8.044572
		6.610405	7.086035		M	A	
10.24021	10.08181	10.9535	11.28853 P	P	P	P	10.14835
	5.729815			A			
6.398449	6.142793	6.378481	7.169382 P	P	A	P	6.426474
		1.865063	6.885155		M	A	
6.647037	5.628358	6.79453	A	P	A		6.257468
6.447878	6.132288		A	A			5.727063

		4.046625			P		
4.506592	4.770907		7.436051 P	P		P	5.871411
			6.767195			A	
7.275435	6.113899	8.355689	8.812593 P	P	P	P	9.076408
5.162138	5.038777		6.571743 A	P		A	6.207047
			2.595488			M	
9.38184	9.24615	9.591276	9.863566 P	P	P	P	9.499854
6.301622	6.377987	6.742495	6.652017 P	P	P	P	6.805685
8.420012	7.765198	9.21949	8.25483 P	P	P	P	8.223791
9.519559	9.395605	8.792555	8.384859 P	P	P	P	9.790401
8.267861	8.346574	7.550932	9.387808 P	P	P	P	8.682734
5.133658		5.799232	4.49593 M		A	M	5.469122
		6.771675			A		
12.18005	12.21967	11.39406	10.65043 P	P	P	P	11.86219
8.415374	8.385226	7.704614	7.749392 P	P	P	P	7.855209
5.789934	5.849722	6.777937	7.829706 P	P	P	A	7.330984
7.035768	7.395576	8.691944	8.304378 P	P	P	P	8.777613
6.627246	5.738603	6.405737	7.756597 A	A	P	P	6.889478
		6.409565			A		
8.940533	9.935191	8.601665	8.276467 P	P	P	P	9.528745
11.49925	10.40007	10.92959	9.918645 P	P	P	P	9.807349
		4.505244			P		
7.648592	8.242678	6.96433	4.525071 P	P	P	P	7.491643
5.615936			6.900399 A			A	3.719434
5.939812	5.453758	7.098844	5.97026 A	A	P	P	6.475416
6.196949		6.870289	A		A		6.214257
6.381312			A				3.76012
	6.904299		7.90691	A		A	
7.767657	7.009668	7.342022	A	P	M		7.296306
5.184117	5.320884	5.483513	6.135731 P	A	P	P	5.767296
7.411352	6.046921	8.410072	7.930193 A	P	A	A	6.798926
5.320863			6.58624 A			A	5.235628
			6.01174			M	
7.899288	7.590881	8.517968	8.838697 P	P	P	A	7.73466
9.694706	8.640718	10.04078	10.16923 P	P	P	P	8.906375
8.42219	9.811313	9.586479	9.68951 P	P	P	P	9.676586
4.836542		6.289159	A		A		4.301296
	5.864404	7.259947		P	A		
	4.670628			A			
6.839357	4.170275	6.631331	6.149556 P	P	P	P	7.171057

5.495146		6.240867	6.407797 A		P	P	3.449108
	8.670166		7.825978	P		P	
9.336505	8.872589	8.31336	8.193691 P	P	P	P	9.511998
5.830278	4.639022	4.017846	5.256591 P	P	P	M	6.395938
10.39971	11.00983	9.851515	10.0885 P	P	P	P	10.88915
	5.001926			A			
5.694796			7.276781 P			P	5.406096
12.16291	12.53627	11.02144	11.6611 P	P	P	P	13.02432
13.17314	12.86934	13.36707	14.88247 P	P	P	P	13.75348
7.911765	7.422412	7.572662	7.197945 P	P	P	P	8.1875
10.01191	8.100019	8.254776	8.158717 P	P	P	P	8.44104
6.465441			6.552071 A			M	5.296823
9.400358	8.356627	9.178479	9.251212 P	P	P	P	8.177736
6.153494	5.453228		A	M			3.679702
9.903981	9.007316	10.63769	9.918663 P	P	P	P	8.72107
5.625572	4.689588		5.787693 P	P		P	6.424517
6.422546	6.571432	5.821301	7.021446 P	P	P	P	6.268101
8.447392	7.834119	8.446475	8.218699 P	P	P	P	7.386992
8.261425	8.442455	7.734204	7.387938 P	P	P	P	8.541575
6.917625	6.993346	5.554376	6.223309 M	P	P	A	5.792301
			3.645457			P	
7.919143	7.536616	8.551348	9.067685 P	P	A	P	8.282099
10.55134	10.47434	11.62939	11.82626 P	P	P	P	10.91843
4.650441			6.932035 P			M	5.837523
		5.452	6.132424		A	A	
4.508447	4.745326	5.056941	P	P	P		5.099388
7.572363	8.293615	7.330989	7.63667 P	P	P	P	7.437326
9.510028	9.018109	8.260316	7.666091 P	P	P	P	9.223265
5.563319			A				4.551669
8.91807	8.457339	8.422973	7.89983 P	P	P	P	8.134952
8.436136	8.682852	8.824612	8.435607 P	P	P	P	8.220616
	6.25417	5.883596		P	P		
	5.687244		7.75618	M		A	
10.24902	9.855196	9.469278	9.346142 P	P	P	P	9.239401
7.202741	7.965251	4.691031	4.037224 P	P	P	P	7.414629
6.460213	6.556069	7.511208	7.120545 P	P	P	P	6.689648
	6.632553		7.458122	P		A	
			2.795264			P	
5.971767	5.5883		A	A			4.880454
2.464275			P				6.171084

	6.798854			A			
6.123521		5.932509	A		P		4.949897
	6.013292			A			
	3.140983			M			
			7.251032			A	
4.601379		5.747814	P		P		5.891196
9.476879	10.13664	8.870139	8.016568 P	P	P	P	9.375067
		5.369545			A		
7.79599	6.774172	8.313059	8.509563 P	P	P	P	8.00346
	6.676733			A			
7.611862	6.797597	5.755651	6.656489 A	P	P	P	4.721762
6.640108	7.019827	5.919436	6.33171 P	P	P	P	6.346196
7.398607	6.594202	6.973475	3.725941 P	P	P	P	7.03953
9.760389	9.885973	9.392636	8.662164 P	P	P	P	10.09901
7.846317	7.85409	8.585849	8.389851 M	P	A	P	8.166794
9.615934	9.392288	9.936227	11.06826 P	P	P	P	9.946093
			6.959546			A	
7.112263	6.530445	6.597064	7.330433 A	P	P	P	6.503163
7.349039	6.700314	7.132297	6.730583 P	P	P	P	6.335817
6.023877	6.742839	5.335678	6.215303 P	P	P	P	5.811284
	5.236632			A			
9.029537	8.728809	9.792689	9.057559 P	P	P	P	8.46046
		6.8359	3.108594		P	M	
6.664949	6.842649	6.485465	4.411047 P	P	P	P	6.220972
6.200685		5.848281	A		P		6.284221
7.854625	7.291251	8.992935	8.006169 P	P	P	P	6.432444
0.706387			P				5.106386
0.843783	5.292211		P	A			5.836345
7.841997	7.388207	6.636967	6.18369 P	P	P	P	7.202283
6.70345	5.306861	6.354958	6.192783 A	P	P	P	5.211603
9.585595	9.549686	10.13375	10.36121 P	P	P	P	9.740285
9.461623	9.808733	10.66654	10.86241 P	P	P	P	9.917001
	4.411634	4.243219		P	P		
5.793177	5.077372	5.108475	P	P	P		4.870319
	6.047112	5.461042		A	A		
7.133229	6.013986	7.804874	7.941126 P	P	P	A	7.581558
		6.473007			A		
6.776156	7.136894	7.493483	7.245543 P	P	P	P	7.85927
5.58456			P				6.746651
5.603334	5.697962		A	P			2.855138

			0.789794			P	
8.276857	8.50996	6.976972	6.37227 P	P	P	P	7.738538
7.336333	6.95646	7.967358	7.128278 P	A	P	P	6.459954
11.65672	11.32934	12.01346	10.86482 P	P	P	P	11.73681
8.294422	6.814115	6.584814	7.186482 P	P	P	P	8.443007
			6.681667			A	
6.195625	5.746071	3.612431	A	P	P		2.909117
	4.588473		2.984918	M		P	
7.195657	7.446679	6.881333	6.475665 P	P	P	P	7.136348
11.15779	10.68808	9.55184	9.315225 P	P	P	P	10.37432
4.424379	5.526741	5.595044	4.978666 P	P	P	P	5.729401
9.015821	8.754318	7.860175	7.732516 P	P	P	P	9.067462
7.008287	6.448291	5.516421	6.598819 P	P	P	M	6.367252
	6.357967		5.556402	P		P	
6.182849	5.538989		A	P			3.887596
10.04952	10.33883	9.693961	8.540963 P	P	P	P	10.217
10.43661	10.52766	9.645368	9.175632 P	P	P	P	9.827598
7.191608	7.96289	7.332309	3.63254 P	P	P	P	7.720788
3.011156			P				6.245928
	6.027628	5.650091		P	A		
12.48994	12.3057	11.98572	11.43065 P	P	P	P	12.16359
9.171095	8.719006	9.798484	10.24238 P	P	P	P	9.525815
8.422285	8.709685	8.178281	7.528044 P	P	P	P	8.636051
9.557851	8.748524	9.504396	9.126778 P	P	P	P	8.538255
6.101026	6.483866	6.092931	5.309302 P	P	P	P	5.850773
6.40233	6.699948	6.739069	7.103727 P	P	P	M	6.761206
7.770804	7.891881	6.217196	6.854411 P	P	P	P	7.456305
		2.239048			P		
6.814743	6.200938		6.020954 A	A		P	5.58211
6.422943	5.288216	6.273224	A	M	P		4.577247
7.57525	7.858206	7.50354	6.302399 P	P	P	P	7.631892
9.036638	9.746462	9.494371	8.899904 P	P	P	P	9.546414
12.15436	12.52116	11.69473	11.43354 P	P	P	P	12.34216
7.543549	8.300723	9.274475	9.165092 P	P	P	A	7.219393
9.318177	9.388127	9.810226	8.65132 P	P	P	P	8.922133
0.344839		5.331335	2.100278 P		P	P	6.467106
4.565839	4.829703	6.325392	M	A	A		6.091045
7.266331	6.480189	7.130177	7.700778 P	P	P	P	7.077518
7.656892	8.124627	8.247639	8.388383 P	P	P	P	7.432279
		7.158512			A		

8.816929	8.478102	9.698216	9.738	P	P	P	8.433575
12.64242	12.78191	11.52272	11.48041	P	P	P	12.92399
9.356259	9.28581	8.703244	7.240465	P	P	P	9.216883
8.237056	9.37386	9.053207	7.153808	P	P	P	8.073648
12.05635	11.946	11.54151	11.01174	P	P	P	12.19514
9.304999	9.33138	10.15057	10.28423	P	P	P	8.703123
5.69368			4.081749			M	5.650649
10.96131	10.38928	11.77484	12.03852	P	P	P	10.12856
11.10049	10.88219	10.01009	9.501296	P	P	P	10.71531
9.17362	8.970646	9.473918	8.851046	P	P	P	8.853909
5.503316			A				2.876214
			7.1472			A	
5.8626	6.120047	6.5152	6.102689	A	P	P	6.307462
9.13108	9.02935	10.9172	10.96732	P	P	P	9.190622
13.84222	14.21209	13.42131	12.76992	P	P	P	14.19305
7.304903	7.139272	6.586402	A	P	P		7.22871
	4.278166	5.937707		P	A		
9.264226	9.75102	10.35018	10.1297	P	P	P	9.488923
7.382754	7.190185	6.500726	6.208083	P	P	P	7.089505
	3.225896			P			
11.55256	11.04575	11.86185	12.3518	P	P	P	11.16461
6.911445	6.60433	7.150555	6.879486	P	A	P	6.929777
		7.8058			A		
8.074462		7.080949	A		P		6.755153
11.62161	11.42003	10.79912	10.80271	P	P	P	11.01875
9.30876	8.976118	8.772841	8.68783	P	P	P	9.319034
8.387524	8.494221	7.67686	7.500164	P	P	P	8.584781
9.390542	8.917178	8.132386	7.851721	P	P	P	8.698761
6.688082	7.42392	5.936665	5.976173	P	P	P	7.337382
9.386135	8.344528	8.901412	9.145902	P	P	P	8.305923
10.75058	9.526753	10.26421	9.316285	P	P	P	9.223499
8.536917	7.604118	8.158621	7.544895	P	P	P	8.702137
6.753722	6.36359	6.745418	4.105214	A	P	P	6.647064
9.230427	9.609077	10.04411	11.71033	P	P	P	10.39732
5.190854	6.081651	6.214079	P	M	A		6.830638
10.98523	8.889336	12.23872	11.7596	P	P	P	8.492681
		2.935905			M		
8.820531	7.814405	7.133613	7.817579	P	P	P	8.530455
6.544739		6.332213	P		P		5.171784
7.563731	6.908113	7.858582	7.131892	P	P	P	5.884646

8.622107	8.625644	7.366205	5.866308	P	P	P	8.077145
5.657073	0.062429	1.048707	6.421429	P	P	P	5.87106
9.613988	9.820425	8.846838	8.068011	P	P	P	9.422885
12.24944	12.64058	11.58815	11.43668	P	P	P	12.58392
		5.143171			M		
6.510405	7.091079	7.09302	6.883248	A	P	M	3.744278
5.736445	6.421923	6.196668	5.24249	A	A	M	6.193121
	5.806459			P			
7.693633	7.670276	8.671958	8.527575	P	P	P	7.772745
12.11336	11.45013	12.90169	12.69809	P	P	P	11.55095
10.19215	9.831405	10.33467	10.53895	P	P	P	9.862337
9.087256	8.384207	9.60638	9.72242	M	M	P	8.430425
7.299068	7.520691	6.616406	6.041478	P	P	P	6.906225
8.736154	9.088864	8.128248	8.515109	P	P	P	9.348325
10.49572	11.66314	10.83267	9.889497	P	P	P	10.29683
5.117234	4.810786	3.247498	7.166796	P	P	A	5.501198
6.278181	7.040268	5.620902	5.974572	P	P	P	6.907293
8.486409	7.33621	9.352323	9.268425	P	P	P	7.390732
8.878994	8.354705	7.526385	7.08628	P	P	P	8.035567
7.046268	6.808995	5.122205	3.940802	P	P	P	7.093213
7.524002	7.628718	7.789537	7.550988	P	P	P	7.109773
8.232636	8.390009	7.954537	6.747297	P	P	P	8.087181
		6.210664	3.817936		P	P	
6.904029	7.081052	8.627751	7.754617	M	P	P	6.858336
8.300799	6.839218	7.729566	8.671825	P	P	P	7.037876
7.834615	7.783504	6.673648	7.880296	P	P	P	7.730599
8.116107	6.747825	5.332208	6.172121	P	P	P	5.145216
8.174051	8.183741	7.7615	7.273005	P	P	P	7.954009
11.49069	11.06619	11.61698	11.17585	P	P	P	10.46901
10.2976	9.516995	9.804576	10.81359	P	P	P	8.391036
7.228399	7.837491	6.154816	6.393863	P	P	P	7.077817
8.843374	8.276321	9.877244	9.260672	P	P	P	8.471471
6.968983	7.484144	7.107785	8.502869	M	P	P	8.121149
9.034618	9.022247	8.071956	7.952307	P	P	P	8.897077
6.418488	8.51085	3.233211	4.346761	P	P	P	7.50681
11.00752	11.08959	10.53881	9.546826	P	P	P	10.90808
		5.238175				M	
11.52371	11.66662	11.2125	10.58249	P	P	P	11.51084
7.598008	7.753438	6.938052	6.426436	P	P	M	7.200509
5.21406	4.588656		6.655618	M		P	4.789914

	5.551699	6.565776	5.556164	P	P	P	
7.044312	5.322752	6.582272	7.453761 P	P	A	P	6.524096
10.77364	10.78887	9.924688	9.864787 P	P	P	P	10.82416
13.64667	14.05064	13.06799	12.38187 P	P	P	P	13.86208
	5.56298	1.156111		A	P		
11.55081	12.293	11.42268	11.76806 P	P	P	P	12.50074
	5.091164			P			
6.953349	7.048197	7.038072	P	A	P		7.1318
9.363145	8.873607	8.254705	8.946159 P	P	P	P	8.32828
	6.272815	5.485419		P	P		
7.256207	5.817608	6.47998	6.918552 P	P	P	P	5.826437
7.345845	8.604585	7.796466	7.501929 P	P	P	P	7.818111
6.059507			5.649723 A			P	3.403753
7.27335	6.188051	6.628601	7.320282 A	P	P	A	6.538691
7.250902	6.532396	8.045852	8.249164 P	P	P	P	6.998648
7.4848	6.668388	8.363228	8.377489 P	P	P	P	6.372687
	5.967802	6.169637		P	A		
6.63892	7.624964	7.777444	7.886976 P	P	P	P	7.772521
	6.451079	3.506951		A	P		
6.97831	7.928034	6.672229	6.938639 P	P	P	P	6.85902
	5.091476		6.71678	A		A	
8.779937	8.351264	9.370849	9.611438 A	A	A	A	8.699714
8.951821	8.530178	7.770418	7.96427 P	P	P	P	8.796924
6.184133	5.729307	4.19403	5.332149 P	P	P	P	6.807295
8.549597	7.022159	8.16882	8.09761 P	P	P	P	8.086581
5.761094	5.882394	8.069969	7.292163 A	P	P	M	5.575129
	5.204717			A			
12.29379	12.80539	11.1194	10.72119 P	P	P	P	12.76461
7.222316	8.160075	7.020441	6.161135 P	P	P	P	7.964045
	6.223685			A			
9.762412	8.65376	8.732389	8.705602 P	P	P	P	8.192568
	5.94354			M			
12.89263	13.05476	12.28332	12.17803 P	P	P	P	13.49749
7.758499	7.204067	6.369926	A	P	P		7.327783
11.40016	11.23861	10.66036	10.36593 P	P	P	P	11.10507
8.62066	8.142527	9.750282	9.253884 P	P	P	P	7.990555
			7.019892			A	
6.347315	4.957642	5.931943	A	P	A		6.50398
8.848777	9.145901	8.04645	5.342483 P	P	P	P	8.170148
5.964276	5.246984	7.688293	8.452553 P	P	P	P	6.96581

7.451847	7.506459	5.966744	7.083751	P	P	P	7.468264
		7.413107			A		
8.417349	7.585015	8.852887	9.458536	A	P	M	7.907753
		7.085129	7.08328		A	M	
9.638142	9.318477	9.769465	8.874169	P	P	P	8.697082
9.590361	9.043144	10.14471	10.15104	P	P	P	8.67196
7.273054	6.864873	8.864687	8.580791	A	A	A	5.901448
9.156948	8.791711	7.955402	7.24757	P	P	P	8.144494
	4.74395	4.777851	6.094303	P	M	P	
9.092741	8.867346	10.72308	11.83172	P	P	P	10.05016
		5.761819	6.252342		M	P	
8.214297	7.554721	8.056453	8.108669	A	P	P	6.839331
9.503206	8.874476	8.04957	8.547753	P	P	P	9.59555
8.485696	7.844417	8.196227	8.161686	P	P	P	7.458348
10.53959	10.19735	9.935767	9.207717	P	P	P	10.00119
9.105834	9.543515	9.455806	7.644549	P	P	P	9.713735
		6.860206			P		
	5.474599		3.963913	P		P	
10.2168	9.621515	10.07844	9.404184	P	P	P	9.136371
4.868782	4.488644		A	M			3.152376
9.99654	9.041196	8.833877	10.2276	P	P	P	8.605565
7.771529	7.466737	8.455421	8.587034	P	P	P	7.504085
8.266203	8.222699	9.579347	9.046031	P	P	P	8.672675
6.282198	5.053372	7.547012	8.171384	P	P	P	6.602729
6.401078	5.870277	7.122066	6.959861	A	M	A	5.97005
		7.286524	7.992874		A	A	
8.402193	8.047944	8.656142	9.038126	P	P	P	8.597212
10.02076	10.02242	9.385133	9.116158	P	P	P	9.77211
6.182449	5.327623	6.453509	A	P	P		6.049049
7.91499	5.660677	7.148578	7.396401	A	A	A	4.203769
	4.115966	5.389576	6.539122	P	P	A	
		5.975898			A		
	5.552527	5.328544		A	P		
7.135922	6.965217	8.06734	P	A	P		7.18098
6.809665			7.941016	A		A	5.689385
10.17705	11.18899	8.583529	9.137071	P	P	P	11.46327
10.21743	11.03269	9.887121	8.908165	P	P	P	10.51361
			6.653495			A	
5.576653	5.474182		6.93906	P		A	5.998359
7.891237	7.501023	8.789341	A	P	P		6.867644

5.436027		6.912207	7.79855	P		A	6.576391
3.711518			P				5.163507
8.022227	7.508302	6.263691	7.459376	A	P	P	3.788294
8.547091	7.223346	6.664684	7.435958	A	P	P	3.856701
9.617674	10.79904	10.25675	9.610457	P	P	P	11.0577
7.44122	6.767098	6.290196	7.66581	P	P	A	6.912192
5.798163		6.251415	A		A		5.107045
8.990268	9.29823	8.20956	7.83469	P	P	P	8.55651
6.885789	5.833877	6.834101	7.365536	P	P	P	7.368702
5.988184	5.450678	3.631552	A	A	P		6.62839
7.475437	6.76935	6.106278	6.921645	P	P	P	8.043518
13.19387	12.93759	11.63762	11.60861	P	P	P	13.10308
4.149414			P				5.364185
			6.814925			A	
12.61887	12.25587	10.75569	11.13313	P	P	P	12.70172
12.41428	12.03051	10.29374	10.74935	P	P	P	12.48572
			2.008516			P	
5.84768	6.059587	5.24968	A	P	P		6.012477
6.480553	5.686637	4.561665	5.219126	P	P	P	5.795019
6.32856	5.683238	6.676858	7.638849	P	A	P	6.951083
8.434114	9.092511	8.785847	9.150524	P	P	P	9.480321
	5.467264		6.905872	P		A	
6.415184	5.486229	6.470805	6.702443	P	P	P	6.22425
9.461939	8.689596	8.627504	7.596682	P	P	P	9.396984
8.960917	8.89076	8.018996	7.424844	P	P	P	9.134385
4.622406		7.277174	2.918772	P	P	P	6.755146
4.873776	5.515922		6.417357	P		P	6.393749
5.423516	5.003455	7.24701	6.481017	P	M	A	5.640278
5.875697	5.798428	5.732764	P	P	P		7.012553
7.564818	6.942032	7.884679	7.202374	A	P	P	6.805758
	7.699437		8.666244	M		A	
5.874681			A				4.617861
8.249914	8.320142	7.349376	6.984106	P	P	P	8.196651
6.25136	5.884311		A	A			5.631779
5.615286	5.032804		P	M			6.98072
7.428792	7.302163	6.722837	6.644291	P	P	P	7.122712
5.68312	5.101681	4.631373	1.07255	M	P	P	5.912251
6.652031	5.573289	5.811091	4.686013	P	P	P	4.99664
6.276012	5.755009	5.288405	6.143376	A	A	P	5.511173
6.0976	5.739032	5.370002	3.374223	A	M	P	5.49169

6.967697	6.921506	6.325847	5.314042	P	P	P	6.16203
7.584145		8.587729	8.484123		A	A	4.662043
	5.091178	2.731194	6.26839	A	M	P	
	4.276239	5.067252		P	P		
12.19465	12.91334	11.90365	11.38062	P	P	P	12.7754
		5.192558	4.468882		M	M	
7.582877	5.960778	6.914794	6.800981	P	P	P	5.670054
9.720085	9.754531	10.38025	10.7876	P	P	P	10.07167
5.813548	6.033773	6.15627		P	P		7.048093
7.637161	7.109792	8.369524	8.623157	P	P	P	7.555849
6.83374	6.623699	5.584626	7.519613	P	P	P	7.177397
6.440724	6.245552	6.642309	5.952811	A	A	P	5.221704
6.394409	5.415054	7.937218	8.27993	A	P	P	6.869097
12.99342	13.07612	12.84041	11.44447	P	P	P	13.1524
10.25477	9.672647	9.132582	8.428701	P	P	P	9.377273
9.433116	9.696528	10.14468	10.46228	P	P	P	9.541926
7.5647		5.232788	7.442684		P	P	6.154945
6.20014	5.192419	5.193529		P	P		5.796222
9.356343	8.609714	9.489932	9.582732	P	P	P	8.58086
6.475574		7.300009			A		5.383361
6.365393	6.486504	6.102647	5.856766	P	P	P	6.105612
8.556759	8.0631	9.178988	8.801897	P	P	P	8.49666
	3.957071			M			
5.42725			A				3.835438
7.496178	8.005457	10.38547	9.913424	P	P	A	7.573475
6.276928	6.703636	8.394216	7.241395	P	P	P	7.051293
6.121444	5.769073	5.983662	6.711546	A	P	M	6.244076
6.934243	6.133098	6.602016	7.510659	P	P	P	6.871823
6.273413		5.926263	A		P		2.689491
	4.67843			A			
6.407561	6.569516	4.822182	6.679013	P	P	P	5.995862
		3.90538			P		
9.05423	7.936725	6.975803	8.53645	P	P	P	8.659157
	5.481708		7.498281	A		A	
			4.074188			P	
8.359897	8.251043	3.785969	6.697079	P	P	P	8.695339
7.936069	7.530021	6.645129	5.930914	P	P	P	6.990926
9.618012	9.07539	9.792375	9.83603	P	P	P	8.643649
8.847357	8.431227	8.958722	9.324126	P	P	P	8.762941
6.818215	7.28525	8.088929	8.505153	P	P	P	6.889276

7.840368	7.407747	8.34121	7.884976	P	P	P	7.298435
6.297418	7.038565	6.712853	6.186997	A	P	M	6.429718
10.63576	10.3333	9.966744	10.19391	P	P	P	10.90537
8.086643	7.772059	8.779386	8.682109	P	P	P	8.094246
7.267613	7.061953	7.585576	6.281793	P	P	P	7.623999
6.419762	4.594906	5.704764	7.447387	A	P	P	5.225869
6.553448		6.600065	A		A		6.36617
10.5295	10.87897	8.672494	8.527665	P	P	P	10.41987
5.960937	6.113756	5.945941	4.296793	P	P	P	7.120683
6.409676	7.942948	6.896172	7.498421	P	P	A	7.870196
10.68206	11.72307	10.31909	8.604124	P	P	P	10.57243
12.89429	12.90101	14.31591	14.2236	P	P	P	12.00608
		9.101898	10.03753		A	A	
5.158704	6.126723	2.535846	1.092661	P	P	P	6.345185
9.170351	8.754424	9.158074	9.194869	P	P	P	8.419496
10.23599	10.64687	9.453745	9.190947	P	P	P	10.21375
	6.10873	3.526206	4.798425	P	P	P	
		6.985372			A		
10.52304	9.885413	11.43877	11.14798	P	P	P	9.774796
6.308443	6.263244	7.04903	P	A	A		6.32085
6.490618	6.606865	6.215991	7.930233	A	P	A	6.458564
7.159154	6.988678	5.431698	5.067382	P	P	P	6.471699
11.00965	11.1587	9.82991	10.29784	P	P	P	11.62547
8.55333	9.197701	8.306478	8.057757	P	P	P	8.858051
8.707009	7.966454	7.207995	6.436404	P	P	P	7.403245
12.22818	11.32813	10.53151	10.75217	P	P	P	11.69969
7.122909	5.888618	7.657031	7.016494	P	A	A	6.220364
7.369324	7.103735	7.08284	A	A	P		6.219582
7.066089	7.189293	7.261279	7.412741	P	P	P	6.937619
7.737467	7.507152	8.330675	7.350459	P	A	P	8.260037
9.923218	8.874082	8.344447	8.87059	P	P	P	9.367782
9.289355	8.25839	8.760338	9.009716	P	P	P	9.079855
11.9524	12.95924	13.02475	12.40165	P	P	P	13.10312
9.96046	8.955363	7.648206	8.375501	P	P	P	8.898104
10.53418	10.55097	9.577152	10.75104	P	P	P	10.77733
7.354281	6.328114	5.657262	7.427964	P	P	P	6.837967
8.868661	9.118498	8.116871	7.680524	P	P	P	8.490117
8.100697	7.076341	7.970716	A	P	P		6.988205
11.83917	12.02226	11.33538	11.13752	P	P	P	12.03387
11.40125	11.57288	12.27366	12.78069	P	P	P	12.02608

8.819468	9.002297	9.288604	9.716614	P	P	P	9.434713
9.943686	9.914787	11.04489	11.2741	P	P	P	9.570106
10.38588	10.04788	10.85632	10.98674	P	P	P	10.06557
9.373448	9.450891	7.972351	8.07171	P	P	P	9.73188
			1.339109			P	
7.166103	6.543791	7.79441	5.76123	P	P	P	6.483468
9.105523	8.635386	8.022949	8.044302	P	P	P	8.693742
6.743949	6.233744	5.201635	7.216531	P	P	A	6.045702
6.278577	7.147098	6.420457	P	P	P		5.943417
8.769668	7.426457	9.466384	9.652545	P	P	P	9.113768
8.288043	7.607019	8.178608	9.125611	P	P	P	8.225022
7.224763			P				8.397159
6.135873	5.59972	5.753954	A	P	P		5.895245
10.82539	10.57862	9.902113	10.20185	P	P	P	10.76997
9.617091	10.3254	7.025092	7.345042	P	P	A	1.429692
10.08664	8.819282	9.772736	9.652013	P	P	P	8.499204
5.794472	7.177871	6.342021	6.07151	P	P	P	6.920354
9.705811	9.155703	9.234952	11.32032	P	P	P	10.43441
7.967308	6.382475	7.844667	7.636719	P	P	P	7.028987
8.991583	11.35321	8.030256	7.822553	P	P	P	9.959934
11.68361	12.17901	11.19878	10.71983	P	P	P	12.25422
11.13608	10.85669	11.3665	12.30399	P	P	P	11.24698
9.859962	8.915749	10.42859	10.24859	P	P	P	9.003255
10.55369	10.37229	9.64393	9.436021	P	P	P	8.77077
7.183336	6.719725	7.924215	7.53712	P	P	P	7.916277
6.033521	5.529598	6.063877	3.177887	P	P	P	4.905605
7.099149	7.057625	8.599622	7.737736	P	P	A	7.787215
9.600898		11.01981	11.47449		A	A	7.709838
7.438003	6.333707	7.860788	8.231862	P	P	P	7.077191
7.553909	8.219206	7.325909	6.269596	P	P	P	7.762889
5.705322	5.025705		A	M			4.663147
		7.005128			P		
			6.90506			A	
	4.037291			M			
	5.32548			A			
7.37293		7.04585	6.934402		A	A	5.633453
12.35518	13.22969	13.53212	13.1885	P	P	P	13.40888
9.15515	9.498277	8.654998	8.756812	P	P	P	10.23109
	4.931588	5.561312	6.713141	P	P	A	
7.705284	7.173747	7.385942	7.653672	A	A	P	7.545796

5.55667			6.813043 A			A	3.152041
9.728791	10.66099	9.483316	8.612896 P	P	P	P	10.25683
12.51802	12.75547	11.20505	11.0225 P	P	P	P	12.61746
6.577629	5.031		A	P			5.357064
8.697633	9.033875	8.314422	7.777126 P	P	P	P	8.910303
10.62358	11.29249	10.8418	11.53714 P	P	P	P	11.82152
7.179315	8.075309	9.706911	9.508075 P	P	P	P	9.155072
10.52034	10.6896	9.912382	8.926574 P	P	P	P	10.34094
6.034932	6.414051	6.460241	6.686658 A	P	P	P	4.860676
9.059227	8.962175	8.112751	6.847413 P	P	P	P	9.091584
6.339153	6.219825		6.998041 A	P		A	5.36853
9.45909	9.270268	10.27758	9.916222 P	P	P	P	8.958672
13.5823	13.25928	12.79552	12.5884 P	P	P	P	13.63191
10.18477	10.28019	9.668761	9.334686 P	P	P	P	10.17577
3.697004			P				6.032552
5.452755			6.509067 A			P	4.409842
7.979812	7.453758	7.366131	6.674534 P	P	P	P	6.884631
7.228857	7.203403	7.216076	7.029222 P	P	P	P	7.721033
			2.335904			M	
5.113502		3.514981	M		P		5.811309
6.707658	6.593494	5.958998	6.37765 A	A	P	P	6.393192
9.397594	8.576511	10.02701	10.05317 P	P	P	P	9.454957
9.230413	9.823701	9.394225	8.552279 P	P	P	P	9.686725
9.615433	9.63677	9.459058	8.605185 P	P	P	P	9.883424
7.262568	6.903563	7.015469	4.209451 P	P	P	P	6.636227
10.10162	9.822718	10.58089	10.63308 P	P	P	P	9.058229
9.755507	8.716236	9.178991	9.103739 P	P	P	P	8.492166
10.78968	10.97682	10.22174	9.654978 P	P	P	P	11.00344
5.676385	5.250771	4.808083	A	A	P		1.616033
9.012914	9.550707	7.577452	8.27289 P	P	P	P	9.22999
6.407825	6.171229	3.168872	4.075562 M	A	P	P	6.893537
11.09087	10.88787	10.22183	10.0668 P	P	P	P	10.75138
10.91581	10.82725	9.897337	9.572012 P	P	P	P	10.50522
			6.471636			A	
9.416892	9.366945	8.167351	7.779044 P	P	P	P	9.374368
	5.238862	4.58626		M	P		
8.692901	9.247111	10.01018	9.058734 P	P	P	P	8.603148
11.25565	9.286612	9.384386	9.351092 P	P	P	P	9.216197
7.172329	6.762142	8.041464	8.021724 P	P	P	P	7.157486
8.466634	8.478316	8.904189	8.631784 P	P	P	P	8.826736

12.29735	12.6262	10.03932	10.70217 P	P	P	P	12.67741
9.171976	9.634747	7.41702	8.163852 P	P	P	P	9.926758
6.41586	6.166032		3.928218 P	P		P	5.886823
7.219826	6.756465	6.769369	2.480813 P	P	P	P	6.938719
	5.01201	7.395614		P	A		
5.678835	5.185194		6.774698 P	P		P	6.827158
12.55021	12.67575	11.86081	11.37411 P	P	P	P	12.49078
7.657507	6.327767	7.293384	8.950932 A	A	A	A	4.74292
9.226769	9.257608	10.47107	11.54535 P	P	P	P	9.506781
11.22287	11.40787	12.20636	12.23365 P	P	P	P	11.08748
12.22947	11.63299	9.634805	11.372 P	P	P	P	10.98482
4.989661	4.941398	6.185226	5.998262 P	A	P	A	5.329663
5.367804			5.664953 A			P	2.990062
		7.013854	7.486975		A	A	
11.02155	11.22506	10.54002	10.11417 P	P	P	P	10.70678
6.110694	7.312349	5.880598	6.521394 P	P	P	P	5.52522
4.46846	6.251562		P	P			6.748176
5.88113		5.991052	A		A		5.548653
8.147918	8.449945	8.765657	7.927845 P	P	P	P	8.140015
14.33305	14.95632	15.15565	15.74557 P	P	P	P	15.20231
14.47557	14.90884	15.14839	15.84205 P	P	P	P	15.25117
10.0887	10.42923	9.510979	9.044335 P	P	P	P	10.55021
6.556724		6.731907	A		A		6.019552
8.296136	8.013502	9.28721	9.844065 P	P	P	P	8.421266
8.954475	9.357196	8.35294	7.84757 P	P	P	P	9.067211
6.256708	6.565	5.785289	5.663842 A	P	P	P	6.314907
12.46337	13.16357	12.1174	11.93851 P	P	P	P	12.99815
5.994169	5.380488	6.034223	A	P	P		6.292169
		8.603095	8.962305		A	A	
9.135054	8.494613	9.804339	9.547251 P	P	P	P	8.449011
8.111329	8.366673	10.37216	9.751262 P	P	P	P	8.207284
			6.820831			A	
7.348383	6.276044	6.597424	6.127005 A	P	A	P	6.016449
10.10426	9.772505	10.77806	10.96829 P	P	P	P	9.753345
7.748938	8.189351	8.330772	9.073553 M	P	P	P	8.116294
6.482839	6.510874		2.832552 A	A		P	6.278574
8.734611	8.442044	7.173526	8.145732 P	P	P	P	8.967969
10.45898	10.91514	8.62552	9.310576 P	P	P	P	10.98018
6.252695	7.000207	5.401298	6.972786 P	P	P	P	6.386571
10.18714		9.888063	10.08091 A		A	A	3.814652

12.39074	10.84063	11.54933	11.59071	P	P	P	11.11972
11.21769	9.455159	10.23179	10.33418	P	P	P	10.06315
7.421666	6.14647	6.414561	7.453044	A	P	P	6.670809
8.531855	8.809976	7.292312	7.092895	P	P	P	8.894327
6.149784		6.850762	6.793716	M		A	5.451952
7.339416	7.651117	7.326642	6.958761	P	P	P	7.083608
5.943348	7.011423	6.708382		A	P		5.602506
7.269351	6.947053	7.275262		A	A		6.288422
10.18152	10.41686	10.41817	11.06087	P	P	P	10.36026
13.56452	13.52551	13.78375	14.81912	P	P	P	13.96313
9.994202	10.83305	11.34016	11.77516	P	P	P	10.70877
7.184394	6.692079	7.097247	8.229859	P	P	P	7.640839
11.54995	10.1034	12.44751	12.9155	P	P	P	9.685694
5.915772	7.701234	5.947334	6.561121	P	P	P	6.536824
9.821785	9.66247	10.25669	10.12911	P	P	P	9.749527
11.40524	11.60034	9.753276	10.19619	P	P	P	11.35727
8.647402	9.120161	7.636449	8.598761	P	P	P	9.847034
6.149897	8.526835	4.960837		P	P		6.521008
9.065769	9.651888	8.613478	7.931103	P	P	P	8.820768
6.792928	6.6924	7.280106	7.420334	P	P	P	7.859991
			3.477076			M	
9.240638	7.67307	8.954453	8.28809	P	P	P	7.903835
		7.141014			A		
7.35753	7.228555	8.183342	8.301224	P	P	P	7.420588
7.46256	6.795917	5.589211	6.254805	P	P	P	6.767373
8.819348	8.095335	8.724122	9.599264	P	P	P	8.872854
8.334818	6.077143	6.783845	5.808353	P	P	P	6.795131
7.689301	7.3012	7.193092	7.128385	P	P	P	6.144377
6.790746	7.373282			P			7.031039
10.09728	9.505199	9.997266	9.5036	P	P	P	8.643518
6.904199	5.908681	7.810261	6.413161	P	A	P	6.202128
8.599175	7.636734	8.736496	8.105808	M	A	P	7.993206
8.157995	8.878091	7.071254	6.981838	P	P	P	7.688199
6.337653	5.898313	6.397705	7.46343	A	A	A	7.091456
	6.288642			A			
8.049205	7.244507	9.146623	9.499378	P	P	P	7.218807
11.48713	11.22829	12.31016	12.71644	P	P	P	11.23633
6.368205	5.834246	7.704768		A	P		6.265073
6.736871	6.67117	7.321659	7.44811	A	A	P	5.912257
6.882851	6.410648	5.06391	4.500747	P	P	P	5.511093

5.64864				A				2.283844
7.868105	8.088514	8.107631	8.556224	P	P	P	P	7.546734
11.05856	12.06196	8.956055	9.37896	P	P	P	P	11.67309
13.3794	14.13236	11.25112	11.29801	P	P	P	P	13.60062
8.727982	7.599732	8.924634	9.530512	P	P	P	P	7.409736
3.13445	6.71425			P				5.890055
8.773291	8.188429	9.239556	9.556337	P	P	P	P	8.4281
8.056768	7.616686	7.323216	5.955932	P	P	P	P	7.195766
7.81067	7.397406	6.341601	6.60936	P	P	P	P	7.497362
7.017144	6.645297	6.107326		M	P			5.735267
7.100175		6.786876	7.602373	M		A	A	6.919523
	5.417613	6.828536		A	A			
5.874377		3.969384		P	M			5.32631
12.17959	11.45524	12.14977	12.15142	P	P	P	P	11.65849
8.074181	7.226011	7.447847	8.063811	P	P	P	P	7.598698
7.221466	7.325497	6.107292	4.343019	P	P	P	P	6.67162
6.318226		6.514921	5.895991	A		A	P	5.285822
11.40235	11.10911	10.15988	10.3366	P	P	P	P	11.37158
	6.81755	3.748265		P	P			
4.799589	4.351361	5.094794	5.465194	P	M	P	P	6.024063
6.101089	4.807704	5.292967		P	M			4.93992
8.367916	8.229284	8.667312	7.822679	P	P	P	P	7.418927
9.752246	8.923156	9.452854	7.239852	P	P	P	P	8.033553
8.230267	8.743029	9.057851	8.241393	P	P	P	P	9.299476
		6.814282					A	
6.222985	7.08378	7.84369	5.901903	P	A	P	P	6.887588
5.310845	5.531397	6.577235	6.176124	A	A	P	P	3.693022
5.866879	6.724677	5.687583		P	A	P		6.910326
10.72634	10.54577	11.49945	11.25563	P	P	P	P	9.99749
8.65439	7.220204	8.85838	8.420338	P	P	P	P	7.518472
10.7057	10.59181	9.787025	9.851748	P	P	P	P	10.55561
9.298512	9.788193	9.637002	8.767815	P	P	P	P	9.725868
7.297991	6.786708	7.988001	7.301212	P	P	P	P	6.931103
7.358569		7.676193	7.98872	A		A	M	5.502817
7.63803		7.681653		A		P		6.59023
5.88568	6.315592	6.445667	6.634344	P	A	A	P	6.717978
8.558586	9.088167	11.31847	10.46992	P	P	P	P	8.18687
8.823649	8.239872	9.204837	8.243136	P	P	P	P	7.464318
10.21335	9.640325	9.245039	9.345156	P	P	P	P	10.08141
12.16473	12.05077	12.83273	13.29283	P	P	P	P	12.20237

7.139464	6.076343	7.486924	8.220711	P	P	P	7.26148
9.437229	8.828506	9.746642	10.25164	P	P	P	8.551009
7.30152	6.248657	8.232876	7.818104	P	P	P	7.053243
8.52783	8.522379	9.118917	8.640584	P	P	P	8.716233
9.446696	8.491215	9.747211	10.12028	P	P	P	8.987849
10.80413	10.47095	11.70386	11.00526	P	P	P	9.284353
6.795603	5.574284	5.6712	P	P	P		6.240488
9.172804	8.521155	8.895059	8.874155	P	P	P	7.888555
9.929078	10.29247	9.04409	8.631705	P	P	P	10.13217
11.24801	11.70402	10.42146	10.60586	P	P	P	11.53649
7.796567	8.189914	6.733551	8.115359	P	P	P	8.636552
6.803887	5.955069	8.004871	7.715367	P	A	P	6.882365
9.09967	8.72436	10.22789	9.366829	P	P	P	9.087877
7.892966	7.940157	7.577438	5.271904	P	P	P	8.004012
13.28242	14.82379	13.37642	12.36405	P	P	P	14.7151
			6.880206			A	
8.701201	8.711984	9.696317	10.39665	P	P	P	8.625464
8.920786	9.448334	8.301663	7.851259	P	P	P	8.876703
6.301222	5.161136	6.601401	7.001124	P	A	A	6.319888
12.30424	11.71185	12.89794	13.27543	P	P	P	11.55257
12.50135	12.01999	11.43744	11.85102	P	P	P	12.24232
13.10275	12.79865	12.34088	11.87908	P	P	P	13.00931
10.34992	9.067563	9.250185	9.270309	P	P	P	8.985131
10.38772	9.444124	9.403888	8.438883	P	P	P	8.768881
10.16956	9.579682	9.094101	8.91108	P	P	P	8.831851
9.689781	11.05205	11.22543	8.880253	P	P	P	11.30217
6.687634	6.389053	7.559096	8.150588	P	P	A	7.447766
11.08425	11.4803	10.10485	9.708624	P	P	P	11.61721
10.04232	9.133036	11.21158	11.79521	P	P	P	9.303763
7.177531	7.347407	7.552339	8.52806	P	P	M	7.225882
	5.6397	5.48543		A	M		
	7.29224	7.865704		A	A		
5.137664	5.785152		6.012544	A		M	6.126012
13.04906	12.76323	13.50488	13.56342	P	P	P	14.10751
13.9499	13.59971	14.4542	14.77081	P	P	P	14.8607
10.83314	11.00293	11.50457	11.90706	P	P	P	11.08395
14.68699	14.56799	15.09958	16.02027	P	P	P	15.4538
14.18788	14.18331	14.68214	15.25399	P	P	P	15.27138
6.155186	5.278151	6.277164	A	P	A		5.125351
8.112549	8.357907	8.279237	6.031621	P	P	P	7.879347

10.37834	9.936888	11.1376	11.92892	P	P	P	10.20109
5.665359	6.387345	5.515379	6.468051	A	P	P	5.568884
9.775824	9.342059	9.670727	10.69784	P	P	P	8.929304
5.14238			A				1.83883
5.071836	7.451589	6.504135	5.480375	P	P	P	6.380084
6.736823	6.445194	7.345323	8.198321	P	P	P	7.435043
7.034135	6.068211	6.399893	6.46499	A	A	P	5.345181
10.98562	10.19557	11.24968	10.77676	P	P	P	9.977951
11.85592	11.87036	10.81271	10.33876	P	P	P	11.26177
7.918178	7.962694	6.90406	6.481091	P	P	P	7.119604
9.668517	10.02071	10.84664	10.27495	P	P	P	9.888326
4.312369	6.757535	6.182644	7.473198	P	A	P	8.122936
9.436418	8.840516	7.557415	7.459469	P	P	P	8.380982
8.951896	7.301076	6.360415	7.288164	P	P	P	7.723395
5.609969			3.399984	P		P	5.197888
8.283891	7.596272	8.164475	8.291009	P	P	P	8.278452
10.50441	10.71753	10.01504	9.214013	P	P	P	10.47249
6.807442	7.601173	7.346398	7.620111	P	P	P	7.852059
7.713759	6.974386	7.395732	8.31211	P	P	P	7.034236
5.572096		4.885634	A		M		3.097502
12.08064	11.82007	11.08537	10.90854	P	P	P	11.81662
7.957672	7.589006	6.929067	6.973499	P	P	P	7.852276
10.92743	10.79748	10.20267	10.26483	P	P	P	10.59622
			6.29406			A	
11.74542	12.08296	12.77349	13.01965	P	P	P	12.00597
10.20945	8.236499	8.812073	8.142355	P	P	P	7.975974
8.498121	8.962003	8.516298	7.587422	P	P	P	8.676974
10.12767	10.16275	11.0739	11.55499	P	P	P	10.4767
7.355408			A				3.802722
7.370121	7.391778	7.458957	7.27621	P	P	M	7.193525
9.307302	9.181864	8.656733	8.018592	P	P	P	8.603553
6.124361	5.890416	6.459657	6.550954	A	P	P	5.939048
12.62735	12.54189	12.03873	11.73049	P	P	P	12.24809
8.203553			9.259546			A	7.9605
			7.35225			A	
10.75691	11.54767	10.85228	10.24368	P	P	P	11.982
8.65337	7.739618	9.415928	8.819719	P	P	P	8.194922
7.913209	7.664125	7.981371	8.114531	P	P	P	7.067252
9.097935	9.950383	9.344147	10.83985	P	P	P	10.67014
5.801138	5.675559	5.985307	7.15107	P	A	P	5.790997

	5.980569	6.424258	6.842873	P	A	A	
8.866648	9.907725	8.213464	9.146168 A	P	P	A	5.771342
12.21095	12.32052	12.79742	13.77952 P	P	P	P	12.65767
7.95533	8.497032	7.952059	9.38337 P	P	P	P	8.652846
9.40143	9.315598	10.49827	10.46647 P	P	P	P	9.040252
11.28756	10.8184	11.50156	11.72514 P	P	P	P	11.04352
7.324267	6.152765	7.316891	6.666377 P	A	P	P	6.323234
11.62197	11.01951	11.58162	11.11487 P	P	P	P	10.78294
	6.376211	7.528993		A	P		
8.110289	7.376918	6.683012	5.845355 P	P	P	P	7.372837
9.682486	5.81384	9.99116	8.510377 P	P	P	P	7.980209
8.989982	9.483393	8.685402	7.618206 P	P	P	P	9.257952
9.323764	9.848735	9.107386	8.245313 P	P	P	P	9.19276
8.249488	8.062934	8.448296	9.570286 P	P	P	P	8.664685
7.075126	6.649974	7.819632	8.272278 P	P	P	P	7.148105
8.793009	7.899963	8.296043	8.043887 P	P	P	P	7.49071
	3.811769			P			
4.03583	4.833724		M	P			5.633257
12.68092	13.18034	11.79317	11.91159 P	P	P	P	12.99898
	5.863175			A			
12.89061	13.34836	13.0606	12.16187 P	P	P	P	13.36737
6.032725			P				7.330165
6.698567	5.455936	5.600372	P	P	P		7.188808
9.457362	8.449175	8.401587	8.020781 P	P	P	P	8.68287
	7.259521	6.474805	7.9919	P	P	A	
11.09935	10.86195	10.10695	9.670756 P	P	P	P	10.91933
13.13833	13.87134	12.57492	12.43935 P	P	P	P	13.82342
6.7316	6.926314	6.48112	6.588698 P	A	P	P	7.112556
		3.274759			P		
12.47049	11.83309	13.35504	13.52412 P	P	P	P	11.76798
	5.808002			P			
5.58693		6.44922	7.045994 A		A	A	6.301166
9.236862	8.81563	9.198946	7.269579 P	P	P	P	9.286303
4.212703	5.682421	5.764113	5.630157 P	A	A	M	5.077765
13.4359	13.96353	12.76349	12.12783 P	P	P	P	13.58734
5.777185	5.494377		6.00512 A	P		A	5.060292
9.867369	9.022962	10.0153	10.10073 P	P	P	P	8.91799
11.74228	11.71396	12.84411	12.82057 P	P	P	P	11.53047
7.999069	8.061592	6.577259	6.775013 P	P	P	P	8.401277
3.390193			7.260916 M			A	6.51427

9.884769	10.04191	9.858118	8.991004	P	P	P	9.788446
7.425924	6.238253	6.62869	6.312512	P	P	P	6.945555
9.003551	8.540557	7.618911	8.33072	P	P	P	8.342233
6.977249	6.124216	8.282612	A	A	A		6.230965
8.629819	7.908802	7.577083	7.988628	P	P	P	9.029797
8.773556	9.117559	8.285286	7.068929	P	P	P	8.774286
8.119485	7.135364	8.306161	7.759724	P	P	P	7.497502
7.173211	7.329052	8.044397	6.869895	P	P	P	8.764339
10.24397	9.649902	9.580183	9.517746	P	P	P	8.5218
6.707003	5.747154	6.880066	6.685764	P	P	A	6.325293
6.02973			A				3.134378
5.023634	5.61822		6.76545	P	A	M	6.691582
5.926684		0.517135	M		M		5.617993
10.78492	9.998545	13.02015	12.26714	P	P	P	9.72971
10.2853	9.493548	9.83445	9.413253	P	P	P	9.037629
5.398012	6.207655	7.335149	7.804534	P	P	P	6.388878
	5.450934	5.620384		A	A		
6.779125	5.863299	5.904187	7.080343	P	P	A	6.666877
6.545018			A				4.057998
7.290135	7.27275	7.453402	8.022838	P	P	P	7.039352
7.860394	8.729966	6.450186	7.649923	P	P	P	7.908584
9.830746	8.23651	8.500171	7.864856	P	P	P	7.920692
12.2458	12.34851	13.17599	12.67137	P	P	P	11.81792
7.846221	6.712402	6.886518	7.298226	P	P	P	7.263111
5.772317	4.637475	6.529953	5.693709	P	P	A	5.530974
7.117074	5.164282	6.070146	6.334327	P	A	P	4.925347
8.026274	7.729788	3.168037	5.664413	P	P	P	7.262683
10.36545	11.33797	11.09583	10.90821	P	P	P	11.70198
10.13914	11.57876	11.49135	10.28396	P	P	P	11.75048
10.28679	11.43596	11.33292	10.46167	P	P	P	11.57665
12.03725	11.56975	12.23171	13.64571	P	P	P	11.70053
10.5881	10.22539	11.36873	12.18387	P	P	P	10.12994
8.75946	8.930422	9.532996	8.898976	P	P	P	8.507566
9.549975	9.402102	8.508449	9.113545	P	P	P	8.835909
5.961405	5.998317	5.969745	5.64736	P	P	P	2.878483
8.753582	8.525801	9.28663	8.003655	P	P	P	7.467108
6.171529	5.102435		A	A			5.918313
11.47543	11.32209	10.93234	10.17533	P	P	P	10.85604
7.233844	6.586844	6.68101	P	P	P		6.040968
8.717877	7.663711	9.145779	9.917644	P	P	A	7.76458

9.872442	9.722902	9.151846	8.023938	P	P	P	9.079837
6.062221		7.208391	7.026352		A	A	4.520584
12.04712	12.02772	11.55304	11.11953	P	P	P	11.92457
7.335025		8.187421	8.890857		A	P	5.533272
9.04338	9.390835	10.52189	10.61675	P	P	P	9.781142
11.13849	10.64089	10.17738	10.90499	P	P	P	11.08498
10.89813	10.45795	11.08258	10.83257	P	P	P	10.16071
9.072297	9.487716	7.772613	7.536988	P	P	P	9.259988
6.786093	6.614794	7.271625	6.98105	P	P	P	7.099915
7.409918	7.536979	6.802523	6.858408	P	P	P	7.162511
7.431156	7.597062	6.962178	7.519761	P	P	P	7.505376
5.542801			A				1.953819
9.740915	9.546497	8.28546	9.239972	P	P	P	9.90278
14.15052	14.83382	13.22591	12.93753	P	P	P	14.7584
10.34046	10.3362	13.02208	12.33312	P	P	P	9.738629
9.857445	9.856255	11.42239	11.35912	P	P	P	9.296026
5.544221	5.19556		A	A			6.090294
6.725693	5.860705	6.712926	6.756802	P	A	P	6.098987
7.517732	4.708656	6.815578	7.119043	P	P	A	6.18422
12.21613	12.37884	11.23418	10.7044	P	P	P	12.24991
	5.947728	5.022963		A	A		
6.194945	6.544023		6.956209	A		M	6.169374
	6.165107			A			
6.611898	6.228086	5.805347	7.141393	A	A	A	6.900895
	5.654439	7.091618		A	A		
6.859946		6.460838	5.515403		M	P	4.432026
10.67153	9.423747	11.26694	11.00957	P	P	P	9.937967
	6.212051	7.392827		A	A		
8.399637	7.622163	8.765328	9.186105	P	P	P	8.372765
6.220743	3.541336	6.773677	A	P	P		3.006642
12.54647	12.04903	11.44278	11.30612	P	P	P	12.10845
7.493588	5.670289	7.376633	6.985093	P	P	P	6.130073
7.393388	7.811877	6.616848	7.329312	P	P	P	9.160836
10.94457	11.05393	10.39642	10.78522	P	P	P	12.32415
10.00513	10.34065	9.606487	9.113009	P	P	P	10.78507
3.761691			P				5.936899
7.608028	7.168734	7.883514	8.148029	P	P	A	7.245964
8.61823	7.672962	7.830092	7.540685	P	P	P	7.2912
7.062177			A				2.744726
8.038979	5.312054	7.664944	7.739332	P	A	P	5.787229

10.37898	10.07076	11.09207	11.13156	P	P	P	10.15171
9.896058	9.109377	11.15423	11.01165	P	P	P	9.233486
9.464183	8.935424	10.38364	9.680007	P	P	P	8.607386
7.176101	6.801026	7.340117	9.152162	A	P	P	7.724407
9.472837	10.75105	8.348638	7.709244	P	P	P	9.697376
11.89912	12.40325	11.74388	11.15318	P	P	P	12.063
8.249349	7.739929	7.691542	6.820155	P	P	P	7.183713
8.155534	7.525725	7.022836	7.040497	P	P	P	7.070169
10.18526	8.520972	9.983369	10.34156	P	P	P	9.499871
6.694179		6.750457	7.693993		P	A	6.423339
10.42975	9.00348	8.524159	8.666253	P	P	P	9.630924
9.530804	9.841481	9.123547	8.491591	P	P	P	9.471512
10.55907	10.77871	11.78447	11.31609	P	P	P	10.75264
13.10046	14.13551	11.13693	12.74198	P	P	P	13.86953
7.624797	7.98973	7.260676	6.889055	P	P	P	8.310917
	6.095504			P			
10.24303	10.08459	10.70876	11.06188	P	P	P	9.792243
9.56667	9.530885	9.016186	9.295386	P	P	P	9.562974
9.021921	7.976514	7.845569	7.585642	P	P	P	8.586427
8.573318	7.869711	7.272318	8.914273	P	P	P	7.89983
6.626791	7.396561	5.449861	6.127935	P	P	P	7.153503
6.962685	7.300008	6.690736	7.935223	P	P	P	7.943988
5.908163	5.211926	3.62514	6.91617	P	M	P	6.004148
8.090618	8.481885	8.557334	9.278176	P	P	P	9.319879
12.06174	12.10799	12.46797	13.18814	P	P	P	12.48167
	5.063261	7.635601	7.740428	A	A	A	
4.700053	2.879473		4.890051	P		P	5.0255
12.29151	13.31562	10.8188	10.64689	P	P	P	12.85252
	6.488612	8.106912	6.794299	P	A	P	
8.009228	7.396526	6.874875	7.222314	P	P	A	6.820463
8.112857	8.267069	8.499058	10.23621	P	P	P	9.186941
10.00796	10.38535	10.06457	9.319913	P	P	P	9.187322
11.28252	10.43305	11.26529	11.40135	P	P	P	10.5662
11.02149	10.28972	11.33557	11.57981	P	P	P	10.74289
7.444355	8.399366	6.904394	5.598075	P	P	P	7.431715
5.906641	4.897936	4.901682		P	P		5.4355
9.86139	9.960062	10.66905	11.8724	P	P	P	10.4375
6.777629		3.698331	6.170227		P	P	5.359009
12.41572	12.66142	13.55185	13.61754	P	P	P	12.93138
8.617664	7.874911	9.781521	9.913684	P	P	P	8.208967

8.978859	8.603094	9.139178	9.41624 P	P	P	P	8.140201
5.825605	6.960338	6.737129	6.501583 P	P	P	P	6.540866
8.859582	6.118858	5.799928	4.307031 P	P	P	P	8.308089
9.490278	8.663411	11.94762	9.773877 P	A	A	M	9.633613
10.56415	10.60909	11.23201	10.79384 P	P	P	P	10.17816
9.132	8.905026	8.95623	8.226228 P	P	P	P	8.783039
13.54925	13.73239	13.37365	13.21364 P	P	P	P	13.53354
5.631089	6.157923	7.036724	6.453619 M	A	P	A	4.988594
7.920528	7.008017	6.838073	6.943344 P	P	P	P	8.169798
	6.387775			A			
9.440617	9.349283	8.42903	8.023242 P	P	P	P	9.90454
9.577211	9.116762	9.648663	9.980979 P	P	P	P	8.685532
9.77445	8.474443	9.084374	9.165179 P	P	P	P	8.215777
10.56179	8.950719	8.448445	8.969918 P	P	P	P	8.005594
9.926498	9.635426	8.94103	10.42076 P	P	P	P	10.23098
9.368978	9.937284	9.559241	7.640521 P	P	P	P	9.409284
6.384089	5.839584		7.347792 A	A		A	6.407091
7.004915	8.80712	6.17883	P	A	P		7.08661
6.614746	6.675095	6.621211	5.399394 A	A	P	M	6.583602
	3.21096			P			
6.470838	5.602683	6.463315	A	P	A		6.060823
9.35126	10.20161	9.333235	7.967098 P	P	P	P	9.499523
6.447034	6.512064	5.076416	6.427207 P	P	P	P	6.14153
7.340385	7.297108	8.784104	8.560681 P	P	P	P	7.222911
6.097977	6.135976	7.107057	A	A	A		6.639547
9.100425	8.966213	10.27167	11.38795 P	P	P	P	9.295548
8.267949	8.243156	9.625572	9.055553 P	P	P	P	8.393398
7.618989	8.909679	9.443695	9.174143 P	P	P	P	8.006988
7.102745	6.489339	6.645202	6.885259 A	P	P	A	5.713191
9.285259	10.2287	9.105858	8.772816 P	P	P	P	10.10593
6.060336	5.239239	5.923285	5.851673 P	M	P	A	6.202379
		6.058262	7.120429		A	A	
6.854408	6.548581	8.950949	9.450172 P	P	P	P	7.36673
12.3459	13.65004	11.92668	11.21418 P	P	P	P	13.47926
6.631778	7.153432	6.61727	5.270788 P	P	P	P	6.408841
8.025775	8.035665	9.350025	9.042987 P	P	P	P	7.388987
6.030079	6.149537	5.034226	6.124522 P	P	P	P	7.047304
		7.651472	8.991948		A	A	
11.97764	12.57227	11.62617	11.29853 P	P	P	P	12.34277
9.932466	9.663856	10.293	10.32459 P	P	P	P	9.151591

9.961957	9.879362	9.82514	9.038051 P	P	P	P	10.20215
13.18941	12.42605	14.03069	14.37009 P	P	P	P	12.16247
6.333754	5.498548	5.37423	6.098829 A	P	P	P	5.059116
		6.399293			A		
6.805331	7.600781	5.02901	5.701373 P	P	P	P	6.955223
8.009624	6.999977	6.628113	6.215072 P	P	P	P	6.373457
7.708685	7.692388	8.80321	9.102617 P	P	P	P	7.403303
10.5269	10.42189	10.33792	9.025977 P	P	P	P	10.3836
7.470387	7.142357	5.672251	6.585321 A	A	P	P	6.504829
8.428494	8.914926	7.517475	6.570563 P	P	P	P	8.145803
11.27107	10.25983	10.97458	10.37956 P	P	P	P	10.1
9.260987	8.949281	9.038818	7.245056 P	P	P	P	8.319562
8.008401	7.196748	7.422424	6.38443 P	P	P	P	7.89204
7.336709	6.316307	7.839575	7.641882 P	P	P	P	6.696064
8.024823	7.356402	7.462413	A	P	M		6.039002
	5.290737			A			
8.390598	8.509532	9.292162	9.207073 M	P	P	P	8.001907
8.964852	8.419227	9.56685	9.317979 P	P	P	P	8.256577
8.128213	8.75713	7.365549	6.755572 P	P	P	P	7.578164
6.053381	5.963723	5.978866	A	P	P		5.504643
7.784546	6.413313	7.267808	8.175128 P	P	P	P	7.224549
7.223887	7.472728	4.12219	6.694504 P	P	P	P	7.502518
7.159652	7.215617	5.628311	5.98047 P	P	P	P	6.963727
9.163649	8.495427	8.842812	9.05041 P	P	P	P	7.989821
6.823985	6.2268	7.505622	7.371366 A	A	A	A	6.02158
10.55739	10.76287	10.34101	8.929362 P	P	P	P	10.3806
8.696161	9.412037	8.515513	7.941714 P	P	P	P	8.951504
10.05287	9.354187	8.336839	8.686326 P	P	P	P	9.028996
			6.351865			A	
8.780152	10.03559	9.666529	9.064566 P	P	P	P	9.715979
7.064693	6.897558		7.194315 A	P		A	6.337183
6.105957	5.533798	5.639167	6.646911 P	P	P	P	7.163251
		7.012609			A		
4.896369	6.093627	6.155942	5.694443 P	P	P	P	6.447587
4.474219	6.800498	7.057274	6.441369 P	P	P	P	7.767529
6.912563	5.17007	6.996333	1.405545 A	A	A	P	5.61714
8.442633	9.335916	8.529542	8.920224 P	P	P	A	9.300488
10.47736	8.855311	9.555129	9.633864 P	P	P	P	8.980789
		1.42836			M		
10.44052	10.58698	8.38586	9.639244 P	P	P	P	10.5471

6.567845	6.211244	7.073788	4.473017	P	P	M	7.010471
7.486767	7.872418	6.877989	7.626324	P	P	P	6.310041
	5.754841	5.25984	6.650157	A	P	A	
7.98292	7.735732	8.826306	8.539989	P	P	P	7.453667
9.76131	10.23336	10.38075	10.71177	P	P	P	9.564389
5.862371	6.044056	4.235962	7.629427	P	P	P	6.515729
7.370982	7.344988	7.773079	6.937627	P	P	M	7.470811
		7.95284	8.307836		A	A	
10.74292	8.736687	9.420184	9.495981	P	P	P	8.975116
6.942085		4.483274	A		P		4.742917
5.594345	6.383828	6.3005	7.082983	A	P	M	6.597852
14.35418	14.71741	15.2395	14.81201	P	P	P	14.8903
12.20985	12.94574	12.01446	11.80178	P	P	P	12.96385
10.27196	10.4972	9.928341	10.09129	P	P	P	10.62085
5.201798		5.37593	P		P		6.247311
11.23866	11.84708	12.85718	13.52883	P	P	P	10.81063
10.27756	9.381518	10.08547	10.58885	P	A	P	10.37363
9.459665	8.901405	10.1624	9.579547	P	P	P	8.820268
12.73583	12.88393	12.30894	12.03053	P	P	P	13.16458
9.341485	10.13312	9.350245	8.689074	P	P	P	9.786919
13.16193	14.01956	12.81772	12.35229	P	P	P	13.83959
12.11887	13.44206	13.13251	12.24094	P	P	P	13.62187
10.15494	11.12632	10.48518	9.207956	P	P	P	10.37636
11.72562	12.05832	11.40248	10.51956	P	P	P	11.83893
11.54908	10.92528	11.98638	12.10274	P	P	P	10.79964
11.88141	11.33416	12.26749	12.44385	P	P	P	11.34
10.41921	10.65875	9.138208	8.821437	P	P	P	10.35865
7.968942	6.687449	7.794227	8.766276	P	P	P	7.90251
7.429288	8.350652	6.449361	7.243507	P	P	P	10.18708
12.41882	11.34578	12.34442	12.17009	P	P	P	11.9853
6.050942	6.143474		A	A			5.987905
7.571363	7.272662	7.657429	7.801326	P	P	A	7.387688
11.07958	10.81935	11.71172	11.07085	P	P	P	10.95717
10.65348	9.773496	10.86913	10.0869	P	P	P	9.556603
9.203617	8.75972	9.29407	9.085168	P	P	P	8.16836
3.336811			M				5.744054
5.452021		5.410752	P		P		6.599089
			7.106542			A	
7.295966	6.340703	6.032108	6.53637	P	P	P	7.31651
	5.652809	5.815607	6.794687	M	P	P	

9.577476	9.530788	9.666538	9.376961	P	P	P	9.438259
5.857517	0.624957	5.817168	P	M	M		6.128354
11.00621	10.07694	10.09593	9.603029	P	P	P	9.624547
5.689417		6.673135	7.386358	P	A	M	7.235806
6.910525		8.395436	A		P		6.915323
8.20966	8.201679	8.591035	8.353107	P	P	P	8.465612
8.622692	8.831897	8.814483	8.136737	P	P	P	7.880171
8.468857	7.936303	8.408599	8.311045	P	P	P	8.728492
8.868904	7.542701	8.021425	7.453474	P	P	P	7.764109
10.52562	8.099343	7.892774	8.874049	P	P	P	8.07982
10.63927	8.306124	8.398587	9.371368	P	P	P	8.271454
10.35173	8.374329	8.723705	9.254501	A	P	P	7.142746
10.43614	8.137174	7.541753	8.952519	A	P	P	6.975262
10.82263	9.025958	8.975834	9.897113	P	P	P	8.513865
8.940976	7.896817	9.826858	8.616946	P	P	P	6.900991
4.722964	0.442123		P	P			4.887601
9.783748	9.554653	10.68497	11.39502	P	P	P	10.2473
	6.436991		4.611378	P		P	
13.14879	12.34052	13.98274	15.04749	P	P	P	12.76736
11.1138	10.9842	12.48364	13.27373	P	P	P	11.17423
11.52459	12.13954	11.18765	10.06895	P	P	P	11.55036
		8.492551	8.906101		A	A	
8.630556	8.011532	7.45108	7.329172	P	P	P	7.675036
7.139437			7.131638	A		P	6.647204
2.529463		5.11343	3.077708	P	M	P	6.381895
		3.787364			P		
	5.596494		4.104155	P		P	
10.75417	11.16751	10.41739	9.578155	P	P	P	10.5257
	5.934753		7.311765	A		P	
11.88593	11.75382	12.73158	13.0005	P	P	P	11.9137
8.128141	7.567013	8.942187	9.227717	P	P	P	8.506983
8.499079		8.82068	9.84687	A	A	A	7.212523
14.52718	14.76623	14.39642	13.6794	P	P	P	14.67491
8.484982	8.35789	8.120731	7.953413	P	P	P	6.809562
9.803484	8.867737	10.05508	9.534866	P	P	P	9.190028
6.37919		6.413891	6.247588	A	A	A	5.470881
7.604682	8.245283	7.658838	9.069779	P	P	A	1.928632
11.2099	11.22433	12.10302	11.42046	P	P	P	11.01519
7.196258	6.958089	5.671635	3.821758	P	P	M	7.244551
8.171883	8.39002	6.959023	7.106371	P	P	P	8.042344

8.236384	7.034251	8.831211	8.093746	P	P	P	8.152752
6.051435	5.738944	6.250803	7.405468	P	P	P	6.098744
7.621052	6.484993	7.494445	7.715888	A	M	P	5.046065
11.24003	11.34559	9.992974	9.896379	P	P	P	10.73014
11.2901	12.11806	11.23655	10.4609	P	P	P	11.87455
11.50362	11.77993	14.06892	15.01877	P	P	P	12.39653
9.487291	8.726375	9.669127	9.206264	P	P	P	8.632937
8.039224	7.01873	7.747862	P	M	P		7.744991
9.300735	10.38175	10.65692	10.26094	P	P	P	9.822157
7.361021	5.152093	6.315695	2.900765	P	P	P	6.922911
6.789468	6.108779	5.246833	5.786019	P	P	P	6.898065
7.699099	8.835489	9.993403	8.980085	P	P	P	9.031799
9.127019	8.699776	8.979754	9.438723	P	P	P	9.62639
8.966572	8.774269	9.365661	8.90239	P	P	P	9.251047
8.55934	9.255749	9.923827	9.729935	P	P	P	9.239116
5.193092			6.155315			A	6.48624
14.56758	14.98282	12.47165	13.4799	P	P	P	15.0475
8.387919	8.205465	8.012263	8.792885	P	P	P	8.28799
11.67884	11.33787	11.3618	11.16399	P	P	P	10.92458
8.640056	7.803173	8.240759	8.978977	P	P	P	8.199638
8.176165	9.06594	6.07285	6.425857	P	P	P	8.661161
7.279422	8.620303	5.751231	3.840238	P	P	P	7.915099
7.423786	8.076464	6.227531	5.932594	P	P	P	7.609377
10.39739	9.254647	10.79565	10.82635	P	P	P	8.726945
	7.560407	8.223961	8.446813	A	P	P	
			7.451373			A	
8.43111	8.160405	9.510617	10.24676	P	A	P	8.067688
6.536641	5.880318	7.089982	7.934678	A	A	A	6.443577
6.679274	7.480144	6.218412	6.915882	P	P	P	7.389805
9.441648	9.103832	7.977166	7.361851	P	P	P	8.426177
9.070835	9.815394	9.611794	8.727942	P	P	P	9.852564
6.616389	6.7244	7.086669	6.875353	P	P	A	6.200621
		6.047804			A		
9.958295	9.623374	10.94218	10.82793	P	P	P	9.435994
6.892005	6.324468	6.578681	7.5941	P	P	A	7.962964
11.39625	11.59715	10.57912	10.67552	P	P	P	11.50185
6.479549	5.969183	7.191422	6.754442	P	P	A	5.887576
10.26625	9.713882	9.806236	11.28697	P	P	P	9.292473
7.439964	7.577344	9.194136	8.087178	P	P	A	6.793395
			6.293632			A	

11.09133	11.53599	12.4818	11.86661 P	P	P	P	11.61474
7.596821	8.792039	8.249169	P	P	P		8.225175
5.806224	4.877692	5.33798	4.008767 A	P	P	P	4.360615
10.18035	9.650186	9.069017	9.017995 P	P	P	P	9.835852
11.42981	11.95125	11.04989	10.17374 P	P	P	P	11.63165
8.000643	9.459302	9.059301	7.574372 P	P	P	P	8.782671
13.63199	13.65672	14.24447	14.64131 P	P	P	P	13.75315
8.959663		8.936196	A		A		6.89397
9.747066	7.836096	9.458816	9.561307 P	P	P	P	7.627867
	6.415623	6.317918		P	P		
9.61871	9.038657	10.40557	10.79016 P	P	P	P	9.607371
6.659381	6.914538	7.221562	7.847049 P	M	A	A	6.797396
11.01587	12.26087	11.16537	9.584668 P	P	P	P	11.57213
11.19113	9.809902	11.24048	11.49812 P	P	P	P	10.0571
10.53764	10.70571	11.05496	11.46915 P	P	P	P	10.66616
11.11417	11.25289	12.95695	12.79762 P	P	P	P	10.83821
5.82696	6.33437	4.964585	5.482045 P	P	P	P	5.966914
13.48161	13.61142	13.30848	12.48795 P	P	P	P	13.42661
12.66438	12.00724	12.79536	12.31503 P	P	P	P	11.86836
		1.809283				P	
10.92165	9.854362	10.27243	10.15403 P	P	P	P	9.913368
14.93649	15.17447	15.94753	16.30714 P	P	P	P	15.08887
14.13061	14.52548	15.30191	15.48718 P	P	P	P	14.28533
15.54163	15.55885	16.02072	16.93509 P	P	P	P	15.64403
11.66668	12.4599	11.22286	10.37733 P	P	P	P	11.48318
9.592191	9.190738	9.841091	9.589681 P	P	P	P	8.567013
14.09526	13.79546	14.47931	14.76427 P	P	P	P	13.82883
8.843331	7.514541	8.72198	8.580579 A	A	A	A	3.37601
12.23186	11.88322	12.80357	13.42026 P	P	P	P	11.52869
12.51091	13.23789	13.19635	12.6264 P	P	P	P	12.85932
7.241778	6.363825	6.860135	6.698891 P	P	P	P	8.353337
	6.718899			A			
11.30541	10.31507	10.67922	10.91592 P	P	P	P	10.84478
12.17765	13.7313	13.23311	13.47291 P	M	P	A	13.39905
8.136801	8.597317	6.945579	6.625032 P	P	P	P	8.655029
7.387275	8.041726	7.739878	6.645059 P	P	P	P	8.010444
	5.234821	6.14507		A	A		
5.862215	5.488877	6.112799	6.707649 P	P	P	P	5.993597
6.657201	7.849244	7.466188	5.345715 P	P	P	P	7.39019
9.699066	8.612167	9.147945	9.076382 P	P	P	P	8.499069

10.52296	9.207433	10.72975	10.10618	P	P	P	9.258108
8.355982	7.625763	9.091953	8.689773	P	P	P	9.375332
5.000206	6.086086	6.405197	A	A	A		3.939456
12.58059	13.79888	13.14092	12.71615	P	P	P	13.55824
8.044395	8.770483	7.674294	7.252588	P	P	P	7.892018
10.78598	10.29554	11.54176	12.0624	P	P	P	10.9139
12.9023	14.42566	13.33577	14.51289	P	P	P	13.89595
9.380968	10.1152	8.245018	7.756379	P	P	P	9.660275
6.611426			7.09428			P	6.707469
		3.046041			P		
10.10494	9.332422	9.909983	10.13818	P	P	P	9.35589
12.26643	11.80021	11.48717	11.20867	P	P	P	11.78514
13.47783	13.47941	12.84919	12.62336	P	P	P	13.5742
8.180795	7.920091	7.871882	7.299288	P	P	P	7.03472
9.937198	9.200992	9.919759	9.254915	P	P	P	8.925664
5.545082	5.422135	2.914632	5.380884	P	P	P	6.509483
7.198065	6.90674	6.985156	6.900444	P	P	P	6.880586
6.063001	6.148262	4.180083	A	P	P		5.79298
10.57712	10.87291	10.67585	10.03727	P	P	P	10.32022
11.38521	11.67656	10.61411	10.16071	P	P	P	11.14806
12.09633	11.04699	12.35726	12.64505	P	P	P	11.64418
6.376627	7.180059	1.931001	A	P	P		7.024178
10.31053	9.894071	10.55653	11.38465	P	P	P	9.969744
7.596191	6.708422		8.573333	P		P	7.308492
10.59692	11.60942	10.12536	9.452184	P	P	P	11.20788
6.993575	8.681191	7.825796	7.058718	P	P	M	8.096442
10.29057	10.90171	10.05361	9.154628	P	P	P	10.63938
7.100707	7.437423	8.694846	8.822646	P	P	A	7.229067
8.071075	9.107299	9.070754	9.119057	P	P	P	9.237292
8.208513	7.958057	8.099387	8.482128	P	P	P	9.376134
12.09194	12.23071	10.17424	10.19135	P	P	P	12.30856
9.879615	10.71494	8.479554	7.951332	P	P	P	9.807602
7.923592	9.936271	8.666827	8.801107	P	P	P	9.509043
11.03775	11.15009	11.81295	13.14907	P	P	P	10.93432
5.995932	5.682278	6.169098	7.971236	P	P	P	7.025504
7.955123	6.726731	8.350896	7.975232	A	P	P	6.590059
8.633768	9.049978	8.318129	8.613135	P	P	P	8.689244
10.53579	10.57392	11.48039	11.52058	P	P	P	10.66963
5.118437		7.035782	P		A		6.213906
7.982523	7.705992	8.390799	8.32366	P	M	P	7.858939

9.080533	9.574487	10.13314	10.68593	P	P	P	9.666995
5.973892	5.437467	5.266344	4.556471	P	M	P	6.119755
9.600092	8.655236	9.460868	10.19926	P	P	P	9.013699
6.645798	6.88533	6.125551	4.156036	P	P	P	6.476371
7.324179	7.082503	8.135878	7.158696	P	P	P	7.265881
10.0073	10.46347	10.31055	11.28696	P	P	P	9.406709
		7.235688	8.13229		A	A	
7.501199	7.020352	7.060038	6.088758	P	P	P	7.265018
8.804887	8.594212	7.80436	8.156027	P	P	P	7.144953
7.707964	6.775695	7.438807	8.426453	P	P	P	7.167035
	5.213447		6.452603	A		A	
11.12083	11.57878	11.61948	12.60578	P	P	P	11.84084
11.97759	12.28153	11.41088	10.87379	P	P	P	11.80967
14.54476	14.83455	14.00638	13.49307	P	P	P	14.70386
10.03664	10.0519	9.595227	9.274069	P	P	P	10.00798
		5.857025			A		
5.548592			A				3.037996
6.580474	6.282096		7.311767	A		A	6.539799
6.758854	6.560209	5.981317	5.882299	P	P	P	6.677123
10.85803	11.29085	11.59252	12.46301	P	P	P	11.51951
10.66578	11.273	11.37538	11.74549	P	P	P	11.33088
			6.418856			P	
9.391222	9.032234	11.99068	11.21726	A	A	M	8.897645
8.516588	8.584618	11.17754	10.24397	A	A	A	8.097434
11.17347	11.40596	11.65776	11.47623	P	P	P	11.20409
11.0547	10.77914	9.306885	9.059813	P	P	P	11.05466
10.64899	10.60046	11.45882	11.88595	P	P	P	10.92432
		6.107112			A		
3.696651		5.568559	P		A		5.292888
9.190935	9.28948	9.706019	10.77511	P	P	P	9.90402
9.760607	10.1032	8.643998	8.465767	P	P	P	9.797246
9.154593	9.725565	8.104287	8.339109	P	P	P	9.75188
7.848184	7.217415	7.674974	7.808852	P	P	P	7.567228
12.55792	12.55395	12.75375	14.06596	P	P	P	12.92032
12.0484	12.37719	12.58299	13.62478	P	P	P	12.56226
7.543446	8.208472	7.522275	5.779433	P	P	P	7.422421
9.854734	8.537524	8.999288	8.5787	P	P	P	8.372841
6.373437	6.529948	6.337189	6.521524	P	P	P	6.300676
	1.256763	5.266388		P	P		
5.350636			A				1.298705

9.783093	9.646318	10.19001	11.11658	P	P	P	9.665058
7.85706	7.50761	7.936471	P	P	P		6.457498
10.28123	9.360765	9.459478	8.505981	P	P	P	8.907722
7.238563	8.797963	8.351056	6.509358	P	P	P	8.393675
11.00271	12.21212	11.72586	11.17903	P	P	P	12.23235
10.72563	10.46543	10.55132	11.84119	P	P	P	10.5162
6.016141	5.906567	6.006521	A	A	P		5.691995
12.47141	12.07059	12.07715	11.6992	P	P	P	12.04642
5.047422	4.066578		6.176201	P		A	6.028078
11.8891	11.56819	11.37044	10.42116	P	P	P	11.32799
8.208736	8.752119	8.675454	7.230916	P	P	P	8.269196
12.92592	12.13308	12.50535	11.91001	P	P	P	11.75475
8.719378	9.357285	8.152515	8.169662	P	P	P	9.467266
6.49024	8.278101	8.028305	7.675068	P	P	P	8.554156
8.314477	8.173136	7.332855	6.977659	P	P	P	7.631057
12.87655	11.60036	14.97909	14.6981	P	P	P	11.33448
13.30892	12.31103	15.09346	15.21085	P	P	P	11.78663
5.693541	5.285505		A	P			4.453478
12.98324	13.32513	12.49525	11.92222	P	P	P	13.00797
8.501047	8.512865	7.241173	6.807907	P	P	P	8.339485
10.26461	9.854025	11.41333	11.35829	P	P	P	10.15796
9.06256	9.297746	9.681144	8.637514	P	P	P	7.937709
10.72827	8.704127	9.529964	9.82449	P	P	P	9.904304
9.35333	8.945505	9.042962	8.315064	P	P	P	8.99088
6.973933	6.340108	7.082775	6.999402	P	P	A	6.590284
10.48933	11.03904	9.21597	9.018039	P	P	P	10.4916
7.922974	8.514376	6.559816	7.071382	P	P	P	7.931878
6.415282	6.450675	3.862491	4.088307	A	P	P	6.548901
7.598249	8.22294	8.337737	8.847769	P	P	P	8.085838
10.94248	10.57394	10.47126	9.971886	P	P	P	10.41131
12.26855	13.18195	12.6537	11.87265	P	P	P	12.85711
5.311312	4.595058	5.210362	4.568287	M	P	P	5.527497
12.07388	12.02679	11.8031	10.82373	P	P	P	12.05205
	5.237119	2.91575		A	P		
8.374711	8.965542	10.96663	10.97017	P	P	P	8.096236
	4.699991			A			
8.949971	9.478764	8.535273	7.732355	P	P	P	8.712389
14.16085	13.75986	12.43059	13.92257	P	P	P	14.46497
		1.086776			P		
7.27929	7.148947	8.968146	8.824484	P	P	A	7.252331

5.942803	6.379138	7.751297	6.233917	A	P	P	P	5.015283
10.62942	10.28099	11.11329	11.45115	P	P	P	P	10.32279
6.13779	7.455099	7.243616	7.404339	P	P	P	P	6.706867
5.858527	6.921619	6.502167		A	P	P		7.104701
11.6465	11.71925	10.41783	10.32619	P	P	P	P	11.50214
6.893515	7.707994	6.860803	6.294939	P	P	P	P	7.136483
11.43522	12.45462	11.18074	10.77886	P	P	P	P	11.99574
6.634826	6.968383	6.500944	7.310668	P	P	P	P	7.672323
12.95019	13.20847	11.66877	11.46761	P	P	P	P	13.31114
7.673723	6.91702	5.632641	5.843714	P	P	P	P	7.50474
8.271797	8.218043	8.85882	7.956085	P	P	P	P	7.922239
		3.873013	5.187137			M	P	
11.27103	10.77819	10.80825	11.35805	P	P	P	P	11.59251
12.18478	11.59403	12.88098	13.10365	P	P	P	P	11.54979
5.17595		4.926133	6.942356	A		P	A	3.755149
8.135554	8.304241	7.929156	7.278637	P	P	P	P	8.436076
		6.220064				P		
8.958665	8.980627	9.515171	9.252563	P	P	P	P	8.806203
	6.759051			A				
5.346115	3.901529		P	P				5.885651
	5.393174	3.339893	6.825597	A	P	A		
6.883669	6.829928	7.077134	5.79601	P	P	P	P	6.735259
			4.120773				P	
12.07621	11.1656	9.213136	10.75411	A	P	P	P	1.443144
8.204745	8.363867	8.03563	7.887175	P	P	P	P	7.922825
12.26187	12.26992	11.79376	10.0332	P	P	P	P	12.66001
9.733266	8.762352	10.9726	11.25901	P	P	P	P	8.805869
	5.758172	6.44293	6.648727	A	P	A		
7.451244	7.901525	8.197015	8.245664	M	P	P	P	6.928302
14.64218	14.08424	15.28728	15.84927	P	P	P	P	14.29108
5.756061	6.716133	5.85109	6.013226	P	P	P	P	6.706609
9.098548	9.003056	10.11048	10.77849	P	P	P	P	10.07387
8.792617	8.588464	9.283175		A	P	A		9.156576
2.659829			P					4.906841
9.867133	10.04429	9.756985	9.054102	P	P	P	P	10.00045
10.87704	12.405	11.9425	10.68895	P	P	P	P	12.14425
9.027873	8.556772	9.851452	10.24104	P	A	A	A	9.149727
			4.624328				M	
8.215098	7.683682	6.323266	5.211891	P	P	P	P	6.799091
10.53896	10.75081	9.431696	8.669987	P	P	P	P	9.511905

8.598557	8.304235	8.821341	7.935206 P	P	P	P	7.303919
12.88521	11.96885	13.26892	12.91388 P	P	P	P	11.77531
10.18826	9.778604	9.065256	8.587047 P	P	P	P	8.768225
9.305007	8.727106	10.16535	9.967318 P	P	P	P	9.707212
	5.240863	6.624334	6.949885	P	P	P	
7.385132	6.760362	6.575897	7.01372 P	P	P	P	6.099277
9.059328	7.959663	7.056605	7.054499 P	P	P	P	8.548785
13.70283	13.95089	12.18046	11.15353 P	P	P	P	13.4836
11.07283	11.00747	11.79098	11.74956 P	P	P	P	11.12161
5.253355	6.049156	5.873069	7.069127 P	P	P	P	7.163066
9.515275	8.844539	9.670911	10.00419 P	P	P	P	8.807292
7.059785		5.678173	6.365639 M		M	P	7.046813
10.6567	10.42071	10.86592	11.23298 P	P	P	P	11.17066
6.770943	6.995666	7.294357	8.18743 P	P	P	P	7.316083
	2.962093			M			
9.798381	8.901923	9.591476	7.762893 P	P	P	P	8.748521
11.88306	12.37785	12.76898	13.1822 P	P	P	P	12.28924
13.36782	13.93688	13.20261	12.71827 P	P	P	P	13.93418
13.3974	14.18675	13.50502	13.08419 P	P	P	P	13.87517
4.66572	5.887518		2.785875 P	P		P	5.663987
14.69194	14.91831	13.71568	12.66102 P	P	P	P	14.45056
		6.339717	7.276821		P	A	
8.82911	9.167051	10.06086	9.80747 P	P	P	P	8.791524
8.670961	9.162286	8.070562	6.30144 P	P	P	P	8.499988
7.04069	6.914658	7.513632	7.71691 P	P	P	P	6.81113
11.81904	12.07415	10.98197	10.58272 P	P	P	P	11.81777
9.545675	10.31449	11.50602	11.04138 P	P	P	P	10.99182
10.21408	10.05338	10.4668	10.38026 P	P	P	P	9.167052
11.05333	11.09499	11.41131	11.86216 P	P	P	P	11.46608
8.489897	8.2847	9.45618	8.81851 P	P	P	P	8.432261
6.526131	6.416845	6.15972	7.996906 P	P	P	P	6.419565
		8.746481	8.641156		A	A	
8.68341	8.535024	7.163141	7.73318 P	P	P	P	8.416389
8.674128	8.612506	8.066001	7.791671 P	P	P	P	8.264138
8.747922	8.077677	7.645354	7.173546 P	P	P	P	7.412655
8.556919	8.175349	6.597373	6.546664 P	P	P	P	8.443195
11.27573	10.85838	11.71537	11.37313 P	P	P	P	10.69086
7.172735	6.808546	6.160204	6.359145 A	P	P	P	5.331782
10.88259	10.8993	12.11446	11.84658 P	P	P	P	9.662112
10.43214	11.2004	10.51704	9.367842 P	P	P	P	10.45569

12.42197	12.55936	11.29189	11.5771 P	P	P	P	12.5988
12.31948	13.30781	12.92372	12.5357 P	P	P	P	13.35898
11.41802	12.32246	12.26628	13.33233 P	P	P	P	12.41718
7.096193	7.277225		8.715937 P	A		M	8.679906
7.154501	6.599673	7.733891	A	P	A		6.04316
6.244961		6.305522	6.484116 A		P	A	6.628391
7.363503	5.358605	6.730879	A	P	M		6.076376
9.375315	9.850208	9.057652	8.913346 P	P	P	P	10.25449
9.231077	9.529141	8.869697	8.192781 P	P	P	P	9.475748
9.159238	9.484506	8.935193	9.265159 P	P	P	P	10.01033
8.761727	9.563448	8.241772	8.20774 P	P	P	P	9.375713
9.489461	10.20683	8.781928	7.769211 P	P	P	P	9.955036
11.82843	12.45613	11.088	10.2929 P	P	P	P	12.00383
8.957829	10.29722	10.33401	8.015458 P	P	P	P	9.748426
8.558757	9.534427	8.663214	7.181268 P	P	P	P	9.038682
8.565729	9.587723	9.997182	7.812011 P	P	P	P	8.881477
11.70119	12.18712	10.73235	9.948327 P	P	P	P	11.77265
6.912762	6.629185	6.717554	4.183023 M	P	P	P	7.257581
	3.525644			P			
	5.247385		2.753786	A		P	
7.625365	9.033625	7.228766	7.557277 P	P	P	P	8.032103
9.359272	9.814346	8.582277	7.069837 P	P	P	P	9.582893
5.074014			A				
12.02174	12.57182	11.25929	10.18394 P	P	P	P	12.12456
5.940764	6.036035	5.926908	5.608977 P	P	P	P	5.851214
9.409493	10.47707	10.39702	6.979091 P	P	P	P	10.26326
6.938536	7.790013	7.928267	8.665941 P	P	P	P	8.570977
11.46161	12.8187	11.03748	11.64266 P	P	P	P	12.11998
11.94894	12.19095	11.37478	11.6795 P	P	P	P	12.03568
13.55856	12.98205	13.59553	14.98334 P	P	P	P	12.1525
13.91155	13.44228	14.9246	15.66062 P	P	P	P	13.29825
13.54542	12.78749	13.45234	14.95928 P	P	P	P	11.99844
6.619962	5.615272	8.029239	8.011838 A	M	A	A	6.273911
6.78266	5.630264	7.74051	6.596644 M	P	A	A	6.398527
8.175529	7.619738	8.99227	9.176741 P	P	P	P	8.668328
10.2623	10.13034	10.79313	10.77881 P	P	P	P	10.73991
8.391542	8.940556	9.754361	8.539882 P	P	P	P	9.308682
8.984521	9.004262	9.631585	8.875671 P	P	P	P	8.817138
5.371254			2.697615 P			P	6.164748
8.558299	9.158753	8.723848	10.06921 P	P	P	P	9.157047

12.50582	12.83183	10.89349	11.85936 P	P	P	P	12.62807
			6.923246			A	
14.68083	14.54738	15.16197	16.21367 P	P	P	P	15.56612
9.585428	8.925554		9.126132 P	P		A	11.05967
12.42883	12.60513	13.695	13.72795 P	P	P	P	12.12329
9.27738	7.667961	10.21552	10.29979 P	P	P	P	9.3922
9.003893	9.415938	9.899129	10.84306 P	P	P	P	9.710689
4.854101	7.187978	7.537767	7.397544 P	P	P	A	7.188147
10.78211	9.394911	10.54608	10.16895 P	P	P	P	9.116443
10.73847	9.752916	10.11545	10.55363 P	P	P	P	9.066134
11.59625	11.21059	11.0944	10.82697 P	P	P	P	11.18459
7.9423	7.288165	5.844264	6.49406 P	P	P	P	7.053809
6.351122	6.545209	6.732896	6.884419 P	P	P	P	5.483771
12.28235	13.56329	14.10666	13.65429 P	P	P	P	14.40892
7.199926	7.637877	7.990046	8.378611 P	P	P	P	8.436137
5.368764			7.161522 P			P	6.190051
	6.116794	6.633535		P	A		
9.387177	9.15049	10.05467	9.944959 P	P	P	P	8.92922
8.237302	8.567563	10.70006	9.685914 P	P	P	P	8.284823
	6.73786			A			
11.12371	10.57455	10.28508	10.66296 P	P	P	P	11.43259
		4.391571			M		
5.21276		5.080754	6.012672 P		P	A	6.234515
10.3021	9.97118	10.48035	10.76884 P	P	P	P	10.30549
7.190983	7.891304	6.911821	6.967379 P	P	P	P	7.383752
9.616136	8.302728	11.27457	11.80419 P	A	M	A	8.625503
5.909848	5.875088		A	A			6.262919
6.205884			A				3.914256
6.637558	5.263186	7.477684	P	A	P		5.684248
6.638841	6.348729	6.687971	5.477425 P	P	P	P	7.037962
6.308991	5.688951		P	A			6.31191
			10.22387			A	
9.367785	8.731378	7.663384	7.651822 P	P	P	P	9.639599
5.927501	6.375079		7.651209 P	A		A	6.945876
8.307582	7.934852	9.120406	8.912061 P	P	P	P	8.232303
8.074927	6.920031	6.771715	7.394722 P	P	P	P	6.976646
9.917438	9.74237	8.495714	10.24242 P	P	P	P	11.00454
		5.417013	6.763885		P	P	
7.819259	7.289574	7.22785	7.098633 P	P	P	P	7.344762
7.295469		8.254771	8.214865 P		A	A	7.374268

6.732812	5.850012	7.976789	6.987015	P	P	P	6.412192
		5.447142	6.605907		A	A	
6.754715	5.746787	11.24288	P	P	P		6.4484
9.167792	8.329691	8.361941	9.186501	P	P	P	8.625993
7.532819	8.464156	7.471095	8.064198	P	P	P	8.198664
11.43294	11.61117	10.87038	11.3578	P	P	P	11.76481
		6.433472	6.62902		P	A	
		5.346114			M		
8.430293	8.983878	10.3155	12.18209	A	A	P	2.64133
8.911444	9.118077	10.29566	10.14312	P	P	P	9.129624
10.84799	10.82385	11.81354	10.89585	P	P	P	10.22798
11.66628	10.65638	11.41708	11.62342	P	P	P	10.60418
7.266125	6.996738	6.700253	6.302122	P	P	P	7.813765
5.190203			A				4.050242
9.640977	8.375403	9.344944	8.811065	P	P	P	8.15061
6.093474			A				4.917553
8.401121	8.328023	8.978005	6.976889	P	P	P	7.869515
10.61401	9.487404	10.5108	9.862294	P	P	P	9.265641
4.418706	7.026387		M	A			6.389987
11.96937	12.14231	13.49414	14.16284	P	P	P	12.30448
7.810581	9.067466	8.248384	7.872059	P	P	M	7.976627
8.412525	10.29505	9.604501	8.702888	P	A	P	2.051295
8.917047	8.12955	9.065178	8.559425	P	P	P	7.946757
9.992388	9.493281	10.60959	10.48854	P	P	P	9.399292
10.01084	9.506285	8.683764	8.588904	P	P	P	9.902596
11.06921	10.10251	10.93869	11.65229	P	P	P	10.00733
12.33963	12.02704	10.20363	9.548755	P	P	P	12.23323
7.908432	5.474612	7.531057	7.331214	P	A	P	8.706038
7.545291	7.153461	10.08886	11.17579	A	A	A	7.563059
8.442402	8.712528	10.0543	9.882625	P	P	P	8.74102
8.092243	8.853089	10.33307	9.881399	P	P	P	8.70245
1.571427			P				5.277866
10.71052	11.75763	10.52794	10.37642	P	P	P	11.19693
6.834334	7.515772	6.879321	P	P	P		6.752356
8.622457	7.031126	8.827989	8.131043	P	P	A	8.256806
9.755128	9.712673	8.545626	8.270042	P	P	P	10.57076
9.3554	9.708221	9.341662	9.476746	P	P	P	10.11708
9.117108	9.452761	9.803827	9.614278	P	P	P	9.359418
5.701099		6.237907	6.906234		P	A	3.190546
9.398232	9.703336	8.819168	8.575446	P	P	P	9.518271

10.52297	10.79536	9.991035	10.05019 P	P	P	P	10.9584
6.948535	7.468484	7.296749	6.310862 P	P	P	P	7.031282
	5.961555	4.666664	5.991441	P	P	P	
			3.384826			P	
10.17117	9.528425	10.49191	9.909451 P	P	P	P	9.677663
9.309882	9.343501	8.54491	8.577319 P	P	P	P	9.278489
8.232293	9.192096	8.498778	8.02832 P	P	P	P	8.225931
10.74405	10.96264	10.28915	10.16913 P	P	P	P	10.58804
5.930135	5.223752	6.016548	P	P	A		6.683
9.520668	9.059371	9.955011	8.450418 P	P	P	P	8.292425
9.847614	9.984012	10.648	11.20489 P	P	P	P	10.55664
9.723901	10.72723	11.71512	12.01046 P	P	P	P	10.2265
3.594067			A	P			5.659129
10.10634	10.01955	10.45043	9.842964 P	P	P	P	9.735029
9.597022	9.771269	8.649504	8.983459 P	P	P	P	9.317008
7.431699	7.040351	6.154002	6.905613 P	P	P	P	7.24245
6.374686	6.248522	6.854533	6.868837 A	P	P	P	5.839611
7.547675	6.648415	7.492971	7.819345 P	M	P	A	7.412867
8.57195	7.652224	9.339537	9.642716 P	P	P	P	7.9111
11.7661	10.45142	11.25396	11.47315 P	P	P	P	10.08365
9.159495	8.634153	8.617599	7.672308 P	P	P	P	8.265237
4.252906	5.381713	4.886951	2.078449 A	P	M	P	5.06279
10.72131	11.48368	10.35203	9.90402 P	P	P	P	11.0369
10.41361	9.718715	10.28609	10.14799 P	P	P	P	9.199584
9.416112	9.673459	10.27772	10.64448 P	P	P	P	10.30918
8.843067	9.413598	9.807449	9.999396 P	P	P	P	9.640444
5.668925	5.175158		3.416466 P	P		P	5.595419
6.390551	7.206598	7.005889	P	A	A		7.030815
9.266006	9.415741	8.05923	8.937367 P	P	P	P	9.342615
7.483527	6.21093	6.822833	7.242477 P	P	P	P	6.134729
7.381439	6.915813	5.648408	6.455884 P	P	P	P	7.493766
8.118602	8.837171	7.974004	7.747064 P	P	P	P	8.428235
11.88609	11.81777	10.32742	10.58539 P	P	P	P	11.91168
10.0119	10.18505	9.087708	9.265174 P	P	P	P	10.00393
8.215859	7.620871	8.66722	9.321577 P	P	P	P	7.633988
6.144921	6.31412	6.706219	A	P	P		2.688021
12.82659	11.17622	12.52942	12.88315 P	P	P	P	10.83728
12.67631	13.10377	13.55199	14.22525 P	P	P	P	12.85162
7.904968	6.992824	6.328294	6.046907 P	P	P	P	7.599238
7.284168	6.892839	7.319082	8.312878 A	P	A	P	7.008438

8.661779	7.514627	9.461376	9.891188 P	P	P	P	8.226753
			8.173745			A	
11.32285	11.57807	10.04958	9.772035 P	P	P	P	11.22974
7.028029	6.420189	6.374313	5.101085 P	P	P	P	6.864432
6.441334	6.536536	7.084582	7.153051 P	P	A	P	7.456725
12.25097	11.35005	12.81917	12.97223 P	P	P	P	11.08454
8.736511	8.476628	10.1894	11.2912 P	P	P	P	8.547
14.8928	14.70773	14.1357	14.29039 P	P	P	P	15.27428
12.06897	11.0283	12.29242	12.55346 P	P	P	P	10.8538
6.834994	6.667503	7.959079	8.614829 A	P	P	A	6.872957
12.74816	11.63076	13.9651	14.75915 P	P	P	P	11.89342
5.936199		5.758333	A		P		1.381219
	8.070658	7.786424	7.492864	P	P	P	
8.288288	7.409469	8.408305	8.003457 P	P	P	P	7.22839
12.35848	12.58784	13.40583	12.41978 P	P	P	P	12.37422
11.62896	11.97427	12.76117	13.00408 P	P	P	P	12.16248
9.71716	9.633964	10.75147	10.66983 P	P	P	P	9.470708
6.938567	7.735025	8.060324	8.22806 P	P	P	P	7.95353
6.303787	5.333974	6.369791	A	A	A		5.901214
11.00323	9.966811	8.559258	9.380896 P	P	P	P	10.2105
10.00398	9.537471	9.179999	9.26103 P	P	P	P	9.678181
7.607606	7.150575	8.27896	8.557705 P	P	P	M	7.771283
9.635307	9.693426	8.962625	7.364991 P	P	P	P	9.121938
9.372436	8.788461	10.15164	10.62159 P	A	A	P	9.049886
5.394763			6.443087 P			A	6.83526
			4.630528			P	
8.147853	7.793082	8.413253	8.699393 P	P	P	P	7.624351
7.784194	7.008872	6.460544	P	P	P		7.191566
6.323272	7.052252	6.831532	2.985729 P	P	P	P	7.116949
8.056184	8.085744	7.518242	8.215039 P	P	P	P	8.924649
	5.538532	6.506108	6.910034	A	M	P	
10.92349	11.04547	10.3814	9.080426 P	P	P	P	10.67337
4.144115			P				5.252331
9.946405	10.97137	8.780268	8.520101 P	P	P	P	10.34975
8.764931	7.752569	8.489142	8.515293 P	P	P	P	8.492317
6.424215	6.182764	6.764097	6.765092 P	A	A	P	6.887464
8.268266	8.319194	8.647387	8.794383 P	P	P	P	9.234554
11.44344	10.56529	11.31319	11.56611 P	P	P	P	11.68631
6.35687	7.568115	8.281323	8.640428 P	A	A	A	8.029526
8.435905	8.28581	7.966302	8.633682 P	P	P	P	9.043499

9.846878	9.385273	9.777069	9.404703	P	P	P	9.101387
13.0195	13.42027	13.35309	13.39481	P	P	P	13.29001
6.335873	7.179573	6.592115	6.378991	P	P	P	6.189953
7.994543	9.450363	8.960313	9.479169	P	P	P	8.167676
7.535798	6.790313	5.879952	4.586894	P	P	P	6.376234
8.646594	8.811229	8.019742	6.794385	P	P	P	8.314503
	6.363936		6.244568	A		P	
10.21503	9.826816	9.457342	8.712335	P	P	P	9.502553
11.88195	11.42554	11.44376	11.31057	P	P	P	11.19187
9.220443	8.672507	7.571926	8.351568	P	P	P	8.855499
10.30644	10.3362	11.20595	11.42871	P	P	P	10.38608
10.20061	10.87129	11.73889	11.16967	P	P	P	10.24132
10.36256	9.97786	8.261849	9.02368	P	P	P	10.73157
6.650716	7.230917	7.012075	6.822405	P	P	P	6.251389
6.625081	5.311636	7.510431	7.807999	A	P	M	6.10332
10.06355	10.46202	9.780667	9.067826	P	P	P	10.12744
5.913993	6.683092	7.011339	6.93407	P	P	P	6.732342
6.703815		8.054797	A		A		5.324172
			3.259389			P	
6.175231	5.965999	6.080353	6.545435	P	P	A	6.026014
10.15394	11.20989	9.126266	8.669384	P	P	P	10.49719
8.639074	7.912308	9.568712	9.991645	P	P	P	6.911741
6.849555	6.38885	7.382461	7.231276	P	A	P	7.301004
8.074023	7.750137	8.202213	8.435739	P	P	A	7.921138
8.104388	7.521719	8.42196	7.592798	M	P	A	6.96213
7.565399	7.302051	6.589523	6.428665	P	P	P	7.449338
11.65704	12.13155	11.56581	10.33688	P	P	P	11.76164
4.133217	4.987413		P	P			5.685342
8.493935	8.332253	8.802622	9.308155	P	A	P	8.062493
11.60512	11.74392	10.76664	10.67632	P	P	P	11.07201
10.20989	8.686678	9.783425	9.749838	P	P	P	9.112475
11.55119	12.02797	12.46755	12.7539	P	P	P	12.02614
13.07037	12.6378	12.26166	11.56739	P	P	P	12.73979
10.02018	10.37449	11.65335	11.60993	P	P	P	10.03263
9.260267	9.785378	8.846308	9.012759	P	P	P	9.872853
4.772301			P				5.993903
7.409464	6.39243	6.575982	5.998754	P	P	P	5.700023
5.365367	5.143671	4.575881	P	P	P		5.676874
5.48879	5.521157		A	P			3.184945
10.85837	10.47152	9.266577	9.742083	P	P	P	10.93764

5.793855	5.685591	5.51081	7.268306	A	A	P	5.750643
11.86188	12.00108	10.98684	10.87966	P	P	P	11.49476
11.68208	12.22111	11.16662	10.94446	P	P	P	12.00218
9.245482	7.903086	9.518649	9.219962	A	P	A	6.917488
7.58189	7.729596	7.520515	8.135436	P	P	A	7.819866
	4.449448			P			
		5.213479	6.095397		P	A	
9.957857	10.4533	9.651006	8.898839	P	P	P	10.11732
5.700275	6.336391		2.033856	A		P	6.242236
8.194764	9.126541	8.610071	6.56511	P	P	P	8.570091
8.508379	8.965834	7.174382	7.658901	P	P	P	8.937276
6.656642	7.341461	6.152279	7.442754	P	P	P	6.944272
11.72522	11.19337	10.55861	11.38634	P	P	P	11.61535
7.960875	6.638712	7.537388	8.306086	A	P	P	7.452448
5.779027		6.340574	A		P		2.851849
13.56242	13.9915	10.75689	12.16029	P	P	P	14.24877
11.89772	10.9372	11.62616	11.14684	P	P	P	9.567806
10.58839	11.01107	11.41429	9.928639	P	P	P	10.60357
8.779749	9.354426	8.63087	8.25903	P	P	P	9.029456
10.52909	10.34983	12.21638	11.94773	P	P	P	10.22206
13.40357	13.03215	11.61467	12.51018	P	P	P	13.48975
7.939551	5.869111	7.254949	7.489631	P	P	P	7.034487
7.599605		6.252233	6.263964		P	P	6.447714
12.11795	12.31187	12.90356	12.66466	P	P	P	11.37541
6.227913	6.333155	6.112466	6.312042	P	P	A	5.165521
		6.5614			P		
6.962581	6.588105	7.014363	A	P	P		6.226334
8.509435	8.272936	8.95956	9.040692	P	P	M	8.618197
10.71222	11.22643	12.02049	11.55576	P	P	P	11.0574
4.819074		6.039811	P		P		6.286973
8.387947	7.899727	7.06233	6.870683	P	P	P	7.471434
10.95838	10.71004	10.21792	9.649539	P	P	P	10.12502
4.131132			P				6.108985
11.3184	12.24873	11.47805	10.65278	P	P	P	11.74726
7.115396	6.897898	7.536787	8.719733	P	P	P	6.502476
6.474499	7.293946	6.391853	A	P	P		6.370395
12.74422	13.10675	12.1181	11.33091	P	P	P	12.99666
9.329622	9.426269	8.589199	8.893567	P	P	P	9.702835
10.79628	11.61301	10.79972	10.39221	P	P	P	11.46496
7.400936	8.268611	8.067448	7.099022	A	P	P	7.251679

8.978108	8.548926	10.13761	10.9114 P	P	P	P	7.965564
9.020962	8.307114	9.457414	9.307293 P	P	P	P	6.791043
9.811467	9.936652	8.524318	8.28471 P	P	P	P	8.505048
7.866962	7.940307	9.068377	10.07603 P	P	P	P	7.289741
		7.476157			A		
			1.315962			P	
		7.292079	8.149262		P	A	
6.51538	6.293265	6.2536	7.442035 P	A	M	P	6.8445
9.717008	7.136545	9.615896	10.03249 P	P	P	P	8.678747
8.386538	6.082413	7.673867	9.076526 P	P	P	P	7.036939
9.133047	8.228384	9.247239	9.995698 P	P	P	P	8.599326
7.23033	6.70749	8.287488	8.164451 P	P	P	P	7.168446
8.12217	8.057155	8.202802	7.758129 P	P	P	P	6.962491
10.62872	10.79413	9.870433	9.354979 P	P	P	P	10.71294
9.583525	9.045491	10.38042	8.765024 P	P	P	P	8.598564
7.632103	7.434304	7.517188	7.535508 P	P	P	P	7.279087
7.540309	7.351039	9.455827	8.452738 A	P	P	P	6.861684
8.128266	7.490828	8.748524	7.660376 P	P	P	P	7.707013
11.97972	12.82765	11.89053	11.73742 P	P	P	P	13.22013
8.637343	8.318664	8.843721	8.298837 P	P	P	P	7.622374
5.784895	4.23052	5.996476	P	P	P		5.863564
6.835311	6.751028	6.977562	7.875458 P	P	P	A	7.102431
8.511341	8.198101	8.777041	8.703244 P	A	A	P	8.341406
6.696753	6.597656	9.347183	7.813867 A	P	P	P	5.661017
12.7811	12.53591	12.80619	14.30962 P	P	P	P	13.5434
8.792698	8.624977	8.682273	9.725391 P	P	P	P	8.39247
10.75735	10.93414	10.1909	9.266416 P	P	P	P	10.69718
7.076797	7.204846	4.494875	6.001587 P	P	P	P	6.677368
10.43099	9.750147	9.704609	10.11117 P	P	P	P	10.6243
9.1776	8.408623	10.15539	10.28668 P	P	P	P	8.752674
12.10277	12.39733	10.74308	10.52321 P	P	P	P	11.81519
8.286452	8.723138	7.000546	6.694181 P	P	P	P	8.24442
8.568794	8.240098	7.512496	6.266895 P	P	P	P	7.517192
9.955815	10.60277	9.49274	8.650252 P	P	P	P	10.09311
1.448818	6.554881		5.254823 P	P		P	5.663923
11.45164	10.11555	10.73846	9.487269 P	P	P	P	9.860092
			7.367187			A	
8.41277	9.159825	7.60748	7.726264 P	P	P	P	9.289556
10.75375	10.71793	11.02984	10.30845 P	P	P	P	10.53432
11.88466	12.56261	11.53512	10.78705 P	P	P	P	12.12703

9.590557	9.103844	10.21469	9.870195 P	P	P	P	9.271981
	4.561491		5.439092	A		M	
5.582841			A				3.071467
10.67083	9.643979	9.203692	10.21326 P	P	P	P	11.1393
10.07376	9.515165	10.50769	11.30482 P	P	P	P	9.904702
11.33781	11.06914	11.17508	10.52945 P	P	P	P	10.00333
		4.358288			P		
6.812685	6.700066	6.861938	6.812512 P	P	A	P	6.768012
9.001679	8.348439	9.501192	9.369758 P	A	A	A	8.701778
9.668121	8.967411	9.97254	9.775324 P	P	P	P	8.864805
11.64466	12.22056	10.71565	10.70032 P	P	P	P	11.79076
	7.529018		4.238873	M		P	
10.68781	10.50087	11.5694	11.40428 P	P	P	P	10.72482
6.367026	4.157451		A	P			5.486329
8.305865	8.943276	9.159531	9.054657 P	P	P	P	8.481279
	6.873141	4.420076		A	P		
12.42692	12.73511	13.36214	14.72323 P	P	P	P	13.32424
6.486503	7.138573	4.724582	2.639581 P	P	P	P	5.958808
8.22506	8.724105	7.693696	6.326907 P	P	P	P	8.340612
6.647932	6.40379	7.191505	7.957392 P	P	P	P	7.082396
	2.75529		6.898962	P		P	
	5.725799	6.210996	6.878411	P	A	A	
8.790085	9.610737	8.004295	8.226399 P	P	P	P	9.191079
		5.430632	3.420206		M	P	
11.15958	11.48932	10.38288	9.252639 P	P	P	P	11.1664
7.169334	7.97152	6.973334	7.115563 P	P	P	P	6.809607
12.50511	12.60295	11.68213	11.55437 P	P	P	P	12.87878
15.16742	15.27543	15.70591	16.75648 P	P	P	P	15.58384
13.60721	12.99202	13.98794	14.17625 P	P	P	P	12.80526
	4.824132			P			
9.016008	8.871205	7.615334	7.143365 P	P	P	P	8.463339
11.26868	12.06041	12.51506	13.34964 P	P	P	P	11.95573
8.73629	8.176223	7.582995	6.984578 P	P	P	P	8.904852
11.15785	10.97636	11.68131	10.97108 P	P	P	P	10.67313
8.214689	8.535848	9.168028	9.380013 P	P	A	A	8.526972
7.492464	7.434881	6.347909	5.878174 P	P	P	P	7.032107
7.478689	6.57308	5.991925	6.038597 P	P	P	P	6.866347
12.37206	12.03924	11.76875	11.68431 P	P	P	P	12.12976
5.815046	7.356425	4.262704	6.377324 P	P	P	P	6.575772
7.429366	6.635823	7.794243	8.527476 M	P	P	A	7.60074

6.882088	7.055394	6.924866	7.369896	A	P	M	7.215602
8.153422	6.909549	7.270398	6.89901	A	P	P	6.698552
11.35173	12.01375	10.7092	9.903569	P	P	P	11.72029
7.958596	9.172855	7.955509	7.927887	P	P	P	9.195095
7.380832	6.615358	6.384419	3.288128	A	P	P	6.493691
12.27353	13.12852	11.65619	11.25633	P	P	P	13.30922
6.236729	5.194449	4.566683	A	P	P		5.930296
6.052673	6.686703	6.491528	7.252417	P	P	P	7.181799
10.08105	8.557429	10.10895	10.41812	P	P	P	8.959516
12.94209	13.00439	14.41538	14.90255	P	P	P	12.94282
		7.292244			M		
	5.790732			A			
8.613482	9.470814	9.156203	8.137423	P	P	P	8.091146
6.393752		7.8502	7.335516	P	A	A	6.145379
	5.14988	6.427136		P	M		
9.146086	9.843493	10.10325	10.08233	P	P	P	10.03655
13.51621	14.3682	14.34145	14.2439	P	P	P	14.9835
8.733487	7.851718	9.48112	9.102481	P	P	P	8.51563
6.895122		7.885752	8.26221	A	A	A	3.749744
8.577569	8.128847	8.695297	8.118935	P	P	P	8.149146
9.397291	10.54522	10.01435	10.51012	P	P	P	10.46131
10.1534	10.88119	10.52262	11.02709	P	P	P	11.2197
9.445941	10.49538	9.810875	8.9926	P	P	P	10.31635
11.83453	11.61232	10.95956	11.06585	P	P	P	12.26469
8.640783		9.570065	9.600801	A	A	A	8.421738
10.98167	11.06906	11.10426	11.34576	P	P	P	10.38137
5.749472	4.359187	6.380325	M	M	P		6.800462
11.81419	12.37967	12.50836	12.45175	P	P	P	12.09335
10.6073	10.72935	10.88913	10.52544	P	P	P	11.03718
7.335247	5.666123	7.298575	8.020676	A	A	A	5.522547
12.26158	12.5952	13.06557	13.07981	P	P	P	12.18581
7.292095	6.819786	6.105831	5.859357	P	P	P	6.872192
8.442365	6.798999	8.449388	9.326903	P	P	A	6.64309
6.32804	6.216091	5.840975	4.568891	A	P	P	6.648501
7.541193	6.001783	6.597671	6.581221	P	P	P	6.341164
13.0934	13.94521	14.13807	13.65401	P	P	P	14.3901
10.29049	10.99732	9.522654	9.677747	P	P	P	10.16796
6.606671	6.525741	6.992151	A	M	A		6.051576
6.394392	6.809316		A	A			6.436515
7.890289		9.111986	A		A		7.316747

8.44906	8.674202	9.49843	9.997656 P	P	P	P	9.058397
6.119539	6.299546	6.360986	7.487064 M	A	A	A	6.767534
12.52965	12.74311	12.1774	11.95598 P	P	P	P	12.94879
14.79248	14.16055	14.66135	14.217 P	P	P	P	13.43519
9.349953	9.435325	11.23435	10.04485 P	P	P	P	9.243436
7.653407	7.454166	10.53754	9.769254 P	P	P	P	7.088417
5.443871	4.268796	6.567319	6.815043 A	P	P	A	2.776316
6.631065		6.740221	5.49011 A		A	M	7.069863
7.269737	6.481316	6.798652	5.796371 P	A	P	P	6.687568
9.13203	7.899482	8.938356	8.627317 P	P	P	P	8.067515
11.22455	11.0731	10.25394	10.15707 P	P	P	P	11.41254
11.96618	12.04	11.36329	10.85186 P	P	P	P	11.85435
7.668332	7.912212	7.392352	6.102554 P	P	P	P	7.353307
8.148236	6.489603	8.589541	8.372754 A	A	A	A	6.551569
9.634983	10.23142	8.227114	9.085759 P	P	P	P	9.877199
9.688719	10.31025	10.54555	11.06465 P	P	P	P	10.44368
11.49112	12.02245	11.14291	10.8106 P	P	P	P	12.73946
13.37871	13.59921	12.57729	12.98099 P	P	P	P	13.87713
12.29935	11.15176	12.06289	11.37124 P	P	P	P	11.12546
6.578937	7.286617	7.437759	P	P	P		6.708654
11.35914	11.45071	12.16281	12.43916 P	P	P	P	11.71434
			6.052577			A	
8.289077	9.041311	8.935179	8.808108 P	P	P	P	8.874831
6.200089	7.540835	7.276207	M	P	A		7.003692
7.902377	9.160449	8.875978	9.837766 P	P	P	P	8.810164
7.751783	8.19599	9.222944	8.688468 P	P	P	P	8.215071
7.192495	6.551361	6.581228	7.790953 P	P	M	A	7.367946
9.271264	9.7065	9.721839	8.035646 P	P	P	P	9.546963
8.860608	8.499833	9.878654	10.13843 P	P	P	P	8.307941
10.7177	9.680016	10.79107	10.24635 P	P	P	P	9.579568
9.014056	8.901816	8.747975	7.392997 P	P	P	P	7.693778
	5.802898			A			
8.538809	8.467353	10.15658	8.721788 P	P	P	P	7.735407
7.074578	7.1624	6.900309	5.59483 P	P	P	P	7.673809
7.475077	7.487392	7.979585	2.119397 P	P	P	P	8.364348
8.400805	8.676467	7.621233	7.573166 P	P	P	P	8.499208
11.88141	11.80568	11.26415	10.14277 P	P	P	P	11.97758
10.91001	10.92348	10.13026	9.933133 P	P	P	P	10.69275
5.237452		6.085962	6.932337 P		A	A	6.227281
6.508928	7.570936	9.337906	9.179603 P	A	P	A	7.656985

9.097446	10.36104	9.426063	8.934753	P	P	P	9.911925
8.621368	8.881413	10.48792	11.01039	P	P	P	8.756167
	5.568821	3.363083	2.621061	A	P	P	
9.835648	11.39849	11.37825	12.60873	P	P	P	12.03588
9.743575	10.82316	9.672252	8.416002	P	P	P	10.43445
	4.364527			P			
7.62571	7.197036	6.306822	6.602626	P	P	P	7.780036
8.707097	8.658663	8.782529	9.075091	P	P	P	8.755508
10.31781	9.242319	10.0892	10.97885	P	P	P	9.799513
8.883255	8.592105	8.138616	9.099572	P	P	P	8.75441
7.436949	7.515231	6.536488	5.991559	P	P	P	8.420515
6.614079	6.8289	7.390048	8.095805	P	P	A	6.565732
11.72314	11.43155	11.877	12.6712	P	P	P	12.07332
12.52667	11.99775	13.13302	12.64363	P	P	P	11.25118
		7.524787	8.063807		P	A	
7.550925	7.184413	8.065292	A	A	A		7.549081
8.585627	8.701487	6.887855	7.238377	P	P	P	8.682223
8.443727	8.43027	9.091044	8.407921	P	P	A	8.084578
	5.419021	5.468199		P	M		
7.912301		7.932506	9.618452		P	P	8.978143
7.740562	7.272955	8.466267	8.758083	A	P	A	8.283877
6.67054	5.828996	5.758897	5.505522	P	P	P	6.806838
7.373336	7.126361	8.025983	P	A	P		6.006515
	6.101685			P			
6.6998	4.784926	1.83673	6.400515	P	P	P	5.663245
5.330899	5.943524	6.586746	5.735264	A	A	P	5.551897
5.087605	4.814416	6.183494	6.188962	A	P	P	5.529009
11.81664	9.38612	10.84363	11.36669	P	P	P	8.886813
	5.570459			A			
8.025933	6.835472	9.43307	9.248124	P	P	P	7.153903
10.64555	10.57734	11.20152	11.64508	P	P	P	10.73099
7.823683	6.535712	7.91318	7.267355	P	P	P	6.844512
9.47599	8.666341	9.870343	9.746609	P	P	P	8.496904
10.93543	9.634461	11.12751	11.92001	P	P	P	9.988106
8.376899	8.192659	9.456074	9.790721	A	A	A	7.649649
9.773015	9.573631	8.51108	7.96451	P	P	P	9.400696
5.490439	6.779898	5.494689	6.917418	P	P	P	7.243226
			8.387491			A	
8.337574	7.861354	8.31952	8.32391	P	P	P	7.760446
4.061518	5.525734		5.96664	P		P	5.267195

			6.595365				A	
9.097582	8.484106	8.758281	8.451984	P	P	P		7.678439
5.929023	6.19347	5.376624		P	P			6.24805
6.215177	6.495364		7.509757	P	A		P	6.890287
9.158591	8.958627	9.885468	10.13236	P	P	P		9.153211
11.00656	10.85162	11.37477	10.59163	P	P	P		10.62255
6.884154		6.805486	7.832962	P		P	M	6.651568
7.334528	8.20158	7.877021	7.536946	P	P	P		7.660142
8.371125	7.462705	8.761509	8.858889	P	P	P		7.807918
5.774797	5.61527	6.506369	6.060228	P	P	A		6.992663
6.576554	6.016929	6.176631		P	P			7.193811
8.158094		9.937373	10.61031	A		A		7.182342
5.758418	6.189425	6.904154	6.383895	P	P	A		6.565109
6.772202	3.471482	6.625163	5.827592	P	P	P		7.146079
12.33066	10.64317	15.0553	14.64292	P	P	P		10.38074
8.720144	8.106125	8.741828	8.485911	P	P	P		8.157504
10.84561	11.10027	11.8225	12.66093	P	P	P		11.55503
5.89752	4.69987			P				6.390239
	2.826931	4.805558		P	P			
8.215361	7.04642	8.483689	8.977918	A	P	A		5.936785
12.0227	11.95136	12.48026	13.44455	P	P	P		12.42937
8.143115	7.734963	6.848204	8.151367	P	P	P		8.798533
5.0944	5.250354	5.677744	5.802369	A	P	P		4.366929
6.458599	4.78682	5.996258	6.382765	A	P	P		6.11251
		4.698448			P			
	5.962829	7.643498		P	P			
	4.67718			P				
	4.32832		5.525207	P		P		
10.38043	9.409025	10.36069	10.08802	P	P	P		9.264
6.596111	6.39259	7.25733	6.786575	P	P	P		6.387374
7.159191	7.16441	7.90834	8.148284	A	A	A		4.600383
		8.178911			A			
6.222418	7.395227	7.122221	8.160835	P	P	P		7.748678
8.635839	9.007074	9.261686	9.793935	P	P	P		8.644444
3.420508				P				5.45038
5.975004			7.225341	A		A		3.239744
6.995649	7.426789	7.514773	8.241346	P	M	P		8.459134
6.372708	6.614963	7.50728	7.30343	P	P	A		7.198326
6.461499	6.46163	5.170362		P	P			6.283414
7.047037	6.896176	6.986267	7.611853	A	P	P		5.894193

7.349183	5.561094	6.150034		A	P	P		6.603626
8.769234	9.610101	9.172731	7.483912	P	P	P	P	8.808518
10.09263	9.92567	9.404757	8.585341	P	P	P	P	9.428549
6.854905	4.894068		5.940095	P			P	6.088905
5.557821			6.689666	P			A	6.201752
		7.02529	6.777753			P	A	
8.471851	9.245058	8.12774	7.386431	P	P	P	P	8.386165
7.661765	8.125933	7.451788	6.912891	P	P	P	P	7.560643
6.396095	6.528976	5.926865	6.828699	P	A	P	P	6.984953
5.675581	4.766969	6.522058	3.801303	A	P	P	P	5.468682
	6.160761				P			
		0.819793				P		
5.765179	2.62549			A	P			5.58884
6.431889	5.255216	5.621696	6.813622	P	A	P	P	5.349407
6.398275	6.574676	6.199138	6.728474	P	P	P	P	5.8925
9.573564	9.44924	10.47339	11.26299	P	P	P	P	9.621209
4.882245			4.329536	A			P	4.674666
8.094873	7.562253	8.337522	8.617754	P	P	P	P	7.525487
13.04696	12.08048	12.18171	12.01571	P	P	P	P	12.93648
8.925735	8.930159	8.686023	8.528072	P	P	P	P	8.683456
5.945058	5.100846			A	P			4.178716
		6.908516	7.846979			M	A	
7.336106	7.917674	7.232035	7.315614	P	P	P	P	7.16443
6.718782	8.037459	7.837869	7.497531	P	P	P	P	8.12226
8.832806	9.448699	9.981151	10.99379	P	P	P	P	9.693923
7.565121	7.799296	7.555513	6.712647	P	P	P	P	7.933796
9.666394	10.67098	10.15089	9.599153	P	P	P	P	10.18849
6.328355				A				3.091834
	2.93678		5.860835		P		P	
8.703691	8.809917	10.53007	10.5077	P	P	P	P	8.803981
5.493896	4.320091		5.877042	A	M		M	5.50024
9.835696	9.295366	10.1826	10.5052	P	P	P	P	9.895974
6.246139	6.758955	7.8292	7.358643	P	P	A	P	6.854677
9.608414	8.610176	9.953594	8.999749	P	P	P	P	8.474495
8.448405	8.538768	9.747959	9.321414	P	P	P	P	8.190896
12.68698	11.33562	13.48073	13.99708	P	P	P	P	11.53711
13.01516	11.98135	13.94616	14.09669	P	P	P	P	11.74017
10.99971	9.311079	9.95013	9.966047	P	P	P	P	9.687768
7.199088	7.015643	7.538828	6.113317	P	P	P	P	6.460417
	5.385886	5.25603			P	P		

11.49975	10.9949	10.67226	10.8883	P	P	P	11.60619
6.307472	5.440459	7.452392	6.205601	P	A	P	6.109261
10.14276	10.46756	10.86525	11.15449	P	P	P	10.63996
12.29791	11.07303	12.69311	12.76727	P	P	P	11.1325
11.36819	11.78043	10.95614	10.13417	P	P	P	11.55513
10.99305	11.38525	10.72153	10.11	P	P	P	11.09433
10.45918	10.78313	10.16162	9.556728	P	P	P	10.56187
11.04342	10.83207	11.40729	12.71796	P	P	P	11.0172
8.974737	9.071339	9.985329	10.5679	P	P	P	9.544642
13.06468	12.67223	13.30071	13.69616	P	P	P	12.82146
	6.587918	7.083313	4.63619	P	A	P	
7.602309	7.99618	8.596696	9.792792	P	P	P	8.480847
8.537034	8.450007	10.28703	9.51361	P	P	P	8.982348
9.9707	8.661867	9.991338	9.748075	P	P	P	8.100966
9.297973	9.394171	9.584012	10.45979	P	P	P	9.995406
8.164145	6.84543	8.130195	7.00234	A	P	A	6.72922
10.81442	11.03515	11.82024	12.72675	P	P	P	11.12076
6.761492			A				4.879798
11.17265	11.07243	10.66749	10.73668	P	P	P	10.86515
9.310677	7.405038	8.119295	8.794864	P	P	P	7.442572
11.01062	11.252	9.935325	9.509041	P	P	P	11.60947
8.904385	8.855358	8.885889	9.987337	P	P	P	8.543065
11.84128	12.48573	11.77706	11.01176	P	P	P	12.18813
10.99957	10.81828	10.3594	9.771466	P	P	P	10.62188
7.793344	7.157343	7.259948	8.349382	P	P	P	5.814026
6.881991	6.400589		8.362525	A		A	6.179725
10.06138	10.14668	9.547853	9.323438	P	P	P	9.300486
10.80603	10.40648	10.84742	10.47059	P	P	P	10.06077
11.40604	11.77177	10.81969	9.958114	P	P	P	11.31029
6.512604	6.79592	5.448041	6.859219	P	P	P	7.357288
7.579356	7.980739	8.652928	7.799233	P	P	M	7.764286
9.84167	8.989328	8.578877	8.339145	P	P	P	8.939109
9.13815	9.003446	10.32852	10.75413	P	P	P	8.875049
9.696799	9.090746	9.295633	9.140034	P	P	P	8.328177
7.579109	7.502028	6.14721	A	P	P		4.904241
12.60263	9.760215	11.62451	12.1941	P	P	P	8.575331
7.208295	7.928589		A	M			8.38391
6.997138	7.586605	7.405871	6.685654	P	P	A	6.576344
10.75199	10.88512	10.19751	9.87524	P	P	P	10.87685
		5.327686			A		

10.07703	10.37053	9.408677	9.255509	P	P	P	10.14323
6.237358	5.562815	5.963117	5.380649	P	P	P	7.386176
7.343857	8.291568	7.824139	7.362993	P	P	P	7.929548
9.094394	8.614218	7.848308	8.84047	A	P	A	7.598157
7.995395	8.645926	7.706995	6.848483	P	P	P	8.268732
10.77495	10.9351	9.950732	9.189486	P	P	P	10.38135
7.04316	5.675167	5.687943	5.64578	P	P	P	6.84717
9.893311	9.623162	10.0279	11.28371	P	P	P	10.1632
9.040732	9.666904	7.786127	8.642531	P	P	P	9.944614
7.890101	8.16575	8.869837	9.378089	P	P	P	8.224833
10.01312	9.484431	10.48426	11.6088	P	P	P	10.92229
7.041707	7.797807	7.543496	5.997421	P	P	P	7.245813
6.68834	3.993788	6.906977	M	P	A		6.182902
11.57704	12.33168	11.46126	10.47506	P	P	P	12.03408
9.451498	8.442845	9.714043	9.939316	P	P	P	8.873648
7.277841	7.310149	6.877335	5.819483	P	P	P	6.823942
8.234653	7.762752	7.186455	7.726453	P	P	P	7.05297
5.431687			A				3.936661
10.8537	11.5473	10.63066	9.8338	P	P	P	11.29112
11.20097	11.38397	10.23549	10.21582	P	P	P	11.68733
8.872685	9.587744	8.24282	8.082597	P	P	P	9.132963
6.135655	6.272092		5.275215	A		P	6.447878
7.706779	6.684448	7.702483	P	M	A		7.12069
	7.413152	6.742831		P	P		
6.61603	6.563227	6.979586	7.140122	P	P	A	6.419204
11.42459	11.81806	10.75333	10.28511	P	P	P	11.55351
8.870879	8.44259	9.708256	9.738071	P	P	P	8.081436
9.731916	9.242556	9.840342	8.454823	P	P	P	8.789716
7.981034	8.876397	6.857627	2.770054	P	P	P	8.125309
7.531615		5.500495	7.344457		P	P	6.615547
10.91255	10.98412	11.62821	12.06763	P	P	P	10.67923
8.733542	8.889239	10.09179	9.169632	P	P	P	8.534965
8.305734	8.116371	8.876839	8.354658	P	P	P	7.806316
7.273107	7.33261	7.718705	8.743741	P	M	P	7.133617
	5.164264			A			
9.184731	9.385456	9.885757	10.42482	P	P	P	9.036134
7.957344		8.104562	A		P		7.770804
7.876856	6.500888	7.179798	8.733885	P	P	A	5.878269
12.14976	12.7736	11.58385	10.57445	P	P	P	12.62062
6.032322	6.41221	4.509587	7.798745	P	P	P	7.494853

8.938839	8.467479	9.515556	9.78878 P	P	P	P	8.158931
8.221937	8.037326	9.247801	8.958822 P	P	P	P	8.093493
8.794136	9.271997	9.838847	9.87796 P	P	P	P	9.179678
			6.609948			A	
6.427674	6.867358	7.794935	8.497531 P	A	M	A	6.934629
7.876315	7.098802	6.499289	8.17027 P	P	P	P	7.64007
7.133662		7.028358	A		A		4.778789
	6.672829	7.934104		A	A		
10.07047	10.61742	10.77088	11.17 P	P	P	P	10.6645
6.452762	8.089792	7.546277	6.428817 P	P	P	P	7.489564
9.024937	9.539094	8.596976	10.3849 P	P	P	P	8.181727
5.71779	6.017521	6.907564	6.579186 P	A	P	A	5.944721
12.44061	13.18246	12.50509	11.71094 P	P	P	P	13.03972
9.666998	9.111679	9.396307	10.0998 P	P	P	P	9.120147
7.619441	7.272192	8.248632	8.758772 P	P	P	P	7.386797
8.249081	7.89889	8.88055	8.860289 P	P	P	P	8.000658
7.842326	8.210188	8.540947	9.639944 P	P	P	A	8.57905
7.259955	6.992648	7.266197	A	A	P		6.116849
7.150351	8.442392	7.93008	5.618097 P	P	P	P	7.750948
10.15876	9.817549	11.07887	10.39627 P	P	P	P	10.17585
8.175735	7.903266	6.937131	7.039715 P	P	P	P	6.950674
7.822766	8.062729	9.252823	P	P	P		8.809321
11.11224	10.07458	11.27476	11.42387 P	P	P	P	9.638397
6.51743	6.274958	6.39653	5.76092 A	P	P	P	5.071966
7.737515	7.973096	8.433887	9.662354 P	P	P	P	8.51892
12.65733	13.05658	13.88338	13.90628 P	P	P	P	12.90347
	4.322655			M			
13.05329	11.80925	15.98988	16.14705 P	P	P	P	8.84513
9.613886	9.067596	9.925591	10.17309 P	P	P	P	9.132402
12.2541	11.30214	13.00325	13.26749 P	P	P	P	11.24486
7.850372	6.88859	5.614897	6.899257 A	P	P	P	4.565268
			6.301346			A	
5.96878	6.570047	6.340886	4.48282 P	P	M	P	6.936384
9.804227	10.58765	9.49564	9.289639 P	P	P	P	10.30813
9.915021	10.58063	9.59237	9.798409 P	P	P	P	10.22341
	5.583146	4.164783		A	P		
4.771896	5.797502	5.629641	P	P	P		5.890395
4.863782	5.376039	7.944356	8.349802 A	A	A	P	7.949782
6.45692	6.811587		7.455336 P	P		P	6.594505
8.248116	8.431643	6.022646	6.507505 P	P	P	P	8.134288

9.1601	9.93447	7.652645	7.545281	P	P	P	9.605092
6.831782	5.619099	7.605674	7.07547	P	P	A	6.599445
11.58635	12.04154	11.32675	11.43282	P	P	P	12.10406
12.10956	12.48956	10.76507	10.7505	P	P	P	11.95393
9.735407	10.43692	9.178381	7.88045	P	P	P	10.15211
14.20555	14.17643	13.65595	14.06394	P	P	P	13.13209
9.411347	10.01787	9.665867	8.279673	P	P	P	9.605368
7.256441	7.595484		M	A			7.515173
7.479042	7.682313	7.322363	8.108035	P	P	P	7.485689
8.091586	8.582808	9.292267	9.333352	P	P	P	8.742513
8.53435	8.632779	8.858467	9.013066	P	P	P	8.822207
5.939169	5.477484	5.801499	5.16295	A	A	P	4.432187
7.390829	8.158925	6.780101	7.276768	P	P	P	7.305308
10.1185	9.74648	9.004003	8.132473	P	P	P	9.620397
7.670548	8.261578	7.674544	6.896284	P	P	P	7.572109
12.67657	11.14811	13.54528	13.97951	P	P	P	11.86181
8.359836	8.40236	9.128417	9.21072	P	P	P	8.651583
10.13933	9.417252	10.24876	10.59936	P	P	P	9.648503
10.07599	9.03663	10.28183	9.452627	P	P	P	8.571305
		6.839327	7.194363		A	A	
9.078129	7.978383	9.22358	9.301279	P	P	P	7.935568
10.70456	10.60215	11.54035	12.29093	P	P	P	11.01331
11.18703	10.68249	13.3249	12.86415	P	P	P	10.37397
6.675928	7.087102	6.924246	7.296092	P	P	A	6.410785
8.922731	9.466209	8.018497	8.746927	P	P	P	9.387246
		7.651097			A		
9.740965	9.949881	10.31572	11.0543	P	P	P	9.88541
8.574545	8.197537	8.426625	8.280175	P	P	P	6.745254
6.687938	5.657121	5.904586	6.630263	P	P	P	5.780613
7.100662	6.557152	7.760107	8.090527	P	P	P	7.560033
10.32246	11.39194	8.787781	9.406846	P	P	P	11.72501
	4.752997	5.083513		P	P		
9.240452	10.635	7.308261	7.777694	P	P	P	10.42276
10.36544	10.69473	10.9816	11.93698	P	P	P	10.84525
6.882832	7.543435	5.997192	7.533331	P	P	P	7.906734
9.89437	10.18594	11.0292	11.79542	P	P	P	10.68102
8.182136	8.10715	9.173468	9.4159	P	P	P	8.688261
5.801876	5.695939	6.682427	A	P	A		6.474222
9.399319	9.253604	9.319862	9.771008	P	P	P	9.681232
9.157966	9.903139	7.51821	7.42388	P	P	P	9.453629

8.100679	7.785307	8.748166	8.698108	P	P	P	8.003692
7.618133	7.024061	8.081133	8.381374	A	A	A	6.063232
6.171127	6.009069	5.782744	5.495213	A	P	P	6.241859
10.16448	10.80431	9.729175	8.986346	P	P	P	10.27753
8.266931	7.541326	8.335575	7.374466	P	P	P	6.360966
7.916495	8.728799	7.720918	7.247307	P	P	P	9.042181
8.909487	8.898487	7.814093	6.98841	P	P	P	9.406603
8.910931	8.522278	9.347005	9.85905	P	P	P	8.739194
8.506628	7.387097	9.035024	8.131419	P	P	P	7.671299
7.736712	7.003916	6.899975	6.277179	P	P	P	6.586982
			2.688098			M	
9.525171	9.996273	10.84905	11.18674	P	P	P	9.797906
	5.413832	6.517981	6.967923	A	A	A	
11.78844	11.96711	11.03324	10.85575	P	P	P	11.78004
6.880146	6.999686	7.072833	8.493738	P	P	P	7.702014
11.7623	11.57243	11.82104	10.96361	P	P	P	10.75523
10.67397	10.41905	9.823441	9.023149	P	P	P	10.04451
7.175058	7.228604	7.930413	8.515199	P	M	P	7.145908
5.379461	4.016173	5.954646	5.844058	A	A	P	5.27619
7.059383	6.467859	7.015916	7.197869	P	P	P	7.044584
7.318711		8.171268	7.49528	P	A	P	7.255805
		3.629183			P		
8.336058	9.267599	8.408702	7.214832	P	P	P	8.965241
9.735425	8.423677		9.572155	A		M	9.182878
7.989472	7.814803	8.686089	8.947256	P	P	P	8.068049
10.45047	9.976468	10.71236	11.02751	A	M	P	9.611486
7.305022	6.983193	7.529356	8.287824	P	P	P	7.12721
10.07632	9.271362	9.650164	9.386234	P	P	P	9.027599
6.311743	7.304072	7.77943	6.99997	P	P	P	7.017535
7.000609		6.373056	5.780352	A	P	P	6.553634
11.12001	9.950806	11.16167	11.24708	P	P	P	10.08566
10.28049	9.009182	10.27314	9.855028	P	P	P	8.848288
10.20505	9.81211	9.399672	9.343866	P	P	P	9.939552
8.305079	7.273468	7.696121	6.91491	P	P	P	7.771204
8.061058	8.946851	7.89074	8.360714	P	P	P	8.449412
9.690558	10.40308	9.679818	8.903957	P	P	P	10.36143
7.39265	5.909097	7.53912	8.429158	P	P	P	5.870562
10.47944	8.983406	10.23212	9.8638	P	P	P	8.670997
	7.030921			A			
5.248657	5.233557	2.82239	5.768801	P	P	P	5.518492

11.83808	11.70427	12.33621	13.66917	P	P	P	12.11865
7.996543	9.421426	8.822419	8.628933	P	P	P	9.097123
7.939251	8.399735	8.265832	8.529365	P	P	P	7.775123
6.73011	6.381035	6.918683	8.33532	P	P	A	7.012202
8.826844	9.864054	10.16935	9.247988	P	P	P	11.5966
	5.121825		7.162986	A		P	
8.149501	7.622415	7.464625	7.536861	P	P	P	8.320793
9.089534	9.814638	10.0089	9.283838	P	P	P	8.733399
11.47736	11.77802	10.67437	10.53484	P	P	P	11.39259
8.665839	9.307502	9.732121	9.757714	P	P	P	8.951227
10.00818	10.86513	9.963035	9.170853	P	P	P	10.21047
6.176114	5.05308		P	P			5.918692
7.026198	7.111709	6.600877	6.492035	P	P	P	6.858678
6.178804	5.96808	7.380346	6.525478	P	P	P	5.439561
9.787001	10.23016	9.707455	9.294725	P	P	P	10.05114
10.00487	9.319512	10.87014	10.38425	P	P	P	8.504
5.869807	6.889547	4.886914	P	P	P		6.903296
7.932454	7.240675	8.174163	8.76154	A	A	P	7.902629
9.269923	7.288154	8.29808	8.493127	P	P	P	7.95556
6.316669	5.815498	6.396582	7.154286	P	P	P	7.394868
9.085073	8.860123	8.793654	8.349013	P	P	P	8.682091
7.088193	6.93638	6.519132	7.128117	P	P	P	7.84459
8.921884	9.079021	9.039905	7.975991	P	P	P	8.930755
5.375703	4.244625		A	P			6.002408
6.844668	6.553395	7.397893	7.335506	P	P	P	6.98768
7.522406	7.360317	7.970552	9.682007	P	P	P	7.475203
8.00388	7.223622	8.094905	8.143594	P	P	P	8.289208
7.385963	8.327561	6.663857	7.521522	P	P	P	7.764514
12.31526	11.94867	11.89854	10.99487	P	P	P	12.24553
12.59811	12.99729	11.57136	10.94423	P	P	P	12.61417
10.10661	10.05467	10.90764	11.15101	P	P	P	10.45071
6.372786	6.078313	7.218507	A	P	A		5.216969
7.466283	6.02599	5.751193	7.234044	P	P	P	7.068915
6.720657	5.370925	6.78301	6.462579	P	P	A	5.698885
		4.987863	4.328288		P	P	
7.05026	6.867845	6.417804	7.540985	A	P	P	7.211118
6.494896	4.262081	6.6411	6.661038	M	A	P	5.651534
11.18106	11.74965	12.08875	12.38638	P	P	P	11.61911
7.573339	7.082439	7.139635	7.807959	P	P	A	7.380957
5.452681	6.588876	6.787894	7.234084	P	P	A	5.764414

9.81536	8.288685	10.26697	9.899603	A	M	P	A	6.747986
6.932561	6.324482	5.812883	7.016505	A	P	P	P	6.547465
7.116132	6.667064	5.404026	7.111618	P	P	P	P	6.99322
9.441765	9.638313	9.251317	9.049567	P	P	P	P	10.07519
9.438644	9.021882	10.93638	10.86888	P	P	P	P	8.807234
8.497438	9.152169	10.33498	11.22292	P	P	P	P	9.417037
8.301285	8.368953	7.546143	7.481798	P	P	P	P	7.98798
10.52387	10.77206	9.953307	9.780134	P	P	P	P	10.5754
8.554244	9.304778	8.170017	7.842087	P	P	P	P	8.503013
8.962271	8.45765	9.784308	9.930596	P	P	P	P	8.779068
7.231017	5.613401	6.977144	7.045428	A	P	A	P	4.44052
7.412851	7.977595	9.400592	9.392413	P	P	P	P	8.132567
10.98939	10.86624	10.48358	10.01352	P	P	P	P	10.5047
12.0996	11.11054	12.99558	13.18047	P	P	P	P	11.01759
6.604547	6.585327	6.0975	P	A	P			6.712843
8.737119	9.033142	8.349909	8.172305	P	P	P	P	8.582969
10.37187	9.407304	11.17736	11.52175	P	P	P	P	9.89109
5.847597	5.729352	5.997957	P	P	P			6.918827
6.115559	6.14737	6.602439	M	P	P			6.550687
9.937462	9.286727	10.71077	10.5795	P	P	P	P	9.464714
7.074759	6.795886	8.928407	7.59332	M	A	P	A	6.83782
8.427669	8.436236	7.08643	6.769923	P	P	P	P	8.11849
6.829372	6.294561	2.868123	6.045012	P	P	P	P	6.662094
	5.428366	5.76235		A	A			
5.67393	5.108696	7.129841	7.377948	P	P	A		6.80252
10.34317	9.900833	9.65653	9.092161	P	P	P	P	9.626545
8.474483	7.984775	9.018464	8.150889	P	P	P	P	7.740584
8.161134	7.662134	8.210101	8.858896	P	P	P	P	7.500231
9.1406	9.869798	8.546863	7.377093	P	P	P	P	9.795294
7.313938	7.414256	5.632305	5.849144	P	P	P	P	7.185905
7.711813	8.197269	8.851511	8.390966	P	P	P	P	7.738161
8.818627	8.329126	8.75758	7.958323	A	P	P	M	7.234084
10.88213	11.63158	10.74293	10.22245	P	P	P	P	11.32527
8.518248	7.727565	7.19849	7.257372	P	P	P	P	7.761499
7.180207	8.252283	7.572989	4.851005	P	P	P	P	7.143934
4.280891	1.718412		A	P				5.470659
8.240811	8.573757	8.366765	8.485462	P	P	P	P	9.539625
4.512254	5.605427	6.678027	6.753424	P	P	A		6.307176
8.885611	8.259526	8.462763	9.058079	P	P	P	P	7.815192
7.340826	7.138109	8.484889	7.765155	P	M	P	P	7.921012

7.242974	7.876075	7.065103		P	P	P		8.252426
7.616644	7.122703	7.61218		P	P	P		6.556389
	4.865979	5.390379			A	P		
10.07396	10.53708	9.257435	8.687775	P	P	P	P	10.1296
13.31132	12.33915	13.04142	12.8302	P	P	P	P	11.74412
7.584309	7.329295	7.07346	6.008134	P	P	P	P	6.849385
7.276712	6.411599	7.611971	6.942718	P	P	P	P	5.981102
7.101868	6.38963	7.706359	7.788914	P	P	P	P	6.46444
6.293689	6.961585	8.772357	8.395561	P	P	P	A	7.132396
6.399088	5.999011	6.721919	5.091964	P	P	A	P	7.12542
8.313682	8.410936	8.125924	7.58229	P	P	P	P	7.309697
10.36585	10.18035	9.907349	8.58313	P	P	P	P	9.772448
11.0337	10.70464	11.80597	12.78472	P	P	P	P	11.04574
	8.562226			P				
8.574153	9.053493	9.803973	9.334229	P	P	P	P	9.499702
8.903758	8.149983	9.34523	8.729797	P	P	P	P	8.047221
10.36012	10.56222	11.23012	11.12024	P	P	P	P	10.49532
9.218378	8.805711	9.226705	8.512203	P	P	P	P	8.216294
	4.098266			P				
9.012215	9.171803	7.219592	8.233254	P	P	P	P	8.914595
6.682007	6.207216	6.655592	6.854313	A	P	P	P	5.765369
7.139751		7.392893			A			6.966765
10.09537	10.06469	10.90343	11.73824	P	P	P	P	10.69992
6.960043	7.462843	5.843275		P	P			6.364253
11.81937	12.59509	11.75772	10.64576	P	P	P	P	12.38038
6.811713	7.083313	5.436159	4.079657	P	P	P	P	6.484867
9.329628	9.224669	8.549938	8.338987	P	P	P	P	9.368916
8.531846	8.88322	7.991607	7.658646	P	P	P	P	8.633075
7.500819	7.528915	7.233334	7.273786	P	P	P	P	7.980676
6.328585	6.270179	5.839906	6.647936	A	P	P	P	6.783568
7.186126	7.14183	8.076205	5.435926	P	P	P	P	6.299805
10.99837	11.14644	10.18037	9.958307	P	P	P	P	10.94974
9.285466	10.08715	10.456	10.84299	P	P	P	P	10.36353
8.261714	9.234262	7.411161	8.626676	P	P	P	P	8.988604
			7.651375				A	
9.439498	9.242042	10.01456	9.836902	P	P	P	P	9.059662
8.46432	8.287823	7.862225	7.343871	P	P	P	P	8.321281
11.46057	10.83701	12.38923	11.73627	P	P	P	P	10.86442
6.845748	7.00569	7.451284	8.369896	A	P	A		5.735836
5.048163	7.152124	6.365903		P	P			5.083408

4.895154	3.388383			A	M			5.068761
10.13847	9.347008	10.44858	8.762697	P	P	P	P	8.965036
9.056253	9.4225	7.823422	7.624274	P	P	P	P	9.46642
9.61788	8.210049	9.485403	9.798913	P	P	P	P	8.8655
8.189919	10.06193	7.563584	8.073457	P	P	P	P	8.547914
6.575741	6.456183		7.39314	P	M		A	6.523112
8.696768	8.860836	9.134561	8.756218	P	P	P	P	8.417926
9.306073	9.047709	9.933855	9.562406	P	P	P	P	8.542026
		1.120427				P		
6.428155	7.458838	8.564034	8.56206	P	P	P	P	6.685794
8.857581	8.52967	6.96029	7.296948	P	P	P	P	9.254297
10.95112	10.87445	10.59151	10.01199	P	P	P	P	10.74715
8.786104	8.038934	8.727186	9.427323	P	P	P	P	9.093549
	4.946298				A			
6.050904		2.929971				P		6.472772
7.542129	7.212188	6.333688	7.119944	P	P	P	P	8.144709
			6.021566				A	
7.243598	6.293121	7.296463	7.040708	P	P	P	P	6.123341
10.38082	8.162724	9.934329	10.39673	P	P	P	P	8.429383
10.33987	10.77805	11.46585	10.83252	P	P	P	P	11.01595
9.653783	9.542724	7.062062	8.557957	P	P	P	P	9.630228
7.15968	6.446437	7.294271	8.432558	P	A	P	P	7.42615
8.422592	8.170223	9.558261			A	P		8.039112
6.959494	5.981957	7.377063	7.782628	P	P	P	P	7.355192
11.07481	11.15184	11.78421	12.07138	P	P	P	P	11.11526
6.018723	5.375598				A			5.200891
8.61411	9.089139	10.18288	10.17076	P	P	P	P	8.938941
8.045951	6.822516	5.786352	6.591969	A	P	P	P	5.599104
5.460251	5.45957	4.776196	6.731039	A	A	P	A	5.405555
	5.293245				M			
11.43733	11.30609	12.09732	12.34678	P	P	P	P	11.29187
7.923758	8.572332	9.282662	9.809314	P	P	P	P	8.157018
9.179832	8.118986	9.098169	9.537364	P	P	P	P	8.86296
			6.804801				A	
8.578023	7.972802	8.02436	7.596862	P	M	P	A	8.217166
7.727564	7.919622	6.726886	7.645537	P	P	P	P	8.611347
6.755548	7.310376	6.137726	5.298425	P	P	P	P	7.342754
8.491441	8.805207	8.296398	8.181869	P	P	P	P	7.838424
6.72271	6.547785	6.006046	8.086238	P	A	A	P	6.755054
		7.558781	8.367731			A	A	

	7.476533	3.467744		P	P		
8.375649	7.590309	8.713041	8.897927 P	P	P	P	7.934639
7.962955	6.863631	6.97959	P	P	P		7.61023
10.12362	8.649594	9.030913	8.759152 P	P	P	P	8.847549
6.809463	5.841891	5.023958	5.480618 P	A	P	P	4.805738
7.321323	6.280914	7.82924	7.431471 A	P	P	P	6.978046
11.67144	10.52928	12.23993	12.68571 P	P	P	P	10.39677
6.976916	7.205028	7.969951	8.145757 P	P	P	P	6.681923
10.76512	10.27045	9.569921	9.701869 P	P	P	P	10.20396
7.595167	7.161829	6.982051	8.10962 P	P	P	P	7.889635
9.145652	8.299202		9.66357 A	P		P	8.961208
10.89926	11.00848	10.5302	9.820233 P	P	P	P	10.9583
7.089129	6.746727	7.756366	8.32803 A	P	A	P	7.425601
	3.994869		3.227343	P		M	
10.67893	9.474839	9.545105	9.841318 P	P	P	P	10.10051
8.475288	6.91161	8.940136	7.368424 P	A	P	P	6.321561
	2.068955			M			
9.799281	10.48228	10.34132	9.954084 P	P	P	P	10.74524
6.62508	6.209053	5.942737	7.605904 P	P	P	P	7.44673
13.33757	13.67549	12.52391	13.16951 P	P	P	P	13.86278
10.78771	11.20902	11.69379	11.51625 P	P	P	P	11.63071
13.30057	11.53699	13.90558	14.41878 P	P	P	P	11.14569
9.745872	9.583349	10.79763	11.06094 P	P	P	P	10.02391
7.229079	6.390029	7.244124	8.040344 P	P	P	P	6.956197
10.8507	9.729813	8.989726	9.999887 A	P	P	P	4.032696
5.712442	6.566627	6.467308	7.161065 A	A	M	P	5.39969
8.676496	8.480869	7.614319	7.417439 P	P	P	P	8.183388
7.991873	6.997324	8.786716	8.608142 P	P	P	P	5.74535
8.510428	8.786694	9.13171	8.851632 P	P	P	P	8.458996
10.38288	8.758044	9.868663	9.522303 P	P	P	P	7.788188
8.512054	7.939722	7.746144	7.872557 P	P	P	P	8.385028
7.192643	5.440423	6.516233	A	A	A		4.85573
10.06404	8.813196	10.15615	11.16432 P	P	P	P	8.86139
9.637515	9.193607	9.613231	10.75149 P	P	P	P	9.292988
9.69247	8.959578	7.938146	7.337028 P	P	P	P	9.124867
10.92536	10.91345	10.04152	9.847138 P	P	P	P	10.53666
8.133576	8.362239	7.687307	7.511205 P	P	P	P	8.016562
10.15076	10.30565	9.383988	9.547144 P	P	P	P	9.926177
7.507752	7.578254	7.516036	4.33953 A	P	P	P	7.173514
7.023494	7.374607	6.649029	6.409042 P	P	P	P	7.687455

6.460995	6.119109	7.919214	7.659703	A	A	P	P	5.734116
6.345532	7.46151	5.60391	6.114523	P	P	P	P	6.802361
6.075081	6.01243	3.75838	P	P	P			6.550596
7.914669	7.488472	9.16056	8.853582	P	A	P		7.559431
9.304608	8.65618	10.00611	9.808656	P	P	P		9.202263
6.070216	5.498262	7.276847	P	P	P			6.045117
5.237756	4.48744		6.085006	A		A		0.888028
5.808727	5.714918	6.333403	6.546239	P	A	A	P	6.173154
8.19807	9.151507	8.395699	6.702606	P	P	P	P	8.419537
6.068962	7.18605	6.576433	6.569031	P	P	P	P	6.859589
10.06501	9.88654	9.271285	8.726192	P	P	P	P	9.691061
9.356949	9.572397	10.16653	9.423833	P	P	P	P	8.873331
9.285216	10.34062	8.800901	9.969969	P	P	P	P	10.61723
8.868851	8.736878	9.573712	9.176662	P	P	P	P	8.536907
11.87191	12.1793	12.70827	12.34239	P	P	P	P	12.29775
7.280299	6.693534	10.48806	10.36616	P	P	P	P	7.639839
9.949298	10.0745	10.80561	11.11877	P	P	P	P	9.969231
7.652628	7.428634	8.388927	8.085855	P	M	A		8.103902
6.813777	6.050302	6.004562	7.292858	P	A	P	P	6.378277
8.853378	8.383842	9.829606	11.24178	P	P	P	P	8.773452
8.241076	7.449159	9.03664	8.690784	P	P	P	P	7.725636
8.217946	7.993902	8.246043	8.446976	P	P	P	P	7.784946
10.3404	9.142822	10.32149	10.57814	P	P	P	P	9.974541
5.132687	4.842456	7.123854	7.964677	A	P	P	A	5.107162
7.869402	7.286496	9.006714	9.435483	P	P	P	P	7.331129
		8.136083	8.835657			A	A	
8.125935	8.54889	9.101778	9.331154	P	P	P	P	9.229143
10.97933	11.50373	10.78291	10.06915	P	P	P	P	11.40649
12.79181	12.65017	12.06794	11.57426	P	P	P	P	12.655
5.038795			M					6.543953
10.84218	10.71715	11.29012	11.55696	P	P	P	P	10.90493
6.260442	6.065266	5.98195	P	A	P			6.626602
4.71689		4.732631	A		P			4.058636
		7.808583			M			
7.063991	7.436535	7.56209	8.536408	P	P	P	P	8.134177
7.703591	7.940677	8.4863	8.383153	P	P	P	P	8.578528
8.493722	9.06353	6.802762	10.61183	P	M	P		9.130974
5.409485			P					6.453472
7.268992	6.66395	8.070995	7.06309	P	P	P		7.603484
	0.797342			P				

10.95903	11.5739	11.88837	12.20224	P	P	P	11.53573
9.219134	8.168163	8.759275	8.412495	P	P	P	8.44997
5.026168	6.04166	4.307624		P	P		7.063888
8.142418	7.0376	7.368797	7.700347	P	P	P	7.685804
	5.229139		7.061343	P		A	
8.650966	9.06144	9.303925	8.714199	P	P	P	8.342755
8.07521	7.091069	7.970151	7.835224	P	P	P	6.82314
10.37399	11.11886	10.35767	9.595155	P	P	P	10.66526
5.944214	3.502462		P	P			6.415888
			7.695497			A	
8.372189	6.851259	7.80477	8.459474	P	P	P	7.455716
8.277558	7.405956	5.484557	7.451947	P	P	P	7.815282
6.634527	6.657094	5.049716	6.416297	P	P	P	6.126198
11.15897	11.22598	10.13033	10.19852	P	P	P	10.91685
10.22318	8.917783	9.577969	9.157689	P	P	P	8.99036
9.59654	10.24599	10.70202	10.96189	P	P	P	9.770294
6.139084	6.654609	6.014058	6.633382	P	P	P	6.327979
			3.177367			M	
5.189731	4.862553		P	P			5.259532
6.47659	7.324945	6.878174	6.736094	P	P	P	7.642555
6.567328		7.153365	6.788684		P	A	6.118454
8.121475	6.762324	8.721814	9.011737	P	P	P	7.324138
7.203899	9.3701	6.852383	6.604469	P	P	P	8.845936
11.63611	12.45853	11.45804	10.63669	P	P	P	12.16601
9.926021	8.687862	7.455142	8.589663	P	P	P	1.620997
11.50544	12.09743	11.44844	10.45087	P	P	P	11.69233
11.08602	12.34385	11.37952	10.549	P	P	P	11.8275
8.053595	8.249022	7.48995	7.301256	P	P	P	6.789883
11.07933	10.50993	9.841289	10.97327	P	P	P	11.52809
12.27795	12.02279	11.06683	11.17488	P	P	P	11.87772
8.899058	8.520093	9.605551	9.276653	P	P	P	8.651904
7.749017	6.042728	7.613502	8.529325	P	P	P	6.890878
12.14064	12.32134	12.61584	13.28807	P	P	P	12.52079
	2.683732			P			
5.080707	1.792875	5.925139	6.955936	P	M	A	2.389396
7.554139	7.046825		A	A			4.383873
11.1953	11.30894	11.34594	10.87182	P	P	P	11.69157
8.015713	8.020653	7.438409	6.488357	P	P	P	7.855802
11.01024	11.21797	10.26097	9.46029	P	P	P	10.78696
11.44617	11.3326	9.520545	9.379132	P	P	P	11.10366

13.55743	13.35107	12.14796	12.14475	P	P	P	14.09962
10.85792	11.2699	11.57301	12.20816	P	P	P	11.38263
	5.951363	7.799251	8.126818	A	A	A	
7.149063	7.937426	6.220748	P	P	P		5.549749
4.284284	4.148403	4.531053	P	P	A		4.932655
6.448282	6.349456	3.7136	4.857219	P	P	P	5.934319
7.122247	5.695894	7.337404	7.60128	P	P	P	7.509631
7.839109	8.219546	8.142678	8.534546	P	P	P	7.788907
12.64496	12.00227	13.0547	14.12502	P	P	P	12.90068
7.734237	6.102482	7.844335	6.965015	P	P	M	6.945332
12.43885	13.00101	12.49541	11.83573	P	P	P	12.8705
	5.382499	6.577378	6.880124	A	A	A	
8.319411	8.764931	8.546902	8.6957	P	P	P	8.597519
5.245198	4.865677	5.796478	M	A	A		5.054406
11.32677	10.72932	11.70449	11.96544	P	P	P	10.46201
5.730791	6.428661	6.216999	6.284421	P	P	P	6.91064
7.790385	6.783318	9.112323	7.111823	P	P	P	8.012011
8.326496	7.042555	6.885502	7.092846	P	P	P	7.252357
8.342329			9.540465			A	8.556004
6.812551		7.581573	7.423053		A	A	6.166779
7.159558	6.450096	7.014169	4.41304	P	P	P	6.616605
10.31085	10.37484	9.679316	9.544221	P	P	P	10.91862
8.236382	8.013956	7.5313	6.897566	P	P	P	8.084314
11.19952	10.74743	10.33905	9.663064	P	P	P	10.43584
8.132736	7.698299	8.639516	8.567203	P	P	P	7.54407
7.200563	6.608469	8.132214	8.136603	P	P	P	6.824671
8.960162	9.308633	10.72109	10.3942	P	P	P	9.052899
6.014216	5.762638	6.263931	6.807522	P	P	A	5.291462
10.33817	9.97831	10.42567	11.6698	P	P	P	10.4196
7.972126	7.465761	8.68223	8.765788	M	P	A	7.478744
12.63936	11.82712	12.91478	13.94107	P	P	P	12.40567
7.61659	6.521772	7.963607	8.298496	P	P	P	7.36427
11.60594	11.88497	10.90886	10.91753	P	P	P	11.98724
9.87813	10.48032	9.476438	10.29071	P	P	P	9.388168
11.66219	11.33396	10.82711	10.8656	P	P	P	11.18882
6.863834	6.535175	7.706029	A	P	A		5.021234
7.811525			8.809706			A	7.168755
9.740692	8.913748	10.33532	9.80817	P	P	P	8.785127
12.02893	10.68194	12.63366	12.66939	P	P	P	11.62373
7.80954	7.062347	7.177756	6.649828	P	P	P	6.57111

14.99724	15.59384	12.08268	13.92703 P	P	P	P	15.82923
7.934512	7.064242	7.699547	8.53897 P	P	P	P	7.197656
8.247474	7.933346	7.695624	5.897446 P	P	P	P	8.165716
7.609324	7.680613	9.273965	8.406738 P	P	P	P	8.660203
8.77761	7.718769	7.769244	7.979636 A	P	P	P	7.1647
7.449486	7.22609	7.862398	8.363428 M	P	P	P	7.331764
5.611135	6.016127	4.858032	6.096684 P	P	P	P	5.580846
10.386	11.55948	10.65299	11.10016 P	P	P	P	11.44893
7.575349	7.213229	5.654741	8.12473 A	M	M	A	8.020312
10.63139	10.44202	10.38284	9.698629 P	P	P	P	10.3088
11.09826	11.50413	12.26818	12.83637 P	P	P	P	11.76945
5.830751	6.131384	6.067083	P	A	P		5.814121
7.340156	7.291377	7.678933	8.337843 P	A	P	M	7.253603
9.34248	8.633953	9.661674	9.357395 P	P	P	P	8.313493
9.807528	9.540401	10.5565	11.18183 P	P	P	P	10.13513
5.936199	6.319816	6.114721	0.865548 P	P	P	P	5.506691
10.91655	10.87565	9.890738	9.51488 P	P	P	P	10.6839
8.533105	9.674418	8.039983	6.978983 P	P	P	P	8.846906
10.56831	9.770409	11.0509	11.38171 P	P	P	P	10.02232
8.149473	8.314538	6.186568	7.481935 P	P	P	P	8.168615
10.42081	9.75948	9.530299	9.53367 P	P	P	P	9.398409
8.078594	7.65184	7.185912	6.78661 P	P	P	P	7.355386
8.624722	7.917094	8.265524	7.613045 P	P	P	P	6.856512
8.319444	8.408308	8.051458	7.95383 P	P	P	P	8.46884
5.929831	6.097265	7.010751	6.273346 M	P	P	A	7.301886
11.59135	13.69013	6.954032	9.66444 P	P	P	P	14.05216
12.84499	12.45932	12.70629	12.56188 P	P	P	P	11.86832
	5.070286			A			
10.20865	9.771391	9.965613	9.401127 P	P	P	P	9.911301
7.368261	6.838765	8.036598	A	P	P		6.419365
11.53619	11.20944	11.36941	11.14062 P	P	P	P	10.7862
7.638841	6.191616	8.30654	6.738625 M	P	A	P	5.841535
		4.506009				M	
	4.518918			A			
8.924099	8.123031	9.10929	10.12804 P	P	P	P	8.733356
7.079695	5.961587	7.25654	5.894329 P	P	P	P	7.20987
7.860755	6.888688	8.031372	7.963782 P	A	P	P	8.670427
7.516184	7.753365	6.960922	5.948154 P	P	P	M	7.064685
11.27052	11.838	11.76905	11.0731 P	P	P	P	11.20632
7.562976	7.354045	8.776163	8.462266 P	P	P	P	6.982771

5.837894		6.667344	6.673847 M		P	P	7.286033
8.516594	6.766975	8.419086	8.242909 P	P	P	P	7.463295
5.473467	6.064153	6.044107	4.008676 P	P	P	P	5.62744
5.804599	5.557127		6.628654 P	M		A	7.100334
8.505815	7.747303	9.082875	9.30178 A	A	A	A	7.28989
	4.362511			P			
9.046965	9.5186	8.71627	8.725909 P	P	P	P	9.380824
10.61139	10.35675	11.07967	12.21118 P	P	P	P	11.14855
12.26366	11.6179	13.15619	13.49669 P	P	P	P	11.74221
6.754516	6.140556	6.81778	7.640589 P	P	P	A	7.323906
10.07247	9.567016	9.914949	10.71794 P	P	P	P	9.566134
10.04564	9.587455	11.07883	10.65243 P	P	P	P	9.823855
8.169278	9.364909	8.423604	7.962013 P	P	P	P	8.117463
8.082624	7.778197	8.851653	8.596519 P	P	P	P	8.362953
13.80521	13.17437	11.68393	12.89161 P	P	P	P	13.83724
6.963043	7.656662	8.987756	7.868004 P	P	P	M	6.054048
6.066767	6.806608	4.798961	3.965048 P	P	P	P	6.860625
7.556343	9.027173	8.020799	6.991032 P	P	P	P	8.673579
7.483845	7.020869	8.801221	9.267399 P	A	A	P	6.379738
12.31943	11.67115	12.64816	12.24944 P	P	P	P	11.89161
8.564675	7.348202	8.144829	7.792363 P	P	P	P	6.678352
8.40449	9.278191	8.235149	8.617833 P	P	P	P	8.678634
6.385146			P				7.495743
12.00543	11.13814	11.02615	11.291 P	P	P	P	12.09774
11.99463	12.53264	12.03333	10.75348 P	P	P	P	12.37086
10.11695	9.91313	10.87401	11.15818 P	P	P	P	10.24878
9.141519	8.110795	9.123317	8.8124 P	P	P	P	8.030156
8.177985	8.14083	7.739484	7.720428 P	P	P	P	7.928924
6.462132	7.998863	6.763456	7.137735 P	P	P	P	7.215419
12.21834	11.12762	11.9644	11.62034 P	P	P	P	10.61557
7.897331	7.380693	8.878846	8.541832 A	P	P	P	7.40386
7.464022	8.269018	8.064365	6.61012 P	P	P	P	8.840478
10.46962	10.30474	9.686326	9.2674 P	P	P	P	10.19009
9.808108	9.291948	9.06336	8.723466 P	P	P	P	9.5789
11.64514	11.94818	11.97336	12.65224 P	P	P	P	11.86278
9.914794	8.916923	9.236394	8.574885 P	P	P	P	8.813241
9.110277	8.632833	8.171392	7.720975 P	P	P	P	8.626851
7.409414	8.514766	7.807261	7.068595 P	P	P	P	7.588935
8.807711	8.628369	9.691382	9.312638 P	P	P	P	8.19618
9.694431	9.870151	9.750546	10.05022 P	P	P	P	9.887121

7.615964	6.327009	7.884974	7.718368	P	A	P	P	6.081753
8.632615	9.216629	9.534414	9.538802	P	M	M	P	8.796922
6.834855	7.12213	6.834725	7.459349	P	A	A	A	6.304678
9.900261	8.343702	8.365247	7.598819	P	P	P	P	8.79408
10.94882	11.67847	10.30745	10.53396	P	P	P	P	11.47993
4.841977	4.909338		3.724371	P			P	6.137008
7.769722	6.523778	7.289241	5.32258	A	P	P	P	7.08082
6.535871	6.884383	7.009279	6.755857	P	A	A	A	7.096389
7.876177	6.66618	7.573664	7.391576	P	A	P	A	8.023226
			7.007527				A	
7.36599	6.972008		6.855036	P			P	6.353804
11.70133	10.19422	11.89348	10.86162	P	P	P	P	9.227978
8.177993	5.885077	8.621054	9.1224	P	P	M		7.383078
6.066526	6.192895		7.404364	A		A		6.351969
	5.730921			P				
		5.066499				P		
11.95856	9.444302	12.32389	11.86805	P	P	P	P	8.7715
8.784013	7.952374	8.089301	7.82781	P	P	P	P	8.010834
12.48126	11.83053	12.52626	12.31494	P	P	P	P	12.20921
10.98324	10.2628	9.818454	9.497911	P	P	P	P	9.863692
10.94127	10.35582	11.28981	11.76441	P	P	P	P	10.71048
5.554729	1.923864		6.744089	P			P	6.69828
9.809622	9.681455	10.75825	11.56573	P	P	P	P	9.523387
	3.950747	6.416619	6.972632	P	P	A		
8.546867	7.619663	10.03008	9.384246	P	P	P	P	8.523925
7.491398	7.272543	8.164266	8.559391	P	P	P	P	7.335974
7.476078	6.876496	8.53101	8.547603	P	P	P	P	9.024893
10.67765	10.46348	10.20337	9.446544	P	P	P	P	10.41173
11.01198	11.38996	10.47552	10.67937	P	P	P	P	11.16183
9.264037	8.256739	8.108164	8.015877	P	P	P	P	7.8268
7.688661	6.055718	8.090465	6.653423	A	P	A		5.837975
8.674943	9.150614	8.49632	8.008615	P	P	P	P	8.348216
10.47475	10.92953	9.880942	9.351957	P	P	P	P	10.36445
13.00842	13.1571	12.0928	11.6932	P	P	P	P	12.88923
	4.672898			A				
		6.59414				A		
	5.225236	1.526788		P		P		
		3.05231				P		
6.449421	7.764233	5.712289	A	P	P			4.675515
9.965241		10.00649	10.26827	A		P	M	7.491473

			6.749551			P	
11.7659	11.93955	11.35462	10.40472 P	P	P	P	11.75993
9.258071	7.870567	9.659841	10.85576 P	P	P	P	8.594306
7.581725	7.75989	7.998235	8.972563 P	P	P	P	8.384498
6.696052	7.015101	7.355262	7.31061 A	P	P	P	6.358433
7.181212	6.627539	6.991596	A	P	M		4.210958
9.509275	9.907858	9.040516	8.54009 P	P	P	P	10.045
8.601295	8.067313	8.767447	9.041986 M	P	A	P	8.240688
8.045995	7.205231	6.235832	7.164169 P	P	P	P	6.917418
8.85464	8.667912	8.719478	9.486593 P	P	P	P	8.803348
8.75227	8.619913	7.761411	8.390753 P	P	P	P	8.814948
10.87318	11.20066	10.42551	9.94502 P	P	P	P	11.25355
9.437953	8.894661	8.858634	10.25347 P	P	P	P	10.8299
10.60311	10.92444	9.9791	9.677434 P	P	P	P	10.97116
6.363647	5.971836		5.20113 A	P		P	5.115466
11.7319	12.37449	12.1623	13.1791 P	P	P	P	12.13731
6.303234	6.079305	5.188935	7.977505 A	A	A	A	6.151984
5.414526			A				4.412568
10.94036	10.85763	10.63418	11.3501 P	P	P	P	10.91517
7.226844	8.811267	7.769053	6.931994 P	P	P	P	7.603916
10.21556	10.16247	11.18443	10.61654 P	P	P	P	10.08164
10.72921	11.08194	10.51595	9.519937 P	P	P	P	11.13318
10.7279	9.723619	10.74274	10.0565 P	P	P	P	9.456441
9.079895	9.182088	10.65236	10.90278 P	P	P	P	9.301964
6.787943	6.495171	6.639422	P	P	P		7.192286
9.368131	8.065528	9.139095	8.98736 P	P	P	P	9.264578
9.240885	10.38331	9.659567	8.7881 P	P	P	P	10.70566
8.858512	8.610826	5.11845	7.180607 P	P	P	P	8.602138
6.945167	6.994623	5.775472	3.839179 P	P	P	P	6.148321
6.035559	6.135656	5.589925	5.219823 P	P	P	P	6.859862
12.1538	10.55898	11.12009	10.72079 P	P	P	P	10.32634
11.06317	12.23825	11.62536	12.11928 P	P	P	P	12.10735
6.808984	6.994169	8.231844	8.839842 P	P	P	P	7.657909
6.028009	6.718302	6.846512	3.996055 P	P	P	M	6.521248
10.67471	10.81456	10.13656	10.06379 P	P	P	P	10.92905
8.979574	8.142622	8.434084	8.92335 P	P	P	P	8.893974
6.788952	6.730758	6.449729	7.627898 P	P	P	P	7.441244
6.321412	3.01419	3.842323	6.219663 P	P	P	P	6.724321
9.748432	10.64355	10.61379	10.50969 P	P	P	P	10.61443
8.387126	7.451849	9.161504	8.910151 P	P	P	P	7.971398

11.54979	11.27013	10.35061	11.48095	P	P	P	12.04654
6.663348	6.190247	2.692629	7.380989	P	P	P	6.665266
5.151398	4.465956	5.921547	6.414651	A	P	P	5.533132
13.11404	13.77528	12.58899	12.07043	P	P	P	13.38933
6.674049	7.139222	7.157856	7.139521	P	P	P	6.838905
11.9367	11.52102	12.62192	12.41092	P	P	P	10.89876
7.007611	7.205728	8.346139	A	P	P		6.517887
9.828131	10.19341	9.131775	8.423879	P	P	P	9.92821
6.532559	6.250314	6.608382	8.96097	A	P	P	5.385668
11.80576	11.97718	11.21977	10.74402	P	P	P	11.63581
5.755518	6.080857	1.561441	P	P	P		6.064321
6.810347	6.307114	2.909047	2.899495	A	P	P	4.721934
13.15145	12.89821	13.16417	13.62757	P	P	P	12.99826
10.89735	10.28246	10.05559	9.648505	P	P	P	9.78917
8.187299	8.415777	7.45777	P	P	P		6.943666
8.441431	7.570424	8.643019	7.734026	P	P	P	8.238318
9.627451	8.907062	8.917781	7.678761	P	P	P	8.615989
	6.324489	7.957549	7.943409	A	A	A	
8.305579	9.243903	9.561161	9.556576	P	P	P	9.807574
9.188982	9.100722	9.193746	8.337412	P	P	P	9.156225
12.47326	12.90796	11.94175	11.62416	P	P	P	12.63308
5.827635	5.68842	6.377707	A	A	A		4.706358
12.00413	13.29905	13.06959	12.07147	P	P	P	13.18209
7.671921	7.133591	6.633273	6.081081	A	P	P	6.292491
10.33351	11.18158	9.650114	9.712792	P	P	P	10.75771
5.808291	5.957524	6.321702	6.639416	P	A	P	6.275421
11.79652	11.96239	11.28789	11.18677	P	P	P	11.96031
9.467925	9.279595	10.31605	9.717798	P	P	P	7.942694
7.081877	7.8268	7.711153	7.0005	P	A	A	7.589748
8.077654	7.596574	9.54706	9.152569	A	P	P	7.407373
11.08314	11.3057	9.675267	9.776449	P	P	P	11.14372
	4.944177			A			
9.7206	10.19876	9.882029	8.636066	P	P	P	9.754193
8.134033	7.450928	7.813435	7.506038	P	P	P	7.018211
7.894112	7.768589	8.925064	8.955791	P	P	P	7.637072
13.28831	13.59105	12.90381	12.19661	P	P	P	13.25218
	5.046805		5.571737	P		P	
11.2579	12.19295	11.72117	10.86908	P	P	P	12.14933
8.94846	8.034326	9.099299	9.027061	P	P	A	8.509513
	6.869359	7.944354	8.501637	P	P	P	

9.766687	10.68245	10.712	9.005293	P	P	P	10.19999
6.57943			A				4.42017
9.906755	10.01326	8.918033	8.66329	P	P	P	9.971292
9.212843	8.309048	9.296235	9.105637	P	P	M	8.335346
6.826754			8.11949	P		A	8.026975
5.923338	5.952854	7.470584	9.068934	P	A	P	6.475485
6.56869	6.23709	7.620569	8.482461	P	M	P	7.062472
8.796934	8.541788	7.60531	6.908217	P	P	P	8.044783
5.642929	2.55355		1.465823	A		M	6.001738
		5.220707			A		
6.735345	5.463276	4.269306	6.51226	P	P	P	6.524721
6.837759	7.021201	7.493255	7.380113	P	P	P	7.266099
9.682705	8.875814	9.387027	8.671822	P	P	P	8.600415
7.870939	8.187634	4.840879	6.940428	P	P	P	6.695993
7.202181	7.391728	7.037426	7.056068	P	P	P	7.363055
6.748642	6.518915		M	P			7.846206
		5.975235				A	
6.722951	6.357441	5.902195	7.520415	A	P	A	6.3717
		8.637531	9.4482		A	A	
		2.561872			P		
	6.743063	4.755918		A	P		
7.418	7.442851	7.621985	8.178438	P	P	A	7.785817
13.4976	13.33715	11.9591	11.53206	P	P	P	13.58958
7.472336	6.814889	7.80904	7.886384	A	P	P	6.8536
	4.268613			M			
7.040852	7.86642	7.258073	8.695456	P	P	P	8.447316
	5.02664			A			
7.895846	8.556029	8.086505	8.594305	P	P	P	9.756418
7.296455	7.722419	5.90584	6.353141	P	P	P	8.438819
6.128192	5.270035	5.306657	A	A	P		5.867013
5.908601			7.276201	P		M	7.723268
11.90795	12.17757	11.45119	10.79235	P	P	P	11.9293
7.726244	6.588412	7.303927	5.836449	P	P	P	6.600677
6.507065	5.969679	5.727059	7.340058	P	P	P	7.088511
7.506366			A				5.832572
8.817334	9.217293	8.811214	8.225654	P	P	P	9.292935
11.40595	10.76279	10.18444	9.935892	P	P	P	10.6165
8.470408	8.368872	7.786929	9.250492	M	P	P	8.811546
9.337425	9.276044	8.289743	8.759157	P	P	P	9.176548
5.767046	5.629614		6.56031	A		A	1.459952

4.320559	6.625149	6.990204	7.471922	P	A	A	A	6.564756
6.757025		7.717221		A		A		5.854136
6.424503	6.000821	6.243521	4.049541	P	P	P	P	6.472488
8.482982	8.67192	6.442952	7.510225	P	P	P	P	8.619246
6.945377	6.440006	6.880283	7.697241	P	P	P	P	7.199972
8.840303	8.637723	9.522703	8.931465	P	P	P	P	8.538218
			6.267993				A	
9.139848	9.167882	7.919018	8.854929	P	P	P	P	8.984758
	4.717514		6.66814	P			A	
7.822142	6.942987	8.734655	8.97206	P	P	P	P	7.423289
		5.966897			A			
6.799856	5.610863	5.748755	7.245423	P	P	P	P	7.409204
6.457027	6.02103	5.312242	5.534083	P	P	P	P	6.237886
5.57165	6.050148		7.292014	M			A	6.282083
6.641449	6.345379	6.530892	7.072221	P	P		A	5.847889
			6.829286				A	
9.030476	9.073893	10.28462	10.36379	P	P	P	P	8.991333
7.018499	6.392765	7.435815	7.471265	P	P	P	P	7.798803
12.0621	12.50453	11.38703	11.43056	P	P	P	P	12.22247
	2.108181		3.360078	P			P	
			6.800821				P	
6.970034	6.473492	4.996333	5.889641	P	P	P	P	6.485408
2.263509			P					6.152845
9.781514	9.323088	10.33538	10.3144	P	P	P	P	9.587297
9.708283	9.36044	10.89942	10.60224	P	P	P	P	9.214607
4.682951	5.799076	6.102717	3.781313	P	P	P	P	5.929884
5.99337		7.868722	7.768524		A	A	A	7.028381
8.691338	8.426157	8.925259	9.728797	P	P	P	P	8.502828
5.472816	5.457178		A	A				1.919663
6.965685		7.69307	A		A			7.460126
	4.655959	6.467112		P	M			
10.13703	9.728982	9.006483	8.889514	P	P	P	P	9.621534
4.496335	7.330692	6.038319	2.356617	P	P	P	P	6.776292
	5.829497			A				
6.668161	6.325303	6.11951	6.300157	A	P	P	A	6.086798
	7.072368	8.730351	9.206309	P	P	P	P	
7.336322	7.969114	6.103567	7.960035	P	A	P	P	8.326489
10.98944	10.4023	10.7678	11.30289	P	P	P	P	11.16656
12.66874	11.90334	11.19332	11.42241	P	P	P	P	12.6111
9.21673	8.780048	11.05613	10.91035	P	P	P	P	8.466186

8.202052	7.927924	8.417603	9.203818 P	P	P	P	8.085425
8.907857	8.602013	9.948508	8.996498 P	P	P	P	8.352661
	2.8133	5.300084		P	P		
7.576687	8.383101	8.000678	8.505456 P	P	A	P	8.658755
		6.34349				A	
	6.615673			P			
9.460487	9.924646	8.348298	8.519098 P	P	P	P	10.09515
	4.67779	6.622706		P	P		
9.689682	10.22761	9.210195	8.66803 P	P	P	P	9.625758
9.49507	8.657491	9.762079	9.858164 P	P	P	P	8.630208
10.8966	10.00503	11.358	11.56367 P	P	P	P	10.181
	5.509886	4.081227		P	P		
9.913678	8.951811	8.209807	7.497229 P	P	P	P	9.552167
	5.472562	6.479168	6.739204	P	A	P	
		6.948289			A		
9.262704	8.943321	10.35851	10.24815 P	P	P	P	8.223672
	5.562321			A			
9.239494	9.082669	8.681104	8.647118 P	P	P	P	8.212182
8.388221	8.771696	8.030266	8.581675 P	P	P	P	8.455646
5.784	5.374003		A	P	P		4.071086
10.55874	11.1524	10.0435	9.651338 P	P	P	P	10.72194
	5.844823			A			
7.584432	6.52962	6.757976	A	P	M		5.682697
6.511065	7.467548	10.67365	10.54571 P	P	P	P	7.239801
11.32146	10.88769	9.203905	9.446216 P	P	P	P	10.60918
9.732939	9.614602	8.299023	7.674142 P	P	P	P	9.41622
6.743587	6.466086	8.159491	7.432528 P	P	P	P	6.609706
11.58824	10.87811	11.19058	12.92303 P	P	P	P	12.0049
7.263598	7.703234	7.232383	7.083035 P	P	P	P	6.562843
		6.422656	6.03964		P	A	
8.018401	6.969176	8.187592	8.353942 P	P	A	P	7.464505
5.464189			4.466991 A			P	5.773136
7.316252	7.321621	7.047027	6.336002 P	P	P	M	7.979154
	8.43286	8.274976		P	P		
8.95739	9.065891	8.240625	8.722541 P	P	P	P	8.937563
10.66994	10.01016	10.87553	11.31479 P	P	P	P	10.00102
10.57062	10.06082	10.80258	9.968142 P	P	P	P	10.01609
7.997874	6.783335	7.756222	6.955285 M	A	P	A	6.797118
11.24004	11.61622	10.58756	10.62935 P	P	P	P	11.66924
14.80881	14.63024	14.09801	16.0004 A	P	P	P	5.368753

	5.737497	1.915727		P	P		
3.478097	5.844247	6.927007	P	P	P		7.465076
8.57741	9.378011	8.74019	8.415854 P	P	P	P	9.297479
10.96527	11.41773	10.91111	9.911755 P	P	P	P	11.09037
9.195103	8.231841	7.302163	6.937017 P	P	P	P	8.104343
10.41742	11.18723	8.965693	8.787648 P	P	P	P	10.65815
11.29976	11.91174	10.01243	10.52514 P	P	P	P	11.51448
11.28079	11.6486	11.1751	10.31997 P	P	P	P	11.1806
8.870397	8.595741	7.975918	7.471567 P	P	P	P	8.638718
9.157525	8.584234	7.981869	7.404799 P	P	P	P	9.151073
6.091923	6.391274	4.9135	3.494479 A	P	M	P	2.869034
5.66749	5.692871	6.339946	5.951083 M	A	P	P	6.826943
	6.340632	2.531655		M	P		
8.438429	8.569547	8.105504	7.303448 P	P	P	P	7.81858
8.338665	7.744633	8.776801	9.866105 P	P	P	P	8.578941
9.436296	7.849995	8.935732	9.34224 P	P	P	P	8.394956
7.041785	6.706305	6.870318	7.120781 A	P	P	P	5.292384
8.374156	9.228611	9.764442	10.27495 P	P	P	P	9.207953
12.16898	11.61399	12.73182	12.58263 P	P	P	P	11.50246
7.575562	7.390683	8.409602	8.55481 P	P	P	P	7.356916
6.615114		7.261289	7.993174 P		A	A	7.365577
4.559941			5.744372 M			A	5.793179
7.910619	7.895605	7.916915	8.834806 P	P	P	P	7.965048
8.766176	7.208274	8.208673	7.63016 P	P	P	P	7.316403
	5.276376			P			
7.846536	7.976075	7.668887	7.590744 P	P	P	P	6.972013
6.292642	5.403123	3.712174	7.400821 A	P	P	P	2.16521
6.867423	7.895595	7.936032	P	P	P		7.9142
7.347267	6.744216	5.201544	7.315788 A	P	P	P	4.749677
6.08595	6.332103	5.773062	5.821313 P	P	P	P	5.701539
6.628557	6.578162	6.25826	4.636393 P	P	P	P	7.409225
5.1694	6.79323	6.698137	6.550371 P	P	P	A	6.134079
10.15622	8.166624	8.030148	8.021287 P	P	P	P	8.866085
8.45196	8.483645	9.738139	9.185274 P	P	P	P	9.278667
10.80963	11.51604	8.438332	9.214501 P	P	P	P	11.39845
4.997418	6.473536		5.997236 P	P		P	5.029396
6.449426	7.021996	6.228938	7.223658 P	P	P	P	7.542925
9.4253	8.581184	9.703654	10.03645 A	P	P	P	8.10301
7.657149	7.507174	5.981121	5.152876 P	P	P	P	7.31307
11.64839	11.19076	11.9608	12.04327 P	P	P	P	10.90194

12.87959	12.77897	10.74446	10.79066	P	P	P	12.22681
11.45159	10.62449	10.19876	9.844153	P	P	P	11.07154
	5.691997	5.472562		P	P		
8.808259	8.150572	8.38591	10.0271	P	P	P	9.400117
5.041103	6.041452	7.47138	6.761457	A	P	A	8.969306
8.156209	7.030363	7.732309	7.937345	P	P	P	6.447582
10.34859	8.895612	9.168335	10.08933	P	P	P	9.211967
8.894851	8.016502	9.176131	10.27808	P	P	P	8.680937
7.982041	8.440132	8.759439	7.63676	P	P	P	8.115953
6.365207		5.987338	A		P		6.639119
11.21385	11.32091	10.35378	8.940573	P	P	P	11.28958
5.889793	6.043746	5.644155	7.028079	P	P	P	5.89127
6.375984	6.054149	3.403383	3.724553	P	P	M	6.358481
8.777161	9.429144	8.343625	8.344639	P	P	P	8.888956
10.92881	10.51423	9.382479	9.481744	P	P	P	10.54405
5.747867	6.521862	5.997283	7.582979	A	P	P	6.763795
6.980856	6.795395	5.661001	P	P	P		5.958397
11.85045	10.69674	12.97206	13.30733	P	P	P	10.48718
9.520645	7.928073	9.603166	10.05665	P	P	P	8.182545
8.942669	8.622357	8.238987	8.441922	P	P	P	8.875172
13.12812	13.46956	13.64228	14.29946	P	P	P	13.70914
10.35541	10.00338	10.54009	10.79364	P	P	P	9.646132
7.505959	5.668916	7.840911	8.239444	A	A	P	6.741409
	5.715786	6.06614	7.16014	P	P	A	
11.30651	11.28008	11.69876	11.86349	P	P	P	11.40152
14.03554	13.37046	14.54146	14.85783	P	P	P	13.18234
9.948403	9.333768	9.861952	9.670404	P	P	P	9.005573
7.572599	7.449048	7.72739	8.328947	P	P	A	5.779461
10.78924	10.55141	11.70473	11.84653	P	P	P	10.34811
5.612403	6.905993	7.388051	3.823096	P	A	P	6.742207
6.641041	6.532627	7.675139	8.188667	P	A	P	7.535478
11.23071	11.12859	10.01163	10.27908	P	P	P	11.16775
10.05961	8.802177	9.22133	9.08907	P	P	P	8.06416
7.950371	7.753968	7.152412	7.00756	P	P	P	7.476792
12.15769	12.02991	12.71932	13.97857	P	P	P	12.59377
					M		
6.515399	6.825484	7.123603	3.763622	P	P	P	6.857688
8.651643	7.27648	9.325727	9.942719	P	A	A	7.853201
10.37242	8.599529	10.50472	10.42487	P	P	P	9.096367
6.369334	4.722455	6.589868	6.983965	M	A	A	6.733737

9.565052	11.04102	9.766914	9.255626	P	P	P	10.61262
8.489829	8.253349	7.044187	7.986527	P	P	P	7.950365
7.033541	6.219351	6.870938	6.614773	P	P	M	8.177076
6.807983	7.019966	6.617044	A	P	A		6.783181
6.7289	7.572949		8.116932	A		P	6.980423
6.91854	6.810979	5.595762	6.355775	P	P	P	7.086224
9.222156	9.597079	10.42928	11.01899	P	P	P	8.954664
5.520949	5.443129	6.016172	5.431351	P	A	P	5.746547
11.75714	11.92769	12.0333	13.62669	P	P	P	12.07526
6.50722	6.806045	6.876387	A	A	A		6.40995
6.689	6.806891	4.381838	5.641751	P	P	P	5.956492
9.775052	10.44679	9.67533	9.416564	P	P	P	10.92674
7.032514	6.538938	6.697245	5.986271	P	P	P	7.714946
12.93891	13.08808	12.06642	11.98614	P	P	P	13.28685
12.91157	12.68185	13.82027	13.75972	P	P	P	12.69053
5.561824	5.172068	4.895052	6.992157	A	P	A	5.876433
13.44141	13.4909	12.49688	12.52971	P	P	P	13.79807
6.133417		6.144234	A		P		2.516272
9.622634	9.513992	9.47585	8.807474	P	P	P	9.15133
5.799577	5.734724	6.61858	6.475919	P	A	A	2.749243
		6.55976				A	
8.352159	8.939625	8.16118	7.730313	P	P	P	8.381652
7.903908	6.735726	8.041141	8.567637	M	P	P	8.412429
9.531606	8.979997	9.67616	8.773973	P	P	P	8.010838
3.450485	4.807012	5.44167	6.595238	P	P	A	6.326462
9.054075	9.578009	7.923944	8.58931	P	P	P	9.438541
	5.33542			A			
5.653001		5.956895	6.506418		A	A	5.079953
	6.799871		7.806998	P		A	
5.942614		6.599091	P		A		5.656325
5.73677			A				3.068775
2.95238			P				6.391644
7.438674	6.800279	7.013541	A	P	P		5.681397
	4.82895			A			
			2.789339			P	
6.122833	7.894199	5.989463	6.396439	P	P	P	7.416786
	6.814878	8.185847	8.336579	A	P	A	
		2.856692			P		
7.796102	8.373934	6.911717	6.848117	P	P	P	8.131638
6.453935	7.481738	6.461103	7.216647	P	P	P	7.784483

8.42338	7.636085	7.41788	7.342527	P	P	P	7.300382
7.041883	7.406135	5.592535	6.207404	P	P	P	7.535049
5.621234	6.523629		A	P			6.949897
6.820732	6.189669	4.924648	6.99211	P	P	P	6.443429
6.058154	5.823128	5.58208	6.17087	P	P	P	6.01781
5.584248		5.639977	7.698266		P	P	6.350604
9.167813	9.504809	11.13871	10.99185	P	P	P	8.415822
	3.601876			P			
7.560634	8.268466	7.396635	7.454298	P	P	P	7.919372
8.69018	9.317411	7.978664	8.069085	P	P	P	8.591644
	3.95181		5.901321	M		A	
9.823926	10.50236	10.93083	11.24819	P	P	P	9.889397
6.701228	5.957158	7.421816	7.038737	P	A	A	6.93857
6.598303	5.93198	7.099052	6.365639	P	P	A	5.703951
7.593057	7.704163	7.032745	7.843906	P	P	P	6.720867
7.75619	6.274349	6.713052	6.291	P	P	P	7.293369
	5.542117			A			
6.0825	5.207432	5.618722	A	A	P		5.888002
6.148212	6.797811	6.441774	6.981305	P	P	P	6.603471
3.90551			M				5.976809
		2.38874			M		
	5.486367		7.53803	P		A	
6.08569	5.736644	5.336695	P	A	M		6.716024
11.48664	13.43646	9.53097	10.41987	P	P	P	12.41664
6.037945	6.476314	6.45015	5.613486	P	P	P	5.678348
	7.523495	8.120807		A	A		
9.519735	9.779957	8.827136	8.212444	P	P	P	9.392927
6.274944			P				7.430691
5.617439	6.455315		7.664394	P		P	6.977771
5.777686	5.363782	7.411978	7.205639	P	P	A	5.473252
	5.321829			A			
6.953823	7.390164	7.184427	6.093715	P	P	M	7.063934
	5.414225			A			
4.848383	4.348254		6.565119	M		P	6.1787
5.927869			A				1.77174
5.331126		5.456323	P		P		6.837174
			6.448528			A	
		5.844845			A		
	5.637123			P			
10.01618	9.602679	10.01051	9.374858	P	P	P	8.85424

		2.710016				M		
9.883684	9.814446	9.909908	10.9308	P	P	P	P	11.25199
6.072501	6.506462	4.963273	5.606107	A	A	P	P	6.372191
5.301846				P				6.304203
5.899463	6.140146	7.059608		P	P	A		5.865118
3.803833				P				5.681497
			7.518242				A	
7.47384	7.443402	7.189329	6.727325	P	P	P	P	6.395004
	5.976447			A				
			7.298104				A	
5.606041	6.438192	5.49122		A	P	P		6.121296
	0.277698				M			
			4.047661				M	
7.197078	7.330855		8.027629	A	A		P	3.476968
	2.982831				P			
2.451736				P				5.284373
3.592064				P				6.248664
3.10289	5.55401	5.28982		M	A	P		5.615121
5.463505				A				1.588722
5.050903	1.307274			P	P			6.316646
5.666841				P				6.820583
		7.634496				A		
6.0287				A				4.724626
7.699456	7.727999	6.845518	6.368321	P	P	P	P	7.579503
7.6082	6.86733	5.701023	6.593104	P	P	P	A	6.461503
	5.524118	5.421917			A	P		
5.922678		7.952163	7.984956	P		A	A	5.552741
9.271351	9.96009	9.250238	7.887173	P	P	P	P	9.652163
8.59035	9.574486	8.259649	7.264211	P	P	P	P	8.808699
6.285832	7.251704	5.728571	5.84439	P	P	P	P	7.214215
9.99915	9.759436	9.40229	9.014459	P	P	P	P	9.818242
7.75786	6.346214	8.09042	7.549046	P	P	A	A	5.383942
	5.432538				A			
6.356558	4.896531	1.949297	5.253904	P	P	P	P	6.241708
7.877792	8.466077	7.146458	6.832245	P	P	P	P	7.395101
			5.93632				A	
8.740407	9.649862	9.363449	8.283896	P	P	P	P	9.493314
6.114142	6.227761	6.276664		A	P	P		5.241332
5.217452		6.121485	5.88795	A		A	A	6.145451
7.461422	6.976761	7.791441	8.124832	A	P	P	A	6.669964

	5.068586			A			
6.569994		5.682314	6.261665 P		P	A	6.707212
	4.474548			P			
			6.636884			A	
		5.533624			A		
4.847635	5.168721	0.914051	A	P	P		4.596622
7.092864	6.453478	6.141746	P	A	P		6.546228
		3.832933			P		
7.00282	5.946561	7.027636	7.93143 P	P	P	P	7.428285
	6.11249		7.087738	A		A	
6.343105	7.191813	7.264096	7.439809 P	P	P	M	6.953563
9.86711	10.02689	9.829772	9.514115 P	P	P	P	10.39396
	4.240457			P			
		5.807206	5.706348		A	P	
6.658805		7.74706	7.944585 P		A	A	7.633071
5.963561	5.767356	4.072783	6.79341 P	A	P	A	5.876393
	6.0347			A			
4.772602			5.41745 P			P	5.998603
6.589346			A				4.962532
5.863979	5.9966	5.500911	4.110406 P	P	P	P	6.36354
7.12543	7.573363	7.70625	6.374657 P	P	P	P	7.273561
6.006633	5.670636	6.647806	7.184555 A	P	A	A	5.470221
8.349631	7.091901	7.774972	6.438191 P	P	P	P	7.299602
	4.871409			A			
5.368409		5.911841	P		P		6.568249
	5.889396		6.400041	P		A	
1.767972			M				6.110535
4.282116		0.255565	P		P		5.295183
5.551408	7.289757	7.403344	A	A	P		3.708749
7.167029	6.469923	6.109445	6.351961 P	P	P	P	7.181202
5.809619		3.33425	A		P		5.188067
5.364599	5.849003	1.899582	M	A	P		5.461488
6.115771	6.302657	6.959372	6.846352 P	A	P	A	6.484073
6.07751	6.377326		P	A			6.538011
6.823937	6.71872	8.076106	7.90235 P	P	P	P	6.464832
8.470728	8.643723	7.658819	7.861316 P	P	P	P	8.736707
7.117065	8.68387	8.183656	7.67291 P	P	P	P	8.313885
6.877691	5.711754	7.175394	P	P	P		6.796776
	7.05854	6.868045	6.532221	A	A	A	
6.928972	7.571111	7.221439	5.581468 P	P	P	P	7.722078

9.236668	9.459971	8.768771	7.721981	P	P	P	9.157564
8.619369	8.128691	9.46916	9.304033	P	P	P	7.088913
6.124215		6.662584	A		P		3.244624
6.811467	6.818976	7.48845	6.537704	A	P	M	5.731406
		6.212197			A		
9.657957	9.80358	9.284648	8.881733	P	P	P	9.455957
9.005116	8.523951	8.77089	8.257963	P	P	P	8.278061
5.266659	5.576972	5.710982	6.743676	P	P	P	6.205179
5.927141	5.865311	6.747259	5.814962	A	P	A	5.338792
8.766313	6.792925	6.882785	6.905976	P	P	P	7.140331
5.871225	5.375982	6.015272	6.523212	P	A	P	5.867458
7.772601	8.170074	7.880685	6.511801	P	P	P	7.716363
8.691387	8.91968	8.026449	7.867286	P	P	P	8.262713
5.485771			A				3.942699
9.185594	9.604172	8.785651	8.145926	P	P	P	9.101453
10.97763	9.468641	10.98875	11.06249	P	P	P	9.019485
10.0633	9.054337	10.24783	10.17028	P	P	P	8.5328
5.445818		6.307375	6.41271		A	A	5.438581
6.867741	6.865837	6.628339	7.351054	P	P	P	7.066626
7.259494	6.613548	6.594552	A	A	P		6.512455
5.130852	5.054323		6.77441	P		A	4.755581
6.24547	5.607444	3.651952	6.946365	P	P	P	5.760771
7.126505	7.341458	7.772151	7.159015	A	P	M	4.095025
8.056361	7.549392	8.24089	10.21366	P	P	P	8.439281
5.38749	5.341466		A	A			2.629614
7.427291	6.86199	6.81957	4.960346	P	P	P	6.545379
4.272004	6.012431		P	A			5.400229
	4.47432	5.501039		P	P		
5.316823			P				6.416334
3.124472	5.56874		4.468356	P		P	6.365064
9.668442	9.702191	9.19701	8.407875	P	P	P	9.63626
7.56878	7.577416	6.598219	6.911681	P	P	P	7.05817
7.74118	7.510998	8.235789	7.555845	A	A	M	8.043625
4.980471			M				6.318001
7.094691	6.073055	7.562503	8.025066	P	A	P	4.400262
	6.142765	4.941707	3.430986	A	M	M	
6.250125	7.477406	6.026397	6.617354	P	P	A	7.399107
10.19937	11.58517	11.90187	10.73108	P	P	P	10.62208
9.003211	9.403227	8.785211	6.926003	P	P	P	8.832776
		6.922813			A		

8.677321	8.738259	9.63069	8.966105	P	P	P	8.856874
9.108719	8.984707	8.165898	7.726669	P	P	P	8.848605
4.996916	4.572053	6.204934	A	P	M		5.572821
5.7873	5.265152	6.311723	6.159225	P	A	P	6.59012
7.44689	7.895684	6.862522	5.77794	P	P	P	7.803093
7.121007	7.963169	7.004041	P	P	P		7.580479
6.308281	5.669756	6.664188	A	P	P		4.820457
6.132898		6.079723	7.00611		A	P	6.237752
		4.268533			M		
			6.321568			A	
6.450476	4.441219		A	P			5.695083
6.658862		5.178791	6.492579		P	A	5.538441
8.478807	8.875202	6.96261	5.958817	P	P	P	8.699912
4.940126	3.834344		6.602966	P		P	5.958108
6.393033	6.255188	7.155984	6.490992	P	P	P	6.947778
		3.793596			P		
		4.57704			P		
6.130434	6.185664	6.899371	A	P	P		5.433662
		5.893284			A		
5.94568		6.540076	A		A		4.370958
9.583735	9.675781	9.830975	8.004982	P	P	P	9.527841
6.612988	7.100781	6.676306	6.203917	P	P	A	7.336155
5.031461	6.664263	7.195659	7.581528	P	P	P	7.378117
7.910714	8.241134	7.475754	6.891777	P	P	P	7.612907
8.487099	8.344764	7.622827	6.912686	P	P	P	8.355118
4.798913			A				0.043866
6.513674		2.973039	P		P		6.31436
5.166133		3.495549	P		P		6.021364
6.852644	6.975303	6.025816	7.012185	P	P	P	7.434225
6.022938		6.992568	7.507548		A	A	6.20581
5.783192	7.394114	4.119344	5.879621	P	P	P	6.213615
	8.790574	7.383881		P	P		
6.44034	6.571263	6.335808	3.628732	P	A	P	6.959238
6.723545	5.610778	7.320598	7.800285	P	M	P	6.262461
	4.693912	2.235183	6.548224	A	P	A	
		5.061446			P		
6.329914	6.338974	6.136636	A	P	P		6.041798
8.648601	8.450629	8.578957	9.357476	P	P	P	8.327449
1.045401			P				5.682989
4.422665	5.840435	6.170412	P	P	P		6.293987

	1.095976				M			
			6.132372				A	
		2.568555				P		
5.018326		0.955691	A			P		4.504115
8.387155	9.031775	8.496499	9.33046 P	P	P	P	P	9.515394
	4.040888			M				
5.976897	5.312846	6.647174	4.265004 P	A	A	P		6.741578
6.540337			A					5.260619
6.757906	7.909481	6.84213	6.897609 P	P	P	P		7.727161
9.752912	10.52734	9.521234	9.430657 P	P	P	P		10.24245
5.885077	5.281445		7.002455 P	P		P		5.785948
7.053674	8.136727	8.819201	8.343233 P	P	A	A		8.188043
5.834441			7.012811 P			A		6.455868
6.611603	7.114058	7.89678	7.276709 P	P	A	P		7.378264
	6.440556	5.724238	6.16318	P	P	M		
	6.053008	5.103366	7.092267	P	P	A		
			6.159557			A		
9.255285	6.955462	6.492531	7.259885 P	P	P	A		6.937916
8.247272	7.281738	7.676576	7.986764 A	P	P	A		7.195978
11.00616	9.625113	10.75558	10.41337 P	P	P	P		9.248156
7.681302	7.790186	7.765522	7.318907 P	P	P	P		8.142758
7.590646	6.966896	6.443606	8.112936 P	A	A	P		7.154816
7.687538	7.176173	7.523442	P	A	A			6.592188
3.94882			M					6.610322
7.640519	9.134513	8.215955	8.183172 P	P	P	P		8.45683
5.329855	3.439455	5.866755	P	M	A			5.931274
9.510687	9.258154	8.560616	8.116879 P	P	P	P		9.36733
5.794606	5.02454	4.476944	A	A	P			1.846359
9.259518	9.190384	9.116826	8.122322 P	P	P	P		8.91958
7.060467	7.425015	7.345046	P	P	P			7.488998
5.755961			4.964642 P			M		6.251505
8.371424	9.1628	8.435234	9.024584 P	P	P	P		9.208228
	6.361098			P				
4.946561			P					6.088548
8.604108	7.34586	8.073837	8.849546 A	P	P	P		7.405874
7.928871	7.45915	9.106341	9.707802 P	P	P	P		8.010419
7.068986	7.327699	7.518315	A	A	P			7.202416
6.705543	6.739384	5.376032	6.020609 P	P	P	P		6.821107
7.790786	7.347602	8.672476	8.432909 P	P	P	P		7.254063
6.248181			A					5.159105

		5.411181			A		
8.374704	7.190298	7.626303	A	P	P		6.85746
7.381086	8.997298	8.442781	7.055612 P	P	P	P	9.002613
7.571247	7.179162	9.429713	P	M	A		8.050665
		6.709415	6.231675		A	P	
4.00384		6.678846	6.41616 P		P	P	6.157355
		2.801592			P		
	4.711706			M			
7.09433			7.059248 A			P	5.36622
6.592863	6.246485	7.585403	7.173224 A	P	P	A	6.830308
4.384318	6.255462		6.019778 P	A		P	5.918641
6.832587	6.743021	6.810113	6.978222 A	P	P	A	6.255262
8.536696	10.15325	9.582454	9.189643 P	P	P	P	9.579433
13.61163	13.18151	12.31477	12.26838 P	P	P	P	12.21212
6.746753	6.294162		6.991569 P	P		A	5.987972
			6.69803			A	
11.43943	12.01839	10.44461	10.05869 P	P	P	P	11.68839
12.39583	11.53186	13.2471	14.17452 P	P	P	P	11.97618
10.84961	10.01311	9.869242	9.912906 P	P	P	P	10.38655
13.64975	14.00505	13.82115	12.80762 P	P	P	P	13.86074
10.52474	10.6208	11.20692	11.5555 P	P	P	P	10.51369
12.2421	12.50342	11.41424	11.47296 P	P	P	P	12.54685
9.023758	9.038077	7.827316	8.383091 P	P	P	P	9.303314
11.50605	11.2949	10.61207	10.84704 P	P	P	P	11.55437
9.358767	9.307823	7.480615	9.375056 P	P	P	P	9.907673
10.77135	11.1398	10.26619	9.743104 P	P	P	P	10.86992
10.88356	9.054213	10.8447	10.82197 P	P	P	P	10.30715
12.48136	12.55832	12.33915	11.61082 P	P	P	P	12.79117
5.734044	6.93899	6.446779	5.198932 A	P	P	P	5.602198
6.666455	5.966635	7.360602	7.876416 P	P	P	P	7.062465
6.855993		9.646709	9.494841 A		A	A	3.854789
6.038689			A				4.280073
11.68782	11.98488	11.24536	10.78101 P	P	P	P	11.97745
		2.152464			P		
4.913958	4.654326	6.022294	P	A	M		6.099151
8.212186	8.161446	7.50436	7.165272 P	P	P	P	8.262017
12.51363	12.74181	11.99888	11.37072 P	P	P	P	12.45803
13.1127	13.02475	12.23352	11.91937 P	P	P	P	12.85233
10.20206	10.61798	9.880561	9.068581 P	P	P	P	9.992335
9.992232	10.65498	9.940519	10.25854 P	P	P	P	10.38471

	6.677914	6.283005		A	P		
11.13541	11.53084	11.07408	10.29953 P	P	P	P	10.77145
11.25928	10.74532	10.97828	9.162706 P	P	P	P	10.38355
9.471456	9.938459	9.280351	8.664071 P	P	P	P	9.559769
6.433949	6.122679	6.102981	6.695683 A	M	P	A	6.247539
11.20093	11.27311	10.89075	10.19501 P	P	P	P	11.07666
10.46802	10.7462	10.57398	9.401456 P	P	P	P	11.028
9.171465	9.667191	10.37226	9.545996 P	P	P	P	9.063668
11.14634	11.68836	10.57196	10.15251 P	P	P	P	11.67597
	4.257494			M			
	5.992802	6.116934		P	P		
11.09081	9.699591	10.57187	10.39409 P	P	P	P	9.571896
9.714306	10.65589	8.763218	7.998274 P	P	P	P	10.17561
9.187798	10.22928	8.551375	8.226731 P	P	P	P	10.2161
7.374239		12.56035	12.49831 P		P	P	13.27214
9.301295	10.77027	9.988186	8.350319 P	P	P	P	9.687511
11.54276	11.10315	12.29206	11.9697 P	P	P	P	10.8947
10.37101	9.15962	8.770763	9.014783 A	P	P	P	7.173243
12.20817	11.86571	11.45927	11.61629 P	P	P	P	11.81776
8.650002	10.82342	10.11699	9.141415 P	P	P	P	10.71765
8.513536	8.638979	8.208791	8.440367 P	P	P	P	8.473413
9.358185	8.545048	9.233944	10.55704 P	P	P	P	8.830221
13.1531	13.96917	13.23686	12.41216 P	P	P	P	13.40829
5.648119	4.84544	4.894023	5.754219 P	P	P	P	5.949885
7.875158	7.753988	6.271458	7.593283 P	P	P	P	7.251689
11.61106	11.59138	12.14043	13.15153 P	P	P	P	11.6622
	2.144918	6.462799		P	A		
11.02104	11.00403	10.40468	9.657304 P	P	P	P	11.36923
9.798377	9.960249	10.74256	9.31297 P	P	P	P	8.952922
7.18844	7.116216	7.165368	6.579814 P	P	P	P	6.555735
9.470343	8.983021	8.269824	8.506792 P	P	P	P	8.633441
9.305484	8.78697	9.887034	10.80412 P	P	P	P	9.248886
7.562006	7.093699	8.800804	8.491853 A	A	A	P	6.914798
12.89232	12.83782	12.02188	11.91261 P	P	P	P	13.05965
9.910826	9.39705	10.63444	10.43919 P	P	P	P	9.388587
13.14448	14.00896	13.1563	12.39023 P	P	P	P	13.67759
11.04296	10.54958	10.10961	9.988257 P	P	P	P	10.61869
9.932508	8.80815	9.724292	9.260351 P	P	P	P	8.640615
6.408853	5.918251	5.582299	M	P	P		5.682576
9.442071	8.882113	8.574278	7.68023 P	P	P	P	9.480423

9.637961	9.381845	10.8051	9.790669	P	P	P	9.454159
8.403659	8.399927	8.09434	7.824879	P	P	P	8.609942
10.98771	10.30428	11.16288	10.61502	P	P	P	10.44769
11.6353	11.5334	11.30777	10.37935	P	P	P	11.03838
9.029667	9.234592	7.503635	7.350984	P	P	P	8.928
6.89004	7.001504	8.077494	6.895981	P	P	P	7.202556
6.533218	7.225527	6.210139	A	P	P		6.799783
6.282182	5.090001	6.689818	7.457382	P	P	A	6.621468
12.4908	12.6028	12.02931	11.91025	P	P	P	12.74129
4.933178	5.424439	6.255933	M	M	A		5.509913
10.86473	11.22289	11.39788	10.29172	P	P	P	10.0892
5.579664	7.767217	5.854247	6.713138	P	P	P	7.181103
11.66444	11.34797	10.97827	10.4519	P	P	P	10.59616
10.2387	10.87316	9.643088	9.552216	P	P	P	10.49418
9.967715	10.99188	10.57136	11.61316	P	P	P	9.75658
8.976531	8.661217	8.208469	8.067957	P	P	P	8.91906
10.32477	10.2815	10.33754	9.331443	P	P	P	10.82577
11.87444	11.01605	10.44114	10.62631	P	P	P	11.89545
10.00204	10.62747	9.503308	9.161253	P	P	P	10.02994
9.455168	10.43316	9.01635	8.673597	P	P	P	9.547321
9.546639	10.34933	10.75375	10.69893	P	P	P	10.60957
11.75971	12.49062	12.61832	11.65759	P	P	P	12.64802
14.36292	14.24993	15.02751	15.12566	P	P	P	14.26688
8.920988	8.141615	9.981137	9.383132	P	P	P	7.705448
10.78069	9.517067	9.438391	9.060946	P	P	P	10.06458
9.98969	10.28804	10.13992	9.498538	P	P	P	10.19137
12.66199	11.71197	12.49538	11.54596	P	P	P	11.10421
8.688528	8.095872	8.870205	8.916323	P	A	A	9.001737
5.289412	6.675421	7.273076	4.521902	P	P	P	6.629587
11.48165	12.20628	12.40015	12.35524	P	P	P	12.71156
10.90009	10.43865	10.37854	10.87348	P	P	P	10.74085
7.666812	7.308278	7.059628	6.755281	P	P	P	6.578309
8.88579	10.20632	9.355954	9.600186	P	P	P	10.48742
12.7579	12.28968	13.4272	14.42709	P	P	P	12.8682
10.60581	10.39091	11.16986	11.90007	P	P	P	10.49114
8.190533	7.457717	7.458592	6.270519	P	P	P	7.480969
5.943268		6.87706	6.84517		A	A	6.368
11.40055	12.42046	11.4794	11.41117	P	P	P	11.14112
8.657126	8.517846	6.846564	7.409145	P	P	P	8.837873
11.70321	11.90779	11.07914	11.54167	P	P	P	12.27833

6.374178				A				1.231701
6.133502	4.932506	5.545852		A	P	A		4.345373
11.63079	11.63712	10.94261	10.57659	P	P	P	P	11.4404
11.61843	11.33075	10.86494	10.79691	P	P	P	P	11.23651
11.54764	11.3607	10.89304	10.72216	P	P	P	P	11.5282
7.865439	8.593415	8.115582	7.337611	P	P	P	P	7.720195
11.68599	11.15328	12.31634	12.99795	P	P	P	P	11.58981
	5.125228		5.036079	P			P	
8.390883	7.963821	8.753179	9.98516	P	P	P	P	7.913471
9.653842	9.03931	9.204916	8.569984	P	P	P	P	9.528156
7.61003	6.014021	6.078186	6.665821	P	P	M		7.467773
13.79635	14.33603	12.64976	13.0202	P	P	P	P	14.46292
7.645719	7.866526	8.948546	8.955318	P	P	P	P	6.886866
6.052473			2.922851	A			P	6.442341
	6.947011			A				
11.10882	10.5864	10.17395	11.5083	P	P	P	P	10.72822
	6.792264	8.400572	8.712445	A	A	P		
9.166302	10.30287	9.055968	8.16376	P	P	P	P	9.780715
7.717434	7.027301	6.866013	7.765945	P	P	P	P	7.444594
6.950625	10.13038	10.37863	9.979665	P	P	P	P	11.19455
					P			
10.45876	10.46886	10.73653	11.76493	P	P	P	P	10.59819
10.87872	10.10749	10.64214	11.27031	P	P	P	P	10.46794
7.1303	7.37569	7.109832		P	A	P		7.992189
13.23176	13.94889	13.30294	12.5602	P	P	P	P	13.8654
	6.337081	5.612541		P	P			
5.65529				A				4.61294
		8.79913	8.176127			P	P	
10.06507	9.427601	9.249695	8.492374	P	P	P	P	9.658439
11.2004	11.39224	11.98154	12.09361	P	P	P	P	10.86663
11.34496	12.02134	11.31949	10.29157	P	P	P	P	11.63249
12.30862	11.92086	11.18145	10.56459	P	P	P	P	11.4787
8.060996	8.673443	7.40562	8.795201	P	P	P	P	8.417603
11.12308	11.94784	12.14829	11.55537	P	P	P	P	12.49577
5.684716		4.824624	6.695424	A		P	A	4.965363
6.639616	6.134548	1.686594	1.844944	A	P	P	P	5.414851
6.110575	6.671014	4.568418	7.33459	P	P	P	P	6.578512
4.66251	2.412211			P				6.195295
9.599002	9.460514	9.504522	8.76858	P	P	P	P	9.849246
9.060528	8.995626	9.250546	8.558476	P	P	P	P	7.425689

7.329054	9.038139	9.260294	8.065226	P	P	P	8.93081
9.533126	8.65754	9.839279	9.872792	P	P	P	8.423013
			5.724189		P	P	
7.380228	8.457261	7.650538	8.214587	P	P	P	8.330262
12.81053	12.49492	12.29907	11.78264	P	P	P	12.45763
11.03779	12.07591	12.98472	14.25013	P	P	P	12.38406
10.68617	9.726888	9.516334	9.946681	P	P	P	11.05615
3.295247	5.004628		P	A			5.816856
6.876073	6.880509	6.898048	6.063384	P	P	P	7.115421
7.444674	8.110914	8.81277	9.110763	P	P	P	8.058422
13.11407	13.80972	12.80325	11.94119	P	P	P	13.27359
12.02427	11.29927	12.06351	13.04579	P	P	P	11.97987
6.830674	7.304456	5.130723	7.536965	P	P	P	7.269618
8.524697			9.079192			A	7.268032
9.859913	9.909404	10.48089	9.541638	P	P	P	10.1435
7.735357	7.38157	7.92235	8.448308	P	P	M	7.151804
10.90308	10.392	9.724299	9.595593	P	P	P	10.6343
11.53224	11.74159	11.25953	10.76705	P	P	P	11.45723
6.732077	5.877675	5.994521	4.870679	P	P	P	6.102605
9.735891	9.796732	8.840948	9.170228	P	P	P	10.14742
			P				4.482111
7.269255	8.114959	7.188136	6.882402	P	P	P	7.585548
9.823084	11.09826	12.07568	12.10554	A	A	P	11.60705
12.27976	11.45991	10.97517	10.728	P	P	P	11.62119
11.58279	11.49475	10.54213	10.52701	P	P	P	11.51299
10.485	11.43337	12.30264	12.66567	P	P	P	12.36356
8.446077	8.392179	7.850962	7.630748	P	P	P	8.765502
11.78494	12.00389	10.16629	10.48224	P	P	P	11.59403
10.29703	10.74988	9.125233	8.108006	P	P	P	10.12318
11.90223	11.57452	12.70238	12.6695	P	P	P	11.58019
5.560918		5.342122	P		P		6.587855
10.87779	10.79209	11.72994	11.24924	P	P	P	10.91917
12.01128	11.71091	12.49396	12.60139	P	P	P	11.9629
10.39589	10.52991	10.74878	9.197465	P	P	P	10.3907
7.381297	7.349789	7.315743	7.163698	P	P	P	6.935444
14.61404	14.68053	15.25911	15.96555	P	P	P	14.89663
9.499089	10.00716	9.091188	8.978553	P	P	P	9.451871
11.29474	11.21819	11.86971	12.44387	P	P	P	11.4991
6.28902	5.972264	7.807119	6.874446	P	P	A	6.44983
11.44818	12.55139	11.0398	10.37634	P	P	P	12.65568

12.47475	11.22724	12.38609	12.37901	P	P	P	11.06393
9.806896	8.88708	9.710846	9.603809	P	P	P	7.99134
10.80837	11.46684	13.59706	14.28375	P	P	P	11.35118
9.854543	10.02524	9.398299	8.490565	P	P	P	9.765548
		5.294779			P		
6.759162	7.217606	7.338358	A	P	P		5.563211
11.31126	11.06935	10.10394	10.5709	P	P	P	11.73095
13.45929	13.3546	12.67113	12.54826	P	P	P	13.31768
9.553076	9.277429	9.522169	10.08075	P	P	P	9.889292
6.501313	6.443228	5.665017	3.500705	P	P	P	5.946982
11.92599	11.91111	11.44705	11.84025	P	P	P	13.01327
9.205102	7.61886	7.978506	7.287853	P	P	P	7.946727
5.752234	6.995298		7.494937	P		P	7.052372
11.26613	12.17491	11.05022	10.44433	P	P	P	11.90077
10.96038	10.81526	10.05047	9.80994	P	P	P	10.59618
12.16353	12.12293	11.82634	11.73608	P	P	P	12.33575
10.35573	10.04516	9.335916	9.243018	P	P	P	10.36191
11.18785	11.55707	10.77286	10.01675	P	P	P	11.02263
14.46917	14.33677	12.48043	13.35965	P	P	P	14.82438
8.755314	8.68886	9.5551	9.262189	P	P	P	8.560305
7.962654	8.604069	7.839873	7.163998	P	P	P	8.483354
6.167186		5.814424	5.120445		P	P	6.644161
9.919262	9.929648	8.570343	7.293451	P	P	P	9.475182
			8.300424			P	
12.81658	12.83229	10.09295	10.71196	P	P	P	13.00219
10.76692	10.51537	11.43882	12.24459	P	P	P	10.9048
6.159895	1.915324	3.718168	6.59115	M	P	P	6.066295
10.67607	10.7663	10.47374	9.674748	P	P	P	10.79943
13.69097	13.85305	13.05268	12.55022	P	P	P	13.76418
12.70655	12.16228	12.65208	11.87373	P	P	P	12.41698
9.641335	9.763106	8.871719	9.255543	P	P	P	8.587273
8.958187	8.919395	8.16073	8.219821	P	P	P	8.740891
8.628338	9.377642	8.549358	7.636149	P	P	P	8.673837
10.04347	10.1281	8.979666	7.940733	P	P	P	9.253878
10.2407	10.54685	9.093442	8.772041	P	P	P	10.4006
9.577543	10.22306	9.395095	8.151478	P	P	P	9.663875
11.50503	11.86722	10.95475	10.35215	P	P	P	11.52815
7.346468	6.09339	7.189868	8.023759	P	M	P	6.680358
11.40983	11.14904	11.99912	12.25237	P	P	P	10.94583
10.20491	10.40962	9.562825	9.184775	P	P	P	10.45391

7.938848	7.621492	7.325552	7.488736 M	P	P	P	6.716043
	6.099949	6.76199		P	A		
8.168695	8.614755	7.85664	7.620394 P	P	P	P	8.974789
11.04534	10.98497	10.28781	10.08625 P	P	P	P	10.91225
10.11771	10.37675	9.621354	9.178615 P	P	P	P	10.04238
		7.61439				A	
10.29584	10.35625	10.98702	11.17543 P	P	P	P	10.30967
8.510397	8.422878	10.06207	10.17424 P	P	P	P	8.587009
9.171836	8.87341	10.47121	11.01922 P	P	P	P	9.227872
9.766283	9.334687	10.27924	9.620531 P	P	P	P	9.664253
11.48774	12.59891	11.57119	10.80608 P	P	P	P	12.29522
6.428751	5.564979		6.616558 P	P		A	4.907397
6.891645			A				5.785902
10.50432	10.46647	9.756853	9.611076 P	P	P	P	10.29825
9.268474	9.773133	10.59725	10.72618 P	P	P	P	9.517114
10.00251	9.886387	9.634289	9.461931 P	P	P	P	9.275128
9.294975	9.764401	8.834209	8.594018 P	P	P	P	9.64465
6.806496	7.139887	6.201374	6.979031 P	P	P	P	6.651923
		7.000659	7.053258		P	A	
10.36236	10.48887	9.618111	9.092052 P	P	P	P	10.46037
9.813889		9.207068	9.481392 A		A	A	7.574022
11.41116	11.67586	11.75639	12.87681 P	P	P	P	12.32408
11.43028	11.23073	11.81058	12.56027 P	P	P	P	11.1734
9.004391	7.033014	9.201851	8.496301 P	P	P	P	8.197429
9.742043	9.651204	8.600697	9.054832 P	P	P	P	9.234709
9.530284	9.262573	10.16502	9.991269 P	P	P	P	9.934093
5.519796			2.780506 P			P	5.626729
11.02283	11.02578	11.65933	11.29734 P	P	P	P	10.86236
11.79843	12.54937	11.9825	11.10403 P	P	P	P	12.54674
10.96054	9.882902	9.206284	6.819439 P	P	P	M	9.884248
12.11363	11.74771	10.9621	10.94621 P	P	P	P	11.81648
10.64357	11.84616	10.80744	10.1205 P	P	P	P	11.61332
9.993948	9.238647	9.905294	9.818257 P	P	P	P	10.01276
11.64506	10.18209	10.85731	10.97677 P	P	P	P	10.6238
10.03105	10.04235	9.340281	8.694931 P	P	P	P	9.750655
5.905134	5.803022	7.305125	7.40129 P	P	M	P	7.305962
8.592009	8.473221	10.06668	9.846543 P	P	P	P	8.78554
11.88614	11.52401	11.13424	11.46392 P	P	P	P	11.58484
6.559354	5.672367	6.505851	A	M	P		4.133589
11.81773	12.92868	12.13448	10.66444 P	P	P	P	12.35821

7.149856	6.854196	5.846996	A	P	P		7.43135
7.947787	8.772572	8.086103	6.280687 P	P	P	P	8.29721
7.961234	7.616107	7.919399	8.650961 P	P	P	P	8.103684
7.847361	9.638451	8.820642	9.415216 P	P	P	P	9.06332
6.352853	11.49399	5.201074	8.949044 P	A	P	P	6.97469
10.78665	12.10771	12.03618	10.87213 P	P	P	P	12.16423
5.208684	4.863926	3.949632	A	A	P		5.514686
8.512625	8.744507	7.890868	7.705997 P	P	P	P	8.744085
13.16774	12.70297	12.07902	11.50337 P	P	P	P	13.11938
11.66104	12.582	12.3853	12.01368 P	P	P	P	12.78372
5.477364		3.077696	P		P		6.165279
12.19404	12.67428	11.82986	11.22419 P	P	P	P	12.57036
9.734898	9.506429	9.968769	9.366508 P	P	P	P	9.591613
9.528399	9.328207	9.502274	10.45352 P	P	P	P	9.079191
9.687471	9.571689	8.534507	8.723671 P	P	P	P	9.952432
10.02387	10.26471	11.31504	10.67765 P	P	P	P	9.68994
7.60211	7.586869	6.7669	6.508232 P	P	P	P	7.45785
	6.433946	6.174899		P	P		
8.567708	7.181313	8.353436	9.50911 P	P	P	P	8.393778
6.799967	4.940184	7.040761	7.034751 M	P	P	A	6.041122
6.369937	6.918117	5.69693	A	P	P		6.518381
9.832478	9.303601	10.18068	11.12296 P	P	P	P	9.209636
7.104394	6.769551	7.285635	8.596205 P	P	P	P	7.700132
8.491362	8.810321	8.023951	7.064721 P	P	P	P	7.735282
9.003033	8.976447	6.660211	7.869303 P	P	P	P	9.116179
8.008956	7.926753	6.644481	6.25583 P	P	P	P	8.10706
8.807081	8.352918	9.455345	8.995229 P	P	P	P	7.929507
5.206688	5.883637		A	A			3.880698
7.925417	7.962118	7.118115	6.840209 P	P	P	P	7.827888
9.488076	10.55346	13.44359	13.28661 P	P	P	P	7.422105
10.63245	10.54443	9.789331	9.542648 P	P	P	P	10.55581
9.327225	9.881011	10.37773	11.37622 P	P	P	P	10.34299
11.10149	11.5476	12.12097	12.26904 P	P	P	P	11.46058
8.416068	7.297536	7.153432	7.353838 P	P	P	P	7.306349
10.34475	11.20017	10.47791	10.20207 P	P	P	P	11.80395
11.40362	12.03566	10.92886	11.48751 P	P	P	P	12.06972
11.1692	11.32219	13.44216	14.00344 P	P	P	P	10.72127
11.55855	11.89394	12.60855	12.78831 P	P	P	P	12.42224
8.320501	7.904874	5.900604	7.662088 P	P	P	P	7.150512
11.66163	12.34841	11.28306	10.66822 P	P	P	P	12.09091

11.61468	12.12354	10.98818	10.93763	P	P	P	11.96553
6.480734	6.614354	6.116334	6.944557	P	M	P	7.146408
5.583778	6.39888	6.247802	P	P	P		6.137199
7.806884	7.600766	6.465719	7.791945	P	P	P	6.916588
9.987381	9.466269	9.917223	10.27599	P	P	P	9.461363
7.355683			A				5.154566
8.103217	9.301886	8.522849	6.537282	P	P	P	8.129112
10.91966	10.72616	9.422633	7.899079	P	P	P	9.311737
9.66676	9.832014	10.29441	11.29114	P	P	P	10.09152
8.958057	8.245276	8.849052	8.185579	P	P	P	9.283834
12.56264	12.74701	11.9348	11.4652	P	P	P	13.13197
9.792455	10.00975	9.499954	8.747026	P	P	P	9.88763
11.59821	11.46558	12.6372	13.23116	P	P	P	11.50722
9.895822	9.759715	10.38287	9.853723	P	P	P	9.417856
8.574823	8.902726	8.249368	8.055515	P	P	P	8.945265
8.439496	7.839061	8.471192	9.353174	P	A	A	7.775075
		1.55668				M	
10.64503	10.65733	10.67239	10.86491	P	P	P	10.86803
5.553629	5.532871	7.648244	5.293607	P	P	P	7.626369
12.52998	12.4011	11.14699	10.94387	P	P	P	12.63729
11.97387	11.988	12.38912	12.60416	P	P	P	12.0846
9.179309	9.159267	9.941145	10.74911	P	P	P	9.333209
7.819501	7.614361	8.527098	9.280759	P	M	A	8.787916
10.88328	11.01008	10.34404	10.15286	P	P	P	10.90356
6.716022	5.842539	6.137574	A	A	P		5.673259
9.333479	10.81289	10.29348	9.413821	P	P	P	10.9014
11.24781	11.60083	11.61052	12.4172	P	P	P	11.52029
11.72639	11.9748	11.61815	11.04113	P	P	P	11.54074
11.08347	10.34855	11.97359	11.4443	P	P	P	9.968701
11.75508	12.6578	11.371	10.74916	P	P	P	11.89097
8.464579	8.94653	8.846687	7.636372	P	P	P	8.836464
8.407159	9.758382	10.02699	9.304231	P	P	P	9.943336
9.173132	8.617284	8.058417	7.2766	P	P	P	8.66857
7.116533	8.113025	7.41811	5.928764	P	P	P	7.821041
11.30578	10.98236	11.73862	12.24339	P	P	P	11.60614
10.48915	10.43642	10.61653	11.77164	P	P	P	10.69185
9.383723	9.003244	9.541391	9.268282	P	P	P	9.37901
9.147816	8.702032	6.989407	7.395504	P	P	P	8.567865
9.166796	7.883542	7.505054	7.936472	P	P	P	8.181272
7.904758	6.70681	8.730196	8.71529	P	P	P	7.195967

11.28796	11.27557	10.6453	10.98288	P	P	P	11.57955
10.65304	8.978743	9.303942	9.110141	P	P	P	9.533432
10.25965	10.60812	10.09757	8.974736	P	P	P	10.23
9.434906	9.097439	9.697426	9.788234	P	P	P	8.820727
10.07872	9.910013	9.514215	8.796912	P	P	P	10.09499
8.453853	8.67205	8.979889	9.966932	P	P	P	8.834718
11.98221	12.25698	11.15079	11.34491	P	P	P	12.35607
14.30959	14.16181	13.73272	13.38392	P	P	P	14.0688
11.89234	11.67283	12.85195	11.93032	P	P	P	12.83464
10.22803	9.50802	9.645359	9.670731	P	P	P	8.727334
10.77915	10.14651	9.180398	9.568328	P	P	P	9.331942
8.577837	8.370419	8.178148	8.754355	P	P	P	9.658304
7.740704	7.628378	6.36227	3.517749	P	P	P	7.113334
11.06246	11.95951	11.14188	10.73683	P	P	P	11.69408
11.88058	12.47156	11.82556	11.1089	P	P	P	12.18057
10.38674	11.26161	10.81881	10.07974	P	P	P	11.48713
9.416299	9.47278	10.42163	10.10187	P	P	P	9.316874
6.918938	7.033587	4.00196	6.96764	P	P	P	7.653851
9.548642	9.986568	8.959279	8.160311	P	P	P	9.872791
11.07262	11.13968	11.53786	12.22668	P	P	P	11.27083
10.98069	11.48592	10.54073	9.834616	P	P	P	11.13219
10.73205	11.53161	11.56042	11.69943	P	P	P	11.80916
9.394389	10.47779	11.4155	11.19042	P	A	A	9.371964
12.36833	12.06551	11.29733	11.38355	P	P	P	12.57878
10.62929	10.95257	10.72143	9.992061	P	P	P	9.672903
9.712214	9.689907	10.04811	10.94517	P	P	P	10.1731
8.674116	8.848043	8.414921	7.685872	P	P	P	8.090528
12.5821	12.03214	11.34931	12.01086	P	P	P	12.59407
12.628	12.47632	11.39557	11.42585	P	P	P	12.1883
10.14273	8.965107	9.256431	9.501879	P	P	P	8.891968
9.163098	8.465162	9.361836	9.240926	P	P	P	8.326763
8.088367	7.420901	7.258571	6.799023	P	P	P	8.1098
8.76002	8.528306	7.784232	7.902309	P	P	P	8.43655
6.130887	6.522168	6.212374	2.809195	P	A	P	6.821094
7.226502	7.571285	6.84803	6.568175	P	P	P	8.034682
7.650345	6.8706	8.752234	8.562741	M	P	P	6.45675
	4.913614	6.803828		P	P		
12.46422	12.12523	11.6442	11.39135	P	P	P	12.0692
11.83618	11.82762	10.24023	10.1381	P	P	P	12.09016
9.906654	9.032426	8.99586	8.38594	P	P	P	8.889094

11.08693	11.27774	10.50856	10.77112	P	P	P	11.01067
10.81459	11.17228	10.18321	9.974488	P	P	P	10.96859
13.01811	13.3407	12.18543	12.08767	P	P	P	13.19731
7.772928	7.515242	7.599406	A	P	P		6.258942
6.824045	7.729458	7.026531	6.712856	P	P	P	6.771683
11.27901	11.49672	12.0085	11.40388	P	P	P	11.47351
8.772132	6.993237	7.560159	8.02589	P	P	P	7.83859
9.895385	9.607711	8.835949	9.215694	P	P	P	9.922474
7.585695	8.004037	6.996463	6.899786	P	P	P	7.937901
9.642941	9.483765	8.44619	8.068967	P	P	P	9.234752
10.13679	12.37151	11.539	10.23579	P	P	P	11.72363
12.30761	10.53772	10.4727	11.98897	P	P	P	5.893717
11.94387	11.13791	10.81958	11.61386	P	P	P	12.23684
	7.042342	6.069261		P	P		
7.498935	8.050262	7.512689	P	P	P		7.236576
9.493708	9.66425	9.143439	8.795846	P	P	P	10.19364
8.628937	6.775842	8.616282	8.784927	P	A	A	6.708743
6.611663	7.079936	7.7061	7.904152	M	P	P	8.129843
		5.467641			P		
9.806884	8.26356	9.362454	8.610422	P	P	P	7.366811
10.19701	10.35438	9.189578	9.247763	P	P	P	10.36966
7.791976	7.728094	6.172087	6.330761	P	P	P	7.38324
8.351349	8.427744	7.036191	7.917145	P	P	P	8.802415
8.815187	7.974744	7.860843	6.766922	P	P	P	7.785986
6.791782	6.458149		A	A			5.63539
7.934351	8.17873	7.359958	7.365106	P	P	M	7.227305
10.12333	10.11948	9.459041	8.677299	P	P	P	9.793667
7.844935	7.667128	8.738353	8.087461	P	P	P	7.104024
		5.296585			P		
	6.219374		8.012471	A		M	
9.663132	9.849873	9.310893	8.372478	P	P	P	9.439238
10.52524	10.46776	11.30228	10.86012	P	P	P	9.458115
11.14483	11.16868	12.10047	12.25986	P	P	P	10.84627
11.07532	10.65733	10.43119	9.726419	P	P	P	10.5731
10.35543	10.72889	8.199327	9.472476	P	P	P	10.72288
11.43852	11.00395	11.49985	11.91259	P	P	P	11.38258
9.574647	9.413463	7.669802	7.848932	P	P	P	9.311543
11.08296	11.04255	10.74101	9.876615	P	P	P	11.1374
11.06152	11.19225	10.6537	9.700484	P	P	P	11.00186
9.07983	8.759332	7.742734	8.482366	P	P	P	9.090816

11.6518	12.15356	11.46407	10.8733	P	P	P	11.74798
11.2046	11.20886	9.846993	10.06061	P	P	P	11.35734
8.951532	8.809078	8.021492	9.094056	P	P	P	8.7618
9.354851	11.04591	9.452855	8.469766	P	P	P	10.24841
7.870622	8.145927	7.058644	6.289326	P	P	P	7.983299
	6.212261		7.512298	P		P	
	3.266423			P			
4.754551			M				6.0751
9.670864	8.897058	8.397161	8.281944	P	P	P	9.153827
9.085951	8.22529	7.405245	7.922868	P	P	P	8.158069
6.456771	6.26283		A	P			5.236825
8.260682	8.82392	6.934765	6.71669	A	P	P	8.359503
7.372675	7.078752	7.423815	7.554888	P	P	P	6.557275
10.39456	10.68143	11.15164	11.96068	P	P	P	11.11123
11.71336	11.0716	10.32969	9.721596	P	P	P	11.09508
9.925785	10.62166	10.93012	11.84805	P	P	P	10.62135
11.48636	12.03704	10.25254	10.55817	P	P	P	12.21709
11.45774	10.49672	12.02374	12.01972	P	P	P	11.46943
5.857617	6.213907	6.545528	P	P	A		6.621922
8.642259	8.714168	8.71199	9.400649	A	P	P	8.559661
7.890918	8.305053	6.586002	7.054188	P	P	P	7.952618
7.905053	7.019472	7.284551	6.716542	P	P	P	6.816207
11.83014	11.11753	12.35681	13.09465	P	P	P	11.31685
9.494714	9.235878	10.22979	10.4665	P	P	P	9.12201
10.81895	11.79975	10.14016	9.551991	P	P	P	11.38053
8.380208	8.650579	8.318293	7.576316	P	P	P	8.657788
9.711433	9.827113	9.272784	8.531521	P	P	P	9.415885
11.21188	10.75129	9.806866	9.729959	P	P	P	11.11286
9.536196	8.734622	8.963624	9.291654	P	P	P	9.839597
9.386586	8.753856	9.930387	9.838882	P	P	P	7.404694
11.83406	11.88916	12.16387	12.88857	P	P	P	11.80671
12.8461	12.30004	13.06053	13.70042	P	P	P	13.14498
6.962001	11.5085	11.43728	10.52323	P	P	P	11.22474
13.11717	12.64361	12.52345	12.16515	P	P	P	12.66873
11.70407	11.93095	12.48841	12.4943	P	P	P	12.24578
	3.201332			P			
10.74035	10.47713	11.04016	11.5085	P	P	P	10.68239
11.41448	11.82318	11.02618	10.04426	P	P	P	11.17692
7.493989	7.21665	6.634925	7.382964	P	P	P	7.465241
9.430467	9.146096	9.319979	8.097316	P	P	P	8.854146

9.454433	8.894032	9.995252	9.298765	P	P	P	8.833628
10.95244	10.43249	9.812727	9.332118	P	P	P	10.44106
8.038058	6.871971	8.383657	9.838084	P	P	P	8.37812
8.823298	8.825418	10.00985	9.868783	P	P	P	8.122444
8.912396	7.066511	7.827159	6.54103	P	P	P	7.352171
8.346692	7.724747	7.184637	6.547973	P	P	P	7.9806
9.68979	8.949905	9.605485	9.054969	P	P	P	8.581584
11.43272	10.12795	9.858528	10.04696	P	P	P	9.35592
8.863091	9.594838	8.594635	8.130478	P	P	P	9.429295
6.976173	7.03619	7.106259	7.268942	P	P	A	6.527093
11.12082	11.61844	11.88081	12.8464	P	P	P	11.66385
7.192067	7.701242	7.607214	7.603443	P	P	P	7.592306
9.152194	9.493438	8.628623	8.170191	P	P	P	8.64444
10.43274	9.800635	9.3974	9.447008	P	P	P	10.16136
9.897281	10.46771	10.00975	8.946851	P	P	P	10.10193
8.41271	8.331888	9.827337	8.899903	P	P	P	8.023959
11.96487	12.2281	11.40649	11.22419	P	P	P	12.2277
8.764759	8.748801	7.764457	7.026298	P	P	P	7.453799
10.71348	11.0512	8.850894	8.529771	P	P	P	10.74889
11.59061	11.57513	12.29594	13.31568	P	P	P	11.91201
8.743501	7.666019	9.146438	9.191758	P	P	P	8.095488
8.265494	7.440711	7.250651	6.702228	P	P	P	7.288312
5.758175	5.825559	5.472869	1.826991	A	P	P	4.612302
11.91864	12.28647	12.3281	12.04321	P	P	P	13.00841
8.750213	8.94068	7.693093	7.54214	P	P	P	8.793824
10.21762	11.5377	10.69826	10.31644	P	P	P	11.64057
5.485816	5.030857		3.208148	P		P	5.618553
11.94881	12.5117	11.9393	11.40299	P	P	P	12.42014
11.73704	12.02247	11.28891	10.65038	P	P	P	11.97989
9.683566	10.04354	9.32586	8.041459	P	P	P	10.44383
10.10564	10.28106	9.351131	9.038838	P	P	P	10.08786
9.747949	10.17714	9.372739	8.92849	P	P	P	9.96147
10.51533	10.324	9.696959	9.950907	P	P	P	10.56282
11.08404	9.404193	11.30638	11.30968	P	P	P	8.605568
7.412661	7.220125	8.34047	8.459038	P	M	A	7.708636
8.046777	9.64686	9.500772	8.861023	P	P	P	9.307732
9.993941	9.776505	8.784458	8.488048	P	P	P	9.310142
11.71689	11.58765	11.11575	10.5802	P	P	P	11.49271
9.423208	9.612351	9.986197	9.578122	P	P	P	9.330284
9.34096	9.82429	9.462707	8.744164	P	P	P	9.289726

11.18282	12.6277	12.15325	11.38233	P	P	P	12.60893
6.276258	6.117191		7.039529	M	P	A	7.325746
11.28331	11.37386	12.4568	12.12915	P	P	P	11.95537
8.66863	7.771488	9.561719	9.931235	P	P	P	8.255211
10.93694	10.80928	10.24698	9.979268	P	P	P	10.59154
9.390147	9.283345	8.429791	8.189466	P	P	P	8.979952
8.869263	9.004449	9.173929	10.02171	P	P	P	8.518776
12.89823	12.39615	10.75646	11.03974	P	P	P	12.96965
10.66836	11.96444	11.54417	11.88517	P	P	P	12.15182
9.933208	8.898191	10.43912	11.18069	P	P	P	10.48
10.23363	9.256098	10.79822	9.857245	P	P	P	9.125129
5.48081	6.119782	6.188958		P	P		6.929268
6.568417	6.659647	6.21281	6.118981	P	P	P	6.710598
9.679014	9.765945	10.16085	10.43167	P	P	P	9.764219
8.327472	8.06101	10.56092	11.01026	P	P	P	7.724192
		5.465233	7.361371		P	A	
11.86202	11.67508	12.92185	12.51021	P	P	P	10.61438
9.392476	9.610974	10.63391	10.54113	P	P	P	9.618897
4.765464			P				6.313758
8.034577	8.246153	7.818234	7.18326	P	P	P	7.203068
11.23162	11.0918	10.92406	10.30945	P	P	P	11.02069
6.635183	4.375121	5.406714		P	P		6.08834
	6.910796	4.41834		P	M		
9.434986	8.435394	8.877022	8.776316	P	P	P	8.201439
	6.875993	4.893736		A	P		
	5.659765	4.879371	5.549475	P	P	P	
6.749532	6.36242		P	P			6.608023
6.700065	6.599113	6.700939	6.348179	P	P	P	6.68501
9.856697	10.04434	10.2565	9.216634	P	P	P	8.716993
6.968167	7.450226	8.529556	6.840369	P	P	P	6.368401
6.080782	3.887417		A	P			6.240446
	5.19293		1.62634	A		P	
7.801919	8.394104	7.628892	6.829022	P	P	P	7.881268
5.321372	6.503611	5.634228		P	P		6.743194
7.179652	6.844944	7.461557	6.230389	P	P	P	6.101508
6.397259	6.214434	6.115414	6.355629	A	P	P	4.829828
	6.441358	5.485314		P	M		
5.787502	5.278212	5.666634		P	A		5.868958
6.113557	5.143111	4.676778	4.619687	A	P	M	5.174273
10.43902	9.163883	9.999419	10.62699	P	P	P	9.079772

	4.067954	3.492536		A	P		
	2.610521			P			
7.925456	7.540333	8.543138	9.11578 P	P	P	P	8.411611
9.847484	9.05272	10.83516	11.49327 P	P	P	P	9.434994
8.012288		9.09392	9.222216 A		A	P	7.14862
6.603364		5.96765	3.726271 P		P	M	6.881635
5.244431	5.718079		P	P			6.592762
7.067974	7.357558	6.949616	5.744272 P	P	P	P	6.675945
	5.796783	6.892066	5.585284	P	P	P	
	5.463602	5.352161		A	P		
9.436439	9.273348	9.931982	10.82529 P	P	P	P	9.307297
7.4718	8.652153	6.422834	5.418459 P	P	P	P	8.477992
8.183748	8.007482	7.810709	6.710012 P	P	P	P	7.719199
6.099213	7.678249	5.805297	6.332162 P	A	P	P	6.75525
	4.113944			P			
6.076127	4.814698	6.167059	5.037539 P	P	A	P	6.750041
6.273105	6.15878	7.382004	7.317047 M	A	P	A	7.018444
6.434941	5.897039	6.877414	5.126072 P	P	P	P	6.69736
10.15068	10.87912	9.291956	9.182989 P	P	P	P	10.43863
11.06588	12.58423	10.83968	10.82849 P	P	P	P	12.18445
6.604161	6.156968	5.731015	4.567429 P	P	P	P	6.302085
7.707815	8.942657	8.637983	8.010591 P	P	P	P	8.591759
8.364496	8.717382	7.401972	7.539973 P	P	P	P	7.648132
	5.042045		4.381555	P		P	
9.098936	9.130732	10.33251	10.98843 P	P	P	P	9.723263
4.311751		5.080493	M		M		5.229691
4.06902			6.011734 M			P	5.898086
5.488086		6.306725	A		P		2.834218
		7.066348			A		
	5.73025		2.342032	P		P	
6.097123	5.809123	3.557861	5.802627 P	M	P	A	6.252722
		1.64364			P		
7.47994	8.149429	8.779004	8.618737 P	P	P	P	7.702056
			6.447019			A	
6.507289	6.930759		7.763058 P	P		P	7.717284
6.746506	5.654016	5.856316	A	A	A		5.640618
	5.58854	6.499967	0.82245	P	P	P	
10.48576	10.51408	10.28909	9.820533 P	P	P	P	10.49744
8.356323	9.275826	8.642745	7.924542 P	P	P	P	8.253471
	2.105418			P			

7.195078	7.221199	6.576692	6.719829	P	A	P	P	7.052208
	5.506738	7.167371			P	A		
	6.755674		6.930693		A		A	
10.49955	10.24199	9.569087	8.606753	P	P	P	P	10.02878
5.158145				P				6.652543
11.16287	11.43239	10.86105	10.25869	P	P	P	P	11.01189
6.111584	4.932322			A	P			5.247671
	4.390039				P			
	5.230634		6.098953		M		P	
	4.80581	6.157917	4.306215		A	M	P	
7.595942	8.476724	6.742832	6.226343	P	P	P	P	8.564888
7.161863	7.15176	8.446885	8.846836	A	P	P	A	6.032431
6.213342	6.629677	6.708236		P	A	P		6.827289
5.581499		6.344033	6.0759	P		P	A	6.993686
5.83875	5.379985		2.005032	A	A		P	6.278678
5.542031	6.187538			P	A			5.773552
6.787656	7.105996	6.92072	6.561242	P	P	P	A	7.080479
7.812975	7.512812	7.070023	7.956402	P	P	P	P	6.798436
7.23901	7.183959	7.598791		A	P	A		6.403159
6.145373			7.086027	A			M	3.424318
			7.179091				A	
4.941705				A				3.060745
4.536721			2.657196	P			M	5.680268
8.13098	8.476189	8.515373	7.012466	P	P	P	P	7.956155
4.954861	5.467951	5.20462	6.437894	P	P	P	A	6.323766
11.42051	12.04906	10.59041	10.55504	P	P	P	P	11.62674
10.87355	11.57594	10.37864	10.45387	P	P	P	P	11.38785
		6.439796				A		
6.394476	4.863532	4.767421		P	P	P		5.979134
5.80794	6.694375	6.282273		P	P	P		6.373176
5.560926				M				7.129592
6.699149	6.501836		8.258281	P	P		A	7.733
6.858845	6.332538	6.608537	5.83248	A	P	P	P	4.928797
	5.328247	6.023151			A	A		
7.046424	8.625982	6.78098		P	P	P		7.903159
4.416366				P				5.963446
			9.245107				A	
	6.480534				P			
6.393301		6.326727	6.837924	A		P	P	2.851082
		4.093462				M		

6.895476	6.913691	6.044384	7.617294	P	A	P	P	7.054805
6.754183	7.299541	7.528952	1.774449	P	P	P	P	6.922004
8.020191	8.829304	6.997595	7.902287	P	P	P	P	8.282057
		6.616899				A		
8.087675	8.360551	8.373026	7.265737	A	P	A	P	7.70275
5.594563	4.136184	4.277335	5.222984	A	A	P	P	3.930386
	5.668612			A				
10.72039	10.51837	10.48457	9.849729	P	P	P	P	10.36495
7.010792	6.914972	7.445171	8.372852	P	P	P	P	7.31822
	6.425607	4.540371		A	P			
6.672542	5.758619	5.148498		P	P			5.923796
9.082849	9.443156	8.448923	9.122595	P	P	P	P	8.809677
4.977001		6.881823			A			4.843936
8.396628	8.810112	8.902127	7.715974	P	P	P	P	8.974875
12.56451	10.85189	11.11469	11.87978	P	P	P	P	11.23305
6.777919	6.548812	7.990288	8.036818	M	P	P	A	6.395854
8.337269	9.021633	7.410919	8.465156	P	P	P	P	9.466858
7.060822	6.110521	6.374332	7.4996	P	A	P	P	6.698539
	6.905578	5.287334		P	P			
	6.255489	6.854557	7.125358	A	P	P	A	
5.792075	6.197202	3.792538	6.233736	P	P	P	P	5.826073
8.590562	8.724286	9.046721	8.601952	P	P	P	P	7.991521
4.962316				A				3.735726
			2.772151				P	
9.935892	9.586323	10.32632	10.0703	P	P	P	P	9.219015
9.577383	8.891023	9.445352	9.456842	P	P	P	P	8.586556
11.17362	10.88545	9.8746	9.548655	P	P	P	P	10.9915
	6.057116	5.87834	7.341593	A	P	P	A	
9.676896	10.35331	8.367713	8.416217	P	P	P	P	10.10565
	5.746464	5.863923	7.484293	P	P	P	M	
	6.732622	6.456211		P	P			
5.331342	7.004551	6.508893	6.651818	P	P	P	P	6.511106
	4.053509		7.680473	P			P	
5.146759	6.155679		5.41185	A			M	2.719934
	6.85566	8.594694	8.125508	7.969658	P	P	P	8.002793
7.525208	7.468113	7.293128	8.035837	P	P	P	A	6.948204
8.427257	8.621199	7.618717	7.657568	P	P	P	P	8.484268
7.288878	7.160761	5.729269	3.385178	P	P	P	P	7.760527
7.526306	7.326793	7.526625	8.305266	P	A	A	A	7.497826
	5.62075			A				

7.699872	8.10184	7.033075	8.02301 P	P	P	P	7.733921
8.542701	8.781751	7.207913	5.953327 P	P	P	P	8.570176
	6.088052	6.839456	7.072345	A	P	A	
9.380956	9.39958	9.934122	11.44307 P	P	P	P	9.468129
7.859839	8.134249	7.420574	6.555883 P	P	P	P	7.683227
12.82424	13.13972	12.10013	11.47399 P	P	P	P	13.06922
5.138949	5.605325	6.528743	6.861431 M	P	P	A	5.539215
7.315074	6.783565	7.011016	6.181755 A	P	P	P	6.24918
		6.604878				A	
8.857497	9.547357	8.307949	8.412919 P	P	P	P	9.042065
8.638575	8.451643	7.158282	7.017834 P	P	P	P	8.640229
6.335943	6.188479	7.522954	7.469508 A	P	P	M	6.201119
	4.82414	6.403012	5.084121	P	A	P	
		6.921596				A	
10.72081	10.44878	11.03993	10.88718 P	P	P	P	10.20017
8.942946	9.003144	9.699266	9.143456 P	P	P	P	8.657627
5.938855	6.86711	6.802466	6.99641 P	P	P	P	6.975631
9.701197	8.836435	10.25217	9.903878 P	P	P	P	9.681536
10.64367	9.39262	10.07245	11.14471 P	P	P	P	9.890698
8.718027	9.126411	8.213221	7.988701 P	P	P	P	9.297792
7.533747	6.084066	6.746131	7.557907 A	P	A	P	6.066573
10.38722	10.18007	9.992699	9.524199 P	P	P	P	9.016709
5.37904	6.004855	7.050221	A	A	P		4.389509
1.632129		6.821001 P				P	5.713238
	3.37211				P		
	3.84766	6.057836		P	P		
7.21339	5.916738	7.539279	8.108141 P	P	A	A	6.196214
8.584537	7.2593	8.619514	8.900613 P	P	A	P	8.168951
8.284881	8.584778	9.174093	10.08329 P	P	P	P	9.089277
4.918389	5.538789	5.248112	5.008362 A	P	P	P	0.650788
	5.182011	1.235012	5.187339	A	P	P	
	8.096136	8.514717	9.054527	P	P	A	
7.428857	7.666118	8.203152	10.0108 P	P	P	P	8.746319
5.976895	6.727875	5.198907	6.775462 P	P	P	P	6.345381
8.46005	8.792626	9.251412	9.064742 P	P	P	P	9.518334
7.177924	5.960699	6.59499	A	P	A		3.976259
10.01167	10.12437	8.710979	8.052838 P	P	P	P	10.03859
6.000076	5.98568	6.083898	4.239224 P	A	P	P	6.188053
6.551446	5.975115	4.697207	A	P	P		4.582428
8.634074	9.356732	8.209287	7.59662 P	P	P	P	9.489662

8.367884	7.7673	7.493795	6.752961	P	P	P	7.08242
		0.776548			P		
7.822662	8.125314	8.593737	9.005091	P	P	P	7.137819
8.732298	8.262698	9.319823	9.426164	P	P	P	8.178494
8.121675	8.31334	6.756686	6.371006	P	P	P	8.040028
7.797574	7.705978	7.779718	8.159861	P	P	P	7.367815
7.756707	6.799494	7.119843	6.314156	P	P	P	6.66813
10.17978	10.39454	11.15782	12.12631	P	P	P	11.08798
10.37449	10.00269	11.22632	11.70499	P	P	P	11.00419
7.050804	6.505715	7.677251	6.661629	P	M	P	6.447525
5.898418	6.387754	6.918307	6.342084	P	P	P	6.928258
8.037148	8.003561	7.476028	7.665722	P	P	P	7.684527
6.424764	5.689302	6.020361	6.670873	P	P	A	5.779756
10.27001	9.496889	10.54044	10.8787	P	P	P	10.34567
8.75266	9.012961	9.625403	8.818564	P	P	P	8.989641
5.569736		5.677445	A		A		5.224376
3.608825		6.950457	P		P		7.265093
10.12124	8.766272	7.738281	7.90705	P	P	P	4.303949
8.518311	8.199375	7.302434	7.035162	P	P	P	7.895713
		7.10297			A		
7.144647	6.81424	7.171113	7.374433	P	P	P	7.131413
11.64603	11.70117	12.1244	12.97462	P	P	P	11.71776
8.301471	7.281397	7.427064	7.816802	P	P	P	6.385205
5.241314	4.843623		A	P			0.926344
7.307054	7.473165	5.903977	7.032855	P	P	P	7.730384
8.51183	8.729295	7.281246	7.307973	P	P	P	8.757481
7.05839	6.20251	5.935837	3.085713	P	P	M	5.535538
6.207969	6.477008	6.494535	P	A	P		7.206368
12.74079	13.06411	12.72801	12.22506	P	P	P	12.798
11.00217	10.5887	11.64595	11.42555	P	P	P	10.70752
11.30401	11.08427	10.11742	9.076336	P	P	P	10.71687
5.945794	6.294037	6.470826	4.052236	P	P	P	5.867778
10.06912	9.940307	8.941413	8.934346	P	P	P	9.644063
9.518845	8.361606	8.983644	9.421428	P	P	P	9.023489
6.412597	6.395498	6.318144	8.119168	A	P	P	7.115533
5.708697	5.033781		6.431368	M		P	2.892534
10.07173	10.33984	9.244643	8.800499	P	P	P	9.647825
8.733443	8.248787	7.66586	8.738787	P	P	P	9.115919
12.05609	10.60435	11.48378	11.74303	P	P	P	10.28303
8.464069	8.723601	8.295281	8.215355	P	P	P	8.914762

	4.820371			A			
		5.001036	6.603549		P	A	
11.83894	11.84527	10.96802	10.27933 P	P	P	P	11.9409
9.260527	8.691526	9.591896	9.845593 P	P	P	P	8.840998
6.922212	6.165068	7.348858	8.808129 A	P	A	A	6.288588
11.11849	10.42	10.9052	11.8553 P	P	P	P	11.0336
9.728369	10.73321	10.47532	10.20846 P	P	P	P	11.01482
9.200817	8.473663	9.758015	10.13187 P	P	P	P	8.099824
6.929932	6.320023	6.037869	6.847146 P	P	P	M	6.756335
7.517738	6.04787	8.70187	8.178358 P	P	P	P	7.194066
11.93515	12.20785	11.08647	10.46775 P	P	P	P	11.84241
11.6742	10.12596	10.81975	10.85292 P	P	P	P	9.615748
6.631895	7.086726	6.763403	7.862618 P	P	P	A	7.805768
6.34418	6.835546	5.834743	5.891024 P	P	P	P	7.019455
	5.960357			P			
7.038911	6.365052		P	A			6.364752
5.650808	6.411486	5.365731	A	A	P		6.808649
7.832994	7.315517	6.334472	7.802435 P	P	P	P	8.129005
7.661051	8.428953	8.247015	8.310067 P	P	P	P	8.785211
	5.419583			A			
9.442456	10.04147	9.060319	8.369609 P	P	P	P	8.963356
8.812761	7.471398	8.238781	9.442212 P	P	P	P	8.08091
4.348201			A				0.7051
7.282714	6.248103	7.014284	8.296609 P	P	P	P	6.669745
9.514819	8.273882	9.584117	9.727463 P	P	P	P	8.520651
12.01432	11.70753	9.580628	10.51172 P	P	P	P	12.30352
		4.377095	7.141187		M	P	
9.570034	9.427252	8.768986	8.887636 P	P	P	P	9.398098
6.995394	6.133691	7.900236	7.268312 P	P	A	P	6.227637
10.23557	9.66326	10.82459	11.72114 P	P	P	P	10.1922
9.756624	10.44266	11.02916	11.47271 P	P	P	P	10.26223
8.966023	8.044833	9.524436	9.69913 P	P	P	P	9.605177
10.33523	9.658297	10.58752	12.72049 P	P	P	P	10.97119
8.851131	7.597038	9.997256	9.326504 P	P	P	P	7.31869
10.19174	10.96779	10.82373	10.60562 P	P	P	P	10.45257
6.381469			A				5.368074
	6.857658		8.012195	A		A	
7.787059	6.952335	7.948707	8.747156 P	P	A	M	7.761547
12.14775	12.23848	11.58341	11.13699 P	P	P	P	11.87005
10.34259	9.33609	10.69293	11.55683 P	P	P	P	9.658448

7.02224	7.023786	3.470063	6.390519 M	P	P	M	6.455458
12.05737	12.04938	10.92133	10.86568 P	P	P	P	12.27227
	5.439896		2.742239	P		M	
			5.391724	P		A	
7.589103	7.492457	8.104593	8.980011 P	P	P	P	7.704795
12.07256	11.46748	11.03356	12.03992 P	P	P	P	12.55106
10.94837	11.77613	11.02538	10.26582 P	P	P	P	11.48821
9.259156	9.184436	9.607641	10.25633 P	P	P	P	9.566563
7.782794	7.515241	7.692545	6.654366 P	P	P	P	7.78364
7.669309	7.61487	6.161683	7.215067 P	P	P	P	7.683817
	4.849731		6.250783	M		A	
5.649053			6.59606 M			A	5.757746
4.366462	5.468595		P	P			6.309941
7.125769			5.046176 P			P	6.846939
8.485753	9.132371	8.005575	8.187636 P	P	P	P	9.365155
8.413721	9.132123	7.653214	6.929601 P	P	P	P	8.59693
10.0019	9.232459	9.453726	8.45803 P	P	P	P	9.477593
7.779664	8.680561	9.024412	9.522618 P	P	P	P	8.607503
11.47547	11.65928	11.56963	12.32193 P	P	P	P	11.7732
7.130629	7.510336	7.828027	8.282961 P	P	P	P	8.611496
10.34767	9.315417	10.53115	11.25127 P	P	P	P	9.617118
9.73567	10.40278	11.04028	10.73945 P	P	P	P	9.944543
9.599245	8.944634	8.602925	8.201344 P	P	P	P	8.720249
12.3621	12.62776	13.26487	13.65105 P	P	P	P	12.7687
9.545102	8.766248	9.840364	10.24659 P	P	P	P	8.999028
11.17578	10.89326	9.443091	9.558666 P	P	P	P	10.95983
8.258148	7.063245	7.27319	6.98908 P	P	P	P	6.638653
7.636476	7.176639	7.41964	A	A	A		6.560171
	5.125279	5.230476		P	P		
8.021436	7.628754	7.070272	6.931865 P	P	P	P	7.667635
11.62017	11.51163	11.03949	10.49631 P	P	P	P	11.32339
8.17438	8.384541	8.003317	9.626 P	P	P	P	8.27695
8.205394	7.841579	8.559939	9.386799 P	P	P	P	8.242875
10.07686	9.988009	9.02945	8.560292 P	P	P	P	9.896744
11.95609	12.21462	11.34362	11.25423 P	P	P	P	12.1329
11.14909	10.83243	10.39412	9.879961 P	P	P	P	10.73892
8.562337	9.317967	8.987758	7.441099 P	P	P	P	9.079604
9.366766	9.288239	8.341939	7.551229 P	P	P	P	8.607632
6.331459	6.119473	6.255965	5.253298 A	A	P	P	5.779648
9.622686	9.856847	11.32898	10.70971 P	P	P	P	9.607261

8.030414	7.101623	7.364648	7.696944	P	P	P	7.629851
9.60727	9.394399	8.591325	8.671484	P	P	P	9.957237
9.250833	8.432867	7.736113	7.674689	P	P	P	8.932467
12.11024	11.51709	12.92276	12.72926	P	P	P	10.97824
7.546629	8.777145	7.671646	7.499709	P	P	P	8.107291
8.043609	8.190632	8.842506	8.060043	P	P	P	8.322735
		3.358153			P		
6.784609	8.440372	7.058505	7.132079	P	P	P	7.990533
6.821922	8.172128	8.20926		P	P		7.811408
12.92226	12.89252	11.93998	11.8946	P	P	P	13.05356
6.787353	6.638395	7.821835	8.021865	P	P	P	6.517624
5.56347	5.23601	5.530442	5.012085	P	P	M	4.003083
7.700101	7.399357	7.398269	7.678922	P	P	P	7.772167
8.621744	8.926876	8.86629	9.841395	P	P	P	8.851998
9.577889	10.14638	7.609355	7.769355	P	P	P	10.16015
5.81538	6.817786	6.890095	3.779739	P	P	P	6.699762
8.246176	7.81056	7.542152	8.360024	P	P	P	7.718954
	6.578445	5.631384	7.631873	A	P	A	
			5.238667			A	
		3.750689			M		
6.214951	6.389713	4.52869	A	P	P		6.24517
5.532689	6.339654	6.613529	6.967211	P	P	P	7.077497
		6.677637			A		
7.619973	7.285867	7.117918	7.469622	P	P	P	6.544354
11.5307	11.51045	11.69979	11.82312	P	P	P	11.24366
6.275382	6.067611		6.926429	P		A	5.897162
11.34283	9.814964	9.649462	9.817154	P	P	P	9.817349
			6.296158			A	
6.176151	7.405075	6.607759	7.741422	P	P	P	7.480026
11.08264	11.66666	10.30545	9.811379	P	P	P	11.41333
8.992952	6.758642	9.011523	9.068675	P	A	A	7.567433
8.258079	7.844552	9.251959	8.894074	A	A	A	6.882388
10.99253	11.16056	9.394974	10.75508	P	P	P	12.08925
10.6015	11.09058	9.127973	9.578111	P	P	P	11.52326
7.613387	6.002722	6.511741	6.23952	P	A	P	5.292311
7.515872			A				2.624506
10.70801	10.59732	9.081015	9.224689	P	P	P	10.58209
6.718587	7.492776	8.350575	8.555437	P	P	P	8.35057
6.037674	5.981166	6.861038	7.678773	P	P	M	5.192917
	5.236261		6.61328	P		A	

6.633059	6.488136	6.894831	A	P	P		5.765376
8.068129	8.304332	7.237553	7.088817 A	P	P	P	7.000508
5.807284		6.649865	6.813335 P		A	A	6.131829
8.454577	9.305233	8.610651	8.469002 P	P	P	P	8.917776
10.88874	9.745355	11.44171	10.91433 P	P	P	P	9.424948
7.754827		8.375739	9.79835 A		A	P	7.697031
	6.790082	5.424309		P	P		
11.79873	11.69712	11.02278	10.52751 P	P	P	P	11.41574
10.7574	10.48144	9.751183	10.36564 P	P	P	P	10.71009
5.6962	5.874712	5.365073	2.683735 P	M	P	P	5.874526
6.746588	7.09927	6.678764	P	P	P		6.451763
8.834215	8.716875	8.643283	7.776187 P	P	P	P	8.162355
			7.112629			A	
		3.343143			P		
9.775443	8.274024	8.912407	8.453523 P	P	P	P	8.336082
4.971999	5.328054		5.932978 A	P		M	2.291528
7.125626	7.952216	7.430627	P	P	P		7.275329
8.608628	9.566756	8.643386	7.35579 P	P	P	P	9.641504
6.656064	7.136263	6.440537	5.574702 P	P	P	P	5.61047
10.92729	10.61012	10.47335	9.721344 P	P	P	P	10.32678
9.556021	9.414948	9.059028	9.784287 P	P	P	P	9.771526
7.54944	7.800097	8.28698	7.203382 P	P	P	P	7.18317
	5.849852	4.542325		A	P		
			5.824525			P	
9.139464	8.881699	8.654909	8.106895 P	P	P	P	8.124801
6.828319	6.206454	5.921	6.795253 P	P	P	M	5.688987
5.548449	6.077085	6.004745	6.129693 P	P	P	M	6.500537
5.592727	6.837347	2.086129	1.572299 P	P	P	P	6.304004
10.2072	10.12731	9.22806	8.556538 P	P	P	P	9.489539
9.563033	11.05243	6.658711	10.02571 P	P	P	P	8.530006
7.503891	7.341948	7.099183	6.695023 P	P	P	P	6.770645
8.618006	8.670924	7.972635	8.76981 P	P	P	P	9.028933
	5.552195			A			
9.735725	9.815835	9.363806	10.41963 P	P	P	P	8.515232
12.27818	11.85991	11.10574	11.57462 P	P	P	P	11.98911
5.627458		7.460284	7.402931 P		P	P	7.289369
7.210992	7.263547	6.831783	3.783818 A	P	P	P	7.24924
10.22038	10.75076	9.758138	9.816984 P	P	P	P	10.29069
		2.104448			P		
7.484682	6.750462		5.579566 A	P		M	6.796465

7.632543	8.058501	7.23867	7.108798	P	P	P	7.886435
9.125304	9.88058	9.725148	9.270227	P	P	P	10.22979
6.508874		6.214076	7.682221		A	P	6.500233
11.00596	11.06216	10.06376	10.10859	P	P	P	11.0986
13.00941	13.10399	13.26165	13.40965	P	P	P	14.06015
10.52137	9.674987	10.2694	9.683849	P	P	P	10.09939
4.119364	5.817938	6.803615	P	A	P		6.595531
		6.615964				A	
		5.962456			A		
5.592342	7.078189	7.365248	8.444053	P	P	P	6.829249
11.0747	10.54887	11.58013	12.02931	P	P	P	11.08628
9.56591	9.648899	10.25743	10.33896	P	P	P	9.670547
	6.513089	5.659296	7.736023	P	P	A	
7.589414	8.434874	8.044291	9.149936	P	P	P	8.802618
8.458522	9.387887	8.078199	8.171078	P	P	P	8.741336
		1.518542	3.607887		P	M	
10.31827	10.3005	9.274391	8.423461	P	P	P	9.654726
11.24325	11.77636	13.01681	12.05075	P	P	P	10.41363
6.585287	6.269266	6.235553	7.164835	P	P	A	6.196593
11.915	11.44274	10.77732	10.33825	P	P	P	11.10299
9.096053	8.121478	7.270577	7.389676	P	P	P	7.335074
8.6297	7.873636	5.899207	6.727319	P	P	P	5.401887
8.390958	7.567624	7.786817	7.182833	P	P	P	7.682768
9.085097	8.843164	8.358592	8.098079	P	P	P	8.526668
6.619658	6.389972	4.435845	6.596334	P	P	P	5.709321
7.36311	7.010871	8.18567	A	M	A		6.329943
8.726096	8.536032	6.3537	6.593645	P	P	P	8.524932
7.069237	6.233656	6.704177	6.34005	A	A	P	6.528062
10.16691	9.930985	9.489564	8.676236	P	P	P	9.689004
7.088888	6.886628	7.638076	8.421506	A	P	P	8.124921
5.338776			A				4.099029
7.97594	6.33196	7.81217	8.18127	P	P	P	6.884852
7.325966	6.265294	5.512317	5.033322	P	P	P	5.650181
6.338644	5.53799	6.421439	7.417396	A	P	A	7.433932
6.708883	6.368344	6.644115	7.296096	P	P	P	7.732947
12.52287	11.43098	12.56643	12.58378	P	P	P	10.62335
6.465497	5.737599	6.872769	7.090435	P	A	M	7.254194
5.468017	3.726276		P	P			6.12964
5.59565	6.241036	6.571822	5.919273	A	P	P	6.42955
8.247657	8.439977	7.571994	8.253793	P	P	P	8.357561

9.269989	9.626043	10.20173	9.512308 P	P	P	P	9.217443
7.914711	8.170134	7.690664	7.195906 P	P	P	P	7.83211
			6.650997			A	
7.0282	7.134339	7.40965	8.385157 P	P	P	P	6.839901
7.223118	6.629326	7.860484	A	A	A		5.255946
9.115414	8.487249	7.472402	7.614857 P	P	P	P	9.0008
10.29972	10.14798	10.08294	9.42848 P	P	P	P	10.06692
9.213967	9.235072	9.631496	10.16534 P	P	P	P	9.24911
13.99899	14.72095	13.57986	13.55682 P	P	P	P	14.89728
		6.844575	5.537282		P	P	
5.48359	6.900046	8.019525	8.404246 P	A	A	A	5.692366
8.199716	7.922761	9.457799	9.964198 P	P	P	P	8.169292
12.07301	11.57381	11.90179	11.77213 P	P	P	P	11.31637
8.488034	8.208423	8.77295	8.795727 P	P	P	P	7.780737
	6.12485	7.617496		A	P		
7.254223			A				6.064676
8.315343	6.888893	8.374619	8.461659 P	P	P	P	7.287563
9.483219	8.090573	8.983298	8.130815 P	P	P	P	7.876239
		3.800458			P		
6.925198	5.960577	7.211873	7.333303 P	A	P	P	6.761929
7.213757	6.471885	8.381247	8.986139 A	P	P	P	5.437913
5.927625			6.813826 A			A	6.000294
6.920677	8.107737	7.369006	6.969946 P	P	P	P	7.930205
9.081432	9.10431	8.509607	9.112706 P	P	P	P	9.333777
6.817837	8.945295	8.828466	9.135462 P	P	P	P	8.269804
5.917692	5.844812	7.452861	A	A	A		5.104622
5.952527		4.866822	A		M		5.458339
7.57509	7.677307	9.066041	A	A	P		7.087045
		6.574527			A		
1.392896		5.877965	6.53756 P		P	M	6.874145
			6.800043			A	
		6.095684			A		
9.160189	10.08705	8.682813	8.158683 P	P	P	P	8.078274
	2.826034			P			
11.25001	12.02277	10.37624	11.62665 P	P	P	P	12.5937
6.080338	6.444056		2.994062 P	P		P	7.33192
6.095472		6.528716	8.04493 P		A	A	7.712048
8.182791	8.356774	9.15528	8.057037 P	P	P	P	7.624718
6.687746	7.693519	7.602884	7.574588 P	P	A	P	6.801227
8.089067	8.621568	8.705003	7.231777 P	M	P	P	7.067577

9.839561	8.810774	9.706209	9.448225	P	P	P	8.830815
6.589249		7.597841	7.47123		A	P	8.705962
			5.818903			A	
	6.952116		6.812387	A		P	
5.555014	6.079083	5.397032	P	P	P		6.674806
		6.388547			P		
6.548288	7.449902	6.503053	6.802182	A	P	P	6.888857
9.183036	9.321808	9.203191	7.702017	P	P	P	8.892462
5.098794		5.827757	A		A		1.410299
12.56793	10.7143	12.2163	11.7606	P	P	P	9.286922
9.149943	9.622582	9.081485	8.231395	P	P	P	9.002851
10.15142	10.44159	9.758302	9.656806	P	P	P	10.20638
8.913118	9.239495	9.797446	9.190473	P	P	P	8.959301
5.175305	6.829479		P	A			5.663069
10.01961	9.662297	10.56545	9.888917	P	P	P	10.42691
	5.634206			A			
7.396406	5.680178	6.706191	6.806413	A	P	P	6.324715
8.464336	6.724302	8.140731	7.593312	A	A	A	6.154848
8.165296	8.715744	7.642394	6.301077	P	P	P	8.558359
6.439227	5.866602	7.202814	A	A	A		6.013752
8.660941	8.511269	9.268634	8.650109	P	P	P	7.89359
6.387939	6.974837	5.761564	8.508562	P	P	P	7.689965
5.218173	4.355855		A	P			1.152885
6.118832		3.904864	A		P		6.169576
6.939551		6.876693	5.823798		P	P	7.190851
7.230009	8.00421	6.752042	M	P	P		7.4143
6.75729	6.609053	6.879773	7.975341	P	P	P	7.37646
7.414599		7.147938	7.567497		A	A	5.686131
	3.493221			P			
8.703393	9.122137	9.754385	9.858184	P	P	P	8.683958
	5.846041	5.629891	3.739352	P	P	P	
6.326555	7.259708	7.947347	7.849089	P	P	P	6.706183
			6.717889			A	
10.16326	9.971012	10.32717	9.349065	P	P	P	9.008303
10.28022	9.770588	10.82766	11.42878	P	P	P	10.22724
10.31156	10.10542	11.52898	12.02106	P	P	P	10.41663
			8.301421			A	
5.552789	6.847824	5.319918	6.71182	P	P	A	6.486587
8.765506	9.730252	8.014605	7.960988	P	P	P	9.108786
8.09678	8.018973	8.913638	9.599182	P	P	P	8.383616

	6.066912	6.222204	5.090562	P	A	P	
6.310904		0.560884	M		P		5.349726
9.012845	7.615298	7.922702	7.230711 P	P	P	P	7.603983
5.084361	4.996419	1.281735	M	M	P		5.925723
6.276583	6.662156	3.426643	6.353127 A	P	P	A	6.261152
9.349177	10.44977	9.153283	8.734586 P	P	P	P	10.27771
7.704908	7.729919	7.755952	8.454469 P	P	P	P	7.939293
6.293239	6.658867	6.343251	6.341466 P	P	P	P	6.015146
6.296329	5.641649		2.15885 A	A		M	5.580442
6.606904		7.036265	6.77315 A		P	A	6.201315
6.650835	4.030897	6.801516	6.740324 P	P	P	A	6.080856
7.731863	7.78095	7.726985	7.948306 P	P	P	P	7.981182
	5.618817			A			
5.918092			6.783257 A			P	5.330664
6.936258	7.001985	6.190524	7.503962 P	P	P	A	7.804221
9.602637	9.524576	9.257907	10.67347 P	P	P	P	10.12489
	6.661604	5.223289		A	P		
5.879854	5.482936	6.194238	P	P	A		5.605439
7.516555		8.210126	A		A		5.882097
6.437516	6.360634	7.372518	6.549307 P	P	P	P	6.787314
		1.853126			P		
10.98727	11.66388	11.37938	12.07398 P	P	P	P	12.00058
8.108656	8.157614	7.93664	6.8362 P	P	P	P	8.278044
7.608943	7.723848	8.625984	9.437973 A	P	A	A	7.856789
6.917206	6.634546	6.464291	6.602738 P	P	P	A	7.209879
5.587929	6.306317	6.284385	5.633192 P	A	A	P	6.551292
3.817817			P				5.223457
5.747757	5.62733		5.014247 P	A		P	5.990842
10.48206	10.30983	9.373043	9.329424 P	P	P	P	10.36551
7.968298	6.942932	7.562914	7.712662 A	P	P	P	6.130362
8.903154	9.429944	8.646318	8.327415 P	P	P	P	8.680409
5.126222	2.806612	5.642799	A	P	P		5.612092
		7.372222			A		
7.799286	7.223115	10.34339	9.748024 A	P	P	P	6.767601
7.933736	7.801756	7.989338	A	P	P		5.430888
5.123807			6.18319 A			A	4.01643
6.417756	6.543647	7.150502	5.061212 P	P	P	P	6.340726
9.335188	9.797571	10.44777	9.98499 P	P	P	P	9.72274
7.732523	7.776042	7.522031	7.179813 P	P	P	P	8.23318
5.601806	6.620871	5.76432	P	P	P		6.156179

5.553924	2.35129		A	P			5.562351
			2.569392			P	
8.364944	9.107249	9.680513	9.900723 P	P	P	P	8.766552
6.211813	7.655254	7.576059	P	P	P		8.001224
5.861985	5.452198	6.444243	5.565142 A	P	P	P	5.620751
	5.092643		6.316051	P		A	
7.557265	7.334154	6.733838	A	P	P		6.512009
	6.194316	5.026576	4.682597	A	P	P	
13.1239	11.86094	12.72465	11.97828 P	P	P	P	11.05706
8.261084	8.957626	8.368966	7.63084 P	P	P	P	8.459774
8.440885	7.575082	7.923028	7.772721 A	P	P	A	6.995845
4.893977	6.005037	7.134329	7.599373 A	A	P	P	6.732976
8.675545	7.724337	7.55954	5.920601 P	P	P	P	6.792305
6.003156		3.389909	P		P		6.271578
6.435756	7.709903	7.585022	7.455162 P	P	P	P	7.735652
7.126137	7.328878	7.331403	P	P	P		5.833122
	6.184751			A			
		6.178623	7.844262		A	A	
5.953464	5.714888	6.325391	A	A	P		4.961958
9.078218	8.785515	7.447491	8.28709 P	P	P	P	8.701818
8.640718	8.235903	7.803888	7.233357 P	P	P	P	6.874138
			4.869599			P	
	2.951003			P			
7.035499	7.152316		4.721809 A	A		P	6.556428
		5.79775			M		
9.457078	10.01915	9.450523	9.558028 P	P	P	P	9.661747
6.168044	6.125193	6.87924	8.185958 P	P	P	P	7.711624
4.776164			A				5.874315
1.452493			M				6.136436
5.75759	5.839429	5.377512	4.916139 A	P	P	P	2.640165
6.219974	5.954862	6.063262	A	A	P		3.119304
7.085225	7.395606	8.23042	7.530017 P	P	P	P	7.05175
6.719097	5.687731		A	A			4.592503
	5.459208	6.049122	7.069372	P	A	P	
		1.110024			M		
		4.881601			M		
6.774791	6.093278	5.158001	7.023538 P	P	P	A	5.875938
5.916011	5.748928	6.125445	4.427753 P	P	A	P	6.804731
7.489369	8.150085	7.710926	8.026585 P	P	P	P	7.500953
7.225436	6.889827	8.81243	8.505299 P	P	P	A	7.177276

5.702646	5.567225	5.916275	3.43497	A	A	A	P	5.59474
6.05118	6.799717	4.048626		A	P	P		5.108507
6.63001		6.95712	5.695149	P		P	P	6.89512
8.488765	8.647862	8.398305	7.404953	P	P	P	P	8.242674
6.801523	6.46585	2.407359	7.353947	P	P	P	A	6.081877
8.142328	7.931395	6.790454	6.013004	P	P	P	P	7.701082
7.503866	7.164852	6.198253	1.159822	P	P	P	P	7.142708
10.03829	10.50071	9.956659	8.787702	P	P	P	P	10.24063
6.891685	7.437595		8.16682	P	A		P	6.602082
			2.600582				P	
5.511256		6.794981		P		A		6.880716
8.575264	8.513818	9.522261	9.532539	P	P	P	P	8.408663
		5.302534				P		
6.805491	7.135819	6.784737	6.874076	A	P	P	P	5.763474
9.26356	10.52327	8.89955	8.102695	P	P	P	P	9.892846
6.753753	7.262576	5.679877		P	P	P		6.412104
	5.529759	6.572321		P	M			
	7.013893		3.310394	A			M	
4.279501				A				2.041947
5.953939	6.24209	5.786038	4.249808	P	P	P	P	6.007055
7.566471	7.294277	6.551019	6.645002	P	P	P	P	7.481422
5.187597	3.892958	5.872318	5.393407	P	P	P	P	6.320601
7.22416	7.489896	7.014472	6.546447	P	P	P	P	7.30825
9.36933	9.66837	8.810577	8.002914	P	P	P	P	9.174543
8.451446	8.505224	7.512356	6.606127	P	P	P	P	7.417118
5.312454		0.727457		P		P		6.3562
		4.626729				P		
5.301027	6.519326	6.822448	7.360149	M	M	P	A	6.529856
11.94235	12.02027	11.05214	10.8378	P	P	P	P	11.73057
		2.791561				P		
	3.160157	3.765225		P	P	P		
5.639054	3.564173	3.843657	6.035763	P	P	P	P	6.446147
7.791514	8.062259	6.848324	6.905996	P	P	P	P	7.681259
8.702163	8.491659	7.378284	6.581322	P	P	P	P	8.55015
11.03965	10.75337	9.927599	10.11708	P	P	P	P	10.95978
7.300191	7.503659	6.418644	6.327857	P	P	P	P	6.076701
				P				
	5.342492		3.546498	P			M	
11.40623	11.47935	10.51827	9.732451	P	P	P	P	10.89016
5.477121	6.105809	6.02542	4.561238	P	A	P	P	5.933904

5.140651	5.763488	6.038875		P	P	P		6.155856
10.12876	10.86128	13.03569	13.10217	P	P	P	P	10.56227
9.357099	9.36595	8.818961	7.738807	P	P	P	P	8.79328
6.439776	3.453465	5.598912	6.367103	P	P	P	P	6.906683
		1.577931				P		
5.69801	5.207188	6.786207	6.405268	A	P	P	A	4.566034
4.75903	5.035494		6.927415	P			P	6.188169
7.972076	7.356633	7.736803	8.728968	P		A	A	7.155791
7.038804	7.107896	6.460185	7.036492	A	P	P	M	6.360892
6.454999	6.002082	6.312141	6.5217	P	P	P	P	5.813242
6.787798	7.235715	6.50056	5.473465	P	P	P	P	6.616286
3.885824	5.656664		7.256003	P			A	6.329985
	6.103798	5.837179		A	P			
6.763949	6.516178	7.124942	7.435843	P	A		P	6.700221
7.151213	7.154117	7.329656	6.082795	P	P		P	7.077048
		4.881684				M		
	5.060051			A				
7.067756	7.095783	6.130819	7.178508	P	P	P	P	7.754791
6.332482	7.121996	6.55472	3.236212	P	P	P	P	6.043913
6.068764		5.738068	4.865417	A		M	P	5.291247
8.413223	8.52457	9.554414	10.23188	P	P	P	P	8.954085
5.792319	6.997064	6.352437	6.984431	P	P	P	P	6.002605
7.536419	6.069011	6.68902	6.842739	P	P	P	A	6.882129
8.034395	8.933927	7.544143	7.098959	P	P	P	P	7.891841
	6.905934	5.668378	2.885839	P	P	P	M	
6.283594	5.762135	5.995043	7.145403	M	P	P	A	6.054933
5.915247				A				4.709376
		6.46253	7.16557			P	A	
6.797209	6.549152	6.918516		A	A			5.681745
	6.66574			P				
6.164362	6.457254	6.276025	2.880861	A	P	P	P	6.402965
9.128005	8.942656	8.902649	7.672732	P	P	P	P	8.283414
4.337011		6.073121		P		A		6.115723
8.137969	8.786894	8.421135	7.097805	P	P	P	P	8.640397
8.230928	9.010077	8.635957	7.064322	P	P	P	P	8.403746
			7.139087				P	
6.627001	6.468887	6.391293	6.516473	P	P	P	M	6.509126
9.824545	9.820259	8.70369	8.661716	P	P	P	P	9.105355
6.238215	6.785424	6.955085	7.359218	P	P	P	A	7.106104
8.313296	6.15826	7.008876	8.151483	A	P	P	A	5.915655

	4.594809		6.535718	P		A	
5.228065		2.324876	A		P		5.125232
2.166312	6.222325		P	A			5.497696
			6.964799			A	
8.193334	8.004452	7.196865	7.884074 P	P	P	P	8.078978
8.182573	8.490999	6.575571	7.531105 P	P	P	P	7.241005
5.903342	6.028613	5.485076	2.873653 A	P	P	M	1.287506
5.385995	5.646086	4.67479	P	A	M		6.570532
9.821298	10.52537	9.74871	9.405603 P	P	P	P	10.17135
7.0076	7.484576	6.848379	A	P	P		6.34628
		5.915664	6.340567		A	A	
	6.378577			A			
	7.301009	3.361167		A	M		
6.885031	7.283408	8.206751	4.33692 A	P	P	P	6.873143
8.026316	8.981109	7.797715	7.630808 P	P	P	P	8.296948
5.707425	6.213853	5.953251	M	P	P		7.454145
5.849348	5.991524	2.895905	P	P	P		6.296557
4.168245		4.769392	P		P		5.309764
		6.730184			A		
		4.381478			P		
9.242327	8.936557	8.710137	8.015054 P	P	P	P	9.081883
			6.772005			A	
7.704766	8.365076	7.256974	6.077745 P	P	P	P	8.093434
8.879681	8.733171	8.929611	7.105938 P	P	P	P	7.560209
		4.856309			P		
9.51322	9.983729	9.933858	8.099791 P	P	P	P	10.22669
6.972742	7.179376	7.281861	7.423787 P	P	P	P	8.056062
8.123729	7.642619	7.833097	6.144602 P	P	P	P	7.676273
6.236367	7.116926	6.968288	6.409818 P	M	P	P	6.702405
			4.076009			P	
	5.839911	7.026041	6.844796	A	P	A	
	5.979784	4.768426	5.399381	A	P	P	
7.437573	6.099925	7.18845	6.822179 A	A	P	P	6.131876
	7.330947			A			
7.013787	6.012884	6.637481	5.63336 A	P	P	P	4.87842
6.919983	7.032857	6.702805	8.601016 P	P	P	P	8.004969
7.07944	6.469966	5.920986	6.490998 A	P	P	P	4.841103
7.262458	6.874613	6.022838	6.809912 P	P	P	P	6.234501
4.626146	5.173657	5.245777	P	P	P		5.976356
8.406357	8.277775	7.346032	7.425241 P	P	P	P	7.269355

6.615144	7.002275	6.915096	6.67587	P	P	P	6.746324
6.275171	6.225317	3.950438	A	P	P		4.72844
8.629282	8.402288	8.649512	9.474021	P	P	P	8.620316
5.150644		5.976321	7.497132	A	A	M	5.830876
6.797257	6.005297	6.406339	A	A	P		6.134079
7.168684	7.711282	6.979769	A	P	P		7.064951
8.098982	8.460885	7.483062	7.566016	P	P	P	8.379232
6.858865	6.356151	6.409626	6.295611	P	P	P	4.836639
		5.671311	6.684977		P	P	
10.47616	7.830088	9.638201	8.581265	A	P	P	6.312769
5.702575			A				3.781589
10.49014	11.26691	10.02137	8.507923	P	P	P	10.75477
5.721425	6.77727	6.651896	5.333779	M	P	M	7.618949
5.886322	4.529688	6.36735	5.938471	P	P	A	5.744965
6.955154	6.956487	6.845054	6.938006	P	P	A	5.872513
6.458725	6.584048	5.868535	7.169076	P	P	P	6.317409
7.19008	7.374719	6.45067	7.531277	P	P	P	7.252149
6.840708	7.718095	6.645562	5.596157	P	P	P	6.988528
5.96153	5.838455	1.899954	A	A	P		5.098326
6.877112	7.526606	7.263137	8.642032	P	P	P	6.922283
9.365141	9.647826	10.06982	8.698278	P	P	P	8.653495
6.014818	5.645839	6.683589	7.40582	A	A	A	3.59523
9.272265	9.402708	9.159482	8.371826	P	P	P	8.209052
		5.776417	6.370075		P	A	
5.824934	6.008201	7.286516	P	P	A		6.586757
7.285673	7.663093	7.000985	5.398447	P	P	P	7.732503
6.961067	7.938016	7.457317	5.326768	P	P	P	7.129476
9.078326	9.432993	8.61853	8.215611	P	P	P	8.320502
6.870073	6.572216	6.663905	7.66314	A	A	M	7.056146
4.864561		3.961605	P		P		6.328641
7.281534	6.06615	7.430632	7.821225	M	P	P	7.51926
11.06911	11.18154	10.51582	9.911597	P	P	P	11.01036
6.043666		6.188763	A		A		4.547317
7.887408			A				5.645381
		6.886544				A	
8.195415	8.790147	7.798769	7.56967	P	P	P	7.964935
8.872932	9.960215	9.050882	8.238732	P	P	P	9.001521
5.677359	6.455626	5.773846	3.689808	P	P	P	6.062545
6.457862		5.872287	4.81302		A	P	5.025027
6.215547	6.018172	7.253943	7.786242	P	P	P	6.827726

8.001371	6.453582	6.776732	5.700644	P	P	P	6.221917
5.848805	5.82305	5.909446	6.980919	P	A	A	6.610225
6.121221	4.861049	5.559405	P	P	P		6.050308
6.156234			3.828399			P	6.620164
	5.91045		4.139009	A		P	
5.383514		5.200186	7.134724		P	P	6.690594
8.796299	8.731844	7.777299	7.625135	P	P	P	8.353284
10.73338	11.33024	12.11752	11.84742	P	P	P	10.8425
7.610399	6.887202	5.751499	6.870931	P	P	P	6.12321
		7.369235			A		
			2.904803			P	
9.35272	8.248874	9.279638	9.957548	P	P	P	8.175395
7.404007	6.861546	5.750095	6.587569	P	P	P	6.704357
9.098847	9.523297	9.277908	8.53341	P	P	P	9.401512
4.933964	5.072113	5.204944	6.171357	A	P	A	4.12718
7.050571	6.754504	7.955597	7.41607	P	P	P	5.818945
		4.999019			P		
		5.41664			P		
6.061859	5.396723		A	P			4.145145
8.24317	7.757235	8.059253	8.39781	P	P	P	8.136221
7.415133			8.250356			A	8.52647
6.434959	5.728882	5.942257	6.058718	P	P	A	4.90528
	5.715549			A			
7.731273	8.885216	8.162116	5.632363	P	P	P	7.794057
3.443432			P				4.858321
	5.610824	5.628801	6.544069	A	P	P	
7.045414	6.333126	5.780834	6.537415	P	P	P	5.492681
			4.775832			P	
4.458282		5.627472	6.331645		P	A	5.701684
9.562466	9.406026	9.018616	8.061138	P	P	P	8.959846
7.264703	5.545136	7.60443	7.85392	P	P	P	6.975752
7.576253	7.036428	7.279662	6.793453	P	P	P	6.014644
9.513968	9.016246	8.295269	8.395516	P	P	P	8.003281
1.086494	5.541477		P	P			6.009702
6.715089	6.387308	7.08447	7.964107	P	P	A	6.127088
8.330923	8.682908	8.558739	8.237463	P	P	P	7.488026
8.665028	7.704244	8.79785	7.055692	P	P	P	7.637018
7.737328	7.042041	7.303179	7.575018	P	P	P	6.568487
6.083706	5.562692	6.50681	6.733429	P	A	P	5.049823
5.631445		4.317084	A		P		5.867017

7.13993	6.897847	6.359549		A	A	M		6.070569
9.652064	9.607566	10.03139	10.88686	P	P	P	P	9.981684
8.425343	7.94662	7.607203	7.011608	P	P	P	P	7.654289
8.1934	7.25158	7.089984	7.122844	P	P	P	P	6.282343
6.342091	7.151756	4.372726		P	P	P		7.501474
6.92722	6.961536	7.27204	3.847282	P	P	P	P	7.131338
	5.059654			A				
8.780073	9.103313	8.069213	7.249778	P	P	P	P	8.399261
6.392914	6.082433	6.500999	7.412043	A	A	P	M	6.460041
4.917321	5.481975			P				6.139928
5.665821		5.95892	6.379	A		P	P	3.304439
8.089524	6.772304	7.242344		P	P	P		7.017934
	5.261765			A				
6.972878	6.466038	5.879369	1.93084	M	P	P	P	5.767576
		2.588669			P			
6.009899	6.693195	3.807564		A	M	P		6.457051
5.989652				A				4.590389
5.916249				A				4.025716
5.611534				A				3.915315
6.869364	6.682388	4.279147	7.533195	A	P	P	P	6.440419
5.141873				A				2.296447
6.181566	5.048814		6.750431	A	M		A	6.159534
6.000132	5.838668			A	A			4.531781
8.003963	7.87459	7.530263	8.234191	P	P	P	P	8.161694
		6.023749				A		
		4.204077	5.27225			P	P	
		5.201734				P		
5.350278	4.959199			A	P			0.435498
5.987711	5.62216	6.252351		M	A	P		6.455149
6.086182	5.90226	6.184368	7.072295	P	P	P	A	6.885484
6.536012	6.969921	6.963919	7.738009	P	P	P	P	6.75735
5.186875				A				2.854164
		7.61317				A		
8.875985	10.27433	8.818335	8.579709	P	P	P	P	10.05857
10.30057	9.165631	9.587407	8.696136	P	P	P	P	8.423676
7.061315	7.359358	7.800498	7.348529	A	P	A	P	6.716709
7.131551	6.681307	7.30726	5.640169	P	P	P	P	5.742096
10.45926	10.11972	10.18672	9.76204	P	P	P	P	10.77646
7.05713	6.366345			M	A			6.674559
6.81656	6.762961	7.216871	6.422168	P	A	P	P	6.362166

6.795343	7.526694	6.732083		P	P	P		6.470677
6.27951	5.019519	6.398037	7.132493	P	P	A	P	6.076554
4.263495	5.455822	3.828888		A	P	P		4.581279
6.722635	6.402065	6.105183	6.327793	A	P	A	P	5.271232
9.320102	9.186036	9.642775	8.721538	P	P	P	P	8.68256
10.21908	9.27758	10.42349	10.14554	P	P	P	P	8.86496
9.192077	8.862262	8.588906	8.415679	P	P	P	P	8.753753
			2.18569				P	
11.40776	11.11005	9.13295	8.576118	P	P	P	P	10.93288
4.315347		3.076844		A		P		5.325694
6.006332	6.831916	6.54069	6.977471	P	P	P	A	6.65315
8.939748	8.114166	9.508744	9.8159	P	P	P	P	8.122776
8.606652	8.299993	9.630048	9.234581	P	P	P	P	7.756252
10.39547	10.79006	10.1362	9.771235	P	P	P	P	10.93114
4.131875	4.520602			P	M			5.25767
9.582558	9.953278	9.527432	8.659655	P	P	P	P	9.314946
7.522709	7.252875	7.617766	7.610125	P	P	P	P	7.733978
8.26109	8.583962	8.95996	10.79746	P	P	P	P	9.680036
8.780244	9.297229	9.059889	7.828836	P	P	P	P	8.904617
6.730984	5.968055	6.461012	5.543728	A	P	P	P	5.389693
9.148374	8.554821	9.23478	10.37588	P	P	P	P	8.900924
6.670633	6.795241	6.732937	5.805816	A	P	P	P	5.546485
6.123027	5.102361	6.013488		A	P	P		3.32812
7.351147	7.21713	8.042242	8.651163	P	A	P	P	7.735965
9.320476	9.703538	9.373239	9.269603	P	P	P	P	9.538979
6.699804	6.523656	5.398539	6.315616	P	P	P	A	6.465935
	4.400569	4.820221	2.218061		P	P	P	
5.613163	6.273164	6.954747	7.428368	P	P	P	P	6.764781
5.505799	6.052801	5.382789		P	P	P		6.423806
	6.050698	6.117319	2.556433		A	P	P	
7.422768	6.902267	6.342536	7.71205	P	P	P	P	8.064446
	5.072677	5.987168		P	P	P		
6.401245			7.573856	P			A	6.789383
	5.731311			A				
5.725886	4.644809	5.945711	6.50737	A	A	M	A	5.768423
		5.29153		P	P	M		
5.978206	6.042014	7.063835	6.168992	P	P	P	P	6.255105
10.05896	10.16498	9.460115	9.323219	P	P	P	P	10.68233
	4.258524	5.865953	3.829131	P	P	A	P	
10.14539	9.946314	10.70921	10.68262	P	P	P	P	10.35581

10.26504	11.08892	10.64642	11.19151	P	P	P	11.30003
6.787689	7.118782	5.530344	5.763957	P	P	P	6.53122
8.144281	8.674005	9.652801	9.509965	P	P	P	7.970652
8.295181	9.885431	8.773289	7.53075	P	P	P	9.293816
5.032369			A				2.685065
8.895156	9.63077	8.016647	8.480132	P	P	P	9.492174
7.948269	8.386002	7.683108	5.953377	P	P	P	8.410673
		6.217607			P		
6.053365	4.958664		A	P			1.309054
		2.593934			P		
5.882422	4.479909	6.297469	7.250363	M	P	A	5.39183
7.432343	7.074808	8.068711	8.025072	P	P	P	7.001269
	6.399001	6.638768		A	A		
11.562	12.25107	10.3232	10.83831	P	P	P	12.23728
5.118933	6.869974	5.456874	3.964091	P	P	P	6.770386
7.302234	8.38216	8.116821	7.386015	P	P	P	8.057185
		6.88938				M	
6.909622	6.341487	6.306494	7.091387	A	P	P	6.989958
8.179529	8.659059	7.992641	7.423095	P	P	P	7.888775
10.52385	9.278548	10.18185	10.61084	P	P	P	9.577639
7.102288	6.8965		7.360355	P		P	6.958828
7.95009	7.956121	7.293086	5.445976	P	P	P	8.041798
8.989144	9.138066	8.188492	7.35747	P	P	P	8.499136
8.012066	8.67239	7.77421	6.524745	P	P	P	7.675084
7.945081	8.28393	7.968038	6.612698	P	P	P	8.173698
	0.807411			P			
6.784472	6.834585	5.846896	7.541467	P	P	M	7.094374
7.176722	6.729771	7.02093	6.309587	P	P	A	4.15683
9.267218	8.544722	8.595544	8.712319	P	P	P	9.293025
		6.259011				A	
7.42418	7.360306	7.901754	8.497515	M	A	A	7.308881
6.35419	6.6201	6.523964	5.300562	P	P	P	7.07337
	5.55986	6.62873		P	P		
7.45361	7.678038	5.66914	A	M	M		7.035904
8.228371	7.010779	7.529195	7.336159	P	P	P	7.126483
11.31049	10.74735	10.8681	10.37862	P	P	P	10.85172
8.905036	8.501487	8.328436	7.804848	P	P	P	8.157058
9.351368	8.993878	7.34382	7.843143	P	P	P	8.158262
7.169437	8.313992	7.682919	7.785467	P	P	P	8.164357
		1.974515				P	

5.515492				A				4.039988
7.055998	5.930529	7.352799	5.751996	A	P	A	P	6.26078
7.41148	7.802912	6.05899	6.380803	P	P	P	P	7.316638
	4.968359		6.76005		P		P	
6.855125	7.591197	7.288245	5.63037	P	P	P	P	6.767838
6.043609	6.283514	7.254428	7.191325	M	P	P	A	6.469946
7.245234	7.578312	5.748591	7.146312	M	P	P	P	7.878034
6.727518	6.818488	6.077979	7.775103	P	P	P	P	6.576121
	5.460477				A			
5.17836	5.624288	5.131739	2.425737	A	P	P	P	4.703975
7.8841	8.378872	8.805256	7.943493	P	P	P	P	7.777223
6.003795	5.315117	3.846984		A	P	P		5.331971
	5.009823	4.870233			A	P		
4.427304				P				6.561392
6.104476	6.484389	6.164597	7.444305	P	P	P	P	6.92433
4.910794		4.302648		A		P		2.895059
7.420629		7.600023	7.701455	P		P	A	6.876709
7.546999	7.996222	6.840045	6.360191	P	P	P	P	7.793294
6.452552	6.157273	7.481232	6.522053	A	P	P	P	6.242661
	6.117401				A			
6.901737	6.737225	5.193258	4.905025	A	P	P	P	6.70158
	4.291925				P			
4.628135				P				5.645459
3.869888				P				5.829263
5.392313	5.746891			A	A			6.301203
		5.739921				P		
8.008913	7.465733	8.491303	8.83641	P	M	A	A	6.816916
5.08016		6.47885	6.736999	P		P	A	6.425908
10.42588	9.011601	9.350074	8.645913	P	P	P	P	9.027262
9.932814	9.257705	10.22515	10.10903	P	P	P	P	10.50793
8.536924	8.181191	8.454517	6.151427	P	P	P	P	8.406455
5.443858	4.229567	4.964358	6.731967	P	P	P	P	6.87715
5.236101	5.520808			P	P			6.440168
			7.281313				A	
7.614906	8.017011	7.096714	7.547585	P	P	P	P	7.65709
4.789994	6.71772	6.645953		P	A	P		6.25156
8.732803	9.019533	8.738916	7.979932	P	P	P	P	8.991677
5.655113	6.779159	6.638342		P	P	P		7.010027
	6.342742	1.576216			P	P		
12.33589	12.28189	10.44863	10.60922	P	P	P	P	12.64327

8.876073	9.176546	7.055955	6.660946	P	P	P	8.426929
6.212354	6.641838	6.229637	A	P	P		6.296483
8.653082	9.115322	7.914197	7.732484	P	P	P	8.61888
8.541039	9.095333	7.482298	6.119409	P	P	P	8.246436
7.903452	8.687415	8.134188	7.065376	P	P	P	8.444107
7.913092	8.846716	7.62228	7.379355	P	P	P	8.233479
11.49393	12.24287	12.50985	13.07511	P	P	P	12.61659
	6.021612	4.682025	3.168814	A	P	P	
12.45459	12.31839	11.81991	11.35171	P	P	P	11.94233
10.14862	9.69049	9.12012	9.34263	P	P	P	8.677045
7.280592	7.200151	7.297527	7.501711	A	P	A	6.467048
3.628938		2.760061	P		P		5.386668
6.764838	7.50944	6.076187	6.770648	P	P	P	7.237063
7.254964	7.021141	6.907637	7.270438	P	P	M	8.266322
	5.046085	6.22569		A	A		
		6.862482	7.009223		M	A	
9.340874	9.101038	8.365212	7.931436	P	P	P	8.077254
		7.481746			A		
4.225338	5.946869	5.771841	5.405231	P	P	P	6.820126
6.702643	6.712404	3.938146	3.968204	P	P	P	6.688627
10.11127	9.403152	8.205751	9.416572	P	P	P	10.23604
8.31343	8.209391	9.618491	11.22211	P	P	P	9.14935
7.079065	6.751266	7.630246	8.466425	P	P	P	7.512496
6.379469			3.290909	A		P	2.540227
6.218131	6.309019	4.798105	6.00294	P	P	P	5.603772
	5.313329	6.198293	6.975721	P	A	A	
9.235189	8.548062	9.96806	9.482765	P	P	P	7.919576
	5.381754		7.428498	A		A	
	4.510186			P			
7.274742		8.317661	9.440598		A	P	7.911547
7.665364	7.64304	6.406403	6.978151	P	P	M	7.729177
6.674694	6.292964		A	A			4.362761
	6.067933			A			
3.409513	6.634953	4.701528	P	P	P		6.407915
7.327842	7.26399	7.289992	6.887594	P	P	P	8.235278
9.981607	10.33025	10.35042	9.621367	P	P	P	9.833831
7.219852	6.669741	6.693439	7.175063	P	P	A	6.29857
7.149833			8.267288	A		A	7.07057
8.319484	6.417366	7.250875	7.191476	P	P	P	7.316565
	5.170816	4.562769		M	P		

7.395346	5.895605	6.583335	7.135361	P	A	P	P	6.625216
6.662203	6.137947	6.436899	5.337876	P	P	P	P	6.980619
4.362443	3.320965			P				5.406731
7.275898	7.642947	6.988604	5.766964	P	P	P	P	6.940517
	4.667334	4.516377		P	P			
5.80727	6.589065	5.787575	6.965948	P	P	P	P	6.950116
	1.580675			P				
4.805131		4.817911	6.409495	A		P	A	2.609706
1.747809	6.360589	5.995246	6.412616	P	P	P	P	6.163068
4.941577	6.010584	5.559177		P	M			6.465087
7.118427	7.471659	7.885306	7.563973	P	P	P	P	7.253891
	5.388643	7.430863		P	P			
6.420898	6.935911	5.96546	6.978488	P	P	P	P	6.152711
6.11454		6.605272	A		A			3.84509
6.209393	6.847572	7.299832	A	P	A			4.265271
8.858049	8.585974	7.636577	7.455511	P	P	P	P	10.24065
7.535472	7.264247	7.069869	7.742684	P	P	A		7.055989
6.426301	5.919718	7.562793	6.403392	P	P	P	P	5.937256
8.772959	8.388231	7.692329	8.776717	P	P	P	P	8.753127
7.934228	8.273322	7.486399	6.806047	P	P	P	P	8.15043
6.854717	6.680652	6.614432	6.544583	P	P	A		5.737814
4.598634	5.649274	5.354973	3.802246	P	P	P	P	5.209579
8.035721	8.555659	6.212145	7.151763	P	P	P	P	7.629876
5.699901			P					6.823268
8.175011	8.206314	8.281721	7.7973	P	P	P	P	8.426212
8.381455	8.564589	8.026785	7.812165	P	P	P	P	8.321501
13.14776	13.53689	13.6462	13.53641	P	P	P	P	13.19324
6.691087	6.244735	5.567033	7.121646	P	P	A		6.40764
			2.969538			M		
7.619284	7.230793	7.200385	7.117719	P	P	P	P	7.312677
7.142841	6.860006	7.064941	5.739104	P	P	P	P	6.711442
10.22608	9.881189	9.268357	8.769035	P	P	P	P	9.339962
6.355956	4.01344		7.926395	P		A		7.471685
8.72414	8.847577	7.955871	6.605562	P	P	P	P	8.555244
9.009116	9.664775	8.571651	7.334346	P	P	P	P	9.189667
5.687408		5.985859	7.454128	P		P	P	6.658876
9.821369	8.855916	9.416523	9.046118	P	P	P	P	8.297619
7.63626	7.886084	7.486366	6.137996	P	P	P	P	7.833127
7.687031			A					6.091812
11.17037	11.12018	11.8197	13.26795	P	P	P	P	12.02829

7.338301	7.892717	7.043737	4.412427	P	P	P	6.949226
7.239795	7.635539	6.302483	A	P	P		6.82005
7.406164	7.904898	7.020484	6.355695	P	P	P	6.7843
6.563135	6.142461	7.262802	4.102149	P	P	P	6.344237
4.084685			P				7.500293
8.401148	9.324561	8.228115	7.916936	P	P	P	8.792411
7.957932	7.300394	8.825361	9.500777	P	P	P	8.496603
			8.079737			A	
9.761122	9.240581	8.282084	7.872325	P	P	P	8.980576
	5.764678	7.341699		P	P		
		2.056669			P		
		4.516455			M		
9.765472	8.741713	8.707272	9.292578	P	P	P	8.48654
		6.856054			A		
5.974953	6.321457	5.984691	2.298656	P	P	P	4.880281
	6.845522	2.975962	3.953571	P	P	P	
7.528387	7.69459	8.144901	8.787572	P	P	P	7.792248
9.86829	10.11465	10.98221	10.86044	P	P	P	9.632584
		5.200025			P		
7.609743	7.588269	6.444791	5.759243	P	P	P	7.350221
7.528785	7.6235	6.775513	7.634081	P	P	P	7.69849
6.562794		6.141554	7.585755		P	A	6.602219
9.473661	9.360914	8.612895	8.43711	P	P	P	9.034355
6.262183	6.160736	6.822925	6.416324	P	P	P	5.212891
9.904282	10.29567	10.71326	11.5496	P	P	P	10.20956
7.969473	9.639937	8.008631	5.201472	P	P	P	8.788681
10.86927	11.82073	10.21128	9.263876	P	P	P	11.36618
8.458412	8.399661	7.541787	6.927041	P	P	P	7.8374
6.693564	5.982754	5.109084	A	P	P		6.225612
	6.284912			P			
7.565351	9.063821	8.435782	6.656673	P	P	P	8.57466
	2.847885			P			
5.310899			A				0.906302
8.398682	7.711525	8.097863	7.61754	P	P	A	6.730808
9.713591	10.58592	11.01536	10.03043	P	P	P	10.45302
	5.801543			A			
7.585188	7.974925	7.18063	6.439536	P	P	P	7.124966
0.291342			P				6.205288
5.737556	4.989779	4.600503	5.000711	P	P	P	6.321967
			6.635068			A	

			5.797777				A	
10.6759	10.37585	10.61352	9.936648 P	P	P	P		10.65409
6.678721	8.022317	7.876877	6.366146 P	P	P	P		7.686481
	6.795932	3.740295		P	P			
11.91031	11.7603	12.42486	13.77417 P	P	P	P		12.61324
	6.266674	8.106417		A	A			
4.877481	4.785363	6.093146	6.669968 P	P	P	A		5.395957
7.24926	7.870519	6.072711	6.457419 P	P	P	P		8.079872
	7.215045	6.88975	5.469739	P	A	P		
8.537783	8.387845	8.757022	6.944152 P	P	P	P		7.502937
5.118673		5.699987	6.604633 A		A	P		5.40388
7.665612	8.320173	7.131276	6.561862 P	P	P	P		7.506152
		4.746341			A			
			1.457973			M		
7.531806	7.461778	7.143098	7.09998 P	P	P	P		6.020709
8.498565	7.516854	7.854725	7.734228 P	P	P	P		7.281995
7.389539	8.308859	7.246481	6.74622 P	P	P	P		7.292356
1.328546	5.737846		P	A				5.674806
	5.378758	5.36389	3.756203	P	P	P		
		4.999253			P			
9.091655	8.738814	8.016546	6.759129 P	P	P	P		8.515914
7.43924	6.832909	3.910433	6.087097 P	P	P	P		7.866608
		5.807201	1.099556		A	P		
7.057571	7.382057	8.251427	6.130244 A	M	P	A		6.923656
	5.346543			A				
5.746535	7.084692	5.428352	P	P	P			6.306865
6.687387	7.868781	7.985981	8.483491 P	P	P	P		7.91409
6.931102			A					5.865862
5.387804	5.921115	4.962184	M	A	P			4.769214
7.592441	8.102307	7.345906	6.496319 P	P	P	P		8.209395
5.103663	6.657108	6.002443	P	P	P			6.755133
6.816488	7.348022	7.937419	7.441138 P	P	P	A		7.297836
8.008328	7.650174	8.521854	7.255096 P	P	P	P		6.642406
11.41351	11.50094	10.77175	9.999213 P	P	P	P		10.53513
5.467726	4.653861	4.937951	P	P	P			6.080778
9.912169	10.29181	10.3858	9.069118 P	P	P	P		10.11706
7.134217	7.149984	7.987758	8.1094 P	P	P	P		7.433502
7.564214	6.942093	6.465275	5.639969 A	P	P	P		6.436072
6.806703	6.124803	5.779952	6.304834 P	P	P	P		6.688956
	2.293018			P				

4.851868			A				0.038664
5.519792		6.177927	6.805716 P		A	A	5.536007
10.58364	10.74409	9.897913	8.999549 P	P	P	P	10.43235
6.244927	6.195481	7.136499	A	P	M		6.907936
6.014525	5.343001		5.613189 A	A		M	5.670404
5.603527		4.860279	A		P		6.534309
	5.707658	4.25796	6.525881	P	P	A	
6.67402	7.677799	7.453096	4.846593 P	P	P	P	7.013971
7.087407	6.556169	6.037957	M	P	P		6.825418
7.582361	6.88449	6.242553	2.713012 A	P	P	M	5.515741
		5.6871			A		
8.095434	7.864507	7.41562	6.601199 P	P	P	P	7.574583
2.328919	4.781436		6.132419 M	P		A	5.52526
5.631887	3.546804		A	P			4.847331
8.694999	9.088391	8.639598	8.544221 P	P	P	P	9.816759
7.956768	8.177839	7.041985	6.378599 P	P	P	P	7.104997
9.080221	7.917155	9.341235	8.290791 P	P	P	P	8.552855
5.95793	7.64395	6.718585	6.530314 P	P	P	P	7.952424
6.82968	8.24857	7.611176	7.159216 P	P	P	P	7.944872
5.802913	6.501968	6.288493	7.123001 P	P	P	P	6.196905
5.583967	3.320308		A	P			5.864209
	5.162413			A			
	5.467777		8.376993	P		P	
7.148011	6.740442	8.758483	8.001926 M	P	A	P	6.504184
6.915701	6.808286	6.930401	8.251414 P	P	P	P	7.324185
7.443129		3.320071	4.220179 A		P	P	6.026331
6.034496	6.192865	6.450302	4.500157 A	P	P	P	5.645385
9.671353	10.10554	10.65177	10.98707 P	P	P	P	9.647048
		4.110735			P		
	5.759811	5.875262		A	P		
6.97055	6.787017	6.257027	P	P	P		5.539877
5.335046	6.514342	6.396799	6.739305 P	A	P	A	6.508635
	5.261945	6.074971	3.488515	M	P	P	
9.941963	9.246591	8.511828	8.288528 P	P	P	P	9.462983
		6.12041	5.730826		A	A	
7.024469	6.573709	6.8564	7.91734 P	P	P	P	7.324147
8.526639	9.106518	8.632626	7.813152 P	P	P	P	9.273946
6.206896	7.334566	6.791295	0.983802 P	P	P	P	6.510076
	6.935205	3.341091		A	P		
9.225407	9.28967	8.699863	8.251143 P	P	P	P	9.344396

5.855895	6.947152	6.877522	7.282043	P	P	P	6.919844
5.704033	4.211231		A	P			2.818493
9.502955	9.446733	10.80766	10.97393	P	P	P	9.89003
6.102542	5.749514	5.921763	A	P	P		5.084408
		9.018342	10.00108		A	A	
6.89534	7.242322	6.796711	3.97674	P	P	P	7.332387
6.366698	7.481697	6.079533	6.66618	P	P	P	6.293697
4.991336			4.758753	A		P	0.880196
8.987075	8.715862	7.969599	8.212274	P	P	P	7.962537
5.874521	5.294018		A	A			4.700227
7.376551	6.934315	7.065823	6.515783	P	P	P	7.682619
9.254992	8.981471	8.217827	7.504659	P	P	P	8.8443
	6.631316	3.563509		M	P		
7.599616	7.499438	6.540741	5.073273	P	P	P	8.015589
8.99811	9.550706	8.067718	8.142518	P	P	P	9.643177
6.638611	6.739178	5.713266	P	P	P		5.861237
7.853718	8.413963	8.752381	7.977174	P	P	P	8.128634
9.43982	10.14542	9.475167	8.87363	P	P	P	9.868114
5.026717	5.656159	5.065595	M	A	P		4.969441
5.716206	5.818853	6.11766	6.012659	P	A	M	5.761896
5.016669		7.088636	A		A		3.397099
7.820156	8.223771	7.285539	6.281612	P	P	P	7.16255
6.762844	6.172678	5.279499	6.95124	P	P	P	6.209423
10.21944	10.08632	9.460477	8.74496	P	P	P	9.427181
7.881793	8.159121	7.3096	6.809281	P	P	P	8.01393
		3.271889			P		
7.301331	7.634878	6.18713	6.931713	A	P	P	6.445697
		5.855953	5.265142		P	P	
7.791827	7.427501	7.412864	6.701495	P	P	P	7.397146
	2.203692			P			
5.002162			2.03974	A		P	5.195925
		1.495706			M		
		3.204093			P		
5.214978			5.8897	A		A	5.033332
	5.498159			A			
8.31564	8.822632	8.521839	7.584696	P	P	P	8.27453
6.474889	6.181733	6.803603	7.545765	P	P	A	7.065406
5.65083	6.626299	8.156979	7.796825	P	A	P	7.016582
		7.656242	8.412652		A	A	
5.893802	6.201493	5.683714	P	A	A		6.897462

6.307263	5.851719	7.50155	8.082402	P	P	P	7.17577
8.020891	8.864989	8.504025	7.709642	P	P	P	8.553587
8.71348	8.446326	8.718511	7.989257	P	P	P	7.614777
6.705919	6.689392	7.228696	6.472119	P	P	P	6.828857
8.085629	7.413744	8.604765	8.105707	P	P	A	8.153317
3.784871		5.398593	P		P		6.025959
12.94906	11.23238	12.94103	12.52294	P	P	P	10.57111
7.625842	8.097599	7.424372	8.214819	P	P	P	7.663538
8.793285	8.941641	8.511601	8.253164	P	P	P	8.159731
6.984726	5.619427	7.027015	6.908733	P	P	A	6.177113
5.909433	6.580377	7.025436	7.482177	P	A	P	6.440554
6.926883	7.007251	6.273897	P	P	P		6.529464
5.62176	0.906751	4.772379	6.103686	P	P	A	5.912298
4.879159	4.858596		P	P			5.746928
5.481549	6.563242	4.282661	P	P	M		5.809197
7.052236	6.520757	6.220935	A	P	P		5.015877
6.447922	5.237048		A	A			4.824722
	6.984484	7.857895		P	A		
8.333987	7.268063	7.689413	6.799816	P	P	P	6.419845
6.067346		6.546581	A		P		4.737195
9.274748	9.568699	8.723298	10.90128	P	P	P	10.25345
11.26002	10.879	10.34157	9.215841	P	P	P	10.41456
11.90767	11.93237	11.28648	10.62037	P	P	P	11.12681
9.056773	8.942125	7.881539	8.18846	P	P	P	8.370001
5.111602	6.149883	6.387323	P	A	P		7.119591
9.18707	8.861787	7.719928	8.075407	P	P	P	9.241788
9.993145	10.27185	10.02253	8.568894	P	P	P	9.708051
	5.760207			A			
5.643916	5.096309	6.343155	6.804512	P	P	A	4.999859
9.806438	10.47168	9.783872	8.820375	P	P	P	9.475929
			6.116733			A	
4.77292		5.387554	7.236182		P	P	5.31381
7.336499	7.16384	7.873904	8.29297	P	P	P	7.505508
5.471123	4.211089		A	P			5.042488
	5.392059	5.793702		A	A		
6.715993	5.382834	2.23617	1.596881	M	P	P	5.368602
8.111755	8.975225	6.897985	7.532144	P	P	P	8.165785
7.144655	8.61892	8.236374	8.340115	P	P	P	8.898506
		6.312961			A		
5.350615			6.356665	M		A	5.140353

9.952198	9.561574	8.815932	9.454598	P	P	P	9.215861
2.652843			P				5.077419
	6.533675		6.527122	P		A	
6.967244	5.95411	7.059672	8.088624	A	P	P	6.674105
8.764613	8.716751	9.649462	8.767839	P	P	P	7.945633
5.831787	7.217495	5.684856	A	P	P		6.200618
10.16916	9.600844	9.724903	9.156753	P	P	P	9.137474
5.265273	6.886303		P	P			5.354098
5.945231		1.463661	2.423181	A	P	P	2.522693
		7.019345			P		
9.72879	9.447845	10.42619	10.50077	P	P	P	8.865745
8.749892	9.43506	10.63161	9.167952	P	P	A	8.425429
11.51304	11.31208	10.07626	10.18424	P	P	P	11.08817
2.006025	4.984463	5.703083	P	P	P		7.009713
6.131642	6.187603	7.394512	6.57648	P	P	P	7.231884
1.200009			P				5.49451
	6.609127		8.091714	A		A	
4.483353	6.040849		6.487653	P		P	5.818854
5.488306	6.530326	7.228087	6.711168	P	P	A	6.632634
	5.230354	6.46627	7.085386	P	A	M	
2.96307			P				5.504496
7.66416	7.892239	5.780798	A	P	P		7.867904
10.56061	11.49261	11.06331	9.530546	P	P	P	11.11475
5.339434	5.401702		P	A			5.994003
8.457011	9.206112	9.679509	8.210335	P	P	P	9.127479
9.187773	10.44387	8.994514	9.037908	P	P	P	9.945899
		2.635136			P		
4.375693	5.950666		5.880138	P		P	5.453188
	2.555806			M			
5.605568			6.992158	P		A	6.09757
7.460123	7.636608	7.307872	6.825208	P	P	P	7.229091
4.636271	6.459912	6.14976	P	A	M		6.47678
9.919706	9.065582	9.393131	9.009685	P	P	P	8.453938
9.764405	9.711305	9.959961	10.20947	P	P	P	9.599925
7.318172	6.827336	6.913397	5.877518	P	P	P	7.134122
10.11145	9.926441	10.05238	11.15502	P	P	P	10.31935
7.268997	6.438232	7.120494	7.185781	P	A	P	6.961415
4.868815	4.89946	6.386859	6.62778	P	P	A	6.163416
3.583235			M				6.078209
7.427037	8.426538	7.389502	7.295453	P	P	P	7.986914

8.330026	10.36375	9.16711	8.675738	P	P	P	9.66209
5.890346		5.980661	6.350898	A	A	A	6.318716
8.563286	7.756704	7.642213	7.06959	P	P	P	7.335253
7.781741	8.173818	8.81247	8.876532	P	P	P	7.915985
8.926342	9.155167	8.395813	8.305438	P	P	P	9.236477
2.398354			M				5.723647
8.203769	7.67314	7.273471	7.266863	P	P	P	7.872622
11.81125	11.76112	12.12708	12.962	P	P	P	12.08781
	5.792698	6.353766	6.960999	P	P	A	
6.296371	6.303097	7.971831	7.947305	P	P	A	6.885741
8.403949	8.992523	7.641957	7.453641	P	P	P	8.439169
	5.366419		5.528358	P		P	
9.185827	9.259727	8.200398	7.489038	P	P	P	9.261057
5.494611	3.840751		P	P			4.790491
		3.877934	6.289222		M	P	
7.618375	8.642036	7.705202	7.135461	P	P	P	7.882354
	5.121973		6.555426	P		A	
1.604234	6.712051	7.323424	P	P	P		6.424152
5.192658	5.718802	5.685134	P	A	P		5.688316
7.002839	6.263983	8.741135	9.043839	M	P	A	7.680283
9.095184	9.066377	9.629334	9.181571	P	P	P	8.731133
	5.391415	5.794828	6.346487	A	P	A	
9.51873	10.39133	9.637647	9.322882	P	P	P	9.895631
9.362514	9.012577	7.260559	8.526509	P	P	P	9.339602
8.577718	7.387945	5.950215	7.523579	P	P	P	8.465068
6.151532	6.088727	5.09674	A	A	P		6.59397
9.779826	10.61805	9.251039	7.775204	P	P	P	9.874553
8.618591	8.058054	8.417388	8.85305	P	P	P	7.777809
8.329515	7.316886	7.94099	7.268902	P	P	P	7.862104
7.460185		5.274469	6.411054		P	P	6.164209
7.475404	6.260178		A	M			6.75136
	6.402213	8.340598		A	A		
7.238923	7.482666	7.090879	7.249103	P	P	A	6.737144
5.930471	6.2296	3.780721	A	A	P		6.227119
6.669936	7.709972	7.068314	9.043408	A	P	A	7.440967
7.513945	7.88284	8.550591	9.507767	P	P	P	7.722632
			8.276629			A	
6.989854	7.298934	8.197062	8.590201	P	A	P	7.82688
8.083444	7.168457	7.977434	8.6644	P	M	P	6.689177
8.477433	8.422778	8.57442	9.184134	P	P	P	9.002536

5.550393	6.459245		P	A			6.708423
			6.950806			A	
		5.603181			P		
			1.97286			P	
9.462665	10.28495	9.667729	8.570189	P	P	P	10.27454
6.030312	6.70126		P	A			6.056751
			6.040002			A	
8.003035	8.017928	8.169866	6.480778	P	P	P	7.180749
5.445619			A				3.814965
6.396212	4.905728		5.999813	A	P	P	6.673818
	6.3966	6.716965	5.929615	A	A	A	
4.640884	6.112155	4.998496	P	P	P		5.877966
5.793609	6.882409	6.878769	7.807842	P	P	P	8.080771
4.86402	5.584385		M	A			6.195597
		4.629889			A		
7.726708	7.994936	6.442992	P	P	P		7.908491
	7.08318			P			
	7.771779		7.5716	P		P	
6.888714	7.269461	7.255798	A	P	P		5.200366
6.211128			A				4.157105
8.852247	8.853964	9.233224	8.940881	P	P	P	8.742158
	5.616765	3.23894		P	P		
		4.640185			M		
6.387826	5.38864	4.285052	A	P	P		6.486045
4.12755			P				6.195187
5.576554			A				3.560232
		6.158175	6.751247		A	A	
7.223389	8.073428	7.32839	6.522176	P	P	P	7.495158
	7.37889	7.322387	6.820685	P	P	P	
11.05734	10.83971	11.52265	11.31042	P	P	P	10.88792
	7.14892	6.112382	6.457488	P	P	P	
6.406653			4.271866	A		P	2.593902
5.433823			A				4.405147
8.016246	6.945852	5.68578	7.72022	A	P	P	6.118566
5.356438		3.686066	6.350528	A		P	5.082222
9.275038	9.65377	10.37407	10.07887	P	P	P	9.091795
	5.191425	6.251633	6.963919		P	P	A
7.773527	6.992348	3.91934	7.112415	A	P	P	4.230681
8.384427	8.114798	6.747627	7.878456	P	P	P	6.796665
7.373661	5.918602	0.880693	6.756818	A	P	P	1.368533

6.256568		6.457085		M		A		6.320464
6.572051	6.258384	4.260846		P	P	P		6.215756
	6.011543	5.228942			A	P		
6.73335	6.3054	7.534926	7.092759	A	A	A	A	5.192235
		6.955112				A		
8.684628	8.009149	10.00013	10.53869	P	P	P	P	8.294734
8.129711	7.53902	7.51373	7.024371	P	P	P	P	6.935134
7.179518	7.816382	8.076803	7.612029	P	P	P	A	7.129681
10.98527	11.64024	11.10705	10.78597	P	P	P	P	12.35998
9.056153	7.750964	8.884381	8.926119	A	A	P	A	7.531537
		6.027076				A		
7.905039	8.428369	7.742971	7.810992	P	P	P	P	7.047887
5.313415	5.914773	6.310941	6.37017	P	P	P	P	6.360479
7.025141	7.752785	6.994986	6.987357	P	P	P	P	6.413403
6.637702	6.093752	5.624257	6.63939	P	A	P	P	7.549042
8.225265	8.701378	8.420621	7.314096	A	P	M	P	8.003569
6.649127	7.142388	6.081686	6.468709	P	P	P	P	7.150299
		2.393752				P		
8.840329	8.851109	8.376485	7.781211	P	P	P	P	7.781392
6.690375	6.200661	7.435669		A	P	A		5.02396
8.448595	7.921006	7.204543	8.005581	P	P	P	P	8.520313
9.369284	8.766588	8.857276	8.465837	P	P	P	P	8.186888
		7.062326				A		
8.702665	8.798697	7.365928	7.600452	P	P	P	P	8.381494
7.408017	7.88985	6.635067	7.026799	P	P	P	P	7.562242
7.463738	7.042947		5.175046	P			P	7.263886
10.81661	11.11119	10.73225	9.829197	P	P	P	P	10.83247
9.158389	8.2953	8.235305	7.070937	P	P	P	P	8.02089
6.48831	7.513399	6.33551		P	P	P		7.177524
9.226817	9.364176	8.857748	7.833214	P	P	P	P	8.57775
7.916602	8.168293	6.795255	6.520228	P	P	P	P	7.697551
10.17843	9.673913	9.538859	9.62122	P	P	P	P	10.65699
		6.920927				P		
7.576361	7.233899	6.49681		P	P	P		7.350866
6.524204	5.299279			A	P			5.913847
9.177839	8.964206	8.305932	8.255688	P	P	P	P	8.068124
		6.89726					A	
5.570551			6.859966	P			P	6.618203
6.906177	5.118987	6.268185	7.200582	A	P	A	P	5.004026
	5.978498				A			

8.615922	9.216081	8.776215	7.674699	P	P	P	7.878501
8.822094	7.890841	9.242642	9.502163	P	P	A	8.259748
8.698154	9.964923	8.381302	8.107529	P	P	P	9.628321
7.026073	6.483027	7.177288	5.084063	P	P	P	6.924664
4.403715	4.41382		P	A			5.337816
10.49081	8.815145	10.05403	9.175768	P	P	P	7.679413
8.449914	9.754285	8.233612	7.44964	P	P	P	8.171603
		8.243756			A		
8.030087	9.121299	8.875555	7.234732	P	P	P	8.787068
			2.345355			P	
6.878384	6.295049	6.922966	8.028307	P	P	A	7.212874
6.692924		7.676858	7.497131		P	P	5.740665
7.127225		7.181131	7.941939		P	A	6.622837
12.31288	12.6936	11.88623	11.21696	P	P	P	12.34753
6.560611	6.919521	6.586434	A	P	P		6.325132
5.121593			A				2.425539
7.046588	7.094543	7.288954	4.956518	P	P	P	7.397303
5.514499			4.264998			P	6.819728
	6.393792	5.681506		P	P		
4.485365	4.986246	0.951487	M	P	M		5.19176
5.590038	6.14688	1.226796	4.189836	A	P	P	6.599894
	6.29362	6.607421	7.242551	P	A	A	
7.083919	7.133905	7.574338	6.05712	P	P	P	6.551504
	4.623444	6.890942	6.505855	P	P	A	
9.451537	9.321125	8.46174	8.181499	P	P	P	9.003194
7.631461	7.708744	6.620263	6.61748	P	P	P	7.138613
9.450088	9.87489	9.03999	8.641887	P	P	P	9.004496
8.590405	8.305516	9.491172	9.820889	P	P	P	8.530831
	5.7862	7.510498	7.556882	P	A	A	
7.257889	6.865882	8.341103	7.134322	P	P	A	6.642524
			4.024516			M	
7.068046	6.642439	6.802175	7.115127	P	A	M	7.494946
8.681224	8.912418	8.095733	8.202505	P	P	P	8.78462
6.546475			A				4.912353
5.662732			A				0.323683
5.464738	4.385995		P	P			5.823935
8.1815	7.552447	7.752	7.314076	P	P	P	8.049749
6.198897	5.426296	6.153334	6.952423	P	P	P	7.417183
6.142915	7.334243	6.633133	7.417868	P	P	P	7.530393
10.71654	10.86549	9.932942	9.222692	P	P	P	10.13994

7.795557	7.965405	8.56669	8.261779	P	P	P	7.454347
7.876987	7.313363	8.408261	7.867368	P	P	P	7.927088
2.669869	6.30347	7.377972	P	P	P		6.050812
	5.925475			A			
5.022615	6.51615	5.251419	6.250329	P	P	P	5.943201
5.765035			M				6.88223
5.765225	6.190819		8.12384	P	A	A	5.646592
6.169704	5.822552	3.447341	7.532899	M	P	A	6.178224
8.850415	9.15278	9.033639	7.925005	P	P	P	8.682379
5.510954	5.343059	6.016033	A	A	P		5.601893
7.651068	6.795756	7.313787	7.406033	P	P	P	7.662977
	5.748357		7.114632	P		A	
			6.2427			A	
7.238336	7.000092		8.360345	A	P	A	6.448703
12.33956	11.897	11.49302	11.51732	P	P	P	11.51123
7.130749	6.626946	7.771247	8.723907	P	P	P	7.387018
	5.861857	5.289317	6.062317	P	P	P	
7.377209	6.941981	6.835859	7.716856	A	P	A	6.469672
6.90725	7.381743	6.843762	6.765347	P	P	P	7.263152
	8.134777	7.054406		P	P		
12.29496	12.1564	11.47503	11.76264	P	P	P	12.11939
5.935813			6.370027	A		A	3.747728
8.319839	9.18058	7.647927	7.889505	P	P	P	9.154635
6.645671	6.663641		5.359068	P		M	7.315681
6.717744		5.690088	4.978652	P	P	P	5.667074
6.594869	6.613108	6.157808	3.242025	P	P	P	6.498799
6.812159	7.820704	6.547322	6.412689	P	P	P	7.257001
			4.886036			M	
6.213675	6.492593		2.355821	P	A	P	5.858195
5.160822	5.660241	6.17421	P	P	A		6.105321
7.763259		9.624689	9.168718	P	P	A	6.56514
12.03208	11.31667	12.74254	12.72392	P	P	P	10.82159
7.166115	7.580387	7.856257	7.535321	A	A	A	6.057201
6.487867			7.27809	A		P	5.388699
5.079456	6.225264	4.975726	7.094631	P	A	M	5.991817
5.130333	4.812065	6.095142	A	P	P		4.549608
5.417147	6.150087	5.189449	7.512953	P	P	M	6.396933
7.270917			A				5.217158
8.152441	8.407292	7.673837	7.636246	P	P	P	7.607171
7.366108	7.286534	6.36407	5.954101	P	A	P	6.833218

	5.326657		6.133019	P		P	
5.557903	4.96946	5.620931	6.702192 P	A	P	A	5.093513
7.663765	6.496097	7.274098	6.641646 P	P	P	P	6.465941
10.18604	10.02797	10.47273	9.910371 P	P	P	P	11.60262
7.116308	7.183368	6.558147	6.48384 P	P	P	P	6.649489
	5.502693	1.87258	5.359536	A	P	P	
7.295379	6.920617	5.551515	6.928464 P	P	P	P	7.165259
10.26058	10.46116	9.750447	9.315312 P	P	P	P	10.40625
6.186738	5.521962	6.721844	6.181448 A	A	A	P	5.428207
7.250831	6.106762	6.958871	7.22767 P	A	A	P	6.978756
5.189822	5.53483	5.549111	5.244179 P	P	P	P	6.220923
8.886535	10.10895	7.930821	7.45487 P	P	P	P	9.614092
7.380784	7.101918	8.262819	7.272678 P	P	P	P	6.808988
6.505096	5.952641	6.969962	6.736203 P	P	P	P	6.40505
	6.243131	6.980169	4.154943	P	P	M	
10.86652	11.89461	10.53304	9.89616 P	P	P	P	11.49963
7.011361	7.141666	5.469799	5.491869 A	P	P	P	4.867279
6.943451	8.402214	7.804287	9.361051 P	P	P	P	8.473737
6.385162	4.778824		6.441865 A	A		P	5.764986
5.823527		7.819106	M		M		7.507736
7.225438	7.066354	6.54059	2.789666 M	P	P	P	6.75166
	4.993081	6.016638		M	P		
5.54653	6.244456	5.549582	3.572684 P	P	P	P	6.039033
7.693724	7.496115	6.850826	8.727906 A	A	P	A	8.085441
10.34094	10.76995	11.43683	11.17195 P	P	P	P	11.31496
7.093039	7.324009	7.187243	6.263373 P	P	P	P	6.978563
8.053519	8.401243	8.365707	7.626218 P	P	P	M	7.847421
12.15944	11.55889	11.40497	10.79008 P	P	P	P	10.97793
7.117324	6.623514	6.855973	6.302257 P	P	A	P	7.119072
11.65668	11.22452	11.11397	10.51742 P	P	P	P	11.20339
8.746572	7.882614	8.172282	6.625341 P	P	P	P	8.788129
5.948945	5.114279	5.039359	5.5227 P	A	P	P	5.077518
	6.196961		6.671047	A		A	
8.727706	9.110106	8.301337	7.625214 P	P	P	P	8.429072
6.12198	6.274311	6.925231	M	A	M		6.013125
6.175647			A				3.052769
7.741841		7.616163	8.174484 A		A	A	2.796891
11.18016	11.16418	11.62228	13.11782 P	P	P	P	11.83958
7.216608	6.988196	3.718871	4.586906 P	P	P	P	7.692409
12.85072	11.84144	10.37023	10.79027 P	P	P	P	12.14309

4.888853				M				6.549242
6.214755	6.021413	5.645135	5.829428	P	P	P	P	6.590683
10.52294		12.47327	12.10606	A		A	A	10.60194
5.320348				A				1.599011
9.070816	8.852538	8.409413	7.829164	P	P	P	P	7.742607
7.630554	7.796078	9.443357	9.612671	P	P	P	P	6.630684
8.1883	8.060219	10.19363	11.41049	P	P	P	P	7.895765
	6.319128	7.254254	7.413076	A	A	M		
9.930076	10.2975	9.665284	9.071804	P	P	P	P	9.832377
		2.383475			P			
7.281626	7.467906	6.661695		A	P	P		4.945272
			6.57487				A	
8.934002	8.964334	7.521349	7.767952	P	P	P	P	8.966557
7.001668	7.145783	5.857004	4.884177	P	P	P	P	7.483081
7.752575	7.795943	7.068366	5.802818	P	P	P	P	7.164413
6.906946	6.796094	6.08907	6.769829	P	P	P	P	7.061341
6.794539	6.045562	5.084524	6.270161	A	P	P	P	6.359299
6.621409	6.885335	7.648743	7.701079	P	P	P	P	7.578168
5.8364	5.264052	2.016756		A	P	P		5.339475
6.687843	6.830013		7.867938	A	P		A	5.947397
8.266974	7.27449	8.502844	10.01367	P	P	A	P	8.030198
5.536908	3.425653	5.328666		P	M	P		5.064281
9.523535	9.072292	10.75497	11.78056	P	P	P	P	10.7112
6.374034	5.197218	6.614977	6.93521	P	P	M	M	6.56147
	2.129975		6.644662	M			A	
6.948741	8.454654	6.667399	7.129951	P	P	P	P	8.252776
			6.024492				A	
	5.137458			A				
8.644276	8.185045	7.738784	7.630907	A	P	P	P	7.89115
9.623326	9.523451	11.99026	11.86293	P	P	P	P	9.887255
5.874021	5.77882		5.253544	P	A		P	4.880776
5.355761	5.55751	5.510092	5.189399	A	P	P	P	5.24933
8.215902	8.42765	7.483175	7.513788	P	P	P	P	7.201446
6.406852	6.922485	6.111383	7.440615	A	P	P	A	6.041587
6.926201	6.643814	7.802403	8.961136	P	P	P	P	7.304551
7.459001	6.482082	7.406663	7.230093	P	P	P	P	6.713741
7.301902		5.864427		P		P		6.547836
7.192332	6.76228	8.497429		P	A	A		6.518843
5.237795	6.321993	4.086135		P	P	M		7.070309
8.033436	7.732493	7.954499	9.060095	P	P	P	P	8.067323

5.954653	5.967008		A	A			2.104478
5.34372			7.495156 P			P	6.368525
5.187585	6.214672	3.468123	P	P	P		5.902209
9.026796	8.874602	7.366897	7.381083 P	P	P	P	9.125104
6.774732	7.824323	3.72452	5.599006 P	P	P	P	7.444021
7.916874	9.170402	5.454238	4.784863 P	P	P	P	8.756249
12.64714	12.55299	13.27757	14.36612 P	P	P	P	13.06092
7.013529	6.395769	6.008939	5.1767 A	P	P	P	6.422421
7.896316	7.260058	7.983738	6.549742 P	P	P	P	6.778565
	5.79761		6.320563	A		A	
8.901896	9.085805	7.969796	8.745527 P	P	P	P	9.09117
		6.630751	6.614383		A	P	
7.532393	8.040369	7.620828	6.299687 P	P	P	P	7.772354
7.545827	7.860678	8.182439	7.239749 P	P	P	P	7.577724
			7.080063			A	
7.452753	7.48123	7.257389	7.455231 P	P	P	P	6.902301
7.21767	6.852305	8.107318	8.009888 P	P	P	P	6.973918
		4.816561			P		
7.62262	8.415136	8.350119	6.06733 P	P	P	P	7.732481
4.381861			P				5.944296
7.094313	6.187121	7.338939	6.817467 P	A	M	P	8.277694
	5.242646		4.613588	A		P	
6.120715	4.246778	6.876163	7.49729 P	P	P	P	6.439289
3.730463	5.361322		M	A			5.685515
5.883363	5.739578	6.836957	6.328406 P	M	A	P	7.03215
6.600587	5.229802	6.947903	7.000979 P	P	P	A	6.566958
6.292283	5.523008	6.191316	6.872381 P	P	P	P	6.506382
	5.184252	6.501657	7.297707	A	A	A	
6.225514	7.227259	6.64377	6.043048 P	P	P	P	7.255375
5.737405	5.816324	4.542517	A	P	P		4.06488
5.800173	4.316829	6.386574	7.009682 P	P	M	P	5.676503
8.873331	9.275807	8.702683	8.116829 P	P	P	P	8.604225
		5.020924	2.916928		P	P	
			6.42093			A	
		5.109385	7.344484		P	P	
7.19307	7.597869	4.969847	3.329659 P	P	P	P	7.312907
8.373127	8.897408	9.278808	8.600927 P	P	P	P	8.93463
4.764066			M				6.656174
2.605353			P				6.457665
10.87721	10.50077	9.766966	9.239249 P	P	P	P	9.680384

8.014914	7.811546	8.382746	8.808066	A	P	P	A	7.636473
8.735959	8.05577	9.48102	7.797672	P	P	P	P	8.85039
6.526308	6.098607	6.191334	5.146665	P	A	P	P	6.583532
7.325472	6.937128	7.376378	6.499079	P	P	P	P	7.038724
4.749049	5.467729			M	P			5.807921
10.26102	10.20497	8.929056	8.709048	P	P	P	P	10.23152
10.21191	9.938244	9.20503	8.062552	P	P	P	P	9.881068
4.910865	5.244291			P	A			6.325125
	5.654714	2.659721	3.64667		P	P	P	
	7.47434	6.638992			P	P		
5.719111	5.548533			P	M			7.221633
8.307946	9.233033	8.058452	7.571653	P	P	P	P	8.737705
		4.2396				M		
6.332387	5.816003	6.399693	6.836708	P	P	P	P	6.072751
4.083042				M				6.857112
	5.048346				A			
5.205096	4.953893		1.869314	P	M		P	4.609565
6.367882		7.438368		P		A		7.152644
7.476796	7.017036	6.839529	6.843213	P	P	P	P	7.348472
	6.988116	3.288815			A	P		
			7.046174				A	
6.580622				A				5.167917
		5.934697	6.735458			A	A	
5.231479				P				6.426687
6.582178	7.241098	6.745164	2.110489	P	P	P	P	6.377527
7.581724		8.274454		A		P		6.819648
8.258835	7.717448	8.482889	9.039605	A	P	A	M	7.936163
6.219727	6.152574	5.979292	7.008717	P	P	P	M	7.341046
4.502495	7.298989	2.341817	5.516037	P	P	P	M	7.299017
7.799306	8.182813	7.957065	7.921654	P	P	P	P	8.74036
5.42594	5.255148	6.289097	7.166061	P	M	P	P	6.825096
10.81203	9.62276	11.85919	12.30934	P	P	P	P	9.112365
4.87196		7.369348	6.929576	P		P	P	6.621931
	5.848182		6.210312		A		A	
	5.782376		6.567755		P		A	
7.154862	7.010887		3.822696	P	P		P	6.625824
6.905322	6.526003	6.475929	5.819063	A	P	P	P	6.413857
7.707314	5.609644	7.150624	7.663468	P	A	P	A	6.983298
	4.12848				P			
9.656543	9.150728	9.065048	9.225054	P	P	P	P	8.618086

9.63212	7.662573			A	A			7.88015
11.45351	11.61245	10.69418	10.75902	P	P	P	P	11.66557
		6.702013	7.072772			A	A	
	2.306307	1.378962		P	P			
		5.155873			A			
5.681391		5.690251		P	P			7.160836
9.641533	8.572619	10.16025	9.635182	P	P	P	P	9.191104
5.775554	5.475676	6.310966	5.797937	P	A	P	A	5.527224
			3.052549				P	
4.733721		2.394376		P		P		5.68293
6.309751	7.420662	6.835654	6.7642	P	P	P	P	7.19097
6.508662	5.436466	4.619419	6.324437	A	P	M	P	6.22669
6.90299	6.899388	6.772729	8.188064	P	P	P	A	7.322311
	3.163513			P				
6.43189	7.068371	5.751569		A	A	P		5.211372
7.871035	5.828301	6.21408	6.758869	P	P	P	P	5.728449
10.43982	10.03902	9.504987	8.700133	P	P	P	P	9.77236
6.293764			7.589582	A			A	6.251829
		4.650092				M		
7.641886	8.217504	7.384789	7.083038	P	P	P	P	7.991467
7.438837	6.525466	6.973175	7.17415	P	P	P	P	6.38707
5.576388		5.584581	7.135076	A		A	P	5.57145
7.909065	8.364888	8.146172	7.273327	P	P	P	P	8.214213
7.443749	6.773734	5.188336	6.416957	A	P	P	P	6.093465
5.327709	4.378151	3.474038		A	P	M		4.750284
8.80176	8.173507	7.65964	7.236633	P	P	P	P	8.299647
		6.339408	6.261608			A	P	
9.187671	9.443981	9.568651	10.1423	P	P	P	P	9.367079
7.20824	7.3971	7.277306	2.47083	P	P	P	P	7.637922
7.038683	7.31904	6.611207		A	P	P		5.169827
	4.378839	1.42755	4.563873		P	P	M	
	5.816396			A				
11.76601	11.68116	11.46462	10.67708	P	P	P	P	11.23868
8.925782	8.725914	8.456225	7.65069	P	P	P	P	8.234897
5.343095			6.876561	P			A	6.173469
5.029664	5.562816	5.587054	0.846077	P	M	P	P	6.255565
	7.670147	7.172587			P	P		
5.901681	6.671681	4.677095		P	A	P		6.373745
8.230879	8.57318	7.659528	6.739914	P	P	P	P	7.740052
	6.075969		5.34885	P			P	

	4.315962	6.21079		M	A		
	2.691905			P			
9.658327	9.696737	7.985205	8.293274 P	P	P	P	9.421552
9.982064	9.178565	8.288318	8.973833 P	P	P	P	9.973365
8.101083	8.693263	8.169028	7.22932 P	P	P	P	8.700356
10.79653	11.88299	12.51661	12.32853 P	P	P	P	12.43928
10.723	11.79435	12.30822	12.12964 P	P	P	P	12.18445
6.463851	6.638903		8.031338 P	A		A	7.209701
	5.933113	5.566251	6.012411	A	P	A	
6.817246	7.139266	6.114146	6.373903 M	P	P	P	6.896275
5.614643			7.049118 P			P	6.63961
9.173975	7.273857	6.861069	8.051839 A	P	P	P	7.498243
7.707571	5.639132	6.67142	5.637166 P	P	P	P	6.711682
7.998661	6.334417	5.050506	P	P	P		7.21365
	6.240655	6.417388	4.85851	P	A	P	
5.940198	5.571255	6.815758	7.441936 M	A	P	P	6.139213
9.249084	9.38667	7.570936	9.05443 P	P	P	P	9.844507
5.08829	5.874199	7.024029	7.87101 P	A	A	A	5.912679
	5.890693	5.208725		A	P		
	3.734781			P			
5.609088	2.095042		P	P			6.057636
3.899498		3.005498	P		P		5.87743
5.362149	5.434342	1.213444	A	A	P		5.654792
		2.901987			P		
	5.43341	5.429421		A	A		
7.672316	8.209841	7.280737	5.461817 P	P	P	P	7.714869
		6.560859			A		
6.622546	7.372644	6.886717	3.999984 P	P	P	P	7.679115
5.320106	6.125782	2.966806	5.986401 P	P	P	P	5.601953
4.530649	5.460069	5.095959	6.80991 P	A	P	A	6.247248
	4.344749			M			
	5.602183			A			
6.291384	5.298494	4.051282	A	A	P		6.271362
		3.560409			P		
6.837645	6.13974	6.045298	A	A	P		5.498541
		7.938428			A		
	5.950337			A			
	2.379341	5.645231	6.63037	P	P	P	
	5.185572			A			
10.29348	10.85462	11.36101	11.54419 P	P	P	P	10.85032

6.396554	6.410783	6.334006	4.675276	P	P	P	6.293548
4.101692		4.199435	M		M		5.136033
	6.350881			A			
		6.342878	5.70922		A	A	
	5.727979	1.617861		A	M		
7.935442	7.284757	8.036274	6.686312	P	P	P	7.722769
6.876007	6.383915	6.463605	6.837343	P	P	A	6.526005
	7.697467	7.110395		A	P		
6.817983	6.806716	7.73004	P	P	M		6.916361
	5.918109			A			
	7.076919	3.910631		A	P		
6.312268	6.104179		4.972008	P		P	7.666392
	5.29561		2.201097	P		P	
6.801822	7.406706	8.142731	8.109026	P	P	P	8.27281
7.569639	7.255479	7.605579	8.611335	P	P	P	7.698192
	3.894623			P			
6.326551	6.56186	7.333127	7.864235	P	P	P	7.416728
6.128684	5.987324	7.121789	7.428742	A	A	P	3.591711
10.98834	10.71415	10.27623	9.320455	P	P	P	10.33366
			6.835871			A	
5.574128			4.947499	A		M	5.898944
5.463224	5.626916	3.357574	A	A	P		5.860467
7.006079	7.001869	7.888575	8.426227	M	P	P	7.04612
6.795782		7.598445	M		A		6.449262
7.183905	6.768649	6.151022	3.472119	P	P	P	7.105849
8.439975	8.184532	7.182307	7.907819	P	P	P	8.794028
	2.520155			M			
9.615279	8.499196	6.826216	7.776438	P	P	P	7.713597
		7.158151			A		
7.112109	6.130943	6.425502	A	A	P		5.470174
6.986179	6.969274	7.600405	8.126479	P	P	P	7.031759
7.883936	7.422699	7.447649	6.06861	P	P	P	6.872106
	6.537548	7.045	6.734296	P	P	A	
6.444724	6.374523	5.209334	6.806987	P	P	P	5.17396
8.346892	7.272138	8.253959	8.546583	P	P	P	7.29431
7.111688		7.084358	A		A		6.655198
8.925674	7.353402	9.649316	7.941904	P	P	P	6.817324
6.413433		6.270664	6.95056		M	A	6.325554
			8.14908			A	
			3.680601			P	

		7.139516	7.361829		A	A	
	5.774767	5.618954	2.073437	M	P	P	
5.348203	5.691476	2.760456	A	A	P		4.874589
	5.266481			A			
10.4912	11.21533	11.1466	11.52588 P	P	P	P	11.49783
6.87047	6.920313	7.204806	7.173461 P	P	P	P	6.319294
9.90083	10.41341	9.393868	8.787168 P	P	P	P	10.008
7.485216	7.271854	6.800768	3.538257 P	P	P	P	7.397917
5.872004	5.785517	6.337277	5.95891 A	P	P	P	4.657864
5.428205	5.813695		A	M			5.856262
5.696577			7.334762 M			A	6.46479
5.616968	4.934334	7.580901	7.774058 P	A	M	P	6.403211
		5.845235			A		
	5.945407			A			
6.536793	5.816745	6.514703	A	P	A		4.898067
7.258576	6.286444	7.625629	7.820426 P	A	A	A	7.185451
7.94543	8.620688	9.671808	8.338408 P	P	P	P	8.517861
7.059924	8.187671	7.7085	P	P	P		7.336127
7.496607			A				5.697548
7.091637	8.396714	7.372708	5.893277 P	P	P	P	8.588533
7.585728	8.800546	7.497668	8.517812 P	P	P	P	9.099753
5.960767	5.971286		P	A			6.274092
		8.085608				P	
6.348603	6.907599		M	A			7.213182
4.369029	4.1042		P	P			6.552256
	5.019699	4.769909		P	P		
7.283351	7.237092	7.044314	8.340374 P	P	P	A	7.885255
5.981006		5.127389	P		P		6.346522
8.640671	8.856683	8.11755	7.262512 P	P	P	P	8.342047
5.527351		6.308562	5.563093 A		A	P	4.057188
		4.412897			P		
10.81308	12.10521	11.07532	9.827388 P	P	P	P	11.63343
6.991944	7.247471	7.493498	3.076292 P	P	P	P	7.339852
9.336428	9.330568	8.858907	8.350104 P	P	P	P	8.993253
6.835361	7.848954	7.544847	5.474308 P	P	P	P	7.247207
8.168575	7.330812	7.182225	7.455981 P	P	P	P	7.432239
6.262899		6.566547	8.079869 A		P	A	5.622393
5.724009	5.379117	5.916729	6.94237 A	P	P	P	4.569871
7.311443	7.040979	5.787491	P	P	P		7.703543
8.588407	7.678067	8.076094	7.841965 P	P	P	P	7.478347

6.247466	6.330372	5.040639	5.440514	A	P	P	P	5.527548
8.364732	8.309725	8.077292	8.038733	P	P	P	P	8.059525
6.938401				A				5.283251
7.741211	8.336004		7.98934	P	P		P	8.918442
5.91369	2.3819	4.248189		P	P	P		6.192389
11.92594	12.01562	9.707694	10.85277	P	P	P	P	11.8552
6.701349	6.187635	7.744189	7.96974	P	A	A	A	5.785501
9.256979	9.104013	8.254519	6.221832	P	P	P	P	8.522482
7.173476	7.053947	6.30921	6.704518	A	P	P	M	7.371743
	5.541119	6.339746			M	P		
6.509265	6.654918	6.652286	7.43195	P	P	P	P	7.519635
8.365448	8.872966	9.128654	9.422098	P	P	P	P	8.620261
6.199148	7.096995	9.701512	8.49091	P	A	P	A	5.930496
4.857049	6.266378	4.685484		P	P	M		6.294746
7.337807	6.22791	6.764486	4.520558	P	P	P	P	7.183234
8.976557	9.990247	9.352121	8.620825	P	P	P	P	9.500452
7.108844	8.437052	6.615533	7.741196	P	P	P	P	6.700552
11.65296	11.75629	10.48938	10.04079	P	P	P	P	11.22065
5.75759			6.255962	A			A	5.989045
		6.915576				A		
9.746136	8.917697	8.499194	8.333812	P	P	P	P	8.583325
6.443058		6.44851	6.86542	A		A	A	4.180931
6.063341			7.480875	A			P	6.586072
10.55464	9.747097	10.01654	11.9709	P	P	P	P	10.88781
7.301585	6.917362	7.421133	7.784291	P	A	A	P	6.360048
	6.331177	6.671502	1.124514		P	P	P	
	8.091491	7.573443	8.448851		M	P	M	
		2.395834				M		
	4.622807		3.826524		A		M	
	5.013786	3.039629			A	P		
		6.142297				A		
9.185185	8.610283	10.4623	8.335478	P	P	P	P	7.524449
6.439784	5.797926	4.607116	4.192129	P	A	P	P	5.654874
	6.105925	8.80243	7.572336		A	A	A	
4.666521				P				5.75991
8.892204	9.328338	8.172969	8.227455	P	P	P	P	8.849994
6.038139	6.119931	6.935416	7.22811	M	P	P	P	6.386837
9.017358	9.293514	8.504975	9.1104	P	P	P	P	9.186473
9.681629	9.404616	8.868403	8.084123	P	P	P	P	8.65968
	5.693417	5.779275		P	P			

8.14198	6.741876	7.99706	8.312416	A	A	M	A	3.982044
		6.799521	7.444293			A	P	
6.08888	6.50996	6.38374	A	A	A			2.765941
5.93467	5.387444	4.143812	5.705552	A	A	P	A	4.744469
4.883988	6.138943		6.774994	P	P		A	6.981113
	5.694398	5.249255	6.797654	A	P		P	
2.725045			5.424764	P			P	5.949288
7.569488	6.567277	6.790422	P	P	P			6.566393
7.855735	6.283618	9.118526	9.478638	P	P		P	7.04366
6.382624	4.087382	8.192254	7.863885	M	P		P	5.635507
6.084321	5.962315	6.650925	7.537607	P	P		P	6.624647
5.91059	5.999543	5.534334	P	P	A			6.597928
0.255853			P					5.882316
6.676136	6.763613	5.621966	1.080323	P	A	P	P	6.563132
8.23524	9.508016	9.159063	8.228186	P	P	P	P	8.953446
	6.674759			A				
	2.206092			P				
8.148399	7.687579	7.424328	A	P	P			5.849754
6.49597	4.667971	6.107648	P	P	P			6.757507
8.877765	8.709505	9.508726	9.159155	P	P		P	8.179274
6.567763		6.54184	7.136901	A		P	P	6.966221
	4.103145	5.888917	5.151968		P	P	M	
7.797192	7.71595	7.1836	7.488698	A	P	P	M	7.275107
7.59911	7.674372	8.426174	9.223518	A	A	A	A	7.711017
	3.425641			P				
8.131819	8.62715	8.439338	8.874839	P	P	P	A	7.967679
5.413483			7.488009	M			A	6.773334
6.710534	6.875789	6.731288	7.717156	P	P	P	M	6.665277
5.902932		5.896649	A			P		4.665831
7.155328	6.799237	6.931219	5.368001	P	P	P	P	6.322591
9.097704	9.943021	8.918459	8.20615	P	P	P	P	9.186761
	3.883401			P				
8.05138	8.060627	8.39507	8.925035	P	P	P	M	8.425868
5.528679	4.545679	6.231642	6.750342	A	P	P	A	5.85505
		2.253907				P		
	6.161029	6.595465	6.863164	A	M		A	
			7.127395				A	
5.885923	5.286638	6.676246	A	A	A			4.968809
5.266919	5.189824	5.083821	A	P	P			5.093113
5.113488	5.618088	5.946932	P	A	P			6.199148

6.119418	6.269533		6.777594	A	P		P	5.30793
5.735062	5.436944	5.994695	7.508922	P	P	A	P	6.50261
6.563591			4.364996	A			P	7.12522
7.283628	7.856873	6.555609	7.217847	P	P	P	P	7.362759
6.438855		6.088679	7.533952	A		A	A	6.590522
		3.793581	1.687358			P	P	
6.605953	7.173228	3.679096		P	P	P		6.78361
4.819028		5.34153		A		P		4.992861
5.882445			4.753029	P			P	5.518765
7.437529	7.919565	6.969594	6.316205	P	P	P	P	7.223553
6.790457	6.982377	7.241422	7.767763	P	P	P	A	7.002753
6.897684	7.292954	5.697135		A	A	P		7.073987
5.931021		7.938505	7.891513	A		A	A	5.268798
6.067552	5.705173	5.784348	6.675879	P	A	A	A	6.747385
5.154884	6.664094	5.428981		P	P	M		5.558505
6.079134	6.871366	5.511211	7.032974	P	P	P	P	7.402497
6.229816	5.99688	6.531833	7.706113	P	P	A	P	6.618866
6.623954	6.860414	4.389118	6.855877	A	P	P	P	6.090983
9.150224	8.320581	8.685099	8.486349	P	P	P	P	7.896197
4.937098	4.896346	4.445785	6.134646	A	A	P	M	5.31321
7.259318	6.92709	8.743765	8.497851	P	P	P	P	7.20885
			6.390842				A	
5.940791		7.020169		P		M		7.341772
		3.523349				P		
7.132412	6.391258	5.274879	6.662977	A	P	P	P	6.643103
6.900412	6.344975	7.362548	7.725996	A	P	P	P	6.806181
6.628865				A				5.591284
7.10764		7.161558		A		A		5.253755
6.030228	5.859026	6.987467	8.089602	P	P	P	P	7.165927
6.21205	4.655658	5.273447	6.267611	P	P	P	P	6.768339
9.189453	8.356633	8.083096	7.595573	P	P	P	P	8.484498
	4.107418				P			
7.531046	7.806245	7.674016	7.853787	A	P	P	A	7.469212
		5.023144				P		
7.400788	8.014713	6.292093	4.67961	P	P	P	P	7.466257
7.144987	7.067941	6.301331	4.096954	P	P	P	P	6.651975
7.050886	6.636144	5.777531	2.300361	P	P	P	P	6.504058
8.468328	8.791176	8.162618	7.178368	P	P	P	P	8.662608
8.337579	7.545435	6.825888	6.641997	P	P	P	P	7.178966
	4.937329	5.507191	6.95763		P	A	A	

	5.186172	5.767173	6.579837	P	A	A	
6.483532	6.742634	5.75155	6.249014 P	P	P	P	6.628619
7.437743	7.715362	6.852987	6.929079 P	A	P	P	7.555153
6.001644	5.290005	4.919859	A	P	P		6.074169
6.944673	6.749281	7.111135	7.12481 P	P	P	P	7.311723
6.714832	7.027152	6.10345	P	P	M		7.073103
5.796203	5.529459	5.154254	P	P	P		6.297456
9.678869	9.676613	9.122939	8.520502 P	P	P	P	9.428135
6.340694	3.922291		A	P			6.317143
8.062636	7.945799	7.875016	7.034023 P	P	P	P	6.574606
3.757299			6.880001 P			A	6.362497
6.653981	5.320421	4.803559	A	M	P		6.353813
7.249851	7.400295	6.699306	6.364038 M	P	P	P	6.222888
		6.103402	4.690452		A	M	
6.835928		6.105146	7.615928 P		M	P	7.695254
8.639794	8.245307	8.744771	9.247686 P	P	P	P	8.191008
6.327033	6.475453	6.715961	6.957508 P	P	P	P	5.788301
8.641622	8.053134	6.798122	6.268745 P	P	P	P	7.89771
6.49952	7.156341		7.174597 A	A		P	7.528561
			7.037993			A	
1.668444			M				5.85242
6.905463	7.782832	8.366417	8.234235 P	P	P	P	7.981161
			7.249981			M	
	6.136366	6.667434		M	A		
8.763347	9.453166	9.502848	10.7632 P	P	P	P	9.333247
5.033646	0.922992		P	M			6.453863
	6.852338	2.496837	5.228465	A	P	P	
10.49554	10.96781	9.902483	9.867036 P	P	P	P	10.8262
5.879643	5.791159		6.75674 M	P		P	6.367252
7.304388	6.227454	5.792238	P	P	P		6.530333
6.336111			7.540921 A			A	5.971269
	7.35464			A			
7.093043	7.552215	7.131368	6.784023 P	P	P	A	6.663508
4.95172	6.170962	4.86358	1.753568 M	A	P	P	6.52972
	7.014206	6.262101		A	P		
	7.551715	8.485892	8.428185	A	A	A	
		7.253141			A		
6.230394			A				1.60144
	5.86897			A			
	2.153611			M			

5.225881	5.645119	6.197499	P	P	M		6.818467
		3.557062			P		
5.787508	7.007029	0.63048	6.502708 P	P	M	P	6.189383
	4.868716			M			
7.964821	6.806655	7.308551	7.154417 P	P	P	P	6.611641
7.768914	8.267495	7.873241	7.215308 P	P	P	P	7.388603
	6.424205	5.584568	5.959749	A	P	P	
5.253724	5.508676	2.332181	6.262514 P	A	P	P	5.519431
5.018918	5.844402	5.557906	A	A	M		5.724795
7.427982	7.345837	7.546545	6.772466 P	P	P	P	7.264041
7.258077	6.875815	4.312795	7.547947 A	P	P	P	6.268486
5.29086	5.543694	6.067088	7.599493 A	M	A	P	5.909444
7.89905	8.590047	6.846231	7.318737 P	P	P	P	8.575871
4.421156			P				6.193082
7.514782	7.505357	8.388203	8.341892 A	P	P	P	7.142753
6.7984	4.159914		A	P			6.052278
7.568991	7.278379	7.215914	3.736733 P	P	P	P	6.968572
6.788588	6.584017	7.300959	8.077906 P	M	A	A	6.417057
5.929839	5.041013	6.602627	6.358062 M	P	A	P	6.396466
5.473325	5.493835		P	A			5.726172
	4.763847			P			
		6.522121				A	
5.961114	6.921837	3.311624	7.011797 P	P	P	P	6.918108
8.29343	8.512342	7.765697	7.122999 P	P	P	P	8.292499
6.077262	4.547884	7.201704	5.671917 P	P	P	P	6.829958
6.150957	6.481939		7.616363 M	A		A	6.792876
5.96936	6.229361		4.551384 A	P		P	5.547744
5.673179		6.28317	6.990859 P		A	P	6.077707
7.046056	6.693354	7.361132	7.65037 P	P	P	A	6.991775
		5.539138	6.655627		P	P	
		4.072949			P		
1.06073	5.812017	5.870516	M	P	P		6.62778
8.444146	7.471198	8.64487	9.233923 P	P	P	M	7.746277
5.531647	6.498997	6.235766	P	P	P		5.799082
		6.005579	7.455988		A	A	
	6.217832	6.778318	5.870378	M	P	P	
6.877504	7.212436	7.627472	8.093111 A	P	P	A	6.934314
	6.052239	4.963527	6.717867	A	P	P	
		2.445065				P	
7.810191	6.835905	6.45201	7.497711 A	P	P	A	6.106224

7.514151	7.564589	6.461114	5.549697	P	P	P	7.016475
	4.563259	5.904488		P	P		
6.586762	6.469309	5.021105	6.869026	A	P	P	6.464344
6.262285	5.302509	3.956859	6.354788	A	P	P	6.460272
7.035273	5.983025	7.567165	6.604422	P	P	P	6.065157
7.37062	6.435853	6.75224	8.361797	P	P	P	7.149645
6.177042	6.363006		P	M			6.641874
9.695909	9.724731	10.63754	10.56312	P	P	P	9.743956
		7.846439			A		
6.96289	6.278005	7.372657	6.146775	P	A	P	6.302791
		5.992923			A		
6.044269	5.743929	6.889029	P	P	P		6.081731
	7.094754	3.412584		A	P		
7.410602	7.685135	5.800972	7.063862	M	P	M	7.527677
8.200333	8.122808	3.061628	6.841925	P	P	P	8.102181
6.388845	5.459866	6.388716	6.320153	P	M	A	5.67246
10.4622	10.21482	9.652641	8.810938	P	P	P	10.10162
	6.462624	8.009246	7.713007	A	A	A	
6.724443	5.165711		6.66112	P		A	6.262781
5.954895	5.288553	5.077636	A	A	A		5.57524
9.396999	9.285026	8.055521	7.603381	P	P	P	9.352098
8.63997	8.380059	7.696019	7.349918	P	P	P	7.757873
9.484418	9.412313	5.481846	8.448402	P	P	P	10.21431
7.773553	7.764535	6.168571	7.102129	P	P	P	7.818645
10.13728	11.40456	4.362376	6.514532	P	P	P	10.29644
			6.278668			A	
5.101923			A				6.170149
5.024044	5.506063		A	P			3.86534
	5.235902			A			
6.210868	6.54569	6.128691	7.267547	P	P	A	7.084611
6.417224	5.638325	5.673072	5.047055	P	P	P	5.346287
5.862133	5.423917	7.008871	7.301327	P	A	A	5.79112
6.743957	6.604799	6.236323	P	P	P		6.813508
5.359953	5.685814		4.875234	A		P	2.999742
6.761371		5.803785	A		P		3.069418
5.997392	4.358165		P	P			5.618507
	7.210236	8.14369	7.872979	A	A	A	
4.92761		6.304082	P		A		5.999675
8.5135	9.314878	8.591362	6.240379	P	P	P	8.106504
7.014447	7.162499	5.705181	6.207006	P	P	P	6.426164

7.945317	8.104269	6.541245	7.016708	P	P	P	7.990379
5.638741	4.776673	4.191011	5.52559	P	M	P	5.967182
7.357216	7.289277	6.825901	5.332655	P	P	P	7.018584
6.271923	4.477024	4.916553	6.013331	P	P	M	5.103371
		5.69066			A		
4.164555			P				6.627049
6.052929	4.82861	6.287502	7.204452	P	P	P	6.334718
8.687027	8.769222	8.692847	7.899366	P	P	P	8.735983
7.643131	6.541628	7.858173	6.808456	M	A	P	6.119113
		6.635523				M	
7.496934	7.883986	6.397107	5.039024	P	P	P	6.541166
	6.587105	4.498049		A	P		
		7.558275	7.26569		A	P	
7.326669	7.597343	6.664389	P	A	P		7.517458
6.749749	7.420612	6.75425	6.962051	A	P	P	5.19019
4.164276	5.864161	6.604197	4.380955	P	A	P	6.316979
8.259846	6.812055	6.483672	7.183025	A	P	M	6.333449
7.567471	7.249895	8.15204	9.517655	P	M	P	8.815772
4.674504	6.098415	4.008028	6.416402	A	P	P	4.516957
	5.243532			P			
	4.228183		6.682673	M		A	
9.242821	9.816148	8.024634	8.399319	P	P	P	10.35745
5.869176	5.587525	6.084694	1.688208	A	P	P	5.824781
8.010504	7.015174	6.585977	6.264529	P	P	P	6.825539
7.162218	7.742885	6.158829	6.656384	M	P	P	5.686813
5.985711		5.782641	A		M		3.917849
5.306086	4.072249	5.398333	P	P	P		5.464175
7.522731	7.286193	6.910458	6.998903	P	P	P	7.683864
7.24601	7.428279	6.134598	5.566963	M	P	P	7.552428
6.781954	6.341671	6.397128	A	P	P		5.503896
5.941122		1.973996	6.699147	A	P	P	5.636897
8.256986	8.15446	6.52428	6.519596	P	P	P	7.755955
7.887114		9.019295	9.824782	A	A	A	8.073042
6.224469		5.001442	P		P		6.828697
6.515349		7.664618	P		A		6.934326
7.574454	7.510701	6.299861	7.15134	P	P	P	7.942231
8.076836	8.149317	7.052903	6.99692	P	P	P	7.829234
	5.636771		4.569619	A		P	
5.61491	5.48285		7.529108	M	A	A	6.362579
6.484994	6.734942	2.323339	A	P	P		6.660667

7.462905	7.991646	7.543502	6.528913	A	P	P	P	5.656128
8.338634	7.899598	8.211873	7.095744	P	P	P	P	7.761261
5.595798	3.971858	5.175003	5.862862	P	A	P	P	5.180601
	3.780037				P			
6.960902	6.576571	6.613898		P	P	P		7.596463
8.766287	9.074654	6.713999	7.386735	P	P	P	P	8.974251
7.262046	8.060575	7.733294	7.389842	P	P	P	P	8.614464
	4.348002		6.587648	M			P	
	4.594286			A				
	2.650773		6.641913	P			A	
		5.881184				A		
3.265796				M				5.888956
6.642031	6.55819		7.279314	A	P		P	6.887344
5.585359	7.046429	5.184783	6.457805	A	P	P	P	5.294699
5.870809	5.394111	2.4536		A	P	P		5.728682
9.130139	8.260418	9.293714	10.64976	P	P	A	P	9.224744
6.816468	6.694677	6.518606	7.153091	A	P	P	A	5.712722
7.474345	6.835375	8.109373	8.140016	A	A	P	A	6.720733
	7.723057	7.78716			P	A		
	4.421149	0.809081			P	P		
7.649591	8.232621	7.43661	7.462659	P	P	P	P	7.554742
5.22557				P				6.551555
6.802331	7.29434	6.728304		A	A	M		7.036934
5.902225	5.440087	5.295126	5.23467	P	P	P	P	6.505058
	4.133344				P			
6.151101	5.967416	6.305963	7.379624	A	A	P	M	6.378394
5.511195	6.119921	5.784888		A	A	P		5.178119
9.452556	9.149021	9.73566	11.62977	P	P	P	P	10.42372
7.314957	6.316025	4.659335	6.585379	P	P	P	P	6.72853
7.617641	8.496539	6.987367	7.478488	P	P	P	P	7.858582
	5.864131	5.528802	6.010146		P	P	P	
5.253481	5.874571	5.886574		P	M	M		6.357674
12.16297	12.75424	11.88193	11.29158	P	P	P	P	12.48593
4.469551				M				5.908147
10.47928	10.37887	11.33738	12.67606	P	P	P	P	10.61945
10.57915	10.3394	11.33139	12.57972	P	P	P	P	10.45453
	7.898975	6.859529			P	P		
			6.387655				A	
	4.976048				A			
5.717247	5.73338	4.499601	2.283602	P	A	P	P	6.044964

	7.481833			A			
			6.405314			A	
4.263281	3.116548	5.560365	A	P	A		4.623331
7.931549	8.355606	9.585179	8.09368 A	A	P	A	5.645845
	5.656996			A			
		2.037928	6.466757		P	A	
6.670446	5.080474	3.219164	6.613669 A	P	P	P	5.634668
			6.030797			A	
8.100424	8.561582	9.678248	9.274406 P	P	P	P	7.91858
7.941688	7.685244	7.044515	8.537897 P	P	P	A	8.293406
		3.591344			P		
		4.143859	6.203487		P	A	
5.403381			2.653815 A			P	3.706081
	1.617889			P			
8.721779	7.979276	7.994204	7.130104 P	P	P	P	7.494223
10.28687	10.28593	9.68515	9.559419 P	P	P	P	9.95637
	5.485758	5.052059	6.253906	P	M	A	
6.243703		5.693571	6.51536 A		P	P	6.932325
		6.511076	6.364629		A	M	
4.772846	5.795388		P	A			5.858958
6.621717	6.822321	6.794499	P	P	P		7.654805
9.111321	9.596663	8.647051	10.49897 P	P	P	P	9.910883
8.88039	10.16374	9.15901	9.082285 P	P	P	P	9.63225
5.929355	6.060963	5.371872	2.392508 P	M	P	P	6.091769
	1.506382			P			
6.559129	6.655969	7.177953	6.295471 P	P	P	P	7.255171
10.44703	11.0313	10.11057	9.588779 P	P	P	P	10.20967
9.89787	10.08649	9.146421	8.509333 P	P	P	P	8.873274
			6.511356			A	
9.244505	9.345923	9.036368	9.02931 P	P	P	P	9.571419
6.409495	6.744027	6.760638	6.856123 P	P	P	P	5.01983
6.514703	6.526347	6.406372	7.742941 P	A	P	P	7.587924
8.440283	8.849386	8.33693	7.153804 P	P	P	P	8.508994
8.85007	7.855506	5.878853	6.374264 P	P	P	P	7.218918
5.045567	4.421731		P	P			6.94069
5.379981	7.121683	5.339236	P	P	P		8.786886
		4.281734			P		
5.965283	5.780109		A	A			4.465352
6.536303			A				5.313176
6.440635	7.687089	6.398139	6.397607 P	P	P	P	6.930327

2.34036			M				5.708195
7.981857	8.278227	8.136086	8.259286 P	P	P	A	7.704175
7.286657	7.234059	5.76119	5.625985 P	P	P	P	6.853143
5.962741	5.766766	5.330481	P	P	P		6.298763
8.378606	8.693994	7.943859	8.306912 P	P	P	P	8.504997
	2.194002			P			
	5.45473			A			
8.501035	8.753939	9.109899	10.64251 P	P	P	P	9.676193
6.871511	6.45736	6.975054	7.19111 P	P	P	P	7.035214
4.609029	4.725915	5.771963	P	P	P		6.009248
5.993121	6.839886	6.020664	7.276039 P	A	P	P	6.786334
4.912459	5.098024	4.190494	6.536616 A	P	P	P	5.225973
11.1946	10.49395	11.36104	12.66639 P	P	P	P	12.24993
	6.229144	0.978088		P	P		
6.838188	7.497278	8.282402	A	A	P		7.061262
	3.052832			P			
7.491142	7.789744	7.383976	6.487582 P	P	P	P	6.849614
4.796465			6.841056 P			A	5.352216
7.570431	8.224718	7.774659	7.980858 P	P	P	P	8.165882
9.441375	9.56454	9.073114	A	P	P		9.370683
	5.35181			A			
6.925452	7.387948	5.843581	4.90219 P	M	P	M	6.214153
6.817856	5.311786		6.661605 A	P		A	6.043805
8.057349		8.194736	A		P		6.946974
5.223129	5.869788	6.173065	5.287186 P	P	P	P	6.323707
			6.12949			A	
6.339119	5.705537	6.362852	6.477266 A	A	P	P	4.448385
		6.328792			A		
	5.361181	0.770841		A	P		
6.213143	5.154074	5.605627	6.315936 A	P	P	A	5.853222
6.264868	5.851051	5.198497	7.255332 P	P	P	P	6.497272
			7.846658			A	
6.83303	5.884069	5.968246	A	A	P		6.445153
		5.873693	6.399565		P	P	
8.602487	7.906767	8.667116	6.882174 P	P	P	P	7.906638
4.989623	5.083642	6.487075	6.119916 P	P	P	P	6.976135
7.286748	7.511514	8.293828	8.260182 P	P	P	P	7.503484
5.955146	6.38417	4.25127	4.997726 A	P	P	P	5.713616
8.245857	8.353977	7.495392	7.395937 P	P	P	P	7.600055
		2.441896	6.286433		P	A	

		6.270355				A	
5.541906			A				2.709463
4.06884		4.442471	5.33538 P		P	P	5.346529
6.751376		7.49342	7.661215 A		P	A	6.871121
5.622701	6.427184	6.386182	6.885413 A	P	A	P	3.786308
		3.400662			P		
6.226429		6.878575	A		P		7.415669
6.249673	6.589284	4.459802	0.754406 P	P	P	P	5.766737
7.229928	6.931624	6.936179	6.423783 P	P	P	P	7.087979
6.19988	5.288078		A	A			1.918732
8.835722	8.568662	11.01355	11.46271 P	P	P	P	7.929996
		6.617866				A	
5.001937			A				0.736435
9.224275	9.988321	9.451369	8.846148 P	P	P	P	9.447662
6.907157	6.423914	9.159948	10.01483 P	P	A	P	7.178547
6.325178			A				5.151718
		7.164437			A		
	6.7138	5.710982	6.288052	P	P	P	
11.8091	11.92967	11.37649	11.11585 P	P	P	P	11.00909
9.413736	9.305064	10.10588	10.8466 P	P	P	P	9.516881
7.426231	7.590043	8.432802	8.949504 P	P	P	P	7.593891
		2.524371			M		
6.070727	6.804082	5.80611	A	P	P		6.351122
	2.013677			P			
6.604533	6.598835	6.296942	7.346621 P	P	P	P	6.433091
8.064968	7.843037	8.316039	9.056823 P	P	P	P	8.508302
7.947871	7.847289	9.157751	8.316316 P	P	P	P	7.916606
		1.717972			P		
4.692165	6.476863	3.494389	P	P	P		6.438886
8.676165	7.540618	7.856186	7.240767 P	P	P	P	7.406002
1.852986	6.150538		P	A			5.820433
6.665406	6.05255	4.993846	6.356656 M	P	P	P	6.428269
5.24604	5.519988		6.886572 P	P		P	6.905434
		6.554014			A		
8.9269	8.535387	8.367706	7.372597 P	P	P	P	8.321553
5.744731	5.664679		A	P			3.170938
8.312724	9.642204	7.971822	7.860891 P	P	P	P	8.69298
9.525715	7.123269	8.610476	7.72791 P	P	P	A	6.426136
		7.194628				A	
6.288676	6.339747	6.833211	7.23809 A	P	A	A	5.931346

	5.926989		7.019573	A		A	
7.481549	7.829511	7.834079	6.497806 P	P	P	P	7.521088
7.707377	7.707913	6.210352	7.451242 P	P	P	P	7.379291
7.639287	7.485786	7.552133	6.134993 P	P	P	P	7.329581
8.111071	7.94346	7.164624	7.783874 P	P	P	P	7.810845
	5.182844	5.695204		A	P		
4.717675		2.000738	P		P		5.555296
		0.918441			P		
			6.198546			A	
6.701262	6.156641		6.051805 P	A		P	6.992109
		5.266898	2.170171		P	P	
		2.547737	6.288216		P	P	
7.467621			A				6.125078
9.95227	7.455949	9.158104	9.140118 P	P	P	P	6.772772
3.863317	4.791624	4.736232	P	M	P		5.056673
4.656788		5.915848	P		P		6.110258
5.316273			5.758192 M			A	5.355481
	0.541437			P			
5.131049		5.848596	2.698061 M		A	P	5.218642
6.075642	5.925146	6.367514	6.198786 P	P	A	P	5.813768
7.140685	7.66149	6.992735	6.377886 P	P	P	P	6.287351
6.372099	6.399503	7.03424	7.219839 A	P	P	A	6.887265
7.556669	7.744756	8.511035	8.31198 P	P	P	P	7.126899
8.972193	9.126109	8.363652	6.041071 P	P	P	P	8.220278
8.530213	8.091017	9.442121	8.303912 P	P	P	P	7.955098
7.449863	7.054745	7.040332	5.688029 P	P	A	P	7.15968
	5.756598			A			
			7.91532			A	
8.694546	9.005845	8.054295	7.94425 P	P	P	P	8.307607
8.435796	8.338626	7.696499	9.377915 P	P	P	P	9.747319
7.057745	7.478587	6.756342	6.668953 P	P	P	P	7.11779
6.910845	6.845547	5.973862	6.525375 P	P	P	P	7.06793
8.792851	9.293694	8.553424	8.777474 P	P	P	P	9.031163
5.117554			6.314397 P			A	5.68712
8.787114	9.549228	7.860871	7.922674 P	P	P	P	9.198653
6.800663			1.771829 A			M	5.804764
8.468398	9.152122	9.088413	9.710967 P	P	P	P	8.644897
	6.037051	6.151527	2.998622	P	P	P	
		8.461072			A		
7.333823	8.155372	7.53294	7.564915 P	P	P	P	8.677666

8.500826	9.173183	6.86879	7.438316	P	P	P	8.661214
		4.7578			P		
11.79112	11.65583	11.04153	10.09381	P	P	P	11.29315
5.882922	5.763605	6.405856	A	A	A		5.068762
4.69545	6.245416	5.475104	6.195288	M	P	M	5.777813
9.235544	8.657411	8.360356	9.288732	P	P	A	7.006769
9.966567	9.642962	9.750884	9.339371	P	P	P	10.45099
6.820317	7.159004	7.517033	8.081999	P	P	P	7.917933
7.210677		8.681174	M		A		8.376061
7.32603	7.421328	6.655108	7.021576	P	P	P	7.190236
2.712379	6.117516		P	P			6.25197
4.310179			M				5.49535
5.489851	6.131714		7.311292	P		A	6.498826
7.503999	7.281361	7.927816	7.995668	P	P	P	6.903845
5.737101	5.868176	4.90296	6.423586	A	P	A	5.434417
0.629959			P				5.395083
5.515223		5.625645	A		P		4.359533
		6.152236			A		
	6.02287			M			
7.450465	7.361232	7.379301	8.669241	P	P	P	7.611418
5.877286	6.224153	4.909799	4.877463	P	A	P	6.26027
7.759426	8.443556	6.63225	7.426721	P	P	P	7.619583
6.298776	6.404483	5.704195	6.541142	P	P	A	7.265707
7.584383	6.776309	6.491584	4.394345	P	P	P	6.826406
	6.480938			A			
6.005406	6.127439	7.413383	7.399247	P	P	A	6.186145
5.780345	5.068429	5.91401	3.68425	P	P	M	5.734017
	4.242801	6.40994	6.527257		P	P	A
7.007552	7.681785	7.508954	6.943774	P	P	P	7.286342
		5.394116			P		
5.93458	6.161782	3.886588	A	P	M		5.250203
6.652931	7.499876	7.846922	8.124282	P	P	P	7.277738
8.438657	8.811042	7.994631	8.230981	P	P	P	8.711915
4.275636		5.570574	P		M		5.573501
6.240177	5.729411		P	P			7.872768
	4.57869			M			
5.199311			P				6.283472
6.527405	6.825165	7.803097	A	A	A		6.446142
7.878379	8.669761	8.188907	7.004458	P	P	P	8.662512
7.228115	6.959647	6.239803	4.50022	P	P	P	6.557474

6.579778	7.504121	7.450105	7.052421	P	P	P	7.754446
		2.070515			P		
7.986649	8.955062	7.038446	7.655455	P	P	P	8.388833
8.495887	8.037002	9.384975	8.457222	A	P	P	7.458635
12.79831	12.71478	10.22737	13.06545	P	P	P	13.1378
8.364062	8.961794		7.25401	A		P	7.780281
10.4504	10.73704	9.898662	10.10006	P	P	P	10.09484
7.898544	8.830902	7.86886	7.188642	P	P	P	7.779705
8.862885	8.387021	8.472978	9.182375	P	P	P	8.887535
8.752891	8.957679	8.471508	7.599961	P	P	P	8.596804
9.962839	10.79316	9.549211	8.721663	P	P	P	10.33814
		0.259232	P		P		4.531901
	5.019309	1.085884		A	M		
9.402158	8.370144	8.263159	6.636504	P	P	P	6.974096
			3.207438			P	
9.151029	9.873159	9.75062	9.966756	P	P	P	9.684308
5.520829			5.357264	A		P	2.726326
6.504561	6.53894	6.558613	5.217805	P	P	P	6.215849
6.926488	6.850555	7.135436	6.911796	A	P	A	6.956265
	6.132309	7.640492	8.351651	P	A	A	
7.083033	6.725065	5.96785	P	P	P		6.832189
	5.537551	5.55229		M	P		
5.639569	6.823515	3.559454	P	A	P		7.211731
		3.857513			P		
5.137408			6.256104	P		P	7.217814
6.319493	6.931273	6.310115	M	P	P		6.88475
	5.36017			A			
7.020606	6.643262	5.322468	6.935085	P	P	P	7.488406
6.531916	7.160793	6.126269	6.704662	P	P	A	6.827493
5.035106	6.314861	4.790157	A	P	P		4.770369
5.653483		5.921343	6.610966	A	A	M	6.069665
5.940126	4.172641	6.101083	P	M	P		6.451867
5.276343	5.710973		5.952191	P		A	6.83925
	6.391733	5.281177	5.242249	A	M	P	
5.449736			6.135925	P		A	5.432849
8.654484	8.154429	8.881402	8.002655	P	P	P	7.562795
	2.752473			P			
		3.064293			P		
8.458381	7.706393	9.006796	8.874703	P	P	P	7.859624
6.187319	5.438645	5.878289	6.704608	P	P	P	5.925703

4.330698	5.412354			M	A				6.22015
8.940806	8.737144	7.540039	7.513447	P	P	P	P		7.655086
7.95062	7.638348	7.13666	3.735012	A	P	P	P		6.802742
5.715571	4.612165		6.02896	P	M		M		4.872892
		5.727023				A			
	5.337949				A				
5.904733	4.793015	6.070897		A	P	A			6.587188
5.69168	5.80047	7.033052	6.29209	A	A	P	A		6.12042
7.802249	9.077827	8.591795	7.948344	P	P	P	P		8.333708
6.047237			6.890283	A			A		4.769357
7.33915	6.566677	6.725661	7.397645	P	P	P	A		7.117467
7.38735	6.815236	6.265805	5.39721	A	A	P	P		5.966419
	5.031656	6.118808	5.314989		M	P	P		
6.188997	6.34788	6.771359		P	P	A			6.428516
	5.413132				A				
		6.519258				P			
7.378413	6.617218	7.299697	6.948036	P	P	P	P		6.351595
8.89708	8.823386	6.914678	7.819969	P	P	P	P		8.82339
9.735312	9.445745	8.350515	8.207745	P	P	P	P		8.884094
5.57672	5.780237	5.232167	6.104045	P	A	P	P		5.655357
7.231304	8.205216	7.395535	7.076951	P	P	P	P		7.152086
8.161387	8.571168	8.13259	6.952444	P	P	P	P		7.829462
			6.899673				A		
7.555038	6.912872	7.972009	8.001132	P	P	M	P		7.467944
9.012402	9.226659	8.873178	8.969544	P	P	P	P		9.098439
8.504625	8.709622	8.148962	6.92483	P	P	P	P		7.81025
7.025705	7.889553	7.557827	6.385261	P	P	P	M		6.970003
6.78495	7.040793		6.375765	M	P		P		7.035202
						M			
8.827179	8.30538	7.983327	8.186332	P	P	P	P		7.639513
6.933188	6.917166	6.774442	6.362815	A	P	P	P		6.736865
4.789353	1.566074	6.604673	7.090929	P	P	P	P		6.671179
5.950763	6.051611	5.88351	1.609819	P	P	P	P		6.662918
7.47718	7.802866	7.423017	6.780741	P	P	P	P		7.779995
8.463769	9.129732	9.09095	7.725817	P	P	P	P		8.455678
5.24223				A					3.872671
4.655959	4.464309	4.766762		P	A	M			5.633573
7.267109	6.668233	6.617874		A	P	P			6.751742
7.565452	7.799669	7.42629	8.014456	P	P	P	P		7.685019
7.042393	6.935436	7.327257	7.34234	A	P	P	P		5.678867

5.177721				P				6.870409
8.196354	8.577866	7.72976	7.180231	P	P	P	P	7.808303
		1.001931				P		
			5.946455				P	
6.62224	5.7919	5.675239	7.436607	A	P	P	A	5.626645
			8.498469				A	
6.079516	4.567051			M	P			5.52357
5.991096	5.18333			A	P			4.564977
4.537499				M				6.675438
7.355988	5.200873	5.984958	6.727551	P	P	M	P	7.386964
6.115729		6.006511	5.209819	A		P	P	5.705525
	4.849188				A			
8.544217	8.037225	7.08247	7.297214	P	P	P	P	8.033601
	5.764768	5.181016			P	P		
6.226479	6.955651	5.85476	6.525043	P	P	P	P	6.843164
5.024688				P				6.668012
	3.372281	6.440304			P	P		
	5.729098	5.464527			A	P		
	5.661819	4.500379	7.049223		P	M	P	
5.074497		6.519044	5.65419	A		A	P	2.672836
	6.714179	5.748452	6.845988		P	P	P	
		7.302622	7.805564			P	A	
		6.169633	6.224066			P	A	
		1.168139				P		
		7.410008				A		
7.208675	7.748186	6.859084		A	P	P		7.872866
8.55556	7.787363	8.123188	8.305456	P	P	P	P	8.471486
1.023109				P				5.925129
	3.807443				P			
8.445756	9.130678	7.969437	7.798981	P	P	P	P	8.84826
8.89059	8.29503	6.969878	6.312939	P	P	P	P	7.901731
9.822765	10.32271	9.395551	7.599333	P	P	P	P	9.437569
			6.973789				A	
			4.830527				P	
7.925468	7.107276	7.889436	7.765924	P	P	P	P	7.137125
7.195897	7.151432	8.057793	7.307874	P	P	P	A	7.340606
6.756106	7.344757	7.094835	3.028835	P	P	P	P	7.16982
6.234411	5.097849	6.720084	7.162077	A	P	A	A	4.91608
6.879269	6.46458	6.796556	5.513358	P	P	P	P	6.803898
6.11738	5.898567		5.974401	P	A		A	6.02145

7.837331	6.792955	6.566937		A	P	M		5.706025
		1.227794				P		
5.716152	5.45072	7.243638	7.802731	P	A	A	A	6.397747
		5.421397				A		
5.176449	5.457956	3.116313		P	P	P		6.557404
6.402389	5.48405	4.588514		A	A	P		3.805906
3.890427	6.317776		7.373733	M	A		A	6.150102
6.787785	8.269019	6.698947	6.067934	P	P	P	P	7.160547
7.288912	7.909489	6.010173	6.38555	A	P	P	P	6.636492
5.764304	6.67332	6.26453	5.773657	P	P	P	P	6.45758
9.130712	8.798752	8.376187	8.241128	P	P	P	P	8.185197
	6.071321				A			
7.698805	8.002079	7.366332		P	P	P		7.630867
7.320443	7.324328	5.693341		A	P	P		6.284496
8.817741	7.895137	8.18477	8.097084	P	P	P	P	7.721627
			7.229489				A	
7.027583	7.060294	6.489988	5.282927	P	P	P	P	7.034156
	3.62132			P				6.28429
7.589146	7.113984	7.422992	7.422669	A	P	P	P	6.471201
6.583396		5.932267		A		P		5.146673
			6.09142				A	
		6.47765				A		
6.938295	7.390817	6.864146	6.683721	P	P	P	M	7.717438
6.053121	6.102539	6.453006	7.144004	P	P	P	P	7.161045
5.790683		2.605431	4.961695	P		P	M	5.505203
7.446314	7.546548	7.004418	8.110273	P	P	P	P	7.466488
8.340459	8.399708	6.992774	4.615624	A	P	P	P	6.837889
8.720038	9.093829	8.768153	8.183848	P	P	P	P	8.078309
6.277232				A				1.610159
	5.536578	0.913123	6.480039		P	P	P	
10.07565	10.78011	9.566257	8.313784	P	P	P	P	10.14711
5.472127	3.55096			A	P			6.162653
11.09425	10.6621	9.997128	10.03839	P	P	P	P	10.91375
7.978938	8.231988	7.134495	7.438823	P	P	P	P	7.582054
7.383029	8.033049	8.044395	8.952607	P	P	P	P	8.512366
6.338341	5.663916	4.68972	6.182491	A	A	P	P	5.727795
5.869067	5.110072	5.60837	4.457747	A	P	P	P	5.542322
8.653363	8.954252	8.448722	7.182948	P	P	P	P	8.334555
	5.500003				P			
	5.662367	5.368978	6.734882		P	A	P	

	6.573797	6.331055		P	P		
6.181284	6.334363		3.431564 P	A		M	5.880881
		6.175597			P		
6.893252	7.007449	6.747602	6.851754 A	P	P	P	5.867177
	2.580394			P			
8.711078	9.193372	6.187181	5.359563 P	P	P	P	8.679914
			6.629539			A	
	4.802153	4.766206	6.442411	M	P	P	
4.004469			M				5.48334
5.836954	5.672488	5.979491	6.06306 A	A	P	P	4.600186
9.615674	10.27391	8.825921	9.004344 P	P	P	P	10.02687
5.151549	5.608592	2.154114	P	P	P		6.095228
8.327795	9.611322	8.44171	8.088996 P	P	P	P	8.957866
5.23937	6.651751	6.046485	6.573344 P	P	P	P	7.282096
10.97545	11.04322	10.59809	9.789377 P	P	P	P	11.11518
4.983749			P				6.49948
5.794628	6.150614	5.80203	6.151322 M	P	P	P	6.464903
4.075333	4.880532	6.346101	3.782443 P	P	P	P	5.725027
		3.48416			P		
			1.400461			P	
	5.894022			A			
8.944575	9.077948	8.381924	7.496156 P	P	P	P	8.879144
3.900107			M				5.173504
9.119746	9.566338	8.884986	7.714382 P	P	P	P	9.010862
2.012462			P				6.009068
0.795859			M				5.073753
9.400369	9.814865	9.073672	8.142284 P	P	P	P	9.197292
		4.26333			P		
			6.903499			A	
6.303563			A				5.278956
3.783789			P				6.048027
	5.916404		5.499391	P		P	
6.639603	6.298864		A	A			5.256839
6.095686	3.902787		A	P			4.20134
	5.302087			A			
2.070307			P				6.406315
4.824368			P				6.631043
		4.068984			P		
6.714708	6.188363	5.395827	A	P	P		6.052724
9.280573	9.055855	6.992779	7.130541 P	P	P	P	8.492353

7.202617	7.174375	7.784063	8.341251	P	P	P	7.068373
6.233618	4.511669		6.866291	P	M	M	6.888316
11.43835	12.24899	11.48793	10.58862	P	P	P	11.92922
	5.664119			A			
5.48589	4.86246		6.892518	A		A	4.984144
10.72008	10.73043	10.09205	9.376062	P	P	P	10.1803
8.864434	8.771151	8.016177	7.570144	P	P	P	8.170722
	5.326441	3.377089	6.31176	A	M	P	
1.591648			6.63719	M		A	5.956348
		1.543976			M		
5.551471		2.466802	6.078492	P	P	P	5.35878
	5.378509		6.754281	P		A	
	4.774558		6.811997	A		A	
5.665405	4.751974		4.021666	A		P	4.899626
		6.616136			A		
4.227228	5.059506	5.479143	P	P	P		6.067933
7.612422	8.390842	7.761022	7.742475	P	P	P	7.339449
7.229492		7.167458	A		A		4.667543
6.597091	6.423986	7.437505	6.802439	P	P	A	7.412458
5.914474			6.631511	A		A	5.684771
6.837849	6.984205	7.518148	8.877563	P	P	P	7.99317
7.406694	7.429345	7.826191	8.437675	P	A	P	7.927803
6.829358	6.203067	7.260069	7.720595	A	P	M	A
		4.753408			P		
7.36613	7.920139	8.617714	8.588566	P	P	A	7.792172
	5.502421	5.454512		P	P		
6.458079	5.665302	6.245461	7.447188	P	P	P	7.359079
4.892197		4.973372	P		P		5.659048
3.493368			M				6.164852
		2.753208				P	
		6.11753			A		
8.601016	7.882795	8.942728	8.237127	A	P	P	A
1.936714			P				7.387625
	6.706418	5.342894	3.537354		P	P	P
5.323015	6.600267	6.098136	6.430604	P	P	P	7.224212
7.412794		7.161907	P		P		6.408482
		3.920732			M		
9.475388	9.183856	10.63977	10.78198	P	P	P	9.393413
6.855795	7.425093	7.647022	9.88741	P	P	P	9.007499
11.16243	11.5332	11.96674	12.98675	P	P	P	11.54594

	6.683679	6.559432	4.893735	P	P	M	
8.714465	9.190485	8.69397	8.604762 P	P	P	P	8.354294
9.429379	9.971677	8.879194	7.797138 P	P	P	P	9.571315
		4.508397			P		
10.98198	11.57068	9.782511	9.262908 P	P	P	P	10.6961
6.179413		5.963985	6.536386 P		A	A	5.609488
9.217975	8.23897	8.927045	8.215166 P	P	P	P	7.992728
12.68234	11.67298	11.93689	11.24173 P	P	P	P	10.76626
	5.521384	2.707948		M	M		
8.074432	6.955598	8.482495	8.105326 M	P	P	A	7.452153
10.25514	9.52004	9.666225	9.2197 P	P	P	P	8.722481
6.350934	6.083065	6.408094	P	A	P		6.803264
5.331514	5.106827	4.757814	P	P	P		6.020912
	6.676602		3.82867	P		P	
12.8972	13.18554	11.95316	12.71993 P	P	P	P	13.49291
6.303553			P				7.357521
		6.709543				A	
5.557262	5.421291	5.459817	P	A	A		5.611612
7.681802	6.994674	8.295524	7.843505 A	P	P	P	6.642308
6.815621		7.376979	7.221882 A		A	A	6.063357
7.706171	7.779039	6.085294	2.390791 P	P	P	P	6.696429
9.231524	10.25675	9.498351	8.21143 P	P	P	P	9.286307
6.380836	6.667465	5.839831	6.352098 P	P	P	P	7.332418
5.949312	5.530845	5.707451	2.098797 A	P	M	P	6.428906
	5.115202			P			
6.805334	7.793803	6.795633	3.840581 P	P	P	P	7.668069
6.701902	6.196236	6.124494	7.402231 A	P	A	A	5.713387
6.500739	6.384965	7.275489	P	A	A		7.09521
5.598121		5.033639	A		P		5.552534
6.879436	6.641879	5.872966	A	P	P		6.17798
4.836847			P				6.472467
8.319751	6.732408	6.503073	8.932973 P	P	P	P	7.9511
4.022332			P				5.565718
	5.324572			P			
8.827484	8.353029	8.101342	7.141295 P	P	P	P	7.825355
6.041915	5.301879	4.094236	5.844974 A	P	P	P	4.700183
	6.225711	6.723733	6.023794	P	A	M	
4.730727			A				2.643869
5.32997		5.960127	A		P		5.389522
7.155298	6.176384	7.662727	7.748052 P	P	P	P	6.779741

	5.231396	5.687063	6.312253		P	P	A	
4.16542			A					1.789855
10.95948	10.75772	8.175332	9.075447	P	P	P	P	10.74532
7.372234	6.925144	4.680421	4.849537	P	P	P	P	7.31667
8.829009	9.209353	10.09306	9.207784	P	P	P	P	8.839602
7.895269	7.092592	6.768741	7.735448	P	P	P	P	7.771587
		6.366121				A		
4.506715		6.757635	M			P		6.257899
6.24087			P					7.262088
7.217534	6.497885	7.166748	A	A	A			3.363131
6.049979	5.996443	3.993894	6.143376	P	A	P	P	6.733345
		5.526513				A		
10.2653	10.11352	9.261739	8.420025	P	P	P	P	9.712643
0.319641			P					5.358943
6.458117			A					2.24891
5.396943	5.774507		7.668991	M	P		A	7.387225
5.922796	4.985868		6.569874	A	P		A	5.176323
9.993648	9.767026	9.007534	8.955562	P	P	P	P	9.598931
7.850087	7.935864	7.37752	6.943422	P	P	P	P	7.221161
11.07847	11.26188	11.62438	11.96633	P	P	P	P	10.91465
5.367892		6.172373	A			A		1.684353
6.523181		6.20713	4.910709	A		P	P	4.614129
5.434595	5.543037		A	P				4.111003
6.94873	5.827868	5.053453	6.244704	P	P	P	P	6.57309
6.101161		4.090521	6.812521	P		P	P	6.250217
7.347814	6.810998	5.357521	5.79151	P	P	P	P	6.876319
			2.625113				P	
		6.984249	8.155986			A	A	
	4.167876			P				
6.065236		4.546137	6.069102	A		P	P	1.389077
	6.716971	7.461062	7.846334	M	A	A	A	
4.560698	6.878644	6.755037	5.798291	P	P	P	P	5.945962
7.126802	7.705859	6.79242	6.821101	P	P	P	P	7.219573
		3.537834	5.738894			P	M	
6.424011	6.444436	7.493587	6.953235	P	P	P	P	7.11482
6.210088		6.756498	A			P		5.08423
8.661013	9.096743	8.320695	7.398613	P	P	P	P	8.589252
8.819282	9.074183	7.986121	6.969261	P	P	P	P	8.854928
6.969505	6.649363	5.395488	2.773982	P	P	P	P	6.396129
6.614378	6.808751	6.160821	7.609877	P	M	P	A	8.01088

7.898634	6.792933	5.375339	6.584847	P	P	P	7.180863
7.128362	8.031907	8.232456	8.079181	P	P	P	7.753628
5.90006	3.615463		5.921368	P		P	5.189291
6.43958	4.760057		3.497573	P		M	4.874907
8.523612	8.35279	9.295204	8.902279	P	P	P	8.329836
5.103334	3.701969	5.062114	6.050746	P	P	M	5.583118
			5.159387			P	
6.598421			A				2.314903
	6.110269	5.46187	6.574335	P	P	P	
			2.779255			P	
10.35108	9.868962	9.892691	8.712017	P	P	P	9.505074
7.676944	7.264151	6.719515	7.297165	P	P	P	7.774744
6.4591	6.151856	6.291222	6.049096	P	P	P	5.379043
5.493629		6.880687	6.88696		A	A	5.428212
6.624585	6.907862	5.915237	8.18646	P	P	P	6.634541
			5.966496			A	
8.261761	8.105688	6.316115	6.346386	P	P	P	7.942043
10.7198	10.43319	8.713227	8.720098	P	P	P	10.83652
11.45248	12.36437	9.196511	9.758276	P	P	P	11.85359
6.013349	6.219125	7.100085	7.014099	A	P	P	5.322455
5.369646	5.811643		A	A			3.469681
0.962785			M				4.871939
			7.232626			A	
0.628088			5.68019	M		A	5.187075
	1.050915			P			
6.276611	5.626938	6.801836	P	A	P		5.71659
7.788401	8.03708	7.281251	5.813821	P	P	P	7.627117
8.352078	7.733707	9.092131	8.50432	P	P	P	7.441936
8.210867	8.018799	7.939972	6.193499	P	P	P	7.242906
8.063925	8.397311	8.355263	7.511832	P	P	P	7.670296
7.962958	8.135882	7.448142	6.338734	P	P	P	7.252228
			6.266788			M	
8.159836	8.372358	8.617644	8.568147	P	P	P	8.163919
5.716413			A				3.915745
10.8479	11.28168	9.931762	10.04846	P	P	P	11.53521
	6.516148	1.896971		P	P		
9.315136	9.085886	9.416549	8.434593	P	P	P	9.265976
		2.894981			P		
5.939034	5.908131		A	A			6.273542
6.512899	5.209862	5.16813	P	M	P		6.440049

6.950339	7.327318	3.980305	6.68834	P	P	P	6.628449
5.152066			P				6.230165
12.31465	13.2643	12.45016	11.5475	P	P	P	12.47838
8.313041	9.427167	8.951892	8.571538	P	P	P	8.606296
7.969988	9.240917	8.833879	M	P	P		8.230763
8.445025	7.620853	8.697018	10.28453	P	P	P	8.481034
			6.280726			A	
	6.179435			M			
6.042025			A				2.906185
6.57275	7.351529		M	A			7.926951
		5.970651			M		
6.389772		6.778658	7.418558		A	A	5.25685
5.901882		6.433908	5.724025		A	A	4.318625
		7.584162	7.957498		P	A	
4.593432			A				3.382692
3.380359		2.019803	P		M		5.360554
	5.601702			A			
7.212055	7.945493	7.170081	6.066266	P	P	P	7.303353
7.769674	7.168152	7.652425	6.464787	P	P	P	7.050912
			7.157763			A	
8.219067	8.565821	7.756598	7.255987	P	P	P	8.503478
5.180207		6.043276	4.77635		P	M	6.309151
8.230263	7.606332	8.084003	6.986576	P	P	P	7.760292
4.421073		4.93413	2.492576		P	P	4.519395
		5.98111	6.097305		A	P	
8.474196	8.159122	9.335054	8.642319	P	P	P	8.175435
4.146061	5.494524	5.409321	P	A	P		5.590295
9.184755	9.498296	8.592757	8.155175	P	P	P	9.277497
7.859757	6.547053	7.504781	A	M	P		6.36559
6.310921	5.630989	6.895571	A	P	P		4.89736
7.285259	6.781528	6.716368	6.671423	A	P	A	6.63775
8.893136	9.158973	8.383741	7.99644	P	P	P	8.699727
6.056979	5.998845	6.873798	P	A	A		5.962346
10.33322	10.47991	11.52639	12.24573	P	P	P	10.77859
11.32958	10.92568	9.94576	10.77191	P	P	P	11.13139
6.950183	6.711251	6.307784	6.420783	P	P	P	5.529779
5.977095			A				3.557243
5.980028	6.144747	4.606484	A	M	P		5.708264
	7.332407		7.198811	A		A	
9.859942	10.01555	9.182916	9.020146	P	P	P	9.805249

8.884131	8.736453	7.54208	7.732759	P	P	P	8.253406
7.331395	7.606823	6.95049	7.687244	P	P	P	7.902907
6.098762			7.253271			P	7.154899
7.296148	7.789325	7.240627	7.103805	P	P	P	7.734665
8.343953	8.822782	9.248649	8.498971	P	P	P	9.465029
7.479796	7.669099	7.416436	5.411463	P	P	P	6.990404
	5.752852	3.291153		P	P		
6.722997	7.285432	6.821593	5.598473	P	P	P	6.815563
	6.490918			A			
	5.919159		4.796675	A		P	
			7.964096			A	
7.56415	6.554399	6.677734	6.483641	P	P	P	6.144192
7.592606	7.114282	7.843305	6.55036	P	P	P	6.835339
6.60087	6.576312	5.127769	8.160684	P	P	P	8.23466
6.087614	6.865403	6.147812	6.75083	P	P	A	6.239379
7.755462	7.48026	5.951585	6.996594	P	P	P	7.534749
		3.77467			P		
7.865049	7.568459	8.514825	9.154446	P	P	P	7.179509
10.70107	11.37425	10.56802	9.656256	P	P	P	10.57828
	6.655201	7.328835	8.127839	P	P	M	
7.365394	6.590582		A	A			5.436423
6.870002	7.199895	6.841785	6.005526	P	P	P	6.216531
11.2489	11.2728	10.64713	9.946517	P	P	P	10.53034
8.210146	8.011323	9.133115	10.21733	P	P	P	8.528416
		6.375818			A		
10.7339	10.30103	9.884986	9.742746	P	P	P	9.908839
6.905044	8.433817	7.998038	7.103895	P	P	A	7.226601
	7.500547	6.074166		A	P		
			3.544201			M	
6.015592	6.259751	9.363396	8.538343	A	P	A	4.33642
		7.575893			A		
6.760319			A				5.742035
5.156124			A				2.19941
6.951019	6.741577	6.331107	P	P	P		7.215154
6.53882			A				5.43183
9.707738	10.34479	10.27289	9.102366	P	P	P	9.704595
5.378664		3.894057	A		P		5.119426
6.782191		6.709823	A		A		5.084294
5.226312	6.33426	1.73058	P	P	P		6.463121
6.00827	5.828527	6.147374	7.011001	A	P	P	5.605221

10.6063	10.59678	9.910533	9.812793 P	P	P	P	10.2217
			7.785735			A	
	5.600907	2.535546	6.69288	A	P	P	
5.456055	5.228733	3.116483	6.668969 P	P	P	P	6.902604
5.418097	5.104571	4.202131	P	P	P		5.060482
	5.46346	4.817499		P	P		
6.587346	8.427862		8.06711 P	P		P	7.820059
7.361111	7.678717	7.251093	7.851389 P	P	P	P	7.168471
5.425698	5.629354		P	A			5.853966
5.675826	5.502131	5.20084	5.522449 P	P	P	P	5.786742
5.738524	6.318326	5.260155	6.545375 P	P	M	P	6.401392
6.892988	6.346996	7.46014	8.674479 P	P	P	P	7.528078
		7.150999	7.796322		P	A	
5.499461	4.525788		A	P			5.62112
7.038742	7.024688	7.229158	2.815979 P	P	P	P	6.551019
8.650468	9.464766	8.939343	8.90091 P	P	P	P	8.746107
6.720138	7.826716	6.335407	6.605335 P	P	P	P	8.308571
5.716242	5.343489	3.999845	P	P	P		6.437091
5.702818	5.443131	5.835011	6.002514 A	A	P	P	5.327404
7.733009	6.961396	8.33079	8.148194 P	P	P	P	7.182422
	7.733547	8.212551	8.694654	M	M	M	
5.70587	5.819243	5.403518	A	P	P		5.897669
5.72432	5.973846	5.728844	P	P	P		7.032953
5.541719	5.944346	6.015498	P	M	A		6.673022
	6.317271			A			
9.305278	9.015628	9.387637	8.032831 P	P	P	P	8.294901
12.84207	12.83905	10.88964	10.72012 P	P	P	P	12.1695
12.07184	12.08696	10.99839	10.17625 P	P	P	P	11.77057
	6.440551	2.034631		A	M		
6.757127	5.989616	6.081664	3.154891 P	P	P	M	7.119149
5.524519		5.883498	A		A		4.980081
6.366198	5.963274	5.563843	A	P	P		6.086044
	4.897751			P			
6.986278	7.118436		5.620849 P	P		P	7.600766
6.603538	5.214055	5.72498	5.279198 A	P	P	P	5.68916
6.708792	6.781135	7.241826	A	P	A		5.215305
6.988381	7.416028	6.744298	7.610148 P	P	P	A	7.478443
5.891384	5.87927	6.526958	6.81412 A	A	A	A	2.690925
			2.171523			P	
2.900243	6.005627		P	P			6.966173

8.014553	8.458021	8.15565	6.821703	P	P	P	8.29305
		4.283001			M		
7.074908	6.679754	7.723415	8.372477	P	P	P	6.700734
9.183427	8.964232	9.648137	8.93668	P	P	P	9.028033
	7.758733	8.530565	9.220593	P	A	P	
5.444675		5.180185	P		A		6.494136
	5.919242	6.506479	7.990078	A	P	A	
			6.263258			A	
7.170268	7.630769	6.86935	P	P	P		7.803295
		5.14485			P		
			6.424631			A	
8.509067	9.960555	9.606933	8.524462	P	P	P	6.889432
7.810524	9.382499	8.402861	6.613244	P	P	P	8.373261
7.628455	6.480862	8.477496	A	A	M		5.50698
5.104776		7.084275	6.776823		P	P	5.989192
6.046467	6.145418	5.711748	0.873433	A	P	M	6.899024
	4.356811	5.874494		P	A		
			6.913176			A	
5.483888	5.382867	5.905244	7.125335	P	A	A	5.790143
	4.595963	5.855098	6.83054	M	A	A	
11.14575	11.53368	9.458686	9.770916	P	P	P	10.81216
			7.608481			A	
	2.104934		6.600795	P		A	
10.46523	10.55213	9.94755	9.418049	P	P	P	9.94705
5.915381	6.168623	6.117256	7.018053	A	P	P	5.777532
6.597932	5.738982	5.88399	6.307129	P	P	M	6.270019
	1.17957			P			
8.171445	6.304223	7.313022	P	A	P		6.84829
6.976434	7.795046	7.542203	8.19903	P	P	P	6.713956
5.181655	5.898122	6.280849	A	A	A		2.842459
7.233747	6.203898	7.784154	6.438539	P	P	P	6.19262
6.14355	6.362227	6.416166	7.438354	M	P	A	6.690149
4.602891			M				5.892423
6.615089	5.968838	3.176894	6.565909	P	P	A	5.219425
6.116126	6.66728		P	A			6.347132
	5.500741			A			
5.267956	6.771813	7.142938	7.2285	P	P	A	5.922427
5.242072	5.51725	6.321669	6.934992	P	P	P	5.478877
9.100747	9.391251	9.345344	9.780437	P	P	P	10.15375
6.777896	6.681671	4.23996	6.309197	P	P	P	5.053766

	1.970442	5.58481	6.632308	P	P	P	
4.188163	5.371805	3.888075	P	P	P		5.858184
8.087109	9.06077	7.645403	6.955405 P	P	P	P	7.967411
8.256616	8.419104	7.78969	7.292292 P	P	P	P	8.133995
5.234703			A				1.721003
7.050633	7.862114	7.526713	6.593224 P	P	P	P	7.551626
7.640955	8.3381	7.413027	7.333702 P	P	P	P	8.270181
6.640991			A				3.064023
5.590959	5.572911	6.252144	A	P	M		2.109723
7.547704	7.253816	7.548871	7.327333 P	P	P	A	7.402906
7.892292	8.505618	6.446282	7.808206 P	P	P	P	8.130164
		5.965849			A		
	5.156969			A			
6.685764	5.71498	5.266758	A	P	P		5.982226
	7.016417	4.959078		A	P		
7.725313	5.350926	4.489047	6.938637 P	P	P	A	6.204728
6.734697		2.960378	A		P		6.080706
7.388736	9.059342	7.422087	7.111208 P	P	P	P	7.857539
4.942314	4.185198	5.479522	M	P	P		5.51113
7.072334	6.689941	6.086747	5.07552 P	P	P	P	7.075211
7.392271	7.563648	6.356449	6.978077 M	P	P	M	6.713271
10.12733	9.425772	7.318434	9.279622 P	P	P	P	9.789686
5.016986			A				3.190474
9.964817	9.761668	9.577415	8.549777 P	P	P	P	9.242714
		6.502994				A	
7.685039	8.147515	8.878279	8.295218 P	P	P	P	7.883698
7.103941	6.760183	6.03886	7.013966 P	P	P	A	6.960012
	5.384675			A			
5.351015			6.525091 P			A	5.881806
3.197614			P				6.170833
4.833466			6.289326 M			A	5.981062
	3.628303			P			
6.558085	5.658511	5.543043	P	P	P		5.692444
5.942378	1.510037	3.716669	A	P	P		5.155422
5.967893	5.403347	4.78084	6.34909 A	P	P	P	4.43729
6.196944	7.219585	6.139956	2.351773 P	A	A	P	6.847058
		2.850315			P		
6.432234	4.833719	6.14411	P	P	P		5.949723
		1.951812			P		
6.651133	7.159878	7.977745	6.851454 P	A	P	A	7.167604

5.655771	7.150994	5.049019	M	P	P		6.209026
	6.097198			A			
5.049583		5.496634	7.063856 A		A	A	4.54566
5.726007	6.013356	5.948314	6.958873 P	P	P	P	5.773734
7.049335		7.277264	8.050041 M		P	P	7.734306
	6.554882			A			
10.22294	10.79217	10.03316	9.121407 P	P	P	P	10.48934
6.357198			7.408036 A			A	6.401235
	6.209182	7.291919		A	A		
7.462111	7.493119	7.27923	4.619167 P	P	P	P	7.559206
5.850682	4.612533	5.453364	6.093047 A	P	P	P	5.09973
		6.265193			A		
7.103223	6.216443	4.756689	P	P	P		6.818236
7.370499	6.273934	3.866367	5.812222 P	P	P	M	6.24055
	9.036015	8.970888	9.696929	P	P	P	
			7.233069			A	
7.000379	6.90975	6.593411	6.750675 P	P	P	P	5.637607
8.593125	8.943809	8.468742	8.794823 P	P	P	P	8.709202
10.50126	9.694091	9.575811	7.86343 P	P	P	P	8.744467
3.268385		6.293238	P		A		6.267619
8.317585	8.529744	10.66305	11.43662 P	P	P	P	8.768811
	6.873869	7.200239		P	A		
6.33766	5.974218	4.678329	5.976935 P	P	P	P	5.530039
	6.915947	5.808919	7.107413	A	P	P	
			5.50294			A	
	6.60979	5.804489	6.941127	P	P	A	
	5.000353	2.505608		P	P		
5.291679	5.391709	5.102292	5.647858 P	A	P	P	6.763377
6.458018	5.869579	6.934017	A	A	A		6.022142
7.118731		6.62073	7.550212 A		P	M	7.086837
	5.971874	6.69375		M	A		
3.593736		4.759053	5.341513 P		P	P	5.455512
7.677947		8.684887	9.081455 A		P	A	7.706575
	5.451739	5.604271	6.942883	P	A	A	
		5.631305	6.459833		A	A	
4.887097		6.132295	6.347929 P		P	P	5.329828
6.626617	6.935667	6.465815	7.034936 P	A	A	P	6.903106
3.903181	5.187303	5.925404	6.978849 P	A	P	P	5.564226
8.940079	9.350781	7.903786	7.972497 P	P	P	P	9.436962
7.595436	7.574444	7.901545	7.607062 P	P	P	P	7.066716

6.441315	5.59072	5.735209	7.073726	A	P	P	P	5.626834
7.286799	6.520626	7.172574	7.14511	P	P	P	P	5.815116
5.38295	5.34402	4.550233	4.830642	P	P	P	P	6.158652
10.3943	11.47055	11.20788	11.60529	P	P	P	P	11.80249
		0.927246				P		
	7.060688	7.769698		P	A			
9.371083	9.588422	7.956483	7.223578	P	P	P	P	9.423357
9.973038	9.060111	9.341555	9.880058	P	P	P	P	8.865606
6.082324			A					4.947786
6.335615	6.241852	4.884922	6.499345	A	M	P	P	5.32005
4.916415	5.475113	5.95252	5.781704	P	A	P	P	5.683994
7.735822	7.245777	8.362556	7.687212	P	P	P	A	7.369407
		3.12202				P		
7.23204	7.105417	7.746423	8.291875	M	A	A	A	7.70053
8.221908	8.544912	6.560462	6.059638	P	P	P	P	8.365324
8.107376	8.097689	9.760666	10.28541	P	P	P	P	8.101182
6.787291	6.703307	7.826424	7.693574	A	A	M	A	5.871402
6.790895	6.567614	3.328925	3.716952	P	P	P	P	7.078895
7.747904	8.526656	9.080169	9.473491	P	P	P	P	9.36085
5.569728		6.450622	M			A		6.000012
		6.969611					A	
7.207732	5.824752	7.115718	7.361192	P	P	P	P	5.702122
7.583587	6.896321	7.491787	8.868237	P	P	A	A	7.915866
5.647852	6.825865	1.992803	P	P	P	P		6.583895
4.63888	5.032099	7.235134	7.433531	P	P	A	A	7.029275
	6.622072	6.070486	6.224566	A	A	P	A	
6.260192	5.599458	2.379146	A	P	P	P		6.195633
	5.954974	4.90648	6.206198	P	P	P	A	
5.909171	7.173374	6.969645	7.054324	P	P	P	A	6.989965
	4.646005	7.110092		P	P	P		
7.184559	6.875417	7.360502	8.488829	P	P	A	P	7.028403
	4.261342			P				
8.118882	9.404557	8.483097	7.557638	P	P	P	P	9.17883
5.922195	5.618491		7.258088	P	A		A	5.962621
6.584995	4.750616	6.473783	6.734641	P	P	A	P	6.860882
8.09898	6.8559	8.517513	9.068132	P	P	P	A	8.241241
6.038534	5.967581	6.381067	6.871713	P	P	P	A	5.932857
	6.016037	5.470884		P	P	P		
6.322321	6.525754	6.199507	P	A	A	P		6.831269
8.86686	8.608892	8.028592	9.165946	P	P	P	P	8.62663

5.528608	4.401683			P	M			6.565376
		2.758106				P		
8.9436	9.619742	8.715307	8.223107	P	P	P	P	9.266199
7.936352	8.045061	8.143182	7.344747	A	P	P	A	6.710724
4.997698			4.748352	A			M	4.772255
10.81124	10.74426	10.21069	9.546138	P	P	P	P	10.65028
4.239367				P				6.085928
	4.627493	5.517282	5.598806		A	A	P	
5.995956	4.451192	5.571338	5.395632	P	P	P	P	5.363683
	6.343085		4.952999		A		M	
5.525398	5.58594	5.425427	4.885047	A	P	P	P	4.294872
7.174176	6.517921	7.652398	7.705608	P	P	P	P	6.286434
7.180781	8.397126	7.797394	8.018115	P	P	P	P	8.702366
4.961872	5.972167	6.608404	6.822065	P	P	A	P	6.844355
6.736149		7.076938	7.093048	A		A	A	5.83581
			6.899302				A	
	4.364142				P			
7.559157	6.646738	5.923465	7.54015	P	P	P	A	6.887967
6.786274	5.543627	6.565922	6.485035	P	A	A	P	6.345487
		2.79817				P		
6.513168	6.714716	6.168125	6.5587	P	P	P	P	6.504978
9.061751	9.680956	7.073706	7.375656	P	P	P	P	9.251338
	5.106305	5.589349	3.679664		P	A	M	
5.975421		5.699645		A		P		4.677828
	4.114451	6.036436			P	M		
6.942846	7.139386	5.476711	6.403041	P	P	P	P	6.684676
	5.729095	3.017041			M	P		
	5.011621	3.987787			A	P		
3.090878			4.1347	P			P	5.969501
	1.307776	6.010025			P	A		
6.048216	5.150909	6.193583	6.658629	P	P	P	A	5.888238
4.013538	5.234334		5.486259	M	P		P	6.532529
			6.891226				A	
10.70202	11.80107	10.83787	9.40091	P	P	P	P	10.94336
8.045731	8.530764	8.435282	8.80203	P	P	P	P	8.068046
10.95752	11.44125	11.31472	10.56441	P	P	P	P	12.02171
	5.228166	5.719648	5.726987		A	P	A	
7.350037	7.978858	6.243352	5.756248	P	P	P	P	7.388697
6.554093	7.39132	6.146033	7.377738	P	P	P	P	6.2241
6.659794	5.8632	6.25314	3.133553	P	P	A	P	6.334726

6.824976	6.708057	9.045436	8.947337	A	P	P	A	6.604892
6.519678	6.453957	5.142537	5.004479	P	P	P	P	6.359136
	5.728509	5.245757	6.240007		P	P	A	
7.682448	7.780973	6.603425	6.691142	P	P	P	P	7.406473
	2.660422				P			
5.063842	4.887666	5.987918	1.661022	P	P	P	P	6.679502
7.215794	6.92449	6.787816	6.102834	P	P	P	P	6.515706
6.780579	6.748005	6.951958	5.033096	P	P	P	P	5.97001
		5.958829				A		
2.070306				P				6.025547
9.731175	9.996481	9.628404	8.664381	P	P	P	P	10.24948
6.423013	7.65608	7.113568		P	P			7.58053
7.729002	6.140773	7.888498	7.671261	P	P	P	P	7.118592
7.31614	7.145977		6.315296	A	P		M	6.59561
6.517483	5.876289	6.48392	7.479446	P	P	P	P	6.637432
7.114867	6.828011	5.895325	5.461804	P	P	M	M	6.851102
6.780837	6.200257	5.923537	4.075266	P	M	P	P	6.362754
6.523955		7.940059	7.498274	M		P	M	6.817096
9.067231	7.69361	7.734488	7.284165	P	P	P	P	8.801748
12.81819	12.87977	10.47549	10.98658	P	P	P	P	13.07293
6.176054	6.638799	6.820685	5.611701	P	P	P	P	6.207025
6.087662	6.532392	7.379037	7.200352	A	A	A	A	2.821696
5.322725				A				1.736816
7.819981	8.055058	8.635458	9.458667	P	P	P	P	8.531109
6.230101	6.113771	2.168912	4.995556	P	P	P	P	7.218415
5.734342	5.632938	4.476249	5.974062	A	P	P	P	5.036895
	7.750624	3.507582		P	P			
6.605436	6.688857	6.122431	6.37436	P	P	P	P	6.144568
4.760779		5.785008		A		A		1.087211
6.548186	6.890861	6.600171	6.45451	P	P	P	P	6.382262
5.543998	2.311077	6.44561		P	P	P		5.783752
		6.053225	6.881086			A	A	
7.952855	8.10486	6.893722	7.244307	P	P	P	P	8.157651
7.93264	8.47737	6.702583	6.281666	P	P	P	P	8.488522
	6.328501	5.960653		A	M			
7.737477	7.507022	7.136987	3.449858	P	P	P	P	7.435432
		4.98473	6.761307		P	P	A	
6.247614	6.246855	5.038281		A	P	P		5.626083
7.058626	7.182401	6.954094	6.019042	P	P	P	P	6.230435
5.811441	5.626291			M	A			4.829873

5.186692	5.038531	5.411454	5.917677	P	A	A	P	6.046475
6.417629	5.562404	6.435531	6.659117	P	P	P	M	6.405984
5.718351	5.48409			A	P			3.874282
9.207737	9.3202	8.503844	8.23824	P	P	P	P	9.163499
10.605	11.73747	9.426801	9.631093	P	P	P	P	11.95772
8.273285	8.363537	6.54653	7.692903	P	P	P	P	9.152789
	6.538895			A				
5.687007	3.215216			A	P			5.966851
7.356117	6.68287	6.893887	6.827828	A	P	P	A	6.849483
	6.074503		1.606322		M		P	
8.220332	8.981784	8.431828	6.960768	P	P	P	P	8.894333
5.33845	5.157195			A	A			1.169225
	1.739928				P			
7.54164	8.722688	7.980671	7.050416	P	P	P	P	7.813521
7.474359	7.561406	7.340809	6.2067	P	P	P	P	7.380996
	5.592728	3.57964			A	P		
6.604757		3.856142	7.138647	A		P	A	3.783933
	5.948294				A			

14DPI_co ntrol_NS	21DPI_co ntrol_NS	28DPI_co ntrol_NS
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7.228128	7.688589	7.510127
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7.730737	8.36467	8.543794
6.336532	6.319718	6.689109
		6.466076
		5.312182
3.31624		
8.294673	9.28298	8.277659
10.57866	10.52798	9.277178
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6.098681	7.95081	5.509924
2.485684	6.755613	
5.620805	6.963	6.403396
9.967963	10.71963	9.587099
	5.547952	
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	6.539659	6.417936
8.370787	8.2766	7.457102
6.558768	6.531607	7.17788
		4.986423
10.87157	10.97634	10.90178
8.192822	8.846861	7.5192
6.065502		5.419255
4.696308	5.660033	6.765404
	5.379574	
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7.742164	6.993964	7.305211
6.624457	7.040059	7.450513

6.100197	6.48503	6.07766
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3.934375	4.31372	5.589044
3.558033		
6.103312	5.708781	6.037542
5.622189	5.191981	
	5.441707	4.907302
12.28512	12.13581	12.67294
5.593891	5.921361	5.930879
4.317908	6.235091	
6.81388	8.286695	
6.164358	6.331463	7.318388
6.377439	5.575413	7.155381
	0.962839	
5.731407		6.591637
10.40446	10.84494	10.42821
		5.742765
	5.087266	
7.476568	7.810984	8.318363
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10.78672	10.69622	11.67814
8.214802	8.082846	7.628769
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6.035379		
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4.082356	6.309861	6.72729
	4.50382	2.515057
6.291462	7.992545	6.559667
8.312958	9.241544	7.969634
6.991378	7.547115	6.301563
6.132509		
4.137811	6.248975	
	5.603276	
7.757942	7.624616	8.603587
9.496641	9.098999	10.02526
		5.854428

9.534575	10.69088	10.06701
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	4.215184	7.135412
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10.44147	9.993703	10.61553
	4.774457	5.097935
5.355665	5.819453	5.552561
5.532385	5.647094	3.46861
		5.605453
6.367987	6.370143	7.008398
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	4.474903	5.162461
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9.969201	9.987633	9.986561
8.427421	8.293331	8.734279
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9.555866	8.798856	8.750877
12.82056	12.54209	12.43293
8.537192	9.874155	8.556755
7.815161	7.842369	7.930255
6.593064	6.747773	6.375489
6.387887	5.742393	6.890811
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7.767388	7.465987	7.976779
9.357101	8.978866	9.076002
7.646774	7.123399	6.789271
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5.682861		

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	6.118221	
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6.712789	6.481935	7.090258
9.823946	9.635763	9.967754
9.17065	9.715768	8.884938
9.11846	10.06211	9.512559
6.703261	8.089445	6.634858
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7.125071	7.692401	7.285955
7.120211	6.600133	7.350118
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6.475215	7.308092	7.181698
4.925733		5.378711
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		5.964481
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7.645525	7.080559	7.632703
5.560451		
7.251955	7.969841	5.031048
8.467911	8.199801	9.452444
7.756678	8.109142	7.914192
6.615461	7.66882	6.738201
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10.65136	10.57227	9.921906
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7.232899	7.694662	7.102641
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6.395994	5.995287	6.319265

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7.239579	7.664679	7.168797
	5.507484	5.509161
	5.426884	6.251957
		1.395085
7.198122	7.672857	
	5.485756	
	5.886157	
9.484062	9.972134	9.097775
		5.169726
7.550865	7.442767	7.999624
7.102305	5.9481	5.033673
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6.460505	6.149165	6.195064
9.892291	9.35547	10.14331
6.211702	5.365731	
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		5.092884
10.44724	9.928923	10.38062
	6.458536	
6.75812	7.29172	7.443838
	4.803741	
7.64306	7.290412	7.535273
7.659317	6.031455	6.624328
	6.408365	
8.751372	9.64413	
7.222354	7.251291	6.319737
10.11798	8.912822	9.662386
5.204238		
7.741252	8.912385	6.814182
5.598494	6.771815	5.705605
	6.794664	

3.143089	5.835637	
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5.627994	5.898379	5.640848
6.112577		5.636778
9.820429	9.743588	9.6146
11.17535	10.91014	11.37736
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	6.69348	
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7.358679	6.571168	6.859061
5.932098		6.585364
5.511866	6.428744	
6.703123	6.677038	6.937907
4.866305	5.979776	6.245363
6.766337		
6.615608	6.199165	6.502769
6.034957	6.651785	6.37238
8.126541	7.561521	9.275976
7.010888	7.839097	6.793443
6.563942	7.066982	6.750302
10.05038	9.560881	9.432862
8.024415	6.970808	7.947894
13.85673	14.13671	13.2403
2.837163		
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6.164146	6.261587	5.736393
5.765573	5.951871	5.363147
5.267257		
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5.943067	6.601469	7.145541
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	5.668439	
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4.897644		
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6.590877	7.849722	5.982417
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9.958939	8.999703	9.718181
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8.237147	8.841099	8.135537
8.725888	9.431531	8.687191
7.448037	7.902624	6.754089
5.356618		
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4.760844		6.243319
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11.34596	11.22617	11.40057
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5.752185	6.915305	6.334851
7.057219	8.156793	7.55769
8.815187	9.575115	8.700638
11.07447	10.81685	11.17982
7.893466	8.14497	7.931612
8.628023	9.239148	8.414558
	5.905074	6.376509
6.622743	5.704565	6.364702
4.714914		
6.360117	7.032128	6.853355
9.748226	9.389437	9.151587
9.048485	9.114832	9.248016
7.713376	7.543509	7.780794
8.384032	8.84282	9.023049
10.61096	10.60171	10.34239
4.325507		
10.69263	10.54923	11.11005
5.683308	4.045826	
	5.51849	
5.397643		6.43636
		3.631194
11.66473	11.19669	11.27299
10.68789	10.2189	10.2259
6.16049	6.350354	7.412853
9.952395	10.46835	9.798405
10.56102	10.10582	10.81502
5.39103		
7.033434	6.558843	6.402551
9.496994	10.51286	9.891721
12.33479	12.42255	12.4903
6.827282	6.829387	7.380258
0.571406	5.912549	
		4.950823
7.197084	7.393819	6.182183
8.655613	8.639141	8.747423
9.226689	9.673172	9.419039

4.436337		5.045415
8.736525	8.832485	8.305625
8.639935	9.173979	8.649306
4.31528		
9.856309	8.962132	9.653
6.822657	7.531611	7.286486
6.641858	6.68889	6.386373
8.043743	8.353384	7.810459
10.35083	10.56408	10.23589
8.703134	9.041265	8.78173
12.39418	12.35331	12.21396
11.7363	11.45827	11.91116
10.61356	10.88285	10.23806
6.179321		6.9944
6.94607	8.133913	7.120581
10.87151	10.85215	11.24097
		5.239589
	6.052625	
5.661924	5.955837	5.5909
9.213926	9.614092	8.541449
10.54526	10.43798	10.4276
10.58969	9.896281	10.78769
6.098497	6.604207	6.007137
6.069524	5.931863	6.294736
9.288197	9.325392	8.762894
7.986978	8.003207	8.114678
8.367808	7.439467	6.373241
9.309568	9.398153	9.413817
7.390872	7.879627	6.569138
8.776444	8.991595	7.986103
5.928739	6.839484	
11.51262	11.45293	11.96405
7.549884	6.647313	7.276319
10.46516	10.70353	10.10718
5.276804	7.158953	
7.786607	8.516291	7.209102
5.689436		6.724651
8.456471	8.014742	8.690953

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	5.846447	
5.555077	6.697066	7.496756
12.0809	12.01963	12.39503
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6.954485	7.365955	6.637587
6.398894	7.963436	7.849155
		9.565413
12.4036	12.29134	12.01693
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10.22756	10.62469	10.53731
	6.064655	
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5.066348	3.490134	2.401739
	6.73557	
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	6.462519	
6.530321	7.51393	6.185027
10.23282	10.11135	10.08996
9.810314	9.37744	9.955129
9.227664	9.614623	9.704855
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9.196454	9.293252	9.390454
7.933082	9.611747	6.622469
8.955586	9.19194	8.906734
7.314789	7.484338	7.991323
8.529391	8.808422	9.509835
9.218202	9.564909	8.816473
11.67442	11.60484	12.22379
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9.085566	9.181261	9.119678
	7.215688	
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9.41448	9.146173	8.7742
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8.959632	9.326365	
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9.312692	9.185877	9.830495
4.78416	5.148725	
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5.992376	6.890362	6.883222
5.079529	5.391343	5.581731
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6.928373	6.081258	7.604138
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7.593952	8.23733	7.882524
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4.732183		
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7.179885	7.555757	6.496293
8.601838	7.031924	8.116605
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	4.728722	6.336818
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3.60243		
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6.121949	6.400204	5.824647
7.079806	7.530676	7.494406
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6.263438	5.033069	
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6.402623	6.964136	
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9.184661	7.813422	10.62308
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11.732	11.59318	11.82685
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9.667425	9.168826	10.21067
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8.902379	9.689244	8.250586
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2.650955		4.965369
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5.59582		6.006656
6.43499		
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8.051662	7.866102	9.555649
7.206869	6.935467	
		3.00869
6.713204	7.293371	7.31488
6.935846	5.843994	5.627226
8.196963	9.241438	7.163331
	5.105833	
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6.117616		6.417205
6.433334	7.25257	8.150732
5.287345	5.792737	
6.451769	6.052275	
9.904946	10.13239	10.73763

9.284814	9.908134	9.964484
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5.649746	6.115554	5.649008
6.345569		6.240056
6.123837	6.548312	6.466386
9.274411	9.214996	9.109617
	5.09455	
4.712135	5.941338	5.695836
9.079229	9.817036	9.317504
6.911781	6.225455	7.620648
6.094607		
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7.843741	8.236759	7.871468
8.709519	8.220726	8.234523
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	6.123663	
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5.679596	4.805752	5.580555
9.29039	10.0247	9.006182
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4.32235	5.871673	5.528445
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6.384011	6.335353	6.212128
6.990374	7.187331	6.559336
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7.591676	8.363991	6.713446
7.453108	7.525267	8.509058
5.518289		
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5.168503	6.042137	
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	6.033906	
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4.657724		
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13.96569	13.36889	14.34645
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	6.45222	7.643675
7.90255	8.545703	7.758014
6.708555	7.030509	6.300498
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		3.294913
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9.379788	9.171569	8.593267
8.21563	7.515815	8.064962
	5.820569	5.507653
4.765242	6.955653	
5.276577	6.430262	6.335919
7.032308	8.003394	7.618128
6.351696	6.471941	5.618323
5.520564	6.406633	6.27771
5.415018	6.214524	6.104043
7.927918		
7.056419	7.556974	7.577634
10.22404	10.77715	10.34904
6.872844	6.363578	6.938914
7.346898	7.614097	7.419871
7.702112	6.562603	7.208871
0.654684		
14.19202	13.91803	14.45117
		6.545442
7.658919	8.142923	6.77488
11.27215	11.5482	10.70489
10.32	10.01002	10.34891
11.08069	10.86498	11.06755
	6.127154	7.144871
10.75846	11.06938	10.75472
4.913424	5.693762	5.573309
7.730175	6.184301	7.602421
3.148964		
2.619842		5.479219

6.661557	6.630639	6.246006
7.358989	7.669334	7.269841
8.94362	8.277198	9.14187
8.015939	8.815588	7.566547
9.874898	9.415322	9.829749
8.61478	8.718551	7.936303
6.724654	7.123105	7.189285
6.42487	5.922874	7.569505
8.020329	7.282527	8.080624
8.697612	9.23497	9.766465
5.844265		
5.9613	8.067227	6.632994
7.298452	7.743681	6.901813
6.078351	6.905808	
		5.672909
9.284185	9.404596	8.433791
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		6.106797
	5.77063	
7.160692	7.4138	6.038926
8.032209	7.687764	8.262796
6.437267	6.007649	6.232883
6.340995		5.775531
9.263555	8.668815	9.507137
6.781601	6.809175	7.401416
13.82051	13.1898	14.07982
7.418453	7.840695	8.298257
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3.744687		
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6.593882	7.940881	8.736774
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8.079414	7.933258	9.069199
7.870183	7.308189	7.817287
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9.577967	9.449348	9.285651
9.302246	8.9929	9.119111
11.63831	11.59195	11.01017
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8.812702	8.290102	8.71449
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8.300715	8.215012	7.553886
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8.81999	8.869704	8.286616
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6.213283	6.608143	6.080473
8.75123	8.226984	9.432404
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7.883143	8.5553	7.643726
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2.988376		2.645322
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7.248156	6.511726	6.331978
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	7.77703	8.091629
9.516434	10.34752	10.10893
8.534111	8.260613	8.309854
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5.059888		
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7.725224	7.906736	8.344879
5.522631	6.434599	6.048171
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9.07222	9.238714	8.50456
5.272673	5.761779	
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6.560207	6.342393	
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9.552746	9.692305	9.127905
9.436532	9.308413	7.866123
9.960475	10.30212	10.01169
	6.737042	
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6.440456	7.39958	6.321154
9.514992	10.06445	9.86353
9.291265	8.894666	7.388336
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9.380821	9.306011	9.419533
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11.31573	11.6186	11.06628
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6.291539	6.113987	7.5573
6.413282	7.649369	
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10.60934	11.09075	10.94967
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	5.66612	
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6.774933	7.29492	6.997517
7.330908	8.568411	7.228712
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	7.242327	6.791852
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7.540595	8.168622	8.344341
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4.91332	6.008976	
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14.27373	13.93485	14.37602
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5.312776	5.835975	
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	5.710367	5.918285
5.240343	6.254952	5.976007
10.07039	9.822706	9.628343
6.226331	7.316134	
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7.123007	7.363417	7.779995
5.727517	6.03572	6.329445
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9.567003	9.012446	9.180548
	5.948627	6.199878
5.27106	6.401266	
8.28097	8.211863	8.246569
	5.647486	
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7.879817	7.899838	8.173144
5.863986		
7.41726	7.009826	6.052033
6.778004	6.628431	6.43392
3.950203	5.636314	6.596674
5.723064	6.096966	6.221896
	6.328117	
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	5.585857	
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5.0035		5.089056
		6.456342
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8.314119	8.075669	7.446112
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6.958203	6.480926	6.821917

7.009329	6.853132	7.518632
6.918308	7.204528	7.339997
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7.403794	7.44955	7.229206
7.010408	7.401189	7.282106
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7.825377	9.439448	6.478418
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11.50143	11.60198	12.09008
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7.102115	6.651815	7.435858
9.438566	9.434228	8.963876
7.54919	8.020089	7.82336
12.52855	12.39916	12.49242
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7.987702	7.589759	
11.88994	11.78072	12.235
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9.623412	9.673739	9.908205
9.668363	8.957924	9.640927
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6.053916	6.462952	6.006084
6.546525	8.326645	
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7.852495	6.612655	7.44716
6.8843	6.543662	
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8.511354	11.95558	3.012531
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7.092532	7.853591	7.280884
4.837753		
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8.899465	8.459125	8.919677
8.383332	8.807664	8.531042
8.681153	9.225812	9.784925
10.86971	10.55911	10.72141
9.635961	9.878625	9.37566
5.896929		6.019661
7.006019	8.730817	
6.285113	6.903605	6.954594
6.602515		
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6.389688	7.160148	6.678556
6.947779	7.768416	7.421674
5.153895	5.809334	
8.355295	8.176623	8.711955
7.32875	7.682507	7.735665
8.616536	9.388568	8.112988
6.258771	6.77365	5.742871
9.967664	10.53071	9.198602
6.467126	6.515189	4.765964
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6.140711	6.455573	7.348883
13.35034	13.2192	13.17772
6.978709	8.081052	7.065244
7.48386	7.958435	7.50081
6.087072	6.388837	5.875104
	6.775142	6.923455
12.52752	12.15337	12.58771
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9.898849	9.69902	10.04822
11.9578	12.10033	12.47684
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7.590405	7.042945	6.779641
7.393657	7.24907	7.386344
10.4834	10.51254	10.54492
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10.40741	9.915738	10.13397
8.716761	8.751089	8.399661
7.671753	8.683544	8.216817
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7.194755	6.733448	
2.709469		
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7.994321	8.223592	8.521316
8.172006	8.489666	6.959281
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6.328254		5.438439
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7.904902	8.276533	7.633214
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	6.208783	5.924299
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	8.189249	
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14.4942	14.11447	14.47134
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9.366076	8.432051	9.912323
8.593488	8.345332	8.606189
13.14779	13.15735	13.07929
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13.99121	14.09854	13.50857
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11.83638	11.89315	11.6052
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7.16112	7.078385	6.597921
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9.700523	9.760009	9.633858
7.789702	7.413766	7.761907
8.347428	8.609103	8.935781
7.261457	8.945548	7.421388
8.665502	9.63733	9.153566
4.555988		
11.70609	12.22792	11.67155
9.123734	9.332459	8.507441
9.662525	5.241696	7.518244
7.98743	7.688742	7.595375
9.057176	8.984371	9.385851
9.697216	9.475399	10.02924
10.52361	10.49277	10.59596
12.45471	12.40108	12.47019
7.086403	6.258344	7.399095
5.837408	5.181306	6.407326
8.401811	9.904595	8.592352
8.07126	9.638452	8.404433
11.49979	12.05911	10.80191
7.312837	8.486036	
6.261217	5.350737	4.5409
9.959175	9.548139	10.06516
10.09065	10.67328	10.0367
9.337287	9.24796	8.512004
	5.966386	3.405294
9.067236	9.870003	9.18116

11.24905	10.88022	11.13466
7.805832	7.932932	7.330222
6.599129	7.249801	6.145936
		5.637145
9.360879	9.464715	9.468309
9.706221	9.563477	9.600446
9.055522	9.845928	7.858708
10.96842	11.1391	11.37506
6.247928	6.544971	
8.357907	8.392217	8.080904
9.889991	9.48455	10.18682
10.21641	9.378465	9.575573
5.077633		
9.954607	9.269033	10.10681
9.656323	10.17728	9.47066
6.990914	7.766567	6.782054
6.07393	5.726925	6.007875
7.218148	7.723122	6.700123
6.337892	6.91	7.143611
9.74709	10.14313	10.60282
8.444635	8.793505	9.475509
5.096094	5.015448	4.956142
11.13159	10.96685	10.97607
9.302094	9.798993	9.349134
9.535584	9.587	9.426136
9.48756	9.352061	8.895792
6.052704		6.317461
7.062156	4.194136	
9.492764	9.609572	9.316064
5.640822	6.544972	5.676063
7.1297	6.875159	7.163783
8.977022	9.075701	8.642617
11.81573	12.69806	11.53028
9.799479	9.719887	10.30484
7.988555	8.023725	8.126437
5.641276	7.292891	
10.06964	10.21625	10.52234
12.89876	12.68079	13.03155
7.80444	8.307395	7.559947
7.518578	7.201267	7.134035

7.745014	6.945724	7.622801
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11.57914	11.63879	11.3417
5.974562	7.114563	7.197475
6.399281	5.788496	5.88106
10.70793	11.15328	10.41997
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14.83413	15.06897	15.4461
10.31237	11.30508	10.96288
7.45396	7.254747	7.389455
11.01436	11.5126	11.44407
	5.657411	
7.578635	9.204971	8.323767
7.708075	7.623496	8.094794
11.75232	11.92587	11.30464
11.80605	12.26338	11.53374
9.770862	9.857604	9.608259
7.737052	7.765333	8.074221
5.513281	5.271175	
9.456395	10.75304	9.998158
10.24129	10.01336	10.51622
7.325173	6.989868	6.531348
10.28242	10.59703	9.377663
8.588259	9.003907	9.189615
		6.141677
		5.734518
7.897333	7.702059	7.486413
7.983983	7.60374	
7.398112	8.801374	5.795592
8.550035	8.750301	8.640719
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11.08265	10.31693	11.06693
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7.676548	8.805545	6.87266
6.660839	5.439681	6.702791
8.361938	8.471765	7.620892
10.66462	10.80342	10.4892
7.220591	6.903047	7.303279
8.532206	9.019483	8.732098

8.193912	9.253862	8.458029
13.2029	12.34662	13.40365
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7.858279	8.333306	8.188055
7.060325	7.622229	6.66593
8.838319	8.409805	8.680104
5.295163		5.894144
9.981342	9.709312	9.942519
11.6181	11.99495	12.31818
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10.03279	9.771232	9.357093
11.04303	10.57089	11.1591
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4.864001	6.126684	6.084568
10.52074	10.15996	10.21421
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	5.320695	
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6.298968	5.838764	5.529496
10.78461	11.00596	10.47927
6.552501	7.075649	7.297303
6.982395	6.289485	7.181021
7.051494	7.804681	6.809253
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7.914166	7.393409	7.462481
12.14637	12.17129	11.54452
5.069907		
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11.89855	11.91027	12.14217
9.466306	9.03703	9.271106
12.01189	11.55589	11.62716
12.7173	13.20309	12.92941
9.815219	9.453646	9.062447
9.692717	9.644877	10.38139
5.606302	6.697591	6.461432
4.883072	5.702696	
5.586994		
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7.468806	7.85875	6.766872
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10.36229	10.1831	10.10043
5.788214		6.514889
9.032986	9.163604	8.028404
9.118072	8.8483	8.499706
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11.69587	11.90382	11.68661
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9.617232	10.43055	9.934818
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13.61861	13.46166	13.69334
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11.0824	10.43052	10.95315
11.9982	11.77854	11.91613
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6.598731	7.874957	
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	7.133407	6.865841
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8.065467	7.98297	7.390166
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13.15162	12.83466	12.83091
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6.291055	5.840968	
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7.67827	7.008456	8.193526
5.892272	6.656747	7.383701
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9.020274	8.955104	9.062563
12.76513	12.58583	12.74576
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8.469521	8.808424	8.04931
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6.127686	7.38081	
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15.1948	14.85716	15.73112
12.62409	13.10131	12.92911
3.738598		
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11.90629	11.62077	11.52926
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6.871689	7.359185	6.807749
13.1952	13.2556	13.16982
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	6.051529	
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14.22082	13.84984	14.51566
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6.07724	6.065334	6.597744
12.38692	11.94883	12.175
6.849137	6.549173	7.161541
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9.283665	8.482694	11.16778
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6.137603	5.586439	
12.07676	11.85581	11.77654
8.459722	8.522415	8.312315
6.962053	7.241355	6.824256
7.721628	7.805829	8.223711
11.44558	11.35641	11.0547
11.50106	11.68415	11.4516
9.482214	10.44453	8.742331
6.032653		6.9471
6.131984	6.017982	
7.893378	8.350196	
5.996873	6.6794	6.137244
11.81975	12.00384	11.44855
7.784874	8.30946	7.457232
7.932742	8.533718	9.08474
9.078094	9.077424	8.013449
	8.1139	8.287787
11.14166	10.5598	11.16167
8.430193	8.866626	8.386064
7.615918	7.865708	8.033858
7.281657	7.636344	7.378327
3.442868		
9.636972	8.755473	8.561478
	6.763753	
5.557747	7.28798	5.565493
12.93267	13.61091	12.47506
6.68013	7.05784	7.398585

8.164167	7.540622	8.337561
7.989921	7.345074	8.069293
8.931651	8.366824	8.977898
		4.098031
6.386263	6.785315	6.553613
7.517061	7.816239	7.598485
	5.200253	
5.91845	6.632634	
10.2809	10.07974	9.994492
7.937897	8.241502	7.373666
8.513696	9.04833	9.12359
6.028595	6.51052	5.383449
12.88445	13.412	12.74948
8.719237	8.945117	8.941667
7.64707	6.783458	7.522125
7.618456	7.258467	8.622001
8.030068	7.813313	8.213613
6.50369	7.174961	
8.28214	9.56662	6.797248
9.899898	9.917843	9.55165
7.926505	8.264883	7.556189
8.006134	7.750829	
10.02928	9.56798	10.02071
6.759787	7.186482	5.992346
7.66083	7.880467	8.081257
12.7313	12.54468	12.87807
6.123308		
7.438656	8.287956	7.991607
8.570795	9.701659	9.093346
10.50323	11.29441	10.61079
6.121655	7.738317	7.446175
		5.235316
6.031564	6.720483	6.347051
10.25784	10.51157	9.97447
10.74726	10.81109	10.42687
5.044932	5.991314	
5.650115	6.747584	
3.383965	6.672813	7.588829
6.145301		6.226788
8.805176	8.112985	8.479747

9.930939	10.9439	9.165631
5.912698	6.536735	3.069119
11.86616	12.38371	12.07226
12.59227	12.24437	12.42345
10.14814	10.04565	10.28108
14.1797	13.70041	14.56509
10.20768	9.757417	9.407446
6.361781		
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8.744617	8.896651	8.257858
8.523024	7.830763	7.732183
2.798302	4.367511	5.2832
7.37239	8.65308	7.43467
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7.839232	8.77305	6.259564
11.13854	13.07689	12.47252
7.701888	8.084984	8.625682
9.303769	9.420585	9.223821
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	5.658839	2.889773
7.437479	8.046764	7.063522
10.66666	10.1636	10.7707
9.97787	10.65426	11.5141
6.0755	6.020639	4.848249
9.444448	9.25116	9.096739
	6.140976	
9.628428	8.860247	9.611043
6.717299	7.975371	6.709089
4.428147	5.509849	6.497038
6.416583	7.161457	7.004051
11.79181	11.69766	11.47347
6.368467	5.513222	
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10.58695	10.16284	10.41261
6.805576	6.547001	7.914033
10.07947	10.10933	10.30487
8.962574	8.702558	8.098782
5.558216	5.398861	
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9.458297	9.54678	8.394994

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7.454997	7.087827	6.715286
5.93698	6.538701	6.550164
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7.489849	7.286534	7.326436
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9.647079	8.903432	8.931257
8.577291	8.234189	8.398993
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6.83473	6.762071	7.196181
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9.791623	9.116526	9.757633
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12.04039	11.71138	12.1084
6.705657	6.261004	6.831933
10.90534	11.33704	10.81093
10.52244	10.56701	10.67824
7.339612	7.167874	6.9957
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6.713813	6.451901	6.165447
	6.83418	7.481421
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7.240856		8.523723
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6.304894	7.308049	6.963022
9.041307	9.417584	9.295192
5.639125	5.339076	6.817896
	6.773777	6.941858
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8.51154	9.257099	8.390082
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7.484701	8.075858	8.344862
8.908432	9.274242	7.665344
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7.975503	8.242684	8.532985
4.29129		
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7.72095	8.366142	10.36501
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8.829519	8.548086	8.792241
9.344094	8.906896	9.048389
11.82549	11.25651	11.81448
9.41751	9.06741	8.706226
10.80382	10.93532	10.47769
6.376947		
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6.003649	6.118437	6.104904
9.919186	10.27065	10.39457
8.418552	8.721017	8.91671
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6.754523	6.954975	7.717166
8.948102	8.703032	8.342523
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8.515352	7.669549	8.470651
8.021802	7.787973	7.683533
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6.83157	7.064431	7.891941
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	6.844506	7.074947
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6.427133	6.931651	5.442797

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9.018965	9.970505	7.822595
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8.213733	7.976771	7.47807
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10.2405	11.27758	10.58228
6.481547	7.161488	
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8.884771	9.23494	9.553244
6.149175	6.799384	
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8.879709	9.111168	9.196222
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4.808584	4.686593	
5.514917	5.600298	5.541439
9.90723	10.6688	9.889724
8.349146	7.864576	8.444277
7.124071	7.671639	7.355108
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7.80457	8.100569	6.269808
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10.34138	10.34601	9.860792
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5.510256		
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7.577815	8.126936	
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7.215682	7.514764	7.107556
9.32235	9.510798	9.505333
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7.68592	8.597971	7.483025
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7.508104	7.740026	7.452529
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6.226241	6.713159	6.708168
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9.505238	9.12066	9.220126
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7.822123	8.591293	8.516729
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6.478575		
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9.501945		9.89475
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5.773273	5.811289	6.427883
6.116112		6.611772
7.501164	7.265647	7.368778
6.224012		
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11.02206	11.26086	11.72815
6.813952	5.979649	5.847419
9.138586	9.728992	8.974904
9.229398	7.944936	11.01904
7.577587	7.312055	8.742119
7.662683	7.786059	8.151732
13.60523	13.31023	14.02635
6.433448	7.022787	6.160243
7.190719	7.090217	6.876073
8.706792	9.524664	7.587396
5.314852	6.208888	7.919525
11.48014	11.22826	12.06424
7.294048	7.083549	7.106922
8.15978	8.350153	8.879659
11.92931	12.30593	12.28524
12.56453	12.79311	12.13799
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8.466548	8.981016	8.107182
7.569214	8.847749	7.302488
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9.172851	9.817591	9.871599
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9.964891	9.832008	9.023911

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10.25991	11.2333	9.389105
9.212077	9.898178	8.680033
	4.292867	

8.561161	8.622836	8.253503
9.628785	10.07096	9.433331
6.530569	6.331493	
5.873008	5.139801	6.220308
8.069567	8.421854	7.461377
7.69836	8.389948	
6.208576	6.583212	
	4.106213	6.286163
	5.729421	
		2.761933
5.585902		
	6.696813	5.6583
9.459791	10.0839	8.584476
5.433519		6.69479
6.744792	6.086066	6.020545
	6.49676	
	7.174923	
5.663652	5.56339	
	3.733993	
	5.361601	
9.380926	9.943274	9.156674
6.889144	7.753303	6.270088
7.036604	7.728206	6.881112
8.059837	8.640037	7.957323
8.385621	8.54086	8.223546
	5.318809	
	5.416346	
6.999055	7.31812	7.652426
	5.958524	5.935045
6.5534	8.045565	6.700163
8.317105	8.721332	
6.909259	6.483602	6.648481
6.392961	5.685225	6.931206
5.674523	5.485828	4.111843
	6.153851	
6.235067	7.553181	
7.861942	8.011645	7.955399
5.703898	6.249014	

4.947278		
	1.608721	
	6.088487	
	5.386941	
8.850264	9.196738	9.237086
5.667147		
5.080192	6.431605	6.27598
8.034347	8.280343	7.345696
10.65276	10.54281	10.21723
5.580922		5.920021
8.174132	7.752901	7.385891
		2.920969
7.119649	6.508014	7.181938
6.056669	7.412112	6.840858
6.2476	6.04251	5.230231
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6.157152	7.561083	6.332647
7.164751	8.065862	7.125464
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8.446783	9.10511	7.990747
5.070315	4.199174	6.361122
5.351733	6.0082	
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5.759122	5.547043	
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7.293747	8.949406	
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9.917767	9.980625	10.38904
7.513489		
8.239176	7.909842	8.846133
8.227425	7.954967	7.950821
5.600354	7.1339	
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7.18174	7.533391	7.14097

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8.401257	9.112682	7.385654
7.402092	7.551938	
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	5.93964	6.959255
	5.571066	
5.867746		
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5.822699	6.813274	3.533607
5.779852		6.363787
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13.46074	13.07387	13.04065
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11.8829	11.67588	11.69993
11.15986	11.25199	11.84297
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12.36217	11.34458	12.68444
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11.45782	11.4121	11.88602
9.610841	9.064547	9.368761
10.42457	11.48431	11.32076
9.022129	10.24459	9.709088
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11.94354	11.78734	11.94543
	5.682177	
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8.074388	8.202559	8.255248
12.88665	12.7553	12.5696
13.01657	12.94601	13.12254
10.16527	10.41312	10.18589
10.8025	10.97181	10.52141

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9.675593	10.81724	8.526177
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9.269256	9.319115	8.489148
11.77632	11.97885	11.05211
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6.318008	6.536438	7.708671
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9.333041	9.084838	9.816584
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7.446575		7.190127
5.741552		
9.259781	9.671849	9.341824
7.985427	8.649774	8.708342
6.517893		
5.658804	8.375699	8.732514
7.010747	6.788826	6.489614
10.54757	10.44325	10.34345
11.63847	11.16585	11.89503
10.84832	10.08042	10.41889
12.42022	12.75606	12.57512
11.55197	11.14971	12.04185
5.98586	4.309236	
7.650743	8.391537	9.02272
8.19635	8.076726	8.229999
6.696621	7.11697	7.579831
10.57241	11.03103	11.48815
8.993066	9.471286	9.159868
11.80374	12.00938	11.04392
8.894735	8.100842	9.278196
9.994629	9.850746	9.831709
10.78094	10.87899	11.24462
8.78125	10.04866	9.476994
8.405293	9.110358	7.649982
11.56275	11.13772	11.32306
12.33371	12.41218	12.56688
12.03129	7.751749	11.67057
13.01533	13.22429	13.34039
11.83609	11.36857	11.67376
5.114209		
10.50213	10.19723	10.46205
11.92131	11.64861	11.60274
7.461654	7.793917	7.255859
9.081488	9.18577	9.198904

8.510699	8.962219	8.178288
10.65575	10.99417	10.36621
7.876053	7.335086	8.286229
8.31814	8.007628	8.469754
8.201592	5.738476	8.607712
8.523767	8.929626	8.361506
8.983212	9.411664	9.163461
8.995373	8.523475	9.345598
9.594401	9.834148	9.355694
6.74185	6.394528	5.99047
11.39972	11.26327	11.51201
7.555461	8.901158	8.881164
9.509979	9.65619	9.159333
10.61875	10.64372	10.79085
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7.09811	6.897239	7.910345
12.37884	12.34173	12.55676
8.72136	9.847862	8.081109
11.35554	11.4338	11.0434
11.75165	11.26461	11.64478
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12.48351	11.40404	12.47004
9.021731	9.298551	8.590905
11.391	12.03712	11.11338
5.185993		5.898113
12.46188	12.04805	12.43616
12.19677	12.33851	12.22679
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10.57295	10.6795	9.764995
10.03417	10.40918	9.531122
10.50545	11.04623	10.91862
8.313047	8.839137	9.244786
7.304794	7.134915	7.668781
9.810304	9.941142	9.156708
9.51204	9.502584	9.571668
11.79443	11.55945	11.81504
9.709162	8.917354	10.36905
9.315908	9.922996	9.847634

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10.94934	11.2671	11.01871
9.738923	10.04204	9.294874
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9.636407	8.826126	9.756221
6.769763	7.397514	7.35356
	5.501269	4.399575
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8.425739	9.06824	7.403815
11.70641	12.12544	11.66253
6.413899	6.043926	
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2.900321	6.614275	
6.696245	6.554789	7.237077
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8.377026	7.775528	8.658296
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5.489611		
4.554487		5.639868
8.30782	8.814033	7.446167
6.370482	7.854046	
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6.463655	6.245137	6.175679
6.538262	7.205228	
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	5.826592	6.990681
6.721767		
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	5.931719	

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5.14808	5.85618	4.717881
6.090219	7.00132	6.453317
		5.614985
8.665032	8.701414	8.696432
9.401358	9.954527	9.304453
7.128693	8.914816	7.139815
4.318667	4.813629	
	6.444464	
7.029364	7.707279	
	5.286093	
	5.92705	5.972627
		5.561449
	2.2189	
8.095614	7.813447	10.63729
5.581468		
12.32289	12.06857	12.23816
5.74089		7.085553
	5.991241	6.021014
6.278281	7.385325	7.882741
5.189099	4.919773	6.959411
4.781473	6.55004	7.222491

8.430573	9.057676	8.346803
	1.93235	7.403676
		4.435404
5.621321		6.989544
6.422534	6.885397	
	7.422905	
7.985663	7.615938	6.249024
9.297079	9.447782	9.111657
	4.447919	
8.766821	10.06614	8.858148
9.918252	10.25017	9.43701
10.57558	10.5146	10.68164
9.088634	9.207974	8.000641
4.331939		
9.617273	8.782056	10.27431
2.918297		
5.913372	5.754664	6.356788
5.615319	6.345059	5.315218
8.603215	8.644959	7.97716
4.837593	6.370987	
8.888865	7.962863	7.893653
6.752185	6.469523	7.667851
5.031396		
	6.705435	
	7.596084	7.40644
7.728732	8.914727	
6.285303	6.704689	6.904585
	5.243681	4.477087
5.893515		
8.901052	8.566678	8.479209
4.696901	4.873803	5.777482
6.954786	6.920421	6.679967
		5.48462
9.725965	9.663443	9.697962
9.587701	9.690083	9.872433
9.898068	9.984845	9.765078
		6.564691
6.475905	7.365875	5.945624
9.397812	10.15282	7.941725
7.586575	7.296907	8.453362

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	6.045447	
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5.281107	5.563951	
6.611859	6.629709	4.42814
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6.643598	7.912052	7.683734
6.650937	7.644908	6.232258
4.657994		5.830907
	5.83458	5.825588
5.533046	5.895585	5.697664
7.319542	7.675532	6.70125
4.588805		
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7.624929	7.974336	7.294345
9.181659	10.10406	9.44192
6.402129	6.945276	
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	5.895218	
6.112148	6.25435	6.847763
	5.714235	
11.69722	11.4101	11.25116
8.337473	7.936917	7.956455
7.489626	6.596966	7.670728
6.262251	5.86164	5.16439
4.909877	6.026349	7.12181
3.096044		5.961702
10.31226	10.50643	10.37592
7.283147	6.367405	7.912119
9.236005	10.26043	8.321344
5.067469	6.118432	
	6.110401	
6.892225	7.761165	7.614894
8.415754	7.9873	
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5.970457	7.157153	6.101859
9.650139	10.02232	8.666367
8.229478	8.544732	7.835747
5.573019	6.913441	

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7.677306	8.127359	
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6.069069		4.981496
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	6.337018	
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5.893954	7.025109	
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4.425751	5.028213	
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4.530722		
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	7.009119	
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7.462106	6.697466	7.518939
6.469883	7.083763	5.745318
4.889296	5.186771	
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	5.406901	
	7.000242	
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6.86131	5.343626	6.11115
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	5.668538	
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6.65215	7.632239	
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6.19611	6.180422	
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8.406709	9.291815	8.388002
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7.474116	7.872553	7.73133
6.501958		
10.43163	10.73163	10.45827
10.40338	10.7093	10.33381
4.698179		
6.65176	6.67951	6.247456
7.725162	8.156033	
6.349237		
8.522375	9.323366	7.735751
	6.598723	
6.203481	6.286703	5.552591
3.41432		
4.929244		5.059174
	5.996109	
8.025474	6.692117	7.520765
6.92936	7.378312	
		5.088106
	5.038469	0.875071
6.852324	7.155001	6.894874
	7.178396	
7.648758	7.228516	8.085443
6.792165	6.838845	7.064916
7.944078	7.230934	6.119126
7.518729	9.026475	8.647657
5.965324	6.340683	6.693892
8.784261	9.752391	8.927048
	6.304921	5.93088
4.786024		5.473803
5.181035		2.438719
7.010671		6.998017
6.562008	6.679415	7.17852
4.675332	6.064722	6.01461
5.822641		
9.493411	9.028023	9.725217

7.628933		
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5.429124	5.05818	
	1.202296	
	6.091641	
8.727393	8.964196	9.292197
3.888799	5.342576	4.86216
		6.399431
	4.726584	
6.807399	7.837123	6.588025
5.931884	6.28034	6.436875
6.600034	7.134993	7.157445
4.388075		
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6.647313	6.484935	6.694095
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		6.083005
	6.208055	
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6.192203	6.85446	6.840685
	5.257968	5.92694
8.605071	6.920523	7.32755
7.068224	7.685686	6.765116
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	4.943528	5.328502
9.389796	8.814181	8.961108
7.753606	7.534802	7.1382
6.89321	8.021099	
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4.581906		
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5.401107	6.209871	6.361243
6.522757	7.3877	
6.007311	6.540239	
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6.330838		7.120132

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	7.194012	
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5.80518		
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	5.592067	
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8.660807	8.174405	8.230736
5.7195	6.107329	6.559996
7.759335	7.115178	7.733086
6.783555	7.097428	6.174289
8.467623	8.555616	8.057462
	5.505567	1.502313

	5.237921	
	5.265521	5.813654
	6.38838	6.623505
5.846793	5.633643	6.535076
	5.440878	
	6.787124	
6.537184	6.490267	6.104971
7.377431	7.201606	7.499306
5.49184		
8.664421	8.750101	8.142381
		1.88011
10.11439	10.47518	9.167619
6.681935	5.709633	6.821892
	6.041247	
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10.8035	11.67021	11.65116
9.029918	9.014987	9.782314
8.227263	7.578224	7.760994
	5.174251	
7.033873	7.475031	
5.321549		
6.371218	6.16411	6.206026
7.457795	7.971391	7.547215
7.944015	7.567346	8.029444
	4.954074	
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8.192327	8.482678	7.841737
3.90268		
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5.521802		6.283799
	5.495507	
8.901482	9.20303	8.389608
5.894045		
8.866325	9.791177	7.966407
5.898791	7.131964	4.702714
		5.680416
5.571648	5.818459	3.276636

5.959755		5.943671
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7.804223	8.294788	7.723421
8.195995	8.817876	7.706355
2.321534	6.036865	
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5.266388		7.158783
	4.06002	5.615675
	5.721597	6.150116
5.923967	5.827777	5.912435
4.898598	5.002675	
	6.098614	
		4.264128
4.730323		
	3.86977	5.420458
5.570438	5.274133	5.817006
7.587053	8.415294	6.443132
6.398456	7.276912	6.116155
7.762127	7.366461	7.297343
8.948183	9.347583	7.856785
8.184591	7.947421	7.874796
7.235184	5.60034	7.346741
1.858412		
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9.429704	9.214417	8.134071
8.374325	7.51896	9.324493
6.808954	6.938131	7.813492
6.196391	7.421516	6.482592
9.11993	9.908046	8.97114
		1.040578
9.068363	9.857381	9.292546
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6.978872	6.797823	6.479885
	5.861809	
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	6.045388	
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5.705417		
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7.560882	7.353293	6.99468
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	6.426533	
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7.047214		
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8.380783	8.666943	7.550481
5.315173	6.097807	6.901861
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5.851311	5.553799	6.786275
6.091771	5.603207	4.278606
7.141563	7.516277	8.045445
	6.668138	
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6.753908	6.812414	7.227823
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	4.392114	
6.248356		
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8.727075	9.331056	8.053959
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9.095387		8.505143
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4.881044		6.111895
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	6.22941	
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	5.896998	6.555743
6.130514	7.22486	5.465642
5.382662	4.947615	
		5.188627
5.785648	5.821605	5.645703
5.002868	4.677056	5.52033
11.52988	11.17969	10.77968
		5.792442
6.395472		5.442065
10.74601	10.95713	10.60068
5.653599	5.894681	5.404042
6.302821	7.690421	6.162705
5.592444		
6.649007	6.559784	
7.217349	6.024894	8.019821
4.774242	5.093262	
7.119636	7.041873	6.999798
5.708025	6.453963	5.65964
5.489883	5.986796	6.338448
4.767837		
2.215758		
5.477061	6.437297	6.468503
5.424062	5.805588	5.640402
9.2419	9.293354	10.07089
4.831912	6.405898	5.961879

5.344367	6.17646	6.142713
5.952122	6.993429	
8.768899	9.661927	7.213629
8.062014	9.306862	8.197994
7.709683	9.251502	7.254026
7.932496	8.734598	8.576534
5.590321	4.878989	
6.488563	6.985067	6.1423
8.126474	8.241809	8.178816
	4.352637	
0.411414		
6.011218	6.324194	
6.947292	6.895277	
6.924268	6.992072	5.808892
	7.237159	
8.411391	9.31993	7.63502
5.674981	5.960685	
7.167464	7.436578	7.149421
7.11313	7.693391	6.700474
9.761377	9.550709	10.66785
9.562269	9.488277	9.590611
		4.159612
7.873241	8.254268	6.903086
6.780585	7.643879	6.181
4.156899		
		2.795949
		5.486876
5.46591		
6.05832	7.928287	
4.823264	5.286447	
4.963239	6.304823	6.318296
6.642228	5.553357	6.923739
	6.029676	
5.978632	6.286824	
	6.367189	
5.546253	5.857208	6.705602

6.643848	7.800683	
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	4.915179	5.549276
5.631789	6.464297	5.820147
	7.706348	6.741742
2.847145		
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		5.888989
4.782538	6.008398	
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5.739631	6.09178	6.246096
	2.149507	
6.669207	6.969171	
6.863912	6.934081	6.190309
7.900541	8.58894	7.917942
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7.09973	8.937766	6.814799
8.85741	10.16663	8.496955
9.018594	9.162757	8.309699
	4.326311	
8.281326	8.770796	8.433845
6.978043	5.997024	
6.782186	6.340017	6.402812
5.980313	7.065726	7.461612
		2.854282
6.144023	7.12896	6.725092
6.113657	5.918839	
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5.324846	5.63669	
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5.780455	5.461227	
	5.613838	5.779904
	6.799225	7.862276
5.667119	6.199165	5.841162
	1.074747	5.370474
	4.908014	5.977174
5.706564	5.875949	6.939536
5.500293	5.857318	5.34469
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7.373463	7.342536	5.647607

6.302794	6.797033	6.795548
7.276079	7.558962	5.912664
4.721957	6.427078	6.333012
11.24985	10.16445	11.40039
	5.628608	
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9.875211	9.759337	9.072075
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6.230037	6.467981	6.008017
3.164542	5.280917	6.122815
7.315134	7.159465	6.509419
	7.869138	
7.163997	6.60587	6.747542
8.428398	8.890918	9.091119
7.655088	6.397162	8.395597
5.991112	6.46681	5.278351
6.496083	5.989458	6.049781
8.677185	8.229872	8.499269
	4.708776	
		4.798098
5.698099	7.135889	6.636297
7.224109	6.819002	6.888461
6.294567	7.956718	
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3.798821	6.180178	5.248128
6.496514	6.249677	
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6.732077	7.036636	6.634814
5.926851	5.62571	
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5.809722		6.067228
6.525975	6.564713	6.987939
7.354893	8.039639	7.017477
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5.948623	7.698354	
5.929321	7.701302	
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7.554984	7.672534	6.960836
		5.828915
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1.747719	5.096094	5.55152
5.663551	5.332385	5.624482
6.5619		7.187686
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6.289414	6.347986	6.140702
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5.857478	2.901811	6.292068
	5.891231	5.596475
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5.76769		
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3.595054	5.305384	6.389391
	6.348903	
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9.719298	10.07076	9.33499
5.721573	5.307185	5.427182
	5.376063	
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7.500472	8.206874	7.204439
4.308731	4.535085	
4.275824	5.114735	
		5.936635
4.11413	4.647039	
5.923894	6.155614	5.658161
6.304546		6.226339
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11.52026	12.01779	10.7113
8.404135	7.927353	7.690402
11.66185	10.78944	11.26488
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7.639731	7.695503	8.263375
6.467177	7.54225	6.669176
4.710789	5.201039	6.080452

5.466887	6.518669	6.142422
5.86146	6.701272	5.97995
6.053359	6.546514	5.692877
6.943034	7.633516	7.173384
5.574362		
5.681727	6.258126	6.178839
6.78796	6.220423	7.174479
6.737376	6.692005	7.582136
	3.452026	
10.28624	10.45019	10.38104
7.307945	8.154221	
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7.499197		7.456801
7.359818	7.243568	6.782114
7.619866	8.072246	6.407346
7.280267	6.781413	6.340803
	6.474646	6.887315
8.914129	8.897666	8.550903
13.06907	13.32659	13.31924
6.714696	7.228517	6.922174
6.070015	5.620906	4.575016
7.446901	6.992198	8.416864
7.101536	6.173799	6.93575
4.516254	5.265206	6.187994
7.272964	7.687213	
6.526279	7.179109	6.201163
	2.777661	
6.482377	7.968091	5.934212
5.593554	5.515875	
	1.76714	5.036292
8.526196	8.599466	7.92336
9.049148	10.09219	7.82367
3.337357	5.86923	
7.878991	8.568225	7.392637
	5.709301	5.067106
6.021369	7.16278	
6.830871	7.781122	7.379914
4.438685		

5.13796	5.913741	4.883201
6.750583	7.40061	6.08873
5.930648		
9.636749	10.03103	9.069784
12.24437	11.53714	12.12665
9.447087	8.632519	9.487063
5.442257		
5.632881		
6.755231	7.543378	5.496379
6.375999		6.641944
8.912056	8.946646	8.388762
4.937815		
5.182347		
8.228943	9.653464	6.999224
7.652226	7.749707	7.414813
5.81278	6.172517	
	6.4731	4.039961
4.039641		