FoldChange	P.Value	ProbeName	GeneName	HS gene ortholog	Hs gene description	IPA_Endocytosis	IPA_term_increases endocytosis by eukaryo	SystematicName	ProbeUID	Row	Col	Start	Sequence
5,431	1,61E-11	A_15_P107148	opn1mw2	RHO	rhodopsin		increases endocytosis by eukaryotic cells	NM_182891	705	11	18	1517	TTCACATCGACATTATGGATTGTCACTCCTTTATTTTTGTTTTCAGCTGATTTGTCAGCA
4,832	3,01E-11	A_15_P171121	c3b	C3	complement C3		increases endocytosis by eukaryotic cells	NM_131243	1006	15	20	4962	GGATGTTTGACATAACTGCATTACGCCTGTTTGCTGATTACAGATAAAAATTAAACACCA
3,404	1,20E-09	A_15_P193006	tgm2	TGM2	transglutaminase 2	Endocytiosis	increases endocytosis by eukaryotic cells	NM_001004647	43125	523	75	2013	GCGATAAACTACACAACATTGAGACCTATGAGAATCTGGTTATCTATGAATAAATGAGCT
2,890	3,14E-09	A_15_P197221	LOC792467	APCS	amyloid P component, serum		increases endocytosis by eukaryotic cells	ENSDART00000066296	36184	440	13	540	TATATCAGCTGGCACAATCTGATGTACACCATTTTTGGGTCCGCAGAAATCAATGAAAAG
2,504	8,08E-09	A_15_P297181	LOC792467	APCS	amyloid P component, serum		increases endocytosis by eukaryotic cells	ENSDART00000066296	37786	458	65	479	CCTAACCACCAATCAGATTAAGACCTACATGGAGGCAAAGAGCAAATACAAACTTGGTGA
2,401	1,73E-08	A_15_P544897	opn1mw2	RHO	rhodopsin		increases endocytosis by eukaryotic cells	NM_182891	9662	120	50	921	GCTTTTTTCTCAAAAGCCTCTGCCTTGTTTAACCCCATTATCTATGTGCTCCTAAACAAA
2,389	1,41E-08	A_15_P107384	zgc:101554	CFH	complement factor H		increases endocytosis by eukaryotic cells	NM_001007418	30859	375	10	2295	TCAGTCCTGCAGCACCCAGAAGAAAGCTGACTATACGAGTGCTTTATTTCTCTTTATTAA
2,231	3,77E-08	A_15_P100433	zgc:86661	LUM	lumican		increases endocytosis by eukaryotic cells	NM_001002059	9599	119	18	1895	AAGGATATTCGACTGTTTTCTACAACCTATGGATATGAACTAAATGCACAGCAGTGCATT
2,210	3,58E-08	A_15_P177451	BC122168	PFN1	profilin 1		increases endocytosis by eukaryotic cells	BC122168	26590	324	38	954	AATCCTACTGAACAAAGCCAAGAGTTGTGACTGCTAGATGCCAAATAAAGAGATTAATTT
1,988	1,86E-07	A_15_P101735	LOC558956	ISG15	ISG15 ubiquitin-like modifier		increases endocytosis by eukaryotic cells	BC151911	6502	81	53	844	AGGGCAAAAGATCGTCTCTCGTAATAAAAGATAGGCTTACCGTTTCATGATGAGAAATGA
1,984	2,21E-07	A_15_P410255	BC151894	PFN1	profilin 1		increases endocytosis by eukaryotic cells	BC151894	42090	509	81	563	GATCTGAGATGCAGAAAACAAACATGAGCTTGAGAAGCTCCACCTTCATTACCTTTGTTT
1,771	1,27E-06	A_15_P150101	zgc:110064	APOE	apolipoprotein E	Endocytiosis	increases endocytosis by eukaryotic cells	NM_001020565	18830	230	56	1002	AACTACATGTATGCGGCTACAGATGTAGCCAATGTAAGATCAATAAAGAAGCATGTACCA
1,765	1,56E-06	A_15_P109105	zgc:110250	HRAS	HRas proto-oncogene, GTPase	Endocytiosis	increases endocytosis by eukaryotic cells	NM_001017623	35671	434	6	570	CAAAACCAGACAAGGTGTGGAAGATGCATTTTACACGCTCGTACGAGAGATTCGTCAACA
1,738	4,53E-06	A_15_P110543	calr	CALR	calreticulin		increases endocytosis by eukaryotic cells	NM_131047	12506	153	59	1444	CAACCTGTTAAACTAGACTAATAAATGTTTGGGTTTTCTGTTCGGTCTCGAGTTGCGCAA
1,700	2,08E-06	A_15_P116801	yrk	FGR	FGR proto-oncogene, Src family tyrosine kinase		increases endocytosis by eukaryotic cells	NM_212781	38969	471	76	2955	TGGAGAATGTGTATTTCAGTTATGCAATGTGTTTGTGCCAATCTATTACACTGAGCTTAC
1,696	5,59E-06	A_15_P195581	cxcl12b	CXCL12	C-X-C motif chemokine ligand 12		increases endocytosis by eukaryotic cells	NM_198068	42006	509	38	3110	CGTTTTGACTCAAATGCCCGATTGCTGTAATGTTTTTGAGCCACTTTAAAAAATATAAGG
1,690	2,52E-06	A_15_P408670	yrk	FGR	FGR proto-oncogene, Src family tyrosine kinase		increases endocytosis by eukaryotic cells	NM_212781	2065	28	80	2959	GAATGTGTATTACAGTTATGCAATGTGTTTGTGCCAATCTATTACACTGAGCTTACTGAA
1,684	3,55E-06	A_15_P161226	tgm2b	TGM2	transglutaminase 2	Endocytiosis	increases endocytosis by eukaryotic cells	NM_212656	26950	327	51	2325	ATGGAAGTCTGACTGAGATTTTAGGCCATATACAGTAAATTCTGCATGCTCATGTTGTTT
1,678	5,78E-06	A_15_P211051	zgc:56558	PRKCD	protein kinase C delta	Endocytiosis		ENSDART00000033819	22963	280	44	2849	GGACTCTGTTTTAGGATGAGAAACTTCACAGTGTCTAATAAACATTTGATGGTGAAAAAC
1,655	7,27E-06	A_15_P115347	tnfsf10l2	TNFSF10	TNF superfamily member 10		increases endocytosis by eukaryotic cells	NM_001002593	19077	234	11	1727	TAATCTGAAACTGACTTTCAGTTTAGCATAACTATGTACGTTACAGTACACTGTGTTCTC
1,632	1,11E-05	A_15_P119413	opn1sw2	RHO	rhodopsin		increases endocytosis by eukaryotic cells	NM_131192	29789	361	57	1275	ACGTAGACCCAATAGGAATTTTTGCTTTTAATGTCAACATTTTTGTAACTTGGTCTTGGC
1,619	5,28E-06	A_15_P170836	tnfsf10l2	TNFSF10	TNF superfamily member 10		increases endocytosis by eukaryotic cells	NM_001002593	783	11	57	1520	CATTCCTAAAGCATGAATCTTGTACATTGACCTAAATGTGAAGATCACTGTGACTTTGTA
1,618	1,21E-05	A_15_P121420	snx5	SNX5	sorting nexin 5	Endocytiosis		NM_214769	21787	265	37	2441	TGACTGAAAAGATGGGACGTCATTTTCGTATGGATTACCCTTATTTTTATGAAAGCTTGC
1,581	1,44E-05	A_15_P101067	itgb1b.2	ITGB1	integrin subunit beta 1		increases endocytosis by eukaryotic cells	NM_212928	920	14	52	2203	ATTTTTAGAAATGCTGTGATGCAAAAATACTACACAGAGTGAATTGTCTTAATGCCTGGG
1,577	1,52E-05	A_15_P147571	ENSDART00000097325	C5	complement C5		increases endocytosis by eukaryotic cells	ENSDART00000097325	16272	199	29	5005	GCAGCGATGCTAACTGCAAACAATATGTCAAAGTTTTGGAAGGATTTGAATTTGAATACT
1,520	4,96E-05	A_15_P106918	vim	VIM	vimentin		increases endocytosis by eukaryotic cells	NM_131872	4000	51	51	1709	CGACCAAAAACGTGATGAGCTTGCGTCTTCTGCACCATTAGACCAAACAACAAACTGACA
1,506	2,91E-05	A_15_P157486	vldlr	VLDLR	very low density lipoprotein receptor	Endocytiosis		ENSDART00000023766	1614	24	12	3065	CTTTCTCATGATGAACATTGTTTCCCAGAGATGCTTCGTGAGTCTTGCTGGGATAAAAAA
1,502	0,000158832	A_15_P133251	scarf1	SCARF1	scavenger receptor class F member 1	Endocytiosis	increases endocytosis by eukaryotic cells	AY732220	15763	194	26	954	TGTGCCTATGAAGAGAAACATCTGTGAACATACTCTTAAAGGGCATTACTTTCTTCTTTA
1,494	3,08E-05	A_15_P113895	shha	SHH	sonic hedgehog	Endocytiosis		NM_131063	4652	60	46	2443	GCTGATGCACAGTTTGGATAGCATATGATGAGTGGCCATACCAGTTAACCTGCCTTTCAT
1,480	4,35E-05	A_15_P205246	zgc:162029	MYH9	myosin heavy chain 9		increases endocytosis by eukaryotic cells	NM_001098177	41360	501	29	2897	GCCTATAAATTGTCAAACTCTGTGCATTGGTAGTGGAATTACTGTATTTGCAACAATTGA
1,480	3,82E-05	A_15_P141671	cxcl12a	CXCL12	C-X-C motif chemokine ligand 12		increases endocytosis by eukaryotic cells	NM_178307	15071	185	12	962	TTCTGAAAACTCATATGCATGCAAGTGCTTTGACACAAAAAGAAGGGCATTGATTTTATC
1,471	5,94E-05	A_15_P112747	anxa1a	ANXA1	annexin A1	Endocytiosis	increases endocytosis by eukaryotic cells	NM_181758	37475	453	79	1105	AAGATCCACCAGATGTCAATATATGCAATAAAAACCCCGTACACAACAAGCAACTATAAC
1,465	0,000457654	A_15_P177511	zgc:103710	C3	complement C3		increases endocytosis by eukaryotic cells	BC122311	21672	263	64	1265	GGCTGTAAGAACACTGCAACAACAATACATACAAATAAAGCGTGACTCTTTTTACTGAAA
1,460	6,16E-05	A_15_P103549	cav2	CAV2	caveolin 2	Endocytiosis		NM_001002150	4211	54	73	1616	GCTGAACACAGCTCAGCTTATGAAAGACAGAACTAAATGCCTCACAGTTCACCAAATAAA
1,447	0,000324432	A_15_P145521	LOC562438	LRP2	LDL receptor related protein 2	Endocytiosis		ENSDART00000007453	6753	86	11	4004	AGCTAGATCGAATGGAAAGGACACAGAAGTATCAGAGGAAAATGTGGTGACGTCTGTGGA
1,430	0,000109622	A_15_P113040	sfrs3	SRSF3	serine and arginine rich splicing factor 3		increases endocytosis by eukaryotic cells	NM_201323	21077	257	16	472	CGCGAGAGGAACCACAAACCATCACGATCTTTCTCCCGGTCGAGGAGTCGTTCCAGATCT
1,426	8,66E-05	A_15_P162531	zgc:56142	S100A10	S100 calcium binding protein A10	Endocytiosis		NM_213003	5707	72	71	481	GCAACTGCAGTTACAATGCATTTTTGCAAATGAGGATGTTTTGTCATTTTTGTCAAGTCA
-1,404	0,000155702	A_15_P264826	LOC100005846	ELMO1	engulfment and cell motility 1			ENSDART00000077742	40651	493	2	370	TAGCAGATATCAAAGCAGTGGTAACAGGTAAAGACTGCCCACATATGAGGGAGAAAGGAG
-1,415	0,0001375	A_15_P120385	zgc:86833	PSMD4	proteasome 26S subunit, non-ATPase 4		increases endocytosis by eukaryotic cells	NM_001002112	2365	31	68	1277	AATTCACACATGGCTTGCTTGCTTCCTCTTTTGCTCTGTTCACAATTGATTAAATATTTG
-1,416	0,000102226	A_15_P108168	zgc:100846	C9orf72	chromosome 9 open reading frame 72	Endocytiosis		NM_205603	15014	184	68	1619	GCATTCTGCACTGTGCCTGCTGCTGAAATGCCAATTTGTGCAATTTTTGCTTTAGAATAA
-1,417	0,000327631	A_15_P114328	sypb	SYP	synaptophysin	Endocytiosis	increases endocytosis by eukaryotic cells	NM_001002501	26426	321	39	650	CAACCTCTGGTTCATCTTCAAGGAAACCGGCTGGATGGCGGCTTTCGCTGGCACCTACAT
-1,446	7,72E-05	A_15_P176116	grnb	GRN	granulin precursor	Endocytiosis		NM_212738	38727	469	38	2257	CCAAAAGTCCAAGGTTGCACTAAATCATCCTCATCCACGTGGTGGAATAATTCTCTCTAA
-1,462	6,09E-05	A_15_P114058	ldlr	LDLR	low density lipoprotein receptor	Endocytiosis		NM_001030283	42720	520	14	2661	CAGAAGACCACAGAGGACCAGGTGCATTTATGCAGAAACAACAGTTCTGATGGCTATTTT
-1,468	8,06E-05	A_15_P148046	gip	APOA1	apolipoprotein A1		increases endocytosis by eukaryotic cells	NM_001100144	16685	204	67	251	AGAAAAACTTTGTGAACTTTCTGCTGAATCAGAGAGAGAAGAAGAGCGAACCGGCTCTGA
-1,468	5,83E-05	A_15_P528837	hmox1	HMOX1	heme oxygenase 1		increases endocytosis by eukaryotic cells	NM_199678	4809	61	42	703	GATGTGTTTGATGATCTTCAGAAATGCTGAGCATCACAGAGGAAGCTTCAAGTGATAAAG
-1,473	3,94E-05	A_15_P119575	psmd4	PSMD4	proteasome 26S subunit, non-ATPase 4		increases endocytosis by eukaryotic cells	NM_001017624	22537	273	82	1440	GTTCATTTTGTATCACTGTTTTCAGTTCCTTTTGTAATAAAGGGCTTTGCTATGGTTGAG
-1,477	4,76E-05	A_15_P106879	arr3	ARR3	arrestin 3	Endocytiosis		NM_200792	3039	39	73	1480	ATGACACTGAACTTAAGCATTGTTCTGATGCTTTTACAATGTCATGTTTATCTCTTCTGC
-1,483	5,53E-05	A_15_P111321	scarb1	SCARB1	scavenger receptor class B member 1		increases endocytosis by eukaryotic cells	NM_198921	27816	337	68	1688	ATTACTACAGTCACCAACCAGCTGAACCATCATCCACATTCACAATATTTAAAAGTTCCA
-1,496	3,86E-05	A_15_P133296	rhoaa	RHOA	ras homolog family member A	Endocytiosis	increases endocytosis by eukaryotic cells	NM_213137	18152	222	52	402	TAATAAAAAAGATTTACGGAATGACGAGCACACTCGACGGGAGCTGCAGAAGATGAAACA
-1,504	4,59E-05	A_15_P117421	zgc:101880	S100A10	S100 calcium binding protein A10	Endocytiosis		ENSDART00000054469	24906	303	24	481	GGTCTTGACATTCTTTGGCCTACAAACAGTATTTTTTCTTGAGCTTGTCCTAAAAACAGA
-1,534	3,95E-05	A_15_P169196	psmd4	PSMD4	proteasome 26S subunit, non-ATPase 4		increases endocytosis by eukaryotic cells	NM_001017624	3782	49	25	943	AAGTGAAGCTCCTAAGGAGGATGAGGAGGATTACGATGTGATGCAGGATCCAGAGTTTTT
-1,555	6,68E-05	A_15_P114288	abcf1	ABCF1	ATP binding cassette subfamily F member 1		increases endocytosis by eukaryotic cells	NM_213186	20763	254	24	3253	CTGTCTAGAATTATGAAATAAGCAGGGCTGTTGACTCATTGGGTTTGGATAGAAACCGAA
-1,594	7,21E-06	A_15_P503397	abcf1	ABCF1	ATP binding cassette subfamily F member 1		increases endocytosis by eukaryotic cells	NM_213186	35844	436	11	532	TGGTGGTGATGATAATGATGATGATGATGACAAACCCAGAAGCAAGAAGAGCTCTAAGGA
-1,595	3,17E-05	A_15_P156271	ENSDART00000026535	DNM1	dynamin 1	Endocytiosis	increases endocytosis by eukaryotic cells	ENSDART00000026535	39082	474	48	1278	GGATTTGCCAATGCTCAACAGAGAAGCAGTCAGATTAAGAAGAAAGCAGCTGGGAATCAG
-1,670	4,24E-06	A_15_P111782	cd36	CD36	CD36 molecule	Endocytiosis	increases endocytosis by eukaryotic cells	NM_001002363	24943	304	42	1608	TCTGCCATTTTGTGGTCTTACTGTGGTTAATTTCAAAATGAAATAGTTTTGTATGTCCGC
-1,797	1,69E-06	A_15_P179256	zgc:86833	PSMD4	proteasome 26S subunit, non-ATPase 4		increases endocytosis by eukaryotic cells	NM_001002112	20348	247	69	347	CGCTTTTGTGGGCAGCCCAGTAGAGGACAATGAAAAAGATCTGGTGAAGATGGCAAAAAA
-1,801	3,71E-05	A_15_P131436	hsp90a.1	HSP90AA1	heat shock protein 90 alpha family class A member 1		increases endocytosis by eukaryotic cells	NM_131328	29578	360	34	210	TCCAACTCCTCTGATGCATTGGACAAGATCAGATATGAGAGCTTGACAGATCCGAGCAAA
-1,849	5,48E-07	A_15_P102524	mycb	MYC	MYC proto-oncogene, bHLH transcription factor		increases endocytosis by eukaryotic cells	NM_200172	22830	277	61	1440	AGGGTGTGGCAAAGTAGTGAGCAATCTTGCATTGATTTATACAATTCACACTGCCTCAAT
-1,860	6,95E-07	A_15_P102590	hsp90a.1	HSP90AA1	heat shock protein 90 alpha family class A member 1		increases endocytosis by eukaryotic cells	NM_131328	20467	250	44	1762	TGTGCAAGATCATGAAGGATATCCTCGACAAAAAGATTGAGAAGGTCACAGTCTCCAACC
3,435	4,57E-10	A_15_P114421	adob	ADO	2-aminoethanethiol dioxygenase			NM_213193	34014	414	12	1594	AGGTTCAAAACACTCACTTGACAAGCTGGCCTACGTGACACTGGACACAAAACCTTTTTT
1,708	2,31E-06	A_15_P111812	adoa	ADO	2-aminoethanethiol dioxygenase			NM_001008634	12294	151	35	1529	ATAAGTGCACCATATAAAATCTTGCTTAATTTATTTTAAAAGACTCTACACAAACACTAA
1,783	1,34E-06	A_15_P206911	zgc:136576	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase			NM_001079977	5409	70	5	3773	CATTCTGAATACACTGAAGAGAAGCTTTTTATTGAGTTTTCCCCCAAAGGAACAATTCAA
1,623	7,68E-06	A_15_P147281	zgc:136576	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase			NM_001079977	22725	277	7	2811	CACAACAGATCAAAAGTAAACTTGCAAGAAGCTCCAGGAACATGCACTAAGCAGGCATCT
1,523	2,14E-05	A_15_P102310	hmgcs1	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1			NM_201085	18251	223	17	3068	CAGGTGGAATTTGTAGCAAAGCAAGCTGTACAGACTATGTCAAAACTGTGTGGGAATCTG
1,534	1,89E-05	A_15_P144951	LOC553326	HACD1	3-hydroxyacyl-CoA dehydratase 1			ENSDART00000029992	8327	103	50	1760	GGTGCTACATTATTTTATTCTTCTGTGCAGCTGAGAAGAGAAAGATTTGTCATCATTAGA
1,772	1,03E-06	A_15_P174821	zgc:163053	BDH1	3-hydroxybutyrate dehydrogenase 1			NM_001089509	37641	456	77	1131	CCACATATGTCCAATCAAGTCAGTATGCAACCTTAATTGAATAAAAGAATCGCATGTCTT
1,736	2,09E-06	A_15_P209151	zgc:163053	BDH1	3-hydroxybutyrate dehydrogenase 1			NM_001089509	18775	229	29	1129	GTCCATATATGTCCAATCAAGTCAGTATGCAACCTTAATTGAATAAAAGAATCGCATGTC
1,673	3,06E-05	A_15_P104772	oxct1b	OXCT1	3-oxoacid CoA-transferase 1			NM_001077150	35602	432	54	890	GCCAGCTATGAAAAAAGAATCGAGAAAAGGTTGGTTCAATCAGGCAAGGAGGAGAAGCCT
-1,424	0,000585929	A_15_P130526	oxct1a	OXCT1	3-oxoacid CoA-transferase 1			NM_001007291	38699	469	24	1139	TCACAATACTTCCTGGAGCTGCTTATTTTTCCAGCGACGAATCCTTTGCCATGATCAGAG
-1,701	2,34E-06	A_15_P118837	oxct1a	OXCT1	3-oxoacid CoA-transferase 1			NM_001007291	36774	446	57	2019	TGTTCTTTCCACATTGTGTACATATCACTTGTACAAAGCAATAAATGTCTATTCGTGACC
-1,645	5,95E-05	A_15_P119952	zgc:92456	HPD	4-hydroxyphenylpyruvate dioxygenase			NM_001003742	21861	266	75	1283	CTTAATCAAGCGTGTGCCATTCATAATAATTTGTACCCAAATGTTTCTTGAACTACAGAC
2,333	1,16E-07	A_15_P468060	alas1	ALAS1	5'-aminolevulinate synthase 1			NM_201287	36309	439	77	2050	AGGCCAGTCACATGTCCATTCCTGTGTGATCAGCATTATGTGTCTGCTCGTCAGTTTTAA
2,220	7,42E-08	A_15_P117006	alas1	ALAS1	5'-aminolevulinate synthase 1			NM_201287	36546	444	26	2059	ACATGTCCATTCCTGTGTGATCAGCATTATGTGTCTGCTCGTCAGTTTTAATAAACTAAT
2,133	8,77E-07	A_15_P160186	alas1	ALAS1	5'-aminolevulinate synthase 1			NM_201287	8780	109	25	1106	AAGTTTATCTTCCGTCACAACGACGCCAAACATCTACGAGAGCTTCTGGAGAAATCCGAT
13,245	2,35E-13	A_15_P210731	alas2	ALAS2	5'-aminolevulinate synthase 2			NM_131682	35683	434	12	2313	CAGAGTCTGAACACTCTAAAGTTGTCACTTTAGTTGTTTTGAATGGGCCCTCTTTCTAAA
10,068	3,78E-13	A_15_P205966	alas2	ALAS2	5'-aminolevulinate synthase 2			NM_131682	5362	67	67	1794	CATTTTAACAGCTCAAGATGTAGATCTTCCATCAGATTACACTGACACTTCAAACCAAAA
2,476	8,80E-09	A_15_P195826	zgc:153357	NT5DC2	5'-nucleotidase domain containing 2			NM_001077143	16676	203	63	2726	CGGTTTTCCAGGAACAAGAAAGATGTCATCTTTTTGTATGTACGTGCTCTACAATTTATA
6,271	4,60E-11	A_15_P100069	zgc:92102	NT5DC4	5'-nucleotidase domain containing 4			NM_001004549	41463	501	81	2109	ATTTACATCAATACAGGGGTTGACATGAAGACTATAAAATGTTTCTACTCCTGTGAATGC
1,533	3,02E-05	A_15_P549377	ENSDART00000104740	NT5E	5'-nucleotidase ecto			ENSDART00000104740	11014	135	61	1972	AACACTCCATCTATGAGCGGGGATCTATTTCACGAGGAATAATCCAGGGATCTGAGTTAT
1,507	2,37E-05	A_15_P210891	ENSDART00000104740	NT5E	5'-nucleotidase ecto			ENSDART00000104740	22950	279	38	2038	CTGCTTAGAAACATTCCTACAAGTGAGCGTCTGCCTCAATAAATGTGTATTTATTTTGTT
6,058	7,91E-12	A_15_P119080	pfkfb3	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3			NM_213397	5451	70	26	3145	ACTAGTCTGTGTTTCATGCACTTTGTTCATAACTGAGATTCTAGAGCATATCAGCAAATA

1,746	1,37E-06	A_15_P148791	zgc:123288	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	NM_001037377	31705	385	20	1392	TCGATTGATTTGAAAGTGGAAGCTGTGAACACACACAGAGACAGACCGACGAACGTAGAT
-1,521	3,32E-05	A_15_P178711	LOC100002625	AKAP6	A-kinase anchoring protein 6	BC142908	34478	418	76	911	AGAGGAGTCTGTTACCTCCACCCAAAAACCTCAAGAGACAATCAGTAGCCCCACAAAAAA
1,424	8,93E-05	A_15_P111509	acaa1	ACAA1	acetyl-CoA acyltransferase 1	NM_001002207	5998	76	48	1556	TGTTTTTTAATTACCCGTGTTGAGGACAAGTGTAATATGCTAAGATTTGTAATGCCTCTG
2,040	1,15E-07	A_15_P103169	zgc:56036	ACAA2	acetyl-CoA acyltransferase 2	NM_213052	32311	392	75	1831	ATGTTGAATTCACTCATTTGACTGTTGTTGACAATAAAGAATCAGCTGTATGCTGCTATG
1,684	2,87E-05	A_15_P115996	ascl1a	ASCL1	achaete-scute family bHLH transcription factor 1	NM_131219	33066	401	35	1483	GCCTCCCTCAGAAAATAAGAATATGCCTTATCTCCATATTTTCTACAGTTTAGTCTCATA
1,521	0,000249031	A_15_P176556	ascl1b	ASCL1	achaete-scute family bHLH transcription factor 1	NM_131231	811	12	71	1109	TGTGGCAGTGTTTTTATACCGGATGAATAACTTTTGTATCAAAGTGTGCACTTGTGTGTT
-1,498	3,34E-05	A_15_P171241	zgc:113200	ACP2	acid phosphatase 2, lysosomal	NM_001013337	39265	475	57	1513	TGCAACACAGACTCAGTGTGTGTGCCTCTGTGGTTTTCTACCAAATGATTATGTAAAAAA
-1,586	1,18E-05	A_15_P582607	zgc:113200	ACP2	acid phosphatase 2, lysosomal	NM_001013337	43493	529	54	695	CTCAAGATGTCATGCAGACGCTGAAGCTGTTGAAGAACTTTGGTTTTCAGATTTTGTTTG
1,509	0,000103763	A_15_P112842	anp32b	ANP32B	acidic nuclear phosphoprotein 32 family member B	NM_212603	22081	270	18	1395	GTGGCAGCCTGTGGCACAAATCAAGGTTGTAGCTACATTTTTACTTTCTGTAAGACAAAA
1,707	4,82E-06	A_15_P104622	zgc:92005	ABRA	actin binding Rho activating protein	NM_001003986	14423	177	16	1985	TGTGTGTGCACACATTGCATGAGATGGCATGTTTAATGCATTCGTGTGAACACGTAGTAA
2,478	1,22E-07	A_15_P103868	zgc:86896	ARPC1A	actin related protein 2/3 complex subunit 1A	NM_001002100	41419	502	58	661	TCTGCTGATCTCCACTGCAGAATATTTTCAGCATATATCAAGGACATCGAGGACAGGCCT
1,642	1,28E-05	A_15_P104931	arpc1b	ARPC1B	actin related protein 2/3 complex subunit 1B	NM_213156	13937	172	23	1379	GGTTCTGGATTAACTAAAAAAGGGAATTTTGTCTGAATCTAAATGCTGGTCATAGATTGC
1,530	1,71E-05	A_15_P102017	arpc4	ARPC4	actin related protein 2/3 complex subunit 4	NM_205537	427	8	22	1191	TATAAAAATCCTCACGCTGGTGCACATGGATCTTACAAACCATATCATGATGATGATGCT
1,449	5,97E-05	A_15_P116868	arpc5b	ARPC5	actin related protein 2/3 complex subunit 5	NM_201509	19005	232	60	1495	CTTCACAATGCAGTAATACAGAACGCAAACACTCAATAATAAACCAAACCGGTATGATGA
4,614	4,98E-11	A_15_P331126	actc1	ACTA1	actin, alpha 1, skeletal muscle	NM_214784	1525	21	47	1265	GGGACAGATTTCTACATGTTATTCGAAGAACATACCCTTGAGTAACAGCAGGAACAGGAC
3,893	1,81E-10	A_15_P117428	actc1	ACTA1	actin, alpha 1, skeletal muscle	NM_214784	17678	216	66	611	GTGATCTTACCGACTACCTCATGAAGATCTTGACTGAGCGCGGTTATTCTTTCGTCACAA
1,703	3,53E-06	A_15_P102134	zgc:112098	ACTA1	actin, alpha 1, skeletal muscle	NM_001017750	1073	16	53	36	TGTGTAGCGGGAGCGCTTCAGCTTTACTTCAGGACTCACGAGAACGAGCAGAGGCAGAAC
2,687	3,58E-09	A_15_P101081	zgc:86709	ACTC1	actin, alpha, cardiac muscle 1	NM_001002066	8915	112	9	1238	GCTCAAATTCTCAACATTACCTCCGCATGTCATGCATGCCGGCAGATTTTGCCTTTATAT
2,197	3,89E-08	A_15_P110054	actc1l	ACTC1	actin, alpha, cardiac muscle 1	NM_001001409	15766	193	28	1167	TCCATCGTCCACAGAAAGTGCTTCTAAATCTTCAATCCTTCTCTGTTCAGTCCAACTAAC
1,603	7,94E-06	A_15_P107356	atf1	ATF1	activating transcription factor 1	NM_199723	3234	43	1	1952	TCGAATCAGGGAGCATACGATGAAAAACAAAACATACAATGTCACTTGTTTTAGGTAAAG
-1,608	6,18E-06	A_15_P107601	atf3	ATF3	activating transcription factor 3	NM_200964	16161	198	57	2516	GTGCAATTGCTTCCAAAAGTCATGATTGAGAAGATGATAGCCTGTCAAATTCAATTAACT
1,583	1,03E-05	A_15_P174081	atf7ip	ATF7IP	activating transcription factor 7 interacting protein	NM_001077603	18867	230	75	3202	TGTTAAAGGTTTTTGTAATGTTTTTTGTCTGGTACCCAGACACTCCAAAATGACACTCAA
1,798	1,61E-06	A_15_P104580	acvrl1	ACVRL1	activin A receptor like type 1	NM_153643	32426	394	49	2379	CAAGAAAGACTTGAACCAGCTTTTTAGGAACAAGAACTGCATTACAGCTCGCACCAAGTA
1,818	1,01E-06	A_15_P170736	acads	ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	NM_001003743	26384	322	17	1431	AAGCCTCACTTGATGATTTCACTGGGAATGTAAAAGCATATCTGACTGTACATAATGAGT
1,543	2,26E-05	A_15_P104922	acox1	ACOX1	acyl-CoA oxidase 1	NM_001005933	13099	162	19	2332	TGGACTTTGTGAAAATGGTTCTGTACTGAATAATTAACATTTGGATGAGGATGGTAAGAC
1,566	1,71E-05	A_15_P257996	ENSDART00000089332	ACSBG1	acyl-CoA synthetase bubblegum family member 1	ENSDART00000089332	37269	452	58	1932	CGCCGGCCAGTGGTTTTGCAGATGTATCACAATGAAATAGAAAATTTTTACAGAGAATAG
-1,624	5,19E-06	A_15_P112797	acsl4	ACSL4	acyl-CoA synthetase long-chain family member 4	NM_200649	21310	260	49	3703	TAAGCAAGAATATACAGCAGTCAAGTGTTTGCGTTGAGAAATTGTGAATTTGCTTGTAGA
-1,449	8,52E-05	A_15_P210781	apeh	APEH	acylaminoacyl-peptide hydrolase	NM_198869	4136	53	35	3293	CTACTGTGCGGGAATCTCTGCATTGTTTCCAATAAAATCTTCAGACTTTTGTAAAGCTGA
1,829	6,79E-07	A_15_P192701	adora2a.1	ADORA2A	adenosine A2a receptor	NM_001039815	17081	209	16	1310	CATATTAAATCAGCTCTGTATGTACAGACAGCTCACTGTGTTGAACTCACGGAGGTTTCC
1,641	8,36E-06	A_15_P118807	adka	ADK	adenosine kinase	NM_212791	25553	311	17	2456	TCGAATGTGTCACGATCAAAGAAATCTGTTGTTGTGTGAGCATAACCTCTGCCAAAATAA
1,434	0,000116362	A_15_P151531	adka	ADK	adenosine kinase	NM_212791	39088	474	51	1850	GCATGAAAAAAGCCAGCCAATAAACTGGTTATTGCAAGAAATAGTCACAATTCTAACAGA
1,422	0,000120995	A_15_P463595	adka	ADK	adenosine kinase	NM_212791	39363	478	23	1627	AAATTGTGAGATACAAACTCTTGACTTCTTTCGGTCATGCTGTATATCTCTCAATTCAGT
-1,891	6,36E-07	A_15_P107904	adkb	ADK	adenosine kinase	NM_198802	19906	243	12	1743	GATGGTTCAGCTGACCAGTTTAATAAAAGGTTTTAATTGTGTACAAGTTGTGTATCTCTG
-1,975	1,72E-07	A_15_P149001	adkb	ADK	adenosine kinase	NM_198802	31927	388	48	1637	GTGTCTTTCAGGTCTGTATTGTTATGAAATGCCAAATTGTATCTTAAGCGCACAATCTTT
-1,424	0,000134754	A_15_P103546	zgc:77905	AMPD1	adenosine monophosphate deaminase 1	NM_200893	34588	419	47	542	GTTGCTCGTATGAAGGATGGTGTGATCTACGTGTATAAAGACGCAGCTGCTGCTGATAAA
-1,621	8,09E-06	A_15_P105123	zgc:77905	AMPD1	adenosine monophosphate deaminase 1	NM_200893	1728	24	70	2231	GAAGCCCATGAGATGACGTCCATGTCTTACTGCAGTTTGCAGTTAATAAGTTTACACCCC
-1,711	1,95E-06	A_15_P115764	ampd3	AMPD3	adenosine monophosphate deaminase 3	NM_199848	17298	212	41	2576	CCTATTGATGATGCACATTTCACTTCCCATGGTGCCTTAAAGGTGTTGGATATAAACATT
-1,608	6,06E-06	A_15_P103201	ahcy	AHCY	adenosylhomocysteinase	NM_199218	4290	55	29	1845	AGTCTGGGTAGCTTGTCCTGTTTTATTACATCCACTTATGAAGACCTGATAAAATAAATG
-1,660	3,25E-06	A_15_P170326	ahcy	AHCY	adenosylhomocysteinase	NM_199218	17617	215	36	1850	GGGTAGCTTGTCCTGTTTTATTACATCCACTTATGAAGACCTGATAAAATAAATGTGGTA
-1,698	5,34E-06	A_15_P110138	ahcy	AHCY	adenosylhomocysteinase	NM_199218	27684	337	2	702	TCTCTGATTGACGGGATCAAGCGGGCCACAGACGTGATGATCGCCGGGAAAGTGTCAGTA
1,642	7,77E-05	A_15_P110886	zgc:91930	AK1	adenylate kinase 1	NM_001003993	26668	324	78	710	CGTGGACGAGGTGTTCGCTATTGTAGAGAAAGCTATCGATGAGCTGAAGTAAACAACACT
1,570	0,000191193	A_15_P273551	zgc:91930	AK1	adenylate kinase 1	NM_001003993	11491	141	50	523	TGTATATCGATGCTAAAGGTGAGACGATGGTGAAGAGACTGATGAAGCGCGGAGAAACTA
1,830	5,73E-07	A_15_P120766	ak3l1	AK3	adenylate kinase 3	NM_213130	41062	497	43	1824	TGTATGGTACAATTTGCAAATCACTGTTTAAATTGTAGTGACTGAAAATTCTGCTTTCGA
-1,511	2,31E-05	A_15_P170656	zgc:85790	AK4	adenylate kinase 4	NM_213299	14157	174	50	1398	CTTGATGTATTAAAATGGACCTATTAGGTACTGGGATAGTACCTTTCGAAAAGGTACCAC
-1,412	0,000110647	A_15_P112877	zgc:85738	ADSSL1	adenylosuccinate synthase like 1	NM_214820	5554	70	79	1325	GGTTCCCATTAAATGGGTCGGCGTCGGCAAATCCAGAGAATGTATGATCCAGATGTTTTA
1,430	8,21E-05	A_15_P107717	zgc:63629	ADGRL4	adhesion G protein-coupled receptor L4	NM_213367	20590	251	22	2338	GTGATACTGCATGCTATGAGTTTCATAACCTGCTGGAGTCAGTAGCTTCAAGACAATAAC
1,421	0,000122159	A_15_P153196	bscv	APMAP	adipocyte plasma membrane associated protein	NM_212608	4354	56	62	1582	AGCCGAGCGACGTATAATGAGCTCTCAGACAGGCTGTTTTTAAATTAAAAGACGTGCCAT
1,415	0,000115617	A_15_P103220	bscv	APMAP	adipocyte plasma membrane associated protein	NM_212608	31911	388	40	1865	AATTCATCATTATTTGTATATGTTGCCGTGTCACTCTTGCCTGATAAACAATGCTGGCTT
-2,958	2,01E-09	A_15_P164381	zgc:112199	ARF4	ADP ribosylation factor 4	NM_001017707	5969	75	34	655	CCTCTGAATGTAGCCTTAGTACTGCAGGACATCTTTAGGACTGCTTTATTTTTTATTCTCA
-1,977	3,25E-07	A_15_P205061	arl13a	ARL13A	ADP ribosylation factor like GTPase 13A	NM_200818	31961	388	65	1828	GGAGAGAAATTGAATGATGGGATGCTTTGTTCAAATATTCATCCCTGATGTTTTTCAATG
-1,431	9,32E-05	A_15_P134501	arl13b	ARL13B	ADP ribosylation factor like GTPase 13B	NM_173272	27806	337	63	1311	CCCCTTTCAACCAATAAACAATGTTTTGACTGAGAACCAAGACAGACTAAACAGAAAAAA
1,418	0,000108777	A_15_P114780	arl3l1	ARL3	ADP ribosylation factor like GTPase 3	NM_200693	23766	289	34	1229	GTGTGGGCATTATGTGCATATGATTATGTAAAATCAGTCTGTTACCACATTTTTCCTAGT
3,072	9,63E-10	A_15_P121020	arl4a	ARL4A	ADP ribosylation factor like GTPase 4A	NM_200860	34806	422	73	841	TTGGTTATAGAGCCAGCAAGCACTTTAGCTGTTTACTTTCATATTGTTTACTCTTCTGGA
-1,461	5,75E-05	A_15_P120937	zgc:77751	ARL5C	ADP ribosylation factor like GTPase 5C	NM_200846	35514	431	9	1139	TATTTAAAGTGAACTGATGATTTGTGTTGTGCGCATGCTGTATGGAGCCTAGTGTTCAAG
1,614	2,15E-05	A_15_P113701	LOC556502	ADM	adrenomedullin	ENSDART00000003505	37084	450	47	327	CTCAACAACAAACTCAAGATTGGGAATGCACCCGTTGACAAGATCAATCCCTACGGGTAT
1,609	8,80E-06	A_15_P189866	LOC567630	AEBP1	AE binding protein 1	ENSDART00000025875	39273	475	61	990	ATTAAGGGAGTTGTGAGGGATAATGAAGGCAACCCTATTACCAATGCCACTGTGTCTGTG
-1,431	8,38E-05	A_15_P362840	ENSDART00000100253	AGRP	agouti related neuropeptide	ENSDART00000100253	13801	170	38	330	TTTAAGGCCTTCTGTTACTGCCGCAGCATGGACAACACCTGCAAAAACGAATATGCATAG
-1,470	4,50E-05	A_15_P205011	akt2l	AKT2	AKT serine/threonine kinase 2	NM_212815	4032	52	67	1763	TTTCTGTCAGGATCACAGTCAGACATGGGCAGGTATTAAAGACTATCAGCTGCTGTCAAA
-1,441	6,76E-05	A_15_P366555	agxtl	AGXT	alanine-glyoxylate aminotransferase	NM_001002331	2511	34	57	642	GGTGCTCCTATCTGTATGGATGAACAAGGTATTGATATTTTGTATACTGGCTCTCAAAAG
1,651	4,19E-06	A_15_P159006	LOC572151	ALDH1L2	aldehyde dehydrogenase 1 family member L2	ENSDART00000102893	6766	85	18	1852	TGTTCATCAACACCTACAACAAAACTGATGTGGCGGCTCCTTTTGGAGGCTTCAAACAGT
3,587	2,83E-10	A_15_P117231	aldoaa	ALDOA	aldolase, fructose-bisphosphate A	NM_194377	18709	228	80	552	TAAGTGGAGGTGTGTGCTGAAGATCACTCCCACAACCCCTTCTAGACTGGCCATCATCGA
-1,737	2,02E-05	A_15_P168958	aldob	ALDOB	aldolase, fructose-bisphosphate B	NM_194367	5746	73	6	667	TGTGTGCTTAAAATCTCTGACAGTTGCCCCTCCGCTCTTGGAATTGCTGAAAATGCCAAT
1,943	2,27E-07	A_15_P171261	aldoc	ALDOC	aldolase, fructose-bisphosphate C	NM_194384	28638	348	63	1249	CGCTGTCTTCTGTACTTTACGGTTGCCGTTGCAAATGTCTCATAATATATCTATTTAAAT
1,850	6,65E-07	A_15_P100837	aldoc	ALDOC	aldolase, fructose-bisphosphate C	NM_194384	20477	250	49	45	ATTGCTTTGAGCCGCTGACATTATGACGCACCAGTATCCCGCTCTCACCGCCGAGCAGAA
2,554	8,21E-09	A_15_P110527	alkbh5	ALKBH5	alkB homolog 5, RNA demethylase	NM_001077387	9174	114	56	1489	AATGAAACTTCGAGACCCACTTTATTTTGTTCTGTGTTTCAAAGGAAATAAAAGGACATCG
1,960	1,64E-06	A_15_P112132	alkbh5	ALKBH5	alkB homolog 5, RNA demethylase	NM_001077387	18133	221	43	337	CAATATTTCGGACTTTGCTCTTGAAAATGGCCGGATTTACCGATCTGCGAGAGAAGCTCA
2,704	4,84E-09	A_15_P493767	CU104710.4	AHSG	alpha 2-HS glycoprotein	NM_001100029	8896	109	85	1427	GGAAGCAGTTATGGCTTTGCCTATTGTATTCCATGGTGCTGTAATAAAATGCTTTCCTTG
1,940	1,13E-06	A_15_P113038	CU104710.4	AHSG	alpha 2-HS glycoprotein	NM_001100029	38415	466	48	412	GCCCAATCATGAAGACACGTATCTTATGGAGTTGGATTTTCTGGAAACTACGTGTCACGT
-1,461	0,000225116	A_15_P163041	zgc:77775	AMDHD2	amidohydrolase domain containing 2	NM_205681	23467	286	50	1635	CCTACATGTTTTTATGATGTGAACCTGGGACACTTCAACTATTTGATTTCAACAATGTCT
-1,497	3,95E-05	A_15_P111013	zgc:92306	ACY3	aminoacylase 3	NM_001002601	16989	208	54	1296	GCTTTGGCTTTTACAATACATAACGTGGTTTAAAGTTATTTTTAATGCAAGGCTGGAAGC
-1,526	1,88E-05	A_15_P291096	ENSDART00000052907	ACY3	aminoacylase 3	ENSDART00000052907	17227	212	5	1326	GGCTCAAAGTTATTTTTAATGCAAGGCTGGAAGCAACTTCTACTGTTTATGCATTTACAA
-1,426	9,49E-05	A_15_P209881	zgc:114148	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	NM_001033729	17301	211	43	1051	TTTCAGAAGAAAAAGGATGCACCTTCAAGGCAAAGTGACCAGGAATGACTCTTGGATGCA
1,601	6,94E-06	A_15_P112185	zgc:110219	ALAD	aminolevulinate dehydratase	NM_001017645	2349	31	60	764	CGGGATGTGAAAGAAGGTGCTGACATGCTGATGGTGAAACCTGGATTACCATATCTTGAT
-2,879	1,69E-08	A_15_P102410	zgc:92137	AMY1C	amylase, alpha 1A (salivary)	NM_001003729	8031	99	71	812	AGTTTAAACACAGTGCGAAAATAGGCACAGCGGTCCGTAAATGGGATGGAGAGAAGCTAA
-3,788	8,77E-10	A_15_P121427	amy2a	AMY2B	amylase, alpha 2B (pancreatic)	NM_213011	21060	257	7	1483	AGAATCAGCAACCAGGAGGAAGACCCATTCATGGCCATTCATGCAGACTCCAAACTTTAA
2,361	2,61E-08	A_15_P198536	LOC567798	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	ENSDART00000007766	23686	287	79	4460	TTTGGTGAAGAATGTTCTCTCTCGCCATAATGTCCACATGGAAAGATCATCCTGGAAGGG
-1,529	2,61E-05	A_15_P117796	aup1	AUP1	ancient ubiquitous protein 1	NM_199690	13830	170	53	1722	ACATGGCAGAGCGATATCTTGAGGTTTATTATGTTGTTAAGGATACGTGTTGATGCAATA
-1,607	1,53E-05	A_15_P115034	LOC569547	ANGEL1	angel homolog 1	XM_692942	35314	427	78	2184	TGTGTTTATTACAATCTACCATGTGAGGAAATCTGACACGGCGTGTATAATTGACAGTGT
1,444	0,000114373	A_15_P222371	ENSDART00000025463	ANGPT2	angiopoietin 2	ENSDART00000025463	26925	328	38	1389	AAAGGTTCGGCATATTCACTAAAGGCTACAACTATGATGATAAGACCAGCAAACTTCTGA
8,737	8,31E-13	A_15_P104133	si:rp71-39b20.7	ANGPTL4	angiopoietin like 4	XM_686956	16470	201	44	2298	AATAAGATGCATTTTCTTTGTAGCGTTACAGCTGTGTTCTTGCCTACTTCAAGCGCTCTG
6,749	4,90E-12	A_15_P198686	si:rp71-39b20.7	ANGPTL4	angiopoietin like 4	ENSDART00000052062	29279	355	50	1030	AGAAGATCCATTCTGTGTCCAAAGGTGGCAACTATATCCTCAAGGTGCAGTTCTCCGATT

1,558	1,18E-05	A_15_P115896	angptl5	ANGPTL5	angiopoietin like 5	XM_689482	25826	314	70	1457	GAACTATGAATATATGACATAGTATAACAGAGATATTGCATCCACATTGGAAGTGCATCC
1,539	6,81E-05	A_15_P180551	angptl5	ANGPTL5	angiopoietin like 5	ENSDART00000079161	42722	520	15	964	CACTTGTCCAAATTAAATCAGTGACTATGAAGATCAGAAGAGTTGAGATCCCGAATTTAA
1,778	2,42E-06	A_15_P100409	zgc:101687	ANGPTL7	angiopoietin like 7	NM_001006073	11715	144	78	1452	AATTGTGATGTTCAGTGTTGCTAGAGTGCGACTTATTACAGGTCAGAGAAATTCACTGGT
1,634	9,14E-06	A_15_P205381	zgc:113016	AGTR2	angiotensin II receptor type 2	NM_001013350	29731	362	27	1691	GCTGTTTTAATGGCATTATGTGGCCAGACTATAAGCTGTTTATTATAATGCCTCGTAAAT
1,663	3,29E-06	A_15_P111514	agt	AGT	angiotensinogen	NM_198063	25389	309	19	1485	TGTATAGTAAATCAATGGACAGCATTAAGACCAGGTCAACCGGTGATATGTTTGTTTAGA
1,635	4,54E-06	A_15_P212366	agt	AGT	angiotensinogen	NM_198063	18920	232	17	1516	CAGGTCAACCGGTGATATGTTTGTTCAGACAAGCTTAATTAAACTAGTCTTTATTCAGAA
2,605	6,22E-09	A_15_P302471	LOC562517	ANLN	anillin actin binding protein	NM_001044987	39625	479	73	4886	TCCAAATGTGGCTTCCATGTATCACGCAGAGCTGCAGTTAAATAAATCAAGCTTTTGACA
1,684	3,77E-06	A_15_P112233	ank1	ANK1	ankyrin 1	NM_001005969	8511	105	59	611	GACGTGACAGCAAGGTGGGCTTTTGAGTTAGATGAGGTGGTTTAAAAAGGGAAATGCAAA
-1,808	7,05E-07	A_15_P206806	ankar	ANKAR	ankyrin and armadillo repeat containing	NM_001007039	27197	331	7	1772	TCCTGGTAATAATAAAGGACCGTCGAAGAAACTGAACACTAGGGGTAGTCAGTCAGCAGT
1,605	1,33E-05	A_15_P100480	zgc:85936	ANKLE1	ankyrin repeat and LEM domain containing 1	NM_214744	30601	371	46	3179	CGTGATCATGTCTCAGTGGGAGTCTCAGTCTTCAGCAGCTGTTCTTAATGTGTATAGACT
-1,507	3,35E-05	A_15_P210616	zgc:112094	ASB5	ankyrin repeat and SOCS box containing 5	NM_001017753	40981	498	1	1431	GGGGACAATTCAATCTAATGTAGTACTTTTGCTAAACATTTTGTTGCCAAACAAAGCATG
1,819	6,35E-07	A_15_P161941	ankrd10a	ANKRD10	ankyrin repeat domain 10	NM_200980	6931	87	17	1137	TCATGAACACAGTACAACTGTGAAAGTAGAGCGGCTCTATGACCAAGAAGTTCTCAGTGC
1,714	1,83E-06	A_15_P116762	ankrd10a	ANKRD10	ankyrin repeat domain 10	NM_200980	19509	237	64	1450	GGGTGCATTTCATTTTCCCCTATAATAAAATGTTAGAATGTTCAGATGTACAAGGAGTTG
-1,413	0,000172442	A_15_P271226	LOC798097	ANKRD34A	ankyrin repeat domain 34A	XM_001338516	11414	142	10	1659	CAGCTATCGACCTTCCGGGAAATACTTACAGAAAAGGTGATGGAGATGAATGGAGATTGA
2,624	8,29E-09	A_15_P200121	LOC793783	ANKRD37	ankyrin repeat domain 37	ENSDART00000103236	42210	511	62	370	ACTTGAAGAAAGCTTCATCATCATCCTCGTCATCCCTCAGTGAACAGCATGTGTTGACCA
1,654	3,46E-06	A_15_P117738	anxa2a	ANXA2	annexin A2	NM_181761	19901	244	9	1265	AACGTGAATCAGCAGTAAGTGAGCTGATATTGGTGCTTTTTGAAGTTATTGCAGAATGAA
-1,484	4,75E-05	A_15_P191386	LOC557578	ANXA5	annexin A5	ENSDART00000032342	43496	530	55	872	TGGAGATTCACTCTACGTGTGTTTTCAGGAAGACACTGATGGAGATTACCAGAAGGCTCT
1,437	0,000193841	A_15_P170441	anxa6	ANXA6	annexin A6	NM_001002038	8690	108	64	2282	GTGATACTGGTGCTTTATTTGTTATCCTGTTTACCCCAGAAATAAACAGATGTGATTGTG
1,440	0,000183596	A_15_P108946	kal1b	ANOS1	anosmin 1	NM_131379	17955	220	37	3000	AGGCTATGGGACTGAGAAGTGCTGCTTTAACAGGCCAATGCTTTCAGACTTAAACGCTTT
1,495	3,02E-05	A_15_P173231	zgc:165571	AGR3	anterior gradient 3, protein disulphide isomerase family member	NM_001099232	882	14	33	490	GACGACATAGACTTCTTGGCAGAGAACATGATAAAAGCCAAGATCCTGCTCAAGGAGGAA
2,290	5,21E-08	A_15_P100639	asf1b	ASF1B	anti-silencing function 1B histone chaperone	NM_207063	38003	462	6	1183	GCACTAGATAAGATGTCAGATGCGCAACTAATTTAACAGACGCAAACAGCAGTACTTTTG
1,480	0,000151534	A_15_P171926	agtrl1b	APLNR	apelin receptor	NM_001030197	34668	421	2	2018	GTTGTGGCTAAACTGCTGTATGATTGTGTTTTATGCAGTACTCTGTGAATAAAATGTGCA
3,099	2,01E-09	A_15_P151116	zgc:112992	APOA4	apolipoprotein A4	NM_001017909	30811	373	71	900	TTCGCCAAGGATAAACAGTCGTGAAAGACTCTAGAGACTTTTAGATATGCGTAATTTATG
-1,414	0,000140504	A_15_P134246	si:ch211-219i10.1	APOB	apolipoprotein B	BC090504	26162	318	73	1305	ATGTTTTGACTGACTTCGACCAGGCCATTGATGTAGATGCAAAGATGGTTTACCAAAAAA
1,549	1,99E-05	A_15_P160686	zgc:153593	APOD	apolipoprotein D	NM_001076582	32770	398	55	559	CAGCAGGGATGCGACCAAAAACTTTGAATGACTAAACTGAAATGTGTTTTAAATGTTTTG
-2,841	2,21E-09	A_15_P118533	BC092811	APOD	apolipoprotein D	BC092811	18581	228	14	721	AGCATGCCCTAAAGCAGCTGCCTTCTGCAGTCTACTACTGTAAATGTGCTTTGTCTGTAT
-3,290	4,88E-10	A_15_P297976	BC092811	APOD	apolipoprotein D	BC092811	42565	517	11	621	TAATAAGGAGACTATCTCTGAGCTGTTGGACATCCTCAAATCCCAAGGCATCGGTACTGA
1,454	6,05E-05	A_15_P206891	zgc:85890	AQP1	aquaporin 1 (Colton blood group)	NM_207059	15397	190	6	879	TGTCCCCGCAGGGAAGTAGCATTTACTATATGACAGTGTGGAAATTCCAAATGTAAAAAA
-1,500	3,85E-05	A_15_P195336	zgc:152755	AQP12B	aquaporin 12A	NM_001045862	6939	87	21	783	CAAGAATCTGCTCTACTCCAAGAAAAATCGATTCCGGCTGCCGAAAGGAAAAACCAATGA
1,497	2,86E-05	A_15_P104846	aqp3	AQP3	aquaporin 3 (Gill blood group)	NM_213468	26165	317	75	1660	TTACGTCTGATAGTGGAGAGATCCTGACATTTATTTGACATTGCAGTTTTTAGACTGTTA
1,689	2,33E-06	A_15_P196526	zgc:152891	ALOXE3	arachidonate lipoxygenase 3	NM_001077346	28810	349	66	2107	GATTGGCAAATTGGGCCCTGTTTATTTTAATTTTAAGAGCAGTGTTTGTCAATCTGATCA
-6,039	5,94E-12	A_15_P150786	arg2	ARG2	arginase 2	NM_199611	10297	128	37	2021	CCTAATAAGGGTAGCTTGATTTGTTGCATTTCAATGTTCCACTAAAACTGTTTTGTTGCA
1,562	1,13E-05	A_15_P100780	zgc:56200	ARMC1	armadillo repeat containing 1	NM_199539	12479	154	45	1060	CTTATCAACATGTGTTTGTCTCATCACAGCTCTGTACTGAAAACTATTCATGTTGTACAC
1,627	5,17E-06	A_15_P211191	zgc:101810	ACTR2	ARP2 actin related protein 2 homolog	NM_001007772	38613	468	64	1331	CAGAGGTCTGTGAATATATCCAGCGTCTGATGGCTAAAATGTATTAATTGTATTTGTGTA
1,625	4,93E-06	A_15_P114645	zgc:101810	ACTR2	ARP2 actin related protein 2 homolog	NM_001007772	27429	334	40	1332	AGAGGTCTGTGAATATATCCAGCGTCTGATGGCTAAAATGTGTTATTGTATTTGTGTATA
1,576	1,15E-05	A_15_P161366	zgc:101810	ACTR2	ARP2 actin related protein 2 homolog	NM_001007772	18402	226	9	1316	AACATGGTTCTGTGGCAGAGGTCTGTGAATATATCCAGCGTCTGATGGCTAAAATGTGTT
1,785	9,89E-07	A_15_P120206	zgc:92034	ARRDC3	arrestin domain containing 3	NM_001004605	33842	411	8	2681	TCTTGGCTTGTTTCTAACTTTTGTACCATTTTGTAAGTCATCTATGTTGTCTCACAGCAA
-1,410	0,00014317	A_15_P178856	zgc:171644	ASPG	asparaginase	NM_001102621	14130	174	36	2466	GGTCCTTGTGAGTCTGTTTTTGTGATTGTAATCGTCACGGCTGAATTTTAGTTTCAATCA
-1,443	9,62E-05	A_15_P440530	zgc:171644	ASPG	asparaginase	NM_001102621	28916	352	35	1170	AGCTGCTCTTTCAAAACTGTCCTATGTGCTGGCAAAACAGAATCTCAGTATAGAAGAGAA
-1,576	1,67E-05	A_15_P284201	ENSDART00000074875	ASPG	asparaginase	ENSDART00000074875	36174	440	8	1638	GTGGAGTCTGTTGAGTTCTTAAAACAGGCAGCTCTGTACCAAACTCAGGTATGGAACATA
1,666	3,85E-06	A_15_P108270	asph	ASPH	aspartate beta-hydroxylase	XM_690883	28731	349	26	3515	TTTGGGTGACCTTTCACAAATCTGTAAACAACTGTAAATGTTTGGTTTGAGCGCTGCAAT
1,653	3,54E-06	A_15_P263416	asph	ASPH	aspartate beta-hydroxylase	XM_690883	6140	77	37	3538	GTAAACAACTGTAAATGTTTGGTTTGAGCGCTGCAATAAAGGTTGGGACAACAAGAGTTA
-2,102	7,75E-08	A_15_P170651	zgc:110112	ASPSCR1	ASPSCR1, UBX domain containing tether for SLC2A4	NM_001017575	146	3	19	1784	CGTCGCTGAGGATGTACAAGAGTCTGTGCTGTAGATCAATAGATTAATTAATAACAATAA
-2,132	9,87E-08	A_15_P162301	c6ast4	ASTL	astacin like metalloendopeptidase	NM_001025180	8334	104	53	867	CACTGATGTTGCTGAACAACCATCAGTCTATCAGATGGATTAAGCACAAAACATCAATAA
-2,810	5,42E-09	A_15_P120851	c6ast3	ASTL	astacin like metalloendopeptidase	NM_001013526	34027	413	19	820	CAGTGCTGAGCAACAGAACTTGGCTTCAGCACCCATGCCTTACATCTGAAAGTACAAAAA
1,571	1,57E-05	A_15_P197456	LOC100003744	ABCB10	ATP binding cassette subfamily B member 10	ENSDART00000088005	15650	192	52	1499	CAAAATACTTTTACTGGATGAAGCCACGAGTGCTCTGGATGCAGAGAATGAGTTTTTGGT
1,646	3,88E-06	A_15_P596157	LOC563039	ATAD2	ATPase family, AAA domain containing 2	XM_686405	2107	30	20	4138	AAGGATTACGACAAGACTGCACTTATACAGGAGATGACAAAGGAAGTCCAAGAGTTTTCC
1,524	3,08E-05	A_15_P191066	LOC562182	ATP1B4	ATPase Na+/K+ transporting family member beta 4	ENSDART00000075278	23795	290	48	2409	GCCAGCTCATGTTTTTAAACACACTCATGTTCTAGCATAAACAATAAAGACGGATGAAAA
1,535	1,60E-05	A_15_P120072	atp1a1a.2	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	NM_131687	5112	66	25	3151	TGCAAACTTATGTTCAGAGACTCTCAAAGAAAAGCGATAAAGAATCTGGTGTATTTCAGC
-1,409	0,000292811	A_15_P121133	atp1a1a.4	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	NM_131689	6666	84	51	2650	AGGGTTCTTTTCCTACTTTGTAATTCTCGCCGAAAACGGATTCCTCCCCTCCGATTTAGT
-1,441	0,000112722	A_15_P212201	atp1a1a.4	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	NM_131689	19620	239	37	3106	GGTGGAACAAGAAACATACTACTAAAACATGAAGCAAACATTTTCAAGGAGACACATATC
-1,420	0,000118924	A_15_P132121	atp1b1a	ATP1B1	ATPase Na+/K+ transporting subunit beta 1	NM_131668	11257	139	15	1381	TATTTTATGGAGTGTGCAGTGCAGTAATCGCATACAGGTGGTCCTTTCCAAGCCATGTTG
-1,522	3,48E-05	A_15_P442765	atp1b1b	ATP1B1	ATPase Na+/K+ transporting subunit beta 1	NM_131671	42350	514	55	438	TTCTGACATCCTACGACCAGGAAAAACAGTTAGACAATATGCAGTTTGAAAACTGTGGAG
-1,692	3,69E-06	A_15_P135196	atp1b1b	ATP1B1	ATPase Na+/K+ transporting subunit beta 1	NM_131671	43646	531	67	965	TACCACGACAAGGACCGCTACCAGGGACGATTCGACGTTAAATTCAACATTAAAAAATCA
1,413	0,000113686	A_15_P120962	atp1b2b	ATP1B2	ATPase Na+/K+ transporting subunit beta 2	NM_131838	6199	77	68	2355	ATAGAGTGACTAGGAGCAGGGACAGCAGATTTATGTTTCGAAGTGAATCCATCCCTGCAT
-1,636	4,90E-06	A_15_P104804	atp2a1l	ATP2A1	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 1	NM_001077533	25912	316	30	3076	ATGTTGAAGTTCCTTGCCCGCAACTATGTGGATGTCTAAACAGTTCTCACCTCCCAGATT
-1,441	0,000127611	A_15_P115272	atp2a2a	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2	NM_200965	29528	359	8	3639	TCTTTTACAGCCGGAGCTGCCAGATCAGTGTTGTAATTATCACAATCAATTGTGGTTCAT
-1,525	3,42E-05	A_15_P152346	atp2a2a	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2	NM_200965	20621	252	37	2798	ATGATCACACTTTACCAGCTGAGTCATTTCCTGCAGTGTTCTCCCGATAATCCTGACTTC
1,411	0,000113909	A_15_P112327	stka	AURKB	aurora kinase B	NM_212566	296	6	26	1138	TTCATATCCATGTTTTAATCTTGTCTGTCTTGTTTAATCCTGTCAAATATATAAAGCTGT
-1,402	0,000177765	A_15_P154986	zgc:113944	ATG14	autophagy related 14	NM_001024812	34922	423	47	1139	TTCCCAAAAAGCTGTGCAACAGTGAGTTCTGTGGAGATAATCTGACTCGCTACCGATTCA
1,676	3,24E-06	A_15_P174701	atg4b	ATG4B	autophagy related 4B cysteine peptidase	NM_001089352	29474	357	66	1637	TGCAGACTGGGTAGGATGGGTCGTGTAATATACAAGAATGATTTTGTCTTCATGTTTAAA
-1,485	0,00022588	A_15_P105351	braf	BRAF	B-Raf proto-oncogene, serine/threonine kinase	NM_205744	17233	212	8	2492	CCGAAGAGCTACGGCCTCAACGGAATTGCTTTAAAATAAAAACATCTCTGCAGGGTGTCA
1,555	1,35E-05	A_15_P106789	birc5a	BIRC5	baculoviral IAP repeat containing 5	NM_194397	2466	33	35	627	TGTCAAGGAACACTCTGTTCTCTTTAAATGTTATCAGTGTTTAAATCTGTGTTCTGTCAC
-1,451	5,73E-05	A_15_P176106	barhl2	BARHL2	BarH like homeobox 2	NM_205740	28740	350	30	1502	GACACTGAGAGACAAATGTATCACAAGTGATGTGACAGACTGAACTTTCACAGAAGCTTT
1,473	4,80E-05	A_15_P148871	bcam	BCAM	basal cell adhesion molecule (Lutheran blood group)	NM_001076627	12594	156	18	1846	TGCTGCACCTTTAACTTTTCCTTCACTGGGGTCAATAAAGGATTCTGTTCTATTTTACTA
-1,459	5,13E-05	A_15_P507457	BC109452	BNIP3	BCL2 interacting protein 3	BC109452	20518	250	70	1557	ACGTGTTCATTTAGTGGTTTTGTATTAACAGAGGGAATGAGCTGAAATAAATGTCTGCCC
-1,464	5,83E-05	A_15_P100272	zgc:73226	BNIP3	BCL2 interacting protein 3	NM_205570	27066	330	25	896	GAAATGGAGCGCTGATTGAAACTAAACAACATCTGTGAACTATCACAGCAAAAGTAAATA
-2,067	9,49E-08	A_15_P117461	zgc:73226	BNIP3	BCL2 interacting protein 3	NM_205570	15221	188	3	2184	TATGATAGGGCCCAATGTGTTTACACTGGTTGGTGTTAAAGATAGTGTTGCTTGTTTTAC
2,578	6,50E-09	A_15_P176726	bnip3l	BNIP3L	BCL2 interacting protein 3 like	NM_205571	14876	181	81	2552	GACCCTTTTTCCTCCCCTGTTGGACAATGACAAGTTTCAAATTAAATTTTAAACAGAAC
1,581	9,25E-06	A_15_P110549	zgc:63614	BCO1	beta-carotene oxygenase 1	NM_200608	40508	492	14	1965	TTGTACAGACAACCTGTAAAACAGGCTATTGCATACAATGTAAATGACTTCTACTCATTG
2,295	2,22E-08	A_15_P108369	upb1	UPB1	beta-ureidopropionase 1	NM_199616	906	14	45	1143	CAGCATGACTTCAAACCCAATGTTATGAAAGATTGAGCCGATCAGAAAAAGCATGAGCTA
1,446	9,26E-05	A_15_P110145	zgc:77123	BGN	biglycan	NM_001001825	26075	317	29	2703	TATGGTGATTAGAATGACAATAAACCGATGCTAAGCACAGTGTGAAAAGCATTGTGTACC
1,913	9,17E-07	A_15_P149371	zgc:91854	BLVRB	biliverdin reductase B	NM_001002686	15944	195	33	844	ACAGGTTGGTACTGATGGTATAGCAGAGATACAATATTCCCAGTCAGTCATTATTATTTC
-1,496	2,90E-05	A_15_P102204	blcap	BLCAP	bladder cancer associated protein	NM_131493	27270	332	44	825	CTACACTGCTGAGATCGCTCAAATGCTGTCAACACTTTTAATTCAATAAAGTTTCTAATG
1,575	2,20E-05	A_15_P121179	bmi1	BMI1	BMI1 proto-oncogene, polycomb ring finger	NM_194366	10315	128	46	2084	GTGTTCATTGTCTTATTGGTCGATTGTAGACTATTGACAGCTGTTGTATTGTGACTGTTG
1,461	5,00E-05	A_15_P161996	zgc:153939	BMP3	bone morphogenetic protein 3	NM_001077765	40787	494	71	3139	GTCTCCCGAGTTGAAAGGATCCCTTTTTAGCAAGGAAAACTCAATAAAGTTTTAAGAATT
-1,495	3,93E-05	A_15_P105447	bcat2	BCAT2	branched chain amino acid transaminase 2	NM_001002676	7035	88	70	3136	AGCTGAAGGGGGCGCTGCTGCACTCAAGTTTGGTTTGTTTTGTTTTCTGATGGTTTTCAA
1,953	2,17E-07	A_15_P161461	zgc:101883	BTG2	BTG anti-proliferation factor 2	NM_001007375	6428	81	15	399	TACGATTGGACTCACAAAAGAGCGACTTTTTTCTCTGCTGCCAAGTGAACTCACCATGTG
-1,615	5,81E-06	A_15_P103119	btg2	BTG2	BTG anti-proliferation factor 2	NM_130922	2420	33	12	1978	TTGAAGCAGAGTTGCTGTTCATGTACATTTTTATAATGAATTTGTGCACATGTAGAGCTG
2,282	8,11E-07	A_15_P104973	zgc:103463	BTG3	BTG anti-proliferation factor 3	NM_001007351	38289	463	69	18	GCGAGGCAGAAGGAGTTTTCCACATGTGGATGAAAAGAAAACACGAAGTTGGACCTGAAT

2,650	4,33E-09	A_15_P177796	BC124681	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	BC124681	15352	187	69	1739	TGTGCTCGCTCTGTCACATACGACGGCATTTTTGGACAAATAAAGAGTTTTGATTCCAAA
1,858	1,02E-06	A_15_P452345	LOC567071	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	BC125843	20628	252	41	2645	AGGACAAATGGAGTCTTTAAAAGGAACGTTCACGCTGATCTCTGGCAGGATTTCTTCCAC
-1,657	3,47E-06	A_15_P102716	bysl	BYSL	bystin like	NM_201106	1120	15	77	1354	ACAGTGCAGTGTGTGTCGCAGTCATGTTTCTGGACTGATTGGGTTATTCTGGTATTACAT
-1,568	1,19E-05	A_15_P157641	LOC795469	CCL19	C-C motif chemokine ligand 19	ENSDART00000057509	42945	521	56	255	AGCAGACTGATTGACCACATACTAGGAAGAGAAAAACCAGCACAAAAACGACCCAGGAAA
1,795	7,97E-07	A_15_P107360	zgc:66439	CLEC14A	C-type lectin domain containing 14A	NM_199786	19681	240	67	1657	ATTAAGCAACATTGGAGATTTATATGTCTGGAGGGTTATGAATAAAGGCGGACATTAAAG
1,528	3,79E-05	A_15_P210301	si:ch211-154o6.6	CLEC4E	C-type lectin domain family 4 member E	ENSDART00000078858	40217	487	36	1040	CCATCGCCTTTAGCGTCTGAACTTCATTGAAATGTGAATAAATGTTGCTCTATTTTTCTA
1,522	1,95E-05	A_15_P163546	si:ch211-154o6.6	CLEC4E	C-type lectin domain family 4 member E	NM_001045039	25573	312	27	1019	CCCATCGCCTTTAGCGTCTGAATTTCAGTGAAATTTGAATAAATGTTGCTCTATTTTTCA
1,717	4,33E-06	A_15_P211941	scyba	CXCL14	C-X-C motif chemokine ligand 14	NM_131627	12044	147	77	1671	CAAACACAACTTAAGTCCAAGGAGTGTAATCTTCGAGCACAGCAATAAACATTTAAGTAA
1,702	5,20E-06	A_15_P212136	scyba	CXCL14	C-X-C motif chemokine ligand 14	ENSDART00000106060	15840	193	66	1610	CAACTTAAGTCCAAGGAGTGTAATCTTCGAGCACAGCAATAAACATTTAAGTAAATCGTT
1,657	3,39E-06	A_15_P108224	scyba	CXCL14	C-X-C motif chemokine ligand 14	NM_131627	3943	52	21	1648	TCTCTGTGTTTGGACTGACCCACCAAACACAACTTAAGTCCAAGGAGTGTAATCTTCGAG
1,568	1,38E-05	A_15_P190706	scyba	CXCL14	C-X-C motif chemokine ligand 14	NM_131627	8566	107	2	481	AGCACTAGGAACCTTGTCAAGTGGTTCAAAATCTGGAAGGACAAACACAGGTCTTTTGAA
2,726	4,63E-09	A_15_P120569	cxcr4a	CXCR4	C-X-C motif chemokine receptor 4	NM_131882	740	12	35	1441	CAAAGATGGATTGAATTATCCATTCCAAGAGCTGCTTTGTCAATTTGAAGTCTTTACAAC
2,178	4,62E-08	A_15_P172286	cxcr4a	CXCR4	C-X-C motif chemokine receptor 4	NM_131882	22629	275	43	1079	AGGACAGGAATGTCATCCGTGTCCACAGAATCTGAATCTTCCAGCTTTCACTCTAGTTAA
-1,944	3,12E-07	A_15_P172151	LOC569005	C2CD4B	C2 calcium dependent domain containing 4B	NM_001089422	24839	302	74	1615	GCCAAATCTGTTTATTTGCCAAAGATGACAGCGACTCCTTTTTTATTAAACACTGTTAAC
1,454	0,000114678	A_15_P103640	cdh5	CDH5	cadherin 5	AY732217	25651	312	67	2772	AACTATCTGTGTGGTTCTAGTTGTAGACGTAGATATTCATTTACTAGACTGTTTAACAGC
-1,616	1,41E-05	A_15_P160101	tceb3	CALCOCO1	calcium binding and coiled-coil domain 1	NM_200121	18182	222	67	1674	TTTTCCAGTGGCATTGCTGACCAAATGCTTTCAGAAGCCAAAGACAGTGTCTTCAGTGCT
-1,925	2,58E-07	A_15_P174116	tceb3	CALCOCO1	calcium binding and coiled-coil domain 1	NM_200121	5518	70	60	2888	GACTTGACAAAGCTGTAAGGGCATTTAAGTGCTTAGTTTCCCATTTTTCTAATAAACATG
-2,064	2,35E-07	A_15_P142906	calcoco2	CALCOCO2	calcium binding and coiled-coil domain 2	NM_001020741	22839	277	66	1961	AAGAGGGTTGCCAGGATTTCACAACAAATCTATCCCATAACTAGCTCCATGATTAAAAAA
1,560	5,43E-05	A_15_P115906	fam26b	CALHM2	calcium homeostasis modulator 2	NM_001003458	9979	123	44	2110	TGTGATTAAAGGATGGCAGGCATGCTATTCGTCAAGCTATATGCTATAAATAAAGTGCTT
1,411	0,000118296	A_15_P119167	zgc:153946	CLGN	calmegin	NM_001077541	5875	73	71	2827	TCTTGGAAATAAATATTTACTATAAAAGTCTGTGCGCTGCTGCCATGACTTCAACCAGAA
1,552	1,46E-05	A_15_P117130	zgc:100997	CLMN	calmin	NM_001003605	18805	229	44	2259	GCACTCTGGATTTACAGTTGAATTGCTGGTATTTAATGTAAAGAATGTGGACTTTCAGTA
1,567	1,03E-05	A_15_P150381	zgc:112420	CAPN2	calpain 2	NM_001017807	32750	398	44	2512	GGTATGCTACTTAAATGAGCGATGAATACTTGAATACTAGTCATGTTTAAAAAGGGCATG
2,939	1,90E-09	A_15_P392690	LOC796693	CAPN3	calpain 3	ENSDART00000063177	2974	40	40	1846	ACATGGAGTTGGATTTCGACAGCTACATTAGCTGCTTAGTGCGACTGGAGGGAATGTTTA
2,440	1,04E-08	A_15_P184061	LOC796693	CAPN3	calpain 3	ENSDART00000063177	18073	221	13	1929	GATGGTGATGGACTTATCAAGCTCAATGTTTTTGAGTATGTATTGCTGAGCATAAACATA
1,609	6,50E-06	A_15_P110184	zgc:85932	CAPN9	calpain 9	NM_212939	23905	292	19	2284	GGTTTAGTGTACTGCAGACAGTGGACGGGTGATTGCTGAATAAACAGATATTTTAAAGAA
1,477	3,75E-05	A_15_P118531	zgc:110603	CAPNS1	calpain small subunit 1	NM_001017899	35969	436	75	1196	GATGTTGGGGATACAGATATCGCCACAAATGTATCAGGATCTGGTGTCAAGTGCAATTTT
-1,417	0,000159133	A_15_P276891	cast	CAST	calpastatin	XM_686446	15185	185	70	3008	AGCATCTTCCTGTGTGAAGATCTGTGGAGACCCTTGTGTACAGAGATGGTGTATACTGTA
-1,684	6,48E-06	A_15_P532237	cast	CAST	calpastatin	XM_686446	31657	383	81	650	TTTGGCTCCTAAAGTCCACTACACTGGACCTGAGATCAAAGAGCCCAAACTGAAATCAGA
-1,750	4,17E-06	A_15_P506347	ENSDART00000081614	CAST	calpastatin	ENSDART00000081614	36979	448	78	125	TCGTGTTGGAGAAAGAGACGACACACTCCCACCAGAATACAGATTCAAAGAGGAAGATCT
1,415	0,000211909	A_15_P120770	zgc:65794	CNN2	calponin 2	NM_213349	32551	396	28	2025	TCATTCCAAAATACGCTTTGTACTAGACATCGGAGATTCGAGGTCTGCTCAGATAAATTA
1,830	6,66E-07	A_15_P118540	calrl	CALR3	calreticulin 3	NM_201465	7450	93	29	1780	AGAAGATCTCAGCCCATGCATTTAATTAGTGATCTTTGACCCCTAAATGGCCAGTTAAAA
1,774	2,17E-06	A_15_P482875	calrl	CALR3	calreticulin 3	NM_201465	3435	45	18	1442	TCAGACCACGCGATCAATCAGTGAGCTTTGACCCCTAAATAGCCATTTAAAGAGACGGTT
1,728	1,88E-06	A_15_P199366	calrl	CALR3	calreticulin 3	NM_201465	9950	124	29	1078	ATCTCAGATGATGTGAAAGAAGCTGAGGAATTTGGAAATGAAACGTGGGGCGCTACAAAG
1,851	5,35E-07	A_15_P520672	BC155741	CASQ1	calsequestrin 1	BC155741	11448	141	28	2367	TGTTTGTTCCAATATGTGGATTGAGTGTTTGTCCCACTGTGATAGGACCTAAAGGTGCTA
1,786	4,15E-06	A_15_P104176	zgc:154027	CASQ1	calsequestrin 1	NM_001076724	24014	291	75	1682	AGCCTTCCACTCGCAGGCTGTTGTTTATGGAGGTTTTATTGCAGGATAAATGACGCTCAA
1,533	3,78E-05	A_15_P117576	zgc:100957	CASQ1	calsequestrin 1	NM_001003620	10301	128	39	1180	TGAGAGTATCTGGTTTGATATGGACGATGATGACATGCCAACAGTTGATGAGCTGGAAGA
1,531	1,78E-05	A_15_P199021	LOC100006915	CASQ1	calsequestrin 1	ENSDART00000056540	2269	31	20	1112	TAAAATTGATCCGGATGACGACGATGATGACGATGATGATGACGACGACGACGATGA
1,510	2,97E-05	A_15_P199016	zgc:100957	CASQ1	calsequestrin 1	NM_001003620	12785	158	30	887	TTGAGGACAATGACAGGCCAACACTGAGGAAAATGCAACCCCACAACATGTATGAGATCT
2,089	2,18E-06	A_15_P275301	casq2	CASQ2	calsequestrin 2	NM_001002682	30681	373	4	660	TGAGATCATTGACAATGCTCTGGAGTTACGAGCTTTTGACCGTATGGAAGAAGACATCAA
1,402	0,000135956	A_15_P194136	capza1	CAPZA1	capping actin protein of muscle Z-line alpha subunit 1	NM_212697	41624	503	81	1244	GACGCACTGAACGTTTTATTGCACAAAGCCCATATGATCAATCGAGTCTATTTTGTTTAC
6,432	4,99E-12	A_15_P599927	cahz	CA2	carbonic anhydrase 2	NM_131110	19591	239	21	955	GATAACAGGAAAGTTGAATCTGATCTTCTAAACTGTCTGCGTTTGTCATAACGCCCATGT
4,078	8,32E-11	A_15_P107954	cahz	CA2	carbonic anhydrase 2	NM_131110	3458	46	29	1233	GGTTTTGTGTGGGTTTATGGCAATGTGTGACTGATGAGATGTGTTGATGCTAATATACCT
-1,698	3,66E-06	A_15_P570427	LOC553246	CA4	carbonic anhydrase 4	ENSDART00000062024	32710	398	24	1465	GGGAAATGAATGATTATAATTACTGTACTGTGTAGCTAACCGTTCAGTCTAAACTGTAAC
-1,772	4,85E-06	A_15_P166346	LOC553246	CA4	carbonic anhydrase 4	ENSDART00000062024	30790	374	60	1489	GTACTGTGTAGCTAACCGTTCAGTCTAAACTGTAACACAATAAAACAACAAACAAGCAAA
-1,641	1,25E-05	A_15_P131656	celip	CEL	carboxyl ester lipase	AF003943	28141	342	64	280	TGTAGGTTATTAGTGACCCCAGTGACCATTAAAATAATTTCTGTCCTTGTCTGCAAAAAA
-2,990	6,78E-09	A_15_P120815	ENSDART00000040598	CEL	carboxyl ester lipase	ENSDART00000040598	15496	190	57	731	TGTCCCTGGGCGATCAATAGAAATCCCCGAAAATTTGCTGAAGAGATCGCCAAGAAAGTA
-4,097	4,29E-10	A_15_P105015	cel.1	CEL	carboxyl ester lipase	NM_199607	4030	52	66	749	TGTCCTTGGGCCATCAGCAGAAATCCAAGACAATTTGCTGAGGAGATTGCAACCAAAGTA
-2,689	5,64E-09	A_15_P116208	cpa5	CPA1	carboxypeptidase A1	NM_199271	942	14	63	856	CAGTGCTCACTCTGAGCCCGAGGTGAAGGCCATTGTGGACTTTGTGAAGTCTCACGGCAA
-3,421	8,36E-09	A_15_P117784	cpa5	CPA1	carboxypeptidase A1	NM_199271	42874	521	19	409	CAACTCATTCATGGACATGCTTGTCGCAGAGAACAGGAACATGGTCAGCAAAGTTGTGAT
-3,983	2,86E-10	A_15_P100059	cpa1	CPA1	carboxypeptidase A1	NM_001020482	28913	351	34	833	CTACCATGGTCCCAGCATTCATTCTGAGCCTGAGGTGAAAGCCATTGTAGAATTTGTGAA
-2,447	2,15E-08	A_15_P118532	zgc:91794	CPA4	carboxypeptidase A4	NM_001002217	39564	480	42	1326	GTTCGTGATCACCCTTATTGAGAGAAATGTGAAAATGTATTGATGCTCTTTAATAAAGGC
-2,494	2,15E-08	A_15_P108469	ENSDART00000066833	CPB1	carboxypeptidase B1	ENSDART00000066833	7021	88	63	1633	TTAAAATTAGACAGGTATGTGCTGCAGATTTGCCCTGTACCTACAAATAAAGCGGTGTTT
-3,759	1,73E-10	A_15_P272306	cpb1	CPB1	carboxypeptidase B1	NM_001110021	26166	318	75	575	GAATGGACTTCTTTGTTCTGCCTGTCTTCAACATTGATGGCTATGAATACACCTGGAACA
1,620	5,16E-06	A_15_P117204	cpn1	CPN1	carboxypeptidase N subunit 1	NM_212770	38451	466	66	1641	TGGACTGTTACTGGAAATTATGTCTGAATATGACAAGGTGTTGATCAGTTTGTCTCCCAT
1,865	4,46E-07	A_15_P102282	LOC564830	CPXM1	carboxypeptidase X, M14 family member 1	BC134205	38457	466	69	966	ATGCCTCATATGTGAACGAGACTCTGAGTTTGTAGCTGGTTTTCTACACTCAGAATGTAA
-1,481	3,48E-05	A_15_P203861	LOC556295	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1	ENSDART00000060266	32996	399	85	2897	TATTACATCTATCCTGGGCAGCAATTACACCTGTGTGGCCAAAAACCCTCTGACCAACTT
1,930	2,48E-07	A_15_P210311	ENSDART00000018235	CROT	carnitine O-octanoyltransferase	ENSDART00000018235	33179	404	8	3200	GGCGTCTCTTGAATATGCATTGATTGTAAACATTTTACAGTAGCAAACTGAAGTGATTTC
1,889	3,57E-07	A_15_P161041	zgc:110643	CROT	carnitine O-octanoyltransferase	NM_001018151	24682	299	79	3192	GGAGACCGGCGTCTCTTGAATATGTTTTGATTGTAAACATTTTACAATAGCAAACTGAAA
1,774	1,51E-06	A_15_P106153	LOC560000	CPT1A	carnitine palmitoyltransferase 1A	ENSDART00000089199	7855	97	66	2157	GGTTATGGTGTATCATATATTATTCTTGGAGAAGACCTTATCAATTTCCACATATCCAGC
1,612	9,96E-06	A_15_P115794	LOC560000	CPT1A	carnitine palmitoyltransferase 1A	XM_683391	39290	476	69	2395	CAGCTTGACATCAAACCTAAACAAAGTGATCCAACTCGTTTCTCATTTCTGAAAAGGGAA
2,723	3,45E-09	A_15_P117834	cpt1al	CPT1B	carnitine palmitoyltransferase 1B	NM_001005940	31471	382	69	1662	CTAGCGAATTAGTGCACTTAGATAAATCGGATTTATGCTGGGGATGAAGTGTAAAAATGT
2,513	7,40E-09	A_15_P167646	cpt1al	CPT1B	carnitine palmitoyltransferase 1B	NM_001005940	39546	480	33	1666	CGAATTAGTGCACTTAGATAAATCAGATTTATGCTGGGGATGAAGTGTAAAAATGTACTG
2,155	5,01E-08	A_15_P167651	cpt1al	CPT1B	carnitine palmitoyltransferase 1B	NM_001005940	5589	71	12	1462	ATCAGACAGGCCATGCAGGACATAAGAGCTCTATTCAACCAAAAAGAGAAGAAGATGTGA
1,813	1,11E-05	A_15_P581667	ENSDART00000083421	CPT1B	carnitine palmitoyltransferase 1B	ENSDART00000083421	6162	78	48	1910	TGCAACTAGCTCAATATAGGGACAAGGGGGGAGTTTTGTCTGACTTACGAATCCTCCATGA
1,938	3,68E-07	A_15_P170161	zgc:114181	CNDP1	carnosine dipeptidase 1	NM_001033737	33214	403	26	779	CATCCACTGGTTAAAGGAGATCATGGAGATTGCTGTTGCAAATTAATAAAACAAGTGTTT
1,784	1,12E-06	A_15_P115391	zgc:165343	CRTAC1	cartilage acidic protein 1	NM_001080178	18885	229	85	1288	GTGAAAGCGCTTCACAGCCCATCTCTGTGTTTAAGGTCAACCAGGGCTTCAGTAATAATT
2,128	4,85E-07	A_15_P441200	crtap	CRTAP	cartilage associated protein	NM_001001406	31739	385	38	1108	AGATGCTGGAATTCGCCAAACAGAAGTTCATGCCAGATGATGAGGGTGAAGTTGTAGAGT
1,756	1,37E-06	A_15_P103288	crtap	CRTAP	cartilage associated protein	NM_001001406	32868	399	20	1397	ATCTGAATCTCAGTCCCTGTCAACTTACTGTATCTCAGAGAAAACAATGTTCTGTGTTCT
1,480	4,01E-05	A_15_P144471	ENSDART00000075398	CILP	cartilage intermediate layer protein	ENSDART00000075398	25857	315	1	3182	TGGTGATAAAGAGGTCACTAGGCAAAGTATGTTCCAGCAGATACAGAACTCACTGGGTCA
1,495	3,40E-05	A_15_P104273	caspb	CASP4	caspase 4	NM_152884	17250	211	17	1721	ATTTGTATTGCTTGGGCTTTAATATCACTGGATGGATCTGTCCTTGTCTGCTCATTCAGT
1,488	3,25E-05	A_15_P106832	caspb	CASP4	caspase 4	NM_152884	8079	101	10	1151	GTATGGAGAAAGATCAACGTTTCAAAGGTCAGGCGAAACTCTTGCCGTGCATTGAAAGGA
1,536	4,86E-05	A_15_P176121	casp8	CASP8	caspase 8	NM_131510	36676	446	7	1483	TGAACTTTGAAGTGAGCAAAAGGATTTTGAAGGGCTACAAGCAGATGCCAGAACCACGCT
1,867	6,62E-07	A_15_P441875	comtd1	COMTD1	catechol-O-methyltransferase domain containing 1	EH500939	35264	427	52	546	AACTTCTAAGTGCTGGTGAAGCTGGAATGTATGACTTTGTGTTCATCGACGCTGACAAGA
-1,692	2,39E-06	A_15_P106744	zgc:55862	CTSB	cathepsin B	NM_201055	21826	265	57	1210	ATGGGGAACCTTTGGTCAGGTGTGACTTAGTAAATGAGCCTTTCAAGCACCATGAAATGT
-1,634	1,80E-05	A_15_P173551	ctsd	CTSD	cathepsin D	NM_131710	39221	475	35	1269	TACACTGTGTTTGACAGGGAGAATAACAGAGTGGGCTTCGCTAAGGCCAAATCAGTCTAA
1,734	1,15E-05	A_15_P140876	ctsl.1	CTSL	cathepsin L	NM_001002368	11682	144	61	1176	AACTGACATTCGCTGTTTTCATTTTTAATGCCCCTGTCTAGGAAAACATGATAATTTGA
-1,501	3,77E-05	A_15_P140851	ctsl1a	CTSL	cathepsin L	NM_212584	28854	352	3	1013	TCTTGTTTAAAGGAGACCCGCCCAGTAACCAGATATAATACCAGGAGCCCACATTAGTGT
-1,556	1,49E-05	A_15_P103675	ctsl1a	CTSL	cathepsin L	NM_212584	6477	81	40	1193	TGACACAGAGTCCTCGAGCTCTAGGTACTGTGTGACACCGTTTTAGGGAATTTATGCAAT
-1,478	3,69E-05	A_15_P499257	LOC558514	CTSZ	cathepsin Z	ENSDART00000074189	411	8	14	841	AAGGAAACTGGTACAATGTCGCCATCGAGAACGACTGTGCATACGGAGATCCAATAGTTA
-1,592	8,41E-06	A_15_P199516	LOC558514	CTSZ	cathepsin Z	ENSDART00000074189	14500	177	56	847	ACTGGTACAATGTCGCCATCGAGAACGACTGTGCATACGGAGATCCAATAGGATGTAAAT
1,838	5,44E-07	A_15_P551517	LOC557070	PTRF	caveolae associated protein 1	XM_680051	32891	399	32	911	AGACTATACAGCTGCAAATGGGTCAGAAAACATTGGGTGTACCCCAGGGTGTGAATTATA
1,706	2,16E-05	A_15_P174926	zgc:158664	MURC	caveolae associated protein 4	NM_001080198	33607	407	57	1208	GCAAGCACTAGATGTGTTTGTGTAATTTCTGTTACCATAAAGCCACATGTGAAATGTATT
1,494	0,000139192	A_15_P109660	zgc:92239	MURC	caveolae associated protein 4	NM_001008579	20122	246	37	2578	GTAAACTAAAAAAGATCAGCTTTCGCAGTATAACCTTGGTGATTAACCATCACTATTCAG

1,661	3,92E-06	A_15_P120557	BC124625	CITED1	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 1	BC124625	2800	38	36	1471	TGCATGCTTAAGGTTCATTCGATTACCCATTGAAAGAAGACCTTCTTTCAGATATTTTCT
4,919	2,62E-11	A_15_P113698	zgc:103418	CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2	NM_001006045	9104	114	20	2185	TATAGATAGACCACTGTGCTTATTATAGTATGCGGTACATGGCAATACTACTGTGTTGAG
-1,450	6,03E-05	A_15_P141931	cebpa	CEBPA	CCAAT/enhancer binding protein alpha	NM_131885	34937	424	54	1981	ACACAGCAAGAAAAAGGAAGCACTTTTTTACAAACTGCGTATGGCAAATGTTATACAAAC
-1,473	5,27E-05	A_15_P577552	cebpd	CEBPD	CCAAT/enhancer binding protein delta	NM_131887	40772	493	64	438	CACCTGTTCAACAATACTGTAAAGCAAGAAAAGCCTGACTTTTACATGTCCAACGCGTTT
-1,488	9,88E-05	A_15_P160661	cebpd	CEBPD	CCAAT/enhancer binding protein delta	NM_131887	38005	461	8	451	TACTGTAAAGCAAGAAAAGCCTGACTTTTACATGTCCAACACGTTTGCGCACAAGAGCGC
1,530	2,54E-05	A_15_P114463	zgc:162651	CD248	CD248 molecule	NM_001099228	11002	135	55	2900	GCAGTATAATGTTTTAATAAGTAACGGTAAGGGGGGAATAAACTTGTTCAAACCACAAACC
1,472	4,17E-05	A_15_P153011	zgc:158279	CD276	CD276 molecule	NM_001080622	4647	60	43	2073	GTAGACATCGCTGTGCCTGACTGTTATTGCGTATGTAAATTAAAAGATCTCATTCTTAAA
2,757	2,94E-09	A_15_P369935	LOC100005092	CD58	CD58 molecule	XM_001344193	32288	391	64	2745	CTGAATAGTGCTTCGCTGTGACCTTTGACAAAAGTGGTGTACCGGGATAACCTTACACTT
-1,489	3,12E-05	A_15_P178436	BC135074	CD59	CD59 molecule (CD59 blood group)	BC135074	794	12	62	922	GTGAAACTTACTGAACCTTTATGCGATCAATAAAAGGAACATGCAGGTTTTATGCGAAAA
1,456	7,88E-05	A_15_P170231	zgc:153684	CLK2	CDC like kinase 2	NM_001076751	13173	162	58	1287	TGTTCCTTCCAGAATGATACGCAAAACGAGGAAGCAGAAGTACTTCTACAGAGGTCGTCT
1,414	0,000109135	A_15_P241316	zgc:101026	CKS1B	CDC28 protein kinase regulatory subunit 1B	NM_001003593	9090	114	13	566	TAATTTCCGAACTTAACCAAGAGATGGTATTGTGCACAACTTCTTTCTGCATCTGTATTT
1,750	1,24E-06	A_15_P140101	zgc:86839	CKS2	CDC28 protein kinase regulatory subunit 2	NM_001002110	9896	124	2	891	CAGGGTTTATATTGAGATAAGGTTTTGACCCTGTCACAGAATTACTTTTAGGGGAAAAAA
1,426	9,16E-05	A_15_P111214	si:dkey-94n12.2	CKS2	CDC28 protein kinase regulatory subunit 2	NM_001044969	5596	72	15	643	TCCATTGCTGAACTGCTGTTGTTTAACATCTCCTACTTGTATCTTGAGCAGTCGACTTTG
-1,491	0,000285593	A_15_P112845	cdkal1	CDKAL1	CDK5 regulatory subunit associated protein 1 like 1	NM_200627	41960	509	13	1951	GGTCTGGCTGTGCTCTGAGCTCCAGACTCGGCCTGGTTTTGTTCTCCACATAAAGCGGTT
-1,511	2,24E-05	A_15_P108392	cdv3	CDV3	CDV3 homolog	NM_212721	9702	119	72	1961	CTTGTCGACATACTGCGAATAATGGATGATCTCTAACAATGTCCCTTTAACCCTTTCATC
1,622	1,00E-05	A_15_P111089	zgc:101711	CCPG1	cell cycle progression 1	NM_001007426	33568	408	37	1141	TTTGCTAACCTGTGCCTGCGGTACCCATTTATGTCTATAACATAGAGCTATATAAAGTAT
-1,687	3,34E-06	A_15_P257286	si:dkey-91f15.6	CIDEC	cell death inducing DFFA like effector c	NM_001045047	16965	207	42	755	GAGGAGAAAACAGAGACAGAGATGATAACACCTGCATACGTCATCAAGCAATTAAAACAT
-1,829	3,03E-06	A_15_P153751	si:dkey-91f15.6	CIDEC	cell death inducing DFFA like effector c	NM_001045047	40023	485	23	1354	GCTGTATTTATTACTGCCTTTGACTGAACACTTTATTGACTTTTCTAATAGCTGTTGCTG
1,662	4,77E-06	A_15_P106443	cdc20	CDC20	cell division cycle 20	NM_213080	29555	359	22	2065	AGTGGTTTAAACTTGTAACAATCACTTGTGTTAGCTTTTTGCAGTGTTTACCATACTAGC
1,532	1,68E-05	A_15_P210476	cdc20	CDC20	cell division cycle 20	NM_213080	31612	383	58	2097	AGCTTTTTGCAGTGTTTACCATACTGGCAGTTTGTTGAATTAAATTCCTCAGTCTCCTGG
1,576	9,38E-06	A_15_P106502	ENSDART00000011657	CDC6	cell division cycle 6	ENSDART00000011657	33731	409	35	1932	GTGTCAAACATTTTTACCTGCCTTTCTAAATGTAGGGCCGTTTTATGTTTTCTTTCAGGT
1,401	0,000146229	A_15_P100627	zgc:101602	CDC7	cell division cycle 7	NM_001007409	34170	415	6	1553	CACTGCAGCATCCACTCTTCAAAGATTTGAGTGAGTAGTGATTGTGCGCATCCACGATTT
1,618	8,54E-06	A_15_P145656	CH211-244O22.2	CDCA2	cell division cycle associated 2	ENSDART00000099566	39798	481	76	2364	GTTTCTGAACCATTCATCCCTCAACCCTCTGAAGAACTAACAACAAACTTGGGAGAGTAA
1,611	8,72E-06	A_15_P192646	DKEY-273O13.2	CDCA5	cell division cycle associated 5	NM_001100947	1437	20	81	1017	GCTGCCAAGATGAACGCTGAGTTCGAGGAAGCTGAAAGTTTTGAACTGTTTGTTGAATGA
2,374	1,46E-08	A_15_P118478	zgc:110113	CDCA7	cell division cycle associated 7	NM_001017574	10411	130	9	1549	TTCTTATTGCTCAGTGGGTTTGCAGACGCTGTTATGACGGCGTGTTTTTACTGCTGTAGA
1,457	5,79E-05	A_15_P105935	crabp1a	CRABP1	cellular retinoic acid binding protein 1	NM_182858	41252	499	58	642	TTCTCTCTCTCTTTGTCCATTTCTGGCACAGATCTGTGTACTGCAAAGATAAACAGTAAT
1,455	5,29E-05	A_15_P111365	crabp2a	CRABP2	cellular retinoic acid binding protein 2	NM_182859	42697	518	77	2480	TTATATAAACAGTTCCAGCAGTCATCACTCATTTCTGTGCATGGACAATAAAAGTTTCTG
2,961	3,15E-09	A_15_P173341	zgc:152925	CENPE	centromere protein E	NM_001076721	33198	403	18	1424	TATGTCAGAAACGTGAGCCATGCTTGAGTCCCTGTCCTTAACAGTGTAATAAAGGGACCT
1,745	1,31E-06	A_15_P121400	cenpn	CENPN	centromere protein N	NM_001002341	21000	256	61	1152	TCATGTATTGAGCAGCCTGAGTTATCTGAAACAGCTGGAATGATCTATGAACCAGCAAGG
1,641	4,45E-06	A_15_P101427	zgc:101125	CENPP	centromere protein P	NM_001003555	28480	345	68	867	TGGAGGCATCGATCGAAGGCTTGATAAGAACCGTGTGTTCGTGACAAGTTGTAAATCACA
1,545	1,41E-05	A_15_P192516	zgc:92404	CRBN	cereblon	NM_001003996	23618	287	43	2364	GTCAGTTAAGTAGCTGTAATAAGAAAACAAGCTGATTTGCATATCTGTGATGTTCAAGAG
-2,087	1,33E-07	A_15_P113219	zgc:92404	CRBN	cereblon	NM_001003996	27422	333	37	2406	ATCTGTGATGTTCAAGAGATTACAAACTGTTCAGATGTACAAACTGATAAATTCACGCCA
2,625	5,69E-09	A_15_P192831	cp	CP	ceruloplasmin	NM_131802	5509	69	56	3000	TAAAGTGTACTGGTATCTGATGGGACTGGGAAATGAGGTGGACATACACACAGCACACTT
-1,807	2,08E-06	A_15_P114147	CH211-244P18.4	CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1	NM_001045032	33395	406	34	754	AATAGGTCAAAACAGCATTAAGGTTCTAATATAAAGTTAATGTTGCCGTCCTTAAGGTGC
1,633	1,74E-05	A_15_P107554	zgc:56093	CHEK1	checkpoint kinase 1	NM_200193	1914	28	3	1670	TGTGACAAAGAGGGTTTTAGTTTTCTACCTCCTAAATAGATTGTAGGGTTCAGAACATCA
-1,720	2,79E-06	A_15_P103044	zgc:63792	CHIT1	chitinase 1	NM_200446	33908	411	42	1939	GGCTGTAGTACAACTGGTTTCTAGAGAGTCAAGGAAAAATTCTCTTGTGAATCAATGCCC
1,596	2,12E-05	A_15_P139551	zgc:65788	CHIA	chitinase, acidic	NM_199603	31435	381	51	1594	GCCAAACATATACCACTGCTTTCTTTTGAAAATGCTACATTTTGATGGTTGGAGAAGTAT
-1,443	8,11E-05	A_15_P108934	zgc:55406	CHIA	chitinase, acidic	NM_213213	33569	407	38	360	AATCCTGCAAACCGTAAAACATTTATTCAGTCTACCATCAAATTCCTGAAAACTCATGGA
-2,809	2,25E-09	A_15_P101682	zgc:55406	CHIA	chitinase, acidic	NM_213213	42077	509	74	1399	TGTTTGATGACAGCTGCAAGTGCTGTGTTTGGCCCAAACCTTAGTGATCATGACTCAAGA
2,424	1,26E-08	A_15_P119113	zgc:92762	CLIC2	chloride intracellular channel 2	NM_001002561	33606	408	56	1276	TTGTATTGTGTGAAGGGGTATTGTGAAGGAGTCATGAATAAGAAAGAGACTGAACTGCTT
-1,704	5,20E-06	A_15_P208291	zgc:101827	CLIC5	chloride intracellular channel 5	NM_001007385	35360	430	16	1771	TCTCAGGTATTATATCTTGCCCTGTCTGGAGTTTTCATAAATTGAAGTGAACAATATCAG
-1,764	1,87E-06	A_15_P141351	zgc:103675	CETP	cholesteryl ester transfer protein	NM_001007360	16339	200	62	1726	CCTTCATAATGTTATTCAGAGGTTGTGTTACCAATATTAAACATTTCCTGATGCTGTCTC
-1,412	0,000249269	A_15_P152156	si:xx-bac7cse.2	CHSY3	chondroitin sulfate synthase 3	NM_001089348	35090	425	48	2267	CGGCTAATGTCAAATGCTGATTTTGTATGCAAATGTTTTGGATTGTGATTTGAACACAGT
-1,417	0,000125415	A_15_P569187	si:xx-bac7cse.2	CHSY3	chondroitin sulfate synthase 3	NM_001089348	41820	508	19	2026	TTGGACTTGATGTACTTTGTTGACAAAAGTGCAGTACACTTTAATGACTGTTTGAATGGA
2,941	1,42E-08	A_15_P104030	lect1	CNMD	chondromodulin	NM_131835	13282	164	28	1551	AGTCGAAATGAACTGCAAAACTGCCAAAAATGCCTTTCTGTATTGGTGTTTTTGTCTTGT
2,682	5,45E-09	A_15_P212236	zgc:153930	CHAF1A	chromatin assembly factor 1 subunit A	NM_001045013	26418	321	35	975	TAATAAAGTGAAGAGACGATCCCTTAAGAGTGTTCAAGAGCAGGAGGAGAAGCAGCGACA
2,497	1,11E-08	A_15_P113857	zgc:153930	CHAF1A	chromatin assembly factor 1 subunit A	NM_001045013	14608	180	27	694	GAACCGACTATACCACTGACAGAGGAGGAGACTGAAAAGGATGAAGCTGAAGATGTAAAT
1,504	6,88E-05	A_15_P141196	zgc:153930	CHAF1A	chromatin assembly factor 1 subunit A	NM_001045013	24947	304	44	2712	ATCTGGATCCTCTGAACAGGACATCAACACATCCTTGCCACAAACAGATCGAGAAACAGA
-1,410	0,000179292	A_15_P296106	flj20508l	C1orf109	chromosome 1 open reading frame 109	NM_173269	9901	123	5	785	GACTGTGCATCAGCATCATTGTAAGAGCAATGCTCTACTGTAATAAATGCAATTCATGCT
-1,443	9,58E-05	A_15_P153176	flj20508l	C1orf109	chromosome 1 open reading frame 109	NM_173269	16789	205	36	791	GCATCAGCATCACTGTAAGAGCAATGCTCTACTGTAATAAATGCAATTCATGCTTTTTAT
1,594	1,36E-05	A_15_P546377	sb:cb484	C1orf115	chromosome 1 open reading frame 115	EH437887	6646	84	41	941	TAACAGGAAAAGATGATCAGAGAAACGACGGCGACTTATTTGAGGGAGTCAGTGAAGCTG
1,587	1,77E-05	A_15_P109196	im:7139423	C1orf159	chromosome 1 open reading frame 159	BC134934	8895	110	84	1562	TTGGTAAATTTACGGTTGGAAAAAAGAGATCGTTGTTGTGTCATAAAGCGAGTGATGCAC
1,405	0,000122696	A_15_P134486	BC092182	C1orf159	chromosome 1 open reading frame 159	BC092182	6136	77	35	1962	GCTTGTGTCAATGGAGTGAGTATTGATCATGTTGAATCATATTTGATGAAGATTTCAGTG
1,608	6,70E-06	A_15_P564217	zgc:153317	C15orf48	chromosome 15 open reading frame 48	ENSDART00000101678	31796	385	67	475	ATTATTCAACTGACTTCAGTTTGACTCCTGGCAAAACCATAAAGCACTGCTCATTTCACT
2,274	3,47E-08	A_15_P118419	BC076207	C15orf57	chromosome 15 open reading frame 57	BC076207	43246	526	65	1025	TGCATCCATGAAGACAGGATTTCATTCAAACATTAGTAGAGATCGTTAAGTGTAACATAC
1,405	0,000139526	A_15_P103851	zgc:91940	C17orf62	chromosome 17 open reading frame 62	NM_001002669	8289	103	31	1245	ATGCAATGCATGAGTACGAATGTAAAGAGCGGATATGGATTAAACTTGTTGAATGTTTG
1,922	2,61E-07	A_15_P170981	si:dkey-184p18.2	C18orf21	chromosome 18 open reading frame 21	NM_001077280	35269	428	54	2046	CACGATACTGCACATTCATTTTTCTACTGGAAAGATTCACTTTTATATGTGGTGTGTTTC
2,097	1,15E-07	A_15_P135886	zgc:112443	C2orf40	chromosome 2 open reading frame 40	NM_001017697	14461	178	36	103	TCGCAAGTGAGAGCAAGCTGGAAAAACTTTTGATGAAACGAGTGGACAGGGATGTAAAGC
2,009	1,45E-07	A_15_P113833	BC076153	C2orf40	chromosome 2 open reading frame 40	BC076153	27714	337	17	488	GCTAACACAACCTATGTTGCATATACTGTCTAATACAAAGGTTTAGCCACCCCTTGATAA
-1,455	5,37E-05	A_15_P190471	LOC565309	C21orf33	chromosome 21 open reading frame 33	ENSDART00000081039	7012	88	58	635	TCCCATCCATGAGATTTTTGATGGCCTGGAACTGATGGTAGCAGATGTTCTCAAACTAGC
-1,507	2,39E-05	A_15_P103105	sb:cb252	C21orf33	chromosome 21 open reading frame 33	EH592105	28483	346	69	752	CTGGAACTGATGGTAGCAGATGTTCTCAAACTAGCCTAACTCTGTTATGTGACATTGTTC
1,647	3,84E-06	A_15_P112246	c21orf59l	C21orf59	chromosome 21 open reading frame 59	NM_200088	21477	262	49	1319	AAGCTTAAAGTATTGAGAGTTATGGTTTCACTGGAAAGAGAGGAAAGTTGAGGGTGAAGT
1,456	5,23E-05	A_15_P104347	c3orf58a	C3orf58	chromosome 3 open reading frame 58	NM_001007436	5584	72	9	1795	AATCATGCCATTGTTGGCTGTAGTCCTGTTTGGGCTTAATAAAGAAGTTTGCACATCTAA
2,078	1,58E-07	A_15_P106734	zgc:77778	C6orf58	chromosome 6 open reading frame 58	NM_213203	6318	80	44	752	GCGTGAACTTGGGAGCATTTATATCGGCGGCTCATTACCACGCAAGCATTGAGCGCGCTG
1,530	2,40E-05	A_15_P199911	chtf18	CHTF18	chromosome transmission fidelity factor 18	NM_001110102	12053	148	81	2072	CGTTTTAATGAAGGTGTGTCCAATGCAGTGCGCAGAAACGTTTACATTCGAGAGTTGCTG
1,484	3,64E-05	A_15_P174076	LOC555570	CHTF8	chromosome transmission fidelity factor 8	NM_001044336	19444	237	31	600	TGGAGTTAGTGCATTTACTGCACACATGCATTGTTGTCAGAAATGTGTTTCTGACAATAA
-3,539	1,19E-09	A_15_P110159	ela2l	CTRC	chymotrypsin C	NM_212835	34565	420	35	362	CAAACTGGAGATTGCTGTTACCATAGGGACACCAATCACTCCTGCATGTCTTCCGGAGGC
-1,840	1,12E-06	A_15_P205871	zgc:92292	CTRL	chymotrypsin like	NM_001004582	24963	303	53	778	GATTGACCAGATCGTTGCCTCCAACTAGAGCTCTTACTCTCTGAAGAAAATGCCAATAAA
-1,592	0,000110608	A_15_P308261	zgc:154142	CELA1	chymotrypsin like elastase family member 1	NM_001099240	41150	499	5	3327	AATGGGGTTTCAAGGACACTGGACCACTGATCTTGGTGTTTCTCCAAAAAATATCTTCTA
-1,811	9,48E-07	A_15_P173931	zgc:112302	CELA1	chymotrypsin like elastase family member 1	NM_001025187	27970	340	62	1309	AAACGGTGTGATGTAAGCTGTTAAACTTTAATAAAAGCAATACATGGTGGACTGCAGAAA
-2,053	1,02E-07	A_15_P150526	zgc:112368	CELA1	chymotrypsin like elastase family member 1	NM_001025474	3282	43	26	861	TAACATCTGCTATTACCAGTAATACAACAAACTTCACATCTAATCTTAGACTGCTTCGGA
-2,092	7,87E-08	A_15_P116148	zgc:92511	CELA1	chymotrypsin like elastase family member 1	NM_001003450	2457	34	30	834	AACATCCTCCATGGCCCGCAATGACAGAAAAAGAAACGTTAACTAACAATAAAACGTTGC
-2,617	7,27E-09	A_15_P212996	zgc:92041	CELA1	chymotrypsin like elastase family member 1	NM_001003737	42595	517	26	841	CCTCGGGAATGCCAACATTTAACATCTGTAAAGGCCAAATATACTTCAATAAACTTTACA
-2,679	5,89E-09	A_15_P113940	zgc:92041	CELA1	chymotrypsin like elastase family member 1	NM_001003737	1011	16	22	840	TCCTCGGGAATGCCAACATTTAACATCTGTAAAGGCCAAATATACTTCAATAAACTTTAC
-2,687	1,25E-08	A_15_P106633	zgc:92041	CELA1	chymotrypsin like elastase family member 1	NM_001003737	39127	474	71	472	TGCTACATCACTGGCTGAAGCCTCACTTACACTGGTGGCTCCCTCTCCGCTCAGCTGAAA
-2,692	4,74E-09	A_15_P209086	ENSDART00000106082	CELA1	chymotrypsin like elastase family member 1	ENSDART00000106082	7274	91	23	770	CGCGTCTCTGCCTACATCAGCTGGATTAATGGCTTAAGAATTCAGATTTGCTTTTTAAAC
-3,414	1,80E-09	A_15_P209091	zgc:92041	CELA1	chymotrypsin like elastase family member 1	NM_001003737	25124	306	52	192	TCTGATCAAACAGAACTTTGTTTTGACCGCCGCTCACTGCGTTGATACCTCAAGAACTTG
-3,689	2,04E-10	A_15_P101676	zgc:92745	CELA1	chymotrypsin like elastase family member 1	NM_001003426	8610	108	24	298	ACAACCATGAGGGTCGCGAGCAGTATATAAGTGTCAGCCGTGCTCATATCCACCCCAACT
-2,110	7,87E-08	A_15_P211831	ela3l	CELA2A	chymotrypsin like elastase family member 2A	NM_001024408	42588	518	22	791	TTGACAAGGTCATGATGAACAACTAAGAAGAAACGAGGATGTCGTTATTAATACCAGAAA
-2,269	3,53E-08	A_15_P599207	ela3l	CELA2A	chymotrypsin like elastase family member 2A	NM_001024408	33393	406	33	735	TAACACTATTAGGAAGCCTACTGTTTTCACCCGCGTGTCTTCTTTCACTGACTGGGTTGA
-3,509	8,29E-08	A_15_P117864	ela3l	CELA2A	chymotrypsin like elastase family member 2A	NM_001024408	32093	390	47	43	AGCGCCTTTGGGTGTGGAAAACCACCCATTGAGCCTCTCGTGTCTCGTGTGGTCAATGGA

-2,218	3,41E-08	A_15_P113799	ctrb1	CTRB2	chymotrypsinogen B2	NM_212618	2808	38	40	784	CCAGACCATTGCTTCCAACTAAAGCAGCAATGAATCCTGTCATCAATAAACTTATATGAC
-2,330	2,71E-08	A_15_P117308	zgc:136461	CTRB2	chymotrypsinogen B2	NM_001045282	21353	260	71	786	GACCATCACTGCAAACTAAATCACCAAGCTAATGTTCATGGTCATAATGTTCATCAATAA
-3,045	1,01E-09	A_15_P108311	zgc:112160	CTRB2	chymotrypsinogen B2	NM_001017724	37469	453	76	1497	GAAATGCCATATTCTGCAACAAAAAGGTCTCTGTAATGAGTAATGTAACATGCTTCATCA
2,021	1,24E-07	A_15_P109080	zgc:85910	CFAP97	cilia and flagella associated protein 97	NM_212778	36895	448	34	1676	CAGTGCCTATTTGTGACAGACACGTATGTTAAAACTATACATAGTTTTAAAGCCATTGCT
1,455	5,71E-05	A_15_P104463	zgc:92247	CLDN11	claudin 11	NM_001002624	3225	42	81	1129	TTTCAGAATAACCGATCAGACTAGATTGCACCAAAATTGGACCAAAGCAGTATTATTTAG
-1,437	7,37E-05	A_15_P120000	cldn10l	CLDN15	claudin 15	NM_131771	22624	276	40	826	AATTGTAAAAAGTAAATCAATTTTCATGGATGCGGCACGTGCTGAATAAAATATGCCCTC
1,607	7,11E-06	A_15_P117602	cldn19	CLDN19	claudin 19	NM_131770	27273	331	46	716	TGATTAACCCTCTGCACTGATGTAAATGACCGGCTCATCATGACGCACTCATTAAAGCTG
1,446	7,30E-05	A_15_P109495	LOC553515	CLDN23	claudin 23	BC081659	6590	84	12	1841	GTATTTTACACTGGGCTCAAGATTTGTGAGGTTTCTTAACAATCCAACTTTGTGTAAATG
4,028	9,08E-11	A_15_P101599	zgc:103419	CLDN5	claudin 5	NM_001006044	34049	413	30	1535	TGCAGGCAGGCTGGTTTGATCATCTAAACCTCCTGATTGTACATAATTGTATGAAACTTT
1,938	2,32E-07	A_15_P108842	zgc:92192	CLDN7	claudin 7	NM_001002340	40328	489	8	1382	TACTAAACACATTTCTGCATTAACTCACACTTGTCATTACTTTACCCATAAGCCCTTTTG
2,795	9,51E-09	A_15_P112672	f2	F2	coagulation factor II, thrombin	NM_213390	40413	489	51	1582	TCGGGAGATGACGAATGATCTTCCAGTCTAGAAGCAAATACAAGGAATAAACACTTTGGT
1,591	6,59E-05	A_15_P113734	f2	F2	coagulation factor II, thrombin	NM_213390	25765	313	40	450	CCACAAGATTGACGAATTTAATGTGACACAGCTGAAGCTACCGGAGAACTTCTGCAGGAA
2,124	1,30E-07	A_15_P170216	zgc:136807	F9	coagulation factor IX	NM_001040310	32679	397	9	1500	TACTAACATTACCAGAATCAGAACAGGACATATGTCTAATGGTGATCAACAGAGTTTGAA
2,744	4,85E-09	A_15_P103427	f5	F5	coagulation factor V	NM_001007208	28713	349	17	6349	TACCAAAACAATGGCAGAAATCCGTCACCATGAGAATTGAGCTGCTGGGTTGTGATTTCG
2,127	6,84E-08	A_15_P102638	f5	F5	coagulation factor V	NM_001007208	27187	331	2	6389	GCTGCTGGGTTGTGATTTCGAATAAACACTTTGCTGTCTATGGTGGATTTTGTTTTTTAAT
1,681	2,79E-06	A_15_P164426	zgc:163025	F7	coagulation factor VII	NM_001089558	28914	352	34	2451	GATTGACAATCAGATTTCTGTGCACTACAGCAATAAAACTAAAGTGACAGACACCAAAAA
1,602	6,53E-06	A_15_P169516	f7i	F7	coagulation factor VII	NM_173228	23951	291	43	1449	GCCCTCAAACTCTTTACTTCCACCCTCATTCTGGATGGATAAATGCATATATAAATATAA
2,171	8,38E-08	A_15_P106615	f10	F10	coagulation factor X	BC056804	8419	105	11	2207	GGAGGTAGAATGGTTCATCAATGCTTCGACCATCATGTCTGAGTTTTAATAAAGATGATA
2,122	6,19E-08	A_15_P520827	f10	F10	coagulation factor X	BC097035	23875	291	4	2206	TCATGGTATATCTAGTAAAATCACATTATGGAGGTAGAATGGTTCATCAATGCTTCGACC
1,486	0,000171156	A_15_P149401	zgc:153334	F13A1	coagulation factor XIII A chain	NM_001077154	22766	277	28	2511	CATCCTTGTCCTTTATGTAAGAAGAGTAATGCTGTACTGCATAGAAAATAAACGACCAAC
-1,449	9,54E-05	A_15_P100633	zgc:73324	COQ10B	coenzyme Q10B	NM_200789	17468	213	44	1018	TGGAAGGATGCTTTTTCATATTTATGATTGTTCTGTTCACACGGTTGACCAAAGGGAGAA
-1,454	0,000107971	A_15_P104517	zgc:112103	COQ10B	coenzyme Q10B	NM_001017747	30266	368	45	823	AAGGACAATCAGGAGAGCGGGAGCTGTGTGCCTGAATATCGTCAGTGCCTGGTCCAAATA
-1,448	0,000247553	A_15_P205661	zgc:153034	COQ3	coenzyme Q3, methyltransferase	NM_001076637	34434	418	54	1606	GTTTATACAGGAGTTCTCCAAGGAGGATTTTGATGCCATTGTGAGCGGATGGACTGAGAA
-1,669	4,45E-06	A_15_P116829	zgc:92578	COQ8A	coenzyme Q8A	NM_001002728	9145	114	41	468	TTCCCGGAGCATCTGATAGATGTGATGCGGCGTGAGCTGGCGCTGGAGTGCGATTACATA
-2,130	8,88E-08	A_15_P207956	zgc:92578	COQ8A	coenzyme Q8A	NM_001002728	14462	177	37	1965	GAGCGATGGTGTTAAAGGCTTTTTTCTAATCTTCCTGCTAATGGCGTTCTTACTAAAAAA
1,688	4,44E-06	A_15_P115012	cfl1	CFL1	cofilin 1	NM_213639	15792	193	41	643	GGGAAGCCTGTCTAAAATTTGATCCACCTGCCTTTTGTCAGTCTGTCGGCCATTATGAAA
1,668	3,01E-06	A_15_P597357	cfl1	CFL1	cofilin 1	NM_213639	42908	521	36	537	ATTGCCAGGTATGAAGTTTGAGTGGCAAATTAATGACCATGCAGATAAAGACGCATCAAG
1,636	4,75E-06	A_15_P180791	ENSDART00000065676	CCDC80	coiled-coil domain containing 80	ENSDART00000065676	33593	407	50	1866	GATGAAAATACTGGCACTTATCATGGCTACACAGAAGAAACAGAAGACAGCTATTTGTAC
1,566	1,15E-05	A_15_P116203	ccdc80	CCDC80	coiled-coil domain containing 80	NM_001007198	24423	297	32	2523	CCTGAGGATGAGTACGGTGGATATGGTTATCATCATCATGAGGGTTACCAGGAAGGTTAT
-1,404	0,000138511	A_15_P297756	LOC567572	CCDC89	coiled-coil domain containing 89	ENSDART00000058248	2236	32	2	434	CAAACTGACCCAAGAGCTTAAGGATTTGGCAGAGCAACATAAGATACTGGAAAATGAGTA
1,484	3,38E-05	A_15_P150961	zgc:162618	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	NM_001089331	41980	510	24	1928	GCACATGTTTGTGCCACTTGCAGATCTGTGTTCATTTGTTTTAGCATCTTTACATTAAAA
1,571	1,15E-05	A_15_P110768	cthrc1a	CTHRC1	collagen triple helix repeat containing 1	NM_001003765	27562	335	24	1100	TCACTGTAATACTGCAATAGTACTCTATTTATTTAGGGGGTTTTCTTTTAGTGCCTGGAT
4,439	1,70E-10	A_15_P104906	col1a1	COL1A1	collagen type I alpha 1 chain	NM_199214	14277	176	26	5407	TAGAAAAGTCCTAAAATCATGAGAGAAGGCACACCTTAGGGGGGTAAAAACAAGAAGATC
4,371	2,42E-10	A_15_P106749	col1a3	COL1A1	collagen type I alpha 1 chain	NM_201478	3515	46	59	5437	ACTTAAAGAAAAAGGGAAAATGCAGAAGAGATAGACCCTCCCATTGGTTCCATCAAAGGA
3,537	3,19E-10	A_15_P106798	col1a1	COL1A1	collagen type I alpha 1 chain	NM_199214	26252	320	35	4260	CCTATTATTGACATCGCCCCCTATGGACGTTGGTGCACCTAATCAGGAATTTGGCATTGAA
3,991	1,08E-10	A_15_P148301	col1a2	COL1A2	collagen type I alpha 2 chain	NM_182968	39731	481	42	4986	CAGAGACCTCTCTCTCAAAACAAACCACAAAGTTTATTGTACCTATTTTGTATATGTGAG
3,535	9,34E-10	A_15_P211731	col1a2	COL1A2	collagen type I alpha 2 chain	NM_182968	34055	414	33	4209	GGACATTGGCCCAGTCTGTTTCAAATAAATAGACTCATGATAAATTAAACGAGAGAAAGA
2,715	1,06E-08	A_15_P113763	col1a2	COL1A2	collagen type I alpha 2 chain	NM_182968	18641	228	45	3675	CGACCCAAACCAGGTCTGCACAATGAATGCCATCAAGGCCTTCTGCGACTTCTCTACTGG
1,679	3,77E-06	A_15_P180121	ENSDART00000077296	COL4A1	collagen type IV alpha 1 chain	ENSDART00000077296	19845	242	66	656	AACATTAAAGGCCGGAAGTCTAAGAACTCACATCAGCAGGTGTCAAGTGTGCATGAAGAG
2,689	3,49E-09	A_15_P120840	col9a2	COL9A2	collagen type IX alpha 2 chain	NM_212579	37639	456	76	3097	GTTGTTTTGCCAGGTTGTTCAGGTTTACCCCAATCAATAAAAAGGAACGTTTTGTAAAAC
1,950	7,45E-07	A_15_P134081	col9a2	COL9A2	collagen type IX alpha 2 chain	NM_212579	8430	105	17	1765	TCAGATCAACACATCATGGACGTGGTTCTGAAGATGCTTCAAGAGAGGTTAGCAGCAGTA
4,223	7,55E-11	A_15_P111375	ENSDART00000055139	COL9A3	collagen type IX alpha 3 chain	ENSDART00000055139	27350	333	1	2922	TCAGTGGGCTTTATCGACCCCAATCCACTAGATATTGGTGCTGTAACTATTAAATATGAT
2,350	2,27E-08	A_15_P119789	ENSDART00000055139	COL9A3	collagen type IX alpha 3 chain	ENSDART00000055139	7423	93	15	1401	AAACATGGTGAACTCGGATCCAAAGGAGTCGTAGGACCCCAAGGAGAGACCGGAGCTAGA
1,943	3,80E-06	A_15_P119490	ENSDART00000055139	COL9A3	collagen type IX alpha 3 chain	ENSDART00000055139	40629	491	76	555	ATGCCTGGATTTAAGGGTCATACAGGCCATAAAGGAAGTAAAGGAGAGTTGGGGAAAGAT
1,831	3,30E-06	A_15_P201966	ENSDART00000041807	COL5A2	collagen type V alpha 2 chain	ENSDART00000041807	30241	367	33	3720	GACATTGGAGGTTCAGATCAGGAGTTTGGAATTGATATTGGGCCTGTGTGCTTCTTGTAA
1,483	3,43E-05	A_15_P495557	ENSDART00000041807	COL5A2	collagen type V alpha 2 chain	ENSDART00000041807	1727	23	70	3436	AGATGACTTTCATCCGTCTACTCTCAAAAGAGGCATCACAGACTATCACTTACCACTGCA
1,695	9,92E-06	A_15_P345675	LOC569755	COL6A1	collagen type VI alpha 1 chain	XM_693161	21727	265	7	5137	AAATGAACATCTATCTTGCCTTTATTTTGGACCCTGCTTGCAACAAAATCTGAGCAATTG
1,664	3,38E-06	A_15_P265756	LOC569755	COL6A1	collagen type VI alpha 1 chain	XM_693161	26833	325	77	5386	CAGAAATGTATTTGAAACTTTGTAAAGGTATTTGAAATAAAGGACGCTACACCCCACCAC
1,492	3,68E-05	A_15_P130226	col10a1	COL10A1	collagen type X alpha 1 chain	NM_001083827	28649	347	69	2478	CCTTATATCTGACTTGAATATTGTGAGATGGTGAAAATGCGAAAAAACAAACTCACAAGC
1,851	5,48E-07	A_15_P151126	col11a1	COL11A1	collagen type XI alpha 1 chain	NM_001079992	23484	285	59	5256	TTTGGGGAGGACAATCAGAAATTTGGTTTTGAAGTAGGACCTGTCTGTTCCTGGGATAA
1,414	0,00039832	A_15_P107299	LOC565402	COL11A1	collagen type XI alpha 1 chain	NM_001083844	42778	520	44	3265	AGGTCCTCTGGGTCCAGCCGGTAGGGATGGAGTTCAAGGTCCAGTTGGTCTGCCAGGTCA
1,524	1,86E-05	A_15_P207321	col15a1	COL15A1	collagen type XV alpha 1 chain	NM_001080091	25426	309	38	3749	CACTTGTGTAGGGTTTTTACTGTAAGCGTTGTTTGTTTGTTGAATAAATCTGGTTTCCAT
1,815	7,21E-07	A_15_P210116	col18a1	COL18A1	collagen type XVIII alpha 1 chain	ENSDART00000053118	10016	123	63	5088	TTCAAAGGCATTGGTTGCATTCGGTGCTTTTTGCTGATGAAACAGCTGCTGACAGTGTTG
2,521	1,15E-08	A_15_P211276	MGC171537	C1QL3	complement C1q like 3	NM_001110109	30317	367	72	643	AAATGGATATGGGATGGAAGCAACGTCACTGTCTTTAATGGTTTTCTCCTTTATGACATG
2,377	1,49E-08	A_15_P113156	MGC171537	C1QL3	complement C1q like 3	NM_001110109	26682	324	85	649	ATATGGGATGGAAGCAACGTCACTGTCTTTAATGGTTTTCTCCTTTATGACATGTAAATA
2,502	9,94E-09	A_15_P404640	ENSDART00000079630	C4A	complement C4B (Chido blood group)	ENSDART00000079630	33792	410	67	4989	CCCACCAAAGACTCAAGTGGAAACATGCAGTATCTGCTGGATTCTAAGACATGGGTTGAA
2,037	1,41E-07	A_15_P203976	ENSDART00000079630	C4A	complement C4B (Chido blood group)	ENSDART00000079630	6422	81	12	5094	TACTGCAAAGAACTGAATGACTTTTTGAAAGAGTACCAAGTTGATGGATGCAATCTGTAG
1,747	1,77E-06	A_15_P173396	c6	C6	complement C6	NM_200638	38880	471	31	2943	CATGCTATAGTTATTTGTTTGTGCATATGGGCATTCTTGATATTGATCTGGAACAACACA
1,420	0,000108466	A_15_P100805	LOC793127	C8B	complement C8 beta chain	ENSDART00000057736	25669	312	76	935	TCCAGACATCATGCAGATGTGGGGAGAAGCCGTCTTCTACAATCCTGAGTTTATAAGCAA
1,768	2,23E-06	A_15_P106040	c9	C9	complement C9	NM_001024435	24718	301	12	877	TTGCAAAGGAGACAAGACCAGTGAAGACTACTGTTAAGACACAGAAAACTACACTACTTT
2,111	1,51E-07	A_15_P164416	cfb	CFB	complement factor B	NM_131338	37827	460	1	1912	AAGGAGGATCACAGTCAAGCTTGGGAAATATCTGGATGCTTGTGTTGAAGATGCAAAAAA
1,452	7,00E-05	A_15_P138196	LOC794857	CFHR2	complement factor H related 2	ENSDART00000105634	17877	217	83	801	TACATGACTTGCCAGGATGCAGAATGGACAGGGAAAATTTATTGTTTGAAGCCCTGTTCA
1,760	2,15E-06	A_15_P178566	BC142751	CFI	complement factor I	BC142751	17928	219	24	1176	ATGGTATTGACGACTGTGGAGACAACAGTGACGAAATGTGCTGCCAGGACTGTCAAAAAA
-1,895	3,28E-07	A_15_P181986	si:ch211-81a5.8	CPLX3	complexin 3	ENSDART00000104637	1273	17	77	281	ACCGGTTCAGAGGACAAACCTAAACAGCAAGACCTCCAGCAAAAATGACAACTCGCTTTT
-1,881	4,29E-07	A_15_P115938	cops4	COPS4	COP9 signalosome subunit 4	NM_205556	11174	137	57	1107	GCATGAACGGATTCATTGACCAGATTGATGGCATTGTGCATTTTGAAACACGAGAGCCGT
3,429	3,24E-09	A_15_P105157	cpox	CPOX	coproporphyrinogen oxidase	NM_001040094	29276	356	48	920	GACTCTGAAGGAAGCCTGTGACAAGCATCATCCTAAATATTACCCAGACTTCAAGAAGTG
2,963	4,10E-09	A_15_P495472	ckmt1	CKMT1A	creatine kinase, mitochondrial 1B	NM_198801	21632	264	43	1619	GTACAAGAATTAAACAGGTTTTTGTGGAAGATGCTGATGATATAACTTGCTGACGGATCC
2,878	2,83E-09	A_15_P118448	ckmt1	CKMT1A	creatine kinase, mitochondrial 1B	NM_198801	15950	195	36	1645	GAAGATGCTGATGATATAACTTGCTGACGGATCCTGAGAGTGTTTATTGTGTGCTTCACT
2,055	2,12E-07	A_15_P107481	ckmt1	CKMT1A	creatine kinase, mitochondrial 1B	NM_198801	5141	65	40	90	TGTTAAAATGGCAAGCAGCTTCGCACGGATTTTGTCAGGTAACAGGAAGGTTGGCATCTT
1,512	5,35E-05	A_15_P176401	zgc:56085	CKMT2	creatine kinase, mitochondrial 2	NM_199816	3477	45	40	467	TGTAATCAAGGACAGACACAATGGCTATGACCCAAGAAACATGAAGCATCCCACTGACCT
1,402	0,000135362	A_15_P193241	crb2l	CRB2	crumbs 2, cell polarity complex component	NM_001045162	233	4	62	5611	GATGATGCAGAATTTTATACAGGCAAGCAGATGAGCTCAGAATATGATCACATATTAGAC
2,240	3,10E-08	A_15_P100884	cry4	CRY2	cryptochrome circadian clock 2	NM_131787	13757	169	16	1549	TTCTGGAGGAGGCGGAGTCACAGTGCACTTCCAAGCGTTTCAGTGGCAGCTCAGACCATA
2,128	6,49E-08	A_15_P137886	cry4	CRY2	cryptochrome circadian clock 2	NM_131787	8762	109	16	1281	AAGTACTTACCTGTGCTGAAGAACTTCCCCTCTCAGTATATTTACGAGCCGTGGAAAGCA
1,494	9,73E-05	A_15_P103946	cry5	CRY2	cryptochrome circadian clock 2	NM_131788	23272	283	36	1491	AACAAAGGTGAAAAGCGCAAAGCGAGTCCATCCATCAAGGAGATGTTTCAGAAGAAGGCA
-1,566	2,77E-05	A_15_P111733	cryaa	CRYAA	crystallin alpha A	NM_152950	14777	181	30	681	GGGGGCCTAGGCTTTAATTTCAGAGGGCATCTAAAGGTGGATTCAAGCAAATCCTCTATT
-1,577	9,48E-06	A_15_P107823	cryaa	CRYAA	crystallin alpha A	NM_152950	660	9	69	1340	GACTCCACATGGGGCCATAAAAAGTGATCAAAGATAATAAAGATGTAACCTTAACCTTTC
-1,461	4,77E-05	A_15_P109998	zgc:92720	CRYBA1	crystallin beta A1	NM_001002586	20158	245	56	943	GTAGCCATTGCAGTTTTCATGGTCAGCTTCTGTATGATATTTGATGAATAAAAACATGAG
-1,737	1,40E-06	A_15_P103590	zgc:101859	CRYBA1	crystallin beta A1	NM_001005965	41305	499	85	1152	AGATGGGATCGTGTGTTTGACCATTCGGAGGAGAGGAGGACGAAGGTTGACTAATAAAAT
-1,534	3,31E-05	A_15_P113660	zgc:92722	CRYBA2	crystallin beta A2	NM_001002584	14720	180	85	637	GCAGAATTCAGCAATAAGAGAACAATATGTCATGCCGTATCAATACTATAGGCAATAAAG
-1,468	0,00042493	A_15_P175256	cryba4	CRYBA4	crystallin beta A4	NM_001018125	40708	493	31	275	ACTCCTTTGGAGGAAGCAATGCTTACCACATCGAGAGAATGACCTCCTTTAGACCAATCT
-1,819	1,37E-06	A_15_P192781	crygmx	CRYGA	crystallin gamma A	NM_001013262	11455	142	31	752	CTGCACCCTTCCCTTCCACAAATACAACTGGAAATAAAGGAGAAATTGATTAAAATCAAA
-1,491	7,12E-05	A_15_P121298	zgc:136220	CRYGC	crystallin gamma C	NM_001033722	38426	465	54	600	AATTCGCCGTGTCCGCTTCAACTAAACCAAATCCCCACATCCGTCAGCTCTTTATACAAA
-1,595	7,12E-06	A_15_P100387	zgc:153846	CRYGC	crystallin gamma C	NM_001076649	39390	478	37	553	CGTATCACTGACATGTGTTAAATTATTAGAATATAGAAGCAAATAAAGTATTATTTTCAG
-2,185	4,77E-08	A_15_P201446	MGC172241	CRYGC	crystallin gamma C	NM_001110106	33471	406	72	493	AGAGATATGGGAGGCATGAGATTTATGAGCATGAGACGGATTACGGATTCCTGTTACTAA

-1,640	4,74E-06	A_15_P199706	zgc:114194	CRYGN	crystallin gamma N	ENSDART00000060885	7844	98	60	306	CAGAATTTCACCGGTCAGTGTGTTGAGACCAAAAACACATCAATGTGTCCAATACTATAA
-1,917	2,79E-07	A_15_P114101	crygn1	CRYGN	crystallin gamma N	NM_001007784	20740	253	13	620	AGGATAACCAGCAAGAAATTCAGCAAGTGTATTGATCCCAAATAAATCGGAGCTTTTGGT
-1,535	3,31E-05	A_15_P141386	ctps	CTPS1	CTP synthase 1	NM_199211	38686	469	17	2041	ACATCCCATTGGGGGAAAGTTAATAGATTCTCTTCATTGTGATGGAGTTTGTTAAGTACC
-1,585	2,70E-05	A_15_P117541	zgc:100914	CTPS1	CTP synthase 1	NM_001003639	13497	166	53	1365	TGGCACTGTGTGAATTTGCTCGTAATGTACTTGGCTGGGAAGATGCAAATTCCACAGAGT
-1,820	7,37E-07	A_15_P139246	si:dkey-72g22.1	CAND2	cullin associated and neddylation dissociated 2 (putative)	NM_001110518	24192	293	81	3459	TGCACTACAAAGGTAAAGGCCGGTTCAGTGAAGCAAGAATTTGAGAAGCAGGAAGAATTG
1,424	8,76E-05	A_15_P104995	LOC572249	CNGA1	cyclic nucleotide gated channel alpha 1	ENSDART00000017375	18214	222	83	78	ATAGAAAATAAGCGTCCTGATGCTGGAGCTCTCTTCAACAACACCAACAACAGCAATAAC
-1,405	0,000183046	A_15_P156966	LOC562675	CNGB3	cyclic nucleotide gated channel beta 3	ENSDART00000088953	10759	133	15	1951	AAGGCAAAGCTGCTCCTACAAAGGATGAAGGAGAGAAGAAGAAGGGATTGGCTTTGTTTG
1,833	5,54E-07	A_15_P173696	ccna2	CCNA2	cyclin A2	NM_152949	20964	256	42	1851	CACTGTTAAAGTGACCTTCCCTTTACATCCAAATAAAAGTGCTGCTGGCCTTTAAAGCAC
2,415	1,71E-08	A_15_P106239	ccnb1	CCNB1	cyclin B1	NM_131513	11734	145	3	1392	TTTACGGATTTCTTCACTGCCATGGGTTGAGCAAAAGTAATCTTTTAATGATTCAAAGTG
1,642	4,30E-06	A_15_P101325	ccnb1	CCNB1	cyclin B1	NM_131513	14245	176	10	624	CTTGTACAAGTCCAGATTAAGTTTAGGCTGCTTCAGGAGACAATGTACATGACTGTTGCC
1,862	2,56E-06	A_15_P109617	ccnb2	CCNB2	cyclin B2	NM_199430	26462	322	57	1397	CTTTTACGGTTTCATGAACTTGCAGGATCTGTATTTTGACCTGTTAAAGCAACTTGAATT
1,419	9,76E-05	A_15_P111190	zgc:153369	CCNB3	cyclin B3	NM_001076719	34304	415	74	1228	GACAGTAAACTCGCCGTCATCAGGAGCAAGTATGCACACAAGGTTTTCTTTGAAGTTGCA
3,485	3,05E-10	A_15_P100423	cdc2	CDK1	cyclin dependent kinase 1	NM_212564	22277	272	34	1127	CCAACCTGCAGTAATGCAATCCGAGTCTTTTGACACGCAATAATCAACCTTCAGTTTGTT
1,988	1,56E-07	A_15_P306636	cdc2	CDK1	cyclin dependent kinase 1	NM_212564	20868	253	79	974	TCCGTATTTTGACGATTTGGATAAGAGCAGTCTTCCAGCCAGCAACCTCAAGATATAAAC
1,611	5,99E-06	A_15_P108536	cdk2	CDK2	cyclin dependent kinase 2	NM_213406	37744	458	44	1416	CGCTTCGTCTAGCCTTAGACTGAATGAAACTGTTTAGACTCCCTGTATCTTTTTGCTGCT
1,457	6,23E-05	A_15_P105830	cdkn1bl	CDKN1B	cyclin dependent kinase inhibitor 1B	ENSDART00000049061	28674	347	82	2180	CCATTTGTGCAAGGTTGCATACTGAGCCTTTTAAGAAATGATGTGGACTGTGTATTGCTT
1,777	1,34E-06	A_15_P102680	ccnf	CCNF	cyclin F	NM_207048	7102	90	20	3322	TGTATGAAGCTGTGAAAGGCCATGGGAACTTGAAAAAAGAGAAAAAAGATGCTTGTTTTAT
1,747	5,44E-06	A_15_P114029	ccng2	CCNG2	cyclin G2	NM_213172	6423	82	12	1668	GTGTGATGTTGTTAACCTACTTGCCAATTTAGTATGTTTCACTTTTAGCCGATGTATGAAG
-1,468	5,25E-05	A_15_P471945	cth	CTH	cystathionine gamma-lyase	NM_212604	23845	289	74	308	TGTTGCCTCTGGATTGGCGGCAACTTTGACCATCACACATCTTTTTAAAAGTGGAGATGG
-1,779	2,58E-06	A_15_P114130	cth	CTH	cystathionine gamma-lyase	NM_212604	40482	492	1	1743	GCGTTTTCAATTCTAAAGGGATCACTTCAGATCTTTGTCTGTGTTACCAGACCCATTAAA
-2,048	1,42E-07	A_15_P174761	cthl	CTH	cystathionine gamma-lyase	NM_001005400	33528	408	17	1110	TTTCACTGAGTAAGGATGAAAGGGAAAAGCTGGGCATCAGTGATACACTCATCCGTCTTT
-1,515	4,29E-05	A_15_P112576	cbs	CBS	cystathionine-beta-synthase	NM_001014345	7507	94	57	2704	TTGCTCTGCATGCTGCTGGAGGTCTCTGCCTCAACAGAACGTCTTATTTTTCTGTTATGA
1,532	1,69E-05	A_15_P163446	cyr61	CYR61	cysteine rich angiogenic inducer 61	NM_001080987	34821	421	81	3438	CAATTCTAGACTCTCGCTTGTATACGAGTGAACGATTATTTGTATTGCAAAGATGTTGAA
-1,615	5,54E-06	A_15_P164791	zgc:85866	CYR61	cysteine rich angiogenic inducer 61	NM_001001826	28637	347	63	804	GTACAGGAATCTCCACCCGAATCACCAATAATAACGCTGAATGCAAACTGATGAAGGAGA
1,430	8,09E-05	A_15_P119555	crip2	CRIP2	cysteine rich protein 2	NM_213497	18520	225	69	1935	TTGTTCTTTTGAGAACTTTCTTATGCAGAGCCTGCATGTCAAGTCCTGCTGCTTCTGTAT
2,002	3,29E-07	A_15_P109044	zgc:63636	CRISPLD1	cysteine rich secretory protein LCCL domain containing 1	NM_200470	19808	242	47	1976	TGTAACAACCTGGCAGGCCAGGAAATCATTATTGCTTTCAAAGAATTTGAGAAATTTACC
2,337	5,06E-08	A_15_P119329	zgc:153291	CYB5R2	cytochrome b5 reductase 2	NM_001045360	635	9	56	1158	CAATTCAAGAAAAACAGGCCAGAAATACACAGCACTGTTGTCTTATTTTGAAATGCATCC
1,666	3,03E-06	A_15_P446355	zgc:153291	CYB5R2	cytochrome b5 reductase 2	NM_001045360	7128	89	34	693	TTCATTTGACGAGACCGTGTGCTCTCTCATATTCGCCAATCAGACTGAGAAGGACATACT
1,733	1,99E-06	A_15_P119785	cyb5a	CYB5A	cytochrome b5 type A	NM_213135	16529	202	73	1248	GCTGCTATCACCATAAGACAAATAACACAAATCATTCAGCTTTATTGTGTCCCAATAAAC
1,507	3,75E-05	A_15_P157221	cyb5a	CYB5A	cytochrome b5 type A	NM_213135	20993	255	58	338	ATCCCTTGTAACAACAGTACAGGAAACAACAAGCTGGTGGTCAAACTGGTTGATACCTGC
19,256	3,16E-14	A_15_P157011	LOC402880	COX4I2	cytochrome c oxidase subunit 4I2	ENSDART00000105691	4042	52	72	456	GTGAACCCCATCACTGGATTCGCTCATAAGTGGGACTACGAAAAGAAGCAGTGGAAATAA
3,070	8,50E-09	A_15_P115818	zgc:153978	COX5B	cytochrome c oxidase subunit 5B	NM_001045357	25673	312	78	435	TGAACACACACACACCTGCAGAAACACTGATGCTTCTGCCATGTACAGCGCTTAATAA
5,599	1,46E-11	A_15_P104789	zgc:92631	COX6B1	cytochrome c oxidase subunit 6B1	NM_001002695	40309	488	83	483	ACGTCATTCCTTATTTAAATGAAAGTGTTGCAGAATCTGCATTAAAATCTCAGGCACTGA
4,921	2,19E-11	A_15_P177856	BC125945	COX8A	cytochrome c oxidase subunit 8A	BC125945	27415	334	33	299	CAGCACAAGAATAAAAAATGAGCATTCCCTCCTTAAGAAGACTATTTAAACCTCTGAATG
2,188	4,25E-08	A_15_P171581	cyp1b1	CYP1B1	cytochrome P450 family 1 subfamily B member 1	NM_001013267	9817	121	48	3109	GCTTGTTTGGATTCAGTGAGGAGTTTAACAAGCCAATGTGAAAAACTGTTTGCAATAAAT
1,518	2,02E-05	A_15_P148661	zgc:136223	CYP1B1	cytochrome P450 family 1 subfamily B member 1	NM_001045256	42798	520	54	1703	ATGTAATTGAAGTGAAATCAACGCACAGGACTTTGCCAAATGAAGGCGGCTAAGAAAACA
1,459	0,000119361	A_15_P136521	ENSDART00000064586	CYP2D6	cytochrome P450 family 2 subfamily D member 6	ENSDART00000064586	32329	392	84	1537	CATTAGGCGGAGAAACACAGTTAAACAGTGAATCTTAATGCTGTATATAAAGTTCCAGAT
-1,820	8,63E-07	A_15_P188336	LOC556280	CYP2U1	cytochrome P450 family 2 subfamily U member 1	ENSDART00000048281	7561	93	85	1281	TTTCTAGATGACCAGGGAAAGATTCTCAGGAAAGACTGCTTTATTCCATTTGGATTGGGG
-2,665	6,36E-09	A_15_P141076	cyp24a1l	CYP24A1	cytochrome P450 family 24 subfamily A member 1	NM_001089458	34470	418	72	2040	GTGGTGGAAATGTAGAGAATGTAGAAAATCACTGGATGTTGTTCACCTTTCATTCTTAAT
-2,935	4,25E-09	A_15_P108884	cyp24a1l	CYP24A1	cytochrome P450 family 24 subfamily A member 1	NM_001089458	32167	391	1	648	TCGAAACCATTTGCTATGTGATCTATGACAAGCGTTTCGGGCTTCTGCAAGACAGTGTCA
1,427	0,000486731	A_15_P132741	cyp26b1	CYP26B1	cytochrome P450 family 26 subfamily B member 1	NM_212666	25886	316	16	2329	CAAGCTATAGAGGGAATGAGGGACTTGTTCCTGCTGCAGATTTTATATCGGAAGACATTT
-1,448	8,29E-05	A_15_P161752	cyp3c1l2	CYP3A43	cytochrome P450 family 3 subfamily A member 43	NM_001007400	23282	283	41	1549	GTTTGGAAACATGTAAAGAGACGCAGATTCCTCTAGAACTGACTCCTGTTTTCCAGCCAA
-1,547	1,60E-05	A_15_P114674	zgc:123110	CYP3A43	cytochrome P450 family 3 subfamily A member 43	NM_001037438	23178	282	73	1632	TCTGATCTTCATACAGCATCACTCTGGTGTCTTAGGAGAACTCAGCGGACAGAGTCTCAG
-1,425	0,000207982	A_15_P200126	cyp4v2	CYP4V2	cytochrome P450 family 4 subfamily V member 2	NM_001077602	43017	523	20	1452	TTTAACATCGTAGCATGTCAAAAGAGGGAAGAACTTCGCCCACTGGGTGAACTGGTATTG
1,579	1,95E-05	A_15_P106000	cyp51	CYP51A1	cytochrome P450 family 51 subfamily A member 1	NM_001001730	42832	520	71	1467	GCGGATGTTCGACTTTGAGCTGGTAGACGGACACTTTCCACCGGTCAACTACACAACCAT
1,565	1,46E-05	A_15_P116988	zgc:63920	CYP7A1	cytochrome P450 family 7 subfamily A member 1	NM_201173	27643	335	66	3161	ACAAAGCTGTTTCTTTGTGGTCTGAAAGTTATACCCGAGTATGGAGGGGAGGAAGGTTT
1,492	3,23E-05	A_15_P118133	por	POR	cytochrome p450 oxidoreductase	NM_001034982	7886	98	81	2194	TATTGCCATCTTGTGATGGCTCTTAATGATAAAAACACTCCGCATCACACAGAATGGCAT
-1,614	5,91E-06	A_15_P102777	ciapin1	CIAPIN1	cytokine induced apoptosis inhibitor 1	NM_001003738	37935	460	56	1058	ATAAAACACTGATACCCAAACAACAAACACACGCAGAAACACTGGCTATATGCTTCAGTT
-1,795	2,84E-06	A_15_P337735	ciapin1	CIAPIN1	cytokine induced apoptosis inhibitor 1	NM_001003738	38372	465	27	512	TTACGGCATCTAAACCTGATTTTGAGGTCGGATCCTCAACACAGCTAAAACTTTCCTTTG
1,612	8,72E-06	A_15_P145611	ENSDART00000083371	CKAP2L	cytoskeleton associated protein 2 like	ENSDART00000083371	22450	274	37	2271	AATGAAGCACTGAGAGACTGTGTCCAGGTTAAACTTGTTTATCCAGAGGAGGTTGAATCA
1,549	2,39E-05	A_15_P108274	dctd	DCTD	dCMP deaminase	NM_001017639	29525	360	6	694	TGTGCAGTCACCATAGAATGAGGAACTTTGATCATGACACTAAGAATGAAATAAAACATTG
-1,462	0,000121806	A_15_P508787	dap1b	DAPL1	death associated protein like 1	NM_131573	4621	60	30	441	TGAACGTGGAGCATCATGACCATCACTTACTCGTAGCATTGAAACAAACTTGCTGTAATT
-1,541	1,60E-05	A_15_P103187	dap1b	DAPL1	death associated protein like 1	NM_131573	23645	287	57	276	GATTTCCCAGAGACTCCAGTTTCTGTGCGACACAGTCGGGTCAGACCGAGCGTGGAGAAA
1,748	1,26E-06	A_15_P108176	dcn	DCN	decorin	NM_131697	35647	432	79	2307	CATTTGTGTTCACGATCTCGTCTGCTCTGCCCGTAGAATAAACTTGTTGTCATTTCCACG
-1,521	2,81E-05	A_15_P109757	dcun1d2	DCUN1D2	defective in cullin neddylation 1 domain containing 2	NM_001002156	5634	71	35	1434	TCATCAGAGTCGGCAGTTCAGCTCAACATCAGTGTTATACTGTATATGTAAATAAAGATG
-1,522	5,58E-05	A_15_P152871	dcun1d2	DCUN1D2	defective in cullin neddylation 1 domain containing 2	NM_001002156	10964	135	36	735	GATGATTTTGTGGAGTTTGCTCGGCCGATCGTTACAGCAGAAAACCTCCAGACTCTATAA
-1,599	8,19E-06	A_15_P117043	rp42-pen	DCUN1D2	defective in cullin neddylation 1 domain containing 2	NM_205538	3594	48	14	1490	GTCAAACGTGTCATCTGCCCTGTTGCGAAACTTGTAACAAACACGGTTCAGTGTTACTCT
1,724	1,94E-06	A_15_P209276	zgc:103654	DHRS13	dehydrogenase/reductase 13	NM_001007363	23636	288	52	984	GAGAGGTTTGTTGGATTAGCATGAGATTGATGGTTTAAAGATTCATTTAACGCATTTGCA
1,696	2,77E-06	A_15_P107699	zgc:103654	DHRS13	dehydrogenase/reductase 13	NM_001007363	28350	345	2	1015	GGTTTAAAGATACATTTAAAGCATTTGCAGTTAATTTAGTGAAACCTGTGCTGCATCTGC
1,438	7,04E-05	A_15_P455820	zgc:103654	DHRS13	dehydrogenase/reductase 13	NM_001007363	20655	251	55	458	AAGGATGTTTGGCGTAAATCACCTTGGTCACTTCTTGTTAACGGATCTGCTGCTGAAACG
-1,429	0,00021982	A_15_P103808	zgc:101565	DHRS13	dehydrogenase/reductase 13	NM_001004641	4091	53	12	922	GGCCAGAAAGCTTTGGCAGATCAGCGAGCGACTGAGCGGCCTTTCCTAAAGCCAGAACAA
2,407	2,60E-08	A_15_P208081	zgc:112176	DHRS7C	dehydrogenase/reductase 7C	NM_001020657	34752	422	45	1358	CCGAAGCATGCGAGAATTCACAAAGGTTCACATATTAATAAATAATGTTATGAGAGCTGA
-1,431	0,000112984	A_15_P210136	rdh1	DHRS9	dehydrogenase/reductase 9	NM_198069	31569	384	35	1065	GTGCTGTTTTGGATTGAACAATTCGATTGCTTTTTGCAACATGGACTCATTATAAATGCA
1,460	5,97E-05	A_15_P194611	dlc	DLL4	delta like canonical Notch ligand 4	NM_130944	31276	380	55	3230	GGGTTTGTAATCCTCTGCAATCAGAGTGTTTTTCAAAATTCACAACAACATAGATTGTTC
1,421	0,000422711	A_15_P206486	dll4	DLL4	delta like canonical Notch ligand 4	NM_001079835	4412	58	7	2970	GCCCAGGGTCTTCTTGGATTGTTTTTAACAATTTGAACTCAACATGGGAAGAAGAAAAAA
2,091	1,12E-07	A_15_P169146	zgc:101771	DCK	deoxycytidine kinase	NM_001007056	24441	298	41	749	GGATGTCAATGATGATTTTAAAGACAACAACATGATGTGCGCTGATATGATTGAGAAGGT
1,426	8,56E-05	A_15_P103134	zgc:110540	DCK	deoxycytidine kinase	NM_001014352	11313	139	43	504	GCTCCGTCTACAGTGACCGATACGTGTTCGCCTCCAATCTCTTTGAGTCCGGAGATTTGA
-1,632	4,54E-06	A_15_P189086	ENSDART00000050651	DNTTIP2	deoxynucleotidyltransferase terminal interacting protein 2	ENSDART00000050651	5111	65	25	1056	TAAGATTACGTCGAGAACATCTGTCAGAATGTGGAATCCCAATAAATCTTCCAATACCAA
-1,689	2,55E-06	A_15_P518847	ENSDART00000050651	DNTTIP2	deoxynucleotidyltransferase terminal interacting protein 2	ENSDART00000050651	8265	104	18	1051	TGGCTTAAGATTACGTCGAGAACATCTGTCAGAATGTGGAATCCCAATAAATCTTCCAAT
-1,439	9,71E-05	A_15_P104271	zgc:92440	DNASE1	deoxyribonuclease 1	NM_001002674	7885	97	81	1054	ATAATCACTGATGTGCTGCTGAAGAAACATGTACAACCCCAAGTGATTTCTAAATTTACT
1,575	9,46E-06	A_15_P152836	zgc:123174	DTYMK	deoxythymidylate kinase	NM_001037110	26755	326	37	740	CTGTGGAGGTGAACTCATCTCTGCTGATGTTTTTATAAACTTCATCTTTTGTTTTTCTGT
1,621	5,16E-06	A_15_P152231	dut	DUT	deoxyuridine triphosphatase	NM_001006005	6251	80	9	393	TGTGGTTGATGAAGACTACAGAGGGAATCTGGGAGTCGTGATCTTCAACTTCAACAAGGA
-2,928	3,72E-09	A_15_P195056	si:dkey-14d8.6	DPT	dermatopontin	NM_001044839	5045	63	77	506	TGCCAAGTTGCAATGCTGAGACTCTCTCAAATGCAAATACAATCAAATTCAAACCTGAAA
1,407	0,000119651	A_15_P102543	dbx1a	DBX1	developing brain homeobox 1	NM_131158	16624	203	36	1181	CTTATTTGGAAAACCTCGCAAAATGATTTTGCTGTGTCGCACAGCTTTTTGTGGGGAACT
1,805	4,46E-06	A_15_P142486	zgc:63938	DIABLO	diablo IAP-binding mitochondrial protein	NM_200346	14116	174	29	1144	TCACCGGCTGTTGTGATATTGCAGTGTACTTCCACAAAAATGCAATCATCTTGTTTTAT
-1,540	1,79E-05	A_15_P153656	dgat2	DGAT2	diacylglycerol O-acyltransferase 2	NM_001030196	14731	181	6	1516	AACCTTATTAAACCACTTTCAGCAGACCACAAATGACCCCAAAAACTCAACAGCAAAAAA
-1,588	7,88E-06	A_15_P366150	dgat2	DGAT2	diacylglycerol O-acyltransferase 2	NM_001030196	35338	429	5	1510	AATAGTAACCTTATTAAACCACTTTCAGCAGACCACAAATGACCCCAAAAACTCAACAGC
1,532	1,77E-05	A_15_P150566	zgc:77734	DBI	diazepam binding inhibitor, acyl-CoA binding protein	NM_199608	40190	488	22	539	GAAGAAGGAAAAACATGTTGTGTTGCCCTTAAGAAATTTTGTATTTGTATCTGAGACCCT
-1,440	9,34E-05	A_15_P120780	dlst	DLST	dihydrolipoamide S-succinyltransferase	NM_201487	13570	167	6	1790	TCGCACAACTCCAGGCCATCCCATTCTGTCTGCCCTTGTAAAGAACCAAAAAATATATGA
1,509	3,13E-05	A_15_P118938	dpp3	DPP3	dipeptidyl peptidase 3	NM_001002683	26271	319	45	2778	ATGTCAAATTGTTCAGTGTGGACGGTGAATACCAACAGTCCCTACCAAATAAAACCAATT

-1,434	8,19E-05	A_15_P155891	zgc:110758	DPH6	diphthamine biosynthesis 6	NM_001013290	18612	228	30	733	TTCAAAAAGAAGATCATCATAGACGCCACAGAGACCGTCATCCACTCAGATGATGCCTTC
-1,457	8,26E-05	A_15_P205126	dlg2	DLG2	discs large MAGUK scaffold protein 2	NM_001012378	26932	327	42	2462	ATGAATAAGAGGTTGACAGAGGGAACAGGCCAAAAAGACATACGACCGTGCCATGAAACTG
1,426	0,000108462	A_15_P119632	dact2	DACT2	dishevelled binding antagonist of beta catenin 2	NM_201586	19877	242	82	2432	CTGCCGCATTAAAGCTTCTAGAGCACTGAAGAAGAAGATCCGCCGCTTTCAGCCAGCATC
-1,473	7,83E-05	A_15_P103093	zgc:92095	DIRC2	disrupted in renal carcinoma 2	NM_001004597	28727	349	24	2967	CAGGGGCGACGTGGCCCTGTCAATGTGTCAATACATGTCAAAGATTTTTAGCACCTTATT
2,218	3,75E-08	A_15_P109699	dlg7	DLGAP5	DLG associated protein 5	NM_001004592	20788	253	37	2992	ATTTCTATACAGTTTGACCTCAGAAAATATTGTATCTTAAAGGTTTTAAAATATGTTGAA
-1,476	5,02E-05	A_15_P132806	ddi2	DDI2	DNA damage inducible 1 homolog 2	AY398334	29116	353	53	1382	AAGCTAGTTAGTGTTTAACACAAGGAATGAATACTCATCACAGATGTGTCGCATTGTGGA
-1,937	2,65E-07	A_15_P206471	zgc:162630	DDIT3	DNA damage inducible transcript 3	NM_001082825	37835	460	5	1197	CAAAACTCAGCCCACCACGCATGCAGACTTCAAATTAAAATATGAAAATAATAAGAAGAG
2,462	2,18E-07	A_15_P194351	zgc:64114	DDIT4	DNA damage inducible transcript 4	NM_200107	42599	517	28	1132	TTGCCAATTTGTTTAAAGATTCAGTTCTTGTGCCCTTGGATCAAATGGAGGAGGAGCTTT
1,914	7,87E-07	A_15_P199281	LOC556995	LIG1	DNA ligase 1	ENSDART00000084174	30205	367	15	3260	TACAAGAAACAGCAGCAGATTCAAAATCAGGGTGACAAACCAGATTTGGAGGACTACTAT
1,649	5,26E-06	A_15_P109372	ENSDART00000084166	LIG1	DNA ligase 1	ENSDART00000084166	22395	273	9	404	AGCAACTCCAACATCAGTGTCACCGTCAGGCATTCCCAAACGCAAGACTGCTCGTAAGCA
1,430	8,21E-05	A_15_P174051	dnmt4	DNMT3B	DNA methyltransferase 3 beta	NM_001025450	17377	212	82	2764	GTGCCTGAAAACGGCCAGGGTTCACATGCGGGTAGATTAATCTTTTATTATCATGAGAAA
1,654	4,15E-06	A_15_P117211	pola2	POLA2	DNA polymerase alpha 2, accessory subunit	NM_199581	29478	357	68	1853	CAAGAGAGTGAGCCCATGTATAGCAGGGCAGGTGGTCAAAATATGAGACCATACAATGTT
1,429	9,31E-05	A_15_P106638	pold1	POLD1	DNA polymerase delta 1, catalytic subunit	NM_001039810	25788	314	51	3479	CTCAAAGATGGAGTCTGTCAAACTCCAGATTGTAAAGAATCTTCATTTTGTAGTGGCTGA
-1,677	2,70E-06	A_15_P104867	dnaja3a	DNAJA3	DnaJ heat shock protein family (Hsp40) member A3	NM_201313	37611	456	62	2248	TTGTTCAAGATCTTTGTTTTGTGTTAAAAGGCTACATCCGTCTGCTTTAGTTGCAGTGTA
1,496	3,45E-05	A_15_P101829	ddost	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit	NM_213093	15872	193	82	1657	TGGTATGGCTTTATACTACAACATGCACTGATGTTTCAGCTCTTGGTATGAAGATTGTTT
2,491	8,78E-09	A_15_P155916	dct	DCT	dopachrome tautomerase	NM_001039975	20537	249	80	1268	GAGTTTGAGCCACTCCTGAACGCTGAGTTCACAAACACAAAATATTCAGGGGAAGCATAA
1,979	2,08E-07	A_15_P205426	dct	DCT	dopachrome tautomerase	NM_001039975	30991	375	77	1337	ACACTGTCCCAAATCCTATGGAGCTTAAAATATGCTGAAACAATCTAAATTTGAACTGTG
1,913	4,32E-07	A_15_P115188	dct	DCT	dopachrome tautomerase	NM_131555	25148	306	64	1599	ACACACACACACTGTCCCAAATCCTATGGAGCTTAAAATATGCTGAAACAATCTAAATTT
-1,439	0,000100874	A_15_P108853	zgc:91929	DUSP2	dual specificity phosphatase 2	NM_001003451	41994	509	32	1947	ATCTTGGGTCATTTTAAAAGTCTGTTGAGTCGAGTGGCGATGGATTGCGAGCGCTAAAGA
-2,366	4,33E-08	A_15_P216996	LOC792623	DUSP27	dual specificity phosphatase 27 (putative)	BC155573	23920	292	27	3264	GCATGGAGGAAGCAGGAAGAGTCAAAGTCACATGATCACAAATAATGCCAAATGATTTAT
-2,435	3,54E-08	A_15_P413200	LOC792623	DUSP27	dual specificity phosphatase 27 (putative)	BC155573	31884	387	27	3249	GATGAAGTGCTGACCGCATGGAGGAAGCAGGAAGAGTCAAAGTCACATGATCACAAATAA
1,888	3,69E-07	A_15_P103350	dtng	DTNB	dystrobrevin beta	NM_199709	33616	408	61	2961	ATTTTACGGAAATGACTCTGGATCGAGGCTGTGATTCACACGCATGTGATTGATGTGCTG
1,470	5,02E-05	A_15_P121105	dtnbp1	DTNBP1	dystrobrevin binding protein 1	NM_201134	10914	136	9	804	GACCACGAGGCTCTGGATGTTTTCCTCAGCTCTGTAGGGGAAGAAGCAGCGCTGTGTCT
1,460	0,00014316	A_15_P141576	e2f4	E2F4	E2F transcription factor 4	NM_213432	32799	397	70	3028	GTCATTATACAGCTAAATACCGGAACTGTTCTTTACTGGAATCCAAATGAAATAAAGGAC
1,901	3,21E-07	A_15_P493942	LOC565952	E2F8	E2F transcription factor 8	ENSDART00000079953	42932	522	48	1966	TAAGGGTTTATTTACAAAACAAAAGCACAATTCGGGCGACGCTTTTTACTATGCTGTAAA
1,515	2,16E-05	A_15_P111660	LOC565952	E2F8	E2F transcription factor 8	ENSDART00000079953	34675	422	5	2270	TGAAATTTAGGGATATTACTATATGCACAGCGTTTATTTGAACTGCATTTACAATCTGAT
-1,790	9,59E-06	A_15_P110281	egr1	EGR1	early growth response 1	BC117642	17908	219	14	3040	AAAGTGACTGTTTATGGCTTCTAAACACATTGAATGCGCTTAACTGCCAATGGGATATTT
-1,435	8,69E-05	A_15_P119871	egr2b	EGR2	early growth response 2	NM_130997	2427	34	15	1940	TTGGACTGTTATACATGTATTTGTTATGAAGTGACTAACGCGGGTCAATAATGTCCTACT
1,469	5,90E-05	A_15_P202781	ecd	ECD	ecdysoneless cell cycle regulator	NM_199891	2104	29	19	1604	ATGACTTTGAAGATGAGGATGATGACGACGATGATGATGACGATGAAGCAGTGCAGAGCA
1,509	2,54E-05	A_15_P193411	zgc:63550	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	NM_200603	32196	392	16	2554	ACCTATGAGGAGATTCTCGCTCTGAAAACGTACTTGCACACATACGAAAGTGAGATCTGA
1,984	3,22E-07	A_15_P142251	egfl6	EGFL6	EGF like domain multiple 6	NM_001002457	41716	506	47	1603	CTGGATCATGTGCTGCTGATCTCTGGAGAATGTTCAGAAGATAAAACACTCGACTTCTAG
1,557	1,33E-05	A_15_P162576	egfl7	EGFL7	EGF like domain multiple 7	NM_001005231	31539	383	20	1175	CCATGTTCTCGTCATGAGTTATGCTTTTTGGATAAGTTGCATTCCTTTTTTACGTCTCAT
5,458	1,37E-11	A_15_P119797	zgc:92314	EGLN1	egl-9 family hypoxia inducible factor 1	NM_001002595	14131	173	37	1873	TCGTAAGCCAAAATTGACACCTAATGTCTGTCTAACAGCTCTGAGTTTTAATTAAAGAAG
5,061	2,00E-11	A_15_P365720	zgc:92314	EGLN1	egl-9 family hypoxia inducible factor 1	NM_001002595	38959	471	71	1807	GGCTGGATTGTTTTTTGCAAGTAAATCTGCGTTATGTCTGTTGTTGCAGACGTCATGTCC
3,394	4,25E-09	A_15_P165246	ENSDART00000090635	EGLN2	egl-9 family hypoxia inducible factor 2	ENSDART00000090635	37014	450	11	1275	TATGCCATCACTGTTTGGTACTTTGATGCAAAAGAGCGAGCTGAAGCGAAGGAGAAGTAC
21,626	1,70E-14	A_15_P103521	egln3/phd3	EGLN3	egl-9 family hypoxia inducible factor 3	NM_213310	5011	63	60	1620	GGTGTTCGACTGTATGAAATGGCCAAACTAAACAGTATGAAAGTGTTTTCAATGATTATC
1,874	4,14E-07	A_15_P135791	zgc:110145	ETFRF1	electron transfer flavoprotein regulatory factor 1	ENSDART00000024936	27461	333	57	1523	GTGAGAAGAACAGAGTGATTGTCCATCTGTATATATGCAATAATAAATGTGTGCTCACTT
2,767	3,12E-09	A_15_P116591	elovl4	ELOVL4	ELOVL fatty acid elongase 4	NM_199972	40808	494	82	2296	AATTCACATGGGAAATACGCAGGATGTTCTCGTGATTTGCAACGTCAGTGTACCTCTTAA
1,446	6,58E-05	A_15_P179276	elovl4	ELOVL4	ELOVL fatty acid elongase 4	NM_199972	40544	491	33	895	GCTTTGATTGGCTACGCCGTTACATTCATCATCCTGTTCGCCAATTTTTACTACCAGACC
1,768	1,28E-06	A_15_P112670	zgc:92749	ELOVL6	ELOVL fatty acid elongase 6	NM_001002570	7658	95	49	922	ATTATCTTCATCAGTTTTACACATGTAAGTGGATTGAACATATTAAGTTGCAAATTAAAT
1,549	1,36E-05	A_15_P171341	si:dkey-103i16.2	ENDOU	endonuclease, poly(U) specific	NM_001044974	30856	376	8	1289	GCTTGTTTACTTTGCGAGATACATTTTGCTAATTTGGTCAACTTCAGAATGCTTTTACAG
5,782	9,89E-12	A_15_P104945	ero1l	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha	NM_200350	23735	290	18	1566	TTGTTGTTGAATTGCACTGCACTATTATGCCCTACATCTCGAGCACTTAAGCCAATTTGC
-2,240	3,02E-08	A_15_P154431	LOC100004902	ERP27	endoplasmic reticulum protein 27	ENSDART00000053700	7093	89	15	13	TTCTAGTGAACGGAGCAGATAAATCCAACAGCCGTGTTCTGGAGTATTTCAGCCTGAAGT
4,166	6,98E-11	A_15_P148231	zgc:153027	ESM1	endothelial cell specific molecule 1	NM_001076741	22307	272	49	1191	ACAGATATGGCATCCCATATTTGACCACATGATATATGTAATGCAGTGTTTTTAATGTGG
1,544	1,96E-05	A_15_P114625	edn1	EDN1	endothelin 1	NM_131519	36600	444	54	999	AACCAAAGACTCTGGTGGAAGATGCACTGTAAAACAATGAAGCTCTGCAATGCCTCCATG
1,401	0,000150428	A_15_P193671	zgc:154079	ECE1	endothelin converting enzyme 1	NM_001077792	29062	353	25	2480	GCTATATTGTAATAGGAAGGAATTGTGCTTTTTGCAGGTGTTTTCTTTGAATACATGCCT
1,607	8,18E-06	A_15_P103241	ednra	EDNRA	endothelin receptor type A	NM_001099445	20294	247	41	1517	TGAAGACCAACAGCAACAGGATGCAGCTGAACCTAACAGCTACAAATGAACCCTGATCAA
4,485	1,34E-08	A_15_P116587	eno1	ENO1	enolase 1	NM_212722	22690	275	74	1687	CAGCGTCAGTATGTGCGTTGTGTTGCTTTTGAGAAGTGTTAGTTCTATATGCGTGGCATA
3,444	6,30E-09	A_15_P472345	eno1	ENO1	enolase 1	NM_212722	7002	88	53	903	TGACCTCTACAAGAGCTTTGTCAAGGATTATCCTGTGGTCTCCATCGAGGATCCATTTGA
1,895	2,15E-06	A_15_P170271	zgc:73056	ENO1	enolase 1	NM_200695	14620	180	33	1219	GAAACTGAGGACACATTCATTGCAGACCTTGTTGTGGGACTGTGCACTGGACAGATTAAA
-2,508	1,16E-08	A_15_P113587	zgc:73056	ENO1	enolase 1	NM_200695	22927	280	26	1635	GCAGATTTTTGAGGACTGTGCTTGTAATAGTGGATACTGTTAAAATAAAAACATCACCTC
1,408	0,000180665	A_15_P187416	dci	ECI1	enoyl-CoA delta isomerase 1	ENSDART00000017962	1906	25	81	987	GAGCGTCAATGGATAACACATTATCCTTTTTGTTTGTTGCTGGAGGATTACTTTATTTGT
1,728	5,73E-06	A_15_P107090	zgc:92030	ECI2	enoyl-CoA delta isomerase 2	NM_001002645	12055	147	83	1611	TACTGTATGTTCCATGTAAGATGTGTGAACATGTAATCATTCGCACTTGATTTAGTCTTG
1,649	1,55E-05	A_15_P152016	zgc:101710	ECH1	enoyl-CoA hydratase 1	NM_001006068	17576	216	15	1405	CAAAAAGCTGCTAAGCCCCTAAAAGCTTAACACCTAGATAAAGATTCATACATAATCAGA
1,572	9,54E-06	A_15_P102356	zgc:112296	EPHB2	EPH receptor B2	NM_001033094	28694	349	7	1951	GGTGAGACTTCTGCCCCAGCTCAACTTTCTTTTCAACTTTCCTTGTACTTTTTAGCTTTC
1,822	3,29E-06	A_15_P149841	zgc:110596	EPYC	epiphycan	NM_001017903	34317	416	80	2087	CCCACAGGCCTACATATGTTTGCCACGTATCCCCATTGGTAACCTTTTTTAAATCGTAAA
1,805	1,58E-06	A_15_P212601	zgc:110596	EPYC	epiphycan	NM_001017903	16434	202	25	2090	ACAGGCCTACATATGTTTGCCACGTATCCCCATTGGTAACCTTTTTTAAATCGCAAAAAA
1,640	2,70E-05	A_15_P102503	zgc:110596	EPYC	epiphycan	NM_001017903	12882	158	79	2157	ATATGCACACTTGAATACACACATAAAAAACTCACACGTATGCATATGCATCAAAACTCC
1,468	4,69E-05	A_15_P174836	zgc:114127	EMP3	epithelial membrane protein 3	NM_001025508	31898	387	34	1011	CTGAAGGGATACTTGTATGGTGGTATCCATACGCTTAAACTTCAAGATGTATTTTTCTAA
2,121	7,28E-08	A_15_P207151	CH211-278B8.3	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	NM_001100093	24111	294	39	4371	ACTGGCGATCCTGAGATCCAACTCTTGATTATTCAGCTGTACAGACAACTGAGCCAGTAA
1,540	1,59E-05	A_15_P114359	erg	ERG	ERG, ETS transcription factor	NM_001008616	6215	77	76	2657	ACAGCACGGCACACACACGGCCTGAGACTGCTGACAAAGGGAAAACACATATAAATTATA
9,159	1,17E-12	A_15_P115769	epb41	EPB41	erythrocyte membrane protein band 4.1	NM_175084	26288	319	54	5000	AATACAAATGCCAGGCTTACGTTTAGCTTATTTCACCCGCTTACACCTATTAACTTGTAA
-1,446	0,000119149	A_15_P364970	zgc:85963	EPB41L3	erythrocyte membrane protein band 4.1 like 3	NM_214812	23918	291	26	3150	TAAGGGCTTTTGGTAGGTTTGTAAAGCGTAGTGTTTATAGAGATCCTCCGTCTTTGACCT
-1,465	0,000123805	A_15_P383555	zgc:85963	EPB41L3	erythrocyte membrane protein band 4.1 like 3	NM_214812	27072	330	28	2775	GAATCTGACAGAGACGCCTCGACACAATGATTCTGCTTTTATTCTGATCTTTACTCGGTG
-1,628	1,30E-05	A_15_P108495	zgc:85963	EPB41L3	erythrocyte membrane protein band 4.1 like 3	NM_214812	26782	325	51	3181	TGTTTATAGAGATCCTCCGTCTTTGACCTTTGACGTCTTTGAGAGGTCGTGCTGTTTTTT
3,071	1,80E-09	A_15_P201081	LOC100005060	ERFE	erythroferrone	ENSDART00000077861	31230	380	31	111	TTCTATCAGCTCTCAGCTAATCTGCTGCTAGAATCCAACTCAGAGTCTCAGAAAAAGGCC
-1,428	8,37E-05	A_15_P207031	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	NM_199745	1380	57	55	1436	TCTTCACAGAGGAGCTTGTATCCACAGCGTCCCTGAAAAACAAAGAGAGCAAGAAGAACA
-1,458	5,01E-05	A_15_P207031	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	NM_199745	1380	297	40	1436	TCTTCACAGAGGAGCTTGTATCCACAGCGTCCCTGAAAAACAAAGAGAGCAAGAAGAACA
-1,503	2,51E-05	A_15_P207031	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	NM_199745	1380	19	53	1436	TCTTCACAGAGGAGCTTGTATCCACAGCGTCCCTGAAAAACAAAGAGAGCAAGAAGAACA
-1,541	1,53E-05	A_15_P207031	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	NM_199745	1380	498	82	1436	TCTTCACAGAGGAGCTTGTATCCACAGCGTCCCTGAAAAACAAAGAGAGCAAGAAGAACA
-1,567	1,63E-05	A_15_P103154	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	BC080208	40254	488	54	362	GAGAATAGAGGCTTCGAGGCTGACAAGGAAGCTGAAGTTGAGGAGGATGATGATGATGAT
-1,594	7,34E-06	A_15_P207031	zgc:66241	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog	NM_199745	1380	474	55	1436	TCTTCACAGAGGAGCTTGTATCCACAGCGTCCCTGAAAAACAAAGAGAGCAAGAAGAACA
2,200	5,44E-08	A_15_P107779	zgc:111795	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	NM_001003872	30807	373	69	2226	CTGTTTGGAAAACCAGGCTGCTGTGATTAATTACATTTGTAAAGTGAACACTTTTCGTTA
1,513	3,49E-05	A_15_P107560	zgc:56608	EBAG9	estrogen receptor binding site associated, antigen, 9	NM_201094	27889	339	20	1218	CAGAGTCTTGTAACTGTACTTTAAACACTGGATTTCACCAGATATGGGTGATCTCAATCA
-1,586	4,37E-05	A_15_P101615	ENSDART00000017726	ETNK1	ethanolamine kinase 1	ENSDART00000017726	36870	447	22	567	AGTGCCGCATGTCTCAGAGACGAGATGATCTGGCTTCAGCAGAACCTTTCTAAACTGGGT
2,249	2,86E-08	A_15_P155421	zgc:85680	ETHE1	ETHE1, persulfide dioxygenase	ENSDART00000043403	27062	330	23	1265	TGTTGACCAGTGCAGAAATACTATTGGTAATCATTTACAATAGCACATCAAATGCTCATC
1,610	6,30E-06	A_15_P111208	zgc:85680	ETHE1	ETHE1, persulfide dioxygenase	NM_212929	2472	33	38	1178	TCCCGTCTACATGTTTGTTTGTTTACAAATATTTTTGGGACATAATCTGTGTGCTGTATC
2,592	1,07E-08	A_15_P111156	eef2k	EEF2K	eukaryotic elongation factor 2 kinase	NM_001002740	8995	111	50	2791	TCTGCTAGTAATGGTAGATGTGCTTTATAAGGGTTTTACGAGTTGTGATTTTTAGCCTGT
1,487	4,30E-05	A_15_P119986	eef1d	EEF1D	eukaryotic translation elongation factor 1 delta	NM_200017	11767	146	19	1485	TGGACTGAACGTATCCTCTTAAATGTCAATTTTGTGCTGTTTTGTATCAAAACCTCAGAA
-1,413	0,000107925	A_15_P115020	zgc:110790	EIF2B4	eukaryotic translation initiation factor 2B subunit delta	NM_001014361	23196	281	83	2015	AAAGGGAACAGTGCATATGTGTGCGCAAGACCATGTTGTACGTATAAGGGGTTTGGTTTA
1,664	4,93E-06	A_15_P150546	LOC561049	EIF3E	eukaryotic translation initiation factor 3 subunit E	NM_001044951	16926	207	21	1478	TGTTGGCCATGAATATCGAGAAGAAGATCAGCCACAGCAACAGAAATGAGACACCGAACT

1,544	1,52E-05	A_15_P112959	LOC561049	EIF3E	eukaryotic translation initiation factor 3 subunit E	NM_001044951	29687	361	5	1799	CAGTTCGGTGTGTTCTCGAATTCATTGTTTGAATATCATAACACCAGAATAAACAATGAG
1,529	1,72E-05	A_15_P210451	ENSDART00000013258	EIF4A2	eukaryotic translation initiation factor 4A2	ENSDART00000013258	33461	406	67	1719	TACAGTATTCCATGTAGGGTTTGGCCCATTTGACAATAAACAGGATGATAATTCTGTCCA
1,510	3,68E-05	A_15_P108055	zgc:77429	EIF5A2	eukaryotic translation initiation factor 5A2	NM_213262	40747	493	51	2310	AGTTTTTCCACACAGCTAGTTGAATGAAGCGTAAGAAGCCACAGTTTTTGGATATGAGGG
1,480	0,000100009	A_15_P211896	zgc:77429	EIF5A2	eukaryotic translation initiation factor 5A2	NM_213262	13422	166	14	2340	GTAAGAAGCCACAGTTTTTGGAAATGAGGGGTGCAATTATAATAAACTCAACTGAAAAAC
-1,572	9,90E-06	A_15_P112052	eif6	EIF6	eukaryotic translation initiation factor 6	NM_200944	41909	507	67	949	TTCACTGTAATATTCATGTATGAACTGCTCGTCACGCTGTCTTTGTGAAAATGCCAAGAC
-1,589	1,93E-05	A_15_P565902	eif6	EIF6	eukaryotic translation initiation factor 6	NM_200944	40901	495	45	182	TTTACAGTGTTTTTGAAGGTGAACTGTCAGAAACGATGCCCGTCATTCATGCCTCTATAG
-1,593	1,27E-05	A_15_P423075	eif6	EIF6	eukaryotic translation initiation factor 6	NM_200944	13299	163	37	407	CTTGTAACGACTATGTTGCTCTCGTTCATCCAGACCTTGACAGAGAGACAGAAGAGATTC
1,420	0,000110021	A_15_P189046	LOC562073	ECM2	extracellular matrix protein 2	ENSDART00000090427	20454	249	38	1381	ACCTGAGACTCAACCACAACTACATCAGCTACGTCACTATGAACTCACTGTGTGATACTA
1,465	4,95E-05	A_15_P170061	eya2	EYA2	EYA transcriptional coactivator and phosphatase 2	NM_001040292	17776	218	31	1176	CCTCCAAATACAAGGTGCTGTTCAATTGTTTACAAGGACTTGTTAAACGTGAGAAAATAA
2,253	8,89E-08	A_15_P101129	sid4	EYS	eyes shut homolog (Drosophila)	NM_001034182	16631	203	40	704	AGAGACGGAGCTCGTTTCCACGACGACAGACTCCACTACATCACTACAGGTGACCATGGC
-1,547	1,51E-05	A_15_P111447	fbxl4	FBXL4	F-box and leucine rich repeat protein 4	NM_001007315	28987	351	72	3039	GCTGTTCGAGAGTTTTAGCATCATTTCAGATCTGAGAGTGACAGTCATGAGGTCTTGGTT
2,044	1,78E-07	A_15_P133621	fbxl5	FBXL5	F-box and leucine rich repeat protein 5	BC054590	7640	95	40	2704	CATATGATGCCTCTATCTTCATCTCAAGCTCCATTCTGGGTTTATTAAAGCGACGGGTCA
-1,654	7,16E-06	A_15_P169481	fbxo32	FBXO32	F-box protein 32	NM_200917	43569	531	28	1600	GATATGGGAATGTTTACCAAAATGGCCTTAATACTGGTGTGCAATACTTTTCTAAGGAAG
1,590	9,56E-06	A_15_P553577	LOC100005140	FBXO40	F-box protein 40	NM_001113657	42315	513	37	1893	ATTTCTGAGCATCTAAAGGTTTGTCCATACTACCAGAAGGAGAGCAAGACAGAACCTGTG
2,034	1,13E-07	A_15_P142781	fbxo5	FBXO5	F-box protein 5	NM_001003869	35124	425	65	1452	TTTTATCTTCCAGAATGTGAAGTGAATTTTGGCCACGTGTGTGGTCACCGCACAGAGTGA
-1,921	3,13E-07	A_15_P149736	zgc:136842	FBXO8	F-box protein 8	NM_001040307	34476	418	75	1722	TGTGCATCGTCACTTATGTCTCGTCTTCTTTTAGAAGAGTAAAACCCACCAGACATTGAA
-1,418	9,83E-05	A_15_P168911	zgc:152955	FAM102A	family with sequence similarity 102 member A	NM_001076613	5364	67	68	2383	AGTGAGATCCTGCATTGTGTGGCTATAATGGGGTCTAATGAAATAATTGTGGAAATAAAA
1,775	1,18E-06	A_15_P178401	LOC559330	FAM13A	family with sequence similarity 13 member A	BC135046	14364	175	71	1610	GTTTCATCTCACCTGTTGATGAACTATCCCCTTCCAAGAACACCACAGACATGAGACTGT
1,711	3,48E-06	A_15_P495647	LOC559330	FAM13A	family with sequence similarity 13 member A	BC135046	24380	297	10	1076	TGAATGAACTAACCAGGCTACGTAAAGACTTGAAAGATCACAAGTTGCTAAAGTCAGAAG
1,654	5,97E-06	A_15_P189116	DKEY-190G11.3	FAM173A	family with sequence similarity 173 member A	NM_001113607	42487	516	49	508	AAATATAACAATGTGACTGTTTTCTTGGCACCCGGAGTGATGGAGGTGTTGGGTAGAAAG
1,501	2,60E-05	A_15_P104790	DKEY-190G11.3	FAM173A	family with sequence similarity 173 member A	NM_001113607	33020	401	12	874	GAAAAGTAGCTTTTCTGTGTTGTGTATTTCTGAACTAAACTGTGAAATAAAGAGCCAGTG
1,407	0,000137727	A_15_P282591	zgc:153444	FAM213A	family with sequence similarity 213 member A	NM_001076713	26706	326	12	581	GAGATGGAGTTTGGGGATAAAGTCCAGAAGTCTGATGTGCTTCAAGCTGTTGAACAGATC
-1,422	0,000117939	A_15_P112422	fam49a	FAM49A	family with sequence similarity 49 member A	NM_001003606	34704	422	20	1338	AACAAAACGACGGCGGCTGGCAAACCTCTGAAACCTGTTTGTTTACAAGAGCAACTTGAT
2,733	1,18E-08	A_15_P164471	fam53b	FAM53B	family with sequence similarity 53 member B	NM_001007187	39849	484	17	1557	CCGTAGTAATATCAGGTAATTCAGTTCCTCACTGGTGAAAACAAAGCTATTAGATCTATT
1,669	3,06E-06	A_15_P177576	LOC795210	FABP1	fatty acid binding protein 1	BC122459	13784	170	29	473	CTCGAGAATATTCCTGAGATATTCCTGTCTATGATAGAGTTAGAGACTATATGACCATAA
-1,439	0,00030569	A_15_P178876	BC150401	FABP1	fatty acid binding protein 1	BC150401	14658	179	53	491	GAGAAGACGAATGCTGATAAAGTCTGAAGTCTTGATTTCTCCTGAGAAAAATACAGAAAT
2,214	4,22E-08	A_15_P113325	fabp11	FABP3	fatty acid binding protein 3	NM_001004682	12338	151	59	578	TGACACCAAAGCAAATGCTCACTGACCCTTTTAAAATGCATTTATTATCAGTCTTTATGG
-1,649	4,22E-06	A_15_P408340	fabp6	FABP6	fatty acid binding protein 6	NM_001002076	9126	114	31	219	AACAAATTCATCGTAGGCAAAGAGAGCGACATGGAGACTGTAGGAGGGGAAGAAATTTAAG
-1,660	3,44E-06	A_15_P116028	fabp6	FABP6	fatty acid binding protein 6	NM_001002076	3157	41	47	439	GTTGAGATGAATGACCCTTTTCTGCTCTGACACTCAATTTACTGAATAAAGTGTACGAGC
1,550	1,50E-05	A_15_P109314	fabp7a	FABP7	fatty acid binding protein 7	NM_131605	13871	170	74	491	CTGGCAACTTGACGATATTACAAGGGAATTTTTATTACACTGTATTGTCATCTGGGAGTT
1,482	3,49E-05	A_15_P115685	fabp7b	FABP7	fatty acid binding protein 7	NM_214807	27838	337	79	498	GGCCAGAAACAGACAGTCATGATGTGCTCTGAAAGCAAAACCTTGAACTTTATTCATCCA
1,682	1,23E-05	A_15_P173546	fabp11l	FABP9	fatty acid binding protein 9	NM_001020558	33207	404	22	420	ATGATAGCGAAATGCACCATGGATGACGTTGTGGCTATCAGGACATACGAAAAAGATGCA
1,703	2,29E-06	A_15_P103127	fads2	FADS2	fatty acid desaturase 2	NM_131645	23917	292	25	1584	AAGATAATTGTGGCACTTTGAATGCGTTTTAAAGAGACGGCTCAAAGATGTGTGTCTCGC
1,510	4,50E-05	A_15_P104437	fads2	FADS2	fatty acid desaturase 2	NM_131645	20433	250	27	1444	TACATAGAAATAAAAAGCGGAGCCGAATCCTCCAATCAGAGCGAGCCTTCACAGACTAGA
1,407	0,000216642	A_15_P119404	LOC100002541	FCER2	Fc fragment of IgE receptor II	NM_001111242	37400	453	41	451	TATATGTGTGCTGCAAACCTGTGAGATCAAATGCAGTCATCCTGCTTCACAGTTTCATTG
1,792	8,44E-07	A_15_P112590	zgc:64101	FERMT3	fermitin family member 3	NM_200904	39075	473	45	2065	ATGAGAATTCAGCATTAGCACTGCACAGTGACTGGCATTTCTTGTACATGTTTTCAACAA
1,447	9,78E-05	A_15_P516787	LOC557898	FRRS1	ferric chelate reductase 1	XM_681052	31358	381	12	2966	ATATTGATTTGTGGACTTGAATGAGAAACTGAAGTGCCTGATAAAGACTGTTACTTTTGC
2,268	1,63E-07	A_15_P116161	fth1	FTH1	ferritin heavy chain 1	NM_131585	27814	337	67	956	TCGTTCACAGTTTGACCTCTCTGCATCTGCATGTGCTGCTTGTGTGATCTGTCAATCAAA
2,062	9,15E-08	A_15_P116685	fth1	FTH1	ferritin heavy chain 1	NM_131585	20726	253	6	996	TGTGTGATCTGTCAATCAAATTATGCTCCAAACCCAATAAAGCAAAACCTCTGGAATCTG
2,591	5,25E-09	A_15_P173126	zgc:56095	FTHL17	ferritin heavy chain like 17	NM_213013	3792	49	30	834	CTTGTCCAAAACCAGCCTGTAGGATTTTCAAATGAGGTTAAGTACAGTGCAAAAATGAAA
2,415	1,18E-08	A_15_P100145	zgc:56095	FTHL17	ferritin heavy chain like 17	NM_213013	3333	44	51	909	ACGCCAAAAGCTGAATTGTTTTACCTCCAAAATGGTGCTCTGTGTCAATAATGCAATAAA
-2,431	1,17E-08	A_15_P113561	zgc:109934	FTL	ferritin light chain	NM_001020531	36597	443	53	754	TTAACATTTAGAGGCTTCATGTTTAAGATCCTGCCTTCTTTGATTAGTCAGCTGATGCCT
-1,852	6,20E-06	A_15_P101038	zgc:92066	FTMT	ferritin mitochondrial	NM_001002378	2596	36	16	120	AAACAACAAAAATCATCTGAAATGGATTCCCAGGTTCGCCAAAACTACGACCGCGACTGC
-2,373	2,06E-08	A_15_P109448	LOC100006523	FTMT	ferritin mitochondrial	NM_001113659	39280	476	64	639	CTGGACAGCTAAATGCAGACATCAGATCATCTGCATGCTCCAAAGTGGCCCTCTATTTAT
2,697	3,39E-09	A_15_P205741	si:ch211-284e20.8	FETUB	fetuin B	NM_001099265	12987	160	47	1246	GTGCTGTCATTTTAAGGTTCAGATTTTTCCAGAATACAGGTTTCTGTCTGCAGTAGCTTT
2,257	2,74E-08	A_15_P117894	fga	FGA	fibrinogen alpha chain	NM_001002039	4838	61	57	2191	ATTCTGCTTGTCTTGAACGTAATACAATGATGATGCAACATACATTTTTACACAACCAGC
2,543	1,26E-08	A_15_P112538	fgb	FGB	fibrinogen beta chain	NM_212774	28849	351	1	1654	GTAAAGGCAAAATGATGGAAATGAGATGGAAACAGTTCTCCTGGTTCTCATTAAAGCTGA
1,903	5,24E-07	A_15_P108310	fgb	FGB	fibrinogen beta chain	NM_212774	19358	236	70	523	ATCAGTACACAGACAGCTTAGAAACCCAGCATGCTTATATTAAGGACACGGTGGACGTCA
1,516	2,15E-05	A_15_P121055	fgg	FGG	fibrinogen gamma chain	NM_213054	8544	106	75	1474	CGCAAGTCCCGATGGTCATGTTTTTAAATTTGATCAACTCAATTCAAATTCAACTGTTCT
1,927	3,60E-07	A_15_P157711	LOC563523	FGL1	fibrinogen like 1	ENSDART00000079566	29848	363	2	1155	GGAGGGATGAAGGAAGAAAGTAATCTTGGTAGATTTGATGAATCCACCTGTTATTTTTAA
1,641	7,40E-06	A_15_P101343	fgf13l	FGF13	fibroblast growth factor 13	NM_205702	11543	142	76	1802	TATATGCATTTTAACCTGCTACCCGCCCGTTTATTATTTGTTGTACATTTAAAAAGCTGC
2,804	7,29E-09	A_15_P246411	fgf19	FGF19	fibroblast growth factor 19	NM_001012246	36247	439	46	570	ATGGACCCTTTCGGAAAGATCTCTCAAATAGTGATCCAGAGTCCCAGCTTCAACAAAAGA
1,584	1,00E-05	A_15_P104834	zgc:162825	FGFBP2	fibroblast growth factor binding protein 2	NM_001089526	29969	363	63	825	GGCTTCCAAACCTGCTTCACCTCGAAAACCTGTAAAGGCCATCACAGTGAGACCCACCGT
1,480	4,37E-05	A_15_P107369	zgc:113456	FMOD	fibromodulin	NM_001030072	13731	169	3	1733	AGAAACTGACCAAGGTCCTGGTGTTTAAACATGTTTGTAGACCTTTCGTGTTGCTCAATA
1,418	9,93E-05	A_15_P105143	fn1	FN1	fibronectin 1	NM_131520	39862	483	25	7646	ACCTGTAAAATCACGCCCAGACATCTTTTCTGATTGGCTGAGTCTACTGCCAGTCTCTTT
1,549	1,57E-05	A_15_P179841	fbln2	FBLN2	fibulin 2	ENSDART00000024992	18762	230	22	2348	AGACATATTATCTCCCTTAATGGATTCAGTTCCTCAATAAAGCAACACCATCATTCCTTC
1,600	6,98E-06	A_15_P117392	LOC553370	FIBIN	fin bud initiation factor homolog (zebrafish)	ENSDART00000058443	25956	315	54	659	ACGACTATCTGAACGTTTAAGACTTCCTGGGCAGACTTCAGTCCCCTTTGGATTGTTCAT
1,706	9,14E-06	A_15_P106173	fkbp10	FKBP10	FK506 binding protein 10	ENSDART00000066367	22496	274	60	1865	AAAGCAAGAGACTCACAATGCTGAGGCTAAAGGAATGGACTAACATGTTTTCTAGTATTA
-1,536	1,56E-05	A_15_P111346	fkbp11	FKBP11	FK506 binding protein 11	NM_001012249	2313	31	42	677	CACGCACAACCTCAAGGCAAGAAGAAGAGCAAAGACAAGAAGAGCAAGAAGAAATGAGAT
-1,558	1,45E-05	A_15_P213041	fkbp11	FKBP11	FK506 binding protein 11	NM_001012249	18022	219	72	663	TCTACAACAAAGCACACGCACAACCTCAAGGCAAGAAGAAGAGCAAAGACAAGAAGAGCA
1,482	6,49E-05	A_15_P502782	zgc:91851	FKBP14	FK506 binding protein 14	NM_001003471	33621	407	64	619	CCAATGACACCCATCATGAAGTGATGGTTGAGGACATCTTTCAGAAAGAAGATGAAGACA
-1,719	4,23E-06	A_15_P365290	fkbp5	FKBP5	FK506 binding protein 5	NM_213149	19324	235	53	1917	ATCGCATAACAGACTTGAATACAGCTGTGTACCCTTATCATGTACTGTACAGTATTCAGT
-1,835	8,56E-07	A_15_P100902	fkbp5	FKBP5	FK506 binding protein 5	NM_213149	35304	428	72	2417	TTCTTTTCAGACCCGCTTGTTCGTTTGATCAAATACTAACTAGTGTTGTTTGCATGTTTT
1,577	1,06E-05	A_15_P175536	fkbp7	FKBP7	FK506 binding protein 7	NM_001004506	35452	430	62	597	CACGATGCTGATGGGACCTTATCACTAAAGGAATACAATATTTACAACCATGATGAACTG
1,592	1,12E-05	A_15_P168176	si:ch211-13k12.1	FKBP8	FK506 binding protein 8	ENSDART00000007856	2907	40	5	1369	CAGAGAAAAGGGCCAAGCAAATGCATTCCAAATATCTGCAATAAAAACAGACTATTACCA
1,801	1,52E-06	A_15_P211936	fli1a	FLI1	Fli-1 proto-oncogene, ETS transcription factor	NM_131348	11012	135	60	2698	CAGCTGTTCATCTCTTATAAGGGATCACTCTCAGATATGAAGGAATTGTCCTATTTTATA
1,675	1,05E-05	A_15_P111027	fli1b	FLI1	Fli-1 proto-oncogene, ETS transcription factor	NM_001008780	30287	367	56	2688	TTGCTTGTGGTATGTTACCAAGTTGAATGGTAATCACCTTTACACTGTAAGCGTTACATT
1,599	6,80E-06	A_15_P109368	fli1a	FLI1	Fli-1 proto-oncogene, ETS transcription factor	NM_131348	18204	222	78	2687	GACAAAACTCCCAGCTGTTCATCTCTTATAAGGGATCACCCTCAGATATGAAGGCTTTGT
1,491	3,34E-05	A_15_P178471	flt1	FLT1	fms related tyrosine kinase 1	BC139515	6983	87	44	2624	TACGGGTCTCTCCCAATGTGATTCGTCCCTTTTTATACAGATTGTTTATGAGTAATATAT
1,414	0,000217018	A_15_P170536	fstl1	FSTL1	follistatin like 1	NM_001017860	4359	55	65	897	ATAATCAAGAAATGACAGAAGAGGAGTGGGTTCAAAGAGTGGCTGAACTCAATAAGCATC
-1,414	0,00039258	A_15_P210876	fstl5	FSTL5	follistatin like 5	NM_001031842	36159	439	1	2644	ATGCTCTTTTTGTGGAGCTCAGTTCTGGCAGTGTCAAAATGATCAAGAGCTTGAAGCAGC
-1,433	0,000141007	A_15_P170131	foxd3	FOXD3	forkhead box D3	NM_131290	32287	392	63	1001	AGCTAAGTCCAAGTCTCCAGTTACAGCTAAATAGCCTGAGCACCGCGTCGATTATCAAAT
1,418	0,000163292	A_15_P110081	foxm1l	FOXM1	forkhead box M1	NM_201097	34142	413	77	3295	AATACTGTTGAATACCGTCATGAAATATGAACTTTGTTGTCTACTTGGCATTTACACAGC
-1,610	7,19E-05	A_15_P148601	foxo3a	FOXO3	forkhead box O3	NM_001009988	36694	446	16	5590	GATCATGTAAACAAGGTAGTGTAAGGCAAGGTGCATGTAAATAAAGCTTGTACAACACGA
-1,430	0,000175026	A_15_P171421	zgc:92354	FOSB	FosB proto-oncogene, AP-1 transcription factor subunit	NM_001007312	30387	370	22	1841	TATGTTGAGCTTCTCAAAAGATCACACTGCTGGGCTAAACCACGTCACAAACATAAAAAA
1,455	5,89E-05	A_15_P138161	ENSDART00000090204	FREM1	FRAS1 related extracellular matrix 1	ENSDART00000090204	15655	191	55	1866	GAAGAGGATCAAACTCGCTCTGTTTGTGTTTTAGCTCAGAGCCAGAAGATGTGGATTCCT
1,632	5,01E-06	A_15_P116112	gbp	FRAT2	FRAT2, WNT signaling pathway regulator	NM_131442	35287	428	63	1268	ACTCTGCATATGCTTCGCAACGAAGTGTTTTTAATAACTCTGGTTGTTCAGAGAGTTTGG
1,433	7,86E-05	A_15_P204616	gbp	FRAT2	FRAT2, WNT signaling pathway regulator	NM_131442	9764	122	19	121	TTTTTTGGAACAGTCGGTGACGGTGGATTCAAAGGAAGTAGACGCTCTCGTGTCGAAAAT
1,563	1,08E-05	A_15_P112836	fzd2	FZD2	frizzled class receptor 2	NM_131140	15653	191	54	2289	ATGTTTCAAAGTTTGGTACTCTTTAGAATCTGAATTTTGTAGCCACTCTCTCTCATTTGC
-1,697	2,15E-06	A_15_P118010	BC055618	FTSJ3	FtsJ homolog 3	BC055618	4321	56	45	1925	AGTCATGATGGCACAATGTATGTGGAAGAATCTGCTTGGTGAGATTTTTAAATAAATGCC
-1,433	8,69E-05	A_15_P119392	fah	FAH	fumarylacetoacetate hydrolase	NM_199601	25402	310	25	2453	CACACTTGAACTACTTTGTTGTTCTGTTACTGAAAAATAACGCAATAAAGTTACTGACCC
1,432	0,000121969	A_15_P205466	gnat1	GNAT1	G protein subunit alpha transducin 1	NM_131868	29280	356	50	1138	CACTTTTCACAAGAGATTGGCTGAATCAACAAAACCCAATGCTTTGCTCCTTGTAGCTCG
1,423	0,000254614	A_15_P452475	gnat1	GNAT1	G protein subunit alpha transducin 1	NM_131868	8377	103	75	480	GTGCTTCGACAGAGCCTCAGAATACCAGCTCAACGACTCTGCTGGATATTATCTAAATGA
1,654	3,54E-06	A_15_P111532	gnb3	GNB3	G protein subunit beta 3	NM_213202	19145	234	46	1773	ACATGCCAGACAGTTCCTCTTAAATATTGCAGTGGTTACTTGAATACCTTTCTAATAAAC

1,669	3,59E-06	A_15_P110628	gngt1	GNGT1	G protein subunit gamma transducin 1	NM_199967	20245	248	14	618	CAAGGCTTAAATGGTGGAGTAATTTAGCTGTTCAATAAAATCACAGTTTTGTGGTAAAGG
1,542	1,56E-05	A_15_P422030	gngt1	GNGT1	G protein subunit gamma transducin 1	NM_199967	13271	163	23	340	GCCCAAAAAAGGACATTCTCAAACACGGATAGACGTTGGTTAACTCTAAATGGCTTTTTT
1,886	3,95E-07	A_15_P114615	gngt2	GNGT2	G protein subunit gamma transducin 2	ENSDART00000024136	34699	421	18	247	TTCAAGGAGAAGGGTGGATGCATAATAACGTAGCCCATGTGATTTCTTGTGGAAAAACTT
1,779	1,15E-06	A_15_P132596	gngt2	GNGT2	G protein subunit gamma transducin 2	AY050507	1439	20	82	148	TAAAAGGAGTTCCTGAGGACAAAAACCCATTCAAAGAAAAGGGCGGATGCATGATCTCCT
1,705	2,36E-06	A_15_P162101	gpr143	GPR143	G protein-coupled receptor 143	NM_200822	24870	303	6	1172	TGTGGTCGGATCATCTTTAATTTACCAGAGCCACGTGCAGGAGATCAAGAAAAACCTGAG
1,547	4,69E-05	A_15_P103551	grk1b	GRK1	G protein-coupled receptor kinase 1	NM_001017711	11779	145	26	1724	CAAAGACGACGAATTCTACACTGAGTTTGCAACTGGGAATGTACCAATTCCATGGCAGGA
-1,768	1,04E-06	A_15_P204266	ENSDART00000088083	GPATCH4	G-patch domain containing 4	ENSDART00000088083	26388	322	19	1364	GACACTAATAATGAAGCATTGATCATGGACACACAAGAGAACAGCAGGAGGAAGAACAAG
1,610	5,87E-06	A_15_P116200	si:busm1-234g15.1	G2E3	G2/M-phase specific E3 ubiquitin protein ligase	NM_001003822	21139	258	47	3087	CTTGTACAGTTTTATTTCTCCTGATGTCTTTGTTTGATATCTTGACAACTCGATAACTGC
1,576	0,000103429	A_15_P116419	zgc:92606	GABARAP	GABA type A receptor-associated protein	NM_001002707	7775	97	25	782	TTTGGAGATACAAAAAAGTTGTAGTAAGCAAGTATATATTACATCTTTCTCTCCCAGGGG
1,573	6,75E-05	A_15_P210276	zgc:92606	GABARAP	GABA type A receptor-associated protein	NM_001002707	17488	213	55	809	GCAAGTATATATTACATCTTTCTCTCCCAGGAGCGCATCATTTGTATTTAATGCAAATAG
-1,649	6,78E-06	A_15_P389310	LOC793200	GABARAP	GABA type A receptor-associated protein	EH485740	4564	59	2	599	CCTTTTACATTTTTATCCTTTTGGTCTCACGTTGAAATCTGATGTTTCATCAGAAGCAGT
-1,726	3,44E-06	A_15_P363370	ENSDART00000073861	GABARAP	GABA type A receptor-associated protein	ENSDART00000073861	3395	44	82	342	CATCACGAAGAAGATTTCTTCCTCTACATCGCCTACAGTGACGAGAGTGTGTATGGAGAA
2,198	3,84E-08	A_15_P112685	lgals1l1	LGALS1	galectin 1	NM_001005958	17772	218	28	796	TAAACTACAGCTGTTGGCAGATGAAAATTAAACCCTGTTTTCACAAATAAACTGAGTCTG
-1,768	1,86E-06	A_15_P120053	zgc:92897	GRIFIN	galectin-related inter-fiber protein	NM_001003430	43629	532	58	601	GGCATGCCGTATAACTGAACTCTATATTCATTTGAATCTCTGAATAAATGAGAGGTCAAT
3,679	4,73E-10	A_15_P108171	zgc:112179	BBOX1	gamma-butyrobetaine hydroxylase 1	ENSDART00000027869	38529	467	21	1062	CTGCACGGCCGAAAGAGCTACCAGTCTCGAGGGCAGAACTTAAGACATCTAGAAGGAGCG
1,593	7,64E-06	A_15_P144391	zgc:112179	BBOX1	gamma-butyrobetaine hydroxylase 1	NM_001017717	14337	175	57	512	TGGATAATAAGGTGTCCATAACTTGGCCTGATCAGCACAGCAGTGAGTTTGATCCTGACT
1,604	1,99E-05	A_15_P158476	LOC556971	GGCX	gamma-glutamyl carboxylase	ENSDART00000099089	38152	461	84	942	TTTTTGATGACAGCCATTGCTTTGCGGAATTTGGCAGTTGGTTTGCCACCGATTGAGCAA
1,616	1,40E-05	A_15_P108288	zgc:56140	GGCT	gamma-glutamylcyclotransferase	NM_213005	17366	212	76	777	CGCAGATCAGGAGGAATGTGCAGTATTTGTGATGTATGGAAGCAGAAGAATTAAATCGCA
1,482	3,43E-05	A_15_P155176	zgc:56140	GGCT	gamma-glutamylcyclotransferase	NM_213005	3110	42	23	531	ACAGAACGGACTTCCAGAAGAGTATCAGGAGAAACTCCGGTCCATCGAAACCAACAAATA
1,626	8,21E-06	A_15_P176776	cx33.8	GJB2	gap junction protein beta 2	NM_212825	34210	415	26	2167	CCAGCGTAATACATGTTCTTTGCGAGTTTGGCTAACAACTAATATTTTATATGAAGGTCT
-1,820	4,40E-06	A_15_P108882	cx35	GJD2	gap junction protein delta 2	NM_194420	30730	373	29	818	GAGGAAGTCCATCTATGAGATCAGAAACAAGGACTTACCGAGGATGAGCATGCCGAATTT
-1,567	1,25E-05	A_15_P146356	LOC566714	GIF	gastric intrinsic factor	ENSDART00000098273	6687	84	62	369	CAAGTTCAGAGGGATGAGAATTTGATCCTGAGGTTCACCACTTGGGCCACAAAGAAATGA
2,035	1,54E-07	A_15_P100366	gata1	GATA1	GATA binding protein 1	NM_131234	2954	40	29	1497	GCTTGTCAGTGATATTTGAACCTGTTGTGTAGTTGAATAGAAAAACATGGCTGAAACTGT
1,921	3,05E-07	A_15_P112469	zgc:112262	GINS2	GINS complex subunit 2	NM_001024439	11307	139	40	665	TAAGAGCAGAATCTTTTCTCAAATAATGGCCACTGCTGGCGCTCGGCGTGTAAATAGTGA
1,534	1,63E-05	A_15_P405035	gins3	GINS3	GINS complex subunit 3	NM_001002874	6745	85	7	722	CAAATGATTGCCAAGACGGACTAAGAAGAGTTTCTTATGAGTGCGTGAGAAAGTGGCCAG
1,515	2,23E-05	A_15_P102183	gfap	GFAP	glial fibrillary acidic protein	ENSDART00000028270	43347	528	47	2526	GTTAGTGTCGGTTCTGTTTGTCAACTAATATCTATGTTCAGTGTCATCACTGCAACTGAT
-1,474	0,000102185	A_15_P101632	LOC563180	G6PC	glucose-6-phosphatase catalytic subunit	ENSDART00000091868	33418	405	46	402	GCTTAGCAAAGGGAAGAAATCAACATCCAATAGCCTATACTTGCGTGGCTCACTTTGGAC
3,911	1,22E-10	A_15_P108859	gpia	GPI	glucose-6-phosphate isomerase	NM_144763	4811	61	43	1977	CCGCTCAATCTGCTGTAGATGGATCTTCATGTTCTCCTTTGGACCAACGAACCACAATAA
-1,727	1,57E-06	A_15_P282206	ENSDART00000078033	GPT	glutamic--pyruvic transaminase	ENSDART00000078033	34438	418	56	1419	AAGGTAGTGTTGGCCAAAATTAAGGATTTTCACCAGATCTTTACAGAGCAGTACTCTTAA
-2,052	9,14E-07	A_15_P171891	got1	GOT1	glutamic-oxaloacetic transaminase 1	NM_213057	36601	443	55	3127	GATTGTGTTTCGCTGTTATTTTCAATGGGATTTATTTGCTCCTACAGTTCATTAAATGGC
-1,437	7,14E-05	A_15_P100963	qars	QARS	glutaminyl-tRNA synthetase	NM_201213	23340	283	71	1500	GACCGTACTTTGACTACATTTATGCATCACAAACCTGTCAATAAAATCTAATTAACCAGG
-1,470	4,20E-05	A_15_P205351	qars	QARS	glutaminyl-tRNA synthetase	NM_201213	8365	103	69	1484	CAGACTTCAGGACAGAGACCGTACTTTGACTACATTTATGCATCACAAACCTGTCAATAA
-1,595	7,14E-06	A_15_P197071	ENSDART00000079655	ENPEP	glutamyl aminopeptidase	ENSDART00000079655	3976	51	39	2378	GCTTTCTGGAACTACAGTAGGCATTACAAATCCTTTGGAACTGTACATTGTTTCTTTATT
1,686	3,81E-06	A_15_P120132	glrx5	GLRX5	glutaredoxin 5	NM_213021	38479	465	81	610	GGAAGTGATGGCAAATCCTGACAACAAAAATCACTGTAAAACACTTGATAGAAAATACAC
1,566	1,10E-05	A_15_P160621	glrx5	GLRX5	glutaredoxin 5	NM_213021	1422	19	74	457	GAACTGCAGAAGCTGGGAATTAGATCAGCTCTTCTAGATCAAGAAAAGGAGTCAAAGTAA
-1,553	4,72E-05	A_15_P150076	gcdhl	GCDH	glutaryl-CoA dehydrogenase	NM_001006024	5090	66	14	1139	TGACAAAAAAGCGGCTCCGGAAATGATATCGCTGCTAAAGAGAAACTCTTGCGGTAAAGC
-1,730	2,62E-06	A_15_P365825	gcdh	GCDH	glutaryl-CoA dehydrogenase	NM_200886	38926	471	54	1347	GAAAATAAACCCATAGTTCTTTCTGAACGTAATCATAAAGCACTTTTGCGTCTGTCTCTG
-1,751	1,23E-06	A_15_P110340	gcdh	GCDH	glutaryl-CoA dehydrogenase	NM_200886	557	9	17	1807	ATTGAGTGCTGGAAGCCCCAGTGACTATTCTTTCATTGTCAATAAAGTCCAATTTGTTTT
1,634	4,49E-06	A_15_P209771	zgc:112293	GPX7	glutathione peroxidase 7	ENSDART00000025676	6026	76	62	877	CAGCTAACATTTTTACTTCTGCGATCTTTCTAAGAGGTGAAAATGGCTTCAATAAAGGTT
1,567	1,36E-05	A_15_P213146	zgc:112293	GPX7	glutathione peroxidase 7	NM_001020501	29331	355	76	892	CTTCTGCAATCTTTCCGAGAGGTGAAAATGGCTTCATTAAAGGTTTTTTAAGTGTTTTCA
1,492	4,43E-05	A_15_P115923	zgc:56280	GPX8	glutathione peroxidase 8 (putative)	NM_200222	33140	401	74	428	TACGGGGACACTGAATCAGGTACTAGCCGAGAAATTGAAGCGTTTGCCAAATCCAACTAT
2,370	3,71E-08	A_15_P112967	zgc:92763	GSTK1	glutathione S-transferase kappa 1	NM_001002560	37520	456	16	996	AGAGAAGTGGATGGGGCCTAATCCAGTCAAACCCATGGCCAAAATGTGATCAGTTTTCAT
1,984	1,62E-07	A_15_P367125	zgc:92763	GSTK1	glutathione S-transferase kappa 1	NM_001002560	9575	119	5	620	AGACAATGTTTGAGAAAGGTTCACTGAAAGCAATGCGCTTTGTGACAGCGGTAGCAGAGA
1,462	4,85E-05	A_15_P206106	gstm	GSTM3	glutathione S-transferase mu 3	NM_212676	21522	262	72	831	GGTTGAATGTGTTCAGGTGAGTGTTGCATTTTGATTTTTCACATTGATTCCATGAAAAGA
1,484	3,48E-05	A_15_P118732	zgc:65964	GSTT1	glutathione S-transferase theta 1	NM_200584	8317	103	45	840	TATATACAGGCACAGTCATGCTTTGGCAGATGAATGCAAGAATCATTCATGTTTCTGTGT
4,275	6,52E-11	A_15_P110249	zgc:76908	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	BC154822	33813	410	78	2	GCAGCAGCATCACTGAAGAAGGTTTAGCACCACAATCCACACTCTTGCAATAATGTCTGA
4,235	1,08E-10	A_15_P111646	zgc:76908	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	NM_213094	29549	359	19	2411	CACGTTGTGTTGGTGTAAAGAGAATAACCGAATAAAGTTACATGAGGTATAAAGGCTACT
3,824	1,30E-09	A_15_P107975	gatm	GATM	glycine amidinotransferase	NM_199531	30546	371	18	808	TCGACGCTGCAGACTTCATCCGGGCCGGCACTGATATATTCGTCCAGAGGAGTCAGGTTA
3,067	1,57E-08	A_15_P120611	gatm	GATM	glycine amidinotransferase	NM_199531	9543	117	74	1625	GCTCTCATCCATTCATGATTCTGTGTTAGGTCAAACTCAATCAAATAAAGAGAAAATCTG
-1,464	4,95E-05	A_15_P105369	gldc	GLDC	glycine decarboxylase	NM_199554	28505	345	81	3250	TGTAGGCTTAACTTACTGGCACTGTTCTCAAACGTTAACCCTAATTTGAAAGATGTAATG
2,584	5,81E-09	A_15_P108956	pygmb	PYGM	glycogen phosphorylase, muscle associated	NM_200472	27127	330	56	1617	GTTTGCTTATATTGTGATAACGCACACAAAACAGACCTGCTGATACCCTTCAAGAGTGCA
2,575	6,56E-08	A_15_P148931	pygmb	PYGM	glycogen phosphorylase, muscle associated	NM_200472	5562	70	83	1652	CCTGCTGATACCCTTCAAGAGTGCATTAAGAGTGTAAAGAAATAAAACAGTAACTAATCA
2,080	1,62E-07	A_15_P143981	pygmb	PYGM	glycogen phosphorylase, muscle associated	NM_200472	29696	362	9	956	GAATACTAAAGAATGGACCAAGATGGTAATCCACAACATTGCCGGCTGTGGCAAATTCTC
1,475	3,85E-05	A_15_P104903	zgc:63701	GYS1	glycogen synthase 1	NM_201180	41527	504	31	2395	GGTGAGCCGTCGTATGTTAAATTGAGGCTTTTTGTGGGAAGATTTCTCCGGTGTCTTTCA
-1,817	1,06E-06	A_15_P113260	gys2	GYS2	glycogen synthase 2	NM_001018679	19164	233	56	1900	TAATCAGCTGACCCAGTTCATGTTTTCATTCTGCCAGAAGTCGCGCAGGCAGAGAATAAT
-1,604	1,08E-05	A_15_P235461	gygl	GYG1	glycogenin 1	NM_001002062	15712	191	85	949	TACATGGGAATAGACTCTTTTGACAACATTCAGAAAAAGCTGGATGTTTTCCTCAAATGA
-1,874	1,08E-06	A_15_P113364	gygl	GYG1	glycogenin 1	NM_001002062	41282	500	73	1359	TCAATGTACCAAGCTGTTACTTAAAGTATTCAGCTGGCACATGTGGTGTTAGGACTACTG
-1,731	3,03E-06	A_15_P497887	ENSDART00000041191	GYG2	glycogenin 2	ENSDART00000041191	32224	391	31	927	GATTATATGGGCAAAGACGCCTTCGACAACATCAAGAAGAAGCTTGATCTGTTCCTCGAT
2,319	1,79E-07	A_15_P211906	BC053302	GP1BB	glycoprotein Ib platelet beta subunit	BC053302	6344	80	57	1182	CATGGAGTTTAGACTGTTTACTGTAAATTACCCTAGTTGGGGATTGAAAATTAGACTGAA
-1,622	9,26E-06	A_15_P117929	gpm6aa	GPM6A	glycoprotein M6A	NM_213200	43292	527	20	1444	TTTTTTAATCATCAAAAGGTATAGAGCCTGATACCAGCAGATGACCTGCTCATTCTGCGT
-1,438	0,00014077	A_15_P211841	gadd45b	GADD45B	growth arrest and DNA damage inducible beta	NM_213031	28751	349	36	1138	AGGACAGTGTTTGTGGAAAACAAAATCTGTCGAGCTAATGAGAAATGCATACTATGAATT
-1,479	0,000113554	A_15_P170826	gadd45b	GADD45B	growth arrest and DNA damage inducible beta	NM_213031	27539	336	12	655	TTCTGCAACGAAAGGATGAAAGAGTCATTCTCTGCGAATGAAAGCAAACGGGCTCTGCAA
-1,538	0,000173748	A_15_P275566	gadd45b	GADD45B	growth arrest and DNA damage inducible beta	NM_213031	15069	185	11	648	ATGCTGTTTCTGCAACGAAAGGATGAAAGAGTCATTCTCTGCGAATGAAAGCAAACGGGC
1,811	1,88E-06	A_15_P109069	zgc:85869	GADD45G	growth arrest and DNA damage inducible gamma	NM_213226	29580	360	35	340	CGCCTTTCAGACATTGTTGGTGACAAAGCTGAAGATTTTGAAGATGCTCACGTGCTT
-1,424	9,22E-05	A_15_P204141	zgc:152753	GIMAP4	GTPase, IMAP family member 4	ENSDART00000013001	24880	303	11	3604	TCTCCCATATCTGGTCAAACGTCTTATGTCATTTGTTATCTGTGAAAATCAATGTCTCTT
1,492	8,08E-05	A_15_P113391	BC142906	GUCY2D	guanylate cyclase 2D, retinal	BC142906	2366	32	68	523	AATGGAAAGCCCCACTAGGACATCTGACAAGAACACAAACATATGAACTCTGAACGCCAG
1,476	4,06E-05	A_15_P146761	LOC792374	GUCY2D	guanylate cyclase 2D, retinal	ENSDART00000097770	15787	194	38	3133	AAGTCAAAATTCGCATTGGACTACATTCTGGTCCAGTGGTCGCAGGTGTAGTTGGCTTAA
1,409	0,000116219	A_15_P209726	guca1b	GUCA1B	guanylate cyclase activator 1B	ENSDART00000007122	12297	151	38	1168	GTAAAGAGCTAAGTTTTTTGAAGGTCCTAATTGTAAAGGCACAGAATCTGTAAATGTCTC
-1,613	1,18E-05	A_15_P155136	ENSDART00000043226	GUCA1C	guanylate cyclase activator 1C	ENSDART00000043226	31384	381	25	381	CCAGATGACATCGTGAGCCTGATCTATGAGAGGATTGATGTTAATAACGAAGGTGAGATT
1,562	1,76E-05	A_15_P110036	h1fx	H1FX	H1 histone family member X	NM_199276	22147	269	54	599	AAAGCCAAAAGCTGCCGCAAAGAAGAAAACTAAATCAAAATAGACTTTCTGACGAAGATG
1,542	1,50E-05	A_15_P119093	h2afx	H2AFX	H2A histone family member X	NM_201073	21568	264	10	518	CAACTCTTCTGAAAAGAGCAATTTCCATGTGTCTGAATGTGATATACGTTAGCTTGTATT
1,530	2,29E-05	A_15_P102171	h2afx	H2AFX	H2A histone family member X	CN503170	23148	282	57	529	AAGGGCCACCCAACTCTTCTGAAAAGAGCAATTTCCATGTGTCTGAATGTGATATAGCTT
1,654	7,31E-06	A_15_P109753	h2afza	H2AFZ	H2A histone family member Z	ENSDART00000062324	31085	378	40	747	GAATCTGTTGAAATGAATCCTGATATGAATCACTCTTGAATTCGACGTCAAGGAATATGT
1,680	3,01E-06	A_15_P598557	zgc:56418	H3F3C	H3 histone family member 3C	NM_201101	35598	432	52	603	TAGTTTAAGTTTATTTTTTGTATTTTTCAGTAGTGGCGGTAGGGAAGGGGTATCTTGTGA
1,429	0,000136322	A_15_P117978	zgc:56418	H3F3C	H3 histone family member 3C	NM_201101	27538	335	12	457	TCGAATCCGTGGAGAACGTGCTTAAACTCTCTACTATTTACTCTTTTTGTGTGGAGGAAT
-1,463	5,81E-05	A_15_P120189	zgc:136363	HDHD3	haloacid dehalogenase like hydrolase domain containing 3	NM_001045267	20680	252	67	993	GGCTCGACTGCAGCATAACACAGACTGAGAGTGTGTAATATATAGTTTAGATTTAATTTA
1,802	8,00E-07	A_15_P179516	BC152295	HPR	haptoglobin-related protein	BC152295	24864	303	2	433	GGATACAACATTGACTATATGCTGCATATGCCACTATTGCTATACTCTAGTTATACCAAA
-1,486	5,68E-05	A_15_P102210	heatr1	HEATR1	HEAT repeat containing 1	NM_199900	30416	369	37	6470	TCAGAAGGTCATTCAAGAAATGGAGACTATCCTCGGTGAACCGCTGCAGAGCTACTTTTA
1,920	2,67E-07	A_15_P114333	hsp90b1	HSP90B1	heat shock protein 90 beta family member 1	NM_198210	11942	148	24	2663	CCAGTTGTGGAGTGCTGACTCCTGTCCACAGAACGATTAAATGTTTCCGGAAAAGGAAAA
1,667	3,16E-06	A_15_P152226	hsp90b1	HSP90B1	heat shock protein 90 beta family member 1	NM_198210	41231	500	46	2140	AATCAACCCCAAACATCCACTCATCAAAGAGATGCTAAGGAGAGTCAACGAAGACGCTGA
-1,428	0,000119101	A_15_P537617	hspa9	HSPA9	heat shock protein family A (Hsp70) member 9	NM_201326	28764	350	42	376	ATACTCTTTATGCTACAAAACGACTGATTGGACGGCGTTTTGACGACGCTGAAGTTCAAA

1,772	1,24E-06	A_15_P140326	hspb1	HSPB1	heat shock protein family B (small) member 1	NM_001008615	40226	488	40	448	TGAGGAGAGAAAGGATGAACACGGCTTCATTTCCAGATGCTTCACCAGGAAATACACTCT
1,524	3,51E-05	A_15_P107871	hspb1	HSPB1	heat shock protein family B (small) member 1	ENSDART00000060162	16711	204	81	764	GAGAGGCTGGATTGCCATGTTGTTGTATTCTCATCTCACTTTTATGTCACTCTTTTATCA
-1,465	5,42E-05	A_15_P196091	hspb11	HSPB8	heat shock protein family B (small) member 8	NM_001099427	12409	275	79	565	TTCCTATTACATACACTCCTGCTGTGAAGAATCCTGCTCTTCAAAACTCAGAGCCGGAGA
-1,471	4,06E-05	A_15_P196091	hspb11	HSPB8	heat shock protein family B (small) member 8	NM_001099427	12409	298	9	565	TTCCTATTACATACACTCCTGCTGTGAAGAATCCTGCTCTTCAAAACTCAGAGCCGGAGA
-1,490	3,19E-05	A_15_P196091	hspb11	HSPB8	heat shock protein family B (small) member 8	NM_001099427	12409	154	10	565	TTCCTATTACATACACTCCTGCTGTGAAGAATCCTGCTCTTCAAAACTCAGAGCCGGAGA
-1,540	1,84E-05	A_15_P196091	hspb11	HSPB8	heat shock protein family B (small) member 8	NM_001099427	12409	478	81	565	TTCCTATTACATACACTCCTGCTGTGAAGAATCCTGCTCTTCAAAACTCAGAGCCGGAGA
-1,551	1,30E-05	A_15_P196091	hspb11	HSPB8	heat shock protein family B (small) member 8	NM_001099427	12409	308	63	565	TTCCTATTACATACACTCCTGCTGTGAAGAATCCTGCTCTTCAAAACTCAGAGCCGGAGA
-2,172	4,67E-08	A_15_P131406	EF583630	HSPB9	heat shock protein family B (small) member 9	EF583630	16658	203	54	604	CCCCATAAACAAGGACAGATCAAACAAAACAGAGGATGAGAAGTCAAACTAGAACAGACG
-1,476	9,58E-05	A_15_P178791	hectd1	HECTD1	HECT domain E3 ubiquitin protein ligase 1	NM_001002504	35198	428	18	2522	TCTGAATTTGTTACTGGCTGGACTGGTAAGAGAGGAAGAAAGCTGAAATCCAAATTGGAA
1,797	1,12E-06	A_15_P117482	hhatla	HHATL	hedgehog acyltransferase-like	NM_200887	1497	22	32	1846	CACTTGCTGTAGCCAAACGCAAACCTGTACAACGATATAATCTTGCACAGACTAACCAAC
1,413	0,000137213	A_15_P148776	zgc:154131	HHATL	hedgehog acyltransferase-like	NM_001077390	36296	440	70	2724	GGCTGCATTTGAAAAGTTTTTACAGATTGCAACCTCTACCATCACTGGCTGCTTTTAAAT
1,584	8,15E-06	A_15_P160691	LOC553328	HELLS	helicase, lymphoid-specific	NM_001037101	18861	230	72	2296	ACATCTGCTGACACGGTCATCATATTTGACAGTGATTGGAATCCTCAGGCAGATTTGCAG
1,418	0,000100592	A_15_P110156	LOC553328	HELLS	helicase, lymphoid-specific	NM_001037101	43392	528	70	3086	CTAAGCCCCTTGACCTAGAATACTGTAGAGCAAATATATCGTTTTGTTTTTCATGTTTTC
1,764	3,11E-06	A_15_P439275	zgc:153411	HEBP1	heme binding protein 1	NM_001045401	30261	367	43	1401	TGTGACCAGGCTTCATGTTTCTCTTCTGATCTGAATAATAAACTCACTGAAATGACAAAA
1,746	2,72E-06	A_15_P143341	zgc:153411	HEBP1	heme binding protein 1	NM_001045401	26420	321	36	1400	CTGTGACCAGGCTTCATGTTTCTCTTCTGATCTGAATAATAAACTCACTGAAATGAAAAA
5,451	2,04E-11	A_15_P520017	LOC564833	HEMGN	hemogen	XM_700557	36179	439	11	602	TGTGCCTGAACAGAGCTCAATTGCAATTCCAATGTTTGCTCCAGCACCTGATTCTTCTCA
8,808	1,99E-12	A_15_P212056	hbae3	HBA2	hemoglobin subunit alpha 2	BC071507	7327	92	50	484	CTGCCTTCATCTCTGATGCGACACTGTATTCGCCTTAATGAGAATGAAAATAATAAATAT
8,523	2,41E-12	A_15_P206756	hbae3	HBA2	hemoglobin subunit alpha 2	NM_183066	31515	383	7	408	AGCTTGCCTTCATCTCTGATGCGACGCTGTATTCGCCTTAATGAGAATGAAAATAATAAA
7,323	3,27E-12	A_15_P111458	hbae1	HBA1	hemoglobin subunit alpha 2	NM_182940	9958	124	33	455	TACAGATAAACACACTTCACTGTGCTCCAAACTCTCTGTTATGTATTGAGACAATAAATT
2,066	1,79E-07	A_15_P290066	ENSDART00000101709	HBA2	hemoglobin subunit alpha 2	ENSDART00000101709	27325	332	73	422	AGTTCCTCGCTGCTTTGTCTGCTGCTCTTGCTGATAAATACAGATAAACTCAAAACTCTC
12,880	2,77E-13	A_15_P193031	hbbe2	HBE1	hemoglobin subunit epsilon 1	NM_212846	37436	453	59	419	TTCCTCGCTGTTGTTGTCTCTGCTCTGCAAAGACAGTATCATTAAGACCTCTCAGATGTG
1,491	3,43E-05	A_15_P106583	hbbe3	HBE1	hemoglobin subunit epsilon 1	NM_001015058	10974	135	41	403	TGCTTGGCAGAAGTTCCTGTCTGTTGTTGTGTCAGCCCTCAGAAGGCAATATCTTTAGAT
12,448	1,96E-13	A_15_P307851	LOC561790	HBZ	hemoglobin subunit zeta	EH578664	2188	29	61	662	GAACGTGGTTTTGTCGATATGGTCAACAGCATGTCAATAAAAACAAACCTAAAACCACTC
11,469	2,10E-13	A_15_P166461	LOC561790	HBZ	hemoglobin subunit zeta	ENSDART00000066383	33258	403	49	77	AATTGGTAACGAGGCGTTTTCCAGATTGCTTTTGGTGTACCCTCAGACCAAGCCTACTT
7,785	2,75E-11	A_15_P193311	zgc:163057	HBZ	hemoglobin subunit zeta	NM_001082834	30803	373	67	661	AGAGGAAGGACGGAATGGTTCTGCCAGATATTATCTTTATCAATGTATATGCTAGCTTAT
27,342	7,70E-15	A_15_P377540	hpx	HPX	hemopexin	NM_001111147	27281	332	50	1971	TGCAGACTAATGTACATGTGTGTTACCACAGAGCCTGTTGTTTGAAGCTTTATCTAAGGA
24,916	1,20E-14	A_15_P114293	hpx	HPX	hemopexin	ENSDART00000020637	40585	492	53	1617	AGAGCCTGTTGTTTGAAGCTTTATCTAAGGACTTGCTTATTTCACCTTTGTCTGCTTGCT
16,966	4,07E-14	A_15_P413855	hpx	HPX	hemopexin	NM_001111147	36201	439	23	1862	TTGATCTCAAAAGTTTATTCCTACCTCTGGTGCTCTGCTCAAATCATCTAGTCTTTGCAA
10,279	2,27E-12	A_15_P383005	hpx	HPX	hemopexin	NM_001111147	26983	327	68	917	CACTGTGATCTTTTTCAAAGGTGATGAGATCTACCACTTTAACATGCACACCAAGAAGGT
-1,443	6,56E-05	A_15_P117587	ENSDART00000028236	HNF4A	hepatocyte nuclear factor 4 alpha	ENSDART00000028236	40264	488	59	3189	ACCAATTGACAATTGCATCCTTCAAAGAGAAGGGTAATTTAAAACATGCAATGTGAACTG
-6,930	2,81E-12	A_15_P114842	hamp1	HAMP	hepcidin antimicrobial peptide	NM_205583	1688	24	49	587	CCTGTGTACATAGACATGTTCATGAATGTTCATTTAGTGTAATGCAAGACTTGTTTGTAC
-8,222	1,53E-11	A_15_P179011	hamp1	HAMP	hepcidin antimicrobial peptide	NM_205583	9832	122	55	197	ATGTGGAGAGTGAAGAACTGCAGGAGAACCAACATCTGACTGAAGCTGAACACAGACTAA
1,517	2,26E-05	A_15_P113787	hes5	HES5	hes family bHLH transcription factor 5	NM_182875	20578	251	16	956	ATGAAGAGTCAATGTTGAACTCCTGTGGAGTTGTGGATTATATGTGATCATTTGTGCATT
1,760	1,60E-06	A_15_P113995	her8a	HEY2	hes related family bHLH transcription factor with YRPW motif 2	NM_199624	15196	186	75	1115	AAATACTCCATACTTGTATATTACAAGAAGAGTCTGACTAGTACCTCATATTGAAGCTGG
1,597	1,01E-05	A_15_P420420	zgc:77366	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	NM_212645	26164	318	74	2016	AAGACTTGTCATGGACTTTGTTGCCAATCAATGATGATTGATCTTTAATTAGGCTCAATG
3,152	7,48E-10	A_15_P120167	hk1	HK1	hexokinase 1	NM_213252	5116	66	27	3944	ACTACTGAATTTGTGTTCTGTGGTTTCCTTTGCAGTTGCCCAAATTATGTAGCATTGTTT
1,612	6,64E-06	A_15_P213871	zgc:85677	HMGA1	high mobility group AT-hook 1	NM_213168	8361	103	67	1933	GTCAGAGAGATGCAAAACGTGTTCACAGACTGTGGTAGAGATCTAGGTTTTATTTTCTTC
1,551	2,20E-05	A_15_P173576	zgc:85677	HMGA1	high mobility group AT-hook 1	NM_213168	2684	36	61	1966	GGTAGAGATCTAGGTTTTATTTTCTTCTGTACGTATTTGTTTGGTGCACTGAATTGACTT
1,501	0,000177187	A_15_P512162	zgc:85677	HMGA1	high mobility group AT-hook 1	NM_213168	16760	205	21	816	TCTCTCAAACAGTTTCAGGCCTTTGGGGATTCACGTTTATTTTTGCAAGTCTAAATCTAA
1,925	3,78E-07	A_15_P196781	ENSDART00000074817	HMGN2	high mobility group nucleosomal binding domain 2	ENSDART00000074817	14795	181	39	594	AAAGTGTTTTCGGAAGGGTTTTCACCATGTTGTTAGCATTTAAACGTACAAATACTGTGT
-1,413	0,000406947	A_15_P109965	LOC100004331	HAL	histidine ammonia-lyase	NM_001089457	6905	88	3	1317	GCGAGACCATATCAGGTGGAAACTTCCATGGAGAATATCCAGCAAAGGCTCTTGACTATT
6,637	3,60E-12	A_15_P102759	LOC559526	HIST1H1A	histone cluster 1 H1 family member a	ENSDART00000077635	25232	307	22	275	ATCATTCAAGATCGGCTCGAAAGCTGCTAAAAAGCCCAAGAAGGCAAAGGCGAAGAGAAA
1,410	0,000239108	A_15_P151746	zgc:110425	HIST1H1B	histone cluster 1 H1 family member b	NM_001020746	37181	451	12	576	CCTAAAGCGGCTAAACCTAAAGCAGCCAAGCCTAAAAAGACCGCAGCGAAGAAGAAATAA
1,440	8,17E-05	A_15_P142051	zgc:163061	HIST1H1T	histone cluster 1 H1 family member t	NM_001089531	30063	366	26	633	GAAGAAAGAGCAGAACTCTTTAATTAAACTGATGTTAAGACATTAGCCCTCTAAATGCGT
1,559	1,28E-05	A_15_P397515	zgc:113984	HIST2H3A	histone cluster 2 H3 family member a	NM_001025176	21527	261	75	1737	ACAACACAAGTGTCATAAGTCAAGTCTGTTGAGTGGTGACAATAAATGGGTTGTTCACAC
1,405	0,000152224	A_15_P168866	zgc:113984	HIST2H3A	histone cluster 2 H3 family member a	NM_001025176	7125	89	32	1743	CAAGTGTCATAAGTCAAGTCTGTTGAGTGGTGACAATAAATGGGTTGTTCACACAAAAAA
-1,608	8,53E-06	A_15_P175581	zgc:165555	HIST2H4B	histone cluster 2 H4 family member b	NM_001098761	17255	212	19	1085	CTTAGTGTGGTAAATGCAGTATCAGCAGGATTTGTGTCATTTTTGACAGACTTTATTGAA
-1,478	6,43E-05	A_15_P116031	hdac9b	HDAC9	histone deacetylase 9	NM_200816	43448	530	31	3547	ATCCACAACTCTCAAAGCTCTTGTAGGATCTTTCTGTGATTTTTCCCATGGCACTATGGA
-1,665	4,87E-06	A_15_P102357	hgd	HGD	homogentisate 1,2-dioxygenase	NM_152966	16115	198	33	1493	TGTGAGAGGTTCAGTTAATCCCAGATGTTCTGTGCATTTAGAATAAGAACAGCCATACAA
1,427	8,52E-05	A_15_P121107	hapln1a	HAPLN1	hyaluronan and proteoglycan link protein 1	NM_001007790	38965	471	74	935	TGTTCGCTTTGTTGGCTTCCCTGACAAAAAGCAGAAGCTGTACGGTGTCTATTGCTACAA
2,151	5,57E-08	A_15_P166901	LOC553472	HABP2	hyaluronan binding protein 2	NM_001110373	36103	437	58	1758	CAGTAGAGGGTTAAATGTCTGTCTTTTAGAACAGGTCATATTCAGACCTTTATGCAAAAA
2,050	1,01E-07	A_15_P394015	LOC553472	HABP2	hyaluronan binding protein 2	NM_001110373	8298	104	35	1753	GACATCAGTAGAGGGTTAAATGTCTGTCTTTTAGAACAGGTCATATTCAGACCTTTATGC
1,715	3,04E-06	A_15_P209981	zgc:92181	HVCN1	hydrogen voltage gated channel 1	NM_001002346	26062	318	22	1024	GGATACTGGGTTTTTCTATATACTGGAGTTATAAACTTGCCTCAGTAGATTATAAGCTGA
1,646	6,11E-06	A_15_P115496	zgc:92181	HVCN1	hydrogen voltage gated channel 1	NM_001002346	22879	279	1	984	GGTCAAATCGCTAGAAAGGGAAATATGTAATCCACATAAGGGATACTGGGTTTTTCTATA
2,863	1,82E-09	A_15_P195511	hao1	HAO1	hydroxyacid oxidase 1	NM_001083542	23201	282	85	1216	AACCCCGAGGATTTGGGCACGACAGATTTAGCATCATGAATAAAACATTTGTGTAAGTCA
1,671	4,33E-06	A_15_P109636	LOC793834	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	NM_001089437	27688	337	4	2731	AGCACTTGTGCTCAGTTTCTCTCTGGACATAGAAAGTGGCCTCAAAAAAGACAATTAAGG
1,621	5,47E-06	A_15_P377580	LOC793834	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	NM_001089437	9567	119	1	2492	GTGCTTGACTAATATTCAGGTAGACTTGGCCAAATGAGAGCCTTTTACTGATTTAGCTTT
1,492	6,67E-05	A_15_P135551	LOC553401	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	NM_001105276	29050	353	19	1897	AAAGGACGCAAGTCTGGAAAGGGTTGTTATGTGTACGGAGCCAAGTCAAAAGAAAAGAAA
1,418	0,00010837	A_15_P496722	hadhb	HADHB	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	NM_200019	3966	51	34	1863	GATAAAGGTTTTGCTCTTAAACACGTGTGCCTCAGATTCAGGCAAGTGAACCTCTGGAGA
4,177	6,98E-11	A_15_P176041	hmbsl	HMBS	hydroxymethylbilane synthase	NM_001024388	12463	154	37	2633	GCAGATTTGTTTGCTTTAACTGACTGTACTTGCCTGTCCTAAATAAATCAAGCTATGTAA
2,818	2,14E-09	A_15_P100482	hmbs	HMBS	hydroxymethylbilane synthase	NM_201154	14627	179	37	1857	AGTGCCTTCCAAATGTGAAATTGACCAGCTATACTATAGCAATTACTTGGCCAGCAACAT
1,895	5,98E-07	A_15_P106857	hmbs	HMBS	hydroxymethylbilane synthase	NM_201154	19738	242	12	530	AATATTAGAGGGAACCTGAACACCCCGTTTAAAGAAGCTGGATGAAAAGGACGACTATGCT
1,566	1,15E-05	A_15_P109672	hsdl2	HSDL2	hydroxysteroid dehydrogenase like 2	NM_199599	16093	198	22	1337	TCACGCAGTCTCCTGCCTTACAAGATGTACATGATGACCTCTTTTCTATATCAGTGTTTT
3,308	6,82E-10	A_15_P181086	hif1al2	HIF1A	hypoxia inducible factor 1 alpha subunit	ENSDART00000065407	37523	455	18	2437	CAGGATTGTGTTTAAAAACGTCTCTTATGCTCAGTAAACCTGCATTTATTTGATGCAAAG
2,563	1,64E-08	A_15_P172786	hif1al2	HIF1A	hypoxia inducible factor 1 alpha subunit	NM_001012371	20453	250	37	1512	TCTTTTCAGACAAAAAGAATCAGCGATACTAACCTGATATCAACCAAGCAGTGGGAGTGA
5,601	9,05E-12	A_15_P105317	hif1an	HIF1AN	hypoxia inducible factor 1 alpha subunit inhibitor	NM_201496	43232	525	58	2056	ATTTCAGTAAGGATTGTAATTCAGAACAAACTACACTTGCCAAGTGTTAACTGTCTCCAT
-1,579	8,75E-06	A_15_P103637	BC122156	IER2	immediate early response 2	BC122156	15236	187	11	1118	CGTGCAGGTCAACGTGAAATAAGCTATACAACAAACATCTTGATGTTATGATTAAGTCTA
2,201	3,81E-08	A_15_P150041	zgc:158343	IER3	immediate early response 3	NM_001080038	29403	358	28	972	TTTGTGTTGCTGAAAGCTGAAATAATACTTGAATCTCATATTGACGACTTCCTGTGTGTT
1,878	3,79E-07	A_15_P289346	zgc:158343	IER3	immediate early response 3	NM_001080038	7892	98	84	624	GCTCTTCTCTATCCAGTCTATCATAGACTTGGTTCTGAGAACTGAACGAACTCTTAAACA
1,472	4,06E-05	A_15_P192956	zgc:110016	ILDR2	immunoglobulin like domain containing receptor 2	NM_001030192	19790	242	38	2244	TGGCTCTCAAGGGAAGCATAAATGTTGATAATGTGCCATTTATTTGTACTGCGCAGTTTT
-1,494	5,78E-05	A_15_P178676	LOC569455	IPO5	importin 5	BC142883	20317	248	53	1477	CGTGTCCATCGAACATTTGTATGATATGCAATCTATCCTGGTTAATCATTTTACAACACT
-1,465	6,89E-05	A_15_P206491	ihha	IHH	indian hedgehog	NM_001034993	21480	261	51	1529	CCTTGGAGCATGATGGACAATGATAGATGAAAATAAGGGAGGAATGAGGAAGTTTCCAAA
-1,510	4,54E-05	A_15_P570517	ihha	IHH	indian hedgehog	NM_001034993	13038	159	73	1522	CTTCCATCCTTGGAGCATGATGGACAATGATAGATGAAAATAAGGGAGGAATGAGGAAGC
1,450	0,000156388	A_15_P107181	id3	ID3	inhibitor of DNA binding 3, HLH protein	NM_152967	19963	243	41	1058	TGTATATGTTTGTGGGGATTGTCTATTTCTACAGACTGTCAGATCAACGAGTTTCATAAA
2,912	1,61E-09	A_15_P121232	BC142841	INCENP	inner centromere protein	BC142841	11385	139	81	1272	AAGATGGCCGTGGCATTTTGCCCACATAATTCACTTCACAAAGAGTGTCAAAATACTCTG

2,367	4,66E-07	A_15_P178621	LOC572121	INCENP	inner centromere protein	BC142801	30385	370	21	1031	ATGGATGTTGAACCTGAACCTGAGGACATGGACAACAGAGAAGAAAAGGTTGATGCAGAA
1,788	8,76E-07	A_15_P102953	insig1	INSIG1	insulin induced gene 1	NM_199869	475	8	46	1631	TAAACCAAAAGTAAGACTAGAAACATTAGCTATCGAGACGTTAAGTGGCACCTTGAAGAA
1,716	3,52E-06	A_15_P173486	insig1	INSIG1	insulin induced gene 1	NM_199869	29659	359	76	862	GTTGGAAATATTGGCAGACAACTAGCTATGGGCTCGACTGAGAAGATTCATAATGACTAA
1,420	0,000150843	A_15_P112525	igf2a	IGF2	insulin like growth factor 2	NM_131433	30982	376	72	1882	ATTTTGATATGAAATCCATAAAAATCAGTCCCAATGAGAGATTACATGCACAACTCGCAG
-1,988	1,76E-07	A_15_P148136	LOC793907	IGFBP1	insulin like growth factor binding protein 1	NM_001098257	39367	478	25	1197	ATTCTCTAACCAGTGTTCTGTTGGGTTAATGTGTGTATATATGTGGATTATACGGTGATT
1,886	3,52E-07	A_15_P142021	igfbp2	IGFBP2	insulin like growth factor binding protein 2	NM_131458	21818	265	53	1592	GCTCCTAACTGTTAACTATTTCAACTACACATTGTGGTTTGTGCAAACTGAATAAACAGT
1,926	2,96E-07	A_15_P101341	igfbp3	IGFBP3	insulin like growth factor binding protein 3	NM_205751	28830	350	76	2801	TCAACGTTCAAGCTAGTTGATCTTCGAGAAAGCTTGCTACCCTCATTCTGTGCAATGCCA
1,540	2,15E-05	A_15_P132396	igfbp3	IGFBP3	insulin like growth factor binding protein 3	NM_205751	22012	267	68	1910	CATTATGCTACAGTGCCCTGAATTACCGCTGCGAAATCGGTGAAGCTATGGCAGTTTTTT
2,669	8,27E-09	A_15_P117386	zgc:85888	IGFBP7	insulin like growth factor binding protein 7	NM_212924	4981	64	44	1220	TTCCTGAAGCATCAGCTGTATCTCTAATGTTTAGATGCTGTTCTTTAAATCCTTAAAGGG
-1,559	1,16E-05	A_15_P103275	itm2c	ITM2C	integral membrane protein 2C	NM_199980	25449	310	49	1735	CCACATAATGGTGTAGCAAAGAACTGGTTTTGTCTGAAATAAATGAGGCGTTTAATTTGA
1,803	7,57E-07	A_15_P144431	ENSDART00000052389	ITGA11	integrin subunit alpha 11	ENSDART00000052389	8159	101	50	4498	GATGTATTGTAGTCAGGGACCCCGATTCTCTTTATCATATACATAAAGTATACCAAAGAT
1,672	1,18E-05	A_15_P190506	ENSDART00000003040	ITLN1	intelectin 1	ENSDART00000003040	27223	332	20	798	CTGGACCTGAAAGAAACATTTAAACAACCCACTCAGTCAGCTGTGCTTCTCTTCTACCGT
1,550	1,34E-05	A_15_P160756	zgc:113924	ITIH4	inter-alpha-trypsin inhibitor heavy chain family member 4	NM_001033104	5682	71	59	2535	CAAACATCAATACTGAAGCTGAAGGAGCAGGTAGTGAAGGCATCTTGGGTGACAATGAAG
2,033	4,76E-07	A_15_P120767	zgc:123068	IFI27	interferon alpha inducible protein 27	NM_001007132	18032	219	77	514	TATGTTGATTCTCCAAATGCATGTTGTTCTTCCGATTGTATCTAGTATGGCTATTAAACC
1,883	4,66E-07	A_15_P175721	zgc:123068	IFI27	interferon alpha inducible protein 27	NM_001007132	2470	33	37	517	GTTGATTCTCCAAATGCATGTTGTTCTTCCGATTGTATCTAGTATGGCTATTAAACCTTT
1,899	3,29E-07	A_15_P105717	ENSDART00000018064	IFI27L1	interferon alpha inducible protein 27 like 1	ENSDART00000018064	12703	156	73	405	CAGAACTGTGGAAGTCGCTGTGAGAATAGTTGATACTGCCTGACATGCCCTTCACTATAT
1,665	6,55E-06	A_15_P197801	zgc:158560	IFI27L1	interferon alpha inducible protein 27 like 1	NM_001007133	43469	529	42	334	TAGCACTCTTGGGTGGTTTGCTCTTATTTAGATTGTTCTTCAGTAGCTGCAGGTGCTGCA
1,629	3,48E-05	A_15_P160826	zgc:153654	IFI44	interferon induced protein 44	NM_001077169	16582	203	15	2063	GCAAGAAAAATGGTGAAACTTGTAAGTAGAATAGCTCACTGTACTTTCTTGTTGATAAGG
1,499	3,98E-05	A_15_P202851	LOC794786	IFIT1B	interferon induced protein with tetratricopeptide repeats 1B	ENSDART00000104730	43323	528	35	1147	CCAGGGACAAATCAATCAACTTCCTCATGAAAGCAGCAGAAATCAAAAACTATTCATATA
1,604	7,59E-06	A_15_P197351	LOC555251	INA	internexin neuronal intermediate filament protein alpha	ENSDART00000027213	5317	67	44	1274	TTTCACCTCAACCCGCAATCCTAAAAAAGAGAGAGAGGAAGAGGGACATCCCAAATCCAA
1,714	1,91E-06	A_15_P139066	si:ch211-239j15.1	IMPG2	interphotoreceptor matrix proteoglycan 2	ENSDART00000086936	19890	243	4	995	TATTCGTATTATAGAGCTTTACGCCAAGGACCGCCAGTTTGCAGATTTTGTCCGACAGCA
1,428	0,000113362	A_15_P136231	ireb2	IREB2	iron responsive element binding protein 2	ENSDART00000104734	3706	47	71	2634	AAGATTCATAGGAATCATTTGGTGGGGATGGGAATCGCTCCTCTTCAGTTTTTGCCAGGA
-1,457	7,66E-05	A_15_P196521	zgc:114185	ISCA1	iron-sulfur cluster assembly 1	NM_001025178	26330	319	75	819	CCAGCGTTACAGTCTGCAAGTCAAACTTAGGAGACAGTAAGATTTGTTAATGCTGTAAAA
-1,604	1,15E-05	A_15_P175501	si:ch211-191d15.2	ISCU	iron-sulfur cluster assembly enzyme	NM_001003632	28687	350	3	447	TTAGCAGACTATAGGCTCAAACAGAAGGATGAGAAGGAGACATTGGCTGAAGCTCGAAAT
-2,694	4,02E-09	A_15_P106754	zgc:110331	ISCU	iron-sulfur cluster assembly enzyme	NM_001017800	35373	429	23	947	AGGGACAGAAACATGATTGTGTTGGTGATTTATGCTGCTGAGATTGTATTTGATGGCCTT
1,691	2,82E-06	A_15_P141791	si:dkey-174c12.2	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog	NM_001025469	21481	261	52	839	ATTTAGACATGTTTGGATATGATGAAGATCATGAAAGGCTCAGCCACCATGTTCACTTAT
1,608	1,04E-05	A_15_P100692	idh2	IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial	NM_199564	2855	37	64	1664	AGAAAAGGAAAGTTCAAGGGCCATGTGAGAAACCCTCTAATAAATCACCAAGTCACCTGG
1,525	3,14E-05	A_15_P175481	idh2	IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial	NM_199564	12645	155	44	1222	AAACTTGATGGAAACCCAGACCTGATCAAGTTCTCTCAAACTCTTGAACGTGTGTGCGTG
-1,462	7,72E-05	A_15_P346420	ivd	IVD	isovaleryl-CoA dehydrogenase	NM_201491	28267	343	43	512	ATTGGACTCAGCTATGGAGCGCATTCCAACTTATGTGTAAATCAGATGGTTCGACATGGA
-1,463	0,000171161	A_15_P101277	ivd	IVD	isovaleryl-CoA dehydrogenase	NM_201491	8850	109	62	2001	GTTGGTCTGTGAAACCTTTGGGTTTTCTGAGCCTTATTAAATCATCGCTCCATGCATCTG
-1,559	0,000160021	A_15_P508907	ivd	IVD	isovaleryl-CoA dehydrogenase	NM_201491	29461	358	59	1068	GCGAAGCTTTTGGACAGAAAATTGGCCACTTTCAGCTGATGCAAGGAAAAATGGCTGACA
1,584	1,02E-05	A_15_P119745	zgc:101070	JAGN1	jagunal homolog 1	NM_001005774	35586	432	46	1071	CATTGCAAGTTGTTACCTCCGATTCAGAAGGTTTGCAGTCTACAGTGTGTTTATACAGAG
2,859	1,85E-09	A_15_P149591	jak2a	JAK2	Janus kinase 2	NM_131093	18621	227	35	4240	GAAGACGAAGTGATGTCTGAGTTTCTTTAAGATCAAGTGTATAAAGCCATTGTGCATTTA
2,148	1,03E-07	A_15_P132541	kpna2	KPNA2	karyopherin subunit alpha 2	NM_001002335	11540	141	75	1467	CTTTGCAGTCTCATGAAAATGAAATGGTTTACAAGGCCTCCCTCAACTTAATTGAAAAAT
2,027	1,29E-07	A_15_P111962	kpna2	KPNA2	karyopherin subunit alpha 2	NM_001002335	7008	88	56	1679	CACGCCACTTATCTTGTTCATGTTTGTCTCTGTTTGGACCTCGTGCTCCAAGTTGTACAT
1,710	1,96E-06	A_15_P119816	zgc:113902	KPNA2	karyopherin subunit alpha 2	NM_001033594	27471	334	62	402	AGGAAGTTGCTGTCAAGAGAGAGACTATCAGATTCAGGAGGTCATCAATGCTGGCATTGT
1,741	1,36E-06	A_15_P141851	krcp	KLHDC9	kelch domain containing 9	NM_001012366	29995	363	76	2430	GGATTTAGATTTGATCTATGAAAAATCATTGAGGTGTCCGTTTTGTATATACATGCCCAC
-1,612	6,69E-06	A_15_P271151	LOC563341	KLHL38	kelch like family member 38	ENSDART00000058941	8947	112	25	1396	GGACAGTGAAGAATGTTTGTGCACCGGCTGCAGTGATTGATGATAAAATCTACATTGTAG
-1,436	8,97E-05	A_15_P198571	kbtbd5	KLHL40	kelch like family member 40	ENSDART00000057022	2282	32	26	1964	TGTGATAGCCATGACATTAAGGGGGAAGGCCTTCCTGTTGGGCAAAACAATAATATTTCC
6,063	3,94E-11	A_15_P114741	LOC553371	KRT13	keratin 13	ENSDART00000066620	26708	326	13	1444	TCTTCCACGTCCCTTGTTAAGTAAAGCACACCAGATTCATGTCGGGTAAAGAAACATCGC
5,934	1,84E-11	A_15_P212321	LOC553371	KRT13	keratin 13	ENSDART00000066620	34271	416	57	1515	GCTGTCAAAATGTGGTGGTTGTCTTTGAGCGTTTACAACAATAAAGCTAACGTCAAAGAA
4,573	6,51E-11	A_15_P108293	LOC553371	KRT13	keratin 13	ENSDART00000066620	8818	109	45	214	TCCATGTCCGCAGCAGGATCAGGAGGTAACTTCGGCTTTGGAGGTGGATTTGGGTCTGCA
-1,493	3,24E-05	A_15_P147936	zgc:136388	KRT13	keratin 13	NM_001040253	24227	295	15	1225	AAGTGTCTCAAGCTCAAGCTCAAGTTCTACAACACGCAAGGTGGTTACCATTGTGGAAGA
-1,511	2,66E-05	A_15_P212576	zgc:109868	KRT13	keratin 13	NM_001017824	23861	289	82	1353	AAGCAACAACAATCCACCTCAAGAGTGCTGAAAAACCAATAAAATGGTCTAACTGTGAAA
-1,699	2,09E-06	A_15_P181706	krt1-19d	KRT13	keratin 13	ENSDART00000010373	20604	251	29	855	TCTGAAACAAGAAGTCGTCACCAGCACCACAGACCTGAAAACATCTCGCTCTGAAATCAA
-1,733	1,47E-06	A_15_P109461	krt1-19d	KRT13	keratin 13	ENSDART00000010373	34090	413	51	1325	ATGCCTGTTTGTATTTGCAGTATATGCACAGAACTGGAAACCAAATAAAACAGCATTTAC
1,402	0,000496066	A_15_P116155	krt15	KRT15	keratin 15	NM_213523	34617	420	61	618	ATGACTTCAAGACCAAGTACGAGAATGAGTTGACCATGCGTCAATCTGTCGAAGCAGACA
2,160	1,34E-07	A_15_P108038	si:dkeyp-113d7.7	KRT17	keratin 17	NM_001083105	32782	398	61	1188	TACTAGTGTATCCACAAGCTCAAGCAAAACCTCCACCACACGCAAAGTAGTAACCATTGT
-1,444	7,88E-05	A_15_P205021	zgc:136902	KRT17	keratin 17	NM_001040359	13547	166	79	1522	CCAAGTAACAAGGAACCGCAGTATTTTGAACACATTAAAAACACTTACTGCTGTGTTTAA
1,688	3,05E-06	A_15_P149781	zgc:77517	KRT18	keratin 18	NM_200568	21639	263	47	1294	CAGGAGACGGTCCTAAAGATCAACAACAACTTCAAGACAATTATAAATTGCATTCAATGA
3,329	9,90E-10	A_15_P115510	krt5	KRT5	keratin 5	ENSDART00000081327	33589	407	48	2298	TTTTACTCTACCTGATTTTGGATGGGCTGATGAGCTGTTCTGTACAACATGGAAACATCA
3,304	1,73E-09	A_15_P374345	krt5	KRT5	keratin 5	NM_131156	22932	279	29	2291	ACCTGATTTTGGATGATGGGCTGATGAGCTGTTCTGTACAACATGGAAACATCAATAAAT
3,265	9,73E-10	A_15_P215851	krt5	KRT5	keratin 5	NM_131156	8928	111	16	2301	GGATGATGGGCTGATGAGCTGTTCTGTACAACATGGAAACATCAATAAATCAGGGTTATA
3,232	1,03E-09	A_15_P132346	krt5	KRT5	keratin 5	NM_131156	13053	159	81	2309	GGCTGATGAGCTGTTCTGTACAACATGGAAACATCAATAAATCAGGGTTATATACAAAAA
2,683	3,84E-09	A_15_P110790	krt5	KRT5	keratin 5	NM_131156	237	4	64	1464	AAGGAGAGGAATCCAGAATTGCATCTGGTGGCAATACTGCAACTATCCACATCCAGGAAT
2,572	6,24E-08	A_15_P105051	ENSDART00000012644	KRT8	keratin 8	ENSDART00000012644	17182	209	68	304	TGGAGGTCTTGGTGGAGGCATGGGCTTCGTTGCGGCTCCTATCACAGCTGTAACTGTCAA
1,884	2,05E-06	A_15_P117519	krt4	KRT8	keratin 8	NM_131509	30271	367	48	2302	TACACATTCCCCTGTATTCAACTGGCTTCCAGAGCATATTTTACATCCCCGGTTATAAAT
1,806	1,04E-06	A_15_P323676	krt4	KRT8	keratin 8	NM_131509	26731	325	25	2111	CTATTTTCTATAAAATGTATATGGCAGTCAGCCAATAACTGATGACATTGCTTGTGGGCT
1,516	2,08E-05	A_15_P206436	khdrbs1	KHDRBS1	KH RNA binding domain containing, signal transduction associated 1	NM_130925	42666	517	62	1921	CCAAAATGTGTCCCTACCAGTTTGTCAATAAAGCATAGTTTTTCTTTTACAGCCTTCAAA
-1,566	1,52E-05	A_15_P145016	LOC562097	KIAA0895L	KIAA0895 like	ENSDART00000082830	10925	136	15	1036	AGGTTTCTTATGAAGACGTGGAGAGACTTCGGCATTCAGCTGTTCTACATGGAACTAGGA
1,607	1,56E-05	A_15_P170931	zgc:66433	KIAA1211L	KIAA1211 like	NM_199273	39041	473	28	3896	CTGAACGCAGCCGAAGGTGTCTTTGTATTTATTTATCTCACTCTTGTATGTTTTATGTAT
1,544	1,51E-05	A_15_P109628	BC155117	KIAA1524	KIAA1524	BC155117	17540	214	81	2956	AGCAGTGGCAAACTCAAGGGCGACGTCACTGCCAACCTTTCTTTGTGAAATGCTTTTAAA
-1,430	8,81E-05	A_15_P367180	zgc:112085	KIF1BP	KIF1 binding protein	NM_001013462	20686	252	70	553	GTCTACATGAAAGAGGATGGTCAACCACCCCTGGATCTTCAAGACTTTTTTGTGCCAGAA
1,677	2,71E-06	A_15_P102248	kdr	KDR	kinase insert domain receptor	U75995	32249	391	44	2263	CATAGCTGATGATGTACTGTCTTCCAAATAATGAAATGTGTATATACTGCCAAATGATGC
1,975	2,25E-07	A_15_P106965	kif11	KIF11	kinesin family member 11	NM_173261	43083	523	54	3452	GTGATATCGTACTGTTACTTTTCCTGTTTCACTAGCGTTTAGGCTTGTTTGTATTTGTTC
1,529	1,72E-05	A_15_P179761	wu:fc51g12	KIF15	kinesin family member 15	BC152018	30	2	25	1154	CCTACAACACACTCACCCTTGACATGCTGGAGATATAAAGTAATGAATATTACACTTTTA
2,428	2,23E-08	A_15_P206741	kif23	KIF23	kinesin family member 23	NM_131355	19191	234	69	3020	CTTCTACAGGCAGCACCCTGAGAAAGCACTGTTTTCATGTAGTTTCACCTGTATGATACT
2,209	1,09E-07	A_15_P106386	kif23	KIF23	kinesin family member 23	NM_131355	9624	120	30	3051	TTTTCATGTAGTTTCACCTGTATGATACTGCTCGCACACAACTGTCAATAAACAGCATTT
2,135	7,09E-08	A_15_P133521	zgc:66125	KIF4A	kinesin family member 4A	NM_200823	9649	119	44	2220	TGCAGCTCATGAGGCAGATGAAGGACGACTCGGAGAAATTTCGCTTGTGGAAACAAAAAA
1,812	9,54E-07	A_15_P119466	zgc:66125	KIF4A	kinesin family member 4A	NM_200823	2832	38	52	5430	TCTGGCTGTATGATGTTGAACAGTCATGGTTGTAGATGATATTCCTATTAAAATCAAGTG
1,550	2,76E-05	A_15_P114236	LOC553438	KIF9	kinesin family member 9	ENSDART00000074175	41572	504	54	1926	ACACTTGCTGGATGTTTGAGATTGGCTGGACATACAGTATAAACAGCTTCTATCTGAAAA
1,460	5,89E-05	A_15_P144646	LOC553438	KIF9	kinesin family member 9	ENSDART00000074175	20376	247	83	1758	ATTACAATGCCTACAACAGGACTCTACAGAGAAGAGGAAGCAGACAGGTTTCTCAGAGTC
1,733	1,91E-06	A_15_P212916	kifc1	KIFC1	kinesin family member C1	NM_131206	23014	280	71	2041	GCTTTTTAATGTTCAGTCTCCCTGACAGAAAGTTTTTAATGTTTTGCAACCATCAAAAGC
1,534	1,78E-05	A_15_P112965	kng1	KNG1	kininogen 1	NM_001005981	4368	56	69	1118	GTTGTGAATAAAGTGTCATTAGTTTCATTGGTGGATTCGCCTGTAATTCACAGTACATTG
2,824	7,69E-09	A_15_P108546	klfd	KLF1	Kruppel like factor 1	NM_130936	40175	487	15	2296	AGTGGATTGTCTCACTGGGACTGACTACTTAATGCATAGGAAAAAAGTACAAAAGTAGCA
2,368	1,50E-08	A_15_P150871	klfd	KLF1	Kruppel like factor 1	NM_130936	4580	59	10	2206	GCGATGGCAAGCTCTGGTAAAAAGACGCAACAACTTCATCTTGAATAGCTTTAAAAAATT
3,105	8,25E-10	A_15_P161496	zgc:153255	KLF11	Kruppel like factor 11	NM_001044941	24472	297	57	1826	GTATTTAATCCCTTTGCCAAAGTCTTTGCATCAGTTCATCTCGTACTTACTCCTTACTGT
2,312	2,76E-08	A_15_P102948	klf11b	KLF11	Kruppel like factor 11	NM_001077604	32927	400	50	1095	TTCCCGCAGGCGCAACTATGTCTGCAATTTCCCAGGCTGTCGGAAAACTTATTTTAAAAG
-1,597	1,59E-05	A_15_P114483	zgc:111859	KLF15	Kruppel like factor 15	NM_212746	3050	40	78	1577	GTGGAGACACAGAGATAGAAAGAGCAAACCAACCAACGGAAGACTTGTGGTACTGTGATA
-1,689	3,72E-06	A_15_P108794	zgc:111859	KLF15	Kruppel like factor 15	NM_212746	10209	126	77	2184	TTACCAGTTTGCCCAGTAGCTTGATGCATACATTGGTGAACTAAAGCACTGAGCAGAGTT

1,536	2,70E-05	A_15_P119736	klf2b	KLF2	Kruppel like factor 2	NM_131857	29865	364	10	3375	GCATGTTCCCTATTGTAAAACATTCCTCAAACGGCGGCACATTCAGTGTCCTCTTGTTCA
2,277	8,92E-08	A_15_P153666	klf4	KLF4	Kruppel like factor 4	NM_131723	40392	490	40	1296	GAGAGGCTATATCTATTTTAAGCAACAAGAGGATTTATATCGACGAGACAACTCCTATTT
2,194	8,54E-08	A_15_P110039	klf4	KLF4	Kruppel like factor 4	NM_131723	39097	474	56	1544	ACATTTGTATCAAGTCAGGGAGTATTTTTCATGAATTTTCAGAATAATTAAAAGCCTTGC
-2,080	5,70E-07	A_15_P146191	LOC565869	KLF9	Kruppel like factor 9	ENSDART00000098473	38034	461	23	91	AAAGTCAAGAAAGCCGGACTCTGTTGATGGTCGCAATGATTCTGCTGGACTTAAACCAGT
-1,477	0,000280943	A_15_P103789	tdh	TDH	L-threonine dehydrogenase (pseudogene)	NM_213245	34377	417	26	1852	ACTTTGTCACTTTCTGATGAATGCAATTTCTGTCATTGCATTTGCCCAAACATAATTTCC
-1,492	0,000273245	A_15_P511952	tdh	TDH	L-threonine dehydrogenase (pseudogene)	NM_213245	35532	432	18	762	ACAACAGACTATGCAGTGCAAATTTTCCACGATGCTGTCAAAACTGGCAAGTTCGAGTGC
1,447	6,88E-05	A_15_P106983	zgc:66107	LARP6	La ribonucleoprotein domain family member 6	NM_199903	8985	111	45	2188	GAATTAAGGCGCTGCGCAGTCTGCTTCCTTACTGTACAAATAAATCACTTCAATCGCAAA
6,343	4,30E-12	A_15_P113715	ldha	LDHA	lactate dehydrogenase A	NM_131246	19576	239	13	2090	CTTTTACTTGAAATGTGTGATTGTAGAATTAAGACACAGCCCGACTGAATAAACATTGTG
2,149	5,54E-08	A_15_P205331	zgc:92882	LDHB	lactate dehydrogenase B	NM_001002474	39425	478	56	837	AAACTGGAAAGAAACCCACAAAAAAGTGGTGGACAGTGCGTACGAAGTGATCCGACTGAA
1,513	2,25E-05	A_15_P102035	lmnb1	LMNB1	lamin B1	NM_152972	29127	354	58	2801	GCTGAGATGCTGAAATTGTATTTTGTACTGCTTTTGTATGTACTGTCTAACAAACACTAG
1,451	8,50E-05	A_15_P143431	lama4	LAMA4	laminin subunit alpha 4	NM_001039065	25280	307	47	5627	AGAAATCTGTGATGGAAACTGGCACAAGATCACAGTGATCAGAGATGGTAGCGTGCTTCA
1,998	1,67E-07	A_15_P110334	LOC100003768	LAMB1	laminin subunit beta 1	ENSDART00000035247	13889	170	83	1383	AGAGTGAATGTAAAATATGCCCAACCTACCTATGAGACTGCAATTACAGTGACCTCGCTT
1,541	1,57E-05	A_15_P108322	lamb1	LAMB1	laminin subunit beta 1	NM_173275	4916	64	11	4366	TGGACAAGCTCTCCAAAATGGTGTCTGAGGCAAAGGTAAAAGCAGACGAAGCAAAGCTAA
1,406	0,000211776	A_15_P159531	ENSDART00000066945	LAMB1	laminin subunit beta 1	ENSDART00000066945	38676	470	11	5184	AATCAGCACATTCTAATGGGGAAATCTCAAGAGCTAGAAGGGCTGGAGAATGAAGCCAGA
1,683	3,58E-06	A_15_P183451	LOC561356	LAMB2	laminin subunit beta 2	ENSDART00000012166	39803	482	78	5277	GAAGATAAAATGAAGGCGATCCTGAACGCCATCAACAGGCAGATTCAGATCTACAACACC
1,604	8,65E-06	A_15_P114025	cmn	LAMB2	laminin subunit beta 2	NM_131014	30482	369	71	3935	CTATTATTTGTTTCTAAAAGCCATTGTTATTTATTTCTTTAGTATCCTGGGGCAAGGCCC
2,187	5,18E-08	A_15_P113770	lamb4	LAMB4	laminin subunit beta 4	NM_173276	3827	50	47	5781	GGGTCGCAAGAGTAAAATTGAAAACAACCCATGCAACTTTGCAGATTCACAGGCGCAGTA
1,464	0,000142211	A_15_P210506	lamc1	LAMC1	laminin subunit gamma 1	NM_173277	10893	133	84	5847	GCAACTTTGTACATTGGCGTAGCAAGACTTTTATCTGATACACTGGTGCTAATAATTATT
1,414	0,000231376	A_15_P118291	lamc1	LAMC1	laminin subunit gamma 1	NM_173277	1202	18	40	5818	GCATTAACACGAGCAAAACTCAACACTATGCAACTTTGTACATTGGCGTAGCAAGACTTT
-1,459	6,44E-05	A_15_P192611	zgc:158293	LANCL2	LanC like 2	NM_001083003	26087	317	35	3220	TCCTCAGGCTAATAATGTCACTTCTGAATGTCACAATAAACTGGGCTTTTTCTGAAAAAA
1,536	2,06E-05	A_15_P101484	ENSDART00000054228	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	ENSDART00000054228	15642	192	47	1005	AAACAGACGTGATGAATTTCACTGATCAAACTCATTGCATCATGAACTTTAATCATGCAG
-1,598	3,50E-05	A_15_P183316	LOC570549	LMOD3	leiomodin 3	ENSDART00000090864	28398	345	26	1806	TATCTCAAAGCAGTACCTCTTCCTAAAATCCTGGAGTCACAGGAAACTAGTCTCTTTTGA
-1,403	0,000204898	A_15_P307916	lim2.4	LIM2	lens intrinsic membrane protein 2	NM_001002407	40876	496	32	424	TTTGAGAGATTCAGTCGTTCCTTCGCTGCGGGAATCATGTTCTTCATCTCCACTTTCTTC
-1,560	1,36E-05	A_15_P204921	lim2.5	LIM2	lens intrinsic membrane protein 2	NM_001013522	38863	471	22	732	CCCACTTATAAAATACAGAGAAAAAAAGACACTGTCAGATTTCACTAGTTGCAATCACAAC
1,636	4,47E-06	A_15_P148076	zgc:158286	LRRC15	leucine rich repeat containing 15	NM_001080682	23416	286	24	2051	GTGTCATAATGTAAAGAAATGTACTGTATTGTGTGCAAATGACTGCACACATTCTGCAAA
-1,915	4,40E-07	A_15_P104712	zgc:85752	LRRC59	leucine rich repeat containing 59	NM_212932	310	6	33	1224	TCCAAAACAGGAAAGGAAAATGGACTTTAAGGAACAGTTGATAATGTTTGCAACCTTTGG
-1,950	2,22E-07	A_15_P208981	zgc:85752	LRRC59	leucine rich repeat containing 59	NM_212932	23156	282	61	1255	GAACAGTTGATAATGTTTGCAACCTTTGGAGTCTTATGTAATGCTGTTTCACAACATCTT
-1,426	0,000130296	A_15_P221181	ENSDART00000105477	LRRTM2	leucine rich repeat transmembrane neuronal 2	ENSDART00000105477	36314	440	79	1464	GTGATCATCAATGGCTATGGGCAGTGCAAATGTCAGCAACTGCCTTACAAAGAGTGTGAA
1,793	1,25E-06	A_15_P169136	zgc:109962	LRIT2	leucine rich repeat, Ig-like and transmembrane domains 2	NM_001020536	27316	331	69	2051	TTTACTAACTCTCAGAGCAGTAGGTGGACTGAACGGGCACTTTAAGAAATTAGTAAAAAA
1,748	3,26E-06	A_15_P365520	zgc:109962	LRIT2	leucine rich repeat, Ig-like and transmembrane domains 2	NM_001020536	19794	242	40	2045	TTGCTGTTTACTAACTCTCAGAGCAGTAGGTGGACTGAACGGGCACTTTAAGAAATTAGT
1,519	3,14E-05	A_15_P114843	lfng	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	NM_130971	18615	227	32	2914	AAATGTTGTCATCTCAGGGATCACAGTCCTGATGTTGTTACCTTGGGCTGCCTTGGTAAT
1,459	6,49E-05	A_15_P121085	ldb3	LDB2	LIM domain binding 2	NM_201505	13507	166	58	722	TTAAAGAACGTGTTATAGACAGTGCTTCCCCAGTGTATCAGGCTGTCATCCCCAGTGAAA
1,440	0,000151534	A_15_P107149	ldb3	LDB2	LIM domain binding 2	NM_201505	30680	374	3	1219	ACTTCTCTCTTTTGTGCTGGCTTGATTGCTTTTTGGATGGTTGTTGAGAACACCATTGCA
1,642	5,41E-06	A_15_P464585	lmo2	LMO2	LIM domain only 2	NM_131111	19059	234	2	813	TCATCAACTCGGACATTGTGTGTGAGCAGGACATTTTTGAGTGGACCAAACTCAACGGTA
1,724	0,000128428	A_15_P149291	zgc:112257	LIMS1	LIM zinc finger domain containing 1	NM_001020670	25842	314	78	1242	TGTGTGTGTTACTGTAATCTCCTTGATCCAGCACAGAATAAATCAGTGTAAAGCAAAAAA
2,257	1,83E-07	A_15_P107222	lipc	LIPC	lipase C, hepatic type	NM_201022	23073	281	18	1555	ACACTTTCACATCCAGTCGGACTTGTCTTTTTGGATGGGGGACAGCTGAATTTCCTGTAA
-1,772	1,46E-06	A_15_P110548	zgc:55345	LIPG	lipase G, endothelial type	NM_200128	35432	430	52	2121	GTCGGAAGAATGGAGAGCTGTTCTGTCTTCATAGAATTGTTGTACATTTTTGTGTCTTATG
-2,511	8,54E-09	A_15_P106261	lpin1	LPIN1	lipin 1	NM_001044353	15182	186	68	94	ATGTCATTGTGGTGCGTCAGCCTGATGGCACACTGCAGTGCTCACCGTTTCACGTCCGAT
-2,588	6,60E-09	A_15_P105446	lpin1	LPIN1	lipin 1	NM_001044353	13079	162	9	2493	GGAGAGCTCATTCAAGAACATGCAAAGACCAACATATCATCTTATGGTCGTCTGTGTGAG
1,557	1,35E-05	A_15_P153831	zgc:153919	LCN15	lipocalin 15	NM_001045415	39229	475	39	985	GACCTGTTTTAGGTTATGGTTGTATGTGGTGCAAAACAAATGGGCAAATTGTATATTTTG
-1,456	5,60E-05	A_15_P138086	LOC568903	LPL	lipoprotein lipase	ENSDART00000048763	38582	467	49	1281	TTTGTATTTGTGAAATGCAAGGAATCGTGGAGGTCTTCATCTAAAAGTGAATTATCGTAC
-2,384	1,47E-08	A_15_P149541	lpl	LPL	lipoprotein lipase	NM_131127	29897	364	26	1793	GAGCACATTCTGCAAGAAACCGCATCTTGAAAATGTTACTGCTGTGCAGTTTTAAAACAA
1,423	9,18E-05	A_15_P113459	zgc:85812	LSM12	LSM12 homolog	NM_214817	31345	382	5	1812	GTATGGCTGTGTGCTAACGGGGTTGCTGTTGGCCTATAGGTTTCTTTCGCAGTATTTTAT
-1,545	1,57E-05	A_15_P111624	zgc:158803	LUC7L2	LUC7 like 2, pre-mRNA splicing factor	NM_001089547	1154	18	16	1077	TGTGAGGTGTGCTCTGCTTACCTCGGCCTCCACGATAATGACCGCAGACTCGCAGATCAT
-1,532	1,86E-05	A_15_P121370	zgc:65749	LYAR	Ly1 antibody reactive	NM_200679	36261	439	53	1085	ACCAACCCCAAGTTTAAGATCTTGAAGGACAGAGTGAGACTGCTCAAATGATGATAATAA
-1,544	1,48E-05	A_15_P443915	zgc:65749	LYAR	Ly1 antibody reactive	NM_200679	35318	427	80	1076	AAGATCAACACCAACCCCAAGTTTAAGATCTTGAAGGACAGAGTGAGACTGCTCAAATGA
1,414	0,000167004	A_15_P195706	si:ch211-124a3.4	KDM4B	lysine demethylase 4B	NM_001082805	15980	195	51	5213	CTTGCATACTGATGGTGGCAAATGTTTATCTGTGCAGAAGTAATAGGAAAGATTCTAATA
1,852	4,72E-07	A_15_P171861	LOC570194	KDM4C	lysine demethylase 4C	NM_001083851	32123	390	62	4912	CGGCAAAGCACATGTCACCTTTTACTTAAAATATTGATCTCTGTATTCATTTGGCATTCT
1,886	3,52E-07	A_15_P108771	zgc:85741	KDM5B	lysine demethylase 5B	NM_001002166	26683	325	1	5220	ACACACGTCATACTTGTAGCAGACAGAAGAGTGTAATGAACTGCCACAAAACCTGCTCAA
1,640	4,10E-06	A_15_P103846	jarid1b	KDM5B	lysine demethylase 5B	ENSDART00000058729	7	1	14	5107	TGTGATGTATACTGTGGCTTTCTTTAAAACAGATCTTTTCCGATGTTAATTCAACTGTGG
1,653	1,13E-05	A_15_P116567	LOC553406	KDM5C	lysine demethylase 5C	BC155574	31319	379	77	2994	GCAGACACACGCGGTCGTGAGTTTGTGTATAAACATTTTCATTTCCATGTTGCCTTTGTT
1,617	7,65E-06	A_15_P342675	LOC553406	KDM5C	lysine demethylase 5C	BC155574	27534	335	10	2979	ATTGGTATTGCTATTGCAGACACACGCGGTCGTGAGTTTGTGTATAAACATTTTCATTTC
1,449	0,0001509	A_15_P100335	LOC553406	KDM5C	lysine demethylase 5C	BC128796	1093	16	63	1620	AATGGTACACAGTCTGGCTGTGAAAATGGAATTGGCAGGGAAGTCGAGTGCACATGAAGTT
1,656	3,58E-06	A_15_P115176	si:ch211-237l4.7	KDM6B	lysine demethylase 6B	NM_001030178	15865	194	78	4457	AGCAGATCAAACCGCTGTTTACTTCACATTGTTTACAATCCTATCAGCAGATGTCGTCTT
1,526	3,59E-05	A_15_P139861	si:ch211-237l4.7	KDM6B	lysine demethylase 6B	NM_001030178	27389	334	20	4264	GATGAGCTGATGAACATGTATGATAACTTTACCCTGTCTGCAGTTCCATGCTGTAGGTGA
2,907	1,59E-09	A_15_P106720	si:dkey-105o6.2	KDM7A	lysine demethylase 7A	ENSDART00000002851	10072	126	6	1764	CAGTCAACGCCGTGGAGATGTACCATAAACACAGGATAAAGCTGGAAAGAATCCCAATGT
-1,743	2,31E-06	A_15_P140646	zgc:64072	LAMP2	lysosomal associated membrane protein 2	NM_199702	42168	512	40	2748	CTGCTGTGTTCTTGTTGGTTTTTCTGCATCAGGGTTTGAGGTTAATAAATGAATAATGAT
3,480	4,53E-10	A_15_P556942	loxl5b	LOX	lysyl oxidase	NM_001102574	12514	153	63	1273	GATGTGAAGTCATTTACACAGGCATTTACATCCAGACCAGAAACTGCATCATAACTGGGT
2,645	4,60E-09	A_15_P148971	lox	LOX	lysyl oxidase	NM_207089	29974	364	65	1342	TGTGCGATGTGATGTACGTTACACCGGAAACTACGCGTATGTTTCTGGATGCCATATATC
2,576	5,60E-09	A_15_P112684	zgc:158414	LOXL2	lysyl oxidase like 2	NM_001080626	9075	114	5	2776	GGTCTTTTTGTAAGCGTTTCAACAAGGTAAGAGGACTTTCCTCAGGTGGGTCATACATCT
2,302	2,60E-08	A_15_P205881	zgc:158414	LOXL2	lysyl oxidase like 2	NM_001080626	14468	177	40	2293	TGGATGTATAATTGCCATATAGGAGGCTCCTTTAGTGCAGAGACAGAAGACACTTTCCCT
1,435	0,000124651	A_15_P175576	loxl3b	LOXL3	lysyl oxidase like 3	NM_001089342	26137	318	60	668	TTCAGCGAAGAGGCTGAGAAGAAGTTTGAGAAATATCCTGGACAACTGAACAACCAGATC
-1,557	3,00E-05	A_15_P238896	mfsd2	MFSD2A	major facilitator superfamily domain containing 2A	NM_001003570	42038	509	54	1608	CTAATATTCATCTCTTATCCCATCAATGAGGAAAAGCGACAAGGCAACCGCAAACTGCTT
-2,327	3,00E-08	A_15_P205116	mfsd2	MFSD2A	major facilitator superfamily domain containing 2A	NM_001003570	4707	60	74	3113	CCAGTTTGTGGTTCTCTGTCAAGATTTCCGCATTCTGATATCAAAAATACAGTTAATGTA
-1,630	4,60E-06	A_15_P140866	zgc:136865	MFSD8	major facilitator superfamily domain containing 8	NM_001045048	38818	469	84	2774	GGTGATTGATGGGTGTTAAAGCACAGTATGGACTTTTCCTGAAAACCTTTAATAAACTAA
-1,969	2,71E-07	A_15_P102057	ENSDART00000061070	MKRN1	makorin ring finger protein 1	ENSDART00000061070	31561	384	31	2264	TGTCGAACTTGGTTGATATGCATATGTTTATACAGAAATGTGCTCGTTTTCTATGGTTCA
-2,048	1,29E-07	A_15_P152496	mkrn1	MKRN1	makorin ring finger protein 1	NM_152978	5991	75	45	1387	TTACTCGATTTCAATCCCTGTTAGAAACTAGACAGGACTGTCTCGTGTGACTGATGGGCA
-2,238	1,08E-07	A_15_P159146	mkrn1	MKRN1	makorin ring finger protein 1	NM_152978	5869	73	68	892	AACTTTGTCATACCAAGCGAATACTGGGTGGAGGACAAGGAGGAAAAGCAGCAACTCATT
-1,629	6,71E-06	A_15_P162291	mdh1a	MDH1	malate dehydrogenase 1	NM_199947	27693	338	6	879	TGATGACCTCATGTACTCCTTCCCTGTAAAGATCAAGAACAAGAGCTGGAAGGTGGTTGA
-1,676	2,77E-06	A_15_P102153	mdh1a	MDH1	malate dehydrogenase 1	NM_199947	28678	347	84	1278	TCTTTACGCACAGTTGTCCTGACTAAAGAATCTTCTGTCATACAACAATAAACGACCATG
1,466	5,63E-05	A_15_P118717	LOC560277	MASP2	mannan binding lectin serine peptidase 2	ENSDART00000035290	29707	361	15	2268	TTGCTGTTTTAAATGTGCTCAATAAATTAAGCTGAATCAGAGGTATACGGGTCAAAAGCA
2,010	2,03E-07	A_15_P206696	zgc:110773	MPI	mannose phosphate isomerase	NM_001033110	9197	113	68	1414	CATGACGAATAACCCCTCCTAAGTGGGAGATTATAAATATTAGAATGACATTTAGTGTTG
2,470	1,13E-08	A_15_P139811	matn3a	MATN3	matrilin 3	NM_001004007	29924	363	40	1738	CTGTACCTGAATTCTGTTAGACTCCATAGAAAACCATCAAATAGAGCTATTCAAACAGTA
2,290	8,42E-08	A_15_P108801	matn3a	MATN3	matrilin 3	NM_001004007	36030	437	21	487	TGCAGGAACCATGACTGGTATGGCCATCAAGAAAGCCATGGATGAAGCATTCACTGAAAA
1,999	2,25E-07	A_15_P119841	matn4	MATN4	matrilin 4	NM_213549	11817	145	45	3241	ATGGCCCCATTATAAGGCTTTGACAGTATATGTGAATTCTTGTACTTTTTGGATATTTCC
1,708	2,28E-06	A_15_P161906	matn4	MATN4	matrilin 4	NM_213549	9284	116	27	2674	GGACATGGCTCATATTGTTCCCTGTTTATACATGATCTGTATTGTACGGTTTGTAGAGAG
1,618	6,17E-06	A_15_P104163	mmp14a	MMP14	matrix metallopeptidase 14	NM_194416	28123	342	55	3286	GTGCTTTGGGTTTTCTGTAGAAACCGGTACTGGATATTACTCGAGTGGTTTTAACAATGA
2,182	4,23E-08	A_15_P121217	mmp2	MMP2	matrix metallopeptidase 2	NM_198067	7341	91	58	2720	GGCTGCCTGAAGACTGTATAGGGTTTGTTGCATGATGGACTCATGTCAAGCAAGTATCAT
1,685	5,24E-06	A_15_P143381	zgc:158401	MXRA8	matrix remodeling associated 8	NM_001080582	22972	279	49	3533	GAGTTCGCTGCCATGTTCAAAGCAGAATCAAATAAATTCAAATAAAAGTTAACCTCTGGA
1,520	1,97E-05	A_15_P320746	zgc:158401	MXRA8	matrix remodeling associated 8	NM_001080582	7899	99	3	3504	GCAGTTTTAGTATTGATGACCTTATTTTCGAGTTCGCTGCCATGTTCAAAGCAGAATCAA

2,802	2,84E-09	A_15_P120517	mcl1b	MCL1	MCL1, BCL2 family apoptosis regulator	NM_194394	16421	201	19	741	GAGAAACACACTTCTAACAATTGGTAGTGTGGCTACATTAAGTGCAGCACTTGCCTATTG
1,598	6,88E-06	A_15_P148736	mcam	MCAM	melanoma cell adhesion molecule	NM_001012367	43266	525	76	3481	CTCTTGTTGCATTTCCTTTGCATTTCTGTTTGGTGTCAGTGGAATTTTTGTTAATGCTTG
1,548	1,49E-05	A_15_P147406	LOC569807	MIA	melanoma inhibitory activity	ENSDART00000074290	35943	436	62	345	GCGTTAATGCCTGCTGAGGTTGAGGTCAAGACTGATAAATGGGGACTTCTACTGCTATTAG
1,446	7,90E-05	A_15_P212956	zgc:91968	MREG	melanoregulin	NM_001002167	22884	279	4	1375	TAAGGTTTATTGAGGAATGTGGAGATTGTACGTGTGAGATGGCGAAGAGAATTTGAATAA
1,620	6,23E-06	A_15_P411830	LOC565942	MELTF	melanotransferrin	XM_689207	29807	361	66	2250	TTACGCATATGATGGAGCATTCAGGTGTTTGGTTGAGGATGCTGGTGATGTTGCCTTTGT
1,470	4,31E-05	A_15_P450935	LOC565942	MELTF	melanotransferrin	XM_689207	8505	105	56	3843	ATCTTATGTATCCAGTATTTCAGTGATTCGACTTCATATCGTTCTGCCAAATCGAAATCT
-1,533	3,43E-05	A_15_P378415	LOC100000736	MS4A4A	membrane spanning 4-domains A4A	EH550393	5349	68	60	819	CAGAGACAGGTGATCTGTGAGTACTACAACAATCTCAATAAGATGATCTGCGGAGGTCTG
-1,432	0,000105329	A_15_P169776	MEP1A	MEP1A	meprin A subunit alpha	NM_001030281	35666	433	4	1862	GTGTGGATTGTGGAGAACATCTTAAATATGTTAATGATGGAAGTAATACTGTGCTACTGA
-1,690	8,33E-06	A_15_P175261	zgc:153272	MEP1B	meprin A subunit beta	NM_001076621	11371	139	74	1749	TTTCATCACACATGACCGTCTGAAGAGCCGAGGCTTCATCAAAGGAGATGATGTCATCTT
-1,453	5,44E-05	A_15_P104811	sepx1	MSRB1	methionine sulfoxide reductase B1	ENSDART00000034489	19552	239	1	2605	TCGCCATTTCAAAACCATTACACTTACGACTGGTATTGTGGCTCAGGGTCACGTAGTCTT
-1,479	3,63E-05	A_15_P160861	CT573048.1	METAP2	methionyl aminopeptidase 2	NM_001100054	3714	47	75	1105	ATGATGACATGGACTGCTCACATTACATGAAGAACTTTGACGTTGGACACGTGCCGATCA
2,593	5,25E-09	A_15_P112700	mthfd2	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_001002181	3236	43	2	2230	CCTGTGACATGCGACACGTCTTATTTGTTTTGCATACTAACATGTAATGCCTTTAAAACA
-1,427	9,28E-05	A_15_P184941	mia3	MIA3	MIA family member 3, ER export factor	NM_001105525	4375	55	73	276	CAGCAGCTTCTCAATGAGAAATCTGATGCTGCGAACAAGATCACAGAATTAAATGACATG
1,653	4,35E-06	A_15_P121252	LOC556677	MFAP2	microfibrillar associated protein 2	ENSDART00000082471	20367	248	78	1505	GCTGTTTACTTGTTTATTTTGTCTTACGGAGAGTTTCACTGAACTCAGGTCAAAGGGTCA
1,643	5,79E-06	A_15_P140201	LOC556677	MFAP2	microfibrillar associated protein 2	NM_001039357	28417	346	35	313	ACAGTGTCTGAACAGCATCTGCTTCTACAGTCTGCGCAGGATGTATGTGATCAATAAGGA
1,459	6,55E-05	A_15_P111132	zgc:158387	MGST3	microsomal glutathione S-transferase 3	NM_001080034	15879	194	85	971	GACTTTCATACATATGCTTTACACTGAATGTACTTTACTATTCAAACATATGAATCATTA
-1,410	0,000125165	A_15_P106483	map1lc3a	MAP1LC3A	microtubule associated protein 1 light chain 3 alpha	NM_214739	4438	58	20	1290	GTTAAATCTCAGATGAAGGGATCGTGATGCACTACTTTGCATGTTGGGTTTCTCAACCTT
-1,411	0,000116296	A_15_P169456	map1lc3a	MAP1LC3A	microtubule associated protein 1 light chain 3 alpha	NM_214739	6056	76	77	1279	GTATGCCTTCTGTTAAATCTCAGATGAAGGGATCGTGATGCACTACTTTGCATGTTGGGT
-1,412	0,000171403	A_15_P472515	ENSDART00000067321	MAP1A	microtubule associated protein 1A	ENSDART00000067321	39134	473	75	1409	TGAGGATGTATCTGTAGTCGAAACAAAGAGTGACTCTGTCAAAGAGAACAAGGTTGAGAA
2,049	1,37E-06	A_15_P114238	mid1ip1	MID1IP1	MID1 interacting protein 1	NM_213439	29608	359	50	1098	TGATTGGGGCCCACATGACTTTTGTTTAGTCTCCCATTTTCCTTTTTGATTTGTCCTTAA
-1,669	1,46E-05	A_15_P302511	zgc:73223	MID1IP1	MID1 interacting protein 1	NM_200832	34681	422	8	155	TGTCTGGACCAAATAATAGCGGATAACCTTCTGTTTGAGCTATCTGGACACCCAGCTCAA
-1,938	2,32E-07	A_15_P114123	zgc:73223	MID1IP1	MID1 interacting protein 1	NM_200832	3323	44	46	709	TATTGGTGGATGTGGGAATTGAGACGAACTGAAGTTTACAATGCCGCTGGACCGCAAAAA
-2,019	1,41E-07	A_15_P290396	zgc:73223	MID1IP1	MID1 interacting protein 1	NM_200832	7383	92	79	606	TGGAAAAGCTGTTTCATTATCATCTAAGCGGACTACACACAGTACTGGCGAAGCTCACTA
1,583	8,30E-06	A_15_P151491	mcm2	MCM2	minichromosome maintenance complex component 2	NM_173257	32979	400	76	2807	GCTCTCGTGGTTTTGTTGACTGTATCTTGCATTGTTTCTGCTGTCAAATTAATTGAATGT
2,055	1,15E-07	A_15_P103444	mcm4	MCM4	minichromosome maintenance complex component 4	NM_198913	313	5	35	2894	TGCGTATTATCCTGCAGGAGTTTGAACATTGACATAAACGATGTGGTTAATATAAATGGA
1,407	0,000335051	A_15_P141481	mcm4	MCM4	minichromosome maintenance complex component 4	NM_198913	21915	267	19	2000	TCAGAGTGAAGAGCAGATTGAAGAGGGAGCATCTGGACATGGCTGTACTGAAAGACTACAT
2,533	1,60E-08	A_15_P169966	mcm5	MCM5	minichromosome maintenance complex component 5	NM_178436	39180	476	14	2189	ATACAGGACTTCGCCAAACAGAAATATCCAGAGCACGCTATTCAAAAGGTCCTTTACCTG
2,141	7,49E-08	A_15_P110803	mcm5	MCM5	minichromosome maintenance complex component 5	NM_178436	27132	329	59	2418	ATTGCTGGAGATATGTTCTGTGTATCATTCTTGCTTGTTGTTATAGCTTTGTGTGGTTTA
2,010	2,79E-07	A_15_P118516	MGC158377	MCM6	minichromosome maintenance complex component 6	NM_001082849	35549	432	27	2170	GGTCAATGGAGAAACTGCAAAACCCTCACTGAGACTGTCGTTTGCTGAGTATAAACGCAT
1,913	3,71E-07	A_15_P193501	MGC158377	MCM6	minichromosome maintenance complex component 6	NM_001082849	22774	277	32	2664	TCAGATTATAAGGATGGGTCTGTCTATCCATTGTTTTTAAGATTGGTGACCTTGCAAAAA
1,870	4,02E-07	A_15_P222036	MGC158377	MCM6	minichromosome maintenance complex component 6	NM_001082849	16777	205	30	1999	TATTATTCGGGTTGAGACGCCTGATGTTAATCTGGATCAAGAGGAAGAGGAGGCTATGGA
1,485	5,29E-05	A_15_P211401	zgc:64116	MIS12	MIS12, kinetochore complex component	NM_200378	2805	37	39	1044	GGGATTTAAATTCATATTAGGACGTCATTGGAGACGTCAGAGGAAGACCTGAAATTTTTT
1,441	0,00014095	A_15_P102956	zgc:64116	MIS12	MIS12, kinetochore complex component	NM_200378	30840	374	85	1104	TAAGATGCTCTGAATCTAAAGTAAAGCACATGGGTTGAGTTGCTCTATCAATTCTAAATG
-1,428	8,63E-05	A_15_P177521	BC122318	MGARP	mitochondria localized glutamic acid rich protein	BC122318	4187	54	61	642	GGAAGATGTAAAAGAAAGCCTCACCTCTTTGAGTTCACTTAATAAACACGCACAACGAAA
2,922	4,48E-09	A_15_P162516	smcr7	MIEF2	mitochondrial elongation factor 2	NM_001076648	24788	301	48	1741	CTACCTAGATGATGTTAGCGATGCTGACTTTGAAGAAGCAAATACTCAATATTAAGACAA
-1,403	0,000140519	A_15_P172366	zgc:114114	MRPL44	mitochondrial ribosomal protein L44	NM_001030260	7024	87	65	1041	GACAGTAAAAACATCATATACATCTGCCTTAAGAGCATTCATCTATTATGCAGATGCAGA
1,757	1,37E-06	A_15_P107387	si:ch211-117l16.3	MRPS18A	mitochondrial ribosomal protein S18A	NM_001030114	31130	378	64	782	AAAGAAGAGATCACCGTGATGCCCTTTAGACGTATGTGTTCATCGTTTTATCCGGGATGC
-1,428	0,000285587	A_15_P118502	zgc:92270	MTERF3	mitochondrial transcription termination factor 3	NM_001002615	39549	479	35	1229	CAGAAGTTGCATTAGCCACTCTTGAAGACTTTGAGAGGTTTCAGAAAACATTGTAGCTGT
1,819	8,81E-07	A_15_P103005	mao	MAOB	monoamine oxidase B	NM_212827	10878	133	76	4322	TCAAAATGTCCAATGGTCTAGTCCTGTAATTGCATCATTTGATCCCTTTGTACAAATCCA
-1,452	6,41E-05	A_15_P379185	BC155327	MUC13	mucin 13, cell surface associated	BC155327	34042	414	26	533	ACTACGACACAAGGTCCATGTGCATCTAGTCCTTGTATTGGAGGCAGTACCTGTGAAAAT
-1,854	4,60E-07	A_15_P101943	BC155327	MUC13	mucin 13, cell surface associated	BC155327	3434	46	17	1964	TGCTTGTGCTGGAACTCAGGTGTACATAAAAGAATCTTAAATCATTTGAGATATTCAAGC
1,802	8,70E-07	A_15_P192491	zgc:158328	MEGF6	multiple EGF like domains 6	NM_001080189	16458	202	37	4962	ATAACGTACAAGAAAAACGATTTTAGGCTGAAACTGTGGTCCTGTGTAGTTTCCAAAAAA
1,764	1,09E-06	A_15_P174606	mus81	MUS81	MUS81 structure-specific endonuclease subunit	NM_213518	11854	145	64	1820	AATCTTGGACCAGCATTAAGCCGCACGATATATCAGCTTTACTGTACTCGTGGACCTTTG
-1,404	0,000145448	A_15_P589337	LOC559917	MSH4	mutS homolog 4	XM_683314	613	9	45	2811	CTGGCTGAGATTCAGATGATAAAAGAAAATGCTACAGAGTTGGTAGAGATTGAGGAGTGA
-1,451	5,88E-05	A_15_P112826	mybbp1a	MYBBP1A	MYB binding protein 1a	NM_001002042	20629	251	42	3819	AGGAGCTGATGGGGGAATAATTGGACAATATTAAATGATAACTGTATGTTCAGCGCAAGAC
-1,540	1,58E-05	A_15_P176781	mybbp1a	MYBBP1A	MYB binding protein 1a	NM_001002042	23509	286	71	3481	TTGTTTGGCGTTATAAAACCAAAGATGGAAAAGGTGAAGAAGGTCCCAGAGGCAGAGCAA
-1,554	9,90E-05	A_15_P178366	mybbp1a	MYBBP1A	MYB binding protein 1a	NM_001002042	35544	431	25	1920	TTTGGACCTGTTGAAGGATTTGCAGACCTGCATGGAGAAAGCTCAGGCTAAGAAATCCAA
1,984	2,34E-07	A_15_P150336	mybl2	MYBL2	MYB proto-oncogene like 2	NM_001003867	24468	297	55	3684	GACATTTCTACTGTCCACCAGTGGAGAATCACTGCTGTAAAATAAACCCTGGTTATCATT
1,414	0,000117713	A_15_P106350	mybl2	MYBL2	MYB proto-oncogene like 2	NM_001003867	20498	250	60	2408	TAGAGTTTGTAAAACAGCCTGTTGGGCCTCACATGGGATGTTTTGAGGACTTAAAAGGAC
-1,929	4,39E-07	A_15_P182221	ENSDART00000052556	MBP	myelin basic protein	ENSDART00000052556	38337	466	9	1515	TCTCATATACTCTGCCTGTATGGACTGTTTCTGAAATAGTGCTGAATAAACATTAGGTCA
-1,995	1,66E-07	A_15_P515052	ENSDART00000052556	MBP	myelin basic protein	ENSDART00000052556	36090	438	51	860	GGTTTTCTTGAGATCCATGTTCAACCTCATGTGATGTGCATTTCTGTATGTTTGTGTTCA
-2,039	1,08E-07	A_15_P432310	ENSDART00000052556	MBP	myelin basic protein	ENSDART00000052556	20572	251	13	490	CTTCCTAGATAGAGATACAATCCAAGTATCTGTTGCTACATGCCTGCAGGGGTACAGAAG
-2,148	5,24E-08	A_15_P436270	ENSDART00000052556	MBP	myelin basic protein	ENSDART00000052556	42320	513	40	533	CTGCAGGGTTACAGAAGCACGTGTTGACTGTATGTGTGCAAACTTGCTGTAATAATTGTC
-1,785	9,76E-07	A_15_P101901	mpz	MPZ	myelin protein zero	NM_194361	17263	212	23	640	TGTTCAGCTTGAGCATGAGCAAACATGGCAAGAAAGGCAAAGGAAAAGAAGGATCACAGC
-2,041	2,91E-07	A_15_P199276	mpz	MPZ	myelin protein zero	NM_194361	32618	395	62	414	ATCCTGATCAAGAACCTTGATTTCGGAGACAATGGAACCTTCACCTGTGATGCCAAGAAC
1,736	1,63E-06	A_15_P163516	LOC566052	MYDGF	myeloid derived growth factor	NM_001098744	29320	356	70	1100	CTCCCAGTCATGCTTTATTCTGATAACCGATGTATCGGAATTTGAATAAATCTGTTATCA
-1,586	9,23E-06	A_15_P134616	LOC553527	MLF1	myeloid leukemia factor 1	BC093317	8117	101	29	930	GGATTATTTCATTCGGAGAGTTATTTCTACAGGAGTACACTTTTATACCACTGAGCTATA
2,441	1,48E-08	A_15_P153786	myoc	MYOC	myocilin	NM_001015062	11808	146	40	1664	CTGTATGCTTGGGATAATTATTACATGGTGTCTTACAGTGTGAGACTTGGCAAGCAGGAG
7,262	2,01E-12	A_15_P107715	mb	MB	myoglobin	NM_200586	41949	510	7	1075	GCTCTTTGGGAGGAGTCGCAGGTGTAAAATCGATGTATTTGAAATGCACTTCAGTGATTG
5,061	2,63E-11	A_15_P188516	mb	MB	myoglobin	NM_200586	1596	24	3	141	TCTGTTCAAGGAGTATCCAGACACTCTGAAGCTCTTCCCCAAGTTTTCTGGGATTTCTCA
1,601	6,79E-06	A_15_P196131	zgc:110761	MYBPC2	myosin binding protein C, fast type	NM_001013511	20021	244	71	7112	ATTGGTGACGATCCAAAGTTCCTGATGCAGAATAACCAGGGAGTTCTGACGCTCAATATC
1,523	3,12E-05	A_15_P119944	zgc:110761	MYBPC2	myosin binding protein C, fast type	NM_001013511	6860	86	65	7721	GTCTTGAAGCATTATCTAGAATGATGTGTTTGTTCAATTGTGTCTGCATTTGTTGTGTTG
-1,815	2,16E-06	A_15_P110951	LOC100002040	MYH4	myosin heavy chain 4	ENSDART00000026257	2837	37	55	4991	TCTGAGGGCTCAAGAGGACATGAAAGAACAAGTTGCAATGGTTGAACGCAGGAATAACCT
-1,891	1,47E-06	A_15_P178891	BC150415	MYH4	myosin heavy chain 4	BC150415	34755	421	47	765	AACTTGCCCAGGAATCTTTAATGGACTTGGAAAATGACAAGCAGCAACTAGAAGAAAAAA
-2,064	1,09E-07	A_15_P511817	LOC100002040	MYH4	myosin heavy chain 4	ENSDART00000026257	8731	108	85	3279	AGCAGGATTGAAGATGAGCAATCTCTTGGTATTCAGTTCCAGAAAAAAGATTAAAGAACTT
1,700	2,27E-06	A_15_P143331	myh6	MYH6	myosin heavy chain 6	NM_198823	2417	34	10	5819	AATAAACTGCGTGCCAAAACTAGAGATGGCGCACCTGGAAAGAAATCTCAAGACGAGTAA
1,932	7,17E-07	A_15_P402695	zgc:77231	MYL1	myosin light chain 1	NM_200000	31958	387	64	583	AAACACATCATGTCTGTCTAAGTCGGAGCTGTGAGGAGACTGAAGCATTTCTCCAGATTC
1,773	1,36E-06	A_15_P107336	zgc:77231	MYL1	myosin light chain 1	NM_200000	42070	510	70	963	TCCCAAAGTCAAAGGTGCTAAATATACTGCCATCAATGGACTGGCTGCAAAACCTCCTTC
1,484	3,59E-05	A_15_P211496	mylz3	MYL1	myosin light chain 1	ENSDART00000103576	31164	377	82	927	TTCAAATAAGAGATGGTGGCTAGGCATGTGATGGTACGGCAATGCTAGATCAGTGGCAAA
1,845	5,38E-07	A_15_P116485	zgc:110679	MYL10	myosin light chain 10	NM_001017871	21693	263	75	9	TCAGGCTTTTTGAGACCAAGAACAGAGTCAGGAGAAGATCTGCACAATGGCACCAAAGAA
1,749	1,56E-06	A_15_P262196	zgc:110679	MYL10	myosin light chain 10	NM_001017871	15578	192	14	583	TCTGTGTTTGTTCATGTCCATTGTGTTCCAGTGTGTTGCGTTCCTCTTAAGCTCTGTACC
1,498	9,14E-05	A_15_P109098	zgc:66286	MYL3	myosin light chain 3	ENSDART00000061955	18219	223	1	24	ATTGAGGATTTAAGGATGCGTTCCAGCTGTTTGACAGGACACCCACCAACGAGATGAAAT
1,429	8,28E-05	A_15_P100753	zgc:66286	MYL3	myosin light chain 3	NM_200516	16496	201	57	543	AGCAGCTGATGGCTGGACAGGAGGACGCAAATGGCTGTATAAACTATGAAGCTTTTGTAA
1,820	6,42E-07	A_15_P110818	cmlc1	MYL4	myosin light chain 4	NM_131692	42503	516	57	729	ACACTGGAAAGCAAATACGTCTTGTCTGTATGTCTTGGAAAGCATCAAATAAAATCCATC
1,674	2,77E-06	A_15_P131831	cmlc1	MYL4	myosin light chain 4	NM_131692	8766	109	18	739	GCAAATACGTCCTGTCTGTATGTCTTGGAAAGCATCAAATAAAATCCATCCAAATGTTAA
1,592	7,42E-06	A_15_P110935	zgc:153867	MYL6	myosin light chain 6	NM_213638	5313	67	42	918	TTATGTACCAGAAAGGCAATAACATTTTGTTTTAATTAACTCGGAATGTTTTCGCGGTCC
1,535	1,62E-05	A_15_P596837	zgc:153867	MYL6	myosin light chain 6	NM_213638	32286	391	63	674	TGACTCCCCAAGAGATAGAGCTCCTGTCCTGTGGTATTCAAACCATATAGCGATATGAAA
1,415	0,000188338	A_15_P111192	zgc:153867	MYL6	myosin light chain 6	NM_213638	38325	465	3	12	CGGAAAACAAGCCGCTGCAAAAATGTCTCGACTTCAGCGAGGATCAGATTCTTGAATTCA
1,757	1,94E-06	A_15_P211626	myl7	MYL7	myosin light chain 7	AF114428	31530	384	15	685	TTGCTATGAGTAGAGCATCATCTCAAACCTATAATAAACTTCATACTCAGTTGCTCTCAG
1,695	2,84E-06	A_15_P171951	myl7	MYL7	myosin light chain 7	NM_131329	12536	153	74	909	GCCCCCTACAGACTGTTAATTGCAATTAATAACTAGACATTTGGTTTAAGGCCCTTAAAT
-1,407	0,000473879	A_15_P134456	BC091968	MPRIP	myosin phosphatase Rho interacting protein	BC091968	17843	218	65	1828	AAATATTCGGTTTTAGAGAAGATTGGTCTCTCGGTCTGCATAGAGTTAAAGCAAAACTTT
1,565	1,11E-05	A_15_P150751	zgc:153767	MYLIP	myosin regulatory light chain interacting protein	NM_001080022	8394	104	83	1338	ACCACCAACAGTGTGCTCAGAAGGACTGGCATCTCAGAGGATTGTGCCAATAAAGAAAAT

-1,649	5,22E-06	A_15_P104384	mylip	MYLIP	myosin regulatory light chain interacting protein	NM_199983	27082	330	33	2444	ACGATATCCAGCAGTCACAGCAGGGGATATTTTTTCAATTTGTACAAGTAGGATTTGTTT
1,685	5,13E-06	A_15_P149696	zgc:77785	MYOZ1	myozenin 1	NM_205678	34087	414	49	1705	CTCTGTCTCCAAGCTAAGCTGCTACATGCCCATTCTTTAATAAATGATCGATTGCGTAAA
-1,432	7,76E-05	A_15_P177006	CH211-214J8.1	NAALADL1	N-acetylated alpha-linked acidic dipeptidase like 1	NM_001098190	29140	353	65	851	TGGAGACTTGTTAACACCTTACCTAGCTGCAAAAGAGGATACTTACAGAAGACCAAAAAA
-1,468	4,34E-05	A_15_P493137	CH211-214J8.1	NAALADL1	N-acetylated alpha-linked acidic dipeptidase like 1	NM_001098190	26832	326	76	845	TGACTTTGGAGACTTGTTAACACCTTACCTAGCTGCAAAAGAGGATACTTACAGAAGACC
2,626	5,29E-09	A_15_P103210	ndrg1l	NDRG1	N-myc downstream regulated 1	NM_200692	35490	430	81	1546	GCTGTTTACATCACACTTGACATTTCTGAATCATTTCTGGTTGTGCAAGACTTCAGTGAG
2,381	4,24E-08	A_15_P196411	ndrg1l	NDRG1	N-myc downstream regulated 1	NM_200692	14989	183	55	881	GGTGGCCTGCCTCAAGTTGATCAGCCTGGCAAACTGATTGAAGCTTTCAAATATTTCATC
1,719	2,52E-06	A_15_P149301	ndrg1	NDRG1	N-myc downstream regulated 1	NM_213348	9059	111	82	2114	TGAAAGAGTGAAGGATCGCCCGGAAAGAGAAAGAGATGAATATAAGCAACTCACCTGCTC
1,456	0,000111235	A_15_P515117	ndrg1	NDRG1	N-myc downstream regulated 1	NM_213348	39264	476	56	743	GTGAATGAAATGAACCAGTACAATCTGCAGCTCTTTGTCAAGTCATACACTAGCCGAAGA
2,879	1,92E-09	A_15_P114917	LOC562651	NMT1	N-myristoyltransferase 1	ENSDART00000079803	19202	233	75	536	TAAAACATTTGATATAGAGTTAAAGATGGTAGAGGCGAACTTCCTGTGCGTGCACAAAAA
2,604	5,40E-08	A_15_P224906	LOC562651	NMT1	N-myristoyltransferase 1	ENSDART00000079803	42005	510	37	304	GGGACACACTTAACCTAACCAACCAGGATCAGCTGAGAGAATTGACGGACTTTCTTAATG
1,440	0,000192883	A_15_P107958	nmt1	NMT1	N-myristoyltransferase 1	ENSDART00000102678	27370	333	11	2641	TTGTGGAAAATACAATGAACGCAACTGAAAACGGGTCTTTAGGATTTTATGATGGAGTGA
1,736	2,10E-06	A_15_P100555	zgc:92417	NADK2	NAD kinase 2, mitochondrial	NM_001003465	18312	224	48	1177	TGCCATTGCTACAATCAGCTTAAACGAGGAGGACCTGCTGCGAACTGTCATTCTTGATTA
1,526	2,49E-05	A_15_P238126	zgc:92417	NADK2	NAD kinase 2, mitochondrial	NM_001003465	16952	208	35	389	ACCATGCTGCTAGTTGCTAGTAAAGTGTATGATAAGAGCAAACCTGTATTGGGTGTCAAT
1,421	9,66E-05	A_15_P162371	zgc:152911	NOXO1	NADPH oxidase organizer 1	NM_001077584	30049	366	19	2181	ACAGGCGGATATTAACACTTTTATTCTGTAACTGCTCAGTTTTTATGTCTGGATCTGAAT
3,090	1,99E-09	A_15_P131111	nppa	NPPA	natriuretic peptide A	NM_198800	10668	132	54	311	ATTTGACACACAGAGAAATCGCCTGCTAGATCTCCTATTGTCGACCCGAAGCAAAAGCTT
2,978	1,27E-09	A_15_P111331	nppa	NPPA	natriuretic peptide A	NM_198800	16663	204	56	450	CAATATGCGGATACAGTGATTTTAAAATGACGGTAACACTTTACAATACGGCTTAATTTG
2,790	3,17E-09	A_15_P164096	nppa	NPPA	natriuretic peptide A	NM_198800	24026	291	81	455	CGCGGATACAGTGATTTTAAAATGACGGTAACACTTTACAATACGGCTTAATTTGTTAAC
5,686	2,84E-11	A_15_P189981	LOC568005	NPPB	natriuretic peptide B	ENSDART00000060765	10658	131	49	307	ACTCAAAGAAGAAAAACTCGGGGTGTTTCGGGAGCAAACTGGACAGAATCGGTTCAATGT
1,553	1,62E-05	A_15_P189986	LOC567953	NPPC	natriuretic peptide C	ENSDART00000074900	399	8	8	78	TTACAGAGTCTAAAGCAGCTGTTAGATGAAGAAGTGAACAAGCCGTTTGAGGAGTCCCAG
1,920	2,67E-07	A_15_P113196	kntc2l	NDC80	NDC80, kinetochore complex component	NM_001003863	26201	320	8	2120	GGTGGAAAACTTCATTAAGAAAGCCAACAGCTTGTAATGCTTGACTTTCCTGTTTTGTAA
3,314	5,30E-10	A_15_P491262	LOC100003066	NDUFA4L2	NDUFA4, mitochondrial complex associated like 2	XM_001342673	37183	451	13	1018	TGTAAAATCATCATCTGTTCAGGACAACAACAACTCATTGATTAAACGTCAGCACTGTGA
-1,521	6,15E-05	A_15_P193816	LOC557021	NUB1	negative regulator of ubiquitin like proteins 1	NM_001113580	26364	321	7	2165	TCACTTTGGTTGAAGTGATTCACTGAGTTTTACTGATTCGTTCTGATTCATATGCTCAGT
-1,671	4,33E-06	A_15_P347100	LOC557021	NUB1	negative regulator of ubiquitin like proteins 1	NM_001113580	41917	507	71	600	CACCACACAAGAGCTGAAGACACAGATAAGTCAGGAGTTTGGATTCACATACTTCGATTC
1,447	0,000214339	A_15_P105205	zgc:56361	NEIL1	nei like DNA glycosylase 1	NM_200283	5730	71	83	1380	CAATCAGAATACTTTTCAAAAAGAAGCTAAATCTGCAAACTACTGAATGTACCACCCAG
1,617	5,69E-06	A_15_P121124	zgc:103553	NEIL3	nei like DNA glycosylase 3	NM_001007335	21404	262	12	1761	AGCGTGAGTTGGACATGACATCTTTTCAAATGCATTAAAAAGCTTTTGAAGCTATGTTTG
1,408	0,000172315	A_15_P166301	ENSDART00000042249	NGFR	nerve growth factor receptor	ENSDART00000042249	38351	466	16	1559	CTGCCTCTGTACAGTACAGGATCCGCTGTTAAACATCCATAAAGCATATGGTTGTATGTC
1,425	0,000116406	A_15_P102055	ntn1a	NTN1	netrin 1	NM_131029	30748	373	39	3127	ATTGTTCTGCTTGCAGTCTTTTTTGATGTATTCGTTAACATGGGAACCTGAGTTTGGCAC
-1,839	8,75E-07	A_15_P102261	zgc:100982	NCALD	neurocalcin delta	NM_001003776	20440	249	31	1418	CGCTGCATACTGTAGGACTGACTAACCGTATAGTTGGACGATATCATTAAGCAAAGAACT
3,233	6,23E-10	A_15_P119710	ENSDART00000054056	NEFH	neurofilament heavy	ENSDART00000054056	1112	15	73	529	AGGAGAGACAGGCTACTCTTGCGGCTAAAAAAGCCAAAGAGGAAGCAGAAGCTAAACTTA
1,764	1,48E-06	A_15_P161081	neurog1	NEUROG1	neurogenin 1	NM_131041	28776	350	48	681	GATACTTGCAAACCGACGTAGTGTACAGCTACCGCAACTTCGTGCCTAGCATCTATTAAT
1,416	0,000101849	A_15_P115134	neurog1	NEUROG1	neurogenin 1	NM_131041	14	2	17	1124	ACAAGACAAAGATCTGGCCTTATGCATTATGTATTTTGACCCGAAGAAACCCTCATCTGT
-1,539	4,82E-05	A_15_P105844	zgc:100871	NEGR1	neuronal growth regulator 1	NM_001003851	32893	399	33	2246	AGGGAAGACAGCCAGAACTGGCTCATATTTCATTTCAAATGACGAAATTATGGACAGTGT
-1,657	9,94E-06	A_15_P130621	zgc:100871	NEGR1	neuronal growth regulator 1	NM_001003851	5867	73	67	972	CAAGGAATCGTCATCAATAACCTCAGCTCCAGATCGGTTCTCACAGTGAAGAACATGACA
-1,847	5,87E-07	A_15_P148271	zgc:136764	NPAS4	neuronal PAS domain protein 4	NM_001045321	40671	493	12	4670	GTGTCGCTGATAAATGTATTTGGTCGTCAAAACAGAGGCATTTATATTAAAGTGCACTTA
-1,635	7,31E-06	A_15_P108520	LOC562714	NFS1	NFS1, cysteine desulfurase	NM_001044993	25498	309	74	2053	AGTATGAGCTCTTCTTTTATTGCAGATCACAGCTTGTGTAGCGTCTGTTGTTGTGATGTT
1,975	8,04E-07	A_15_P100324	mibp	NMRK2	nicotinamide riboside kinase 2	NM_131693	37406	453	44	626	CGGTTTGCCAATCGAATACTTGGATGGCTTGAAAACAAAAGATGAAATTTACAACCAGGT
1,521	1,98E-05	A_15_P137536	mibp	NMRK2	nicotinamide riboside kinase 2	NM_131693	7797	97	36	461	CCTTTGCTTGACGTCTTTGACAAATCTTACTACATCACCATCCCATATGAGGAGTGCAAA
-1,681	2,22E-05	A_15_P598982	zgc:103408	NMRK2	nicotinamide riboside kinase 2	EH501172	20325	248	57	485	AAGACATTTAGGACTTGAATCATTTGTTGTATTTATGGACCCATGTGGTTCATGAACCCT
-1,812	7,06E-07	A_15_P153446	zgc:103408	NMRK2	nicotinamide riboside kinase 2	NM_001004618	20926	256	23	610	AAGGACGAGCTCTATAACCAAGTTTATGAAGACATTCAGAACTCTCTGTTGAACATCTTA
-1,931	2,64E-07	A_15_P219031	zgc:103408	NMRK2	nicotinamide riboside kinase 2	NM_001004618	31059	378	27	417	TGACGTCTATAACAAGTGCTTCTACGTCACCATTCCATATGAAGAGTGCAAAAGGAGAAG
-1,433	0,000108665	A_15_P167481	LOC557254	NOB1	NIN1/PSMD8 binding protein 1 homolog	ENSDART00000027115	26072	318	27	1127	AATGTCTAGAAAGGCTCGTCAGAAGACTAATGTGTTTGATCCAGATTACCTGGCCAGCAG
1,864	3,63E-06	A_15_P396525	zgc:56466	NIPSNAP3A	nipsnap homolog 3A	NM_200264	25795	313	55	864	CAGTAATTCAGATAACCATGTGTAATCTTGGCAGTACGTTGATATGTTTTGCTGATGGA
1,774	2,77E-06	A_15_P102092	zgc:56466	NIPSNAP3A	nipsnap homolog 3A	NM_200264	18563	228	5	880	CATGTGTAATTCTTGGCAGTACGTTGATATGTTTTGCTGATGGACAAATAAAAAGTGTGA
-4,046	1,01E-10	A_15_P186571	Capon	NOS1AP	nitric oxide synthase 1 adaptor protein	ENSDART00000073787	7909	100	8	244	AACCGAGGAGAAAGACCTAAAACAGACACCATGCCTGCAAAAACAAAGTACAATTTAGTC
1,749	1,59E-06	A_15_P105189	ndpkz3	NME3	NME/NM23 nucleoside diphosphate kinase 3	NM_130928	1785	25	19	536	AAACACTCTTGCGTTCATCATCAAACACACACACAGCTTTATCTGATAGCTGCTTATCAA
-1,411	0,000127104	A_15_P117166	noc3l	NOC3L	NOC3 like DNA replication regulator	NM_001002863	39203	475	26	2481	TCACATCACCACACACACAGCAGGAACCATGAACAGATGATTACAGTATGGTGTAAAATA
-1,482	0,000255906	A_15_P134071	noc3l	NOC3L	NOC3 like DNA replication regulator	NM_001002863	28079	342	32	1452	TGTCATTCAAGGAGAAGAGGAAAAAATTTATCCAGGATGCAGCGGAAGTGGAAGAAAGCAG
1,753	1,24E-06	A_15_P171091	zgc:158618	NCAPH	non-SMC condensin I complex subunit H	NM_001080196	34089	414	50	2430	CACCAAGAGGAAAAAACTCAGCATGGTGCAGTTTGAATAATGTTTGCTTTTAAGATTAAG
1,457	0,000174529	A_15_P168981	si:dkey-202b22.2	NCAPH2	non-SMC condensin II complex subunit H2	NM_001044991	17015	208	67	1807	ACAATGGAGCTCACTTTATTGACTACTCAGAGGGCTCACGAACGTCTCAAAACCTACAAC
-1,643	4,04E-06	A_15_P112992	nol14	NOP14	NOP14 nucleolar protein	NM_001003831	40337	490	12	2908	TCTGCACATTTATTCTCAGTGGAATGTTTTATATGTGACTCTTCAGAGAAATAAACCACG
1,449	6,58E-05	A_15_P194416	zgc:153630	NPRL2	NPR2-like, GATOR1 complex subunit	NM_001045847	22564	276	10	1474	CCTCTGGCTACTGTAAAATGTGTGATCTACAATGTGTTAGCTACAGCATTAAAATAAAAC
-1,943	5,16E-07	A_15_P103985	nsfl1c	NSFL1C	NSFL1 cofactor	NM_001007446	33126	402	66	1569	AAAGAACCGAAGCGAAGATCTAACAAGTTTATGCTTTTAGAGTAACTGCTGAATATATAT
1,440	9,03E-05	A_15_P258551	si:ch211-147d7.3	NSL1	NSL1, MIS12 kinetochore complex component	NM_001025521	33766	409	54	860	CTGTAGCTCAGATGGAAATTCGTGTTTCACCACTTTCCTTTTCCATTAAATCTGTTTAAT
2,499	1,01E-08	A_15_P109440	nfe2	NFE2	nuclear factor, erythroid 2	NM_175043	21177	257	67	1224	AATGATGGCAACATTTACTTGGTGCCACGGAATGCAGCACTGGCTGGTGAATGAATGTTT
-1,421	9,75E-05	A_15_P224896	zgc:77060	NFIL3	nuclear factor, interleukin 3 regulated	NM_001002218	17432	214	25	3926	ACCAGAAGCCTCATACATTCAATTTACAAATGGCTGTACTTGCTCTTAATCTCATAACTA
-1,547	1,45E-05	A_15_P169431	zgc:77060	NFIL3	nuclear factor, interleukin 3 regulated	NM_001002218	12059	147	85	4463	GCCATTGTCCAGACAAGAAGAATATCTAATTGAACTAAACTGTTACTCGCATTTTAATGG
1,448	6,36E-05	A_15_P142731	DKEY-266F7.5	NUGGC	nuclear GTPase, germinal center associated	NM_001100099	27274	332	46	1162	CAGTCATTGGTTGTGTAGGTCCAATTACACATTAAACATTAATTTCTGTGACATGTTTCC
1,419	9,66E-05	A_15_P563112	ENSDART00000005194	NUMA1	nuclear mitotic apparatus protein 1	ENSDART00000005194	30939	376	50	1430	AACTACAGCTTCACAGAAAAATTCAGAGCTTCAAAACAAGCTTCATCAACAAGAGAGCTT
3,477	7,56E-10	A_15_P170361	zgc:92186	NARF	nuclear prelamin A recognition factor	NM_001002342	27280	331	50	1881	TTGCACCTAAATGATGTCATGCATGGATGGGCAACTAGCCATCACACAGATGCTAAAGTG
1,714	5,36E-06	A_15_P151741	whsc1	WHSC1	nuclear receptor binding SET domain protein 2	NM_001082551	16103	198	27	5280	TTCAGAGTTTTAAAAGTGAATCATGACGGGCTTCTTGTGATACAAGAAATAAAGCTGGTT
2,437	1,33E-08	A_15_P118726	zgc:55307	NCOA4	nuclear receptor coactivator 4	NM_201129	36801	445	71	2731	TTTCTTCTGTCAGGATTGTGCCAGACCGCTGGATTGCGCACACATGTACTATTTAGGTA
2,317	2,74E-08	A_15_P365130	zgc:55307	NCOA4	nuclear receptor coactivator 4	NM_201129	36404	442	40	2554	CATCCGCCATAAACAAACCACTGATACTGCTTTGTGAACATGTAGACAGGATTTAATCTT
-1,590	2,39E-05	A_15_P109764	zgc:92434	NR4A1	nuclear receptor subfamily 4 group A member 1	NM_001002173	23379	286	5	2710	GTGCGGTACCAGTCAGACTATAGAAGAATCATATTTGTATGTATGTATTTTGAGGATGTA
-2,153	5,48E-08	A_15_P134816	nr5a5	NR5A2	nuclear receptor subfamily 5 group A member 2	NM_001077272	34809	421	75	1926	GCCGTTTTAACTTGTATTAAAGCACAAATTTCTAACCTCTCTAAATCACAGATGCCCATC
-2,181	9,36E-08	A_15_P101460	nr5a5	NR5A2	nuclear receptor subfamily 5 group A member 2	NM_214779	30747	374	38	1559	AGATTTTCCCTGCAACTCACTGCTGACTGAAATGCTTCATGCCAAGCACACATGAGATCA
-2,201	3,79E-08	A_15_P142176	nr5a5	NR5A2	nuclear receptor subfamily 5 group A member 2	NM_001077272	32326	391	83	1961	CCTCTCTAAATCACAGATGCCCATCTCATATCAATAATGTCAAATTGTTTACAGAATTGG
1,579	8,74E-05	A_15_P108422	nutf2	NUTF2	nuclear transport factor 2	NM_001003598	38148	461	82	669	TTTTGTATGTTGTGGCATGCACTGGTTGACAATAACTTCAGTTTGGTAATAAATCTGTTC
-1,719	2,21E-06	A_15_P378665	zgc:153192	NUCB1	nucleobindin 1	NM_001045463	19683	240	68	1508	TGAACTTTTCATAGCATAACCAGATCAAAACAGCTCAAAGTAACAGTAAACGCTTCTCAA
-1,763	1,11E-06	A_15_P192881	zgc:153192	NUCB1	nucleobindin 1	NM_001045463	31653	384	78	1299	CTAATGGGGAGCTTAAGTTCCAAGAGGGCATCCAGAAACTAATAAATGAAGACCGTCAAG
1,433	0,000116086	A_15_P100486	LOC567446	NUSAP1	nucleolar and spindle associated protein 1	ENSDART00000003314	23809	289	56	728	GAATTCAGTTAAAGAGCTGAAGACCCTGTCAGAAAAGACACTGAAGAAACCCGAGGCAAA
-1,523	2,95E-05	A_15_P115612	zgc:56457	NOL12	nucleolar protein 12	NM_200290	28149	342	68	1433	AGTTTTTCAGCCTTTTCTATGTGCTGAGAGCTGCGTTACATCATCATTAAAGGAGCCGTG
1,498	3,24E-05	A_15_P188606	CH211-114L13.8	NXNL1	nucleoredoxin-like 1	NM_001110760	23408	286	20	663	CAGCATGACCGACCCCATCAGAAGAATCAAATATAAAGTGGAGGACGAGAAGAAGAAGAA
-1,617	9,86E-06	A_15_P148881	zgc:162229	NUDT6	nudix hydrolase 6	NM_001089522	26605	323	46	548	AAGAATGCTTGGAAGTTTCCCGGGGGTCTTTCAGATCTCGGAGAAAACATTGCTGATACA
1,673	4,99E-06	A_15_P165651	ENSDART00000100214	NUFIP2	NUFIP2, FMR1 interacting protein 2	ENSDART00000100214	11166	137	53	1707	AGGAGGTCTAGTTGGGGGTCGTTTGATCTAAAAGCTGCTGTAATTTATCACACTAAAGGT
2,049	1,29E-07	A_15_P102999	zgc:153815	OLFML3	olfactomedin like 3	NM_001077251	27300	332	60	1411	ATGTACAGGGCTCAACAATGAACACTTTATCTCAGTTTGCCTGGAGCAGAACTAATAAAT
1,810	8,17E-07	A_15_P237616	zgc:153815	OLFML3	olfactomedin like 3	NM_001077251	28334	343	79	1197	GCTTGGGACGATGGCTATCAAATCCTCTACAAACTCCAACTAAAAAAGAAGCTAGAGGTG
1,555	1,65E-05	A_15_P117254	pvalb4	OCM2	oncomodulin 2	NM_212783	28284	344	52	546	CTGTCTTAAATATGAGTTTTGCTTACTGTAAAATCTGATGCACTTTTACGGGAACGAAGA
1,506	5,61E-05	A_15_P132286	pvalb4	OCM2	oncomodulin 2	NM_212783	40916	496	52	350	ATGAGTTCGCTGCCTTTGTTAAGGCATAAATTGCTTCTCACCAACAACACCTCTTGCTCC
-1,508	2,90E-05	A_15_P108421	pvalb8	OCM2	oncomodulin 2	NM_182937	26927	328	39	761	AGAGCGCACATGGGCATCGAGCAAATGTAAAACTACCTGAAAAATTACTGAAGTCAATAA
-1,555	2,52E-05	A_15_P115654	pvalb5	OCM2	oncomodulin 2	NM_207167	35860	436	19	605	CGCTTCTGTAGTTATTGAATATGAAACTGCTTAATCAAATAAAATCTCCAAGTGAAGGGC
3,085	9,02E-10	A_15_P113881	opn1lw1	OPN1LW	opsin 1, long wave sensitive	ENSDART00000065941	15785	194	37	1610	AAAGAGTGATTGGTAGATGCCTGCCCATGTACAGCATGTAATATGGTTCTATTTTTTCTT
2,720	4,62E-09	A_15_P119429	opn1lw2	OPN1LW	opsin 1, long wave sensitive	NM_001002443	28646	348	67	1208	AGGGAAGAACTGGACTTTCAGACTCCAAGATGCAATAGTCTTGACTGTACATATGTAGGC
1,613	8,72E-06	A_15_P205196	zgc:85772	ORC4	origin recognition complex subunit 4	NM_213183	9739	122	6	1335	CGCATGACACTCACACTTTAGACATTTCCTTGTCTGTATATAGGTTTGTTTGCAATAAAA
1,459	9,03E-05	A_15_P121229	orc5l	ORC5	origin recognition complex subunit 5	NM_213198	29734	361	29	1553	ACAATTTATCCAAGGGTCTCCTTCCTTAAGGGGAATTTATCGTGTGGCACACTGTAACCT

1,422	9,50E-05	A_15_P106764	orc6l	ORC6	origin recognition complex subunit 6	NM_212671	34533	419	19	1307	GACATGACTCATTTGCTTCCATTTGGATTTTAATGTGAATAAAATGGGTGTTCTTGACAC
-1,742	2,12E-06	A_15_P174241	oat	OAT	ornithine aminotransferase	NM_207077	24270	295	37	1883	CTTTCTTCCAGAAACTCTTTCACAACCTTTGCCCGATACTATCCAGGACATAGATGACAG
2,699	3,54E-09	A_15_P201681	LOC794667	OTC	ornithine carbamoyltransferase	ENSDART00000089526	7614	95	27	1008	ATGGGTTTAATGGTGTGCATCCTGACAGACTATAGGCCACAAATTCCCACACTCAAATTG
-1,431	7,87E-05	A_15_P144761	oaz2l	OAZ2	ornithine decarboxylase antizyme 2	ENSDART00000083569	18065	221	9	569	TATGGTCTACACAATACAACAAACTCACTCATCTGAGGAATAACTGCAGAACCTTCACCT
-1,733	8,81E-06	A_15_P103003	zgc:56053	OVGP1	oviductal glycoprotein 1	NM_213050	30661	371	78	1593	GTACTGGTTATATATTCACTCACATCTAGTTTTCCTCTTGTTGTGCAACAAAACTATGTC
1,977	2,38E-06	A_15_P156501	oxsr1b	OXSR1	oxidative stress responsive 1	NM_201175	26035	318	8	1831	CCAGCCCATAGGATTACAAATGGAGTTGCACAAAGAATTTGTAGGAATCCATTAAAATAA
1,538	1,60E-05	A_15_P101476	oxsr1b	OXSR1	oxidative stress responsive 1	NM_201175	2099	30	16	4372	TCATGGCCTTCGTGTTCTTTATAAATAAGGTGACGGGAGGAGGTGGCGTTCACTACTAAA
1,620	2,09E-05	A_15_P106741	c20orf149l	PPDPF	pancreatic progenitor cell differentiation and proliferation factor	NM_200008	37799	457	72	687	TTTACACGTGTAACCGTTTGTTACTTGTTGTCGTCTTATCCTATGTTTTTCAGCACAATA
-1,423	0,000482681	A_15_P344225	zgc:158746	PANK1	pantothenate kinase 1	NM_001083841	27778	337	49	678	TCAAGGTCTGCTGTACGTTGATTCAGTCGGGTTCAATGGCCATCCAGAATGTTATTTTTT
1,410	0,000169607	A_15_P103781	BC152272	PTMS	parathymosin	BC152272	21117	258	36	551	ACAGACATTCCTTTGCCGCTACAACATCTTCTTTTATTGCACTGAGGCCCATAACATCAT
1,468	4,40E-05	A_15_P105154	pth1a	PTH	parathyroid hormone	NM_212950	36999	450	3	584	TACAGAAGAAAAATGCTGTAGGACCAAATGTTTCTGAAGAGAGAAGCTTTTATTTACGAC
-1,434	0,00010076	A_15_P115624	pth2	PTH2	parathyroid hormone 2	NM_212949	14499	178	55	420	ATGAACTAACGTCAGGGCAGGAGGGAGGACACAGTAAGTGTCAATTAAAATATACTCTTG
-1,596	7,86E-06	A_15_P111657	tip39	PTH2	parathyroid hormone 2	NM_205577	20369	248	79	810	GTGTGGGAGAAAAACAAGAATTTACTCATTACTTCATGAGTAAACAATTAAAGGGGTAGG
-1,746	1,38E-06	A_15_P284006	tip39	PTH2	parathyroid hormone 2	NM_205577	15923	196	22	689	GAGAGACAAAAATGGCTCAACTCCTATATGCAGAAGCTCTTAGTAGTTAATTCAAAGTAA
1,513	2,72E-05	A_15_P145131	zgc:162217	PARVA	parvin alpha	NM_001110471	9396	116	83	1891	GCTTTTCAAGCTTTATGTGAGATAAACAGCAGTCAGTGATAGACAGAAATAGAGCTTATT
1,915	4,18E-07	A_15_P133511	BC046015	KIAA0101	PCNA clamp associated factor	BC046015	20022	243	72	427	GAGGATGAAGATGATGATGAATGATCTCTCTTTGAGTTTCTTCAGTGTAAATCTTTG
2,236	4,16E-08	A_15_P109818	pbk	PBK	PDZ binding kinase	NM_001002387	21551	263	2	1590	CATGTTGCATAAGGTCTTATGTACTCTGCTGATTTCAGACATGCTCTCGATCATACTGTA
-1,426	0,000130125	A_15_P117349	pdzk1l	PDZK1	PDZ domain containing 1	BC066762	14816	182	49	1859	TAGCTACGATTAGTGAAGGCATCTAATCCATTGGGGATCTACAACAACAAATCTATATTT
1,452	0,00018848	A_15_P119172	ppib	PPIB	peptidylprolyl isomerase B	NM_213019	36784	446	62	961	CTGGGTCCAGATCAAACTATCATTCCACAAGGTCACGCCAACCTGCTTTTGTAAACGAAT
1,474	6,09E-05	A_15_P102875	rds4	PRPH2	peripherin 2	NM_131567	2060	27	78	2259	ACATTTGACTTTGCAGTAATATACGTTTTTGTGGAATTCTTGGATCATGTAGTCAACTCC
2,419	1,39E-08	A_15_P196416	zgc:92891	PRDX2	peroxiredoxin 2	NM_001002468	2946	40	25	871	ATATTTGGTACTCTGTGAACATAGCTGGTTTTAAATTCTCTCAAGTTGTTGGCTTTCTGG
1,609	1,46E-05	A_15_P150206	prdx3	PRDX3	peroxiredoxin 3	NM_001013460	42159	511	36	943	GATAGGGAACGGGATCTGTTGTGATTTATGTATTTGTTAAGCTGTTCAAATAAAGTCAGA
2,144	5,33E-08	A_15_P398265	LOC570477	PRDX4	peroxiredoxin 4	NM_001089425	14986	184	53	727	AGTGATACGATTATCCCCGACCCTGCAGGCAAACTCAAGTACTTTGATAAACTCAACTGA
1,740	2,05E-05	A_15_P176306	LOC570477	PRDX4	peroxiredoxin 4	NM_001089425	26093	317	38	815	TTTGTTTTGTTCTGGTTTCTGCGTTCAAAAGTGCAGAATGAATAAAAGGGGAGTTTTGAT
-1,546	0,00053934	A_15_P206991	zgc:112318	PRDX5	peroxiredoxin 5	NM_001024406	24942	303	42	713	CCGCACAAATCTTTTCATTCTGACTGTTACGTATTGTAACCTATAGTATTTACCCAAGCA
-1,623	5,23E-06	A_15_P379260	zgc:112318	PRDX5	peroxiredoxin 5	NM_001024406	1145	17	12	484	ACTTTCTGGCTGAGGTCTAAAGAGCTACATCCAGCTTACAACCAATTCATCAGTCACTCT
-1,445	6,30E-05	A_15_P118232	zgc:91986	PHF20	PHD finger protein 20	NM_001004114	3659	47	47	531	TGATGGAAGGAGCAATCAGCAAGCTCGAAAGCGTGCCGATCAGAACGAAAAAGAATTGAA
1,940	7,32E-07	A_15_P163956	zgc:113291	PBLD	phenazine biosynthesis like protein domain containing	NM_001017897	2578	36	7	990	CTTCATATTATCAGAGCTGTTATGTGATTCCATACAGTAAGACCACAAATATTGCAATGC
1,939	2,37E-07	A_15_P103458	zgc:101129	PBLD	phenazine biosynthesis like protein domain containing	NM_001003759	27993	339	74	900	ACAAATCATTCTTCAGGGAACTCTTAAAGTCTAGTCAAGTCGTGCAAATCATTGAATCTG
-1,778	1,49E-06	A_15_P101511	pah	PAH	phenylalanine hydroxylase	NM_200551	39335	478	8	2031	CGACTGCTTACGCAACTCAACATACTGCATATTTTGTTGTAGATGCAAAACTGAAATGTC
1,865	8,41E-07	A_15_P113559	zgc:77867	PCK2	phosphoenolpyruvate carboxykinase 2, mitochondrial	NM_213192	985	16	9	2939	GTTGAGCTAAGGTTGAATGATGGACCAAAGAGGACCGCCCAGTCTTATTCAGTGAATGTT
1,780	2,29E-06	A_15_P207816	zgc:110298	PFKL	phosphofructokinase, liver type	NM_001017596	10243	127	10	1613	AAACACCCCCACAGAGGTCAGACACACTACTTAAACATTCATCAGTATTCATTCAAAAAA
2,304	1,37E-07	A_15_P108648	MGC162168	PFKM	phosphofructokinase, muscle	NM_001089417	16451	201	34	822	TGGCAATCGTTTGAATGTCATCATTGTGGCCGAAGGAGCTTTGGATCGACACGGCAAACC
1,451	7,25E-05	A_15_P117637	pfkm	PFKM	phosphofructokinase, muscle	NM_001004575	10676	132	58	2444	GTGACTACACAGAGCAAACACTTCAAGAGAACGATCAGGAATGTAGCTAGTTCTGTTGTG
3,504	3,05E-10	A_15_P199396	LOC561416	PFKP	phosphofructokinase, platelet	ENSDART00000033381	17572	216	13	2031	AAGATCGCAGCTAAAGCCATGCAATGGATCTCCAAGAAGCTCAAAGAGTTTTACAGAGAC
3,896	1,51E-10	A_15_P112909	pgm1	PGM1	phosphoglucomutase 1	NM_201025	27357	334	4	1890	GATTGTGTCACGTTTACGGTGCTCCACATGTACAAACAAAGATCTATATCTATTATGAAT
1,405	0,00016419	A_15_P103207	pgm2	PGM2	phosphoglucomutase 2	NM_212886	894	14	39	3298	ATGTAAAGCTGACCAGTCAGTCCACCATCTTTTTCATGTAAACAGATTTAATATGTTTCG
3,315	4,82E-10	A_15_P116144	pgk1	PGK1	phosphoglycerate kinase 1	NM_213387	37441	454	61	1774	CGACCTGCAGCTTGTGAGATAGATGTTTCGCACTGGAATTGTTATGAGGGGCTAATGTTA
5,252	1,37E-11	A_15_P105204	pgam1	PGAM1	phosphoglycerate mutase 1	NM_198804	25154	306	67	1086	TTTGAAGAATGTGTTTGGTCGTGTTTTCTCAAGCACACAGATTTTCACATTAAACCATTG
1,426	0,000287915	A_15_P109893	zgc:66482	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	NM_198374	23376	285	4	1974	CCCATTGTTCGTTGGATTGTACAACTGCTTAAGGTTAAAGAAATGATTATTTTTTGGCAG
1,587	1,76E-05	A_15_P135186	pla1a	PLA1A	phospholipase A1 member A	NM_207056	17229	212	6	1550	AAGAACATTCATATTGGACGTGGAGTTCCATGGTCACATGACTTTGTACAGGTGTGCTAA
-1,648	5,89E-06	A_15_P101145	plaa	PLAA	phospholipase A2 activating protein	NM_212690	24614	299	45	2544	AATTTTCACATTTTGATGCTGAATGGATCTGGATGAATGCATGATGTGAATAAACACTGC
-1,444	6,26E-05	A_15_P106978	lypla3	PLA2G15	phospholipase A2 group XV	BC066589	7612	95	26	2171	AACAATGCAGAGTTAACTGGCTATCTGTTACTCACAAAAACAGATGTTGCATACATGCCC
-1,455	5,74E-05	A_15_P140271	zgc:92249	PLA2G16	phospholipase A2 group XVI	NM_001002623	29340	356	80	1335	CGGTTGGTTTGACCAAATTAATCTTCAAGTAAACTGCCATGTTTCTATTTTTTGAGCCATT
1,417	0,000190356	A_15_P195691	zgc:158396	PLCD3	phospholipase C delta 3	NM_001099423	8570	107	4	6568	AGATGTAGTGCCTTTTAAAAGCATGCCTACGTTTTATAAATGTGCAAAGCTAATTGTACC
-1,862	4,90E-07	A_15_P110076	zgc:100903	PLTP	phospholipid transfer protein	NM_001003519	8534	106	70	1726	CTTAGGGCAGAAAAACTGATTGATAATGCTCGAATTTGCTTTAATGCTGATAAGCAGCGC
1,499	2,77E-05	A_15_P209941	ENSDART00000076362	PHKG2	phosphorylase kinase catalytic subunit gamma 2	ENSDART00000076362	11116	137	28	2250	GCTACTGCATGCAGTTTAGAATGAATGATATGTAATCGCTGATTTATAAATCTCTTCCAC
1,496	2,95E-05	A_15_P102397	zgc:55863	PHKG2	phosphorylase kinase catalytic subunit gamma 2	NM_200962	17705	215	80	2250	GCTTCTGCATGCAGTTTAGAATGAATGATATGTAATCGCTGATTTATAAATCTCTTCCAC
1,578	9,17E-05	A_15_P106890	psat1	PSAT1	phosphoserine aminotransferase 1	NM_199819	15224	187	5	1563	TTTCATCTGGAGTAGTAACGTAGGTAAAATAACCATCATGTGGATATGTAAGAGCATGTT
1,485	0,000258012	A_15_P211436	psat1	PSAT1	phosphoserine aminotransferase 1	NM_200895	2344	32	57	1545	CTGGAGTAGTAACGTAGGTAAAATAACCATCATGTGGATATGTAAGAGCATATTTGCAAT
2,871	1,78E-09	A_15_P111360	pim1	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	NM_131539	40560	491	41	2323	AAGCTTTCCTGTAAATACTTGTGTATTGAATAATGTGATGTGGCCGCTGTCACGTGATGT
-1,864	4,26E-07	A_15_P133631	pinx1	PINX1	PIN2/TERF1 interacting, telomerase inhibitor 1	NM_001013265	32486	393	80	916	AGGCAGATGAACAGCAGACTGTAGAAATCGAGAATCAGGACTCTAAAGTTTCAGAGAAAA
-1,959	1,94E-07	A_15_P119340	pitrm1	PITRM1	pitrilysin metallopeptidase 1	NM_213487	29506	357	82	3323	TGAACAGAAGTATTGAAAATAGTGCTGAGCTCACTTGTTTATTTCAGTAAAGCAGCGTTT
-1,579	9,14E-06	A_15_P143941	ENSDART00000077352	PLAC8L1	PLAC8 like 1	ENSDART00000077352	24851	302	80	300	TCCTGGTGCCAGATTTCTCGAGAAATGAACATCCGAGAGCAAAGTTTGACATTTGTCACT
-1,426	0,000140289	A_15_P149796	zgc:114201	PLAC8	placenta specific 8	NM_001033097	13813	169	45	727	GGGGTCGACAGTAGAATGAACCACCCTCCACTCAATTTAACTAATAAATATTTCATGAAT
-1,828	5,81E-07	A_15_P157571	zgc:114201	PLAC8	placenta specific 8	NM_001033097	14504	177	58	301	GCCTGTCAGCTTAAGAGAGACATCGACATTAGAAAGAGTAACGGCACGCTGAAATTATGA
2,094	7,92E-08	A_15_P174126	zgc:136228	PLVAP	plasmalemma vesicle associated protein	NM_001030244	4267	56	17	1757	CGTTTTATGGCACCAGTCAATATTTAATATCGATGGAATCCGATTCTTTACTGTGATGTA
1,624	7,00E-05	A_15_P194411	zgc:110385	PLGRKT	plasminogen receptor with a C-terminal lysine	NM_001033098	11263	139	18	1109	CATCCGCATGTAAAGCGTCTCCTGATGAAGTGATGAGTAAATCGTCTGTGTGTCCTCAAA
1,446	6,30E-05	A_15_P188041	LOC569386	PECAM1	platelet and endothelial cell adhesion molecule 1	ENSDART00000084729	19678	239	66	2288	CTCATGCTGAACATTTTTCATATTGGATTGTTTGCTGTTTTGTGATGATTGTGTGTCTAG
1,601	1,08E-05	A_15_P105837	pdgfrl	PDGFRL	platelet derived growth factor receptor like	NM_200314	43075	523	50	724	AACCCCAAAATCAAAGTCTCGCTACACAGAGAAGTTCCTGCAGTGGAAATTGCTGTGGAT
1,766	1,11E-06	A_15_P120341	plxnd1	PLXND1	plexin D1	NM_205697	5549	69	77	2666	CTGTAGATAATCTGCTCAAATCTTTAATCTGGTTCTGGAGAAAGGGAAATTCATCAATAA
1,623	4,73E-05	A_15_P107698	wdr51a	POC1A	POC1 centriolar protein A	NM_213049	19729	241	8	1658	CTTTTATAATGTACACTGTGAGTATTCTTCACATAAATGTGGTTAAATCCACCCAGAAAT
1,900	3,64E-07	A_15_P119355	plk1	PLK1	polo like kinase 1	NM_001003890	14051	172	81	2075	ACTGACGTCATAAATTGTATAGCTATGAGTTCACCATCGGCTCTCACTTGAGTCTGAGGG
2,546	2,55E-08	A_15_P113198	pabpc1b	PABPC1	poly(A) binding protein cytoplasmic 1	NM_200882	31538	384	19	2685	GGGAGGTGAGAACTGGCAGAACCAGCAATGTGAAGTTATTTTAAATCGAAAATATGCTTG
2,263	3,20E-07	A_15_P164401	pabpc1b	PABPC1	poly(A) binding protein cytoplasmic 1	NM_200882	20005	243	63	2337	ACAAACTCTACTGGTGTGCCAAGCGTTTAAGCCAAGGGTTTGCAACCTTGAATCTTCACT
1,593	9,19E-06	A_15_P105323	phc2	PHC2	polyhomeotic homolog 2	NM_152958	40275	487	65	3343	TTATCCCAACCTTCAATGTGTGCACTCACATTTGGAAAGCTAGTGCAGCTCGTGTGTCTA
-1,476	5,01E-05	A_15_P166586	LOC568267	KCTD17	potassium channel tetramerization domain containing 17	ENSDART00000078476	30647	371	71	306	ATTAAATTAATCAAAGAGAGGATTCTTGAACGCGACTCAAAGGCCACGCAGCAGGTACCG
-1,439	8,23E-05	A_15_P173451	si:ch211-244h7.6	KCNJ1	potassium voltage-gated channel subfamily J member 1	NM_001045169	29058	353	23	1730	CGGTGCTTTTGTGAATCACTCTGGGATGTTGTTTCTTATTACAATTGTACATTTCTTGTA
-1,403	0,00014205	A_15_P275731	DKEY-79C1.2	PJA2	praja ring finger ubiquitin ligase 2	NM_001105116	27501	333	78	587	TGTTGACTCGCTTGACGATTCGCGCTCTAGTTTATTTAGAAAAAATCGTATGAAACAAAT
2,556	6,35E-09	A_15_P100971	prelid1	PRELID1	PRELI domain containing 1	NM_200366	8724	107	82	1265	AAAGCAGCTGCCAGAAAGGATTGCAGTGGATGGACGGCAATGTCCAATTACAAGTGTTAA
-1,941	4,55E-07	A_15_P174486	c20orf45	PRELID3B	PRELI domain containing 3B	NM_199734	11539	142	74	1572	CCAGCAGCAGTGAACACAGCCAAAGCGGTTTACACATGTGGAAATAAACTAACGTTCATA
-2,051	1,24E-07	A_15_P366070	c20orf45	PRELID3B	PRELI domain containing 3B	NM_199734	9055	111	80	1472	ATTAAGTTATTTGCAGGAATGTACCGTGGTGGAGAGATCTGAAGGGAAAGTCCAGTTTGT
2,344	1,70E-08	A_15_P196446	silvb	PMEL	premelanosome protein	NM_001033918	39810	482	82	1703	TGTCGTATCAGCAATGGCTGCTGTAGCTTTTGCGTATAAGCGTCTTAAAGGGTACCAAAG
2,041	1,57E-07	A_15_P154091	zgc:136622	PMEL	premelanosome protein	NM_001045330	21658	263	57	2331	TTGCTTTTACATACAAGCGGTTTAAGGAGTACCATCCACTGAGAGAAGAAAGCGAGGGCA
1,753	2,08E-06	A_15_P103899	prim1	PRIM1	primase (DNA) subunit 1	NM_201448	30142	366	67	1433	CTTCTGAAGAGATGGACACTTTACTTCTCTGAACCATATCTTGAGGGATCAAATGATGTA
1,633	7,94E-06	A_15_P209721	prim1	PRIM1	primase (DNA) subunit 1	NM_201448	37090	450	50	1334	ATGGCTCGATCTCGCAAAGGAGAGATGCTGAAGAAGAGTGATCTTCAGAAGGATTTTTAA
1,632	9,36E-06	A_15_P139751	prim1	PRIM1	primase (DNA) subunit 1	NM_201448	3862	49	65	1331	TCAATGGCTCGATCTCGCAAAGGAGAGATGCTGAAGAAGAGTGATCTTCAGAAGGACTTT
1,560	1,14E-05	A_15_P209716	prim1	PRIM1	primase (DNA) subunit 1	NM_201448	1328	19	27	1449	CACTTTACTTCTCTGAACCATATCTTGAGGGATCAAATGATGTATGAAACAATGCCATTT
1,474	5,97E-05	A_15_P117621	zgc:110727	PRIM2	primase (DNA) subunit 2	NM_214782	8036	100	73	1909	GTAGAACCTAAGGAAAATACAGGGCTCTTACTTGTATTCACTGTTTAAGACACAAACTGT
1,573	9,92E-06	A_15_P192906	si:ch211-237l4.5	PCOLCE	procollagen C-endopeptidase enhancer	NM_001030181	1466	21	17	1274	TCACAATCACCCAAGCTGGAGAAACCATGTCTGTCAAACTCATGATGCCCTGCAAGAAAT
1,589	8,60E-06	A_15_P148461	pcolce2b	PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_200460	24779	302	43	1657	GCTGGATGAGTTACTCCTTGTCTATAAAATATTTTGATAGAAAGGGATTCCTAGTTGTGA

7,869	1,31E-12	A_15_P120443	zgc:152876	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	NM_001077742	4533	58	71	2616	AATCGGTGCTGACGTTTGAAAACAGTGTGTGGTTTGTTTTCTAACTGCTTGATGTTGCTT
1,465	0,000297537	A_15_P121051	pgrmc2	PGRMC2	progesterone receptor membrane component 2	NM_213104	34452	418	63	2129	GGAACTACAAGTTTGGACAAATATTTTGTCTTTGCTGGGGGAGGGGGTGAGGCGAAATTT
1,558	5,08E-05	A_15_P179436	zgc:171925	PROK1	prokineticin 1	NM_001105698	20884	256	2	807	AGTGTCATATTTCTGGTTGAATTCCATCTTCAATATGCTGTGCATTTGTTGAAGGCTTAG
-1,410	0,000130076	A_15_P100570	prlra	PRLR	prolactin receptor	ENSDART00000039549	37617	456	65	1638	ACGTCTCATCAGGTTGTCAATGATTACAGCCAGGACTTTGAAAGCTATGCTGATCAATGC
1,852	5,63E-07	A_15_P105183	pcna	PCNA	proliferating cell nuclear antigen	ENSDART00000076304	21953	267	38	885	CATGTCCGCAGATATTCCACTAGTGGTTGAGTACAAAATTGCAGACATGGGACACGTCAA
1,774	5,13E-06	A_15_P322966	pcna	PCNA	proliferating cell nuclear antigen	NM_131404	36391	441	34	627	ATTGAGATGAATGAGCCAGTGCAGCTCATTTTTGCATTGAACTACCTGAACTTCTTCACC
1,477	4,80E-05	A_15_P104409	pcna	PCNA	proliferating cell nuclear antigen	NM_131404	13479	165	44	720	AGAATGTCCGCACATATTCCACTAGTGGTTGAGGACAAAATTGCAGACCTTGAACACGTA
-1,572	2,26E-05	A_15_P192766	pa2g4b	PA2G4	proliferation-associated 2G4	NM_212641	25519	309	85	1362	TTCAATACCTCCTCTTTTAGTTGTCAAAGACACCACCACGTTTGCTTGTCTGTGAGCGAG
-1,582	1,91E-05	A_15_P209741	pa2g4b	PA2G4	proliferation-associated 2G4	NM_212641	9029	111	67	1880	CATTGTTTATCCACTAAACTGACTGACCAAATTATCCTGCCATTTTATAAGCGTTCATCT
-1,981	2,45E-07	A_15_P495107	pa2g4b	PA2G4	proliferation-associated 2G4	NM_212641	33643	407	75	638	TTAAAGCAGCATGTCATTGATGGAGAGAAGACTATCATTCAGAACCCCACCGACCAGCAA
1,523	2,45E-05	A_15_P101935	BC090182	PRRG2	proline rich and Gla domain 2	BC090182	32906	400	39	948	TTCGAGATGGTGGTCATGCGCCACAGACAAATGTAGTTTCAGTCACTGTTTGGCTAACTT
1,489	3,24E-05	A_15_P204826	LOC565522	PNRC2	proline rich nuclear receptor coactivator 2	ENSDART00000075326	6216	78	76	2447	GAATGTAAAGTCACGCTATGGACGTGGCTTGTTTTCAAATGCTGAAGAAAAAATATTTTG
1,411	0,000119779	A_15_P582207	LOC565522	PNRC2	proline rich nuclear receptor coactivator 2	ENSDART00000075326	13524	166	67	1784	TTGCTTGACCAGATTTGGTTACAAGTGCCATAAATCATTGCGTAAGGCATTAGCGTATAT
7,871	2,07E-12	A_15_P120689	p4ha1	P4HA1	prolyl 4-hydroxylase subunit alpha 1	NM_214691	10897	135	1	2188	CTTTAATCCTGAGGCAAATGCAACATTTGTCTTTTTCCTTTTATGTGTGTGAATGGAAAC
5,721	1,26E-11	A_15_P116212	p4ha2	P4HA2	prolyl 4-hydroxylase subunit alpha 2	NM_001007285	42616	518	36	1818	ATTCTCCAGTCAGGTTCACCCGGGGAATCGTGTCATTGTTTATGTAATGCTTAAATTATT
4,711	9,03E-11	A_15_P140051	p4ha2	P4HA2	prolyl 4-hydroxylase subunit alpha 2	NM_001007285	33854	412	14	1385	AACTACTACAGGTTGCGAACTACGGCGTCGGGGGTCAATATGAACCACATTTTGATTTCT
2,543	2,15E-08	A_15_P132671	p4ha2	P4HA2	prolyl 4-hydroxylase subunit alpha 2	NM_001007285	8335	103	54	747	AACACCGAAAGCAGATGTGCTGGATTATCTCAGTTACTCTGTCTATCAGATGGGGGATCT
-1,497	0,000123502	A_15_P438055	psap	PSAP	prosaposin	NM_131883	7096	90	16	2182	TAATGGTTGTCGATTCTGTCATTGTGCTTCTTTAATGATTTGGAGGAGGGGGAAGGTGATG
-1,633	3,20E-05	A_15_P118275	psap	PSAP	prosaposin	NM_131883	25575	312	28	2288	GATCGCTCTCACTTCCTAAATGTCAGATTTTCTTTCCACTGTTCAGACTGAGGCTGTTTT
1,705	4,64E-06	A_15_P118515	ptgds	PTGDS	prostaglandin D2 synthase	NM_213634	106	2	63	369	GTTGACGCCAAGTTTGACGAGTACGCTATTTTTCACACCATCAAGACCAAAGGAGGAGTA
1,417	0,000171379	A_15_P281316	zgc:153154	PTGDS	prostaglandin D2 synthase	NM_001045413	13149	161	46	1171	ACTTCTTTTTTCTCTTTGTTGGTTTTGTTTGCTGCCGATGGATTAAATAGGTTGGCAAAA
1,495	3,98E-05	A_15_P365850	ptgs2b	PTGS2	prostaglandin-endoperoxide synthase 2	NM_001025504	8170	102	55	1799	CAGTCAGATCGAAATGTCAACCCAACTGTTTTACTAAAAGAAAGGACATCTGAGCTCTGA
-2,368	7,69E-08	A_15_P117814	try	PRSS1	protease, serine 1	NM_131708	13955	171	33	671	CCCAGAGGAACAAGCCCGGTGTTTACGCCAAGGTCTGCACTTCACCACCTGGATCAGAAA
-2,991	2,31E-09	A_15_P110812	zgc:66382	PRSS1	protease, serine 1	NM_199605	6505	82	54	773	CAGCCTCCAAATATGCAATACATCCATTTTCTTTGTTTTGGAGATAACACTTGTGAAAAT
-4,617	3,33E-11	A_15_P100839	zgc:92590	PRSS1	protease, serine 1	NM_001007054	21491	261	57	532	TGTTCTGACAAGAGCCCAGTGTGAGGGTGCGTATGGATGGCAAATCACTAAAAACATGTT
1,544	1,46E-05	A_15_P187676	ENSDART00000029262	PRSS27	protease, serine 27	ENSDART00000029262	12267	152	21	789	AGCGAAAGTCAAACGCCTCTGGTTACAGTCCTGTCTTTAGCATTAGTGCTCATTTGGAGA
-1,549	1,30E-05	A_15_P116386	psmc1a	PSMC1	proteasome 26S subunit, ATPase 1	NM_200033	32232	392	35	1662	ACTTACTCTTGCCGTAACCCTCTGTTGTTCATTTGTGCTCAATGCCAATTAAATATGTTT
-2,820	3,28E-09	A_15_P100455	psmc1b	PSMC1	proteasome 26S subunit, ATPase 1	NM_001002091	31295	379	65	1390	TCGCTCCTCCTATTAACACTTCTATGTCAAAGCTACGCATGTTCTTGTCTGCCAGTTTGT
-1,727	1,68E-06	A_15_P106517	psmc2	PSMC2	proteasome 26S subunit, ATPase 2	NM_200966	9011	111	58	1377	TGTTTGTTTTCTGCCTGATATAATTCAAAGATTCCTGTCGTTCTGTGATGTCACTTATCC
-1,669	5,66E-06	A_15_P102231	psmc3	PSMC3	proteasome 26S subunit, ATPase 3	NM_001002064	686	12	8	1496	GTGTTCTGATGGAGACAGATCAGCCAAATTAGACTGGACTGCCTCACAGTGAAGACTTAT
-1,855	8,48E-07	A_15_P110002	psmc4	PSMC4	proteasome 26S subunit, ATPase 4	NM_199750	36135	437	74	1445	TGGTCAAAAAACAAACCAACTTGTACATCTGGTGAGCATTTGATGTATTCAGTTTAACAG
-1,554	1,51E-05	A_15_P100559	zgc:92464	PSMC5	proteasome 26S subunit, ATPase 5	NM_001003740	6808	85	39	1179	GCAGAAAGACAGCGAGAAAAACATGTCCATCAAGAAACTCTGGAAGTAAACGTTACACTC
-1,702	3,49E-06	A_15_P106273	psmc6	PSMC6	proteasome 26S subunit, ATPase 6	NM_001003832	15457	190	37	1453	CGGCTCTTTAGCATTCTGTGTGATCAGTTGTATAAACTGTGTTTGCCTGGCCTGCTTCTT
-1,795	0,000270771	A_15_P225421	psmd1	PSMD1	proteasome 26S subunit, non-ATPase 1	NM_201184	33550	408	28	631	GCAGAACAAAAAGTTTCGCAATGAAGTTCTGCGCGTTTTGGTCAAGCTGTACATGAACCT
-2,139	2,23E-07	A_15_P110826	psmd1	PSMD1	proteasome 26S subunit, non-ATPase 1	NM_201184	31514	384	6	3056	TTTTTTACGTTGTTTCCTCCACTTGGCCACTTAAGGCATGTTTTACATGATGCATTTCGG
-1,463	5,60E-05	A_15_P187731	LOC561267	PSMD11	proteasome 26S subunit, non-ATPase 11	ENSDART00000084448	27155	330	70	1777	TTTTATTGTCGAGCGGAAAGGTTTGAATAAGCTGCTGTCATCAGGATGGGCTTGTGAGCT
-1,477	6,14E-05	A_15_P107937	psmd11b	PSMD11	proteasome 26S subunit, non-ATPase 11	NM_199592	40654	494	3	2559	GTGTGGGCAGATTTAAATATGAGGAAAAACTGCTTTGTTTTATTTTTGTATGCGTTGGCC
-1,737	1,90E-06	A_15_P106167	psmd13	PSMD13	proteasome 26S subunit, non-ATPase 13	NM_200948	18841	230	62	1152	TAAACAAACACAGCTGACCTTTCAAGAGTCCCTCACTTCTTCTCTGTGTATCTGCATTCT
-1,935	2,74E-07	A_15_P113880	zgc:162272	PSMD14	proteasome 26S subunit, non-ATPase 14	NM_001083573	24608	299	42	980	GTGTTCCATTGATTTCCCCCATCCATCTCTGTTTGTGCATACATGTTCATATTCTACAAC
-2,022	1,25E-07	A_15_P116537	psmd2	PSMD2	proteasome 26S subunit, non-ATPase 2	NM_200546	4196	53	66	2961	GCGAGCGTGTGAGTTTATGCTGATTTAAACATGTTTTGCTTGTTTTTGTTACTTGTTACT
-2,083	8,78E-08	A_15_P194186	psmd3	PSMD3	proteasome 26S subunit, non-ATPase 3	NM_200572	5122	66	30	1195	TACACACTGATCATCCGACTGAGACACAACGTCATTAAAACTGGCGTGAGGATGATCAGT
-1,768	1,03E-06	A_15_P100140	psmd6	PSMD6	proteasome 26S subunit, non-ATPase 6	NM_200291	34451	417	63	1260	CAGCACCAGGCGTTTGACCAACATCCACGTCTTTTCTTGTGAGCAACTTGACTTTTGTTT
-1,545	1,38E-05	A_15_P114365	zgc:86762	PSMD8	proteasome 26S subunit, non-ATPase 8	NM_001002131	38599	468	57	1381	ATCCTGTAATGGGATAAAAATCCCCCAAATTGTCAAAAGGAAGTGACAGTTCATAGTAAA
-1,611	5,80E-06	A_15_P108087	zgc:86762	PSMD8	proteasome 26S subunit, non-ATPase 8	ENSDART00000005431	27523	335	4	1255	AAACTTCACTGCTTATTCAATGTAATCCCAGGAGTATTCATTGAATTATTGTACTCTCCG
-1,683	1,01E-05	A_15_P226546	zgc:86762	PSMD8	proteasome 26S subunit, non-ATPase 8	NM_001002131	7241	91	6	617	AGATTGCAGGTTGTATCGAGAAAGCATATGAACAGATTCAATTCAATGAAGCCACGCGGG
-1,426	0,000130589	A_15_P111266	zgc:92775	POMP	proteasome maturation protein	NM_001003424	9808	122	43	488	GATCCTGTAGGTTGTGTTGTGTGCATTGTTTAACCGGTTTCTAATAAAATGTCAAATGTG
-1,735	1,71E-06	A_15_P102032	zgc:92726	PSMA1	proteasome subunit alpha 1	NM_001003427	40179	487	17	916	AGTGCGCTGTCAAACATGTCTTCTGTCTGTGAGGGGAAGAGTAATAAAGCCGTTGTTTGT
-1,515	2,24E-05	A_15_P112562	si:rp71-45k5.4	PSMA2	proteasome subunit alpha 2	ENSDART00000051750	40382	489	35	708	CTACAGCACTACAACTGCTTACACAGTTTCGCATTTCGGTTTGGTTGTTTGTTTAAATTC
-1,972	2,37E-07	A_15_P111074	zgc:114044	PSMA3	proteasome subunit alpha 3	NM_001030187	39788	481	71	585	GTTGCGCGATTGGAAAAGCCAAACAAGCTGCCAAGACAGAAATCGAGAAACTACAGATGA
-1,885	2,45E-06	A_15_P171191	psma4	PSMA4	proteasome subunit alpha 4	NM_214697	17613	215	34	909	CGCTGGGATTCGTAAAAAAGTTCATATTGCTCTGTCTGTCCATCTGTCGATTTCTTTATT
-2,144	1,98E-07	A_15_P153506	psma5	PSMA5	proteasome subunit alpha 5	NM_205708	9671	120	55	965	ATTTCTATAGTTCTGTACAAGCACAGGACAGCAGATCTTGTCATTGAATTAAATGGGGGG
-1,511	2,51E-05	A_15_P105460	zgc:92716	PSMA6	proteasome subunit alpha 6	NM_001002589	35739	434	43	243	ACACAGAAAAAAGTCCCAGACAAGTTGCTGGATTCATCAACCGTCACGCACTTATTCAGA
-2,014	1,38E-07	A_15_P143266	psma6a	PSMA6	proteasome subunit alpha 6	NM_153655	398	6	77	538	AGAAGAAGATCAAGAAGAAACTGGACTGGACCTTTGACCAAACAGTGGAGACTGCCATCA
-1,921	5,20E-06	A_15_P109743	zgc:77139	PSMA8	proteasome subunit alpha 8	NM_213166	21004	256	63	1131	TCGACCACTGCTCAGAATTCTGGGAGAATGTGCTCTGACTGATGTTTCCTAATAAACTGT
-1,731	1,51E-06	A_15_P110217	psmb1	PSMB1	proteasome subunit beta 1	NM_001003889	29806	362	65	814	TTCATTCTGCTCTCCTTTTTATATTCTGTCTCGAGAATAAATACCATACTGGTGTCAACA
-1,402	0,0001294	A_15_P106758	psmb2	PSMB2	proteasome subunit beta 2	NM_001002609	6492	81	48	666	ATGAGCCGCTGCTGTTTTTCACTCTCTTTTGTACTAAAATAACCCTCTGTGCTCTAATAA
-1,750	1,41E-06	A_15_P104914	LOC573095	PSMB3	proteasome subunit beta 3	ENSDART00000022499	941	13	63	361	AAAGAAGGTCGTCAGATCAAGCCAAGGACCTTCATGAGCATGGTGTCCAATCTTCTGTAT
-2,233	3,13E-08	A_15_P118425	zgc:110330	PSMB4	proteasome subunit beta 4	NM_001017801	18727	230	4	821	GCTCTTAGCACCTCCAGATCACTATTGTGTTGTCAAGAATACAGTTAGACTTTTCTCTCT
-2,342	9,66E-08	A_15_P511077	zgc:110330	PSMB4	proteasome subunit beta 4	ENSDART00000076928	3105	41	21	763	GCTCATTTGGTCAGTGGTTTTGAATGAGTCCTGTTTGCCACATCATCATCTTCAGACATG
-1,658	3,94E-06	A_15_P210521	psmb5	PSMB5	proteasome subunit beta 5	ENSDART00000056554	23991	291	63	761	AGAGTCTCACAGGAAGACGTGCTTCAGTTGCACCAAAAATACCAGATTCATCAGAAAAAA
-1,620	4,15E-05	A_15_P107267	psmb6	PSMB6	proteasome subunit beta 6	NM_131152	32702	398	20	505	GAATGAGCAAAGAAGAGTGTCTGAAATTCACTGCAGGAGCTCTGACTCTGCCCATGGAGC
-2,320	2,05E-08	A_15_P193011	psmb7	PSMB7	proteasome subunit beta 7	NM_131675	23245	284	22	885	TGTCCCACAAGTCTTATGTGGAGGTTTACTTTTTCACTATGTACAATAAAAGAAGTTGCA
-2,114	6,99E-08	A_15_P100991	zgc:55398	PDIA2	protein disulfide isomerase family A member 2	NM_201048	2581	35	9	1737	TATGCAACATGAGCAAGATTGATGTCATGTTCTCTGCACTAGACAATTTGTATAAACTAC
1,594	3,69E-05	A_15_P108276	pdia4	PDIA4	protein disulfide isomerase family A member 4	NM_199779	35708	434	25	2209	GTACGTTCTTTTGTTTCTGGGATCAAAACATTGAGTATTTTCATTCCAAACTAAGCACTG
1,509	3,29E-05	A_15_P152461	pdia4	PDIA4	protein disulfide isomerase family A member 4	NM_199779	10233	127	5	2036	GAGTTCAGCAAATTTGTGGAAAAACACGCAACGAAATTATCACACAAAAAAGATGAGCTC
1,537	1,73E-05	A_15_P108473	zgc:91999	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	NM_001003498	16625	204	36	1572	ATGACATTCAGACATTTTCACATATCAAAATCTTTTTGGTGGCAAACAAATTCAGTGCCC
1,455	8,29E-05	A_15_P195221	zgc:91999	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	NM_001003498	30008	364	82	995	AGGAAAGAAACCAAAAGCCCACAAAGGAACCGATGACAAAGCTGTGATGATTGGAGGTGT
1,427	0,000150129	A_15_P209196	ENSDART00000067806	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	ENSDART00000067806	27859	340	4	722	AAAGAAACCAAAAGCCCACAAAGGAACCGAGGTTAAAGATGTGATGATTGGAGGTGTGCG
4,807	6,91E-11	A_15_P192631	MGC162126	PPP1R15A	protein phosphatase 1 regulatory subunit 15A	NM_001082921	17186	209	70	1377	AACGCATTGTGTTGTGTTTGATTTTATAAATGCATTTTTGGAGAAGCTCATCGTTCTTGG
-1,561	1,22E-05	A_15_P186326	zgc:123237	PPP1R27	protein phosphatase 1 regulatory subunit 27	ENSDART00000054297	8982	112	43	1491	TCTGATGGTTCTTTTGAAAATATCATGCTTCCAGCAGGTTAGTCTTTGATGCTTTCTTTG
-1,678	4,09E-06	A_15_P174831	zgc:123237	PPP1R27	protein phosphatase 1 regulatory subunit 27	NM_001037104	42452	515	31	811	CCGATGACAGCAATTAAGACAGGATTTAAACTTGCTTCTACAATGAACTTTTCTCTTTTG
1,422	0,000111864	A_15_P116827	ppp1r3b	PPP1R3B	protein phosphatase 1 regulatory subunit 3B	NM_212709	39490	480	4	1773	ACAGAACCACTTGAAAATGTTGTAAAAAAGTTCTCTCAGCGGTATTCGGTATGTTCAAAT
3,512	1,84E-09	A_15_P552892	LOC799144	PPP1R3D	protein phosphatase 1 regulatory subunit 3D	NM_001110412	15107	186	30	634	GGGGAGGATCCGTTCATTCCAGAGCATGTCTTATTTCGACTGCTAATGAATGCAGAGTTA
1,497	2,76E-05	A_15_P368990	DKEY-266M15.3	PPP6R2	protein phosphatase 6 regulatory subunit 2	XM_693835	25290	307	52	1451	GGAGCTCAAGATGGAAGAAGACGTTTAGTATTGATCATTTCAGGCTGATCTGAATATTTT
1,414	0,000104074	A_15_P116470	zgc:56239	PPME1	protein phosphatase methylesterase 1	NM_199937	16264	199	25	1585	GCATTATGTTGTGTTTAAAGTGTTGGTCGTTGCTGATTTCAAGGGAAATAATAAAGTGAG
-1,467	4,38E-05	A_15_P592417	LOC100005132	PPEF2	protein phosphatase with EF-hand domain 2	XM_001344226	25812	314	63	2223	GAGGAAGAAAGCTCTCAGACCGCTGACTCATTACTTCAGTATCTTGATTTGTTGATGTGA
1,732	1,71E-06	A_15_P141891	zgc:153678	PPM1H	protein phosphatase, Mg2+/Mn2+ dependent 1H	NM_001077455	631	9	54	1871	AGGCGGAACCAACAGTGTTTTGTTTGTCCTTTCAGGATATTAATTTATCCTCTGAATGTT
-1,562	3,33E-05	A_15_P180706	zgc:171765	PPM1N	protein phosphatase, Mg2+/Mn2+ dependent 1N (putative)	NM_001103117	22580	276	18	1512	ACTGTATAATTTCTGCTTACTATCAACAAAAAGATGCTCGAAGATCTAGATTAGCCCAGG
1,459	6,58E-05	A_15_P102574	zgc:55664	PRC1	protein regulator of cytokinesis 1	NM_200234	29049	354	18	2202	TTTAAGAAATACTCTAGAGCTCATTCTCAGTGTTAGCTACTTTCTCAAAATCACAGGATG
2,245	3,21E-08	A_15_P105303	ptp4a3	PTP4A3	protein tyrosine phosphatase type IVA, member 3	NM_213181	26851	328	1	1745	TCAACAGAGATGGGATGGTAAAAAATGACCCTGTGTGAATGAATTCTGAGATGAGACTGT

1,469	0,000192832	A_15_P569267	si:dkey-78k11.1	PTPN22	protein tyrosine phosphatase, non-receptor type 22	NM_001099420	42747	520	28	2798	TTTGGAACTCGTTTTGGAAAGCCAAAAGGACCTCGAAATAAGCCAGAAACCTGGGTCTAG
-1,658	5,75E-06	A_15_P168761	zgc:123165	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	NM_001030067	26751	325	35	1996	CACGCTGTCGTAACAACTTGTTTGCAATATATTGTCAGCATATGAAATCTTTGGCTTCAT
-1,644	1,32E-05	A_15_P341645	plp1b	PLP1	proteolipid protein 1	NM_001005586	13470	165	39	1411	AGAGAGCGTGATTGTTGTCAGATGTAGGTTTGCATTGTGTGAGACACAGAGACTCATTAT
-1,854	4,94E-07	A_15_P105275	plp1b	PLP1	proteolipid protein 1	NM_001005586	25977	316	64	1548	TTAGCAGTATGCTGAACCTGATCAATGATGGTGCTCGGTCAAAACAACTAATCATTTTTT
1,599	7,35E-06	A_15_P140001	ppox	PPOX	protoporphyrinogen oxidase	NM_001039979	17787	217	37	1497	GTCAATGATGTTATATTTAGTGGGCGGACGGCAGCTGAGGGTCTTGTCGGAAAAATATGA
1,918	3,22E-07	A_15_P114998	zgc:86785	PSMC3IP	PSMC3 interacting protein	NM_001002124	15636	192	44	684	TGGGATTGAAACAGACGAGGACCATAAAGTGACAATGCCCAACATCTGACGAAAAGGCAA
2,727	5,36E-09	A_15_P209891	zgc:101740	PNP	purine nucleoside phosphorylase	ENSDART00000024204	43348	527	48	1008	GTTCATGCAAAAATGGTGATAATCCCATGATTTGCTCACCTTAAAGGGCTATAAAACCC
2,361	3,48E-08	A_15_P108245	zgc:101740	PNP	purine nucleoside phosphorylase	NM_001004628	34522	420	13	1058	GTTCATGCAAAAATAGTGATAATCCCATGATTTGCTTACCTTTAAAGGGCTACGAAACCC
2,745	2,82E-09	A_15_P105148	LOC794083	PDK2	pyruvate dehydrogenase kinase 2	XM_001332558	25512	309	81	2708	AGATGATCAGAGGCCATATTTAAGGCTGCATTTTCTTTGTGGCCAAATGTAATCAATGGT
1,618	7,29E-05	A_15_P166716	ENSDART00000008010	PDK2	pyruvate dehydrogenase kinase 2	ENSDART00000008010	36315	439	80	1122	TTTAATAAGACTGCTCGACGAAATTATGAAGTCACGCAGGGGGCAGATGACTGGTGTGTA
1,499	2,77E-05	A_15_P182791	si:rp71-57j15.4	PDK4	pyruvate dehydrogenase kinase 4	ENSDART00000077121	24923	304	32	1120	TTCCTGTCTTCAACAAGTCAGCCTTAAGGCACTATCAAACCAGCACAGAAGCGGATGATT
-2,015	1,30E-07	A_15_P194511	pklr	PKLR	pyruvate kinase, liver and RBC	NM_201289	26686	326	2	1711	GCTGATCTCAGTTTGATTTACATTTACAGCATCATGTGTCAGTCCATTTTACAGCAATAA
2,710	5,45E-09	A_15_P194371	pkm2	PKM	pyruvate kinase, muscle	NM_199333	22222	271	7	1449	TCTTTACCGTGGTATTTTCCCCATATACTACAACAGCCCATCTAATGATGTGTGGGCCGA
1,562	2,29E-05	A_15_P151326	zgc:92037	PKM	pyruvate kinase, muscle	NM_001003488	22819	278	55	1787	GTGGAAATTCTTTTCATCCGCATTGTACTGTATGTGTCTACAGTGACATTTTTGTATCCT
-1,484	3,66E-05	A_15_P185001	qdpra	QDPR	quinoid dihydropteridine reductase	NM_001110469	11415	141	11	558	TTCTTCCGGTTACCTTGGATACACCAATGAACAGGAAATTCATGCCTGACGCAGATTTCG
-1,492	2,96E-05	A_15_P104828	zgc:92926	RAB40B	RAB40B, member RAS oncogene family	NM_001002524	7873	97	75	1957	GCTTATGTTTCAGATTTACACTGCAAGCAAACAGAAATTTCTAACATGCTACCATATCAG
-1,431	0,000120271	A_15_P515902	rab6b	RAB6B	RAB6B, member RAS oncogene family	NM_001034179	23545	287	6	2048	CCAATTCTGTTGTAAATACATCAGCTGTCGTTTTCGAACAGGCTTTATTACCAGAAATGC
-1,481	4,29E-05	A_15_P134086	rab6b	RAB6B	RAB6B, member RAS oncogene family	NM_001034179	21168	258	62	2054	CTGTTGTAAATACATCAGCTGTCGTTTTCGAACAGGCTTTATTACCAGAAATGCAAAAAA
1,455	5,73E-05	A_15_P192486	rad54l	RAD54L	RAD54 like (S. cerevisiae)	NM_201144	36116	438	64	1902	ATTGTGGAGAGATTCAACAACCCCTCTAGCCCAGAGTTCATCTTCATGCTGAGCAGTAAA
1,440	0,000170601	A_15_P112610	rhot1a	RHOT1	ras homolog family member T1	NM_212704	10600	131	20	2973	ATGTAACTTTTGAGTGCAGTTTTTCCCTCTTTAAGACCACGGGATTGTTGCGCTTGTGGG
1,422	9,16E-05	A_15_P195831	zgc:65909	RASD1	ras related dexamethasone induced 1	NM_200532	39129	474	72	1138	GAGAACGGGAGTTGACATGTCAGCTGTTTACATTTTTATTTGAGTAAATCAACTTGAATG
-1,665	3,19E-06	A_15_P188556	LOC100006464	RASD1	ras related dexamethasone induced 1	ENSDART00000034898	32077	390	39	1046	GTTTGCCAGAAAGCAACAAAAAACAACTTTATTCATCATTTGAGCATGGATCAGAGTGTT
1,534	1,64E-05	A_15_P103260	rbb4	RBBP4	RB binding protein 4, chromatin remodeling factor	NM_212595	20759	254	22	1903	ACCTGTCAGGTGATGTTCAACGTCTTTTTAATATTGTGACTTTTCAATGTCTTTTTCCTG
1,629	1,05E-05	A_15_P201576	zgc:173949	RBBP6	RB binding protein 6, ubiquitin ligase	NM_001105146	41243	499	53	403	AACAGAAGATTTGTTGGACATCAAGCTGGACGATGGGGTAAACCTTCACCAAGAGGTGAT
1,435	0,000119691	A_15_P118774	zgc:91850	RBBP6	RB binding protein 6, ubiquitin ligase	NM_001003472	33969	412	73	726	CCCTCTAAAGGGGTAACTGGGTTTTCTAAGCTTATGGTTGCTGTGAACTTGAGCTCTTGA
1,736	1,60E-06	A_15_P416545	ENSDART00000092941	RLF	rearranged L-myc fusion	ENSDART00000092941	38602	467	59	3126	ACTTGTACACCTACCTTGAATACAAGGTCTCCTGCCAAAGCAGCACACAGCAAAAATGAG
1,638	5,90E-05	A_15_P217396	ENSDART00000092941	RLF	rearranged L-myc fusion	ENSDART00000092941	15997	196	59	5226	GATTCAAAGGAGAAAGAAGGGATTGAGTTTTCAGAAGAGCCGCTCCCTGACAGAAGTTTG
1,603	6,53E-06	A_15_P202366	ENSDART00000092941	RLF	rearranged L-myc fusion	ENSDART00000092941	6853	85	62	6027	GAGAGGCCAAAGTCCTTTGCCTCCATTTTCGATCTCTTGCCCTCTGAAACTAAAGTATAA
1,460	5,60E-05	A_15_P134201	BC090460	RAMP2	receptor activity modifying protein 2	BC090460	35861	435	20	1752	GTTTTGGACATCTGTGTCAAACACTTTGGAGAACCACTTTTAAGAGTCTGTGAATAATTT
1,855	4,81E-07	A_15_P101141	rgs4	RGS4	regulator of G protein signaling 4	NM_199274	10049	123	80	2472	TTGGCAGATTTAACATATCAAACTACAGATGCTCCGGTTCAAATAAATGGCCAAACATGT
1,650	6,59E-06	A_15_P186581	rgs4	RGS4	regulator of G protein signaling 4	NM_199274	20828	254	58	649	TTAGAGAAGAAAGTAAAGCGACAGATTTCTGACTACAGTCAGTGTTTGCCTAGTTATGCC
2,140	5,54E-08	A_15_P230341	zgc:64006	RGS5	regulator of G protein signaling 5	NM_199962	25725	313	20	1826	CCGTGTGCATAATGTATTGCAGAACACCTCTGGTGGGATATGGGTATAGGAACATGTTTG
2,443	1,54E-08	A_15_P170411	zgc:136859	RELL2	RELT like 2	NM_001040301	14848	181	66	1767	CCACACAATGAGTCTTAAATTGCACATGTAAACTTGTGCGAATAGCTAAAAACGAATTGT
1,726	1,57E-06	A_15_P110564	zgc:92286	RNLS	renalase, FAD dependent amine oxidase	NM_001002607	18878	230	81	1296	GACAGAGCCTGATGCCTCAAACTGGATTTAACAATGTCTTGAGCTATGGTGTTCTGGATG
1,628	1,34E-05	A_15_P116513	rpa2	RPA2	replication protein A2	NM_131711	1242	17	61	995	TCTTTAGACCGCAATGTATTAATTGACATGTGTTAAACCTTGCATTGCGTATTTAGATGC
2,838	1,34E-08	A_15_P101031	zgc:64022	RERGL	RERG like	NM_200365	34269	416	56	1367	AACTGTTTCGTTTGATGCATTGGTAACAACTGTCAAACCCAGATTGTTGTGTGTATAT
1,509	2,57E-05	A_15_P115079	zgc:77264	RCOR2	REST corepressor 2	NM_205638	43554	532	20	2684	CAAAACGTATGTATGTGAGAACTGTTAACTTGTGAACTGGATTTGCTTGTGACTATTTCT
1,500	2,70E-05	A_15_P100216	rcn3	RCN3	reticulocalbin 3	NM_001002158	37083	449	47	1460	AATATTACGTCTTCCACTTCTCAGGAATTCAGCACTGAATACAGGTCCAGCTTCGTTTGT
2,154	1,41E-07	A_15_P163326	rtn2b	RTN2	reticulon 2	NM_001029959	39079	473	47	1677	CCTGTGTTTGTACATCTTTTGTGCGACATGACCCCCAGTAAACACGTGTTTTCAATGTTA
1,488	3,20E-05	A_15_P132921	rtn2b	RTN2	reticulon 2	NM_001029959	15908	195	15	748	ATGGTTTGGGGCTTATGAATGAGCATTATGATTTACAGTACATTTCTCAAGGTGCTATGA
-1,597	9,72E-06	A_15_P194456	rtn4b	RTN4	reticulon 4	NM_001040335	8376	104	74	3172	CTGAACTCTGCGATGCGTTTTCTCTTGTTGATGATATTAATAAAGCTCTGCTGGTCTTGA
-1,677	5,33E-05	A_15_P132916	rtn4b	RTN4	reticulon 4	NM_001040335	32470	393	72	2813	GAGATCGATCAGTTCATTTCCATGATCAACACTCAGATGAGAGAGGCTTTGGGGAAGGTT
-1,509	2,31E-05	A_15_P164071	zgc:158792	RD3	retinal degeneration 3	NM_001080631	27111	330	48	1484	TTACCAGTCAGCTCACCATGGTTCCAGAAAGCAGGTAAGACAAAAACAGAAGCCAAAAAA
1,437	9,87E-05	A_15_P108097	zgc:110660	RGR	retinal G protein coupled receptor	NM_001017877	40416	490	52	282	CGTTATTGCTTTCCTTAAAATCAGAGAATTGCGGACCCCAAGTAATTTCCTCGTGTTCAG
1,429	8,15E-05	A_15_P115780	zgc:73336	ROM1	retinal outer segment membrane protein 1	NM_200794	16252	200	18	4862	AAAGAGGGTGTAGATGATGCTCAATGCTCCGCTATGAAACACTGTACTCGCAGAAATCTG
1,463	0,000112436	A_15_P206036	zgc:158340	RRH	retinal pigment epithelium-derived rhodopsin homolog	NM_001079657	39859	484	23	1953	TCTTCATTAAACCTGGTTTTTCTGCTCTGCCCAATTTTAGTTTCAGGTAAAATCCAGATT
1,908	3,74E-07	A_15_P108795	rlbp1	RLBP1	retinaldehyde binding protein 1	NM_205690	24781	302	44	1250	AGAACGGAAAAGCACTCAGCCTGGTCTAAGTGTTACAAGCAAACTATATATGATGTTCAG
1,803	6,16E-06	A_15_P446290	rlbp1	RLBP1	retinaldehyde binding protein 1	NM_205690	40856	496	22	563	TTAGAGCTTACTGTGTGATCCTGGAGAAGCTTCTGGAAAATGAGGAGACTCAGATCAACG
-1,655	7,96E-06	A_15_P198956	LOC100001180	RBP1	retinol binding protein 1	ENSDART00000056577	3338	43	54	348	GACGAGTTACATGTGGAAATGAGAGTCTGTGGAGTGGTGTGTAAACAAGTTTTTAAGAGA
-1,834	2,24E-06	A_15_P166156	ENSDART00000082203	RBP3	retinol binding protein 3	ENSDART00000082203	16705	204	78	1871	AGCATTTTTCCGGCCAAAAATAAGTTGTTCATCTGGGCCTGGAACGGAAGCCAAATGATA
1,480	6,73E-05	A_15_P179631	rbp4l	RBP4	retinol binding protein 4	BC152210	10532	129	71	7	TCTGTGGAGTTGGTATAAAAGGGCTCTTGGTCAGTTTAGACAACACAGCCTTGTGGAGAA
1,704	1,99E-06	A_15_P119690	rbp1a	RBP5	retinol binding protein 5	NM_199528	24743	302	24	1106	GTCGTGATTAATTTGCAGTTGTCAAACATTGTCTGAAAGTGTCAAAATTTGTAAGCTCTG
2,435	1,60E-08	A_15_P186046	LOC569308	RBP7	retinol binding protein 7	ENSDART00000103491	7323	92	48	345	CTTTACCTGGAACTTACATGCGAAGACCAGATCTGCAAACAAACCTACAAAAGATCTGCC
1,657	3,40E-06	A_15_P186066	LOC555864	RDH10	retinol dehydrogenase 10	ENSDART00000041177	17909	220	14	891	ATGTATCCATTCATTGAGACCATGAAGAAGAGAGGAGGCAATAGCCCACTGAAAGCTGAT
-1,973	1,84E-07	A_15_P174381	rdh12l	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	NM_001009912	14857	182	70	913	CACTTGAGTAAACCTCAACAAGCCGTCATGTGGTTCACAAAGCCTTTCACCAAGACATCA
1,722	1,21E-05	A_15_P118708	rdh5	RDH5	retinol dehydrogenase 5	NM_001030101	29881	364	18	580	CTCAAAGTCAACATGACTGGTGTGATCGAGACCACCATGACCTTCTTACCACTTGTGAAA
1,477	3,88E-05	A_15_P113767	rs1	RS1	retinoschisin 1	NM_001003438	22977	280	51	1200	TTATGAGCCTGTACTGTTAAACTGTGTTTGTGGCTTACCTGAGAGACAACACAATTGAAT
-1,675	3,84E-06	A_15_P142661	zgc:162132	RHCG	Rh family C glycoprotein	NM_001089577	28654	348	71	1387	AAGATGAAGAGAGTATTCCTCCCGTTCTAGAGTACAGCAGTCACATGGTCGGAAAAAACC
1,466	0,000117351	A_15_P181016	LOC100004997	ARHGEF2	Rho/Rac guanine nucleotide exchange factor 2	ENSDART00000078306	32736	398	37	2131	AGGAACATCTTTACACTGATGCCACTGTGCCGGTCAACTGTGCATCTGAAATGAAGAAAC
1,754	1,20E-06	A_15_P168986	rnaseh2a	RNASEH2A	ribonuclease H2 subunit A	NM_200226	25733	313	24	1172	CACAAGTCGGATTCATCCAACACTGCAGATGATGAATTGTGCATGACAAAGTATTATATT
2,176	5,43E-08	A_15_P105466	rrm1	RRM1	ribonucleotide reductase catalytic subunit M1	NM_131455	17095	209	23	2448	TAAAGCTGCAATGGTGTGTTCACTGGAGAACCGTCACGAGTGTCTGATGTGCGGATCATA
3,360	1,61E-09	A_15_P154211	rrm2	RRM2	ribonucleotide reductase regulatory subunit M2	NM_131450	26518	324	1	1285	TTTCACTCTGGATGCTGATTTTTAAAGACTCAATCTGAGTGCTTCAACGGACACTTAACA
2,868	5,11E-09	A_15_P210961	rrm2	RRM2	ribonucleotide reductase regulatory subunit M2	NM_131450	26152	318	68	1937	AGCATCTTCCCAAACCAGAACAGGGTTCGAGACATTGCCACACTGTCCATCAAATTTTTT
-1,563	1,33E-05	A_15_P193481	LOC560815	C14orf169	ribosomal oxygenase 1	NM_001089388	34813	421	77	1643	ATTGATCTTCACCGCTGAACCGCTAACAGCTCAATAAAGCATCGAGTACTCTACCTTGAA
-1,802	1,67E-06	A_15_P119244	rrp12	RRP12	ribosomal RNA processing 12 homolog	NM_001030276	17346	211	66	3601	AGGAAAATTGCAGCTGATCTGGATGATGACCTGGATGTTGAGCCTGCACTGAAATATAAA
-2,098	6,14E-07	A_15_P134066	rrp12	RRP12	ribosomal RNA processing 12 homolog	NM_001030276	25052	306	14	3084	TAGGAAATTTGGATTTGAGCTTGTCAAAAGCATGCTGCCGGCTGAGCAACACAAGGTTCT
5,319	2,10E-11	A_15_P103822	zgc:112118	RFESD	Rieske Fe-S domain containing	NM_001017740	12183	149	64	683	GGGATTCACTGCAACGGCTTGACTTTCAAGACCACATTTCTCAGCTAAACACTGATGGAT
1,443	6,66E-05	A_15_P115882	zgc:153310	RNF225	ring finger protein 225	NM_001076668	9942	124	25	1328	GTTGTTTTAAGAGCAAGAGGGAACAATGCAATGATGACATCTACTCTGACCTACAATGAA
1,611	6,10E-06	A_15_P366130	rnf24	RNF24	ring finger protein 24	NM_001007352	43658	531	73	1526	CAAACACACGTCGACTGCTTTGAGTTCAAGGCTGTACTTGATAAGAATCTGAAACTAACC
1,527	2,27E-05	A_15_P171221	rnf24	RNF24	ring finger protein 24	NM_001007352	34573	420	39	1532	CACGTCGACTGCTTTGAGTTCAAGGCTGTACTTGATAAGAATCTGAAACTAACCAAAAAA
2,924	3,08E-09	A_15_P160726	zgc:113070	FAM65C	RIPOR family member 3	NM_001012499	15239	188	12	3110	AGACACTGACGTTTGTATTGGACACATTCCATATGTGTGTACATGTATTGCCAAGTATTT
1,967	5,81E-07	A_15_P453860	BC090313	RBM15	RNA binding motif protein 15	BC090313	764	12	47	1559	GTTTAATGTTGATGTGTTCTGATGATGAGTGTTGCAGTAATAAACACATGAACAGCTCGA
-1,453	5,68E-05	A_15_P344075	LOC567058	RBM6	RNA binding motif protein 6	XM_690347	25699	313	7	4685	GGTTCAGCAGGTTGAATATTACTGTAGTGAGTCAATAAATTGTCTCAACATGACTGTAAC
-1,590	2,74E-05	A_15_P118011	polr3e	POLR3E	RNA polymerase III subunit E	NM_212754	91	1	56	3162	GTCTGTGTGTTTTAATCATTCCACATACTCGCAAAATCATCGCTCCACGTCCGACAGTCA
-1,619	8,26E-06	A_15_P108082	zgc:101594	POLR3GL	RNA polymerase III subunit G like	NM_001004639	4227	53	82	480	GAAAACAATCACAGGTACCAAGCAGCAACTCAAGCAGAGACCAAAAGTAGCTGCATCCAA
2,695	3,58E-09	A_15_P115534	rpepa	RPE65	RPE65, retinoid isomerohydrolase	NM_200751	16688	203	69	1609	ATGGGATGTACAAACCATAAACCCGCTGAACACACTAGCACTGATCCTGACTGACTGTAA
-1,423	8,93E-05	A_15_P118353	zgc:110543	RUFY3	RUN and FYVE domain containing 3	NM_001014335	8233	103	2	1721	ACGAAGCTTGAACACGGCTGCTGGAAAACTCCTTCAGAGGCAGCAATAAAACCATTGTTA
-1,532	6,32E-05	A_15_P181871	zgc:91995	S100A5	S100 calcium binding protein A5	ENSDART00000053397	35606	432	56	4	AGATGCTCATCAAGACCTTTCATAAGTACTCGGGGAAGGAAGGAGACAAGTATACGCTCA
-1,714	1,84E-06	A_15_P100245	BC155173	SCCPDH	saccharopine dehydrogenase (putative)	BC155173	12724	155	84	1761	TTTAGAGACCAGTGAACCAGTGAATTGTCTGAAAGATTGCAGAATACTGTTCTTGTTTGT
2,855	5,52E-09	A_15_P120662	srl	SRL	sarcalumenin	NM_001077531	31714	386	24	1284	CAGTGCTCCTACATTGGCGGTTGCCTGCTGGAGAAGATCGAGCGTGCAATCACCCATGAA
1,955	1,02E-06	A_15_P120684	srl	SRL	sarcalumenin	NM_001077531	3423	46	11	473	TATCGTAATGGCTGCTGACAGCTCTCGCTCCTTCTCCCCGCTGGAGAAGTTTGGCCAGAA
1,570	2,97E-05	A_15_P120089	zgc:100924	SGCG	sarcoglycan gamma	NM_001003748	28867	351	10	3745	ATTAGGCTGGGCAATAAAGGAGCTGGTCAAAAACTTTGAGTCCATTGAACTTAAATCATG
-1,484	3,39E-05	A_15_P104338	sdad1	SDAD1	SDA1 domain containing 1	NM_173230	19704	239	79	2201	TGTGGACCATTGTGTAAAGGAAGACAGTAAACAGACTTGGCTGTGTGGGTTTTCATGTTG

-1,486	6,60E-05	A_15_P601692	sdad1	SDAD1	SDA1 domain containing 1	NM_173230	34160	415	1	467	CTTTTCTTCGAGCTGCTGCGCTGTCACGACAAACTTCTGAGAAAGACTTTATATACCCAT
-1,456	5,22E-05	A_15_P109228	zgc:111821	SPP1	secreted phosphoprotein 1	NM_001002308	15588	191	20	1333	TCGAACTGCTGCCAAACTTGTTCAGATGCAGTTTCATCTCAACAATGTCTTCCTGTTCAT
-1,702	2,90E-06	A_15_P162746	zgc:111821	SPP1	secreted phosphoprotein 1	NM_001002308	9278	116	24	1080	TGAGTTAGACGACAGACGGCAGTGCACAAAGATGCAGCTCATACACTGAAAAGAAGATTC
2,640	1,41E-08	A_15_P101419	sparc	SPARC	secreted protein acidic and cysteine rich	NM_001001942	2533	34	68	687	CTTTGAAAAGAACTACAACATGTACATCTTCCCCGTTCACTGGCAGTTTGGCCAGCTTGA
2,623	5,86E-09	A_15_P101323	sparc	SPARC	secreted protein acidic and cysteine rich	NM_001001942	9983	123	46	1603	GCCACAATGTGAGCACTATGAATCTCTTTACATAAATAAAAGCTACTGAAATGTCCAAAC
4,991	3,13E-11	A_15_P106503	sepn1	SELENON	selenoprotein N	NM_001004294	11842	146	57	2745	CATGGGCTCTATTAGATCACCTCTGTAATCTGCTTTTGTCAGAGGGAGGAGATGCAGAAT
4,173	1,92E-10	A_15_P175341	sepn1	SELENON	selenoprotein N	NM_001004294	19826	241	57	2079	TAGGGTAGCAAGATTGTGCTTGGTCACCTCAATGAAAGCTGAAAGATGTTAAAGAGACAG
1,512	3,03E-05	A_15_P105895	sepn1	SELENON	selenoprotein N	NM_001004294	38875	472	28	1250	GAAGGAGGTGAACCCATTCAGTTTGTGTTTGAGGAGATAGTCTGGAGTGAAGAGCTGAAA
-1,676	6,31E-06	A_15_P331161	LOC558648	SELENOO	selenoprotein O	NM_001044871	35924	436	52	1978	GTGCTTAGAAACTACATCGCCCAGAATGCAATAGCAGCAGCTGAAAATGGAGACTTCTCA
-1,797	1,31E-06	A_15_P194971	LOC558648	SELENOO	selenoprotein O	NM_001044871	22268	271	30	2022	AAATGGAGACTTCTCAGAGGTCCAAAGAGTCCTGAAAGTGCTGGAAAAGCCTTTCTCAGT
3,478	5,38E-10	A_15_P104008	sepp1b	SELENOP	selenoprotein P	AF322072	28329	343	76	1046	ACACTAAACTTCTGATTTCCCCCCTTTTTGGGAAAATGTGATTGTGCTGAACTAAGTGGT
1,979	1,70E-07	A_15_P546417	sepp1b	SELENOP	selenoprotein P	AF322072	24226	296	14	669	AGTACAGAGCCAGTAACTGCTGCTCATCATCATCATCATCAACAACATGAGCCTCATCAT
1,441	7,49E-05	A_15_P175801	sema3d	SEMA3D	semaphorin 3D	NM_131048	14526	177	69	2584	GGTTTGAAGGGTGATCCACTGAATGTGGATTAAACAAACTGTAAACCAATTATAAAGACT
-1,541	3,56E-05	A_15_P119378	sqstm1	SQSTM1	sequestosome 1	NM_213173	1483	22	25	1749	TTGTTAGTTTGAATAAACAGATGGAATCGGATCGATGTCGCTGTTGGTCTTCTAAAATTC
-1,566	1,25E-05	A_15_P119639	serinc1	SERINC1	serine incorporator 1	NM_199727	11868	145	72	2105	TATTGTATTAGGCACGCCAGTGATTTACTAGATGGCTGTACCAAATGTTTCTTTTCCTTC
-1,669	7,92E-06	A_15_P150616	serinc1	SERINC1	serine incorporator 1	NM_199727	14817	181	50	1625	ACACGGCTTGGGTTTCCTTTGATGTGATGTTAATATTTCCTTCATCAACTTGTGTTCTTC
1,435	8,59E-05	A_15_P100235	zgc:110621	STYX	serine/threonine/tyrosine interacting protein	NM_001024390	401	8	9	765	TGAAGCGAACACTAGAGGAGGATGAAGATTTCGGAAGTATGCAAGTCACAGCAGCACAAA
2,870	1,78E-09	A_15_P146244	ENSDART00000051469	SERPINA1	serpin family A member 1	ENSDART00000051469	41471	504	2	792	TTTACAGGAGTTTCAGAGGAAACATTTTCGTTTCACAGTGTTTTTGCATAAAGCCACTCTG
1,466	5,04E-05	A_15_P161246	serpinc1	SERPINC1	serpin family C member 1	NM_182863	22366	272	79	1884	GTGGTTATCGTGAAGATGGCATTCACATTATTAATGATTAAACTTTCTGATTCCTGTACC
2,685	3,60E-09	A_15_P104979	serpine2	SERPINE2	serpin family E member 2	NM_200184	40995	498	8	1466	ATGTTTGCAACTTTTGTATAACTTCATCTGAGATGGCTTCTTTGTCCTCAATAAAGCATC
1,885	3,52E-07	A_15_P108358	zgc:92072	SERPINF1	serpin family F member 1	NM_001004539	10351	128	64	1806	GTTCAAATTACACTCAAATCAAGTTCAGATCACATTCCCATATGTACATTTATCACCAGC
2,042	1,19E-07	A_15_P154086	zgc:158410	SERPINF2	serpin family F member 2	NM_001080010	13065	161	2	1520	GTCTGTCCCCACTGGGAGGCAGATTTAGTATATCTACTTAAAGTAAATTTTTTAAGATCA
1,764	1,27E-06	A_15_P412200	LOC560308	SERPINF2	serpin family F member 2	XM_683705	18242	224	12	1703	GTTCATTTTAATGATCAGTTAACTGCCTTTTCTCAGGTGTTACATGGCTATATGCCAAAT
1,467	0,000126612	A_15_P417330	zgc:158410	SERPINF2	serpin family F member 2	NM_001080010	12139	150	40	637	TCTCAGAAACTGTATGACTCAGAGCCGGCCACTTTGACTGATGTTAATGACGTCAATGAA
-1,581	8,61E-06	A_15_P423125	serbp1	SERBP1	SERPINE1 mRNA binding protein 1	NM_214714	41225	500	43	1345	ATGATGGAAGACTGTCATCCATGCCATTCACCCTTGAGGACTGAATTTTACCGGTTTTAG
-1,586	9,29E-06	A_15_P601457	serbp1	SERBP1	SERPINE1 mRNA binding protein 1	NM_214714	18572	227	10	1332	TTCAGCAGATGAAATGATGGAAGACTGTCATCCATGCCATTCACCCTTGAGGACTGAATT
-1,452	5,72E-05	A_15_P118556	sgk1	SGK1	serum/glucocorticoid regulated kinase 1	NM_199212	2273	31	22	2095	CAGAAACAGGCCAGTCTGTCTCAGCAACACATTCCATTGAACAAGACTGTATGGTTATTT
-1,479	0,000105939	A_15_P131381	sgk1	SGK1	serum/glucocorticoid regulated kinase 1	NM_199212	25285	308	49	1100	AAATCAAGAACCACATGTTCTTCTCTCCCATCAACTGGGACGATCTGAATGCCAAGAAGC
-1,575	9,52E-06	A_15_P113750	zgc:154030	SGK1	serum/glucocorticoid regulated kinase 1	NM_001077302	5648	71	42	2684	TTTCATATCATTGGACCAATAATGTGCTATACGTCGTTCTTTAGATAACTACGAACATGG
-1,674	3,76E-06	A_15_P404150	zgc:154030	SGK1	serum/glucocorticoid regulated kinase 1	NM_001077302	34228	415	35	2566	GACTTGGGTACGATGTGAACAATTTGTCATCATTGGGACGAATGAGCGGTATCGGCTTAA
-1,486	4,81E-05	A_15_P130311	sesn1	SESN1	sestrin 1	NM_001002660	23598	287	33	1592	TGTCGACCTTCTTAATTAATAGTTTACTGTTGTTGTTGATGTTGCTACAGTGGGACACTT
-1,568	8,77E-05	A_15_P177436	BC122140	SESN1	sestrin 1	BC122140	27609	336	47	841	TCATGCATTTGTATAAAACCCATGCCTGCTGTGTAAATGTACTTGTGTGGAAGTTGTAAA
-1,599	1,81E-05	A_15_P176731	sesn1	SESN1	sestrin 1	NM_001002660	24373	297	6	3021	GGAGGTTTTAAGTCAGACTTGAGAGACTGATGTCAGTTACTGACACTTTTATAAGAAAAT
1,858	4,51E-07	A_15_P109981	sesn3	SESN3	sestrin 3	NM_213519	20784	253	35	3623	TCTCCACTCATGATGCATTTATACGTTTCCAAAAATGTAAGCGCTGGAACTGCTTTCCAG
-1,417	0,000100365	A_15_P202726	zgc:63842	SETD3	SET domain containing 3	NM_200054	30757	373	44	1836	GAGAAGCATGACCCAAGTGCCAAACGAACTGAAGGTGAACCAAAAGATGCTGACAAATAG
-1,616	1,47E-05	A_15_P131226	setd7	SETD7	SET domain containing lysine methyltransferase 7	NM_001002456	24289	296	47	1798	CTGTATGCATTGGGAAATGAAAGAAAGGGATGTGTTTGAGAATATGGTGCAATGTTCAGA
-1,639	8,06E-06	A_15_P193646	setd7	SETD7	SET domain containing lysine methyltransferase 7	NM_001002456	18255	223	19	1854	CAGAGGAATCTTTTTACTGAGCTTCATCCTTTGATATGCAGAAGCTATCAACAAAGAATT
2,365	3,18E-07	A_15_P207101	shbg	SHBG	sex hormone binding globulin	NM_001007151	29907	364	31	948	GTTAAATCGGAAACTCTGGACTTTCTCTCCATGTGGAAAAATGGGATGCTCCTGACATTT
2,109	4,33E-07	A_15_P366320	shbg	SHBG	sex hormone binding globulin	NM_001007151	15383	188	84	652	CATGCTCTTCAGAAATCAAGAAAGGGAGCTATTTTCCAGGAACTGGAGTGGCTGTGTTTA
1,523	2,72E-05	A_15_P104144	c6orf83	SFT2D1	SFT2 domain containing 1	NM_200372	11802	146	37	2484	TATATTAACAAGAAAAACGTTTCACATGAGCCTGTGCACCAAATAAATAACTGCTTTGTT
1,504	2,54E-05	A_15_P164181	zgc:154065	SGK2	SGK2, serine/threonine kinase 2	NM_001076564	12221	150	83	1660	TCTGTCAAGAGTGTGGTAGAAAGAATCAGTTATTTAAAGCCAATGCACGTTTATGGGATA
1,704	2,64E-06	A_15_P117794	zgc:158742	SH3GL3	SH3 domain containing GRB2 like 3, endophilin A3	NM_001081691	24028	291	82	1381	ACGTTCCACTGTACACTGATGACCAACACTAATCTCACTTCAACAGACAAATAAAACTGA
1,442	6,92E-05	A_15_P117924	zgc:63829	SDR16C5	short chain dehydrogenase/reductase family 16C member 5	NM_214771	30657	371	76	1302	AGTAGACACAACTTCAGCCATATGCGCTTACTTTGCATCCAATAATCCGTTTTCATAAAG
1,492	3,18E-05	A_15_P150836	zgc:158297	SGO1	shugoshin 1	NM_001080620	23382	285	7	2216	AATCCTTTGGCAGCTCTAAATGACTCTAGTGCTTTTATGTCTTATGATTTTAGTTGTGAC
-1,491	9,61E-05	A_15_P100785	zgc:103539	SIRT4	sirtuin 4	NM_001005988	6922	88	12	1150	ATGATCAAGATTTTGGAGGTTAAAGTGTGATACAGAATACATCACTTGCACTGAGTAAAG
1,477	3,76E-05	A_15_P119663	sirt5	SIRT5	sirtuin 5	NM_001002605	34146	413	79	1533	TGCTTGTCTGCTTCTCCTGTGTCACAGCAGATAAACAGCAGTCAGTGATAGAGACAAACA
1,401	0,000175744	A_15_P107014	snrpd1	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide	NM_173252	35349	429	11	566	GATTCTGCAAGGGTGTCTGGTTATTTTTCTACATTCTTACCAATAAAAACTGCTTGATTG
1,476	3,82E-05	A_15_P114273	snrpd3	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide	NM_001002081	29103	354	46	407	CCAGGACGAGGAAACGTTTTCCAAAAAAGGCGCTAGTTTTACTGATGTATCTTTTTAAAT
1,442	0,000168594	A_15_P147861	zgc:113342	SMTNL1	smoothelin like 1	NM_001013321	16669	204	59	1225	CCGGAACAGATTCAGCCATGAAGACTGAACAAGAGACAGATCAGAATGAAAATGTAATAA
-1,623	2,74E-05	A_15_P391680	LOC563485	SOGA3	SOGA family member 3	XM_686846	29026	354	6	3731	TACAGTGCGCATGTATGCTACACGCATAACATGTATTTGAACATACATGGCAACGACTTC
-1,466	4,48E-05	A_15_P119815	slc1a3	SLC1A3	solute carrier family 1 member 3	NM_212640	24600	299	38	1971	GGTTTGGTGTTATTAATTCAAAGCATGTCGTTGTGGAAACTGTTTGTTAAAAATGATGGC
3,024	2,84E-09	A_15_P160816	slc10a4	SLC10A4	solute carrier family 10 member 4	NM_001044803	30446	370	52	698	TTTGATTCTACATATGGCGCGGTAATAGTGAGCGATCCGAATGTCATTGTGCTCGAGTCA
1,928	3,20E-07	A_15_P113295	slc11a2	SLC11A2	solute carrier family 11 member 2	NM_212574	16650	203	50	2645	TGCTGTTGCCGTTGTTTTAAACACATTCCTGACTGTCAGAAATGCAGAAGTGTGTGTTTG
1,656	4,96E-06	A_15_P160191	slc11a2	SLC11A2	solute carrier family 11 member 2	NM_212574	30584	372	37	1594	ATCAACATGTATTTTGTGATTGTGTACGTGACGGATCTGAACAGCACCGTCCTCTACGTG
-2,027	6,47E-07	A_15_P106113	slc13a2	SLC13A2	solute carrier family 13 member 2	NM_213452	21761	265	24	2254	TCTGGTTTCATAAGTTGGTTTTCTGGTCTTCCATTTGTGCTGGTTCACGAAAATTTAATA
-1,411	0,000153182	A_15_P142201	zgc:152684	SLC15A2	solute carrier family 15 member 2	NM_001039828	22787	278	38	3121	GTCAGGGACGGAGTGATTCATGACACTCTTTGAAATAAACTTGTATATATTTGTAACACA
-1,537	3,30E-05	A_15_P103785	zgc:63767	SLC15A4	solute carrier family 15 member 4	NM_200957	34201	416	21	2732	GGCATTAGATTCCTACTAGCTTGTTTTTAAAGATTTTGATCATAAGTTGTAAGGCCAAGC
1,437	0,000101668	A_15_P208226	zgc:158478	SLC16A10	solute carrier family 16 member 10	NM_001080028	9	1	15	2322	TGCCACACTGCTGTCAGTGCAGTTCTGCTCCACAATCAATAAAGATAAATGTTTGTATTA
5,866	8,47E-12	A_15_P106623	slc16a3	SLC16A3	solute carrier family 16 member 3	NM_212708	36776	446	58	2892	TCAGACACTTGAGCTATTTTTTTGGTTGTGCCTTAAGTCTTGTAGTGGTACACAATTTTGT
5,267	2,09E-11	A_15_P409825	slc16a3	SLC16A3	solute carrier family 16 member 3	NM_212708	38334	465	8	2889	TGTTCAGACACTTGAGCTATTTTTTGGTTGTGCCTTAAGTCTTGTAGTGGTACACAATTT
2,029	1,17E-07	A_15_P499912	LOC561627	SLC16A3	solute carrier family 16 member 3	ENSDART00000038525	15890	195	6	1443	TTTCTTAAAGAGGAAGATGAGAAAGAGAAAACCATCACCTGCAGTGCAGAATCTGACCTC
-1,493	3,96E-05	A_15_P105768	zgc:114041	SLC16A6	solute carrier family 16 member 6	NM_001029972	14747	182	14	1383	ACTGAGACTACAGATCTCAAAGCAGATGTTTAAAAGCCAGGGAGGATTTTTTACCAGTGT
3,667	8,74E-10	A_15_P166601	ENSDART00000078325	SLC16A8	solute carrier family 16 member 8	ENSDART00000078325	19106	234	26	1173	TATGAACTGATTTTTTACATGGCTGGCGGAGAGCTGATCACTGCTGGAATATTTCTGGCC
1,549	2,11E-05	A_15_P143451	slc16a9b	SLC16A9	solute carrier family 16 member 9	NM_001003552	31000	376	81	2464	GGCACCTTCGGATGTAATGGATCTTTGAAACTGCCATTGTTATTTATGTTTCTTTTTATG
-1,645	4,28E-06	A_15_P120017	slc2a12	SLC2A12	solute carrier family 2 member 12	NM_200538	23585	288	26	2218	GTATGGCATGAGATGCCTTGTATAATCATGTTACACAATTGTGAATCAACATGTTATGTG
4,691	3,70E-11	A_15_P102046	zgc:92476	SLC2A3	solute carrier family 2 member 3	NM_001002643	31248	379	41	3644	TTTCATGGTGGCTTTTCCTGAATGTGTGTCCAAATCATGAGTGGTTCTGTGTACAGCTGT
-1,708	1,18E-05	A_15_P106522	slc20a1a	SLC20A1	solute carrier family 20 member 1	NM_213179	10586	131	13	2453	CACATCACACTCTTACTCTGTGATTTTTGTACGTTTAAGGTGCTTAGTATTTTTAGCTGT
-2,023	1,41E-07	A_15_P112798	zgc:64076	SLC22A2	solute carrier family 22 member 2	NM_213150	28085	341	36	2750	TAGGGCTTGAATGTTGTGAACTGTTTGTATGGTGGAACACAAATAAAGAGACTTTCTCAA
-2,172	1,39E-07	A_15_P112347	zgc:66036	SLC22A4	solute carrier family 22 member 4	NM_200849	30641	372	67	1626	CTGCAGCGAGCACTGAGGACAAGAGCAAAGTTCTGCAGGAAGTCAAATTATAACTGGATA
-1,530	5,47E-05	A_15_P194251	zgc:63958	SLC22A7	solute carrier family 22 member 7	NM_200349	9791	122	34	1643	GCCTGGATTGGAGGCCTTCAAGGAGACAAAATGAATTTGACTCGAGAAGAAAATGAATCT
-1,416	0,000143458	A_15_P109111	slc25a12	SLC25A12	solute carrier family 25 member 12	NM_212782	13109	162	24	2686	TCCACTGATCCCCAAAACAAAGTCATGATTGGTTTGAAACGTAGGAAATAATTTAAATGC
-1,747	2,63E-06	A_15_P101805	slc25a25	SLC25A25	solute carrier family 25 member 25	NM_213257	27360	333	6	2411	TACTGGCAGTATTGATTGGGGTTTGAGTACACTAATTTCAACAAGTCTCCATGGGGAGCT
-2,402	1,53E-08	A_15_P105957	ucp4	SLC25A27	solute carrier family 25 member 27	NM_199523	30606	372	48	2408	AAAGTGAGATCGCCTCATTGCTAGAAGCTCATAAACACCTGAAGATAAGCTTCAATAAAA
-2,461	1,51E-08	A_15_P534252	ucp4	SLC25A27	solute carrier family 25 member 27	NM_199523	17310	212	47	1909	CAATAGTTTTGGTAATTAGGCAAGTCATTAAACAGCACTGGTTTGTGCTGTAGTTAATCA
-1,447	6,15E-05	A_15_P539587	slc25a28	SLC25A28	solute carrier family 25 member 28	NM_213119	28562	348	24	2567	TTTCATTTTTTGGGTGAACAATTCCTTTAATATGCTAGTGAGGAGGCTGTCCTGTTAGTG
-1,486	4,29E-05	A_15_P110950	slc25a28	SLC25A28	solute carrier family 25 member 28	NM_213119	20107	245	30	2654	ATTTATTCTGAGTTCCAGACTGTTCACCAGAGCAAACCTGACCCCTATAATGTATTCCCA
1,501	2,58E-05	A_15_P115516	slc25a3l	SLC25A3	solute carrier family 25 member 3	NM_200715	19447	238	32	1254	GTCTCTCCTTTGGTGAATGTTGGACTGAATATTTAAACTAAATCATATTTAGTGGCCCAA
-1,962	1,96E-07	A_15_P121224	slc25a33	SLC25A33	solute carrier family 25 member 33	NM_213157	2807	37	40	1542	GTTTCATCCGTTTACTGTATATTTGGCTGTACAGAAAAGAAGGGCTTCAATGCGTATGCT
-1,652	5,40E-06	A_15_P109068	zgc:65857	SLC25A34	solute carrier family 25 member 34	NM_200580	445	8	31	1117	CCACAATGCACCTGGAAGGAGCGTTGTCCCTCACCGCCTTCTCTACAGACTCTTTACATT
-1,593	8,52E-06	A_15_P151011	slc25a43	SLC25A43	solute carrier family 25 member 43	NM_001004497	38388	465	35	1060	CGCTACCTAAGAAACAGAAAATCACACAAAGCACAGAGTTCATCAATAGGAAACCGTTGG
-1,585	8,43E-06	A_15_P107466	zgc:158435	SLC26A1	solute carrier family 26 member 1	NM_001080667	18170	222	61	2550	AAATAGGGTCATGAGAATGCATAATAGATCTGTGACTGTACATTCCCTATACTGTCTTTT
1,662	4,91E-06	A_15_P116814	slc26a5	SLC26A5	solute carrier family 26 member 5	NM_201473	32757	397	48	3373	TGTTTTATTGGGGGGTAATGAAGACCAAAGTTCAACAATCAGTTGCAACGGCAGTGTATT
-1,809	1,14E-06	A_15_P185901	LOC559448	SLC26A6	solute carrier family 26 member 6	ENSDART00000103833	33029	402	16	2336	TGATGCAGTTCTGTATTGTGTAAAGCATCATGGAGCTGCAACCATCAACGGCCATGAGAA

1,429	0,000116529	A_15_P188581	zgc:153860	SLC27A1	solute carrier family 27 member 1	NM_001077248	31259	379	47	1985	CAGGCACATTTAAAATCCAGAAAACCCGCTTACAGAAGGAGGGATTTGACCCTCATCAGA
-1,531	1,85E-05	A_15_P365295	zgc:112138	SLC27A4	solute carrier family 27 member 4	NM_001017737	5505	69	54	2376	CTATTCATTTTCACAGCACACCTCTCTTACAAAACAGGACTGAAGAAGCATTCAGCCATC
-1,622	7,52E-06	A_15_P195796	zgc:112138	SLC27A4	solute carrier family 27 member 4	NM_001017737	38008	462	9	2387	CACAGCACACCTCTCTTACAAAACAGGACTGAAGAAGCATTCAGCCATCGTGAAAACAAA
1,777	1,16E-05	A_15_P172706	zgc:110527	SLC29A2	solute carrier family 29 member 2	NM_001012501	2084	30	8	1686	GCGATGTACACTGATGTATAGCACTTTTATCTATGGTTTAAAAAGTCTCATGTAGGACAG
1,586	2,00E-05	A_15_P209501	ENSDART00000011551	SLC29A2	solute carrier family 29 member 2	ENSDART00000011551	40258	488	56	1794	GTACTGTTCCATAGGACTGTTCATGTTTAACATGTTTTATGATTTTACTCCTTGCGTTGT
-1,434	7,83E-05	A_15_P520182	zgc:55813	SLC3A2	solute carrier family 3 member 2	NM_201514	22432	273	28	1552	CTTGCACAGCTAGAGGTGAACCCAGGAGAAGGTATAATGCTGAAGTTTCCATACACATCT
-1,517	2,34E-05	A_15_P107639	zgc:55813	SLC3A2	solute carrier family 3 member 2	NM_201514	6552	82	78	634	GTTCTGGCACAGTTTAAAGAAGTCATTACGGCTGCACACAAGAGAGGCATCTCCGTTATT
-1,473	4,88E-05	A_15_P117466	BC076442	SLC31A2	solute carrier family 31 member 2	BC076442	35820	434	84	1052	ATTTTGGGAAATTGCATTGCATCACGTTTGATATTAGTGTCGCAGTAAACTTCTTACATG
-2,283	4,92E-08	A_15_P102375	slc34a2a	SLC34A2	solute carrier family 34 member 2	NM_131624	31256	380	45	2356	ACACACTGTGAGATCTGGTGATTGTTGTCGTACTTGTTCCAGTGTGAAAAGGATACTTGT
-1,462	4,70E-05	A_15_P152211	zgc:110140	SLC35E4	solute carrier family 35 member E4	NM_001017857	10894	134	84	2152	CACAATTTTAAAGCATAAAATATAACAGGGATCATGCCGTGTCGCTGTCTTGTGAAAAAA
-1,430	0,000102462	A_15_P205176	si:ch211-132p20.4	SLC38A2	solute carrier family 38 member 2	NM_001045104	13616	167	30	4546	GCCATTCCTGCGAATGATACGCTCTTGTTTCAATGAAACACTATGTATATCATGTAATTA
1,470	4,93E-05	A_15_P117273	slc38a3	SLC38A5	solute carrier family 38 member 5	NM_001002648	31512	384	5	2580	TCACAATCTAACACAACATCCATGAAAACGAACACATTCGTGGAAGTTCATGGATAAGTA
2,366	2,63E-08	A_15_P115339	slc39a13	SLC39A13	solute carrier family 39 member 13	NM_001005306	10989	136	48	1447	TAATGAAAGAATTGGCCTTGACAGTTAGGTGCTTGAATCTGCCAGTATATGATTTTAAGC
11,416	2,20E-13	A_15_P119878	slc4a1	SLC4A1	solute carrier family 4 member 1 (Diego blood group)	NM_198338	15345	188	65	3230	TCGATTGTACCCCCGTCCTGTTTCCACAGGTGATGCCAATGCAAAATATGTGCCTTTATA
7,606	6,98E-12	A_15_P194071	slc4a1	SLC4A1	solute carrier family 4 member 1 (Diego blood group)	NM_198338	35819	433	84	2767	GAAATGAAATGTCTGGATGCTGATGACGCAAACGTGAAATTTGATGATGAAGACGACTAA
1,967	1,92E-07	A_15_P187196	slc4a1	SLC4A1	solute carrier family 4 member 1 (Diego blood group)	NM_198338	10439	130	23	1949	TTGGAGATTTTGGTGTCCCCATCGCCATCTTCTTCATGATTGCTGTGGATATCAGCATCA
1,827	5,92E-07	A_15_P102507	slc40a1	SLC40A1	solute carrier family 40 member 1	NM_131629	19563	240	6	3674	CATCGCAGTGGGAGGATTATAGAACTTTAGTCTTGTATTGTATCTCACTTCGACTGAAAT
1,607	1,33E-05	A_15_P201931	slc40a1	SLC40A1	solute carrier family 40 member 1	NM_131629	29428	358	41	930	TTTAAGGCAGGACAGAAGGATAGCGATGACCAAGAGCTGAAACACCTCAACATACAAAAA
-1,808	7,39E-07	A_15_P101406	slc43a1	SLC43A1	solute carrier family 43 member 1	NM_199897	30828	374	79	2807	GTTTTTGGAGAACATGCAAGAGAGCATCCATGTACAAAGTGCAAACAATGTCACGTTTGA
-1,459	4,92E-05	A_15_P113884	slc5a1	SLC5A1	solute carrier family 5 member 1	NM_200681	1608	24	9	2412	TCAATGCAAAGCTTTTTCAACTGTCTCACATCTACCAAATTACTGTTAGATAAGTTGGAG
-1,539	1,65E-05	A_15_P173901	slc5a2	SLC5A2	solute carrier family 5 member 2	NM_212926	33580	408	43	1968	AATGTTAACGCACTTATAATGATGACTGTGGCCGTTTATTTTTGGGGATTCTATGCATGA
-2,022	1,58E-07	A_15_P108695	slc5a2	SLC5A2	solute carrier family 5 member 2	NM_212926	21641	263	48	2226	AGGTTGGGAAACACTGAAACTCTTTGAATTCTTCTACACAATCTGTTAATCAGCGCATTT
-1,619	9,17E-06	A_15_P222291	slc5a8l	SLC5A8	solute carrier family 5 member 8	NM_001034969	43065	523	45	1668	TCTCCTGTTGGCATAATTGTGACCATGTTCATCGGACTAATAGTTAGTGCAATCTCAGGT
-1,633	4,93E-06	A_15_P192966	slc5a8l	SLC5A8	solute carrier family 5 member 8	NM_001034969	41248	499	56	1897	AAGAGAAAGACCAGCAGGAGAAGATCACAAAGCTTTAAATGTAACATAAAACCATTTTGC
1,474	5,05E-05	A_15_P107039	zgc:92111	SLC51A	solute carrier family 51 alpha subunit	NM_001004546	376	6	66	1434	GAGCTGGATAAAGGTCAGCATTCTTTCATGTTGCTAAATTGTACGTTCGTATAATATCCT
1,514	2,38E-05	A_15_P365960	slc6a13	SLC6A13	solute carrier family 6 member 13	NM_001004533	28128	341	58	2424	GTAATTTAAAAGGATATCTGTAGGTCACTTACGTGGAAGTACATGACTTAGAACGGTTTT
1,415	0,000135212	A_15_P120441	slc6a13	SLC6A13	solute carrier family 6 member 13	NM_001004533	15117	186	35	2420	TGGTGTAATTTAAAAGGATATCTGTAGGTCACTTACGTTTATGTACATGACTTAGAACGG
-1,656	4,23E-05	A_15_P140526	slc6a19	SLC6A19	solute carrier family 6 member 19	NM_199736	5630	71	33	2463	GGCCATGTTTCCCGACGAGTTCAATAAATATTTGTCTATGCCAATAAATTTGGTTCATTT
1,431	0,000121688	A_15_P188881	slc6a8	SLC6A8	solute carrier family 6 member 8	ENSDART00000037922	14704	180	76	1732	AGCTCTCTGGAGCTAAGGGAACATTTAAAGAGCGTTGGGAAAATCTGACCAAACCAGTGT
1,626	8,31E-06	A_15_P155111	nhe1	SLC9A1	solute carrier family 9 member A1	NM_001113480	29	1	25	1686	ATCTCTAAAGAACGAGAGGCAGAAATCCGGAAAATGCTACGAGCTAACCTGCAGAAAACC
2,229	3,85E-08	A_15_P116194	sri	SRI	sorcin	NM_200373	11139	138	39	1006	TATCATGTGGGTTGTTATGAGCAACTTGTAATTGTGACAAGTGCTTAACTTCTAATCAAC
2,091	8,96E-08	A_15_P210256	sri	SRI	sorcin	NM_200373	5342	67	57	1239	CCATCATAGTGCTTTGTAACATCTTTGTGTTTCACGATCTTTAAACAGACCATGATATGA
1,688	1,16E-05	A_15_P169581	zgc:158337	SOWAHC	sosondowah ankyrin repeat domain family member C	NM_001080006	25505	310	77	1620	CAGACAGGGCCGAGGCTTAAAGTTCACATTTTAATGTCAATAAATTGAATCTTGTTTGAA
1,671	4,18E-06	A_15_P100405	zgc:110417	SPC24	SPC24, NDC80 kinetochore complex component	NM_001024440	33051	402	27	864	ACACATTTTATTGTTAAGCCTTCAGATTTCCACAGAGCAGTGAATCTGATCCTATCAAAT
2,862	2,65E-09	A_15_P110927	sptb	SPTB	spectrin beta, erythrocytic	NM_131525	10553	130	81	7262	TTTTATACCAGAGTCACATAACACATTCACTCTGTATACAAATAAAAGCACAGGAACCTG
1,965	2,43E-07	A_15_P179526	BC152302	SPACA4	sperm acrosome associated 4	BC152302	34877	424	24	1047	GTTTAAGTTGCCATTATAATGTGTGCTGCCATTTCAATATGAGAGCAATAAACTGGTTCA
1,445	8,36E-05	A_15_P161621	zgc:154064	SPATS2	spermatogenesis associated serine rich 2	NM_001077726	40375	490	31	2623	GTCCGCTGATCGCTGATCGGCTTCCCTCATGATCAATAAAGAAGGATTGGTAGCAAAAAA
-1,432	0,000164208	A_15_P195191	spg21	SPG21	SPG21, maspardin	NM_213395	30140	366	66	867	AAGTCAACCTGTACATACAAATACATCTGCGTCAGTTTCACGGTACACGTTACGCAGCCA
1,902	6,30E-07	A_15_P201396	ENSDART00000102139	SKA3	spindle and kinetochore associated complex subunit 3	ENSDART00000102139	10505	129	57	1450	CAGCAGTTTGAAGCCGTAACACAAAGGCTCTACTGACTTTTTTATAATTACAAACACTTT
1,794	1,71E-06	A_15_P179356	zgc:171223	SPDL1	spindle apparatus coiled-coil protein 1	NM_001104942	43192	525	38	1463	TTCCAGAAGAAAACTCTGCATCTGTAAAAGACGAAACCACAACCCAGGATACCGAGCTAA
1,401	0,000139023	A_15_P102878	sox11b	SOX11	SRY-box 11	NM_131337	30514	371	2	2553	ACCATCTGCGTTTTGTAGCAAAGGAAATGAGTTACATGTCGTCATGCTGAAGTCTGTATC
-1,406	0,00017503	A_15_P111240	LOC794757	SSX2IP	SSX family member 2 interacting protein	ENSDART00000088027	35293	428	66	915	TGCAGGAAAACATAGAACTGAAGAAAGTGCTTCAACAAATGAAACGAGAGATGGTTGGAC
1,845	7,45E-07	A_15_P208746	zgc:158162	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	NM_001083029	25903	315	26	3058	TCCGTTTGGGAACTTGTTTTTTAAATACCACCGCAGGATTTCGTGAACTTCTGAAGTATT
3,638	3,49E-10	A_15_P193026	zgc:153307	STC1	stanniocalcin 1	NM_001045457	12693	155	68	906	TTAATTTCAGAGCAGTTCGAACTTTGCCATCAAGCACACATACATAAGCGCAAATTGAAA
1,573	1,39E-05	A_15_P114719	ENSDART00000079215	STC2	stanniocalcin 2	ENSDART00000079215	36355	442	15	1014	ACAGTCATTCCAGCACTCCCAAACTGTACATTTCGCAGGGTAAATGTGGTGCAGCTTTTT
2,808	2,22E-09	A_15_P149586	zgc:136942	STMN1	stathmin 1	NM_001040375	35151	426	79	850	GACTGTTCTTTGTACAAGACTGAGAAAAGAAAAGATTACCTTGTCGACTTTACTGTACAA
1,470	0,000109371	A_15_P101984	Slbp	SLBP	stem-loop binding protein	ENSDART00000008197	34109	414	60	1003	AAAGAGAAGGTTTTGTCATCATCACTGAATTCACCGTTCTCCCACTTTTCTTTTTCGGGTC
1,666	3,78E-06	A_15_P199131	LOC563729	SAMD7	sterile alpha motif domain containing 7	ENSDART00000084958	27830	337	75	917	GTAACGTTATGCAATAGGGGCTCTAAAAAGTTGATAGACTGTTAAATGCTGGATTTTTCT
-1,547	1,87E-05	A_15_P121066	LOC564868	SOAT2	sterol O-acyltransferase 2	NM_001111180	34124	413	68	942	TGAGGTTTATCCGCGAAACCCAAACATCAGATGGAGGTTTGTGGGCATGAACTTTCTGAA
1,456	5,45E-05	A_15_P103844	zgc:136689	STRA6	stimulated by retinoic acid 6	NM_001045312	36429	441	53	2810	GATATTTCCGTCTATTTTGTCTTGTTCTGCGCTACCTACGGCATGTGATTGAAACGAAAT
2,628	4,52E-09	A_15_P118073	smc2	SMC2	structural maintenance of chromosomes 2	NM_199542	29087	353	38	3779	AGTGTTTGTATTAAAAGCATTTGGACACATTCAGTGCATCTAATGCATGTGAAATAGCTC
2,363	1,33E-07	A_15_P151021	smc2	SMC2	structural maintenance of chromosomes 2	NM_199542	30429	370	43	3542	TTCACCAATGCAAACGTGCTCTTCAAGACCAAATTTGTGGACGGTATCTCCACAGTCACT
1,497	0,000116309	A_15_P103359	smc2	SMC2	structural maintenance of chromosomes 2	NM_199542	32822	397	82	2386	GGTTCAAAAGAAGGCAGAGGAGAAATACAACGTTCTGGAGAACAAGATGAAAAATGCTGC
2,072	8,64E-08	A_15_P107585	smc4	SMC4	structural maintenance of chromosomes 4	NM_173253	39392	478	38	4082	ATCACCTGTTCTGCTTTCACATCGCTGTGCTCCTGTGAGCCTTTTACATGTCTCCCGTTA
1,915	3,06E-07	A_15_P133426	smc4	SMC4	structural maintenance of chromosomes 4	NM_173253	8999	111	52	1402	ACACACCAAGAGCAAAACCAAGAAACTGCAGAAACAGCTTCAGAAAGACCAGGAGAAGTT
1,490	5,38E-05	A_15_P113720	ssrp1a	SSRP1	structure specific recognition protein 1	NM_212802	25772	314	43	2414	AGATTTAATTCAGGGAAGTGTGGATTAGACCTGCTTGTAGAGGGTTTTTCCTTCTTTTTA
1,414	0,000137875	A_15_P194726	zgc:109973	SUB1	SUB1 homolog, transcriptional regulator	NM_001020540	34473	417	74	623	GGATAGAGAGATGACTGGTTTTAGCTTGTGCCCTGAATTTTCAATAAAGTTGATCGAAAT
-1,480	7,64E-05	A_15_P321121	sucla2	SUCLA2	succinate-CoA ligase ADP-forming beta subunit	NM_213026	20543	249	83	808	GATTCTTCTGGAATTGTGATGTGTATGGATGCTAAGATCAACTTTGATTCAAACGCTGCC
-1,919	2,70E-07	A_15_P106478	sucla2	SUCLA2	succinate-CoA ligase ADP-forming beta subunit	NM_213026	4117	54	25	2026	CTGACGTGAAGCCACCGGATGCGGAAAACAATAAAAATACCAACACCTCTCATGCTTGAT
1,576	2,24E-05	A_15_P111246	sulf1	SULF1	sulfatase 1	NM_001003846	8791	110	30	4514	TAACTAGTGGTGTTGGAACAATTTTGGCTTCTGGAAAGCCAAGAAGCTGTTTTGAAATAA
3,367	1,16E-09	A_15_P107748	SUMF1	SUMF1	sulfatase modifying factor 1	BC078369	26453	322	52	1143	TATGCTGGAAATCCTCCACACCTCCACAGGTCTTGGGGTAGGATTTGGGTAAAAACAAAA
2,466	9,25E-09	A_15_P111081	zgc:136465	SUMF1	sulfatase modifying factor 1	BC095053	11888	145	82	1149	CTCTGATGTTGATCCATAACCTCAAACATCACTAATCTCACTGTCTTACACTTCAAACTA
1,417	0,000109257	A_15_P105111	zgc:136465	SUMF1	sulfatase modifying factor 1	NM_001040340	21933	267	28	186	ATGACGAGCTGAGGTCTCATGGCTATGGCACCGGTGTTGAATATTTGCGTGGTTTTTATTT
6,502	3,96E-12	A_15_P102683	zgc:113156	SQRDL	sulfide quinone oxidoreductase	NM_001017881	22042	267	83	1455	CTGTCAGTGATGTGCCTGCTTTAAAATATAGTTTGCTAACAATTTCTTATAACAGTGCTG
1,448	6,93E-05	A_15_P107010	sult1st1	SULT1A1	sulfotransferase family 1A member 1	NM_182941	5064	66	1	349	TTCCTGGAGTCTTGTTTCAAAGTGATAGCATCAGGAACGGAACTGGCTGATAACATGACC
-1,714	4,31E-06	A_15_P108867	sult1st3	SULT1A1	sulfotransferase family 1A member 1	NM_183348	11890	145	83	1318	AGAAATTTCACTGTGAACCAAAAACTTCAGACTGCATGTTCAGGTAAAAGTTTTGTATGG
-1,536	4,59E-05	A_15_P153096	zgc:111843	SULT6B1	sulfotransferase family 6B member 1	NM_214686	40830	495	9	1069	GCACAGACTCACTGTCATTAAACCTCATGGAGTGTGTTTGCTAACATTTATTAAAATGAA
1,440	7,01E-05	A_15_P105831	sae1	SAE1	SUMO1 activating enzyme subunit 1	NM_001002058	5338	67	55	1324	TGCCACACGTCAACTAATGCCAAGAGCAACCAGAACATTTTGTCCACACACTCTTGAATA
1,475	8,85E-05	A_15_P201676	LOC571373	SENP7	SUMO1/sentrin specific peptidase 7	ENSDART00000089539	22137	269	49	1206	GGCTCTCTGGGAAATGATGCTGCAGATGATAGGACAGATTATGGCAATGTCATTAAGTGA
-1,853	5,01E-07	A_15_P119415	socs3	SOCS3	suppressor of cytokine signaling 3	NM_199950	32889	399	31	1802	GAAGATGCATTTAGACCTTTTGTAAAGACATCTCAACCATGTTTGACGATGGATGTGACT
1,549	2,83E-05	A_15_P131146	DQ840139	SUV39H1	suppressor of variegation 3-9 homolog 1	DQ840139	43403	527	76	246	TATAAAGCCTCCTCATGTTTATGTTGCTTTTGGAAAATGGACCGTGAAGCTGGAGTGTTC
1,421	9,75E-05	A_15_P140451	zgc:136593	SUV39H1	suppressor of variegation 3-9 homolog 1	NM_001083541	16022	195	72	1145	AAGATTGATCCAGTAGATGCCGAGAGCACAAAGATGGATACTAATTTCGGTGTGATGGGA
2,575	6,08E-09	A_15_P194901	zgc:110822	SRPX	sushi repeat containing protein, X-linked	NM_001014326	30087	366	38	1569	TATGTCAGAGTGGACGGTCTACTACCAAAGCAATATTAATGTAATAAAGGCCTGTTTGAT
-1,453	5,48E-05	A_15_P141256	zgc:109926	SZRD1	SUZ RNA binding domain containing 1	NM_001030076	33439	406	56	1357	TTAACGGAAAAGATGAGTTGTGTAAATATTTGTCGTGCTGGGAAGAACTGAAGGGAGGGT
1,521	2,41E-05	A_15_P105234	smarcad1	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	NM_001110104	38813	470	81	1802	ACATATTGTGCTCTGTTTAGCCTACTCGGGTTGTTTACAGATTTGTGACTTCAGAGTTTG
-1,406	0,000121438	A_15_P107948	zgc:162081	SYNGR2	synaptogyrin 2	XM_691842	35088	425	47	1004	CTGATGTGTGTGTAGTGAAGTATCAGCTCAGAATAACACAGATAATGTCCTCCAGCTCTC
-1,849	5,99E-07	A_15_P147911	zgc:153950	SYNGR2	synaptogyrin 2	NM_001080585	32531	395	18	3298	CACATAATTGCTGTCCTTCTGTTCATTTACTTTGTAACAACAGTTATTGCACCAATGTCT
-1,650	3,70E-06	A_15_P180961	LOC568900	SYCN	syncollin	ENSDART00000101151	15090	186	21	290	CAAAAGGAAGTTTCTTGCTGGTGTTGTCTACCACCTGAAAGAAGTGAAGAGAGGCCTGTT
-1,493	2,91E-05	A_15_P161541	zgc:153017	SYBU	syntabulin	NM_001077173	8941	112	22	2537	GTACAGCGAACACTTGTTATGTGCCTGAGCTATGTGCAATATTTTTGTTAATATGATATG
1,891	2,01E-06	A_15_P148746	zgc:110133	SNCG	synuclein gamma	NM_001017567	3060	40	83	1011	GATGGTCCAAAAAAGATGAGCAACTGATGTCTGTAAAGTGTGGTTATAAAATGATGCTCT
1,802	7,56E-07	A_15_P197531	zgc:110133	SNCG	synuclein gamma	NM_001017567	16508	201	63	257	TAAACACAGTTGCCCAGAAAACAACTGACCAGGCAAATCTCATGAGTGATACTGCTGTGG
2,195	5,95E-08	A_15_P107499	tbx6	TBX6	T-box 6	NM_131052	31616	383	60	2737	TGGGATTATTGGTTGGTTCCTCACTCTCACAGTGCTCAGGGTTTTGACATTGTTGCCTTT

1,899	4,07E-07	A_15_P168831	tbx6	TBX6	T-box 6	NM_131052	32507	396	5	2471	AGACTGACATCAACAGAGAAAGCCCGCAACTCAACCGCAAAAATACCAAAACTATTTTTT
-1,433	7,77E-05	A_15_P107412	zgc:73347	TCP11L2	t-complex 11 like 2	NM_213020	17997	220	58	2606	CGTCTACAGGACAGACCTTCAGTTTAATATTATTGCAATATATATGTACCGTTTCAGATG
1,683	2,79E-06	A_15_P118288	tal1/scl	TAL1	TAL bHLH transcription factor 1, erythroid differentiation factor	NM_213237	30469	370	64	2434	GTAACCAGTCTTGGTACCTTTAAGTCTTTTATTGGGTATTAAATGCGCAAACAAACAAAC
-2,089	7,64E-08	A_15_P107888	si:dkey-34f16.1	TXLNB	taxilin beta	ENSDART00000026106	28095	341	41	1504	CAGATCAACTGGAATCAACACAAGAGCAATCCTCTACCACAAAAGTCATTGAAGAGAAGC
1,893	7,35E-07	A_15_P208511	LOC563506	TIPARP	TCDD inducible poly(ADP-ribose) polymerase	NM_001045019	13899	172	3	2039	CAGAGTTATCCGTACTTCATCGTTCAGTATGAAGAGGTAGGCAGTACAGTGGCTATCTGA
1,802	1,89E-06	A_15_P169141	zgc:153056	TIPARP	TCDD inducible poly(ADP-ribose) polymerase	NM_001045436	20313	248	51	1089	GTTCAGTGAGAAAACAAACAAAATTGGTAAGAGGGAGGGACTGGTGTGACTTTCACCTAA
1,766	4,16E-06	A_15_P194196	tnc	TNC	tenascin C	NM_130907	22591	275	24	5529	GCAGAGATGAAGATCAGACCTGCCAACTTCAGGAACTTTGAGGGAAGAAAAAAGCGATCA
2,427	5,98E-08	A_15_P109993	tnw	TNN	tenascin N	ENSDART00000077178	38982	472	83	3376	TGTTAAGCTATAATGTCCTCCATCTGGATGTGTACTGTAGTTGTACTATAATTCCTGACA
1,941	6,26E-07	A_15_P198921	tnw	TNN	tenascin N	ENSDART00000077178	12661	155	52	2547	ATCCAAACAGAAGTTCAAACTTACCATTGGCAGCTACAAGGGAAATGCTGGTGACGCCAT
-1,845	5,59E-07	A_15_P120835	zgc:77495	TESC	tescalcin	NM_213328	14365	176	71	2018	CGGCATATGTTACAGGATACACATTATAATGCCCACTGTATGGATATACGTCAAAATAAA
1,475	3,92E-05	A_15_P112382	zgc:92266	TSPAN33	tetraspanin 33	NM_001002617	20813	253	51	1504	TGTCTTCCTTCTGTTTGGAGAACGGAACGTTCATTCAGTGGATCCCAATGTTTTGTTGTT
3,800	1,88E-10	A_15_P209216	thop1	THOP1	thimet oligopeptidase 1	NM_001005930	20886	256	3	2091	CAGGAAACTAATTGCACTTAAAAATACACAAGATACTGAGACTGATACCGAGTTCTCTTT
3,746	2,13E-10	A_15_P172046	thop1	THOP1	thimet oligopeptidase 1	NM_001005930	18444	226	30	2116	ACACAAGATACTGAGACTGATACCGAGTTCTCTTTCTGAAAATTAAATGTGATGTTTCCA
1,652	3,64E-06	A_15_P199471	LOC569944	THEM6	thioesterase superfamily member 6	ENSDART00000083520	16667	204	58	751	AAACCTGGATCATGCCATATTATGACTTGTGCAGATTGTAAGATTATGAATAGCCATGAA
1,480	3,68E-05	A_15_P174181	zgc:110680	TXNDC12	thioredoxin domain containing 12	NM_001020824	1533	21	51	2138	GCAAATTGTGAGGGAATTGCCTTTGCCATACTGTATTTTCTTAACATGTAAAATAAGGCT
1,896	5,34E-07	A_15_P119236	txndc5	TXNDC5	thioredoxin domain containing 5	NM_213016	5911	76	4	2943	GAGGGGTACACACACTGCCCGGGGGTTTTTGTACAAAAATAAAAAAGGCACATTGTGACA
2,220	3,74E-08	A_15_P406510	txnip	TXNIP	thioredoxin interacting protein	NM_200087	24552	299	14	2479	GTGTGCAGTTAATCTTGAAGACATTTTGATCAACATTTCACTTGTGGAGATCTTCCTGAA
2,200	3,88E-08	A_15_P106217	txnip	TXNIP	thioredoxin interacting protein	NM_200087	32859	400	15	2515	TTCACTTGTGGAGATCTTCCTGAAATTTGTTGATTGTGTGTGTGTTGTTTTGTTTCTTCA
-3,557	3,24E-10	A_15_P161971	txnl1	TXNL1	thioredoxin like 1	NM_201138	31110	377	54	928	CAAAAATCAACTATTTGACGTTTATCGGGACTCCAGTGCAGGCCACGAACATGAACGACT
1,435	8,04E-05	A_15_P207166	zgc:110025	TMX3	thioredoxin related transmembrane protein 3	NM_001020557	8434	105	19	1320	CTCCGAAGCAAAGAAAGAGGATTAACATGGACTGTTTGTTTACTTTGTATTGTGTTAATC
-1,412	0,000136043	A_15_P190801	LOC563265	TSTD1	thiosulfate sulfurtransferase like domain containing 1	ENSDART00000105898	1709	23	60	282	GGATTCAAGAACGCTCGTAATTATGCTGGAGCCTACAAGGAATGGTCAGAAAAAGAAGGC
1,425	0,000150893	A_15_P171516	thy1	THY1	Thy-1 cell surface antigen	NM_198065	8206	102	73	613	CTGAAATCCAAAGTCTTCTGACTGTTTTAATTTCAGTATGTGTACACTGGTTCAGGTTGT
1,437	8,71E-05	A_15_P139646	tk1	TK1	thymidine kinase 1	NM_199832	7741	98	7	1563	GAAGCACTGCCAAACACTGACGTCTCAGGAGTAATAGTCAATAAAACAAATAGATTATAA
2,021	3,30E-07	A_15_P119814	tyms	TYMS	thymidylate synthetase	NM_131760	35289	428	64	995	TGAGATCTATGATTATGACCCACATCCTACAATCAAAATGCAAATGGCTGTTTAGACCTA
1,428	9,33E-05	A_15_P191541	LOC555433	THEMIS	thymocyte selection associated	ENSDART00000002928	39552	480	36	2403	AAACCTGTTCTGAGACCTGTGCATAGAGTTAATTAAACCTTAAGGTGTTTCTGTAAAGAA
1,419	9,65E-05	A_15_P212521	LOC555433	THEMIS	thymocyte selection associated	ENSDART00000002928	30666	372	80	2397	GTTCAAAAACCTGTTCTGAGACCTGTGCATAGAGTTAATTAAACCTTAAGGTGTTTCTAT
1,445	0,000104256	A_15_P141011	zgc:92287	TMPO	thymopoietin	NM_001002606	32198	392	17	1106	ATAGGGTTTTAAAACTTTAAAAAGGATGTGTTGTCGGCTAGCCCTTTGCATGGATTTTTT
1,526	2,16E-05	A_15_P119443	tmsb	TMSB10	thymosin beta 4, X-linked	NM_205581	30932	375	47	319	TGAGGAATGTATTTCACCCTGTGAGTTCAGAAAACCAAATAAAATGCACCTCATTTTTGA
1,839	5,47E-07	A_15_P104901	zgc:56292	TRIP10	thyroid hormone receptor interactor 10	NM_200224	27795	338	57	2366	AGTCATATTATACCTGTGTTGTTATCACTACTGTTAGATCAAATAAAGCTTCGCTGATGG
1,706	2,17E-06	A_15_P106314	trip13	TRIP13	thyroid hormone receptor interactor 13	NM_200582	23166	282	66	1531	GATGAGCTGCAGTTTCGATGTCTGACTTTGGCAATGGCACTTTTATTTGCATATCAAACA
2,065	9,84E-08	A_15_P100223	LOC796294	TFPI	tissue factor pathway inhibitor	ENSDART00000047653	15105	186	29	2112	GAGCTGTTACTCTTAAGAAGACATATTGGACTCCACTGACAGTGGTGAAAATGCATACTT
1,805	1,16E-06	A_15_P108604	hdr	TNFRSF10A	TNF receptor superfamily member 10a	NM_194391	1787	26	20	1176	ATTCTCAGTGGACGAAGGTACAGTATGCTTTTCAGTTTCATTTTGTCCATTGCTAAAGTG
1,753	6,51E-06	A_15_P106641	zgc:85914	TNFRSF1A	TNF receptor superfamily member 1A	NM_213190	38184	463	15	2359	TGTGTAAGAGCAGAGCTGTTAGTAATTGCATTTGTGTTGCACATTCTTTCTGTGTATCAA
1,560	1,13E-05	A_15_P102219	LOC445411	TICRR	TOPBP1 interacting checkpoint and replication regulator	NM_001003887	24206	296	4	5794	TTTTTTAAATGTGGCATGGATTTTAACGTTCGGCAGCTCACAGCATCTATCATAATGTGA
-1,480	5,82E-05	A_15_P106200	top1mt	TOP1MT	topoisomerase (DNA) I, mitochondrial	NM_001001838	36704	445	22	1795	TGGGCCATCGACATGACGGACGAGAGCTTCCAGTTCTGAACACGCATACCAGCACACACA
2,557	2,16E-08	A_15_P174396	top2a	TOP2A	topoisomerase (DNA) II alpha	NM_001003834	30821	373	76	4770	ACTGCTGGAAAGAAAGCAAAGAGCTGGGAGGATGATGAAAGCTTTCAGTTGGAAGAGACT
-1,457	5,56E-05	A_15_P140466	zgc:136900	TIGAR	TP53 induced glycolysis regulatory phosphatase	NM_001039836	31071	378	33	1944	CTAGTCCTTCAGGACCAAGTTTGTCCATCCCTGATTTAGACAGTATTGAGTCTTAGTAAA
-1,438	7,36E-05	A_15_P141346	zgc:153625	TFB1M	transcription factor B1, mitochondrial	NM_001076769	23590	287	29	1640	GAAGAAAGTTGTGTATAAGGTTTGACATTGAAACACTCAGTAAAAGCTTTTCACATGGTG
1,413	0,000133049	A_15_P116535	zgc:91796	TFCP2L1	transcription factor CP2 like 1	NM_001002214	27742	337	31	1890	AAACGTTGATAAAGTCTCCTCTAACTGGAAATAATCTGTTTCATATTGGACAGGTTCTGT
-1,491	3,02E-05	A_15_P117292	tob1b	TOB1	transducer of ERBB2, 1	NM_212974	19502	238	60	1143	ATGGCTAACTGAGGAGCGATTGTTGGCGTAAAAAGGAAAACGAAAGGCAAAGACGCACTT
6,262	5,26E-12	A_15_P210471	tfa	TF	transferrin	NM_001015057	21459	262	40	2073	CATCAAACAGTCAGATGTGATCAGGTTTCTGTTTTATCACAAAAGGGGATGAAATGAAAT
6,097	5,99E-12	A_15_P596772	tfa	TF	transferrin	NM_001015057	13435	165	21	2050	ACCTATCTTACGGTCAACAAACACATCAAACAGTCAGATGTGATCAGGTTTCTGTTTTAT
5,982	6,23E-12	A_15_P112659	tfa	TF	transferrin	NM_001015057	37511	455	12	2059	ACGGTCAACAAACACATCAAACAGTCAGATGTGATCAGGTTTCTGTTTTATCACAAAAGG
5,673	8,40E-12	A_15_P324426	tfa	TF	transferrin	NM_001015057	23924	292	29	242	CAGTAGATGGAGCAAATGTTTTCACTGGTGGACTAAATAATTATCTGCTCCGTCCAATCA
5,018	7,34E-11	A_15_P106533	tfa	TF	transferrin	NM_001015057	21220	259	4	620	TGATGACGGAGCCTTCCAGTGCCTGAAAAATGATAATGGACAGGTTGCATTTGTTTGCCA
6,983	2,85E-11	A_15_P139541	tfa	TF	transferrin	NM_001015057	30802	374	66	2026	TGGGCAACTGTATTAGCTCCTAGTACCTATCTTACGGTCATCAAACACATCAAACAGTCA
1,902	3,90E-07	A_15_P171111	tfr1b	TFRC	transferrin receptor	NM_001009918	536	7	77	2340	ACAAGATGTACGTGACAAAAAGGCAAGCTTCGACATCGACCAGGTGCTAAACAAATTCGC
1,575	1,02E-05	A_15_P172511	tfr1a	TFRC	transferrin receptor	NM_001009917	37017	449	13	2006	CATCCGAAACAGCGATCTTGATGACATGGAGCAGTGTCGCATCATCAACAATCGCATTAT
3,533	2,61E-10	A_15_P115554	tacc3	TACC3	transforming acidic coiled-coil containing protein 3	NM_212581	21552	264	2	3085	ATGAGCTGCTGCTTAAAGTGCAAAAGCATGGTTTTTAATGCTTTTCCCTCCTTTTTGTGT
1,847	6,72E-07	A_15_P119930	tgfbi	TGFBI	transforming growth factor beta induced	NM_182862	40825	496	6	2941	TCACTGAGCTGAATTCACAATGTGGTGGATTGTCATAATGTGTTGATTAATGTGTGTGGC
-1,560	1,19E-05	A_15_P365355	zgc:112355	TGM1	transglutaminase 1	NM_001030096	25591	312	36	2245	AGCAGCAGTTTACTGTAAAGGCTCTGCTGTCGCATTACACTGACAGAGCAACACTAATAA
-1,591	9,55E-06	A_15_P137266	LOC793448	TGM1	transglutaminase 1	ENSDART00000041912	3853	50	60	1787	TGGATGCGATTGTGTTGTGGGCAAAGAAGTGCCAGTCAAAATCACTTTCCAAAACCCACT
-1,675	2,50E-05	A_15_P472140	LOC793448	TGM1	transglutaminase 1	ENSDART00000041912	37195	452	19	1605	GAGCTCAAGGCTACTGAAACCAAGGTTCTGGAGTGGTCTCTGAAATATGAGGATTACAAG
1,492	4,18E-05	A_15_P100104	trpc6	TRPC6	transient receptor potential cation channel subfamily C member 6	NM_001030282	3260	44	14	2441	AGGAGATCAAACAGGACATTTCAAGCCTTCGCTATGAACTGCTGGAGGAAAAGTCACACA
-1,769	1,14E-06	A_15_P104131	BC124699	TOMM6	translocase of outer mitochondrial membrane 6	BC124699	29521	360	4	401	TCAACAGCGAAGGGAATAAATCCCAACAATTGGATGATTACAAATTGTAAATTTCTGCTG
1,511	0,000129647	A_15_P132571	tram	TRAM1	translocation associated membrane protein 1	NM_153669	31581	384	41	1495	ATACCTGCAAAGAAAACATGAGAACTGTGGGGGGCGGGAAAGAAAAGTAACTTATTTTTT
1,417	0,000207322	A_15_P110596	tram	TRAM1	translocation associated membrane protein 1	NM_153669	22845	277	69	2150	CAAAATACAACCAAGTTGACCAACAAGCAGTGAATACGTTAATAAATGTCGTTTTCACAG
2,261	4,76E-08	A_15_P118164	zgc:103456	TSPO	translocator protein	NM_001006032	12531	154	71	807	CACTGCACCTATTTACTCATGTTTAGATCAGTTTATTTGCTCTTCAAATCAACTGTTTGC
1,648	1,55E-05	A_15_P153121	zgc:158825	TM6SF2	transmembrane 6 superfamily member 2	NM_001080661	40727	494	40	1205	CATCCTACCTATGGGCCAAACCAACAATGAGAAGAAATTAAGTTAAACTGACTACAAAAA
1,560	1,24E-05	A_15_P547967	zgc:158825	TM6SF2	transmembrane 6 superfamily member 2	NM_001080661	11274	140	23	1191	GACTACTTCCTTCCCATCCTACCTATGGGCCAAACCAACAATGAGAAGAAATTAAGTTAA
1,909	3,05E-07	A_15_P265846	LOC568324	TMCO4	transmembrane and coiled-coil domains 4	XM_691648	27085	329	35	1965	AACACAACTGAAGCACGAGATCAATTAGGCAATGGTAAACCTGCCATTTCTGAGCCAAGA
-1,559	1,19E-05	A_15_P190576	LOC556714	TMED9	transmembrane p24 trafficking protein 9	ENSDART00000040383	9899	123	4	594	GTTGGATTCTGGCAAATGAAAAACCTCAAAGACTTTTTCATCGAAAAGAAGTTGGTTTAG
1,907	3,08E-07	A_15_P101307	zgc:110086	TMEM11	transmembrane protein 11	NM_001017400	9750	122	12	1107	TTTACTGTACCCTGCCTTTGGTGCGTCACATTTTCATTAAACAGTAGGAGATTTAACCTC
1,600	6,69E-06	A_15_P100226	zgc:153439	TMEM14C	transmembrane protein 14C	NM_001045438	23161	281	64	374	CAGAAACCTCAGAAATCATGATACTGAAACAAAAATCATGTCTGCTATTGTTCAAAGTGA
1,852	6,06E-07	A_15_P153811	zgc:153018	TMEM179	transmembrane protein 179	NM_001076639	39576	480	48	2032	GAATGCCATCACTTGACCAGCACAGATCACTTTATAACAAATGCAGTGCATAAATTAATA
-1,586	1,12E-05	A_15_P108955	LOC553226	TMEM198	transmembrane protein 198	ENSDART00000061723	25348	308	82	1150	GAAGTCTTCATCAATCACCAGCAGAGACGAGTGCAGCTAATGCGAATCCGTCAAAAAGAG
1,440	0,00013089	A_15_P177571	zgc:158860	TMEM205	transmembrane protein 205	NM_001080686	28795	349	58	1090	CCTGCGTTTCTATCAGTTTCATGCTCAACCTTAACTGATATTATTATGGATATTCACAGT
1,611	6,42E-06	A_15_P208371	tmem38a	TMEM38A	transmembrane protein 38A	NM_200900	39123	474	69	691	TCTTCACACTTTTCATGGTCTCATCCAAGGTGTTCATGACAGCTCGTCACTCTCATGGAT
2,432	1,52E-08	A_15_P195601	zgc:110647	TMEM45A	transmembrane protein 45A	NM_001020617	13642	167	43	1717	GCCGTAATTGTTCTTTGGAAAGCTTATCAAATATTTGACTGAAAAAAGGACAGCCATTGT
1,645	3,87E-06	A_15_P176991	BC097189	TTR	transthyretin	BC097189	32966	399	70	1112	CGAGCTCAGTCTATTACACACCACAGCGTTACTTTCTGAATGGACATTTAAATGTAATAT
1,456	6,66E-05	A_15_P106487	zgc:162523	TRDN	triadin	NM_001089561	13394	164	85	594	AAGAGGAGGATGAAGGCGAGCGTCATTTTGTGAAGAAAAAAGGAGAATTCCTGCCACCAA
-1,492	4,03E-05	A_15_P119740	zgc:76966	TRIB3	tribbles pseudokinase 3	NM_212869	43333	528	40	2089	GTGTACACTACATTTGTTGTTTCAAGGGGTGATGTACCTACAAGCGAGTATTTTGTT
2,524	2,39E-08	A_15_P193701	tpi1b	TPI1	triosephosphate isomerase 1	NM_153668	2415	34	9	751	GGCGGAGCTTCCCTAAAACCAGAGTTTATCGACATTATTAACGCAAAAGCATAAAGACAT
2,469	6,48E-08	A_15_P193701	tpi1b	TPI1	triosephosphate isomerase 1	NM_153668	2415	134	21	751	GGCGGAGCTTCCCTAAAACCAGAGTTTATCGACATTATTAACGCAAAAGCATAAAGACAT
2,465	3,54E-08	A_15_P193701	tpi1b	TPI1	triosephosphate isomerase 1	NM_153668	2415	270	41	751	GGCGGAGCTTCCCTAAAACCAGAGTTTATCGACATTATTAACGCAAAAGCATAAAGACAT
2,459	4,57E-08	A_15_P193701	tpi1b	TPI1	triosephosphate isomerase 1	NM_153668	2415	179	38	751	GGCGGAGCTTCCCTAAAACCAGAGTTTATCGACATTATTAACGCAAAAGCATAAAGACAT
2,458	5,29E-08	A_15_P193701	tpi1b	TPI1	triosephosphate isomerase 1	NM_153668	2415	214	24	751	GGCGGAGCTTCCCTAAAACCAGAGTTTATCGACATTATTAACGCAAAAGCATAAAGACAT
-1,489	3,80E-05	A_15_P194691	zgc:136833	TRIM55	tripartite motif containing 55	NM_001039982	17994	219	57	1012	AATGCTAAACCCCTTCTGCAAAAAATTGCAAAGGCATCGAATACCTCACACCTGGAGAGA
-1,444	7,00E-05	A_15_P366285	zgc:56376	TRIM63	tripartite motif containing 63	NM_201095	27481	334	67	1358	GTTGTTCTTAAAAGTCATCTTCCTACTTTTGTTTCGCTCAGAAATGAGTCACTGTTGTTT
-2,234	1,19E-07	A_15_P147811	zgc:86757	TRIM63	tripartite motif containing 63	NM_001002133	31198	380	15	1035	GTACTAACAAAAATGGACTTTGGAGTTGGTGGTATTGATAATGATGATGATGAGGAGGAG
-2,582	2,07E-08	A_15_P119618	zgc:86757	TRIM63	tripartite motif containing 63	NM_001002133	34918	423	45	1444	CACTTGCACTTGACTGTAATGCAATGCTCATTTTCATTGGATAATTCAGTGGAAATAAAG

-1,438	8,89E-05	A_15_P148116	zgc:103570	TRMT10C	tRNA methyltransferase 10C, mitochondrial RNase P subunit	NM_001007332	25484	309	67	808	ATCTGGACTGGGATTGTGGAGCTAAAAATCTGACTCTGGATCAGATGATCCGCATTCTGA
-1,423	0,000105732	A_15_P112485	zgc:92277	TYW3	tRNA-yW synthesizing protein 3 homolog	NM_001002611	37653	456	83	1272	GGCTCATTTGGGCGACTTGGCTCATTAACAGTCCACTCTTTCTGCCATGAGAAATCAAAA
1,613	6,62E-06	A_15_P593357	LOC795944	TROAP	trophinin associated protein	XM_001334580	24058	293	12	2603	GCTGACAGGAAACACTGTGTGCTTGTCTATTGTGTAAAGTCTGTAATAAATCTATATATG
2,002	1,43E-07	A_15_P104093	tmod4	TMOD4	tropomodulin 4	NM_131196	20750	253	18	1317	TGCAAACTTGAACAAGATGCTAGATAGTTCATTTTCTGGTAATATGGTGCTTCCACACAC
1,724	1,96E-06	A_15_P109860	tpma	TPM1	tropomyosin 1 (alpha)	NM_131105	22847	277	70	1080	TTCTGTGAAATAAAATTTCCTCCCATCTGTGTAAGCTCCCCACTCCTTTCTCTTTAGT
1,595	7,94E-06	A_15_P113180	zgc:77592	TPM3	tropomyosin 3	NM_205676	23374	285	3	1250	GACTGGTGTTGGGCAACCAAGCATTTACCCATCTTCAATTGCACATGTATTATATCTCAT
1,583	8,59E-06	A_15_P102851	zgc:63734	TPM4	tropomyosin 4	NM_199675	24691	300	83	1594	TTGGTTATTTAGTGGGACCATTTTGTACACATGGTGCCTGTAAGGCCCGTTTAACTGTTG
1,629	6,01E-06	A_15_P118352	tnnc1	TNNC1	troponin C1, slow skeletal and cardiac type	NM_181498	19524	238	71	1617	TGAAGTTGATGAACAATAAAAAACTTGACAGCCAGTTAGAATGCATTCAGATATGAAGGG
1,411	0,000126147	A_15_P108824	zgc:86932	TNNC1	troponin C1, slow skeletal and cardiac type	NM_001002085	39350	477	17	707	GAAGTGAATCAGTCTTGTCATACTGCTGCCCTAATTATTCGTGTTATTTGTGCTCAAGTA
1,522	3,36E-05	A_15_P193931	tnnc	TNNC2	troponin C2, fast skeletal type	NM_131563	6159	77	47	830	CTTTAGTCTAGATTTAGTCTAGATCAGCAGCTTGTTATCGCTGCATAGACCAATGCCAAA
2,772	2,84E-09	A_15_P173666	zgc:103458	TNNI1	troponin I1, slow skeletal type	NM_001008613	12713	156	78	835	TTGCCAGTGTGTTCAGTAAACTACAAAAAAGTAGGCCTTTTTAAGTTCACGTTACACTAT
-1,572	1,16E-05	A_15_P148906	zgc:112242	TNNI1	troponin I1, slow skeletal type	NM_001020668	42042	509	56	447	CCAAACACAAAGAGTCCATTGACTTTAAAGCAAACCTAAAGACAGTGAAGAAAGAAGAGG
1,535	1,59E-05	A_15_P211721	zgc:92053	TNNI2	troponin I2, fast skeletal type	AF539738	37206	452	25	751	GCTTTCAGTGCCTCAATTAAGCATTTGTTGTATGCAGCCTGCAAATCCTAGAAGGTCTGC
1,487	6,24E-05	A_15_P101048	Tnni2	TNNI2	troponin I2, fast skeletal type	NM_205742	25913	315	31	127	TTGAAGAGCCTGGTGCTCTCCATTGCCTTCAATCTGCTGGATGCCGAAGCCAAGCAGCAC
1,772	1,79E-06	A_15_P446310	zgc:114184	TNNT2	troponin T2, cardiac type	NM_001025179	19744	242	15	653	AACGATAAACTGAAACGGCAGAAATATGACATAAATCAGCTGCTTTGCCGCGTCAAGGAT
1,687	4,87E-06	A_15_P158911	LOC556703	TNNT2	troponin T2, cardiac type	ENSDART00000067351	25073	305	25	659	TCTTTCTGAAGATAAACTGAAGGAGAAGGCCAGTGAAATGTGGCAGTGGATGATGCAGTT
1,685	2,45E-06	A_15_P100007	zgc:114184	TNNT2	troponin T2, cardiac type	NM_001025179	20222	247	3	814	TGTTTGTTTGATGGAGATACGTTTAAAATCATTTTTCTGAACGTACAAACATGCTCTGGC
2,578	5,57E-09	A_15_P170661	tnnt3a	TNNT3	troponin T3, fast skeletal type	NM_131565	39978	483	84	598	TCTGAGAAATTTGAACACATGGAGAGGCTGAAGAGACAGAAGTACGAGGTTACTACACTG
-1,469	5,95E-05	A_15_P114150	zgc:63488	TDO2	tryptophan 2,3-dioxygenase	NM_199856	21643	263	49	1576	TTGAATGAGGCACATGATGTAGGTTTCTCTGGTTGTTTGTAAATATATGATACACTCTAC
-1,427	0,00047238	A_15_P116639	zgc:65895	TSC22D1	TSC22 domain family member 1	NM_200574	40024	486	23	2097	ATGTGCATGTTTCCTTTAAACATGTGACGTTGTACAGTTGCACTCAACAGCTGCACAGTG
2,810	2,28E-09	A_15_P106537	tsc22d2	TSC22D2	TSC22 domain family member 2	ENSDART00000061315	18462	225	40	3104	TTCGATGGTGAAGGGTGAATTATTTTGGTCTCGGAGGAAAAGTCCCAGTTATACGTAAAA
1,896	3,61E-07	A_15_P139271	ENSDART00000104684	TSC22D2	TSC22 domain family member 2	ENSDART00000104684	27195	331	6	999	ACTCTGTTTTGGAGAGGGAAAACGCAGTATTGAAATCTCTGGCCAACAACGAGCAGTTGA
1,537	1,54E-05	A_15_P348830	zgc:153012	TSC22D4	TSC22 domain family member 4	NM_001077734	591	9	34	1235	TTAGGTTAGGTAACTGGCTCTTCCTGTCTGCTAGTGAATAATGATCTGATCTGTAACGAT
-1,417	0,000117351	A_15_P210696	dt1p1a10l	TSR2	TSR2, ribosome maturation factor	NM_173284	31825	385	82	1041	GCACACCAAGAGAAAAAACTGCAGTTACAGAGCTTGTTAAATGATTAACATCATCATTTC
-1,451	6,81E-05	A_15_P118225	dt1p1a10l	TSR2	TSR2, ribosome maturation factor	NM_173284	39818	483	2	1010	CCAGCAGCAGTGGTGAATATGCTGTTTAACAGGCACACTAAGAGAAAAAACTGTAGTTAC
1,438	7,02E-05	A_15_P210251	ttk	TTK	TTK protein kinase	NM_175042	6426	81	14	3117	CATACAAGATGTCAGGCAAAACCGCTTCCACATTATCACTTCATTCTACATGCCTCTTTT
1,425	0,000100184	A_15_P102068	ttk	TTK	TTK protein kinase	NM_175042	2774	38	23	3115	CGCATACAAGATGTCAGGCAAAACTGCTTCCACATTATCACTTCATTCTACATGCCTCTT
2,471	2,06E-08	A_15_P110343	tuba1	TUBA1C	tubulin alpha 1c	NM_194388	37048	449	29	1404	ACTTACCAGTTGTCAACTGGCTAAAAGGTCAATCCTTGCGACACTTTTAGAAAAAATAAA
1,593	2,04E-05	A_15_P103091	tuba8l4	TUBA4A	tubulin alpha 4a	NM_200185	24431	297	36	1403	TATTAAGTTGATGGCTTGCTGACCCTTGCACAACCTAGCAAGACAACTCATGCCTGACTT
1,493	3,50E-05	A_15_P210071	tuba8l3	TUBA4A	tubulin alpha 4a	NM_001003558	42681	518	69	1463	GATGTTTGCAACAACGACACAACTGCTACTTGAAATTCCATTTGCATTACAATTGGTTTT
-1,522	0,000285586	A_15_P118678	tuba8l2	TUBA4A	tubulin alpha 4a	NM_200691	3767	50	17	511	CGGGCACTACACCATCGGCAAGGAGATCATTGACTCTGTGCTGGACCGCATTCGCAAACT
1,509	4,77E-05	A_15_P119881	tuba8l	TUBA8	tubulin alpha 8	NM_212772	336	6	46	1730	TTTGTAAGCTGTCTTTGTCTCTCACACATGGTGTAAGTGATCAATGCAGTTTCAGAATAA
-1,415	0,000106771	A_15_P116464	zgc:92701	TUSC2	tumor suppressor candidate 2	NM_001002402	16630	204	39	996	TGTATACCAAGCAGAACTCCAGAGAGGATTTTCGTAGAGGTAACGTCGTTAGGGTTAGTA
-1,425	8,74E-05	A_15_P137941	zgc:92701	TUSC2	tumor suppressor candidate 2	NM_001002402	8631	107	35	1000	TACCAAGCAGAACTCCAGAGAGGATTTTCGTAGAGGTAACGTCGTTAGGGTTAGTACAAA
2,919	1,95E-09	A_15_P110475	tyrp1b	TYRP1	tyrosinase related protein 1	NM_001002749	34088	413	50	1835	CATGAGGTTATGCACTGCTTATGAATGCCCTATGAACACATGACAAAGTTATTGTACAGT
-3,713	3,04E-10	A_15_P382380	zgc:154059	TAT	tyrosine aminotransferase	NM_001077554	4894	62	85	1965	TGTTACATCCCACCCCCCAACCCGAAAAAGCTATTTAAATAAAAGTGTATCAAGATTTTT
-4,558	3,77E-11	A_15_P111952	zgc:154059	TAT	tyrosine aminotransferase	NM_001077554	22173	270	67	1415	AGATGATGATCGAGGCATGTATTCGCATCAGAGAATTTTGCGCACGTCACTATCGACCTA
2,060	1,50E-07	A_15_P207786	tpst1l	TPST1	tyrosylprotein sulfotransferase 1	NM_200202	39000	474	7	1798	GCTTTTGTCTTGTGGTTCTATTTGTATGCATGCATGTCACAGTAAATGTGTCCTAAAGAG
-1,741	1,92E-06	A_15_P104908	zgc:73238	UQCC2	ubiquinol-cytochrome c reductase complex assembly factor 2	NM_200758	37354	454	17	570	TGGAAGAGCTGCTGTAGAGTTGAAGAAATGTGACAATTCAGGAAAATCGTATTCAGTTTT
-1,443	0,000147308	A_15_P164266	zgc:158399	UBAP2	ubiquitin associated protein 2	NM_001082481	40095	486	59	2896	TGGAACAGTATATAGCAAGAACCAGACTTTTGAAAAGCAGGGTTTCCCTACAGCAGCTGG
1,744	1,49E-06	A_15_P205326	zgc:153687	UBE2T	ubiquitin conjugating enzyme E2 T	NM_001077295	34804	422	72	642	CCAAAAAAGTGTGCTTGTAGCAGCTCTATTTCACTGATGACTGATATACAATTTTGAGTT
-1,507	2,75E-05	A_15_P193091	zgc:162907	UBTD1	ubiquitin domain containing 1	NM_001089401	43124	524	74	1879	GCTAATTGGGAATCTGAAAGAAAAACACTTGTCAAATCTCACTGTCAACATTTCACATGT
-2,424	1,19E-08	A_15_P110415	MGC162578	UBFD1	ubiquitin family domain containing 1	NM_001082830	16176	197	65	573	AGCTAAGGAGCGTCTGCCAACAGTGCCTTTATCAGGAATGTACAACAAATCTGGTGGTAA
-1,747	1,84E-06	A_15_P194881	ubl7	UBL7	ubiquitin like 7	NM_200360	20189	279	2	582	AAACCTGCTGGACACGTTGATCAGGTCTCACCCGTCGCTGGTTAATGCCATTATATTAAT
-1,759	1,81E-06	A_15_P194881	ubl7	UBL7	ubiquitin like 7	NM_200360	20189	350	10	582	AAACCTGCTGGACACGTTGATCAGGTCTCACCCGTCGCTGGTTAATGCCATTATATTAAT
-1,786	9,42E-07	A_15_P194881	ubl7	UBL7	ubiquitin like 7	NM_200360	20189	246	71	582	AAACCTGCTGGACACGTTGATCAGGTCTCACCCGTCGCTGGTTAATGCCATTATATTAAT
-1,824	8,67E-07	A_15_P194881	ubl7	UBL7	ubiquitin like 7	NM_200360	20189	292	68	582	AAACCTGCTGGACACGTTGATCAGGTCTCACCCGTCGCTGGTTAATGCCATTATATTAAT
-1,841	1,11E-06	A_15_P194881	ubl7	UBL7	ubiquitin like 7	NM_200360	20189	477	4	582	AAACCTGCTGGACACGTTGATCAGGTCTCACCCGTCGCTGGTTAATGCCATTATATTAAT
-1,427	0,000111267	A_15_P108713	uba1	UBA1	ubiquitin like modifier activating enzyme 1	NM_213062	3656	48	45	4053	ACATGATTTTACTCTGTAATGGGAGCACTTAGTGTGTTAGTGAATAAAGTTGGAAACGTT
1,546	1,64E-05	A_15_P148666	uhrf1	UHRF1	ubiquitin like with PHD and ring finger domains 1	NM_213077	30149	366	71	5014	CCTTGATGTTTTTCGCTTGTTACTATAGTATTTGCTAAATAAATGCCTAATGGCTGCAGA
1,452	5,75E-05	A_15_P304326	uhrf1	UHRF1	ubiquitin like with PHD and ring finger domains 1	NM_213077	39932	483	61	4867	CAGGTGCATTTTTGCGTCGATCCTGGATCTGGTTTTAAGCGTCTTGATTTTACAAAGGTT
-1,722	4,91E-06	A_15_P115710	zgc:92173	UBE3A	ubiquitin protein ligase E3A	NM_001007318	23384	285	8	3946	ACTGTGGTTTGATCCACTGCTGATGGCGCTAACATAAAAGGGGGAAACAGAACTTGATAT
1,442	0,000168539	A_15_P102351	usp1	USP1	ubiquitin specific peptidase 1	NM_199579	43211	526	47	3124	AGCTAGATCTCTGAGCAATAAATAACACCCTTCGTGTAGAGTCTCTATTACTACATGGTA
-1,401	0,0001621	A_15_P173651	MGC163140	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	NM_001098386	14368	175	73	3412	GTGGAATCCTAAAGATTTGTTCTTGGTCCTTGGTGATTTATAAAATTCAAGTCAATGGAC
-2,135	6,87E-08	A_15_P194636	usp14	USP14	ubiquitin specific peptidase 14	NM_199973	22303	272	47	1632	ACCGTAAATGCCATTTCAGAGCACTGTCTGTATAGATGTGCAAAATAAATTTCTCGTGTC
-1,457	9,29E-05	A_15_P107099	usp5	USP5	ubiquitin specific peptidase 5	NM_214755	31263	379	49	2604	GAGAAACCACCGAAGGACCTGGGATACCTGTACTTTTACAGGAGAGTGATGGAATAAACT
1,492	7,10E-05	A_15_P109312	ugdh	UGDH	UDP-glucose 6-dehydrogenase	NM_001110402	3409	46	4	1658	CCAAAGTAATGTGTGACCATTGCTGGAAATCAACAGACTCTTCTGTTTGTAAAAGTGCAT
-1,455	0,00020485	A_15_P264991	ulk1	ULK1	unc-51 like autophagy activating kinase 1	XM_682116	15621	191	37	3798	TAACCGCAGCTGTAAATACTGTACATTCTGCATGTGTGTTTTTTATTTTGGAGTGAATGC
1,564	0,000138386	A_15_P115948	zgc:85838	UCMA	upper zone of growth plate and cartilage matrix associated	NM_212934	35493	429	83	1226	TACTTCTTGCAATCCAAACATATAACATGTTGTAAATCTTTCAATTTGGTGAAATAAAAC
1,441	0,000147005	A_15_P108811	zgc:77421	UPRT	uracil phosphoribosyltransferase homolog	NM_207091	39556	480	38	1086	TCATGCTTCTCCATGATACCACTGGGATGAAAACACACCATTTCTGAACATTCTGGAGTG
1,807	8,85E-07	A_15_P376630	zgc:158663	URAD	ureidoimidazoline (2-oxo-4-hydroxy-4-carboxy-5-) decarboxylase	NM_001080172	43255	525	70	689	ATATTTGTGATATGGGCCTGTAGGCTATACGTTCTCTGTACATTTACAATAAAGTTGAAG
1,752	1,30E-06	A_15_P142611	zgc:158663	URAD	ureidoimidazoline (2-oxo-4-hydroxy-4-carboxy-5-) decarboxylase	NM_001080172	29159	354	74	696	TGATATGGGCCTGTAGGCTATACGTTCTCTGTACATTTACAATAAAGTTGAAGTGATAAC
-1,717	2,00E-06	A_15_P101502	uppl	UPP2	uridine phosphorylase 2	NM_200144	16616	203	32	1519	TCTTCATCCTCTGGTACAGTAATGTAGATGTTGGACTGAAGCAGCTAATATTCATTTACA
4,003	1,60E-10	A_15_P142801	urod	UROD	uroporphyrinogen decarboxylase	NM_131347	38640	468	78	1101	ATTCGTGGAGGCTGTACATAACCACTCTCGCCAGCTTCTCAAACGCTAATAAAAAAGTCC
-1,471	4,37E-05	A_15_P288671	zgc:153384	UTP18	UTP18, small subunit processome component	NM_001076764	43388	528	68	1721	TGTACAGTTCCTGACCGTGATGATCAATGTGTTTGAGTACACTGCTGAATAAACACACAC
-1,487	3,60E-05	A_15_P194476	zgc:153384	UTP18	UTP18, small subunit processome component	NM_001076764	36187	439	15	1735	CCGTGATGATCAATGTGTTTGAGTACACTGCTGAATAAACACACACACACTCAAAAAA
2,270	2,52E-08	A_15_P204471	LOC795272	VPS72	vacuolar protein sorting 72 homolog	ENSDART00000085653	17357	212	71	1017	ACTCCAGCAGACACCACTGCAAAGAGCCTGAAGCAGAAGATCATTATTAAACAAGCCATC
-2,003	3,90E-06	A_15_P193431	vcp	VCP	valosin containing protein	NM_201481	36545	443	26	2060	TTCTTAAAGCTAACCTCAGGAAGTCTCCAATCTCAAAGGATGTGGACCTGGACTTCTTGG
3,269	5,88E-10	A_15_P206256	zgc:158875	VCAM1	vascular cell adhesion molecule 1	NM_001083835	9611	119	24	2849	CAGTTTGCTGTACTCAAGTTGACAACACAAACAAATTCTGTATTTAATTCAGTGTGGTGA
2,706	4,59E-09	A_15_P147821	si:dkey-14d8.3	VEGFA	vascular endothelial growth factor A	NM_001044855	4244	56	5	2248	TGTGCAGTGTTATTCTTGCCCCATTTTGTCTGCAAAACTCCACACTGTTGTTCTGAGAAA
2,687	2,36E-08	A_15_P158881	si:dkey-14d8.3	VEGFA	vascular endothelial growth factor A	NM_001044855	41454	501	76	1223	AGAAGAAGGTTGTTTGTTCAAGACCCAGAGACATGTCAGTGCTCCTGCAAACACTCTGAA
2,669	4,06E-09	A_15_P113354	vegfa	VEGFA	vascular endothelial growth factor A	NM_131408	12537	154	74	2479	AGCTCGGTGGAGAAGTGTTGGGATGACAAACAAACATTCTCTTTGTGTGCCACGTTTTCA
1,431	8,25E-05	A_15_P158466	vcanb	VCAN	versican	NM_214688	12909	159	8	4693	TTCAGTGAATCTCAGTACCGCCATCGCTGGTCAAAAACAGCAGAAGAACTCAAACACTGA
-1,464	5,11E-05	A_15_P102485	vdr	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	NM_130919	9666	120	52	1432	ATGCCGGAGCCAGAACATCAATGCGGCAATGAGAGTGCTCTGGGGGCTGAGAAAAAGCCT
2,358	1,89E-08	A_15_P100717	ENSDART00000075935	VTN	vitronectin	ENSDART00000075935	38141	461	78	1431	ATTTGAACAGCATTGTTGGATTAGAAGTCATTCATGAGCCATTAATCGCTGTCAGCATTG
1,920	4,35E-07	A_15_P119259	ENSDART00000075935	VTN	vitronectin	ENSDART00000075935	2690	36	64	1070	ATCGCTCTTCTGGGAAGACTTCGGACTGGACTATGAGGAAAGGTATTTGGAACAGAGAAA
1,494	2,88E-05	A_15_P108721	vdac1	VDAC1	voltage dependent anion channel 1	NM_001001404	909	13	47	1479	GGATTTAGCAGGATGGAGTCCTTCCTTACGTTGAATAAAACGTTCGACCTGTATCACACC
1,615	1,30E-05	A_15_P106646	zgc:158722	VHL	von Hippel-Lindau tumor suppressor	NM_001080684	39513	479	16	503	TAAAGAGATGTATTTGCCAGCATCTCTTGAAAATGGGCAAGTCGCAAATGCCAAGATCAC
1,454	5,48E-05	A_15_P520862	LOC568379	VWA1	von Willebrand factor A domain containing 1	XM_691704	12224	149	85	1841	TGAACAGCAGAAACTTTCCACAAATGGACAGATGGAGCTGTTTGAACACTCATCAGCCAT

2,414	1,20E-08	A_15_P103020	zgc:153112	VWDE	von Willebrand factor D and EGF domains	NM_001076771	28157	342	72	613	CACCGGACCGCAGTGTGAAGAGAGGAAGAAGCTTTACTGATGTCAGAATAGTCTGATCTC
2,409	1,29E-08	A_15_P208781	zgc:158671	WFDC1	WAP four-disulfide core domain 1	NM_001080703	25458	309	54	2160	GTGCAGATGTGTTTTACTCCACGGATGTCTGATAAGCTACACGAATCTGACTTGTGGAAA
1,624	5,11E-06	A_15_P375905	DKEY-238O13.6	WFDC1	WAP four-disulfide core domain 1	NM_001100000	5080	66	9	812	AAACTCAGATGGACGAAGTCTGAGACACAAGTCCTTCAAAGATTATAAGGATTATACAGG
2,469	1,95E-08	A_15_P118458	wsb1	WSB1	WD repeat and SOCS box containing 1	NM_199633	36947	447	62	3282	GCTGTTCCCAATTCGTCAAAAGGAAAAGTCATCTGACAAGAATGTACTTTTTTCTGTCCT
1,942	3,06E-07	A_15_P149171	wsb1	WSB1	WD repeat and SOCS box containing 1	NM_199633	8718	107	79	3339	CCTCCAAAAGTTGGAGTTTCTGTTTGTTTGTTTGCTTGTTTGTTTGTTTTGATTGTCAGA
1,852	5,78E-07	A_15_P341460	wsb1	WSB1	WD repeat and SOCS box containing 1	NM_199633	8521	105	64	1753	TTTTTCTTCTGGCACAACTTGTATAGCACCTTATAGCTAGGTGAATGTGGTGCTTTTAGC
1,571	1,05E-05	A_15_P144496	LOC570063	WDR76	WD repeat domain 76	ENSDART00000075588	23308	284	54	1241	TAAAATTAAGGTATATCACGAGAGCGGTCGCCTGCTCCACACTTTACAAAACACGGAGCA
-1,404	0,000251768	A_15_P142706	wdr82	WDR82	WD repeat domain 82	NM_199551	31503	383	1	1919	AGCTGACAGAGGAATATCTGTATGATGAGGTCCATCCTAAACAACATGCCCACAAGCAAG
1,687	4,50E-06	A_15_P104490	wif1	WIF1	WNT inhibitory factor 1	NM_131229	33380	406	26	1819	AAGCCAAAAATGGTTTAGTGTGACTTCCATTAGCCTACACAAATAAAACGTGTTTTCATG
-1,408	0,000228124	A_15_P132261	LOC553286	XIRP2	xin actin binding repeat containing 2	AF429955	936	14	60	118	AGATTTCAAGACTCTAGGCTGAAATAGGAAACGTGCAGAAAGTCATCAGAGAGGATGAGG
1,411	0,000118631	A_15_P107563	zgc:85702	YBEY	ybeY metallopeptidase (putative)	NM_212594	12746	157	10	647	GGACATTTGCTGCGGAGATGCACTACTGATGAATCAAAACCACAAAACAAGCCGGAGTTT
1,676	9,57E-06	A_15_P413905	LOC793098	YME1L1	YME1 like 1 ATPase	XM_001332041	30617	371	55	1369	ATTGTGATTGGAGCTACAAACTTTGCTGAAGCTCTGGACAATGCTCTAGTGAGACCAGGT
-1,555	2,18E-05	A_15_P119370	zfand5b	ZFAND5	zinc finger AN1-type containing 5	NM_200949	25675	312	79	1677	TTTTCCAGGTTTTGGGTCTGGCTGCTCAGTGCTGTTTTGTTTTAGAGATTTGAGTTTACA
1,739	3,10E-06	A_15_P404590	LOC572136	ZBTB40	zinc finger and BTB domain containing 40	XM_695817	19999	244	59	1369	CCAGCTACAGAGGACTGGACAAATGATGTATTATTAAAACTGTACAATAAAATCCTCATG
-1,497	3,92E-05	A_15_P110789	zcchc9	ZCCHC9	zinc finger CCHC-type containing 9	NM_198370	29522	359	5	968	ATAAACATCCCCCTGATGAATCTGAGACTGGAACATCACACATGATTTGGTCAGAATTGT
1,737	2,18E-06	A_15_P100773	ENSDART00000042588	ZFYVE21	zinc finger FYVE-type containing 21	ENSDART00000042588	29867	364	11	1318	TTAGAGCAGCCAGACTGCCAGGACTCATATTAAACTTTGTTCTAGGTCATCAGGTTTGGT
1,632	1,19E-05	A_15_P193699	prkcbp1l	ZMYND8	zinc finger MYND-type containing 8	NM_199641	36732	445	36	3106	CAAACTGTAAGAAAGAGGCCATTTTCAACTGTTGCTGGAACACGAGTTACTGCGATTACC
1,586	8,04E-06	A_15_P118539	prkcbp1l	ZMYND8	zinc finger MYND-type containing 8	NM_199641	28858	352	5	3985	GTGGGCATGTTTCTTTTTTCCTCTTGTCTTGTGGACTCTCTTGTTTACATACTGTAAATA
-1,591	7,54E-06	A_15_P406770	LOC564460	ZMYND8	zinc finger MYND-type containing 8	ENSDART00000040235	10486	129	47	547	TAGAACAGCATCCAGACTATGCAGAGTATATATTTCACGCCATGGATATCTGCACTTTAG
2,093	8,63E-08	A_15_P109056	znfl2a	ZNF134	zinc finger protein 134	NM_194390	15390	189	3	592	ACCTGATGACGCACTACAAACACAAGCCGCTCCTCTGCTCGGTGTGCGGGAAAGGGTTTA
1,565	2,86E-05	A_15_P447010	blf	ZNF22	zinc finger protein 22	NM_001012485	30602	372	46	1284	AATCACATGTGCTTTGATTGTGGGAAGACCTATTTTACGAAGAATGAACTGAAGCTGCAC
2,404	2,77E-08	A_15_P141881	si:busm1-189a20.4	ZNF292	zinc finger protein 292	NM_001030212	36807	446	74	7840	ATCCTACTCAAGCAGCTTCAGGAAATGCGACCCACAGTGATCCTTCAGAAAGAGAAGTAA
1,603	8,48E-06	A_15_P177346	si:busm1-189a20.4	ZNF292	zinc finger protein 292	NM_001030212	35714	433	29	6052	AAAGAGATTCTGCCCATAGCCCCTTTTACACAAAATCCTTCAGCACTGCTTCACAAAGTA
2,369	1,52E-08	A_15_P141651	zgc:158367	ZNF395	zinc finger protein 395	NM_001080054	35311	428	76	2534	GTACTTCCAAAGTGTTTCCTTTAATGAACCGTCTGAGATCTGTTCAAGATGAAAGTATAA
-1,472	4,33E-05	A_15_P202346	znf593	ZNF593	zinc finger protein 593	NM_200817	11181	137	61	245	CTTGAAAACCTTAAAGGAGCATTTCAAATCCAAACCCCACAAAAAACGGATTAAAGCAGC
-1,483	6,17E-05	A_15_P104011	znf593	ZNF593	zinc finger protein 593	NM_200817	5225	65	82	503	TGTTAATTTATGGAGATGGAAAATCTACATGTAAAGGTCCTCAGCTGGCACAGTGTCAAT
-1,501	2,67E-05	A_15_P202341	LOC559352	ZNF593	zinc finger protein 593	ENSDART00000082237	757	11	44	247	AATCCAAACCCCACAAAAAACGATTAAAGCAGCTTAGGGAAGAGCCATACACACAGGCTG
1,660	4,03E-06	A_15_P295766	LOC100004980	ZNF654	zinc finger protein 654	XM_001344108	43350	527	49	3577	AAACTGTGCTGAAAAAGAAGATTGCGCCTGAGGAGCAAAAAGAGGATGGAGATGCTGTAA
2,302	2,11E-08	A_15_P171586	znf750	ZNF750	zinc finger protein 750	NM_001017786	4728	59	85	2393	GAGTGGGTGGTGGCATTTTTACTCAATAAAGTAGCAAGCCAAACTTGTAATATTTGAATA
-1,455	0,000171319	A_15_P150846	zranb1	ZRANB1	zinc finger RANBP2-type containing 1	NM_001077768	1482	21	25	1657	ATATTATAAGAGCTTCAGAGGAGAGACGCTGGGATACACACGCTTTCAGGGTGTTTACCT
1,450	6,00E-05	A_15_P185746	zgc:56597	ZRANB2	zinc finger RANBP2-type containing 2	ENSDART00000065108	39607	479	64	528	GAGGACGATGATGATGATGATGATGATGAAGATGATGCAGATTTGTCCAAGTTCCCGGTC
4,744	1,42E-09	A_15_P204546	LOC555835	ZP3	zona pellucida glycoprotein 3	ENSDART00000102798	35239	428	39	1364	GAAAAAAGGCAAGTTTGTGGAGCCCCGCAGAATATTTGAGGAGGTATTTGGACTGGACTA
-1,557	2,91E-05	A_15_P113021	zgc:77346	ZER1	zyg-11 related cell cycle regulator	NM_212901	37722	457	33	3314	TGATGTACTGAAGTCAGACGTCTACACAACACTGGCTGTAAAGAGAGATGAATATTCATG
14,051	4,32E-12	A_15_P367940	LOC100007672		#N/B	XM_001346031	31815	385	77	1862	TAATGCATTTCACAGACATATGGATTCCCAAGACTGGAATGACTCTTGGAGGGTGAAGAA
12,644	2,28E-13	A_15_P402330	LOC568476		#N/B	XM_701353	2294	32	32	703	TAGAGTGTGCTAGATTTCACTGCTGTGAAATAAAGCTATATTTGCTCGATCTGTGTGGTC
6,229	5,26E-12	A_15_P226221	TC317454		#N/B	TC317454	3250	44	9	1439	TGGTGCAGTTATATCCTGGCTGTCAGAAGAGAGATTAAAATAAGAGTTGTAGTGAAAAAA
6,165	5,06E-12	A_15_P506692	LOC569901		#N/B	XM_693317	43622	531	55	1331	GGACTGAAATCCTGAGTTTTGCACTTAGCTTTAACACATTCCAGCACTCGTAGCATGAGT
6,094	6,32E-12	A_15_P106524	wu:fc15e02		#N/B	EH438071	18014	220	67	637	AAGGAGCTCTGCGTTAGAGATGTACCATTCGACTATTGAAAGCACAGCCCAATGCACAAT
5,630	1,54E-11	A_15_P118620	TC346406		#N/B	TC346406	13719	167	82	362	ATGCTTTTCAGATGGCAAAATCTTTCTCACTTTTGATTCAAATAAAAAGCCAGTCACTCC
5,556	1,31E-10	A_15_P350060	wu:fc15e02		#N/B	EH438071	37977	460	77	429	ATCTAAAATCACAGCACCGGGTTTCTACTTCAGGACTCTCTTGCTTTAGTTTAGCTCTCA
5,449	1,64E-11	A_15_P469685	TC354942		#N/B	TC354942	31502	382	85	396	GGCAAGAGTCTGACAGAGATTTCTTTCCCAAACTGCCAATAAAAGCAATCTTTAATGTCC
5,062	8,33E-11	A_15_P498117	LOC569901		#N/B	XM_693317	1635	23	23	1339	ATCCTGAGTTTTGCACTTAGCTTTAACACATTCCAGCACTCGTAGCATGTGTGCCGTACA
4,840	9,45E-11	A_15_P468660	ENSDART00000077505		#N/B	ENSDART00000077505	31584	383	43	2537	GATCAAACTAGAGACACAACATGAAAGACAGAGAGTGGAGGAAATGACTGCTGATTTTAT
4,837	1,44E-10	A_15_P459450	EH585008		#N/B	EH585008	25644	311	64	493	TAAATGTTACGTAAAACATGTTGTGTAACAGCATCCAGAATCCAGTAAAAGCGCTCTTTT
4,720	2,92E-11	A_15_P261176	LOC571517		#N/B	CO920562	21140	257	48	398	ACCTGTGGCTGTTATGAACAGAAATATCGTGATTGTTTTATTTTACTCCGTGAAGATTGC
4,648	5,92E-11	A_15_P100432	TC321730		#N/B	TC321730	10469	130	38	596	CTGCTCACACAACGAGAAGTACTTCGGTGAGAACTGGAGGAATTAATGAGGCTCTTCTAA
4,602	4,69E-11	A_15_P110873	TC365323		#N/B	TC365323	22608	276	32	1188	TTTATACATGTTATTCGAAGAACATACCCTTGAGTAACAAGCAGGAACAGGACGAGGTAG
4,509	4,20E-10	A_15_P438070	LOC557772		#N/B	XM_680892	5516	70	59	39484	ATCTGGAGAAACAGAAGGAGGAGTTTGAGCTCATGCAACAAAATCCTGGAATCCAGAAGA
4,414	5,62E-10	A_15_P112852	wu:fb60g12		#N/B	CK866844	16474	201	46	426	GGGCCCAGCTGAGGCAACTCAGCCCCATAAATGTTTAAAGAAAAAGAAATAAAGATCATG
4,378	9,67E-11	A_15_P336265	TC362338		#N/B	TC362338	22249	272	20	942	AACAAGCTGATGATCTGGACATGCGAATGATTGCGCACAGAGAAACAAAGAGATGAGGTA
4,309	4,77E-10	A_15_P132691	AY193833		#N/B	AY193833	8403	105	3	252	GACCCACGGGATCAAATGGGGGTTATCTGTAAGAATTGAAATATTGCAAATATTCTGATA
4,282	5,66E-11	A_15_P413585	LOC557772		#N/B	XM_680892	25100	306	39	41768	CAGAGAAAAGGAAGAAGAGCTAAGATCCATGCGTGCTGATATTGAAAGACAGCTAAAATC
3,929	1,78E-10	A_15_P102414	LOC568005		#N/B	CN023754	21083	257	19	628	ACCATTTGAAGCGCATTTTAAGGTTATCCGACACAATATTTTTACAGTGTCATTATCTCC
3,915	2,78E-10	A_15_P106213	AY880252		#N/B	AY880252	20293	248	40	1911	GAATGTGTTTGCTGTAATTGCATAAAACAATGCACTGTGTTCTAAAACACTCTCCAGAGA
3,871	1,92E-09	A_15_P112737	TC331860		#N/B	TC331860	29582	360	36	514	AGATCACATGCATTACGCGGGAGGGAATATAAACGCAAATAACGGGATCCGGCAATTCAT
3,825	6,79E-10	A_15_P218371	TC347987		#N/B	TC347987	11284	140	28	673	CATGCATGCAGTGCATCCATTGTGTGCATGAATTTATAAGTCAGTGCTATCATTTCTGCA
3,730	2,01E-10	A_15_P150276	zgc:158580		#N/B	NM_001080618	15324	187	55	1105	CACTCAACAGACCTAAACAGTTATCTGATGAGAATTGCGGTTATTTAATCTTTTCTAACC
3,725	3,48E-10	A_15_P179701	BC152081		#N/B	BC152081	11989	148	48	592	TCTGGATGTAGAAGAACGAAGAACATCTCAAGTGGAAAAAGAAAACTTCTCATGTATTCA
3,652	6,42E-10	A_15_P182716	LOC557772		#N/B	ENSDART00000077766	14932	184	25	3051	CTTCTTATCGTTGAGATTCAGGAACAAAGAGAGGATGTGAATAAAAGGTTAGAGGAGACA
3,618	1,07E-08	A_15_P333144	TC361332		#N/B	TC361332	35802	434	75	987	AAGATGAAATCAACAAGCGTGCCGCAGTGGAAATGAATTTGTCCTGCTGAAGAGGATGTT
3,451	4,45E-10	A_15_P107927	LOC566445		#N/B	ENSDART00000101146	7198	89	69	1955	TGCAAAATTGTGTTTCCTTGCATCACTTTCTTGTACAATAAAGAAAAATCCATCCTGGTC
3,442	4,52E-10	A_15_P602957	TC358225		#N/B	TC358225	7527	94	67	613	GGCTTGATGAAGCTGTTTCTGTACAACATGGAAAACCATCAATAATTCAGGGTTATATAC
3,419	5,58E-10	A_15_P288446	LOC561704		#N/B	EB861253	18459	226	38	465	CACAGACTGACGCCTCTTCGAGATCATAACTCACTATTGCTGCTAAATGAAGATGAAAAC
3,357	6,47E-10	A_15_P234736	EH581707		#N/B	EH581707	32168	392	1	600	GCCGATACGATAAATCATTTGACACACCTGTGTTTTCATAGCAATGGTGCTGTCTGTGCA
3,322	4,03E-09	A_15_P384240	ENSDART00000077550		#N/B	ENSDART00000077550	32193	391	15	3529	CAGACATACAGAAATACAAGGAAGAACTACAAAGTGTCACTGAAGAACTCCTGACAAAGA
3,230	5,83E-10	A_15_P209666	zgc:123103		#N/B	NM_001037120	21989	268	56	986	GCAAAATAGTCCACAGAATAGTCCACCTGACAAAATAGTGGCAAACAATTAATTACAGTT
3,222	7,98E-10	A_15_P541787	TC323531		#N/B	TC323531	18956	232	35	1139	GTGTATAGTATGGAGATTCCCGAGTGTCTTGTTGATAAATATTGTCTGAAAGGAGATTTT
3,128	7,81E-10	A_15_P213016	zgc:123103		#N/B	NM_001037120	24698	301	2	1008	CCACCTGACAAAGTAGTGGCAAACAATTAATTACAGTTTAATAAATGTCTCACTCAACAG
3,095	1,38E-09	A_15_P419055	TC340781		#N/B	TC340781	38649	467	83	747	AATTATTTTGTTTGTAGACCAATTGTTTCTGTAGACTTTACAGAAAGCACCTACCCGTGT
2,979	8,67E-09	A_15_P342340	TC327287		#N/B	TC327287	17923	220	21	2193	ATTTGTTCCAAACTCAAAGGAAGATATACTGGAGAGTGTTGGGGGAAAAAACAACCATGA
2,976	9,32E-09	A_15_P383730	TC356827		#N/B	TC356827	42961	521	64	731	TAGTATATGAAGGGTCCAGAAGCAGAACCACATGTCAAATTGACCATACATCATCTAGAGCCG
2,972	1,68E-09	A_15_P102047	LOC555334		#N/B	XM_677825	41985	510	27	1087	ATTAAGTCAAGTGCTGATCTGAACTGTATGTGCATAGTTGAGAAAACTGTGGTTCTGTTT
2,970	5,83E-09	A_15_P212506	zgc:123103		#N/B	BC124096	17985	220	52	1205	GAAAACCACATGTTTTTCCCCCAATAAAACAAACACAGTTTTTGCTCATTTTTGTCACCT
2,960	1,58E-09	A_15_P116142	A_15_P116142		#N/B	A_15_P116142	35724	434	35	0	ATATTTGATCTGCTAAACTGAGATCATCATCTAAACAGCACATATCATGTCTCCATGAAG
2,921	1,89E-09	A_15_P114739	TC336848		#N/B	TC336848	4926	64	16	557	TATACGTCAACGATGCCCTCAGTAACGTATTAGTGCTTTAAGGCTCTTCTGCCAGAGGTT
2,901	5,18E-09	A_15_P536082	TC360041		#N/B	TC360041	4062	52	82	1027	CTGATGAACCTGATCCAATACGACAAGACGCAATAAACAGAACCTCTGGATTCTCACGCA
2,879	7,54E-09	A_15_P306021	TC353258		#N/B	TC353258	32403	393	38	1045	AGAGCTTTATTCAGCCACTGGAGCTGTGCTGGGTGGTTTATATTATGAAGAGATCTGCTT
2,850	1,91E-09	A_15_P229961	EB982158		#N/B	EB982158	28848	350	85	563	GTTAGATGAGCACCAATGTGTGCTTTGTATTCGAGAACCTATGAGGTTTATCTGCAAGAA
2,836	5,05E-09	A_15_P111982	wu:fa55f06		#N/B	CK028201	24650	299	63	199	AAACGGTGTTCAGATCGCGCTTCATTCCTGCTGTACAGATACATTTTGGGTGTCAAACAT
2,823	2,31E-09	A_15_P384520	TC357075		#N/B	TC357075	27156	329	71	1340	TTCCATAGTAAGAAAAACAATTACTCTGGAAGTCAGTGTTTACAGGTTTGCTGCTTTCTT
2,821	5,59E-09	A_15_P104991	zgc:136930		#N/B	NM_001039819	8554	106	80	1516	CAGCCCAAACGTGAAAAGTCAAGTCCCATCCACTGTTTCTCCAATAAAGCTGCATTGTGA
2,752	2,86E-09	A_15_P349300	LOC564151		#N/B	XM_687500	21249	260	18	508	ATAAAGAAGAGAGGAAAACGAGTGTCCCGCATCTCAATGGATAGCGATGAGGATGAGCAA
2,748	4,76E-09	A_15_P566072	TC338327		#N/B	TC338327	12956	159	32	398	CTCCTCTCTGAGCTTTCTCTGTGAATTTACTGTTCTCTAAACTGCCAATTAAACTGATAA
2,708	5,80E-09	A_15_P430445	CF348313		#N/B	CF348313	35933	435	57	714	TTCACCAAATGAGGTCTTTCACCTTGAATGTGAGCGTGCATATGTTGATGTAATCTGCTG

2,696	5,25E-09	A_15_P281436	TC344281	#N/B	TC344281	27685	338	2	1886	GGTTCATTATGTACTACTCTATTTCAGTGTATATTTACTTGAAATGGCCCGTATAGGCGA
2,650	1,29E-08	A_15_P106753	TC357892	#N/B	TC357892	37983	460	81	203	CAATCCTGATGTTTGGGTCAAGTGACAAAACTGATAATCTCTCCTTGAATAACATGAAAA
2,630	1,26E-07	A_15_P101138	TC319349	#N/B	TC319349	23150	282	58	279	ATCTGGGCAAAGGGGTGAAAAGAGCTGTTAAATATGTAAATGAGTTCTTGGCCCCTGCTT
2,611	4,90E-09	A_15_P118042	ENSDART00000082372	#N/B	ENSDART00000082372	33902	411	39	1977	GTTTTCTGTGTTCAGGAGAGAACTGTGTACATTGAACAGAGTTTGTGAAGTAAATATGCA
2,582	1,00E-08	A_15_P184826	si:dkey-7c18.24	#N/B	NM_001082832	16040	195	81	615	ATGTGACTATGTGACATTGCTAGGAACATGGAACCCCATGGTCATGCTAGAGATTGTCAC
2,566	1,13E-08	A_15_P207721	si:dkey-7c18.24	#N/B	NM_001082832	35457	429	65	713	GGGAAGTCAAGACACAACCCACCAGAAAAATTCTCATTTAGTTGAGAAAGAAATGGTGTT
2,551	6,42E-09	A_15_P111276	LOC795119	#N/B	DT882146	13783	169	29	708	CAATGGTGCTAATGTTTACACCCTGTCAAAGTTGCTATTTTATTACTGCTTTATTACTGC
2,542	6,51E-09	A_15_P184831	si:dkey-7c18.24	#N/B	NM_001082832	6868	86	69	526	TCGATGGCTAGATCCGACTCAGTGGAGTGTAACACAAGCAATGAGAAAAAACACTCTGCT
2,513	5,45E-08	A_15_P108046	TC359747	#N/B	TC359747	37758	458	51	892	TTGTTCAAGACAAACTGTTCAAAATATGATGCATTTCTGAAATTTTTGCCATGTGGGACG
2,492	4,28E-08	A_15_P156321	cyp1c1	#N/B	ENSDART00000019953	41920	507	73	2935	GTTTACACTGAATGTTTTTGCAAGCTCAGTGCATGAAGCTTTCTGAAGAAAATCAGTTTTT
2,475	8,74E-08	A_15_P110105	TC361324	#N/B	TC361324	14829	182	56	316	CCCCCAGAACACTGATGACGGCACAAACTTCGCCCAACTGATCAAGGACAGGGGCATTGT
2,457	9,71E-09	A_15_P219246	ENSDART00000080442	#N/B	ENSDART00000080442	37121	449	67	555	AAACCAGCTGATTACTCCCTCAAAGTGGTGAGAATGAAGATCAGACCTTCTTTCTCACAA
2,446	1,54E-08	A_15_P320876	TC344958	#N/B	TC344958	31963	388	66	946	ACATTAGTGTAAAGTGTTCAGAACCGCTGGAAAACATGTTTGGTCTGTTTAATACTCTAC
2,427	1,31E-08	A_15_P364555	ENSDART00000037713	#N/B	ENSDART00000037713	27022	329	3	1971	GATGGTGATGGACTTATCAAGCTCAATGTTTTTGAGTGGCTTCAACTGACAATGTACGCC
2,397	4,19E-08	A_15_P203566	LOC563311	#N/B	ENSDART00000016487	40647	491	85	1488	TTCGATTATAAAATCTCTGCCAAACCCAGGGGAAGCATTTTTGTGCTGTCTAACCCACTG
2,380	3,32E-08	A_15_P534377	TC359499	#N/B	TC359499	8104	102	22	1115	GTTAAGAGAAAAAACAGAGTACAGTCTTTTACTTCCTTCAAATCAAAGAGAGGGGAGATG
2,345	2,98E-08	A_15_P116912	TC306740	#N/B	TC306740	30703	373	15	1361	GTTCCCAATAAAGAGCACTTTGTAGGATCCCATTTTGGGCCGATGTCTTTATCTACACTA
2,335	1,88E-08	A_15_P107847	LOC791523	#N/B	ENSDART00000077221	24507	298	74	319	ACTTCCCTAACCGTCAAGGCTCAGAGAAGTACAAGTATATGAATTTTACAGGCCAAGCCA
2,331	2,91E-08	A_15_P111743	ENSDART00000079523	#N/B	ENSDART00000079523	38435	466	58	1577	AGCCTAAACCAATTGAAGCTGGCTCACGATTAACTTCTTGAAAGGTTAATTTGACTATAA
2,328	2,79E-05	A_15_P496107	TC313168	#N/B	TC313168	162	3	27	869	CAATGTGAACTCTCCATTGCGCTCTCACAAAGCTGGTAAAGAGAATTATATTACAACCCG
2,320	2,38E-08	A_15_P562492	TC337014	#N/B	TC337014	43002	523	12	1888	CATCATCAAGTGTGAACGTTTGCCTGACCAATAAATCCACAATCACCGTGTGTGAAAAAA
2,315	2,55E-08	A_15_P510652	zgc:123103	#N/B	NM_001037120	39997	485	9	790	GAAGTTTAATCGTCAGTATGAAAGTGAGAAGGGGCATGAGGAACGAGAGAACCTCTTCCT
2,309	5,49E-08	A_15_P287511	LOC563311	#N/B	XM_686678	2779	37	26	1635	ACACTGAAGCCATTCGATTATAAAATCTCTGCCAAACCCAGGGGAAGCATTGTAAATTGA
2,262	4,77E-08	A_15_P488120	TC349926	#N/B	TC349926	25927	315	39	1469	GTAAAACATTGCATATAATCTCACCTATAACCTTGCTCATAACTCTTGGAATGGTTTGCA
2,256	3,57E-08	A_15_P536142	CT732399	#N/B	CT732399	33309	404	74	570	TCAAATGTCGGTCAGATGTTTGTAAAAGTGCTTTTTCTGTGTGTTTGACGTACCCGGCGT
2,253	4,63E-08	A_15_P215231	LOC557772	#N/B	XM_680892	2793	37	33	25437	GAGGAATTAATGCAGAAAATGGAAGCACTGAGCATGGAAGACTTCCAAGAAGCAAGTAAG
2,230	3,50E-08	A_15_P264431	wu:fb78a10	#N/B	EH503877	17075	209	13	804	TGTGAAGTCCCCGATGTTCAAATTGGATTTCTTGTCAAATTGCAAAATCTTGTTTTGTGA
2,218	2,98E-07	A_15_P100799	TC326093	#N/B	TC326093	13624	167	34	1560	AGCACAATGGTGTGTTGTACAAAGCACCACATCTCGTAACCCCCCCTCTGAAACGAATAAA
2,193	4,02E-07	A_15_P516942	CO923279	#N/B	CO923279	607	9	42	580	TGTGTGTTAGATCATATGCATGTGAACGAGTGTGAAGTCACTGGGTGTGTTGTGTTCAAA
2,188	4,15E-08	A_15_P105552	TC306241	#N/B	TC306241	23671	287	71	1499	ACAGGGTACCATGCAGGCTTTGTGAGATTTATTTCATCCTGTCCACCAAATGACAACTGT
2,172	4,07E-07	A_15_P382250	TC356358	#N/B	TC356358	36082	438	47	619	AGAGGGATAATTACCAAGTGGCCAGTAGGTGGAACATTTGATTTAATTAACCTTAGAGAT
2,152	1,17E-07	A_15_P310441	ENSDART00000073976	#N/B	ENSDART00000073976	33067	402	35	4167	AAATTCGAGATGAACAAGCAGCTTTCAGAGCGAGGATCCCTCATAATCTACCTGGACAAG
2,147	1,03E-07	A_15_P265161	LOC100005506	#N/B	XM_001344503	41404	501	51	668	TTTACTCAACATGGACATTCTGCCTCAGATACTGGACGTCCTGCACAAGCAACACAACAT
2,146	5,35E-08	A_15_P394195	EH448159	#N/B	EH448159	12891	157	84	798	AGTTTTGCGTTTTTGGCGGTTTTGCGCCATCTTGTGACTAAATAAAGCGCTCTTCATCAA
2,143	5,53E-08	A_15_P544397	TC324584	#N/B	TC324584	15927	196	24	3102	AGCGGGCTTTTTCATCATAGTGTTAGCACTTCAAGTCTTCAATAAATGATATAAATCCTG
2,136	7,37E-08	A_15_P186116	LOC556386	#N/B	ENSDART00000023506	28050	342	17	1305	AATCAGCAGGATGACCCTGGAAAAGAGGTTGTAGAGGCATTGAAAGCAGCTGAAGACAAT
2,135	1,17E-07	A_15_P113509	LOC100006823	#N/B	XR_030042	26066	318	24	5501	GTGAGATGAGCCCTACATTTTTAGTAGTTTTTCTTTATCCTGAGCAAAGTAATTTCCAAC
2,131	5,82E-08	A_15_P100537	TC323575	#N/B	TC323575	17839	218	63	1405	TTTCATGGGGTGCAAGAATGTCTACTTCAAAAACATTTCCCACTTTTATGTTTAGTATCC
2,124	7,56E-08	A_15_P430325	EB865652	#N/B	EB865652	5693	72	64	380	GAAATGGCTAAAGGATTACTCAAGGAGAAAGAATAACCTGCAATATTCCTGAAAGGATGG
2,123	6,10E-08	A_15_P145996	LOC558956	#N/B	ENSDART00000079420	12840	158	58	402	ATGAAGTTGCAGGACTATGACATCACCTCATTGAGCACCATTCACATGACTCTCCGTCTA
2,091	1,63E-07	A_15_P107796	zgc:101560	#N/B	NM_001005998	25344	308	80	1435	TATTTGTGCATTTGTTTTTATTTGATTTGCCTGTTTGGCTTGAACACAATATTAAATTAT
2,083	8,56E-08	A_15_P322221	CT694511	#N/B	CT694511	23336	283	69	231	GAGCACCACATCAGGTGCACAACCTGTACAGCTGTATCAAAGCTGCAGAAGATTTTGTTT
2,065	3,66E-07	A_15_P120732	TC361450	#N/B	TC361450	32509	396	6	182	ATAAATATGACGGACTGAGGACAGTTTTCATCAAGAGTGGAGAGCTTCATCAAAATCGCT
2,064	9,81E-08	A_15_P257676	wu:fb60g12	#N/B	CK866844	43313	528	30	433	GCTGAGGCAACTCAGCCCCATAAATGTTTAAAGAAAAAGAAATAAAGATCATGAACTGAA
2,060	1,02E-07	A_15_P540477	LOC799369	#N/B	XM_001339697	33083	401	44	2839	GTTGTCCAAATTAAATCTTTAGCAGTGCACATGGACCCTTTTCACATTTCTGGCTCTCAG
2,053	1,60E-07	A_15_P183216	ENSDART00000105181	#N/B	ENSDART00000105181	6009	75	54	1724	CAGACTTCTAGCAAAAGCTGAAGAAAATAAAAGCACGCTCTTATATGAAAGTGTCATTTG
2,049	1,01E-07	A_15_P110676	TC357542	#N/B	TC357542	40715	494	34	777	CCAGTTAAGCTTGCGACGGTACGAAGCAAGTCATATGATTTCAGTAAATGAGGCGAGTAG
2,042	1,56E-07	A_15_P347020	TC333221	#N/B	TC333221	4182	54	58	1178	AGGCATGAAGTACATGGTCGGAAAAGAGTGGAGGGACTTCTTTGATGTTGTCATTTTGTC
2,024	2,25E-07	A_15_P487455	TC349713	#N/B	TC349713	35161	426	84	851	GAGCTGTAATGGAGCATGTGTCTGCTAAGAGGAACTCTGTATGTAATCTCTATTAAATAC
2,019	3,84E-07	A_15_P349820	TC334287	#N/B	TC334287	37988	459	84	542	ACTGGGCAGAGGACTTATGCAATAAAAACAGCACCACCTAAGAGAGCTTATTGAAAACAA
2,017	1,26E-07	A_15_P110518	A_15_P110518	#N/B	A_15_P110518	43072	524	48	0	TTTAAAACCTTTTTTAAATTGGGAACAAAGGTGTTTGGGCATAACCTCAGGGGAATAATG
2,011	8,24E-07	A_15_P536237	LOC557081	#N/B	ENSDART00000076635	36213	439	29	1642	CGGATGTGAAAAGAGCTCTGTCAGATTTTGGCATTGAGGTCAGAGAACTGAAACTATTAG
2,007	1,60E-07	A_15_P222601	ENSDART00000058602	#N/B	ENSDART00000058602	34974	424	73	852	CTGGAGAGCCTCAAGTTGCGAGCTCGGGTTCATATTGATGTTTACAAAAATCAGGTTTAG
1,999	4,57E-07	A_15_P117464	LOC561143	#N/B	NM_001044954	31783	386	60	2117	TCAGTCTCCCTGACAGAGTTTTAATGTTTTGCAACCATCAAAAGCATATTGTAATTCAAC
1,998	1,45E-07	A_15_P108560	LOC555251	#N/B	XM_677718	10541	130	75	1750	TGGTAAGCACCATGGCATATTACAAATAAGGGACCAAACCACTGATTTAACTGTAACACA
1,994	1,57E-07	A_15_P182006	ENSDART00000104622	#N/B	ENSDART00000104622	36303	439	74	1500	GCAATAACTCTTGCCAAAGTGATGCTAAAGACTTTTTCTGCTACAAATACTCTCCTGGTT
1,991	2,16E-07	A_15_P118151	CK352708	#N/B	CK352708	32243	391	41	491	CAATGTTTCTTGTGCCATAGTTGTGTGGAAACAGTTTAACTGGCCAGAAGTGTTATGTTT
1,987	1,62E-07	A_15_P243016	LOC100001731	#N/B	XM_001341638	21237	260	12	1117	AAGGTGGTGGTTCAGGGAGGAGCATATGAACTGAATAAGCAGATAAAGCCATTTGAATAA
1,986	1,62E-07	A_15_P115977	TC358599	#N/B	TC358599	7666	95	53	990	AAAGACCCTAAAGCAGGGTTTCTATGACAAGCCGATTGGACATTTAATCTATAACCTGTA
1,958	4,23E-07	A_15_P110799	LOC570408	#N/B	ENSDART00000058964	30361	370	9	197	CAGTCTGAAGGATGTTGTTGAGGAACTGAAGAAAAGCCCAAGAGTGGAGAGCTTCATCAA
1,956	2,03E-07	A_15_P320846	TC344944	#N/B	TC344944	15825	194	58	765	GTTGTATATAAACCGGAAACGGTGACTACATGCCCCATAGTTACACAATAAATCTATATT
1,952	1,45E-06	A_15_P311646	CK400617	#N/B	CK400617	20470	249	46	602	CCAGGAATTTATGCTTCATTTCAGCGAGAACTCAATTTAAGAAACAGAAATTGATGTGGA
1,952	2,26E-07	A_15_P591492	LOC793857	#N/B	XM_001333656	13543	166	77	3567	TGTTGAAATTGTTGTACGAAAACCTCCAGGTATACCACTACTCTGGACCCAGCAACTACT
1,951	2,07E-07	A_15_P582457	TC320471	#N/B	TC320471	27463	333	58	775	GTGGAGCCTGAGATTTTACCTTACGGTTGCCGTTGCAAATGTCTCATAATATATCTATTT
1,945	2,19E-07	A_15_P145506	LOC569485	#N/B	ENSDART00000081770	25377	310	12	1078	TAACTGTTGGATCGATTAGTGCTGTCGGCTCAGTCATTATTGTGGGATACTGGTACAGCT
1,944	2,74E-07	A_15_P279201	TC343522	#N/B	TC343522	37056	449	33	977	GGTCACATGACTGAAAATTTCGAAACACAGGTCACGTGACTAAGCGATTAATCATCATCA
1,939	2,30E-07	A_15_P507352	LOC563411	#N/B	XM_686768	31210	380	21	3755	ATGTATACCATGTACACGATGTAGACTTGATTGTGTTGCGGAATTGTGAATAAACTTTGT
1,913	2,90E-07	A_15_P465715	TC353689	#N/B	TC353689	7672	95	56	1232	CTGGACAGAGGATATGAGAGACACTGATCTGTACAGCTGTTTGATTAAAACACATTTTGT
1,911	2,46E-06	A_15_P177581	BC122460	#N/B	BC122460	21662	263	59	331	CCCTTCTCCATCTGACTCAACATGATTTGCTTAACACTTCTTAAAAGGAATGTCTAAAAA
1,896	3,70E-07	A_15_P104191	TC316146	#N/B	TC316146	29571	360	30	113	AGCTTACGTGGGGTGGCTTTCAAGTCAACATCATAGATTGACTGACCTTTGATGATGTGA
1,894	3,34E-07	A_15_P339680	TC363378	#N/B	TC363378	12025	147	67	1244	AGCATTACACTGACACATAGCCACAGGAAACCCAAACGCATAGATAACACCTTAGTCTTC
1,886	3,72E-06	A_15_P422975	TC342139	#N/B	TC342139	35907	436	43	934	GTGTGTTGCCCTTTTAATTGTCTGAGAGTGTAATAAACACCTGTGTTGTGTGTTAAAAAA
1,883	3,97E-07	A_15_P436275	TC350121	#N/B	TC350121	27464	334	58	891	TTGTAACCCGTAGGGGAAATCATGTATTCAAATGCAAATAATAAAGCAAGCTACAGTCTG
1,870	6,50E-06	A_15_P534012	TC359377	#N/B	TC359377	9367	115	69	859	ACCAAACACTTGAGGACCAGGAAATGGACTGACAATTCTGGGAGTTTTTGGGGAGAAATG
1,863	6,93E-07	A_15_P111279	CK362411	#N/B	CK362411	22728	278	8	516	AACACTTCGCAGTACTGTAAAGGTTCCGGTTCTGGAAACTGATCAGCAGAATGCAGGATT
1,836	4,25E-06	A_15_P214541	TC346698	#N/B	TC346698	8231	103	1	888	GGGCAGACATAATAGACGCACCTAATGTGTATCGTATCGTACTGCATTTCTGTATTGCAT
1,835	5,48E-07	A_15_P208721	cyp1c1	#N/B	NM_001020610	34199	416	20	2615	CTCGGATTTGGAGCAAAAGTGCATTTAATTATGCTTGCGTAAAACTGTATAACAATGTGA
1,835	6,26E-07	A_15_P115756	TC345990	#N/B	TC345990	13932	172	20	345	TACAAAGAACCTTTTGTACCAAAGAAGGAGAATCGTTCCATCCTGGTCCCAGAGGGCTTT
1,835	5,67E-07	A_15_P114846	TC311288	#N/B	TC311288	9444	118	22	434	TTCACAAGAAAAAGAAGTCTTCTCTTGTGTTCAGCCTTCCAGGTGTAAAGAAGCCTCTCG
1,835	5,49E-07	A_15_P309431	DT059977	#N/B	DT059977	954	14	69	629	TATTTGGAGCCCATGTACATAACAAACTGTGAAATATTTTTGATCTCCAGAAGAGAGGGT
1,832	6,16E-07	A_15_P138896	ENSDART00000078111	#N/B	ENSDART00000078111	26064	318	23	2181	TTCCTGCAATTAAACTGAGGAGGACACAGCAGACCTGGATGAAGACCAAAGATGAATCTA
1,829	5,85E-07	A_15_P113001	CT654504	#N/B	CT654504	27448	333	50	150	ATGTTGTCTGTTCATGCACAATATTAACATATCGGATGTCGTTCACAAGCCATTTCATAT
1,818	1,12E-06	A_15_P310806	LOC100001587	#N/B	XM_001341521	20478	249	50	1039	CCAAAAACGTCAAGGGGACTTAAAAACAACCTCACAATCCTGAAAACCTATTTATAAACT
1,811	8,37E-07	A_15_P510147	BC154008	#N/B	BC154008	27858	339	4	818	CCCATAAACCTCATCATAGAGACAGCAGAAGTCACTCCTAATAGTTTTAATGTGTCAAAA

1,811	6,84E-07	A_15_P572922	EH496483	#N/B	EH496483	7349	91	62	656	ACTGGCCAGATTGCTATTTGCCTGTAGGCTTCAGTTTTTAATTTAAAACAGGTTTTAACA
1,804	8,07E-07	A_15_P556872	LOC562659	#N/B	XM_701053	19824	241	56	1967	GACTGCGCTGAACGGGCACTGCCATGTACTTTGATACTGCTATACTGAATAAACATCTTC
1,799	7,97E-07	A_15_P117633	TC327887	#N/B	TC327887	25431	310	40	700	ACCAAACACCCAACATCGCAGATCTGAGCACTGAAGAGAACCACGCACTCTACATGCTCA
1,791	1,58E-06	A_15_P114197	wu:fb02c12	#N/B	CN511483	2589	35	13	735	GATTAAGGAACTGAGCCAGACTTGTCTAAAACATTTTGTGATTTTTGTGTGTTATTCCTG
1,791	8,60E-07	A_15_P134851	BC095625	#N/B	BC095625	26672	324	80	654	GATTGTCAATCCTGCACTTGTTAGCTCGCTATAGGACCAGATAAAATCCTGACTTAAGTA
1,770	2,15E-06	A_15_P111574	LOC564821	#N/B	XM_688151	10115	125	29	5218	TCTAAAAGGTGCATTATTATTGCTCGTTTCCATTATGTAAATCAAGTATTCCCTCTAGCG
1,757	1,35E-06	A_15_P603492	TC358397	#N/B	TC358397	13360	164	68	948	GAAAGAGGGGGGTGTCACTATATATGATGGTGATATTTACTAGCTGAAAATAGTGGACACT
1,756	5,07E-06	A_15_P376360	LOC793641	#N/B	XM_001333398	29041	353	14	1779	GGTCAAGTCTCATCTCCTGTGTGTTATGGAGGAAGAACAAGCGAGGTAGTGAAAACTTAG
1,752	3,00E-06	A_15_P532632	TC358937	#N/B	TC358937	6934	88	18	849	TGAAACTTTGCATAAAACCTGGTCTATAATCTCACCTATAACCTTGCCCATAACTTCTTG
1,752	2,00E-06	A_15_P267626	LOC793590	#N/B	XM_001333357	23079	281	21	3267	AAAGAGACTGTTGCAGTGATGGACAGTGACTCTGCAGTCATTCCAGCTGAAGAAACATGA
1,748	2,81E-06	A_15_P528412	TC324913	#N/B	TC324913	3861	50	64	982	GTGTACTATGGTCACACTAGATCAGGGGTGTGCTATACAAGTCCCTGAATGTCTTGTTTG
1,743	1,35E-06	A_15_P139281	LOC565222	#N/B	ENSDART00000075430	41174	500	17	339	AGACTTGTTGAGAAGATCCGCATGAGATGCTATAGTGAAAACCTGGGAGAGAATAACAGG
1,735	1,44E-06	A_15_P106303	TC301719	#N/B	TC301719	17523	213	73	6604	TTCGTGTTTGACCCTACCCTGCTATTGACTAAACCACTGACCCTATACAAAACCTGTGTA
1,732	2,35E-06	A_15_P111115	TC357954	#N/B	TC357954	33510	408	8	609	AATAAGTTGTGCACTGTTCATATTTACTGTCCATTTGTTGTTTGAGTTGAAAGCATCCAC
1,726	3,88E-06	A_15_P118244	ENSDART00000102609	#N/B	ENSDART00000102609	23756	289	29	977	ACGTGCAAAAATTGCTGCTCTGGATAAAACCAAGCAGGATCTGACTGCCCTCATAAACCA
1,719	1,69E-06	A_15_P110344	LOC561810	#N/B	EH556952	29231	355	26	589	TGTGCTGCTCTTATTCAAATCAACAGGACTGCTTTGGTAAGCATTTGTAGTGAAAATGCA
1,718	2,88E-06	A_15_P469485	TC354877	#N/B	TC354877	35133	426	69	711	ATTCAAGAGATCATATTCACAATTTGCATTTTGTTTATTTGCCTTTTAATGCCCGGACGC
1,716	8,94E-06	A_15_P111569	TC341801	#N/B	TC341801	9546	118	75	921	AATGCGAAATTATTTTGGGATTCTCCTGAATTTCACGGATGTTCCTTTGAAATGTGGATT
1,708	2,72E-06	A_15_P475045	TC336111	#N/B	TC336111	31729	386	32	1301	CTGAACGGGCACTGCCCATGTACTTTGATACTGCTATACTGAATAAACATCTTCATTGCC
1,704	2,07E-06	A_15_P537482	TC360478	#N/B	TC360478	16013	196	67	632	CAGCAGGGGATTCATTTCTCTTGGCGCTGATGACCATTGCAGTGGCATTACATTTATTCT
1,701	2,08E-06	A_15_P111944	TC331259	#N/B	TC331259	43055	523	40	1903	GTGGTGCCATGCATTTTCACTGAACTAATTCAAAGCATGCTTCATTTAATACATGTCTGC
1,700	2,39E-06	A_15_P212011	2-sep	#N/B	BC067625	19309	236	45	2074	GACTTGAAGAGAGTTAAATGTTACTATTTGGTCATGAAATCTGTTGTCAACATTCCAGTC
1,691	4,28E-06	A_15_P117854	zgc:136538	#N/B	NM_001045237	8625	107	32	1481	AAACTTTATCATGAAGCTTGTTTGTTTTAAGGTCAGGTATTCTGTGACACTATTACTCGG
1,690	2,37E-06	A_15_P445465	ENSDART00000098582	#N/B	ENSDART00000098582	15426	190	21	2721	AAAGTGGTGGCGGTCAACTCACTTGGCAGAGCAGAGTGTTCTTCGACATTAAAAGTGAAA
1,688	4,64E-06	A_15_P310906	LOC563620	#N/B	XR_029316	35892	435	36	7116	CAGAGCCCACATAAGCACTACACAGATGTATTAAACCGTTATTTTATGTGAAATGTTACG
1,686	8,33E-06	A_15_P551617	im:7144880	#N/B	EH997715	21297	259	43	656	CCAGATTAGAGCGGCATGACTAATTTTACACTGCAATGGAAGAGCTTATATGAAAATGCA
1,685	7,94E-06	A_15_P179046	BC152493	#N/B	BC152493	34338	417	6	426	TGGAGATTGAACGAGGTATTTCCTTTTTCTTACATAACATGGGGTTAGAACTTCATGTTA
1,672	9,67E-06	A_15_P183956	LOC796348	#N/B	ENSDART00000067662	31460	382	63	534	AAGCCATATGAGTCTGGAGAGTCATGCTCTAAATGCCCTGAAGAATGTGAAAACAACATC
1,671	2,84E-06	A_15_P563417	TC337358	#N/B	TC337358	34268	416	55	1392	CTGACTGTTGTAGCAGAATCTGCTTTTTCAATTTGTTGTTCAAGTGACTCATTCAATCAA
1,670	0,000351511	A_15_P382450	TC356436	#N/B	TC356436	39151	473	84	361	TCATCTCTCCTGTAGTGTGTGTTCACTGTAGTCTCCTGTAGTGTGTAGTGTGTGTTCACT
1,666	3,13E-06	A_15_P138201	ENSDART00000105631	#N/B	ENSDART00000105631	17681	215	68	1413	ATTGTGGATCCTCTCCGTGCTATTCAGATACTGGCTAATGCTCTTGCTATTGTGCCTTGA
1,666	3,73E-06	A_15_P145576	ENSDART00000099771	#N/B	ENSDART00000099771	20272	248	28	6747	GCTGCTCATTATAATATGAGCTTCTTATTGGAGACCATTGACTGGATCATCAGTATGAAC
1,663	3,58E-05	A_15_P502012	si:dkey-7c18.24	#N/B	NM_001082832	34826	422	83	240	ATACTTTAATAAAATTTTCCATTTTCCAAATTTTCCATCATTGAGCAACTGCCCGGAGGG
1,661	3,39E-06	A_15_P165373	LOC100006993	#N/B	ENSDART00000101046	32388	394	29	2205	TATAAAGACGATCATGTCATTGTGTATCTGAAGGAGGTCCCCAAACATTTTCCTGTGAAT
1,651	5,67E-05	A_15_P483490	TC348445	#N/B	TC348445	27362	333	7	710	AATAAATTAGGAAATTACCCATATTTACCTTCGGCCGACTAGCCTCAATCAAGTTTGGTT
1,647	8,42E-06	A_15_P546527	LOC793330	#N/B	XM_001333032	25378	309	13	1677	GGTCATATTGAAAGACGTTGTAGGACTGTAGAAGGACCACAAGGGCCTTTAAACTTATAG
1,647	1,17E-05	A_15_P475655	TC336350	#N/B	TC336350	26102	317	43	489	GGTTCAAAAATCTGGAAGGACAAACACAGGACGTTTGAAGCCTAAATGTTCTACATTATG
1,647	4,26E-06	A_15_P254121	DT065034	#N/B	DT065034	27276	331	48	691	AATGAGCTAAATGCTTCGACAACACAGAGTTGTCTCTACAGAGCACCTCATAAGCAGTTG
1,646	4,34E-06	A_15_P118290	LOC562744	#N/B	EH585602	31557	384	29	462	GGTTCATTGTAGTGTGTTTAACTGCTTAGTATTGCATGATTGAGTTGTTGACAAATGCAG
1,645	7,57E-06	A_15_P277051	TC342770	#N/B	TC342770	11133	138	36	1622	TGTGCTGATCCACCTGCCCAAAATCAAAGCAACAAATGGCAATAAACTAACTCCATGGGG
1,639	5,68E-06	A_15_P334864	TC361879	#N/B	TC361879	27256	332	37	122	AAAGGATGGCAGAAGCCAGTGTAGATGGAGCCAAAATGACAGAGTCTCCAGTTGAAGATA
1,632	5,07E-06	A_15_P206481	zgc:136586	#N/B	NM_001040297	35934	436	57	1068	AAATTGTTCAGTTCTGGTATGCAGAGAGGAGTTGCCGAAAAGAGGAAGTATGTCTGGGTG
1,631	9,35E-06	A_15_P568322	ENSDART00000078111	#N/B	ENSDART00000078111	15059	185	6	2155	AGTAACAGCACTAGACGTCCTTTTATTTCCTGCAATTAAACTGAGGAGGACACAGCAGAC
1,630	1,55E-05	A_15_P108513	TC360850	#N/B	TC360850	36324	440	84	648	CAGCAGCAGAAGGAGGAGGAGAAGTTAAACCATTAAACGACTGCAATAGTTTAACAAACA
1,628	5,70E-06	A_15_P432845	TC331521	#N/B	TC331521	7297	91	35	768	TTAGATGTTCTGTGTGTGATGGTAGTACCCGTATCATGCATCTCTGTCTGTGGTGTCACT
1,621	5,12E-06	A_15_P243556	LOC100000968	#N/B	XM_001341031	31308	380	71	1242	ATAGAAGAAATGGTCGTGTGTCAGGCGTTCAAGAAATGGAGTGAAGAGCTCTGCGAGAAA
1,606	1,60E-05	A_15_P114204	sep2	#N/B	BC067625	39697	481	25	1954	GGGATATGTGGATGAAAACTATTTTAGCTTATTCCTGTGGTTCAAGCAAACCTCCATATC
1,606	7,17E-06	A_15_P110083	ENSDART00000073559	#N/B	ENSDART00000073559	8561	106	84	1768	AGTTGACGCCTGCATGGCTAACAATACATCCGATCAGGAAGGACATGTACCTCAAACTAA
1,589	1,54E-05	A_15_P199156	ENSDART00000084879	#N/B	ENSDART00000084879	39275	475	62	1609	GTCGTGGAGTTCAAGAACAAAAAGACAAAACCAAACCCATGACTGGGAATGATCCAAAAA
1,582	8,40E-06	A_15_P106689	TC347763	#N/B	TC347763	22784	277	37	1042	ATCATGCGCTTCATCTGTTACATGTGGAAGTCAAGCATATTGAAATACAGAAGAGCAGAC
1,581	9,76E-06	A_15_P119636	TC307542	#N/B	TC307542	19449	238	33	1218	ATGGTTTACTGACCTGAAATGACTGGAAGTATCAACTTTGTGCTACAGTGTGACATGCTA
1,581	2,13E-05	A_15_P190441	LOC553434	#N/B	ENSDART00000042831	1256	17	68	1750	TTGCGGCAAATCCGACAAGGAAACACCAAACAGCGCATTGATGAATTTGAATCCATGTGA
1,580	8,58E-06	A_15_P113905	TC354382	#N/B	TC354382	14629	180	38	727	ATGAGGGCTCCGACACAGGTGTCTTGAACAAAATAAACAGTCAAATCTCTCACCGTGCTT
1,579	9,33E-06	A_15_P290751	LOC100004951	#N/B	XM_001344093	30711	373	19	2346	GGTATTACAGGCCGAAGTGACGGCAGTAAAATTATTGCACTGGGTCTCTACTTCATTTAG
1,577	1,22E-05	A_15_P598437	BC153670	#N/B	BC153670	22287	272	39	562	TCTTCAGGAATGAAATCTGAGGTGTTTCCCCTGAAACCTGACTTGATCTCGTCGGAAAGA
1,576	1,52E-05	A_15_P349325	TC334097	#N/B	TC334097	11241	139	7	598	GTAAAATGTGTTTAAGCTCACATTAGGAGCATTTAACACCGAATAAAGCCCATAATCAGT
1,570	1,06E-05	A_15_P362945	ENSDART00000099215	#N/B	ENSDART00000099215	2863	37	68	678	TTCTCTGGCGGAGTGACTGTTGGAAATATTGGCAGACAACTAGCTATGTTAGTTTCCTCT
1,565	1,14E-05	A_15_P156811	LOC559861	#N/B	ENSDART00000081036	16193	198	73	2585	GAAGATAGAGGAAGAGCTGGGCAAACACACTCAAATGATTGCCATGATTCACAGTCTCAG
1,565	3,09E-05	A_15_P164866	ENSDART00000010518	#N/B	ENSDART00000010518	43014	524	18	2557	GCTCCAGAAACACTGTCAGATTAAAGAGAATACATAACAATAAAACAAGTTTAAGACCGC
1,561	1,21E-05	A_15_P110405	ENSDART00000080061	#N/B	ENSDART00000080061	1674	24	42	627	ACACAAACAAACACGCGACAGGGAGGTGAGAAGCACTACTAAACACCCTACACACACATA
1,560	1,15E-05	A_15_P104029	TC355032	#N/B	TC355032	21962	267	43	581	AGTTCACTTCCAATCATGCTCCTGATCTAATTATGTGCCAGAGGACTGACGCGCTTTTTA
1,559	2,08E-05	A_15_P260536	LOC100002378	#N/B	XM_001342143	24763	301	35	1260	GACTTCAACAGAAAGGCCAGAGGATTTGCTTCATCTACAGGAAAAACGGAAGATGTTTGA
1,559	1,40E-05	A_15_P296606	CT667563	#N/B	CT667563	10816	133	44	769	AAACCCAACGTGGCTCACCTAAAAGTGTTCAAGTTATTTTGGACTTTGAGCAGCTTTGGC
1,558	1,16E-05	A_15_P434620	TC332203	#N/B	TC332203	7581	95	10	857	TTCCTTCATTGACAAGGTGTCGCTTCTGTATCAGCTGAACATATTACTCGAGACAAAATG
1,554	1,22E-05	A_15_P597432	LOC555997	#N/B	CT700514	32776	398	58	713	TGAATATTTGGTGATTCTCTTGGTTTAACAATAAATAAAGACTGGGATGACCGCAATGGC
1,549	3,14E-05	A_15_P109991	LOC572562	#N/B	XM_696353	321	5	39	1406	TCATTCAGTGGCCAATGGGGGTTTGTTGGGGTGCTAGAAATAAAAACGAATTATTTATGT
1,545	0,000147135	A_15_P289496	LOC560707	#N/B	XM_684104	10238	128	7	1568	GAACACATCAGAAGGGACCTGTTTCCTTGAGAATGTTTTTCTCAAAGGAAAAATCAATTA
1,545	1,89E-05	A_15_P311261	CN509070	#N/B	CN509070	20091	245	22	617	ACATATCCAGAACTTAACCTGCCTTAAGCAGGTTAGCGGTGCAGTGAAAATATCAGGTGC
1,544	1,50E-05	A_15_P528117	TC324808	#N/B	TC324808	24364	297	1	1302	AAATAATAACAGCGGTTCCCCTGTGAGGGAGTGTCTTTCAAAATAAAAGACAAGGGCATG
1,540	2,90E-05	A_15_P308226	LOC559757	#N/B	XM_683124	35299	428	69	1637	GTGTTCAGCCAGTTTATCACTTATTCTGAACCATGACAGCTTTTAGTTAATATCAGGTTT
1,537	0,000161042	A_15_P563497	TC337389	#N/B	TC337389	38586	467	51	759	CAATTCTTTAGTCATGTCTTTTGAGTGTTGTGCATACTGAGTGCGTATTAAAGCCTTTAT
1,535	1,62E-05	A_15_P436000	TC350034	#N/B	TC350034	3086	42	11	588	ATTGAAGATGATCCTAAAGGAATGGCTGGGAATTCAACATCGACAAATTACAGAAAGGTG
1,522	4,02E-05	A_15_P266301	CT702692	#N/B	CT702692	8577	108	7	741	GAGACACACATTGCACATGATCATTCTCAACGTTTGTGAAAGAGTTTGTGTGAGTGGTTC
1,521	1,93E-05	A_15_P367705	TC308620	#N/B	TC308620	29457	358	57	1539	CACCACATCTTTTTCATGAATTTGCGCACACCGGCGGGAATTTACACCGACATAAAATTT
1,520	3,39E-05	A_15_P134156	BC090263	#N/B	BC090263	27147	330	66	1180	GCTTTTGATGTTTTGTACAATGCGTGTCTTTCAGCCTTTGTAATAAAATGTGTAACAGAC
1,516	2,49E-05	A_15_P191836	ENSDART00000104372	#N/B	ENSDART00000104372	11566	143	3	1500	AAAGACGTTCTGAGTTACCTGAAAGCTGGACTCATGAAACTGTTTCTTGGTGACAAATGA
1,516	2,72E-05	A_15_P154791	ENSDART00000097173	#N/B	ENSDART00000097173	3038	40	72	292	AAGATTCAAATGTGCAAATGCCTGTGAAACAGACTGAGAATCTGGCTGAGGCAAAGGCGT
1,515	5,84E-05	A_15_P432875	TC331538	#N/B	TC331538	37111	450	61	407	GAAAAGATGCAATATTAGAATGGCTGCCGTCGTTTGCATTTCCAGCAGTTGATCTTCTTC
1,514	0,000155326	A_15_P339655	TC363371	#N/B	TC363371	33779	410	60	599	AAGCTACCATTTCATGTTTCAGCAGACCTCCGGAGGTGTTTTCATCTGGTATGGTTGGTA
1,512	2,20E-05	A_15_P596142	CT694511	#N/B	CT694511	3543	46	73	605	TCCTCTCTGCATTTTTAAAAGTCTGTTCTTTTCTCAGCATTTGTTGGACTGTTCAAAGAG
1,507	2,38E-05	A_15_P550722	LOC555593	#N/B	XM_678143	9676	120	58	2368	ATGCCTAGATGTTTGAGCGATATTCTTCCCAGATGTCACGAATTGTATATTGCTGAATGT
1,507	2,38E-05	A_15_P183554	LOC100000514	#N/B	ENSDART00000104084	2278	32	24	435	AAGAAAACCATTGAAGGATTTCTGGGTAAACCTGGATCTGTGGTCAGAAAACTGATAGAA
1,506	2,50E-05	A_15_P332894	TC361261	#N/B	TC361261	21179	257	68	351	GCTGCTGAAAACCCCCATCATATATGTATTGGGCACAATTTCATTAAAATACGAAAGTCT
1,503	2,53E-05	A_15_P110031	TC303668	#N/B	TC303668	40468	489	79	2211	TTTATTAAAGCATGTGCAGCAAACAGTGAGGTAATGCTGGCTCTCACGTCATGTATTTAA

1,503	3,61E-05	A_15_P100856	TC326854	#N/B	TC326854	39949	484	69	2171	GTGATGTGAAGAGATGCTTACATAATTGTAAAGCCCCTTGGGTGTATGGCGGCACACAAT
1,502	2,61E-05	A_15_P449600	wu:fc56c01	#N/B	DN895678	28488	345	72	708	GCAATTTGGCACCATCTAAAGGTAAAAATGGATTTGTGTGCTTAATCTGTGAAGTACTGT
1,500	4,55E-05	A_15_P299806	LOC571908	#N/B	XM_695552	24724	301	15	735	GGATTATCCACAGCTTTTACAGTCATACTGTATAACCAGAGGAAGTCCTTTACAGGTTAT
1,499	6,22E-05	A_15_P111120	TC310103	#N/B	TC310103	28485	346	70	2642	AACGTGTCTATCCCCAATCTACACTGTATGCAGAACAATTCAAGAGGAACAGAAGCGTTT
1,497	4,24E-05	A_15_P437230	TC350410	#N/B	TC350410	39809	481	82	589	GACTAAACCTTTATAACAAGTGTGTATTCAAGCTTTTAACCTTGTGTCATTGCAGTGTTC
1,495	5,03E-05	A_15_P106017	TC342968	#N/B	TC342968	5835	74	50	330	GTTCATTTACAGTATGTGGCTGGCTGCTAATCACATTTTTAGGTATCATACTTGTTTGTA
1,495	7,65E-05	A_15_P523462	CT640242	#N/B	CT640242	3688	48	61	602	ACAGATGTGAATTCAGCTGGAGAGATCGGACCTGTCAAAAGAGCGAAAGAGAGTGTGAAA
1,494	2,94E-05	A_15_P406310	LOC564688	#N/B	XR_030032	11638	143	39	3223	TTATGTTGTGAGGAGATGGATGCATGTGGACTCATCTCACAAATAAACAACTGGAGAGTG
1,494	3,43E-05	A_15_P108474	EB793690	#N/B	EB793690	39044	474	29	96	GTATTTCCCTTCAATACAGTAACCTTCACTGGGTGCCCGCGGGGTCTTAAAAAGTCTTAA
1,492	0,000290113	A_15_P415260	TC329467	#N/B	TC329467	1883	25	69	723	TGGATGTTGCATCTTGGAAATGAAGAATTGGGACTGTGCCAGTATTCTGTTTCCACCATG
1,491	3,01E-05	A_15_P580847	TC319766	#N/B	TC319766	42265	513	11	691	AATCCAAATCAGTTTTATTAAAACAAAGCAGCTGCTTTTGTTAAAAAACCCACGCGTCCG
1,491	3,48E-05	A_15_P114729	zgc:110339	#N/B	NM_001017792	37455	453	69	910	CTTATTAATTATTCATGTTTCCGCCTGTTTGTGTCCACTAAACCTGAGCCGTTTGTACTT
1,488	4,51E-05	A_15_P104065	wu:fj05f05	#N/B	DN898964	39511	479	15	287	CTGGCTTGTGGCTTCTCTTTGGAGTATTCTTACTAATAGAGATACAAAAATAAAATACAT
1,488	3,37E-05	A_15_P575402	LOC100000210	#N/B	XR_029607	39441	478	64	2081	CTGAATAAATTCCTGCGCATTTCTTGTACAAGAGCACTGTTATGGTATGTTGATCTTCCC
1,487	3,29E-05	A_15_P110248	si:busm1-211o13.10	#N/B	NM_001005318	15781	194	35	840	TGATGTGGGAAATTTGGCATCGTATGTTGAATGTGACAAATACTTCAAGGACCAACTTCA
1,486	0,000131387	A_15_P599587	wu:fb98c10	#N/B	AI588251	18083	221	18	460	TTTATTTCTGATTCCTTCACACGCACATTTAAACCGGCGCATCATTTGTAAAATATACAG
1,484	3,84E-05	A_15_P408400	LOC100004862	#N/B	DT078355	28428	345	42	687	AGCCCAATGTTACTGTTATCAGGGTCCCCACAAGTCATGGAGTTCCTGTAATGTATTTCC
1,483	0,000419236	A_15_P580417	TC319537	#N/B	TC319537	24305	296	55	725	GATTTGGTATAAGTGGATCAGCAGGGGCTAATTATAAGCAAACAACAACAAATATCATCA
1,483	4,28E-05	A_15_P594282	LOC100001632	#N/B	XM_001341552	10140	125	42	940	GATTTTGACAGCGCGCAGAGAAAACTAAGGGAATGTGAGTCGGTAAGAATCATCACCTGA
1,482	3,85E-05	A_15_P422190	TC341875	#N/B	TC341875	223	4	57	783	TGACATGGGATGTCAAAATGCTCTTGCGCAGAGTTTGTGAATGAGTAGCCACATTAGAAG
1,482	3,46E-05	A_15_P130426	AB055669	#N/B	AB055669	6617	83	26	148	CTGTTGTAAAACAACCTGTTCATTTTTGTTTATTTTTAAAGGCTGAGCGCAACTTTTCCC
1,479	4,18E-05	A_15_P138191	ENSDART00000079311	#N/B	ENSDART00000079311	29936	363	46	849	AGAGGATACCACTATATGAAAGTGACATGTCTCGACGGGAAGTCGGACATTAAATCATGT
1,474	3,95E-05	A_15_P179106	sep2	#N/B	BC151880	6623	83	29	1728	GTGTTGCCAGAGAGATTGCTGATTTCTGAAGTACTTATCTCTTGCCTGCATGAAGTCTTG
1,472	4,89E-05	A_15_P432155	TC331214	#N/B	TC331214	16969	207	44	954	GTTTACAGTCCATTATGTCAAATGGTCAAAGGGAGCGATTTGACAGACCATGTGCAGTTG
1,470	4,79E-05	A_15_P463675	AI618406	#N/B	AI618406	5949	75	24	301	AAGAGAGAAAGAGGATTCTAAGAGTCTATGAAGACATGGGCTTTGCCTCTCTGATAATCT
1,469	5,39E-05	A_15_P217811	TC347818	#N/B	TC347818	32203	391	20	389	GCTGCTAGTTTCCAAACGCTCAATTTCATGCTAACAAAAGATACATGTTCTGATGCTGTG
1,468	4,41E-05	A_15_P443575	zgc:113858	#N/B	NM_001025490	21412	261	17	1022	TCTGATGTGTCTGGCGATTATGCTGACTGTCTAAAGATGATTTGCGGAGGAGACGACTAA
1,463	0,000102231	A_15_P118902	TC350734	#N/B	TC350734	15517	189	68	443	TTCATAAGGCAGATCTCACAACATGGAAACGATTTGGTCTGAGATAATCACAGAGTTTTT
1,463	4,95E-05	A_15_P118537	ntd5	#N/B	ENSDART00000060004	21222	259	5	1619	TTACATGAAGAGTAGAGTAGACCTGTGTGTATTATAGCATAAAAAGCCTTGCTGAAGCAG
1,462	4,87E-05	A_15_P113584	TC335902	#N/B	TC335902	24783	302	45	861	AGCTGATATCGTTGGAAAATACGCCAACCGAATGTACTCAGACACCAGGTCGTTCATGTT
1,462	0,000101396	A_15_P102840	LOC799801	#N/B	XM_001335170	37684	457	14	913	ACCTGCTTTTGTAAACGAATCTTCAATAAAGGATCCAGGTTTTCTTAAAGGATGTGGTCG
1,460	6,11E-05	A_15_P117046	opn1mw1	#N/B	NM_131253	6655	83	46	1450	TTTTTTGGTCATTGTATTGTCTGCAAAAGCTGTCTGACTTGATCAGGTCAGATTCTGTAA
1,460	5,26E-05	A_15_P105770	CO350465	#N/B	CO350465	13763	169	19	504	TTATTGCATGACTTGAAAGAGTGCAGAGAGATGGCTGCACACAAAACAGAAGAGACAACA
1,457	0,00012177	A_15_P326466	CT722749	#N/B	CT722749	31072	377	34	735	ACCTCTTATTTGTGCCAGCGGTGTGTCTGTAAATGTGAGTGCATCTTTTTTCCCTCTCCT
1,455	8,62E-05	A_15_P322276	TC345421	#N/B	TC345421	10340	127	59	577	AGAAATGCAGCCCTGAAGGCCTTTAACACTGCGATTTGCTACTAATATGAAATGAAAATA
1,455	6,37E-05	A_15_P107324	TC348736	#N/B	TC348736	3099	41	18	108	AATTTTAAAATCATTTCCAGCCGTTCACATCTGAATTGTTCACCTACTAGGGATTAACAC
1,455	5,29E-05	A_15_P467640	TC354284	#N/B	TC354284	16817	206	50	340	ATACAGAGCAAATGTTTCAACGTTGTATCATTGTCTCAGTGACCACAATAAAGAGGCCAA
1,454	5,66E-05	A_15_P102920	LOC573469	#N/B	XM_682119	8061	101	1	2342	GCTGTTTATCTGTCCTCTGTTCTTTGTATAAAAGCTTTTGGATGAGAATCTTTTAACGTG
1,454	5,89E-05	A_15_P260226	LOC797793	#N/B	XM_001338222	8665	107	52	660	TTCAAGATAGATTTAACTGCAGAACAAGAACCTCAGAAGATCATCACAGCTGTGTATGAG
1,450	5,78E-05	A_15_P498217	LOC100007551	#N/B	XM_001345944	17265	212	24	678	TGGAAGAACGATAATGAAACTCCCATGAAATTCATCACCATGAAGATCAAACCTGTGTCC
1,447	0,000241625	A_15_P433000	TC331590	#N/B	TC331590	24539	299	7	720	GATCAAACATGGAGTGGAGACTCCATAAAATCCTCTTATAAACTTCTAGAAGATTCTGTT
1,445	6,94E-05	A_15_P253371	DN900457	#N/B	DN900457	39051	473	33	104	GTATTGGGTTGACACTGGCTTATGTCTCCTTTGTAAACAATAAAATATTCCAGTAATGCT
1,439	9,32E-05	A_15_P433275	TC331681	#N/B	TC331681	35464	430	68	460	TTAAATGTTTACCTTTGTCTGCCTTCTAGCTGAGAGAAGCTGAAGGAGTGACACACCTAA
1,439	6,88E-05	A_15_P202141	LOC793949	#N/B	ENSDART00000019912	16315	200	50	531	TCTCTTGTGACCTTGGTTGACTTGCTCAAATGCTTTAAAGTCATGCAGTGTATTTTTTGT
1,438	7,28E-05	A_15_P253091	DN893503	#N/B	DN893503	13915	172	11	726	GTGCTGATGATTTACTTCTGAAGTTTTGCCTTCATCTAAGACGTTTGCTGCTGGATGTAG
1,433	0,000157891	A_15_P175216	zgc:112496	#N/B	NM_001013465	3811	50	39	780	AGACTGAATGACCAGAAAGACAGAATCAAGCAGCACTTAATCACAAAATATCCAGACATT
1,431	8,69E-05	A_15_P132241	AF423762	#N/B	AF423762	20381	248	85	160	GAACCAGTAGGGTGTCTGTCCTTTTCTTTCTTTGCTTTTTTTCTTTTAAATGTAAACAGTC
1,426	0,000128714	A_15_P102709	TC311443	#N/B	TC311443	13240	164	7	2267	AAAGTGTTGAAAGCCTGTGTGTGTTGGGCTCTGTGTCCGTGAGATTGCGGTATTGAATAA
1,425	0,000402981	A_15_P119628	TC321019	#N/B	TC321019	36738	445	39	975	GAACTTTTTCTCCAACCCAAAACTTAGCGGCTTATATGATAGTAAGGGTGAGGTTGTCCA
1,425	8,91E-05	A_15_P581152	TC319911	#N/B	TC319911	27595	336	40	4311	GCTGCATGGTTACATGGATTGAGCACTATTGCCTGTAAATAAAGCTAAAGAAATCAGATT
1,421	9,51E-05	A_15_P204901	LOC569378	#N/B	ENSDART00000101737	36074	438	43	887	CCCACTGACACGCTTGTAGTATTACAGTAAGAGTTTGTTTTTATTTGTTGTGTGGAAAAT
1,420	0,000146457	A_15_P586397	EH513206	#N/B	EH513206	7949	99	29	826	TCCTAAATATCCTGTCGCTCCACTGCCGCCTGTGTGGATGTTCAATAAACAAAGAAGAAA
1,420	0,000101483	A_15_P112968	LOC560869	#N/B	XM_684268	21312	260	50	1919	ATGTGTATGAGGATTCCCTCTGAGACTGTATGCTGTTGTAAGGCATGTATTTGCTGTTTT
1,419	0,000107166	A_15_P113208	zgc:92275	#N/B	NM_001002612	9306	116	38	1625	AACAGTGCAGTTGTTTTATCATACAACATGTGCAAAGCCAACAATAAAGCAAATGCTAAA
1,417	0,000128167	A_15_P400230	TC330420	#N/B	TC330420	41513	503	24	1448	CTCTCATTTTCGCATCACGATTATTATTGTCGAATCCTGGGAGGTGATTCCTTTTGTTGT
1,415	0,00012568	A_15_P289391	LOC556736	#N/B	CK396210	20099	245	26	342	GCTCTGATACAAGGCGGGGAAAATATTGTTTGGCCATTCAAATGAGAGAAAGAAAGAATAA
1,414	0,000104941	A_15_P112715	LOC564600	#N/B	XM_687930	35148	426	77	1981	TCAGGAGCTCATCTTTTGCCCATTTGCTTATCAAAGCTATTGTACACAACCATAATGTGT
1,414	0,000114252	A_15_P473075	TC335377	#N/B	TC335377	3834	49	51	461	ACTTTAAATATGTTTGTCTGCAGTATGTTTTGGCACCCATAAAGGAGAAATGAGCAACAT
1,413	0,000108722	A_15_P540132	TC322849	#N/B	TC322849	27583	336	34	536	GTATTCTTCCAAGTAGCACAATATTGTTGTAGGCCATTTATGGTGCATTTATGGTAGTAA
1,412	0,000113031	A_15_P101947	ENSDART00000023359	#N/B	ENSDART00000023359	32949	400	61	3365	TTATTTGGTTGATATGGACCAATGAATGCAAACGTTAACTGGATATTCTGTTAAAGTGGC
1,412	0,000108844	A_15_P376850	LOC569378	#N/B	ENSDART00000101737	27193	331	5	657	TGGATGTAGGTACAGTATGAAAGGGAAGGATTTTTATGTGGCTTGATTCAGTCTCATATG
1,411	0,000221062	A_15_P119542	LOC100000237	#N/B	XM_001336581	30901	376	31	1930	TGCATCTTGATCAGATATAAGAGTTTTGTTTATTTCCTTTGAAACAACTGCAATAAACAC
1,409	0,000123065	A_15_P108927	TC341652	#N/B	TC341652	13364	164	70	391	TTGAACGTGAGTTACGTTGTGGAAACGCAGCGTCTCCATTAGTGTAGAAAAGGAAGTCCT
1,407	0,000142137	A_15_P594272	ENSDART00000079311	#N/B	ENSDART00000079311	16110	197	31	811	ATTACTATGATTGCAAGGATGGATGGACTACCGCTAATAGAGGATACCACTATATGAAAG
1,407	0,000146808	A_15_P548197	LOC565641	#N/B	CK353663	37381	454	31	589	GTGTTGTATATGAGCTCAAATGAGCATCTGCTAAACAAATCAATAAAGTAATGACCAGTG
1,405	0,0001632	A_15_P116131	LOC568957	#N/B	ENSDART00000028029	31288	380	61	537	TACCCAACAGGACGGGTGCGACTAAAAGATCCACAGGGAAAAGTCATTATGGACACTAAA
1,402	0,000291454	A_15_P382465	TC356445	#N/B	TC356445	11778	145	25	1064	TCAAGCACCAGTGCTTAAAGTGACACTTCACCCAATAATGTACAAGCACGCATACACTGT
1,401	0,000163296	A_15_P512177	TC308992	#N/B	TC308992	10096	125	19	771	TCGAAGATTACAAGTGAAGTCGGCTGATGTTCGCCGTGTCCGTTAATTAGTAATAGCTGA
-1,400	0,000179475	A_15_P342195	TC327234	#N/B	TC327234	34887	424	29	1150	GGTCTTGCTTTACAAAATGTTATATTGATGTTTCATTGAAGTATGTCATGTTCTGTGGGC
-1,401	0,000177495	A_15_P109449	LOC798254	#N/B	CK398525	7688	96	64	298	GAACTGGGATCCCCACCTCTCCAGGCACAACTCACTCACTGTGCACTCATATTGCAAAGA
-1,401	0,000152681	A_15_P524497	CT704283	#N/B	CT704283	29432	358	43	469	AACACTCAACACTCACTCAGAGATCACACCGACATATGATTCAGATACAGGAATAGCTAG
-1,403	0,000127205	A_15_P121355	zgc:77748	#N/B	NM_200858	7945	99	27	1459	TGACTGATGTGTAACTAGCGAGCTTGCGAAATATACCCTTTTTATACAATCATGCAAATG
-1,406	0,000140022	A_15_P383715	TC356823	#N/B	TC356823	23776	289	39	330	CGTGTCTCTGTCTTGTTAGTCTCTTTAGCTCAGGTCACAGTAAAATTCACTGTCATTTCT
-1,407	0,000216818	A_15_P454070	BI880206	#N/B	BI880206	31298	380	66	499	TTCATGATGATCCACAACTTGACTCTCCCAGTAGATTCAACTTGTTAGGCCCTTTCAGGT
-1,408	0,000148532	A_15_P471315	TC334729	#N/B	TC334729	40237	487	46	579	GGATGGATGAATGGATGGATGAATGGAATGAAAGCAAGCCAATAAAAATGTTTTACTCTC
-1,415	0,000109399	A_15_P325396	CT701933	#N/B	CT701933	29248	356	34	534	GATGCACGGATATAGGGTGATGCTCATCTAAGAACTCTTCAAGACTCCAGCATGACTTTT
-1,415	0,000185531	A_15_P201331	LOC553307	#N/B	ENSDART00000061403	15	1	18	1315	TGGGAACTTTGGTCCTGAGAGAACACGAGATCTATCCTAATAAGAAGAAAAGGAGGAAGC
-1,416	0,00010288	A_15_P160556	ENSDART00000103676	#N/B	ENSDART00000103676	2558	33	81	1718	TGTGAAGGAGCGCAACAGGCTGAAAGAGAAACAAAGGAGAGACTTCCTGCGAATAAAGTT
-1,419	0,000282434	A_15_P529257	TC325258	#N/B	TC325258	20320	247	55	1487	GTACTGTTATTCTCAGTAAGTTAAGTCAACTCCAACCGTTTGAGGAAATAGATTGCAACT
-1,420	0,000161102	A_15_P405770	LOC797987	#N/B	XM_001338399	43129	523	77	847	CTTCCATGCTGTATAATGGTGTTGGATAGCTTTCAAAGGTGCATAAATCCATTGTAAAAC
-1,420	0,00010149	A_15_P305916	LOC562980	#N/B	XM_686350	33712	409	25	2198	TGTACGTCATGCTTTGCTCTTGGTTAATGTGCTAATTTCTATAAATCATGCTATTCCGAG
-1,424	8,92E-05	A_15_P253216	CT734835	#N/B	CT734835	31095	378	45	746	TGGAAATACACCATCCGTCTCTAATCAGCCACCGTCACAGGGTCTTGTGTTATTGTATAG
-1,425	8,88E-05	A_15_P322016	TC345320	#N/B	TC345320	39916	484	52	711	TTTACATTTGAGATGTGCATGTGTGTTTAAAGACTGACCTAATAAACCTGGACTTAAGTG
-1,425	9,49E-05	A_15_P474260	TC335820	#N/B	TC335820	36598	444	53	774	AGTCCGAGTCAACTAATTGTACAATGTGGACTTGAAAATCAAGTCATTGCACTGTTTGTT

-1,426	0,000101129	A_15_P348870	TC333923	#N/B	TC333923	31580	383	41	668	TCTGCACTGTTGTGTTATACACTAAACTGATGGTTCTTTCATGTTTAAGTGCCTGAAATC
-1,427	0,000104721	A_15_P101768	TC302023	#N/B	TC302023	25713	313	14	3876	CTTGGTTAACACAATCGTGCAGTATTTAGAAACCAGCTGCTTGCGTCATGTCTGCCACTT
-1,428	0,000159277	A_15_P223481	ENSDART00000102516	#N/B	ENSDART00000102516	24534	300	4	1128	ACTGGGACAGGGCACACAGAGAAAGACGAGGGCATTTTCTCCAAATTAAAGAAAATGTTT
-1,428	8,60E-05	A_15_P212631	BC134075	#N/B	BC134075	3294	43	32	1279	ATGCTTGCAAAACTGTCAGGTCAGTTTTGACCCATGGGAGATAATTTAAGTTGCTTCTTT
-1,428	8,83E-05	A_15_P358755	CT720011	#N/B	CT720011	18503	226	60	574	TAGGTTTACCATTTTTCACTGAGTCCAAACAAAGTTACACAGACACTGAAGTGTTTCAAA
-1,429	8,04E-05	A_15_P440820	TC351573	#N/B	TC351573	27236	332	27	739	TATACATTACAAAGTACAGATTGTTGAGGCAACAGCATTTTCTAGATATTGTCATTGGGC
-1,432	0,000131755	A_15_P470285	TC355133	#N/B	TC355133	7022	87	64	221	GGATTTGGCAGATTTTGACAACTCTGTATGAGACCAATAGAAAACATATGCAATCGTAAA
-1,433	0,00010003	A_15_P103611	TC335042	#N/B	TC335042	13663	168	53	2469	GTTCAGATACCTCTATCTGTTGTACACGGTATGTTGGAGGAATAATAAAACATGTTTGTG
-1,433	7,59E-05	A_15_P104412	TC316955	#N/B	TC316955	33893	412	34	6144	TCACGGCTAGGACATCCCATTGTGTGCAATTAGCAGGTAAAGGCACAACATGGTATCATT
-1,439	0,0001674	A_15_P262756	wu:fk29f02	#N/B	DN900405	29277	355	49	773	TTCATTGCATCCTATGGGACTCGAAATCATGTTCATGTATGAGCTAAAATATGCGTTAAA
-1,440	7,27E-05	A_15_P167076	ENSDART00000090720	#N/B	ENSDART00000090720	27	1	24	1691	TTAATAAGGATGAAAGCGAGAAAGACTCTGACTCTCCAGAATCGTTGCCTGACAGTACTG
-1,442	0,000218883	A_15_P586422	CF594957	#N/B	CF594957	26811	326	65	876	ACTTGGACAACAAATGTGTTGCCCGCTGTCGTAAGTTGAAACGTACAGTCTTCTGTTTAA
-1,446	0,000176355	A_15_P229361	EB944063	#N/B	EB944063	38275	463	62	495	ATTCTGGTGTTTTCCAACTGAAAGGGATAGTTCTCCCAAGAATGAAAATTTACTCACATT
-1,447	9,00E-05	A_15_P253431	DN900113	#N/B	DN900113	14148	174	45	525	AATCTTCATGATGATCCACAACTTGACTCTCCCAGCAGATTCAACTTGTTAGGCCCTTTC
-1,449	6,21E-05	A_15_P575272	wu:fj56b03	#N/B	EH444465	14349	176	63	704	CTTTAAGTCAAGGGGAGAAGTCTGTCACTGTAGTTAAGACTTCCCTCAAAAGAGGCAAAG
-1,451	5,59E-05	A_15_P424590	CT654522	#N/B	CT654522	36962	447	70	806	TCCGGCGCTTTCAGCAGTGAGTGAATTCTGTGAATCTAGAGAAATGACAGATCAATATCC
-1,453	6,68E-05	A_15_P346450	TC333028	#N/B	TC333028	30557	371	24	651	AAAGAATCTCAAATCCAACAACCAGTTAGATCCTATTCTCTCAATACCCTGATAGTCAAA
-1,455	5,88E-05	A_15_P189936	ENSDART00000060919	#N/B	ENSDART00000060919	13892	169	85	2268	CCAAAGTGTTTGACAAGTTCCAGTTTGAGAGAGTGGGCTACTTTTCAGTGGATGCTGACA
-1,460	0,000341915	A_15_P113062	TC340968	#N/B	TC340968	16151	197	52	271	GAGGAAGCAATGCTTACCACATCGAGAGAATGACCTCCTTTAGACCAACCTCCCTGCTCC
-1,461	5,45E-05	A_15_P188666	LOC793064	#N/B	ENSDART00000040156	9423	117	12	2397	TGGGTGGAGTTTCAGAATAAATTCTACCGCGGATCTGGATACAAGTTCAACCCTTTCTCC
-1,462	0,00011221	A_15_P551972	AL928334	#N/B	AL928334	28915	351	35	450	CAAAGTATTAAAGAGGAGATAACATTTGATGGGTAATGATGAAGTTGGATTTACCACCTC
-1,463	0,000156147	A_15_P154856	LOC571046	#N/B	ENSDART00000098962	7810	98	42	1298	TTTCTACGCCATGAACTCTACAGCCAACTATGATTTCGTCTTGAAGAAGCGAGGTTTCCC
-1,466	4,43E-05	A_15_P231466	CT607900	#N/B	CT607900	28461	346	58	720	TTGATGCCACCTTTCCTGGAGTCTAGCAGATGTTTCAGGTCCAAATATAATCTTCATTAT
-1,467	0,000251902	A_15_P465660	TC353676	#N/B	TC353676	21354	259	72	912	CTAACGGATTCTTCAGCAGATGAAATGATGGAACGTCATCAGCCATTCACTGAGACTGAT
-1,467	5,33E-05	A_15_P533637	TC359258	#N/B	TC359258	14232	176	3	852	TGGGGCTATTTTGTCTTTGGACTTAATCTGATTTCCTTTCTTGACTATGTCGAACGACAT
-1,468	4,44E-05	A_15_P593857	wu:fc84c07	#N/B	CT617800	20112	246	32	418	GTAAATGAGAAAATATGTTTTTGGTGAACTGTCCCTTTAAAAGAGTGCACTCAACTCTGA
-1,470	4,27E-05	A_15_P229106	EB932425	#N/B	EB932425	6560	82	82	431	GGGATCATTCCTAACTGATTTCCCATGGGATTTTCAAGAGTGCGCCAGACCATATTTATT
-1,471	9,09E-05	A_15_P104153	LOC572703	#N/B	XM_702050	27465	333	59	1439	TCATGCCTTCTGAACACACTGAGAAACAGACGGAGCAACACAAGGTTTTCTCTAGTCAGT
-1,472	4,05E-05	A_15_P270601	LOC568605	#N/B	EH448452	1346	19	36	799	ACAGAGACTGCCGTGTGGATTTTCCATTAGTCTATGCCCGCGTCTCTTACTTTCGAAAAT
-1,476	4,05E-05	A_15_P570942	wu:fj62d01	#N/B	EH506070	32495	394	84	888	GGGAAGGGAGGCTCGAATAATGTCTTCTGTCAAGCCTATGAACTTAACAACCTCAAAAAG
-1,479	3,62E-05	A_15_P137526	ENSDART00000081879	#N/B	ENSDART00000081879	28781	349	51	1289	CCAACGCTAAAGACATGCATCTGAAGGGACGCAGACACAGACTGCAATACAAAAACAAAA
-1,480	4,66E-05	A_15_P311301	CN843308	#N/B	CN843308	25915	315	32	599	AATAAACAACAACAGGATTTGAGGCTGGCCTATTCACACTACAAGTGATAACTATTTCTA
-1,481	4,86E-05	A_15_P204706	ENSDART00000058653	#N/B	ENSDART00000058653	19140	233	44	854	CTACTGTGCTGTTACTGAGGGCTTAGAGAGCAAATCTGGTAGCTACTTCAGTTACTGTTT
-1,484	3,74E-05	A_15_P376770	LOC572300	#N/B	XM_701519	40941	495	65	472	GGGATGGCATTTATTTTCCTGGATCAAAAGTCTTATTAGTTTTGCTCTTGGTCTCTAAAA
-1,487	3,47E-05	A_15_P280331	TC343896	#N/B	TC343896	30386	369	22	614	TGATTTACAGTGCATATACCTTTCTGTCCATAAACGCTTTGAGTTGTCTTCCGTATGATT
-1,491	3,22E-05	A_15_P103488	TC344354	#N/B	TC344354	35398	430	35	159	ATATAACACCAGCTATATCTCAGCATCAGAACATCGTAGAGAGACGGGGGTTGGCTTGTT
-1,491	4,77E-05	A_15_P432450	TC331335	#N/B	TC331335	25758	314	36	925	AAGAATTCCAGTTTGTCAGCAGATAGAGTCGCCACATAAAACATTCCTTTGCATAGTGGC
-1,494	5,69E-05	A_15_P165946	LOC565961	#N/B	ENSDART00000051966	30358	369	8	2679	ACTATCGTCATATGCATTATTGCTGGTGTAACCACATGGGCAGTGAGACGAAGAAGACCT
-1,501	5,42E-05	A_15_P373835	EH441663	#N/B	EH441663	39158	476	2	612	CGCAGACTGGAGGAACAGATGCAAAATGAGATCCTTGCAGAAATTCAGAGGAGAGAAGAT
-1,502	5,13E-05	A_15_P308701	LOC567050	#N/B	XR_029248	42202	511	58	3604	AGGCAGAGATTTTACCCTCATCTTCTTTTCACGTCAGCTGTAGACACATAGCGTGAAAAT
-1,504	2,67E-05	A_15_P486085	TC349263	#N/B	TC349263	20424	249	23	500	CACGTTATCTGGACAGATTAATCTTGTTTGTAACAACTCGACCACAATAAATGTCACTCT
-1,504	2,60E-05	A_15_P113522	ENSDART00000084309	#N/B	ENSDART00000084309	17093	209	22	1468	AAGTGGTCAACTATGATTTTGTGTCCTTCAACACAGACATGTGGAGTTTGGGCGTCATCA
-1,505	2,43E-05	A_15_P288191	LOC796964	#N/B	XM_001337347	5563	69	84	1413	CCAGATTTGATTGACCAATCAGAGGAAATGGGCGTTTTAGAACCGCCTACATGTGGATAA
-1,508	2,79E-05	A_15_P596582	LOC559158	#N/B	XM_682474	40305	488	81	1177	GAATACTGCCAACCTCAATGCCAGCAACCAACTTTATTATTTATACCTCAGACTTGACTG
-1,509	2,40E-05	A_15_P371035	CT616419	#N/B	CT616419	916	14	50	663	GAAGTGTAGGGGTTTTGTGTCGTGCCTGCAGTAAAAACTCAATCAGTTTCCAAACTGTTA
-1,510	0,000103917	A_15_P446890	ENSDART00000083254	#N/B	ENSDART00000083254	25303	307	59	1050	AAGCTGGATCTCACTGGAAATTATCCTGGACCATCAGGATTATCGTGGTTCTTTAAGTTA
-1,511	2,63E-05	A_15_P101094	TC305906	#N/B	TC305906	39917	483	53	1908	CTGCAGATTCCTTCATTTGAATGTTTTGGCGTGATGATCATCAGTCTCTAGGAATAAAAG
-1,520	3,08E-05	A_15_P118786	LOC556060	#N/B	XR_029509	29992	364	74	2362	CTCAGCTTAAGAGTATCTACAAGAAGGCCGGCGTGGGGAAGGAGAAGCGTGAAGTGACGT
-1,520	0,000108323	A_15_P584057	ENSDART00000105400	#N/B	ENSDART00000105400	28779	349	50	1020	CTGGTCTTTGCTAAGGAATCCTCAAAAGGCTCTTATGAGGTCGACAATTTTCAGCTCAAA
-1,522	1,93E-05	A_15_P510902	TC340199	#N/B	TC340199	3578	48	6	357	ATATAAACATGAGGTCGACATGTCACCTGAAGCTGTTGACATTTTTGTCAATAATACGTT
-1,531	3,15E-05	A_15_P558232	ENSDART00000097188	#N/B	ENSDART00000097188	33641	407	74	666	CAAGGTTTCCTGGAAAAGGATCCTGTTAAGGCCAAGAAACTGTCAAAGACCATCACTGAC
-1,533	9,31E-05	A_15_P556182	CO917745	#N/B	CO917745	32875	400	23	832	ACTGACTCGCTGATGAATGGTCCATGAGCTACACGATGGGAACTATGAACTGGTGTATAT
-1,539	2,26E-05	A_15_P322806	TC345604	#N/B	TC345604	3634	48	34	1064	TGAATTGATTACAGAATGAATAAAAATTGCACATGCTGTACTGGAGGGACAAAGCGAACA
-1,542	1,45E-05	A_15_P543312	TC324146	#N/B	TC324146	42541	516	76	1655	GCGTTTATCAACACACTGAATAACAAATACAGAAATAAATGAAGTTTGTGCTGGTCTGTG
-1,545	2,26E-05	A_15_P262711	LOC562083	#N/B	XM_685480	2318	32	44	2386	GCTCTTGAATATGCAGATTATTAAACTCTGGGTAGCTGTGCAGTAGCCCACTGATGATGA
-1,548	2,61E-05	A_15_P116859	TC302933	#N/B	TC302933	14469	178	40	2864	TTCAGTAACTTTTCACAAGCTATATGAGCAGCTTTAGTGGTGGGGTTTATTGCTAGGCCG
-1,549	6,76E-05	A_15_P504112	EB942354	#N/B	EB942354	37761	457	53	599	TTATGAATATTGAATATGGACCACCACAAAGCTGAACAATAAATGTTGGTTCTCACGCTC
-1,550	1,68E-05	A_15_P558092	EH484715	#N/B	EH484715	38872	471	27	859	GTTTCATTTCTTCACATTATGGTTTCCCTTTGGCAAAAGCTTCAAATGATATCTGAGCTG
-1,552	1,59E-05	A_15_P302596	TC352184	#N/B	TC352184	40594	491	58	710	CATAAATGAAGTGAAATGAGAGATACATCATTTCAGAAGTGGATGTCCTAGGTTTTCAGT
-1,556	1,18E-05	A_15_P112114	LOC567050	#N/B	XR_029248	13503	166	56	3737	TCTTTGTACAGTAAGCTTGTCTGATTTTCCACTCCTTTGTTCGACCCCTTTACCTTTCAG
-1,565	1,32E-05	A_15_P113563	LOC798769	#N/B	XM_001336604	30301	368	63	611	GACTGCTATACAGTACATGCTGGCTATGCAAAGATTGAAATTATGAAGAAAAAAGCCTCA
-1,570	7,57E-05	A_15_P506367	TC322767	#N/B	TC322767	31607	384	55	698	TCTGCGCCGGTTCGGAAAATTCCAAATTGAACTTAAAACAATCGATTACAATTTGGTCCC
-1,572	1,04E-05	A_15_P231866	EE685937	#N/B	EE685937	4993	64	50	587	GCATTCGAAGCCATCATTTAAGACAAGCGGTGCCTTTTGAGCATGCTCAGAATGAGATTC
-1,574	1,17E-05	A_15_P135271	LOC553286	#N/B	ENSDART00000064047	3331	44	50	118	AGATTCAAGACTCTGAGGCTGAAATAGGAAAGCTGCAGAAAGTCATCAGAGAGGATGAGG
-1,578	9,36E-06	A_15_P115352	TC303096	#N/B	TC303096	23028	280	78	2840	TACGCAGCGGATGTCGCAAACCATCTCTGGGAAAAAGTTGAGACAGTATAGAATGCAAAA
-1,581	2,13E-05	A_15_P313596	CT601355	#N/B	CT601355	32704	398	21	415	TCGCTCTAGACTATGGTCAACTTGTGAAGTTACTCATACACCTCCGCTCATGGCATATTA
-1,582	3,53E-05	A_15_P256481	EB950891	#N/B	EB950891	19981	243	50	515	CATATATTTAAGGAATTAGCTGTTGAAACCTGAGCCAACGTGGGATCCTAAAGATATGTT
-1,586	8,82E-06	A_15_P557582	LOC100001502	#N/B	XM_001341447	41926	507	76	1423	TTAGCGCTTCCAGCTGACCACATATCTTCGTATGGACAGTTTTTACGGTGTTAGCAGTTT
-1,591	7,88E-06	A_15_P536507	TC360174	#N/B	TC360174	2338	32	54	357	AGTGGCGGTAGATCCGCTGTTTATACGAGGAGTCCCACTGATATTAAAGTGGCGTTAAAA
-1,592	8,16E-06	A_15_P493622	TC311921	#N/B	TC311921	12209	149	77	762	ACTGGAGTTTGGCTGACTGTAAACTATGGAAGCACATTCTTCGCATGATAACCAGAGCCA
-1,594	1,47E-05	A_15_P107556	LOC798702	#N/B	CT662555	11823	145	48	468	AGGGTCCGACAAGGACTGGCTCTGGAAGTGAAAAAGAAATAGGTAGCCTGGCTCCCTCCG
-1,601	1,98E-05	A_15_P472055	LOC100000459	#N/B	XM_001340626	28332	343	78	3755	GGAAGCATGCTACATTTCCTTGAGTGTGAGATTAATTTTAATAAAAGGGGCATCAGCAGT
-1,602	1,57E-05	A_15_P378680	LOC570160	#N/B	EH504865	13939	172	24	610	GCTGGAGGCGGTTCGGCCCAAAACTGCCCTAATCACAGATATTTTACAATAAACTTCGAT
-1,602	6,88E-06	A_15_P556722	LOC100000158	#N/B	XM_001337155	11416	142	11	3070	TAATGTTTCGAAAATATGGTGGCACTTTGTAATAGCGCTGAATGGTCAAGGATTTTACAG
-1,603	1,31E-05	A_15_P119270	CD606624	#N/B	CD606624	29627	359	60	255	TGGTTAGAGCGTGGTGCTAATAATGCCAAGGTCGCGGGTTCGAGCTCCGTATTGGCCAAA
-1,611	1,08E-05	A_15_P332394	sb:cb322	#N/B	CK028151	29790	362	57	615	AAACAAAGCGTGATTCACCTGTTGTAAAAAGCCAAAGTGATTTTGACTGGGTGTTTAGTT
-1,611	5,81E-06	A_15_P405910	LOC796302	#N/B	XM_001336575	11824	146	48	1949	TCAGAAAATGTTCATTAGGCTAACATTTCACCCATTTTAAGTGAGTTTGAAGTCATGCAG
-1,615	6,96E-06	A_15_P104698	LOC100001232	#N/B	XM_001338430	15568	192	9	939	AAATTCTAGTGTGTTTTCCACACTGACCTGAAAACTGCACAAAAGAGCTATAGCAAGCAC
-1,616	7,20E-06	A_15_P590472	LOC799650	#N/B	XM_001339948	10109	126	25	2060	AATTAATATTTGCTCGCTCAGGGCGTCAGTATCCATTACATACACTGACTGCTTTTACTG
-1,616	5,44E-06	A_15_P592432	LOC798023	#N/B	XR_029436	39688	482	20	1237	AGCGTCAGCACACTCAACATTAACTCAGCTATACTATATGACAGAAATACAGCCAATCAG
-1,617	6,32E-06	A_15_P208246	zgc:153102	#N/B	NM_001077310	31947	388	58	1777	CTACTTAGTTTAACAAACAACTGTTGTATTCAGCAGAGTTATTCAATGCATGAAGAGCCA
-1,618	5,43E-06	A_15_P110206	CK359992	#N/B	CK359992	11590	143	15	115	AGCTTGTTTCAAATGAGCACTGGGAGAAAGAACTGTACTAAAGAATGTCTGTGACATCTA
-1,622	4,14E-05	A_15_P565882	TC338244	#N/B	TC338244	128	2	74	632	TGTAGTGACGAGTGTAACGTCTGATCATCACATAATAAACTATACTCTGATCCTGAAAAA
-1,627	2,37E-05	A_15_P275756	ENSDART00000099515	#N/B	ENSDART00000099515	34881	424	26	1731	GTATACTTGATGGAGCAATGTTGCTGAGAATGAAACGGGATGAAATCAGAGCGATATGTC

-1,629	5,05E-06	A_15_P291826	LOC799650	#N/B	XM_001339948	18679	228	64	2066	TATTTGCTCGCTCAGGGCGTCAGTATCCATTACATACACTGACTGCTTTTACTGCAGTTG
-1,630	1,07E-05	A_15_P106926	BC155792	#N/B	BC155792	33109	401	57	699	GGCAGAGTCCCCAGAGACAAAGCCAAAGCTTCCGATGAATAGACTCATATCAGACTTATA
-1,638	4,24E-06	A_15_P293986	TC364254	#N/B	TC364254	31222	380	27	477	AAACTTGTTAGGATTTAAGGGGGTTCAGTTCTTACCAGTAACGAGCAGATTGTCATTTTT
-1,653	3,50E-06	A_15_P115758	si:ch211-240l19.8	#N/B	NM_001082930	1446	21	7	314	ACAAGACTTTCGACGATCATTTGGGCACTTGCAACAAATTAGTTCAGTATGGGTCTTTCG
-1,667	1,34E-05	A_15_P434895	TC332319	#N/B	TC332319	36725	446	32	523	CAAGGAGATTAAAGAAGTGATTGAACTTCCAGTCAACACCCAGAATTGTTTGAGCTCTTG
-1,669	8,19E-06	A_15_P590422	LOC100007711	#N/B	XM_001341234	40126	485	75	809	AACTGATACATATGCGATTTATGAAGAAATTGACTATGACCAGATCTCAGATGATCAGCT
-1,672	2,86E-06	A_15_P346465	LOC799650	#N/B	XM_001339948	19609	239	30	2114	TTACTGCAGTTGTGCTGTTTATACGAGGAGTCCCACTGATATTAAAGTGGCGTTAAAACC
-1,679	0,000454051	A_15_P503647	TC321490	#N/B	TC321490	3127	41	32	694	ATGCTAATCATGCTAGATCATGCTAATCATGCTAGCACATGCTATTCAGCTAGATCATAC
-1,696	2,37E-06	A_15_P493577	TC311897	#N/B	TC311897	11022	135	65	724	GTTATGCGCATCTAGCATCTAACGTTAGTCACCTAAACTCACACTTAGCTTTGTTTTGAT
-1,701	1,46E-05	A_15_P106780	TC344906	#N/B	TC344906	34333	418	3	1601	CAGAAAAAGTCATGATGTTGTAAAGGGTTTTTGTTACCTTTCTAGCCCCTTGGTTCCTTT
-1,715	2,08E-06	A_15_P591077	LOC569489	#N/B	XR_028944	28989	351	73	1734	ATCAGTGTTGTTTATTTGTGTTCAGCAGATAACTCTGTGATTAAAAGTACACTGCGGGGT
-1,722	1,65E-06	A_15_P253146	DN893839	#N/B	DN893839	20321	248	55	732	AAATGTTGATGGTCCAGGATCAGCAATAGTGAACTAGATATTAAAGTTTGAGGACAAACT
-1,725	1,85E-06	A_15_P310581	CT610857	#N/B	CT610857	6785	86	27	834	AAACGTGGATAGATAGCCAGCAGGACATTTGAGTTTCAGCATCACAGCATCGACTGTGTA
-1,736	1,44E-06	A_15_P538302	si:ch211-240l19.5	#N/B	NM_001030152	33119	401	63	441	ACAAGTATGAGTTGAGATGATTTGTACCAAAGCTTATTTGAGACAAATTTCCACTGCAAG
-1,740	1,46E-06	A_15_P441150	TC351688	#N/B	TC351688	6222	77	80	313	GTATTATTGTGTAAACCTACCATAAATCAAACAAATACATAAAACTGGCCTGGCCTGGCG
-1,743	2,36E-06	A_15_P116802	LOC569609	#N/B	XM_701410	35188	427	13	325	TGTTAAATCGTCATTTGGTGAGAAGTTTCCTGAGGTCACTGCAGCGTCTCCATCTACCAA
-1,756	1,33E-06	A_15_P237416	ENSDART00000022933	#N/B	ENSDART00000022933	11168	137	54	345	AAAGTGAAGGAGAACCTGAGACGAACGTCATTTACAAGTTCTGGAGAAAAGGAGGTGTAA
-1,762	1,50E-06	A_15_P569147	TC334013	#N/B	TC334013	35008	426	5	1205	TAACCATTGAGAAGCATTTTATTTCAATAAAGCCCAAAGGAAGGATGATCTTCAGTGACA
-1,777	9,79E-07	A_15_P173841	si:ch211-240l19.5	#N/B	NM_001030152	12485	154	48	451	GTTGAGATGATTTGTACCAAAGCTTATTTGAGACAAATTTCCACTGCAAGTAGATTGATG
-1,789	1,18E-06	A_15_P107809	LOC561538	#N/B	XM_684946	21797	265	42	5392	AGGGGAACCTATTGCAGGTATGGCTGTCCTGCATCTGTAATCTTCTTGTACAGTTTTGTG
-1,810	6,89E-07	A_15_P346120	TC332902	#N/B	TC332902	2220	29	77	880	AAATAGAAATGTCACGCATGGCGTCAAGACGATGCTTAGCGCGAAAACCCCTTTTAACTC
-1,840	5,26E-07	A_15_P545427	BC152580	#N/B	BC152580	34381	417	28	175	GTTCTGTTTGGGCATGGTTATCATATTCAGCAAAAAACTCAGATGTGGAAAGTCCTCTGC
-1,938	2,52E-07	A_15_P515302	TC310832	#N/B	TC310832	18667	228	58	849	AACACCGAGCATCTAAACGACTGAGAGACATTCAGAGGGTAAAGAGAAAACCAAAAACAG
-1,972	1,76E-07	A_15_P117867	CK697851	#N/B	CK697851	27369	334	10	217	TCGAGCAGCCCTAGTTCTACTGCTGTAGAAGTCCTTCAGTGCTATTGTAAGGCTCTTAAA
-1,979	2,32E-07	A_15_P272131	TC314185	#N/B	TC314185	22194	269	78	727	TTGTCTGCCTTTGATTTAGTTTGCTTCGGTAATCGAGCAAATCAACAACAGTTCTACCAC
-1,981	3,21E-07	A_15_P306101	TC353277	#N/B	TC353277	43249	525	67	711	TGATGCGATACGTCTTGTAGTCTCCCTTTAAATTAGCTGAGTGATCATTTCACATATACA
-1,992	1,48E-06	A_15_P113065	TC322836	#N/B	TC322836	19568	239	9	2406	AGCCCTGCATTTCTGAGAAAAGGGGAATCTGAATTTTGAGAGTACAAATTAACTTACAAT
-2,060	2,69E-07	A_15_P600272	LOC571764	#N/B	XM_695385	13761	169	18	2506	ACACACACAAATGAATATCATTACACAGCTGTGTACTGAAAACACACACACAATGAGCAT
-2,105	9,05E-08	A_15_P582022	TC320295	#N/B	TC320295	7575	95	7	593	GATTTTTTGTTGTTGTTGTTGTACGGACTTCTCTCGGCACCCACAAATAAACATCTACGT
-2,121	6,34E-08	A_15_P103323	TC309508	#N/B	TC309508	11214	137	78	884	CACTTTTGATTTGTTTCCTGTCACAGACTTTTAAAGCACCTCAGAAGTTCTTTCATCTGG
-2,138	6,55E-08	A_15_P102081	TC325806	#N/B	TC325806	15562	191	6	661	CTGGACAGCTAAACTCAGATCATCTGCATCCTCCAAAGCCTCAGTTGTACTCTATGCTTT
-2,213	7,52E-08	A_15_P105066	TC347047	#N/B	TC347047	24701	302	3	251	CATCACGTGGTGCATCTAAATATTGTGGACTGCTGATATTCTACTGCATTGATTGTGATG
-2,381	3,82E-08	A_15_P106371	LOC796842	#N/B	XM_001337202	7811	98	43	2291	ACCCCTGCCCTAGGTGATATCATTGAGATGATTGTCTTGTAAAACTCATAAATATGCTTA
-2,562	8,75E-09	A_15_P377595	LOC100000361	#N/B	CN503237	10706	132	73	719	CAAAGCAGCATATGACAAATGTCAGGAGAACAGTGTGATAAAACAACTGAAGAATGAGGC
-2,652	6,42E-09	A_15_P111079	TC310191	#N/B	TC310191	22015	268	69	722	TTACTGCATTGAATTATTTTCTTTGTAGCTGCTGATTCCAACAAGCTTCAGTGTCTGGAG
-2,708	9,95E-09	A_15_P106535	TC306742	#N/B	TC306742	27563	336	24	515	TCGCACACAGACTGGTGGGTCAACCTCGCCACAGCTAAAACAAGCTTTGCTGCCTGTGGT
-2,745	6,81E-09	A_15_P496952	TC313638	#N/B	TC313638	18163	221	58	2098	AAATTCATTATGACATGATTTTTGTCTGACATTTGTACAGAGACCCTGGAATGGACTAGA
-2,839	6,32E-09	A_15_P120360	TC359093	#N/B	TC359093	8431	106	17	637	ACTCCGAAAAAGTCATCAGACACCCCAGCTACGTTAAGACCGTCTCTCTGCCTTCAAGCT
-2,899	2,22E-09	A_15_P130321	BC086847	#N/B	BC086847	31038	377	16	1571	CTTTATAGATCTGCAATTCATCTGCAATGTCTGTCTTTGGTTTGTAGATAAAAACCTGTG
-3,252	5,41E-10	A_15_P274886	TC315630	#N/B	TC315630	8053	99	82	673	TGACTACACCCTGGTTTACTCCTGCACTGATTTTGACAATCTCTTCCATGCTGATATCCT
-3,298	4,89E-10	A_15_P510937	TC340210	#N/B	TC340210	31172	379	1	358	TGTGTCTTTTGCTAGTACATGGGCAGATGGCATGAGATCATGAAGTTCCCTTCACCATTC