

Supplementary Table 1. Detailed chromosome-wise information regarding all markers present on the RH II map. Cytogenetic locations shown in bold represent work from this study.

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	1CA01	1q11-q12	F: ATTTCAAAAGCGGAAGAGCA R: ATAGAGGAAGGCTGGCAACA	110	2.0	58		AF043198
microsatellite	1CA16	1	F: TCACTGGGGGGTATATGCAT R: GATCCTACTCCACCTGAAGTGG	121	3.0	58	Chowdary et al. 2003	AF043200
microsatellite	1CA20	1	F: TGGACAAAATGCAAAAGTCA R: TCCACTACACAGGAAAACGAA	194	1.5	50	Chowdary et al. 2003	AF043202
microsatellite	1CA21	1	F: TGTCTTTCTCTGCCCTGGTT R: TCTTGCATAAAAGGAATACGC	243	3.0	58		AF043203
microsatellite	1CA22	1	F: TGGGCAAGAGGACAAATAGC R: TGGCAGCCTTGGTTTGTACT	208	3.0	58	Chowdary et al. 2003	AF043204
microsatellite	1CA25	1q17.3	F: TCCAATTTTCCCCAATGGTA R: CTGCATTTTGACAATGGTGG	206	3.0	58	Chowdary et al. 2003*	AF043205
microsatellite	1CA28	1	F: CCTACGCCCACACTCACATA R: TGGACTTTTCTTACCCCCAAA	213	1.5	58	Chowdary et al. 2003	AF043208
microsatellite	1CA30	1p16	F: TGGGGAGGGGTTGTTCTAG R: GCTCTCCACTGCATGCATAA	130	3.0	58	Chowdary et al. 2003*	AF043209
microsatellite	1CA32	1	F: AGTTACCAAATGTCTGCATTGC R: TTCATCTGTAAAATGGGCAGG	107	1.7	58	Chowdary et al. 2003	AF043210
microsatellite	1CA36	1	F: TGGACCAGGACAGAGGAAAC R: GCCTTTAAAACAACCTCCCCC	191	1.5	58		AF043211
microsatellite	1CA40	1	F: TTGAAAGCCGTGTTTTTGTG R: ACCCCATGTTCTGACAAGGA	226	1.5	58	Chowdary et al. 2003	AF043213
microsatellite	1CA41/ 1CA24	1q15-q16	F1: CTGGTCAGGCCTATTACCCA R1: AGATATTGGGGGCGGAAG F2: AGATATTGGGGGCGGAAG R2: TGGAGGTCAACTGGCTATCTC	245/ 205	1.5	58	Chowdhary et al. 2003*	AF043214/ AF179211
microsatellite	1CA43	1q17.1- q17.3	F: ATGGCATGATTTGCTTCTCC R: TGGAAACAACCTAAATGTCCA	122	1.5	58	Chowdhary et al. 2003*	AF043215
microsatellite	1CA44	1p16	F: GGCAGCACACCAAATCAAGT R: TCCTGCAAAAACAACAGAGGA	203	2.0	58	Chowdhary et al. 2003*	AF043216
sequence	1STS01	1	F: CAACAGAAGGCACTTCAAAGC	115	1.5	55	Perrocheau et	DX010625

tagged site	(FLJ11186)		R: GGAGTTGCAAGCACGATTTTA				al. 2006	
apobec-1	ACF	1	F: GAATGGATTTAGGGCTCAGAC	229	1.5	60		ECA576521
complementati			R: GAGAGAGAACCAGGAGAGAAC					
on factor								
actin, alpha 2,	ACTA2	1p13^a	F: CCACCCCATTTCTCCCATATC	325	1.5	58		
smooth			R: TCTTCCATTTCTCTCTCCCC					
muscle, aorta								
actin, alpha,	ACTC1	1q24-q27	F: GTGCCTTGCTCTCAGTCCACC	179	3.0	58	Lear et al.	G62166
cardiac muscle			R: GGTTGCAAGTCCTGGTCTGGTT				2001*	
1								
actinin, alpha	ACTN2	1	F: GCCTGGTGTAACCTCCACCT	1328	1.5	58		
2			R: GATGACTTCCAACAGCAGCA					
adducin 3	ADD3	1	F: CTCAGTCACCGCAAATATCC	~1075	1.5	58		CD528586
(gamma)			R: TACTCACTCGTTTAGCAAGCTC					
adenosine	ADK	1	F: GGTTCCTCCCGGAGTCAGTAT	165	1.5	58		
kinase			R: GTCTCATTTCCAAAAAGTATGTCA					
angiotensinoge	AGT	1q11-q12	F: GAAGACTCAACTTGCCCTCCACT	212	3.0	58	Fetal cDNA	
n			R: GCCACATTTACCAAGGACAAATG				library, clone	
microsatellite	AHT021	1q14-q15	F: TCCAAGTTGCTGAATGGATC	199-215	2.0	58	#1109	
			R: ACGGCCTGATTCTCTCTTTG				Swinburne et	
							al. 1997;	
microsatellite	AHT026	1p13	F: CTGATGTGGCTCAGTCTCCA	202-210	3.0	58	Chowdhary	
			R: TTCTTGGATTTTGGCAAAGG				et al. 2003*	
microsatellite	AHT040	1q15-q16	F: GCAAGTTCAGCACCTCCCT	230	2.0	58	Swinburne et	AJ271511
			R: TTTATGACACCTGCTGAGAACG				al. 2000*	
							Swinburne et	AJ271525
							al. 2000;	
							Chowdhary	
							et al. 2003*	
microsatellite	AHT058	1	F: CAGTGATGAGCCGCAAATAG	163-198	2.0	58	Swinburne et	AJ507675
			R : TCTACCTATAATCCGCCTCCC				al. 2000	
microsatellite	AHT069	1	F: ACCGCTGGACCTTCCTTC	192-194	1.5	58	Swinburne et	
			R: ATCGTAGCATCCCTCACATACA				al. 2003	
microsatellite	AHT085	1	F: GTGCCAATCACTATCCAGTTTG	153-160	1.5	58	Swinburne et	
			R: CGACCAGAATATCAAACAAGTG				al. 2003	

microsatellite	AHT113	1	F: CATGGATGTCAGCTCAGGG R: GGTCAAACAAAATAATGGTTCC	110	1.5	59		
microsatellite	AHT121	1	F: TTGAAGGCCTCTCCAGAGAG R: AGGTCAGAAAGTCCTTGGAGG	182	1.5	61		
aldehyde dehydrogenase 1 family, member A3	ALDH1A3	1q17.2	F: CCATCAGGGAGTGTTCTTCAA R: CCTGACGTCAAAGGGGTCT	145	1.5	55	Perrocheau et al. 2006*	DX010430
arachidonate 5-lipoxygenase	ALOX5	1p13-q14	F: CCATGCAGGACCTGACCTAT R: GTCGTCCCGGTAGAAAGTAGT	64	1.5	58		AB218723
alpha-kinase 3	ALPK3	1	F: CCTCCTCCACCAGTGTAAC R: TGGACTCTTGGAACCTTTGG	107	1.5	60		
ankyrin 3	ANK3	1p13- p12.3	F: CCTTGGTACACATAGAGAGCAT R: GGTTAATGATTCCCAGAATGGC	113	1.5	58		
ankyrin repeat domain 1	ANKRD1	1p14-p13	F: ACTGATGCTGGAAAGCTCAC R: GCACTCGCCTATTATGCTAC	314	1.5	58		
ankyrin repeat domain 2	ANKRD2	1	F: GAAGGCAGGAAGGTAGTGAG R: GATGAATGGATGGATGGATGG	256	1.5	56		
annexin A2	ANXA2	1q21.3- q22	F: GTGGGGATGACTGAAGCCTGT R: CACTGCCAACTCCTTGGAATGT	234	3.0	58	Chowdhary et al. 2003*	G62155
annexin A7	ANXA7	1p12.3- p12.1	F: GCCGTCCTCACAGTCTTAT R: GAGCTTGACCTCCAGGATA	~856	3.0	58	Chowdhary et al. 2003	
annexin A11	ANXA11	1	F: AACGAGTATCAGCGAATGAC R: TGAGCCTTTCAGCAAAGAAG	~1200	1.5	60		CD528344
AT rich interactive domain 4B	ARID4B	1	F: TGGAAAGTGCTATGTGGAGG R: GGAATGGGAACTAAACGAGG	151	1.5	56		
arrestin domain containing 4 microsatellite	ARRDC4	1	F: TTCCTCTCGTCTGATTGTTCC R: CAATCCAGGATGGATGGAGT	189	1.5	60		
microsatellite	ASB08	1q16-q17	F: GACAACGTGGCAGCTCACTGCC R: GCAAGTAAGCCATATGTGCATGCG	143	3.0	TD 64	Breen et al. 1997*	X95323
microsatellite	ASB12ms	1q12-q13	F: TCAGCAATAGAAGCCAGCTCC R: TCCTATGGAGGTGACCTTCCC	171	3.0	65	Breen et al. 1997*	X95327

microsatellite	ASB41	1p14	F: AAAGTTCACTTAGTCCTTGG R: CCACCTGTTTGCACCTTGC	129-159	3.0	TD 64	Irvin et al. 1998 ; Lear et al. 1999*	AF004771
beta-2- microglobulin	B2M	1q23^a	F: CACCCCAATGTTTCTCACT R: GGTCCCTCCTGCCTACTAGC	194	2.0	58	Shubitowski et al. 2001	
BCL2- associated athanogene 3	BAG3	1p18-p16	F: CGTCAGGAAGGTTTCAGACC R: GGGCTCTTCTCCATGTCC	187	1.5	61	Perrocheau et al. 2006*	CX595296
BTB domain containing 1 caspase 7	BTBD1	1	F: CAAGAAGGTAGCGACGTGTG R: AGACCAACTTGTCTCTGGCATA	239	1.5	60		CX599403
	CASP7	1	F: GAGATCCATCACGACCAACC R: CTCAGCATCTTTGTCTGTTCC	~650	1.5	58		CD466307
cadherin-like 23	CDH23	1	F: CATCATGCTGATTGCCAGAC R: GCTGTGTGACAGAAGGCTCA	157	1.5	58		AB218725
centrosomal protein 27kDa	CEP27	1	F: GCAAAGATGGATATTTTGGTGA R: AAAGGTAAAGGAGGTATCATAACATCA	158	1.5	58		DN506056
cofilin 2 (muscle)	CFL2	1	F: CCATTTCTCCAGCTCAGTCA R: GCATTCCGTGGGTTCTACATA	185	1.5	58		
cingulin-like 1	CGNL1	1	F: CAGTCGGAGCAACAGTTCAG R: TTGAGCAATTCCTTCGCTTT	180	1.5	58		CX594868
BAC end sequence	CH241- 102E24_SP6	1	F: CTTGGAACCCTAAGTTGCTG R: GCTGGAACCTTGGGATATTAAC	545	1.5	60		AJ584137
BAC end sequence	CH241- 102F21_SP6	1p13	F: ACCGATTTGCTTAGCCTTCC R: CAAACCATCCCATTGATCTCC	541	1.5	58		AJ584173
chromodomain helicase DNA binding protein 2	CHD2	1	F: GCTCAGACGAATGACAGTGAC R: CGGATCTCCGCATCAGTAAA	173	1.5	60		CX602471
carbohydrate synthase 1	CHSY1	1	F: TGTGTATTGGGCGTGTGTTT R: TTTGTCCCCAACACAAGTGA	171	1.5	60		CX594281
calcium and integrin binding 1	CIB1	1	F: CAAGTCCCCTATGCCTTCC R: CTCAGGTCATCTCTGTTCAAGG	213	1.5	63		
C-type lectin domain family 14, member A	CLEC14A	1	F: GGCTCCAAAGACCTTCTCTTC R: CAAGCCCTCAAACCTGGTACTT	279	1.5	54		

CDC-like kinase 3	CLK3	1	F: CAGCCCCATTTTCTCCAAC R: GTACCAGGGGTACAAACAGTAAG	199	1.5	58		
chymase 1	CMA1 (CYH)	1	F: GAATTGCTCCTCTGCAGGTC R: CCTGTAGGTCCCACCTCTGA	200	1.5	TD 60	Chowdhary et al. 2003	AF130752
collagen, type XIII, alpha 1	COL13A1	1	F: CTCGAGGCAAACCAGGAGAC R: CCCTTTCTCCCCCTTCTCT	61	1.5	58		AB218726
microsatellite	COR006	1q25	F: GTTCTGCACATCCTGCTCTT R: AGTGCCCTGAAACTGTATGG	187-199	3.0	58	Hopman et al. 1999; Chowdhary et al. 2003*	AF083449
microsatellite	COR046	1q17.1	F: TGTTTGCAAAGATATTGGGG R : ACCTGGTCAGGCCTATTACC	245-259	1.5	55	Ruth et al. 1999 ; Chowdhary et al. 2003*	AF108363
microsatellite	COR053	1	F: AATTGACTGTGGAAGCCTTG R: GGCTGAGGAGTAAGCTGAAAG	173-197	3.0	55	Ruth et al. 1999	AF108370
microsatellite	COR059	1p12.3- p12.2	F: ATGAATGGCAAATTGAAGGA R: TTCTGTTTAGGGGCTCTTAGG	265-277	3.0	58	Ruth et al. 1999; Chowdhary et al. 2003*	AF108376
microsatellite	COR063	1	F: CAGAGCAATCCTTCTGTCACG R: GTTGTTTATCATTTGAAAGCCG	130	1.5	58	Tallmadge et al. 1999a	AF142600
microsatellite	COR079	1	F: TGCTGCCAGATCTTCTGAAT R: TGGAGAGCGTGAAATTAACC	202-212	1.5	58	Tallmadge et al. 1999a	AF142616
microsatellite	COR100	1	F: CCCAGAGGTTTCAGAGGG R: ATTCTAGGGCATATTATGACAA	188-220	3.0	58	Tallmadge et al. 1999b	AF154953
chemokine (C-X-C motif) ligand 12	CXCL12	1	F: GGCCACCTTCACATTATCTG R: CGATTTGACCTTCCTTTCTGAC	370	1.5	60		BM781275
cytochrome P450, family 1, subfamily A, polypeptide 2	CYP1A2	1	F: ATCCAGGAGGAGCTGGGTTAG R: GAGTGTCGGAAGGTCTCCAG	202	2.0	65	Chowdhary et al. 2003	AF134063
cytochrome P450, family	CYP19A1	1q22	F: TGAAGGTGATGCTGGTTTCA R: TGTTGAGGCACTTTTCTGA	169	3	58		AF031520

19, subfamily A, polypeptide 1								
discs, large homolog 5 (Drosophila)	DLG5	1	F: TTAAACAGCCAAGGCAGCAG R: TTCAAAGCACAGAAAGGCAAAG	404	1.5	58		
dynammin binding protein	DNMBP	1	F: CCAGAAACTGACTTGGTTGAA R: CAGTGCTTTAGGGGCTTTTAG	175	1.5	62		
early growth response 2 (Drosophila)	EGR2	1p13- p12.3	F: ACTGTTAAGCAAGTTCTGAACC R: ACATCACACAAGGCACCAAG	155	1.5	60		CD471350
eukaryotic translation initiation factor 3, subunit 10 theta	EIF3S10	1	F: AGCACTTGAAGTCATTAAGCC R: TACGCTCCTTCTCTCTCTCC	~1200	1.5	58		
exocyst complex component 8	EXOC8	1q13	F: TGGGAAGTTGATTAAAGACCAC R: TATGATTCCAAGCTCAAGCG	252	1.5	60		CD465126
exosome component 1	EXOSC1	1	F: GCCCTAAGACCCACACTAAAG R: GAATGAAATCCACTGAAAGGTT	250	1.5	62		
fumarylacetoac etate hydrolase	FAH	1	F: CACTTGCCAGTGGCTACCAT R: TGCAGGCACCATATACAGGA	234	1.5	60		CX599712
feline sarcoma oncogene	FES	1q14-q15	F: CACCCAAGGTCACACATCAG R: AATGAGACGCACAATGTTGG	201	1.5	58	Lear et al. 2000* ; Chowdhary et al. 2003	AF130763
fibroblast growth factor receptor 2	FGFR2	1	F: ATGCTTAGAGCTGGAAGGAC R: GAGGAGAAATAAGCCCCAAC	377	1.5	58		
FK506 binding protein 3	FKBP3	1	F: ATTCCACCAAATGCAAAACTC R: GGGGATCAAGTAAACAAGTCCT	198	1.5	58		CX604401
furin	FURIN (PACE)	1q16	F: ATGGAGCTAGGCCCTGGTT R: CCATGCTTGCGTGCCACA	150	2.0	58	Godard et al. 2000*	

GTP cyclohydrolase I feedback regulator	GCHFR	1q23-q24	F: GAGTACTACGTCAATGACCCTCCT R: GTGCCCTGTCTGCTCCTC	150	1.5	58		CX597457
glutamate dehydrogenase 1	GLUD1	1q13-q14	F: GCAAAAATAAAAAGCCCACTG R: GGAGGTTACTGCATTCTTTGG	92	1.5	58		AB218733
glyceronephos phate O- acyltransferase	GNPAT	1	F: CTTACAGAGGGAAGAAAAAAT R: TAGAGAAAACAAGGCACA	198	1.5	56		
glutamic- oxaloacetic transaminase 1 general	GOT1	1p14	F: GAAGGTGGAGCAGAGGATTG R: AAGAGCTGGGCTGTCATCTC	84	1.5	58		AB218734
transcription factor IIA, 2 hect domain and RLD 2	GTF2A2	1	F: CTGGCTCCAATACTACAGAATGA R: AAAGGTAATGTAAGAGGCTACAGAGG	201	1.5	58		CX604586
equine EST	HERC2	1	F: GCAATATTTTGTGGCCGTTT R: GCTCACTGCCATCAATCAGA	151	1.5	58		
	HEST16	1q21-q23	F: GGCCTTCATAGGACTTTTCATAAAC R: GAGGCTGAAGGACAATTCAATTCAAGC	50	2.0	58	Godard et al. 2000*	
hypoxia- inducible factor 1, alpha subunit inhibitor	HIF1AN	1	F: CAAGGGCCGATACAACCTAGC R: CTCCAGGGTCATGGCAAG	154	1.5	62		
hexokinase 1	HK1	1	F: CCACTCTGCATGATTTGATTC R: TGGCATTGATACATCCCAAAAG	303	1.5	60		BM780491
microsatellite	HMS07	1q25	F: CAGGAACTCATGTTGATACCATC R: TGTGTGTAACATACCTTGACTGT	172-182	3.0	58	Guérin et al. 1994; Chowdhary et al. 2003*	X74636
microsatellite	HMS15	1q21-q23	F: ATATCTCTTGCTGTCCTACTTTCC R: AATGTGACACGTAAGATAGGCCTC	213-237	3.0	TD 64	Godard et al. 1998*	U35401
heterogeneous nuclear ribonucleoprot ein F	HNRPF	1q11	F: TTGCCACTCACGAAGAAGC R: ATCCACCCATGCTGTTCTCG	234	1.5	58		

microsatellite	HP27	1	F: TGTTCATTCAACCATTCTGCCC R: AAACCCTCCACTACCCCATTC	136-152	1.5	58	Swinburne et al. 2005	
microsatellite	HTG12	1	F: CACTAGAGTCAGGGGGGGTGGGCT R: TTGGAGTACTCTTTCTCCCTTCCC	111	1.5	65	Marklund et al. 1994	AF169296
HtrA serine peptidase 1	HTRA1	1	F: GATAGACCCGCAGGCAGAAGC R: AGGCAACTCTGGCCATTTGGA	295	2.0	58		G62160
insulin- degrading enzyme	IDE	1	F: GTGACATTTCCCATACCTGA R: TGATAACAGACTCCCAGGAC	102	1.5	58		
insulin-like growth factor 1 receptor	IGF1R	1	F: TCCAGACAGGAGTACAGGAAGT R: CGACCCATTTCCAGAGAGAG	105	2.0	65	Caetano et al. 1999	AF097585
iron- responsive element binding protein 2	IREB2	1	F: TCGTCTTTGTGATTGTGTTCG R: AGGCCAAATATCATGCAGGT	464	1.5	60		
interferon regulatory factor 2 binding protein 2	IRF2BP2	1	F: AGAGAGACTCGTGACTTTCC R: CTAGAAGCATTTCTGATTTGCC	336	1.5	62		CD535568
potassium large conductance calcium- activated channel, subfamily M, alpha member 1	KCNMA1	1	F: TCCAAAACAACCAGGCTCTC R: CCGAGGATGAAGAAGACCAT	93	1.5	58		AB218740
kelch domain containing 2	KLHDC2	1	F: GAGAATGCCTCTCATCACTTG R: TTCACATGCACATTAACCA	120	1.5	58		CX596933
La ribonucleoprotein domain family,	LARP6 (<i>FLJ11196</i>)	1	F: AGTACATGGGGGACGAGTCTT R: GATTTTCTGGAGACCCCTTTG	205	1.5	55	Perrocheau et al. 2006	DX010626

member 6								
microsatellite	LEX020	1p15	F: GGAATAGGTGGGGGTCTGTT R: AGGGTACTAGCCAAGTGACTGC	192-215	2.0	58	Coogle et al. 1996	AF075622
microsatellite	LEX030	1	F: GGAGGGTGCAAGGTGCTA R: GGCAGGTCAGAAGGGACA	173-179	1.5	55	Coogle et al. 1996	AF075632
microsatellite	LEX039	1	F: CCTCTGTCCCCACTACTCTC R: TTGATCTCCACTCCCAATG	181-187	3.0	58	Coogle et al. 1996	AF075641
microsatellite	LEX058	1q17.1	F: GCAATCCGCTAGATAGAGTG R: ACCTTTACTTTACGGGTCACA	224-236	2.0	55	Coogle & Bailey 1997*	AF075665, AF075664
microsatellite	LEX077	1	F: GGTCTCTATGGATCTCTTTGTG R: GACTGATAAAACATGGAAGGTT	181-199	5.0	58	Bailey et al 2000	AF213363
lipase, hepatic	LIPC	1q21.3- q22	F: CCTCTTCATCGACTCCTTGCT R: GAGGCTCTTGCTCTTCTTGC	169	1.5	58		
lysyl oxidase- like 1	LOXL1	1	F: TCAGCTGAAGAGGGAAGGAGCC R: CCAGTGACCTGCCCCTTTCTGT	282	1.5	58		
LysM, putative peptidoglycan- binding, domain containing	LYSMD2	1	F: GGAGCAGATTAAGGGCAAA R: GGACTGGGAGGAGAGAGGTC	204	1.5	58		CX597257
lysosomal trafficking regulator	LYST	1	F: ATCCAGTTCAGAGACGAGCG R: TGACCTGTTCTCGGGTTTCC	~180	1.5	58		NM_000081
mitogen- activated protein kinase	MAP2K1	1	F: AAGTGGATTTTGCAGGTTGG R: GGTGAAATGCACGTGTGAAC	181	1.5	58		CX601814
kinase 1								
mitogen- activated protein kinase	MAPK6	1	F: TCCTAAGGCTGTCCACGTACT R: TTCCATGCACACAAGTCTAACA	201	1.5	55	Perrocheau et al. 2006	DX010525
6								
MAP3K12 binding inhibitory protein 1	MBIP	1q26	F: ATAGTTGTGCAAGAACCGATG R: CTTCTACGGCCTGATTACCAC	~407	1.5	58		CX597715

methylnalonyl CoA epimerase	MCEE	1	F: CCTCAATCATGTAGCAATAGCA R: TGAAGCAGTTCCATCTTGGTA	150	1.5	58		
microfibrillar- associated protein 1	MFAP1	1q23-q24	F: CTGCCGTACATGTGACACTGG R: CCTTTATTCTCGACACACATACA	368	30.0	58		G62192
multiple inositol polyphosphate histidine phosphatase, 1	MINPP1	1p13 prox	F: GAAGAATTCCGAGTGCAGATG R: TCACATTCTTCACTGGTATGACAA	140	1.5	55	Perrocheau et al. 2006	DX010642
multimerin 2	MMRN2	1	F: CCCAAGGATCGGTAATAAAGA R: AGGCCACCTATAACCACTG	218	1.5	60		
mitochondrial ribosomal protein S11	MRPS11	1	F: CTGCCATTAAGGGACTGACC R: GCTTCTTTCCCTCACAGC	119	1.5	60		DN505125
myosin, heavy chain 6	MYH6	1q25-q26	F: AGTTGCAGAACCCGAGTGAC R: ACAAGGGGAAACCATGTGAG	200	2.0	58	Caetano et al. 1999; Milenkovic et al. 2002*	AF130771
myosin VA	MYO5A	1q23	F: TTGTCAAAGTGTGAATTTG R: GGTGACAGGAAAGATGTG	~500	3.0	58	Mariat et al. 2001*	
necdin homolog (mouse)	NDN	1	F: CGTGTAACCTTTGTTTCAGTACAGTGC R: TACACACCATCCGTCCCATA	235	1.5	58		CX605730
NADH dehydrogenase 1 beta subcomplex, 8	NDUFB8	1	F: TGTATATCAGGAACCGTGTGG R: CTGGTAGGTGGGGTAAGTGTC	131	1.5	58		DN507469
nei endonuclease VIII-like 1 (E. coli)	NEIL1	1	F: GAAGAAATCCAAGGGACTGC R: CTGCTGGGCTGTAGTTTGCT	287	1.5	58		
neogenin homolog 1 (chicken)	NEO1	1	F: GAAGGACCTAAACGCCATCA R: CAAAGGGAAGCTGCTTTGAC	248	1.5	58		CX603891
NHL repeat	NHLRC2	1	F: AGGGAATTTTGTTCAGTCAGC	150	1.5	60		

containing 2 nidogen 2	NID2	1q28	R: AAGATACAGTGACGGGAAGGA F: TGTTTGCTATGGATTTTGTCTG R: AGAGCCTTCTCTGACCTTGTC	103	1.5	58		CX603999
nucleoside phosphorylase	NP	1q26-q27	F: CATTCCCAGTGAGGGTTTTC R: CGGATCAGCATGATATCACC	110	1.5	58	Godard et al. 1998*	
nuclear receptor binding factor 2	NRBF2	1p13- p12.3	F: CAGAAGAGTGAGCCAACAGAG R: AAGGGAGGAAGATTGGGTATC	353	1.5	60		
neuregulin 4	NRG4	1	F: TTCTCCCAAGCTTCAGCATC R: GGAAGTAGATGGCTCCAATGA	102	1.5	60		CX596376
microsatellite	NVHEQ031	1	F: AACTCAAAAGCACAAAGCCCACAC R: CAACACAGTGATGACCCAGGTAGG	128-130	2.0	58	Roed et al. 1998	AF056394
PDZ and LIM domain 1	PDLIM1	1	F: CCATTTCTTTGTGGAAGATCA R: ATTGTAAAAGCAGGCATCACA	283	1.5	60		
phosphatidylin ositol 4-kinase type II	PI4KII	1p14 .1	F: GCTCTCCCAAAGACCACA R: ACATTGCCCTCATCCAGA	171	2.0	58		
pyruvate kinase, muscle	PKM2 (PK3)	1q21.1- q21.2	F: GCAACCTGGGTTCTGTGTTT R: CCTGCCAAATTGCTCAAAAT	207	2.0	58	Chowdhary et al. 2003*	AY008802
plasminogen activator, urokinase	PLAU	1	F: TCTCTTCCTCTTTCCCAGCA R: ACCGACCCAGGTAGACAATG	209	2.0	58		AY008803
pancreatic lipase-related protein 2	PNLIPRP2	1	F: AAGCGAATGGGTACCTCAAG R: AGTTGGGGCTTGGAGAGATT	~1000	1.5	58		AF359386
pinin	PNN	1	F: GCACACGGAGAGACCTTATC R: GCAACAGTGGATTCTTGTTTG	~274	1.5	65		
polymerase (DNA directed), gamma	POLG	1	F: TCAGAACCAAGATGCCAACA R: TCTAGGGCACTGCATCACAG	178	1.5	60		CX598342
peptidylprolyl isomerase B	PPIB	1	F: GTCACTGGTGTCCGAGGCTTT R: TCTGCTCTTCGGTTTGCTGC	834	1.5	61		

protein phosphatase 1, regulatory subunit 3C	PPP1R3C	1	F: ACGGCCTTTGACAAGTTCAG R: GAAGACGTGAATGTCGGTGA	228	1.5	58		AB218745
perforin 1	PRF1	1	F: ACTATGGCTGGGACGATGAC R: AGCACTTGGCATGGTAGGAG	80	1.5	58		
prolactin releasing hormone receptor	PRLHR	1p16-p15	F: GCTGATCGTGCTGCTCTACA R: AGCAGGTTGAAGACGTGCAG	717	1.5	58		
prosaposin	PSAP	1	F: AGCCATCCTTCGTGTGCT R: GGGTAGCTGACTCCATGTTCT	426	1.5	60		
retinol binding protein 3	RBP3	1	F: TGCAGAACTCCTTGAACGAC R: AGGTCTAGCACCAAGGCAGA	234	1.5	58		AB218747
ret proto-oncogene	RET	1	F: TTTGGTCTTGCAATGGACAG R: CTAGACCCAAAGCCAGCAAG	201	2.0	58	Chowdhary et al. 2003	AY008809
retinal G protein coupled receptor	RGR	1	F: CCTTGGTGTTCTTTGTGTGG R: AGTCTAGGGTGCAGCACGTC	68	1.5	58		AB218749
Rho-related BTB domain containing 1	RHOBTB1	1	F: CTGGAGTAAAGGGTTTGTGTTGG R: TTCGTGATCTCCTGGTTCAT	276	1.5	58		
RAR-related orphan receptor A	RORA	1	F: ACTACATCGACGGGCACAC R: CAGTTGGGGAAGTCTCTCCAT	198	1.5	55	Perrocheau et al. 2006	DX010571
RNA polymerase II associated protein 1	RPAP1	1q23-q24	F: TGCTGCAGATGAAGAGATGG R: CTCACCCTGCTCCAGAAAAG	156	1.5	58		CX605214
ribosomal protein, large, P1	RPLP1	1	F: GGAGCCTCATCTGCAATGT R: CTTTGCTTCCACTTTCTTCTCC	263	1.5	63		
ribosomal protein S17	RPS17	1	F: TGTCACCCACCTGATGAAAC R: TCAGCATCTCCTTAGTGTCAGG	~670	1.5	60		DN508793
ryanodine receptor 2	RYR2	1q13	F: AGCTTTGAGTGCTACAGACATGG R: GCTGAGCTTTGGTAAGTGAACAG	182	1.5	58		

ryanodine receptor 3	RYR3	1q24	F: GAAGGCCTGATGAAGGAAATC R: CCAGGATGACACTGAGGTGTT	199	1.5	55	Perrocheau et al. 2006*	DX010573
SAR1 gene homolog A (<i>S. cerevisiae</i>)	SAR1A (<i>SAR1</i>)	1	F: GACAATGCAGGCAAAACC R: CATTCCAGCAATTGTCAGC	658	1.5	58		
surfactant, pulmonary-associated protein A1	SFTPA1	1	F: ATTTTGTGCTGCATGCTCTG R: CTATCACCCACAACCTGGGCT	360	2.0	58		AF400580
microsatellite	SGCV02	1q14	F: CCTTGAGTTGCACTTGGAGTC R: CTGCTCATATACCTGGGGATT	123	3.0	TD 64	Godard et al. 1997*	U90585
microsatellite	SGCV25	1q14	F: GCCCATATTAGTAGGACTGTG R: GGCCATATTCAGCAGAGCT	210	2.0	58	Godard et al. 1997*	U90603
solute carrier organic anion transporter family, member 3A1	SLCO3A1	1	F: TGTTCCTGGAGCACGTTCTGT R: TCCCTCCCCAGATTGTCTAA	238	1.5	60		CX596998
slit homolog 1 (<i>Drosophila</i>)	SLIT1	1p14	F: GTGGTCAGCTCTGTGAGACC R: GTGAACTGCAGGTAGGTGTCC	199	1.5	55	Perrocheau et al. 2006*	DX010584
synuclein, gamma	SNCG	1	F: AAGACCAAGGAGGGTGTGTG R: CGCCACGTTCTCCACCTC	395	1.5	60		
sorbin and SH3 domain containing 1	SORBS1	1	F: AGTGGATCTCGCTGACTGTAG R: GTGGAACGATCTGACCAACT	175	1.5	58		
spastic paraplegia 21	SPG21	1	F: TCATACTCTGACCCCGCTGATC R: TTAAATTTTCCTTCCCACTCACG	224-228	1.5	58		
signal peptide peptidase-like 2A	SPPL2A	1	F: GCATCAGCAATGAGCCTGTA R: CAGCCCCAAACAACAGCTACC	592	1.5	58		
serglycin	SRGN	1	F: GAAGTGCGCTGCTCTAATG R: GGTAAAGTGGTGTGAAGTCCTG	142	1.5	58		
suppressor of var1, 3-like 1 (<i>S. cerevisiae</i>)	SUPV3L1	1	F: GTTCGAGACCTCCAGAAAGAG R: GGTACTGCGTGTTCTTCTAGC	177	1.5	62		

tubulin folding cofactor E	TBCE	1q12-q13	F: CGTTACCATCGCACTAATAGAG R: ATGACAATCCAGAAGGTGAAAG	~ 410	1.5	58		
tight junction protein 1	TJP1	1q16-q17.1	F: CATTCTATGACACACACAAGGTC R: TGATTGATTAACAGAATGTGGTG	285	3.0	58	Chowdhary et al. 2003*	G62194
microsatellite	TKY002	1q17.2-q17.3	F: TTCCCTCCCATGGTTATTTTTC R: TCTCTACTTTCATATACATTTGG	113 - 119	4.0	58	Sakagami et al. 1995*	
microsatellite	TKY007	1p12.1	F: CAAGGGACGTGTTGTAGTTG R: TTATACCAACTGGAGGATGG	152	2.0	58	Hirota et al. 2001*	AB048318
microsatellite	TKY013	1q12	F: ACTGTTCCCTTTTTAGCACC R: TTAGGAAACAGGACTACTGG	137	2.0	58	Hirota et al. 2001*	AB048324
microsatellite	TKY015	1q12	F: GGATTTTAGAAGTACAGAGGG R: CATCCTACTGAGAACAATGCG	149	2.0	58	Hirota et al. 2001*	AB048326
microsatellite	TKY106 (RC09)	1	F: CTAATCTTCCTCAGCACACACA R: GGTGGCCATGTATCTTTAGTCTCC	109	2.0	58	Mashima et al. 2001	AB053345
microsatellite	TKY281	1	F: GCTTGGACAAGCGAATAATGAC R: GATCAGTCACTGCCAGTGG	178-194	2.0	58	Tozaki et al. 2000b	AB033932
microsatellite	TKY295	1	F: GTCAAGTGTCAGTAGCTCTG R: GTTTCTAGGCTGATGCTGTA	205-227	1.5	58	Tozaki et al. 2000c	AB034604
microsatellite	TKY318	1	F: ACAGAAGTGGAGATGGTTTG R: CCACAGGTTCTACTGTCTTG	152-170	1.5	58	Tozaki et al. 2000c	AB034627
microsatellite	TKY342	1	F : AAGCAAGTAAGAGGAATGTG R : GTTGGATTGTGTTAACCTAGTC	166-178	1.5	58	Tozaki et al. 2001	AB044843
microsatellite	TKY370	1	F: CCATATCTAACCCTGATAG R: CACACCACCTGGAAATGAG	319-323	1.5	58	Tozaki et al. 2001	AB044870
microsatellite	TKY374	1	F: GCACTTTTGACAGTCCTTG R: GTACAATCAGAGGTCCAGAG	153-161	1.5	58	Tozaki et al. 2001	AB044874
microsatellite	TKY405	1	F: AATGAGGTAAACTTCCCTG R: AATTCCTCAAGTTTCTCCCT	135	2.0	58		AB103623
microsatellite	TKY410	1	F: GGAGGAGGAGAGAGTGGGCTAC R: CTGGACTTTGGACGGATTTT	298-310	1.5	58	Tozaki et al. 2004	AB103628
microsatellite	TKY466	1	F: TGGAACACATTCTCACCAG R: GTTCTCCTTCCACCCCAAAT	311-323	1.5	55	Tozaki et al. 2004	AB103684
microsatellite	TKY492	1	F: TGACGCTTACCAAGGAGGTC R: ATCCTCAGAAATGCCTGGAA	218-228	1.5	58	Tozaki et al. 2004	AB103710

microsatellite	TKY530	1	F: ACAAAGCTGTGTGACAGACCA R: TCGTTTCTGCATCTCTTCCA	25-270	1.5	55	Tozaki et al. 2004	AB103748
microsatellite	TKY534	1	F: TCCTAATAAACTACTAATAC R: AGAGAAAATGCCCTAATACC	136	2.0	58		AB103752
microsatellite	TKY558	1	F: TGGCGGATGCTAGATGTAGAG R: GCTGTGGAAATGACCCAGTT	240-244	1.5	50	Tozaki et al. 2004	AB103776
microsatellite	TKY577	1	F: CTGATGATCTGCTGCACAAG R: CAGCCCCTAATCACATAAAC	140	2.0	58		AB103795
microsatellite	TKY597	1p14	F: AGTGCCAAGGAGGCTGTCT R: TCTTCTCCCATGAGTCACC	136-148	2.0	58	Tozaki et al. 2004	AB103815
microsatellite	TKY659	1	F: TTCAAGCAGCAGTAGCAGGA R: CGAGGAGGGTTTTGTTC AAG	129-141	1.5	50	Tozaki et al. 2004	AB103877
microsatellite	TKY670	1	F: GTTGCTTTGGGACCAGTCAT R: TCCAGCCCAGTCAGGTCAT	149-153	1.5	58	Tozaki et al. 2004	AB103888
microsatellite	TKY702	1	F: AGGAAGTGATATAATGGGTC R: AAATGCTAGGGTGTGTAAGC	113	2.0	58		AB103920
microsatellite	TKY704	1	F: CATTTAGCGATCTCTGCCAG R: CAAATCTGCTTATAGCCTCC	100	2.0	58		AB103922
microsatellite	TKY706	1	F: AGGCACTAGGCAGGGACTTC R: ACCCAGGTGGTCTTGTT CAG	155-171	1.5	56	Tozaki et al. 2004	AB103924
microsatellite	TKY707	1	F: ATGTCCCCTATGAATAGGAT R: CATGCATCTCCATGCCATTG	122	2.0	58		AB103925
microsatellite	TKY728	1	F: AGGAAGATTAGCAACAGATG R: CCTGAGTACTTTTGTGTATG	90	2.0	58		AB103946
microsatellite	TKY776	1	F: CCTCCCAGCTTCATATACAG R: AGCTTCTTGCCAAGTCTAAC	198	2.0	58		AB103994
microsatellite	TKY791	1	F: AAAGAGGAGGATTGCAACAG R: TTGAAGTGAGCTCTTCCTAC	249	2.0	58		AB104009
microsatellite	TKY803	1	F: TCCAGGTGTTGGTATTAACCAA R: GGATTGTGGGTACCAAAACAT	204	2.0	58		AB104021
microsatellite	TKY812	1	F: AATTTCCCTTTGCCCTACT R: AGTAAGTCCTACAAACACCC	106	2.0	58		AB104030
microsatellite	TKY886	1	F: GATGCTCTGTAAATGTAAAGGC R: GGTGGGAAGATGGAAAAACC	104	2.0	58	Tozaki et al. 2004	AB104084

microsatellite	TKY899	1	F: AGCAACAGAGTAATGCCAAG R: TAGGCGGGTTTTAAACATGG	113	2.0	58	Tozaki et al. 2004	AB104104
microsatellite	TKY933	1	F: GTCCCCTGATGGATGAATG R: AAATGGCAGGATTTTCCTTCG	104	2.0	58		AB104151
microsatellite	TKY941	1	F: GTACATGCTCGCATGTGAG R: CAAAAGGCCTCCCATATCG	119	2.0	58		AB104159
microsatellite	TKY962	1	F: TCTGGGTATTCAACTGAAGG R: TCCTTCTGTTTATGGGTGAG	226	2.0	58		AB104180
microsatellite	TKY980	1	F: TTTATGCATTTGGTTGCCTTG R: GGCTATGGTTACCTTATGAG	125	2.0	58		AB104198
microsatellite	TKY987	1	F: CTGTTTGTAGTGGCATCCCTG R: AACCAGGGGCAATTATTCC	140	2.0	58	Tozaki et al. 2004	AB104205
microsatellite	TKY1005	1	F: GAGACGTGAATCAGAAGATTC R: AAGACTGGCACAGATGTTAG	117	2.0	58		AB104223
microsatellite	TKY1016	1	F: CAATTGGTCTCTGAGGTCAG R: ATGGCGGTGGATGCTAAC	244	2.0	58		AB104234
microsatellite	TKY1020	1	F: GCCTTCCTCTAGATGTAAAC R: CCCAGAACTGAGAGAAAATAC	172	2.0	58		AB104238
microsatellite	TKY1043	1	F: ATCAAAGGCACTTTCCATCC R: GCAGCCCTTAGGCTTTTAC	203	1.5	62		AB104261
microsatellite	TKY1077	1	F: TCCTTTCCTTTCAAGTGCAG R: GACATCAGGTACTAGGAGAG	124	2.0	58	Tozaki et al. 2007	AB104295
microsatellite	TKY1689	1	F: ATTATCAGTCGTGATGCCAG R: TACATGCTAGTTTTAGCCTC	148	1.5	58		AB215632
microsatellite	TKY1785	1	F: GGATTTATGACAGATGGAGT R: GTTTCCTTGGATGGAGAGTG	202	1.5	58		AB215728
microsatellite	TKY2220	1	F: GAATGTACCAGGCTAGAAAG R: GTTCCAGATGCTAGAAGGC	208	1.5	58		AB216163
microsatellite	TKY2278	1	F: TTGTTTTGTGGAGGGGATG R: TCGCCTCAGAGGTCTGAAG	181	1.5	58		AB216221
talin 2	TLN2	1	F: GACGGAAGTTCTTTTACTCTGATCAG R: CCAATCCCCACCCAAGATA	1308	1.5	62	Tozaki et al. 2007	
TM2 domain	TM2D3	1	F: CCCAAAAGAACTTCGTCATCA	159	1.5	60		DN506665

containing 3 transmembran e emp24 protein transport domain	TMED3 (P24B)	1q17.1	R: CCAAGCAATGAATGTGGTC F: CCCTTGGGAAACACCATCTA R: ACTCTGTTCCCCCATGTCTG	189	1.5	60	Perrocheau et al. 2006*	CX605575
containing 3 transmembran e protein 23	TMEM23	1	F: ATGGGTTTAGGAAGGAGATGA R: CAGCCACTGAATTAGCCATAG	284	1.5	58		CX599668
tropomyosin 1	TPM1	1	F: CTCCCAAGACCCTTTCATCA R: TTTACACTGAAATGAAGAGCTTCTG	159	1.5	58		
thyroid hormone receptor interactor 4	TRIP4	1	F: TTGTCAATTGAGAGTGCTGAAGA R: GGACTGCTGCAGAACATCAG	150	1.5	58		
tetraspanin 3	TSPAN3	1	F: ACACAGGTGTTGCACAGAGC R: GCCTGGAGGTAACAGAAGCA	210	1.5	60		CX602714
uveal autoantigen with coiled- coil domains and ankyrin repeats	UACA	1	F: GGGATGAAGGCAAGCTGATA R: TTTCTGTCGGAATGGAAAGG	156	1.5	58		
microsatellite	UCDEQ440	1	F: TGTTCGGACAGTGTGGAT R: GCAGGGTATGTGTGTGCT	100	1.5	58	Eggleston- Stott et al. 1999	U67410
microsatellite	UCDEQ487	1p12.1- p11	F: CCCTGGGCGGTCACATGT R: AACCTGCCTCCCTTGGGTCTC	135-149	1.5	55	Eggleston- Stott et al. 1997; Chowdhary et al. 2003*	U67417
microsatellite	UCDEQ493	1	F: ATTGGATATTTAACACCAAATGC R: CCCAGCTCAGTGACTCCATT	199	1.5	58	Chowdhary et al. 2003	U67418
microsatellite	UM002	1	F: AGTGGCAGCATAAAGATG R: TTTTGGTCCTTGTAGGAG	240-260	5.0	58	Meyer et al. 1997	AF195124

microsatellite	UM004	1q22	F: AGGTCAGGTTCACTTTTTTC R: AGGTCAGTGTGCCTAGTTG	92-117	3.0	55	Meyer et al. 1997; Chowdhary et al. 2003*	AF195126
microsatellite	UM026	1	F: CCCAAAATCAATTAGGTCTC R: ATCAGTTGCTCTCTACTTTTC	208-220	1.5	58	George et al. 1998	AF195573
microsatellite	UM041	1	F: TGCCCTTCCATGAACAGAC R: TCCCTCTCTCTCTCTCCTTCTC	105-115	2.0	58	Swinburne et al. 2000	
microsatellite	UM043	1	F: CCTCAATCTTTTCTTCTCC R: TCAAGAGAGACGCTACAC	145-150	1.5	58	George et al. 1998	AF195586
microsatellite	UMNe086	1	F: GAGTCTGGATGTAGGCCTGTCC R: TGGCCTTCAGGGTAAGAGAGTAAG	176	1.5	58		
microsatellite	UMNe090	1	F: CGACACTTCCACAGTCATCTC R: TCCGTGCTTTTAAGCAAGTTCC	149	1.5	58	Wagner et al. 2004a	AY391285
microsatellite	UMNe099	1	F: GAGAAAGGAACACGCAAACC R: CCCAGGAACCACAGACAGG	201	1.5	60		
microsatellite	UMNe111	1	F: GGTAAGGTGAACTTTTGTATTTCTC R: GATCAAAGAATTAAGTTACTTAATTAGGC	116	1.5	58		
microsatellite	UMNe115	1	F: TCCTCCTACACTGGCCATATC R: TTTCCTATCGGAGTGCTTGC	166	1.5	58	Wagner et al. 2004a	AY391296
microsatellite	UMNe120	1	F: TAATGTACGCGCTTTGTTC R: AAGCACATTGAAAGGTTAAGGG	137	1.5	58	Mickelson et al. 2003	AF536254
microsatellite	UMNe196	1	F: ATGAAAAAAGGCATACCCCC R: TCTTATCAGGTTGATGGTGTGC	131	2.0	58	Wagner et al. 2004a	AY391319
microsatellite	UMNe247	1	F: CACAGGCATGCTCACAGTG R: AAAGCCCAGTTTGCATTTTG	200	2.0	58	Mickelson et al. 2003	AF536315
microsatellite	UMNe318	1	F: CAGGGCTAGTCAACAGGCTC R: TGGGGTGTAATGACTACCAGG	209	2.0	58	Wagner et al. 2004a	AY391336
microsatellite	UMNe334/420	1	F: GTTTGAGAAGCACTGACTGGG R: TGTCAGTGGGGAGGAGAAAC	243	2.0	58		
microsatellite	UMNe381	1	F: ATCCCGGTAGGTGCCTAGTT R: GGATGGGCAGACAGAAGTCT	151	2.0	62		
microsatellite	UMNe448	1	F: CCATTCTGCCCTGATTGG R: TTCAAGACCCCTCAATCTGC	164	1.5	58	Mickelson et al. 2004	AY731396
microsatellite	UMNe467	1	F: TTTCTGGAGGTTTCATTACATG R: AGGCTATGTGAGAGAGAGGGC	115	1.5	62		

microsatellite	UMNe471	1	F: GAGCAATCACTTCCTCTGTGG R: CCTTCTTCCCTCAACACAGC	271	1.5	60	Wagner et al. 2004b	AY464495
microsatellite	UMNe486	1	F: CAAATTATTGTTCCCTCTTGCC R: GACTACTGGGCTTCACAGGC	217	1.5	60	Mickelson et al. 2004	AY731402
microsatellite	UMNe498	1	F: TCCCACAGCCTGAATTTTG R: GCCAACCTCATAAAATGAGAGC	~250	1.5	55	Wagner et al. 2004b	AY464506
microsatellite	UMNe520	1	F: CTTCTTCCCCTTTGGTCTC R: GCCGTTACTAGTGGATCGTAGC	~150	1.5	55	Wagner et al. 2004b	AY464515
microsatellite	UMNe548	1	F: GACTCATGGTGAGTTAGGGAGC R: GCAACCTGGTGGTGATGAC	~300	1.5	58	Wagner et al. 2004b	AY464523
microsatellite	UMNe591	1	F: CAGCAGAAAGAAATGTTGATGG R: ACCTACACACTGCTCATCAAGC	283	1.5	58	Wagner et al. 2004c	AY735287
vinculin	VCL	1	F: TGCCTGAATGTCCTTCCTTC R: CTGGAAGAACTTGGAGAGCAA	246	1.5	58		AB218753
voltage-dependent anion channel 2	VDAC2	1	F: GATCATCCTTGGGCCATTTTC R: GCAATCCTATCAAATCAGCAC	246	1.5	60		
microsatellite	VHL134	1p12.1	F: CTGGGAACAGAATCAAGACTTG R: TAATATGCATGTATCTGATAGCTC	157-163	3.0	58	van Haeringen et al. 1998; Chowdhary et al. 2003*	Y08448
microsatellite	VIASH034	1	F: TGAGTGTTTGCGTGTGTGTG R: TCCCGTCTCCTCTCTTGTTTC	113	5.0	55	Chowdhary et al. 2003	L23549
vacuolar protein sorting 13 homolog C (S. cerevisiae)	VPS13C	1	F: TGGTCCTCATTCAAGAAATGG R: TCATTGAGGTCTCCATTAATTCTG	285	1.5	58		
X-prolyl aminopeptidase (aminopeptidase P) 1	XPNPEP1	1	F: ATCCAAGTGCTTCCCTACAAG R: ATGGCTTCACTCACAGCATAG	119	1.5	62		
zinc finger,	ZDHHC6	1	F: AGGATGGTTCCCTAGAAACTG	202	1.5	58		DN507548

DHHC-type containing 6 zinc finger protein 248	ZNF248	1	R: CTTGGAGGAAAAGAACACCTT			
ZW10	ZWINT	1	F: AACTTGCTTTCACCACCAAC R: TGGCTATGACTGAGGACATTC	304	1.5	58
interactor			F: GCAATGGAAAGAGCTGAAGG R: GTGCTTGCTTCTTTTGGGCC	67	1.5	58

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	2STS01	2	F: CTGGAATCGGTCATCACCTC R: ACACGCTGAAGTCCTCGTTC	160	1.5	60		
sequence tagged site	2STS02 (ACADL)	2p18	F: TTGCCAGGGAGGAAATAGTG R: CCCCAGAGAATTTGCTTCAA	105	1.5	58	Mariat et al. 2001*	
sequence tagged site	2STS03	2	F: CACACTGGGAGATGATTGG R: TCCAGTTCACGAAGTGTTG	453	1.5	55		BI961554
microsatellite	A-14	2q14-q21	F: CAGCTGGGTGACACAGAGAG R: GTCATCACTACTCCCTACAC	212-238	2.0	58	Marti et al. 1998*	Y10238, Y10239
ATP-binding cassette, sub-family E (OABP), member 1	ABCE1	2	F: GTAATGAAGCCTCTGCAAAT R: CGTTTGACAACCTCGAGCAG	388	1.5	58		CN789500
acyl-CoA thioesterase 7	ACOT7	2	F: GACTTCCTGTCGCCCATGT R: GGATGTTCTCGGACATCACG	112	1.5	55	Perrocheau et al. 2006	DX010633
angiotensin II receptor-associated protein	AGTRAP	2	F: GACTCCATCGACGCCATAAG R: TGAGACCAGCCGTAGGGTAG	100	1.5	60		
microsatellite	AHT012	2	F: ACCCAAAGTCATGGGAATCA R: TTGTTGCCGACAACATGC	104-116	3.0	58	Swinburne et al. 1997	
microsatellite	AHT035	2p15.1-p16	F: TGACTTAGAGCTTTTGCTCCC R: CCAGAAGTCCAGGCATTTGT	125-141	2.0	58	Swinburne et al. 2000*	AJ271520
microsatellite	AHT065	2	F: AATGCAGGAAAATTATTGTCCC R: TGACTTATGAAGAGGACAGAGC	175-195	1.5	60	Swinburne et al. 2003	
microsatellite	AHT067	2	F: CGGAGTTGGTATTTAACACACG R: ACGCACCAACTTCTGAAAGG	238-248	1.5	58	Swinburne et al. 2003	
microsatellite	AHT073	2	F: AACAGGACTGCAGAGACTCCA R: CTCCCTCACTAAACTGTGACCC	144-156	1.5	60	Swinburne et al. 2003	
adherens junction associated protein 1	AJAP1	2	F: GCTTTCAACAGCTTTGACTTCC R: GACCCCTTGAGTCTGCAGTG	228	1.5	55	Perrocheau et al. 2006	DX010528
alkaline phosphatase, liver/bone/kidney	ALPL	2p14	F: GAAAAGAAAGTGTCAGACTGCC R: GCTCCATGTTTCCTGACAGG	190	1.5	58	Mariat et al. 2001*	
microsatellite	ASB13	2q14.3-q21.2	F: CTCTGAAAGAGCAGGATTGG R: GTCTTCTAAGTGGTAAGAGCC	125	2.0	58	Breen et al. 1997*	
microsatellite	ASB17	2p14	F: GAGGGCGGTACCTTTGTACC R: ACCAGTCAGGATCTCCACCG	130	2.0	55	Breen et al. 1997*	
microsatellite	ASB18	2p17-	F: TGCAGACAAAGCTGGACACTC	205	2.0	58	Breen et al.	

ATPase type 13A2	ATP13A2	p18 2	R: CTGCTGAGAAAGCTTCTGC F: GCTGGCACTGAGGAACATTG R: CTTCTTAGAGGCCCGTTTGG	262	2.0	58	1997*	BI961820
brain-specific angiogenesis inhibitor 2	BAI2	2p15.1- p15.3	F: TCTTTCATGCATTTGGAAGG R: TAACACTGGATCACGGACTG	209	1.5	58		AJ871799
chromosome 1 open reading frame 165	C1orf165	2	F: GAAATGGCACCAGCTACAAGTA R: TTGTGGCAACTCCTGTGACG	116	1.5	62		NM_024603
CAP, adenylate cyclase-associated protein 1	CAP1	2	F: TCGCTTTCAGCCTTTGGGAG R: TCCTTTAACTGGCCTGGGTGA	468	1.5	60		BI961765
capping protein (actin filament) muscle Z-line, beta	CAPZB	2	F: TCTTAAGAACGACCTGGTGGA R: GGTGGTGATGCGAGTTGTTAT	190	1.5	55	Perrocheau et al. 2006	DX010445
carbonyl reductase 4	CBR4	2	F: CCTCTTTCTTCCGAGTTTGC R: CCAGTCGGTAGCCTTTCC	124	1.5	54		
complement factor I	CFI	2	F: CTTCGGCTGTGCATATTCCAT R: TCCCTTATCAGTGCCCAAAGA	141	2.0	58		
BAC end sequence	CH241-100C12_SP6	2	F: GCAGACCTCAATCCTTTGC R: ACCTGGGACCCTGAGAG	200	1.5	57		AJ542755
BAC end sequence	CH241-100C12_T7	2	F: GCCTCATAGCTCCCTTGG R: TTCCAAGTGGTGGCAGAC	279	1.5	57		AJ542756
BAC end sequence	CH241-100G3_T7_MS	2	F: GGGTGAACAGTAGGGGAAAC R: GAGCCCCCTCTCTACAACAG	193	1.5	65		AJ542943
BAC end sequence	CH241-100K16_T7	2	F: CAGCAAAATTATCCGATGC R: ACTGCCTCCAATCTGATAGC	505	1.5	56		AJ543083
BAC end sequence	CH241-101D21_T7	2	F: GACAAAACGATTATTCAACTGG R: TACCTCAGCCAACAGAGGAC	502	1.5	57		AJ576582
BAC end sequence	CH241-102M22_SP6	2	F: TCTTGGAAGTCAGCAGGTC R: GGTGGGACACCTGTGTAATC	500	1.5	58		AJ584460
chloride channel 6	CLCN6	2	F: GCCACTAGAACACGTTACC R: CGTCCACATCATCTCTCTCC	105	1.5	56		
chloride intracellular channel 4	CLIC4	2	F: AACTTCACGTCTTCCCCTGA R: AGGTAGGCGGGTAAAAGAA	196	1.5	58		BM781110
clusterin	CLU	2	F: GAGTACCGCCAGAAGAACC R: CAGATTACAAGGCCGTTTTAT	503	3.0	58	Lindgren et al. 2001	L46797
cannabinoid receptor 2	CNR2	2	F: AAGAAGGTCTTTGCCTTCTGC R: TTCACATCAGCCTCTGTCTCA	203	1.5	55	Perrocheau et al. 2006	DX010454
microsatellite	COR026	2	F: GGCGTCCAACGTAAAGTAGA	224-228	2.0	55	Murphie et	AF101395

microsatellite	COR035	2	R: CCTCTTCGGAAACTCTGACA F: CAAACTCACCGTATTTACGGC	205	3.0	55	al. 1999 Murphie et al. 1999	AF101404
microsatellite	COR037	2	R: TTGCTTTCTCACCTCCTTTG F: GAGCAATTTCTGGGTCTGAG	225-245	2.0	58	Murphie et al. 1999	AF101406
microsatellite	COR041/065	2	R: CACCCCTCTCTTTGTTTGTC F: CAACTTGGGTTCTCGCTTAG	223-241	2.0	58	Ruth et al. 1999	AF108358
microsatellite	COR043	2	R: TCCGGAAAGTGCAAAGTTAG F: ACGCTCATTTCATAGGCTCTGAC	127-129	2.0	55	Ruth et al. 1999	AF108360
microsatellite	COR049	2	R: GCAGGAGTGGTGTTTGTTTCAC F: TGACATTCACAATGACCAGC	190-192	2.0	58	Ruth et al. 1999	AF108366
microsatellite	COR051	2	R: CGGCCTGCACTATAGACTTC F: GTATGGGAGAGAGCAGAATCAG	290-292	2.0	58	Ruth et al. 1999	AF108368
microsatellite	COR078	2	R: GGTGCTAGATGTGCTCATTACT F: TGCAGGGTGAAGATATGAGC	230	2.0	50	Tallmadge et al. 1999a	AF142615
microsatellite	COR090	2	R: ACCTATGTGCACGCACTCTC F: GGTTTGTCTCTTTGAGGTGTG	81-103	2.0	58	Tallmadge et al. 1999b	AF154943
microsatellite	COR094	2	R: TGCTCATATCTTCACCCTGC F: GAAGGGTAGAACAGGGCAGAC	283-291	2.0	58	Tallmadge et al. 1999b	AF154947
microsatellite	COR108	2	R: CAGCTCTATAATTCTGGGAAGC F: CAGTCCCAACCCCAAATC	235-237	1.5	56	Swinburne et al. 2005	
microsatellite	COR109	2	R: AGCCTAGACTGGCCATGAG F: GTCGAAATCTGGCTCTCAAG	216-217	1.5	58	Swinburne et al. 2005	
carnitine palmitoyltransferase II	CPT2	2p17-18	R: CATCCAGAGGCATTCAAGAG F: CCAGATGGCCTTTCTGAGG	170	1.5	58		
colony stimulating factor 3 receptor	CSF3R	2	R: CTGAAGCTCCGCAGCACT F: GTTTAGCTCCGTGGTGTTC	600	1.5	62		BI395101
cathepsin B	CTSB	2	R: TCAGAATGGACACATGGTGGC F: CTTCCAAAATGTGGCACCTC	102	1.5	55		AY817460
cytochrome P450, family 2, subfamily J, polypeptide 2	CYP2J2	2	R: TGACCAGCTCATTTGACAGC F: TGCTAGGCACTGAGGATATAAC	238	1.5	54		
DNA fragmentation factor, 40kDa, beta polypeptide	DFFB	2	R: CTACTCTACACGCACATGAC F: GAGAAGAAACGCACCATTGTT	196	1.5	58		DN510949
24-dehydrocholesterol reductase	DHCR24	2	R: GCTTTGTCAGGGGTTTGTAGA F: TGTGGAGCCCTTGGTGA	898	2.0	58		
			R: TGCAGATGTGCTGGAACAG					

dehydrogenase/reductase (SDR family) member 3	DHRS3	2	F: CTGAAAAATGCCTGAAGGAGA R: AGCTGTCTGGTACACCTCCTC	107	1.5	55	Perrocheau et al. 2006	DX010576
endothelin converting enzyme 1	ECE1	2	F: CAAGGATGGGAACCTCCG R: TGTAGTTGCCGTACTGCC	95	2.0	58	Chowdhary et al. 2003	
eukaryotic translation initiation factor 2C, 1	EIF2C1	2p15-p16	F: TGAGCCCCCAAGACTACAC R: TGAAGATACCAAGGGAGTGG	113	1.5	60		AJ891045
eukaryotic translation initiation factor 4 gamma, 3	EIF4G3	2	F: TTCCTGTTCTCCGAAGCAC R: TGTTTCATCATTCGCTTTGTCC	102	2.0	50	Chowdhary et al. 2003	
enolase 1	ENO1	2	F: GCTTCCTTAGAACCGCTACAG R: CACGGCTCCAGACACTTG	134	1.5	58		CX602735
exosome component 10	EXOSC10	2	F: GCTGCCAAGAAGAGAGAAC R: GGATCAAACCTGGGAAGAAG	1050	1.5	58		BI961526
fatty acid amide hydrolase	FAAH	2	F: GACTGCAGTAACCCCTCTTT R: GGTTCCCTGTGGGTTTGAG	196	1.5	55	Perrocheau et al. 2006	DX010472
fatty acid binding protein 2	FABP2	2q22-24	F: CGGTTAGACAACGGAAATGAA R: TCCAAGAACAATGCTCACTCC	572	1.5	58		
Fas associated factor 1	FAF1	2	F: TTGCCACTTTTAATTGATTTTC R: CATCATATTCACCACCCAAAG	504	1.5	57		AJ543260
family with sequence similarity 54, member B	FAM54B	2	F: CTTCAAGTTCAGGAGCCGGT R: TGGTCCCGATTCTTCTCACT	630	1.5	58		NM_019557
filamin binding LIM protein 1	FBLIM1	2	F: AAGTGTGGCAAGTGTGGC R: GGATTCTCACAGATGCTGCA	203	1.5	58		
farnesyl-diphosphate farnesyltransferase 1	FDFT1	2q13	F: CTGCGAGCTCTGGACACTCT R: CGTTGGGAAGTCCTCTAGCA	156	2.0	62		CX598027
fibrinogen alpha chain	FGA	2q14.3-21.2	F: GACTCTGTCCTTCGGGTGTA R: AGCCTCCTCCGTAGACTTCC	259	1.5	58		
fibrinogen beta chain	FGB	2q14.3-21.2	F: TCGGAAATGACAGAATTAGCC R: GGTTTTCTCCCACCAGTTGA	213	2.0	50		
fibrinogen gamma chain	FGG	2q21	F: ACTTCTCGGGGTATTGCAG R: AGCCAAAGATTGAGCAATGG	191	2.0	58	Caetano et al. 1999; Lindgren et al. 2001* Godard et al. 2000*	AF134218
fucosidase, alpha-L- 1	FUCA1	2p15	F: CATTGGACCAACTAAAGATG R: TAGATAGCCTCCCCATTGAT	100	1.5	55		
guanine nucleotide binding protein, beta	GNB1	2	F: ACACACCGGGGATGTTATGAG R: ATCCGCACGAAGGTCAAACAG	229	1.5	60		CD467307

polypeptide 1								
guanine nucleotide binding protein-like 2	GNL2	2	F: CACCAAGGCGGTCATTAAAGC R: GCAAACACCTTTTCAGTGAGTCCC	300	2.0	58		BI961871
G protein-coupled receptor 3	GPR3	2p14	F: AATGAACGGAGAAGCAGAAAGGC R: ACTGCGGTGCAGGTTGGAGG	100	2.0	58	Mariat et al. 2001*	
hypocretin (orexin) receptor 1	HCRT1	2	F: GTATCTCCCAAAAGAACACCC R: AGGTTTCCCCAGAAGACAC	105	1.5	56		
histone deacetylase 1	HDAC1	2	F: AAGTTGGCTTGAGCAGACCTCT R: AGGATTTTGTCTTATGGCTGCTTAA	301	3.0	58	Chowdhary et al. 2003	
high-mobility group box 2	HMGB2	2	F: GATCCCAATGCTCCTAAAAG R: TTGCAGTATCCCCAATGGAT	182	1.5	56		
microsatellite	HMS16	2q13-q14.1	F: AGTGTAATCAATGGATGAGTGGAC R: TGTGTGTCGAAATGGCAGGCATC	148	3.0	58	Godard et al. 1997	U89806
heterochromatin protein 1, binding protein 3	HP1BP3	2	F: GCAGCTGGGACTTTAGGT R: CCAAAGAAAGAGCCAGATG	641	3.0	58	Chowdhary et al. 2003	
heparan sulfate proteoglycan 2	HSPG2	2p14	F: CGTCTGCCCCAGGTATCAC R: CTGTGGAGGACAGAGACGATG	104	1.5	55	Perrocheau et al. 2005*	AY817475
microsatellite	HTG19	2	F: GTATGTGCTGTACCTTCTGC R: ATGAGAAAGACGATAGATGATAT	130-144	3.0	58	Lindgren 2000*	
5-hydroxytryptamine receptor 6	HTR6	2p12-13	F: CTCACCTTCTTCTGCCCTC R: AAGGCGGGAACAGGAAATGG	350	1.5	59	Prause et al. 2006*	
ISG15 ubiquitin-like modifier	ISG15	2	F: CTTGTCTGTCAGAACTGTGAC R: CCTCGAAAGTCAGCCAGAAC	166	1.5	60		BM735112
potassium channel tetramerisation domain containing 9	KCTD9	2	F: TGCTGATCTTTCTCGTTTGG R: GATCAGCTCGCTCCAGATTC	110	1.5	60		
KIAA0922	KIAA0922	2	F: CACTCACTCACAGCACTGAC R: TCCCTGCTTCATTCTTGGCT		1.5	60		
kinesin family member 1B	KIF1B	2	F: TTTTGTTCATAGTCCGTCGCC R: ACCAGTCATTTCATGTCTTTGTC	209	1.5	58		
kelch-like 2	KLHL2	2	F: GCCACTTCTGAGGAATGA R: CTGATCAACGCACATAGC	314	1.5	58		BI961843
lysosomal associated multispanning membrane protein 5	LAPTM5	2	F: GGGTGGACCATTCTCCTG R: AGATGACGGCCAATTTGAG	183	1.5	55		AM072953
leucine proline-enriched proteoglycan 1	LEPRE1	2	F: TGATGGACGGCGTCATCTCT R: CTTGAGGGCTTTGAAGACAG	319	1.5	58		NM_022356

lipoprotein lipase	LPL	2q12^a	F: CAGAAGCTCCAGTCGCTTTC R: CCTCCATTGGGGTAAATGTC	137	2.0	60		AZ575478
leucine rich repeat containing 41	LRRC41	2	F: CTTCGCAGATTATGTCAGCAC R: CTAAACCCAGTTGTGGGAATG	217	1.5	65		CX599691
MAD2 mitotic arrest deficient-like 2	MAD2L2	2	F: GCGGGCTCATAAAAGCAG R: AAGAGCACTTGCAGTCAGGG	118	2.0	58		BI961750
mannosidase, alpha, class 1C, member 1	MAN1C1	2	F: CGAGGCCCTTCTGGTTTAACTC R: ACTCCCTGTAGATGGGGTCGT	137	1.5	55	Perrocheau et al. 2006	DX010506
microtubule-associated protein 9	MAP9	2	F: TTTCTGACACCTCAGTAGATGAA R: AGGGATTTATGACCACGTCTT	210	1.5	54		CX600044
matrilin 1	MATN1	2p15	F: CTTTAAGATGTTTGCTGTGG R: GCCGTGTAGAAGTAGTGCTC				Godard et al. 2000*	
mitochondrial trans-2- enoyl-CoA reductase	MECR	2	F: CTGCTATGGGCGGATCAGAT R: GCTTGGGAAGGATGCCGTAA	553	1.5	58		NM_016011
mitochondrial ribosomal protein S15	MRPS15	2	F: TCCACGCTGCTCAAAGACTA R: CTGGGGGTATTGACAAGTGG	725	1.5	60		BC031336
methionine sulfoxide reductase A	MSRA	2	F: GTTCTTTCAGAGCACGGCTA R: ACCCAGTGGACAGGACACTC	153	1.5	60		
matrix-remodelling associated 8	MXRA8	2	F: GCAGCGTCATCAACGTCAT R: GATGAGCAGCAGGATGAAGAG	101	1.5	55	Perrocheau et al. 2006	DX010526
NMDA receptor regulated 1	NARG1	2q21.3	F: GTTAGAGCAATGCAGCAGGTG R: AAGCTTTTCCCTTACGCTTTG	199	1.5	55	Perrocheau et al. 2006*	DX010627
nuclear autoantigenic sperm protein	NASP	2	F: AAGGCTCAGAAGAGGAGGAT R: TATCCCAGGCAAGCTCTAGG	550	1.5	58		NM_172164
neuroblastoma, suppression of tumorigenicity 1	NBL1	2	F: CCAAAAACATCACCCAGATC R: TGTAGCTGAAGCACTGTCCC	213	1.5	58		NM_182744
nuclear transcription factor Y, gamma	NFYC	2	F: ATGTTTCATCCAGTCAGCCAAC R: GTTGTGCACCAGTGTCTTAGC	198	1.5	55	Perrocheau et al. 2006	DX010535
NK3 transcription factor related, locus 1	NKX3-1 (NKX3A)	2q13	F: CTTCTCGCACACTCAGGTCAT R: GAGAAGGCCTCCTCTTTCAGA	229	3.0	58		
nicotinamide nucleotide adenylyltransferase 1	NMNAT1	2	F: TGTGTGGGGCAGATTTACTG R: ATCATTTCCAGCCCGAGTA	116	1.5	54		
natriuretic peptide precursor A	NPPA	2p14- p13	F: GATAACAGCCAGGGAGGACA R: CTGGGGAAGCCACAATTAAG	210	2.0	58	Caetano et al. 1999; Milenkovic et al. 2002*	AF134229, X58563

nardilysin (N-arginine dibasic convertase)	NRD1	2	F: GTATGAGCTGGAAGAGGATGG R: GGTAAAGCGTCGATGTGAAAG	152	1.5	58		CX605734
oxysterol binding protein-like 9	OSBPL9	2	F: GCTCATGGAATAGTCTAAAGCG R: CATCATCTCTATCATCGTGTGAA	533	1.5	58		NM_148904
poly(A) binding protein, cytoplasmic 4	PABPC4	2	F: AAGCTGAGCTTGGAGCCAAA R: CTTTGGATTTCCTACTGGGA	329	1.5	58		NM_003819
protocadherin 18	PCDH18	2	F: GTAAGCTTCATGGACATGGT R: CCATTTTCTCCAAGATCAGG	304	1.5	58		CF368035
PDZ and LIM domain 2	PDLIM2	2q13	F: GAGCTGTACTGCGAGAAGCA R: ATCCCATGCCCACTTGTTAC	152	1.5	60		CX596726
phosphogluconate dehydrogenase	PGD	2p12-p13	F: GCCTTTGAGGAATGGAATAAGA R: GTACTCCAGGGCGGAGATG	168	1.5	55	Gu et al. 1992*; Perrocheau et al. 2006;	DX010555
polo-like kinase 3	PLK3	2	F: ATGCCCTTCTGGTGCAAGTA R: AAACCTGGAGCCCTGACTCT	100	1.5	60		
procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	PLOD1	2	F: GGTTCTGCGTTACAAGTCT R: CAGGCTTGCCGATTAGG	169	1.5	58		
prepronociceptin	PNOC	2q13	F: CATGTGGTGGCTGCTCTTTA R: CCTCTTCTGCAGCTGCTTCT	156	2.0	58	Chowdhary et al. 2003	AY011855
phosphatidic acid phosphatase type 2B	PPAP2B	2	F: CCGGATCTATTACCTGAAGG R: TCTGGCTGAAATCAGGGTTG	200	1.5	58		NM_003713
protein kinase, AMP-activated, alpha 2 catalytic subunit	PRKAA2	2p18-p17	F: AAAAGGAAGAAAGTAGTGGG R: CAGTAATAGCAGTAAAAGCAG	364	1.5	60	Dranchak et al. 2006*	
PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	PRPF38A	2	F: AGAGTCCAAGACGTCACCGC R: GGAGACTTTGAGTGGCTCCTG	587	1.5	60		NM_032284
surfactant, pulmonary-associated protein C	SFTPC	2p13	F: CCACATCCATCTCTCCCTGT R: GAACCCGAGTTCATTCAGGA	202	2.0	58	Shubitowski et al. 2001	AY008813
solute carrier family 10, member 7	SLC10A7	2	F: CGAGCACCTCTCGTTAATATC R: CCTTGACACCATCCAAGAC	106	1.5	59		DN504501
SWI/SNF related, matrix associated, actin dependent regulator of	SMARCA5	2q21	F: GAAGCTGAAACTATGAATACATA R: CTACATACTATGTTTCTAGCTCG	164	3.0	58	Lear et al. 2001	G62205

chromatin, subfamily a, member 5								
spermatogenesis associated 5	SPATA5	2	F: TCAAGAGAAGAGTGGGCTACA R: ACACGTGATGCCTACAGGTTTG	393	1.5	58		CX605537
serine/threonine kinase 40	STK40	2	F: CACGGATGACTTCTATCAGC R: AAAGCAGAGAGTACTCGGTG	473	1.5	62		NM_032017
stathmin-like 4	STMN4	2q13	F: GGACCTGAACTGGTGTGTCAT R: TCAGCTGCTTCCAGTTTCTTC	186	1.5	55	Perrocheau et al. 2006*	DX010591
TBC1 domain family, member 9	TBC1D9	2	F: GGCCATCTTTCCAGTTAAATCAG R: CAATAAAGTAAAGGAGGGTGCTG	317	1.5	58		BI961809
transcription elongation factor B (SIII), polypeptide 3	TCEB3	2	F: ATCAAGTACGATCTCTGCTCCC R: AGGAATTATCATGGCCCCACAC	199	1.5	58		
testis nuclear RNA- binding protein	Tenr	2q22- 23	F: CAATGACTGGTTTCAGAGTTC R: GTGCAAACCTGGTGCAAGG	921	1.5	62		AJ693294
microsatellite	TKY003	2p15.1- p15.3	F: GGTTACACAGGAGTCAGGGA R: CCTTCTGGTTTGCCTCGTCTC	162-168	2.0	58	Tozaki et al. 1995*	AB048314
microsatellite	TKY024	2p14- p16	F: GATCCAACAGCAGCAACAGCAG R: AGTGGCATGGCATGAGCTTC	151	2.0	58	Hirota et al. 2001*	AB048334
microsatellite	TKY313	2	F: TGTAGTGCCAGAAAGTAAGG R: GACTCCTGCATGTCTTTAAC	120-122	1.5	58	Tozaki et al. 2000c	AB034622
microsatellite	TKY335	2	F: TGAGAGTAGTAACCTGCATC R: TAGGCAAGTCTCAGTTTTCC	268-274	1.5	58	Tozaki et al. 2001	AB044836
microsatellite	TKY340	2	F: CAGGCTTTGGGTTTCATTATG R: TCAGTCTCCATTATAGGAGG	147-169	1.5	56	Tozaki et al. 2001	AB044841
microsatellite	TKY358	2	F: GAAGCAGTGCCTCTTATGTG R: CAGAACAGTCAGGACTTGAC	173-183	1.5	58	Tozaki et al. 2001	AB044858
microsatellite	TKY381	2	F: AGGTGTTGAAGTCTAAATCC R: TGTCCCTTGGTCACTTAATC	204-216	2.0	55	Tozaki et al. 2001	AB044881
microsatellite	TKY384	2	F: TGCAGCAAGAAACCTAAACA R: CTTCAAGTTGTAATCAGGCTC	114-120	1.5	54	Tozaki et al. 2001	AB048290
microsatellite	TKY474	2	F: TGTCCTACTTCCCAGCTACG R: CCTGCCTTTGCAGTTCAGTG	153-157	1.5	55	Tozaki et al. 2004	AB103692
microsatellite	TKY483	2	F: AAAACAGATTCCTTAAATATACACAA R: TTACAGTTCAACGGCCTGTC	203-209	1.5	58	Tozaki et al. 2004	AB103701
microsatellite	TKY497	2	F: CAGGAAACTGAGGCTTGAGG R: GCCACATCTATGCAGCTTGA	288-300	1.5	58	Tozaki et al. 2004	AB103715

microsatellite	TKY511	2	F: AGGAAATGAGGACCGAGAGG R: TGCAGGCCTTGTTACTTGTG	195-213	1.5	58	Tozaki et al. 2004	AB103729
microsatellite	TKY605	2	F: AGTGCCATCTTGAATTGCTG R: CGATGAAATTGAGGATTTATGGA	158-162	1.5	58	Tozaki et al. 2004	AB103823
microsatellite	TKY615	2	F: CCAGACCCACCCAAAAGATA R: GGGCAAAGTGGTCTGAGAAG	243-263	1.5	58	Tozaki et al. 2004	AB103833
microsatellite	TKY645	2	F: CGATATAAGGAAGATGGCATAAAG R: TCTCTCTCCCAATCTTTCATC	122-124	1.5	58	Tozaki et al. 2004	AB103863
microsatellite	TKY701	2	F: TTTTGCAGTATGGCTCATGG R: CTGAATGGGAATTTGAGGTGA	221-225	1.5	56	Tozaki et al. 2004	
microsatellite	TKY718	2	F: GGTGTGTTTCACTCCATCCTG R: CCTACTCCAGAAAGCAACTC	143	2.0	58		AB103936
microsatellite	TKY777	2	F: TGTCTGCCTTAGAGGAGG R: TGATGGTGTGAATGGTGTGTTGG	97	2.0	58		AB103995
microsatellite	TKY784	2	F: GATCAGTACTTTGCAAATGGATAAC R: GTAACCTCCAAGGCTACGTTC	202	2.0	58	Tozaki et al. 2004	AB104002
microsatellite	TKY842	2	F: ACATTTGACGTGACCTCTCA R: GGCAAGCTCAGTGTAGTAAA	106	1.5	62	Tozaki et al. 2004	AB104060
microsatellite	TKY850	2	F: TGGTTTGCTGGTTTTGCCTC R: AGACATAGGTATTGACTGGG	152	2.0	58	Tozaki et al. 2004	AB104068
microsatellite	TKY903	2	F: TCAAGTTCTTGCAATCCCAG R: CTGAGCCTCACAGATGAAC	218	2.0	58	Tozaki et al. 2004	AB104121
microsatellite	TKY944	2	F: CACCTCTGCACATTTTTTCTC R: GCTGCTTCAGGAAGAAGAG	146	2.0	58		AB104162
microsatellite	TKY965	2	F: ACAAGGGCTACTTTAAGTGC R: TATTTGCACTCTGAGCACTG	234	2.0	58		AB104183
microsatellite	TKY974	2	F: ATGCCATCTCTAGCTGCTG R: TGTCTAGGCACTGACCATC	270	2.0	58		AB104192
microsatellite	TKY1054	2	F: AACATTTACACACGTGCAGC R: AAGTCTGTTGGTTTTGGAGG	208	2.0	58		AB104272
microsatellite	TKY1142	2	F: CTACATTGAACATCTATTGCTC R: AAGAATGCCCCCTCATATAG	301	2.0	58		AB104360
microsatellite	TKY1171	2	F: TTTGCAGACCTGACAGCTG R: GCCATAAGTCTGGGTGATG	252	2.0	58		AB104389
microsatellite	TKY1192	2	F: TTTCATTCAACTCAGTGCCA R: TCTGGGTAGCCTAACCTTG	198	1.5	58	Tozaki et al. 2007	AB215135
microsatellite	TKY1907	2	F: TGTCCAAGAGCTTAAAATGC	217	1.5	58	Tozaki et al.	AB215850

microsatellite	TKY2565	2	R: GATCAATTCCTCCACTCAAT F: CCCGCAGAAATTGACATTTA R: TGCCTTCCATTCTATCAGGA	228	1.5	58	2007 Tozaki et al.	AB216508
microsatellite	TKY2717	2	F: GTTTCTAGCCCCCAGTTCTC R: TCTTCAGGTAGAGACAGGTAAGC	218	1.5	58	2007 Tozaki et al.	AB216660
microsatellite	TKY2970	2	F: ATTTGAATCCTGATGGCAGA R: AACAAAGCAGCCAGCTAAAAA	227	1.5	58	2007 Tozaki et al.	AB216913
toll-like receptor 2	TLR2	2q14.3- q21.1	F: CAGGAGCTGGAGCACTTCAA R: GAAGAATGAGAATGGCAGCA	229	1.5	60	Musilova et al. 2005*	
transmembrane protein 34	TMEM34	2	F: TGCAGAGAATGTTACGAAGC R: GTGGACAGCAACATAAAGGAG	145	1.5	58		CX596283
transmembrane protein 59	TMEM59	2	F: AACTAAGGTGACTGACGGCATC R: AGTTACCCAAATCTGTGAAGACTG	227	2.0	58		
tumor necrosis factor receptor superfamily, member 18	TNFRSF18	2p12	F: GGGAGTTTTCTGTTTTGGCTTC R: ACGGCATTGTGCGTCTTGTT	308	1.5	60		CD535912
TNFAIP3 interacting protein 3	TNIP3	2	F: GTCTGGTAATGTTTCACTCTGGCA R: GTTTCAAGAAGTGGCGCATAATCC	156	1.5	58		BI961939
translocation associated membrane protein 1-like 1	TRAM1L1	2	F: GGGACTTGTTCTCCTGATGAT R: TAGGCTTGGATAGTGCAACTG	276	1.5	58		
tetratricopeptide repeat domain 4	TTC4	2	F: TGCCTCCAGTCCATTATTTTC R: AAGGACAGCATTCAAATCAGG	900	1.5	54		CX601532
microsatellite	UCDEQ380	2	F: GTGGGATGGGGTAGGAAC R: ACTGGGAAGTGCTGCAAA	129-133	2.0	58	Eggleston- Stott et al. 1999	U67403
uncoupling protein 1	UCP1	2q22	F: AACAAACAGAAGGCTTGACGG R: ACCAGGGCCTCCTTCATTAG	220	1.5	58		
UDP glycosyltransferase 8	UGT8	2q24	F: TCTGAAGGCAGAGACATCG R: GGCCGGTTTGGTTAGGAT	639	1.5	58		AF129810
microsatellite	UM007	2	F: GGGAATAGAGAAAGGTGAAG R: TTAGAGTTCCTGCTCCTCC	115-150	2.0	58	Meyer et al. 1997	AF195128
microsatellite	UM029	2	F: CTTTCATCTTTTGGCCCC R: CTGTCTTGCTTTCCACC	190	2.0	58	George et al. 1998	AF195576
microsatellite	UMNe076	2	F: CCCTCAGGTTGAGGACTCAG R: AGGTGACAACCTGGATTTGC	98-102	2.0	58	Roberts et al. 2000	AF191706
microsatellite	UMNe080	2	F: GGGTTTGGGACTTTTGTCTAGG	125	1.5	58	Mickelson	AF536242

microsatellite	UMNe129	2	R: TCCAAGGACGACAGTACTTCTCTG F: GGACTTCCCAGCCTCCAG	169	1.5	62	et al. 2003	
microsatellite	UMNe205	2	R: GCAGGGTGCTATTTTGAGATG F: TGGAGAAAAGGCTGATTCTAGG	187	2.0	58	Mickelson et al. 2003	AF536257
microsatellite	UMNe226	2	R: GCCATGGAAACCATGGAG F: TAGAACAGGCCAGAAAAGTTGTG	200	2.0	58	Mickelson et al. 2003	AF536288
microsatellite	UMNe236	2	R: CAGAATGAGGCCAAGAACTTG F: CAGAACGTGCAAACCTTAACTGC	155	2.0	55	Mickelson et al. 2003	AF536302
microsatellite	UMNe242	2	R: TTTGTTGAACTGACAAAATCCG F: CCCACCACTCCATTCTGC	169	2.0	58	Mickelson et al. 2003	AF536307
microsatellite	UMNe323	2	R: GCAGAACATGCGAACTTAACC F: GATCCTGCAGGAAAGCATGT	185	2.0	58	Mickelson et al. 2003	AF536312
microsatellite	UMNe330	2	R: CCGCTCGGAATATTTTCATTG F: AAACATGGAACCAGAGGGG	129	1.5	58	Wagner et al. 2004a	AY391338
microsatellite	UMNe336	2	R: TCTCCAGCGTATTTGGTTAGTG F: ACCTTCTCTTTGGAAGGAAATG	119	1.5	58	Wagner et al. 2004a	AY391341
microsatellite	UMNe374	2	R: GAGACCTAAGCATGGAGCATG F: AATTTTCATATGGTTTCCATGCC	194	2.0	58	Mickelson et al. 2004	AY731385
microsatellite	UMNe396	2	R: TAAGCACTGCGTTAATGTTCTG F: CAGATTTTGGTTATGAGGAGCG	168	1.5	58	Wagner et al. 2004a	AY391356
microsatellite	UMNe405	2q13	R: TGCTGTAGAAGCAGTAGGTTCCG F: TTTTCCATCTGGGAATCAGG	234	2.0	58	Mickelson et al. 2004	AY731392
microsatellite	UMNe411	2	R: ACATAATGCTTGGAAGAGGTGG F: GATCTGGGAGAAACAATCTGAC	175	2.0	58	Wagner et al. 2004b	AY464481
microsatellite	UMNe433	2	R: ATTGTGTTTATTGCCATGTTGC F: AACTGAGGCCAGCTGGTG	400	1.5	62	Wagner et al. 2004b	AY464485
microsatellite	UMNe449	2	R: TCAGCAGCCACTGGTTTTTC F: AGTAATCCAGGAGTCCTCCTCC	334	1.5	60		
microsatellite	UMNe488	2	R: TTGAGCCACTGTGGTAAATCC F: TGTTAAGCACACTTTGACCCC	319	1.5	60		
microsatellite	UMNe513	2	R: CGACACAGTGGTAGTGGGTG F: AGAATCTCACTTAGCTCCGCC	300	1.5	58	Wagner et al. 2004b	AY464512
vesicle-associated	VAMP3	2	R: TGGGAAATCTTACCTTTGT F: TGGGAAATCTTACCTTTGT	114	1.5	56		
membrane protein 3	UMNe554	2	R: ACTCTCTATGATAAGCTGTA F: ACTCTCTATGATAAGCTGTA	157	1.5	62	Wagner et al. 2004c	AY735267
microsatellite	VHL123	2	R: ATTCCCTACACAGCACTTGGC F: ATTCCCTACACAGCACTTGGC	149-161	1.5	62	Wagner et al. 2004c	
microsatellite	UMNe563	2	R: GATTATCTAAGTCAATATTC F: GATTATCTAAGTCAATATTC	125	1.5	55	Wagner et al. 2004b	AY464529
			R: TTCTCCATTAAACACACGCG					

WAS protein family, member 2	WASF2	2	F: GGATTCTTGGGTGTGTTTGC R: CGGAATCTTCAGGTCCTGG	306	2.0	58		BI961530
Yip1 domain family, member 1	YIPF1	2	F: CGGTCCGTTGGGTTCTAGTTA R: CACAGAAAGCAGCATGTGAAG	149	1.5	55	Perrocheau et al. 2006	DX010463
zinc metalloproteinase (STE24 homolog, S. cerevisiae)	ZMPSTE24	2p15- p16	F: TTTGCAGGCTTTTACAGAATG R: TTACTACGTCTCCGTGAAGC	185	1.5	59		AM072944
zinc finger protein 330	ZNF330	2	F: GGATGTTTGTGATCCAAGC R: GCATCTGACTTTTATCCTGTGG	253	1.5	58		CX600513
zinc finger, UBR1 type 1	ZUBR1	2	F: ACATCGTGCACTACGACTGC R: ACTTGGTGTGGCGTTCTGA	504	1.5	58		NM_020765

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	3CA001	3	F: GGGCCTATGCATTTTTCAAT R: AACTGTTGCATGGGGAATGT	177	1.5	58		AY820143
sequence tagged site	3STS01	3	F: GGCTGGACTCTTGGTCTGTC R: CATGCCTGTAGTCCCAGCTA	290	1.5	52		BG193780
ATP-binding cassette, sub-family G, member 2	ABCG2	3q13	F: CAGGTGGAGGCAAATCTTC R: GCCACTTTATCCAGACCTAA	1524	1.5	TD 58		BE487863
adducin 1 (alpha)	ADD1	3q26	F: ACTGCTTTGAGCTTCCTGGCG R: GAAAGGACGTAGGACCTGTCCTCC	250	3.0	58	Lear et al. 2001*	G62182
alcohol dehydrogenase 1A, alpha polypeptide	ADH1A (<i>ADH3</i>)	3	F: GTGCTATGCCTTGTCGTTT R: CACCTGCCCAGATTCTGATT	204	2.0	58	Chowdhary et al. 2003	AF134056
alcohol dehydrogenase IB, beta polypeptide	ADH1B	3q13-q14.1	F: GGAGTGGGCCTGTCTGTTATC R: GAAAAATCCACACCTCCATTG	191	1.5	55	Perrocheau et al. 2006*	DX010429
microsatellite	AHT022	3p13	F: AAGCACAATGTGGGTTAG R: TCCACGTTACACATACCTCA	189-197	2.0	58	Swinburne et al. 1997*	
microsatellite	AHT036	3p16	F: TGCTGCCTCCAGTGTCCCT R: TAGATTTACAGGCGGGTG	133-144	2.0	58	Swinburne et al. 2000*	AJ271521
microsatellite	AHT090	3	F: ACGTTTTCCAGTTCCTGATACC R: GTTCTTTGCTGTCTGGGGTC	109-111	2.0	58	Swinburne et al. 2003	AJ507707
microsatellite	AHT097	3	F: AGTTCGGTAACCTTGCCCATG R: GTTCATGGGCAGAATGGC	151-165	2.0	58	Swinburne et al. 2003	AJ507714
microsatellite	AHT118	3	F: GATCAATAGGTGAGATGCGT R: GGTCTTCTCCTGCCTTCAGA	283	1.5	61		
AKT interacting protein	AKTIP	3p15	F: CTTACTGTATTTTTATGGCAGGAGA R: TTCTCTACAAAACACATTAGTCATTCA	100	1.5	58		

albumin	ALB	3q14.3	F: CGGATTCCTTGGCGGAAAGAC R: GGAAGGTGAATGTTTCAGCCT	110	3.0	58	Godard et al. 1998*	
anaphase promoting complex subunit 4	ANAPC4	3	F: CGCTTTCCGACCTGTTTC R: GCCAAGGCAATGAGATCC	107	1.5	59		
microsatellite	ASB23	3q22.1- q22.3	F: GAGGTTTGTAAATTGGAATG R: GAGAAGTCATTTTAAACACCT	129-153	2.0	55	Irvin et al. 1998; Lear et al. 1999*	X93537
bromodomain containing 7	BRD7	3	F: AGACCACCAGATTGCTCAGG R: ATGGAAATCCCCATTGCTTT	431	1.5	58		CX596327
chromosome 16 open reading frame 61	C16orf61	3	F: GCAATGTGATGCGAAAGAGA R: CTGCCCAACAGACAGTCAGA	224	1.5	58		DN507164
C1q and tumor necrosis factor related protein 7	C1QTNF7 (CTRP7)	3q25	F: GCCAAAGATGTTTGTCTTGCT R: CGTCTCTACCATCTCGTCCTG	209	1.5	55	Perrocheau et al. 2006*	DX010458
core-binding factor, beta subunit	CBFB	3	F: AATCTTTCATCACCCAGC R: GAAAAGGGATACTGGAGC	162	2.0	58	Chowdhary et al. 2003	
cyclin I	CCNI	3	F: GGTGCTCACCAAAGAAACATGTAAC R : CATCAGTACATGGTTCTGACCTGC	311	3.0	58	Chowdhary et al. 2003	
BAC end sequence	CH241- 100F24_SP6	3	F: GGCTGCTTTGTAGGAATAC R : CAGACAGAAGCCAGAGAC	261	1.5	56		AJ542905
BAC end sequence	CH241- 100F24_T7	3	F: TCACTGGGCAGATTCCAC R: AATGCATTTCCAGCCTGTG	216	1.5	56		AJ542906
cytokine induced apoptosis inhibitor 1	CIAPIN1	3	F: GCAAGCTCCATTCCAAG R: TGGTGAGAATTCAGAGGG	116	2.0	55		
C-type lectin domain family 3, member A	CLEC3A	3	F: CCTCGGAAGTTGAAAATTGG R: TTTTCCCCAAGCCTAAATTG	161	1.5	58		CX600199
cappuccino homolog (mouse)	CNO	3	F: CCCATTACGTTTCAGGAACTG R: AGCAGGGAAAGTGGTCCTC	133	1.5	58		CX605498

CCR4-NOT transcription complex, subunit 1	CNOT1	3	F: GATGCCAGAGCAAATCAGG R: GCACATTCCGTGCAAATC	694	1.5	63		
microsatellite	COR005	3	F: CAATTCCTGGCATGCTGTAAG R: GATGCTCACTTCCATGAACC	198-200	2.0	58	Hopman et al. 1999	AF083448
microsatellite	COR028	3	F: TAAAGAGGAAGGCAATGGAC R: ACCTTTTGTGCTAGGCACTG	227-241	2.0	58	Murphie et al. 1999	AF101397
microsatellite	COR033	3	F: CCTCCCCTACTTCCTCTCTG R: CATTTTCTTTCCAGGTTCCC	219-243	2.0	58	Murphie et al. 1999	AF101402
cytochrome c oxidase subunit IV isoform 1	COX4I1	3	F: GTCCCACACACCTTTGAAGAG R: AGTCCCCTTGGCAGAGAAG	100	1.5	58		
casein kappa	CSN3	3	F: TCCCGCCTATAATAATGCCA R: CTTGCCATTGAGGAATTTGG	263	2.0	58		AF165600
chemokine (C-X-C motif) ligand 6	CXCL6	3	F: CAGATGAAGAAGCTAGGAAATAGG R: GAAAGATACACCATAAGCGTCTAC	216	1.5	58		
chemokine (C-X-C motif) ligand 9	CXCL9	3	F: AGTAATGAGGAAGGGACGCTGT R: AGAAGGGCTTGGAGCAAATCTGT	100	1.5	58		BI961648
DEAH box polypeptide 15	DHX15 (<i>DDX15</i>)	3	F: GACATGAGCAATTTCCCACAG R: AACCAACGTGAAGAGCACAAAC	178	1.5	55	Perrocheau et al. 2006	DX010462
docking protein 7	DOK7	3	F: ACTCTCCACCTCTGCAATGAC R: CGCCCTCAAAGATGAATCC	127	1.5	56		
family with sequence similarity 114, member A1	FAM114A1	3	F: GCCTAGCAGTGGTTCTTTACC R: TCAGTAAGCGTGTCTCAGTC	219	1.5	58		
F-box and leucine-rich repeat protein 5	FBXL5	3	F: TAGCATACAGCTCTGCAGTT R: GCAGAATCTGAAATGTCAGTT	1035	1.5	60		
fibroblast growth factor receptor 3	FGFR3	3	F: AGCGGATGGACAAGAAGCTG R: TTCACCTCCACGTGCTTGA	586	1.5	TD 62		AB059430
fucokinase	FUK	3	F: ACTGACCAAGGAACACAGC R: GAAGGGAGGGGTTACGGTAG	389	1.5	58		
GABA(A)	GABARAPL2	3	F: TACCGGTGCATTTGTAGCTG	202	1.5	58		DN507256

receptor-associated protein-like 2			R: TACCCACCTCCCTCACTTCA					
growth arrest-specific 8	GAS8	3	F: CGAGAGGAGCGCAACTACTTC R: TAATCTCCACCTGGTGCCTCT	151	1.5	55	Perrocheau et al. 2006	DX010490
golgi apparatus protein 1	GLG1	3p13-p12	F: TCATGTTAGAGCAGCAGCAGGTA R: GGTTCTGGAAGTATTGGTAATTCCA	203	2.0	TD 60	Lear et al. 2001*	G62189
gonadotropin-releasing hormone receptor	GNRHR	3	F: CAAACAGTGCCTCTCCTGAA R: AGCTAGGGGCCTTGTGATG	440	1.5	TD 62		AF018072
glutamic-oxaloacetic transaminase 2, mitochondrial	GOT2	3p15-p14	F: TCTCCCAGCTGGATCTCAAT R: GCGTGCAGGAGAATAATGT	203	2.0	58	Lear et al. 1998*; Chowdhary et al. 2003	AF052648
GrpE-like 1, mitochondrial	GRPEL1	3	F: GTTGCAGACATTTTGGAGAAG R: CAGCTTGTACCCCACTTTGT	264	1.5	60		CX595321
microsatellite	HMS61	3p12	F: TGCATCTGACCTAATGTGGC R: CGTCAAACCATGCTGTCACG	200	3.0	55	Mariat et al. 2001*	
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	3	F: GTCAACTTGTCACCCAATC R: CTAGGCCAAGTACCAGTGT	170	3.0	58	Chowdhary et al. 2003	
haptoglobin	HP	3p13	F: CCCATCTGCCTACCTTCAAA R: TACCAGGTGTCGTCCTCCTC	320	1.5	58		BM780758
hydroxysteroid (17-beta) dehydrogenase 11	HSD17B11 (<i>LOC51170</i>)	3	F: GCTCTGGCAGTCCTCGTTTCT R: GCATTGAAATGTGAGGTATGTCTCAA	406	3.5	TD 60	Chowdhary et al. 2003	
microsatellite	HTG02	3	F: GATTGGCAACAGATGTAACTCGG R: CCCCATGAGAACTAACAATGTTAG	99-107	3.0	58	Ellegren et al. 1992	AF169163
insulin-like growth factor binding protein 7	IGFBP7	3	F: AAGGTGCCGAGCTATAAACC R: ATGGATTGGATGAAAAGAAGC	114	1.5	58		DN508698
interleukin 8	IL8	3q14.2-q14.3	F: GATCCATGAGTCCCTGTTC R: GTTAATGTGCTTCCACCAG	117	1.5	58	Nergadze et al. 2006*	BI961686

lysyl-tRNA synthetase	KARS	3p13-p12	F: CTGTTTCCTGCCATGAAACCC R: TTCTCTCCTCTGGTTGCTGACC	223	3.0	58	Lear et al. 2001*	G62187
kinase insert domain receptor	KDR	3	F: GAATGAGGGCCCCCTGATTAT R: CTGAAAACGTGGGTCTCTGA	493	1.5	58		
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	KIT	3q21	F: TTGGCATGCAGCTATTGAGT R: CCTCGCATAACCTTCATCGT	202	3.0	58	Lear et al. 1998*; Chowdhary et al. 2003	AF053636
microsatellite	LEX007	3	F: GGTAGGGCTCTGGGATGA R: AACACTGGGGAAAAGTCAG	188-198	2.0	58	Coogle et al. 1996	AF075610
microsatellite	LEX057	3	F: TGGTCCCCTAATCAAATCAGA R: ACGGCATCCCACATAAAATAG	157-167	2.0	58	Coogle & Bailey 1997	AF075659
lipoic acid synthetase	LIAS	3	F: AGCCCTACAATACTGCAAAG R: CTCAGCTCCTCCATCAGG	180	1.5	58		
hypothetical protein FLJ20425	LYAR	3	F: CCCCAAAGTGAGGGAACCTT R: GATATTCCACACCTGCTCCA	~274	1.5	54		DN504824
mitogen-activated protein kinase kinase 1 interacting protein 1	MAP2K1IP1	3	F: TCTTATCTACTTTTGCCCTTGC R: TGCAGTTCCTGGTAGGTGTTA	100	2	50		
membrane-bound transcription factor peptidase, site 1	MBTPS1	3	F: CATTCTGTCTTTGCCTTCC R: GCTCTCTTCGGCTCTCACAG	191	1.5	58		CX596016
melanocortin 1 receptor	MC1R	3p12	F: CAGCAGCTGGACAACATCAT R: AAGCGATGAAGAGGGTGCTA	205	2.0	60	Raudsepp et al. 1999*; Chowdhary et al. 2003	AF252541
matrix metalloproteinase 2	MMP2	3p15	F: ACTCCCACTTTGATGACGAC R: GAAGAGGAAAGGGAACCTTGC	350	1.5	58		

M-phase phosphoprotein 6	MPHOSPH6	3	F: GGTGCCTCGTGAAAGTTAGC R: AGCAAAGCAAAGGAGGCATAA	157	1.5	58		CX601025
Mof4 family associated protein 1	MRFAP1	3	F: GACCAAAGGAGGAGAGAGGTA R: TGAATTAGGTTGTCCAAACAGA	101	1.5	56		
nuclear factor of activated T-cells 5	NFAT5	3	F: GGAAAACCAAAAAGGAACTGG R: TTTACTGAGCCACGGCTACC	153	1.5	58		CX597950
microsatellite	NVHEQ102	3	F: CAACTGGGCCTCAATCTTGG R: AGGGTTGGGGTCATCATCC	150-170	1.5	58	Penedo et al. 2005	
OCIA domain containing 1	OCIAD1	3	F: TGGAGATACTTGGGATGAGTG R: GAATATCCTTGCCCTGTAACCTT	296	1.5	58		CX601897
protocadherin 7	PCDH7	3	F: ACTCAGGGCGTCTCTGAAGAT R: GCAACAAGCCAGTCTCAACTC	193	1.5	55	Perrocheau et al. 2006	DX010549
platelet-derived growth factor receptor, alpha polypeptide phosphorylase kinase, beta	PDGFRA	3q21	F: TGGCTAACAACATCTCAAACAT R: CTTCAGCTCTCGGTTCTCAG	152	1.5	58	Raudsepp et al. 1999*	CX605007
	PHKB	3p16	F: TTAGCCCAACCTCTACA R: GAGTATGCCAGCTACAAT	399	3.0	58	Chowdhary et al. 2003; Perrocheau et al. 2006*	
peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	PPARGC1A	3q23	F: AGACCAGTGAACTGAGGGACA R: GATTTGGGTGGTGACACAGA	229	1.5	60		
protein phosphatase 3, catalytic subunit, alpha isoform	PPP3CA	3	F: CAGCAGTTGGATGTTCTTG R: AGTGCTGCGACTGTAAACG	349	1.5	TD 62		CD467720
proteasome subunit, beta type, 10	PSMB10	3	F: GAGGCGTAGACTTGACAGGA R: TCCTCCAGAACTGCCAGA	222	1.5	58		
proteasome 26S subunit, non-	PSMD7	3	F: TCCATGGTTTGAAGGGACTC R: CCATTTGGTCGTTGGTCTTT	189	1.5	58		CX594573

ATPase, 7 replication factor C1, 145kDa	RFC1	3	F: CTATTTTGGGACCTGACGACT R: ACATTTTCATCTGTCCAAGCC	772	1.5	50		
ras homolog gene family, member H	RHOH	3	F: GAGCAGAAGCCAACAGAGA R: GATGGAACCTCAGCATCTTCC	628	1.5	TD 62		CD465079
ring finger protein 4	RNF4	3q26	F: TTCTGAAGGAGCAGGAACTTG R: GCCCTCCTCAACTCCAAGTAG	175	1.5	55	Perrocheau et al. 2005*	AY817482
ribosomal protein L13	RPL13	3	F: AAGAACTCAAATTGGCCACC R: TGGCCTTCTCCTTCTTG TAG	650	1.5	58		
SEC31 homolog A (<i>S. cerevisiae</i>)	SEC31A	3	F: GGTACTGGAGCTGAAGGCTG R: CAGGTCCTCAGAATGGTTGG	~1000	2.0	50		BI395133
microsatellite	SGCV18	3p14- p13	F: TGGGGAAGAGGGATTCAT R: AAATGCCAAGCCTATCTATGC	157	1.5	TD 60	Godard et al. 1997*	U90596
solute carrier family 2, member 9	SLC2A9	3q26	F: TACAATGAGTCGTGGGAGAGA R: TCCAATCAGCTTCACTATTAACG	132	1.5	58		CX595350
solute carrier family 12, member 4	SLC12A4 (<i>KCC1</i>)	3p14	F: GCCGCGGGTACTTCACGTGGAG R: GGGGCCTCCTCACACCAAGAACTG	~400	3.0	58	Hanzawa et al. 2002*	AF425261
SPARC-like 1	SPARCL1	3q13	F: CCAAAGCAGAAGTGGAAGAAG R: TGGTGTTACCGTCATCAGTAGG	177	1.5	55	Perrocheau et al. 2006	DX010589
sulfotransferase family 1E, estrogen- preferring, member 1	SULT1E1	3	F: TGACCATTCTGCATACTTTGG R: GATTTGGGATAGGTGGCAAT	129	1.5	58		
THAP domain containing 6 microsatellite	THAP6	3	F: GTCTGCGGAATGTTTTAGACC R: CGTTCTATGCTTTCCTGACAA	151	1.5	58		
	TKY353	3	F: TTCTTACTTAACAACCATCG R: TGTCACCTGACAGATGAATGG	161-179			Tozaki et al. 2001	AB044853
microsatellite	TKY427	3	F: CTGATTTCCCTTGTGGCATG R: ACTAGTCAGCAGATCTGTGA	149	2.0	58		AB103645
microsatellite	TKY434	3	F: CAAACACTTTGTTGGCCGAC R: TCATCCATCAGTGTCCTG	194	2.0	58		AB103652

microsatellite	TKY447	3	F: TCGGCCTTTAAAACCTAATCC R: GGAGTAAATTGGAGGCAGCA	198-218	1.5	58	Tozaki et al. 2004	AB103665
microsatellite	TKY450	3	F: GTTCTTCCTTCCCAGCACTT R: CATTGTAAGTCGGGGACCAT	113-119	1.5	58	Tozaki et al. 2004	AB103668
microsatellite	TKY528	3	F: AGTGCCACCTCTGCTCTGTT R: TCTTGCTATTGGTGCCCTTT	290-300	1.5	58	Tozaki et al. 2004	AB103746
microsatellite	TKY569	3	F: TGGCCTGTTGTTGATCTCAG R: GCAGTGGGAAAATACTTTGAGG	191-196	1.5	58	Tozaki et al. 2004	AB103787
microsatellite	TKY590	3	F: ACGCATGCGCACTACAGATA R: CACCTCTGGCATTTTGAAT	230-258	1.5	58	Tozaki et al. 2004	AB103808
microsatellite	TKY651	3q12- q13	F: CCCTCTGTACCTTCATTCCAA R: CACTGCTGTTTGACCCTGTG	209-211	1.5	58	Tozaki et al. 2004	AB103869
microsatellite	TKY780		F: AGAACCACCCCTCATTGG R: GACACAGCGGACACTTGATA	250	2.0	58	Tozaki et al. 2004	AB103998
microsatellite	TKY837	3	F: GCGACAATCTTCCTCAAGCA R: GACTATTGCCACTACATGAC	147	2.0	58		AB104055
microsatellite	TKY840	3	F: AGAATTTAGGTGAACCTGGG R: GGACAATCTTCCTCAAGCAA	111	2.0	58		AB104058
microsatellite	TKY874	3	F: GTGAATTAAATCCCCCTTCC R: GCTCCAGCTCCATAGGTAAT	177	2.0	58		AB104092
microsatellite	TKY905	3	F: TGTTCAAGGAACAGAGAAGG R: ACATGTCAAAGGACATGGAC	202	2.0	58		AB104123
microsatellite	TKY910	3	F: ATAAACCACATTTAGGGGCA R: AAGGAGAACCCAGTCAGTC	229	2.0	58	Tozaki et al. 2004	AB104128
microsatellite	TKY937	3	F: TCCTGCGGAAATACATTAGG R: AGTTCAAAGTGGTCCCATAG	146	2.0	58	Tozaki et al. 2004	AB104155
microsatellite	TKY990	3	F: GATCAGACATGGTCTCTTTTG R: TGCCCTCCTATAGGACTTC	220	2.0	58		AB104208
microsatellite	TKY1037	3	F: ACTGTTAAATGAATTGTCAAGTGG R: GGCCTCATAACATACTTTGG	176	2.0	58		AB104255
microsatellite	TKY1082	3	F: GAATCTAAGCTTGCCCTTTC R: CTGAACCTCGAACTTTAAGGTG	125	2.0	58		AB104300

microsatellite	TKY1085	3	F: ACCAAACTCAAGGTTAAGCTC R: TGAAGTCTACCTTCAAGTGG	189	2.0	58		AB104303
microsatellite	TKY1129	3	F: CTAGCAATTCCTTTCTGGGA R: ACATGCTCACTTAACCACTG	241	2.0	58		AB104347
microsatellite	TKY1146	3	F: TGCTCCAAGACACCAATTTG R: CGCGTGAAGTAAACCACTCG	356	2.0	58		AB104364
microsatellite	TKY1150	3	F: TGGCCTTTGGACATTACATG R: TGGCTGTCATCGCCATTG	185	2.0	58		AB104368
microsatellite	TKY1154	3	F: GAGTCACAGACCATCAGATG R: ATAAGTGTGATGTCCCTGAG	167	2.0	58		AB104372
microsatellite	TKY1174	3	F: AAGAGTTGAGGGTTCAGAAC R: CAGGGTGCCTAATGACAAG	96	2.0	58		AB104392
microsatellite	TKY1323	3	F: TCATTTCTACCTCCTTGGAG R: GACTGAGTCCCAAAGCAAAG	195	1.5	58	Tozaki et al. 2007	AB215266
microsatellite	TKY1918	3	F: TGAAAGTTACGTAGCAGAGG R: GCCTTGTAAGTCTGCTAAG	196	1.5	60	Tozaki et al. 2007	AB215861
microsatellite	TKY2482	3	F: CAGATTTCTTCCACCCTGAA R: ATGGTGCATAATGAGGAGGA	270	1.5	58	Tozaki et al. 2007	AB216425
microsatellite	TKY2924	3	F: TAGCCTTTGCTAAGCCTGAA R: GGGAAAGGTGCTCTGTTGTTA	205	1.5	60	Tozaki et al. 2007	AB216867
microsatellite	TKY3084	3	F: CTATTGGACCCAGTGACCTG R: TGACATCACCTCTTCCAAGG	250	1.5	58	Tozaki et al. 2007	AB217027
microsatellite	UCDEQ437	3	F: CTGTTCTGGGCAGGCTTCTCTA R: TTGCTGGCTTGGCTGGTC	167-191	2.0	58	Eggleston- Stott et al. 1997	U67408
ubiquitin carboxyl- terminal esterase L1	UCHL1	3q22	F: GCTTCCCTACTTGTTAGAACACAGC R: CAATTAAACCACATCCAAGGCC	187	2.0	58	Lear et al. 2001*	G62176
microsatellite	UMNe068	3	F: AATTTCAAAGTCCAGCTCTTGC R: GGGCCCAAGAATAAAGAAGG	121-133			Roberts et al. 2000	AF191701
microsatellite	UMNe082	3	F: GAATCCAGCAATCTCTAAAGCTG R: ATGGGCACAGATGTTAGCTCAG	~180	1.5	58		

microsatellite	UMNe113	3	F: GATCTCATTGAAGTATTCTTACCAC R: CATCCATGAAACCATCACCA	136	1.5	62		
microsatellite	UMNe158	3	F: AATTGAGAGCCAAGATGACACC R: GGCACCATTTGAGGAAGATG	146	1.5	60	Wagner et al. 2004a	AY391305
microsatellite	UMNe175	3	F: GCATAACGTCAGCCATGTTG R: AAGCAACCCAAGTGTCCATC	153	2.0	58	Mickelson et al. 2003	AF536274
microsatellite	UMNe178	3	F: TGGCAGATAAAGCCCTTACC R: GATCACATAGTGAAGGTGTTAAACG	107	2.0	58	Wagner et al. 2004a	AY391312
microsatellite	UMNe182	3	F: TCTCTGCATTTCACTTCTCGG R: TGAGAGAAGAGCCCAGGAAG	132	2.0	58	Wagner et al. 2004a	AY391315
microsatellite	UMNe231	3	F: TAGTCGTTGTCCACCAGCTG R: GATGGAATGACACAGCACATG	230	2.0	58	Mickelson et al. 2003	AF536304
microsatellite	UMNe251	3	F: CTGGTTCCCTTACAGGACACTCC R: ATTATCCATGTGACCCGTCTG	370	1.5	55		
microsatellite	UMNe311	3	F: GATATCCTACACCGAGGACTGC R: TCGTTCTTTGCTGTCTGGG	179	2.0	58	Mickelson et al. 2004	AY731384
microsatellite	UMNe317	3	F: CAAGAACAGACCTCTTCCGC R: GCGGTTACCAGACATGGG	161	2.0	58		
microsatellite	UMNe439	3	F: TGCAGTCTGTCCATGTAGCTG R: AATTGTCAAACTGTGGACGG	330	1.5	58		
microsatellite	UMNe516	3	F: TCCAGAAACTCTACTCTTAGGG R: TGCCTTCATTCAACATTATG	306	1.5	58		
microsatellite	UMNe527	3	F: GCAAACGTAGTGTACTTGTGCC R: TCTCATCCACAGCACCAAAG	209	1.5	62	Wagner et al. 2004c	AY735261
microsatellite	UMNe529	3	F: TTTCCCCACAGATGGCTAAG R: AGAGCAGCAACACCTGGG	286	1.5	58		
microsatellite	UMNe538	3	F: GAAGGGCAGAGAAGCAAATG R: AGCCCTTTGGTGATTACAC	~350	1.5	58	Wagner et al. 2004b	AY464521
microsatellite	UMNe541	3	F: AGGCAGCGAGCTAACTCTTG R: CAGATGCTCTGTCTGTCCTCC	216	1.5	58		
microsatellite	UMNe557	3	F: TCAACAAAGTGAAACATCTTTG R: TAACAGCATTTGTCAAGAGAGC	152	1.5	55		

microsatellite	UMNe576	3	F: CCACTGCAGTGTACAATAGAGC R: ATGCTTCATTGCTGTGAACTG	~300	1.5	58		
microsatellite	UMNe600	3	F: GAGCAGTGGTGCAGAATTTAC R: TAGAAGAATGCATGGCTCATAC	148	1.5	50	Wagner et al. 2004c	AY735292
Vac14 homolog (S. cerevisiae)	VAC14	3	F: CCTGCAGCTGCTAGATGTGA R: GTGGGAGAGCAGCTGGAA	103	2	55		
microsatellite	VHL063	3	F: GCTTTTAAAATGGTATGAATCTCCA R: AAAGAAGGAATCAGGCAAACACTCTA				van Haeringen et al. 1998	
vacuolar protein sorting 35 homolog (S. cerevisiae)	VPS35	3	F: TGATGCGGTCACAATTCAGG R: ACACATCGCAGGTGCAGAATG	320	2.0	58		BI961559
WD repeat domain 1	WDR1	3	F: GTCACCATGCAAAGATCGTC R: TGGATCTTGACCCTGGTCTC	124	1.5	55	Perrocheau et al. 2006	DX010610
YTH domain containing 1	YTHDC1	3	F: CAGATCTGCAAGGAGTGTTATC R: ACCTCCCAGCATTTTAGCAT	233	1.5	60		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
ATP-binding cassette, sub-family F, member 2	ABCF2	4	F: CTGTGGGCAGTGCATGGC R: TCACGAGGATGGTAGGGC	96	1.5	52		
aryl hydrocarbon receptor	AHR	4	F: GGATGCATGGATATTGTGTTTC R: TTGTCTACCCGCATCTGAAC	102	1.5	58		
microsatellite	AHT006	4	F: GAAGATGTCCGCTTTGATAT R: CACTGGCACATCCAGATTTG	121-131	1.5	56	Binns et al. 1995	
microsatellite	AHT009	4	F: TAACCATGTCCCTGCAATGA R: TCAGAACTGTCCTTGTGAAAGC	186-190	1.5	54	Swinburne et al. 2005	
microsatellite	AHT013	4	F: CTTCTCAGGTGCATAGGTTG R: TCATTAAAAATAACAACCTGCCCC	142-146	2.0	58	Swinburne et al. 1997	
microsatellite	AHT042	4	F: CATTTCGCATTTTCAGTTCAGG R: AAACCCACTCACCTATCACCC	87-99	3.0	58	Swinburne et al. 2000	AJ271527
microsatellite	AHT043	4	F: ACACAAGTGACAGGAGCGTG R: TGGAAGCATGCAAGAGGTC	168-186	3.0	58	Swinburne et al. 2000	AJ271528
microsatellite	AHT061	4	F: TCTGCATCCTCATGTTCAATG R: TTGACTTATTTCACTCAGCCCA	226-234	2.0	58	Swinburne et al. 2003	AJ507678
microsatellite	AHT084	4	F: TGGCAATCTGCAGGGAAC R: GATCTTGTGATTGTGTGTGTG	87-171	2.0	58	Swinburne et al. 2003	AJ507701
microsatellite	AHT108	4	F: ATCTCTGGGCTTCAGAGG R: ACTGGCCATCTGAAGGCAT	326-337	1.5	58	Swinburne et al. 2003	
A kinase anchor protein 9	AKAP9	4	F: GTAAATACCTGAGGGCAGAAAG R: ACTCTGACAGCAGACCGAAAC	205	1.5	58		
ankyrin repeat and MYND domain containing 2	ANKMY2	4	F: TAGAAAACAAAGGGGCAAGG R: CAGGAAGAGCCACATGAAAG	506	1.5	58	Dierks et al. 2006	CX596863
ankyrin repeat domain 7	ANKRD7	4	F: CCATGATCTTCATTCCCTCTG R: AGACTCACTGCTGGGAGCAC	98	1.5	58	Dierks et al. 2006	CT006390
anillin, actin binding protein	ANLN	4	F: CAATTGTACAGTCGGCAGAT R: ACACAGAGTGTGTCCCTGCAT	141	1.5	55	Perrocheau et al. 2006	DX010431
acyloxyacyl hydrolase (neutrophil)	AOAH	4	F: CTGTTGGCAGATGTCTTCT R: GGTCTCCAAACACCTTTTC	327	1.5	58	Dierks et al. 2006	BI961651
ADP-ribosylation factor 5	ARF5	4	F: TGGGGTGAAAGGCAGGAAG R: TTACCTGACCCGAATTCAAAAC	105	1.5	52		
ADP-ribosylation factor-	ARL4A	4	F: TCGACAGCAGTTTGTAGCAG	495	1.5	58	Dierks et al.	AJ584157

like 4A			R: TCACTTCCACTCAGGAGGAG				2006	
microsatellite	ASB03	4p12- p13	F: AATTCATCTCAGTGTCTACCAGC R: TTCATTTTCTACATGCACTACAGC	197	2.0	58	Breen et al. 1997*	X95318
microsatellite	ASB22	4q21	F: GAGGAATGTGAAATACAGGAGG R: TTTGTGGTCTTCCGTGCACC	159	3.0	58	Breen et al. 1997*	X93536
microsatellite	ASB29	4	F: CTGGCCCATAAAAAAACAACACTG R: TGTATGGTTGTCAGCTCAAACC	123-135	2.0	58	Breen et al. unpub.	X93543
ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F	ATP6V1F	4	F:CTAAACCGGGATGACATTGG R: AGTCCCCTAACGCAGGTCTT	201	1.5	58		
Bardet-Biedl syndrome 9	BBS9 (<i>PTHB1</i>)	4q21.3	F: AGCCAAGCTACATTCTGCTG R: ATCACTTGAACGTGGAGGAG	170	1.5	60	Dierks et al. 2006*	AM072941
BMP binding endothelial regulator	BMPER	4	F: CTGAATCTTGAGGGTGGAG R: AGTCGAGTGGCAGGTCTGAA	155	1.5	52		
2,3-bisphosphoglycerate mutase	BPGM	4	F: GGGCTTAGTCAGTGTCTCAG R: GGGCCTCTGGTCTTAACTATC	260	1.5	62		BI961532
chromosome 7 open reading frame 10	C7orf10	4	F: CCAGTTCGCCCAGGAGTAG R: TGGGATGACAGCAGGTTACA	134	1.5	51		
chromosome 7 open reading frame 23	C7orf23	4	F: TGTGACAAGGATACAACACTGGAG R: ACCCCTAAAGGGAAACTGTTC	320	1.5	58	Dierks et al. 2006	CX598762
calcium channel, voltage- dependent, alpha 2/delta subunit 1	CACNA2D1	4q12	F: AACTAAAAGACCAACACCA R: GACCCACATTCCCTACTAC	147	1.5	56		
Ca ²⁺ -dependent activator protein for secretion 2	CADPS2	4	F: TGCTCATTTTCATGTGCTTCC R: CGTGCATAACCGTAGAGCTG	335	1.5	58	Dierks et al. 2006	AJ542841
caldesmon 1	CALD1	4	F:GAATGACAGGCATCTCCACA R: TAAGCAGGAGCACAGCAAGA	244	1.5	58		
capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2	4	F: CTTTGTGATATTCGCCCAGTTC R: AGCATTAGACCTTGGCCTTG	252	1.5	58	Dierks et al. 2006	CX596422
chromobox homolog 3 (HP1 gamma homolog, <i>Drosophila</i>)	CBX3	4	F: AACCAAGAGGATTTGCCAGA R: CTGGACAAGAATGCCAAGTT	500	1.5	54		
coiled-coil domain containing 132	CCDC132	4	F: CAGCCTACTGACCCTCAAGC R: TGCAGCTTGTTGTTGTTTCA	1200	1.5	58		
cell division cycle 2-like 5	CDC2L5	4	F: AGCAACTAAGGCTGCTGAGG R: GTTCCACCACTTGAGGGAGA	168	1.5	53		

cystic fibrosis transmembrane conductance regulator	CFTR	4q22	F: CCATGGTTGGAAAGCTGATT R: GGGTTCTTCGAATGATTGTT	163	2.0	58	Shubitowski et al. 2001; Mariat et al. 2001*	AY008775
BAC end sequence	CH241-100K23_T7	4	F: CTGTTTCATCCTCGGGAGTAG R: TTTGGTTGATTTAAGTTTCAGG	496	1.5	57	Dierks et al. 2006	AJ543097
BAC end sequence	CH241-100O5_SP6	4	F: TCACCATTTGAGGGAGAGAG R: CCTTAGCAAACCTCAAAGC	377	1.5	58	Dierks et al. 2006	AJ543269
BAC end sequence	CH241-112H8_SP6	4	F: TCTTGGTTCCAAAAATCCACA R: TTATGGCAGCTCTTGCACTG	201	1.5	63		CR955466
coiled-coil-helix-coiled-coil-helix domain containing 3	CHCHD3	4	F: GGCCCAAATTCTCCAGTGT R: CTGTTTGGCCTGATTGACG	100	1.5	58		
chloride channel 1, skeletal muscle	CLCN1	4q26	F: GGTGGCCACGATGGACATCC R: ACTAGCCCAGGATTTCTGGGACTC	120	2.0	58	Mariat et al. 2001*	
cordon-bleu homolog (mouse)	COBL	4	F: TCAGAAACCCAACAGCCTTT R: CTTAGGGGGACCAGGCTTAA	120	1.5	54		
collagen, type I, alpha 2	COL1A2	4	F: GAAGAATGTTGATGGTGCTAGAAG R: ACCATGGGAAAGGATGAAAAC	205	3.0	58	Chowdhary et al. 2003	G62185
microsatellite	COR047	4	F: GAGACAAGCAGAAGCTCAGG R: CGGACTGTCTGAGGAACTG	249-253	2.0	55	Ruth et al. 1999	AF108364
microsatellite	COR057	4	F: GGAGGAGAGGAAGAGAGTGG R: ATCCAGGGCTCTCCATAGTC	227-243	2.0	55	Ruth et al. 1999	AF108374
microsatellite	COR089	4	F: CCTGCCATAAATTTGTTTCC R: TCCCTACCTCATCTCCACAC	272-290	2.0	58	Tallmadge et al. 1999b	AF154942
carboxypeptidase, vitellogenic-like	CPVL	4	F: TGACCAGAGTTACTACGGGAAG R: TAATTATTCATGATTTTCAGTTAACCAC	164	1.5	58	Dierks et al. 2006	DN511041
cAMP responsive element binding protein 5	CREB5	4	F: CCAGCTCACCCTCACAGAA R: CTGGAGAAAAGCACCAAAGC	278	1.5	54		
cytochrome P450, family 51, subfamily A, polypeptide 1	CYP51A1	4	F: ACCTAATCCGGTAGGTGACAC R: AGTTGCTAAGCCCATGCCAG	223	1.5	50		
DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	DDX56	4	F: CAACCTTCCTATCCCCCAATC R: CCCTACAGCAGCAACCTTTC	207	1.5	58		
dihydrolipoamide dehydrogenase	DLD	4	F: CCCACTGATGATAAAAACAC R: AGAATGAAAAACAAAGCACC	265	1.5	56		
DnaJ (Hsp40) homolog,	DNAJB6	4	F: CCTTTGGTTCACTGGGTCAT	750-800	1.5	55	Dierks et al.	

subfamily B, member 6			R: CTCTTCTTTGACCATTCTCGAC				2006	
DnaJ (Hsp40) homolog,	DNAJB9	4	F: TGATACCACCAATCAGCACAC	442	1.5	58	Dierks et al.	CX600182
subfamily B, member 9			R: GGCAAATTCAATCTTTTCTTGG				2006	
epidermal growth factor	EGFR	4p11-12	F: AAAGCACCCCTTCAGAAGAAC	246	1.5	58		
receptor			R: TAGCAGATCCAGACCATTCC					
engrailed homolog 2	EN2	4q27	F: GAACCCCAACAAAGAGGACA	147	2.0	58	Caetano et al.	AF134060
			R: TGAGACTCGTTGAGGCTGAG				1999; Lear et al. 2001*	
hypothetical protein	FLJ20323	4q13	F: TGTCTGCATGCACGTGTAAAT	191	1.5	55	Perrocheau et al. 2005*	AY817468
FLJ20323			R: TTTTCCCATTACAGGAAAAGTCA					
hypothetical protein	FLJ22374	4	F: TTGGGTCTCTGGCTTACACC	185	1.5	58	Dierks et al.	CR957559
FLJ22374			R: CTACCTGCTCCCTGGACATC				2006	
filamin C, gamma	FLNC	4	F: GCTTTACCTAACACACCGTTC	223	1.5	52		
			R: ACATGCATCCAACTAATCCTTC					
forkhead box P2	FOXP2	4	F: TTGACGGAGTAAAAGGGATTG	463	1.5	58	Dierks et al.	AJ885834
			R: TGAATGCTCAAAATGCAAGC				2006	
glycyl-tRNA synthetase	GARS	4	F: GGCAGAAATCGAGCACTTTG	99	1.5	58	Dierks et al.	CX594065
			R: TGGGCTTTTGCTGAATACAAG				2006	
glucokinase	GCK	4p14-p13	F: GTACCCCTGGCCCTTCTTAG	201	2.0	58	Shubitowski et al. 2001;	AY008787
			R: CTAGATCAGGCTGGGTGTCC				Chowdhary et al. 2003*	
GTPase, IMAP family	GIMAP4	4	F: GGACAAGAATGTTTGGTG	142	1.5	62		BI961493
member 4			R: CTCAAGCTGTGGGGTTATG					
GLI-Kruppel family	GLI3	4	F: GGAAGGGAAATGAGAAATGGAG	241	1.5	58		
member GLI3			R: TGCACAGTCCAACGTGATAG					
G protein-coupled	GPR37	4	F: CCTCCTCTTCTGTCTCTGCAA	199	1.5	55	Perrocheau et al. 2006	DX010498
receptor 37			R: GCAATGAGTTCCAACAGAAGC					
glutamate receptor,	GRM3	4	F: GGCCTGTTTCTTATTAACGAA	154	1.5	50		
metabotropic 3			R: GAACACCAACTTCACTCCTG					
HMG-box transcription	HBP1	4	F: GAGTTGGCCTTTCCTTGACC	407	1.5	58	Dierks et al.	CX596143
factor 1			R: TGCAAGTGTTGCACTGTCAC				2006	
HERPUD family member	HERPUD2	4	F: ATGATGGGCAAAATGCAAAC	580	1.5	58	Dierks et al.	CX597132
2			R: TTAATCCAGGCCTTTGAAGC				2006	
3-hydroxyisobutyrate	HIBADH	4q21.1-21.3	F: GTTAGGGCTTGACCCAAAACCTC	101	1.5	58	Dierks et al.	
dehydrogenase			R: CATCCATCACCCAGGTACAG				2006*	
microsatellite	HMS09	4	F: GCAACAGATATTAGCTCAGGGCC	107	2.0	58	Godard et al.	U89805

microsatellite	HMS19	4q21	R: TGCTGTTCTTTTGCTGTGAAGGG F: CTAACCAGCACAGAATGAATGGC R: TAAAAGAACAGTGGAGAGTAAAGTG	86	4.0	58	1997 Godard et al. 1997; Godard et al. 1998*	U89808
microsatellite	HMS56	4	F: CAACCCCAATACCACCTCTGCC R: CCGGGAGTGCAGTGGGAGAC	123-150	2.0	58	Chowdhary et al. 2003	
microsatellite	HTG01	4	F: TTTAATGATTCTTTACTCCAGATT R: TGCTAAGCAATGGAATGATGGGTG	200	2.0	52	Ellegren et al. 1992	AF169162
microsatellite	HTG07	4	F: CCTGAAGCAGAACATCCCTCCTTG R: ATAAAGTGTCTGGGCAGAGCTGCT	124	3.0	58	Marklund et al. 1994	AF169291
microsatellite	HTG09	4q21.3	F: TGTGGGAAGAGTGTCAATAGCTGT R: AGGCATCTGGTTTGCTGCAATTTC	130	2.0	58	Marklund et al. 1994; Godard et al. 1998*	AF169293
microsatellite	HTG22	4	F: TACTACATTTTCATCCTCCACAT R: GGAGAACTTCCCAGAGAGCA	150	2.0	58	Lindgren 2000	
insulin-like growth factor 2 mRNA binding protein 3	IGF2BP3	4q21.1- q21.3	F: ACCAGCGTGTCTTTCATTTTC R: AGAAATTCACACCAGGTTGC	198	1.5	58	Dierks et al. 2006*	AM072950
insulin-like growth factor binding protein 1	IGFBP1	4p12	F: GAGCAGCTCCTGGACAGTTT R: CCACTTTTGTATGTCGGAGA	123	3.0	58		
interleukin 6	IL6	4q14- q21.1	F: TTGAGGTAAGCCTACACTTTCC R: TGGGCACAGAACTTATGTTG	~200	1.5	61	Musilova et al. 2005*	
inhibitor of growth family, member 3	ING3	4	F: AAGAGGGACGAAGAACATCAAG R: TGACGAACTGGCATTCTGTG	158	1.5	58	Dierks et al. 2006	CD464595
inhibin, beta A	INHBA	4	F: GCTACCACGCCAACTACTG R: CAAGCGGTATTGGTTGATG	104	1.5	58		BI961669
integrin, beta 8	ITGB8	4	F: CATCCATGTGCTGTCTTTGAC R: ATCAAGAGCGAGATGAGACG	900	1.5	54		
kelch repeat and BTB domain containing 2	KBTBD2	4	F: ATGACAAGGGAATTCAGTGC R: GCCTAGATACGCTAACC GAAC	516	1.5	58	Dierks et al. 2006	CT008293
potassium voltage-gated channel, Shal-related subfamily, member 2	KCND2	4	F: TTGTCCTTCAAAATGACTCCTC R: TGGCTGTATGTGTGTGCAAG	159	1.5	58	Dierks et al. 2006	CT007157
KIAA0895 protein	KIAA0895	4	F: TTGGAGTAACTTTCCCTTGC R: TTTGAAAAACAGTCTGCGTTC	504	1.5	57	Dierks et al. 2006	AJ543064
laminin, beta 1	LAMB1	4p13-12	F: GCACCCACAGCAGTTACAG	420	1.5	58	Dierks et al.	DN872515

leptin (obesity homolog, mouse)	LEP	4	R: ATCTGGGCCTTCTCTGCTTC F: TGGGAAGGACAGGAAGACAG	199	2.0	58	2006 Caetano et al. 1999	AF097583
microsatellite	LEX033	4	R: AGAGCAAGAGCTCAGCAAGG F: TTTAATCAAAGGATTCAAGTTG	182-197	3.0	55	Coogle et al. 1996	AF075635
microsatellite	LEX050	4	R: TTTCTCTTCAGGTGTCCTC F: ATAGTCTGGGGTTAGGTAAGG	112-126	2.0	58	Coogle et al. 1997	AF075652
microsatellite	LEX061	4	R: TCTAGCCCAATGTAAATGC F: TCAGTGTTCCCATCTGTA	148-166	3.0	55	Coogle & Bailey 1997	AF075661
limb region 1 homolog (mouse)	LMBR1 (<i>C7orf2</i>)	4q27	R: TGAAATCACACCTTTACTTTA F: TTGACCTGCTTGAGACTTTG	141	1.5	55	Perrocheau et al. 2005*	AY817456
LSM8 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	LSM8	4q22	R: TGAAAAGCTCTTCTCGCACAG F: TCCACAAAGAGACTCACAACAG	532	1.5	58	Dierks et al. 2006*	AJ583991
membrane associated guanylate kinase, WW and PDZ domain containing 2	MAGI2	4p15-13	R: AGCCATGATTTTAATTTGGTTC F: TGAATACGCAACCTACACCAAC	147	1.5	54		
MyoD family inhibitor domain containing	MDFIC	4	R: CTGATGATGACAAAGCCGAAG F: TATATGGCCATCACGACTGC	403	1.5	58	Dierks et al. 2006	CX594432
mesenchyme homeobox 2	MEOX2	4	R: ACAAAGCTTGCAATTTTGACC F: CAGGCTCTGCAAACCAACTG	151	1.5	53		
mesoderm specific transcript homolog (mouse)	MEST	4	R: AGCCCAAGCTGGAAGAGTT F: ACTTCAGTGCTTAGAAGCGTGTCC	169	3.0	58	Chowdhary et al. 2003	
myeloid/lymphoid or mixed-lineage leukemia 3	MLL3	4q27	R: GTACAGGAATTGCTAAGCTACATGAGG F: TTCACATAGTACAGCCCAGG	164	1.5	54		
membrane protein, palmitoylated 6	MPP6	4	R: TGACAGGAACATACATGGAAAG F: ACGATTACCTCCATCAAGC	1000	1.5	51		
myotrophin	MTPN	4	R: CTCCCACATGAAGCAGACCT F: GCAATTGCAGTGTTTTTGCAT	214	2.0	53	Chowdhary et al. 2003	
myosin IG	MYO1G	4	R: TTCTGATGTACATGAACCAGGAT F: CTACGTCCGCTGCATCAAG	158	1.5	54		
N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	NAPE-PLD	4	R: TGAGCAGGAATCGAGAGTAGG F: TGGATAAAGACCCACCTTGC	508	1.5	58	Dierks et al. 2006	CX605596
			R: TTCCATAGGAAGTCACAAATCC					

NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	NDUFA4	4	F: CAGCAAACCTGAAGAAAGAAGGTC R: CGTGCATTTAGAGGGGGAAT	135	1.5	54		
neurogenic differentiation 6	NEUROD6	4	F: GGGCATGGGACTCTTGATAA R: GCCAATTACTCAGCCCACAA	438	1.5	54		
nucleotide-binding oligomerization domain containing 1	NOD1	4	F: TGTTGTCCAAAGCCAAACAG R: ACGCCGTAGTCGTTGAGATT	376	1.5	54		
nitric oxide synthase 3	NOS3	4q26-27	F: CCATCAGGAGATGGTCAACTATG R: TGGCCACTTCCTTAAAGGTCT	240	1.5	58	Perrocheau et al. 2006*	
neuropeptide Y	NPY	4q21.1-21.3	F: AAGCGACTGGGGTTGTCC R: GTGTCGCAGCGCTGAGTAGT	150	1.5	58		
microsatellite	NVHEQ029	4p14-16	F: GAGATTTTGCCCCAAAGGTTA R: CTCTTCTTTCTTCCCCAGGTCT	91-113	2.0	58	Røed et al. 1998	AF056393
neurexophilin 1	NXPH1	4	F: CTCGGGATGAAGGTGAACAT R: GCTGACTGGGCAGAAATTACA	187	1.5	54		
poly (ADP-ribose) polymerase family, member 12	PARP12	4	F: ACTCCTCCATCACTGTATCTC R: GCCCAGAAACCATTAGGAATTG	151	1.5	56		
piccolo (presynaptic cytomatrix protein)	PCLO	4	F: GTGGATACAAGCGTCCAAACT R: TGAAGTCTATGCTGGAGACT	155	1.5	50		
phosphoglycerate mutase 2	PGAM2	4p12-13	F: CAAGGACGCAAAGATGGAAT R: GTGGTGGGATGTCAAAGGAG	236	1.5	55		
PHD finger protein 14	PHF14	4	F: AGAACCCGAGGACGAAAAC R: GCAAGTTGCACATTCCGTTC	260	1.5	58	Dierks et al. 2006	CX594630
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	PLEKHA8 (<i>FAPP2</i>)	4q21.3-q22	F: CCAACAAGGCAAAGTTTACCAC R: TCAGCCACAAGAGGGCTTC	105	1.5	55	Perrocheau et al. 2006*	DX010473
polymerase (DNA directed), mu	POLM	4	F: TTCTGCAAGGCAAGGAGGGGC R: TCGCACCCACCCCTGGAGTT	122	1.5	60		
paraoxonase 1	PON1	4q13-14	F: GGTGAACCATCCAGATTTTAAG R: GGCAGAAGTTTGTGTCTGATG	102	1.5	55		
paraoxonase 2	PON2	4q13-14	F: ATGGTATCAGCACTTTCATAGACA R: AAGCTCATGTTTGATTGTTTTAGA	678	1.5	55		
protein phosphatase 1,	PPP1R3A	4	F: TCCAGGTGCGAGAAGAGTTT	267	1.5	55		

regulatory (inhibitor) subunit 3A			R: CGAATAACGCCCTTCACACT					
protein kinase, AMP- activated, gamma 2 non- catalytic subunit	PRKAG2	4q26- q27	F: ATGACAACATGAGCAGAAGAG R: CCACCCCCAACCTATTAAATC	460	1.5	60	Dranchak et al. 2006*	
proteasome (prosome, macropain) 26S subunit, ATPase, 2	PSMC2	4p15-13	F: TTCAGAGGACCCGAAGTACA R: ATCTTAGGAGGCAGCGGAAT	630	1.5	55		
protein tyrosine phosphatase, non-receptor type 12	PTPN12	4	F: TCTGCATGGTCTAAATCTTTGTGTAC R: AACACACACAAGCTAAGAGAATTCAAC	271	1.5	58	Chowdhary et al. 2003	
scinderin	SCIN	4	F: TGTCTGAAACTGCCACAAA R: GTAAAGCCGAGGTGGATGGT	500	1.5	54		
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEMA3C	4p16	F: ACTCCTTCTTGAACGTAAGAGCC R: CCTCACACGGAGTGAACATTCA	249	2.0	58	Chowdhary et al. 2003	G62198
microsatellite	SGCV23	4q27	F: GGCTTAAGATATGGGTGAGTAAGG R: GCCCACCTCTTACTTTTCTCAA	218	3.0	58	Godard et al. 1997*	U90601
src kinase associated phosphoprotein 2	SKAP2 (SCAP2)	4	F: TTTGCCAACTGATGACCAAC R: GCAAATAATCAAGCAAAATGC	474	1.5	58	Dierks et al. 2006	CD528759
solute carrier family 25, member 13	SLC25A13	4	F: TTTTAGGGGTCAGCAGCTTG R: TCTCCCTTTCCCCATCTTTC	525	1.5	58	Dierks et al. 2006	AJ543018
sorting nexin 13	SNX13	4q14	F: TCCATTATTATCCTGGTGGAAG R: GTGATCCCAAACACAACATTC	365	1.5	61	Dierks et al. 2006*	AM072955
sclerostin domain containing 1	SOSTDC1	4	F: CTGGATTGGAGGAGGCTATG R: TCTCTGTGATGCTGGACTGG	243	1.5	59		
sorcin	SRI	4	F: AGGTAAAGTCCCCAGGCTGT R: GGAAATTCACAACACCTTGCT	800	1.5	55		
SFRS protein kinase 2	SRPK2	4	F: ACACGGCATTAAAGACCAACC R: GTGCTCAGAAACCACACAG	526	1.5	58	Dierks et al. 2006	AJ885367
six transmembrane epithelial antigen of the prostate 1	STEAP1,2	4	F: AAAAGTGATTTGCAGCCTGG R: AGGATAGGCAGTCAAGCTAC	115	1.5	58		
T-box 20	TBX20	4	F: TGTGGAGAAGTCGTCCTGTG R: CCCAGCTCATGGAATTTGTC	215	1.5	54		
T cell receptor gamma	TRG@	4p15-	F: AGCTCCATAAGGCTGGAACA	176	2.0	58	Caetano et al.	AF134235,

locus	(TCRG)	p14	R: TGACTTTCCAGTCACGGTCA				1999; Lear et al. 2001*	L38392
testis derived transcript	TES	4	F: AAGTGCCACGAATTGTCTCC R: TTTTCGGCCAATTTGTTCTC	200	1.5	58	Dierks et al. 2006	CX597165
transcription factor EC	TFEC	4	F: TCCAAAGAGAGCAGTAGGAGAAG R: CACCGACATAGAATTGCTTCC	106	1.5	55	Perrocheau et al. 2006	DX010594
microsatellite	TKY210	4	F: CGGAAATGACCAGTTTGCTT R: AGGTTGCCACGGGATTAAGT	240-280	1.5	53	Swinburne et al. 2000	
microsatellite	TKY223	4	F: GCAAGAAATCAACGCAAAAG R: CCGATTCAAGTAGTTCAGGGATG	170	1.5	53		
microsatellite	TKY300	4	F: CAGTTGTTATCATGAGGGTG R: AGTGACAAGAGCTCAAAGTG	150	1.5	50	Tozaki et al. 2000c	AB034609
microsatellite	TKY337	4	F: AGCAGGGTTTAATTACCGAG R: TAGATGCTAATGCAGCACAG	200	1.5	53	Tozaki et al. 2001	AB044838
microsatellite	TKY354	4	F: AGTGAGGTCTTCCTTGACTG R: TGTTAGATGGTGGTAAGTGC	156-188	1.5	58	Tozaki et al. 2001	AB044854
microsatellite	TKY363	4	F: CTCAGACTAAGCGGTACTAG R: ATGGATACATTCTGGGGAAC	184-192	1.5	52	Tozaki et al. 2001	AB044863
microsatellite	TKY375	4	F: ACCAAGAGGAAAAGCACTTG R: CTATAAGGAAGGCGGGAAAAG	170	1.5	50	Tozaki et al. 2001	AB044875
microsatellite	TKY430	4	F: TTTTGGTTAGGCCTCTGTAC R: CCCACTCTCCTATAAACAGT	156	2.0	58		AB103648
microsatellite	TKY552	4	F: CTAGAGGTGCCTTCCCAGAC R: ACCACCAAGACGAAAGGTGA	148-156	1.5	58	Tozaki et al. 2004	AB103770
microsatellite	TKY586	4	F: GCAGATTTCTCCCCACTCC R: TTATGTGGGGCTGAGAAAGG	100-105	1.5	53	Tozaki et al. 2004	AB103804
microsatellite	TKY639	4	F: TGCTAAGAACTTGCAGTAGA R: TGGTATATCACATAGCCAGT	208	1.5	56		AB103857
microsatellite	TKY661	4	F: CGAGGTCTTGGAACCTATCC R: TTCACTTCAGACAACCTATTGAAGA	150	1.5	53	Tozaki et al. 2004	AB103879
microsatellite	TKY720	4	F: CAGGAGTATCCAGAATTGCAGA R: CCAGCTGTGTGTAACGCAAT	220	1.5	53	Tozaki et al. 2004	AB103938
microsatellite	TKY772	4	F: ATCAATAGAGAACGAGCAGC R: TGAAGCAGTGACAGAATGCC	142	2.0	58		AB103990
microsatellite	TKY797	4	F: CACCCCAATCGATGTCTGAAG R: CCATGCTGTGGTGGCATC	148	2.0	58	Tozaki et al. 2004	AB104015
microsatellite	TKY810	4	F: CCACCTACGATGGGTTCAT	259	2.0	58	Tozaki et al.	AB104028

microsatellite	TKY818	4	R: CCAAGAGCACTGATACAGAG F: GCAACAGATGTTAGCTCAGG R: TATGGTGCATCATTTTGAGACT	99	2.0	58	2004	AB104036
microsatellite	TKY820	4	F: ATCGCAGGTAAGGTACAGAC R: GCTGACTCTCCCCAAAGAAT	167	2.0	58		AB104038
microsatellite	TKY830	4	F: ATTGGAATGTCAGGTGTAGC R: AGGCAGGCCAGTTTGATTG	143	2.0	58	Tozaki et al. 2004	AB104048
microsatellite	TKY833	4	F: TTTTGGTTCGAGTCCTTGGA R: GGGAAGTGGTTGTAGACAAG	149	1.5	62	Tozaki et al. 2004	AB104051
microsatellite	TKY922	4	F: CCACTTTGTTGAACCCGTTT R: TGCAGACTACACAAGCTTTTC	120	2.0	58		AB104140
microsatellite	TKY935	4	F: TCCTACAATACTCTTCTCGC R: AGTCGGACTTAGTGTTTGTC	201	2.0	58		AB104153
microsatellite	TKY942	4	F: GAAGGGACCTTGTCAGAAG R: TGACTGGAGCAGTGTGAAG	212	2.0	58		AB104160
microsatellite	TKY953	4	F: CCTAGGATGGTGAATGTAAC R: GGGCCAGACAATCAAGTTC	209	2.0	58		AB104171
microsatellite	TKY958	4	F: ATCTCAACTCCAAGTCTCAG R: TTCCTGAGAAACAACAGCTC	222	2.0	58		AB104176
microsatellite	TKY977	4	F: ATCTACCCAGTCTCCTATAAG R: ATTTCTTGTCTCCACTTTGAAG	119	2.0	58		AB104195
microsatellite	TKY1030	4	F: AAGTAGGGAACCGTAAAGAG R: TGAGTCCTCAGAAAACTAAGC	93	2.0	58		AB104248
microsatellite	TKY1044	4	F: GTATGCCTCTGTGATGCTC R: ACAGCTTCAAGTCCTTGAAAC	162	2.0	58		AB104262
microsatellite	TKY1059	4	F: TGGGGGTAATAAGTACAGTG R: AGCAACAGATGTTAGCTCAG	87	2.0	58		AB104277
microsatellite	TKY1063	4	F: TGAGAATACCACAGTGCAAC R: ACAACAGATGTTAGCTCAGG	232	2.0	58		AB104281
microsatellite	TKY1079	4	F: TTCTCATACCTGTTTCAGGTG R: TAGAATGGAGAAGGGGAATC	166	2.0	58		AB104297
microsatellite	TKY1089	4	F: CTTCTGTTGATTTGGGTTGAG R: GGGACTTTACTGGACAGTG	243	2.0	58		AB104307
microsatellite	TKY1099	4	F: TGCAAAATGGAGGAAGACTG R: AAATCTGGGTACTGAGGTTG	193	2.0	58		AB104317
microsatellite	TKY1110	4	F: AAGTTCATGTTGGACACTGC R: AGCATGAACTGAAGTCCATC	162	1.5	58		AB104328

microsatellite	TKY1717	4	F: CAGAATCCTATCGTGACTTC R: AATGGATGGAACATATGAGC	281	1.5	58	Tozaki et al. 2007	AB215660
microsatellite	TKY2101	4	F: AGTCATGGAATTTTCCGTGC R: AAGGGGTGCTGTAAATAATG	176	1.5	58	Tozaki et al. 2007	AB216044
microsatellite	TKY2805	4	F: GCGCCAACTGTAGTTTGAAT R: CGAAAATGTTTCTGGCAAAT	601	1.5	60	Tozaki et al. 2007	AB216748
microsatellite	TKY2982	4	F: CCGATGTTAGAATCAACAGGA R: TTGGGTTGTGATTTCTGTCA	278	1.5	58	Tozaki et al. 2007	AB216925
microsatellite	TKY3083	4	F: TGGCAGTTTTTTGCTGATAC R: GGGCTAGACAAATGCTGAA	99	1.5	58	Tozaki et al. 2007	AB217026
T cell receptor gamma variable 10	TRGV10	4	F: TCACTGCTGGAAGCATTAC R: CCACCATCCAGCACAGTAG	450	1.5	58	Dierks et al. 2006	CD535783
microsatellite	UMNe054	4	F: AACTCACTTCTTCCTGCTCG R: CCAAGGCTCTTTGCCAAGAC	107-127	2.0	58	Roberts et al. 2000	AF191691
microsatellite	UMNe063	4	F: GGATTTTCTTCTTTTGAATGGC R: TTTACAATAGCCAAGATGCGG	128-142	2.0	58	Roberts et al. 2000	AF191696
microsatellite	UMNe101	4	F: CATTTTAATCAACATTTTCCATCTG R: GCAATGCAGTGAGATGATGC	100	1.5	60	Mickelson et al. 2003	AF536247
microsatellite	UMNe104	4	F: TGATTTTTGTTCAGCCTCTATGC R: CCTAGAAAGGTGGGAAATAAATTG	156	1.5	60	Wagner et al. 2004a	AY391291
microsatellite	UMNe110	4	F: TCTTTCCTACCCTCCATGACC R: GATCTAGTACAACACTCCGTGTG	141	1.5	58	Wagner et al. 2004a	AY391293
microsatellite	UMNe112	4	F: TGCCCAAATATTGAGCAAGG R: TCTCTCCTCCCCTTTTGTG	155	1.5	55	Wagner et al. 2004a	AY391294
microsatellite	UMNe138	4	F: AGCTGGAAAGGACCACTTT R: AACCAACAGGGGGTTTCC	148	1.5	58	Mickelson et al. 2003	AF536259
microsatellite	UMNe172	4	F: CCAGACACAGACCTAGCACC R: CCAGCAAAGGAGGAGGAAG	190	2.0	58	Wagner et al. 2004a	AY391310
microsatellite	UMNe174	4	F: TCTGCATCCTCATGTTCAATG R: TCGAAAATGGCAAGATTTCC	184	2.0	62	Wagner et al. 2004c	AY735237
microsatellite	UMNe192	4	F: TAAGCCTGTCCATCCCTGTC R: TCAAAGAGCATCTCACGGG	164	2.0	58	Mickelson et al. 2003	AF536280
microsatellite	UMNe199	4	F: TCCAGCAAATGGTAAGGTAGTG R: GATCTCTCTCCACCCTATACCA	124	2.0	58	Mickelson et al. 2003	AF536284
microsatellite	UMNe224	4	F: ATGCTTAGCAAGGCCGTG R: TCCAAAGATAGCGGCAGTG	152	2.0	58	Mickelson et al. 2003	AF536301
microsatellite	UMNe249	4	F: CAAGAGAAGGAAGCTGGGG	124	1.5	58	Mickelson et	AF536317

microsatellite	UMNe256	4	R: AAAAATGTGAAATGTGCCTTCC F: GGCCACACGACTACTTTCAC	142	2.0	58	al. 2003 Wagner et al. 2004a	AY391329
microsatellite	UMNe377	4	R: ACTTCTGGAAGACAGCTGGC F: CAGACATGGCACCCTTG	240	1.5	58-62	Wagner et al. 2004b	AY464468
microsatellite	UMNe404	4	R: AGGATATTGTGTTTCCCTCAGG F: TTGGAACCTTTTAGCAAAGAACC	166	2.0	55	Wagner et al. 2004c	AY735245
microsatellite	UMNe544	4	R: GATCCATTCCCACATATGGC F: GCCAGGTGTCCCACGTAC	189	1.5	58	Mickelson et al. 2004	AY731411
microsatellite	UMNe551	4	R: CTGGACCAGCCTCACTCTTC F: GATCTAGTGAGGGTTGGAGGG	215	1.5	62	Wagner et al. 2004c	AY735266
microsatellite	UMNe561	4	R: AACCCAGAAAGACACGTTCTG F: ATGCCAAAGCAGAAAAAGATG	162	1.5	58		
microsatellite	UMNe587	4	R: TCTTCACCTCAGCCCGTC F: TTGGTCAGAATAGGTAGTTATG	254	1.5	58	Wagner et al. 2004	AY735285
microsatellite	VHL057	4	R: AGATGGATATGTACATGGATAC F: GGCTCCTAAACATCCAGCAG	105	1.5	62	van Haeringen et al. 1998	
microsatellite	VHL088	4	R: GTGAGGCTCCAAGTACCTCT F: CCACCTTCACAATTATCAGTGAC	120	1.5	62	van Haeringen et al. 1998	
vacuolar protein sorting 41 homolog (S. cerevisiae)	VPS41 (<i>CH241-103G20</i>)	4	R: TGGTCCTCATCATCTAGTTCCT F: CCCACATTTACCTCATCAGC	391	1.5	58	Dierks et al. 2006	AJ618811
Wiskott-Aldrich syndrome-like	WASL	4	R: AGTTTTGAGTTCCAGTTTCCAG F: ACCTGCAAGATGTGGCTTG	302	1.5	55		
zinc finger, C3HC-type containing 1	ZC3HC1	4	R: CCAGACTCATCCACACCAGA F: CATGCAGCTCTCCCTGATAA	197	1.5	58		
			R: GGCTCCGAGTCATCATCCT					

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	5CA001	5	F: GCTGATGCAGTGC GTTGTAA R: CCCTCCATAGACAGCATTGG	215-217	1.5	58	Penedo et al. 2005	
sequence tagged site	5STS01	5	F: TTTCCAAGTGGTGGTAGGC R: CACGGTCTTGTTCTCCACT	107				
sequence tagged site	5STS02	5	F: GCCCTAAGACAGCAGATTGG R: GTGAGGAGGGAGGTTGACT	1161	1.5	60		CX595941
sequence tagged site	5STS03 (DIA1)	5q17	F: TGTCGGCCAGCACATCTACC R: CCTCCAGCGGGAACTTGGG	180	1.5	65	Mariat et al. 2001*	
acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ACADM	5	F: GCCTGGGAAC TTGTTTAATG R: CCCTGTACATCCATAAGCCAAT	719	1.5	58		NM_000016
adenosine A3 receptor	ADORA3	5	F: CCAATTCCGTTCTGTTGTGA R: GCCAGGACAAAGCAAACAAG	241	2.0	58		AY011243
amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	AGL	5	F: CGATTAGGCCCAACTTTACAG R: TGATTATCAGCACCAACACG	803	1.5	58		NM_000646
microsatellite	AHT024	5p16	F: TCCACTAATATCCCTCCACCC R: CTGTACCGCATGTGCAGC	197-199	2.0	65	Swinburne et al. 2000*	AJ272106
microsatellite	AHT050	5	F: GTTGGCTGGTTTTTGCATTT R: CGTACACACATTTTCACCCA	299-305	1.5	58		AJ507667
microsatellite	AHT066	5	F: ATCCATTTTCACCAAGTGTGG R: GTTTGTCTCCAAGCTCAGGC	277-281	1.5	58	Swinburne et al. 2003	AJ507683
microsatellite	AHT068	5	F: GGGAGGAAACCCAGTCAATT R: GGTCCCTCATCACTTCCACA	296-308	1.5	58		AJ507685
microsatellite	AHT107	5	F: ATCTAACCAGAGCGCAACGT R: CCCGACACAGAAGATGGG	133-178	1.5	58	Swinburne et al. 2003	AJ507724
adenosine monophosphate deaminase 1	AMPD1	5q12-q13	F: CATCATGGTGCTCAACAACC R: TTTTAAATTCAGGCCATGAGAGA	900	1.5	58		
anterior pharynx defective 1 homolog A (C. elegans)	APH1A	5	F: CTGACTCCTCTAGTGGAATG R: CTCGTGTCTGGGCTCATATCT	209	2.0	58		BI961757
apolipoprotein A-II	APOA2	5p15-p14	F: GAGCTTTGGTTCGGAGACAG R: TGTCAGCTGCTCCTTTGACTT	586	1.5	56		
microsatellite	ASB10	5	F: GTTGTCTAGGTGCAGAATCTGG R: GTTATGTCTCCCCTTTCTCTACC	146	1.5	58	Breen et al. 1997	X95325
activating transcription factor	ATF3	5	F: TCCTCATCGAATCCTCCTTTT	203	1.5	55		DX010613

3			R: AGCCTTAAATCCTGGAGTGGA				et al. 2006	
ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide	ATP1A2	5p13-p12	F: CTGCCATCTCCTTGGCCTAT	352	1.5	60		
ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	ATP1B1	5p18	R: AGGTGAAGAAGCCACCCAGT					
breast carcinoma amplified sequence 2	BCAS2	5	F: CATGCTGGTGCTGTGTCTTT	300	1.5	58		
B-cell CLL/lymphoma 9	BCL9	5p12	R: TCCATTGTTTTAACCTGACTGAA					
brix domain containing 5	BXDC5	5q14-q15	F: CTGGGTATCCCTGGTCAGTAA	105	1.5	55	Perrocheau et al. 2006	DX010437
chromosome 1 open reading frame 43	C1orf43	5	R: TCTTTGTTTGCTTCTCCGTGT					
complement component 4 binding protein, alpha	C4BPA	5	F: GATCAACATGCCCCATTCTCT	193	1.5	55	Perrocheau et al. 2006*	DX010439
complement component 4 binding protein, beta	C4BPB	5	R: GTCTGGGATTTTTGGCACAT					
calcylin binding protein	CACYBP (SIP)	5p17-p16	F: CTCAATTTATTGGAAGGCAG	346	1.5	58		NM_025065
calsequestrin 1	CASQ1	5p13-p12	R: GAATCAAAGGTCCCTTTCTG					
calsequestrin 2	CASQ2	5	F: ATCCCTGTTCTTAATGGGC	123	1.5	58		NM_138740
CD2 molecule	CD2	5q11	R: CTGTCTCATAGCCATCCAGC					
cell division cycle 7 homolog (S. cerevisiae)	CDC7	5	F: GTATCAGAGGCCAACAAAAGAG	126	1.5	58		CX597654
cadherin, EGF LAG seven-pass G-type receptor 2 (Drosophila)	CELSR2	5	R: CACCTGAAATCTTCCTGACAA					
BAC end sequence	CH241-100A3_SP6	5	F: CCTGTGCTGGTGAATGGTGAAT	118	2.0	58		BI961786
BAC end sequence	CH241-101I11_T7	5	R: CTAGGCACTGGCTCCAATTGCT					
BAC end sequence	CH241-101P7_T7	5	F: GGGTGGAAATCAAGAGAGAAGC	196	1.5	55	Perrocheau et al. 2006*	DX010655
chloride channel, calcium	CLCA1	5q15	R: CTCCAGCAGGAAATGGAGAAT					
			F: CTGCTTTTCCTGATGGTGCTA	198	1.5	55	Perrocheau et al. 2006*	DX010446
			R: CTGTCTTTGTGAGGCCTTGTC					
			F: CCTTGAAGATGAATGAGGTTGA	111	1.5	56		
			R: GGTGCTCTTTCACAACTCCA					
			F: TCGTAACTCTGTCTCCTGAC	378	3.0	58	Lindgren et al. 2001*	X69884
			R: TCCCGAGACACTGGGCAA					
			F: TCAGAAATTTACTCCTTTATCC	60	1.5	58		
			R: TTGCCAAGTATTATCCTACTA					
			F: GTCGTCTTCCGCAACGAGAG	844	1.5	60		CK834787
			R: CAGCCCAGCATGTAGTAGAA					
			F: GACAGGAAGCCCTGAGAAAAC	500	1.5	60		AJ542693
			R: ACACCCAGTGTGGATGCAAG					
			F: TAAGATGAGGGAGAGCGAGGAG	743	1.5	62		AJ576757
			R: GCCAGGCACGAGAAATACAG					
			F: GTGGCTTTTCATCACTTTTATAGC	555	1.5	60		AJ577078, AC114496
			R: CTTAATTGTTCCGTCCTGTCC					
			F: CGAATTGAGGAGACCCAGACTA	240	1.5	64		AM114457

activated, family member 1			R: ATACTTCCTTCGGCAGCACAATC					
coatomer protein complex,	COPA	5	F: AGATTTATCCTTTCCCTCCCCAC	124	2.0	58		BI961783
subunit alpha			R: CCAAGGAAAATAGGGAATGGCTA					
microsatellite	COR023	5	F: CGTTTAGCACCTCTCATGAAC	269-275	2.0	58	Murphie et al. 1999	AF101392
			R: TCTTTGCAAAAATAGGGCTTG					
cathepsin K	CTSK	5	F: CAGAGATTGCCATTCCGTTT	191	2.0	55		XM_041899
			R: ATAGAATCAGCCCCAGGACA					
cysteine-rich, angiogenic	CYR61	5	F: GCTAGACAGCTACAGCCTTCC	182	1.5	58		DN508934
inducer, 61			R: CCCTCCCCAAAAGCTACAT					
death effector domain	DEDD	5	F: CACAGACTCCCTCAAGCAG	113	2.0	58		BI961869
containing			R: GCAGCATCAAGTTCCTCAG					
DEP domain containing 1	DEPDC1	5q16	F: CTAAGTGTGTTTGGCTTACCTG	378	1.5	56		
			R: CACCCCCCGAAAAAGTCATC					
endothelial differentiation,	EDG1	5	F: GAAACTCCATAACGGGAGCA	223	2.0	58		AY011735
sphingolipid G-protein-			R: CAGAATGACGATGGAGAGCA					
coupled receptor, 1								
coagulation factor V	F5	5	F: AGATTTTGTTCATTCCCCTAACC	201	1.5	56		
			R: CTGCTCTACGCTGAAGAAAC					
Fas apoptotic inhibitory	FAIM3	5	F: GAAGTCAAGCTGGAGGGAAC	205	1.5	60		
molecule 3			R: CCACTAGGAACAGATTCTGTC					
Fas ligand	FASLG	5	F: AGGTGCGGATGTAAGACAG	302	1.5	56		
			R: TCACTTCTAAGCAAGACTCAAC					
feline leukemia virus subgroup	FLVCR	5	F: CTGATTTCTCTGAAACCTG	61	1.5	56		
C cellular receptor			R: CAAATTCATTACCCATTAGAAC					
fibromodulin	FMOD	5	F: ACTTCCCCACAGCCATGTACT	200	1.5	60		
			R: GAAAACCTTCCTGCCACCTTA					
far upstream element binding	FUBP1	5	F: TGTGTAGAAATGAAAATTGGTTTG	159	1.5	55	Perrocheau et al. 2006	DX010486
protein 1			R: TGTAAGACACAAAACAGGCATT					
glucosidase, beta; acid	GBA	5	F: TGTCTGCAATGCCACGTACT	201	2.0	58	Chowdhary et al. 2003	AF134220
			R: GCACAATTCAGTTCAGCAG					
guanylate binding protein 1,	GBP1	5q14-q15	F: ATCCGAAAGTTCTTCCCAAAG	186	1.5	55	Perrocheau et al. 2006	DX010492
interferon-inducible			R: CTTGATGCCTCCTGAGAGAGTT					
guanylate binding protein 2,	GBP2	5	F: TGTTCTTATTTTCCCCATGCC	150	1.5	54		
interferon-inducible			R: AGTGGAGAGGTTGAAATAGAGG					
ganglioside induced	GDAP2	5	F: AAAGTATGACTTACTCATTTCC	118	1.5	56		
differentiation associated			R: TCCTCCTAAACTATCTAAATCC					
protein 2								

gap junction protein, alpha 5	GJA5	5	F: AGGTCTGGCTCACAGTCCTC R: GACGGTGTGGAGACGAAGAT	199	2.0	58	Chowdhary et al. 2003	AY008788
guanine nucleotide binding protein, alpha inhibiting activity polypeptide 3	GNAI3	5q13	F: CAGTGTGGAGTGTGAGACCA R: ACAGTTGCTCCAATTCCAATG	182	1.5	55	Perrocheau et al. 2006	DX010495
glutathione S-transferase M3 (brain)	GSTM3	5	F: AAGATCACCCAGAGCAATGC R: TTGTCAGTTGCATGCGGAAA	226	1.5	54		NM_000849
general transcription factor IIB	GTF2B	5	F: AAAGCTTTAGAAACCAGTGTGG R: CCACAGCTTTACGGGCTATA	124	1.5	58		NM_001514
hippocampus abundant transcript 1	HIAT1	5	F: GCACTTGGAAGTATGCAGA R: ACAATGGGAACACCGAGGTA	480	1.5	58		CK951802
hemicentin 1	HMCN1	5	F: ATGACCTGGAATGTGCCTTG R: CTTAAGGCAAAAGGAACAGTCTG	181	1.5	58		NM_031935
microsatellite	HMS05	5	F: TAGTGTATCCGTCAGAGTTCAAAG R: GCAAGGAAGTCAGACTCCTGGA	102-108	2.0	58	Guérin et al. 1994	X74634
microsatellite	HTG15	5	F: TCTTGATGGCAGAGCCAGGATTTG R: AATGTCACCATGCGGCACATGACT	130-146	3.0	58	Marklund et al. 1994	AF169299
interleukin 10	IL10 (CSIF)	5	F: AGCATCCTAGGGAACGAA R: TTCACAGAGAAGCTCAGTAAAT	202	3.0	58	Lindgren et al. 2001	U38200
integrator complex subunit 7	INTS7	5	F: GATCTGGCAAACCTTGGTGAA R: AAATGCTTCTCACTTTGTTGAGTA	995	1.5	58		NM_015434
influenza virus NS1A binding protein	IVNS1ABP	5	F: TTCTTCATGGGCGAAACAGC R: GGAGACATGGGCTTTTCTATT	112	1.5	58		NM_006469
jumping translocation breakpoint	JTB	5	F: TCTGTGGTGGCAGAAGAGTG R: GAGCTGCATGTGATTTTCTCC	888	1.5	60		CX602145
KIAA0907	KIAA0907	5	F: TTGGCTTGGTGGCTTATG R: CGGCATCCCTAACTTCTG	288	2.0	58		
keratinocyte associated protein 2	KRTCAP2	5	F: CTCCTTTGCCTCCTGTTGG R: GTTGCTGGTACAGAGTCGAG	362	3.0	58		BI961691
laminin, gamma 1	LAMC1	5	F: GCTCCATGGTAGGCACTATGA R: TCCGACAGTTCGGTATCATTC	216	2.0	58	Chowdhary et al. 2003	AF134225
LAG1 homolog, ceramide synthase 2 (S. cerevisiae)	LASS2	5	F: ATCACCCGACTGGTCATCCT R: TAGAGCTCCAGTGGGTACACC	194	1.5	58		NM_181746
leptin receptor	LEPR	5q17	F: CCGTTGTTCTGTCCTGATCTT R: AATGATAGGCAGTCCGAAGG	159	3.0	58		
microsatellite	LEX004	5	F: AATAGCAAATCTCCCACTTCA R: GTCCTCACAACTCATCATAA	275-293	2.0	50	Coogle et al. 1996	AF075608

microsatellite	LEX014	5q16-q17	F: AACCACCTCTTTTCGTCAACCA R: GCCCCTATCCCTACGAAGAA	197	3.0	58	Coogle et al. 1996; Lindgren et al. 2001*	AF075616
microsatellite	LEX034	5	F: GCGGAGGTAAGAAGTGGTAG R: GGCCTAAGATGAGGGTGAA	245-257	3.0	58	Coogle et al. 1997	AF075636
microsatellite	LEX069	5	F: TTTCTTTTTTCCCACTTAAAGC R: TGGGACTTAGCAGTATGAAAC				Coogle et al. 1999	
latrophilin 2	LPHN2	5	F: GTGAAAAGCTCTTGGTTGCAC R: TGGCATAACTGGCTTCAAAGA	202	1.5	55	Perrocheau et al. 2006	DX010517
leucine rich repeat containing 39	LRRC39	5	F: GAATGGCAACTTCATAGAACTGGT R: CCAAGCTGGCACAGTGACTT	1096	1.5	58		NM_144620
mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2	5	F: GAGGAAGAGGCAGAGGTTAG R: GAGAGGAAGCAGGAAGAGAG	309	1.5	60		
mesoderm induction early response 1 homolog (Xenopus laevis)	MIER1	5	F: GAGTTTCGGACGTGGTTAAG R: TGAGGGAGTTCGGATTTTCC	118	1.5	58		NM_020948
neutrophil cytosolic factor 2	NCF2	5	F: TTTGCATCTGACCATGTCCC R: AGCCGATGTTAAAGCAAATCC	146	1.5	58		
NADH dehydrogenase (ubiquinone) Fe-S protein 2	NDUFS2	5	F: TCCCATACTTTGACCGGCTA R: GGTTCAAAAGCCGTGTGATT	319	1.5	60		CD468843
nerve growth factor, beta polypeptide	NGFB	5	F: TCACTGTGGACCCCAAACTT R: TCCTGTGAGTCCTGTTGAAGG	147	2.0	58	Chowdhary et al. 2003	AF134228
nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1	5	F: GGCTTTCAATGCTTTTTTCCT R: CCAGTGATTAATTTGACATGGC	178	1.5	60		
microsatellite	NVHEQ122	5	F: GAGGAGGGTTGGCAGCAGAT R: CCAAGGGGGCACAAGACATA	203-207	1.5	58	Penedo et al. 2005	
oviductal glycoprotein 1	OVGP1	5q13	F: AGGGGAGTGGTAAACAGAATG R: TGAGAAAGGCAAAATGCGAG	260	1.5	58		
phosducin	PDC	5	F: TTCGGTTTGTCAATATCTCACC R: AACACTGAGGAAAAAACAGGG	316	1.5	58		
phosphodiesterase 4B, cAMP-specific (Drosophila)	PDE4B	5	F: ATCAGAGCATGATACCCCA R: TACCATACAGCTGGCATGCT	217	1.5	62		CN792407
phosphoglucomutase 1	PGM1	5q17	F: ATTCTTCTCATCTGCTGTACC R: CATCTGCTGCTCCATCATC	116	1.5	56		

phosphatidylinositol glycan anchor biosynthesis, class C	PIGC	5p17-p16	F: GCTGACTTGAAGAGTGCCCTA R: AGGCAGACAGAAGCAAAGATG	215	1.5	55	Perrocheau et al. 2006*	DX010557
phosphatidylinositol glycan anchor biosynthesis, class K	PIGK	5	F: ACCTTGGGTAAACATTTGTCA R: TTAGCGTCATTTAGCACTCG	154	1.5	58		CX600327
pyruvate kinase, liver and RBC	PKLR	5	F: AGATACGCACTGGGATCCTG R: CCAGCTCCACTTTTGATTCC	197	2.0	58	Shubitowski et al. 2001; Chowdhary et al. 2003	AY008804
phospholipase A2, group IVA	PLA2G4A	5	F: GGGCCAGAGGAGATTAATAAAG R: GAGACAGGTGAAAAGAGGTAAC	550	1.5	60		
pleckstrin homology domain containing, family A member 6	PLEKHA6	5	F: AATCTTGACTGTAGAGCCCC R: GCAAGTGGTGGCAAACATAC	430	1.5	60		AJ584242
protein phosphatase 2, regulatory subunit B', alpha isoform	PPP2R5A	5	F: TTCCTAAGATTGTTTCCTCACG R: GGAAGCCTACTTCATTTCTTTT	284	1.5	58		CX594395
proteoglycan 4	PRG4	5	F: TTATCCAAAGTCTGGTACAACCTG R: TGTCTACAAACTGTAATAAATGTGA	216	1.5	60	Chowdhary et al. 2003	AY246746
protein kinase, AMP-activated, beta 2 non-catalytic subunit	PRKAB2	5p12	F: GGACGAGGAATAGAGACCTG R: GCCAGCAACAAATGACATTAC	351	1.5	60		
prostaglandin-endoperoxide synthase 2	PTGS2	5p16-p15	F: GACCGAGTTAAATCAGGATGA R: CGCTTCACTGTAATGCCAG	435	3.0	58	Lindgren et al. 2001; Musilova et al. 2005*	AF027335
regulator of G-protein signalling 5	RGS5	5	F: GTTCTGGATTGCCTGTGAGG R: TCTTTAGGAGCCTCCGTTTG	108	1.5	58		NM_003617
regulator of G-protein signalling 16	RGS16	5	F: TTAAATCAATGTCCCCACTTCC R: TGTCAACCATAACCCAGAG	109	1.5	56		
ring finger protein 2	RNF2	5	F: GCCATCCTTTTCTCCTCTC R: TTGTTTGATTCTCTTTCCCAGG	328	1.5	60		
RUN and SH3 domain containing 1	RUSC1 (NESCO)	5p12	F: CTGGTGGAAGCAGCTGACC R: CCAGGCACTCCAAACAGTCTC	190	1.5	55	Perrocheau et al. 2006	DX010644
S100 calcium binding protein A1	S100A1	5p12	F: GTGGACAAGGTGATGAAGGAC R: TGTTACAGGCCACTGTGAGG	100	1.5	58		
S100 calcium binding protein A7	S100A7	5p13-p12	F: CTTGGCCAATGTCTTTGAG R: GTTCTTGCGGTCTCTGG	183	1.5	58	Leeb et al. 2005*	AW260999

S100 calcium binding protein A9	S100A9	5	F: GCGCGACATAGAGACCATCATC R: GCTCTTTTTGAACCAGCTGTTTG	107	2.0	58		BI961525
serpin peptidase inhibitor, clade C, member 1	SERPINC1 (<i>HEST007</i>)	5p17-p16	F: CAGGGGTTGGCTACTCTGCCC R: AAATGAGGAAGGCAGTGAAGCTGC	165 bp	1.5	58	Perrocheau et al. 2006	AW735739
SH3-domain GRB2-like endophilin B1	SH3GLB1	5	F: GAGTGAATTTGATCGTCAAGC R: CTGGAGGTCTAACATGTACTGG	539	2.0	62	Chowdhary et al. 2003	
solute carrier family 16, member 1	SLC16A1	5	F: GGCAAAGAATGAGGGAAGAAC R: AATTAGCAAACATTGGGGGG	888	1.5	60		
Jun dimerization protein p21SNFT	SNFT	5	F: GTCTTTTCCACACCCTTACATC R: AGAGGAAGTGATTCTGCATAAC	225	1.5	58		
sterol O-acyltransferase 1	SOAT1	5	F: GTGCTCTTCATGTTCTTTGG R: GTGCATACCACTCTTGAGA	1031	1.5	58		BI541987
synaptotagmin XIV	SYT14	5	F: ACAACACCAAGTGAGGTTCC R: TGCCATCTAATGGCTAATATGC	405	1.5	60		AJ542913
tudor and KH domain containing microsatellite	TDRKH	5	F: CCTTTGCCTTTCTTTTCACAC R: GACATTTCTCTGCCGCTAAC	324	1.5	56		
microsatellite	TKY041	5p18	F: TGGACAAGTGCTCTGTAATG R: TTCCATGAGTCTGGAGTTGG	160	2.0	58	Hirota et al. 2001*	
microsatellite	TKY271	5	F: CAGTGAAGAGTGAATGGATA R: GCAAATGGCAGAAATTCCTT	112-124	1.5	56	Kakoi et al. 2000	AB048313
microsatellite	TKY331	5	F: AGAGTGGGAGATGTTTATGC R: CACTGAAATGAACACATCCTC	288-298	1.5	58	Tozaki et al. 2001	AB044832
microsatellite	TKY334	5	F: AAGTCCAAGGCTAGTTTCAC R: ATCTTTGTGCTACTTTGTGTAC	139-149	1.5	58	Tozaki et al. 2001	AB044835
microsatellite	TKY389	5	F: TGCCAATGTGTCTCTCTTTTC R: CGCACTGTGGTGTATTCTGG	172	1.5	58		AB048295
microsatellite	TKY456	5	F: GCTGGATGGATAAATGAATGG R: TGTTCGACTGAGCAGAGAGG	176-198	1.5	58	Tozaki et al. 2004	AB103674
microsatellite	TKY464	5	F: CCTATTCCACTCCTGGGTCA R: TATGTCCCGAAAGCAAGACC	235-243	1.5	58	Tozaki et al. 2004	AB103682
microsatellite	TKY489	5	F: AAACCCATCACATACGCACA R: TGCAAATGAAATGCTGTTCC	175-191	1.5	55	Tozaki et al. 2004	AB103707
microsatellite	TKY508	5	F: CAAAGCCCGCAGGATAAATA R: GCATTGCAAGTGCAGAAGTC	171-177	1.5	58	Tozaki et al. 2004	AB103726
microsatellite	TKY521	5	F: TCTTCTCAGGATTTGGGAGGT R: CCCTTCTGAACGGCTTATGA	217-223	1.5	58	Tozaki et al. 2004	AB103739
microsatellite	TKY525	5	F: TGAGTGCGGTACCTTTCCAT	225-235	1.5	58	Tozaki et al.	AB103743

microsatellite	TKY544	5	R: GGAACCGTGCTGGGATACTA F: TGACCCAGTAAGCAGCCTGT	273-315	1.5	58	2004 Tozaki et al.	AB103762
microsatellite	TKY616	5	R: TGCCAGGGGAAGAACATTTA F: ACCCTGGACAGGCGCCAGAC	157	2.0	58	2004	AB103834
microsatellite	TKY644	5	R: AACAGGGCGACTGGGACGAC F: TAAGTGTCCGCAGACTTTAG	142	2.0	58		AB103862
microsatellite	TKY673	5	R: TAGGACAAAGCACACTATGA F: TCCAGTTTAGGGGTATATGT	176	2.0	58		AB103891
microsatellite	TKY731	5	R: CCATGATGCTGACCTCTTTG F: GGGCACAGACCTACTCCACT	236-258	1.5	58	Tozaki et al.	AB103949
microsatellite	TKY739	5	R: GCAACAGCATCCCAGAATTT F: TTTCCAAACAAAGGCACACG	186	2.0	58	2004	AB103957
microsatellite	TKY774	5	R: GCAGAACGTGTGCACTTAAC F: ACCATGCTCTTTCCAAACTCAA	92	2.0	58	Tozaki et al.	AB103992
microsatellite	TKY801	5	R: CGAGGTGGGTTGTACATTTA F: TCCCTAAGCTAATTCCATCC	151	2.0	58	2004 Tozaki et al.	AB104019
microsatellite	TKY847	5	R: GCGCTTGCTCATCTAAAAGC F: GATTGCATTTGGCAAAGTCC	197	2.0	58	2004	AB104065
microsatellite	TKY887	5	R: CCTACACACCACTCATCAAG F: GAGAACTAGATGCCACCC	100	2.0	58	Tozaki et al.	AB104105
microsatellite	TKY889	5	R: TGTTGGAGTGTGTAGGCT F: CATCCCAAACAAACAGCAGA	179	1.5	58	2004	AB104107
microsatellite	TKY911	5	R: GCAGCCAACTCAAAAACCTCC F: GATCTTTAGAATCAGCTTGTTG	140	2.0	58	Tozaki et al.	AB104129
microsatellite	TKY1078	5	R: CTCGCCACGTTAGTTGATG F: CTTCTTAGGTCAAGAGCTA	187	2.0	58	2004	AB104296
microsatellite	TKY1108	5	R: TTCCTCTACATGACTGCATC F: CGGAGATGTGAAAACCTTGG	164	2.0	58		AB104326
microsatellite	TKY1117	5	R: ACTGAATTGCCCCATTTGTC F: ATTAACAACTGCCCCCAG	256	2.0	58		AB104335
microsatellite	TKY1163	5	R: CCAGACTTCCAAAGGTGAAC F: TGTGGGTATGAGTGAGGTG	220	2.0	58		AB104381
microsatellite	TKY1175	5	R: TCCTTAGAACATGCTCTGAC F: TTATCACCAGTTTCCAGAGC	203	2.0	58	Tozaki et al.	AB104393
microsatellite	TKY1777	5	R: CTTATTCCACCCACTAATTACAC F: TGATGGCTAAACTTGAGAAG	294	1.5	58	2004	AB215720
			R: AATACCCATAGGAATTGAGG					

microsatellite	TKY1909	5	F: TAATTATAAGCTCCGGACAG R: AGATAGAGGACAAACCCCA	249	1.5	58	Tozaki et al. 2007	AB215852
microsatellite	TKY2544	5	F: TGTCCATTTACACCCTACCTG R: GTTGCTGACAGCCTTGTTTT	174	1.5	58	Tozaki et al. 2007	AB216487
transmembrane and coiled-coil domains 1	TMCO1	5	F: AGATGAGCACCATGTTTCGCG R: TTCCACTTCTGCCTTCAGTC	546	1.5	58		NM_019026
torsin A interacting protein 2	TOR1AIP2	5	F: GCCCTGAGTGTTATCCTGAT R: GGGTTAAAGCCAGCTACTCTA	184	1.5	58		NM_145034
tropomyosin 3	TPM3	5	F: GCCCTAGTCTCCAATTCTCCA R: TCAGCTGCCTTCTTCTCTGC	888	1.5	62		CX601529
translocated promoter region	TPR	5	F: CAGTTTCATATCTACATGCC R: ACACCTGTAAGAGAAAAAAG	136	1.5	54		
TRAF3 interacting protein 3	TRAF3IP3	5	F: CTGCGACTTTTGGAGAATGA R: CTTGTAGGTGTTGGGTGTCTG	100	1.5	58		
thyroid stimulating hormone, beta	TSHB	5q14-q15	F: TGCTTATTGCCTCACCATCA R: TACCAGCTCAGCACATCCAC	391	2.0	58	Milenkovic et al. 2002*	AF165601
thioredoxin interacting protein	TXNIP (VDUPI)	5p12	F: CCAGCAAGATGATGTGGTATGG R: AACCCCTTCCAAAAACCTTG	178	2.0	55	Lear et al. 2001*	G62161
UDP-N-acetylglucosamine pyrophosphorylase 1	UAP1	5	F: TTCACCGTACCGTTTCTGAG R: GTCTGGCTTAATTAAGTGTCCC	1141	1.5	58		NM_003115
microsatellite	UCDEQ304	5	F: CGCTTTCCTGCTGTCACC R: GAGGGACTGTGGGGGAGGT	97-115	2.0	58	Eggleston-Stott et al. 1999	U67402
microsatellite	UMNe108/163	5	F: AGCTGCTAGCCAGGCAGAGA R: GATCTTGTTCAGGTGCTATAAA	105	1.5	60	Mickelson et al. 2003	AF536251
microsatellite	UMNe190	5	F: AGATGAAGGCTGCTCTGAGC R: GATCAGTTTGAACATTTACAGTGTG	91	2.0	58	Mickelson et al. 2003	AF536278
microsatellite	UMNe220	5	F: TTGATGATACAGTGTTGGAGGG R: TTAACCATTACACCACCGGG	293	2.0	55	Mickelson et al. 2003	AF536299
microsatellite	UMNe230	5	F: TGGTCTAGAGTACACATACACCAAC R: TTTCTCCTTCCACCCAG	109	2.0	55	Wagner et al. 2004a	AY391324
microsatellite	UMNe237	5	F: TTAAAAGCAAGCCAGAGGGA R: GATCTTCATGTAAACACACACAGAT	109	2.0	55	Mickelson et al. 2003	AF536308
microsatellite	UMNe255	5	F: TAGGAGGACCAGAGAGGAACC R: TCCAGAAGCAAAAATTGAGGC	181	2.0	58	Mickelson et al. 2003	AF536319
microsatellite	UMNe306	5	F: TTGTGGACGTAGCACTGCTC R: CTTTAACCCAGACTCTTCCCTG	217	2.0	58		

microsatellite	UMNe361	5	F: AGGGAATAACTTATGAACAGATGAA R: TCTTTATGGAAATTCTCTCTGAACC	169	2.0	62	Wagner et al. 2004a	AY391349
microsatellite	UMNe383	5	F: CCATCCACATTATCACAAATGG R: CACCAAGGTATGGAAATGACC	151	2.0	58	Wagner et al. 2004b	AY464473
microsatellite	UMNe412	5	F: GATCAAAATACAGAAGATTACGTG R: TGATGCTCTGGAAACCAGTC	170	1.5	58	Wagner et al. 2004b	AY464482
microsatellite	UMNe454	5	F: GGGAGAAACACCTACAGAGTGG R: AGACTGAATTGCCCCATTTG	244	1.5	60	Mickelson et al. 2004	AY731397
microsatellite	UMNe455	5	F: TGAGGTACTGTGCCTTGCTG R: CTGGGAAGACAGAGCCAGTC	130	1.5	60	Mickelson et al. 2004	AY731398
microsatellite	UMNe477	5	F: GTCAAGGAACAGCTGAAGGTG R: TTCCTGAGCTAGGGTAGGAGC	322	1.5	60		
microsatellite	UMNe481	5	F: ACATTGGGCCAGTTGCTTAC R: ATTGTTGGGACACCAGATTACC	130	1.5	55	Wagner et al. 2004b	AY464499
microsatellite	UMNe515	5	F: CTCTGACCTCACTGTCTGCG R: TATTCGGGGAGCTGCAAG	130	1.5	55	Wagner et al. 2004b	AY464514
microsatellite	UMNe534	5	F: ATGTTGTTGCAAATGGTAGGG R: TCCATCAATCCCTCTTCTGG	249	1.5	62	Wagner et al. 2004c	AY735262
microsatellite	UMNe536	5	F: CTGGCTGGAGACAGTCCTTC R: ACGCTGACCACAGTTCGAG	125	1.5	58		
microsatellite	UMNe555	5	F: AGACCTCTCTCATGAAC TTCAG R: GGAATCAGGAT TTCAGTTATGG	120	1.5	62	Wagner et al. 2004c	AY735268
microsatellite	UMNe582	5	F: TCTTGACCTTCTTTACTTAGTACACA R: CCTGGGCATAGACCTACACA	175	1.5	58	Wagner et al. 2004c	AY735282
microsatellite	UMNe604	5	F: AGACTTGCCCAGCAGCAC R: ACCTCCAGCCCAGCTTTC	240	1.5	58	Wagner et al. 2004c	AY735294
ubiquitin specific peptidase 1	USP1	5q17	F: CAACCAACGACAGCTATGGA R: CACACCCCTTACTTCCTCCTC	194	1.5	55	Perrocheau et al. 2006	DX010606
vascular cell adhesion molecule 1	VCAM1	5q14	F: GACTGGCAGCTGACCTATGTC R: AGTCTGATGAATCAACATCGTAGC	262	2.0	58	Lear et al. 2001*	G62179
microsatellite	VHL66	5	F: TCTTTAAAATTTGATGCACAATGGT R: GGGGAGAATTTACTTATCTTGAC	102-108	3.0	58	Van Haeringen et al. 1998	Y08440
WD repeat domain 42A	WDR42A	5	F: TTACCTCTTCAACTCCTCTC R: TTGTCCCCCTCCATGAACT				CB448605, XM_066690	
wingless-type MMTV integration site family,	WNT2B	5	F: CTAAAGGGACAGACGGTTGTG R: CAGGTTTGATCCAGCCACTCT	190	1.5	55	Perrocheau et al. 2006	DX010611

member 2B								
zinc finger, RAN-binding domain containing 2	ZRANB2	5	F: GTCTTTTACAGCAGCTTATC R: CTTTTTACGTCCAAACTACAG	175	1.5	54		
microsatellite	ZuBeEq2	5q15	F: GTTGGAGATACGGCCACATT R: CCCGTTAGGGTGTTTCTCCT	160	1.5	64	Klukowska Rotzler et al. 2006; Horsemap database*	AM040154
zinc finger, ZZ-type containing 3	ZZZ3	5	F: CTCATGGTGTGTGAATGTTAGA R: CTACCACTGGCACTTTTCAC	113	1.5	58		NM_015534

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	6CA001	6	F: GTGCCTGCTTCTCCCTAATG R: CTTGGGGGCTGGTATCATAA	249-253	1.5	58	Penedo et al. 2005	
sequence tagged site	6STS01	6	F: CCAACAATTCTTCAATTCAGTG R: TCCCAGTAAGGAAATAGCATTG	250	1.5	60		
adiponectin receptor 2	ADIPOR2	6	F: GCTTGAGTATCCCATGAATGA R: ATCACCTCCCTTTGTACCATC	115	2.0	56		DN507534
ADP-ribosylation factor-like 4C	ARL4C	6	F: GACCTGTCCTACCAAATGGAC R: CCTAAGTTCAGTCAGCCATCA	200	1.5	60		CX594150
activating transcription factor 7 interacting protein	ATF7IP	6	F: CCTTGCAGAAACCATTAGTGA R: CAAAAGAACCCTCCATCTTCT	212	1.5	58		
ATG9 autophagy related 9 homolog A (S. cerevisiae)	ATG9A	6	F: CAGCACCATGACAGGCTCT R: TGCATATACAGGGCATGCAG	239	1.5	58		
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	ATIC	6	F: GAGCAGGACAGCAGTCTCGTA R: TCGCCGATAGTTCCAGTAACA	169	1.5	55	Perrocheau et al. 2006	DX010434
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	6	F: AGGTAGCGCTGGTGTATGGT R: CCTGGGTGAAGCGAAAGATA	150	1.5	58		
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C2	ATP5G2	6	F: TGCTGAGCCGATCACTGTCT R: CAATGAACTGGCTGCTGTGT	698	2.0	58		BI961853
ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E1	ATP6V1E1	6	F: GGTGAGGGGTCAGATAGTGG R: GCCCAAACAGCTAACAGTGA	183	1.5	58		CX604368
C1q domain containing 1	C1QDC1	6	F: GAACCTCTAATCTCGCTCCTG R: GCATAGGCAGATACCAAGACC	217	1.5	58		CX597695

calcium binding protein 39	CAB39	6	F: ATTAGACAGACACAACCTTCACAAT R: GGCCTCAAACCTGGATGTTAC	~ 120	1.5	58		
coiled-coil domain containing 91	CCDC91	6	F: AGTCCATCTTTCTCCAGCTTC R: TGCTGTTGTCTGCATGTGTAT	125	1.5	54		
cyclin D2	CCND2	6	F: GGAGTGGGAACCTGGTGGTGC R: CGGTGGCACACAGAGCAATG	175	1.5	65		
cyclin T1	CCNT1	6	F: GCCCTGCAACATCTCCACA R: ATGCCAGGCTGCCAAGAAA	217	2.0	58		
CD63 molecule	CD63	6	F: CTTATCACGCTGGTGGGA R: CCAGGATCAAAGCAGTGT	231	2.0	58		BI961928
cyclin-dependent kinase 2	CDK2	6	F: GCCATCCCAGTCTCTGAAAG R: TTTAAAACAGGCCCTTCCT	163	1.5	60		
cholinergic receptor, nicotinic, gamma	CHRNA3	6	F: CCCTCACCACCAATGTCTG R: CCCCTCTCTCTGCTACATCG	178	2.0	58	Chowdhary et al. 2003	AF130751
C-type lectin domain family 2, member B	CLEC2B	6	F: ACATGATTGGATTGGTTTCC R: CATTCTTCAACGGTGTCAAT	130	1.5	50		DN505051
cytidine monophosphate N-acetylneuraminic acid synthetase	CMAS	6q21.2	F: GTGTGGGTTTCAACAGACCAT R: ACTGATGGCGTCTCACAAC	~434	1.5	68	Perrocheau et al. 2005*	CX596382
collagen, type II, alpha 1	COL2A1	6	F: CAACGTCCAGATGACCTTCCT R: CAGCCATCCTTCAGGACAGTA	201	1.5	55	Perrocheau et al. 2006	DX010616
collagen, type IV, alpha 4	COL4A4	6	F: AGACAGACGGACAGCAGTAG R: TGAGGGAAGGAGAAGTAGTGG	196	1.5	58	Wagner et al. 2006	DQ001082
coenzyme Q10 homolog A (S. cerevisiae)	COQ10A	6	F: AGGTGGTGTCCAATGTCCAG R: CCCATGAAAACAGCAGAGGT	151	1.5	58		
microsatellite	COR010	6	F: TTGAAGGGTGGAGTAGGG R: GACAAGAAGGGATGAAGGAG	289-299	2.0	58	Hopman et al. 1999	AF083453
microsatellite	COR019	6	F: GAAAGGTCAGAACAGGCAGA R: CTAGGAATGTGTGTACATGTGTT	220-222	2.0	58	Hopman et al. 1999	AF083462
microsatellite	COR070	6	F: CATCTGTTCCGTGGCATT R: TTCAGGTGTGGGTTTTGAATC	267-295	3.0	58	Tallmadge et al. 1999a	AF142607
microsatellite	COR088	6	F: GAGCCAGCTTGTTCGTGTATT R: GCACGAAGAAGAACCAAGA	276-290	2.0	58	Tallmadge et al. 1999b	AF154941

carbamoyl-phosphate synthetase 1, mitochondrial	CPS1	6	F: TCAAATGAGATTCCAAGGGAAG R: TGAGGGACAGTAAAGAGATGAC	242	1.5	58	Wagner et al. 2006	DQ001083
cullin 3	CUL3	6	F: CATATGTAGCATAAAATGCGC R: CCTGTTTTTCATACAGTATTGAAA	294	3.0	58	Chowdhary et al. 2003	G62174
dynactin 2 (p50)	DCTN2	6	F: CTCTCCCCTTCCCGAACAC R: GGGAGGTCGGCGTATTTAG	100	1.5	58		
DEAD box polypeptide 47	DDX47	6	F: GCTTTGCTACTCCGAAATCTT R: ACATCAGTTGCCAGAAGAATG	~651	1.5	50		
desmin	DES	6	F: GCAGCCAACAAGAACAATGA R: CCTTGAGGGCGTCGATCT	103	1.5	58	Wagner et al. 2006	
diacylglycerol kinase, alpha 80kDa	DGKA	6	F: TCGCTCCTCCAATTTCTTTG R: ATGTGTTTGTGGGGTGTGTG	239	1.5	60		
DnaJ homolog, subfamily C, member 14	DNAJC14	6q22-q23	F: CTTCTTTGCAGCTCCTCAGC R: TGCTGTACACAGCCCTTTTG	183	1.5	60		
eukaryotic translation initiation factor 4B	EIF4B	6	F: ATCAGTGCAGTGCCTTTACC R: AGGGCACTGAGCAAGGAAT	101	1.5	58		
v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4 (AC092680)	6	F: AGAACCCCTCCCATTGAATC R: GCACATCTTCTCCCTTCTTTTG	584	1.5	62	Wagner et al. 2006	AJ584440
FK506 binding protein 4, 59kDa	FKBP4	6	F: CGAGTTTCTCTGATGAGGATG R: GTGCCAAGTCAAAGTCATTCA	~746	1.5	58		CX602041
fibronectin 1	FN1	6p15	AGGCTGCACATTCAGTTCC R: GGAAAATCGGCAATTCGTAG	196	2.0	58	Mariat et al. 2001* ; Chowdhary et al. 2003	AF130764
GABA(A) receptor-associated protein like 1	GABARAPL1	6	F: GGGCAGGTATGAGGTAGGATA R: CTTGGCCTGACAGCATAAACT	387	2.0	58		BI961792
guanine nucleotide binding protein, beta polypeptide 3	GNB3	6q13	F: CTCTGTAGCCAGGGCAGTGT R: GGAGGCTGTCACAGAAAAGC	173	1.5	66		
glucosamine (N-acetyl)-6-sulfatase	GNS	6	F: TTTGTAGAAGTCTATAACCTGACTGC R: GGTCAAAAACCCCTGGAGTG	184	1.5	58		
histone deacetylase 4	HDAC4	6p12	F: GTACGAGCGGCATGTCTTTAT R: TCAGTAAGACGCAAACGTTCC	195	1.5	55	Perrocheau et al. 2005*	AY817472

high density lipoprotein binding protein	HDLBP	6p12	F: ACCCACAGAGTCAACTACAC R: TTTTCCTGCTTTGGCTGC	124	1.5	58		
microsatellite	HTG31	6	F: CTCTGTAACCCCTTATATCCTTA R: TGTTGATTGCTCCTCCCCCT	162	2.0	58	Lindgren et al. 1999	
interferon, gamma	IFNG	6q23-q24	F: TGGGGAATATATTTTTAAACTCATCA R: CGGCTACCCACTCCCTAGTT	203	2.0	58	Chowdhary et al. 2003; Musilova et al. 2005*	AF130766
insulin-like growth factor binding protein 6	IGFBP6	6q22	F: CCGCAGACATCTGGACTCAG R: GTAGAAGCCCCGATGGTCAC	100	1.5	58		
Indian hedgehog homolog (Drosophila)	IHH	6	F: AGCTGTGAGGCCAGGAGAC R: CGCTGGTTCTGAGTGATTGTT	199	1.5	55	Perrocheau et al. 2006	DX010636
inhibin, alpha	INHA	6p14	F: GCAGCATTGTGCTTGCATC R: GAGAAGTGGAAGGAAGAGGG	121	1.5	60	Mariat et al. 2001* ; Wagner et al. 2006	D50327
insulin receptor substrate 1	IRS1	6	F: GTGAGTCCTAGCACCAACAGG R: GGAACCAGACACAGAAGCACT	219	1.5	55	Perrocheau et al. 2006	DX010515
killer cell lectin-like receptor subfamily A, member 1	KLRA1 (LY49)	6q13	F: CAGGAGGAAATTCTACAAAACC R: AAAGATCCCCTGTTTTTCGAT	~200	1.5	55	Takahashi et al. 2004*	AB120393
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS	6	F: GTGGAAGTGGAACCTTTTGGATAAAA R: CAGCATTGAGAAATTAACAGCATACAA	284	2.0	58		
lactate dehydrogenase B	LDHB	6	F: CCTGGAAACTAAGTGGATTACCC R: CTTGAGTCGCCATGCTCTC	151	1.5	58		
LEM domain containing 3	LEMD3 (MAN1)	6	F: AAGACTACTTTCGCCACC R: AGTTCCTTATGGGCTACTG	209	3.0	58	Chowdhary et al. 2003	
microsatellite	LEX065	6	F: GAAGGCACAATTCAATCTACT R: GCCCAGTCCCATTCTAAC	144 -156	2.0	58	Coogle & Bailey 1999	
LIM domain and actin binding 1	LIMA1	6	F: GAGAGACCTGCGTGGAATGT R: TTGTTGCAATAGGAGCAACG	106	1.5	58		
leucine-rich repeats and immunoglobulin-like	LRIG3	6	F: TCACTTGAAAGCTCGTTCTTC R: TGGTCCCATTCAGTCTATGTG	174	1.5	58		CX594173

domains 3							
Equine skeletal muscle EST	M6PR	6	F: GTGGGCCAGGGTCAAGAG R: ATTGAAGACGTGAGTCTCGTTGAGT	150	1.5	58	
microtubule-associated protein 2	MAP2	6	F: TGTATGCTGGGATTCCAAGGT R: TTTGCAAATTTTGATTGAAAAACA	150	3.0	58	
hypothetical protein MGC50559	MGC50559	6	F: AAATTCTTACTAGGGTCAATGTCA R: ATCCTGATGTTGTCAGAGGAA	127	1.5	58	DN506262
matrix metalloproteinase 19	MMP19	6	F: CTCAGGTCAGCTGGATGATG R: GCACCTCTTGGAAGGTCAAG	460	1.5	60	
myosin, light chain 1	MYL1	6	F: GACCAGGGCAGCTATGAAGA R: TGGCTAAGACATGACGGAGTT	100	1.5	58	Wagner et al. 2006
myosin, light chain 6	MYL6	6	F: GTCTTGCTTTAGGGTGGTCC R: ACACAGCAGAGGCAGAAAAGT	214	2.0	25	BI961490
nucleolin	NCL	6	F: TGCAGAGAAAACCTTGGAAGA R: CCAAGTGCTATTCTTTCCACCT	121	1.5	58	
NADH dehydrogenase 1 alpha subcomplex, 10	NDUFA10	6	F: GACAGAACGCAGCAAAGTGA R: TGGCGTACAACCAGGACT	1013	1.5	TD62	
ninjurin 2	NINJ2	6q12-q13	F: AGAAGAGCGTGGCAGAGAG R: CAGAGAGATGCTGATGAGAGTG	134	1.5	56	CX596080
nucleoporin 107kDa	NUP107	6	F: AAAAAGCATGAAGCTGCAAAA R: AAGCTCTAATGCACAGATGTTCTC	151	1.5	58	
microsatellite	NVHEQ081	6	F: TTCTGGATGAAGTGCAGCC R: GGACAGTGGAGGTGGAGGATA	166 -181	2.0	58	Bjornstad et. al 1999
microsatellite	NVHEQ082	6	F: TGTGGCAGCATCCCACAAAC R: CCTCCATTTTTGTCGGTTAGCG	127-141	2.0	58	Bjornstad et al. 2000
ORM1-like 2 (S. cerevisiae)	ORMDL2	6	F: TGGCGTACACCATCTTGGTGTA R: TTGTTTTTGTTGGGAAAGG	160	1.5	58	
poly (ADP-ribose) polymerase family, member 11	PARP11	6	F: CTATTTTGCTAGAGATGCTGCTT R: GCTGCAAGCTCACACCAT	95	1.5	54	DN504980
paired box gene 3	PAX3	6	F: GTTATTTTGCCCCGGTTTCT R: AAGAGGAGCCCACCTGATTT	187	2.0	58	Chowdhary et al. 2003

phosphofructokinase, muscle	PFKM	6	F: TCTCCACCTACCATTACGG R: GGCCCATTCCTTTCTTTTC	204	2.0	58	Chowdhary et al. 2003	AF134231
phospholipase C, delta 4	PLCD4	6	F: CCGAGGTCCATACCAAGAA R: GATGAAAGGAGGCTGGTCT	378	1.5	TD58		
protein phosphatase 1, regulatory (inhibitor) subunit 7	PPP1R7	6	F: AACCTGGAGACGGTGTACCT R: TTGGGTTTGTGACTGTTGCTA	~ 230	1.5	58		
prickle homolog 1 (Drosophila)	PRICKLE1	6	F: CAGCCACTGTTTGATGTCCT R: CGTACTCCTCCAAAGCACAG	153	1.5	58		CX603902
protein kinase, AMP-activated, gamma 1 non-catalytic subunit	PRKAG1	6q22	F: AGCAGAGGTAGGGAGGCCA R: AGCAACAAGGGAGAAAGCGA	137	1.5	60	Dranchak et al. 2006*	
protein kinase, AMP-activated, gamma 3 non-catalytic subunit	PRKAG3	6p14-p13	F: CAAGCTCTTGGTGTCCACAG R: AAGAATCAGAGGCAACAATTTCG	169	1.5	60	Dranchak et al. 2006*	
proline rich 13	PRR13	6	F: CCTGTACCTTGTGTCAGTGG R: CAAATGGACCCCACTTTCC	116	1.5	58		BI961720
prostaglandin E synthase 3	PTGES3	6	F: TTGATCTTTTTACAGTATTGATCC R: CATGACTGGCCAGATTCTCC	1000	1.5	58		
parathyroid hormone-like hormone	PTHLH (PTHrP)	6	F: CACAGCGGAAATCAGAGCTAC R: AGTTCGCCGTTTCTTCTTCTC	226	1.5	55	Perrocheau et al. 2006	DX010565
RAP1B, member of RAS oncogene family	RAP1B	6	F: CACAAGGCCTGAGTTGCAGTA R: GGCCACCTCAAAGGAGTTGTA	119	2.0	62		BI961717
RAS-like, estrogen-regulated, growth inhibitor	RERG	6	F: GTCAAGCAAGCCATTAACAAG R : CAGACATTTCCAGAGTCAGA	186	1.5	58		CX598283
microsatellite	RKJ06	6q22	F: GTGGCTAGGAAAAGTTAGCG R: CAAGTCATACGCAATGTTTAG	225	3.0	58	Chowdhary et al. 2003*	
ring finger protein 25	RNF25	6	F: CCTTTGGAACCCGAGTCAAC R: TGGCAGTTCCTGGGTATCAGT	309	2.0	52	Wagner et al. 2006	BI961897
secretogranin II	SCG2 (SGII)	6p13-p12	F: CAACTCTCAGATGATGTCTCC R: CCTAATTCTTGATCCTTGTC	600	1.5	60	Milenkovic et al. 2002	
sodium channel, voltage gated, type VIII, alpha	SCN8A	6q22	F: GCCCATTGAGCACTTCTACG R: TTCCTTTTACTGGATACGGTCTT	174	2.5	50		

subunit								
splicing factor, arginine/serine-rich 2, interacting protein	SFRS2IP	6	F: CTCGGTGGAAGGAAAGATG R: TGTCAGCAGAATTTGGATCAT	153	1.5	58		
silver homolog (mouse)	SILV (<i>PMEL17</i>)	6q23	F: AGTACCGGGACCCTGATCTC R: CTGCAGTAGGCACTTGTCCA	199	2.0	58	Rieder et al 1999.; Chowdhary et al. 2003	AF076780
solute carrier family 38, member 2	SLC38A2	6	F: GCTTTAAGAGCACATTTATTGTATGTT R: CCTTAGAGCCAGATGACCAA	167	1.5	58		
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a- like 1	SMARCAL1	6	F: CGCTGCCTTCCGCAAGTTCG R: GGGGTCCACTCCAGAAAGGTCG	132	1.5	58	Wagner et al. 2006	BM414611
sarcospan	SSPN	6	F: CCTTTGTGTACCAGGATGTGA R: CGGAAGTTGTTAGGGAGCATA	186	1.5	58		CX605718
SH3 and cysteine rich domain 3	STAC3	6	F: GCTGAAGCGGTTATTCAGGA R: GTGGCTCCTCCTCCTCTTCT	155	1.5	58		
signal transducer and activator of transcription 6	STAT6	6	F: CCTGTGTGACAACCCAAG R: CACAGCCACATAGACCCT	140	2.0	58		BI961587
microsatellite	TKY025	6	F: AATCTCATGGCAGAATACCG R: GACTCTGGGAAGGGCTAAGG	100	1.5	58	Kakoi et al. 2000	AB048335
microsatellite	TKY026	6	F: AACGCATGCAATTGGCCCAG R: TGCTGTTGCTGCTGGATTGC	100-103	1.5	58	Kakoi et al. 2000	AB048335
microsatellite	TKY027	6	F: TACTTGGTCCAGCAGCTGTC R: TCAGAAGCACCTGTCTGTGC	160	1.5	58	Kakoi et al. 2000	AB048335
microsatellite	TKY028	6	F: TTCAGCAGGGTCTCATGCCAC R: TTCGGCTCTGGTTCAAGAGG	276-357	1.5	58	Kakoi et al. 2000	AB048335
microsatellite	TKY029	6	F: CTCTTGAACCAGAGCCGAAC R: TAGAAAAGCGTTGCAGAGGC	121-127	1.5	58	Kakoi et al. 2000	AB048335
microsatellite	TKY030	6	F: CCAGTCCACTGCCCACCCAC R: GTGCATGGTGGGAGCTACTG	193	2.0	58	Kakoi et al. 2001	AB048336

microsatellite	TKY111 (RC11)	6	F: TATGGCGATTTCTGGTCTGTGTC R: GATGACAACACTGGGAAGAAAGAG	125-131	2.0	58	Mashima et al. 2001	AB053346
microsatellite	TKY284	6	F: CTGGACTAGAGTCAGATTGC R: AACAGGATCCCCCAATGCC	159-175	2.0	58	Tozaki et al. 2000b	AB033935
microsatellite	TKY312	6	F: AACCTGGGTTTCTGTTGTTG R: GATCCTTCTTTTATGGCTG	251-270	1.5	58	Tozaki et al. 2000c	AB034621
microsatellite	TKY323	6	F: CGGAAAGCTAAGAAGACTGG R: AAATTGGCAAGTTTTTCCCC	130-141	1.5	58	Tozaki et al. 2000c	AB034631
microsatellite	TKY360	6	F: CGTGATATGCACGAGATGTC R: GATCAGTTCAGAATCAGCTG	236-240	1.5	58	Tozaki et al. 2001	AB044860
microsatellite	TKY377	6	F: GTTTACATAGTGTCCTACTTG R: TGGTAATGGGGAAATTACTC	134-140	1.5	52	Tozaki et al. 2001	AB044877
microsatellite	TKY411	6	F: AGGACCTGATTCCCTAACATG R: CTGTGGGCCACTTTGAAAAG	134	2.0	58		AB103629
microsatellite	TKY412	6	F: GTGTGGGACAGGAAGTTTGG R: ATTCTTGGGTCCCCTCATCT	234-248	1.5	55	Tozaki et al. 2004	AB103630
microsatellite	TKY543	6	F: AGGAAAGCGGTGTGGTACAG R: CACACAAGACGGACGAATGT	263-267	1.5	58	Tozaki et al. 2004	AB103761
microsatellite	TKY556	6	F: GCAGAGGGTGAAGCCAGTAA R: TAATTCCTGCTTGTCGCAA	202-250	1.5	58	Tozaki et al. 2004	AB103774
microsatellite	TKY570	6	F: TCTCCGCAGCTCAAACCTTC R: CTCAAAGGTGCCTGAGAAGC	159-177	1.5	58	Tozaki et al. 2004	AB103788
microsatellite	TKY595	6	F: GCAGAAGCCACTTCCTCAGA R: AGGCAGCAAGCTTGTGAAAT	187-193	1.5	58	Tozaki et al. 2004	AB103813
microsatellite	TKY723	6	F: AAGAAGTCAAGGGGAGTTGGA R: GGGGTTTCTTCTCAGCATCA	146-152	1.5	58	Tozaki et al. 2004	AB103941
microsatellite	TKY744	6	F: CCTGCCTTTGCTCTAGAAACC R: GGCTCCCAAGGGACTAGAAG	251-259	2.0	54	Tozaki et al. 2004	AB103962
microsatellite	TKY829	6	F: ATCTATAAAAAGCCTGGGCA R: TAGCCAGGTCTCACTTTATG	160	2.0	58		AB104047
microsatellite	TKY843	6	F: GCAGCACCCACAGAAAATA R: TTGGCAACTCCATGCAAATA	163	1.5	58		AB104061

microsatellite	TKY863	6	F: ACATACAGGCCATTTGATGG R: CTCATCAAGCCATGCTGTGA	198	2.0	58		AB104081
microsatellite	TKY952	6	F: GATCGGTAAGTGTCGGGAC R: TAAAATGACTGGGTGGAGAC	216	1.5	62	Tozaki et al. 2004	AB104170
microsatellite	TKY1001	6	F: TCTCAGAAGCCATCTGGAG R: ATCGATGCAGAACACGTGG	252	2.0	58	Tozaki et al. 2004	AB104219
microsatellite	TKY1013	6	F: TACCCGCTATTCCAGACTC R: AGAGACCTGACCCTTACTC	188	2.0	58		AB104231
microsatellite	TKY1087	6	F: ACCAGCAATGAAGGACTATC R: AGCAGAAGACTTTGGGAAC	196	2.0	58	Tozaki et al. 2004	AB104305
microsatellite	TKY1090	6	F: CATCCCAGGGACAAACATC R: CAGGGACAATCTTAGACAAAC	174	2.0	58	Wagner et al. 2006	AB104308
microsatellite	TKY1113	6	F: GATCAGAGGGAGGAAAGAG R: AAGAGATGAACAGAATCAGTG	206	2.0	58		AB104331
microsatellite	TKY1159	6	F: TAATGTCCTCAAGGTCCATC R: AACCTGAGTATCCACTGATG	188	2.0	58		AB104377
microsatellite	TKY1162	6	F: TTTAATTATCACTCCCTTGACA R: TGACTCTGGTTTCTGACTTC	123	2.0	58		AB104380
microsatellite	TKY1235	6	F: CACTGTTTCTGCCAAAATC R: CCTATAGCTGAATACTCTCC	134	1.5	60	Tozaki et al. 2007	AB215178
microsatellite	TKY1433	6	F: ATTTCCTTAGGAAGTAGACC R: ATGAGCAAAGTTAGCACTTG	172	1.5	58	Tozaki et al. 2007	AB215376
microsatellite	TKY1474	6	F: CTTCAGTCAGTCTCCTGAG R: TTAAACTGCTGTTGCCAGC	147	1.5	56	Tozaki et al. 2007	AB215417
microsatellite	TKY1613	6	F: GTTCAGATGTTTGGAGGATG R: GATTTATCCCCTGATACAGA	262	1.5	58	Tozaki et al. 2007	AB215556
microsatellite	TKY1745	6	F: AGGTAGACCAATCAGTTAGA R: TCTGAAAGTGACAAAGCTGC	226	1.5	58	Tozaki et al. 2007	AB215688
microsatellite	TKY1892	6	F: TAATTTATCTAGCTCCCTGC R: AGATTCTCAAAGCCATCAGA	129	1.5	58	Tozaki et al. 2007	AB215835
microsatellite	TKY2582	6	F: CTGATTCCAGCTACAGGACAA R: GAATGGCATGGACAGTAGGT	232	1.5	58	Tozaki et al. 2007	AB216525

microsatellite	TKY2815	6	F: TCCGTGCATCTGGTGATAG R: ATTTAGGCTTTTCCCCTCCT	247	1.5	58	Tozaki et al. 2007	AB216758
microsatellite	TKY3193	6	F: CTAATCACTCATGGTGGTG R: GATCAGATTCTCCTTGAAAGAA	218	1.5	56	Tozaki et al. 2007	AB217136
microsatellite	TKY3278	6	F: CCTGGTTTTACTTGGCAGTG R: ACATACTTAGCTCTGGAAAACACA	240	1.5	58	Tozaki et al. 2007	AB217221
transmembrane 7 superfamily member 3	TM7SF3	6	F: CGTTGCAGATTCTGAAGAGAA R: TGGGTAAATCGGCCATAGAG	154	1.5	58		
transmembrane protein 4	TMEM4	6q23	F: CCTCACAGAGCTGCTAGAGGA R: AACTTGAGGGTGCCACTGAT	174	1.5	55	Perrocheau et al. 2006*	DX010598
triosephosphate isomerase 1	TPI1	6	F: AGAAGGTCGTTTTCGAGCAA R: CCAGCAAGGGGATTAAGTCA	120	1.5	61	Chowdhary et al. 2003	
tetraspanin 8	TSPAN8	6q24	F: CTCCGCAGACAAATTACTCC R: TATGCAGCCACTCACACCT	111	1.5	56		
microsatellite	UCDEQ465	6	F: AACCAGTCCCTACATAGAAC R: CTCACAACCAAGCATACA	200-206	2.0	58	Eggleston-Stott et al. 1999	U67414
UDP glucuronosyltransferase 1 family, polypeptide A1	UGT1A1 (HMS70)	6p12	F: CATCATGCGCCTCTCCAGCC R: CTGGTACCAGTGTAGGTCGTGGG	~140	1.5	65	Mariat et al. 2001*; Wagner et al. 2006	
microsatellite	UM015	6	F: AGTCTGGCTGAGGATACTG R: GGTGAGAAAGGAGATAAATG	153-163	3.0	58	Meyer et al. 1997	AF195133
microsatellite	UMNe087	6	F: CCTCCAAATTCCTTCCCTTTTAG R: GCTCACTTTAGCCATGTCAAGC	146	1.5	62	Wagner et al. 2006	AF536243
microsatellite	UMNe177	6	F: GCTGGGACATAAAATTTTCATCC R: GTCTGTCTTTTTCATCTAGGCC	162	2.0	58	Mickelson et al. 2003	AF536276
microsatellite	UMNe195	6	F: CAAAGAAGTGGCCCTCGTAG R: GATCTGGCCCCAGAGAAAAA	~550	1.5	55	Wagner et al. 2004a	AY391318
microsatellite	UMNe197	6	F: CTGGTTGAAGCTTGTTTCTCTC R: CCGCTTGTCCAGTGACATAG	188	2.0	58	Mickelson et al. 2003	AF536282
microsatellite	UMNe203	6	F: GTAACAAAGCCCCTAATTGCC R: TGAGCCAACACAACACTTCTG	131	2.0	62	Mickelson et al. 2003	AF536286

microsatellite	UMNe216	6	F: CTAGGCTGCCACTTGGAGAG R: ACATACATAGACACACAGGCGC	101	2.0	55	Mickelson et al. 2003	AF536297
microsatellite	UMNe233	6	F: AGAACAGTACATGCTGTGGTCC R: CTGTGAACCGTCTCATGAGTG	141	2.0	58	Mickelson et al. 2003	AF536305
microsatellite	UMNe248	6	F: GATAATGCCTCTTGCTCTCCC R: AAGATGAAGAGAGGTTAGCCTAGTG	110	2.0	58	Mickelson et al. 2003	AF536316
microsatellite	UMNe337	6	F: CTTTAATATGCCTGCCACTTCC R: TTGGGAAGTCCAGGATCTTG	215	2.0	55	Wagner et al. 2004a	AY391342
microsatellite	UMNe427	6	F: GGAAGTGGAGACTCAGCAGG R: TGCATAGACAACCTGCCTGG	128	1.5	58	Wagner et al. 2004c	AY735247
microsatellite	UMNe472	6	F: TGAGTTGTTGTAGCGTGTTG R: AGGCAGTGTGATAAATGTGGG	~300	1.5	60	Wagner et al. 2004b	AY464496
microsatellite	UMNe556	6	F: CTAAATGAATGGAGGGAAGGC R: TGACTCCAGCCAGAGGATG	325	1.5	62	Wagner et al. 2004c	AY735269
ubiquitin specific peptidase 15	USP15	6	F: GCACATTTCCCGTATCGACT R: AAGCAAAGCCATGATCAACA	245	1.5	58		
vitamin D receptor	VDR	6q21.3-22	F: AGGACCAGATCGTACTGCTGA R: AGTCTTGTTGCCACAGGTC	264	1.5	56		
von Willebrand factor	VWF (HMS55)	6q12	F: GCCATGTCTTGATGTGGTGG R: TAATGGAATATCACCACCGG	180	2.0	58	Godard et al. 2000*; Mariat et al. 2001	
WNT inhibitory factor 1	WIF1 (WIF-1)	6	F: AAGTACGTCTGTAGCGTGATGGT R: TCTCTGGGATCAGGAGAAAGTC	344	3.0	58	Chowdhary et al. 2003	G62206
YY1 associated factor 2	YAF2	6q21.2-q21.3	F: GCCAAGATTGAAAAATGTGGA R: GTGAAGACGACCTGGACATTC	197	1.5	55	Perrocheau et al. 2006*	DX010659

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	7CA001	7	F: CGATGTGGATGTGCATGAGT R: GGTGGGTGTGCTGTAATGCT	154	1.5	58		AY820149
sequence tagged site	7STS01	7	F: TGTCACCACAGTCATTTGC R: GAGGAAACAGTGACTTCATTACC	562	1.5	TD51		CF722812
sequence tagged site	7STS02	7q14-q15	F: CACCCAGTGTAATCAACCCAG R: GCCTGTCAGTTCCTTTAATAC	155	1.5	56		
ATP-binding cassette, sub-family C, member 8	ABCC8	7q17-q18	F: ACTGAAGCGGAGAGCTACGA R: TCTGGATCTTGCTTGGTCT	202	1.5	64		
acid phosphatase 5, tartrate resistant microsatellite	ACP5	7q12	F: CTGGTCTTGAACAGGGACTTG R: AGAACGGCATAGGCTTTGTG	205	1.5	55	Perrocheau et al. 2006	DX010426
	AHT019	7q17-q18	F: CATTTCTCTGGTGTATCTCCCA R: GGAATAGTCATAGTCCACGACC	137-145	2.0	58	Swinburne et al. 1997	
apolipoprotein A-IV	APOA4	7p15	F: TCTTCAGCACTCTCAAGGAGGAGA R: CACGTGTCCTCAAGCTCATACAAG	198	1.5	58	Lear et al. 2001*	
apolipoprotein C-III	APOC3	7p14 (TAMU)	F: CAGCTATCTGCCTGGAGGAC R: ATGCTGGTCAGCGTATCCTT	217	2.0	58	Shubitowski et al. 2001; Chowdhary et al. 2003*	AY008771
brain-derived neurotrophic factor	BDNF	7	F: AGGCTCGAGAGGCCTGAC R: GCTTCAGCTGGCCTTTTCGAC	382	2.0	64	Momozawa et al. 2007	
baculoviral IAP repeat-containing 2	BIRC2	7p15	F: CCATTTTCAGGGCACATCTTT R: GATGGCCATGGGATATCAAC	248	1.5	58	Brinkmeyer-Langford et al. 2005*	
baculoviral IAP repeat-containing 3	BIRC3	7p16-p15	F: CCGGAAGAATAGAATGGCACT R: TGAATATGGTGGCTGCAAAAT	191	1.5	55	Perrocheau et al. 2006	DX010440
complement component 3	C3	7p16	F: CCACCCCTCTCTTCTCATTTG R: ATCTGGCTTCTGCTTCTGGA	200	2.0	58	Millon et al. 1993*; Caetano et al. 1999	AF097579

chromosome 19 open reading frame 19	C19orf19	7	F: GCCTACAGCCCAGAGAAAGT R: CTGCTGGGCTTGATGAAGAT	164	1.5	58	Brinkmeyer- Langford et al. 2005	BF080172
cell adhesion molecule 1	CADM1 (<i>IGSF4</i> , <i>IGL</i>)	7p13-p12	F: CAGGGTAACCAGCAAGAAGG R: CTGCCCTAGGAGAGGGAGAG	135	2.0	58	Home et al. 1992, Mariat et al. 2001	L07573
ClpB caseinolytic peptidase B homolog (E. coli)	CLPB (<i>SKD3</i>)	7q14-q15	F: TCCTTCTTCAGCTGCTTAGGTC R: GGTCTCGGTACGTCCTCTCTG	194	1.5	55	Perrocheau et al. 2006	DX010582
microsatellite	COR004	7	F: GAGTGTGACGGAGGACGA R: AGGGAGCAAACGCAAGAC	292-312	3.0	58	Hopman et al. 1999	AF083447
microsatellite	COR095	7q13dist^a	F: TACCTCTGGTGGTGATGCTT R: CCCACACTTACTCCCATCAC	206- 216	2.0	58	Tallmadge et al. 1999b	AF154948
microsatellite	COR106	7	F: CTTCCACTTGTGTCTTCTCCC R: GCAATCCTAACC AAACTCC	135-137	1.5	58	Swinburne et al. 2005	
Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	CTR9	7	F: CAAGTGTGGCAAGTTACAGG R: GCTCCAGTTCTTTCACAGC	340	1.5	58		
defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	DCUN1D5	7	F: TGCTTCAACTTTCAGCTCTGG R: ACAAAGGGCCCTCAACAAAACCTTC	~350	1.5	55		BI395196
dipeptidyl- peptidase 9	DPP9	7	F: CCAAAGCACGTTTCTTG GTT R: TATTCAGCGGTCACATCCTG	160	1.5	58	Brinkmeyer- Langford et al. 2005	
dopamine receptor D2	DRD2	7	F: GATGTGCACAGCAAGCATTT R: CCATGCATGCACATACACAC	207	2.0	58	Chowdhary et al. 2003	AF134061
v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	ETS1	7p14.3	F: AGTGGACAGAGACCCACGTT R: CTTTCTGCAGGATCTCCAGGT	192	1.5	55	Perrocheau et al. 2005	AY817465

hemoglobin, beta	HBB	7q15	F: CCTGGGCAGGTTAGTATCCA R: ACCAGCAGCTTAAGGGGTTT	146	3.0	58	Milenkovic et al. 2002* ; Chowdhary et al. 2003	AF134224
Equine EST	HESTG07	7	F: GGCAAAGTGTTTCATCTGTTTTTC R: TACGACATATTCACCTTGGACAATG	~200	1.5	58		AW735737
microsatellite	HTG20	7	F: CTGGTTTACCTTCCCTACAG R: CCAATGGTTCCTCTGAGAAG	170	3.0	58	Lindgren et al. 1999	
microsatellite	HTG33	7	Lindgren pers comm.	~200	2.0	58		
5-hydroxytryptamine receptor 3A	HTR3A	7p14.3-p14.1	F: GCAATGACCCTGTCTCCCTG R: AAATGCCCCGCTGTTGCCTG	296	1.5	65	Prause et al. 2006*	
interleukin 18 binding protein	IL18BP	7	F: CTTCCATCACTTCAGCATCC R: CGTGAAAACACAGGAGAAGC	268	1.5	58		
insulin receptor	INSR	7p16	F: CTGTGGGACTGGAGCAAACA R: CCTCCATCTTGTGAATTCC	100	1.5	60	Brinkmeyer-Langford et al. 2005*	BM255680
lactate dehydrogenase A	LDHA	7q18	F: TGCACACTCCAAGCTGGTTA R: TGGATTGGAAACAACAAGCAA	160	1.5	58		CX603334
microsatellite	LEX015/038	7	F: GCATTCCCATCATCACAT R: CCTGCCTTGCCTCTTTCT	132-145	2.0	50	Coogle et al. 1996	AF075617/ AF075640
microsatellite	LEX045	7	F: AATCGAAGGGCCGCAGAGTT R: CCAAATGCCAGCCTCCTG	233-258	2.0	58	Coogle et al. 1997	AF075647
Ion peptidase 1, mitochondrial	LONP1 (PRSS15)	7p16	F: ACTGCTTGAGCTGCTGGA R: TTGGCCGTGCAGATGAAC	180	2	60	Brinkmeyer-Langford et al. 2005*	CK947971
neural cell adhesion molecule 1	NCAM1	7	F: ACACACACACACGCACACAC R: AAGTGAGTGGGCAACAAAGG	144	2.0	58		AF025992
nuclear factor I/X	NFIX	7q11-q12	F: ATCAAGCAGAAGTGGGCATC R: TCCCCGTCAGTACTTTCCAG	245	1.5	60	Brinkmeyer-Langford et al. 2005*	AW659814

nucleoporin 98kDa	NUP98	7	F: TACCTGAAGGGGTTCTTGGA R: AAGGCCAAGGAAAAGGAAAA	178	1.5	58		
olfactomedin 2	OLFM2	7	F: ACTTCATGGTGGACGAGAGC R: GAGTTGGTGACGTAGAGCAC	185	1.5	TD60	Brinkmeyer- Langford et al. 2005	BF078883
paired box gene 6	PAX6	7q18	F: GCCTAATTCAGGCCACAGAA R: CATGAAATGTGGCAACCAAG	194	2.0	58	Godard et al. 2000*	AY008800
phosphodiesterase 4A, cAMP-specific	PDE4A	7	F: CTCATGTACAACGACGAGTC R: ACCCCTGAGCTGGTCACTTT	426	1.5	58	Brinkmeyer- Langford et al. 2005	AV595552
polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	POLR2E	7	F: CAGACGCTGGAGGAGTTCAA R: CGGTGGGGTCGTCATTGT	106	1.5	55	Brinkmeyer- Langford et al. 2005	CD471676
polymerase (RNA) mitochondrial (DNA directed)	POLRMT	7p16	F: TGATGACCGTGGTGTACGG R: CAGAGAACATCTCCTGGAGG	346	1.5	58	Brinkmeyer- Langford et al. 2005*	CF722762
POU domain, class 2, transcription factor 3	POU2F3 (OCT11)	7p14	F: TGGGCTACCAGGATCTTCTTT R: TGTGTGAAGCCAGCTTAATG	168	1.5	55	Perrocheau et al. 2006*	DX010425
parathyroid hormone	PTH	7	F: ACCTGGGCAAACATCTGAAC R: TCCACATCAGCTTTGTCTGC	199	2.0	58	Chowdhary et al. 2003	AF134233
radixin	RDX	7	F: ACGCCTAGCCACAATTCAG R: ACTGGCATGAAGAACATAGGG	332	4.0	50		
ribosomal protein S15	RPS15	7	F: CAACGGCAAGACCTTCAACC R: TCACGGGCTTGTAGGTGATG	185	1.5	63		
microsatellite	SGCV28	7q14-q15	F: CTGTGGCAGCTGTCATCTTGG R: CCAATTCCAGCCCAGCTTGC	157	1.5	58	Godard et al. 1997	U90604
SRY (sex determining region Y)-box 6	SOX6	7	F: CAGCGTGAGTCCAGTTCTTG R: GCTCATCTCCTGCCTACCTG	186	1.5	59		
thyroid hormone responsive	THRSP	7q15-q16	F: AGCGCTACCCCAAGAACTG R: GCCTTGAGCATGGTGAAGTAG	178	1.5	55	Perrocheau et al. 2006	DX010595
Thy-1 cell surface antigen	THY1	7	F: GGGAGAGAGACCAGCACTCA R: GCCCAGTTTTCTTGTGAGGA	202	2.0	58	Chowdhary et al. 2003	AF134236

microsatellite	TKY005	7p13-p12	F: GTCAGAGTTCTCCAGAAAAGTC R: ACAGATAGATATTCTCTCTAG	107	2.0	60	Hirota et al. 2001	AB048316
microsatellite	TKY012	7p14.3	F: GAAAAAGTGACACAACAGCTT R: ACTAGAGGAATGAGATGTGT	88	2.0	58	Hirota et al. 2001*	AB048323
microsatellite	TKY034	7p14	F: GCCACTGTAATGGTCTGAAG R: GGAAGGTAGAGCATTCTCAG	160	2.0	55	Hirota et al. 2001*	AB048340
microsatellite	TKY035	7p14	F: CCTTCCCCTCTCTCCAAAG R: TTAGAGCTGTGCGATGTCAA	122	2.0	58	Hirota et al. 2001*	AB048341
microsatellite	TKY272	7	F: CTTGAAGATTCAAGGTCATGG R: ATATCATAGCAAATGGCAGG	100 - 116	2.0	58	Tozaki et al. 2000b	AB033923
microsatellite	TKY282	7	F: TTACATCTCTGCACTCTCCC R: GGTCTCATGCAAAACGCAGG	147-155	2.0	58	Tozaki et al. 2000b	AB033933
microsatellite	TKY283	7	F: GGAAGTCATCTCTTTCCAGC R: AATACATGATTCTCTGCCTGC	203 - 207	2.0	58	Tozaki et al. 2000b	AB033934
microsatellite	TKY338	7	F: GGACTAGTTAAATCAGTGGG R: ATGGGACTAGAACTCAGTTC	214-254	1.5	58	Tozaki et al. 2001	AB044839
microsatellite	TKY348	7	F: AGATACATACACACGTGCCC R: CCTGAAAGGTAACCACAAAG	108-128	1.5	56	Tozaki et al. 2001	AB044849
microsatellite	TKY380	7	F: CCCTATTGTCCTTTATAGGTC R: TTACGGCAAACACATTGGTG	119-131	1.5	50	Tozaki et al. 2001	AB044880
microsatellite	TKY461	7p14.1-p13	F: ATGGCCCATCGTAAGAAACA R: GAGGGAGGAAGAAAGGAAGG	162-168	1.5	58	Brinkmeyer- Langford et al. 2005*	AB103679
microsatellite	TKY476	7	F: GCATCTAGAAACTGTTCCAC R: TCATTGCCAACTCTAGGTAC	230	2.0	58		AB103694
microsatellite	TKY506	7	F: CTCCTTCATGCGTGAATCCT R: CAGTGACAGAAAACAGGATGG	187-195	1.5	50	Tozaki et al. 2004	AB103724
microsatellite	TKY512	7	F: CATTACAGTTGCTGTGGAG R: GAATACCTACAGTACAGCGT	157	2.0	58	Brinkmeyer- Langford et al. 2005	AB103730
microsatellite	TKY574	7	F: AGGAACATTGGCAAGAGATG R: TGCAGTCTCTGTATTTGGAT	97	2.0	58	Brinkmeyer- Langford et al. 2005	AB103792

microsatellite	TKY588	7	F: AGGCCACGGAGGATAGAAC R: GTCTTCATTCTGGTACCAG	206	2.0	58		AB103806
microsatellite	TKY613	7	F: CCAAGAAGGGCTGACTTCAC R: GCCTAGACCTGGGGTCTTTC	244-250	1.5	58	Tozaki et al. 2004	AB103831
microsatellite	TKY618	7	F: GTTTTCCATAATGGCTGCAC R: GCAATTCCAATTAGTATCTCAGCA	100-106	1.5	58	Tozaki et al. 2004	AB103836
microsatellite	TKY624	7	F: GTGACAGGAAAGTAGAGGTC R: GTTAGATACATACAGTCT	142	2.0	58		AB103842
microsatellite	TKY638	7	F: CGAAATATAAGGATGGACACCTG R: CCCATCTTCAACTCCTCCAA	131-151	1.5	58	Tozaki et al. 2004	AB103856
microsatellite	TKY690	7	F: GCGGATCAGGATCAACTAGC R: GGGCCCTGACAAGTTCCTAT	193-199	1.5	58	Tozaki et al. 2004	AB103908
microsatellite	TKY703	7	F: TTCAGCAAGAACCACAGCAG R: CCTGGGGTATCAGGTCATTG	181-197	1.5	56	Tozaki et al. 2004	AB103921
microsatellite	TKY724	7	F: TGCATGGGAGAATTACTTCTTTT R: TCTAGGATGGGAGCAGGAAA	288-300	2.0	54	Tozaki et al. 2004	AB103942
microsatellite	TKY757	7	F: TGCAGCCTTTATATTGGAGGA R: CCCCCAGTAGTTGGCTGTAT	113-135	1.5	50	Tozaki et al. 2004	AB103975
microsatellite	TKY822	7	F: ATATATGCTGTGAGCCAACG R: GCTTTCTCACAGTCCTCAAT	249	1.5	62	Tozaki et al. 2004	AB104040
microsatellite	TKY839	7q17-q18	F: CCTTCCGTCCAAACCACCAG R: TCTCTCCACACAGGAAATGA	144	1.5	58		AB104057
microsatellite	TKY858	7	F: CCCCCAGCTTTACTGAGATA R: CATCACTGCCAACTCTAGGT	206	2	58		AB104076
microsatellite	TKY884	7	F: CATCAAGTTCAGGGCCAATC R: CCTTGAACCTTCTGCCTTGC	92	2.0	58		AB104102
microsatellite	TKY927	7	F: TTGGCCCAGTTTCCATTTC R: CCATCGTGGGTAGATATCG	304	2.0	58		AB104145
microsatellite	TKY931	7	F: ATAGCCATGCTATGTTTCACG R: TAGAAATGAGGAGACGGAGG	253	1.5	58		AB104149
microsatellite	TKY946	7	F: GATCCTAGGGCTTTGTGCG R: CATACCATGGAACACTGCTC	110	2.0	58	Brinkmeyer- Langford et al. 2005	AB104164

microsatellite	TKY957	7p15-p14.3	F: AGAAAGTCAGGGAGCAATC R: CCTTTGAGACCACTCCAAAC	145	2.0	58	Brinkmeyer- Langford et al. 2005*	AB104175
microsatellite	TKY986	7	F: CTTTCCCTCACGAAGATGAC R: TAGACTCCAGAATGGCATAAC	118	2.0	58	Tozaki et al. 2004	AB104204
microsatellite	TKY1007	7	F: GAGAGATTTGCTCTGCCTC R: ATATCCTGCACCTACCTTTC	275	2.0	58		AB104225
microsatellite	TKY1029	7	F: TAGCTTTGAGCCTGAAAGTC R: TATCTCTAAGATGGCGAGTG	281	2.0	58		AB104247
microsatellite	TKY1058	7	F: GATCCCCATTGACCATATGT R: TTTAGAATGTTCCCAGGGAG	100	2.0	58		AB104276
microsatellite	TKY1062	7	F: ATCAACCCCTCTTCATCTTC R: AAAGTGGCTCCATTCTTTCG	140	2.0	58		AB104280
microsatellite	TKY1097	7	F: TGATACAATCCACAGAGCTC R: AATCTACCCACGTCCTAAAG	112	2.0	58		AB104315
microsatellite	TKY1107	7p15	F: AGGGGGATGATTGAAAACAG R: TCATGACACTACCTTTCCTG	197	2.0	58	Brinkmeyer- Langford et al. 2005*	AB104325
microsatellite	TKY1112	7	F: GATCACAGTGCGATGACTTG R: AAAATTACCATGTGACCCATC	149	2.0	58	Brinkmeyer- Langford et al. 2005	AB104330
microsatellite	TKY1147	7	F: CTCTGGACTTTGGTTCACCTC R: ATGTACGTCTGCATAGATGC	176	2.0	58		AB104365
microsatellite	TKY1177	7	F: GGGGAAACAGGAGACAAATT R: AAACCACCCAATCTGTGGC	128	2.0	58		AB104395
microsatellite	TKY1294	7	F: TCAACCATGTAATGCTGGAG R: TAGGCCTAAGTGTTCACAAGA	174	1.5	58	Tozaki et al. 2007	AB215237
microsatellite	TKY1518	7	F: GAACATAATCCCCATCTCAC R: CTCCTTCACTCTGCATCTTG	266	1.5	58	Tozaki et al. 2007	AB215461
microsatellite	TKY1929	7	F: GAAGGTCTCTATAGTAACGG R: GGTTTAGGAACAAGGGGCTG	132	1.5	58	Tozaki et al. 2007	AB215872
microsatellite	TKY2165	7	F: CTATGGGAGCATTGAGGAG R: GATTCCAGTGTGGAACAACCT	223	1.5	60	Tozaki et al. 2007	AB216108
microsatellite	TKY2366	7	F: ACGGGCAATTTTCATCGTTTC R: AAATTTTCAGCTTCTCCAGC	228	1.5	58	Tozaki et al. 2007	AB216309

microsatellite	TKY2512	7	F: GCTGGAGCCTGTGATAAGAA R: ATGACCTCTACCGCACACTC	215	1.5	58	Tozaki et al. 2007	AB216455
microsatellite	TKY3464	7	F: CTTCCCAGTTTCAGGCATTA R: TCCACAGAGCATGAGTCAGA	233	1.5	58	Tozaki et al. 2007	AB217407
tripeptidyl peptidase I	TPP1	7	F: CTGGAAGATGGTTTAGGGAAG R: CTATGTGTCATCCCAGACTCC	270	1.25	60	Pascual et al. 2002	BI395244
thyroid hormone receptor interactor 10	TRIP10	7	F: TACCCATCATCGCCAAGTGT R: TTCATGGGCTGGCTGAAGT	250	1.5	58	Brinkmeyer- Langford et al. 2005	BP455004
tubby homolog (mouse)	TUB	7q16	F: GGGCTGGAATGTAACCAGAA R: TCTGGTCCATGCACAATCAT	209	2.0	58	Chowdhary et al. 2003	AF097580
uncoupling protein 2	UCP2	7q14-q15	F: GACCCCAAGCCTTCTACAAA R: CCTCTTCAGCTGCTCGTAGG	464	1.5	52		
uncoupling protein 3	UCP3	7q14	F: GATGAGCTTCGCCTCCATC R: GCCAAAATCCGGGTAATGAT	337	1.5	60		
UEV and lactate/malate dehydrogenase domains	UEVLD (<i>FLJ11068</i>)	7q18	F: CAATTCGTTTGTGGATTTTGG R: TATTCTGCCTTGAGCATCCAC	116	1.5	55	Perrocheau et al. 2006*	DX010480
ubiquitin-like, containing PHD and RING finger domains, 1	UHRF1	7	F: GGGAACCTCGTTCACGTACAC R: TGTTGGTGTGTTGGTGAGTTTC	100	2	60	Brinkmeyer- Langford et al. 2005	BP169308
microsatellite	UMNe074	7	F: CGATGGATGTGCTGTAAACG R: TGCTGCCTTCTCCCTCAC	139-143	1.5	58	Roberts et al. 2000	AF191705
microsatellite	UMNe093	7	F: CGCAGAGTTGGAGACACCTG R: GGTGCCATCCACTGAAACAC	167	1.5	58	Wagner et al. 2004a	AY391287
microsatellite	UMNe100	7	F: CTGATGCAGAGGCATTTCTG R: CGTCAGCTGAGGCAACTATG	183	1.5	58	Wagner et al. 2004a	AY391289
microsatellite	UMNe333	7	F: GGCTTCTGCCTTGTTGTCTC R: CGGCACAGATGTTAGCTCAG	144	1.5	62		
microsatellite	UMNe356	7	F: GATCTCCCAGTCCCCCAC R: TGACGGCTGAGTCAGAACC	177	2.0	58		

microsatellite	UMNe359	7	F: GTGTGACGGAGGACGAGG R: TGGTGCCATCCACTGAAAC	140	2.0	62	Wagner et al. 2004a	AY391348
microsatellite	UMNe425	7p12-p11	F: GAAAGAGCAAGGAGCCAAAG R: GCTTGCAAATGTTTGGGG	213	1.5	58	Brinkmeyer- Langford et al. 2005*	
microsatellite	UMNe459	7q14	F: CTTTTTGGAAGACATCACTCC R: TTAGTCCAAAATACAAGCAGGC	142	1.5	60		
microsatellite	UMNe565	7q12-q13	F: GAGAGCTAACCAGAATTGCCC R: CTATACCGTCAACTCTCCTGGG	~300	1.5	62	Wagner et al. 2004c; Brinkmeyer- Langford et al. 2005*	AY735270
microsatellite	UMNe574	7	F: AAAGTGGTTTCTGCCACCAC R: ATTGGATATTGGTCAGAGTGGG	~150	1.5	58	Wagner et al. 2004c	
microsatellite	UMNe606	7	F: TGCCTTTACCTTACAAACAC R: ATCCAAGAATATCATATTGGC	150	1.5	58	Brinkmeyer- Langford et al. 2005	
microsatellite	VHL108	7	F: TTTCTTTCCCTCAGGCTGGA R: GACCTAAGAGAACCCCTTAAGT	191	1.5	58	van Haeringen et al. 1998	Y08445
extracellular link domain containing 1	XLKD1 (<i>LYVE-1</i>)	7q16-q18	F: TCTCCAGCTTATCCACTTTCAA R: TCTCAGGCTCTTCTTGATGGA	211	3.0	58	Chowdhary et al. 2003*	
microsatellite	ZuBeEq11	7	F: CCAAAGACTAATTACCATCTGCAC R: TGGATGAACATCAAGGGAGA	208	1.5	TD 63-55	Klukowska- Rotzler et al. 2006	CR957095

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	8CA001	8	F: AATACCCGTGCTTTCAAGGT R: CCGGGATGTGGAGCTACG	134-150	1.5	58		AY820145
sequence tagged site	8STS01 (PAI2)	8q23	F: GAGGACGCCTTCAACAAGGG R: TCTGCCACAACTGTGGGCC	200	1.5	TD 65	Mariat et al. 2001	
acetyl-Coenzyme A acyltransferase 2	ACAA2	8	F: CGTCGAGGTGGAAAATATGC R: TGCTCTGAAGGTCACCTGTTT	161	1.5	58		CX597606
adenosine A2a receptor	ADORA2A	8	F: CCACCCTCCCCAGACTTTCC R: GCACCGCTCCATTACAACCTCC	303	1.5	60		AY394857
microsatellite	AHT003	8	F: CAAACATCAGTTAAGAGTGA R: CTCTAATCCAGCAGTGTTCA	123-137	1.5	50	Binns et al. 1995	
microsatellite	AHT005	8	F: ACGGACACATCCCTGCCTGC R: GCAGGCTAAGGGGGCTCAGC	150	1.5	58	Binns et al. 1995	
microsatellite	AHT025	8p17- p16	F: TCCCACATGCCACAACATAGA R: TTCCCCCTTGCTTTTAAAAC	172-176	2.0	58	Swinburne et al. 2000*	AJ272107
microsatellite	AHT130	8	F: TGCAAGAGCCATTTGATGTC R: CCTGTGCTAGAAAGGGAGAA	244-248	1.5	58	Swinburne et al. 2005	
microsatellite	AHT131	8	F: GAGGGGTTGGCTACAGAATG R: AGATTGCCCAACAATTCAGG	183-188	1.5	58	Swinburne et al. 2005	
alpha-kinase 2	ALPK2	8	F: AGCCGCTTCTAAACCAGTCA R: AAGTCCTTGGAACACAACC	197	1.5	60		
microsatellite	ASB14	8	F: CTCCATGAATTCTCGCAGGTTGG R: CCATGGGCCATATGCACACTGC	120	2.0	58	Breen et al. 1997	X95329
activating signal cointegrator 1 complex subunit 2	ASCC2	8	F: CGTGAGACAACCCAGGAAC R: GCTGTGGGATAAGGCACTG	333	1.5	58		CX603744
ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	ATP2A2	8p14- p12	F: TGGCAACAATTTGTGCTCTT R: GCAGGCATTTGCTCGTTCTA	916	1.5	58	Muller et al. 2006*	
ATPase, Class II, type 9B	ATP9B	8	F: GCCAATTCGTCATGCACA R: TGAGGAAGCCCTGGTACAGA	308	1.5	58		DN505743
ataxin 2	ATXN2	8p14- p13	F: TGAGAAATGTTGGAGGCTAGG R: TGTTGTCGAGACTGGAATGG	394	1	55		AY788863

breakpoint cluster region	BCR	8p17	F: AGAACCTCACCTCCAGCGAG R: TCCCGGAACATGCGGTAG	105	1.5	62	Mariat et al. 2001*	
coiled-coil domain containing 5	CCDC5	8	F: GTTGCTGCGTGGTTGAAAA R: ATTCGCTTGCCTTCTGTTTC	163	1.5	60		DN504612
cadherin 2, type 1, N-cadherin (neuronal)	CDH2	8q14-q15	F: TCAGTCCACTGCCACTGTGT R: TTTGCTGCATATATCGATCTGG	199	2.0	58	Chowdhary et al. 2003*	AY008774
CNDP dipeptidase 2	CNDP2 (<i>FLJ10830</i>)	8q21.3	F: CCTGGACGAGCTGATTTTTG R: CGTAAGTGATGCAGGGCTTC	110	1.5	55	Perrocheau et al. 2005*	AY817467
catechol-O-methyltransferase	COMT	8	F: CTTGCTGAGACCTTGACACC R: TCAAGGAGCTCTGCATACCC	251	1.5	62	Momozawa et al. 2005	AB178284
microsatellite	COR003	8	F: TAGGGAAACTCCTCAAAGCC R: GAAACCAAAACCTTCATCCA	186-206	3.0	58	Hopman et al. 1999	AF083446
microsatellite	COR012	8	F: TCTAGGAAAGACCCATCACG R: AGTAAGTGAGGCCAAGGAT	162-176	2.0	58	Hopman et al. 1999	AF083455
microsatellite	COR056	8	F: AGATTCCAGGCATTAGGACC R: TCAGGGACAATCTTCCTCAAG	184-210	3.0	58	Ruth et al. 1999	AF108373
microsatellite	COR097	8	F: GGGATTTCTGAGATGCTGAA R: ATGGCTGGCTAGAGTTTGTG	236-242	1.5	58	Tallmadge et al. 1999b	AF154950
cytochrome b5 type A	CYB5A	8	F: CGGACAAGGCGGTGAAGTA R: TTGGTCAAATCGTACACCTTGT	103	1.5	60		CX594805
DiGeorge syndrome critical region gene 14	DGCR14	8	F: CTACAGGCGGTCATCCAGA R: GGCTCTCGGGACATCTTG	155	1.5	58		
desmocollin 2	DSC2	8	F: GTCTTTGTGGCCTAGCTGGA R: GTTGCTTGTTGCCCTAGAA	205	2.0	58	Chowdhary et al. 2003	AY008781
erythrocyte membrane protein band 4.1-like 3	EPB41L3	8	F: TCAGAGCCAAGCCTTAAACTG R: TTCGCTATGCAGAAACGTACA	150	1.5	60		
family with sequence similarity 38, member B	FAM38B	8	F: TGGAAGGACAAGCCTCATTC R: CCTGAGACGTCAGTGGTGTTC	115	1.5	60		CX600321
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 1	GALNT1	8q16	F: CGAAATGTGGAAACAAATCAG R: TCTAATTTCTTTGTTGGCAGTATAAG	642	1.5	58	Perrocheau et al. 2006	CX598432

galanin receptor 1	GALR1	8	F: CTTCTTCACCGTCTCCATGC R: GAAGAGGCGCTGGTGGTAT	193	2.0	58	Chowdhary et al. 2003	AY008783
GCN1 general control of amino-acid synthesis 1-like 1	GCN1L1	8p15	F: TGGAGAAGTTGGAGAAGCTGA R: TTGAGGATACAGGGGATGATG	166	1.5	55	Perrocheau et al. 2006*	DX010493
G protein-coupled receptor kinase interactor 2	GIT2	8p15	F: TGAAAATTCTGAACCTCAGGAA R: GGATGGTTCACCTCTCCCATT	192	1.5	55	Perrocheau et al. 2006*	DX010494
immediate early response 3 interacting protein 1	IER3IP1 (HSPC039)	8	F: GAATTCTCCCTGAGATCAGAG R: AAAAGTGTACCGGACTGTCAC	310	3.0	58	Chowdhary et al. 2003	
laminin, alpha 1	LAMA1 (LAMA3)	8q12-q13	F: CAACATCTTCCAGAGGGCTCAT R: CCATTTCCCGTCATTGAACTTC	152	3.0	58	Chowdhary et al. 2003	
microsatellite	LEX023	8p13-p12	F: GGATGAAACAGGGAAGGAAA R: CCAACGGATTCATGAAAGCTA	246-268	2.0	58	Coogle et al. 1996; Lindgren et al. 2000*	AF075625
microsatellite	LEX029	8	F: TGGGGTGTCACTGCTTCTC R: ACTGAGGGCCAGGTTTCTAA	260-268	2.0	58	Coogle et al. 1996	AF075631
lipin 2	LPIN2	8q13-q14^a	F: AAAGCTTCCTGCTTACCTTGC R: GAGCAAAAACCTCTCTCCGTGTC	155	1.5	55	Perrocheau et al. 2006	DX010521
methyl-CpG binding domain protein 2	MBD2	8	F: TTGGTCCAGGTAGTAACGATGA R: GACAATGAAAGCCTTGCAGA	158	1.5	60		CX605069
malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2	8	F: TGGACAGAACACACTTATTCAGTT R: CCCAGTAACCTTTTGTGC	235	1.5	58		
molybdenum cofactor sulfurase	MOCOS	8	F: TAACCCTCACAGCCAGAACG R: GCCTCTGCCACCAGTTTAAAG	1082	1.5	55		
metallophosphoesterase 1	MPPE1	8	F: CAACAGTGTGCACTGGAAG R: CACAAGGACTGGGGCTGAC	298	1.5	60		CX601769
asparaginyl-tRNA synthetase	NARS	8	F: GCTGGACAAACCGAGGGTAT R: TGCCTATTTGGGATAGTGAGG	776	3.0	50	Chowdhary et al. 2003	
NADH dehydrogenase flavoprotein 2, 24kDa	NDUFV2	8	F: CTCCTGAGAATAACCCAGATACTCC R: GCAGCCATCCATTCTGTCTT	235	1.5	60		CX594923
pescadillo homolog 1	PES1	8p17-p16	F: GGGTGTTTGACTATGTGAACG R: ATCTCCTTCCTTCTCCGACAC	110	1.5	60		CX602171

piwi-like 1 (Drosophila)	PIWIL1	8	F: TACTCTGGCCAACAAGG R: AGGCTGTGAGAAAGTGGTAG	351	2.0	58	
protein kinase, AMP- activated, beta 1 non- catalytic subunit	PRKAB1	8p15	F: GTCTTCTGAAAACCTCACTCTG R: GTATCTGGTGTGCTGTCTC	146	1.5	60	
proteasome 26S subunit, non-ATPase, 9	PSMD9	8	F: ATCTTCTCTTGCCCTGGACT R: CAGTGTTTCCACCACCTAGAA	112	1.5	58	CX599547
protein tyrosine phosphatase, receptor type, M	PTPRM	8q12- q13	F: CATCCCTGCTCCCAAGTTAG R: CACCGGTTTTTCTCATGGTT	925	1.5	60	CX596065
retinoblastoma binding protein 8	RBBP8	8	F: TCAACTGTCCAAAGACAACCTCA R: TCCTTTAATTTTGTCCAAAGATCC	179	1.5	58	
ring finger protein 10	RNF10	8	F: CTGAGGGTCGGAAGCAAAAG R: GAATTCTGGAAGCTGGGCACAG	250	2.0	58	BI961511
Rho-associated, coiled-coil containing protein kinase 1	ROCK1	8	F: GCATGCTAACCAAGATATTGAA R: TGTGTTTTAAGGGTTCGTTCTG	420	1.5	58	CX604958
arginine/serine-rich coiled-coil 2	RSRC2 (<i>FLJ11021</i>)	8	F: CCTTGCCAAAGCATCTTTC R: GGAACGCAAGTAACTCCTCA	167	3.0	58	Chowdhary et al. 2003
squamous cell carcinoma antigen recognized by T cells 3	SART3 (<i>SCCA3</i>)	8p16- p15	F: GTGACACTTGTTTTATAGCAATTCTG R: CAAAATACATCCATATTTGAATGC	241	2.0	58	Lear et al. 2001*; Chowdhary et al. 2003
strawberry notch homolog 1 (Drosophila)	SBNO1	8	F: CACCAGTTATTTACCTGCTC R: TCATCCAGGGTATTAGGAGGA	~263	1.5	58	DN507503
scavenger receptor class B, member 1	SCARB1	8	F: GGTAAGACCTCCAGTCCTTC R: CGGATTTGGTAGACGATGG	125	1.5	54	CX595686
scavenger receptor class F, member 2	SCARF2	8	F: CCTGGATAACACACTCAACTGC R: GTGGTGTGCAAGGAGGAGA	105	1.5	60	
serpin peptidase inhibitor, clade B, member 2	SERPINB2 (<i>PAI2</i>)	8q23	F: CCGGAATTTGGCAGACTT R: CCATTCATCCTTCCGTTCTC	106	1.5	58	Mariat et al. 2001*
splicing factor, arginine/serine-rich 8	SFRS8	8p13	F: GTGGCTGCGGTTACAGAA R: CAGGTAAGAGACTGCTGGTCA	174	1.5	58	CX599637

microsatellite	SGCV32	8q14-q16	F: TGTTCCAAAATGGAGGGTGAGCC R: CCACAGGCTCTTAAAACCAGAAGC	139	3.0	58	Godard et al. 1997*	U90607
solute carrier family 15, member 4	SLC15A4	8	F: CATTCTGTGAGGTACGACCA R: GCCCGACATTTATGGCTAC	170	1.5	58		
SMAD family member 2	SMAD2 (<i>MADH2</i>)	8q21.1	F: CTCTCCCGTAAAGGAGGAAGA R: GAAGCAGCACACACACACCTA	196	1.5	55	Perrocheau et al. 2006*	DX010522
small nuclear ribonucleoprotein D3 polypeptide 18kDa	SNRPD3	8	F: TGGGACGTGGAAACATCTTC R: ACCCCCGAACTGAGATAACC	100	1.5	54		DN508752
T-box 5	TBX5	8	F: CTACCGCTCCAGCTACCC R: GCTATTGTCACTCCACTCTGG	496	1.5	64		CX593794
thyroid hormone receptor associated protein 2	THRAP2	8p14	F: CAGAAGGCAGTCAAGCTCAACC R: CTCAGACAGACACGCACAGCAAC	416	2.0	58		BI961576
microsatellite	TKY359	8	F: ATAATCAGCATGCCTCTCAG R: AGGAACATTTCTTACCTTAC	191-203	1.5	54	Tozaki et al. 2001	AB044859
microsatellite	TKY362	8	F: GACCTCTCAGCGTAGATTAC R: GCTGTTTCAGGTCCAACAG	186-190	1.5	50		AB044862
microsatellite	TKY391	8	F: GCCGAAAACAACCTGCATACTG R: CTTTAGGGCCAATTATCTCC	182-188	1.5	54	Tozaki et al. 2001	AB048297
microsatellite	TKY409	8	F: TCCTCAGAGCCCCGAAAATTA R: ACTGTTGACGGCCACTGATT	326-340	1.5	58		AB103627
microsatellite	TKY436	8	F: CCAGAAATCCCGAGTAGCTG R: GGTCTTTCCAACCACATACACA	144-154	1.5	58	Tozaki et al. 2004	AB103654
microsatellite	TKY458	8	F: CACACACTCTTGGGGAAATG R: AAGCCACCCAGAGCCAGGTG	133	2.0	58		AB103676
microsatellite	TKY468	8	F: TTCCCTAAAGGCAACCACAG R: TGTGGAATCAATGTTCTGCAA	284-296	1.5	55	Tozaki et al. 2004	AB103686
microsatellite	TKY470	8	F: CCGAGATCACTCAAACCTGAT R: AGAGACCAAAGGATAGGTAG	197	2.0	58		AB103688
microsatellite	TKY509	8	F: CCTGATTGATGTATCTCCAC R: TTGATGAGGACGTTATGCTC	237	2.0	58		AB103727
microsatellite	TKY513	8	F: CCCGCTTCAGTGAAATGTCT R: CCAAGTCAAAACACCGTAACAA	232-246	1.5	50	Tozaki et al. 2004	AB103731
microsatellite	TKY573	8	F: CAGAATGAGGCGTTGAATCC	252-260	1.5	58		AB103791

microsatellite	TKY620	8	R: AGAGGCTTTAGGCTGGGAGT F: GGACTTGGTCTGGTGA CTCC R: CCATTGTGATTCTCCGTC ACT	155-169	1.5	58	2004 Tozaki et al.	AB103838
microsatellite	TKY653	8	F: ACTGGCTCCAAAGACCATG R: CGTTGAGGACATTCTCTCAC	225	2.0	58	2004	AB103871
microsatellite	TKY669	8	F: CCCAGTTTTCCATCGTGAGT R: TGA CTGCTGGCATT TGTTC	186-200	1.5	58	Tozaki et al.	AB103887
microsatellite	TKY813	8	F: CCACCAATCTGTGGTTCTAT R: TGATGTTCTCCTTGCCGAAA	197	1.5	62	2004 Tozaki et al.	AB104031
microsatellite	TKY894	8	F: TCCCATTTACCATAGCATCA R: AGCAA ACTA ACCAGTCCTC	232	2.0	58		AB104112
microsatellite	TKY901	8	F: TGCCCAAGACACTGGTTTG R: TACCACAAAGTCAAGGTCTG	264	2.0	58	Tozaki et al.	AB104119
microsatellite	TKY904	8	F: AAGATTGGCATGGGTGTTAG R: GGCTGCACCATTTTACATTC	159	2.0	58	2004	AB104122
microsatellite	TKY923	8	F: ATTCAGCATGGTGATTGTAGT R: TGTTGGTATGAACATTTCGTGC	298	2.0	58		AB104141
microsatellite	TKY932	8	F: ACTTAGAAGAGGAGAAGACTC R: GATATTGTTGCAAAGGGCAG	205	2.0	58	Tozaki et al.	AB104150
microsatellite	TKY955	8	F: GCAGAATCATGGAGATGGAG R: ACCACATGGATAGCTTTACC	205	2.0	58	2004 Tozaki et al.	AB104173
microsatellite	TKY961	8	F: TCAGTCCAGAGGTTTCAGTG R: CAAGGGAGAATCGAAGCATC	164	2.0	58		AB104179
microsatellite	TKY985	8	F: ATTGGCATGGATGTTAGCTC R: AAAGTGCATGGTCTGAATCC	101	2.0	58		AB104203
microsatellite	TKY994	8	F: AGTTGCTACTAGAGATGCTG R: CTGCAATGGTCCAGAAGAC	118-124	2.0	58	Tozaki et al.	AB104212
microsatellite	TKY1045	8	F: CACTCCAGTCTTCCTGAAAC R: GAATTCTAGTTCGGTCCCTC	120	2.0	58	2004	AB104263
microsatellite	TKY1051	8	F: GTTGGCCTTAATACTCATGC R: AATAGACATAGAGTGCCCTG	96	2.0	58		AB104269
microsatellite	TKY1056	8	F: CATGCTCTTAGCTACTATGC R: TCATGCTGTTAGCATTGTGG	123	2.0	58		AB104274

microsatellite	TKY1157	8	F: AAAGGTGCCATTTTCGGGTC R: CAAGCCTTATTTGTTGAGTGC	181	2.0	58	Tozaki et al. 2004	AB104375
microsatellite	TKY1161	8	F: AGATGGGACACGGATGTTAG R: TGTAATAATCATGTGGGCCTG	284	2.0	58		AB104379
microsatellite	TKY2159	8	F: GCTAGTCATGGAGAAATCTA R: ATATTGGACAGAGCAGGTC	147	1.5	58	Tozaki et al. 2007	AB216102
microsatellite	TKY3255	8	F: TTTTATACCTGCCAATGGTG R: TGAAACAGAGCTGTGAACAG	110	1.5	58	Tozaki et al. 2007	AB217198
microsatellite	TKY3280	8	F: CCCTGTGAATGAGAATTCAC R: ACCACCTGTCCATGTGACA	123	1.5	58	Tozaki et al. 2007	AB217223
two pore segment channel 1	TPCN1	8p14	F: ACTTCAGCACCTGGAGAAC R: ATGAAGAAGACGCAGGACCA	375	2.0	61		AY847946
thymidylate synthetase	TYMS	8q12- q14	F: GCCCTGCTCACCTACATGAT R: TCCATGGAAGGTTACAAAGTGA	194	2.0	58	Lear et al. 2000* ; Chowdhary et al. 2003	AF130786
ubiquitin-conjugating enzyme E2L 3	UBE2L3	8	F: AGCCTGGAAACTCCCACCTTT R: TTAGAACCAACCCCCACACT	160	2.0	55		
ubiquitin protein ligase E3B	UBE3B	8	F: CCTGGACTTCTGGAGAACAGTGTC R: CCAGAGGAACTGAGCATTTAAGGG	151	2.0	58		BI961658
microsatellite	UCDEQ046	8	F: GCCAAACGCTGGAGGGTT R: CCACATTCACACACATGCACAC	230-238	2.0	58	Eggleston- Stott et al. 1996	U25171
microsatellite	UM033	8	F: CATTGTCCTGAGCAAGTC R: CTATCCGTCAAGTGTTTC	126-140	2.0	58	George et. al 1998	AF195579
microsatellite	UM034	8	F: TTGAAACCCTTCAGACCC R: CAGAGAGCAAGTGTGAG	102-117	2.0	58	George et. al 1998	AF195580
microsatellite	UMNe070	8	F: TGGGCATTATTTACAGTATGC R: TACATTAGGCCTGGAATGGG	150-152	1.5	58	Roberts et al. 2000	AF191703
microsatellite	UMNe164	8	F: AAAGAGGAGGATTGGCAATG R: ATCTCCAGTGTGACAATCTCTACC	105	2.0	58	Wagner et al. 2004a	AY391307
microsatellite	UMNe211	8	F: ATCCATGTTCTTGTGAATGGG R: CAATCTAGGTGCCAAACAACCTG	149	2.0	62	Mickelson et al. 2003	AF536293
microsatellite	UMNe238	8	F: CCAGCACCCTGTTCAAGAC R: TCTAGCCATATGTTACCCTGCC	198	2.0	58	Wagner et al. 2004a	AY391326

microsatellite	UMNe385	8	F: GGATGCCAATCTCCTTTTCAC R: CTATGTCTTTATAAGCGCGCG	156	2.0	58	Wagner et al. 2004c	AY735244
microsatellite	UMNe479	8	F: TACGGTAGGACCAATGCCTC R: GCCGTCAGAGAAAAGACAGG	~200	1.5	58	Mickelson et al. 2004	AY731401
microsatellite	UMNe526	8	F: GGCTGTCAGGGGTCACAC R: ACATTGATACAATCCATCCACC	147	1.5	60	Wagner et al. 2004c	AY735260
microsatellite	UMNe532	8	F: TAACATCAATTGGGCAAAACG R: GTAGCAAAAGGGGTGTGTGC	233	1.5	58	Mickelson et al. 2004	AY731408
microsatellite	UMNe545	8	F: TCGCTCTCCTCTCTGTCTC R: TATGGCTGCAGATTCCACTG	197	1.5	62	Wagner et al. 2004c	AY735265
microsatellite	UMNe578	8	F: TTCACACGCTCGTTCTCATC R: TTGTGCAAAAAGAGCCTACTTG	~125	1.5	58	Wagner et al. 2004c	AY735279
microsatellite	UMNe579	8	F: ACAAGGTCACGCCTGAGC R: TGTGGAAACTCTGACTTGGG	~225	1.5	58		
VAMP-associated protein A, 33kDa	VAPA	8	F: TAGCAGATGTCAGTTGCACATTC R: AAGGAGAAAATTTACACTGTAAGGC	254	3.0	TD 60		G62203
microsatellite	VHL073	8	F: GGTCATTCTCCCAAAGCAAAAC R: AAGAGAAGGTGGATTTCAGAGG				van Haeringen et al. 1998	
vacuolar protein sorting 33 homolog A (S. cerevisiae)	VPS33A	8p14-p13	F: CAAGTGGCCAATATGATGATCAGGATG R: ACAATGAAGGGAACCAGCAC	800	1.5	58		
WD repeat and SOCS box-containing 2	WSB2	8p14	F: CGCTGCTCTCCTTCAGTG R: GCACCTATTAAGAAAGCCAAAG	122	1.5	54		CX602847
X-box binding protein 1	XPB1	8	F: TCCAAGCAGAGAACACCTACC R: ATGGAGAAAGCACCTTCCAA	157	1.5	58		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	9STS01	9	F: CATGACACCTTTTGA CTCTTC R: TGAAGCCCAAAAGGGAAC	130	1.5	58		
actin-binding Rho activating protein	ABRA	9	F: AACCAAAACCGCTGAAAGG R: AGTCCACCAGTCCGTGTTTC	209	1.5	60		
microsatellite	AHT053	9	F: CACTCATCAAGCCATGCTGT R: TGCCACAGAGTAGCTGATGC	286	2.0	58	Swinburne et al. 2003	AJ507670
microsatellite	AHT096	9	F: CCCTATGCCAGGCACTGTAT R: GATCTTATAGCTTCTCACTACA	241-251	2.0	58	Swinburne et al. 2003	AJ507713
microsatellite	AHT104	9	F: CACTGAACTCACAGAAATGGAGAG R: TAACCATGCTGTCCATTACATC	149-151	1.5	58	Swinburne et al. 2003	
ankyrin repeat domain 46	ANKRD46	9	F: GCTTTGACCCAAACATTCGT R: TATCCACATGGCCACAGAGA	165	1.5	60		CX599917
microsatellite	ASB05	9q16-q18	F: TCGAGGAGCTCATGACCTGG R: TTGTACA ACTCTCCACCATAGC	115	2.0	58	Breen et al. 1997*	X95320
microsatellite	ASB21	9	F: TCTTTGGGATTTTCCCTGCAGC R: CTGATTGATGAGAAGAAGGC	168-178	2.0	58	Irvin et al. 1998; Lear et al. 1999	X93535
ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d2	ATP6V0D2	9p15-14	F: CCGAGCTGTACTTCAACGTG R: CAGGGTCTCGCACTGGAC	113	1.5	60		CX594477
ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	ATP6V1C1	9	F: ATTGATTGCAACTTGCTGGA R: TGGACCACTACGGGAGAACT	170	1.5	62		CX597400
antizyme inhibitor 1	AZIN1	9	F: TCATGGCATGTCAATTTTGC R: CAGAACCACACACGTTACCT	313	2.0	58		
carbonic anhydrase III, muscle specific	CA3	9	F: CTGACCACTGGCATGAATTTT R: CCGTTGTTCAGGATGGTCTT	151	1.5	65		
coiled-coil-helix-coiled-coil-helix domain containing 7	CHCHD7	9	F: CAGGGAAAGCTGTTCCACTTAC R: TATGGCATCTTTCCCATTGC	955	1.5	58		DN510885
chromodomain helicase DNA binding protein 7	CHD7	9	F: GTTTGACCGGCTTCTCACTGG R: GCGGAGAGAGGGCTATTCAAC	366	1.5	58		
chromatin accessibility complex 1	CHRAC1	9	F: CGATGAAGCCGAATCCTAAA R: GTCGGGCTTACTTCCCTTTC	219	1.5	58		CX592924

COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	COPS5	9	F: GAAAATGCAATTGGCTGGTA R: CTAAAGGCGCCAAGATTAC	807	1.5	60		
microsatellite	COR008	9	F: TAAGTGCTGAGTCTGGGACC R: TGGTAGATAGCGTCTGGAGG	240-264	1.5	58	Hopman et al. 1999	AF083451
microsatellite	COR013	9	F: TTCCCCTGGGTCCTAAATAC R: CCTTTTCCCCATAGGTCTGT	248-254	2.0	58	Hopman et al. 1999	AF083456
microsatellite	COR093	9	F: GAACCTGGGCTGCTGAAG R: GGCACCAAAAGGGAATTAGT	251-263	2.0	55	Tallmadge et al. 1999b	AF154946
microsatellite	COR098	9	F: GCAACAGATGTTGGCTCAG R: GGAGATGTCCTTGACCACAG	235-251	2.0	58	Tallmadge et al. 1999b	AF154951
cysteine-rich secretory protein LCCL domain containing 1	CRISPLD1	9	F: GGGCAGCCAGAACTTTGTAT R: AGGTACCACAATATGGCAACA	195	1.5	60		CX594553
eukaryotic translation initiation factor 3, subunit 6	EIF3S6	9	F: CATGTTGGCAGACAAACTGAA R: GGCCAACATCTGGCTTCTAA	196 + Intron	1.5	60		
exostoses (multiple) 1	EXT1	9	F: AGCTGGTTTGGCTACATGC R: CAAAGTCGCTCAATGTCTCG	113	1.5	58		
fatty acid binding protein 4	FABP4	9	F: ATAAGCCAAGGGACGTTGAG R: AACAACACAACCAGGCTGAA	153	1.5	60		
fatty acid binding protein 5	FABP5	9	F: GGAATGGGATGGGAAGGAA R: CCCTGTCCAAAATGATGCT	850	1.5	58		
ganglioside-induced differentiation-associated protein 1	GDAP1	9p13	F: CATTGATTATCTTGAACAGAC R: AGCACTAAACCACCATCATG	214-222	1.5	54	Blechynden et al. 2002	
gamma-glutamyl hydrolase	GGH	9	F: TTGAAGAGGATAAAGCGCTGA R: CGCCATGAGAGGCAAGTTAT	165	1.5	62		CX603845
microsatellite	HMS03	9	F: CCAACTCTTTGTACATAACAAGA R: CCATCCTCACTTTTTCACCTTTGTT	151-169	2.0	58	Guérin et al. 1994	X74632
microsatellite	HTG04	9	F: CTATCTCAGTCTTGATTGCAGGAC R: CTCCTCCCTCCCTCTGTTCTC	129-139	3.0	58	Ellegren et al. 1992	AF169165
microsatellite	HTG08	9	F: CAGGCCGTAGATGACTACCAATGA R: TTTTCAGAGTTAATTGGTATCACA	188	3.0	58	Marklund et al. 1994	AF169292
KIAA0196	KIAA0196	9q16-q17	F: AGCACACGTGCCTAATTTCA R: TGCAGTTATATGAGCGGTTGA	151	1.5	58		CX596975

Kruppel-like factor 10	KLF10	9	F: AGAATCTGCTTCCGGGTACA R: ACTGGGCTCTTCTCCTCCTC	304	1.5	60		CX605713
microsatellite	LEX019	9	F: TTCCCTTTTTCCTCACATCCT R: TTTTAGGTTTCATCTATGTTGTTGC	157-161	3.0	58	Coogle et al. 1996	AF075621
microsatellite	LEX070	9	F: CATCTCATAACCGTGGATTGA R: ATTCGCCTCTTGACAGTCTG	233-250	2.0	58	Coogle et al. 1999	
leucine rich repeat containing 14	LRRC14	9	F: GTTTACCCGCAGATCCACAC R: CTTCCCTCTGCTGTTCAAGG	617	1.5	58		
lymphocyte antigen 6 complex, locus H	LY6H	9	F: TGCATGTGAGTGACTGCTTG R: ACCTAGAAGTGCGGGATGTG	350	2.0	58		BI395116
MCM4	MCM4	9p13-12	F: TGTAGACATGAGGAAGATTGGTAG R: CAGTCCGGGGATCAGTTG	194	1.5	60		DN506988
minichromosome maintenance deficient 4	MTDH	9q14	F: CCAGACGGGAAACGTGAATA R: CCCAAATGTCTTCCAGCACT	239	1.5	60		CX594650
metadherin	MYC	9q16	F: GGTGAACCAGAGCTTCATCTG R: AGGTACAAGCTGGAGGTGGAG	205	1.5	55	Perrocheau et al. 2005	AY817477
v-myc	NBN	9q13-14	F: GCAGAATGGCCTTTTCCTTAAC R: TCCTCCAAGTTGCAATACAGC	644	1.5	60		
myelocytomatosis viral oncogene homolog	NOV	9	F: AGAAGAAGCAGAGCATATCAGCAGA R: CTTGTTCGTGAGTTTGCATAATTATGG	243	2.0	58		
nibrin	NSMAF	9p13	F: TGGCAGAGAGTAGCTGAGAG R: GCTAATCCTTCCCCAGGTTC	231	1.5	58		
nephroblastoma overexpressed gene	NUDCD1	9	F: CTCCCATGTCCACTGTCCTT R: CCAGCCACCACTGAATACCT	236	1.5	60		DN509026
neutral	PENK	9	F: TGGAGTAACTTTTCGCCTTCTTC R: GGGCTTCATGAGAGGCTTAAA	194	1.5	55	Perrocheau et al. 2006	DX010554
sphingomyelinase activation associated factor	PKIA	9	F: CCTGGCTGGAATGCATTTAT R: ACATCCAAACACAAGCCACA	181	1.5	60		
NudC domain containing 1	PPM2C	9	F: GTAAGGAGGCGTCCAAACTG R: CTTGAGCCTCCAAGGAGATG	156	1.5	60		
proenkephalin	PRKDC	9p12	F: ACATGGCACCACCTCATCAAA R: CGCAATGTGCACAATTAACC	187	2.0	58	Bailey et al. 1997;	U97529
protein kinase inhibitor alpha								
protein phosphatase 2C, magnesium-dependent, catalytic subunit								
protein kinase, DNA-activated, catalytic								

polypeptide							Caetano et al. 1999*	
RAD21 homolog (S. pombe)	RAD21	9	F: GCAATATTGGCGCATGTAATAA R: ACCATCCCTAAGCACAGTTGTT	213	1.5	59		CX595401
ring finger protein 19	RNF19	9q14	F: AAGGCAAGCTCACAGATGAAG R: CAAGAATTCTCTGAAGGAACCAA	218	1.5	55	Perrocheau et al. 2006*	DX010467
ribosomal protein L7	RPL7	9	F: AAGCGAATTGCCCTGACAGA R: CCACAGGAAGTTGTTTGCTTCT	500	1.5	58		
ribosomal protein L8	RPL8	9	F: AAGGCAAAGAGGAACTGCTG R: TTTATTGAGCCCCAACACT	617	1.5	58		CX604741
ribosomal protein S20	RPS20	9	F: GAAAGGACCAGTTCGGATGC R: CACGTCTTGGAACCTTCACC	503	1.5	58		
scribbled homolog (Drosophila)	SCRIB	9	F: GGAGCTGGTCCTACTTGTGC R: TTGGAGATAAAGATGCCCTCA	165	1.5	55		
snail homolog 2 (Drosophila)	SNAI2	9p12-p11	F: ACAAGCAGCTGCACTGTGAC R: TGAGTTCTGATGTGTCTTGC	184	1.5	55	Perrocheau et al. 2006*	DX010585
TGFB-induced factor	TG	9q16	F: AGTGATGGGGATGCTCTCTG R: GCTTGCTCGGCCTGTACTTA	210	2.0	58	Caetano et al. 1999	AF130785
microsatellite	TKY291	9	F: TCTGACTTGTTGTTGGAGTG R: AACTCAACACCATGTTCTGC	81-85	1.5	58	Tozaki et al. 2000b	
microsatellite	TKY293	9	F: CACAAACGTACTGTTACGGC R: ATAGACCACCGGAAACTGAG	78-90	1.5	58	Tozaki et al. 2000b	
microsatellite	TKY452	9	F: TATTATGCCACCAGGCCAGT R: TGACCATGGTGAACCAGAGA	266-278	1.5	55	Tozaki et al. 2004	AB103670
microsatellite	TKY453	9	F: CTTGTGGAAAAGTTGCATGG R: GACATGGCACATTCATGGAC	232-258	1.5	58	Tozaki et al. 2004	AB103671
microsatellite	TKY457	9	F: GCCTCAAAGTTGGGTGAAAA R: ACTCCCTTTCCGAGATTGGT	273-287	1.5	58	Tozaki et al. 2004	AB103675
microsatellite	TKY465	9	F: CCTACACACTGCTCTTCAAG R: TCAAGGGTAATAACCTGCTG	196	2.0	58		AB103683
microsatellite	TKY505	9	F: ACACCAAATTTTCCCACACA R: TCTGTGCCACACAACCTTA	195-213	1.5	58		AB103723
microsatellite	TKY529	9	F: AGCATCCCTTTCTTCCCACT R: GGAAAGAGGTGCTGGTTGAG	146-158	1.5	58	Tozaki et al. 2004	
microsatellite	TKY533	9	F: CACTCTCCAGCTGGGTAGC R: AGGTGATGGGCTGGATACAC	232-240	1.5	58	Tozaki et al. 2004	AB103751
microsatellite	TKY540	9	F: TCCCACAACAGTTCCTCTCC	166-192	1.5	58	Tozaki et al.	AB103758

microsatellite	TKY627	9	R: GAGATTGTGGGGGCATCTTA F: GTGGGATAGGAGGGAGAGGA R: CGAAGAGCTTGCTAGTTACCC	215-227	1.5	58	2004 Tozaki et al. 2004	
microsatellite	TKY676	9	F: ACCATGTTTCTGAAACACTC R: ACCATTGCTTGAGCTAATTC	192	2.0	58		AB103894
microsatellite	TKY699	9	F: TGA CTGACATGTATACTGGT R: AACTGACACAGGTTTCAGTC	132	2.0	58		AB103917
microsatellite	TKY714	9	F: AATTCACCTATGTATG R: CGGGATAGACTGATCCATTG	106	2.0	58		AB103932
microsatellite	TKY805	9	F: TGCCTTTTTCTCTCATCACC R: AGACTAGTCTGCAAGTTCAG	199	2.0	58	Tozaki et al. 2004	AB104023
microsatellite	TKY878	9	F: GCTTAGCATAATGTCCAAGC R: TCACAATAGCCAAGACATGG	203	2.0	58	Tozaki et al. 2004	AB104096
microsatellite	TKY879	9	F: CTCAATGCTCTCGAAAGTCC R: TGCAGCCAGACTGAGAAG	243	2.0	58		AB104097
microsatellite	TKY895	9	F: CTGGGTAGACTGGAACATG R: TCTATAATCACCTGTGGGAG	90	2.0	58		AB104113
microsatellite	TKY916	9	F: TCTGATAACAGCAATGCCAG R: AAACAGAACTAAGTGGCCAG	119	2.0	58	Tozaki et al. 2004	AB104134
microsatellite	TKY939	9	F: GAGCAAGTGTGAAGTAATGC R: AATTTTCCCCACAGTGTCAG	286	2.0	58	Tozaki et al. 2004	AB104157
microsatellite	TKY1010	9	F: AAGAGAAGCTGTGGATATGG R: TTGTGGATACCAGAGAAGTG	253	2.0	58		AB104228
microsatellite	TKY1138	9	F: GAAGATTGGCAACAGATGTTG R: AGTAAACCCTGCTTGAGTAG	174	2.0	58		AB104356
microsatellite	TKY1831	9	F: ACAAGATGGGTGTAAGTAGT R: ATGCTTTTCCATTGGACAGT	186	1.5	58	Tozaki et al. 2007	AB215774
microsatellite	TKY1884	9	F: ATGAATGAAAGCCATTCTCC R: TATTCTGACCAATCACTTCC	243	1.5	58	Tozaki et al. 2007	AB215827
microsatellite	TKY2223	9	F: TAAGCAGGAAAGAGAAAGAC R: TGTTATCTCCCTTTCTGACT	208	1.5	58	Tozaki et al. 2007	AB216166
microsatellite	TKY2231	9	F: CAACAGAAGAAACGAGCGAG R: CAATGGAACCTCTGCCTTTG	129	1.5	58	Tozaki et al. 2007	AB216174
microsatellite	TKY2459	9	F: AATGCATTTTGTGCACCCG R: TTTGGGTTGTCTTTTTCCAG	172	1.5	58	Tozaki et al. 2007	AB216402
microsatellite	TKY2519	9	F: TCCTTTTAGGGACACAGTGC R: CCAAATCAAGCAGCTGATAA	223	1.5	58	Tozaki et al. 2007	AB216462

microsatellite	TKY2750	9	F: ACTTGGAAGGGACCTGAGAG R: GATCTCAGAAGGAGGGCTTC	178	1.5	60	Tozaki et al. 2007	AB216693
microsatellite	TKY2751	9	F: CTACACTACAATTTGGGCAC R: GTCACCTCCCCAGGAATCTC	247	1.5	60	Tozaki et al. 2007	AB216694
microsatellite	TKY2874	9	F: TCTGCAGGAAAAGCAGTCTT R: CCCTCTTTGAACTCCCAA	172	1.5	58	Tozaki et al. 2007	AB216817
translocation associated membrane protein 1	TRAM1	9	F: TCTGTGGGCAGTCTTGTGTTG R: AAAGCAGAATGTTCCCTCCA	559	1.5	60		
thyrotropin-releasing hormone receptor	TRHR	9	F: CTTTGTCTGGGCTTTCACATC R: TGAATCCGTAGAGGACAGTGG	200	1.5	55	Perrocheau et al. 2006	DX010603
microsatellite	UM037	9	F: TCATTTTATCCTCCACCTC R: AAAAGGGCGTAATATGG	108-118	2.0	58	George et al. 1998	AF195582
microsatellite	UMNe103	9	F: GGTAAATTAATCCAAGGTATTTTATTC R: AGAGGAAGACTGGCACAGATG	152	1.5	58	Mickelson et al. 2003	AF536248
microsatellite	UMNe123	9	F: CTCCAATTCTGCCTAGCAG R: GGGGCCATAGGTAGACTTTAGG	156	1.5	58	Mickelson et al. 2003	AF536255
microsatellite	UMNe155	9	F: GAAAGAGAAGAACCCAGCCC R: TAATCTTTGAAAGTGACGCGC	135	1.5	62	Mickelson et al. 2003	AF536267
microsatellite	UMNe189	9	F: GATCAAATACCCTCTGCAAAGC R: GGCTTCATATCCTCCCTTACC	148	2.0	58	Mickelson et al. 2004	
microsatellite	UMNe204	9	F: TAATTAATGTAGCGCCAACCTG R: TCCAAGCAAAGATAAACAGTGG	125	2.0	58	Mickelson et al. 2003	AF536287
microsatellite	UMNe212	9	F: CCACATAATCACATGGGTGC R: GCTCCACTCATAGCTGAGGG	105	2.0	58	Mickelson et al. 2003	AF536294
microsatellite	UMNe322	9	F: TCATGTGAGGCTCCTCTGG R: TTCATAAATCATCGTTAATGCCA	105	1.5	58		
microsatellite	UMNe342	9	F: TCCACTCTCCCAAACCTCTG R: TGCAGCTATCATTTTACCATGG	207	2.0	58	Mickelson et al. 2004	AY731388
microsatellite	UMNe393	9	F: CAAATTTCTTAAGGCCTTACCC R: CCTAACGAGAATGTGAGGAGG	163	2.0	62		
microsatellite	UMNe438	9	F: GATGGTTCACGCTTTTCACC R: CTCTGGGTGATTTATTGGAACC	254	1.5	58		
microsatellite	UMNe493	9	F: GAACAGAAGGAAAAGCCATCC R: ATGGAAGCTTTGCTCCTAAGG	108	1.5	55	Mickelson et al. 2004	AY731403
microsatellite	UMNe496	9	F: AGCCCCCAAATTCTCAG R: GAAGCTGGTGAACAAAAGGC	154	1.5	58		
microsatellite	UMNe507	9	F: TGTCCAGCTGAGCCCTTC	200	1.5	60	Wagner et	AY464510

microsatellite	UMNe518	9	R: TGTGTATGTGTGTGCATGTGC F: TGGCCAAAAAATCTCATATCC R: GCCTTAGCACCCTGACTGG	296	1.5	58	al. 2004b	
microsatellite	UMNe540	9	F: ATTCTCAGGTGACCAATCGC R: AAAATTTCCCAGGGTGTTC	371	1.5	58		
microsatellite	UMNe577	9	F: CCGTGCCTTTTTCTCTCATC R: ATGAATGGTTACTGGTGACCG	250	1.5	58	Wagner et al. 2004c	AY735278
microsatellite	UMNe580	9	F: CCCTGTTGCCACCAACTC R: ACAACCCAAGTGTCTTGATG	242	1.5	58	Wagner et al. 2004c	AY735280
ubiquinol-cytochrome c reductase binding protein	UQCRB	9	F: TGCAGATGATACAATACATGAGA R: TTTGTCCACTGCTCTTTAGGC	151	1.5	60		DN504187
microsatellite	VHL126	9	F: GACCCAACATTGTATGTAAGCG R: TGTGAATAGATATAAGTTGCTTGC	85-87	2.0	58	van Haeringen et al. 1998	Y08447
microsatellite	VHL219	9q16	F: ACTTATTGGTTTATCTTTGCCATC R: CTACATCTCAGTGTTCTTATCTG	100	1.5	62	van Haeringen et al. 1998	
zinc finger protein 706	ZNF706	9	F: GACACCTTTGACTCTTCTCAGACCTT R: TTTATAACAAGGATGGACTGATTTTCAG	203	2.0	58		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequenced tagged site	10STS01	10	F: GGGATAGCAGAACCACCAAA R: CATCACTGTGGTTGGCTTGA	235	1.5	58		AB218742
sequenced tagged site	10STS02	10	F: CCCACTTTGTAGTGACGTG R: ACCCAGAGTATTCCATAGCTTG	755	1.5	60		
sequence tagged site	10STS03	10	F: CCTTCAGGAACATCAAGACC R: CGTTCAGTTCGTCCTTCT	196	1.5	58		
microsatellite	AHT015	10p13dist	F: GGGTCCTGAGCAGGTCTTTT R: GAAGTAATGGCGGTCATGCT	139-154	2.0	58	Swinburne et al. 1997; Chowdhary et al. 2003*	
microsatellite	AHT049	10	F: TAATTGCCAAATACCACACAAA R: TGTCTTGTTCTCAGGCTCT	296-311	1.5	58	Swinburne et al. 2003	
microsatellite	AHT086	10	F: CCCAATGAAGTCCAAGATGG R: GAAATCTCTAGCAAGACCCAGG	195-216	2.0	58	Swinburne et al. 2003	AJ507703
microsatellite	AHT126	10	F: GGTTCCCAGGCACAACCTACA R: TTTCCAAAAGGGACATGAGG	166-180	1.5	58	Swinburne et al. 2005	
microsatellite	AHT132	10	F: GATTCTTCTGCCACCAGAA R: GGAATTCTTCACAAAGAAGACCT	153-169	1.5	58	Swinburne et al. 2005	
adenosylmethionine decarboxylase 1 arginase	AMD1	10q21	F: TGCTGTGTTGAGGACCAGTGC R: AGTCCAACACCAGGAAGAGAGAA	267	2.0	58	Lear et al. 2001*	G62175
	ARG1	10	F: TGAAGAAAGGTGGGACATCA R: TTTGCCAAAATGGGAAATGT	236	2.0	58	Chowdhary et al. 2003	
microsatellite	ASB06	10p13	F: GGCACAGATGTTAGCTCAGC R: ATGGAACCAGCCTGGATTGC	198	1.5	65	Breen et al. 1997*	X95321
microsatellite	ASB09	10q21-q23	F: GTGCGCATGTATGTGCGTGCC R: ATTTCCACAAGGGACATGAGG	94	3.0	58	Breen et al. 1997*	X95324
aurora kinase C	AURKC	10	F: TCGATGACTTTGAAATCGGG R: CAGTCCTTCCTTCTCTATCTG	134	1.5	58		CK463294
branched chain keto acid dehydrogenase E1, alpha polypeptide	BCKDHA	10p13	F: GAGAACCAGCCCTTCCTCAT R: TTCTTGCGGGACTGCTTCCT	436	1.5	60	Brinkmeyer-Langford et al. 2005*	J03759
chromosome 19 open reading frame 2	C19orf2	10p15	F: AGAATTTTTGTGCGCCCTCCT R: TTTTCTGCTGCAATCTGGC	153	1.5	60	Brinkmeyer-Langford et al. 2005*	CK464292

complement component 5a receptor 1	C5AR1 (C5R1)	10	F: ACTACACGTTATCCGGGTCG R: ATCTGGTGCCAGAACTACCG	144	2.0	58	Pascual et al. 2002	BI395175
calpain, small subunit 1	CAPNS1	10	F: TGAGGCCAATGAGAGTGAG R: CCATCAGTCTTCAGATCAGG	408	1.5	58	Brinkmeyer-Langford et al. 2005	BP434626
CASP8 associated protein 2	CASP8AP2	10	F: GATTTGCTTCCCCTGTTATTGGTC R: ATCCTTGGCTACGCAAAGCC	336	2.0	60	Chowdhary et al. 2003	G62191
CD164 molecule, sialomucin	CD164	10	F: GAGTGCTGCAAGGATACAAG R: CAAAGACACAGGGAGAAAGG	290	1.5	60		
CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG	10p15	F: GCCCATGGATCGAAACAG R: TGCTTCCAAGCGATCATTC	151	1.5	58	Perrocheau et al. 2006*	
glycoprotein hormones, alpha polypeptide	CGA	10q23	F: TGACAGCGTGCTCTTGTTTC R: TCCCACCTGCATCTAAGTCC	186	2.0	58	Caetano et al. 1999; Milenkovic et al. 2002*	AF130749
BAC end sequence	CH241-100C6_SP6	10	F: GCAGCACAATTACAGATGG R: GTCTCCTTTTGCTGTCC	261	1.5	57		AJ542789
BAC end sequence	CH241-100D21_SP6	10	F: ATTACACGCTCTGGGTTTGAG R: TATTTGCCAACGATTTACAG	166	1.5	60		AJ542818
BAC end sequence	CH241-100E2_SP6	10	F: TAGACCCTTGGTGGCATC R: CAAGATCTTTGTGCCTCATC	206	1.5	60		AJ542867
BAC end sequence	CH241-100J10_T7	10	F: GCAGCTGTTTTACAGGAGAG R: TCTGACTTGGCTTCAACTGC	162	1.5	60		AJ543029
BAC end sequence	CH241-100N24_SP6	10	F: CTTCCACAACCCTGAAGAGC R: GTCTCAATGCCCAGTGTCTG	215	1.5	58		AJ543219
BAC end sequence	CH241-101E16_T7	10	F: AGAATGATCCCTCGGATG R: TGGGTGATTCTCCACAAC	213	1.5	59		AJ576607
BAC end sequence	CH241-101F16_T7	10	F: TGGCTCCCAGAAAGTTTCAC R: CGTGGAGTTGGAGAGTGTTG	227	1.5	60		AJ576648
BAC end sequence	CH241-101G24_T7	10	F: GCGCTTGATTGTCAATTTG R: GAATCCTTGGGAATTCCTG	249	1.5	56		AJ576705
BAC end sequence	CH241-101L6_SP6	10	F: TGTCGCTGAACTTTCTTCC R: AATGGTGCTGGATTCTCC	282	1.5	59		AJ576917
BAC end sequence	CH241-101M4_T7	10	F: GATTTAGGGCAGGCAGAC R: GGAGACGTTGCTGTGATG	290	1.5	61		AJ576958
BAC end sequence	CH241-102A14_SP6	10	F: TTTCTACGAAGCACAGC R: TTCAAGGAAGGGAAATGC	216	1.5	56		AJ583945

BAC end sequence	CH241-102D7_SP6	10	F: TGGCAGTTCTACCCAAATC R: TTGCAATTGTGTATGTTTGC	204	1.5	58		AJ584104
BAC end sequence	CH241-102D24_SP6	10	F: TGGGGGAAATTATTGGAG R: ACCACCTTTCCATTTTGG	227	1.5	57		AJ584092
creatine kinase, muscle	CKM	10p13	F: AGGTGTGGACAACCCAGGTA R: GAGCACAGCACCAATAGCAC	200	3.0	58	Caetano et al. 1999; Chowdhary et al. 2003*	AF130753
cleft lip and palate associated transmembrane protein 1	CLPTM1	10	F: GATGAAGAGCTGTGGTCGTG R: ATTCAGGGAGATCCTGATGC	225	2.0	58	Pascual et al. 2002	BI395231
cannabinoid receptor 1 (brain)	CNR1	10	F: GCAATTGTGATTGCTGTGCT R: ACCACAAGGATCAGGACCAG	338	2.0	58		AY011612
collagen, type X, alpha 1	COL10A1	10q21-q22	F: CGACCCAAGAAGTGAATCT R: ACCCGGTCATTTTCTGTGAG	204	1.5-3.0	65	Caetano et al. 1999; Mariat et al. 2001*	AF130754
microsatellite	COR015	10p13prox	F: GGTGTGGAAACATTCCGTAT R: ACTGCATGTGTGGGAGAGAT	217-237	1.5	60	Hopman et al. 1999; Chowdhary et al. 2003*	AF083458
microsatellite	COR020	10	F: TCTCTACCGCAAGTGAAACC R: CTGAATTGTAGGACATCCCG	150-164	1.5	60	Hopman et al. 1999	AF083463
microsatellite	COR045	10p13dist	F: TCTCTACCGCAAGTGAAACC R: CTGAGCCCTTAACCTGTGGA	150-164	3.0	65	Ruth et al. 1999; Chowdhary et al. 2003*	AF108362
microsatellite	COR048	10p14-p13	F: GATTGGGATGCAAAGATGAG R: CAAGAGGATTGGGAACAAAGG	167-189	2.0	58	Ruth et al. 1999; Chowdhary et al. 2003*	AF108365
microsatellite	COR083	10p13prox	F: TCATCCTTGGGACTGTACTTG R: AGTGTTTGTGTTCCCTGCCTC	272	1.5	58	Tallmadge et al. 1999b; Chowdhary et al. 2003*	AF154936
microsatellite	COR085	10	F: GTCATGACGTCTGGCACTC R: AGCTCCCATGTAGCCTCAC	150	1.5	58	Tallmadge et al. 1999b	AF154938

elongation of very long chain fatty acids-like 4	ELOVL4	10q13	F: TGGGCCTTAAGTCTAGCAGACA R: AGCACATTTGCCTTTTTCTCC	107	1.5	55	Perrocheau et al. 2006*	DX010623
epididymal sperm binding protein 1	ELSPBP1	10	F: AGTATGGGGGAAATTCCTTC R: TCGGGCACCAGAGCTTGTT	108	1.5	55	Brinkmeyer-Langford et al. 2005	AJ539176
EPH receptor A7	EPHA7	10	F: GTCCCTTAAGTCTAGCAGACA R: TGCTGTATAATGTACACTGCCT	151	1.5	58		
ethylmalonic encephalopathy 1	ETHE1	10	F: ACTGTCTGATCTACCCTGCTCA R: TTGACAAACTCCTCACAGCTGA	823	1.5	58	Brinkmeyer-Langford et al. 2005	BP434586
F-box and leucine-rich repeat protein 4	FBXL4	10	F: TGGATCTGTGGAGGTGTAAGA R: CCAGCTCTTCAATGTCTGTGT	213	1.5	59		CX598415
four and a half LIM domains 5	FHL5	10	F: CTGCTCTCACCAAGCACTTACT R: ATGGTTGCAGGATCGTCTACT	109	1.5	58		CX594212
ferritin, light polypeptide	FTL	10	F: CCATGAAAGCCGCCATTGT R: CCTCTGGATGTTGGTCAGATGG	353	1.5	58		
FYN oncogenes	FYN	10	F: CCTTCCTGTTGGTTCCTGAC R: CTGCTCGGAGGAAGAAATCC	164	1.5	58		CD528503
gap junction protein, alpha 1	GJA1	10	F: TGTGAGAGACTTAGAGGAAATGC R: ACTCCTGAAACCTCTTTCAATCT	250	1.5	58		
glioma tumor suppressor candidate region gene 1	GLTSCR1	10	F: CTGGTCATCCAGAAGAACCT R: GGTGTCAGCTGGTAGAGCTT	248	1.5	58		CK465846
glucose phosphate isomerase	GPI	10p15	F: CTGGGACATCAACAGCTTTG R: GCTCCTGCTTGATGAAGTTG	261	1.5	58	Milenkovic et al. 2002* ; Brinkmeyer-Langford et al. 2005	X07382
glycogen synthase 1 (muscle)	GYS1	10	F: AAGGCTCGAATCCAGGAGTT R: GGTCTTGTTCCAAGTTGAAGT	413	1.5	58	Brinkmeyer-Langford et al. 2005	BX926004
HBS1-like (S. cerevisiae)	HBS1L	10	F: AAGAGATTACTGGCAAACCTTGG R: CACCACTGAGACCACTCGTAG	630	1.5	59		DN508599
histone deacetylase 2	HDAC2	10q21-q22	F: CCTTTCAAGTTCCTCTTACA R: CTCATCATTCAAATGGGAGATA	180	1.5	58	Perrocheau et al. 2006*	
hairy/enhancer-of-split related with YRPW motif	HEY2	10	F: GAGCGGCTCCTTGAGAT R: CCTACAGCGAAACCCGAC	141	1.5	58		

GLI-Kruppel family member HKR1	HKR1	10	F: AATGTGGACGAGGCTTTAC R: TCCTTGCACACATAAGGCTTG	170	1.5	60	Brinkmeyer-Langford et al. 2005	CK834051
microsatellite	HMS23	10p15	F: GATCCAATATTGTAAACCCCGCC R: CCTTCATAACCCTTATTGCAGCC	95	1.5	TD 60	Godard et al. 1997	U89810
heat shock transcription factor 2	HSF2	10	F: AGGGGAGTACAGCATCATCG R: TCTGAGTTGGTTCTGGGTCC	102	2.0	58		
5-hydroxytryptamine (serotonin) receptor 1B	HTR1B	10q12	F: CGCCCTTGACCTCTACTTTC R: CGGCGGAGAGGTTGACTTGA	250	1.5	55		
inhibitor of Bruton agammaglobulinemia tyrosine kinase	IBTK	10	F: TGAAAGAAAAGCTGTGGAAG R: CACTTCAATCACTCATGATTTCC	250	1.5	58		BM781379
leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	LILRA5 (<i>ILT11</i>)	10p12	F: TAAAGAGCGAAATCCAGTGC R: AGTGGGGCCGAGATAGTAAC	125	1.5	58	Takahashi et al. 2004*	
killer cell immunoglobulin-like receptor with 3 domains and long cytoplasmic tail gene family	KIR3DL@ (<i>KIR3DL</i>)	10p12	F: TGCAATCAGGACAAAATGTG R: TCACAGGACCCAAGAAGAAG	150	1.5	58	Takahashi et al. 2004*	
kaptin (actin binding protein)	KPTN	10	F: CCAAGACCTCCGACAGAAAA R: ATGAACGTGATCCCCACAAC	491	1.5	60		BE236872
laminin, alpha 2	LAMA2	10	F: TCGATGAAGACAGAAGGCATA R: TAACAAGGTTCCACACACAGC	150	2.0	63		
microsatellite	LEX008	10	F: AAAGTGTGACAAACGGTTAGGAC R: CGAAAAAGCCACTTGAGGTC	403-419	3.0	65	Coogle et al. 1996	AF075611
microsatellite	LEX009	10	F: AAAGCCGTAAAGATTGGGACA R: TCCATTGTGAGGGTGTAACA	366-379	3.0	58	Coogle et al. 1996	AF075612
microsatellite	LEX062/066	10p12	F: GCTCTCAGTAACCTCGATGTT R: ATTAAGGAGAAGGTGGAAAAGAC	209-215	3.0	65	Coogle & Bailey 1999; Chowdhary et al. 2003*	AF075662
leukocyte	LILRA@	10p12	F: GCCAGTACAGATGCTACGGT	450	1.5	55	Takahashi et	

immunoglobulin-like receptor gene family	(LILRA)		R: CCAGATCTCAGAGCGACATT				al. 2004*	
lipase, hormone-sensitive	LIPE	10	F: TTCCTGCAGACCATCTCCAT R: CTGTATGATCCGCTCAAACCTC	266	1.5	55	Brinkmeyer-Langford et al. 2005	AJ000482
mannosidase, alpha, class 1A, member 1	MAN1A1	10	F: CAGGCTATAAAGGTTAAGCCAG R: GAGAAAGGAGCCAGACACAG	162	1.5	58		
mannosidase, endo-alpha	MANEA	10	F: TTCAGTGCATACTGATTTTGACAG R: CAGCTGCCTGTTTCTTAATGC	120	1.5	58		BM781108
mitogen-activated protein kinase kinase kinase 7	MAP3K7	10	F: TGGCAACCTGAAATGTAAAACC R: GCCCTAGAAAATCTCAGTGTCC	129	1.5	58		
malic enzyme 1	ME1	10q12-q13	F: GTGCAATTTTGGCCAGTGGC R: CTTATCCGTGATATGCCTCAG	150	3.0	58	Godard et al. 1998*	
mitochondrial ribosomal protein S12	MRPS12	10	F: AAGCCCAAGAAGCCCAACT R: ACGACGGTGAGCTTGACG	173	1.5	60		BI961235
myeloid-associated differentiation marker	MYADM	10	F: ATAGCAGCAAAGGTGATGG R: GGTACAGTAACCCGCACGAC	322	2.0	62		BI395226
natural killer cell group 7 sequence	NKG7	10p13-p12	F: GTGAGCTTCCTGGTCCTGTC R: GAGAAGAACGTCTGGATCTG	259	1.5	60	Brinkmeyer-Langford et al. 2005*	BM734829
nitric oxide synthase interacting protein	NOSIP	10	F: GGAGGAGCAGAAAGAGTTGC R: CAGCGCTTTGTCTTGTCTT	286	1.5	60		CD535503
nuclear receptor subfamily 2, group E, member 1	NR2E1	10	F: CATCTCCCTAACACTTCTTTCC R: GAAATATCCGTAGCAGAGTGG	161	1.5	58		
nudix (nucleoside diphosphate linked moiety X)-type motif 19	NUDT19	10	F: ACTGACTACCTGATGTTGCCCT R: GTGCTCCATAACACACCTGAAA	116	1.5	59		CX599185
nucleoporin 62kDa	NUP62	10	F: TGGAGAAGGTGAAGCTGGAC R: CGAGTTCTGGTCGATCCACT	341	1.5	58	Brinkmeyer-Langford et al. 2005	BM089312
microsatellite	NVHEQ007	10	F: TCAGCGACAATCTTCCTCATACA R: ATTCACACCTCCCCCAGAAAT	122-126	3.0	65	Røed et al. 1997	AF011402
microsatellite	NVHEQ018	10	F: GGAGGAGACAGTGGCCCCAGTC R: GCTGAGCTCTCCCATCCCATCG	112-142	3.0	65	Røed et al. 1997	AF011404
microsatellite	NVHEQ067	10	F: GCTCACTCAACTCCCAGAG R: GGATTAGATTACCCAGACAACT	187-195	2.0	58	Bjornstad et al. 2000	AJ245764

programmed cell death 5	PDCD5	10	F: CAAGGTTTAATAGAAATCCTCGAAA R: CGTCATCTTCATCAGAGTCCA	426	1.5	60		BX914933
paternally expressed 3	PEG3	10p12	F: GCTCACTAAAGGTTGGGCTA R: GATCATGCATACTAGAGAGAACC	245	1.5	58	Brinkmeyer- Langford et al. 2005*	BU745796
peroxisomal biogenesis factor 7	PEX7	10q22-q23	F: CGCTATGCCTGCTTGAGGTAC R: TCAATAGAGTCTACGGAGCTCCAG	330	1.5	60	Lear et al. 2001*	G62199
phosphoglucomutase 3	PGM3	10	F: TCCACACCCCAACTCTAACC R: ATGCAATCCTCACAAAAACCC	125	1.5	58		
pleckstrin homology domain interacting protein	PHIP	10	F: GCCCTACTAAGGACAAAATTCC R: GCCAGACAAGACATCACAAAAG	147	1.5	58		
protein kinase (cAMP- dependent, catalytic) inhibitor beta	PKIB	10q22	F: AAGCCCAAAGATGAAGGAAAA R: TTGGACATCATGGTTGTAATCC	202	1.5	55	Perrocheau et al. 2006*	DX010648
proline-rich nuclear receptor coactivator 1	PNRC1	10	F: CCAAAATCCCTGGACTCTTGAA R: TGCCTTAGCACACACTTAAAT	269	1.5	58		
processing of precursor 4 , ribonuclease P/MRP subunit (<i>S. cerevisiae</i>)	POP4	10	F: TACAGTCTTTTCTCCCTCT R: GAAACAATAGCGCCGTGAAG	313	1.5	60	Brinkmeyer- Langford et al. 2005	BP172676
popeye domain containing 3	POPDC3	10	F: TAGCGAAACTCTGATGATGGA R: GCAAGATGATAAATGGCTCCT	194	1.5	58		
POU domain, class 2, transcription factor 2	POU2F2	10p14-p13	F: TCTGGTGGAAGTCTGCCTCT R: GCTTCCTCGCCCTCTTTC	398	1.5	58	Brinkmeyer- Langford et al. 2005*	BM734940
protein phosphatase 5, catalytic subunit	PPP5C	10p13	F: AGTACACAGCCCAGATGTAC R: TCCGCTCGATCTTCCTGATG	280	1.5	58	Brinkmeyer- Langford et al. 2005*	BP161170
PR domain containing 1, with ZNF domain	PRDM1	10	F: TCTCCCGTGTCATGTAGCTC R: TTCCCCTACCATTTTCCACC	135	1.5	58		
prolyl endopeptidase	PREP	10q17	F: GCTTTCCACCGTTAAACC R: AAGGGCTCGCTAAAAAGGAG	143	1.5	58	Perrocheau et al. 2006*	BI961439
presenilin enhancer 2 homolog (<i>C. elegans</i>)	PSENEN (<i>PEN2</i>)	10p14-p13	F: TTGTCCCGGCATACACGGA R: TACCCAGGGGTATGGTGAA	355	1.5	58	Brinkmeyer- Langford et al. 2005*	BX921838
RALBP1 associated Eps domain containing 1	REPS1	10	F: CAAAGGCACAACCCCTCT R: CTGTGATGCAAGAACAGCAG	133	1.5	60		CX594615
REV3-like, catalytic	REV3L	10q21	F: CGACAATGTATGAAGCTTCTGG	118	1.5	55	Perrocheau	DX010569

subunit of DNA polymerase zeta (yeast)			R: TAAGTTCAAGGGATGGCACAC				et al. 2006*	
ring finger protein 146	RNF146	10	F: GTAGTGCATTTTCGGGAGTTG R: ACGAGGACTAGACAGCAAAGC	508	1.5	60		CX602891
v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	ROS1	10	F: TTCTTCTTCTCCCGACTCCC R: TGAAC TTGCTCATGCTTTCC	201	1.5	58		
ribosomal protein L13a	RPL13A	10	F: CATGAACACCAACCCATCC R: TGCCATCGAACACCTTGAG	343	1.5	58		
ribosomal protein L28	RPL28	10	F: CTGATCAAGAGGAACAAGCA R: ATCTCCGCTTCATCACCACC	285	1.5	60	Brinkmeyer-Langford et al. 2005	BM780607
ribosomal protein S5	RPS5	10	F: TACATCGCGGTGAAGGAGAA R: GCTTCTTGCCATTGTTACGG	148	1.5	58	Brinkmeyer-Langford et al. 2005	BI961498
ribosomal protein S17 pseudogene	RPS17ps	10	F: TGTCACCCACCTGATGAAAC R: TCAGCATCTCCTTAGTGTCAGG	190	1.5	60		
ribosomal protein S19	RPS19	10	F: CCCAGCCATTTTAGCAGAGG R: TCCCTGAGGTGTCAGTTTGC	602	1.5	63	Brinkmeyer-Langford et al. 2005	
SEC63 homolog (S. cerevisiae)	SEC63	10	F: AACCAGAAACAGTGCAGAACC R: AATGCACCATCCCATTTCTTG	153	1.5	58		CD471880
microsatellite	SGCV17	10q17-q21	F: GGCCCAACGTCTATAGAAAGATGT R: CCCCCAAATGGCTATTTTCTAA	138	3.0	65	Godard et al. 1997*	U90595
microsatellite	SGCV20	10p14-p13	F: GGAAAAATTTGCTTATATATGCATAC R: GGAAAAAGAACGTTTCACCTTAGCTG	168	3.0	65	Godard et al. 1997*	U90598
microsatellite	SGCV30	10p13prox	F: ACTGGAGGGGTGAAACAGATTGAGA R: GGAAGGGAGGTCATCAGAA	160	3.0	58	Godard et al. 1997*	U90605
serum/glucocorticoid regulated kinase	SGK	10	F: AACCTGTGTGAGAGTGAAAAAC R: GGAGAAAGCGACTTGGA CTG	153	1.5	58		
solute carrier family 7, member 9	SLC7A9	10	F: TAACAAAGATGCCACTCCCC R: CATCGTACCAAGCTCTGCAA	346	2.0	58		AF425262
solute carrier family 7, member 10	SLC7A10	10p15	F: GGTCTTCAGCTTCATCTCGG R: ACATTGTAGGGAGGCATTCC	274	2.0	58	Hanzawa et al. 2002*; Chowdhary et al. 2003	AF425263
sphingomyelin	SMPDL3A	10	F: GACCCTACTTACCACATCACAGA	107	1.5	59		

phosphodiesterase, acid-like 3A			R: GGGGAATCACACAGAACATCT					
striatin, calmodulin binding protein 4	STRN4	10	F: GCTAGGATGACTGACC R: CGACCTGCCTCTGTACCTTC	700	2.0	55		BI395151
transforming growth factor, beta 1	TGFB1	10p14-p13	F: ACTGCTCCTGTGACAGCAAA R: ATCAATGGTGGCCAGATCAC	228	1.5	58	Perrocheau et al. 2005*	
microsatellite	TKY023	10	F: GCACACGAATCTTAGGGTCG R: CAGAAGCTGGACGATGGTTC	169	2.0	58	Hirota et al. 2001	AB048333
microsatellite	TKY365	10	F: TCAAGACCTTTTACGACCTG R: CCTACGATAGACAGAGGAAAG	155-171	1.5	58	Tozaki et al. 2001	
microsatellite	TKY460	10	F: CAACTAGAAGGACCCACAAG R: AGACTTCTCCATCAGGCAC	188	2.0	58		AB103678
microsatellite	TKY471	10	F: AAATCTGCGCCTCTGAAGAT R: TTCACCCAACCCCTCATAAA	215-227	1.5	55	Tozaki et al. 2004	AB103689
microsatellite	TKY496	10	F: ATCATTCTGCGGCTAAAGG R: GATCAACCAGGGAGGAGGAG	220-240	1.5	60	Tozaki et al. 2004	AB103714
microsatellite	TKY503	10	F: CCCATCTCAACCCAGGTAAA R: TGTGAACATGGCTCTAGTGGA	116-128	1.5	55	Tozaki et al. 2004	AB103721
microsatellite	TKY537	10	F: TCAGGGGTTCTCTTCAGTG R: TTGCCTGGTGTCTAGGTTCC	162-172	1.5	50	Tozaki et al. 2004	AB103755
microsatellite	TKY580	10	F: AGAAATGGAGGGAAGGGAAA R: GCAGTGGCTGTGTGGAATAA	192-196	2.5	57	Tozaki et al. 2004	
microsatellite	TKY592	10	F: TGCAGTGGGTACGTGTGTAA R: GGGCAGACTTCCAAACAGTC	149-163	1.5	58	Tozaki et al. 2004	
microsatellite	TKY601	10	F: CGAGGGGGAATTTTGTGTTGT R: ATAGAGCCATGCAGGGGAAA	205-219	1.5	60	Tozaki et al. 2004	
microsatellite	TKY614	10	F: CCGTGAGGAGTTTTAGACAG R: ATGTTAGCTTAGGGCCAATC	104	2.0	58		AB103832
microsatellite	TKY632	10	F: CGACGGATGAATGGATAAAG R: ATGTTGTTGCAAATGGCAAG	164	2.0	58		AB103850
microsatellite	TKY689	10	F: ATACCACAGCACAGCACACC R: TTTCTGGTACCCCACTTA	232-238	1.5	58	Tozaki et al. 2004	
microsatellite	TKY722	10	F: CATTTGCAACATGCCTCTTT R: CATTACGCAGCAGATAAAGGA	104-122	2.0	54	Tozaki et al. 2004	
microsatellite	TKY751	10	F: ATGTGTGTGAGCGTGTGTG R: AGGCACCAGAATTTTGGAA	156-167	1.5	58	Tozaki et al. 2004	
microsatellite	TKY773	10	F: GAGAACGGCCTTAACCGT	245	2.0	58		AB103991

microsatellite	TKY838	10	R: CCTTGCAACCAAAGCCGTTTC F: AGAAACAGAACCACTAGGAG	148	2.0	58		AB104056
microsatellite	TKY855	10	R: TCTATTATCAGGTGCCAAGG F: GATCTTGGCAGAAATGCCTG	142	2.0	58		AB104073
microsatellite	TKY867	10	R: TCAAGCAAATAGGAGCTGAG F: AGCTAATGTCAGTAGGTTGG	215	2.0	58	Tozaki et al. 2004	AB104085
microsatellite	TKY918	10	R: TTCCAAGCATCTTAAGGAGG F: TGATGCCCAGGGAACAACT	274	2.0	58		AB104136
microsatellite	TKY964	10	R: TGTTGTAGTACTTGTCCAGG F: CCCAATCTCCTGCTTAAGT	191	2.0	58		AB104182
microsatellite	TKY999	10	R: AATTGATGACTAGGGCTCAC F: TGAGAGTATCAGGCAAGAAG	132	2.0	58		AB104217
microsatellite	TKY1034	10	R: AACTTTGGCAGGTAGAGTAG F: GACCTGTTAGTGTAAGTTCTG	158	2.0	58		AB104252
microsatellite	TKY1050	10	R: ACACCTGATGCAATGCTTTC F: GCATTATCACATGAGCTAGC	137	2.0	58		AB104268
microsatellite	TKY1101	10	R: AGGAGAGAGGAACCCAAG F: TCTGGCCTTTTCCCATTATC	183	2.0	58		AB104319
microsatellite	TKY1765	10	R: ACAGAATGTACGGTTCATG F: AAACATTCTCACTCCAATCC	219	1.5	58	Tozaki et al. 2007	AB215708
microsatellite	TKY1995	10	R: TTGGGTGACTCATCTTGAAT F: CCAACCACTGGCTTTTAAAG	157	1.5	60	Tozaki et al. 2007	AB215938
microsatellite	TKY2470	10	R: ATGTCTGGCAAAAAGCTACAG F: AAAATGCATCCATTCTTCA	144	1.5	56	Tozaki et al. 2007	AB216413
microsatellite	TKY2521	10	R: TCACCCTATTTGTTGGGAAA F: TTATGAAGCCAGAGGCAAC	290	1.5	58	Tozaki et al. 2007	AB216464
microsatellite	TKY2859	10	R: GAGCTGCTGTCTAACCAGAAA F: ATGGTGCCGCCTAAAAGTAT	164	1.5	58	Tozaki et al. 2007	AB216802
teashirt family zinc finger 3	TSHZ3	10	R: GATATTGAAGATGCTCACATGG F: CAACGACCAAGCCATAGACT	245	1.5	58		AW417891
microsatellite	UCDEQ412	10p13prox- p12dist	R: TGGAAGGGGTGGAGGACTT F: AGAGGAAGGCGACAGGTC	188-208	3.0	58	Eggleston- Stott et al. 1997; Chowdhary et al. 2003*	AF000011
microsatellite	UCDEQ482	10p14-p13	R: CATCCGTCCATCCATCAG F: CACAGCCCTGACCACTGA	115-125	1.5	58		U67416

			R: CCAAAACAGCCCTGGACT				Stott et al. 1999	
microsatellite	UM028	10p13prox-p12dist	F: GCTCTGCCTCATTCCTTATC R: TTGAGGACGGAGTGTTG	127-129	1.5	58	George et al. 1998; Chowdhary et al. 2003*	AF195575
microsatellite	UM040	10q21-q23	F: CTCTTGTAACATGTCTCCTTGTC R: TACTTTCTCTCTTCCAAACC	250-270	3.0	50	George et al. 1998; Chowdhary et al. 2003*	AF195584
microsatellite	UMNe209	10	F: CCAAAGGTTTCGTAGTTTCCC R: TAATTGGCCAGGAAATGCTC	200	2.0	58	Mickelson et al. 2003	AF536291
microsatellite	UMNe265	10	F: GATCTGACACCACCACCCTC R: ACCATAAAAAATCATCACCTCG	180	2.0	58	Mickelson et al. 2003	AF536323
microsatellite	UMNe267	10	F: AGCCTCCATATGCTTTGTCTG R: GGAATTGACTCAGTCCTGAAGG	150	2.0	58	Mickelson et al. 2003	
microsatellite	UMNe372	10	F: ACGTTACAGGTGGGGAGATG R: CTTGGCTTCCAGGAAAACAC	127	2.0	58	Wagner et al. 2004a	
microsatellite	UMNe426	10	F: TGGCTTTTCATCTGAACTGTTC R: TGGCCTGGGAGGTTATTTTG	139	1.5	50	Mickelson et al. 2004	AY731393
microsatellite	UMNe506	10	F: AGGGACGTGACCTAACATGG R: CAGCACAGCCTCCTCTCC	142	1.5	60	Wagner et al. 2004c	AY735257
microsatellite	UMNe543	10	F: GGCAGGATTTCTCTCTTTCC R: TCTGCACTCCTGTGTTCACTG	190	1.5	62	Wagner et al. 2004c	AY735264
WNT1 inducible signaling pathway protein 3	WISP3	10	F: GGAAGCAGTTTTGTGTCATTGG R: GTCACAGTACAGCCCTTTGTG	173	1.5	58		CX598720
zinc finger protein 536	ZNF536	10	F: CTTGTGTCCGATTGTCCTGT R: CACATTTTGCTTCAATCACC	209	1.5	55	Brinkmeyer-Langford et al. 2005	AV593008
zinc finger protein 543	ZNF543	10	F: TTCACCCACCGCTCCAATTT R: CTTCTCCCCAGTGTGAATCC	390	1.5	60	Brinkmeyer-Langford et al. 2005	BP437102

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	11STS01	11	F: TCTTCCACGAATACTAGTGTCTG R: CAAGGACCCTCAACACCATC	101	1.5	58		
sequence tagged site	11STS02	11	F: TGCCTGTTGGATTCTGTTTTTC R: TCTGATTCTGGACCTTTCCG	233	3.0	58		BI395131
alanyl-tRNA synthetase domain containing 1	AARSD1	11	F: GCTTCTCCAGGACTATGTCAGC R: ATTCTGTGGTCACAGGAGGC	102	1.5	59		CX594725
acetyl-Coenzyme A carboxylase alpha	ACACA	11q12	F: TCCTGACTTGTCAGAGACCC R: CTAATCCCCACTTAGTGCCC	633	1.5	60		AJ543302
angiotensin I converting enzyme 1	ACE (ACE5)	11p13	F: GCCCAGGAGGATGTTTAAGGA R: CTTGCCGTTGTAGAAGTCCCA	140	3.0	60	Milenkovic et al. 2002*	AF264016
acyl-Coenzyme A oxidase 1	ACOX1	11	F: GACAAGTAACGCTGCTATCG R: ATGCCACACACCAACTTTCC	~1070	1.5	60		CD535625
microsatellite	AHT016	11	F: ATGTTGTGCAAATGGGATGA R: TGCCCATTGATTGATGATTG	123-146	2.0	58	Swinburne et al. 1997	
microsatellite	AHT044	11p14-p13	F: CCTCCACATGAGGTGCATTT R: GACAATGAGAGAGGCCAACC	160	2.0	58	Swinburne et al. 2000; Chowdhary et al. 2002*	AJ271529
microsatellite	AHT076	11	F: ACTGAGCGGCCATGACTC R: GAGGATTGGTGGCAGATGTT	162-168	1.5	60	Swinburne et al. 2003	AJ507693
microsatellite	AHT125	11	F: TCCCCTCTTCAGACCTCTCA R: CAAGCAAAAAGAGGAAGATTGG	247	2.0	60		
microsatellite	AHT128	11	F: ACATGGCACATTTCGTGGAC R: TCTGGGTACGCTAGCGATG	306-320	1.5	58	Penedo et al. 2005	
adaptor-related protein complex 2, beta 1 subunit	AP2B1	11	F: CCGGTCATCTTTAGGGTTGTA R: GCAGCGTTATCTGAAATCAGC	162	2.0	58		
microsatellite	ASB35	11	F: ATGCATGAGCAGAGTGTTCTTCC R: TAGTACTTCTCTCTTAATATAAGC	170	4.0	58	Lindgren et al. 1998	

XIAP associated factor-1	BIRC4BP	11	F: ATGTCGCACAGTCTCAG R: CATCTTTCTCTGCCGTGGA	116	1.5	55	
breast cancer 1	BRCA1	11	F: CTATGCGCAGCAATTGAAAA R: GCAAATGACTGACGCTTTGA	212	2.0	58	AF284010
carbonic anhydrase IV	CA4	11	F: ACGGGATAGGGTGGGAGAG R: CAGAGTGGGTTGAAGCAGG	138	1.5	60	
calcium channel, voltage-dependent, beta 1 subunit	CACNB1	11	F: AGTCAGAGACTGGGTTCAAG R: ACATGGGCAAACTATAAGAGG	131	1.5	56	
chemokine (C-C motif) ligand 2	CCL2	11	F: CTTCTAGCATTCCCTAAATGCC R: TTTCCACAATAGCGTTTTTAGC	303	1.5	60	AJ251189
CD300c molecule	CD300C	11	F: TGAAGTTTGCGGGGTGGT R: ATCTGTGCTGGAGAGATGACCCA	~800	2.0	55	BI395096
cerebellar degeneration-related protein 2-like	CDR2L	11	F: GTTACAGGTTCCAGGGGTCT R: CCTGCTCTGATTGGCTACAG	~250	1.5	59	CX596675
BAC end sequence	CH241-100B11_SP6	11	F: GCAATGGGTAAGGCAGTTAAG R: GTGAGTGGCACATAAGAAGG	471	1.5	60	AJ542709
BAC end sequence	CH241-101A18_SP6	11	F: CTCAGATTGTAGGAAAGACCAC R: GGCAGAGGTTAAGTAGGCAG	216	1.5	60	AJ576445
BAC end sequence	CH241-101K01_T7	11	F: ATGTAATGCCCCGTCCCAGTC R: GCCTAATGTGCTTGTCTGGAG	567	1.5	60	AJ576859
BAC end sequence	CH241-102B10_SP6	11	F: CATTTTCTTATTTGCTGCCTCC R: CATTTCTCCCTTAACCCCTTTC	571	1.5	60	AJ583985
BAC end sequence	CH241-102M09_SP6	11	F: GCAAGTCTGTCTCAGTTTTCTC R: TTGTCCATACACCCAGTCCC	288	1.5	60	AJ584478
BAC end sequence	CH241-103P20_T7	11	F: GCAGACAACAGCAGGTAAAG R: GGAGCCACTGGAAAATGAAC	245	1.5	60	AJ618911
cholinergic receptor, nicotinic, epsilon	CHRNE	11	F: GCTTGAACCTACCCCTTTCCTG R: CCGTCAGATGAGGGCAATTC	125	1.5	56	
collagen, type I, alpha 1	COL1A1	11q11-q12	F: TGTCCAGCAATGCCCTGA R: GCAAAGAAGGCGGCAAG	268	2.0	60	
colony stimulating factor 3	CSF3	11	F: TATTTAAACAGCAGTGTTCCCC R: TATCGTGAAGTTGGCTACAATG	504	1.5	58	AF503365
chemokine (C-X-C)	CXCL16	11	F: CATCCATGCCAATGAAACC	131	1.5	58	

motif) ligand 16			R: CTGCCACTGTAACTGATGTCC					
microsatellite	D-8	11p13-p12	F: TTTTGTGTCTCAGGAGTGTG R: AGTCTGATGGTGGAGGAAGG	95-105	3.0	TD 64	Marti et al. 1998*	Y10241
DEAD box polypeptide 5	DDX5 (<i>HLR1</i>)	11p13	F: GAACTCTGCAAAAGAGGGC R: AGAGCATTTCAAATGGAGAGTC	99	1.5	56	Lear et al. 2001*	
elaC homolog 2 (E. coli)	ELAC2	11q14.3-q15	F: CCGAAGTTGAACGCTTGA R: CCGAATAGACCACCTTCCA	217	2.0	58		
enolase 3	ENO3	11q14.3-q15	F: GGTCCTGAAAGCTGTGGAAC R: GTCCCATCCAGCTCAATCAT	279	1.5	55		
eosinophil peroxidase	EPX	11	F: CCCCAGGACAGTGAACAAG R: CCACAAGCCACCATTCTGAC	120	1.5	56		
ecotropic viral integration site 2A	EVI2A	11q12-q13	F: AACAACAACAAAATCGCTATGC R: CGCTTGCCTACTTGTGTTTGA	140	3.0	TD 60	Chowdhary et al. 2002	AF130762
fatty acid synthase	FASN	11p14	F: CACCGGGTGAAGGCTGGCACT R: GGTTTAATCGTGGGGAGGCTCC	296	1.5	55	Lear et al. 2001*	G62204
galanin receptor 2	GALR2	11	F: ATCGTGCCCATGTTATTTGC R: GGTGAGGAAGATGAAGAAGTG	246	1.5	58		CD467026
gastrin	GAST (<i>GAS</i>)	11q12	F: ATGTGCTGATCTTTGCGCTG R: AGGACTTTGATCCCCCTTCCTC	302	1.5	60	Milenkovic et al. 2002*	Y09440
gem (nuclear organelle) associated protein 4	GEMIN4	11q14.1	F: AGTCTGACTGGGAGCACGTT R: GTTGCCACAGAGAAGAACAC	200	1.5	55	Perrocheau et al. 2005*	AY817471
growth hormone 1	GH1 (<i>GH</i>)	11	F: TCAGGATGTGGGCGCCTTC R: TGGGCGTTCCTGGATCGAGTATCT	372	4.0	58	Caetano et al. 1999	AF097589
guanylate cyclase 2D, membrane	GUCY2D	11q15-q16	F: ATGAGCACTGTGCGGATTCT R: AGGGGGACGGAGGACTTAG	201	2.0	58	Shubitowski et al. 2001; Chowdhary et al. 2003*	AY008791
hepatic leukemia factor	HLF	11	F: TTGGAATACATGGACCTGGAG R: GGCTCTGCACACAGTTTGG	193	1.5	55	Perrocheau et al. 2006	DX010505
microsatellite	HLM2	11q14-q15	F: CCCACCTCCCCATCTCCCAACC R: AAGCCAGTTCCTCAGCCCCACC	123-137	1.5	58	Vega-Pla et al. 1996; Chowdhary et al. 2002*	U36494
microsatellite	HTG26	11	F: CCTGGAAACCATCATTCTACT	141	2.0	58	Lindgren	

integrin, alpha 2b	ITGA2B	11	R: CTCCAGGCTGAGTTATTTGTA F: CACTCCCTAGCTGTGTGTTTC R : AAAGTCACTGCCCAAATGCC	154	1.5	56	2000	
microsatellite	LEX068	11p13 prox	F: AAATCCCCGAGCTAAAATGTA R: TAGGAAGATAGGATCACAAGG	154-168	3.0	58	Coogle & Bailey, 1999; Chowdhary et al. 2002*	
lectin, galactoside- binding, soluble, 9	LGALS9	11	F: GGTGGCCTGTACCCCTCCAA R: CGGACCACGGTGTTCATCAA	390	1.5	60		CD528716
ligase III, DNA, ATP-dependent	LIG3	11	F: CTTTCTTTGAGAGGCTCCAC R: AGGAAATTCTGAGGTTCCCTG	268	1.5	58		
Meckel syndrome, type 1	MKS1	11	F: TGCCCACCCTACTTAGCTTG R: CATGTCAGATTGCATCAGCTC	420	1.5	60		U97315
MAX-like protein X	MLX	11	F: ATAGGAAGCTCCAGCCATCCAC R: TCCCCCAGCTAGGAAGAAGAAC	145	1.5	60		
monocyte to macrophage differentiation- associated	MMD (<i>HESTG03</i>)	11	F: GTGGTCTGGTTGGTGTATCAC R: GTACTGATACTGCTTTAAAAAGTGG	~200	1.5	52	Godard et al. 2000*	X85750
myosin, heavy chain 3, skeletal muscle, embryonic	MYH3	11	F: TCAGCCCAGATTGAGATGAAC R: TCCTTCTCCAGTTTCTGCTTG	188	1.5	55	Perrocheau et al. 2006	DX010531
myosin, heavy chain 4	MYH4	11q14.3 -q15	F: GTCCATGAAAGGCCATGAAC R: TAGCCTCACTGCCCTCTTAG	211	1.5	58		
myosin, light chain 4	MYL4	11p13- p12.3	F: TGTTTTCGACAAGGAGAGCA R: AGACAGGGTGGATCAGGATG	196	1.5	58	Caetano et al. 1999; Chowdhary et al. 2002*	AF130773
neurofibromin 1	NF1	11q12- q13	F: ACAGTGGCCTCATGCACTC R: CTGTGCCTTGTTGGAGGATT	221	1.5	58	Caetano et al. 1999, Mariat et al. 2001*	AF130776
nucleolar protein 11	NOL11	11	F: ACCAGTTCTCCTTCATGGATGT R: TCACGTTTCTCTCGCTACTGAC	114	1.5	59		CX605913
N-ethylmaleimide- sensitive factor	NSF	11	F: CGTTAGAACAGATCAAGAACGA R : TGCATCATGTTTACCACCT	96	1.5	56		

microsatellite	NVHEQ040	11	F: TGGCATCTGAATGGAGAATG R: GATTATGATGCTACAGGGGAAAG	144-158	3.0	58	Røed et al. 1998	AF056395
microsatellite	NVHEQ090	11q14	F: TCTATGTGTGTCAGAATGAGGAGGT R: TTTTGCAAGGTAGATAGATGCC	99-105	2.0	58	Røed et al. 1998	AF056397
oligodendrocyte myelin glycoprotein	OMG	11q14	F: AGTGTTGTAACTCCTTCCCGCG R: ACATACACAGGGAGGAAACTGGG	273	1.5	60	Lear et al. 2001*	G62156
procollagen-proline, 2-oxoglutarate 4-dioxygenase, beta polypeptide	P4HB	11	F: GACGAGCTGACAGCAGAGAA R: AGGACAGCCATCTTCACACC	219	1.5	58	Chowdhary et al. 2002	AF130777
phosphodiesterase 6G, cGMP-specific, rod, gamma	PDE6G	11	F: CGAGCCTGTCCTTTGTTTTTC R: CCCAGGAAGAGTGGCTACAG	195	2.0	58	Chowdhary et al. 2003	AY008801
phenylethanolamine N-methyltransferase	PNMT	11p12	F: GTGTGTACAGCCAGCACGTC R: AGTGTGGTGATGTGGTCCAG	355	1.5	58		AB071422
proteasome 26S subunit, ATPase, 5	PSMC5	11	F: GGAGTTGGGACAGACAACAG R: TGTGCTAGATGCTAGGGATAC	152	1.5	60		
recoverin	RCVRN (RCVI)	11q14.3-q15	F: GGCAGAGTTCCAGAGCATCTA R: CCACGTCGTAGAGGGAGAAG	197	2.0	58	Chowdhary et al. 2003*	AY008807
sodium channel, voltage-gated, type IV, alpha subunit	SCN4A (HYPP)	11	F: GGTCTTCATCATCGTCTTCACG R: CACAATGGACAGGATGACAACC	118	4.0	58	Caetano et al. 1999	
sarcoglycan, alpha	SGCA	11q13	F: AGGAAGTGTTGCCCTCGTC R : AGGAGAAGGGTGAGGCAGAG	540	1.5	66		
microsatellite	SGCV13	11q12	F: GGACTAAAGCCCAACCATCCAGC R : CTCACCAGTAAGGGGTTATGGGGC	162	2.0	58	Godard et al. 1997*	U90592
microsatellite	SGCV22	11p14	F: GGAAATCACTGCCCCAGCCTG R: GGTGGTTGGGAAAGGGTTGAGGC	112	2.0	58	Godard et al. 1997*	U90600
microsatellite	SGCV24	11p12	F: CTACCATTGAAGAGGGGTGGC R: GAAACGAGCAGGAAGTGAATCTCC	121	4.0	TD 64	Godard et al. 1997*	U90602

skeletal muscle and kidney enriched inositol phosphatase	SKIP	11	F: GGCTTCATCCAGTAGATCC R: GTGATATGCCTGAGACTGAG	332	3.0	58	Chowdhary et al. 2003	
SR Y (sex determining region Y)-box 9	SOX9	11p14	F: CAGCGAACGCACATCAAGA R: TGGGGGTCGTTGTAGTCGTA	161	1.5	60		
thyroid hormone receptor associated protein 1	THRAP1 (TRAP240)	11q13	F: CCAGGGGTGTAAGCATGAACTT R: TATTTTCACCTTTGGAGCAGC	200	1.5	58	Chowdhary et al. 2003	
translocase of inner mitochondrial membrane 22 homolog (yeast)	TIMM22 (TIM22)	11	F: CCGGTGAGAGTAATTGCCTCTG R: CAGGACTGAAGTTTTGTGGAGCTT	350	2.0	58	Chowdhary et al. 2003	
microsatellite	TKY010	11p12	F: GATCTTGGACTCGCTCACC R: GATCTAATAGGATGTGTG	180	2.0	55	Hirota et al. 2001*	AB048321
microsatellite	TKY032	11q12	F: GTTCTGCCTTTTGGCTTAAT R: TAGTAATGGGATAATAGGGC	125	2.0	58	Hirota et al. 2001*	AB048338
microsatellite	TKY033	11q12	F: TAGATTAGGTGCCTGGCACG R: CCTCTCCCCCAACTCCAGAG	86	2.0	58	Hirota et al. 2001*	AB048339
microsatellite	TKY276	11	F: TTAGCACTTTATCTCCCTGC R: TGTGTCTGCAATTTACTCTG	87-101	2.0	TD 60	Tozaki et al. 2000b	AB033927
microsatellite	TKY304	11	F: CTGGTGGCATCTTCTATTAC R: ATATATTCTGCAGGCACAAG	128-136	1.5	58	Tozaki et al. 2000c	AB034613
microsatellite	TKY343	11	F: TAGTCCCTATTTCTCCTGAG R: AAACCCACAGATACTCTAGA	166-188	1.5	58	Tozaki et al. 2001	AB044844
microsatellite	TKY424	11	F: ATACAGGAGTGCGCTTTTCC R: AAACCATCCTCCACCTTTCC	158-174	1.5	58	Tozaki et al. 2004	AB103642
microsatellite	TKY490	11	F: CAGCAGCATCAAACCTAGCA R: TGTGAGTGACTTGGGGGAAG	177	1.5	58	Tozaki et al. 2004	AB103708
microsatellite	TKY551	11	F: GGAACAGATCCTCCCTCAGA R: GAGGCCTTGCATGTGGAC	265-269	1.5	55	Tozaki et al. 2004	AB103769
microsatellite	TKY626	11	F: CCAGCTGAGCCCATTTTAGA R: GGGAGGAGCTGAGAAGATTTG	237-239	1.5	58	Tozaki et al. 2004	AB103844
microsatellite	TKY630	11	F: ATGGCAGGACTCAGCCTCT R: AGCCTTCCTCCACAAGACTG	165-180	1.5	60	Tozaki et al. 2004	AB103848

microsatellite	TKY646	11	F: CACCGGTAGAGCCTCTGAAT R: GCACAGTGACCATCTGGAAG	198-224	1.5	58	Tozaki et al. 2004	AB103864
microsatellite	TKY648	11	F: ACCCATCCATGCTGAAAAGA R: CGAAAGGTATTTGGTGTGTCTC	278-282	1.5	58	Tozaki et al. 2004	AB103866
microsatellite	TKY710	11	F: TCAGGAGTTTGGATAGATTTTGC R: TGGAATAACTGAAATGTCCAACA	210-216	1.5	58	Tozaki et al. 2004	AB103928
microsatellite	TKY906	11	F: CCATGGTGCCTAGTTTAATC R: GCAGTCCTGGTTGAAAATCG	225	2.0	58	Tozaki et al. 2004	AB104124
microsatellite	TKY908	11	F: GCATTTGGAGGGCATCTTAG R: ATGCCAAATAAGCAGTTGGG	267	2.0	58	Tozaki et al. 2004	AB104126
microsatellite	TKY954	11	F: AGCTCCTCAGGAATCTAATG R: GGACATGTTAACACCTCTCC	123	2.0	58		AB104172
microsatellite	TKY960	11	F: GATCATGGTCTGCATGTGG R: TGATTCAGACACGGAAGCC	192	2.0	58		AB104178
microsatellite	TKY978	11	F: TGGCAGTCCAGTATCCATC R: GAACGTGGACACTTAACTGC	213	2.0	58		AB104196
microsatellite	TKY988	11	F: TCCCAAAGTGAGACTCCTG R: AGAGCTGCTAAATGTAGGTG	222	2.0	58	Tozaki et al. 2004	AB104206
microsatellite	TKY1004	11	F: TCTGACTTCAGGTTGTTCTTC R: CACCTATATGCCAACCAGA	212	2.0	58	Tozaki et al. 2004	AB104222
microsatellite	TKY1028	11	F: ATGGAGCTGTTAGTGAGTTG R: CCCAACAAGGCAGACAATC	102	2.0	58		AB104246
microsatellite	TKY1312	11	F: TCCATCTCTGTTCCAATACG R: GAAACAGGCAAGAAAACCAC	147	1.5	58	Tozaki et al. 2007	AB215255
microsatellite	TKY2446	11	F: CGCATACATTTGCTCACAAG R: TAACTCTGCCTCTCCAAAGC	161	1.5	58	Tozaki et al. 2007	AB216389
microsatellite	TKY2455	11	F: GGCCAAATGGACAATTAGAG R: AACTTGATGTTTCGGTGGTC	104	1.5	58	Tozaki et al. 2007	AB216398
microsatellite	TKY2674	11	F: ATCCTAATCCTACAGGGAG R: AAGTCATAGGGGCAGATAG	215	1.5	60	Tozaki et al. 2007	AB216617

microsatellite	TKY2944	11	F: GATCCACATATGAACTCCTA R: TTACCCCTATGCATTTGTCA	114	1.5	58	Tozaki et al. 2007	AB216887
microsatellite	TKY3288	11	F: GATCAGCTTCTCCCCGACAC R: ATTTCCCTCAGCCAGAGCTA	170	1.5	58	Tozaki et al. 2007	AB217231
microsatellite	TKY3493	11	F: CATTTAATCAAGCGCCAACT R: CCTGGGTAGTTCTGTGCAGT	246	1.5	58	Tozaki et al. 2007	AB217436
microsatellite	TKY3518	11	F: CTGCAGCCAAAATCACTTCT R: TACCGAGAAACACAGGAAGG	151	1.5	58	Tozaki et al. 2007	AB217461
transmembrane protein 49	TMEM49	11	F: TTTCTGAAAGCAGTTTAGTCC R: TTGAAGGTGGGAGAGGAAGG	381	1.5	62		CD471078
microsatellite	UCDEQ039 (CA39)	11p14-p13	F: GCCCTTCACCGATTTAATA R: GAACCCAGCACATTATCGGG	188	2.0	58	Chowdhary et al. 2002*	U25168
microsatellite	UCDEQ439 (CA439)	11p14-p13	F: GTTGATGCTCAGAGGAAGGC R: GGTGCACAGTCCACAAGAAA	207	2.0	58	Eggleston-Stott et al. 1999; Chowdhary et al. 2002*	U67409
microsatellite	UMNe085	11	F: GGACATGGCACATTCATGGAC R : AACTTGTGGAAAAGTTGCATGG	191	1.5	58		
microsatellite	UMNe096	11	F: CATCCATGTTGTTGCAATAGG R: AGCCAAGACATGGAAGCAAC	150	1.5	62		
microsatellite	UMNe116	11	F: TCAAATCCCGAGCTAAAATG R: GATCACATGGGAGAAAATACAC	153	1.5	58	Wagner et al. 2004c	AY735236
microsatellite	UMNe128	11	F: TCCATTTTGTCTCTGTCTCCG R: GGCACATTCATGGACATCC	121	1.5	58		
microsatellite	UMNe143	11	F: AGAAAGGGTAAACAAGAAGCCC R: GACACCTCTGCATCACACATG	~110	1.5	58	Wagner et al. 2004a	AY391301
microsatellite	UMNe201	11	F: TATGTGTGAAC TTGGTGGTAGC R: TGCATAAACATACGCTCATGC	143	2.0	58	Mickelson et al. 2004	AY731380
microsatellite	UMNe240	11	F: GACAAGCATCAGCAAAAAGC R: TTGATGACCTTGAAAAGGGC	215	2.0	58	Mickelson et al. 2003	AF536300
microsatellite	UMNe259	11	F: TCAGGGCTAAACTTCCATTCC R: ACTGAGCGGCCATGACTC	144	2.0	58	Mickelson et al. 2003	AF536321
microsatellite	UMNe314	11	F: AGGCCCTTGTATATCCCAC	153	2.0	58	Wagner et	AY391335

microsatellite	UMNe365	11	R: GAGCTGGGAGTGGAAGGAG F: CCCTCGTCTCAGACTTCTGG	201	2.0	58	al. 2004a Wagner et al. 2004a	AY391351
microsatellite	UMNe378	11	R: GAGGCCTTGCATGTGGAC F: CTAGGGACTCTGGAAAGGGC	251	2.0	58	Wagner et al. 2004b	AY464469
microsatellite	UMNe398	11	R: CCACGTAACCCAAGTGTGTG F: TCCGCAGATACTCACACAGG	105	1.5	58		
microsatellite	UMNe423	11	R: CCTATATCTACCTTTCGCTGGC F: TGGAAAAAGGAATTTGCAGG	252	1.5	58		
microsatellite	UMNe443	11	R: TCTGTGGAGAAGATGATTGGG F: GTGAATAGTAACCAGCCCATCC	300	1.5	58	Wagner et al. 2004c	AY735251
microsatellite	UMNe514	11	R: GTATATGTGAAAGTGGGGGTGG F: GGAATTTTGGTTCTCTGACAGG	~250	1.5	58	Wagner et al. 2004b	AY464513
microsatellite	UMNe558	11	R: GAACTCTGTGTGTGCATGTGC F: TTGGGAGGAGAGTGCACAG	~200	1.5	58	Wagner et al. 2004b	AY464526
ubiquitin specific peptidase 32	USP32 (<i>USP6</i>)	11	R: GCTGAGGCTTTTTTACGCC F: GGTATAATGTGATGAAGTCAGAC	435	2.0	TD 60	Chowdhary et al. 2003	G62170
microsatellite	VHL060	11	R: TGTTTGGATAATAGTTACAGATAA F: GACTGTTTAACCACTACGTGA	~150	1.5	62	van Haeringen et al. 1998	
microsatellite	VHL78	11	R: CACTACATAGCTTCAAAGTGGA F: CAGGTCTTCTGGAGGAAACC	~110	1.5	58		
WD repeat and SOCS box- containing 1 zinc finger protein 207	WSB1 ZNF207	11 11q13- q14.1	R: CTAAGGGCAAAGGAAACAGG F: TTGGCGTGAAGCAGGGAC	198	1.5	60		CD528403
			R: CGCAACGACACAGAAGGG F: TGGAACAGTTACAGCCCTCA	370	2.0	65	Chowdhary et al. 2003	
			R: AGCCAAGCTTCCGTCAATAAG					

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
actinin, alpha 3	ACTN3	12q14	F: GGAGGACTTTTCGGGACTACC R: GAGCAGCCAGTCCTCATAGC	308	1.5	58		
adrenergic, beta, receptor kinase 1	ADRBK1	12	F: GCCCGCTCTAGAGATGAGAA R: CCCATCTTGGACATGTAGCC	189	2.0	58	Caetano et al. 1999	AF134059
microsatellite	AHT027	12p13	F: GAGCAAGTCTTCCTTCCACG R: ACGTGCACACCTGTACGTGT	101-109	2.0	58	Swinburne et al. 2000*	AJ271512
microsatellite	AHT056	12	F: TCAAATGTTTGCTTGGAATGG R: TCTCCATCTCCACATAGGCC	96-112	1.5	50	Swinburne et al. 2003	
microsatellite	AHT122	12	F: ATTCAATTACACAAACCCCA R: CACTACCTTCCCCTACGTTCC	157	2.0	61		
beta-1,3-glucuronyltransferase 3	B3GAT3	12	F: GTGGATCCCAAGGACCTAGA R: CATCTTGGGCTTCTCTGTCC	791	1.5	65		
CD44 molecule (Indian blood group)	CD44	12	F: GACGACAGAAAGGCAAGTGG R: CACCCCAATCTTCATGTCC	153	1.5	58		
ciliary neurotrophic factor	CNTF	12q13	F: AGCTTACCGTACCTTCCATGTTAT R: AGCTCTTGCAGCACCTTCAG	261	1.5	58		
microsatellite	COR009	12	F: CGGTGTTCTTATTTTCATGGA R: GGAACGAAACACAGTGGAAC	122-130	3.0	58	Hopman et al. 1999	AF083452
microsatellite	COR030	12	F: CTGGCTGTTTAGCATTCCAC R: ACTGGCATCTCAGTTTGGAG	233-241	3.0	55	Murphie et al. 1999	AF101399
microsatellite	COR058	12	F: GGGAAGGACGATGAGTGAC R: CACCAGGCTAAGTAGCCAAAG	206-228	2.0	55	Ruth et al. 1999	AF108375
dopamine receptor D4	DRD4	12	F: AGACCCAGAAACAGGCAA R: GCTTTCCTCGACCCAAACC	433	2.0	60	Momozawa et al. 2007	
eukaryotic translation elongation factor 1 gamma	EEF1G	12	F: CGTCATCCTCTTTGGAACC R: CCTGATTGAAGGCTTTGC	453	1.5	58		
F-box and leucine-rich repeat protein 11	FBXL11	12	F: TGGAAAGATGGAGGCAGGGT R: CGCACGTAAATTGGTCAGCAG	270	2.0	58		
F-box protein 3	FBXO3	12p14-p13	F: GGTGAATTTCCAATCATCAGC R: CGAGCTATAGACACCCTGAATG	188	1.5	55	Perrocheau et al. 2006	DX010476
HRAS-like suppressor 3	HRASLS3	12	F: CTCAAGAAACAAGCGACAAAAGC R: CACAAACCAAACCTCAAAGC	113	1.5	58		
interferon induced transmembrane protein 3	IFITM3	12	F: TCGTGGCCTTCGCCTACT R: ATGTTCAAGGCACTTGGCAGT	1000	1.5	58		BI961736

insulin-like growth factor 2	IGF2	12q14	F: AGCCGTAGGGTGATTGACAG R: GTATCTGGGGGAGTCGTCCT	162	4.0	58	Raudsepp et al. 1997; Lindgren et al. 1998; Caetano et al. 1999	AF097586, AF020598 AF020599
leucine rich repeat and fibronectin type III domain containing 4	LRFN4	12	F: GCCAAATTTTCCTGAACTG R: CCATTGGGAGTAAAGTCA	162	1.5	58		BI961933
lymphocyte-specific protein 1	LSP1	12	F: GAGCAAGAAAAGCCTCTGG R: CGAGCACCTTCTCATATTTCC	285	1.5	58		
MAP-kinase activating death domain	MADD	12	F: GCCATTTCCGTATGGTCTGC R: AACCATCTCTTGCCCACTGC	211	1.5	58		
membrane-spanning 4-domains, subfamily A, member 1	MS4A1	12	F: GTGTGCCAGGAGTTGTGCTA R: GCATCACTGCAAAAATGCTC	204	2.0	58	Caetano et al. 1999	AF130748
NAD synthetase 1	NADSYN1	12	F: CGAACAGACACAAGATGACC R: CGGTGTGGTAGAGAAATGG	102	1.5	58		
phosphorylase, glycogen	PYGM	12q14	F: CCCTGACAGACCAGGAGAAG R: GCCAGCGCGAAGTAGTAGTC	160	1.5	66		
recombination activating gene 1	RAG1	12	F: AGCACATGGCTCACAGAATG R: CCCGAAAGATGAACTGGAAA	227	2.0	58		AF447516
recombination activating gene 2	RAG2	12	F: GTGTTCTCTTTGGAGGACGG R: TCTGTATAGGTTGGCAGGGC	260	2.0	62		AY011974
microsatellite	RKJ12	12	F: CTTGCGTAATTCTGGATCAGC R: CAGCAACAACAGCAACAACA	200	4.0	60	Chowdhary et al. 2003	
retinal outer segment membrane protein 1	ROM1	12	F: CAGGTGAGTCAGCAACGTGT R: GTTCTCCCTCCCCATTGAT	195	2.0	58	Shubitowski et al. 2001	AY008811
ribosomal protein, large, P2	RPLP2	12	F: CATCAAGAAGATTCTGGACAGC R: CAATACCCTGGGCAATAACG	600	0.5	58		
secretoglobulin, family 1A, member 1	SCGB1A1	12q13	F: CTGAAGACGCTGGTGGACTT R: CAGCTTCTAAATCCTAAGCACACA	450	1.5	58		
microsatellite	SGCV08	12	F: GAGTTCATTCTTTTTTCGTGGCTG R: GGAAACACCCTAAGTGTCCCTTG	128	1.5	50	Godard et al. 1997	U90590
microsatellite	SGCV10	12p13	F: CATCCATCCTTTCCAGCTCGATATTC R: CAAGACCGTAACTCAGGAGCCC	172	3.0	58	Godard et al. 1997	U90591

tyrosine hydroxylase	TH	12	F: TGAATGCAACCACATGACCT R: GAAAAGGAGCCGAGTGAGTG	241	1.5	58		AB167791
microsatellite	TKY286	12	F: TCCTTAACAACAAAGACACC R: ATGGGCATATTAAGATGCAC	94-112	2.0	58	Tozaki et al. 2000b	AB033937
microsatellite	TKY404	12	F: TTGTCAGTGTGTGAGGAGATCA R: TGCAGAGCAGCAATTTCATT	190-196	1.5	55	Tozaki et al. 2004	AB103622
microsatellite	TKY482	12	F: TAAAGAAAATGTGATACACATAC R: TTGCATTTCTCTCTCTGATTTATTTT	198	2.0	58		AB103700
microsatellite	TKY499	12	F: GATGCCCTCTGGCTAGTGTT R: TAGAGACCCACCTGCTGCTT	122-178	1.5	55		AB103717
microsatellite	TKY683	12	F: CAATGGTGAAAATCTCTTTCCAG R: AGGTACAGCCCTGGTGTAATA	160-174	1.5	58	Tozaki et al. 2004	
microsatellite	TKY734	12	F: TGGCGTCTCACACACAAAAT R: TTCAGCAGGGTGGATAAAGG	172-184	1.5	50	Tozaki et al. 2004	
microsatellite	TKY769	12	F: CCAGCGTGCCACCTGTTC R: GTCAGTGTCTTTCTCCTGT	243	2.0	58	Tozaki et al. 2004	AB103987
microsatellite	TKY823	12	F: AGGGTTCACACAATTGATTG R: AGTGCCTCCCAGTGATTAG	114	2.0	58		AB104041
microsatellite	TKY1075	12	F: AGTACCATGTACTGCATAGC R: AATTGCTTAGCCTAGCAGAC	107	2.0	58		AB104293
microsatellite	TKY1143	12	F: GAGCACTGGTTTTGTATAGC R: GTTTTGATTTGCCCATGCAC	226	1.5	58		AB104361
TNF receptor-associated factor 6	TRAF6	12p14-p13	F: ACAGTTAGAGGGTCGCCTTGT R: GATTTCAAGTGCATCCCAAAG	198	1.5	55	Perrocheau et al. 2006	DX010602
microsatellite	UCDEQ411	12	F: TGCTGCGAGTCAGTGGCT R: ATGCCTCACATCCCTGGGT	77-93	2.0	58	Eggleston-Stott et al. 1999	U67405
microsatellite	UCDEQ497	12	F: GTGGGAGGCAGCAGGAAC R: CCCCAGACACCGTGTGAT	105-109	2.0	58	Eggleston et al. 1999	U67419
microsatellite	UMNe109	12	F: TGGCTCAAATTCTGTGGTTG R: TTTTCCTTCCCTCAATATCTGTATC	180	1.5	55	Mickelson et al. 2003	AF536252
microsatellite	UMNe165/193/260	12	F: CAGCCCTGGTCTAAAATTTACC R: TCAATGGTGAAAATCTCTTTCC	160	2.0	58	Mickelson et al. 2003	AF536272
microsatellite	UMNe168	12	F: CACCAAACCCCACTGAATTC R: CACTACCTTCCCCTACGTTCC	149	2.0	58	Wagner et al. 2004	AY391308
microsatellite	UMNe191	12	F: GGTGATGTGTCCACACTTGC R: CGAAAAAGATAGTCCACCGG	142	2.0	58	Mickelson et al. 2003	AF536279

microsatellite	UMNe223	12	F: GTCTGTCCCAGACATATACCCC R: AACCTGGGCAAGGGAAAG	112	2.0	58	Wagner et al. 2004a
microsatellite	UMNe329	12	F: TGTTTGCTTGGAATGGTCAG R: TCTCCATCTCCACATAGGCC	104	2.0	58	Wagner et al. 2004a
microsatellite	UMNe331	12	F: TAGCCATGATATGGAAACAACC R: ACTGTCCATCCATGTTGCTG	158	1.5	64	
microsatellite	UMNe391	12	F: ATCAGGTCTGAAGGTGGCC R: GAATCTTATTGGTCCAGCTTGG	187	2.0	62	Wagner et al. 2004b
microsatellite	UMNe469	12	F: CCACGCTCCCATCTTTTG R: CTTTCATGCTCTTTTCTCCCC	156	1.5	60	Wagner et al. 2004b

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	13STS01	13	F: AGCTGACCGTCAAGACCAAG R: CGACTGGGTGGCTGACTT	~900	1.5	55		BM780447
actin, beta	ACTB	13	F: CGACATCCGTAAGGACCTGT R: GTGGACAATGAGGCCAGAAT	332	1.5	58		
microsatellite	AHT030	13q13	F: TCACCGCTCACCTTTTGAC R: CGTGCAGGTGTACATTTACATG	181-183	2.0	58	Swinburne et al. 2000	AJ271515
microsatellite	AHT095	13	F: CATTCTCCAGGGATTAACATTG R: ACCATAATGAGCTAAGGAAGCA	217-233	2.0	58	Swinburne et al. 2003	AJ507712
aldolase A, fructose-bisphosphate	ALDOA	13	F: CATCAACCTCAACGCCATC R: GGCATGGTTAGAGATGAAGAGG	327	1.5	58		
actin related protein 2/3 complex, subunit 1B, 41kDa	ARPC1B	13	F: CAAGTAACACAACCCTGAGTC R: GCTCTCCACACTATCTCCAAAC	190	1.5	52		
microsatellite	ASB01	13	F: AGCAGAAACCCACTCAAGCC R: GCATAATACCCTCAAGGTC	153	2.0	58	Breen et al. 1997	X95316
microsatellite	ASB37	13q11-q12	F: CCTGCAACTTTTTCCCAGCC R: GGCAGATGTTAGCTCATGGC	125-138	1.5	TD 64	Irvin et al. 1998; Lear et al. 1999*	AF004767
ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1	ATP2A1	13	F: CCCTCCTCCATCTCTTTGAA R: CTGAAGATGCGTCGCTATGA	545	1.5	58		
autism susceptibility candidate 2	AUTS2	13	F: GACACACCTCAGTGGGAACC R: CCATCAGTTACCGCACACAG	167	1.5	54		
alpha-2-glycoprotein 1, zinc-binding	AZGP1	13	F: CCCAGGAAAAGAGAGGACAC R: TGGGCCAGACGATTATTACTG	503	1.5	58		BM780848
bifunctional apoptosis regulator	BFAR	13	F: TGACGTCTGAGGTTTGATGC R: GCTGTGTTGTCCCAGCTCTA	189	1.5	63		CX602272
chromosome 16 open reading frame 53	C16orf53	13	F: GACCGCTGTTGGAATCTGA R: GCCGTAATGTCTCCATGACC	158	1.5	58		CX597497
chromosome 16 open reading frame 63	C16orf63	13	F: GAGGCGTGTTAGGGCATTTA R: TGCCATGAGGACAGATGCT	173	1.5	63		DN507486
chromosome 16 open	C16orf72	13	F: GCTGAAGTAGCTCGGCTAGG	146	1.5	62		DN504887

reading frame 72			R: GATGTGTTGGCTTGGGTT					
calcium regulated	CARHSP1	13	F: TGCTGGACACCCAACAGG	~863	1.5	63		CX593894
heat stable protein 1, 24kDa			R: CCTTGGATCGACAGAAGCAT					
chaperonin	CCT6A	13	F: TAGGCTCATTTTTGTGGCAG	381	1.5	58		
containing TCP1, subunit 6A			R: AGAAGTTGAGACACTTACGTTG					
BAC end sequence	CH241- 102019_T7	13	F: GAGCAGGGAGAAGAGACG	243	1.5	59		AJ584539
			R: CCCATCTTGGCTTACCTG					
BAC end sequence	CH241- 106P18_T7	13q16	F: ACCAACCCCTAGCTTAGAGTG	152	1.5	58		CT008340
			R: CAACTGAGGCAACATTAGCAT					
coenzyme Q7	COQ7	13	F: GAAATTCGGGATGAAGAGC	~811	1.5	58		CX604694
homolog, ubiquinone (yeast)			R: CATCCGACCTGGATAATGCT					
microsatellite	COR069	13	F: AGCCACCAGTCTGTTCTCTG	265-283	2.0	55	Tallmadge et al. 1999a	AF142606
			R: AATGTCCTTTGGTGGATGAAC					
coronin, actin binding protein, 1A	CORO1A	13	F: CCTCCTCATTTCCTCAAG	284	1.5	63		
			R: GGAGCTTCCTCATCTCTTCC					
CREB binding protein	CREBBP	13	F: CATTCCAGCAGGAGGGATAA	534	1.5	62		CX594454
			R: GGTCCTGAGTGACATGTTTCG					
hypothetical protein DKFZp434J1015	DKFZp434J1015	13	F: GTGCTCTCCAAGGTCCAAAG	266	1.5	58		CX597697
			R: CTACCGTCCTGCTCTTACGG					
eukaryotic translation initiation factor 3, subunit 8, 110kDa	EIF3S8	13q13	F: AGAACCTGGCTCTGCAGCTA	295	60	1.5		CX604676
			R: GGACAGAAGTGACGCAATCA					
elastin	ELN	13p13	F: CAGGCCTGTAGGCTGCTTAT	182	3.0	58	Milenkovic et al. 2002* ; Chowdhary et al. 2003	AF130761
			R: CACCTGTGAAGAGGGCAGAT					
erythroid associated factor	ERAF	13	F: GTGACCGTGGTGAATGACTG	163	1.5	58		
			R: AGGACTTCAGGAAGGCCCTA					
guanine nucleotide binding protein, beta polypeptide 2	GNB2	13	F: CTGAGCTTTTGTTTTGCCTG	158	1.5	56		
			R: GTCCTGTTTCCTATCCCCTG					
G protein-coupled	GPR30	13p15-	F: GCTGGTCTTCTTCGTCTGCT	212	1.5	51		

receptor 30 glucuronidase, beta	GUSB	p14 13	R: TCAGCTTGTCCTGAAGGTC F: CCAACGAAGCAGGTTGAAGT R: AAAACTGCTGCCCGATAGAG	198	2.0	58	Chowdhary et al. 2003	AF134223
hemoglobin, alpha 1	HBA1	13qter	F: CTGTCGAATCTGAGCGACCT R: GTGGATCGAGGGAGTGTCTAG	170	2.0	58	Oakenfull et al. 1993*; Shubitowski et al. 2001; Chowhary et al. 2003	AY008792
huntingtin interacting protein 1	HIP1	13	F: CTGTTCTACCGCTCCAGCA R: CTCTAGGACTGGCTCGCTGT	171	1.5	54		
hematological and neurological expressed 1-like	HN1L (<i>C16orf34</i>)	13	F: GAACAGGCTGCAGAACAAACA R: AAGCCTTTGAAAGCAAACCA	225	1.5	62		DN506642
interleukin 4 receptor	IL4R	13	F: GACTACATCAGCATCTCCAC R: CTTGAAGGAGCTGTTCCAC	370	1.5	58	Solberg et al. 2004	AY081138
KDEL endoplasmic reticulum protein retention receptor 2	KDELR2	13	F: TCAGTCTGCCAGCGTAAGTG R: AAGGCAAGATGCATTAAACAG	205	1.5	58		CX605749
microsatellite	LEX041	13q12- q13	F: TATTTTCTGAATGCTTCTGTGC R: CTCTACACCCAATGCCTGAT	149-162	3.0	58	Coogle et al. 1997	AF075643
leucine-rich repeats and calponin homology domain containing 4	LRCH4	13	F: CCTCATTCTGGCCACTGTATG R: CAGAGGGTCGGAAAGAAAGAC	246	1.5	62		BI961649
methyltransferase like 9	METTL9	13	F: AAGACTTCGGCCTCCACGTG R: GAAACCATCAGAAATTTTGG	211	1.5	60		CX602521
hypothetical protein MGC11257	MGC11257	13	F: TCTCCACCTTGCTGGCTTAC R: TAGGAGAGCAGCTGGAGCAC	172	1.5	58		CX600886
microsatellite	NVHEQ098	13	F: TGCAATGACCATCAGAACTTC R: CGGTGGTTTTTGAAATGAA	167-169	4.0	50	Roed et al. 1998	AF056398
phosphorylase kinase, gamma 1 (muscle)	PHKG1	13	F: GCATCCACAAGCCCACAT R: ATGTTGGGGTGCCCTGAA	151	1.5	58		
P450 (cytochrome) oxidoreductase	POR	13p13	F: GGGAACAAGACCTACGAGCA R: CTTCCACCCCAAAGTGTTCA	~600	1.5	58		
protein kinase C, beta	PRKCB1	13q13	F: GACACCTCCAATTCGACAAA	174	1.5	55	Perrocheau	DX010562

1			R: ACACTCCAGGCTTACAATGGA				et al. 2006*	
PRKR interacting protein 1	PRKRIP1	13p13-p12	F: GCCCAAGAAAGAGCCACAA	~1200	1.5	58		
protamine 1	PRM1	13q14-q15	R: TTACATCTCGGACAAATTCTGGG F: CCTCCTATGAGGTCACATG R: CCTCGCAGACCAGAGCTGT	407	3.0	58	Lindgren et al. 2001*	L10654
retinoblastoma binding protein 6	RBBP6	13	F: TGATGAAGCTGCTTTTGAACC	175	1.5	62		CX605509
serpin peptidase inhibitor, clade E, member 1	SERPINE1	13p13-p12	R: GCTCCTGTTACGCCTATTT F: GGAACAAGGATGAGATCACCA R: ACCTGCTTGACTGTGGTGTG	115	1.5	58		AF508034
microsatellite	SGCV03	13q12	F: GATGGCAACCCTGAAACAAG R: TTTGCCATGTGTGAGGCTAC	249	1.5	61	Godard et al. 1997*	U90586
PI-3-kinase-related kinase SMG-1	SMG1	13	F: ACACGGAGATTGTCTTTCTGC R: TTCCTTGGCTGTGATTCTTC	196	1.5	55	Perrocheau AG 2006	DX010586
specific E3 ubiquitin protein ligase 1	SMURF1	13	F: TTGAGTCCATTCAAAAAGTCC R: CAGGAAGGTGGCTTTAGAGG	401	1.5	58		CX599658
STIP1 homology and U-box containing protein 1	STUB1	13	F: GCAAAGACATCGAGGAGCA R: GATGAATGCGTCGATGACC	205	1.5	58		
THO complex 6 homolog (Drosophila)	THOC6	13	F: GGCCCAGCACTTACTCTCTG R: GGCTGCTGGTTGAGGCTA	301	1.5	62		DN507406
microsatellite	TKY031	13p15	F: CTACTCACCAGCCTGCAAAG R: CTGCTTGTCTTCTCATCTCC	95	2.0	58	Hirota et al. 2001*	AB048337
microsatellite	TKY371	13	F: AACGTGGGAAAGTGCTTCTG R: CTGTCCAAAGACAATCCCTG	164-182	1.5	58	Tozaki et al. 2001	AB044871
microsatellite	TKY416	13	F: GTCCAGGGACTGAACTTTTCG R: AGCCCGGAGCATCTTGTAAGT	132-142	1.5	55	Tozaki et al. 2004	AB103634
microsatellite	TKY421	13	F: CCTTGTAGGAGGCGAGTCAG R: GCCACTTCCTACCAATGCTC	270-292	1.5	58	Tozaki et al. 2004	AB103639
microsatellite	TKY500	13	F: CAACCCAAATGTCCACCAAC R: TGGTACTCTGTTTCTAGCAG	275	2.0	58		AB103718
microsatellite	TKY561	13	F: TCTGCTCAGTTCCCAACACA R: ACTGCACAGAACAGGGCTTC	294-306	1.5	58	Tozaki et al. 2004	AB103779
microsatellite	TKY581	13	F: AAGAAGGGCTGGTGACCTCT R: GGCAGCACTATTGGCTCTTC	165-179	1.5	60	Tozaki et al. 2004	AB103799

microsatellite	TKY585	13	F: GCAGCCTGAGGAAATGAAGT R: TTATGACCCCCACTCTCCTG	122-136	1.5	58	Tozaki et al. 2004	AB103803
microsatellite	TKY594	13	F: CAGAGGGAAGAGCCAGGAG R: AAAAGGTGATGGGCACAGTT	115-135	1.5	58	Tozaki et al. 2004	AB103812
microsatellite	TKY693	13	F: CAGAGACTGCTGTCAGCTCCT R: CACAAATGCAGAACCCACAA	201-217	1.5	56	Tozaki et al. 2004	AB103911
microsatellite	TKY835	13	F: AGATTGGCACAGACATTAGC R: ATTTCCAGATGGGAAAGAGG	255	2.0	58		AB104053
microsatellite	TKY852	13	F: CTGACCTGCATTGACCTTTA R: CATTGTGTATGCTGACTGGC	105	2.0	58		AB104070
microsatellite	TKY979	13	F: AGTAACGGCTGCTATTGTAG R: TCCAAACCAGTTCCTATGTC	237	1.5	58		AB104197
microsatellite	TKY981	13	F: TCACAGCATTAGCATTGCAG R: CAGGAGGGAAGAATACAAG	116	2.0	55		AB104199
microsatellite	TKY1025	13	F: TCCCTACTTCTCTTGAATGC R: AATGCAGTTCTCTGATGACC	120	2.0	58		AB104243
microsatellite	TKY1047	13	F: ACAGGAATGGACGAGAATTC R: AGAAGAATCTCTGGGTATGG	156	2.0	58		AB104265
microsatellite	TKY1092	13	F: GGGAAAGGAAGGTCAATATAC R: AGAGCCAGGCTGATTCTTG	220	2.0	58		AB104310
microsatellite	TKY1176	13	F: GATCTGGAGTTGCAAACCTCA R: AAGGAAGTGGGAATTGGAGC	173	2.0	58		AB104394
microsatellite	TKY1398	13	F: TGTCTGAAATATGGGGCTG R: TCCAGAGAAGGCTAATTTG	175	1.5	58	Tozaki et al. 2007	AB215341
microsatellite	TKY3276	13	F: GGGAGACGAGAGAGAAAAGG R: ATGTTCCAGAGGGGAGACAC	165	1.5	58	Tozaki et al. 2007	AB217219
transformation/ transcription domain- associated protein	TRRAP	13	F: AGAGCCTCTGGCACATAAGAC R: CCACCCATCACACAAGAGG	311	1.5	58		CR955442
tuberous sclerosis 2	TSC2	13q16	F: TATCCCTCCAAGTGGATTGC R: AGTCGTCCACGGAAGAGATG	328	1.5	62		CX601414
ubiquitin-binding protein homolog	UBPH	13	F: TGCCATGCAGAAAGTCATGT R: GGCTCCTTCTGTTCTCCTC	183	1.5	63		DN507077
microsatellite	UM030	13	F: CCGTGAAGTCACAGACTTAG R: ACAGTTTCTACAACAACTGA	127-143	2.0	58	George et al. 1998	AF195577

microsatellite	UMNe126	13	F: CAAGCTGCACTGTGGTGG R: TGCAGCTCAACAATGGTACTG	174	1.5	58	Mickelson et al. 2003	AF536256
microsatellite	UMNe133	13	F: CCAGGTATGTCACTAGGTGTGG R: TCCCTGTCCTTGCTGTGTC	174	1.5	58	Mickelson et al. 2003	AF536258
microsatellite	UMNe145	13	F: ACAGCCACTCCCCATTACC R: TCCAAAAATTTCTCATGCC	110	1.5	58	Mickelson et al. 2003	AF536261
microsatellite	UMNe217	13	F: CTTTGAGTTCACCAGTTCTCCC R: AACCAAAAGGAACCTTGGTGG	151	2.0	58	Wagner et al. 2004a	AY391320
microsatellite	UMNe276	13q13	F: CATGCTCTCCATGACTTTTCC R: CACCCAGGACTCCCACAG	154	2.0	58	Wagner et al. 2004a	AY391331
microsatellite	UMNe278	13	F: CAATTATGTGGGCACTGTGC R: AGCAGATACCTGACATCATTGC	185	2.0	58		
microsatellite	UMNe305	13	F: ACAGTTCACAGCGGCCTC R: GAGAGGGAGCAAGCCCTC	162	2.0	58	Wagner et al. 2004a	AY391333
microsatellite	UMNe344	13q13	F: ATCAGCGCACACCTAGTAGAG R: GAGACACTCTGTAGGGGATTGG	130	2.0	55	Wagner et al. 2004c	AY735241
microsatellite	UMNe364	13q16	F: TCCATACCCCTGAACTGCTC R: AGAGCTAAATGAGAGGGGGC	156	2.0	62		
microsatellite	UMNe431	13	F: CAAGGTAAGGGTCAATCAGAGG R: AAGGGTCAGGTGCTAGAAAGC	270	1.5	58	Wagner et al. 2004c	AY735250
microsatellite	UMNe451	13	F: GGCAACAGATGTTAGCTTAGGG R: TCAGGTGTTTCCAACCTGTTCC	268	1.5	60	Wagner et al. 2004b	AY464488
microsatellite	UMNe462	13	F: GATCTGGAACCCACATGG R: ATGTTGCAGAGAAAGGGGG	303	1.5	62	Wagner et al. 2004b	AY464491
microsatellite	UMNe552	13	F: ACCTCTCTGTGCTTCAGTTTCC R: TTCAGTGAACCACTTTGTTCTG	~300	1.5	58	Wagner et al. 2004b	AY464524
microsatellite	UMNe601	13	F: CTCTAAACCCAAGGATGAGATG R: CACAGCTCACATTCTCTGCC	108	1.5	58		
vasorin	VASN	13	F: GACCTCGGTCTCCTCATCTG R: TGTGTTACCAGCACACAGCA	162	1.5	6		CX594894
microsatellite	VHL161	13	F: GTTCCACCTTCCTCTGGATC R: GTGTGTCGCTAGGATTCAATCA	175	2.0	58	Van Haeringen et al. 1998	Y11661

microsatellite	VHL47	13	F: GTTTGCTGTGGTTACCAGGCAGA R: GCAAATTGAATATTTGAAGTTGAGAC	126-144	4.0	58	Van Haeringen et al. 1998	X86449
vitamin K epoxide reductase complex, subunit 1	VKORC1	13	F: GGCATCTACTCTGCTGTTGCT R: ACCTCCCGGAAGCTGAGTAT	156	1.5	58		CX600422
WD repeat domain, phosphoinositide interacting 2	WIP12	13	F: GACTGTGGCAAGCAATCAGG R: ACAGCAGCAACACAAATGGG	166	1.5	58		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	14STS01	14	F: AGAGAAAAGAGAGTGTGG R: GAATCTGCATTGTAACAAGG	211	1.5	50	B. Brenig, personal commun.	AY008801 AY008799
sequence tagged site	14STS02 (<i>SOD2</i>)	14	F: GAAGTTGACTGCTGTATCGGCTG R: GGTTAGGACAGGCAACAATCTGG	101	1.5	62		BI961637
sequence tagged site	14STS03	14	F: TTGCGAATCTCTTCAAGGGC R: CTGTCATTGCTGTCAACCAC	500	1.5	60		
adrenergic, beta-2-, receptor, surface	ADRB2	14q14dist- q16prox	F: CTCGTCCATCGTGTCTTCT R: GGCTTTGTGTTCTTCAAGC	202	2.0	58	Caetano et al. 1999, Chowdhary et al. 2003*	AJ507700
microsatellite	AHT029	14q13	F: ACTCATTTCATTCACAAATCCCC R: AGAAAATTCCCTCCTGTCCC	270-292	2.0	58		AJ507705
microsatellite	AHT083	14	F: CTGACTATCCCCCAAACACA R: ATGGCATTGCTTACATATCCTG	102-114	2.0	58		
microsatellite	AHT088	14	F: TCACATGTGCCCTATGAATCC R: CCTGTCAATGGAGGAATGGA	307-318	2.0	58	Swinburne et al. 2003 Swinburne et al. 2003 Perrocheau et al. 2006, Goh et al. 2007*	
aldehyde dehydrogenase 7 family, member A1	ALDH7A1	14q22.1	F: GAAGATCCAAGTACTAGGAAGCT R: ATCCACGTACTCTGAAGTTCT	1045	1.5	58		DX010433
annexin A6	ANXA6	14	F: TGAGAAAGTGCTCATTGAGATC R: TCTTCTGGAAGTGCCAGAG	1032	1.5	58		
arylsulfatase B	ARSB	14	F: GCATCAAATAATCTTGCCCTGT R: GTATCAAATCCTCGGCGTGT	162	1.5	55	Perrocheau et al. 2006 Caetano et al. 1999, Goh et al. 2007	
BCL2/adenovirus E1B 19kDa interacting protein 1	BNIP1	14	F: AATTTAAGTCCATGTCGGGG R: CAATATAGAGGACTGTCGCAAGA	132	1.5	58		AF115747
C1q and tumor necrosis factor related protein 2	C1QTNF2	14	F: AGCTTTCTCGGTGGCAGTG R: GCGTGATGTCGTAGGTGAAGTAG	158	1.5	58		
calcium/calmodulin-	CAMK4	14q23-	F: CCCTTTCTCAGGGCAGAAG	199	2.0	58	Caetano et	

dependent protein kinase IV		q24	R: CCTTTGTGTGTCCAGCAATG				al. 1999, Chowdhary et al. 2003	
calnexin	CANX	14	F: AGATGGGTGCTATCCACCAG R: GGAGAAAGCACTGAACAGCA	328	3.0	60	Chowdhary et al. 2003	
calpastatin	CAST	14	F: AAGACGGAAAGCCTGTGGA R: TCACCAAGTTTCTCACGATCC	566	1.5	58		BI961829
coiled-coil domain containing 100	CCDC100	14	F: CCTTCAGAAATCCAGACAGAG R: CTTCTGCAAGAGCTTGCATA	681	1.5	58	Goh et al. 2007	BI961752
CD14 molecule	CD14	14q16-q21	F: CTCAACTTGTCTTCGCTGGG R: CAGATTACTCACCACGGGCAG	132	1.5	58	Goh et al. 2007	
CD74 molecule, major histocompatibility complex, class II invariant chain chromodomain	CD74	14	F: GCACAGATTAACAACGCAGG R: GCAAATGTGTTGGACTTGGG	201	1.5	58	Hopman et al. 1999	AF083445
clathrin interactor 1	CHD1	14	F: GCAGATGGACCATAGAGCTT R: TCCGACTACTCCAGGTATGC	135	1.5	58	Swinburne et al. 2000	
microsatellite	CLINT1 (ENTH)	14	F: ATGGCCCCCTCTTGAAAT R: GTTCCAGAAGTCATGGCTAAGT	140	1.5	58	Goh et al. 2007	
microsatellite	COR002	14	F: CTTGAGCACCCAGTAACACC R: CCAGGAATCTTCTCTACCGA	224-232	2.0	58	Hopman et al. 1999	
microsatellite	COR103/104	14q12-q13	F: GGGAGTGTGTCCAGTTTGTC R: CCABATAAAGCCCAAATCCT	167-169	2.0	58	Swinburne et al. 2000	
cofactor required for Sp1 transcriptional activation, subunit 9	CRSP9	14q15	F: CATCCTATGCAGTTTGATCAC R: TCTGTCCAGTACAATTGTTGC	400	1.5	58		
colony stimulating factor 1 receptor	CSF1R	14q15-q16	F: GAGTTTATGAAGGAGGTG R: GTGTGAGAGTGATGTTAG	174	1.5	50	Caetano et al. 1999, Beck et al. 2005*	
colony stimulating factor 2	CSF2	14	F: CTGGGACCTTCTTGAGATGC R: TCTGTCCTCCACCAGTAGGG	194	2.0	58	Caetano et al. 1999	AF115750
casein kinase 1, gamma 3	CSNK1G3	14	F: GGCAACATATCTTCGTTATGTAA R: CTGGTTTTTGGATTGTTGCA	998	1.5	60	Goh et al. 2007	
chondroitin sulfate	CSPG2	14q26-	F: TTCGCTTACAAGAAAGGCCTGA	282	3.0	58	Chowdhary	

proteoglycan 2		q27	R: CAGCATTTCATACATGAACATTCAAAAC				et al. 2003*
chondroitin sulfate synthase 3	CSS3	14q22.1	F: GGAAATCCTCCCACTGATGA R: CACCTGCACCTAGAAGATCA	112	1.5	58	
cytoplasmic FMR1 interacting protein 2	CYFIP2	14	F: TCTCTGGCTATCTTCGCTACAG R: ACATGGTGCAGTAGTGCCTG	156	1.5	58	
DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	DDX46	14	F: TGATAAGAAGAAAGGTGAGCTG R: GATACCCTGTAAGGGCTGTC	775	4.0	55	
dimethylglycine dehydrogenase Dmx-like 1	DMGDH DMXL1	14q27 14	F: AGTACACTGAGGCCAAAGCAA R: AGAGCCCACTGACTCGTTGA F: AGTAGCTTATAAGCAGCCTG R: GATCCAATTCTACAGTCAG	506 306	1.5 1.5	58 60	Goh et al. 2007* Goh et al. 2007
dihydropyrimidinase-like 3	DPYSL3	14q14dist- q16prox	F: GTTTCCTCAAGCCTTCTCCCTTA R: GCTACCACAGATCACAGGGAGATAG	114	4.0	60	Chowdhary et al. 2003*
dual specificity phosphatase 1	DUSP1	14	F: CTGCGAACTGTCCCAACCAT R: TTGGGGGAGATGATGCTTCT	716	1.5	58	Perrocheau et al. 2006
early B-cell factor 1	EBF1	14	F: GAGGTTGGATTCTGCTACAGAG R: TTAACCAACACCCTGCACTT	173	1.5	58	Goh et al. 2007
ephrin-A5	EFNA5	14	F: ATGACACCGTCCATGAGTCAG R: GGATGAGCAGTTAGGTGGATCT	198	1.5	55	Perrocheau et al. 2006
fibrillin 2	FBN2	14	F: CTAACCGAGGGGATGTTCTT R: CTTTCCTCCATGTCTAGAGCA	1003	1.5	55	Goh et al. 2007
F-box and leucine-rich repeat protein 17	FBXL17	14q24	F: TTGGGCGATACAGCATGACA R: CATCAGCCCCAAATATCTCAGA	119	1.5	58	Goh et al. 2007*
fem-1 homolog c (C. elegans)	FEM1C	14	F: TTCTTAAGCTGCATCCAAGG R: TCCAGCAAGTCACTAGCAGTT	292	1.5	58	Goh et al. 2007
fibroblast growth factor 18	FGF18	14	F: GCAAGGAGTGTGTGTTTCATC R: GCTTCATGAAATGCACGTCC	159	1.5	58	Goh et al. 2007
gamma-aminobutyric acid (GABA) A receptor, gamma 2	GABRG2	14	F: CTACCATTGATATCCGCCCA R: GAGGTAGGAGACCCAATAGACC	263	1.5	58	
G protein-coupled receptor 98	GPR98 (<i>MASS1</i>)	14	F: TCAAAGCTAGTGATCATCCA R: GGACACTGTTCTAAATTCCG	1205	1.5	58	Goh et al. 2007
glutamate receptor,	GRIA1	14	F: TTGAGGGCAATGACCGTTAC	114	1.5	58	Perrocheau

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ionotropic, AMPA 1			R: GGGCTCCGTATTTTCCATCA				et al. 2006	
hyaluronan and proteoglycan link protein 1	HAPLN1 (CRTL1)	14q27	F: AAGCCAAGGTGTTCTCACAT R: AGTCCTTCAATCACCTCACAC	298	1.5	58	Milenkovic et al. 2000, Perocheau et al. 2006	
histidyl-tRNA synthetase	HARS	14	F: TTGCTCGAGGACTGGACTACT R: AGATCCGCTCTACTCCAATGC	198	1.5	55	Perrocheau et al. 2006	AF115752
heparin-binding EGF-like growth factor	HBEGF	14	F: CCCAAGGTGCTGATGTCAAAG R: GATTATCCTCTGCTGCGCTGA	235	1.5	58		
hexosaminidase B (beta polypeptide)	HEXB	14q27	F: ACGCTGTGGCTTACCATTTT R: TCATGAATGCTTCAGGTCTCC	137	3.0	60	Caetano et al 1999, Chowdhary et al 2003*	
hexokinase 3 (white cell)	HK3	14q13	F: AGTGGGGCTCCTTCAGTGAT R: CACCAGCTCACCCAGGTACA	656	1.5	58	Shubitowski et al. 2001, Goh et al. 2007*	AY008793
microsatellite	HMB1	14	F: GTGTGTATGCTTCCCAACCCTT R: GTTATAAAGCACTATGATCTCA	118	58	2.0	Goh et al. 2007	Y07729
3-hydroxy-3- methylglutaryl- Coenzyme A reductase	HMGCR	14q27	F: TGTGGCCAGCACTAACAGAG R: CCACCAAGCTGCCAGAGTAT	193	2.0	58	Shubitowski et al. 2001, Chowdhary et al. 2003*	
hyaluronan- mediated motility receptor	HMMR	14	F: AAGTATTGAAAGGACCAGTATCC R: CTTAACTTTTCTAGCTGAAGCAG	890	1.5	50	Goh et al. 2007	
hydroxysteroid (17- beta) dehydrogenase 4	HSD17B4	14	F: TGGGTCTTCTGGGCCTTTCA R: TCAACCGTGATCCAGCTTGA	96	1.5	58	Marklund et al. 1994	AF169295
heat shock 70kDa protein 4	HSPA4	14	F: GAACAAGCAGAGTCTGACCA R: TCAGGAAGCTTCTTGTCTGA	458	1.5	58	Lindgren 2000	
microsatellite	HTG11	14	F: CAATGATGGTACTTTGCATATTAA R: ATCGGCATGCACACTCATAGGTAG	110	4.0	60	Marklund et al. 1994	
microsatellite	HTG29	14	F: CTATTTCCAGTCTTTGTGTGT R: CCATAATAAAACATTAAAGATCAG	110	3.0	58	Lindgren 2000	
5-	HTR4	14	F: GAGCATGCCCACCAGATC	139	1.5	58	Goh et al.	BI961569

hydroxytryptamine (serotonin) receptor 4			R: AACCCATGATGATGCACAGG				2007	
interleukin 12B	IL12B	14q14- q15	F: TCTTAGGCTCTGGCAAAACCT R: TGTGAAGCAGCAGGTGAGAA	114	1.5	58	Goh et al. 2007	
interferon regulatory factor 1	IRF1	14	F: GTGAATCCTGTTCCCAAAGA R: GCTTAGCGGAGACGTTAGTG	236	1.5	58	Goh et al. 2007	
jumonji domain containing 1B	JMJD1B	14q21	F: TATGGCACATCTATGCAGCC R: GAATTGGGTCATGATCAGGG	388	1.5	58		
KIAA0372	KIAA0372	14	F: ATTTGAAAGCTGGTCAGCAT R: CACTGTATATGGATTCTGGGTTC	1077	1.5	58	Goh et al. 2007	
kinesin family member 3A	KIF3A	14q21	F: TTGCATATGGACAAACCGGA R: AACCTTTGTGTCTGATCCTTGC	358	1.5	58	Goh et al. 2007*	
La ribonucleoprotein domain family, member 1	LARP1	14	F: ATGAGCAAGAGGAAGTGGAT R: GCATGTAATGTGGTGTCTGG	162	1.5	58	Coogle et al. 1997	AF075645
lymphocyte cytosolic protein 2	LCP2	14	F: CCTTGCCACTTCCAAACAAA R: TGGTCGGGTAATATAAGAAACG	702	1.5	58	Coogle et al. 1997	AF075649
microsatellite	LEX043	14q13- q14	F: CATTAAAGCAACAAAAGCATC R: GGAAAAGCATGACAAGACACT	238-246	3.0	60	Coogle et al. 1997, Chowdhary et al. 2003	AF213364
microsatellite	LEX047	14	F: TATAATAATGTGTCTTGGTGTG R: TGTTAATCAGGGTTCTCC	237-245	3.0	58	Coogle et al. 1997	
microsatellite	LEX078	14q27	F: TGTGCGCATTTAACCAGTGT R: TTCATGCACTCCACTTCAGC	230	1.5	60	Bailey et al. 2000, Lear et al. 2000*	
lectin, mannose- binding 2	LMAN2	14	F: ATGACACCTTCCTGGCTGTG R: AGGCTCCAAAGTAGTAGCCG	247	1.5	58	Goh et al. 2007	
methionine adenosyltransferase II, beta	MAT2B	14q14	F: TTCATTGGTCTGGCAACGAA R: TCAAGCTGAGCATTTCTTGGA	663	1.5	58	Goh et al. 2007*	
methylcrotonoyl- Coenzyme A carboxylase 2 (beta)	MCCC2	14	F: TAGGAAGGTTGTGAGGAATCTA R: GCACCAACTATTCCATACAAT	216	1.5	50	Goh et al. 2007	
MADS box transcription	MEF2C	14	F: CCAACTTTGAGATGCCAGTCT R: TTACCTGCACTTGGAGGTCTG	169	1.5	58	Goh et al. 2007	

enhancer factor 2, polypeptide C	MEGF10	14	F: CCATTGCAGGCATCATCATT R: GCAGGGGTGTAGGTAACCTGCT	121	1.5	58	Goh et al. 2007	
multiple EGF-like- domains 10	MFAP3	14q16	F: AAACCATGGAGTTTGCTCGT R: CATCTGAATCTCCTCCTGGT	234	1.5	58	Goh et al. 2007*	
microfibrillar- associated protein 3	MYOT	14	F: ATGAAGCTGGAGTGACCACA R: AAAGTTGGTCGGACACGTAA	315	1.5	50	Bryan et al. manu	
myotilin	NR2F1	14	F: CCTGTCCGGCTACATCTCG R: CTTCTCCACCTGCTCCTGG	373	1.5	62	Goh et al. 2007	
nuclear receptor subfamily 2, group F, member 1	NR3C1	14q16- q21	F: GAAAGCATTGCAAACCTCAA R: TCTGTTTTCACTTGGGGCA	~100	58	1.5	Goh et al. 2007	AY392091, AY392092, AY394747
nuclear receptor subfamily 3, group C, member 1	PAM	14	F: TACCAAGAATGCCAGGTTCC R: CGTGATGGAAGAAGAGGACTG	~200	62	1.5	Shubitowski et al. 2001, Goh et al. 2007	AY008799
peptidylglycine alpha-amidating monooxygenase	PCSK1	14q26	F: GGTTGTCTGGACCTCTGAGTAT R: AACTGCTCCAGGTCCTG	153	1.5	58	Goh et al. 2007*	
proprotein convertase subtilisin/kexin type 1	PDE6A	14	F: GGGCCAAGGTCATCTCAGAC R: AGCCTGCAGATTCTCCTGAA	137	2.0	58	Shubitowski et al. 2001	
phosphodiesterase 6A, cGMP-specific, rod, alpha	PJA2	14	F: CTTCCAGAGACCCTTGTCTT R: GCCAAATTGAGACACAAGGT	541	1.5	54		
praja 2, RING-H2 motif containing	PPIC	14	F: TTGGAGACAAAGATGTTGGC R: CCTTGATGACACGATGAAACT	577	1.5	50	Goh et al. 2007	
peptidylprolyl isomerase C (cyclophilin C)	PPP2CA	14	F: GAGCACAGTACTCCAGAGTGTGAGAG R: GCTCCAATGATTGTTTGCTGCT	340	3.0	58	Perrocheau et al. 2006	DX010568
protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	RARS	14q14	F: CCATAGTAAAATCAGATGGAGGT R: CATTGTCCACAACATAGATAATCA	111	1.5	58	Goh et al. 2007*	
arginyl-tRNA synthetase	RASA1	14q12	F: TGCTGGAAGTGTGAAAGAAAA	210	1.5	55	Perrocheau	
RAS p21 protein								

activator			R: ATGGTTGAATGGGTAACATGC				et al. 2006	
Rho-guanine nucleotide exchange factor	RGNEF	14	F: TAATGCAAACAGAGATGCATC R: AGAAGAAATGCCTGTGGATT	156	1.5	50	Goh et al. 2007	BI961565
Equine pseudogene	RPL7ps	14	F: AAGCGAATTGCCCTGACAGA R: CCACAGGAAGTTGTTTGCTTCT	135	1.5	58		
ribosomal protein S14	RPS14 (LOC153195)	14	F: CAGGTGGCTGAAGGAGAAAATG R: GAGTTTGATGTGGAGGGCAGTG	856	1.5	65	Goh et al. 2007	BI961565
ribosomal protein S23	RPS23	14	F: CGCTTTAAGGTTGTCAAAGTAGC R: TTACTACCACGCTTTCACCATC	105	1.5	59		
secretory carrier membrane protein 1	SCAMP1	14	F: ACATCCAGCTTATACACAGATTGC R: GTTCTTCTGGCGCTTAAGA	996	1.5	58		
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	SEMA6A	14	F: TGGAGATGAACACATCGCGT R: GCTCGGAGCGAACTGGTACA	186	1.5	50	Goh et al. 2007	
SH3 domain containing ring finger 2	SH3RF2	14	F: CTCCGGGAAGCCTGAACAG R: CCTCCGGAGGTCTGTCTGC	133	1.5	58	Perrocheau et al. 2006	DX010583
solute carrier family 25, member 46	SLC25A46	14	F: TCATTACATCATCAGCTCAG R: TTGGTAATCTGTAAAACAGC	399	1.5	58		
solute carrier family 26 (sulfate transporter), member 2	SLC26A2	14q15	F: AGGCAGACATGGACTCAAAGA R: CCAGATGTGGAGGATTAGCAG	200	1.5	55	Brenig et al. 2004*, Perrocheau et al. 2006	
SMAD family member 5	SMAD5	14q21	F: CATCTGTACTATGTTGGTGGA R: GCTCATATACTGCCTCAAAC	214	1.5	58	Caetano et al. 1999, Goh et al. 2007*	AF130781
synuclein, alpha interacting protein	SNCAIP	14	F: ACAGCTGATGCAGAGGTCAC R: GCTTTCTGCGCTGTCCATAC	145	1.5	58	Goh et al. 2007	AY008814
equine pseudogene	SOD2ps	14q22.3-q23	F: GACAAACCTGAGCCCCAAT R: CTTATTGAAGCCGAGCCAAC	148	2.0	58	Caetano et al. 1999, Chowdhary et al. 2003*	AF115756
SRY (sex)	SOX30	14	F: GTTTGGGCAAGGATCCAC	100	2.0	62	Goh et al.	

determining region Y)-box 30			R: AGTTTGTTCCTACTCTAACCCGA				2007	
secreted protein, acidic, cysteine-rich	SPARC	14q21	F: ACCCACTAACGGTCCCATT R: CTGGCAGCCAATACCCTAAA	199	2.0	58	Caetano et al. 1999, Chowdhary et al. 2003	
sequestosome 1	SQSTM1	14	F: AGGATGACATCTTCCGCATT R: AGACACTGCACTTGTAGCGG	966	1.5	58	Perrocheau et al. 2005	AY817486
ST8 alpha-N-acetyl- neuraminide alpha- 2,8-sialyltransferase 4	ST8SIA4	14q25	F: AGTTTGCTGCAGATGTGGGA R: CCTCCTTTGACCATGAAAGCA	172	1.5	58		
serine/threonine kinase 10	STK10	14q13	F: AGATGCAGCGCTACAACCAG R: CTTGATCTTCTCACGCTGCTC	176	1.5	55	Perrocheau et al. 2005*	
synaptic vesicle glycoprotein 2C	SV2C	14	F: CAAGACGGGATGTCAGATTACC R: GAAACAGCTGATCCCCGAA	634	1.5	58	Goh et al. 2007	
TAF7 RNA	TAF7	14q21	F: AGATGCTTGTCTCCACAGTT R: CTCGTCACTGTTCTAGTGAGTCA	377	1.5	58	Goh et al. 2007*	AB104254
polymerase II								
thrombospondin 4	THBS4	14	F: ACATCGACAGTTACCCCGAC R: GCCATCTCTGTCTGCATCTTCT	342	1.5	60	Tozaki et al. 2004	AB104271
microsatellite	TKY267	14	F: CCACTGCCAAATGAAACAAA R: CCACACATTTTCAGGAAAGAA	97-113	1.5	50	Kakoi et al. 2000	
microsatellite	TKY317	14	F: CTTGAGGAACATGTCATAGC R: AATGCTCTCACAATTTACCC	141-155	1.5	58		AB217464
microsatellite	TKY329	14	F: GCAGATTATTCCACATACCC R: CCTAACTGTTTATGGGTGAG	127-153	1.5	58	Tozaki et al, 2001	
microsatellite	TKY376	14	F: ATGCTTCACAGGGTTATCTC R: CTGGTGAGATTTGCAGTCAG	192-214	1.5	58	Tozaki et al, 2001	
microsatellite	TKY390	14	F: CCCTTTGTTGGGTAGAATAG R: TTATGCCTACCTCATAGGAC	220-224	2.0	50		AB103653
microsatellite	TKY395	14	F: ATGTCCCTTCTCAGCTTTG R: CTGGCGTCATTTACACATC	193-207	1.5	52		AB103656
microsatellite	TKY435	14	F: GTTCGTCTGTTTCTAGCCTC R: TATCTCCACATGGTACTCTC	205	2.0	58		AB103658
microsatellite	TKY438	14	F: TCCCCGAGAAAGGTGTGAGAC R: AAAACTGTACAGGGCAGGT	277-295	1.5	55	Tozaki et al. 2004	AB103691
microsatellite	TKY440	14	F: TTCCTATCTTCGAGGCCAGA	221-231	1.5	58	Tozaki et al.	AB103709

microsatellite	TKY473	14	R: CTTGCCAACACCCATTCTCT F: AAAGAGGCAATGTCAGTCAG	243	2.0	58	2004	AB103745
microsatellite	TKY491	14	R: AGAGGTTGGAGGGATAAATG F: CCTCTTGGGACAGAGGACAG	256-268	1.5	55	Tozaki et al. 2004	
microsatellite	TKY527	14	R: TCTCTCAGGAGCCTGTGTTG F: AGGGGTGTCAAATGCAGTC	149	2.0	58	Tozaki et al. 2004	
microsatellite	TKY584	14	R: ACAATTCCTTTTCACTGGGTG F: AGCCATTAGCCAAGGATGC	134-136	1.5	58	Tozaki et al. 2004	
microsatellite	TKY636	14	R: GACCAGGGATGTGGGTACAG F: TAATCGAGGGGGCCTTAATC	188-216	1.5	58	Tozaki et al. 2004	AB103874
microsatellite	TKY647	14	R: CGCTCTCTCTAAAGGCTCCA F: CTGGGAAGCAGCAGGAATAA	96-98	1.5	58	Tozaki et al. 2004	
microsatellite	TKY656	14	R: GCTAATGGAAAGGCCACAGA F: TTGTCATCACAAATGGCAGG	131	2.0	58		AB104005
microsatellite	TKY749	14	R: CGACGGATGAATAGATAAAG F: TGGGTTCTGTCTTCTCTCTGT	222-228	1.5	58	Tozaki et al. 2004	AB104059
microsatellite	TKY787	14	R: CCAGGCTCGAGAGACTTGTT F: AAAACAGTCCCTACCTTGAG	234	2.0	58		AB104062
microsatellite	TKY841	14	R: TGTGTGTGATTTAGCTAGCA F: ATCACTGATAGTCACCAAAGTG	148	2.0	58		AB104100
microsatellite	TKY844	14	R: ATGTGGATTAAGATAGAGCTGC F: TCTACCATAGCTCTACAGGA	153	2.0	58	Tozaki et al. 2004	AB104148
microsatellite	TKY930	14	R: GAGACAGAACCTGCTACCTT F: TTTGGACTTGCTTGGCCAG	147	2.0	58	Tozaki et al. 2004	AB104189
microsatellite	TKY948	14	R: AGAGAAGCAAAACCAGTAGG F: GATCGTCCCTCCACCTTG	102	2.0	58		
microsatellite	TKY971	14	R: CCTGCCAAACATCAGTATTC F: GTCGACAGAGCCAGGAAG	86	2.0	58		
microsatellite	TKY1036	14	R: GGGACTGTCAATTAACCCTC F: TTCCCTGTTTAGCTCTTAAAC	188	2.0	58		AB104332
microsatellite	TKY1053	14	R: GCAGTAAAGATGGTATCTCC F: ATACTGGCTTTACGTCACAG	92	2.0	58	Tozaki et al. 2004	AB104363
microsatellite	TKY1114	14	R: ATCACCACCAGAGTTAATGG F: GTTTATTAGGTCAGTCTTCC	247	2.0	58		AB104369
microsatellite	TKY1145	14	R: GCAAGCTCATTGCCAAGAC F: TGGCATCCACATAAAACAG	257	2.0	58		AB104374
			R: ACTGATTTGCACAGAAGGAG					

microsatellite	TKY1151	14	F: TCACGCAATTCCAATCTTTGG R: TGCCTACCAATTTGTAGGTG	259	2.0	58		AB215620
microsatellite	TKY1156	14	F: AGTGACAATCTTCCTCAAGC R: ATGGTTGAGAGGAAACTTGC	197	2.0	58		AB215933
microsatellite	TKY1677	14	F: TGACCCAGATGAATCTCTTA R: CATTCACTGCCGTCTAAGTA	174	1.5	58		AB216467
microsatellite	TKY1990	14	F: ACACTTTGTAGGGCACACT R: ATCAGTACAGTGGGAAGTTG	245	1.5	58	Kakoi et al, 2000	
microsatellite	TKY2524	14	F: TCCATGCGAATTAGTCCATT R: TTTGTTTACCCACACCTTCC	233	1.5	58	Tozaki et al, 2007	AB216996
microsatellite	TKY3053	14	F: TCCTTTTCAGCCATTTGTTGA R: TCTAACCAGAAAGTGAAGC	99	1.5	58	Tozaki et al, 2007	
microsatellite	TKY3521	14	F: TGGTACTCCTTTTGCTTCCA R: CGCACCAACTTAACCACTCT	238	1.5	58	Tozaki et al, 2007	
transmembrane protein 161B	TMEM161B	14	F: GTTTACTCTGAATTACCATCAGC R: ATGCCACAGTCAGATACTGG	202	1.5	50		
transportin 1	TNPO1 (<i>KPNB2</i>)	14	F: GCAACATTGAACAGCTGGTA R: CATGCTGAAAGCAAGCTTTT	215	1.5	60	Goh et al. 2007	
tripartite motif- containing 36	TRIM36	14	F: AGAATATCGAAAGGGAGCTC R: TTGATTGGAGTTGTCTGATC	161	1.5	50	Goh et al. 2007	
sequence tagged site	TUDPEc277	14	F: AAGAAAGAGGGTCAGAGGGC R: AGGAAAGCTGATTTTTCATGGTG	388	1.5	60		BI395242
ubiquitin- conjugating enzyme E2D 2	UBE2D2	14	F: TTTACCCCTTACATCCAGATAGA R: TGTGACAAGCCAATTCTCCA	545	1.5	58	Goh et al. 2007	AF195134
microsatellite	UM010	14q14	F: TACAGCCATTGGAAATCTAC R: CACCATTACATTTTCCCAG	110-120	3.0	58	Meyer et al. 1997, Chowdhary et al. 2003*	
microsatellite	UM016	14	F: TTCCTCCACTATCTCTCCCTC R: GCAAAAATGCACAGCCTC	200	2.0	58	Meyer et al. 1997	
microsatellite	UM032	14q14dist- q16prox	F: AAATGGTCAGCCTCTCCTC R: TGTCTCTCTAGTCCCACTCCTC	141-149	2.0	58	Swinburne et al. 2000, Chowdhary et al. 2003	AF536266
microsatellite	UMNe125	14	F: TGGGTCCTGAGACCATAAGC R: TCCTCCCTACCTCCTCACTG	143	1.5	58	Wagner et al. 2004a	AF536277

microsatellite	UMNe154	14	F: CAGCAATCAAATTGACCAGC R: TGGCTCCTCTCAAGTTGAGC	143	1.5	58	Mickelson et al. 2003	AF536281
microsatellite	UMNe187	14	F: GCTCCCTCCGCACTACTTC R: CTCCTATTCCAGACAGTGGAGG	108	2.0	58	Mickelson et al. 2003	
microsatellite	UMNe194	14	F: ACTGGATGCCTGGAATTGAG R: GAATAAGTTGGGACCCCTCC	120	2.0	58	Mickelson et al. 2003	AF536306
microsatellite	UMNe227	14	F: ATAATTTCCCTTGCCAACACC R: CTGTAGACCCAAAGGAAGATGG	186	2.0	58	Wagner et al. 2004a	AF536309
microsatellite	UMNe234	14	F: TATGCACAATTAAAGGCCTGG R: AATGACCCAGAGACAGGCTG	189	2.0	58	Mickelson et al. 2003	AF536314
microsatellite	UMNe239	14	F: ATCAAAGGTTTCATCAGTTGGTG R: TTCTTTCACTCAGCGTGGTG	171	2.0	58	Mickelson et al. 2003	
microsatellite	UMNe244	14	F: TCCAAGGGTTTGTCCAAAAG R: TCTCTTGGTTGAAAATGGGG	173	3.0	58	Mickelson et al. 2003	
microsatellite	UMNe315	14	F: CAGGCAATAAAAAATCTCCAACC R: TCACAGACGCTCCATAAACG	129	2.0	58	Goh et al. 2007	
microsatellite	UMNe321	14	F: ATCATATGGTATTTGTCTTCCTCTG R: CTCAAAAAGATAAATGCACCCC	178	1.5	62	Goh et al. 2007	
microsatellite	UMNe406	14	F: GGCAACAGATGTTAGCTCAGG R: ATGTGCTCTCGAGATGAAAATT	96	2.0	55	Wagner et al. 2004b	
microsatellite	UMNe458	14	F: GACCTACATTTCCTTGTCAGCC R: TTA AAAACAAAACCCACTACCCTG	171	1.5	60		AY731399
microsatellite	UMNe460	14	F: CCATCAGTGATGTTGCAAATG R: AGTGTCCATCAATGGATGAATG	153	1.5	62	Wagner et al. 2004b	AY464502
microsatellite	UMNe474	14	F: CCAAAGGGTGGAATTGATG R: TTTTGCCTCTCTCACCATCC	300	1.5	58	Mickelson et al. 2004	AY731412
microsatellite	UMNe489	14	F: ACACAAACCTAGCACGACTCG R: TTGTTATAGCAGCCCAAATGG	400	1.5	60	Wagner et al. 2004b	AY735281
microsatellite	UMNe550	14	F: GAGTATCACTGCTCCCAGGC R: TTTTGGGGACTGTCATTTAACC	122	1.5	55	Mickelson et al. 2004	AY735283
microsatellite	UMNe581	14	F: TCATCAAGCCATGTTTTAGTG R: TTGCTGACAGTCAGGGTGAG	150	1.5	58	Wagner et al. 2004c	CX593585
microsatellite	UMNe584	14	F: AAATTTGTCCCATGTAATTCCC R: TCACTGTTGGGAAAGGAACC	100	1.5	58	Wagner et al. 2004c	
voltage-dependent anion channel 1	VDAC1	14	F: CCCAGTCCATCACCTCTTTTAG R: AGGTCCTGAATTATTGGCTTCA	104	1.5	59	van Haeringen et al. 1998	

microsatellite	VHL162	14	F: GCTACTCTTTTACTCCTACTGC R: CTCTCGATGTAAGTGCTTGTGC	~100	1.5	62.0	van Haeringen et al. 1998	Y08451
microsatellite	VHL204	14	F: ACTGAAGTTGAGAATCATTAAATGG R: ACTTCCTCGACATCCTTCCCT	~100	1.5	62.0	van Haeringen et al. 1998	
microsatellite	VHL209	14	F: TCTTACATCCTTCCATTACAATA R: TGATACATATGTACGTGAAAGGAT	84-98	3.0	60	van Haeringen et al. 1998	
Yip1 domain family, member 5	YIPF5	14q21	F: GGAATCATTCTCACTGCTGG R: TTAGGGCAAAGACTCCGTAT	139	1.5	58	Goh et al. 2007*	CT009210
YTH domain containing 2	YTHDC2	14	F: GACAGAAGTGGCATAGCTTA R: GCTCTTCTGAAGACATAGGC	180	1.5	58	Goh et al. 2007	
zinc finger, FYVE domain containing 16	ZFYVE16	14	F: TAACAAGTATCAGAGGCCGA R: CCCATTTCCATATGAATCAAC	819	1.5	55	Goh et al. 2007	
zinc finger protein 608	ZNF608 (<i>KIAA1281</i>)	14	F: AAGGACCATCTCAGCAAGAAT R: AAAGTGCTGCACTCCATCCT	164	1.5	55	Goh et al. 2007	
microsatellite	ZuBeEq13	14	F: TTGGGTCTAGGAATCTCTGACT R: ATCAATGTTTTTCCACCCTCTA	246	1.5	63-55	Klukowska-Rotzler et al. 2006	

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	15CA001	15	F: CTCTGTGCCAGACCCTGTTC R: GGTCTGCTCGAACGTCATTT	139-143	1.5	58	Penedo et al. 2005	BI395220
sequenced tagged site	15STS01	15	F: GATTTCTGACTGGACCGAG R: GAAGTTCAAGGGCGACAG	352	2.0	58		
sequenced tagged site	15STS02	15q13	F: TCAAGTGCATCATCCTCACC R: CCTGAGGCTCACACTCTTCC	567	1.5	58		
ARPI actin-related protein 1 homolog B	ACTR1B	15	F: AGGCAGCAGAGGTGTTTTT R: GAAAGTCGACTCCCTCTTGC	619	1.5	58	Wagner et al. 2006	AW260913
acylphosphatase 2, muscle type	ACYP2	15	F: ACACAGAAGATGAGGCTAGG R: TGGAATTGACTTTCTCTTCAGG	114	1.5	60	Wagner et al. 2006	
adducin 2 (beta)	ADD2	15	F: ACAAGGGGAACAGAACAAAC R: GCGAGCAAGAAGCAGAAATC	220	1.5	58	Wagner et al. 2006	
AT rich interactive domain 5A	ARID5A	15	F: GGAGGGCACTGTCGAAAGA R: CCCACTGAACTTTGCCAGC	170	2.0	58		BI961816
microsatellite	ASB02	15q21.3-q23	F: CCTTCCGTAGTTTAAGCTTCTG R: CACAAGTCTGTTCTCTGATAGG	182	2.0	58	Breen et al. 1997*	X95317
microsatellite	ASB15	15q21.1-q21.3	F: GTCCCAAAGGGACTCAGGAAGG R: TGGATGCCAGTGCATAGACAG	144	3.0	58	Breen et al. 1997*	X95330
microsatellite	ASB19	15q21.3-q23	F: GAGTTGGAGCTCAAGTCTGTC R: GTTTAGCAACTACAGCGTAGG	193	2.0	58	Breen et al. 1997*	X95334
microsatellite	B-8	15q14-q21.3	F: TCCTCAGTCCTTTCTCATGC R: AGCTGAAGGCAATCTGTACC	80-102	2.0	58	Marti et al. 1998*	Y10240
carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	CAD	15q25	F: ATGATGGTACAGAAGGAGC R: TGTGCTCACCTCGTAGAA	650	1.5	60	Godard et al. 1998*	
capping protein (actin filament), gelsolin-like	CAPG	15	F: CATCTCCCGCATGCAGTA R: TTGAAGATGGGACTCTCGC	655	2.0	58	Wagner et al. 2006	BI961838
CCAAT/enhancer binding protein zeta	CEBPZ	15	F: TCTTGGCTCAAACTCAACTC R: TGTATTCAACTATGTGAGGCA	146	1.5	58	Wagner et al. 2006	DQ001079
BAC end sequence	CH241-100A9_T7	15	F: AGTGACAAACGCTTTTCCAG R: CTGACAAGGGGGGTATTGTG	647	1.5	58	Wagner et al. 2006	AJ542706

BAC end sequence	CH241-102M19_T7	15	F: TTGGTGATTTGTTGGGAGGG R: TAGGTGAGGTTGAAGGAAGG	553	1.5	58		AJ584457
copper metabolism (Murr1) domain containing 1	COMMD1	15	F: TCTGGAAGAGCCATAAGACAA R: CTGAGTGCCTTGACTGTGATT	120	1.5	59		CX601484
microsatellite	COR014	15	F: CTATCATGTCAGGGACCAGG R: CTGCCCTAGTTAGCAACCAA	143-167	3.0	55	Hopman et al. 1999	AF083457
microsatellite	COR042	15q26	F: CAAATGTGCTCCATCTCCAAC R: GCCAGCTCCCTTACTCTGTA	153-155	2.0	58	Ruth et al. 1999; Wagner et al. 2006*	AF10835
microsatellite	COR075	15q27	F: GCCCTAGTTAGCAACCAACA R: AAGATTGATTCCTCAGCACG	192-214	2.0	58	Tallmadge et al. 1999a; Wagner et al. 2006*	AF142612
microsatellite	COR076	15	F: GTCCTCACTCCTCTCACTGG R: ACAGTCTGTCCACAGGGAAG	208	2.0	60	Tallmadge et al. 1999a	AF142613
microsatellite	COR077	15	F: AGGGAGCATTTGAACCAAGT R: CAATGGTGGTAGAAGCAAGG	152-154	2.0	58	Tallmadge et al. 1999a	AF142614
catenin ,alpha 2	CTNNA2	15	F: CCATCATGGCACAACCTACCAC R: CTGTCGTCCCATTTAGCCACT	112	2.0	58	Wagner et al. 2006	
development and differentiation enhancing factor 2	DDEF2	15	F: CGAAGAGCAGTACACCCAAG R: GCCGTCAACTCCTTTGTAAAC	120	1.5	59		CX598654
DEAD box polypeptide 1	DDX1	15q26	F: GCATTCATAACTAGCCTCACC R: AAACGATGAGTCCATCACTTAC	141	1.5	58	Wagner et al. 2006*	DQ001086
EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	15	F: AAGACTTCCCATCTGAAC R: AGTCAGGAATCTTCTTAGAG	132	1.5	58	Wagner et al. 2006	DQ001088
eukaryotic translation initiation factor 5B	EIF5B	15q12	F: ACTGTGAAGAGCTGAGAGCC R: AAACATCCCCACCCAAGAAC	101	1.5	58	Wagner et al. 2006*	DQ001099
F-box protein 11	FBXO11	15	F: GCTGCAAAAGTGGCTGAATG R: AATGAACGGCAAGAGCAATG	114	1.5	58	Wagner et al. 2006	DQ001124
FOS-like antigen 2	FOSL2	15	F: AGGGTAGATATGCCTGGCTCA R: GTCTTGATCACACCGGGTCTC	206	1.5	55	Perrocheau et al. 2006	DX010485
follicle stimulating	FSHR	15q23	F: TGTTATGTCCCTCCTTGTGCTC	585	1.5	60	Milenkovic	S70150

hormone receptor glutamine-fructose-6- phosphate transaminase 1 hexokinase 2	GFPT1	15	R: GAAGCATTTCAGTCAGCAATGCC F: GCCATAGAAGTTGGAGGAAC R: CAGACAATCCCAAACAAAGAAC	132	1.5	58	et al 2002* Wagner et al. 2006	DQ001093
microsatellite	HMS01	15q27	F: CCAGCAATTCTTGAGTGCC R: ACTCACCCAACTTCATTTTCC F: CATCACTCTTCATGTCTGCTTGG R: TTGACATAAATGCTTATCCTATGGC	142	1.5	58	Wagner et al. 2006	DQ001095
microsatellite	HTG06	15q26- q27	F: CCTGCTTGGAGGCTGTGATAAGAT R: GTTCACTGAATGTCAAATTCTGCT	170-180	2.0	58	Guérin et al. 1994; Wagner et al. 2006* Ellegren et al. 1992; Breen et al. 1997*	X74630 AF169167
inhibitor of DNA binding 2	ID2	15	F: GCCCAGTATAAACAGACTTTGC R: AAGAGTTCACAAGGTTTCACTCA	200	1.5	59		CX602301
interleukin 18 receptor accessory protein	IL18RAP	15q12	F: TGGATGACCAAACACTGAAAC R: TCCACCAATCTCTCTACTCAC	355	1.5	58	Wagner et al. 2006*	CD467478
interleukin 1, alpha	IL1A	15q13- q14	F: ATGCCTGACACACCCAAAAC R: GAAAGTCAGTGATAGAGGGTTGC	172	1.5	55	Perrocheau et al. 2006	DX010514
interleukin 1, beta	IL1B	15q13	F: CTGCATGCTGCTCATCACTT R: TGGGGTACATTGCAGACTCA	212	2.0	58	Caetano et al. 1999; Milenkovic et al. 2002*	AF130767
interleukin 1 receptor antagonist	IL1RN	15q13- q14	F: TATTCCCAGCACGTCGATG R: CAGAACAGCATCAGATTCCAA	403	2.0	58	Lindgren et al. 2001*	D83714
intersectin 2	ITSN2	15	F: CAGCATTGGGAACACAGAG R: AGGTAAAATGAGTGACAACAGG	120	1.5	58	Wagner et al. 2006	DQ001100
microsatellite	LEX046	15	F: ATAAGCCAATCCACTTTTCC R: ATTACCACCCATTTCCTT	115-127	3.0	58	Coogle et al. 1997	AF075648
microsatellite	LEX051	15	F: CCTACGTGTCTCTTTCTCTTT R: GTAACGCAATAATACAGCACT	130-144	2.0	58	Coogle et al. 1997	AF075653
luteinizing hormone/choriogona dotropin receptor	LHCGR	15q22	F: GCCATAGACTGGCAGACAGG R: AGGCAGCYGAGATGGCAA	190	2.0	60		
latent transforming	LTBP1	15q24	F: CCTTTTGCTATGTTTTTCTGCC	141	1.5	58	Wagner et	DQ001106/

growth factor beta binding protein 1			R: GCTGAAGTGTCTCTTTTGGTCTG				al. 2006*	DQ001107
mitogen-activated protein kinase kinase 3	MAP4K3	15	F: TGAGGAGAGGAGAAGGAAGG R: GAAAGGAGAAACAAGGGGC	129	1.5	58	Wagner et al. 2006	DQ001108
methionine adenosyltransferase II, alpha	MAT2A	15	F: AAGCAAAACAATCAGCAAGAC R: AGGGACGGAAAAACAAGAAC	170	1.5	58	Wagner et al. 2006	DQ009808/ DQ009809
multiple coagulation factor deficiency 2	MCFD2	15q22	F: CTGGGGAGAGACCATTACCC R: CAATTCAGCTCTGATTGCACA	392	3.0	58		
malate dehydrogenase 1	MDH1	15q21.3	F: AGAAAGAACATAGCCTTAGCAG R: GAAAAAGTCACCTCCACCAG	200	1.5	58	Milenkovic et al. 2002; Wagner et al. 2006	DQ001109
c-mer proto-oncogene tyrosine kinase	MERTK	15	F: GTTGCGAGATGACATGAC R: TACATCTCATGGTTCTGGAC	916	1.5	50		CF767046
MOB1, Mps One Binder kinase activator-like 1B (yeast)	MOBK1B	15	F: CTCCAGCTCACAGAATGGAC R: GAAACACTGGACTGCCTGC	399	2.0	58		BI395139
myelin transcription factor 1-like	MYT1L	15	F: GCCCGACAGAACTGTAAGAC R: ATTCAATATACAGCACTTGCCC	143	1.5	58	Wagner et al.2006	DQ001112
nuclear receptor binding protein 1	NRBP1 (NRBP)	15	F: CAACGTAAGTCCCTTTGGC R: TCCTACGAGTGAAGAATCCC	115	1.5	58	Wagner et al. 2006	DQ001114
microsatellite	NVHEQ083	15	F: TTGTTGCTGTTGCTGGTG R: TGGAATGGAGGATGAACAGATA	121-123	2.0	58	Bjernstad et. al 1999	AJ245771
poly(A) polymerase gamma	PAPOLG	15	F: AACTGAGCATGCGTTCA R: TGTGTCTCATGCCATCCT	370	2.0	60	Wagner et al. 2006	AK023034
paired box gene 8	PAX8	15	F: TTGGGGGAATCATGACAGAG R: AGGATGTGGTGTATGAGGAAG	214	1.5	58	Wagner et al. 2006	DQ001116/ DQ001117
pellino homolog 1 (Drosophila)	PELI1	15	F: GATCATTTGGGTTCACTCAGG R: CACAGGACTTGATTTTCCTTGC	172	1.5	55	Perrocheau et al. 2006	DX010553
pleckstrin	PLEK	15	F: CCCCGTGAGGAAAGAAGAGTAGG R: CGAGGAGCAGGAATAGTCTCATGG	104	2.0	58	Wagner et al. 2006	BI961655
proopiomelanocortin	POMC	15q25	F: GCCCTATAAAATGGAGCACTT R: GCTTAAACAGGCCGAGTATCT	250	1.5	57		CX598023

protein phosphatase 1, catalytic subunit, beta isoform	PPP1CB	15q25	F: CAAAGACGATATTAAGGTCAAG R: AAGGAGTAGAAAAGTCAGCA	215	1.5	58	Wagner et al. 2006*	BM414639
prominin 2	PROM2	15	F: GCGACTCCTTTCCAGCCCAC R: TCAGCCCTTCCCCTCAGCTC	95	1.5	58	Wagner et al. 2006	DQ001104
RAB10, member RAS oncogene family	RAB10	15	F: GCGGACTTTCTGCTCAGG R: GTCCCTCTCACTACTGCCAAC	350	2.0	55		
RAN binding protein 2	RANBP2	15	F: CCACCCCAATTTCTATCCC R: AGTCCTAAACACCCAGCTTC	164	1.5	58		
receptor accessory protein 1	REEP1 (<i>FLJ13110</i>)	15	F: CACATTTCAAAGGCCAGC R: TGTTGACTAGGGAGTTGGTTC	397	2.0	58	Wagner et al. 2006	
REV1 homolog (S. cerevisiae)	REV1L	15	F: GGTCCAGTTTTTCCAAATC R: GGAGCTGTGGAGTTCAGTAA	440	4.0	60	Wagner et al. 2006	
Rho-associated, coiled-coil containing protein kinase 2	ROCK2	15q26	F: TTTATAAGAGCACGTCCCATT R: ACTTCCGATAGCATAGGTAACC	169	1.5	58	Wagner et al. 2006*	DQ001119
ribose 5-phosphate isomerase A	RPIA	15	F: GCTTCATTGTGATTGCTGATT R: ACTGGGACGTAGGCCATT	800	1.5	62		DN507232
radical S-adenosyl methionine domain containing 2	RSAD2	15q27	F: CATCTCCTGTGACAGCTTTG R: TCTGTTCCCTCATATCCTCTTC	179	1.5	58	Wagner et al. 2006*	CD471892
reticulin 4	RTN4	15	F: CTGTCTTGACTGCCATGTG R: CAAGTCTGTGCGATGCAGT	606	1.5	55		
microsatellite	S22	15	F: ATAGGTAATCCCTGGTGGGC R: TTTCATCTAGCTACCAGCCTCC	biallelic	1.5	58	Swinburne et al. 2005	
sema domain, immunoglobulin domain , 4C	SEMA4C	15	F: TGA AAAA ACCCAAAGAAGGTG R: AGTGGACCACGTTTCCTGAAG	133	1.5	55	Perrocheau et al. 2006	DX010579
septin 10	SEPT10	15	F: TGGCCATCTGATTGCATTT R: CCAGGTTCAAAGGTATTTGTCA	330	2.0	58		
surfactant, pulmonary-associated protein B	SFTPB	15	F: CTACCCACGCCAGAGTTAC R: CGTGAAGGTATGAGGGGTGT	206	2.0	58	Shubitowski et al. 2001	AY008812
microsatellite	SGCV06	15q24	F: GGGCCTGGTTTTCTTCTAA R: GCATTTGTGGCCTGTGTCATA	167	3.0	58	Godard et al. 1997*	U90588
microsatellite	SGCV21	15q23	F: GCACCAACTCCACTTTTGTCCAG	120	2.0	58	Godard et.	U90599

solute carrier family 1, member 4	SLC1A4	15	R: GCTGAGTATTTATGTTGCTCTAAAGC F: AACACCAATCTCGCCATAAC R: ACTGAAAACCAACACAACCC	129	1.5	58	al. 1997* Wagner et al. 2006	DQ001121
solute carrier family 3, member 1	SLC3A1	15	F: CAACTTCACTGCGTTTGTAGG R: CAGTCTTTCTCGTGGTTCTGA	120	1.5	60		
solute carrier family 8, member 1	SLC8A1	15	F: AGAAGGCAATGAAACCGG R: TTGGTAGTCTCTCCATTG	250	1.5	60		DQ329035
solute carrier family 20, member 1	SLC20A1	15	F: ACATCTGTACACAGAGAAGCC R: CTCAGAAGCGAATGCCAAG	225	1.5	58		
spectrin, beta, non-erythrocytic 1	SPTBN1	15q22	F: TGGGGCTTTTCGAAGTTACTG R: CAAAGGTTCACTGCCAAACA	200	2.0	58	Lear et al. 2000*; Wagner et al. 2006	AF130782 AF218582
sulfotransferase family, cytosolic, 1C, member 1	SULT1C1	15	F: TGTCATACCACAGACTGGG R: TGAGGGTAAGGTGGAATGAG	243	1.5	58		
TBC1 domain family, member 8	TBC1D8	15	F: CTGAAAATGACCGAGACAGC R: GGCTCATTTTGGGCAACTC	622	1.5	58		BM029703
TIA1 cytotoxic granule-associated RNA binding protein	TIA1	15	F: CCTGCATATGGAATGTATGGC R: GCTGCACTCCGTAATTTGGTC	974	3.0	50	Wagner et al. 2006	BI961840
microsatellite	TKY011	15	F: ATGAGAGAGGTCACCAAAAT R: CCCTGCCAACAAAAACCTTG	130	2.0	55	Hirota et al. 2001	AB048322
microsatellite	TKY104	15	F: GAAAAGACATCAGCAAGTGGTC R: GCCTAAAACTAACTTCCAGAAGG	153	2.0	58	Mashima et al. 2001	ABO53343
microsatellite	TKY327	15	F: CCTGGTATATCTCCTAACAC R: GATCTAGCTATTTCTCTCGTG	87-91	1.5	58	Tozaki et al. 2001	
microsatellite	TKY369	15	F: GCCATGTAGTTTACTCGCAC R: GAGTGTGAGAACCCTTCAGAG	104-140	1.5	58	Tozaki et al. 2001	
microsatellite	TKY383	15	F: CTTCTTCCAATCTCTATGC R: TTTCTATACGGCAGGAGAAG	160-172	2.0	55	Tozaki et al. 2001	AB044883
microsatellite	TKY392	15	F: CCCGTTTAAAGTAGCAACAC R: CACCTTACTCTTTCAAGTGG	121-129	1.5	58	Tozaki et al. 2001	
microsatellite	TKY433	15q26	F: TCCCATCTCCTTTTGTCTGC R: GCCAGAATGAACTAAGACCCTCT	292-296	1.5	58	Tozaki et al. 2004; Wagner et al. 2006*	AB103651

microsatellite	TKY518	15	F: GATCCCCCACTGGCCTTA R: ACGAACTCCAACAAATGCAA	149-165	1.5	55	Tozaki et al. 2004	AB103736
microsatellite	TKY531	15	F: ACCACTTAAACCGCGCTTC R: GGTCTTTTAAGCTCTGCTCG	160	2.0	58		AB103749
microsatellite	TKY541	15	F: GAGGAGGGGCTTTCTCTCTC R: TGCAAAAAGCCAACATTTCC	106-124	1.5	58	Tozaki et al. 2004	AB103759
microsatellite	TKY565	15	F: GGGGCGTTAAGGCAGTAAG R: ATGCGCTTCAGCATCTCTTT	192-208	1.5	58	Tozaki et al. 2004	AB103783
microsatellite	TKY571	15	F: ACAGCACAGCAGCAAACAAA R: CAGTGGGCCCAGGTGTATAG	122-130	1.5	58	Tozaki et al. 2004	
microsatellite	TKY629	15	F: TCAGTCCCTGGTCTGAAAAA R: GTCCCTACCTGGTTCCCAAG	186-188	1.5	58	Tozaki et al. 2004	
microsatellite	TKY743	15	F: ACAAGGTGCCACAGTCAACA R: TTGGGCTTGAGAGGAAAGAA	170-206	1.5	50	Tozaki et al. 2004	
microsatellite	TKY779	15	F: GAAATTTGGGGAGCCAAAGG R: TATACAGAAGCCAGTTCCAG	146	2.0	58		AB103997
microsatellite	TKY795	15	F: AGAGTAATGTGGTGGAGGAG R: TTTTGTGGCTAGGTTTGGG	151	2.0	58	Tozaki et al. 2004	AB104013
microsatellite	TKY814	15	F: ATGCAAAGTCCAGAAACAGA R: TGGGGAACCTCTAAATAACG	155	2.0	58		AB104032
microsatellite	TKY815	15	F: CCATGGAAGGTCACAAGATG R: TCTGTACTTTCTACCACAGC	237	1.5	62		AB104033
microsatellite	TKY861	15	F: GACTCCAGTGTGTTTAGAGG R: CAGGACTGCCACAGCTTC	241	2.0	58		AB104079
microsatellite	TKY885	15	F: TCAAAGTGAAGCTTCCTGG R: TGGAAACTCATCCTCTAAGG	230	2.0	58	Tozaki et al. 2004	AB104103
microsatellite	TKY926	15	F: GATCATGTACTGGGCACAG R: ATGAGCAACCGGGTGTAAAG	89	2.0	58	Tozaki et al. 2004	AB104144
microsatellite	TKY976	15	F: ATCAATCTGAGGGCCACAG R: CATTTCCATTTGCAGAGTCAC	177	2.0	58		AB104194
microsatellite	TKY1015	15	F: ACTGCCTTCAAGTTTCATCC R: TGGAAACAGCCTAAGTGTTTC	149	2.0	58		AB104233
microsatellite	TKY1033	15	F: AGACATGGATTTAGGGAGTG R: GCAGAGCCATGCTAAACTG	146	2.0	58	Tozaki et al. 2004	AB104251
microsatellite	TKY1091	15	F: ACAAGTGGAAAGAAGTGAG R: CCATCTGCAGAAGTAATCCA	140	2.0	58	Tozaki et al. 2004	AB104309
microsatellite	TKY1095	15	F: TTGAGTTGTGTCCTCTCATC	158	2.0	58		AB104313

microsatellite	TKY1165	15	R: CTCAGTTCACAAGGCTTGAG F: AAGACCAACACCGTAAAAATC R: CCTACCAGAGTCCAGATTC	300	1.5	58		AB104383
microsatellite	TKY2469	15	F: TGTTATTTGGAGAGAGCTTG R: GTGGAAGATTAAAGAACTGTG	207	1.5	60	Tozaki et al. 2007	AB216412
microsatellite	TKY2783	15	F: GCTGATACCAGTGGAGGCTA R: AGGTGGTCTTACTTGCACGA	249	1.5	58	Tozaki et al. 2007	AB216726
microsatellite	TKY2810	15	F: GAGCCTTGAAAAGAGGGAAC R: GGCAATCACCTAGCTTGAGA	221	1.5	58	Tozaki et al. 2007	AB216753
microsatellite	TKY2891	15	F: TAGGGGTGCCTGAAACAATA R: CTGTGTCCCATACCTTGAGC	204	1.5	58	Tozaki et al. 2007	AB216898
microsatellite	TKY2955	15	F: ATATCATGGCCAGATTCAGC R: CCATTCTTGGAAGTCCACAT	242	1.5	58	Tozaki et al. 2007	AB216935
microsatellite	TKY2992	15	F: TGAACGTGGTAAATTGCAGA R: CCAACTCCAGTGAATAATTTTGA	185	1.5	58	Tozaki et al. 2007	AB217345
microsatellite	TKY3086	15	F: GAGTCCCCCAGGATTAACAT R: TCAAGAAATATCTCTAAAGAACAAAGA	156	1.5	58	Tozaki et al. 2007	AB217029
microsatellite	TKY3402	15	F: GTCACCTGAACCTTACTTC R: CCCTCTTAAGAGCTTCTTTC	116	1.5	58	Tozaki et al. 2007	AB217469
microsatellite	TKY3526	15	F: TCTCACTTTCAACTGGAAGA R: AACAGCTGATACAGCAATTC	113	1.5	58	Tozaki et al. 2007	AB217469
thymosin, beta 10	TMSB10	15	F: TTCCTAAGAACCTGGAGGATTTTC R: AAACCGAAGAATTTGGCAGTC	193	1.5	55	Perrocheau et al. 2006	DX010599
microsatellite	UMNe084	15q26	F: ACAGTTGGATATCCGTGGGAAC R: TCTGTTATGTGTTGCCCTCTGC	216	1.5	58	Wagner et al. 2006	AY391284
microsatellite	UMNe102	15	F: ATGCATGCTCATTGCAGAAC R: GCACAAAGAAATTTCCAACTCC	191	1.5	58	Wagner et al. 2004a	AY391290
microsatellite	UMNe149	15	F: AAATGATTTGATAGCACCAGGG R: TTTCTATGCATAGACAGCAAGG	114	1.5	58	Mickelson et al. 2003	AF536263
microsatellite	UMNe156	15	F: AGACTAGCTTCAAATTGCCCC R: TCAATTGCCTATGCTTGAAGG	126	1.5	58	Mickelson et al. 2003	AF536268
microsatellite	UMNe198	15	F: CAAGAACTGGCATCAGAATTTC R: TCTTGGGTCTCACTCACTCTCC	152	2.0	58	Mickelson et al. 2003	AF536283
microsatellite	UMNe219	15	F: GTGTCCACTGAAGGATAAAGGG R: TAGCATAATGGCCCTCAAGG	164	2.0	55	Mickelson et al. 2003	AF536298
microsatellite	UMNe222	15	F: ACCGCATTCTCTTTCAGGTG R: CTGGGTAACTGACTGGAAAAGG	151	2.0	58	Mickelson et al. 2003	AF536300

microsatellite	UMNe245	15	F: TTGCATAGGGACAATCCTACG R: ACAAACCCTACCACTCGGC	104	2.0	55	Wagner et al. 2004a	AY391327
microsatellite	UMNe250	15	F: ATGTTTCAGTGCCTCACCTCC R: GTCTTCGCATTTTAGCCTGC	202	2.0	58	Mickelson et al. 2003	AF536318
microsatellite	UMNe275	15	F: GTCAACAAAGAGCCTGCTCC R: TCTGCAAAGTGTTGTTGTGATG	221	2.0	58		
microsatellite	UMNe373	15	F: AGGCCACTCAAGCCACAG R: CACCTCCTCCTCCAAATGAG	265	2.0	58	Wagner et al. 2004a	AY391355
microsatellite	UMNe388	15q27	F: ATCCTAGGGTAGAGCCTGCC R: TGGGCCTTTACTCCACCTC	237	2.0	58	Wagner et al. 2006	AY464474
microsatellite	UMNe575	15	F: CTTTTGAGGAATCTCCATACCG R: GGACCAGGCTGTTTCTGAAC	300	1.5	58	Wagner et al. 2004c	AY735277
microsatellite	UMNe605	15	F: GTTCTGTCACCTTCACTTGCC R: TTCCTAACCCTCCAGGGTG	285	1.5	58		
vaccinia related kinase 2	VRK2	15q22	F: TGTCTCTCCTTCTCTCCTAC R: ACACACACATACACAGACATTC	225	1.5	58	Wagner et al. 2006*	DQ001125
xanthine dehydrogenase	XDH	15	F: CAGGGAATCCCTTCCACTAC R: CTGGAGCCAACATCCATGAC	900	1.5	58	Wagner et al. 2006	BI961081
zinc finger protein 36, C3H type-like 2	ZFP36L2	15	F: CTTTGCTTCTCTGTCTTTCC R: CGAGCCACGACGAATAAC	150	1.5	58		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	16STS01	16	F: GAGGCCAGATTTGATTCCAAC R: TAGATGGTAACTCCTTGCCA	1333	1.5	TD 58		CF722812
abhydrolase domain containing 5	ABHD5	16	F: CTAAACGCGCAGCCTAAGTC R: CCTGTCCTGCTTTTAGTCACTC	164	1.5	58		
acetyl-Coenzyme A acyltransferase 1	ACAA1	16q21.3	F: CAAGATACCTTTGCACTGGCT R: GCACAATCTCAGCTTGGA	1164	1.5	58	Mariat et al. 2001*	
aminoacylase 1	ACY1	16	F: GAGGAGGCTGAAGGCTGAG R: CGCTGCACAAACAGTTTCAT	191	1.5	58		
microsatellite	AHT014	16	F: GAGAAGCAATCACACACACACA R: GCTCTTTCCATGGGTGGTAG	138-151	2.0	65	Swinburne et al. 1997	
microsatellite	AHT037	16qcen ^a	F: ATTTACCCACTCCCAACC R: TTTCGTTTGCACAAATATGG	206-218	2.0	58	Swinburne et al. 2000	AJ271522
microsatellite	AHT038	16q21.1	F: TTCATGGCCTTCAAACTCC R: CCAGCTGGGGATACTTACCA	130-140	2.0	58	Swinburne et al. 2000*	AJ271523
microsatellite	AHT060	16	F: GGTCAAGCTTTTGGTTTTTCC R: CCTAAGGAAGAGCTGTTCTTGC	282-308	2.0	58	Swinburne et al. 2003	AJ507677
microsatellite	AHT063	16	F: CCATGTGTTCACAACTCGG R: GAGGGTTGGAACCTTTCAGTCC	108-110	2.0	58	Swinburne et al. 2003	AJ507680
microsatellite	AHT081	16	F: AACTCAGGGGCAGACAAATG R: TTGGAACCTTTCAGTCCAGGG	198-200	2.0	58	Swinburne et al. 2003	AJ507698
microsatellite	AHT091	16	F: TAGCTGTCTGCAAAGGCTCA R: CCAGTGTTCCACATGCCTC	108-118	2.0	58	Swinburne et al. 2003	AJ507708
ADP-ribosylation factor 4	ARF4	16	F: TCGCTCCGTTAATTCCTGTCCC R: GCCGCCTCCTTTCAAGCTCC	126	1.5	60		CD466539
Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	16	F: TTGTTCCCAGAATGAGTCGTG R: GACCAGGGCTGGAAGCAGAT	107	1.5	54		

basic helix-loop-helix domain containing, class B, 2	BHLHB2	16	F: CTACTTGCCCATGCTGGAGAAG R: GTTCATGAATCTGGTGAGGGCTG	100	1.5	58		BI961704
chromosome 3 open reading frame 10	C3orf10	16	F: CTTGTCAATGTGTTTGAGGCAT R: CAAGTTGAGGAGTTTATTCGGG	361	1.5	59		CX594448
calcium channel, voltage-dependent, L type, alpha 1D subunit	CACNA1D	16	F: GAAGGCTTAGGACGGTACGC R: CTGTAGCCAGGCCCAAAGTC	209	1.5	55	Perrocheau et al. 2006	DX010443
chemokine (C-C motif) receptor-like 2	CCRL2	16	F: CGGGAAGAAGGGAGGTGTTA R: GAGGAAAGCGTCTCCATGTC	626	1.5	TD 55		CD465256
CDV3 homolog (mouse)	CDV3	16	F: TGGTACAATGGACAGCCTCA R: GGGGTTGTGTTATTGAAGAATA	207	1.5	60		
BAC end sequence	CH241-100I1_T7	16	F: TGCTACCAGAAATAGCAACAC R: ACATATTGCAGGCAATGCAC	520	1.5	60		AJ543004
BAC end sequence	CH241-100N15_T7	16q16	F: GCCCTTTCTAAGCAACAATCAC R: CATCCTCAATGGAGCCTCAC	539	1.5	60		AJ543200
BAC end sequence	CH241-101A11_SP6	16	F: CTCCAGAAGTCACATCACTAAC R: GAATAAGTGGCAGTGGGAATAG	574	1.5	58		AJ576431
BAC end sequence	CH241-102N14_T7	16	F: GCTAGACCTTAACTTCTGCCC R: TACCTGCCTTCAATGCTGCC	293	1.5	60		AJ584489
BAC end sequence	CH241-111J21_SP6	16q14	F: CAAAAATTCTTCCCCATTAG R: TCCAAATTTCCACATCTGAAG	600	1.5	58		CR956118
cell adhesion molecule with homology to L1CAM	CHL1	16	F: CTACCCAGGTCCAATTTATCCC R: GGCAGACGAAGTTACATACAG	205	1.5	58		
cytokine inducible SH2-containing protein	CISH	16	F: CTGGAAGTCCTGGCACTGA R: TCTGCGCAGATGGAGCTCT	169	1.5	58		BI961934
coatamer protein complex, subunit	COPB2	16	F: GTTGCAAGGAAGAATTGGGTT R: GAACTCTCTCCAGAGTATTG	288	1.5	58		

beta 2

coatamer protein complex, subunit gamma	COPG	16	F: GCAGGTGACAGCCAGAAGTT R: GGGACAAGATGGTTTTAGGG	375	1.5	TD 62		BM780459
microsatellite	COR039	16	F: ACGTTGGCTCTGCTTTATGT R: ATCCAGGCTCTGAATCCACT	254	2.0	58	Murphie et al. 1999	AF101408
microsatellite	COR052	16	F: CAGGTGGTGCTAGTTTTCCA R: ACCACTGCTTTGAGGACCTAG	230-232	2.0	55	Ruth et al. 1999	AF108369
microsatellite	COR064	16	F: TCCATACATGTGTGAGGGC R: AAGATGGCTTACAAGGATTATG	188-198	3.0	55	Tallmadge et al. 1999a	AF142601
ceruloplasmin (ferroxidase)	CP	16q25	F: ATTGAGCCAATCGGAGTGAG R: ATGATACACAAGCGGGTTCC	200	2.0	58	Godard et al. 2000* ; Chowdhary et al. 2003	AF134057
cysteine-rich with EGF-like domains 1	CRELD1	16	F: CGCCTGGTAGAGGTGCTT R: TGAAACCACCAGCTCTCCAC	101	2.0	58		
cartilage associated protein	CRTAP	16q21.1	F: CCATCCTCTGATCCAGCAAAGAT R: GAATGAGTGAAAATAGACTCCCTCTG	274	2.0	58	Chowdhary et al. 2003*	
catenin beta 1	CTNNB1	16	F: TGTCGATTAATTCCAGGTCAAG R: TTGTTGGTGTGATCCTGTTC	204	1.5	58		
deleted in azoospermia-like	DAZL	16q22.3	F: TCGGTAAACATCCAAAGTCCTC R: GAAACCTCCAGACGCTTGCTA	135	1.5	54		
dynein, cytoplasmic 1, light intermediate chain 1	DYNC1LI1	16	F: ACCTATATCACAAAGGCCTC R: CTTTCATTTCTTCAGGAGGA	180	1.5	58		
eukaryotic translation initiation factor 1B	EIF1B	16	F: CTGTTTCAGGGCATTGCAGAT R: GCTGAATAACCTCTCCGTATTC	530	1.5	58		
forkhead box P1	FOXP1	16q14-q15^a	F: ATACCAAACCTAACCAGCAACC R: AAAAAAGTAACACTCCCGTCC	228	1.5	60		CD528822
FERM domain containing 4B	FRMD4B	16	F: AAACCTCTTCGCTCATCAAATCC R: TTTTCGCCTCCAATGTCACC	~ 685	1.5	60		CD471098

ghrelin/obestatin preprohormone	GHRL	16q13	F: CTGGGTGGACTTGACCATG R: TGCTAGAAAGGAGGCGTTC	~300	1.5	58		
galactosidase, beta 1	GLB1	16	F: AACGACACTCAAAAGCCAAGA R: GGCAAAATTGGTCCACCTA	196	2.0	58	Chowdhary et al. 2003	AF130765
golgi autoantigen, golgin subfamily a, 4	GOLGA4	16	F: GAAAAGCTGTTGCAGAGG R: CTTCATGTTGCTTTGCTTC	124	2.0	58		
G protein-coupled receptor 175	GPR175 (TPRA40)	16	F: CAGTTCGATTTCGGCCAGTG R: TCGCTGTCCGTACTGTTGATG	89	1.5	55	Perrocheau et al. 2006	DX010601
glutathione peroxidase 1	GPX1	16q21.1	F: TTTTCGGCCCCCTCAATATTCC R: AGAAGAGAGAACTGAGGGCCAA	244	3.0	58	Milenkovic et al. 2002*: Chowdhary et al. 2003	
glycogenin 1	GYG1	16q25	F: GTGATTCTGCACATCTAACCTT R: GAGTATCTGCATCCATGAATAC	~110	1.5	58	Godard et al. 2000*	
microsatellite	HMS74	16q21	F: CTGGTGTGGCCTACACGCCA R: CCACCCTCACCCCTATGGGC	~200	1.5	58	Mariat et al. 2001*	
microsatellite	HTG03	16q13	F: TAACCTGGGTGCAAAGCCACCCAT R: TCAGGGCCAATCTTCCTCAC	119-129	2.0	50	Ellegren et al. 1992; Godard et al. 2000*	AF169164
microsatellite	HTG13	16	F: TTAGCACGGGGAGATCGGATCCTG R: GGTCTCCCTCTCCATTCACCCTGC	120	2.0	58	Marklund et al. 1994	AF169297
microsatellite	I-18	16q23- q25	F: CAACAAAGATGTTGCAAGGG R: TGTGCCTCTTGTCTCTTAGG	113-187	3.0	58	Marti et al. 1998*	Y10244
interferon-related developmental regulator 2	IFRD2	16	F: CTTCAAAGCCCGGACCAAG R: CTGTTAAAAATGCGGGCAAG	115	1.5	55	Perrocheau et al. 2006	DX010513
inositol hexaphosphate kinase 2	IHPK2	16	F: TGCTCACCTGCTCACACCT R: ACACGACCTCAGACACAAGC	900	1.5	TD 58		BM780272
interleukin 17 receptor D	IL17RD	16	F: ATACTGGAGGAGCTGAAGTC R: GAAGGAAAAGGGACGATC	699	1.5	TD 58		BE750478
integrin, alpha 9	ITGA9	16	F: CCCATAATTCTCAAACCCACC R: AATCGCAACAAGAAGTCTCTCC	500	1.5	60		AJ543268

inositol 1,4,5- triphosphate receptor, type 1 microsatellite	ITPR1	16q14- q15	F: CCACAACCCACAAAACAAAC R: CCTTGCCTTATCCTTCACAC	120	1.5	60	Perrocheau et al. 2005*	
	LEX048	16	F: CATAGTGCCCTCAAGTTC R: TGAATTGGATAAAGAAGATGTA	164-168	3.0 - 5.0	58	Coogle et al. 1997	AF075650
microsatellite	LEX056	16	F: GACCTACAGGCCACTCATCAA R: GGCAGTTTCCTCCATCCTTA	213-229	2.0	58	Coogle et al. 1997	AF075658
microsatellite	LEX059	16	F: TGAAATGTACCTTCTCAGAG R: ACTTCGTGGTGGACACTTGC	229-235	2.0	58	Coogle et al. 1997	AF075660
lactotransferrin	LTF	16q21.3	F: AACCCGCTATTATGCTGTGG R: GCTGGCAGAGAAGAAGTTGG	~400	2.0	58	Chowdhary et al. 2003*	AJ010930
microtubule- associated protein 4	MAP4	16	F: TGATAAACTGTCTCCTCTAGCC R: GCTGAGTCATCAAACACAAAG	113	1.5	58		
muscleblind-like (Drosophila)	MBNL1 (<i>MBNL</i>)	16	F: TGAACAGGCAAACCAAACAG R: TGTGGGGTTGTCTGATAAGTG	244	4.0	TD 60	Chowdhary et al. 2003	
microphthalmia- associated transcription factor	MITF	16q15- q16	F: AACCAACCTCGGAACCGGGACC R: AGCAACAAATGCCGGTTGGC	292	1.5	58	Ward et al. 2003	AF401626
mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	MLH1	16	F: CTGACATGCAGCAGATCAAC R: TGAATGAGATTATGCTGAGCC	134	1.5	58		
microsatellite	MPZ002	16	F: GATCCCCCCTATTTTATATACAG R: AGGTTCTCATTCTACCTACAAGG	77-101	3.0	TD 60	Breen et al. 1994	Z28342
microsatellite	NVHEQ216	16	F: TTGGACTACTGTATTTGGTC R: TGATCTCTCCATAGCATAAT	142-144	2.5	57	Penedo et al. 2005	
p300/CBP- associated factor	PCAF	16q22.3	F: ACAGTGAAAGTGAGCCGTAG R: TAGCACAGGATAGTCAGCAG	184	1.5	53		
programmed cell death 6 interacting protein	PDCD6IP	16q21.3	F: GAGGAATTAAACCCACAAGTGAAAT R: AATTAAACCAAATCAATAAACCAAGAGA	155	3.0	55	Chowdhary et al. 2003*	
procollagen-lysine, 2-oxoglutarate 5-	PLOD2	16	F: TGCGATGTATCTTGTTC R: GGTGAAATATTCCCCTGA	408	2.0	55		

dioxygenase 2

peroxisome proliferator-activated receptor gamma	PPARG	16q12-q13	F: GGGTGTTCAGTTTCGCTCAGT R: CACCAAAAGGCTTTCTCAGG	235	1.5	62		
proteasome 26S subunit, non-ATPase, 6	PSMD6	16q16	F: CAGATTTATTGCTGCTGGGAG R: TTATACAGTTGAACTGGGCAC	~ 364	1.5	60		CD535869
parathyroid hormone receptor 1	PTHRI	16q21.2	F: CATTGCACACGCAATTACATC R: CGGTGCCCCGAGTAGAGAAC	100	1.5	55	Muller et al. 2005*; Perrocheau et al. 2006	DX010564
v-raf-1 murine leukemia viral oncogene homolog 1	RAF1	16	F: AATCCTTCCTTACGAGTGCC R: ATTTCTCCCTACCTCACACC	178	1.5	58		
retinoic acid receptor, beta	RARB	16q22.1	F: ATGCGAGCTGTTTGAGGACT R: TTCCCAGAAAGATCCCAAGTT	149	3.0	58	Chowdhary et al. 2003	AF134234
RNA binding motif protein 5	RBM5	16	F: CCTAAAAATTGAGAATGCGCC R: AGGAAGAACTTTGCCAGTGG	171	1.5	60		
RNA binding motif, single stranded interacting protein 3	RBMS3	16	F: AGGTGAAAGTGGTAACAAACAG R: GAGGAAACAACAAGCCAAATAG	563	1.5	60		AJ576782
raftlin, lipid raft linker 1	RFTN1	16	F: AAAAATAACCCCCAAGCCCC R: AGTCACAAGAATCATTGAGCC	589	1.5	62		AJ543037
rhodopsin	RHO	16q12-q13	F: CACTTCACCATCCCCTTGAT R: AGCTGCCTGTAGGGACACAG	178	2.0	58	Chowdhary et al. 2003	AF130780
ribosomal protein L29	RPL29	16	F: CACAACAAGAAGGGCCTGAAG R: CTGGGCCTTGTTTGTGACTT	120	2.0	58		BI961709
ribosomal protein SA	RPSA	16	F: GACTTCTGGTGGTAAGTATCC R: AGCATCCACCACATCAGACC	175	1.5	66		

SATB homeobox 1	SATB1	16q22.3	F: CATGGCAGGAGAACAGAACT R: ATAACCTTCCTCGCAGAGCATT	202	1.5	58	Pascual et al. 2002	BI395227
solute carrier family 6 member 20	SLC6A20	16	F: CTGAGCGTGGACATTACAGAAG R: TGTATTGGACTGTGTGCATTCC	88	1.5	56		
solute carrier organic anion transporter family, member 2A1	SLCO2A1 (SLC21A2)	16	F: AGACCCCTCCCAAAGCATAC R: GCAGAGCCTTCAGAATTTGG	302	3.0	58	Chowdhary et al. 2003	
sarcolemma associated protein	SLMAP	16	F: ACTGCAGAGGTTACACATCA R: TCTGTTGGTCCTCACATTGT	293	1.5	58		
stromal antigen 1	STAG1	16	F: CAGTGGTGATTATCCCCTTACC R: AAAAGCTCTGACCTGGGAGTC	181	1.5	55	Perrocheau et al. 2006	DX010590
transferrin	TF	16q23	F: CCACAAGAGGCTGACAGAGAC R: AGAAGCCCCCAGATCAAGTC	140	2.0	58		BI395139
transforming growth factor, beta receptor II	TGFBR2	16q21-q22	F: GAGCTTTATCACTCATGGGTCATC R: CATGAGTACTGCGGAAGTGTTCC	207	3.0	58	Lear et al. 2001*	G62195
transketolase	TKT	16	F: AGAGCAACATCAACCTCTGC R: TGGGTAAAAGACGGTTGACG	267	1.5	58		
microsatellite	TKY279	16	F: AATGAATGAGACTTGAACCC R: TCTGCTGTTTTAGGCTCGG	119-133	3.0	TD 60	Tozaki et al. 2000b	AB033930
microsatellite	TKY311	16	F: CAAACAGGTCGCATCATTAG R: CGCATCTCTGCTTTTCAGAG	244-263	1.5	58	Tozaki et al. 2000c	AB034620
microsatellite	TKY341	16	F: TATCCAGTCACCCATTTTAC R: TTGTGTCAGTACACTCTATG	157-171	1.5	58	Tozaki et al. 2001	AB044842
microsatellite	TKY347	16	F: TCAACATTTGCTCCAAATTCC R: CCTCAGGTACATTTGATATG	191-199	1.5	56	Tozaki et al. 2001	AB044848
microsatellite	TKY349	16	F: GATCAATCAATCAATCAATATC R: TCAGTAAGTGACCAGATTCG	119-131	1.5	58	Tozaki et al. 2001	AB044850
microsatellite	TKY350	16	F: TCCTAGGGAATTCACAGTTG R: TAACAGAACTACAAGGCC	184-214	1.5	58	Tozaki et al. 2001	AB044850
microsatellite	TKY388	16	F: TCTAAAACAAGGCACAGTGAG R: TCAACACATCCTCACTGTTAG	185-191	1.5	54	Tozaki et al. 2001	AB048294

microsatellite	TKY406	16	F: CCACTAGGGGCCAGTGATT R: GAACTCCACCCTTTGGGATT	119-137	1.5	58	Tozaki et al. 2004	AB103624
microsatellite	TKY445	16	F: CCTGGGCTAATTCCCATTTT R: CCAGCTCTTTGAAGGTAGCA	298-308	1.5	58	Tozaki et al. 2004	AB103663
microsatellite	TKY532	16	F: ACAAACACTCGTGGTTGCTG R: TATTTTCAGCAAGGGGCAAC	182-201	1.5	58	Tozaki et al. 2004	AB103750
microsatellite	TKY563	16	F: TGCAGGATCCGAGGAGAG R: AGAGTGTCCCCTCGCCTTAC	177-195	1.5	58	Tozaki et al. 2004	AB103781
microsatellite	TKY637	16	F: TCTCTGCTTTTCAGAGTCTG R: AGGCTAGGTCCAAAAATCTG	171	2.0	58		AB103855
microsatellite	TKY667	16	F: GAAATGATCCCAAGGGACAC R: GACAACCATGTCTTGGCAC	71	2.0	58		AB103885
microsatellite	TKY687	16	F: CAGCCTTCCATGGGAAGTAGT R: GTGCTGCTGCAGTATTTTGG	197-227	1.5	58	Tozaki et al. 2004	AB103905
microsatellite	TKY719	16	F: CTCATAACTGTGTGCCAATTCC R: TGGTCATCACTTTTCTGTTGAA	159-169	1.5	58	Tozaki et al. 2004	AB103937
microsatellite	TKY781	16	F: GATCCAATTGGAGCCTATCA R: TTTTGCAGCTTCTTAAGCCC	206	2.0	58		AB103999
microsatellite	TKY800	16	F: TAAATGTTGCTGCACTTGGG R: TCTTTCTATGACGTTGGGCA	255	2.0	58	Tozaki et al. 2004	AB104018
microsatellite	TKY802	16	F: GGAGGAAAGAGCTGAATGGA R: TCATCCAGTTCACCCATCAG	100	2.0	58	Tozaki et al. 2004	AB104020
microsatellite	TKY871	16	F: CACACTACTCATGAAGCCAT R: ACTTGTCCCAGCACTGTTTG	253	2.0	58	Tozaki et al. 2004	AB104089
microsatellite	TKY921	16	F: TTA CTCCACTAGCACCAAAG R: CATTTTAGAGAATAGGGAATC	86	2.0	58		AB104139
microsatellite	TKY936	16	F: ACCACTGTACTGAATACTGG R: ACAAAGCATCTCCTCGAATAG	120	2.0	58	Tozaki et al. 2004	AB104154
microsatellite	TKY1032	16	F: CCATCGACGAATGACTAGTG R: TCTCAGATGGTAGGATGTTC	120	2.0	58		AB104250
microsatellite	TKY1066	16	F: ACCTTCCAAGTGCTCAGTG R: ATAGTGCTGTCCAGTAGAAC	114	2.0	58		AB104284

microsatellite	TKY1069	16	F: TTTGAACCACCAACCAAAGG R: CCCAAAGGGAAAGGATGATG	139	2.0	58	Tozaki et al. 2004	AB104287
microsatellite	TKY1086	16	F: TATGACCTGATGGTATGTGG R: GTTAGCTCAGGTGCCAATC	282	2.0	58		AB104304
microsatellite	TKY1131	16	F: TCTCCAATAGAGATAGCACC R: GCAGAATAAGGTGGGATTCA	224	2.0	58		AB104349
microsatellite	TKY1149	16	F: TCTGTTTCCCACCTCACTG R: ATCCCCCATCTCCCTTCT	280	2.0	58		AB104367
microsatellite	TKY1930	16q22.1	F: ATGGTGGCTTGTATTTTTCG R: CCCGTTACACATTTAGGTTG	286	1.5	58	Tozaki et al. 2007	AB215873
microsatellite	TKY2022	16	F: ATCTCTCAGGTGAGCCCTT R: AGGAAAGTCAGGAAGGTTTC	198	1.5	60	Tozaki et al. 2007	AB215965
microsatellite	TKY3372	16	F: TTGCTGGGTGCTCAAAGTAT R: GGAGCTGACAAAACAGAGGA	153	1.5	58	Tozaki et al. 2007	AB217315
transmembrane protein 16K	TMEM16K	16	F: GGAGTTATTCCTGCAGTTTGGT R: GCCATACACCAATACTGGCT	170	1.5	64		
TATA element modulatory factor 1	TMF1	16q15- q16	F: TGGACTTGTAAGTGGTCAAA R: TACACACCCAAGTTAATGAA	133	1.5	56		
topoisomerase (DNA) II beta 180kDa	TOP2B	16q22.1	F: AGGTCCTCCTCATGAAGGAA R: TGGAATGCCAGCACTGAGTA	164	1.5	56		
equine EST	TUDPEc039	16	F: AAGCTAACCCAGAGAACAAGG R: TGTGAAGGAAATGGAAAACG	237	1.5	58	Pascual et al. 2002	BI395107
microsatellite	UCDEQ505	16	F: ATCACTCTCTTGTTGAGATAAC R: GGGATTTCTTCTTTCTC	175-197	4.0	50	Eggleston- Stott et al. 1997	U67421
microsatellite	UM042	16	F: GGCATCCCACATACAAAG R: GAAGCAACAGTCAATTCAG	218-226	1.5	58	George et al. 1998	AF195585
microsatellite	UMNe122	16	F: CCATGTGTTCACAACTCGG R: TGGAACCTTCCAGTCCAAGG	100	1.5	62	Mickelson et al. 2004	AY731378

microsatellite	UMNe213	16	F: CTGAATATCCAAAGTTCTTCTGTG R: GGTATACAACAAAGTACGGGGGC	150	2.0	58	Mickelson et al. 2003	AF536295
microsatellite	UMNe264	16	F: GCAATGCTAGCACAGGGG R: CCTCTCTCTCTTTCCCCCTC	101	1.5	58	Wagner et al. 2004a	AY391330
microsatellite	UMNe277	16	F: AGGCGATGGTGACATCTTTC R: CTACACACGGGATAAAATTCGC	158	1.5	58	Wagner et al. 2004c	AY735240
microsatellite	UMNe348	16	F: TCTAGTTGTAGGGAGCCTAGGG R: CATATTAGAGTTGCCCAATTGC	150	2.0	58		
microsatellite	UMNe468	16	F: TTCGCATAGAGCTGTTCATGG R: GTTATAGCAGCCCTAATGGACG	247	1.5	58		
microsatellite	UMNe562	16	F: TTGGTTTAGGTTTTTAATTACTCTG R: GGTGTTGAAACAACCTGGCTG	~150	1.5	58	Wagner et al. 2004b	AY464528
microsatellite	UMNe566	16	F: TGCTGTGACTATGCTGTGTCC R: ATCAGCTGGTCAATGATGAGG	~250	1.5	58	Wagner et al. 2004c	AY735271
microsatellite	UMNe585	16	F: ATGAGAACACTGGGTGGGAG R: AAGGCCCTCAGGGAAATG	~400	1.5	58	Wagner et al. 2004c	AY735284
ubiquinol-cytochrome c reductase core protein I	UQCRC1	16	F: CTGTGTGTGAGGACATTGGA R: CAGACCTCACGTACCACACT	464	1.5	58		
microsatellite	VHL145	16	F: GCAAGCACAATGAATACTCATG R: AGTTTGGTTTCTGGAGAATTGTC	93-109	1.5	54	Swinburne et al. 2005	
WD repeat domain 51A	WDR51A	16	F: AGCAGCCCTCTCTCCTATAC R: CATTGCCACAGAGAAAGCCC	598	1.5	62		AJ576546
wingless-type MMTV integration site family, member 5A	WNT5A	16	F: CCATATTTTTCTCCTTCGCCCA R: GAGCCCAAAGTCACGATTCA	142	1.5	60		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	17STS02	17	F: ATATCACGTCCATTTCCGTTTC R: TATTGACACGTTGTTAGCTGGG	139	1.5	59		CX594220
sequence tagged site	17STS03	17	F: CCTCAGTTCCATCTGTCTCC R: GGCTAGGTCCCCAAATATCC	314	1.5	58		
sequence tagged site	17STS04	17	F: ACAACCGAGGAACGAACATC R: CAGAGGGTGAGTAATCCCACA	175	2.0	62		BM414763
microsatellite	AHT102	17	F: GGCCATACCAAGCTGGAATA R: ATCCCTTCGTTTCATTCAGCA	273-295	1.5	58	Swinburne et al. 2003	
asparagine-linked glycosylation 5 homolog (S. cerevisiae)	ALG5	17	F: CCATTTTGGAGCTGGCTA R: GCTAATTCACCTTTCCTGGGTTG	103	1.5	62	Lee et al. 2004	BI961590
basic, immunoglobulin-like variable motif containing breast cancer 2, early onset	BIVM	17q26	F: AGGGCAACTATCCATCTTTCAA R: GCAACAAGAGAGGAGCTCAAAT	132	1.5	59		CX596367
	BRCA2	17q14^a	F: GTGACACTCCAGGTGTGGAT R: GCCGATCTTCTGCTTCTATCA	700	4.0	50	Chowdhary et al. 2003	AF317283
chromosome 13 open reading frame 24	C13orf24 (<i>PIBF1</i>)	17	F: GGGAAGTACAACCTTAGTGCAGA R: CAGTGTGTGAGATTTCTTGCA	124	1.5	62	Lee et al. 2004	BM781341
chromosome 13 open reading frame 27	C13orf27 (<i>LOC93801</i>)	17	F: GATGCTGTTTGTGTTGGTACC R: AGGCAGAAAAACCCATGAGA	134	1.5	62	Lee et al. 2004	
coiled-coil domain containing 70	CCDC70 (<i>DKFZp434K1172</i>)	17	F: GGGAAGAGATGTGGACTTTCC R: TAAGGCGTTGTCCTCTTTCC	230	1.5	58	Lee et al. 2004	
cell division cycle 16 homolog (S. cerevisiae)	CDC16	17q27	F: CTGGGATTTTCAGGGAATTTG R: GTTTCTTCCAAGGAGGGTCTG	115	2.0	63	Lee et al. 2004; Perrocheau et al. 2005*	BM735064

claudin 10	CLDN10	17q26	F: GGCCACATCTGTCATGTCTT R: ATTATGGGAGGGCCTTGATG	184	1.5	58	Lee et al. 2004*	
ceroid- lipofuscinosis, neuronal 5	CLN5	17	F: ATGTAAAAGCCAGCCCAGA R: CCCAGATAAGTAGGTTCTCCA	172	1.5	58	Lee et al. 2004	
component of oligomeric golgi complex 6	COG6	17	F: AACTCCCACCACCTGATCTT R: AGGAGAGGATCCAAGACACA	157	1.5	62	Lee et al. 2004	
microsatellite	COR007	17q12- q13	F: GTGTTGGATGAAGCGAATGA R: GACTTGCCTGGCTTTGAGTC	153 - 175	2.0	58	Hopman et al. 1999; Chowdhary et al. 2003*	AF083450
microsatellite	COR032	17q22dist- q23	F: GCCCTCTTAGAGCATTTTCC R: CAGAGATGGCTGGAGTAAGG	247 - 253	3.0	58	Murphie et al. 1999; Chowdhary et al. 2003*	AF101401
microsatellite	COR067	17	F: AGGCTGGGAAATGACAAATG R: TGTGCCTGGAGCTGTTCTAA	212	3.0	58	Chowdhary et al. 2003	AF142604
microsatellite	COR072	17q13	F: TTCCTCATTGCTTCCTGAGT R: TCACTGGATAGTCTGCTGAGG	155	4.0	60	Tallmadge et al. 1999a; Lee et al. 2004*	
microsatellite	COR105	17	F: TTTCTCATTGCTTCCTGAG R: CCCAAGGTCTGTCTTGCTCTC	174 - 192	3.0	58	Swinburne et al. 2000	
crystallin, lambda 1	CRYL1	17	F: CGAGTGCCTTACAGTTCCTTCT R: ATCATCAGGATCAAACAGGCTT	354	1.5	59		CX594359
cullin 4A	CUL4A	17q27ter	F: GAGGACAGTGAGTTGCGAAG R: GAATTTGTCTCCATCTTCCAC	105	2.0	60	Lee et al. 2004*	BM781050
cysteinyl leukotriene receptor 2	CYSLTR2 (CysLT2)	17q15^a	F: TCACAAGCACACTGCCTTTC R: CTGATGCTGGTGACATGGAG	191	1.5	60	Lee et al. 2004	BI960974
dachshund homolog 1	DACH1 (DACH)	17	F: CCACATTTGCGCTCTATGC R: CCAGGCTCAAAGAACTAGGC	219	1.5	65	Lee et al. 2004	
dopachrome tautomerase	DCT	17q26	F: CACCGGTACCATTTGTTGTG R: GCCAATGAGTCGCTAAAAGC	180	4.0	50	Chowdhary et al. 2003;	

DAZ interacting protein 1	DZIP1 (<i>KIAA0996</i>)	17q26	F: CTTTGGGTTCCTGACAC R: AAGGATAGAAGAGCTGGG	848	2.0	60	Lee et al. 2004* Chowdhary et al. 2003; Lee et al. 2004*	
endothelin receptor type B	EDNRB	17q23-q24	F: TGGTGCCAATCATTTGAAGA R: GTTTTGGCAAATGCCTCACT	197	2.0	58	Godard et al. 2000*; Lee et al. 2004	
EF-hand domain family, member A1	EFHA1	17	F: CGAGTCTTCGTTGATTTCCCTTT R: AGCATGCTGTGCTACTGTGTCT	156	1.5	59		CX605170
ephrin-B2	EFNB2	17q27prox	F: AGGGGCAGAAGGAAGATAGG R: ACTGAGCATTGGGACCACTT	169	1.5	62	Lee et al. 2004*	BM781257
esterase D/formylglutathione hydrolase	ESD	17	F: GCTACCCATCTTGTGAAGTCC R: GCAGCTATGAAGTTATCAGG	116	1.5	55	Lee et al. 2004	
exosome component 8	EXOSC8	17	F: ATGAGCCGAGCAGTTACAAGAC R: TGTTTTGAAAATGTGGTGGTTG	101	1.5	59		CX595111
coagulation factor X	F10	17q27ter	F: GAGACCTACGACTTCGACAT R: CACCTCCAGCATCTTGAG	198	1.5	58	Lee et al. 2004	
fibroblast growth factor 14	FGF14	17	F: GACAACAGGAATCTGGTAGAGC R: GGCTTGGGTAGAAAATGAGC	197	1.5	63	Lee et al. 2004	
hypothetical protein FLJ10154	FLJ10154	17	F: GCGACAGCGTCAACAAAAA R: CACTTCAACATGAAGCTACCA	160	1.5	60	Lee et al. 2004	
fms-related tyrosine kinase 1	FLT1	17	F: TCCTGGTCTTTGCCTGAAAC R: AGCCAGTGTGATTTGCCTGA	133	2.0	62	Lee et al. 2004	BM735444
glypican 5	GPC5	17	F: CCACCAAGTGGGAACCTT R: CCTCTTGACTTCTCCACTTCC	113	2.0	53	Lee et al. 2004	
glypican 6	GPC6	17q25	F: ATCGGGGCTGTGATTCTTC R: TGAATCCCTTGGCACCGTA	115	2.0	58	Lee et al. 2004*	
microsatellite	HMS25	17q25-q26	F: CAAACATAAAATATGCATGTCCATGT R: CTTTTGGATATGTAAGGCTTGAGG	124	3.0	58	Godard et al. 1997; Chowdhary	U89811

et al. 2003*

microsatellite	HMS41	17q21.3-q22	F: AAAGTCTTCATTTGAAGTTTCCTAAG R: GACTAAGTAGATGAGATGTGTTTGG	113	3.0	58	Godard et al. 1997; Godard et al. 1999*	U89812
5-hydroxytryptamine receptor 2A	HTR2A	17q21.1	F: GCTCTTTTCGTGGCATTTTTTC R: AGAGCAACCATAGTGCAGTCA	628	1.5	64	Momozawa et al. 2007; Prause et al. 2006	AB264327
integrin, beta-like 1	ITGBL1	17	F: CGGAAATGCGTGTGAAAT R: TCGTCTGTTTGACCTGTCCT	219	3.0	55	Lee et al. 2004	
integral membrane protein 2B	ITM2B	17	F: TCCATTGCACAGATATGGGTTA R: AATAACCTTGGCATCTGCTG	192	1.5	62	Lee et al. 2004	BM781143
potassium channel tetramerisation domain containing 12	KCTD12 (LOC115207)	17	F: TCCCACTGCACATCCTGT R: CAGACTGGATCGCATGAATCT	295	1.5	58	Lee et al. 2004	BM735319
Kruppel-like factor 5	KLF5	17	F: GTCCAGATAGACAAGCAGAG R: CAGTAGTGGATGCGTCGTTT	193	1.5	62	Lee et al. 2004	
Kruppel-like factor 12	KLF12	17	F: ACACAAACTGAGCCAGTGGA R: AAGGGGCCCTGGAGTTAATA	216	1.5	62	Lee et al. 2004	
kelch-like 1 (Drosophila)	KLHL1	17	F: CTGAGGAGCTCCATAAAC R: TGGAAGCAGTGGCAGTCTTA	158	2.0	58	Lee et al. 2004	
karyopherin alpha 3	KPNA3	17	F: AACCAGCAACAAGTTCAAGCT R: CCAGCCATTATCAGAATGTT	260	1.5	62	Lee et al. 2004	
lysosomal-associated membrane protein 1	LAMP1	17	F: AGTATCAGAGCTACTGCTGGGG R: TGTACACAAACAAGTGCAGACG	153	1.5	59		CX594321
LATS, large tumor	LATS2 (RP11-56904)	17q12-q13	F: CGCTGTAAATAACGACATGG R: CCGATTCCTGTGTACTGGTTT	121	1.5	62	Lee et al. 2004*	BM414633

suppressor, homolog 2 (Drosophila) lymphocyte cytosolic protein 1	LCP1	17	F: CCGAAAAATTGGAGCAAGAG R: GAAAACCTCTGGAACGGCTTG	226	1.5	58	Lee et al. 2004	BI961466
microsatellite	LEX067	17	F: GTTGCTAAAATTGTTCCAGAC R: CCAATAAAAGGAATCACTGCT	200	2.0	56	Coogle et al. 1999	
microsatellite	LEX076	17	F: TTACCTCAGCCACAATCTTCTT R: TTGCCAGACACAGAGAAGTG	222 - 226	2.0	58	Bailey et al. 2000	AF213362
lipoma HMGIC fusion partner	LHFP	17	F: GGTGAAAGATGGCATCCAG R: TGCACAGGATATGAGCACCT	172	1.5	65	Lee et al. 2004	
ligase IV, DNA, ATP-dependent	LIG4	17q27	F: GGGTGGAATGATGTCTCAT R: TCTGGCTTCTCTGTTCCACA	211	1.5	55	Lee et al. 2004	
LOC144997	LOC144997	17	F: CAGATGGGAAAATGCCTTGA R: ACATTTTCTAAGGTATGGGC	104	2.0	62	Lee et al. 2004	
myotubularin related protein 6	MTMR6	17q12- q13	F: GGGACGGGAATCTTAATATTTG R: TTCTCAGGCCATATGTGAGCAC	190	3.0	58	Chowdhary et al. 2003*	G62207
MYC binding protein 2	MYCBP2	17	F: ACGGCTTTGCAGGATGGTAG R: AGCCAATGCAAGTGAAGACCC	138	2.0	58		
neurobeachin	NBEA	17	F: GAATTTGGGCTCAGTCAG R: CAGGAGTTGGAAGTCATT	278	2.0	58	Lee et al. 2004	
Nedd4 family interacting protein 2	NDFIP2 (<i>KIAA1165</i>)	17	F: GAATGGCAGAGTGTTTATGC R: TGTCAGGTCAGAAGTCAATG	239	1.5	58	Lee et al. 2004	
microsatellite	NVHEQ024	17	F: CCACTGTGGAAAAGACTGAAAG R: TGTACTTCCTTGAAACCCAACA	161 - 163	2.0	58	Roed et al. 1997	AF011405
microsatellite	NVHEQ079	17q14- q15^a	F: ATTGCTGTGCTGAGATGG R: GCAAATTGCCTCTGTATCACAC	190	2.0	58	Bjornstad et al. 2000	
PAN3 polyA specific ribonuclease subunit homolog (<i>S. cerevisiae</i>)	PAN3 (<i>RP11- 502P18</i>)	17	F: GGGAGCCCTCTTTTCCATAG R: ACGGGTTGTCTTTCTGTGC	160	1.5	60	Lee et al. 2004	BM734723

protocadherin 9	PCDH9	17q22 dist	F: GCTGAACTGGAGGAGCAAAG R: CACAACCCCCAACAAAGGT	211	1.5	58	Lee et al. 2004*	
protocadherin 17	PCDH17	17q22 prox	F: GGGCAAGAAGAAGAAGATCA R: CGGTTTGAGATACATCACCT	187	2.0	62	Lee et al. 2004	
phosphoglycerate dehydrogenase like 1	PHGDHL1 (<i>LOC94902</i>)	17	F: TCTTTGTCGCCTCGCTTGTG R: CTTGGACACTTGAGCCCATC	155	1.5	62	Lee et al. 2004	BM781094
polymerase (RNA) I	POLR1D	17	F: AAGCAAAGCAGAAATAAACCCA R: TACAAAGGTTCTTGCAGGGATT	198	1.5	59		CX603903
polypeptide D RAN binding protein 5	RANBP5	17	F: CTTACGCAGTGA CT CAGTTTGG R: CATAAAGGAAAACATCGGGAAA	250	1.5	59		CX602694
retinoblastoma 1	RB1	17q15	F: CGAACGTGTGCTCAAAAGAA R: AAATTGGCAGGAAAGGGATT	201	2.0	58	Chowdhary et al. 2003	AF130779
ring finger protein 6	RNF6	17q13- q14	F: GTCACAACCGCTGCTTCAGT R : TCCTCCCAGAGATGATCCAG	265	3.0	58	Chowdhary et al. 2003*	
Sequence from clone RP11- 477B16	RP11-477B16	17	F: TGCCATTGTTCTGACCTAG R: ATCTGCCCTCCCCTGAATT	117	2.0	62	Lee et al. 2004	
sarcoglycan, gamma	SGCG	17q13	F: AGTTGGTTCAGGGA ACTTGG R: GATCCGTGGAAGATGCAGTT	163	2	58		CX598910
SLIT and NTRK-like family, member 6	SLITRK6 (<i>DKFZp564O1 278</i>)	17	F: CCAGATTGACCTTGAGGA R: TCATCTGTCACTGTGTTCTT	99	2.0	55	Lee et al. 2004	
spastic paraplegia 20	SPG20	17q14- q15	F: TCAAGAAGAAAGGGCAAAGGTA R: CCCTATTTAGCAAACCTGCATC	158	1.5	59		CX605041
START domain containing 13	STARD13	17q14- q15	F: AGGTCAC TCCCCAGAATGGT R: GCATTTGCTTTTGCTTCCTC	160	1.5	61	Lee et al. 2004	BI960825
TBC1 domain family, member 4	TBC1D4	17q23	F: GTCCAGGCTCCTTCATGACT R: CTCTGGCTACAAATCCTAATG	137	2.0	65	Lee et al. 2004*	
thrombospondin, type I, domain containing 1	THSD1	17	F: AGTCAGCCTGAGACTTGACACA R: TTACAAAGGGAAAGGTT CAGGA	210	1.5	59		CX593698

microsatellite	TKY102 (RC01)	17	F: ACCCTGATGGTGGTTTTTCAG R: AAAGTGTTCAGGGGATTGCT	213	2.5	50	Chowdhary et al. 2003	AB053341
microsatellite	TKY103 (RC03)	17	F: TAAAGTGATAGCGACCGATGG R: TAGTAGCTCAGGGCCAATCTT	145	2.0	58	Mashima et al. 2001	AB053342
microsatellite	TKY287	17	F: ATCAGAGAACACCAAGAAGG R: TCTCTGCTATAGGTAAGGTC	224-240	2.0	58	Tozaki et al. 2000b	AB033938
microsatellite	TKY328	17	F: AATCCCTTCGTTTCATTCAGC R: CTGACCCACAAATGATTTCAG	131-155	1.5	58	Tozaki et al. 2001	AB044829
microsatellite	TKY356	17	F: TCAATCACACGAGCCAATTC R: GATCATAGGATGATTAGCAC	157-171	2.0	55	Tozaki et al. 2001	AB044856
microsatellite	TKY373	17	F: GGCCAATGATTAAGTACTC R: CAGGTTGCACTAGAGTTCTC	166-176	1.5	58	Tozaki et al. 2001	AB044873
microsatellite	TKY379	17	F: TAGCCTGACCATAATTTTGC R: GAACAATGGCATCCTCAGTG	213-231	1.5	58	Tozaki et al. 2001	AB044879
microsatellite	TKY481	17	F: TGGACTTCATCGCTATTCTG R: TGGTCTACTTGCCTGTGAGG	160	2.0	58		AB103699
microsatellite	TKY546	17	F: TAGGATGGGGCACCAAGTAG R: CATTCCTAAGGGTGGAGCAC	244-248	1.5	55	Tozaki et al. 2004	AB103764
microsatellite	TKY684	17	F: TTTGCAGGCTTTCTGTATTTTT R: TTCTGTTTCGTTTTCCCTGAA	230-246	1.5	50	Tozaki et al. 2004	AB103902
microsatellite	TKY792	17	F: CAGTTCCATCCATCAGTGAC R: ATTCCCAAAGGGCCTTTTTC	149	2.0	58	Tozaki et al. 2004	AB104010
microsatellite	TKY796	17	F: GTTTACAGAGCACTGGAAGG R: TAAAGGAATTTCCCAGGGC	100	2.0	58	Tozaki et al. 2004	AB104014
microsatellite	TKY825	17	F: TTTGGAAAAGACAGAGGTGC R: GGAAAAGAACCCACCCCA	254	1.5	62		AB104043
microsatellite	TKY826	17q14- q15	F: TCCATTTGAAAAGGGTCAGG R: CTCTTTCCAACACTCCCTTG	98	2.0	58		AB104044
microsatellite	TKY865	17	F: TCATAACTGCATGAGCCAAC R: TTATTAACCAAAGTGCCACAG	202	2.0	58		AB104083
microsatellite	TKY869	17	F: TTATTTATCATGGGGCTGGC R: CTCCTCATAGTTCCTGAGAC	251	2.0	58		AB104087

microsatellite	TKY893	17	F: GTTCTCCAGAGAAGCAGAAC R: ATAACATGGACCGATTCTGTG	109	2.0	58		AB104111
microsatellite	TKY924	17	F: TTCACCTATGAGTTTGAGGTA R: CGTCATAATGCAGACTCTTTG	168	2.0	58	Tozaki et al. 2004	AB104142
microsatellite	TKY951	17	F: ACGGCAAGTGAAGAGAAGC R: TAGTCTATTTGGCTGCTAAAC	284	2.0	58		AB104169
microsatellite	TKY969	17	F: TCATACCAATCATACCCAGC R: TTCCCCACTTCTATGCTTTC	242	2.0	58		AB104187
microsatellite	TKY983	17	F: ATCTTGTTCCCTGCTGTATC R: TGAGGGGAAATACAAAGAAGG	154	2.0	58		AB104201
microsatellite	TKY1071	17	F: CAGTGCATCCTAACCAATAC R: AAAATTCTTCGAAGTATTTCTTAAG	172	2.0	58		AB104289
microsatellite	TKY1102	17	F: ACCTGCTATGTAGTCTGAAG R: AGCTCTCAAATCCTTCATCC	123	2.0	58		AB104320
microsatellite	TKY1128	17	F: TGGACATGTCACAAGAATCC R: ATGTTGGTCCTCATGCCTG	252	2.0	58		AB104346
microsatellite	TKY1133	17	F: GATCAGTAGTAAATATTTTCATC R: GTGACGGAATCCCACATAC	111	2.0	58		AB104351
microsatellite	TKY1301	17	F: ACCAAAGTGACAGCACTAAG R: CTCATTTGGCTTCCTTTTGTG	138	1.5	58	Tozaki et al. 2007	AB215244
microsatellite	TKY2347	17	F: CCTGCATTTACGTCTTCAGT R: CCCCTCTCCCAAATTTAAAG	282	1.5	58	Tozaki et al. 2007	AB216290
microsatellite	TKY2549	17	F: ATCCATTCAACCATCAATGC R: ATTTGCTGCTTCAAGTTCCA	203	1.5	58	Tozaki et al. 2007	AB216492
microsatellite	TKY2567	17	F: GATCAGACCAGTTCTGGGGG R: TCCAGGGAGTTTAACTCAG	171	1.5	58	Tozaki et al. 2007	AB216510
microsatellite	TKY2597	17	F: CAGTGAGGTTCCCTTTGTGTTG R: AACCCAAGCCTCAGTTCTTT	196	1.5	58	Tozaki et al. 2007	AB216540
microsatellite	TKY2700	17	F: TCCTCTGCTACCTGAATGCT R: AAGTGGAATGGTGGTAACG	178	1.5	58	Tozaki et al. 2007	AB216643
microsatellite	TKY3156	17	F: CCATATGGGACTTGAGGAG R: CTGGTGGGATTACAAGGAG	114	1.5	58	Tozaki et al. 2007	AB217099

transmembrane 9 superfamily member 2	TM9SF2	17q26	F: CTAAATACACCTCTTCCCGCAC R: ACCTACCGAGCCTAGAAAAATCC	256	1.5	59	Lee et al. 2004	CX600656
tripartite motif- containing 13 microsatellite	TRIM13 (<i>RFP2</i>) UCDEQ014	17 17q21.3	F: GCTTGGATACCTTGGAAGT R: CCTGCAAGATGGTGTGAG F: GCATTTGCTCACTGGCTAC R: ACTCCTCCACTCCACCTA	204 134	2.0 2.0	62 58	Lee et al. 2004 Eggleston- stott et al. 1996; Lee et al. 2004*	U25266
ubiquitin carboxyl- terminal esterase L3 microsatellite	UCHL3 UMNe52	17 17	F: TGCCATAGAAGTTTGCAAGAAG R: TGGTGTTTCCATTATTGACAA F: TGTCTGCTGACAGATGAATGG R: CATGGCTGAATAATATTCCGTG	114 88 - 104	1.5 2.0	55 58	Lee et al. 2004 Roberts et al. 2000	AF191690
microsatellite	UMNe162/ 246	17	F: TGCATTCTGTGTTTCATATGGTC R: ATGGAAAGGCAGGATTCATG	123	2.0	58	Lee et al. 2004	AF536271
microsatellite	UMNe176	17	F: TTTTGAGGGGTGTGTTACAGC R: TTACCAGAGTTCTTACCTGGGG	107	2.0	50	Mickelson et al. 2003	AF536275
microsatellite	UMNe235	17	F: TGAAGGCAATGACCAATATCC R: CACCAACAAAAGTATCTGCCTG	178	2.0	58		
microsatellite	UMNe384	17	F: AGTCAGGAGAGACAGTGTAGGC R: TCATGGAAGCATTTCCCTAG	251	2.0	58		
microsatellite	UMNe521	17	F: GTACCGAGCTCGGATCTGAG R: TCTGCAGAATTCCAGCACAC	137	1.5	62		AY735258
microsatellite	VHL179	17	F: CTGTCATCCATCTGCAGTGTTT R: GAATATCTGTAAACTCGTGGAGG	110	1.5	62	van Haeringen et al. 1998	
vacuolar protein sorting 36 homolog (S. cerevisiae)	VPS36 (<i>CGI-145</i>)	17q14- q15	F: TAAGCTCGTGGGAATGTCTG R: TTGGGTAAAACCGCAAGC	190	2.0	60	Lee et al. 2004	
WW domain binding protein 4	WBP4	17q21.3	F: GGAACCTCCAAGCACTGAAAA R: GATCATCACCTCGTTGCCTTA	191	1.5	62	Lee et al. 2004*	BM780424

zinc finger, MYM-type 2	ZMYM2 (<i>ZNF198</i>)	17q12	F: CCCAGTGTGGGTACACTGCTA R: ATGCTCGTACGGGTTCTTTT	204	1.5	61	Lee et al. 2004*	BM781014
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Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	18STS01	18	F: AGAGACTGGTGGGCAAGAAA R: CGTGGTCATCCATGAGAACT	207	1.5	55		DX010503
ARP3 actin-related protein 3 homolog (yeast)	ACTR3	18	F: CGGACTTTACTCAACCTATCTC R: ACCACCACTCAATTCCTCAC	~350	1.5	60		BI961286
activin A receptor, type I	ACVR1	18	F: GTGAATGACAGTAGTCACAGG R: CAGGTACACAGAGATGGAAAAG	155	1.5	58	Wagner et al. 2006	DQ001074
microsatellite	AHT080	18	F: AGAACTGAGGAAAGAAGAGGGC R: TCCCTGAGACTTAATTTCTCA	155-165	2.0	58	Swinburne et al. 2003	AJ507697
microsatellite	AHT115	18	F: GAACCCAAGAGGAGTCCACA R: ACACACCTCAAGCAAAACACC	133	1.5	58	Wagner et al. 2006	
aldehyde oxidase 1	AOX1	18q26	F: GGAAGTGTCCCCATTTGTCTC R: TGCACATGCTGGATCAAAGC	127	1.5	60	Mariat et al. 2001*	
activating transcription factor 2	ATF2	18	F: TATCAGCAGGCAGTACCTTCAC R: ACATACACACACACAAGGCCAC	185	1.5	58		
bromodomain adjacent to zinc finger domain, 2B	BAZ2B	18	F: TCGAGATATTGTGGAGAACTGG R: CTGATGCAACCCTCCTTTCTA	~100	1.5	58		DN510366
bridging integrator 1	BIN1	18q12-q13	F: TGGAGAGGGAGAGAGGAAC R: GACACAGGCACACTCAGG	305	1.5	58	Wagner et al. 2006*	DQ001077
basic leucine zipper and W2 domains 1	BZW1	18	F: GTGTTTCTTAGCTCCTTGTC R: CAATGTGTTTAGCCCTGATCC	101	1.5	58	Wagner et al. 2006	DQ001078
CD28 molecule	CD28	18q26	F: ACTCACTTTAAACAGACCCAAG R: AATACACAGAGCACAATGGAC	273	1.5	60	Mariat et al. 2001*; Wagner et al. 2006	CD528733
BAC end sequence	CH241-101P3 (AJ577071)	18q25	F: TCCGTAACATCAAATCGGAAC R: GTGAATATGGAGTGAAGTGGAG	591	1.5	58	Wagner et al. 2006*	AJ577071

BAC end sequence	CH241-111C11_SP6	18	F: CAGCTCAGGCAAATCTAGG R: GGAAC TTCCACATCAGC	198	1.5	58		CR956033
BAC end sequence	CH241-111C11_T7	18	F: GTAGGCAGGACCACG TTC R: TTCGGGTCGTGGTATGAG	228	1.5	57		CR956863
cholinergic receptor, nicotinic, alpha 1	CHRNA1 (<i>CHRNA</i>)	18	F: GGT TTGGCTTGACGAGTAGG R: TGTTGATGCTTTGCACCTTC	205	3.0	58	Caetano et al. 1999; Chowdhary et al. 2003	AF130750
cytoplasmic linker associated protein 1	CLASP1	18	F: CAGACCCAATAGTAGAACATCG R: GGCTCCATGGTGGAATTCA	300	1.5	TD58		CD464645
collagen, type III, alpha 1	COL3A1	18	F: GACAGCCACAAAAATGGATGA R: CACCTTTTACTCCAGGCTGC	286	1.5	58	Wagner et al. 2006	DQ001081
microsatellite	COR096	18	F: CCCCTCTTTTGCTTGAGAAT R: GCGTGTATGTGAGGATTGAAG	307-319	3.0	58	Tallmadge et al. 1999b	AF154949
chemokine (C-X-C motif) receptor 4	CXCR4	18q21	F: GGACCATAGAAAAGGGAAGT R: TACATTACAGGCGCTGCTATC	255	1.5	58	Chowdhary et al. 2003*	
DEAD box polypeptide 18	DDX18	18q15	F: AAATAGGACGTAGGCCAGAG R: TCCAATCACAACATCCATCAG	127	1.5	58	Wagner et al. 2006*	DQ001087
dipeptidyl-peptidase 4	DPP4	18	F: CTTTCCCATCACCC TTTCTGT R: CCAGACTGGCACAGTTTCTG	200	1.5	55	Perrocheau et al. 2006	DX010468
dynein, cytoplasmic 1, intermediate chain 2	DYNC1I2	18	F: GTGTGGCCCTTGTATGGAAT R: GCTGACAGTGGAGTTCTTTG	1103	1.5	TD58		CK954736
eukaryotic translation elongation factor 1 beta 2	EEF1B2	18	F: CAGATATGGCAAAGCTGG R: CTCAAAAGCAGTGATCCG	561	2.0	58	Wagner et al. 2006	BI961819
erythrocyte membrane protein band 4.1 like 5	EPB41L5	18q15	F: CCTCCAGTAATCAGACATAA R: GCATATTTACACAAGCC	144	1.5	58	Wagner et al. 2006*	DQ001101/ DQ001102
FAST kinase domains 2	FASTKD2 (<i>KIAA0971</i>)	18	F: GGACAATTGCCAAAAGGATG R: GCTTCACCACAGCATGAAGA	159	1.5	58	Wagner et al. 2006	

frizzled-related protein	FRZB	18	F: GGA CTAGCAAAGGAAAATTGC R: AAGGATCTGTACCCAGACCAA	180	1.5	59		CX603714
glutamate decarboxylase 1 (brain, 67kDa)	GAD1	18	F: GAGCCATCTTGTGTAGTCTTC R: ATGCATATTACTCAGTTGCCC	148	1.5	58	Wagner et al. 2006	DQ001092
grancalcin, EF-hand calcium binding protein	GCA	18	F: CACAGGAAAGATGGGATTTAATG R: CCATAGCAGCAATAGCTTGATTC	140	1.5	55	Perrocheau et al. 2006	DX010631
glucagon	GCG	18q22	F: GGGCATGAAGTTATACAGCTTG R: TGAAAAGCCTGATAGAAACCTG	110	1.5	58	Wagner et al. 2006*	AY008785
growth differentiation factor 8	GDF8 (MSTN)	18	F: TGA CTGTGATGAGCACTCCA R: TCTGGGGTTTGCTTGGTGTA	190	2.0	58	Caetano et al. 1999; Chowdhary et al. 2003	AF097584
growth factor receptor-bound protein 14	GRB14	18q23	F: GGCCACAGCACATTGTTTATC R: GCCGACTAACTATGGATTCTGC	213	1.5	58	Wagner et al. 2006*	DQ001094
microsatellite	HLM3	18	F: GAAGGTAGAAAAGGAGGGCTAGAAC R: TCTAGAGGACCATTCTCTGGGCTGTG	123-131	2.0	58	Vega-Pla et al. 1996	U36495
microsatellite	HMS46	18	F: GTCTCAGCCAAAAGGTATTCAAGC R: TGGCACCAATATAGGTCACCTGG	141	3.0	58	Godard et al. 1997	U89814
microsatellite	HMS75	18q25	F: CCCTATTGTTCTGGAATCG R: GGAAAGTAACGTTAGAGTTTGGG	~150	1.5	58	Mariat et al. 2001*	
homeobox D10	HOXD10	18	F: GCAACAAAAGAGCACAAATGAG R: TCACTGGATGAAAGGCAAGG	104	1.5	58	Wagner et al. 2006	DQ001096
heat shock 60kDa protein 1	HSPD1	18	F: TAACAGAGAAGCCACTCCAG R: TGAGAAGATTATGCAGAGTTCC	249	1.5	58	Wagner et al. 2006	DQ001097
microsatellite	HTG28	18	F: AATCAACTAATATTAGGCCTCCT R: GAATACAGTTCTAGGGGCGT	180	3.0	58	Lindgren et al. 1999	
isocitrate dehydrogenase 1	IDH1	18	F: GCAGTACAGATCCCAAGTTTGA R: GTAGTTCTTACAGGCCCAGATG	120	1.5	58		CX594417
integrin, alpha 4	ITGA4	18	F: TGAATGTTCCCTCCGAGA R: AGTAGCCGAACAGGGTGTTG	186	1.5	55	Perrocheau et al. 2006	DX010516
integrin, alpha V	ITGAV	18	F: TTGTTTTACTCCCCACC R: CAGACACACAAAAAGTCTCC	274	1.5	58		

kinesin family member 5C	KIF5C	18	F: CAGCTCAGCAGGAGATAGAG R: GCCTATCCTATCCTTCTTCCTC	93	1.5	58	Wagner et al. 2006	CD468079
kynureninase	KYNU	18	F: CATCCCATCAAACACTAAATAC R: CACATCCACACTGCTCAC	155	1.5	58	Wagner et al. 2006	DQ001103
microsatellite	LEX016	18	F: GTGGGGCCGGTATAGTGATTG R: ACCCTAACTGATAACTGATAGA	171-185	2.0	58	Coogle et al. 1996	AF075618
microsatellite	LEX054	18	F: TGCATGAGCCAATTCCTTAT R: TGGACAGATGACAGCAGTTC	164-182	2.0	58	Coogle & Bailey 1997	AF075656
low density lipoprotein-related protein 1B	LRP1B	18	F: CTTAGCAAGGTCACAAAAGGG R: GCAGAAGGGCAAGAAATCAAC	126	1.5	58	Wagner et al. 2006	DQ001105
low density lipoprotein-related protein 2	LRP2	18	F: CTGCAAACCTTGTTAGAGAAGA R: GCCTTACCTTCAGATAGCTTCA	~ 310	1.5	58		DN508963
minichromosome maintenance deficient 6 homolog (S. cerevisiae)	MCM6	18	F: GATTGAAAGGCTCGACAGAA R: CCCAGGAAGATACACACATCA	334	1.5	58		
mannosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	MGAT5	18	F: CCTTTCCTCCCTAGCGATAC R: TGTCATAGCCATAGCCCCAAAAC	105	1.5	58	Wagner et al. 2006	DQ001110
myosin IB	MYO1B	18	F: CCTTGAAAAGAATTTCCCTTGC R: AGAAGATGAGCCACAAGACC	127	1.5	58	Wagner et al. 2006	AK000160
NADH dehydrogenase Fe-S protein 1	NDUFS1	18q26	F: GAGACTTCTTCCAATCTGTTCC R: TGATGTTATTCTCCCAGGCG	1161	1.5	58	Wagner et al. 2006*	BI395134
nebulin	NEB	18q21	F: TGACGTACGTAACAGTCAACGA R: CCAAATTCTGGAGGTGATCC	151	3.0	58	Lear et al. 2001* ; Chowdhary et al. 2003	AF130774, G62157
nuclear factor	NFE2L2	18	F: TACAGTCCAACCCATGTCACC	219	1.5	55	Perrocheau	DX010645

(erythroid-derived 2)-like 2 N-myc interactor	NMI	18	R: TGATCTTTTCGACAGGGAATG				et al. 2006	
			F: CAGATCATAGCTGCCATAGAG R: CATTGTGAACATGCAGCAC	1192	1.5	TD58		BM735031
nuclear receptor subfamily 4, group A, member 2	NR4A2	18	F: CAGCAGGAGATAGAGAGACAG R: GCCTATCCTATCCTTCTTCCTC	88	1.5	58		
microsatellite	NVHEQ077	18	F: ATAATCTCACCGTTGCCTACTA R: TTAGCTATGCTTCATATCACCC	134-136	2.0	58	Bjornstad et al 1999	AJ245767
microsatellite	NVHEQ133	18	F: CTACCTCCGTCTTCTCCAAC R: CAGGGGATGGTGGTCTC	167-191	2.0	58	Penedo et al. 2005	
origin recognition complex, subunit 4-like (yeast)	ORC4L	18q22	F: CCATACAGCTTTTAACTCAGCC R: GCCAATGCTTTTCAGTAGCAC	154	1.5	58	Wagner et al. 2006*	DQ001115
pyruvate dehydrogenase kinase, isozyme 1	PDK1	18	F: CAGTAGAAAGACTCCCCGTGT R: CTGAACACCAAATCTCTTCCA	~200	1.5	58		CX602628
protein C	PROC	18q13	F: CATCATGCACCCCAACTACA R: GCGGTTTCTCTTGGTCTCAC	202	2.0	58	Murakawa et al. 1994; Godard et al. 2000*	D43753
PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	PRPF40A (FNBP3)	18	F: AAAAACGCACAGCAACTAGAC R: TTGATGTCAAAAGGTTACATAGTAATG	349	1.5	58	Wagner et al. 2006	DQ001090/ DQ001091
pleckstrin homology, Sec7 and coiled-coil domains, binding protein	PSCDBP	18	F: TTGCAAGGACATCACCTGGGAG R: TGTGTTGCTGAGGTTTGGGG	118	1.5	58	Wagner et al. 2006	DQ001118
proteasome, 26S subunit, non-ATPase, 14	PSMD14 (POH1)	18	F: AGGTTGGCTTTTCTTACCAGTT R: AATTTGTCCACTTTGATGTATTCT	427	1.5	58		

splicing factor 3b, subunit 1, 155kDa	SF3B1	18	F: CAACTTCTCCCAGACCTTTTTC R: AACCCATTATGGTAAAGACAGC	102	1.5	58	Wagner et al. 2006	DQ001120
microsatellite	SGCV07	18q21	F: GAATTTGAATGTATCTATTCTGAATG R: GTGAGTTTTCAAGCTGGCATATTC	132	3.0	58	Godard et al. 1997*	U90589
Sjogren syndrome antigen B	SSB	18	F: TGGATTATTTTGGAGTGGAATC R: ATGAAGCCAGGATGTCTCG	123	1.5	58	Wagner et al. 2006	DQ001122/ DQ001123
sperm specific antigen 2	SSFA2	18	F: GAATGTGTGGCAGTAGAAG R: GAGGGACCAGAACATACAG	1502	1.5	TD58		CB042018
TRAF family member-associated	TANK	18	F: GTTCTGTGTGATGATTTGGGG R: CTGGGCAACAAATGTCTTAGG	458	1.5	TD58		BI961543
NFKB activator tissue factor pathway inhibitor	TFPI	18	F: GCTGGAATCTGTCTGAGGTT R: CAAGCGTTCCTGCATTCTTC	~130	1.5	58		CX604782
microsatellite	TKY016	18q26	F: GGTTATGGTTTGGTATCTGTC R: AAAACAATGGCTTCCTGGTCA	~120	2.0	58	Kakoi et al. 1999	AB048327
microsatellite	TKY017	18q26	F: CAACTGTATGTTGACAGCACA R: CGGCCATATTAGGTTTATCTG	127	2.0	58	Hirota et al. 2001	AB048328
microsatellite	TKY101	18	F: TCTGAAATACCGTGTGCCT R: TTCTGCCTCCCTCCAACCTT	~200	1.5	58	Mashima et al. 1999	
microsatellite	TKY303	18	F: GTAACCTGGGTGCATCTCTG R: GAATAAGGATACAGCCACGC	127-129	1.5	58	Tozaki et al. 2000c	AB034612
microsatellite	TKY322	18	F: TGCAAACACTTGTGAACCTGC R: AACCTAGTGTAATTGCTACC	203-224	1.5	58	Tozaki et al. 2000c	AB034630
microsatellite	TKY407	18	F: TCCTGCTGTGAGTTCCATGA R: CATCTTGTGCTGGGGATCTT	230-232	1.5	58	Wagner et al. 2006	AB103625
microsatellite	TKY426	18	F: TCCCTCCATGTCTCTTTCCTT R: ATTTGAATTACCGGCGGACT	138-142	1.5	58	Wagner et al. 2006	AB103644
microsatellite	TKY449	18	F: GAGCCAATTCCTTATAATAC R: TTTAGTCACCTGGACAGATG	182	2.0	58	Wagner et al. 2006	AB103667
microsatellite	TKY545	18	F: GCAGCTTCCCTCTGTCCAC R: TGACCTACGGCTTTGGTTTT	130-138	1.5	58	Tozaki et al. 2004	AB103763

microsatellite	TKY589	18	F: TATCCTGGATTGGGGTCTG R: TGCAGGGAGGTGGAGCCG	115	2.0	58	Wagner et al. 2006	AB103807
microsatellite	TKY608	18	F: AGCAACAGATGTTACCTCAG R: AAACCTTCTCTTTTCCCCTAC	108	2.0	58	Wagner et al. 2006	AB103826
microsatellite	TKY692	18	F: TTCCCCACTAGATCCTGACA R: TGCTCTGTAATCTGGCAAGC	112-138	2.0	50	Tozaki et al. 2004	AB103910
microsatellite	TKY741	18	F: CCTTCCTTCTCCTAACTCAGTCC R: TGGAAACCAGGAATAGGTGTG	97-115	1.5	50	Tozaki et al. 2004	AB103959
microsatellite	TKY909	18	F: GAGTCACACTTCTGGGAAG R: GCTACCAAACAACACTTGGT	188	2.0	58	Tozaki et al. 2004	AB104127
microsatellite	TKY943	18	F: CACGGTTAATGAGGACCTG R: TAGTGTTGCCAGAGAACTTG	217	2.0	58		AB104161
microsatellite	TKY1008	18	F: GACCAGACGTTTATCCCATC R: TGAAGTCCTCACTCTACTTG	166	2.0	58		AB104226
microsatellite	TKY1055	18	F: AGAAGGTCATCAAACGATGC R: GCTGTTGAGATATTGACAGC	112	2.0	58	Wagner et al. 2006	AB104273
microsatellite	TKY1260	18	F: GTGCAAAATATTGCCACTGC R: AAGGTTAATTGAGGCAAGGC	121	1.5	58	Tozaki et al. 2007	AB215203
microsatellite	TKY1913	18	F: CACCTAAGTGTTGCTCAATG R: CTCAAAGTCCATCCAAGTTG	164	1.5	58	Tozaki et al. 2007	AB215856
tumor necrosis factor, alpha-induced protein 6 equine EST	TNFAIP6	18	F: CGGTGGCATCTTTACAG R: ACGCTGACCATACTTGAG	112	2.0	58	Wagner et al. 2006	BI961885
	TUDPEc010	18	F: CCCAAATTCACCCCGGTTCTAC R: GGAGTAAGCAATGCAGAGGGT	242	2.0	58	Wagner et al. 2006	BI395085
microsatellite	UCDEQ136	18	F: CTTTGGGCCTTTCTCCAT R: CGAGCCTGGGAGTGATAC	111-121	3.0	58	Eggleston-Stott et al. 1997	U67401
microsatellite	UCDEQ387	18	F: ACCCCCCGCCCCAGCAC R: TGCCCCGTCAATTCTGC	78-88	3.0	58	Eggleston-Stott et al. 1999	U67404
microsatellite	UMNe50	18	F: GTTGGAAGAGAACAACGAAAGG R: GCTAAATTTCACTCCATCAGGG	121-131	2.0	58	Roberts et al. 2000	AF191688

microsatellite	UMNe089	18	F: TCCTGTGTCCTTCTGAGATACCC R: ACCAGGGAATCTTGGAGAAATG	174	1.5	58	Wagner et al. 2006	AF536245
microsatellite	UMNe095	18	F: TGTCCAAATAAATTTAGTCAAAACAG R: ACCCATGATTTCATCACTGC	179	1.5	58	Wagner et al. 2006	AF536246
microsatellite	UMNe097	18	F: TGTCAGGTGGCATTCAAATC R: TAACCAACAATGCCCAAGTC	202	1.5	58	Wagner et al. 2006	AY391288
microsatellite	UMNe114	18	F: AACCCAAAAAGCATTGAGAAG R: TCTGCACCAGTTTTGTACGC	129	1.5	58	Wagner et al. 2006	AY391295
microsatellite	UMNe180	18	F: TGGAAAATCCTCACAACACTGC R: TATATTTTCCTTTTGCCTGTGC	148	2.0	58	Wagner et al. 2006	AY391313
microsatellite	UMNe243	18	F: TCCATCTATCAGTCTACTTTCCAGC R: GAACTAACACACCTCATTTTTCCC	151	2.0	58	Wagner et al. 2006	AF536313
microsatellite	UMNe263	18	F: TCTCTTCCCTCTTCCCCCTC R: ATAATGATATTGGCTGCCTGTG	165	2.0	58	Wagner et al. 2006	AF536322
microsatellite	UMNe307	18	F: ATTGTCCCTGCTCCATGAAG R: GTCCCCATGCTCTCCATG	139	2.0	58	Wagner et al. 2006	AY731383
microsatellite	UMNe308	18	F: TCTTTGTTAAAACACGTATACCACA R: TATTGTCTTGAAAGAAATCGTTGC	162	2.0	58	Wagner et al. 2006	DQ013266
microsatellite	UMNe442	18	F: TACAGGTTTTCCCATGAACAC R: ATGGATGGGCTTAGGAGGTC	170	1.5	58	Wagner et al. 2006	AY464487
microsatellite	UMNe501	18	F: CCCATGATTTAATTGTCTGCTG R: TCCAAGTTTTTCCCGAAATG	296	1.5	58	Wagner et al. 2006	AY731404
microsatellite	UMNe505	18	F: CCAGAAAGGCTGTGTTCTTACC R: TGCTGCTTTGAGAATTGTGG	~250	1.5	58	Wagner et al. 2006	AY464509
WD repeat domain 12	WDR12	18	F: GCTGTCCCTAACGTCACATAC R: TGTATCCCACAGTTTGACCAT	~ 200	1.5	63		
zinc finger E-box binding homeobox 2	ZEB2 (<i>ZFHX1B</i>)	18	F: GAATTCACAGCGGTGAGTAG R: TTGGTAGTACCACAGGTCTC	181	1.5	58	Wagner et al. 2006	DQ001126/ DQ001127

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	19STS01	19	F: GCACAGCGTACTTAAGGTAGT R: GCTAAGAGCACAGTATGTCA	467	1.5	62		BM780472
ATP-binding cassette, sub-family C, member 5	ABCC5	19	F: ATTGTATTTATTCCATATTCATGTAA R: CTGTTATTAGCACAGTGCTTAT	218	1.5	54		
ATP-binding cassette, sub-family F, member 3	ABCF3	19	F: AGAAGCTAGAGAAGGCTGAG R: TGGCTGGCTGATGCCTCTT	269	1.5	58		
abhydrolase domain containing 10	ABHD10	19	F: CTTTCCTTAGTCGACCAGAC R: ACTCCTCAATTGCCAATGCT	129	1.5	58		
alpha-2-HS-glycoprotein	AHSG	19	F: GCTGACAAAGCAAGTTCTCC R: GGTCCCTCAGGCACTTTG	260	1.5	58		BM780497
microsatellite	AHT041	19q13	F: CGGAGGACAACTTCCTCTG R: GTCCTTGAAGAAGCCTGTGC	243-255	2.0	58	Swinburne et al. 2000*	AJ271526
microsatellite	AHT052	19	F: AGTGGAACCTCCTGTTTTTCCTG R: GATCCTGGGCAATGAGGC	252-254	2.0	58	Swinburne et al. 2003	AJ507669
microsatellite	AHT055	19	F: GGGAGATATTTCTTGGCTTGC R: AATACACCCAGCTACGCACA	156	2.0	58	Swinburne et al. 2003	AJ507672
microsatellite	AHT094	19	F: CACCTCCATCACATTGGTCA R: GGCTGGAGTCAGCTGACATT	232-240	2.0	58	Swinburne et al. 2003	AJ507711
microsatellite	AHT106	19	F: GAAACGATGCCCTCGTTCTA R: GCATCAGGTACCAGGAAGGA	197-213	1.5	60	Swinburne et al. 2003	
microsatellite	ASB07	19q14-q16	F: CTGGAAATTACAGTGGTCTTCTGG R: AGGTTTTTCAGGGGCTTGCGAAGC	153	2.0	58	Breen et al. 1997*	X95322
microsatellite	ASB11	19q21-q22	F: CCACCTATGTGTTTCAGTTCACC R: GCACCAATGTTTATAGACTCCC	139	2.0	58	Breen et al. 1997*	X95326

microsatellite	ASB25	19q21-q23	F: GGAAACATTGGTACAGAGGC R: TGAACCCAACCTTCCTGCTCC	70-94	2.0	55	Irwin et al. 1998, Lear et al. 1999*	X93539
ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	19	F: GCCTCTTCTATTTCGTTCTTCAC R: GGTTTGTGTCTGCTGTTCTG	355	1.5	54		BM781440
beta-1,3-N-acetylgalactosaminyltransferase 1	B3GALNT1	19	F: CACTTCACACTTCGAGAGC R: GCATAACCTGCCAAAATGT	781	1.5	58		AY253340
butyrylcholinesterase	BCHE	19	F: TTCTCTTGCGATTTCTTCTGC R: GTCAAGGATTGTGGCTTTTTG	199	1.5	55	Perrocheau et al. 2006	DX010614
B-cell CLL/lymphoma 6	BCL6	19	F: ACAAATGCGAAACCTGCGGA R: CCACAGATTTACAGGGATAG	523	1.5	58		
calcium-sensing receptor	CASR	19q21-q22	F: GGCACAATTGGATTTGCTTT R: CTCCCAGGTGAGCAGGTATAG	377	1.5	58		
coiled-coil domain containing 80	CCDC80	19	F: AAGACGTACCAGCCCATTG R: GCCTGCATACTCATCTTCTG	233	1.5	58		CB441880
BAC end sequence	CH241-100C11_T7	19	F: GTCTGACCTCCATTTTTGTCTG R: CCATCTTCAAAGAGCATCTCAC	651	1.5	58		AJ542754
BAC end sequence	CH241-100N17_T7	19	F: CAAATTTTCCCTCTCCTTACCC R: TGCTGATAGCCTTGAACAAAC	533	1.5	56		AJ543204
microsatellite	COR044	19	F: CTGAGGCTCTCAGGAACAAG R: GTTGATGGAAAGGCCTACAA	152-190	2.0	58	Ruth et al. 1999	AF108361
microsatellite	COR092	19	F: GGCAAGAGCCAGGTATTTTC R: ACTGCTTGGACGAAACTGAG	183-199	3.0	55	Tallmadge et al. 1999b	AF154945
coproporphyrinogen oxidase	CPOX	19	F: AAGTTTGGCCTCTTCACTCC R: AGTTCTCTGAGGGTGAATGC	736	1.5	58		CK949021
discoidin, CUB and LCCL domain containing 2	DCBLD2	19	F: CTGTCTGCTTCCTTTTGCTG R: TCCCTTACTGATGACGACAC	450	1.5	58		BM781107
Filamin A interacting protein 1-like	FILIP1L (DOC1)	19	F: AAATCACAAGTCCGACCACAG R: CAAAGGTTGCCATGGTAATTG	192	1.5	55	Perrocheau et al. 2006	DX010465
fragile X mental	FXR1	19	F: ACAGTGGATGTTCTGAGGA	340	1.5	58		

retardation, autosomal homolog 1			R: ACTGTGTGGTTTCTGGATGG					
hairy and enhancer of split 1, (Drosophila)	HES1	19	F: AGCCTATCATGGAGAAAAGAC R: TGTCATTTCAGAAATGTCCG	385	1.5	60		
microsatellite	HMS08	19	F: GGTGAGGAATTATCTCTTTGAAGG R: GCAGGTAGGATTGGATAGGTACAT	207-215	2.0	58	Guérin et al. 1994	X74637
HRAS-like suppressor	HRASLS	19	F: GTATTCAGCAGAAAGGCCCT R: CCTTCTCCATAGCGAAGCAAA	218	1.5	60		
histidine-rich glycoprotein	HRG	19	F: TCCAGGTAAACGACACTTTCC R: ACATTGGTCAGAGGCTGATTG	187	1.5	55	Perrocheau et al. 2006	DX010508
microsatellite	HTG23	19	F: GTCCTTCAGAGTTGTCCCTG R: GGAGAACAACCTTGCCTGAG	191-199	2.0	58	Lindgren 2000	
microsatellite	HTG24	19	F: CTCAGGGCTAATCTTCCTCA R: TGTAATTTCTCCTATGGAAGCA	180	2.0	60	Lindgren 2000	
interleukin 1 receptor accessory protein	IL1RAP	19	F: CGATGACTGGGGACTAGATA R: CTCCTTACTAATGCGGTTCT	214	1.5	62		CB446872
IQ motif containing G	IQCG	19	F: TGAGGAGAAGCTAGAGTTCTGGA R: GCAAGTTCTTGAAGGTGTGCT	120	1.5	55	Perrocheau et al. 2005	AY817463
kininogen 1	KNG1 (KNG)	19	F: ACCTAAGGCCCTGCGAGTATGT R: AGACAGAACTTTATTTACCCAGCAA	226	4.0	58	Milenkovic et al. 2002*	
lysosomal- associated membrane protein 3	LAMP3	19	F: GTATAGGCTGATGAGGTGGTG R: CCCTGGTAACTACAAACAGCA	178	1.5	58	Pascual et al. 2002	BI395182
microsatellite	LEX035	19	F: CCCAGCATATCAAAGATGTT R: GCTCAGTGACTTCAAGCAG	247-275	3.0	58	Coogle et al. 1997	AF075637
microsatellite	LEX036	19	F: CCCAGCCTCTTCAATATCCA R: CCCTAAGGGGATTTAGCAGTT	190	3.0	58	Coogle et al. 1997	AF075638
microsatellite	LEX040	19	F: TTTGGCCGTTAGTCGTGT R: GACAAATCGGAAAGTTGGAA	130-136	4.0	50	Coogle et al. 1997	AF075642

microsatellite	LEX073	19	F: CCAGCCATCCACTGGTAGAG R: GGGAAAAGGGGAACCTTCTA	218	2.0	58	Bailey et al. 1999	AF213359
microsatellite	MPZ003	19	F: CCTAGAGTCCATCCTTGCATC R: TTGTGGGAGCTGTTTTCTTCTTGG	170	2.0	58	Breen et al. 1994	Z29484
myoneurin	MYNN	19	F: AGGAAGCATAGTGGAGAGAAGC R: TAGAGACAGCAAATGCCTTCC	148	1.5	55	Perrocheau et al. 2006	DX010532
N-acetylated alpha-linked acidic dipeptidase-like 2	NAALADL2	19	F: CATCATCAAACAAAAAGCAGC R: CTGTCTCACCAACAGAGAAAC	299	1.5	60		AJ542929
microsatellite	NVHEQ011	19	F: GGCCCCACCCACTAAATATCACTG R: CGGGGTCTTGGAATTTATGAAGG	118-128	2.0	58	Røed et al. 1997	AF011403
poly (ADP-ribose) polymerase family, member 15	PARP15	19	F: CCACATGGACACCAAGAATG R: CCACAAATAGCTTTGGATGC	~200	1.5	62		BI961550
protein S (alpha)	PROS1	19q25	F: TCGGATAVAGGCCHTAAGTCT R: CTGGAAGGCCACCCAGGTAWG	208	1.5	62	Milenkovic et al. 2002*; Ward et al. 2003	AY301023
schwannomin interacting protein 1	SCHIP1	19	F: CTGATAGAGACACTACTGAAG R: CTACTTGCATTTTGGCCATTG	132	1.5	60		
sorting nexin 4	SNX4	19q21	F: CTTAACCTCAGTGATGAGCC R: GTGCTTGGCTTCTGAACATA	200	1.5	56		
TBC1 domain family, member 23	TBC1D23	19	F: GAGAAGGCAGCAGAATTACTTT R: CAGTTGTATAAATCGCTGCGT	152	1.5	58		
transducin (beta)-like 1X-linked receptor 1	TBL1XR1	19	F: TTTCTGGATGATAGAAATCAATGC R: TCATTCAGCGTTTACCTTTGG	100	1.5	55	Perrocheau et al. 2006	DX010593
microsatellite	TKY004	19q21	F: TCTGTGTATGTGAGTGTATA R: GATCGAGGTATTCCTGAGTG	87	2.0	55	Hirota et al. 1997, Hirota et al. 2001*	AB048315
microsatellite	TKY009	19q23	F: CAGTGATTTTCTCTCCTCC R: AAAATGCTGACCTGTAGGCA	103	2.0	58	Hirota et al. 1997, Hirota et al. 2001*	AB048320

microsatellite	TKY372	19	F: CATCTAACTCCATTTCCCAG R: TATCTAAAGCCCCATGCTAG	142-154	1.5	54	Tozaki et al, 2001	
microsatellite	TKY419	19	F: CTGGAACCAAAATGGGTCACG R: AATGACACTCGTGAGGTGAG	258	2.0	58		AB103637
microsatellite	TKY422	19	F: CAAATCTTCAGACTCTTTAGTCCTTG R: GACTGCAGCCCTAACCTCAC	234-256	1.5	58	Tozaki et al. 2004	AB103640
microsatellite	TKY444	19	F: TCCTCAGCCCATTCAAATCT R: ATCAACCCACTGGCCAATAA	134-152	1.5	58	Tozaki et al. 2004	
microsatellite	TKY448	19	F: TTCTTTTGCTCTCCCTCTCG R: GGAAAGACAGAGTAAGTGCGTGT	140-162	1.5	58	Tozaki et al. 2004	AB103666
microsatellite	TKY510	19	F: AAAGAATGGAGGATTGGCAG R: AGGAGGGGAAGTGTTTATTC	170	2.0	58		AB103728
microsatellite	TKY538	19	F: TGGATGGAAGGGAAACAAGA R: TTGAAGAGGGTGGAGCAAAT	151-165	1.5	58	Tozaki et al. 2004	AB103756
microsatellite	TKY606	19	F: ACATGCCAACTCACCACTG R: TTCATCCTACGAGGGCTCAG	108-114	1.5	58	Tozaki et al. 2004	
microsatellite	TKY679	19	F: GCATATTCCAAATAACGGTG R: AGAGCCACTTTATCAGTTG	179	2.0	58		AB103897
microsatellite	TKY686	19	F: TTGATCCAGCCCCTTCATAG R: TTGGGTCTCCGTGTTACTCC	284-286	1.5	58	Tozaki et al. 2004	
microsatellite	TKY713	19	F: TATCTTCCTTCCCTGAGTAG R: CCCAAGGCTAACTTACTTAG	112	2.0	58		AB103931
microsatellite	TKY730	19	F: CTCCTTGAGTAACAGTCAC R: GACCTTATCAGTGCCCTTG	278	2.0	58		AB103948
microsatellite	TKY738	19	F: CCCGCAAATACACCACTGT R: GGGTCCTTTCAGCCTCATCT	209-223	1.5	58	Tozaki et al. 2004	
microsatellite	TKY783	19	F: TAGACAACTGACCAGTGCAA R: CTGGTTGCTCCTGTCTTAAA	149	2.0	58	Tozaki et al. 2004	AB104001
microsatellite	TKY817	19	F: TATAAACAAGGGCAGAGCGA R: GAGTGAATTCCCTGCTTCTC	155	2.0	58	Tozaki et al. 2004	AB104035
microsatellite	TKY992	19	F: TCTGAACTGTTGGCTTACTC R: TAGCTAGTATGTGGCAGAAC	101	2.0	58		AB104210

microsatellite	TKY1038	19	F: GGCAGTCTTGCATTCTCTG R: TTTCTGGGTGTAGAACCAAG	249	2.0	58		AB104256
microsatellite	TKY1132	19	F: CCTCTCAAACTCGGTGTC R: GTTTCCCCTTAACTCCATAC	259	2.0	58		AB104350
translocation protein 1	TLOC1	19	F: TGGAAGGTGATGGCTCTTCT R: TGTGCCTCCTGGTCTGATAA	388	2.0	55		
microsatellite	UMNe071	19	F: GGAAATTTGGGAGACAGTATGC R: GGCAGAATTGTGACTAGAACCC	142	1.5	58		AF191704
microsatellite	UMNe083	19	F: AGCTCCTGAAAGAAGAGAGCC R: TGGAACCCAGTAACATGAAGC	300	1.5	58	Wagner et al. 2004c	AY735234
microsatellite	UMNe098	19	F: AGGGGAAATTTGGGAGACAG R: AAGCGTACAGCCAGTTTTGG	165	1.5	58		
microsatellite	UMNe106	19	F: AATCCTGTGAGGCAGGAGTG R: TGTCTGGGCATCTCTTAGGG	200	1.5	58	Wagner et al. 2004a	AY391292
microsatellite	UMNe221	19	F: AGACCTTGAGAAGCTCTTGCC R: CCCTAGAGTCCCATCCTTGC	188	2.0	58	Wagner et al. 2004c	AY735239
microsatellite	UMNe319	19	F: TTCGTGCAATCTGTTGCTTC R: GATCACAGTCCCTGGTACTGG	154	2.0	58	Wagner et al. 2004a	AY391337
microsatellite	UMNe324	19q24- q25	F: TTCCTCAGCAAGAAGAGGGA R: TTCAAAGTCCTTATGAGAATTCCC	143	2.0	58		
microsatellite	UMNe325	19	F: GCGAGGTAGGAGTTCTCCG R: GATCCAGCCGTGTTTTGG	192	2.0	60		
microsatellite	UMNe351	19	F: TGAGAAGCTCTTGCCAATCC R: TAGAGGCCATTTTTGCATCC	150	2.0	58	Wagner et al. 2004a	AY391344
microsatellite	UMNe440	19	F: CCTTCATGGAAGTACAATCTG R: GCCAACCTGAAAGGAGGAG	387	1.5	58	Wagner et al. 2004b	AY464486

microsatellite	UMNe500	19	F: CAGCCATCATGGACAATGAG R: CAAGTCTGGTTCCTTTTGTGC	300	1.5	55	Wagner et al. 2004b	AY464508
microsatellite	UMNe590	19	F: GGGAGATATTTCTTGGCTTGC R: TGAAAATACACCCAGCTACGC	156	1.5	58	Wagner et al. 2004c	AY735286
microsatellite	UMNe592	19	F: TCCAAACTGTGTGTGTGTTTGT R: TGCACATAGAACAGGGCAAG	163	1.5	58	Wagner et al. 2004c	AY735288
microsatellite	UMNe599	19	F: AGTCCATCCTTGCATCCAAG R: AGACCTTGAGAAGCTCTTGCC	184	1.5	58	Wagner et al. 2004c	AY735291
uridine monophosphate synthetase	UMPS	19q21	F: CTAAACGGCTTATAGAAGGGG R: CTTACAGAAGGGAGAGAATC	300	2.0	50		
microsatellite	VHL011	19	F: CGGCACCAGGTCATCACCACG R: GAGTCGGGGCTTTGTTTGACAG	110	1.5	62	van Haeringen et al. 1998	
zinc finger and BTB domain containing 11	ZBTB11	19	F: GGAGATGCCACATTTCTCTCCTC R: AATTGTAGGTCAGCCACACAGCTAC	316	4.0	60	Chowdhary et al. 2003	
zinc finger, matrin type 3	ZMAT3	19	F: CATCTGTGTATGCTGTTGGGGC R: TGAGCCATCAACATAAGCAGGG	211	3.0	55		AF201736, G62159
zinc finger protein 148	ZNF148	19	F: ATGGAAAGGCATAAGAGAACC R: ATACACGATCTGTTCTGGAAA	290	1.5	58		
microsatellite	ZuBeEq9	19	F: CCATAATTCTTTCCCTCCA R: TCTGAGTGCCACAGCAAGTC	224	1.5	63-55	Klukowska-Rotzler et al. 2006	CR957324

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	20STS01	20	F: GAGGCAGCTGTGTTTCCTCAT R: AAAAGCAGGCAGTGGAAAGA	110	1.5	60		
activator of basal transcription 1	ABT1	20	F: ATCTTGCCCTTTGAGCGTCAG R: CAAAGGCCCAAGAGCTATCC	159	1.5	58		
microsatellite	AHT018	20	F: TTTTCCAGTGACTCTGAGTGTG R: GTTGTGGGAAAAGTCTGCTGGC	168-178	2.0	58	Swinburne et al. 1997	
microsatellite	AHT109	20	F: AGCAGAGCTAAAAATGAGGCC R: TTGGCTGAGTTTTTGTCTTTTG	163-187	1.5	56	Swinburne et al. 2003	
microsatellite	AHT111	20	F: CAGCCCATGGATAGCCAG R: TGCTGCAAGATAAATGCCTG	268	1.5	61		
HLA-B associated transcript 3	BAT3	20	F: AGAGTCAAACATCATTAAGCTGG R: TGGCAAAGAGACCAACAAAG	129	1.5	58		
bone morphogenetic protein 6	BMP6	20q14 ^a	F: CAGAGATGGCCCTTATGACAA R: GATTGCGACTCTGCTGTCTG	116	1.5	55	Perrocheau et al. 2006	DX010441
biphenyl hydrolase-like	BPHL	20	F: GATTTTGGACCCCAGATTAAG R: CATCCTTTGCATCCCTTTC	136	1.5	59		
chromosome 6 open reading frame 62	C6orf62	20	F: GATCTCTTTCCCCAAGTTG R: CTATCATGGTTTCTGCAGC	146	1.5	58		
cyclin D3	CCND3	20	F: TTCCTCTTTGCTTTGCTTTCC R: TCATCCCTGTTTCATCCCCC	293	1.5	58		
BAC end sequence	CH241-100D3_SP6	20	F: CTGGTGCCAGTTTGTTTG R: ACACAGAAGGAGGGCTTG	256	1.5	58		AJ542823
BAC end sequence	CH241-100D3_T7	20	F: GCCTTTCAAGTCCTCTGG R: TGGCAGCAGTTAGCTCAG	208	1.5	60		AJ542824
BAC end sequence	CH241-100F12_SP6	20	F: AGAACTTCCCAGCCATTG R: CAGGTGGGTGTCAGAATG	287	1.5	61		AJ542881
BAC end sequence	CH241-100H23_T7	20	F: TTTCTGACTGCCTACAGAGC R: AAGGCAGAACACTCTGAAAGTC	172	1.5	60		AJ542975
BAC end sequence	CH241-101E21_T7	20	F: CACGCTCAACAGAGAAGCAG R: TCAGGCCCATCGTTTCTTAC	218	1.5	60		AJ576619
BAC end sequence	CH241-101H13_SP6	20	F: GATGGAGCTCTGGAAGCAAC R: GAAATGACCATGGGAAATGG	227	1.5	60		AJ576722
BAC end sequence	CH241-101K12_T7	20	F: CCCAACAGAGCTGGAATTTG R: ATCACTCCGACTGGGTTGTC	162	1.5	60		AJ576843

BAC end sequence	CH241-101N2_SP6	20	F: TCCATTTTCCTATGCCTGTC R: GTCCCTGCCCTAGAATTG	201	1.5	59		AJ576997
BAC end sequence	CH241-102A12_T7	20	F: TGGCTGGCAGATTACTTGTG R: AGATGCTCGTGGGAAAACAC	196	1.5	60		AJ583942
BAC end sequence	CH241-102E20_T7	20	F: AAGCTACCCTACCACCAAC R: ACCTGCTCCTTCTTGTGC	264	1.5	60		AJ584133
BAC end sequence	CH241-102G5_SP6	20	F: GATTTCTGTCCGGATTGC R: TGGTTAGGCCAGGAAGTC	272	1.5	59		AJ584229
BAC end sequence	CH241-102I4_SP6	20	F: CCATTTACTAACGGATGCTG R: TTTTCTGTGGAAGAACATGC	216	1.5	60		AJ584316
BAC end sequence	CH241-103M18_T7	20	F: GAACGCAGGCTTTAGGTGTC R: CTCACCTGTACTGCCAAGTCC	160	1.5	60		AJ618884
colipase, pancreatic	CLPS	20	F: AAACAGAGGCTCCCCAGAGT R: AGTGTCTGCAGAGGCACAGA	200	2.0	58		AF097592
cytidine monophosphate-N-acetylneuraminic acid hydroxylase	CMAH	20	F: TCCAAGGGAAAAGAGAGAGAAA R: ATGATCCTGGAGTGGAATCAA	148	1.5	58		
collagen, type IX, alpha 1	COL9A1	20q24	F: TGGAAAATGCCTGCTTTCTA R: TAATGCAGTTGATCCCACGA	200	2.0	58	Godard et al. 1998; Caetano et al. 1999*	AF130755
collagen, type XIX, alpha 1	COL19A1	20	F: CTGTAGTCGTTGATGGTGGAA R: ACAAGAGACGGAGTTCTCGAT	106	1.5	59		
microsatellite	COR029	20	F: CTAGAAGGGTTTCCCAAAGG R: TCGAGCTCCTGAAGAACATC	222-228	3.0	58	Murphie et al. 1999	AF101398
microsatellite	COR050	20	F: TCTGTTGCCTTTATCCACAA R: ATGAAAACCCTGGGAATAGC	283-297	1.5	58	Ruth et al. 1999	AF108367
cysteine-rich secretory protein 1	CRISP1	20q22	F: CCCCAATCACAGAATATCC R: TCAGCTAGCCTAGAATCTG	891	1.5	58		ECA315379
cysteine-rich secretory protein 2	CRISP2	20q22	F: ATCAGTGAGCTCAACTAAGAC R: TGGGCCTACTATACTTTGTTG	1135	1.5	58		ECA459963
cysteine-rich secretory protein 3	CRISP3 (SGP28)	20q22	F: TGTGGCAAGTAAGAATAAGG R: ATCCTGACTACTTTCAACAC	1417	1.5	58	Chowdhary et al. 2003*	ECA459964
endothelin 1	EDN1	20	F: TGCCAAGCAGGAAAAGAACT R: TTCCAGCCTTTCTCCATAGTG	209	2.0	58	Caetano et al. 1999	AF130760
major histocompatibility	ELA-A	20	F: GACTTCTCTTTCTGCAGCTGG	193	1.5	65	Bailey et al.	BI961794

complex, class I, A major histocompatibility complex, class II, DM alpha	ELA-DMA	20	R: CACGAAGTTAAGACAGGGAGG F: TTTGTCTCCGCGGTTGATGG R: CCAAGCCAACAATGATGCCC	450	1.5	57	1979 Chowdhary et al. 2003	
major histocompatibility complex, class II, DO beta	ELA-DOB	20	F: TTGTGATTCAGGCAAAGGCTG R: TGTTCCACTGCTCAGCATCTGG	175	1.5	55	Chowdhary et al. 2003	
major histocompatibility complex, class II, DQ alpha 1	ELA-DQA	20	F: CGACTCAGATGACCACATTG R: GGGGACACATACTGTTGGTAG	260	1.5	57	Chowdhary et al. 2003	AF115329, U92522
exocyst complex component 2	EXOC2	20	F: GTGATTTCCCCCATAACCC R: CTCCTTCAGAGTCAGTTTCCC	259	1.5	58		
FK506 binding protein 5	FKBP5	20	F: TTTTCCTTGCAGGTGTGACTC R: AGTGAATGTTTCCTTGCGTTG	273	1.5	58		CD470964
glutamate-cysteine ligase, catalytic subunit	GCLC	20	F: ATGAGCATCAACACCATCATC R: GTGTCCACATCCACTTCCAT	180	2.0	62		DN507482
guanosine monophosphate reductase	GMPR	20	F: CACGGACAAGTTTACGAAT R: TGGAAAAGATGAGCAGCATAAC	130	1.5	59		
glycosylphosphatidylinositol specific phospholipase D1	GPLD1	20	F: TTGCTTCTTACCCTGCCAAG R: GGTGGCCCCTCATTTTATTT	250	1.5	60		
glutathione S-transferase A1	GSTA1	20	F: TCAAGTTTTGATAAAGCAGG R: GTTTCCTTAGTGTACAACTACTC	118	1.5	60	Milenkovic et al. 2002	
microsatellite	HMS04	20	F: GCAAACAACGTGCAATAGAT R: AATTCATCCCAATTGGCTGG	106-112	3.0	58	Chowdhary et al. 2003	X74633
microsatellite	HMS42	20q24	F: TAGATTTCTTAAGTGCCAATAGTGG R: GAACTGCTATAGATATACCTAACTC	135	2.0	65	Godard et al. 1998*	
heat shock protein 90kDa alpha (cytosolic), class B member 1	HSP90AB1	20	F: CTACTTGCAGACCAGTGTCC R: CACAATACACAACATCCAAACC	195	1.5	58		
heat shock 70kDa protein 1A	HSPA1A	20	F: TGAGGCATACCAGACCCAAG R: AAAGCAAAAAACAGGACAGAGG	251	1.5	60		
microsatellite	HTG05	20	F: TGCTAAGCCTCAGCACATACA R: TGGAAATAAGGTTAGCAGGGATGC	79-95	3.0	58	Ellegren et al. 1992	AF169166
intestinal cell (MAK-	ICK	20	F: GAGAGCCCTAACCTAAAATCAG	425	1.5	58		

like) kinase			R: CGCCAAGAGTATGGTATTAC					
inositol 1,4,5- triphosphate receptor, type 3	ITPR3	20q21.2 ^a	F: CCGTGCTCAGATCTGCTGTAGA R: GGCCAAAGGATGTGTAAAACTTTAC	246	1.5	60		G62183
potassium channel, subfamily K, member 16	KCNK16	20	F: TGCTGTGACGGAGTCTATTG R: TTTGCTTCCACAGGCATCTAC	100	1.5	58		
kinesin family member 13A	KIF13A	20	F: AGACTCGGCCATGTATAAAAG R: GTTCCAACTTAGCATTCTTCC	148	1.5	58		
microsatellite	LEX011	20	F: ATTCCCAGTGAAGTATTGCCA R: AGAGATGGGTACCTGGGATTC	242-244	2.0	58	Coogle et al. 1996	AF075614
microsatellite	LEX052	20	F: GGAACGGAAGAGTGTAGTTTT R: CATTTATTTCATCAGCGATTG	196-225	2.0	58	Coogle & Bailey 1997	AF075654
microsatellite	LEX064	20	F: ACCCTTTCCGCAGACAA R: CACATCAGAGCCCATCTTCTC	197-209	2.0	58	Coogle & Bailey 1999	
microsatellite	LEX071/072	20	F: CTTTATTCTACTCTTTGGTCC R: CCGATATTTCACTGATTATT	185-204	3.0	55	Bailey et al. 2000	AF213358
mutS homolog 5 (E. coli)	MSH5	20	F: AGTGTTGGGTGTGCAGATGG R: ATCGAAAGTAGGGCTCCTCC	133	1.5	58		
methylmalonyl Coenzyme A mutase	MUT	20q21	F: CCATTCAAGTGCTTGATGATAT R: CATCACACTTATAACATGACAACA	228	1.5	60	Lear et al. 2001*	G62188
nucleolar protein 7	NOL7	20	F: AGGCAGAAGCGAGAGAAG R: GGGACAAAGGGGGACAAG	133	1.5	58		
neuritin 1	NRN1	20	F: TTCAAGAGAGATGTCCACGAG R: CCTTGTGATCTATACCGTTGG	359	1.5	58		DN509784
nucleoporin	NUP153	20	F: AAGCAATCCAGCTCCTTTAGC R: CTGTGGTTCCAAAACCTGAAGC	197	1.5	55	Perrocheau et al. 2006	DX010542
microsatellite	NVHEQ005	20	F: GGCATGTGCTTCCCCTCAC R: CCTCTTTCCACGCAATCACTCTA	151-155	1.5	58	Røed et al. 1997	AF011401
microsatellite	NVHEQ021	20	F: CCAGAACCTGGACTGAACAGTGTC R: GAATGTGCTTGATGCAGAAGAAGG	151-161	2.0	58	Bjornstad et al. 2000	AJ245762
protein kinase C and casein kinase substrate in neurons 1	PACIN1	20	F: CTATAGGGCAGTGGGGGAAT R: ACAGGCTGCTGGATAGCACT	145	1.5	60		
PHD finger protein 1	PHF1	20	F: GTGGGGTCGGTTACCTGTC R: CAGGTACATCCCAGCTGTAGG	202	1.5	55	Perrocheau et al. 2006	DX010556
pim-1 oncogene	PIM1	20q21.3 ^a	F: TTTGTCGTCCATCTCCATCC R: CCTCCCAGGGGTTAGAAAAC	210	1.5	60		

prolactin	PRL	20	F: CAACTGCTAAGCCCACATCC R: GATGAGACCCATTACACCCAAG	122	1.5	58		
peripherin 2 (retinal degeneration, slow)	PRPH2 (RDS)	20	F: TGTCTGCGTCCTCTTCAACA R: ATTGTTGCCACAGCATTTGA	199	1.5	55	Shubitowski et al. 2001	AY008808
run-related transcription factor 2	RUNX2 (CBFA1)	20q21.3	F: TCTTACCCCTCCTACCTGAGC R: ACGTCGGTGATGACAGGAA	101	1.5	55	Perrocheau et al. 2006*	DX010447
serpin peptidase inhibitor, clade B (ovalbumin), member 1	SERPINB1	20	F: TGGACCAAACCTGAGAATCTG R: TCCTCATTCAGGTCCACAAAG	215	1.5	55	Perrocheau et al. 2005	AY817484
serpin peptidase inhibitor, clade B (ovalbumin), member 9	SERPINB9	20	F: TTAGCCACCTGGTGATACCC R: ACCAGACAATGGAAGGCAAG	228	1.5	60		M91161
solute carrier family 17 (sodium phosphate), member 2	SLC17A2	20	F: TCTATGCTGCCTACTACATCC R: CACTTGAATTACACCAGTCTCC	268	1.5	58		
SFRS protein kinase 1	SRPK1	20	F: CTAGACTTGCGCTAGACATTAC R: GCACCACTTTTTCCTTTGCC	292	1.5	58		
signal sequence receptor, alpha	SSR1	20	F: AGATAACGCCATTACCGCCGGA R: AACACGAGCAGGAGAAGCAGAA	116	1.5	58		
transcription factor AP-2 alpha	TFAP2A	20	F: TGCCCTGGAAAGCAATGTAT R: CTCGCTCCTCTCCCTCTCTC	180	1.5	60		
microsatellite	TKY008	20q21.1	F: TTCAC TTGTGCATGAAGCTG R: GTTCCCAATGTGTGAGGAAT	148	4.0	55	Hirota et al. 1997, Hirota et al. 2001*	AB048319
microsatellite	TKY273	20	F: GATCACTGGCGAGGGTAAGC R: TATGTTCCCGATTTCGCAAGC	174-194	2.0	58	Tozaki et al. 2000	AB033924
microsatellite	TKY321	20	F: CACTGTGTAACTAACACC R: TGTGACTTCAAGAAGACGACG	96-120	1.5	58	Tozaki et al. 2000c	AB034629
microsatellite	TKY477	20	F: CCCCTCTCTCTCTCAAGTGC R: CTCCTGGGTGGGAGAACTTT	108-134	1.5	58	Tozaki et al. 2004	AB103695
microsatellite	TKY507	20	F: CACCTGCCTACAGTCCAAGC R: TTTGTGCTTAATGCCTTTGTG	129-141	1.5	55	Tozaki et al. 2004	AB103725
microsatellite	TKY539	20	F: GCTTTACGGCATTAACACA R: ATTGATGGTGGCAAGGAGTC	192-206	1.5	58	Tozaki et al. 2004	AB103757
microsatellite	TKY547	20	F: TTGCTCAGGAAGCAAAGGAT R: AAAATGAGGCTTTTCGCACAT	224-238	1.5	58	Tozaki et al. 2004	AB103765
microsatellite	TKY649	20	F: AGGGGATAAATTCCCTCACC	208-214	1.5	58	Tozaki et al.	AB103867

microsatellite	TKY666	20	R: CACGTCCTGCAAATTTCTGT F: TACCTGAGGGTTACTGTATG	132	2.0	58	2004	AB103884
microsatellite	TKY694	20	R: AGTTGCATTGTTAGAAGCCA F: CCGCACAGACTTCACAAAGA	91-111	1.5	50	Tozaki et al. 2004	
microsatellite	TKY821	20	R: ACACACCCATGAACCCACTT F: ATTCACTCTACTAGGCCTG	111	2.0	58	Tozaki et al. 2004	AB104039
microsatellite	TKY848	20	R: AGACTGGGGAAGTTGAGTG F: AGAGGCACTCACAAC TAGAA	249	2.0	58		AB104066
microsatellite	TKY912	20	R: TTTCTCATCTCACAGATGGC F: TCTGTGGTGCTTTGTATGG	288	2.0	58		AB104130
microsatellite	TKY925	20	R: AGTCACCACTTCATGAACTC F: AGCAAGATTGGCAACAGATG	114	2.0	58		AB104143
microsatellite	TKY940	20	R: TCTGCCATTTTCAGAGAGTTAG F: TAGATATCAAGAGAGCCAGG	122	2.0	58		AB104158
microsatellite	TKY995	20	R: AGGTCAGGTAGGGTGCAAG F: TTTAGTGAACATCTGCCGTG	273	2.0	58		AB104213
microsatellite	TKY1024	20	R: CAGCTGGCAAGTTTCTTTAATG F: AACACATATTTGGAAAAGGCAC	97	2.0	58		AB104242
microsatellite	TKY1040	20	R: TGATTCTCTGGAGTTAGTG F: TAGAAAGTAGGGGAAGATGG	217	2.0	58		AB104258
microsatellite	TKY1070	20	R: TTCTGGTTTCCCTGAATGAG F: CAGTCTTCCTCAGCAAAGAG	154	2.0	58		AB104288
microsatellite	TKY1115	20	R: CTCTTTCCCTTCTGGACTTC F: GAATACACACGGGTAGGTTG	252	2.0	58	Tozaki et al. 2004	AB104333
microsatellite	TKY1116	20	R: ATGGCAGCCTACAGTAAAAG F: ACGCTAGTATGAAGGTCAAC	254	2.0	58		AB104334
microsatellite	TKY1405	20	R: GTGATTACCATGAGGTTTCGT F: GGACAGCATTTCTAAGAGAG	109	1.5	58	Tozaki et al. 2007	AB215348
microsatellite	TKY1517	20	R: TGGCCAGAGAAAACGTCTC F: TAAAAGTGTGGGCATGTATG	176	1.5	58	Tozaki et al. 2007	AB215460
microsatellite	TKY1798	20	R: CAAAACAACAACCTCAGAGC F: GGCTTTTGGTTGGTTAGTAC	180	1.5	58	Tozaki et al. 2007	AB215741
microsatellite	TKY2230	20	R: CCATGTGGCTTAGATATCTG F: GATCAAGACATGCGGTATAG	237	1.5	58	Tozaki et al. 2007	AB216173
microsatellite	TKY2258	20	R: CTAAATGGGTACTGGAGTC F: CCAATGAGAGGGAGAGAATG	157	1.5	58	Tozaki et al. 2007	AB216201
			R: TGCTCTGAGTGTAAGCCGT					

microsatellite	TKY2503	20	F: ACCATAAGGGGGCAATTTAG R: AGCCCTGGAAAAATGAGAGT	213	1.5	60	Tozaki et al. 2007	AB216446
microsatellite	TKY3403	20	F: TTGGACGAGTATCAATTTGC R: CACCAATGGGAAAAGAAATGA	120	1.5	56	Tozaki et al. 2007	AB217346
tumor necrosis factor	TNF	20q16- 21.1	F: CTTCTCGAACCCCAAGTGAC R: GAGACAGCTAAGCGGCTGAT	548	1.5	58		
tumor necrosis factor receptor superfamily, member 21	TNFRSF21	20	F: CTTTCTCCAACGGGTACACA R: ATCAGTCCACGAATCTTCTCC	154	1.5	59		CX600724
triggering receptor expressed on myeloid cells 1	TREM1	20	F: CTGGTCCTTACTGTCCTGTTTGC R: CTGCCAGATGGATGTAGATGGAG	104	1.5	62		BI961625
tripartite motif- containing 27	TRIM27	20	F: TTGAAGGAGCATGAGTATCG R: GATGTTGCAGGAGAACTGTGT	102	1.5	58		CX603302
ubiquitin protein ligase E3 component n- recognin 2	UBR2	20	F: CCAGGGACACCCTCTTCTAAC R: ATTTTGGCCTTTGTACATCC	209	1.5	58		BM780968
microsatellite	UM011	20	F: TGAAAGTAGAAAGGGATGTGG R: TCTCAGAGCAGAAGTCCCTG	150-180	3.0	58	Meyer et al. 1997	AF195130
microsatellite	UM013	20	F: TGCCACATTTGCCCTGGTT R: ACTGAAACACACCTCCTCTCCG	190	2.0	58		AF195132
microsatellite	UMNe056	20	F: TCTGTCTGCAGCTAAAGAGGC R: GCGGGGTACATAAAGACTGTAGC	193-201	2.0	58	Roberts et al. 2000	AF191692
microsatellite	UMNe064	20	F: TTGCTTTTCTTCTACACTCCC R: TTGACCTAAAGCTCAATGTGTG	145-147	2.0	58	Roberts et al. 2000	AF191697
microsatellite	UMNe065	20	F: TCCTTCCACTCCCCTCAAC R: TCCCTGAAAAACCTTGGTTG	126-146	2.0	58	Roberts et al. 2000	AF191698
microsatellite	UMNe067	20	F: TCCTTACCCCTTTGGAGATG R: CAATGGTGTGCTCCATGAAG	171-175	2.0	58	Roberts et al. 2000	AF191700
microsatellite	UMNe094	20	F: TCTCCTCACCTTTGCTCAC R: GGGCGGGGTACATAAAGACTG	173	1.5	58		
microsatellite	UMNe119	20	F: GTTTTCATTCTGACGTTGATG R: AATCCCTAGGAAGACAGGAGAC	109	1.5	58	Mickelson et al. 2003	AF536253
microsatellite	UMNe151	20	F: CATTTCAAGGGCTACTTTGACC R: CATACGTTTTGCACCCTCTC	151	1.5	58	Mickelson et al. 2003	AF536264
microsatellite	UMNe170	20	F: GGGTGTTAAGAATCCTGCTCC R: CTAGGCAAACCTACTGACCCCC	138	2.0	58	Wagner et al. 2004a	AY391309

microsatellite	UMNe214	20	F: TCCTTCCACTCCCCCTCAAC R: TCTCTCTGGCCATCTGGC	165	2.0	55		
microsatellite	UMNe225	20	F: GATCTCTTGCTGTGTGTTTGTG R: TCAATTTTCAACAAGATGGAAACG	154	2.0	55	Wagner et al. 2004a	AY391322
microsatellite	UMNe272	20	F: AATACTGCCAGTGCCATTGC R: AAGGCTAAGAAGGATGGAATCC	172	2.0	58		
microsatellite	UMNe274	20	F: CAGTGTACAGAGTTAGGATGCACA R: TTCACAAAAGATGTATGAAGTCACA	139	2.0	58		
microsatellite	UMNe301	20	F: TTTTGGGGTCCAGAATAAACC R: TAGACAACCAAATGCCAAAGG	140	2.0	58	Wagner et al. 2004a	AY391332
microsatellite	UMNe304	20	F: AGATGGGCATGGATGTTAGC R: GGTTCCTGAATGAGAACG	199	2.0	58		
microsatellite	UMNe341	20	F: TCCAACTTTTTGCATATGTTGC R: ACGTTTGAACCTCAATCCAACC	223	2.0	58	Mickelson et al. 2004	AY731387
microsatellite	UMNe380	20	F: TTCCACATATACGTGTGTGTATGG R: AGTACCAGGAATAAGAAATGGGC	154	2.0	58	Wagner et al. 2004b	AY464471
microsatellite	UMNe418	20	F: CCCTTAACAACCACCCCC R: TTGGGAGACAGGACTTACCG	200	2.0	58	Wagner et al. 2004b	AY464484
microsatellite	UMNe428	20	F: AGGTCCCTCTCAACTCTATCCC R: TACACTAGCGTATAAGGGCACG	152	1.5	58	Wagner et al. 2004c	AY735248
microsatellite	UMNe456	20	F: TAACCTCCCAGGTCCAACCTG R: TCGTCAGCACTTACAATGACG	274	1.5	60		
microsatellite	UMNe480	20	F: CCACTGGTAAACGTCCCCG R: TTTCTGGAAATTTTGCCAGG	200	1.5	55	Wagner et al. 2004b	AY464498
microsatellite	UMNe484	20	F: GGGGAGCATTATCTGATACAGC R: AGGCTTAGAAAATTGAAAGGGG	250	1.5	55	Wagner et al. 2004b	AY464501
microsatellite	UMNe494	20	F: GCTCTTGGGAATTGTTGGTG R: CCAAGAAACATTTGGGATGG	150	1.5	55	Wagner et al. 2004b	AY464505
vascular endothelial growth factor A	VEGF	20q21.3	F: ACGTCTACGCGCAGCTACT R: TGCATGGTGATGTTGAACTCC	181	1.5	55	Perrocheau et al. 2006*	DX010658
Werner helicase interacting protein 1	WRNIP1	20q13- q14	F: GCCGTTTCGTTGTTTTAGG R: CAAAGCTGCCGGATATTTTC	218	1.5	58		CD528438

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	21CA001	21	F: TCATGCTGAAATCAATGCAAA R: TTCCTTATGGCAACAACACG	295-311	1.5	58		AY820151
sequence tagged site	21STS01	21	F: CGTGACAATCGTGTGGTG R: TTCGGTCATGGTCTGGATG	~800	55	1.5	Goh et al. 2007	
sequence tagged site	21STS02	21	F: AGAGTTGTCGGGGATTTTGT R: TTTGGAAGCAGTTTTAATGGAGA	195	1.5	55	Perrocheau et al. 2006	DX010651
ADAM metalloproteinase with thrombospondin type 1 motif, 6	ADAMTS6	21q14	F: GCCTAGGAAATTTGATGTTGCT R: AGCACAAGTAGCTGAGCATTCT	635	1.5	58	Goh et al. 2007*	
adenylate cyclase 2	ADCY2	21	F: GAAGACCACGTGGCATTTTT R: CGAAACACATGAACAAGTAGCC	166	1.5	58	Goh et al. 2007	
microsatellite	AHT010	21	F: CTCCTAGTACCATTTTGAAC R: CAAAGTAGAGCAAGACTGGC	124-126	1.5	56	Swinburne et al. 2005	
microsatellite	AHT077	21	F: TTCACCATTCTTCCCCATC R: GGAAAAAGGGATTTTCTAAGCC	117-121	1.5	56	Swinburne et al. 2003	
microsatellite	AHT078	21	F: CCTCTCGCAGAAGCACAAAT R: GCTCCCTGCTGACTTCTGAG	191-195	2.0	58	Swinburne et al. 2003	AJ507695
A kinase (PRKA) anchor protein 8	AKAP8	21q12	F: ACCAGCGTTTGGACATGATG R: ATAGTCGTAGCTGTAGCTGG	710	1.5	58	Brinkmeyer-Langford et al. 2005 ; Goh et al. 2007*	BI774186
brain abundant, membrane attached signal protein 1	BASP1	21q18	F: GGGTCCTGGATTTTAAAGATCAATG R: TGGCATCGAGATACATGTGGATAG	302	3.0	58	Chowdhary et al. 2003*; Goh et al. 2007	
brix domain containing 2	BXDC2	21	F: AAGAAGATGCTGCTCTGGTA R: CAGCTGTGATGGATCTTATG	403	1.5	58	Goh et al. 2007	
C1q and tumor necrosis factor related protein 3	C1QTNF3	21	F: CAACCATGCAGTGTGAAGC R: GAAGAGCAGGAAGCCTGCAA	115	1.5	58	Goh et al. 2007	
chromosome 5 open reading	C5orf22 (<i>FLJ11193</i>)	21	F: TATACCGGGCCATAGGCTCA R: ACGGTGTCTGCTGGCATATT	109	1.5	55	Goh et al. 2007	

frame 22								
chromosome 5	C5orf23	21	F: GGGAGAAATTTGAATCAGCAG	103	4.0	50	Chowdhary et al.	
open reading	(<i>FLJ14054</i>)		R: GCCCTTTATTCCTTGTGCATA				2003	
frame 23								
chromosome 5	C5orf38	21	F: GGACATACGTGAATTTGTTGG	231	1.5	58		
open reading			R: AAATATCAAATTTGTTTCCACTTCTT					
frame 38								
complement	C6	21	F: CTAATAATGGCCGCCCCAC	1035	1.5	58	Goh et al. 2007	
component 6			R: GGCTCCAGGAAGACCAACAA					
complement	C9	21q17	F: GTTGCTCGTTGTGGGTTTCT	196	2.0	58	Godard et al.	AF115746
component 9			R: CGCAAATTTTCTCCCTCTTTC				2000*; Chowdhary et al. 2003	
cyclin B1	CCNB1	21q13- q14	F: CAAAATACCTACTGGGTCGG	704	1.5	58	Goh et al. 2007*	
			R: AATTTCTGGAGGGTACATTTCT					
cadherin 10, type	CDH10	21q17- q18	F: TGACATTCATGCCACAAGAAG	198	1.5	55	Perrocheau et al.	DX010449
2			R: ACAACCGACATTTTCAGGAACA				2006*	
cadherin 12, type	CDH12	21	F: ATCAAAGGCTACAAGAAAATGATATG	196	1.5	50	Goh et al. 2007	
2			R: CCAAACATGTCTGCCAAGACT					
cadherin 9, type 2	CDH9	21	F: GGATAGTGAGTCTGACACAAG	98	2.0	55	Goh et al. 2007	
			R: ACCTGTATACTCTTCCAACAAG					
cartilage	COMP	21q12- q14	F: TCGTGCAAACAATGAACAGC	570	1.5	60	Mueller et al.	AF325902
oligomeric			R: TCCACATGACCACGTAGAAG				2005a*; Brinkmeyer- Langford et al. 2005	
matrix protein								
microsatellite	COR068	21	F: AACCAATTGTGAGATTTTTGCT	144-156	2.0	58	Tallmadge et al.	AF142605
			R: GGCTAGTCCTGGATCATGTG				1999a	
microsatellite	COR073	21	F: GCCAAGACATGGAAACAATC	180-198	2.0	58	Tallmadge et al.	AF142610
			R: GTTCTCAAGGTGCATCCCTA				1999a	
CREB regulated	CRTC1	21	F: CAGCCTCTCTAAAGAACTGAC	129	1.5	58		CB445064
transcription			R: TTGAGCATGTGCAGTCCATC					
coactivator 1								
disabled homolog	DAB2	21	F: ATCCTTTCCGTGACGATCCT	412	1.5	58	Goh et al. 2007	
2 (Drosophila)			R: ATGGCTATGGAGTCATGTGG					
DEAD (Asp-Glu-	DDX4	21	F: ATGTTCATCGAATTGGGCGT	291	1.5	58	Goh et al. 2007	
Ala-Asp) box			R: TTTCTTCCAACCATGCAGGA					
polypeptide 4								
DEP domain	DEPDC1B	21	F: TGGATATCACTTTATCTGCTCCA	136	1.5	50	Goh et al. 2007	

containing 1B DIM1 dimethyladenosin e transferase 1- like dynein, axonemal, heavy chain 5 endothelial differentiation, lysophosphatidic acid G-protein- coupled receptor, 4 EGF-like, fibronectin type III and laminin G domains erbb2 interacting protein excision repair cross- complementing rodent repair deficiency, complementation group 8 F-box and leucine-rich repeat protein 7 F-box protein 4 FK506 binding protein 8 hypothetical protein FLJ13611 follistatin	(<i>XTP1</i>) DITM1L (<i>HEST014</i>) DNAH5 EDG4 EGFLAM (<i>FLJ39155</i>) ERBB2IP ERCC8 (<i>CKNI</i>) FBXL7 FBXO4 FKBP8 FLJ13611 FST	21q13 21q18 21 21 21 21 21 21 21 21 21q16	R: TTGGAGAGTTTGGCATCTGT F: CTTGACTTGAGTTTGAAACATTC R: CTTGAATGACTAGTGTTAGGAG F: AATGACCGACCTCACTGCTT R: CCATATTGTCCAGAGCCCAG F: CTCTTCCTCATGTTCCACACA R: ACAGCCACCATGAGCAGGAA F: TCGCTCTGCACACTAACAGG R: CTGGTGTTACTTGGCTCCG F: CCACAGTCTGCACCTCAAATA R: TGATTTTCTGTGCTCTCTGATCTAG F: ATAGTCATCATATGTCTCCGGT R: GTTGTACTTTGGGTCCTCTAGTA F: CCAAGTACTGCGGCAAGCTG R: CAAGACTTGAGGCTGAGGCG F: CCGTCCTATGTATGGAGCTGTCT R: CATCAATCTGCCTCTGAGGC F: AACTCCTACGACCTCGCCAT R: GCCTTGATGTTGTCAGGCTG F: GCAGGCATCATTAAGGGAGTA R: CAGTATCTGGGATTGCCTCC F: TGCCCTGACAGTAAGTCTGAG	~250 527 365 146 164 1150 199 176 642 1309 124	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5	55 58 58 58 58 58 58 58 58 58	Godard et al. 2000* Goh et al. 2007* Brinkmeyer- Langford et al. 2005 Goh et al. 2007 Goh et al. 2007 Goh et al. 2007 Goh et al. 2007 Goh et al. 2007 Goh et al. 2007 Goh et al. 2007	AW735741 CK461960 CB427408
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growth differentiation factor 1	GDF1	21	R: ATCCGGAATGCTTTACTTCC F: CTCAAGGTCCTGTATGCCA R: TGTACAGGAACCAGTAGAGG	124	1.5	58	Brinkmeyer-Langford et al. 2005	BM286244
glial cell derived neurotrophic factor	GDNF	21	F: TTTTCAGGTACTGCAGCGGC R: GGTCGTCATCAAAGGCGATG	141	1.5	55	Goh et al. 2007	
growth hormone receptor	GHR	21q16	F: TTGGCCTCAACTGGACTCTA R: CCAGGACTATCCACCCCTTC	114	2.0	58	Caetano et al. 1999a; Milenkovic et al. 2002*	AF097588
GEM interacting protein	GMIP	21q13-q14	F: GTTATCCGCTCGCTGAAGA R: ACAATGCCCAGGTTGTTGG	460	1.5	58	Brinkmeyer-Langford et al. 2005; Goh et al. 2007*	BE682381
granzyme A	GZMA (CTLA3)	21q14-q15	F: ATGTGGCTATCCTTCGTCTC R: TTCCGGCACAAATCATATTC	402	1.5	58	Chowdhary et al. 2003*; Goh et al. 2007	
hyperpolarization activated cyclic nucleotide-gated potassium channel 1	HCN1	21	F: GATACAGTTTTCTATTGGACCTG R: GGGATGGATGAGATGAAGTCA	146	1.5	58	Goh et al. 2007	
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	HMGCS1	21	F: ACTGGGCACGGATCTTTTT R: GGACACATATGCAACATGCCT	147	2.0	65	Chowdhary et al 2003	
heat shock 27kDa protein 3	HSPB3	21	F: AGTTTCAAGCTCGCGGTTTG R: TACTGTCGGGTGAAGCTTCTTG	298	1.5	58	Goh et al. 2007	
microsatellite	HTG10	21q15	F: CAATTCCCGCCCCACCCCGGCA R: TTTTATTCTGATCTGTACATTT	93	1.5	TD 60	Marklund et al. 1994; Goh et al. 2007*	AF169294
microsatellite	HTG32	21	F: CCTGAAACCTCAGTAAACAGA R: TGTGGCTTTGGTGTGGAAAC	150-160	2.0	58	Lindgren 2000	
5-hydroxytryptamine (serotonin) receptor 1A	HTR1A	21	F: GGAGAGAAGAGGGGAGAGGA R: GACTCCAGCTGGGAAGTGAG	232	1.5	62		

interleukin 7 receptor	IL7R	21q17	F: TGGAGTGAATGGAGTCCAAGT R: TATAGCCACACCACCCTGGA	150	2.0	58	Caetano et al. 1999a; Chowdhary et al. 2003*	AF115754
insulin-like 3 (Leydig cell)	INSL3	21q13-q14	F: GAACTGCTACAGTGGCTGGAAGG R: TCAGTGGGGACAGAGGGTCAG	~200	1.5	59	Brinkmeyer-Langford et al. 2005*	
Janus kinase 3 (a protein tyrosine kinase, leukocyte)	JAK3	21	F: CTGCGGTTGGTCATGGAGTA R: GAAGTCGGCGATCTTGACGT	486	1.5	58		BE753801
jun D proto-oncogene	JUND	21	F: ATCGACATGGACACTCAGGAG R: GCTGAGGACCTTCTGCTTGA	210	1.5	58	Brinkmeyer-Langford et al. 2005	CA779483
kinesin heavy chain member 2A	KIF2A (KIF2)	21	F: AGGTTCAAGTGGTGGGATTA R: CATGTAGTTTTCTTTCCCTTCTA	548	1.5	50	Goh et al. 2007	
Kruppel-like factor 2 (lung)	KLF2	21q12-q13	F: AGAAGCCCTACCACTGCAAC R: CTACATGTGCCGCTTCATG	173	1.5	58	Brinkmeyer-Langford et al. 2005	BI132469
microsatellite	LEX031	21	F: CCCATTAAGAACTTTTCATCCTG R: GGCAAGCCCCACAAAATTAT	252-256	2.0	58	Coogle et al. 1996	AF075633
microsatellite	LEX037	21	F: GGATTCCTCAACCTCCTAAA R: AGGGATAAGTGACCACCAC	189-197	3.0	58	Coogle et al. 1997	AF075639
microsatellite	LEX060	21	F: TTGCAGAAGGAGCCAATC R: AAGGCATTTCGAAATCTAAAT	145-161	3.0	58	Coogle & Bailey 1997	AF075667
similar to microtubule associated testis specific serine/threonine protein kinase U6 small nuclear RNA associated (S. cerevisiae)	LOC375449	21	F: CTTGACCACATATTATCCCC R: CTGTCTTCCATCCTCACTC	120	1.5	58	Goh et al. 2007	
mesoderm induction early response 1, family member 3	LSM4	21	F: GGATGCCCCGAGTGCTACATT R: GCCCTTCTGCTGCTTCTGCT	140	4.0	50	Brinkmeyer-Langford et al. 2005	
myosin X	MIER3	21	F: TAACTTCTAACCGGCCTGAG R: GGAGGAAAGCTATCATCCAA	253	1.5	58		
	MYO10	21	F: GCCATCAAGATATTCAACTCCCT R: TCTGCTTGATGAGCTGGCAG	136	1.5	55	Goh et al. 2007	

nicotinamide nucleotide transhydrogenase	NNT	21	F: CCAGATTTTCGGATTTACCTCA R: ATAGGCAACCAGAGACCCACT	199	1.5	55	Perrocheau et al. 2006	DX010536
natriuretic peptide receptor C/guanylate cyclase C	NPR3	21q17	F: AGATGATGCTCGCCCTGTTC R: GCAAGCCTTCCTCCTGGAAG	132	1.5	55	Milenkovic et al. 2002*; Goh et al. 2007	
poly (ADP-ribose) polymerase family, member 8	PARP8	21	F: TCCTGCAAAGCCGTAACCTTA R: TCTTGTGCAGACATGATCAGTA	998	1.5	58		
phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	PDE4D	21q14	F: TGTTTGTCTGTTTACAACCA R: AAACAAGCTCTAAGGTGACA	209	1.5	58	Goh et al. 2007*	
pelota homolog (Drosophila)	PELO	21	F: TGGTTATGCAGGAAGGCCTC R: TAGTCGCAGAACTGCTCCCT	241	1.5	58	Goh et al. 2007	
phosphoinositide-3-kinase, regulatory subunit 2	PIK3R2	21	F: AGGGAGAGTACACGCTGAC R: TTGGACACTGGGTAGAGGAG	656	1.5	58		AV663221
polo-like kinase 2 (Drosophila)	PLK2	21	F: TGTGGTACCCCAAATTATCTTTCTC R: TGTCATCCAACTGGGACGA	762	1.5	58	Goh et al. 2007	
polymerase (DNA directed) sigma	POLS	21	F: CGACATCAGCTTTAACATGGA R: GCAGGAGGAACTGTTTCAGT	1216	1.5	58	Goh et al. 2007	
protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1	21q16-q17	F: CCAATTGCATTAAAGAATCATTAGC R: TTTTGTTTTCAAAGATAATACTGGTGA	175	1.5	58	Dranchak et al. 2006*	
prolactin receptor	PRLR	21	F: ATGTCCAGACTACAAAACCG R: ACATAAAGTGGATCCGAGGA	170	1.5	55	Goh et al. 2007	
regulatory factor X-associated	RFXANK	21	F: TGTCCATCCACCAGCTTGCA R: GGCTTGTTGATGAGGTTGT	300	1.5	58	Brinkmeyer-Langford et al. 2005	CK459113

ankyrin- containing protein succinate dehydrogenase complex, subunit A	SDHA	21q19	F: CACTACATGACAGAGCAGGCC R: ACCAAAGGCACGCTGGTAG	445	1.5	58	Goh et al. 2007*	
sema domain (semaphorin) 5A	SEMA5A	21	F: AACCTGACGGAGATCCATGAC R: TTGGAGTTGTACTGTGCGGTG	197	1.5	58	Goh et al. 2007	
splicing factor, arginine/serine- rich 14	SFRS14	21	F: CCCAACTTTTCCAGACTCTC R: ACTCTGGGTGTTTTCAAAGC	151	1.5	58		CB450106
microsatellite	SGCV14	21q13	F: CCCCAGTGGTTCCATTTAGATGT R: GGGGAGAGCATTTTGGTGA	188	3.0	58	Godard et al. 1997*	U90593
microsatellite	SGCV16	21q13	F: AATTCTCAAATGGTTCAGTGA R: CTCCCTCCCTTCTCTCTA	190	2.0	58	Godard et al. 1997*	U90594
S-phase kinase- associated protein 2	SKP2	21	F: CCGACCAGAGTAGCAACGTT R: CATTCCTTTGCTCTTCAGC	198	1.5	58	Goh et al. 2007	
solute carrier family 27 (fatty acid transporter), member 1	SLC27A1	21q13- q14	F: TTCAACAGCCGCATCCTGC R: CTGTGGGCGATCTTCTTGCT	~305	1.5	60	Brinkmeyer- Langford et al. 2005*	CK837240
threonyl-tRNA synthetase	TARS	21	F: ACCACCAGTGTGCAACAATAC R: ACCCCAAGATGGCTCTATGG	284	1.5	58	Goh et al. 2007	
microsatellite	TKY021	21q13	F: AGGTGAACCCAGAGAGTCC R: AGTGAGGCCTCGGTTGGGAG	117-132	2.0	58	Kakoi et al. 1999; Chowdhary et al. 2003*	AB048331
microsatellite	TKY280	21	F: GAGGAGACCAAAATAACAGG R: ACTCCCTGCTTTGCACTCTG	309-321	3.0	58	Tozaki et al. 2000b	AB033931
microsatellite	TKY296	21	F: CTCTCACTTCCAAGACACTC R: ATCAAACGTACAGGAAGAGC	254-273	1.5	58	Tozaki et al. 2000c	
microsatellite	TKY306	21	F: GTTTGTGGTGCTTTGTAGC R: CTCTGCACTTGCTGAACATC	266-279	1.5	56	Tozaki et al. 2000c	
microsatellite	TKY355	21	F: GTTCTGTACCTTGATGGTAG R: TGGACATCTTTCCACAAGC	275-283	1.5	58	Tozaki et al. 2001	

microsatellite	TKY418	21	F: TGAAATCAGCTAGGAGACTG R: TCTGTCCTCAACTCTGATTG	124	2.0	58		AB103636
microsatellite	TKY520	21	F: GCAGTTTCTGGCATTGTGTG R: TGATGTGAAACGTGTGCTTG	182-184	1.5	58	Tozaki et al. 2004	
microsatellite	TKY623	21	F: CAGTGTGGGTGGGCTTTATC R: ACCACTAGGGTGTGCATGTG	263-281	1.5	60	Tozaki et al. 2004	
microsatellite	TKY671	21	F: AGGCAACATGAGAAGGCACA R: ATAGCACCTGTTCCCTGGAG	100-116	1.5	58	Tozaki et al. 2004	
microsatellite	TKY677	21	F: ATGGAAATTGCCTGATTGGA R: AAAGGAAGATTGGCAACAGA	116	2.0	58		AB103895
microsatellite	TKY678	21	F: TAAAAGAAGGGGTAATGGG R: TGTGGTGCTTGTTCAGCA	207	2.0	58		AB103896
microsatellite	TKY709	21	F: CTTTTCTGGGGCTGTGTGTC R: CAAGGGGGAAGATGATGATG	121-143	1.5	56	Tozaki et al. 2004	
microsatellite	TKY721	21	F: TCAAATGGTTCAGTGAAAATGG R: CCTCCCTCCCTTCTTCTATT	143-183	2.5	56	Tozaki et al. 2004	
microsatellite	TKY806	21	F: TGGAAGTGTGATGATGTTGC R: TCTTTCTTCCCTTCCGAGAG	180	2.0	58	Tozaki et al. 2004	AB104024
microsatellite	TKY824	21	F: AATGGTATTTGCAATAGATTTGGG R: GCAGAAAACAGTTTGATAAAATGC	161	2.0	58		AB104042
microsatellite	TKY868	21	F: TGGGCTCAGCCCAGACAG R: GTGGTTAAGGTAGTTTCAGAG	177	2.0	58		AB104086
microsatellite	TKY907	21	F: CTTGTCGTCACAAATGGCAG R: ACCTGCCAAAGAATGAATGG	125	2.0	58		AB104125
microsatellite	TKY1018	21	F: TCAAAAAGGCAGAAAGGGTC R: TCTTGTTTCATGCAGCTCTAC	175	2.0	58		AB104236
microsatellite	TKY2049	21	F: TTAAAGGGCAGAGGGTACA R: ACAGTCAAGCACAGGCTTC	223	1.5	60	Tozaki et al. 2007	AB215992
triple functional domain (PTPRF interacting)	TRIO	21	F: GTCCAACCTCAACACGACCTACC R: AGGTCTCTTCCACGCTGTCTG	181	1.5	58	Goh et al. 2007	
testis-specific serine kinase 6	TSSK6 (<i>SSTK</i>)	21q13	F: TCAAGCTTACCGACTTCGGC R: GACCATGACGTAGAGCACGA	170	1.5	60	Brinkmeyer-Langford et al. 2005*	BI344525
tetratricopeptide repeat domain 33	TTC33 (<i>OSRF</i>)	21	F: TTTCAAGTAGCCCTTCACATC R: ACAAACAGCAACAATCTCATCA	198	1.5	58	Goh et al. 2007	

microsatellite	UMNe139	21	F: AGACACAGGTTTAGGTGGATGC R: GATCAAGCACATAAGGGACAC	100	1.5	58	Wagner et al. 2004a	AY391300
microsatellite	UMNe147	21	F: CAGACCTACTCCAGTCATCAGC R: AAACAAAGAGACTTGAAGTGGC	180	1.5	58	Wagner et al. 2004a	AY391302
microsatellite	UMNe179	21	F: GATTCAGGAGTTTGTGTGATGG R: AGAACTTCTATTACATGGTTCACAC	106	2.0	58		
microsatellite	UMNe206	21	F: GATCAAGCACATAAGGGACAC R: CATATCCATAGCTTTTTGACCC	154	2.0	58	Mickelson et al. 2003	AF536289
microsatellite	UMNe229	21	F: CTTCTCTGGACAAAGGGGTG R: CATGAATTTGCCAGTTTGATG	123	2.0	58	Mickelson et al. 2003	AF536303
microsatellite	UMNe327	21	F: TTTTCCTTCCTCATTGGTGC R: GAAATGCAGGGCTAAGGATG	157	2.0	58	Wagner et al. 2004a	AY391339
microsatellite	UMNe432	21	F: CTGACGTCACTGGCAACG R: GCGGAGTCCCACATAACG	282	1.5	58	Mickelson et al. 2004	AY731394
microsatellite	UMNe464	21	F: GTTCCATTTGCGAAAATTTAGC R: CGTTTGCTTCTAAGCCGTTT	~300	1.5	58	Wagner et al. 2004b	AY464492
microsatellite	UMNe509	21	F: GGGCATTCTCAATCTTTAGGC R: GAGGATGCAAAGGAATAAGGC	~200	1.5	55	Wagner et al. 2004b	AY464511
microsatellite	UMNe539	21	F: GGTTTCCAAATGAGTGGTTTG R: CAATTTAAGATTCAATTGGGGAG	126	1.5	58	Mickelson et al. 2004	AY731410
microsatellite	UMNe564	21	F: GAATACAGGGGCTTTTTCTGC R: TTCTGCATCTTGATTGCAGTG	~200	1.5	58	Wagner et al. 2004b	AY464530
microsatellite	UMNe603	21	F: TTGTCCTGAGTGTTTCATTCCC R: AAGCTGCAAAAAGATAGATGCC	186	1.5	58		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	22STS01	22	F: GAAACATACCGAGGCACCAC R: GCAGGGGCTCTAGAACTCAG	500	1.5	60		BI961508
acyl-CoA synthetase short-chain family member 1	ACSS1 (ACAS2L)	22	F: AAGTTTCTAGATACAAAAGGCAGAGG R: TCATTAGCTTCCCTGAACGAC	517	1.5	60		BM781307
adenosine deaminase	ADA	22	F: AGGCAGGGTTAATGTGACCA R: GGGAAAGCTTCAAGATGGTG	219	2.0	58	Caetano et al. 1999	AF135790
adhesion regulating molecule 1	ADRM1	22	F: CTGAGATCATGGCACCTATCC R: CTTGTTGGCTGCCTCCAC	400	1.5	60		BM780744
S-adenosylhomocysteine hydrolase	AHCY	22q15-q16prox	F: GGTTTAAGAGAATGCCCAGCTC R: TACCTGGCCTGTGGACTTGATA	161	3.0	58	Chowdhary et al. 2003; Gustafson-Seabury et al. 2005*	
microsatellite	AHT031	22q18-q19	F: TCTTGCTGCATTTCTTGG R: TGCAGGAAAAGTTTGATGACC	109-123	2.0	58	Swinburne et al. 2000	AJ271516
microsatellite	AHT110	22	F: TATGCCACATACATCTTCCTGC R: TTCTCCCGAGCACACTCC	203	1.5	60		
agouti signaling protein (mouse)	ASIP	22q15-q16prox	F: GCAGCCAGGCTAATGAGAAC R: ACAAAAAGGAGCAAAGCCAGA	198	2.0	58	Godard et al. 1998*; Chowdhary et al. 2003	AF179635
ATP synthase, H ⁺ -transporting, mitochondrial F1 complex, epsilon subunit	ATP5E	22q19	F: GGAAGTCATTAGCTCCTGTCA R: CATGAAGAGCCTGGAACAAGT	~300	1.5	62	Gustafson-Seabury et al. 2005	
ATPase, Class II, type 9A	ATP9A	22q18	F: GTCTTGGCTCTTAACGCTCAC R: TCGTGGCTTGTTTGTTGTAG	~160	1.5	58	Gustafson-Seabury et al. 2005	
attractin	ATRN	22	F: CCACAGCAGATGCGTTAATC R: CTGACACTTTCCCCCATTG	122	1.5	59		AW260909

BCL2-like 1	BCL2L1	22	F: TCCCTTCAGAACCTTATCTTGG R: TCCCGGAAGAGTTCATTAC	519	1.5	60		BI960951
bone morphogenetic protein 2	BMP2	22q14dist-q15prox	F: AACTCCTCTGCATGGTGTGT R: TGTGGGGCCTAAGTTCTCTA	204	1.5	58	Gustafson-Seabury et al. 2005	
BTB (POZ) domain containing 3	BTBD3	22	F: AACATGGCATGAAGGCTAGTG R: AAGCACTCTGATGCACAAGG	382	1.5	60		CX604284
chromosome 20 open reading frame 7	C20orf7	22	F: CAAGAACCTCGGCCTCAG R: TCCTCCTTCAGGTAGTCAAACCTTC	159	1.5	59		CX598272
chromosome 20 open reading frame 24	C20orf24 (<i>HEST20-5</i>)	22	F: AGCTGCATGGAACCTGGA R: CGACAGCTCCAATCAGCA	198	1.5	58	Gustafson-Seabury et al. 2005	
chromosome 20 open reading frame 30	C20orf30	22	F: TTTGATGACTAGCACCCACATC R: CCCATAACACTGCTACTCTCCC	289	1.5	59		CX600131
chromosome 20 open reading frame 39	C20orf39 (<i>FLJ14220</i>)	22q13	F: CAAGGGGGACTTCCACCAG R: GCTCATAGGTGGTTGCTCTTG	144	1.5	55	Perrocheau et al. 2006	DX010628
cadherin 4	CDH4	22q19	F: GGCCAGGAAATGAGTGTCTA R: AATCAGCGTCAATGCTTTTC	172	1.5	58	Gustafson-Seabury et al. 2005	
centromere protein B, 80kDa	CENPB	22q14dist-q15prox	F: CAGGAAGGTCTCGGCATC R: GTATGAAGGAGGGCACATCA	285	1.5	60	Gustafson-Seabury et al. 2005	
microsatellite	COR001	22	F: GGCAGCATCCACATAAAACAG R: GCTCACTATTACCACGATGATTGATTC	123-137	2.0	58	Hopman et al. 1999	AF083444
microsatellite	COR016	22	F: CAGCTCAGTAGATGATTGTCCA R: GCAAAGACAAGGAGGTTAAGTT	177-196	2.0	58	Hopman et al. 1999	AF083459
microsatellite	COR022	22q15-q16prox	F: AAGACGTGATGGGAAATCAA R: AGAAAGTTTTCAAATGTGCCA	254-264	2.0	58	Murphie et al. 1999; Gustafson-Seabury et al. 2005*	AF101391

microsatellite	COR107	22	F: TCTCAAGTATTGATTTTGGGG R: TGCAGAAGCTATTTCTGGTG	260-272	1.5	56	Swinburne et al. 2005	
carboxypeptidase X (M14 family), member 1	CPXM1 (<i>CPXM</i>)	22q14dist- q15prox	F: ACGTGGCAACACATCTCCTA R: TGGTGATCTTCATTTCGTTCTC	167	1.5	58	Gustafson- Seabury et al. 2005	
cleavage stimulation factor, 3' pre-RNA, subunit 1	CSTF1	22	F: ACCATCAGTCTCTGCTGCTG R: CCAAAGCTGGCACAATGAC	273	1.5	60		CX600101
cathepsin A	CTSA (<i>PPGB</i>)	22q17	F: GAAAGGTCCCCTCAAGGAC R: GCGTGAACCAAGATCAGAAC	112	1.5	58	Gustafson- Seabury et al. 2005	
DEAD (Asp-Glu- Ala-Asp) box polypeptide 27	DDX27	22	F: TGAGAAAGTCCGAAAGAAAAGG R: CTTCCCCTTCAAGGTCTTCC	380	1.5	60		CD528389
docking protein 5	DOK5	22q18	F: GTTTGCTCTCTTCCTTCATGC R: TGAGAAGCTACAACCAACCAA	~200	1.5	58	Gustafson- Seabury et al. 2005	
destrin	DSTN	22q12- q13	F: CAAGCACTAAGCTGGGAAGTA R: CGACGGAGTAGGTCACAAAG	194	1.5	58	Gustafson- Seabury et al. 2005	
endothelin 3	EDN3	22	F: GTCCAAGTCCCAGAACCC R: TGATCCAGATGATGTCCAG	162	2.0	58	Chowdhary et al. 2003	
erythrocyte membrane protein band 4.1-like 1	EPB41L1	22	F: CAAGGATCGAGAAGCGAATC R: GGCTTCTTGTCCTCTCCTC	500	1.5	60		CX603690
eyes absent homolog 2 (<i>Drosophila</i>)	EYA2	22q18	F: CGGGTCTTACTCAGCTTCAG R: GCCTTATACGTGTCTGTCTGC	191	1.5	58	Gustafson- Seabury et al. 2005	
FK506 binding protein 1A, 12kDa	FKBP1A	22	F: AGCCATCATGACAAATCCTTG R: CCAGGAGACTCGGAGATCAG	116	1.5	55	Perrocheau et al. 2005	AY817466
GNAS complex locus	GNAS (<i>GNAS1</i>)	22	F: AAGCAGGTTTAACGCACAGG R: GGCCCTGAACCTCTTCAA	199	2.0	58	Caetano et al. 1999*; Chowdhary et al. 2003	AF134221

hydroxyacid oxidase 1	HAO1	22q14	F: CCATTGTCATTTGGACCTGT R: TGCTATTGGGTAGTTTATGCAC	189	2.0	58	Gustafson-Seabury et al. 2005	
histidyl-tRNA synthetase 2	HARS2	22	F: AACCTGCGTGTGTTTGAGG R: ATGAGCTCCGGCCTGTAAG	215	1.5	60		CX601399
histocompatibility (minor) 13	HM13	22	F: GAGTTTGACACCAAGGACCTG R: CCAGAAGACGTCATAGATAAAGAGC	400	1.5	60		BM735454
microsatellite	HMS053	22	F: TCATTACTGATGACATTTACTCAGC R: TGTTATAAATCTGAGATAGTGATGC	196-198	1.5	54	Swinburne et al. 2005	
microsatellite	HMS47	22q18	F: CCTGCTGAGGACCTTGGAAGCT R: ATGTATTTTCAAGCTAATATCTGCC	196	3.0	58	Godard et al. 1997, Godard et al. 1998	U89815
microsatellite	HTG14	22q14	F: CCAGTCTAAGTTTGTGGCTAGAA R: CAAAGGTGAGTGATGGATGGAAGC	141	2.0	58	Marklund et al. 1994	AF169298
microsatellite	HTG21	22	F: ATTACTTCCTCCAGGTATCTCAG R: AGGCAGGGCTGGGAGACGT	151	3.0	58	Lindgren et al. 1999	
itchy homolog E3 ubiquitin protein ligase (mouse)	ITCH	22	F: GACGTTTCTGTTGGGAACTG R: AAAACAAATGGCTAAACCAAGG	248	1.5	58	Gustafson-Seabury et al. 2005	
integrin beta 4 binding protein	ITGB4BP	22q15-q16prox	F: CAGCAAGGTATCCAGAGCAT R: AGGGAATATGGGTGACGAGT	284	1.5	60	Gustafson-Seabury et al. 2005	
inosine triphosphatase jagged 1 (Alagille syndrome)	ITPA	22	F: TGCCAGAGTACCAGGGAGAG R: GAGGGCATTGAAGCACAGAC	710	1.5	60		CX601964
	JAG1	22q14	F: CCGCAGACGTTTCGAGGAA R: TCACAGTGTGACACGGCAGT	258	2.0	62	Gustafson-Seabury et al. 2005	
kinesin family member 3B	KIF3B	22	F: GCCACTCTCTGCTTTTCCTG R: TTGCGCTACACACAATAGCC	283	1.5	60		CX596463
microsatellite	LEX002	22	F: AAAAGGAAGACTGGCGACAG R: GGTGGGGGAAAGAATGGT	127-131	3.0	58	Coogle et al. 1996	AF075606
v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB	22	F: TCCTGGCTTCCTGAACTTTG R: TCGAGCAGGCAATAAAACTG	272	1.5	60		BM735497

matrilin 4	MATN4	22	F: TCGTGGACTTCCTAGACGTG R: TGCTGCCTTTAAGGTTCTCC	550	1.5	59		CX598714
matrix metalloproteinase 9	MMP9	22q17	F: GTGGGTGTACACAGGCAAGTC R: TGCTGAACAGCAGCACCTTAC	125	1.5	55	Perrocheau et al. 2006	DX010527
myosin, light chain 9, regulatory	MYL9	22	F: GCCAAGGACAAAGACGACTA R: CCTGTGTTACATTGGCTGTG	230	1.5	58		
N-ethylmaleimide-sensitive factor attachment protein, beta	NAPB	22q12-q13	F: GGTGAACACACCCACACAG R: CGGGGAAACACTTATGTACC	172	1.5	60	Gustafson-Seabury et al. 2005	
p21(CDKN1A)-activated kinase 7	PAK7 (<i>HEST20-2</i>)	22	F: AGCACAACTCTCCTATGTCTGG R: AAGGCCATGAGAATTCCAGTC	279	2.0	58	Gustafson-Seabury et al. 2005	
prodynorphin	PDYN	22q15-q16prox	F: TTGGAATAGGACGTTTGAGC R: TCTTGTCTCATGGCCTCTGTA	~210	1.5	62	Gustafson-Seabury et al. 2005	
phosphatidylinositol glycan anchor biosynthesis, class T	PIGT	22	F: GGCCTGCTCAAGTGGAC R: AAGAGGGGGCTCTCTTCC	400	1.5	58		CX604421
phospholipase C, beta 1	PLCB1	22	F: CAACCATACAAAGCCCCATC R: GCTCAGTTTTACCAAATGCC	227	1.5	58	Gustafson-Seabury et al. 2005	
phospholipase C, beta 4	PLCB4	22	F: CGCAGACCAGCAACAGTAGT R: TCCATGGAATTTGTGTCCAG	108	2.0	58	Gustafson-Seabury et al. 2005	AY011799
phospholipase C, gamma 1	PLCG1	22q16-17	F: GCTTTGGCCACAATTTTCAT R: TGCCCCTAGTGAGAAGCTGT	242	1.5	58		
prion protein	PRNP	22q14dist-q15prox	F: CTTTTGGTGGAATTTTATAGGA R: ACTCAACAGCACATTGAAAGG	493	1.5	58	Gustafson-Seabury et al. 2005	
protein C receptor, endothelial	PROCR	22	F: CCTACACCCTGCAGAAGCTC R: TGGGAGAAGAAAGGAGTTGC	620	1.5	60		CX601326
proteasome, subunit, alpha type, 7	PSMA7	22q19	F: GAATCGGTCAGGAAGAGAGG R: GAACGTGCAGGGACTTTG	~220	1.5	58	Gustafson-Seabury et al. 2005	

proteasome, inhibitor subunit 1	PSMF1	22	F: GGCTTGGAGGTGCTGTTC R: CTCCCAAGCCGTAGTAGCC	112	1.5	59		CX602082
protein tyrosine phosphatase, non-receptor type 1	PTPN1	22	F: GCCTCGTTCCTGAACCTTCTC R: CACAGCCAGGTAGGAGAAGC	800	1.5	60		CX595178
protein tyrosine phosphatase, receptor type, T	PTPRT	22q16-q17prox	F: GGATGCTTCTAACAGCCTTG R: GTTGTGGTCTGGGTCAAGTC	171	1.5	60	Gustafson-Seabury et al. 2005	
RNA binding protein, autoantigenic	RALY	22q15-q16prox	F: CCTTCTGCTCACTAATTTTATTCC R: CACTACGCACTGGCAAGG	230	1.5	58	Gustafson-Seabury et al. 2005	
ribosomal protein S21	RPS21	22q19	F: GAATAGCCAGCTTCTCTGACA R: GACACACCAAAGACACAAGG	~210	1.5	58	Gustafson-Seabury et al. 2005	
ribosome binding protein 1 homolog 180kDa (dog)	RRBP1	22	F: TGGTCTTTGGTGGATTTATGG R: CAGGAGCAATGACCACAGG	327	1.5	60		CX600901
Sec23 homolog B (<i>S. cerevisiae</i>)	SEC23B	22q12-q13	F: GGAATAAGTGGAAACCAAGTTC R: CTTACTATGGAGGTGAGTGAGTG	208	2.0	60	Gustafson-Seabury et al. 2005	
serine incorporator 3	SERINC3 (<i>TDE1</i>)	22q15-q16prox	F: AGACCCTTCTCCCTCTCAAG R: CCTCCACCACATCGTATCAG	190	1.5	60 62	Gustafson-Seabury et al. 2005	
splicing factor, arginine/serine-rich 6	SFRS6	22	F: TCCACGTTTATACTTGGCCTCT R: TGCCACCATTTCTTTAGAACCT	117	1.5	59		CX596991
microsatellite	SGCV01	22	F: AGTCACCACCACTCACCTTGT R: CCAACACAGGATACGGATGA	187	2.0	58	Godard et al. 1997	U90584
microsatellite	SGCV19	22q19	F: GCCCCACCTGCTCCACC R: GGGGCAAAGTGGAATCC	143	2.0	58	Godard et al. 1997	U90597
serum/glucocorticoid regulated kinase 2	SGK2	22q15-q16prox	F: GAAGAGAAGGGGGACAGACT R: CCTCAGAACCACCTGGAAG	206	1.5	60	Gustafson-Seabury et al. 2005	
signal-regulatory protein beta 1	SIRPB1 (<i>SIRPB</i>)	22	F: TCCTCCTAGGCACAAAGGTG R: AAGGCGATGGATGAGAGCTA	1150	1.5	60		CD528661

solute carrier family 32, member 1	SLC32A1 (<i>VIAAT</i>)	22q15-q16prox	F: GGCAGCATGGTTGTAATAGTC R: TGTATGTATTCTTCGGGGTCA	178	1.5	58	Gustafson-Seabury et al. 2005	
snail homolog 1 (Drosophila)	SNAI1	22q18	F: GCTAGGAAGTGGTGAAGCTG R: TGTGGAGTAAAACCCTGGAA	321	2.0	58	Gustafson-Seabury et al. 2005	
small nuclear ribonucleoprotein polypeptides B and B1	SNRPB (<i>SNRPB1</i>)	22	F: AAATGTTCTCTCTCCCAGCC R: AATGCCCAATTCCCACCTTC	110	1.5	58	Gustafson-Seabury et al. 2005	
small nuclear ribonucleoprotein polypeptide B	SNRPB2	22q12-q13	F: TGACCTTGGGGTCTATTTGT R: GGCGTATCGGAGATCATAAA	239	2.0	58	Gustafson-Seabury et al. 2005	
syntrophin, alpha 1	SNTA1	22q15-q16prox	F: CCTTTCTGCGCTTATTTTCA R: GGGTAAATCCGAACCTTGACA	383	1.5	60	Gustafson-Seabury et al. 2005	
SRY-box 18	SOX18	22	F: CGAGTTCGACCAGTACCTCAA R: GATGCAGGCGCTGTAGTAGAC	173	1.5	55	Perrocheau et al. 2005	AY817485
v-src sarcoma viral oncogene homolog (avian)	SRC	22	F: TCACCTTGGGAAAACACAC R: AGTGGATGGGGACCACAAAG	158	1.5	58	Gustafson-Seabury et al. 2005	
TAF4 RNA polymerase II	TAF4	22q19	F: TGGGAGGTAGGCAGCAAGT R: TAACGGTCAGGGATGGAAG	~290	1.5	58	Gustafson-Seabury et al. 2005	
transcription factor 15	TCF15	22q13dist-q14prox	F: CTGCAAGAGAGATGAGGAACA R: GCCGGAACGTAAGTGTGAC	~200	1.5	58	Gustafson-Seabury et al. 2005	
transcription factor-like 5	TCFL5	22	F: CTCTCATTCGACATCCATCTGA R: GCAATCCAATATCCTGGTG	500	3.0	50	Gustafson-Seabury et al. 2005	
TGFB-induced factor 2	TGIF2 (<i>DAP4</i>)	22	F: GGTTCGCCTCACAACATAAAC R: ACATGGCAGCTTCAAGGTTA	288	4.0	TD 60	Gustafson-Seabury et al. 2005	
transglutaminase 2	TGM2	22	F: GCTGGTCACTAACCAACAAGG R: GTGGCTCAAAGGCACACC	411	1.5	60		BM780537
transglutaminase 3	TGM3	22	F: GCTGCTTGCTGACTTCTCCT R: GCAAACAGTCCAGACCGACT	450	1.5	60		BM735536

TH1-like (Drosophila)	TH1L	22	F: CAGTGGTAGCAATGGGTGTG R: TTAACAAGCAGCTGCAGGAC	500	1.5	60		CD535792
microsatellite	TKY285	22	F: ACCAATGGTAAACATGGCAG R: CTGAAGAGGCAAGGAAAAGG	164 -174	2.0	58	Tozaki et al. 2000b	AB033936
microsatellite	TKY308	22q14 (prox to HTG14)	F: GATCGCGCGCACGCGAGCGC R: GTTAGTCTTAGTGATGTGC	99-125	1.5	56	Tozaki et al. 2000c	AB034617
microsatellite	TKY345	22	F: GTCACAGTAAGGCTTACATTC R: TTGATTGAGAATGGAGAGCG	152-172	1.5	56	Tozaki et al. 2001	AB044846
microsatellite	TKY498	22	F: GGTGGGAGCATTATCTTTGC R: CTGTCTTTGTGCGTTTGGAG	274-276	1.5	58	Gustafson- Seabury et al. 2005	AB103716
microsatellite	TKY548	22	F: CAGCAAGACGTCTGTCCATT R: TACCCTGGGACTCATGCTCT	194-200	1.5	55	Gustafson- Seabury et al. 2005	AB103766
microsatellite	TKY554	22	F: GGCCTTCCTGACTCCAATTT R: AGCGTTTGCTGAAACCCATA	259-263	1.5	58	Gustafson- Seabury et al. 2005	AB103772
microsatellite	TKY560	22	F: ATCCACCCTCTGCTCCTCTC R: CCAAGGGAAAAATGGAAAA	164-182	1.5	58	Gustafson- Seabury et al. 2005	AB103778
microsatellite	TKY567	22	F: AGCCCTATCTTTACCTTCTC R: GAGGCGCTATTAAGTATTC	138	2.0	58		AB103785
microsatellite	TKY572	22	F: GTGTAGCGCATGATCCAGTG R: CCCCAGCCTGACCTTCAT	100-110	2.0	58	Tozaki et al. 2004	AB103790
microsatellite	TKY582	22	F: AGGCAGCTTGACTACCCTGA R: AAAGTCTCCCCTGCGTGTT	147-159	1.5	58	Tozaki et al. 2004	AB103800
microsatellite	TKY593	22	F: TGGATGAGAGAAGGCAAAAC R: CTGTATGAACCGTCTCCAAG	172	2.0	58		AB103811
microsatellite	TKY596	22	F: AGGGATGTCCTCCCTAAGA R: TCACCACTTCCAGGGAGTCT	122-136	1.5	58	Tozaki et al. 2004	AB103814
microsatellite	TKY695	22	F: TGCCATGCAAAGAAGTGAGA R: TCCTTCCCCACTCTGCTTTA	165-187	1.5	50	Tozaki et al. 2004	AB103913
microsatellite	TKY785	22	F: TTAGGTGTCAAGTCTAGGAC R: GTGGGGAAGACGCTAAAGAG	192	2.0	58	Tozaki et al. 2004	AB104003
microsatellite	TKY1009	22	F: ACAATGTCTGCAACTCACTC R: GCACTTTGCCACATTTGTTTC	119	2.0	58		AB104227

microsatellite	TKY1093	22	F: ACATCAGTGATGTTTCACAGC R: GGGCATGCAGCTTCTTTAG	332	2.0	58		AB104311
microsatellite	TKY1106	22	F: TGCCACAACCTAGAAGGATTC R: GCAGAACGTGCGAACTTAAC	278	2.0	58		AB104324
microsatellite	TKY1158	22	F: AGCTCCACTTGTCAAACATG R: AGAGCCCTCACTCAATAAC	192	2.0	58		AB104376
microsatellite	TKY1160	22	F: AATATCCCCTTAATGGCCGAC R: ATTGGGAGAATCTGGAACAG	211	2.0	58		AB104378
microsatellite	TKY1315	22	F: CATTGTCCAACCTAGACCATG R: GGAGCCTAGAAAAAGTACAG	206	1.5	58	Tozaki et al. 2007	AB215258
microsatellite	TKY2105	22	F: GCACTCTTGGTACAAATCTT R: ACCCTCATGAGAGGAATTTG	245	1.5	58	Tozaki et al. 2007	AB216048
microsatellite	TKY2468	22	F: CGGCAGACACAACGACAG R: AGAAGCACCCACTCTCCTCA	148	1.5	58	Tozaki et al. 2007	AB216411
microsatellite	TKY2844	22	F: TTTCTTGTTGAACGCAAACA R: GACATGACGGCTGTCTCTTT	174	1.5	58	Tozaki et al. 2007	AB216787
transmembrane 9 superfamily protein member 4	TM9SF4	22	F: CTCCCACCACAAGACAAAGC R: GGACAACGGCATATTTATTTACAAC	423	1.5	62		CX600477
topoisomerase (DNA) I	TOP1	22	F: TCCCATTCACTCTTCTCCCC R: ATCCAGCCAAGAAAAGGCTC	113	1.5	58	Gustafson- Seabury et al. 2005	
microsatellite	UMNe077	22q15- q16prox	F: CAATGGGGACTTCTCAGATAGC R: AGGGAGGTTGAAGAGTTTACC	135-143	2.0	58	Roberts et al. 2000	AF91707
microsatellite	UMNe105	22q15- q16prox	F: TGTGTGGCCAGTTTATAACCATAC R: AAACAAGCCAATCCCAAAAG	210	1.5	60	Mickelson et al. 2003	AF536249
microsatellite	UMNe137	22	F: CTGCTTTTTACTGCTTCAGTGC R: GATTTGAGTCGAGGTCTGCC	137	1.5	58	Wagner et al. 2004a	AY391299
microsatellite	UMNe183	22	F: AGAGAACAGGAGAAGACATGCC R: ACCCTGTCTCATGGAAGCTG	106	2.0	58	Wagner et al. 2004a	AY391316
microsatellite	UMNe208	22	F: AGAGCAGAACGCAACTTTCC R: AGGAGATGCGCATATGTGC	140	2.0	58	Mickelson et al. 2003	AF536290
microsatellite	UMNe215	22	F: AACTGCAGCCTGGTGAGC R: GACCTCCTCCTTTCTCTTCTG	197	2.0	58	Mickelson et al. 2003	AF536296
microsatellite	UMNe355	22	F: TCATGCAATTCTGAAAAAGAGC R: CAGAGCAAATCTTCCTCACC	182	2.0	58	Wagner et al. 2004a	AY391346

microsatellite	UMNe358	22	F: TACTGCTAAACAAAGAGTGCGC R: TCATGCGTTTCTTTTGTGTTAG	138	2.0	55	Wagner et al. 2004a	AY735243
microsatellite	UMNe441	22	F: GATAAACTGTCCTCCTGCTGAG R: GGCAGAAAGTTCTGTGGAGTG	150	1.5	62	Mickelson et al. 2004	AY731395
microsatellite	UMNe466	22	F: CAGGCCCTGCTAACTCTC R: TAAGGAAGACACTGCCTGCC	371	1.5	62	Wagner et al. 2004b	AY464493
microsatellite	UMNe490	22	F: TTGAAAAGGACACGTGCAAG R: TAGGCCACCTTCCAAAATTG	~300	1.5	55	Wagner et al. 2004b	AY464503
microsatellite	UMNe499	22	F: CTGCAGCCCGTGTGTATG R: TTAAAAGGGACTTGAGAGGGC	~100	1.5	60	Wagner et al. 2004b	AY464507
microsatellite	UMNe537	22	F: TGCATTACGGGAAAGGAATC R: CTGAACTGCACACTGAGAAATG	129	1.5	58	Mickelson et al. 2004	AY731409
microsatellite	UMNe607	22	F: AAGACCATCTTTGCAGTGTGG R: TTCCTTTGCCCTTGGGATATG	220	1.5	58	Wagner et al. 2004a	AY735295
5'-3' exoribonuclease 2	XRN2	22	F: GACCCTCTGTTCTCACCCCTTA R: GAAGTGGAGGCATAGCAAAAG	158	2.0	58	Gustafson- Seabury et al. 2005	
tyrosine 3- monooxygenase/try ptophan 5- monooxygenase activation protein, beta polypeptide zinc finger, CCCH- type with G patch domain	YWHAB ZGPAT (<i>KIAA1847</i>)	22	F: CCCAATGCTACACAACCAG R: CCGAGAAATTGAGTGCCAG	~1000	1.5	62	Gustafson- Seabury et al. 2005	BI961675
zinc fingers and homeoboxes 3	ZHX3	22	F: ATCTGGTTCACAGCCCAAAG R: TGACCACCTTCACAGCAGAC	416	1.5	63	Gustafson- Seabury et al. 2005	BI961508
zinc finger, NFX1- type containing 1	ZNFX1 (<i>KIAA1404</i>)	22	F: GGGCGTAAATCATACTCTGG R: GATCTCCTCAAAGTTCATCAGG	373	1.5	60		CD464197
				112	1.5	55	Gustafson- Seabury et al. 2005	

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
ATP/GTP binding protein 1	AGTPBP1	23	F: TTAGAAAGTAAGTCATTTAA R: AAATCTATAAGCAACACCTGGT	~275	1.7	58		
microsatellite	AHT039	23q12	F: CCATTTTCTCATCACAAGCG R: TGAATCCCTGCTGCTTCC	79-102	2.0	58	Swinburne et al. 2000*	AJ271524
microsatellite	AHT072	23	F: TCTGCCCCCTCTTCATGTATACC R: TCATGAATGAAATGCTAGGTGG	229-240	1.5	58	Swinburne et al. 2003	AJ507689
microsatellite	AHT114	23	F: TGCAGCCCTCTTAAGCCC R: AGTGGAAAATGACCGATGCA	243	1.25	61		
microsatellite	AHT117	23	F: AGAGACAGGAGAATGTTGAAGG R: AACATTTGACCTCACTTGGTG	190	2.0	61		
aldehyde dehydrogenase 1 family, member A1	ALDH1A1	23	F: GGGCCATTAAGAGAAAGA R: TATATGACCCCCAAGTCC	161	3.0	58	Chowdhary et al. 2003	
aquaporin 7	AQP7	23q17-q18	F: TAGGTGGCATCATCTACTTGG R: GGATTGAAGGTCTGCTGGT	183	1.5	58	Perrocheau et al. 2006*	
microsatellite	ASB39	23q15	F: ACAGCTGCCTGGATATGTGG R: GCAGAGAGAAATAGAGATGC	156-172	2.0	58	Irvin et al. 1998; Lear et al. 1999*	AF004769
BAC end sequence	CH241-2L11_SP6	23	F: GCCACTCCATGCTGACTGTA R: CTGCAGGTCTGGATCACTCA	244	1.5	58		CT864967
BAC end sequence	CH241-32E21_T7	23	F: GACCTGCTCCATTACCCCTA R: TAGTGCACCCAAGAGCAGTG	152	1.5	58		CT957034
BAC end sequence	CH241-34H11_T7	23	F: AGTTCGTGGCAGCAGAAAAT R: ACTTTCCTGCTGGGAGCAT	208	1.5	58		CT958587
BAC end sequence	CH241-42I2_SP6	23	F: TGCTGGCTGCCTTAGGAATA R: TGGACTGTTGGTCTGAGCTG	176	1.5	58		CT964212
BAC end sequence	CH241-80K19_T7	23q18	F: TGCATAAAGGATGTGCGGTA R: CTGGTGGTGGTGATGCTATG	153	1.5	58		CU011085
BAC end sequence	CH241-92F11_SP6	23	F: GAGGCAATGGAAACACTGCT R: TGGGCCAATTCTATCACTCC	201	1.5	58		CU013797
BAC end	CH241-115F18_T7	23	F: TTCACCCCTCATTC AACCTC	103	1.5	58		CT007279

sequence			R: CGTCTTCTGATGGGTTGAGC					
ciliary	CNTFR	23q19	F: CCCAACACCTTCAATGTGACT	346	1.5	58		
neurotrophic			R: TGATAGCTGTGGCATTGTGG					
factor receptor								
microsatellite	COR060/055	23	F: TCCTTCCTTCTCTGGGTCTT	200-226	2.0	58	Ruth et al. 1999	AF108377/ AF108372
			R: AGCAGTATGTTCCAAGCGT					
cathepsin L1	CTSL1	23	F: ACTCTTTCTGGCTGCCCTTT	300	1.5	60		
			R: TGCTTCCCTTGGCTGTATTC					
death-associated	DAPK1	23q13	F: ATGGTGTTGGTCAGTGAGGTC	210	1.5	55	Perrocheau et al. 2006*	DX010461
protein kinase 1			R: GACGGAGAAGATCAAGTGCTG					
dedicator of	DOCK8	23	F: AGTTGGAAAAGGACTTGTTGGT	161	1.5	58		CX595911
cytokinesis 8			R: TGCCCAGTATAGCCAAAATCT					
fructose-1,6-	FBP1	23q12-q13	F: GTGAAGAAGCTGGATGTCCTC	108	1.5	58	Mariat et al. 2001*	CX594820
bisphosphatase 1			R: CACTATTATGGCGTGTGTGTCTT					
growth arrest and	GADD45G	23	F: GAGCCGAGGACTCTACAAGTG	212	1.5	58		DN511281
DNA-damage-			R: CAGTGCAGACCGCTCAGT					
inducible, gamma								
growth arrest-	GAS1	23	F: CCAGTGGTGTTGAACAATGC	626	1.5	60		
specific 1			R: GGATGGAGCACATGTACAG					
microsatellite	HP13	23	F: CCTAAGCACTGCCTTCAGCATC	134-138	1.5	58	Swinburne et al. 2005	
			R: GATCATCACTCCATATCCACTCCC					
microsatellite	LEX053	23	F: TTGTGGAGCTGTGTCTGCAT	202	2.0	58	Chowdhary et al. 2003	AF075655
			R: TTCAAATCCTAGCTCGTCCAA					
microsatellite	LEX063	23	F: CGGGGTGTGCATCTCTTAGG	241-249	2.0	58	Coogle & Bailey 1997	AF075663
			R: TGGCGAATGCTGAATCTGG					
leucine rich	LINGO2	23	F: CTCATGGGTGAATCATGTGC	189	1.5	58		CT941726
repeat and Ig			R: CCTTCACCAGCAGAAAGAGTG					
domain								
containing 2								
LOC158345	LOC158345	23	F: AGCCAGAGTTGCCCTTGTA	199	1.5	58		CT950695
			R: AAGCCCATCATTCATTTTGC					
NADH	NDUFB6	23	F: GGTACACGCCAGACGAGA	129	1.5	58		CX594959

dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa microsatellite	NVHEQ026	23	R: ATTCCTCCATAGGCCACATC					
opioid receptor, sigma 1	OPRS1 (<i>SIGMAR1</i> , <i>SR-BP1</i>)	23	F: GGAAGTGGAACCAACTATGACA R: TGGAGGTTTAAAGGGACGCTAT	140	1.5	58	Roed et al. 1998	AF056392
phospholipase A2-activating protein	PLAA	23	F: CGTCCTCACCATATGCCTTAC R: TCTAGGCCAGGGCTGGTCTCC	253	1.5	65	Lear et al. 2001	G62162
patched homolog 1 (<i>Drosophila</i>)	PTCH1	23	F: CTGGCTACATTGACCCTGAAC R: TGGTTCTGACACTGAGGCATA	240	1.5	58		DN509052
protein tyrosine phosphatase, receptor type, D	PTPRD	23	F: TGGTGATCTTTCCTTTTCTTGG R: GTATTTGAACTGGGCAGCAAT	137	1.5	58		CX605711
RAN binding protein 6	RANBP6	23	F: GGTAGGGGCAGAAACACAAA R: GGAGAACTTTCTGGGCAATG	168	1.5	58		CU017459
microsatellite	SGCV04	23q19	F: TGGAATGTGCAAGAACTCGT R: GCACCCATCTCCATTACTT	161	1.5	58		
small nuclear RNA activating complex, polypeptide 3, 50kDa	SNAPC3	23	F: CGACGCCTCCTCCTAAAC R: CAGCTGTGTGCCTTTGATTAT	213	3.0	58	Godard et al. 1997*	U90587
spindlin 1	SPIN1 (<i>SPIN</i>)	23q18-q19	F: ACAATGACAGTTTTGCACCTG R: AGTCACCATCCAAGCGTAGTT	181	1.5	58		DN504823
serine palmitoyltransfera se, long chain base subunit 1	SPTLC1	23	F: TGTGGACCCATCAGAAGACTGTTT R: ATGGAACACGAAGACCTCTGAACTA G	240	4.0	TD60	Chowdhary et al. 2003*	
tight junction protein 2 (<i>zona</i> <i>occludens</i> 2)	TJP2	23q15prox	F: CCAGAGAAAGATGCTGGCTA R: CGTGAAGGGAGAGAAGATCA	214	1.5	58		CX599930
microsatellite	TKY269	23	F: ATAGCTGCCTTCCAGGACTGT R: GGCTTTGCATAAAGCTTCAAA	169	1.5	55	Perrocheau et al. 2006*	DX010597
			F: ATTTGGGATGTCCTGAACAA	120-126	1.5	50	Kakoi et al.	AB048311

microsatellite	TKY301	23	R: TGCATTTCAGAGACTTTGTCA F: AATGGTGGCTAATCAATGGG	197-213	1.5	58	2000 Tozaki et al.	AB034610
microsatellite	TKY339	23	R: GTGTATGATGCCCTCATCTC F: GATCAAGCGTTAAGAAAGTTG	140-158	1.5	58	2000c Tozaki et al.	AB044840
microsatellite	TKY346	23	R: TGGAATCCATGACCAAATC F: CACAGCTCAGGTCCTACTTC	178-184	1.5	58	2001 Tozaki et al.	AB044847
microsatellite	TKY367	23	R: GTTCAGCAGAATTCAGTGAG F: GTTTTTGTCCATTGCTCTGG	236-242	1.5	58	2001 Tozaki et al.	AB044867
microsatellite	TKY385	23	R: AATTATGTTGGCCAGACTGG F: TAGTACGTACAACAGCTCTG	143-155	1.5	58	2001 Tozaki et al.	AB048291
microsatellite	TKY441	23	R: CACTTGCATCTTCCTAAAGC F: TGTCCTCCAGGAGAGGGAAG	190-210	1.5	55	2001 Tozaki et al.	AB103659
microsatellite	TKY486	23	R: TTTTGAACGCTGATTGCAG F: CAGCTTTTGTGGGAAGAGG	140-166	1.5	55	2004 Tozaki et al.	AB103704
microsatellite	TKY536	23	R: AACTCATCAGTCCATTGGCTTT F: GCAGTGTCAATGTACTTTCG	145	2.0	58	2004	AB103754
microsatellite	TKY542	23	R: GTGTGGGACAGCAATAG F: GGTGCCTAACCCAGATATGC	162-174	1.5	58	Tozaki et al.	AB103760
microsatellite	TKY568	23	R: CCCCATCAATTTCTGCTTTT F: TTCCTGACGTGAAGGCATTA	217-257	1.5	50	2004 Tozaki et al.	AB103786
microsatellite	TKY881	23	R: TGCCCTTCCTGCCTAGTAGA F: GTGGTAGATGAAGAGACGTG	206	2.0	58	2004 Tozaki et al.	AB104099
microsatellite	TKY947	23	R: TACCTCCCCACTCCCCAA F: AAACCTCCCCTATCCAGTC	285	2.0	58		AB104165
microsatellite	TKY1122	23	R: GTTAAAAAACAATTTAAACTGTG F: GTTAGTGAAGCTTAAGCTGC	288	2.0	58		AB104340
microsatellite	TKY2261	23	R: ACGAGGGCGTTACCAATAG F: GGTAACATACCCCTTAGTTG	120	1.5	58	Tozaki et al.	AB216204
microsatellite	TKY2321	23	R: TCATGTTCAGCCTCTGAGTG F: GAAGTAACTAGGGAGTCAC	259	1.5	58	2007 Tozaki et al.	AB216264
microsatellite	TKY2336	23	R: ATCACACTACTAGTGAGGG F: AAGTCTGTCATGAAATGGGA	152	1.5	58	2007 Tozaki et al.	AB216279
microsatellite	TKY2433	23	R: GATCTTTTAGGGAAACAAAGC F: TGGGAGGAAAACATGAAAAA	286	1.5	58	2007 Tozaki et al.	AB216376
			R: AATAACCAAGCCTGATGCAA				2007	

microsatellite	TKY2485	23	F: GTTTTTGCTGGCACCTTTTA R: GGTGGGAAAAGATGGAGAGT	161	1.5	58	Tozaki et al. 2007	AB216428
transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4	23	F: CTGCTGGAAGATGCGATG R: ATGACAGCGATGGTGAGAAG	~700	3.0	58	Chowdhary et al. 2003	
transmembrane channel-like 1	TMC1	23	F: AATTTGGGGATCCACATTCA R: ACAGCAGTAAGCGCCTCAGT	240	1.5	58		CT951751
tyrosinase-related protein 1	TYRP1	23q14-q16	F: GCGCCAACTCCACAGTATTT R: TATGCTGATGACCAAAGGGG	332	2.0	58	Rieder et al. 2000	AF395448/ AF395447
microsatellite	UM018	23	F: AGATAGGGAAAGAACGAAG R: GGTTAGTGTCGGATTAGG	~200	2.0	58		AF195135
microsatellite	UM019	23	F: TACTGCCAGCACTTGTACC R: TCTCTCAGTTTCTCTCTCTGTC	134-180	2.0	58	Meyer et al. 1997	AF195136
microsatellite	UM022	23	F: AAATAGCCACCAGCACGCAC R: GCAGCAAATCATCAACCCAG	125-140	3.0	58	Meyer et al. 1997	AF195138
microsatellite	UM027	23	F: TGCAAGAATTGTGAGGGAC R: GTGCTCAGTTAGTGGTATTC	235-239	1.5	56	George et al. 1998	AF195574
microsatellite	UMNe51	23	F: TCTCTGCTCCAGATGGCC R: AACTTTCTCATCCCCAACCC	158-160	2.0	58	Roberts et al. 2000	AF191689
microsatellite	UMNe069	23	F: CCTCTTAAGGATGCTCACAGTG R: TGCATGGGTGTATGGGTATG	122-130	2.0	58	Roberts et al. 2000	AF191702
microsatellite	UMNe142	23	F: ATGGAGTGGAATGATTGGAG R: CAGTGAATGGCACATTTTAC	150	1.5	58	Mickelson et al. 2003	AF536260
microsatellite	UMNe159	23	F: TTGCAATCCTTTCCCCTTC R: GATCATTCACTTGTGTGGAAAG	141	1.5	58	Mickelson et al. 2003	AF536269
microsatellite	UMNe357	23	F: GATCCAGTAACAAACAAGCTAATTT R: TCAAATGATTTCTTACTGAGGATTC	210	2.0	58	Wagner et al. 2004a	AY391347
microsatellite	UMNe473	23	F: GATCCAAACCGGCAAAAAC R: TCTGCTCCCCACCAAGTTC	~270	1.5	58	Wagner et al. 2004b	AY464497
microsatellite	UMNe524	23	F: TATGGTGGCAAATTCTGCTC R: CTTAAGCATTATAGCAGCAACC	~100	1.5	55	Wagner et al. 2004b	AY464517

microsatellite	UMNe560	23	F: CTCATCAGCCACGCTGTG R: GGGGACACAATTCAATCCAC	~175	1.5	58	UMNe560	AY464527
microsatellite	VHL121	23	F: AATGCACATGCCATAGTGCTC R: GCTTCCCAGACTCTCATTTGG	122	1.5	58	van Haeringen at al. 1998	
very low density lipoprotein receptor	VLDLR	23q15dis	F: ATGGCCTAACGGGATTACAC R: TTAGTGCGAGAGGATGAGCTA	767	1.5	62	Milenkovic et al. 2002	

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	24STS01	24	F: TACCTCCGAAACCCTGTGTA R: GAGCCCTTTGTAGAAGACCTG	272	1.5	58		CX604630
sequence tagged site	24STS02	24	F: GGACTCATGAACTCCTTCACG R: CCTCAAGAAGATCCTCATCG	102	1.5	58		
activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	AHSA1	24	F: CAAGTGTGAGGTGACAGAGGT R: CCAGTTTAGTTTGATGCTCCA	106	1.5	58		CX595858
microsatellite	AHT004 (HMB4)	24q14	F: AACCGCCTGAGCAAGGAAGT R: CCCAGAGAGTTTACCCT	190	2.0	58	Binns et al. 1995; Godard et al. 1998*	Y07733
microsatellite	AHT032	24q14-q15	F: CCAAGTCCTGCTTCCATGAT R: CCTGTCTGGGTCAGAGGATG	138-142	2.0	58	Swinburne et al. 2000	AJ271517
microsatellite	AHT071	24	F: GCAATTGAAACAGAGGAAAACA R: GGACAGAACTTACCGAACCC	243-249	1.5	58	Swinburne et al. 2003	AJ507688
microsatellite	AHT119	24q14	F: GACAACCACCCGAGGTTG R: ATGACCCATAGTAGGAAACCCA	264	1.5	61		
bradykinin receptor B2	BDKRB2	24q16	F: ACTTCCTCATGCTGGTGAGC R: TCTGCATCTCGTTGTTACGC	336	1.5	58		
calmodulin 1	CALM1	24	F: TTGAGCACAGTCAGGCATTTTGT R: CCTGAGGTAAACCAATTTTAAATGTGT	149	2.0	58	Chowdhary et al. 2003	
CDC42 binding protein kinase beta	CDC42BPB	24	F: TCGTAGTCAGAAGCTGGACAT R: TTCAAAGGAGAGATTCGTGTC	127	1.5	58		CX595283
microsatellite	COR024	24	F: CAAAAGTGATTGCCTTCGAT R: TTGGAAGCTGGGTGATTG	201-213	2.0	58	Murphie et al. 1999	AF101393
microsatellite	COR025	24	F: ACAGAGCTGACTGCCTATGG R: TCCTCTTCTCAGGGAGACCT	172-176	2.0	58	Murphie et al. 1999	AF101394
microsatellite	COR061	24	F: TTAAGAGTGGCAGACCGACT R: GAACGCTTCTTAAGTGGCAGA	188-210	2.0	58	Tallmadge et al. 1999a	AF142598
microsatellite	COR087	24	F: CCTAATCATCAATGGCTAACTG R: CAATCTGTCCATAACTGGCAC	181	2.0	58	Tallmadge et al. 1999b	AF154940

deiodinase, iodothyronine, type III	DIO3	24q16.3	F: TGCTAGACTTCCTGTGCATCC R: GCCTGCTTGAAGAAATCCAAC	205	1.5	55	Perrocheau et al. 2005*	AY817462
microsatellite	EA2C4	24	F: CAAAGCTGTGCTCTGGGTTT R: AGCAGGAGGAATGGCAGTTA	253	3.0	58	Gralak et al. 1994	Z29341
fibronectin leucine rich transmembrane protein 2	FLRT2	24q15- q16.1	F: GGGGCATTTGTAAAGGGATT R: GCCTTTACTGAATATATCAACAAGGTA	304	3.0	58	Chowdhary et al. 2003*	
hypoxia-inducible factor 1, alpha subunit	HIF1A	24	F: CCTAAATGTCCTGCCCACCCT R: TCCAACCACAAAGAGCAAAAGG	290	2.0	58	Chowdhary et al. 2003	G62202
microsatellite	LEX032	24	F: CGTAGTAGGGTTTTGGGTCC R: TTGCGTTTCAATTTTAAATGAC	254-267	3.0	58	Coogle et al. 1996	AF075634
microsatellite	LEX042	24q15	F: ACATACAAACCTGCTCAACAT R: CCTACACATCGCTCATCAA	217-227	3.0	58	Coogle et al. 1997	AF075644
microsatellite	LEX074	24	F: AAGAGTGCTCCCGTGTG R: GACAATGCAGAACTGGGTAA	148-168	2.0	58	Bailey et al. 2000	AF212260
mediator of RNA polymerase II transcription, subunit 6	MED6	24	F: GCCAGAACTGTGAAATCTGA R: AATGAGGCATAACGATTGACA	156	1.5	58		DN507485
numb homolog (Drosophila)	NUMB	24q15	F: GATCCCGTCTGCAACTT R: GGTGGCCTGTCTTAGAGA	365	3.0	58	Chowdhary et al. 2003	
phosphatidylinosito l glycan anchor biosynthesis, class H	PIGH	24	F: GCCTACCTTACCAACTGAGGA R: AGTTTCCCATTGTCTTGTTC	136	1.5	58		
sel-1 suppressor of lin-12-like (C. elegans)	SEL1L	24	F: TCGAGATGTCTTCACCCAAC R: CTGCCCTGCTGTAAGCTAT	118	1.5	60		
serpin peptidase inhibitor, clade A, member 1	SERPINA1 (PI, AAT7)	24q15- q16	F: CAACACTCACACTGAGATCCTG R: TCAGCATCCCTGAAGTTGATGG	200	2.0	58	Godard et al. 1998; Lear et al. 1999*	AF034077
sine oculis homeobox homolog 6	SIX6	24q14	F: CTCTTCCTCGGCCCTTAG R: CCTTACCCGCTTTAACCCT	184	2.0	55		

(Drosophila)

solute carrier family 8, member 3	SLC8A3	24	F: TCAGGGGACGTGCCAAGCA R: ATATAGAGCCAGATGTAGGCA	650	1.5	56		DQ329036
SPARC related modular calcium binding 1	SMOC1	24q14	F: GAAAGTCCACTCATGTGACCA R: ACACACCAGCAGTAGCCAGT	150	1.5	60		CX602091
spectrin repeat containing, nuclear envelope 2	SYNE2	24	F: TAGTGGAACGTCAACCTCAAG R: ACATGCACCTTCTCTTCAGC	106	1.5	58		CX597180
microsatellite	TKY036	24q14	F: TGGCTTTTCCTGCTGACTCAT R: TGCTGGGAGGGCTCCCTTTC	183	2.0	58	Hirota et al. 2001*	AB048342
microsatellite	TKY037	24q14	F: CTCAGGGCCAACAATCCTG R: TCGGTTGTTTCTGAAACTGC	151	2.0	58	Hirota et al. 2001*	AB048343
microsatellite	TKY307	24	F: CACAGTTCTATCCAAGCGAC R: TAACCATGTCAACAGAGAGG	247-257	1.5	58	Tozaki et al. 2000c	AB034616
microsatellite	TKY357	24	F: ATCTTCCCTAAAATCGCCAC R: TCTCAGGGATGGTAAATCTG	143-163	1.5	58	Tozaki et al. 2001	AB044857
microsatellite	TKY394	24	F: TTGAAGTTGAAGAGCTTGCG R: TGCCAGAGAATCAGTTATGG	154-174	1.5	58	Tozaki et al. 2001	AB048299
microsatellite	TKY524	24	F: AGTTGTGGCTTGCTTTCTAC R: TTGCACTTGAGCACTTAGTC	241	2.0	58	Tozaki et al. 2004	AB103742
microsatellite	TKY564	24	F: GCCCAGGCAAATACATCATT R: TGAGCTGTGAGCACTCCTTG	267-281	1.5	58	Tozaki et al. 2004	AB103782
microsatellite	TKY631	24	F: AGGAAAGCTGCAGGCATAAA R: TTCTGCTGCCAGAGAGAACA	101-115	2.0	58	Tozaki et al. 2004	AB103849
microsatellite	TKY756	24	F: TGAAGGGAGCATCCGTTACT R: GGTGGATCTGCCCTCAGTAG	139-153	1.5	58	Tozaki et al. 2004	AB103974
microsatellite	TKY782	24	F: TGGACTTGACTTTCACAAGG R: GCAACACATGGGCTCAGAAA	154	2.0	58		AB104000
microsatellite	TKY831	24	F: CATCAATGGATGGACGGATA R: CTGTCACAAATGGCAGGATT	142	2.0	58		AB104049
microsatellite	TKY849	24	F: GATCTTAAAAGTCCTTACCACAC R: CACAGATTTAATTGGCACGTGA	159	2.0	58	Tozaki et al. 2004	AB104067

microsatellite	TKY857	24	F: CTTAGAATGCTCTGTTTCTGAG R: TGCTGTATCCCCTGAATCTA	163	2.0	58	Tozaki et al. 2004	AB104075
microsatellite	TKY864	24	F: TGGAGCATCGTCAGTTAAGG R: GCACAGACACAGGCTAGCAG	109	2.0	58		AB104082
microsatellite	TKY982	24	F: ATAAC TTTCTCTCAGCCAC R: GTTGATGAGAGCCCAGAAG	232	2.0	58		AB104200
microsatellite	TKY998	24q14	F: GAATATCTGATTAGGCTGGC R: AAAGATGCCCTGTTGACTG	148	2.0	58		AB104216
microsatellite	TKY1014	24	F: CACATCAATGAACCAAAC TCTC R: GAGTCTAAGACTCCAGAATTG	155	2.0	58	Tozaki et al. 2004	AB104232
microsatellite	TKY1083	24	F: AACCTGTTGAAACCCACAAC R: GTCTAAGAGCAACTCCCAG	248	2.0	58		AB104301
microsatellite	TKY1594	24	F: CCAGAGGCAGCACAATTGA R: CCTGGAAAACGGTAAGTACT	153	1.5	58		AB215537
transmembrane emp24-like trafficking protein 10 (yeast)	TMED10	24	F: CATTTGTACTGGGTTTCCTCA R: ACCAGAAGCCACCTAAACACT	216	1.5	60		DN509189
microsatellite	UCDEQ467	24	F: CCCC GCAGCCAGCCTGTT R: TTGTTCCCA GTGTAGGCACTCT	88 - 108	2.0	58	Eggleston- Stott et al. 1997	U67415
microsatellite	UM012	24	F: GGAATTTAGACTATGACTGAGG R: GCCACCTGAACACTTTTAC	100 - 110	3.0	58		AF195131
microsatellite	UMNe152	24	F: ACAGGTGTT CATCCAAATTTTG R: AAAGTAGAGGAAGACAGGCACG	144	1.5	58	Wagner et al. 2004a	AY391303
microsatellite	UMNe210	24	F: AAAAGGGGAAAAACTCCTGAATG R: TCTTTTCCCAA AAGTGTCGG	197	2.0	58		AF536292
microsatellite	UMNe389	24	F: AGGGAACAGCAGCCACAG R: AGTTCATCCTCGACAGGG	190	2.0	65	Wagner et al. 2004b	AY464475

microsatellite	UMNe533	24	F: CTACGAGAAGTGCTTCAAAAGG R: TGAAATCTGATGATTCTAGCCC	~250	1.5	58	Wagner et al. 2004b	AY464519
microsatellite	UMNe569	24	F: ATGTTATACACTTCATATATATGCTT R: TGAGGAAAAGATGGAGTTGT	~200	4.0	50	Wagner et al. 2004c	AY735273
vaccinia related kinase 1	VRK1	24	F: GGACTATGCCGAAAAACCTC R: CCATTCTCCACAACACTGAAG	114	1.5	58		DN506868
tryptophanyl-tRNA synthetase	WARS	24	F: AGTTACAAAGCTGCCACAGG R: GTCCACAAAGTCCTCTCCAG	114	1.5	60		

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
v-abl Abelson murine leukemia viral oncogene homolog 1 microsatellite	ABL1	25q18-q19	F: GCAGCCTCTTCCTGTTTCAG R: ACTCCCCGACTGAACGAACAC	202	1.5	60	Shubitowski et al. 2001	AY008765
microsatellite	AHT007	25	F: CCTTAGATCCGAGAAGGAGA R: GAAGCCTCACTCCATCCAGG	121-133	2.0	58	Swinburne et al. 2000	AJ507668
microsatellite	AHT051	25	F: ACCTACACACCACTCGTCAAG R: TGCCTTATATTCCTTGTGTGTG	146-181	2.0	58	Swinburne et al. 2003	
angiopoietin-like 2	ANGPTL2	25q18-q19	F: GCAACTACAACTGCTGGTGA R: GTCTCTGTCCAGGGTGCTG	185	1.5	58		CX604237
microsatellite	COR018	25	F: AGTCTGGCAATATTGAGGATGT R: AGCAGCTACCCTTTGAATACTG	249-271	2.0	58	Hopman et al. 1999	AF083461
microsatellite	COR080	25	F: CGTGCTGCCAGAGGTAAATA R: ACTGAGATGAGGTTTGCTGC	198-206	2.0	58	Tallmadge et al. 1999a	AF142617
catenin (cadherin-associated protein), alpha-like 1	CTNNAL1	25	F: CGATGTTGGAGGTTATCTTGG R: CTCGCCTGAGTTGACAGTTC	103	1.5	58		
dopamine beta-hydroxylase	DBH	25q18-q19	F: CGAGCCCATCGTCACCGAG R: CCAGGGCCAGGCGGCCAG	~180	1.5	65		
exosome component 2	EXOSC2	25q18-19	F: GGTGAAACGGCAGAAGACTC R: GTGCTCAGGGGTAGGGTAGAT	100	1.5	67		DN506159
golgi autoantigen, golgin subfamily a, 1	GOLGA1	25	F: CAGGACCCACGTACCAG R: CTAGAAGTTGCTGCTCCAAGC	115	1.5	58		CX604753
heat shock 70kDa protein 5	HSPA5	25	F: TGAGAACACGGTCTTTGACG R: TGTTGCTCAACGTTTTCCAG	195	2.0	TD60	Caetano et al. 1999	AF134222
nipsnap homolog 3A (C. elegans)	NIPSNAP3A	25	F: CTGCATCATTTTCACCATTTG R: CCACCTCCTTCAAATAAAAGTG	130	1.5	58		
microsatellite	NVHEQ043	25	F: TGACACAAGATAAAAGCCCCAGG R: GATTGGGAAAAGAGCACAGCC	135-159	2.0	58	Roed et al. 1998	AF056396
pregnancy-associated plasma protein A, pappalysin 1	PAPPA	25q17-q18	F: TCACTGTGGGATTCTCATGG R: ACAAGCTTGAGCCTCCTTT	221	2	58		

RAB GTPase activating protein 1 stomatin	RABGAP1	25q17-q18	F: TGAGTTGAGCTTCATTCTTGAG R: GTTTTCTCGTCATCACTTCCA	164	1.5	58		CX595444
	STOM	25q17	F: AATCAGTGTGGATGGTGTGGTC R: GCAATCTCTTCTCTGTCAGAGAGG	~180	1.5	65		
syntaxin 17	STX17	25q13	F: GAGCGGGTATATTTTCGTTGTT R: TGTCCACACATCTCAAGACCT	181	1.5	58		CX598896
surfeit 2	SURF2	25	F: CTTCTGGGAACCTGAGTCCA R: TGTTGTCTCCGTGCTCAGTC	267	1.5	58		
microsatellite	TKY018	25	F: TTTTCGTGACTTAACCCCTCC R: CTTCCCTGAGCAGAGATG	136	2.0	58	Hirota et al. 2001	AB048329
microsatellite	TKY292	25	F: CCTCAACATCCTTCTAGACG R: AGTACACGTTGAACGTTACC	124-134	1.5	58	Tozaki et al. 2000c	AB034601
microsatellite	TKY302	25	F: TACATGGTGAGAAATAAGCACC R: ATCTGCATCCTAGCTCACTG	95-101	1.5	58	Tozaki et al. 2000c	AB034611
microsatellite	TKY316	25	F: CACATTCTTCCGGTCACAAC R: TGTTTAGGGACACTAAACGC	282-294	1.5	58	Tozaki et al. 2000c	AB034625
microsatellite	TKY429	25	F: AACAAATGGACAAGCACGTAC R: GTCCTTCAGGGAAAATCTGTG	111	2.0	58		AB103647
microsatellite	TKY575	25	F: CAGACCTGAGTCCCAGAGGA R: CCATTCCAGGAAATGACCTT	206-208	1.5	58	Tozaki et al. 2004	AB103793
microsatellite	TKY771	25	F: CAGTCCTCTCACTCCAACCT R: GGACAGGTAAAGGTGGTATG	198	2.0	58	Tozaki et al. 2004	AB103989
microsatellite	TKY851	25	F: GGTCTTCTGGACAGAAAGTG R: AGCATCATCGTTATTCCCCT	255	2.0	58		AB104069
microsatellite	TKY1064	25	F: GGATTAGGGAAGACTTCTCA R: TCAGTTTCATGCCTTCACTC	190	2.0	58		AB104282
microsatellite	TKY1065	25	F: TAGTTAATGGTCAAGCCAGG R: GTCTTCCCTCTCACTCAATG	116	2.0	58		AB104283
microsatellite	TKY1096	25	F: ATTCAAAAGCCAAGCCCTTG R: TAAAACAGGAGCGGTTTCATG	277	2.0	58		AB104314
microsatellite	TKY1104	25	F: GACCTACGGCTAGAATATAC R: GGTACCTACTTCAGGATTAG	197	2.0	58		AB104322
microsatellite	TKY3347	25	F: AGTTTCTCTCTCCCCTGCAT R: GGCAGGTCTAGCCTTTCTTC	239	1.5	58	Tozaki et al. 2007	AB217290
toll-like receptor 4	TLR4	25q17	F: GTGCAATACCCTTACAGATGC R: ATGCTTTCACCTCTCCCATAC	196	1.5	58		

transmembrane protein 15	TMEM15	25	F: GTCCCAGGTATCGTCTTTGAC R: GATGTGTGTCAGGATGAGTGG	183	1.5	58		
transmembrane protein 38B	TMEM38B	25	F: CCAGGGCTATTCTTTCCCTACC R: GCTATCAGCATGTGTGACTCC	100	1.5	60		DN507625
tropomodulin 1	TMOD1	25q12-q13	F: CAGAAGGATCAGACCACCAAG R: CTCGCTTTTCCCCTGTGTAG	130	1.5	66		
TNF receptor-associated factor 1	TRAF1	25	F: GGAAGCTGCGTGTGTTTGAG R: TGTTCCAGGCTCAGGATGTG	127	1.5	58		
thioredoxin	TXN	25	F: TGGTGGCTTCAAGTTTTTCC R: GCCCCCAAGGATGTTAATTT	187	2.0	58	Caetano et al. 1999	AF134237
microsatellite	UCDEQ405	25	F: ACCTCGTCTGGCTGTTGTAAG R: ACTTGCTGTGCGACTCTG	256-274	2.0	58	Eggleston-Stott et al. 1997	AF000010
microsatellite	UMNe160	25	F: TGGAAGGATTCTCCCCAAG R: GTTGCTCCAATGCCATACTC	114	1.5	58	Wagner et al. 2004a	AY391306
microsatellite	UMNe339	25q17-q18	F: TCATTTTGCACGAAAGAAAGC R: GAAGTGAAAGGCTTAAGCTGC	103	2.0	58		
microsatellite	UMNe362	25	F: GAGAGAGAGAGTATGCGCGC R: GATTCCAAAGGCTATCCACTC	117	2.0	58	Wagner et al. 2004a	AY391350
microsatellite	UMNe416	25	F: ACTTTCTAGCCTGCCCTATGG R: CCTAACCCTCATCCACTTGTG	134	2.0	62		
microsatellite	UMNe525	25	F: CAACCACTCCCTTTCTCCAG R: AATGGCCAAAGGTAGCCAC	152	1.5	62	Wagner et al. 2004c	AY735259
microsatellite	UMNe598	25q18-q19	F: CTGTCCTTAGTCTGGTCC R: GATCCTCATTTTATACCC	146	1.5	50	Mickelson et al. 2004	AY735290
microsatellite	ZuBeEq12	25	F: CTTCTTGACCCCAACACGCTCACA R: GCATCCTGCTGGGACCCTCTTTGA	193	1.5	68	Klukowska-Rotzler et al. 2006	CR956107

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
sequence tagged site	26STS02 (4ES)	26	F: CGCATTCGAGAATTCGCAC R: GAAATCGCGTTATTACCGAC	109	2.0	55		
sequence tagged site	26STS03 (GP2)	26	F: CGCTTATGCAGAGAGCCATG R: GAGTGCGTGAGTAATGAGTC	177	2.0	55		
microsatellite	A-17	26q13-q14	F: GTGGAGAGATAAAAGAAGATCC R: GGCCACAAGGAATGAACACAC	95-111	3.0	58	Marti et al. 1998*	X94446
ADAM metalloproteinase with thrombospondin type 1 motif, 5	ADAMTS5	26	F: CGTGGTGAATAAGAGGTCACA R: GCCCAGGTGATGTTCAATAAC	177	1.5	58		CX598584
amyloid beta (A4) precursor protein	APP	26	F: AGAACTAGACTACCGCCGCA R: TGGGTCACAAACCACAAGAA	374	2.0	58		AY011366
BTG family, member 3	BTG3	26	F: GTCACTACCCTCCTCCTGTTC R: GGTTCGCCCCATCTAACTTT	261	1.5	58		CX595745
chromosome 21 open reading frame 34	C21orf34	26	F: TAGGCAAAGCATGTGAGCTG R: GGGGAAAAGAAGGAAGGAAAC	462	1.5	58		AJ618767
carbonyl reductase 1	CBR1	26	F: TGAGACCATCACAGAAGAGGA R: GCTCACCATTGTTTGACTTTC	357	2	62		CX603498
CGG triplet repeat binding protein 1	CGGBP1	26	F: GAGTGGTCATTTGGTGCTTAGTC R: TACCTCAGAAATCTGATAGCGTG	240	3.0	58		G62184
BAC end sequence	CH241-100G23_SP6	26	F: ATCCATCAAGATGCCCTGTG R: ATCACCCCATTGGTACTCAC	392	1.5	58		AJ542940
BAC end sequence	CH241-102G11_SP6	26	F: TCCCAAAATGTGTTTCACCTC R: TGCATAGCTCATTATGATACTGGAA	696	1.5	58		AJ584196
BAC end sequence	CH241-109H15_T7	26	F: TGAATGAATATAATTAACATGGGAAG R: TCGGTTTAATTGTAAATTTAGGAACC	356	1.5	58		CT006207
BAC end sequence	CH241-111N13_SP6	26	F: CCCCAGGAACAGGTCTGATA R: TATGGGCGAAGGAATTC AAG	325	1.5	58		CR955725
BAC end sequence	CH241-112C9_SP6	26	F: GGTGTGGTTGTAAGGGCAAC R: ACATGGCATGCATCGTTATC	567	1.5	58		CR955681
BAC end sequence	CH241-	26	F: TTCCCTCCCTGATATCTTTCC	349	1.5	58		CR957276

BAC end sequence	112M19_T7		R: TGAAATGGTAGCCGTCTAGG					
	CH241-112P17_SP6	26	F: TGGAGATACTGCTGCACGAC R: GGTTTTAGAAACAGCCATTTGC	557	1.5	58		CR955487
BAC end sequence	CH241-113E17_SP6	26	F: ACATTTGCCATGCATTCCTC R: GGACGTGAGAAAATGGAAGC	656	1.5	58		CR955553
BAC end sequence	CH241-114I13_SP6	26	F: TTCTAGATTTAAAAATTTTCCTGTGG R: GGCAGAGGAGCAGAAACAAC	443	1.5	58		CT006985
BAC end sequence	CH241-115F4_SP6	26	F: ACTTACCGTAATGGCGGTTG R: CCCCCATCCTGTATCTCCAC	291	1.5	58		CT007664
microsatellite	COR071	26	F: CTTGGGCTACAACAGGGAATA R: CTGCTATTTCAAACACTTGGA	178-200	2.0	58	Tallmadge et al. 1999a	AF142608
microsatellite	COR099	26	F: GAAAAGAAATTCCAGGTCC R: CCTTGGAAAACAATGACTGG	158-160	3.0	50	Tallmadge et al. 1999b	AF154952
cystatin B	CSTB	26q16	F: AGGTTGGCGATGACGACT R: CCTGGCTTTGTTGGTCTGAT	101	1.5	58		DN509356
Down syndrome critical region gene 1	DSCR1	26q15	F: GTCCTTTGGAAATACCTAATGCCG R: ACGTCACTAGGAACACTTGACAGCT	206	3.0	58	Chowdhary et al. 2003*	
dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	DYRK1A	26	F: ACTTTCGAGCGGTTGAATTG R: AACTACTGAATTCCTTGTGATATTGC	444	1.5	59		CX592800
microsatellite	EB2E8	26q15	F: GGGGTTGTGGAGAATGTCTG R: CCACAGGTTTTTCATGGGTCT	197	3.0	58	Gralak et al. 1994; Lindgren et al. 2001	Z29340
v-ets erythroblastosis virus E26 oncogene homolog (avian)	ERG	26	F: GCTCCAACTCCAACGTATCA R: CCGAGGGGTACTTGTAGAGAG	270	1.5	63		CX597452
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	26q16-q17	F: TCCTTGCTTGGCTGAGAATC R: AGAGCATGAAGCCCAGCTTA	208	1.5	60	Lear et al. 1998	AF053637 AF134064

phosphoribosylglycinamide formyltransferase	GART	26	F: TGCTCAACATACACCCATCC R: AAAGCCACCATGCAAACAG	500	1.5	60		CX601789
glucan (1,4-alpha-), branching enzyme 1	GBE1 (<i>GBE1</i> exon2)	26q12-q13	F: CCAACATGATGGTTCTGACC R: GAGTGCGTGAGTAATGAGTC	232	1.5	58	Ward et al. 2003*	AY301014
microsatellite	GBEm1	26	F: GGAAAGACATCTTGCACCAC R: TGCACCCATAACGCAAAG	230	1.5	65	Ward et al. 2003	
5-hydroxytryptamine (serotonin) receptor 1F	HTR1F	26	F: GTGATGCCCTTCAGCATTGTG R: TGCAATYCTACTTGCTTGTCT	433	2.0	58	Ward et al. 2003	AY301022
interferon gamma receptor 2	IFNGR2	26	F: TTCATGACCAACTCCATTGTG R: TCTATTTGTACTGGGATGCTTGG	700	1.5	60		BM781196
interleukin 10 receptor, beta	IL10RB	26	F: TACCACCTTGATGGAATGTGA R: GTCATCCACAGGACAGAAGG	127	1.5	58		
junctional adhesion molecule 2	JAM2 (<i>JAM</i>)	26	F: TTTCAAGCACACAAAATCCTTT R: TTTGCAAATGTAAGACAAAGCTG	120	1.5	55	Perrocheau et al. 2006	DX010637
potassium voltage-gated channel, Isk-related family, member 2	KCNE2	26	F: ATCCAAGCGACGAGAACACT R: GGTGGCCTTTGGTTCCTCTA	115	2.0	58		AF387764
potassium inwardly-rectifying channel, subfamily J, member 6	KCNJ6	26	F: CTGGGGGAAGGGTATTTGAG R: ATGCTCATGGATGCTTTTCC	548	1.5	58		AJ885649
microsatellite	LEX044	26q13-q15	F: TTGGGCTTCTTATCTTGTTAC R: GGCCATATGATTTGCTTT	191-205	3.0	58	Coogle et al. 1997; Lindgren et al. 2001*	AF075646
LOC391271 protein	LOC391271	26	F: CCCCCGGAATTATTCTTCAC R: CTGCTTGAGAATTGGAAGTGG	587	1.5	58		AJ584005
MORC family CW-type zinc finger 3	MORC3	26	F: ATATTATATCTGAAGCCAAGGATGC R: ACTGACATCCAACCTTTTTCATAAGC	500	1.5	60		CX596098
myxovirus	MX1	26q16-	F: CTGAGAACAACCTGTACAGCCA	~200	1.5	60		

(influenza virus) resistance 1 microsatellite	NVHEQ070	q17 26	R: TCCAGCACGGAGCTCTTG F: GCTGGTCAAGTCACACTGTG R: AACCTCACCCCAAGTTGTAT	189-203	2.0	58	Roed et al. 2000	AJ245765 AJ576675
oligodendrocyte transcription factor 1	OLIG1	26	F: TCAGGACTGTCACCTGCAAC R: CACCAGAGAAACCCACCATC	693	1.5	58		
POU domain, class 1, transcription factor 1	POU1F1	26q12	F: CTGGAGAGACACTTTGGAGAA R: TCACYCGTTTTTCTCTCTGYC	121	2.0	55	Ward et al. 2003*	AY301021
roundabout, axon guidance receptor, homolog 1 (Drosophila)	ROBO1	26	F: AACCASTTACAAYAGTTCCAG R: GCAGATCGACAGCCAATTC	107	1.5	55	Ward et al. 2003	AY301019
roundabout, axon guidance receptor, homolog 2 (Drosophila)	ROBO2	26q14	F: TCCAAGRCACAGCTGGARG R: CAGTTTCCTCTAATTCTT	231	1.5	58	Ward et al. 2003*	AY301020
runt-related transcription factor 1	RUNX1	26	F: GGATCTGCTTGCTGTCCAAG R: AAACAAACAAAAATCCCCAAAC	391	1.5	60		CX598164
S100 calcium binding protein B	S100B	26q17	F: GTAACAGAGACGACCCAAGGA R: CCAGCCAGCTAACACGTATG	196	1.5	58		CX604272
SAM domain, SH3 domain and nuclear localization signals 1	SAMSN1	26	F: CTCCGCTTTTTTCAGGTCAAG R: AACAGGAGGAGAACGAGACG	595	1.5	58		AJ885556
SH3 domain binding glutamic acid-rich protein	SH3BGR	26	F: TAGGAAGAAGCAGCAAGAAGTC R: CCCAGGAACATTCTCTCTCAT	118	1.5	60		
T-cell lymphoma invasion and metastasis 1	TIAM1	26q15	F: AAGCAAGTCTCTTGGGAGGAG R: TCTCCTTGATGTCATCCTGCT	188	1.5	55	Perrocheau et al. 2006	DX010596
microsatellite	TKY275	26	F: TCTCAGTGGATATAACTAGC R: GAGATGGATACAGATAGAAG	144-154	3.0	50	Tozaki et al. 2000b	AB033926
microsatellite	TKY386	26	F: GGACAAGTCTATAGCAAGAG	311-313	2.0	55	Tozaki et al.	AB048292

			R: GCACTTGTCTCCCTAATTTTC				2001	
microsatellite	TKY502	26	F: ACGGAAAACGTATGCCACTC R: AGTGGGGACTTTGTTGAGGA	220-228	1.5	55	Tozaki et al. 2004	AB103720
microsatellite	TKY664	26	F: TACTGCCCTTGGCTGACTCT R: CAGAACATGAACCCCTCCAG	241-261	1.5	58	Tozaki et al. 2004	AB103882
microsatellite	TKY766	26	F: ACTTTGCACCTGTGCAAAAAG R: CTGATTCTTGGCATCTGGAAA	100	2.0	58	Tozaki et al. 2004	AB103984
microsatellite	TKY767	26	F: GTGAACATGACAGTTCATATGG R: GACTACACTCTTTCCTTGTCT	90	2.0	58	Tozaki et al. 2004	AB103985
microsatellite	TKY778	26	F: CTTAGATGGAGTCCTCCTAC R: GGGTTCCTTTTACCTTCTCC	208	2.0	58	Tozaki et al. 2004	AB103996
microsatellite	TKY794	26	F: CAAACGCCCAGCAGAGTG R: AGTCTGCAACTAACTCTCAG	199	2.0	58	Tozaki et al. 2004	AB104012
microsatellite	TKY846	26	F: TCAAACCATCTGCTCAGAAG R: AAATCCCAATCTGAGGGTAG	188	2.0	58	Tozaki et al. 2004	AB104064
microsatellite	TKY934	26	F: TTCCAGTGGTTAGGATGTAG R: TTGAGCATAGTGATAGCATATG	141	2.0	58	Tozaki et al. 2004	AB104152
microsatellite	TKY1017	26	F: ATGTCAAGGTCTAGTGTTCC R: GCTCCTTCCTCTGGTGTA	124	2.0	58		AB104235
microsatellite	TKY1155	26	F: TGACAACCTGATATCAGCTCAG R: ACCTTTTACACATGAGCCAG	281	2.0	58		AB104373
microsatellite	TKY1233	26	F: CTCTAGGAAGCCAGAACTG R: CACCTTCCCGTCTCTAATG	179	1.5	58	Tozaki et al. 2007	AB215176
microsatellite	TKY3385	26	F: CACCAGGGAAAAGTACATGG R: TCCCTCACCTCTGGTTATGA	180	1.5	58	Tozaki et al. 2007	AB217328
ubiquitin protein ligase E3A pseudogene 2	UBE3AP2	26	F: TGCACAGTTGCATGACTTTC R: CCAGCGCCTATTTATCCAAC	617	1.5	58		AJ885744
microsatellite	UM031	26	F: GCTCAAACCAACCTTTCAAAC R: TCAGGCCTTAAAACAGACACAC	~200	1.5	58	George et al. 1998	AF195578
microsatellite	UMNe66	26	F: GAATCCCATCTTTCCTTTCAG R: ACGTGGAGAATTATCCTGCG	124	1.5	58	Roberts et al. 2000; Ward et al. 2003	AF191699
microsatellite	UMNe127	26	F: TTATAAATCACCCTGTTTACACAC R: TCTTGAAGCAGGATGGGC	135	1.5	58	Wagner et al. 2004	AY391298
microsatellite	UMNe153	26	F: GTGCTGGAGTGAGCTGACC	~150	1.5	58	Mickelson et	AF536265

			R: ATCCAAATCGGAGACCATATG				al. 2003; Ward et al. 2003	
microsatellite	UMNe188	26	F: GTTAACAAGGATTGTTTTGGGC R: TGC GTTTCTGCTTCTCCC	132	2.0	58	Wagner et al. 2004	AY391317
microsatellite	UMNe434	26	F: TCTGCTGTTGGCCATCATC R: ACCTGCCTGCAAAACCTTC	268	1.5	58		
microsatellite	UMNe444	26	F: CGGTCTTGCTTGGGTTAGTC R: AAGGGTCTTCTCAGCAGAAGG	273	1.5	58		
microsatellite	UMNe542	26	F: TGAAAGAGACCATAACGATGC R: CACGACTTAGAGACGTGTGAGC	252	1.5	62	Wagner et al. 2004	AY735263
microsatellite	UMNe547	26	F: CTGCCATTTCATCAGAAAATCTC R: TCAATCATTTTGTACTCATGGC	~150	1.5	58	Wagner et al. 2004b	AY464522
microsatellite	UMNe559	26	F: CTTCCCATTTCTCTATCACCCC R: CTGTTCTCCCAATTCTTTCTGG	160	1.5	58		
microsatellite	UMNe588	26	F: CGCAGGTAGACTGTGTTAGGC R: CAAGACTGGAAATTTCAAGGG	144	1.5	58		
ubiquitin specific peptidase 16	USP16	26	F: ACCCTTAGAAATAAACCTTGAGC R: CTGTCCTTGCTGCTGATAGCC	489	1.5	58		
ubiquitin specific peptidase 25	USP25	26q13	F: AGCTGCTTGATTGTTCTACGG R: AGGAAGGCAAGGGCTAAGAAC	200	1.5	55	Perrocheau et al. 2005	AY817489

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	27CA001	27	F: CGATCCAGGGTTCTGTGAGT R: TCCATTCCCTCAGGCATCTTC	251	2.5	58		
sequence tagged site	27STS01 (<i>Fell Pony Syndrome</i>)	27	F: GTGTGAACAAGGGTGATCTGG R: CAAGCCTGGTCTCGTAAACGC	430	2.0	58		
sequence tagged site	27STS02	27	F: GATGCCAGCAGTGATGAAGA R: CCACAGGCTCTGTCTCCTGT	160	1.5	60		CX595237
adrenergic, beta-3-, receptor	ADRB3	27q12-13	F: GCAACCTGCTGGTAATCGTG R: CTCATGATGGGCGCAAAC	364	1.5	56		
aspartylglucosaminidase	AGA	27	F: GTCTGGAGAAACCACACTGG R: TCCTACTAAAAGCGTGTGTGC	~729	1.5	58		CX600750
microsatellite	AHT074	27	F: GAGGAAAGATTGGCACAGATG R: ATGGGATGAACCACAGCAC	119-121	1.5	62	Swinburne et al. 2003	AJ507691
microsatellite	AHT082	27	F: TGCCTATTGTTTGAGGAGGG R: GCCAGTACAAATTGGGCAGT	203-209	2.0	58	Swinburne et al. 2003	AJ507699
ankyrin 1, erythrocytic	ANK1	27q14	F: GTGGCTCATTTCTGTCTC R: AACTCGAGATTGCTAAGTGG	307	2.0	63		
microsatellite	ASB38	27	F: TGGGGTTGCCCTTGTTACC R: TCAGAGGATGAGGCACAGC	111-119	2.0	58	Irvin et al. 1998; Lear et al. 1999	AF004768
microsatellite	ASB5	27	F: CAAAAAGGCAAATATTGGGATAC R: CTTGATCTTCCTATGTAGTTTCTG	1335	1.5	58		
ash2 (absent, small, or homeotic)-like (<i>Drosophila</i>)	ASH2L	27q14-q15	F: TCCTGTCTACCTTTCATGACCA R: GATGTTTCATCCTGCGTTCG	428	1.5	60		
caspase 3	CASP3	27	F: TGGTACAGATGTGGATGCAG R: GCAACAATCCCCTTTGAAG	577	1.5	58		CD467628
CDKN2A interacting protein	CDKN2AIP (<i>FLJ20036</i>)	27q16	F: TGGAACTAAAGCCACCAACAG R: GTCCCAGCTGGCTTCTAAGAG	203	1.5	55	Perrocheau et al. 2006*	DX010482

BAC end sequence	CH241-10E15_SP6	27	F: AGAGCATTGAAAAGGGAGCA R: TTTGTTGGTTACCCCAAACC	203	1.5	58		CT839565
BAC end sequence	CH241-34I24_SP6	27	F: AAGGGATCAAGTTTCCCACA R: CAGTTGGTTGGAACAATGCTT	222	1.5	58		CT958650
BAC end sequence	CH241-3I14_T7	27	F: GAGGCCTGAGACCTGCAGTA R: AGTCTTGGCCACCAATCTGA	211	1.5	58		CT826489
BAC end sequence	CH241-84O15_SP6	27	F: TTGCTTATGTGCTTGCTCTGA R: ATGCGAGGAATGTTTTTCAGC	229	1.5	58		CU016897
ceroid-lipofuscinosis, neuronal 8	CLN8	27	F: GCTGTCGTCTCCCTGAAC R: CTAGATAGTGGCCGGCTTTG	347	1.5	60		CX603545
microsatellite	COR017	27	F: GAAGGCCTGAAGCATTTACA R: CGTAATGTTGACCAAACCTTCA	235 - 253	2.0	58	Hopman et al. 1999	AF083460
microsatellite	COR031	27	F: CAATTGCCATTTGTTCCAGTG R: GCTTAAGAAACACCAGGCAG	214	1.5	58	Murphie et al. 1999	
microsatellite	COR040	27	F: GTGTTGGGACACGAATGAAT R: AGGCTGTCTCCAGAGTCCTT	275-289	2.0	58	Murphie et al. 1999	AF101409
ER lipid raft associated 2	ERLIN2	27	F: TGGTGGTGTGATGATCTACTTTG R: AAGCGTGTGTACACTGCAGAA	317	2.0	62		
dCMP deaminase	DCTD	27	F: ACAGCAGACCGACTCAGAAG R: GTTATGTGTAACCTGCGAGACGA	115	1.5	58		CX603647
deleted in liver cancer 1	DLC1	27	F: GGCTGGTGGAGCTGATTTAG R: CTTCTCCAGGCCATTTTCAG	391	1.5	64		CX598743
coagulation factor XI	F11	27	F: AGAAGGGGGATTGGGTACAG R: TTCTGGATGCTGGTGTTTGA	218	1.5	52		CT974651
fibroblast growth factor receptor 1	FGFR1	27q14-q15	F: AGATAGGGGATTTGCAC R: TGAAATTTATGGGCTAGAAC	210	2.0	55		
farnesyltransferase, CAAX box, alpha	FNTA	27q14	F: GCAAACACAGCACAGAAAGTG R: AGGAAACAATCACATTACTTAGAGC	248	1.5	60		CX597111
GIN5 complex subunit 4 (Sld5 homolog)	GIN54	27	F: CCAAACCCGATCTAGATTTCCT R: GTACTGCTCCAGAGGCAACC	265	1.5	60		DN505633
general transcription factor IIE,	GTF2E2	27	F: AGTCAATAATCCCCAAAATTGAAGT R: GCAGTCCTTCCTCTATGTCTTCT	155	1.5	58		DN506260

polypeptide 2, beta 34kDa microsatellite	HMS45	27q16	F: TGGTAAACTGTGCATGATTGG R: AAAGGAAGATTGGCAAACCA	215	3.0	58	Godard et al. 1997*; Chowdhary et al. 2003	U89813
indoleamine- pyrrole 2,3 dioxygenase microsatellite	INDO	27	F: CTTGCTCATTAGAGTCAGGC R: GCAAATGGTAGCTTCTCAGGG	124	1.5	58		
	LEX005	27q16	F: AAGGCAATGCTTATCAAATGC R: TTACCCGCAGTGACTTCTATT	245-265	3.0	58	Coogle et al. 1996; Lindgren et al. 2001*	AF075609
myomesin 2, 165kDa	MYOM2	27q18	F: CGAGGACATTGGGGATAATG R: GGATCCAAGACAAAGCTGGA	245	1.5	60		
neuregulin 1	NRG1	27	F: TAGGAAATGACAGTGCCTCT R: TCAGGTCTATACCACCTCAC	242	2.0	62		
pericentriolar material 1	PCM1	27	F: AGCCCGAAGAAGAAGTGGA R: TACTGTTGCCGGATCTACTGG	224	4.0	58		
platelet- derived growth factor receptor-like PDZ and LIM domain 3	PDGFRL	27q16-17	F: AAAGGAGCCAGGAGAGAACAG R: TTCCTTTACATCGAAGCTCCA	206	1.5	55	Perrocheau et al. 2006	DX010552
RNA binding motif protein 13	PDLIM3	27	F: CCCTTCTTCTGTCAGTACTC R: TGAGTACAACTGCATAGGTGTA	148	1.5	60		
	RBM13 (<i>LOC84549</i>)	27q15-16	F: CCAGCAGAATCAGGCAGTC R: CCATGTTTCTTCTTGATTCCA	159	1.5	55	Perrocheau et al. 2006*	DX010520
solute carrier family 25, member 4	SLC25A4	27	F: AAGGGATCATTGATTGCGTG R: AGTAGGCAGCTCTGTAGATA	420	1.5	60		
sperm associated antigen 11B	SPAG11B	27	F: AGAAAGCGGAGAACTGC R: GAACAAAGCAGTTTAATGTGG	95	1.5	58		AJ786157
steroidogenic acute regulator	STAR	27	F: AGGTCACTCCCCAGAATGGT R: GCTTCCTCTTCCCTGAGTTTG	110	1.5	55		BI960825

microsatellite	TKY288	27	F: AGTATGACAGCCCACTCTCG R: ATGCATTTCAAGGAAGCCAG	139 - 157	2.0	58	Tozaki et al. 2000b	AB033939
microsatellite	TKY315	27	F: GATGCCTCGAACTAGCTTG R: GATCTTCCATGTTTTTGTGTTGG	89-105	1.5	58	Tozaki et al. 2000c	AB034624
microsatellite	TKY431	27	F: TCCAAATGAGCATCTGCATG R: TTTGCTTGCTTAATTGCCAC	159	2.0	58		AB103649
microsatellite	TKY437	27	F: TCCTGGGAAGGGTCCTTATT R: GCTCATTGCTACTGGGGTGT	167-183	1.5	58	Tozaki et al. 2004	AB103655
microsatellite	TKY480	27	F: CAGAGGGCAGAGGATTTGTC R: AGGGACGAGGACCAAATGTA	263-281	1.5	55	Tozaki et al. 2004	AB103698
microsatellite	TKY576	27	F: ATTGCAGCCAATTTCTACG R: GCAGGGCATATGACAAGAAA	270-276	1.5	58	Tozaki et al. 2004	AB103794
microsatellite	TKY603	27	F: TTTTCTGTCTTTTTCACCTTCA R: AACCAGCTTGCAAATCCTGT	181-199	2.0	60	Tozaki et al. 2004	AB103821
microsatellite	TKY612	27	F: GAAAGTAAAATCCTAGCAGGAGGA R: AATGATGACATGAGCGGTGA	282-284	1.5	58	Tozaki et al. 2004	AB103830
microsatellite	TKY764	27	F: GGTGACCTTTAAAGTCCCTT R: TGCAAGCAAACTTGCCTTG	261	2.0	58		AB103982
microsatellite	TKY789	27	F: CATGAGGAGAGGAACAAAGG R: CATCTCTGCTTTGGGAAGGC	200	2.0	58	Tozaki et al. 2004	AB104007
microsatellite	TKY804	27	F: GGATGGGTCAAGTGAAAGAG R: TTCCTATGACCTAGTGAAGC	250	2.0	58	Tozaki et al. 2004	AB104022
microsatellite	TKY828	27	F: CTCCTTCTGGCTCTACTATT R: GCATGGATTAAGGTGTATGC	186	2.0	58	Tozaki et al. 2004	AB104046
microsatellite	TKY1137	27	F: ATCCAAGGAAGAATAGGGTG R: GGGTAAGTTACTCCACATGA	221	2.0	58	Tozaki et al. 2004	AB104355
microsatellite	TKY1152	27	F: GGAAGGATAGTTTATGCAGC R: AACCCCAATCCTGAAATCAC	222	2.0	58		AB104370
microsatellite	TKY3012	27	F: ATCACATCCTTGGGCATTTA R: CCAAAGCATCCTCCATTCTA	304	1.5	60	Tozaki et al. 2007	AB216955
TM2 domain containing 2	TM2D2	27	F: CAAAACCTCTTCCTGGATATCAGAC R: GAAAAAGCAATGTACAGAAATAAAGA	250	1.5	60		CX596200

transmembrane protein 66	TMEM66	27	F: CCTGTGATGCTGTAAGAAGC R: CCACTGAAGGACTCAAAGC	249	1.5	58		
microsatellite	UCDEQ005	27	F: AGCGGAAGTGCTGCGAAAG R: CCAGCATCTCTGGGCAGG	236-238	2.0	58	Eggleston-Stott et al. 1996	U35423
microsatellite	UMNe117	27	F: TCCCTTAAAAGTTCTCCCTTCC R: TGAAAATTATTGTTTGCCCTTG	139	1.5	58		
microsatellite	UMNe161	27	F: TTGTCATTTCAAGTCTTTTCC R: TGAAAATTATTGTTTGCCCTTG	157	1.5	58	Mickelson et al. 2003	AF536270
microsatellite	UMNe186	27	F: TATAAACCTCCCTGATTTGCC R: TGATAGAAGGAGCTAAGCCTGC	149	2.0	58		
microsatellite	UMNe258	27	F: TGCCTATTGTTTGAGGAGGG R: AGCCAGTACAAATTGGGCAG	207	2.0	58	Mickelson et al. 2003	AF536320
microsatellite	UMNe313	27	F: AGAACCTGTTGGAGATACGAGG R: ATCAGAGTGGAGACATGGGG	179	2.0	58	Wagner et al. 2004a	AY391334
microsatellite	UMNe379	27	F: ATCCATGGAGTCTCGGAGTG R: ACAAGCAAACAAGCAAAAACC	161	2.0	58	Wagner et al. 2004b	AY464470
microsatellite	UMNe476	27	F: GAGTCATGTTACCATCCCC R: TTAGACGGTCAGCCAGCAG	~200	1.5	58	Mickelson et al. 2004	AY731400
microsatellite	UMNe523	27	F: GTTCCTGATATTGAAAACACCC R: TTTTGTGGCATTACTTCCCTAC	243	1.5	58	Mickelson et al. 2004	AY731406
microsatellite	UMNe553	27	F: TCTCAGTGCGGAATTAACCC R: GAGAACTGGACCATGAAAGAGG	~250	1.5	55	Wagner et al. 2004b	AY464525
voltage-dependent anion channel 3	VDAC3	27	F: TGACACAGGGAAAGCATCAG R: CCTGTGTTCTGGTACAAATATGG	963	1.5	58		DN505151
microsatellite	VHL149	27	F: GGAGGCGTTCTGGTCACGTT R: ACTTCAGCCTGTTTGCAGTCA	100	1.5	62	van Haeringen et al. 1998	

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
aconitase 2, mitochondrial	ACO2	28	F: TGCACCAACTCCAGCTATGA R: ACATCCCTCAGGATCTGTGC	394	1.5	58		
apoptotic peptidase activating factor 1	APAF1	28q15	F: TGAGAAAGGTGGGACACTGA R: GGCTACGTCCAATAGTTAAGCAA	155	1.5	62		
arylsulfatase A	ARSA	28	F: AGGCTACCTCACAGGAATGG R: GCTCCACTCAGGTGTCTGGT	210	2.0	58	Caetano et al. 1999	AF130747
activating transcription factor 4	ATF4	28	F: CGAGAAGCTGGATAAGAAGC R: CAGGTACTGGATCTCCTTGG	178	1.5	58		CX602876
B-cell translocation gene 1, anti-proliferative	BTG1	28	F: GTACTGGAAGTTTTATGACAAGA R: TGCTAACACCACAGTTGAGA	208	1.5	58		CX600800
cysteine and glycine-rich protein 2	CSRP2	28	F: CTTGTTTCACGCTCAGTAAAGG R: CCGCAGAGGTTTCACAGTAGT	109	1.5	50		DN508680
cytochrome P450, 2d region, gene family	CYP2D@ (<i>CYP2D</i>)	28q18	F: ATGACATCCCGTGACATTGA R: CTACTGCATTCCCACATCCA	200	2.0	58	Caetano et al. 1999; Mariat et al. 2001*	AF130756
decorin	DCN	28	F: TGGACAAAGTGCCCAAAGAT R: TTCTTCAGGTTCTTAAAGTCTCCA	103	1.5	58		
DEAD box polypeptide 17	DDX17	28q16	F: CAGGCCAATACACCTATGGTC R: CAAACTGTTGTGACATCACTGG	204	1.5	55	Perrocheau et al. 2005	AY817461
FLJ21963 protein	FLJ21963	28	F: TGGCAAGGAAGATCCTTTGA R: CATTGACAAGGGCAGACAGA	311	1.5	58		
GLI pathogenesis-related 1 (glioma)	GLIPR1	28q12-13	F: GCCTGGATGGTTTCTTTAGTC R: GATCGGAACCTTGTTGTGCAT	113	1.5	58		DN505358
glycosyltransferase 8 domain containing 2	GLT8D2	28	F: CACTGGAATGGAAGACACAAG R: CGGTGTTATAGTAGGCTGCAA	189	1.5	58		CX601670
microsatellite	HTG30	28	F: TCAAGGCAAATCTTTCCCAG R: GTAAAATAACAAGTTGTTCCAG	242	2.0	58	Lindgren 2000	
insulin-like growth factor 1	IGF1	28q15	F: CATTTCAAAGATGGGCATTC R: TACCAACTCCAGGACCGTTT	227	1.5	58		U85272.1

IKK interacting protein	IKIP	28	F: GTGAAGAGCCGGAAGAAGTC R: ACGTCCCCAGAGAGAGCA	151	1.5	54		CX602699
KIT ligand	KITLG	28q14	F: CCCCACTGGGTCCCTATAAT R: AAGGCCAAGTGCAATACCAG	261	2.0	58		AF165596
KRR1, small subunit processome component, homolog (yeast)	KRR1 (<i>HRB2</i>)	28	F: CAGGATGATGTCGCATGT R: AACTGTGTTTCCCTGAACC	~246	1.5	56		CX599475
lectin, galactoside-binding, soluble, 1	LGALS1	28	F: CTTTGTGCTGAACCTGGG R: CCACCATCCTTGCTGTTG	111	1.5	58		BI961629
lumican	LUM	28	F: CAGGTGCGTTTACTTTCCTCT R: GTCAGGTTTACCAGTCCATCA	487	1.5	58		
minichromosome maintenance deficient 5 (S. cerevisiae)	MCM5	28	F: CTGCGGAGAAGCTGAAGAAC R: GTGATGGGGATGCTGGAG	94	1.5	62		DN507453
methionyl aminopeptidase 2	METAP2	28	F: GCTTTCAGGACTTTCAGATGTT R: GAGGATATAGGTGCAGAACTGG	187	1.5	58		
myogenic factor 5	MYF5	28	F: CTGTTTCAGAGCCCACTAGCC R: GTCCGCTGGTCGTGTATTTT	294	2.0	58		AF411602
nuclear transcription factor Y, beta	NFYB	28	F: GGCAGAATTGTAGTGAGACGTT R: ACATTTTGTGTTGACCATCTG	152	1.5	58		CX595848
microsatellite	NVHEQ054	28	F: AGATGTCCACCTTCTCGCTG R: CGGGGCTTTTAGGAGGTAAC TA	172-186	2.0	58	Roed et al. 2000	AJ245763
pro-melanin-concentrating hormone	PMCH	28q15	F: CCTTTGTCGAAGATATGGGATT R: CAGCAGGTATCAGACTTGCCAAC	212	2.5	58		
peroxisome proliferator-activated receptor alpha	PPARA	28q18	F: AGTGACGTCCTAGAGACC R: TCACTGTCTGTCAGTTCCAG	292	1.5	58		
PWP1 homolog (S. cerevisiae)	PWP1	28	F: AAAGCTGCCTAGAAATGTTCC R: TGCAGAGAGGAATGTCAGG	90	1.5	58		CX598419
suppressor of cytokine signaling	SOCS2	28	F: CGAATACCAAGATGGGAAGTT R: GTTCGCTTATCCTTGACAT	123	1.5	58		

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TIMP metallopeptidase inhibitor 3	TIMP3	28q16	F: GCTTCCCTCGGACACTAACT R: CGGGTGGAATAGGTGATGT	184	1.5	58		CX594408
microsatellite	TKY299	28	F: TGAAGTTTGAGCCTGGACACC R: TGCAATGTCCTGGGAAATCC	120	1.5	58	Tozaki et al. 2000c	AB034608
microsatellite	TKY333	28	F: CCTTCACTAGCCTTCAAATG R: TTGTGTTTAGACAGTGCTGC	109-127	1.5	56	Tozaki et al. 2001	AB044834
microsatellite	TKY364	28	F: TTCACAGCCGTCATTCAAAC R: GATCCTAAACAAGCTGCAGG	102-116	1.5	52	Tozaki et al. 2001	AB044864
microsatellite	TKY425	28	F: CCTGGGTGTCGTGTGTTTTA R: TTCCTCTCTCCTGCCTCATC	109-125	1.5	58	Tozaki et al. 2004	AB103643
microsatellite	TKY467	28	F: GCGAACAGTTGCTGAACACT R: TGCCTTTGGCTCAGAAAAAC	234-254	1.5	55	Tozaki et al. 2004	AB103685
microsatellite	TKY485	28	F: GGTGGTGGTGAGGATAAAGAC R: TTGTAAGAGTTCTGCCATCCA	150	2.0	58		AB103703
microsatellite	TKY493	28	F: CATGTGGATTGTTAGAGCTC R: GATCGTTGAGAAAGATGTGTG	179	1.5	58		AB103711
microsatellite	TKY515	28	F: AGGCCAGCAGTGTTTCCTCTA R: GGCTCAGGTACGTTCCCTTC	145-151	1.5	58	Tozaki et al. 2004	AB103733
microsatellite	TKY768	28	F: TTTGGCTTGAATGGGGAAAG R: ATTCAGTAATCGAACTGGTGTG	114	2.0	58		AB103986
microsatellite	TKY808	28	F: CCTGAGTGCTTTTGAAGTGG R: ATACTTTTTGCCAACTACAAAATA	128	2.0	58	Tozaki et al. 2004	AB104026
microsatellite	TKY872	28	F: TGGGGCTTTGGGAGACAT R: CAAGGCCAGAATTTCTTGAAGT	124	2.0	58	Tozaki et al. 2004	AB104090
microsatellite	TKY873	28	F: ATTCCTATCTCTGGAGAACC R: AGATTTGCCTGAAAGTCAGC	223	2.0	58		AB104091
microsatellite	TKY877	28	F: GATCTCTGTCTTCATCTGTCTA R: AGTCAATGTAAAGGTTCTTGGC	210	1.5	58		AB104095
microsatellite	TKY1023	28	F: GTACCCCCAAATAAAATGTGC R: ACTTTAATCACTCCCCACTC	121	2.0	58		AB104241
microsatellite	TKY1060	28	F: AAAATGAGGTCATGCTGGAG R: CAAGTAGAAGCATCACCCCTG	167	2.0	58		AB104278

microsatellite	TKY1080	28	F: ACAAAGCTGCTGAGAGAAATG R: TCACTGCATACAAGCCAAGTA	200	1.5	58		AB104298
microsatellite	TKY1153	28	F: CTTCGCAGAAAGACATTGAAG R: TCAAATGAAAGGCAACAAGAT	290	1.5	58		AB104371
microsatellite	TKY1168	28	F: GTCTGAAGGACAGATGGTTG R: GGACTGTATATGACCAAAGC	101	2.0	58		AB104386
microsatellite	TKY3400	28	F: AAGTCAGAAGCCAAGCTTTC R: CGCTCAGATACGCAGAGTG	115	1.5	58	Tozaki et al. 2007	AB217343
translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22	28q16	F: TGTACCCCTGACCATAGGTG R: CTGCTCTGTCCTCCACAGTC	196	1.5	58		DN510491
tryptophan hydroxylase 2	TPH2	28q12-q13	F: CATTGTGGGGCTTAGCAGTC R: GGTTCCTTTATGGTATTTTAC	138	2.0	57		
thiosulfate sulfurtransferase	TST	28	F: GTGACTCCCGTGCTTAGTGA R: GGCCAAGTTTATTCCAGTGC	129	1.5	58		
microsatellite	UCDEQ425	28q18	F: AGCTGCCTCGTTAATTCA R: CTCATGTCCGCTTGTCTC	230-250	2.0	58	Eggleston- Stott et al. 1997; Lindgren et al. 2001	U67406
microsatellite	UM003	28	F: GGAGGGACGATAGAGAGTAAG R: GCAGAGATAACGGACATGG	135-160	3.0	58	Meyer et al. 1997	AF195125
microsatellite	UMNe166	28	F: GTAAAGGGGAACCAAGAATTCC R: GGGCCTGGTACCTCATAAGC	127	2.0	58	Mickelson et al. 2003	AF536273
microsatellite	UMNe345	28	F: CCAATCTGCTTTTTCACCTTGC R: ATACTGGTAAGGGCACCGTG	196	1.5	58	Mickelson et al. 2004	AY731389
microsatellite	UMNe354	28	F: AACTGTCCCAATTTTCCCG R: CTTCCGTTCCCTCCCTCTACC	~250	2.0	58	Mickelson et al. 2004	AY731390
microsatellite	UMNe465	28	F: CTGTGACTAGGCCAAGGTCTG R: GGGACTAGCTAGACCCTGGG	~200	1.5	58	Wagner et al. 2004	AY735253

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
acyl-Coenzyme A binding domain containing 5	ACBD5 (<i>LOC91452</i>)	29	F: CCGACTGCTTGTAATGAATC R: TGTGTCTGTCTAAAGGGATCT	248	3.0	58		
aldo-keto reductase family 1, member C3	AKR1C3	29q16	F: GTCCTGTGTGCAGATAGTGTGGC R: GATTCACATAGGAAAGAGATTTGGG	173	3.0	58	Chowdhary et al. 2003*	G62200
Rho GTPase activating protein 12	ARHGAP12	29	F: AAACAAGGGGAACGATACATC R: GGAATTATTTGGCAGTCCCAC	171	1.5	58		CD535148
ADP-ribosylation factor-like 5B	ARL5B	29	F: AGTATGGGGGGCAGGTATGA R: CCTGTAAGCCTGAGACACAAT	134	1.5	58		BC024163
microsatellite	ASB43	29q16	F: CCCGGGGGATCACTTAGTAG R: TCCTTGACTCTCCACTCATCC	101	3.0	TD60	Irvin et al. 1998; Lear et al. 1999*	AF004773
BMP and activin membrane-bound inhibitor homolog	BAMBI (<i>NMA</i>)	29	F: ACGTTCTCTCTCCTCCCAAG R: CGTAGGGCACTCCATTAATAAAG	400	1.5	58		
B lymphoma Mo-MLV insertion region	BMI1	29	F: CGCAAAACCGATCAAAGGAAA R: AGCAATGGGAAATGAAGACAC	466	1.5	58		CD468823
chromosome 10 open reading frame 97	C10orf97	29	F: TATCTTGCTGCTTTGTCCTG R: ACCTCCTTTTATCATCTAACCC	298	1.5	58		BC002225
BAC end sequence	CH241-101F21_SP6	29	F: CTTACCAGTCCGCAGAATCAG R: TGCCACATGATAAGAGCCCC	619	1.5	58		AJ576657
COMM domain containing 3	COMMD3 (<i>BUP</i>)	29	F: CCTGCATATTCGGTGACCT R: CTAATCTCTGGGTGGGATTG	157	1.5	58		
microsatellite	COR021	29	F: CTGTAGCCAGCCCTGACAGT R: GATGGTGGGGTATTTGTCCA	202	2.0	58	Murphie et al. 1999	AF101390
microsatellite	COR027	29	F: CAGCTCTGCAATTTCTCCTC R: AATGACCAAGGCATTGAAAG	219-243	5.0	TD60	Murphie et al. 1999	AF101396

microsatellite	COR082	29	F: GCTTTTGTCTCAATCCTAGC R: TGAAGTCAAATCCCTGCTTC	196-226	2.0	58	Tallmadge et al. 1999b	AF154935
cAMP responsive element modulator cubilin	CREM	29q13	F: TCATGCTCACATTACCAAG R: ACGTACAGTGAAGCATTTTAGG	386	1.5	60		CD535436
FERM domain containing 4A glutamate decarboxylase 2 GATA binding protein 3 GDP dissociation inhibitor 2 microsatellite	CUBN	29q14	F: TGCCTTGTGGTGGAACATTTA R: GGTGGGTCCTGAAACTCTAAG	202	1.5	55	Perrocheau et al. 2006	DX010619
	FRMD4A	29	F: ATCCTTCCTAGCCCTGAGTTCC R: ACTTCAAAACACACCCATTCCC	658	1.5	58		AJ576877
	GAD2	29q14- q15	F: AAGTAGTCCCCGAAATAGTGAT R: TACAATAGCATTTCGGCACAG	356	1.5	60	Perrocheau et al. 2006	DX010491
	GATA3	29q15- q16	F: TCCAAAAAGTGCAAAAAGGTG R: ATACTGGAAGGGTGGTGAGGT	200	1.5	55		
	GDI2	29	F: AGATTTACAGGGTCATGC R: CAGCTCTCCAAGGCCATA	736	2.0	58		
inter-alpha (globulin) inhibitor H2 kinesin family member 5B microsatellite	HP12	29	F: TCACACGAAACCAGTCACGGGAG R: ACAGACACTGCTGGAGTCTCATGG	132-148	1.5	58	Swinburne et al. 2005	BM780631
	ITIH2	29	F: CAGTGGGAAAGGTTTCATCG R: TTATAAGCCACCGTGCTGTC	194	1.5	62		
microtubule associated serine/threonine kinase-like myeloid/lymphoi d or mixed- lineage leukemia translocated to10 membrane protein, palmitoylated 7	KIF5B	29	F: CCTCCTTTCCCTGAAACTCC R: ACATGAGTAACGTGAGTTACAC	234	1.5	60	Coogle et al. 1996	AF075620
	LEX018	29	F: TTCATCACTTTCTGCTTCC R: TTCTCTTCCTTTGCTCATCCT	228 - 242	3.0	58		
	MASTL (<i>FLJ14813</i>)	29	F: CAATGATGAAACACCACAACA R: TGCACCTTGAGCATTATCAGATA	513	1.5	60		
	MLLT10	29	F: GCTGAAGTCATTGCACCAAC R: GGGCTGGGATTTGTTGTTATT	103	1.5	58		AB218743
	MPP7	29	F: AAGCCCTCTTTGACTATGACC R: CACCACGTTGCATCATCTT	118	1.5	58		
								CX597390

neuroepithelial cell transforming gene 1	NET1 (<i>HES1G05</i>)	29qter	F: GGCTCAAAAACAGTATGGCTTG R: GCCTTTTCAAATTGGCATGTCTTTA	~150	1.5	65	Vaiman et al. 2000	
optineurin	OPTN	29	F: ATGTCCCAACCAACCACTTAG R: CTCCTTCTGTTTCTCTGTCC	~1230	1.5	62		BI961284
sequence tagged site	29STS01	29	F: GCCCCAAATGTGGAGAAGT R: AGTACAACCTCTGGAGGAAG	137	1.5	58		
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	29	F: GCCTACATGACGAGATGGAAC R: CAAACCAACGAACGACTACAC	450	1.5	58		BM734895
plexin domain containing 2	PLXDC2	29	F: GGTGGCTCTTATACTGTGTTC R: GCACTGTCTGCTTAAATTTCTC	434	1.5	58		AJ576646
Sec61 alpha 2 subunit	SEC61A2	29	F: ACAATGGTTTGTGACCCTCC R: TCCCTGACTGCTATCTACCC	256	1.5	60		
supervillin	SVIL	29	F: ACGCTTGCTTTAAGAGAACC R: TTCATTTGCCTCTGCTGTCC	372	1.5	60		
microsatellite	TKY112	29	F: GCCTGTCAACAGATGAATGG R: TTCATGGCTACGTAGTATTCC	89-107	2.0	58	Mashima et al. 2001	AB053347
microsatellite	TKY325	29	F: ACCTTAACAGCACTTAGAAG R: TGGATGAACCATGAATAGTG	173-193	1.5	58	Tozaki et al. 2001	AB044826
microsatellite	TKY332	29	F: CAAGGACAACTTCTCAGGAG R: AATAAGAAAGGAGCCAGTCG	211-225	1.5	58	Tozaki et al. 2001	AB044833
microsatellite	TKY478	29	F: GCCTGGGTACCTTTGTTGAA R: GGAACAGAATGGGAGTCCAG	110-130	1.5	60	Tozaki et al. 2004	AB103696
microsatellite	TKY628	29	F: TGACACACAGGACCATCTCG R: AAGTGCCTGAGACCCCATTT	222-232	1.5	58	Tozaki et al. 2004	AB103846
microsatellite	TKY715	29	F: CAGTTTCACAGGAGAGAGAGTCC R: CTGGAGTCCCACCTCCAAC	224-246	1.5	58	Tozaki et al. 2004	AB103933
microsatellite	TKY819	29	F: CACCACAGTGTGACTCTGTT R: CTGGATAGGACAGACAGTTA	209	2.0	58		AB104037
microsatellite	TKY859	29	F: GATCAAGACGTGAGGAACAAAT R: TACAAAATAGAGGAGTACTGGC	150	2.0	58		AB104077
microsatellite	TKY900	29	F: CTTGTTGTCAAGAGGCAG R: ACCTAAATGTCCTTTGGTGG	126	2.0	58	Tozaki et al. 2004	AB104118

microsatellite	TKY913	29	F: TAATTTTGCATGCCAGCTG R: AGGTAACAACCTGAACTTGC	176	2.0	58	Tozaki et al. 2004	AB104131
microsatellite	TKY989	29	F: CTTGCAGAAGACATGATTGTC R: AGAAACCTTGCTGAACTGAC	118	2.0	58		AB104207
microsatellite	TKY1866	29	F: TTGTCTCCCAAGTCAATG R: TATCACCTGGAAGACAAGAT	244	1.5	58	Tozaki et al. 2007	AB215809
microsatellite	TKY3085	29	F: GATGACACACTCAGGTAAACACA R: CTTTCATGCTTCACTGTGTGC	238	1.5	58	Tozaki et al. 2007	AB217028
microsatellite	UMNe218	29	F: ATTTTGTACCCATGCCAG R: GCCATCTGTATCCTGCCATC	139	2.0	58	Wagner et al. 2004c	AY735238
microsatellite	UMNe253	29	F: CAGAAAGATTTCTTCTTTATGGC R: ACTACACTGCCTCTTGGAATATCC	222	1.5	58	Wagner et al. 2004a	AY391328
microsatellite	UMNe602	29	F: AATAGTCCAAAGGAGCAAGACG R: TTCAGAGTAAGAGAGTGGCGTG	161	1.5	58	Wagner et al. 2004c	AY735293
microsatellite	VIASH39	29	F: AATGTGATTATAGCAGATAGGGTT R: CTATCCAATCTTCACAATCATGTA	154-158	5.0	TD60	Ewen & Matthews 1994	L34845
vimentin	VIM	29	F: TTCATGCCTCCAGTTCACA R: TTTGGAAGACAGCTCGAACA	197	2.0	58	Caetano et al. 1999	AF135018
WD repeat domain 37	WDR37	29q16	F: AGGGTTGCCCTTCAAATTATG R: ACACAGGAAGAGAGGGAAAC	221	1.5	60		
zinc finger E-box binding homeobox 1	ZEB1 (TCF8)	29	F: CAGACGATGAAGACAACTC R: CTCCTTCTCTTGCACTGCT	97	1.5	58		AB218752

Name	Symbol (Alias)	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
adenylosuccinate synthase	ADSS	30q12	F: GCCTAATCGTCAAAATAACACC R: TTTTCTGCTGAGACCATTGC	362	1.5	58		
microsatellite	AHT023	30q15	F: TGCTGACATCTGCTATTGTGC R: CTCATCATTTTTTAAGGGCAAG	197-207	2.0	58	Swinburne et al. 1997	
microsatellite	AHT062	30	F: AGAATGTTGGGAGCACATAAGG R: TCCATGACACAATCTCTGCC	285-287	2.0	58	Swinburne et al. 2003	AJ507679
calcium channel, voltage-dependent, L type, alpha 1S subunit	CACNA1S	30	F: AGGCAGTGCCCATTCCAGAA R: TGAACCAGGTGGCATTGACG	769	1.5	58		NM_000069
CDC42 binding protein kinase alpha	CDC42BPA	30q13	F: AGTGAGGTTACTGGCGTGTTG R: CTCAAACGCACTTCTCCAGAC	195	1.5	55	Perrocheau et al. 2006	DX010558
cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	CDC73	30	F: AATGAAGAAGGTCACAGATCGA R: AACGCTAATTTAACCAATGGAGA	191	1.5	58		NM_024529
cytochrome b5 reductase 1	CYB5R1	30q15	F: GATCCTACTTGGTTCGGAGG R: GGGCAGAGAGGTAGACATGT	868	1.5	58		NM_016243
degenerative spermatocyte homolog 1 (Drosophila)	DEGS1	30	F: GTTGTATTTTGGGCATACGC R: TTGGGGTTGATGAAGAGAGG	335	1.5	60		
dual specificity phosphatase 10	DUSP10	30	F: GAGCATGCTACCTCAGTCCA R: TGAACAGGCCTTTCTCGTAG	194	1.5	58		NM_015434
epoxide hydrolase 1, microsomal (xenobiotic)	EPHX1	30	F: ACACCAGAGGATCGACAAGG R: GAAGTGGGGGTATCTGTTGAGA	160	1.5	58		NM_000120
estrogen-related receptor gamma	ESRRG	30	F: AACTCGCTCTGTGTTGTTGC R: AAGGGATGTGCCAATTTCTG	289	1.5	TD58		BU746640

fumarate hydratase	FH	30	F: TGCACATTGCTGCTGCAATA R: GCCCAATTTTGATGATCTGG	114	1.5	58		NM_000143
G patch domain containing 2	GPATCH2	30	F: GCCTAAGAGGAACAGCAAAGA R: ATAGCTGAAAGTCGCTGACAA	249	1.5	58		DN509877
H2.0-like homeobox 1 (Drosophila)	HLX1	30	F: CCGCCTTTCAAGTGAGGCCAG R: AGCCGAGGACGATCCGCTTTC	136	1.5	60		
microsatellite	HMS18	30	F: CAACAATGAAAATTTGTCCTGTGC R: GTAAATGAGTAGACAATCATGAGG	170	3.0	58	Godard et al. 1997	U89807
heterogeneous nuclear ribonucleoprotein U	HNRPU	30q13	F: CTGACAATAACTGGGAAGGC R: CCTCCACAAATAATGCAACC	132	3.0	58	Chowdhary et al. 2003	
microsatellite	HTG27	30	F: ATATGTCATATTTGAACAAGTCG R: GCACTGAAATCGAACATCTAA	150	3.0	58	Lindgren et al. 2000	
isoleucine-tRNA synthetase 2, mitochondrial	IARS2 (<i>FLJ10326</i>)	30q13	F: GTGTTTTTCGTACTGGGTGGA R: GGCTCAATCACAATGATCACC	157	1.5	55	Perrocheau et al. 2006	DX010479
lamin B receptor	LBR	30	F: TAAGAGTCTGCTCGTCTCGG R: TGGATCAGCAGCAAGGTGAAG	~1100	1.5	58		
microsatellite	LEX025	30	F: CAATCGTGGCCCGGTAAC R: TTCACTCCAATCCTCAGTCA	139-156	2.0	58	Coogle et al. 1996	AF075627
microsatellite	LEX075	30	F: TCTGAAAAGTTGCAGTTTGAGAA R: TACAGTGTATTGGGGGCACA	219	2.0	58	Bailey et al. unpub.	AF213361
neuron navigator 1	NAV1	30	F: ATCGCTCGCCCTTCCACTTC R: TGGCTTTGGCCTTCTCCTTTTC	~500	1.5	60		
presenilin 2 (Alzheimer disease 4)	PSEN2	30	F: TGTCTCTCTGATGTTGCTG R: CATGAGCGCACTGATCATG	867	1.5	58		NM_012486
regulator of G-protein signalling 1	RGS1	30q15	F: CAAAGTCGTTTGTGCATTTCAG R: TTGCAAAATCAATCTTGTCATCC	239	1.5	54		
regulator of G-protein signalling 2, 24kDa	RGS2	30	F: GCTGCTTTACAACCTGCCAG R: TGATGCTTCCCTCAACACCCC	251	1.5	60		
regulator of G-protein signalling 18	RGS18	30	F: AAGAAACAAGCAAAGAAGCCAA R: TACCGGAGTGGGTCTCTTCA	~560	1.5	60		
signal recognition particle 9kDa	SRP9	30	F: AGAACAGACCAAGCTCAAGATG R: AACCATTCAATCCGTTTCCA	72	1.5	58		AB218754

TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	TAF1A	30	F: CAGGAAGAAAATTAAGCGGATG R: GCAAAGAGCAAAGACAGTGA	262	1.5	58		
microsatellite	TKY658	30	F: AGGCGCAAGAACTCACTCTG R: GCCAGTTGTCAATTGTGTGG	261-277	1.5	58	Tozaki et al. 2004	AB103876
microsatellite	TKY762	30	F: TTCTTCGTCCCAAATCCAAA R: TCGCTGCGACTACTTTTGAG	185-192	2.0	54	Tozaki et al. 2004	AB103980
microsatellite	TKY897	30	F: GCTGTTCAAGTCACTCTCAG R: ACCCTTCCCGATGTAACTC	174	2.0	58		AB104115
microsatellite	TKY1022	30	F: AGAGAGGCAATCTACTCTTC R: TTGGAAGTCTTGGGGTATTG	188	2.0	58		AB104240
microsatellite	TKY1178	30	F: TGCCTGATGCTCTAGTGTG R: CGTTAGAGGTGACTGTGTAC	183	2.0	58		AB104396
troponin I type 1 (skeletal, slow)	TNNI1	30	F: TGAAGCTGAAGGTGCTGGAC R: TCCACGTTCTTCCTCCAGTC	1100	1.5	TD60		
microsatellite	UCDEQ455	30	F: CCCCTTCACACTCCTCTC R: CAGCAAGTGGGGAATCTA	154-166	2.0	58	Eggleston-Stott et al. 1999	U67411
microsatellite	UMNe078	30	F: CCTATTGCAAATGATTACACC R: AGAGATTTCAAGGAAACATTCC	134-152	2.0	58	Roberts et al. 2000	AF191708
microsatellite	UMNe088	30	F: GATCTTTTCCCTCAGGATGACG R: GGCAAGAATTCAAGTTCTATCCAG	201	1.5	62	Mickelson et al. 2003	AF536244
microsatellite	UMNe340	30	F: TCTGTCTGTCTCGCGCTG R: ACTGTGTACTGGTCCAGGCC	133	1.5	58	Mickelson et al. 2004	AY731386
microsatellite	UMNe463	30	F: AACCACAGACTTTTGGGCC R: GTAAGTCAGGGGTGTGAGAGTG	145	1.5	60		
microsatellite	UMNe530	30	F: AATGAAGCCAAGTGAATGGG R: GTCTGAACCCTGTAACCTCACC	224	1.5	58	Mickelson et al. 2004	AY731407
microsatellite	VHL20	30	F: CAAGTCCTCTTACTTGAAGACTAG R: AACTCAGGGAGAATCTTCCTCAG	89-107	4.0	TD64	van Haeringen et al. 1994	X75970

WD repeat domain 26	WDR26	30	F: ACTCTCTGCTAGATATCACACC R: CTTTTCACATAGCTTGTTGCC	440	1.5	58		AJ618802
zinc finger CCCH- type containing 11A	ZC3H11A	30	F: ACTTCGGTTGCTACTTCCTTT R: CTGTCCATTGCTTTATCAGACA	298	1.5	58		CU004011
zinc finger protein 281	ZNF281	30q15	F: GCGTTTGGTTCTCAGTTCAAG R: CACTCCTGGGACCTTACCTGT	202	1.5	55	Perrocheau et al. 2006	DX010612

Name	Symbol (Alias)	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
microsatellite	AHT033	31q15-q16	F: CTGAGGGCGTAAGTCGAGTC R: GTTAATAGGAGCGGTTGTTTGG	149-169	3.0	TD 60	Swinburne et al. 2000	AJ271518
microsatellite	AHT034	31q16	F: CTCAGGGCGAATGTTCCCTC R: CCCCACCATGAGTCAAAAAC	121-142	3.0	58		AJ271519
brain protein 44-like	BRP44L	31	F: GTCTTTAACCCAGCTCTCTGC R: GTTGGTTGTCTCATGGTCATT	240	1.5	59		
chromosome 6 open reading frame 55	C6orf55	31	F: AGCCCTCGACTTCAGCTTAC R: CACTTCTGCTGGCGTATTG	104	1.5	59		CX596424
BAC end sequence	CH241-100B15_SP6	31	F: GTGGATCCCATTCTGGAG R: GAATGACCTGCTGTTACCC	270	1.5	60		AJ542717
BAC end sequence	CH241-100I20_SP6	31	F: CAGCTTCTGCTGTTCAAG R: GTGCCATATGGGAAGATGC	296	1.5	59		AJ543005
BAC end sequence	CH241-100J19_SP6	31q16-q17	F: GGGGGAAATTTTCTGACTCTG R: TTGCAATTTTCATTTGGCTTC	501	1.5	58		AJ543044
BAC end sequence	CH241-101A08_SP6	31	F: TAGGCGTGGGTTTAATGGAG R: TTTCTGGTAAATGCCCAAG	209	1.5	58		AJ576467
BAC end sequence	CH241-102M02_SP6	31	F: GTAGCACGAGGACCAACACC R: TGCGGTTAGGTTGAGAAGTTG	223	1.5	60		AJ584466
BAC end sequence	CH241-102M06_T7	31	F: ACATGACCCCAGAGGAACTG R: CTGAAGATGGCCAAGGAGAG	172	1.5	60		AJ584473
microsatellite	COR038	31	F: GCTGGAAAAGAGCAGTTTCA R: TGACATTAACTCCCGCATCT	202-208	2.0	58	Murphie et al. 1999	AF101407
estrogen receptor 1	ESR1	31q16	F: CAAGGAGGAAAGCAGGGTAG R: TGGGCAATCAGAAATGAATGAG	611	1.5	60		
fucosidase, alpha-L- 2, plasma	FUCA2	31	F: GCTTAACTGGACTGCTCTGAA R: TGCTAGAAACTTGACATTTGCT	178	1.5	59		CX604953
human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	31q16	F: CCCTGTTCGAGATAATTCACCA R: TGATTTCTTTCCCAGGTGACA	211	1.5	55	Perrocheau et al. 2006	DX010504

katanin p60 (ATPase- containing) subunit A 1	KATNA1	31	F: CAAAAGGCAGGGAAGAGC R: GTAATGTCCGCACCTGAATAAC	115	1.5	60		DN507055
mitogen-activated protein kinase kinase kinase 4	MAP3K4	31q13	F: GGATAATGGAGCTGCTGGAGT R: GCCAGCCAATGTGTGATAAAT	207	1.5	55	Perrocheau et al. 2006	DX010524
protein-L- isoaspartate (D- aspartate) O- methyltransferase pleiomorphic adenoma gene-like 1	PCMT1	31	F: CAGTGGTCCAGGGACGAACTG R: TCCTTTGCATCCCTCCTCTACC	228	3.0	58	Chowdhary et al. 2003	G62181
plasminogen	PLG	31	F: CATGTGTTGTGCCAATCTGTC R: TTCTTCCATTTTCGGAGGAATC	248	1.5	58		BI961408
		31q12- q14	F: GTGCCTCGAGTCCCAGATAG R: CCTTGGGGTTTCTCTTAGGC	203	2.0	58	Lear et al. 2000*; Chowdhary et al. 2003	AF097581
proteasome subunit, beta type, 1	PSMB1	31q12	F: AACCGATTAAGGCTAACAGCAC R: AACATGCAGAATGTGGAGCAC	201	1.5	55	Perrocheau et al. 2006	AY817481
ribonuclease T2	RNASET2	31	F: GATAGAGCTGTGCCTCACCA R: TGGATTTCACTTGCTTTTCAA	225	1.5	58		CX601446
SPARC related modular calcium binding 2	SMOC2	31	F: TGAAGGGCTTGATCTCCTTT R: GACCCCAGCCACACACTG	~150	1.5	58		
sorting nexin 9	SNX9	31	F: CGTGTTTAAGAAAAGTGCAGAG R: AAAATGAGAGCAGTTGGAGAG	225	1.5	58		
thrombospondin 2	THBS2	31	F: TTTGTCTGCTTGTCATTCTC R: TCCAGCAAAATGGCTCTAAC	230	1.5	58		
microsatellite	TKY105	31	F: TCGGGACAGGAAAGGAAGCT R: GGTATCCAGAATGAAAGACCCC	196-204	1.5	50	Mashima et al. 2001	AB053344
microsatellite	TKY274	31	F: CATTCTGGAATTGAAACCTC R: GGGAGTTCTGTTCTGAATGG	112-132	2.0	58	Tozaki et al. 2000b	AB033925
microsatellite	TKY278	31	F: CTAGGGAATACAGAGAGAGC R: GCCACTCCGGTAACAAAATC	104-132	2.0	58	Tozaki et al. 2000b	AB033929

microsatellite	TKY368	31	F: TTCAAGCCAGCAAAATTATAGC R: GTCAGGATAATTTTCAGCCC	251-263	1.5	58	Tozaki et al. 2001	AB044868
microsatellite	TKY668	31	F: GCTGTAATGTACCGCTGGT R: TAGGCAGCTGCGATAAGACA	159-175	1.5	58	Tozaki et al. 2004	AB103886
microsatellite	TKY755	31	F: CGAAGCTTCCACTCTTTTCC R: CCGAATTATCCCTGCCCTAA	220-238	1.5	58	Tozaki et al. 2004	AB103973
microsatellite	TKY919	31	F: GATTGGCAACAGATGTTAGC R: GGAAAGCCTGACATCCTTTC	94	2.0	58		AB104137
microsatellite	TKY1011	31	F: TCAGGTATGAGGAAAAGGTTG R: TCACTATCTTCAGCCTTTCC	103	2.0	58		AB104229
microsatellite	TKY2302	31	F: CTTCTGAGGTCATTCCATGG R: TCAGGAAATTCTCTGGAAGA	112	1.5	58	Tozaki et al. 2007	AB216245
microsatellite	UMNe157	31	F: TTCAACTGTGTGAGTGTGAATG R: AGCTTTTGTCCAGCAGGAAC	94	1.5	58	Wagner et al. 2004a	AY391304
microsatellite	UMNe181	31	F: TTAAGCAACCCAGTGTGTGG R: AGAGAAGAGAATCGGGGGAG	149	2.0	58	Wagner et al. 2004a	AY391314
microsatellite	UMNe368	31	F: TCCCAGAAAGCAACACTCAC R: TGTCAGTTCAGATTTTTGGCC	292	1.5	58	Wagner et al. 2004a	AY391353
microsatellite	UMNe382	31	F: CTTCATCTCCGCTAGGTTGG R: ATTAATGATAGCGTTGGGGG	212	2.0	58	Wagner et al. 2004b	AY464472
microsatellite	UMNe424	31	F: GGCATCACAAGAGAGGTAGAGG R: TTCACAGCCTAGACCCATCC	168	1.5	58	Wagner et al. 2004c	AY735246
microsatellite	UMNe546	31	F: AGGAGGAAGGGACAGCTCTC R: GCCCTTATTCTCCCAGGAAG	129	1.5	58		
microsatellite	VIASH21	31q14-q15	F: AAATGATAACGCCAAGTGCTCT R: ATGTGAGTGCCAGCTTGTGAT	247-249	2.0	58	Swinburne et al. 2000, Lindgren et al. 2001*	L10926
villin 2	VIL2	31	F: AGCAGTTTCATTTACGCCTTC R: ATGTCCCTCCTTCATGCCTC	171	1.5	58		
vasoactive intestinal peptide	VIP	31	F: TGTGTAAAATGTAACTGAATGGAACG R: GCAATGATAATCAAACGCTTTATTTTC	200	2.0	58		
Wilms tumor 1 associated protein	WTAP	31	F: TCTGTGGCACACTGTGTCTTC R: GAGAGCATCCACAGCATTAGC	418	1.5	58		CD468561

Name	Symbol	Horse chr.	Primers	Product size (bp)	MgCl ₂ (mM)	T _a	Reference	Accession No
acyl-CoA thioesterase 9	ACOT9 (<i>ACATE2</i>)	X	F: CTTTCATAGTTTCCTGGCTAAG R: CCTTACGGTGTTTTGAACAG	138	1.5	50	Raudsepp et al. 2004	
acyl-CoA synthetase long-chain family member 4	ACSL4 (<i>FACL4</i>)	X	F: CATCGGGATGAAATTCTC R: TTCATGACAAGCCAAACC	162	3.0	58	Chowdhary et al. 2003	
AF4/FMR2 family, member 2	AFF2 (<i>FMR2</i>)	X	F: CCCCAGTGTCTCTCAACAAC R: CCCCCTAACACGTTGCTAGT	133	1.5	58	Raudsepp et al. 2004	
angiotensin II receptor, type 2	AGTR2	X	F: TCTTCCTCTATGGGCAACCT R: TGCCAGGGATTCTTCTTTG	189	1.5	60	Raudsepp et al. 2004	
microsatellite	AHT028	Xq15	F: CCTGGCTTATAGATGGCTGC R: ATTTGGAGATGGGGGTCTTT	217	1.5	60	Swinburne et al. 2000*	AJ271513
microsatellite	AHT079	X	F: AATTCGTTCCAGCTTTGGC R: CCAGGGCAGAGAGAATCTTG	157-159	2.0	58	Swinburne et al. 2003	AJ507696
microsatellite	AHT099	X	F: TTCTTGGGCAGGGGATTT R: GGGGTGAGTTGGCTGTATTC	167-171	2.0	58	Swinburne et al. 2003	AJ507716
microsatellite	AHT124	X	F: CCAGCTGTCACTCACCTCC R: CCCTGGCATGATAAAACACA	222	1.25	60		
A kinase (PRKA) anchor protein 4	AKAP4	Xp13	F: GGTTTCCAACATGCACTGAG R: TCTCCTTGATTTCCTTACGG	346	3.0	58	Raudsepp et al. 2004*	
aminolevulinate, delta-, synthase 2	ALAS2	Xp14	F: GGCTACGCATGAACCAATCT R: GTTAGGCCAGCTCATTCTGC	195	2.0	58	Milenkovic et al. 2002*; Raudsepp et al. 2002	AF133200
aldehyde dehydrogenase 2 family pseudogene	ALDH2ps	Xp13	F: TTGCCATTATCCAGGGTCTC R: GGGAGGTCATCTGTTGGGTA	202	2.0	58	Raudsepp et al. 2002*	AF133203
amelogenin (X-linked)	AMELX	X	F: AGCAACCAATGATGCCACTT R: GAATATCGGAGGCAGAGGTG	197	1.5	60		AB032193
angiomotin	AMOT	X	F: CTGGTAGACCCCCTGATTTA R: CAGTGGACAGGCAGGATACC	153	2.0	58	Raudsepp et al. 2004	

androgen receptor	AR	Xq12	F: GGAGCCCGGAAGTTAAAGAA R: ACCGTCAGCTTCTGGGTTG	102	1.5	58	Milenkovic et al. 202*; Raudsepp et al. 2004	AY032721
Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ARHGEF6	Xq27	F: AGCATGTTTTTGGGACTTGG R: GGCAAACAGGAACCCATTTA	190	1.5	62	Raudsepp et al. 2004*	BM734718
arylsulfatase E	ARSE	Xp25	F: TTTGACCTCTCAAGAGACCCTTCT R: ACATTGTCCAGCCTGTCCAGCTGCA	155	1.5	58		
aristaless related homeobox	ARX	X	F: GAGCAATCAGTACCAGGAG R: AACAGCCGCATTTTGCAC	128	1.5	60	Raudsepp et al. 2004	
ankyrin repeat and SOCS box-containing 12	ASB12	Xq11	F: CCTCATGGACATCACCAAGA R: GCAGCTAAGGTGGCCATAA	228	1.5	58	Raudsepp et al. 2004*	
acetylserotonin O-methyltransferase	ASMT	Xp25	F: GTTCTCTTTGCTGCCTGTGA R: CAGCAGCTTCAGGGACACAC	150	1.5	60	Raudsepp et al. 2004	
ATG4 autophagy related 4 homolog A (<i>S. cerevisiae</i>)	ATG4A (<i>AUTL2</i>)	X	F: GACCTGGAGGAAGATTTTCG R: GTATGCTGTTGGCATATCAG	147	1.5	60	Raudsepp et al. 2004	
ATPase, Cu ⁺⁺ transporting, alpha polypeptide	ATP7A (<i>MNK</i>)	X	F: CACAGCAAAGGAGTCCATCA R: CGGTTTCTTGAGTGAGAGGC	360	2.0	58	Raudsepp et al. 2004	AY011430
biglycan	BGN	X	F: CACTGTTCTCCAGGGGATTC R: GGGGGCTAGTGGTCTTGAAC	226	2.0	58	Raudsepp et al. 2002	AF135019
baculoviral IAP repeat-containing 4	BIRC4	X	F: TCAGAACACAGGCGACACTT R: ATCCGTGCTTCGTAATCTGC	155	1.5	63	Raudsepp et al. 2004	
bone morphogenetic protein 15	BMP15	X	F: CTCCACCCTTTCCAAGTCAG R: ATGGCATGATTGGGGGAATT	140	3.0	58	Raudsepp et al. 2004	
CD40 ligand	CD40LG (<i>TNFSF5</i>)	X	F: CAGCTGGCCGTTAAAAGACA R: CCTCCCAAGTGAATGGATTG	203	1.5	60	Raudsepp et al. 2004	
CD99 molecule	CD99	Xp25	F: CCGGGTAGATGATGTGGACT R: AAAACGGTTCAATGCCCTTT	192	1.5	60		CX598338
CD99 molecule-like 2	CD99L2	X	F: GCAGAGACTGGCACCATC R: CTGTATGCTGAAGCAGAACT	111	1.5	58	Raudsepp et al. 2004	
centrin, EF-hand	CETN2	X	F: GATCGAGATGGAGATGGAGAAG	144	1.5	59		CX599736

protein, 2			R: GACCAGGTTTTCACACAATAGCA					
BAC end sequence	CH241-144B9_SP6	X	F: GGAAGTGGCTCGCTCAGTAG R: TAATGCCACAGGGTTTTTCC	160	1.5	58		
BAC end sequence	CH241-178I7_T7	X	F: ATCGAGCGAGTTGTGCAATA R: TCCAAGTGGCCTTGAATAGA	154	1.5	58		
choroideremia	CHM	Xq15-q16	F: ATTAACCCCCAACCTCCAAT R: ACTGAGGGAGTTCTCCTTG	173	1.5	58	Raudsepp et al. 2004*	
chloride channel 4	CLCN4	Xp24-p23	F: CATCCTGCTTGGGGTCTTT R: GAAATGAGCTCGCTTGTGCT	192	2.0	58	Raudsepp et al. 2002*	AF133199
claudin 2	CLDN2	Xq21dist	F: ATCACCCAGTGTGACATCTA R: CAACAGGAATGAAGCCCAG	243	1.5	58	Raudsepp et al. 2004*	
chloride intracellular channel 2	CLIC2 (<i>HESTX-11</i>)	Xq29	F: CAGAGAGTGAGCATATCAGAGAGG R: CTAGGTGTTGAATCCCATGCTAAG	108	2.0	58	Raudsepp et al. 2004*	BI961616
connector enhancer of kinase suppressor of Ras 2	CNKSR2 (<i>CNK2</i>)	X	F: AGAAGGAGTGGCCATTATGA R: AACCAGGCAAGCAGACTCTT	105	1.5	60	Raudsepp et al. 2004	
HESTX-2, collagen, type IV, alpha 5	COL4A5	X	F: CTCTTACCACTTAGATGCCCCC R: GCATCAAGTGAGAAGATGACAGC	322	3.0	58	Raudsepp et al. 2002	G62201
microsatellite	COR074	Xp24-p23	F: GAAAAGCGTATCTTCTCTTAGTC R: GGGCGATTCATCAGAATCTA	281 - 291	2.0	58	Tallmadge et al. 1999a; Raudsepp et al. 2002*	AF142611
microsatellite	COR091	X	F: GGTGATTCAAGGTTAATGGC R: TGTATCTGTCCACAGCATGG	205	2.0	58	Tallmadge et al. 1999b	AF154944
cofactor required for Sp1 transcriptional activation, subunit 2	CRSP2 (<i>TRAP170</i>)	Xp14	F: TTTCATCAAAAAGACCATCAGTCTTT R: TTGCTTCCTTGGGATGAGTTTATAAC	300	2.0	58	Raudsepp et al. 2002; Chowdhary et al. 2003*	AF135802
CTP synthase II	CTPS2	X	F: GTCTTAAACGATGGTGGAGA R: CCTGGACAGCATCAGTAATG	~1200	2.0	56	Raudsepp et al. 2004	

cullin 4B	CUL4B	X	F: TTCCTGCTTTAATTAGGGTCCA R: ATTGAGCATTGTGTTTCCAGTT	150	1.5	60		AF513243
chromosome X open reading frame 6	CXorf6 (<i>F18</i>)	Xq29	F: TCATGGTATCCTGCATGTGC R: CAGGTTGGCAAGAATGGAGT	200	2.0	58	Tozaki et al. 1998*	AB009590
chromosome X and Y open reading frame 3	CXYorf3 (<i>DXYS155E</i>)	Xp25	F: GACATCCCCATGCTGGAC R: CTCGCCCTTGAACATGAG	171	1.5	58	Raudsepp et al. 2004	
doublecortex; lissencephaly, X- linked	DCX	X	F: CAAACAGGGCAGCAATGTC R: TTTGAAGGAGGTTTCAATGC	198	1.5	60	Raudsepp et al. 2004	
DEAD box polypeptide 3, X- linked	DDX3X (<i>DDX3</i>)	X	F: GAAGCTGATCGGATGTTGGA R: GGTCTCCACAAACACTAAGG	~600	1.5	58	Raudsepp et al. 2004	
diaphanous homolog 2 (<i>Drosophila</i>)	DIAPH2	Xq17- q21prox	F: GCCTGTGAAGAACTGAAGAA R: CCCAAAGACTGGGCATTTC	107	1.5	60	Raudsepp et al. 2004*	
dystrophin	DMD	Xp16	F: TCTGGAGTGAGTCTGTCAAA R: GAACCCAGTACCTGAAAACA	187	1.5	58	Milenkovic et al. 2002*; Raudsepp et al. 2004	
ectodysplasin A2 receptor	EDA2R (<i>XEDAR</i>)	X	F: TGGTTATGGAGAGGGTGGAG R: GGGATGCACTCTTGGTCCT	766	1.5	58	Raudsepp et al. 2004	
EF-hand domain (C- terminal) containing 2	EFHC2 (<i>FLJ22843</i>)	X	F: GAGGATCAGTTTTATACTGTGC R: CATGTAAGGATCTTCTGGAC	165	1.5	58	Raudsepp et al. 2004	
ephrin-B1	EFNB1	X	F: GAGCAGCTGACTACCAGC R: CTTGCGCAGCTTCAGTAGC	~450	1.5	55		
EGF-like-domain, multiple 6	EGFL6	X	F: CATTTTTGAAGCAGAACGTG R: TCCACAGATAAAGGGCCATC	102	1.5	58	Raudsepp et al. 2004	
eukaryotic translation initiation factor 2, subunit 3 gamma	EIF2S3	Xp22- p21dist	F: CAGGTGCTTGGTGCAGTTG R: TTTGTCTCCTTCAGTACGTACACC	102	1.5	62	Raudsepp et al. 2004*	
FYVE, RhoGEF	FGD1	X	F: GACAGACGGCATGTCTTCAA	165	1.5	55	Perrocheau	DX010477

and PH domain containing 1			R: CTCTTCCATCTCCCTGTCCTC				et al. 2006	
fibroblast growth factor 13	FGF13	X	F: CTGTGGAAGTGTGATGTTG R: TGTTGTTTAGGGGTAACCACTC	141	1.5	58	Raudsepp et al. 2004	
fragile X mental retardation 1	FMR1	Xq28	F: GTACCTGGGGTCACTGCTA R: AGCCTCAATTCTCACCTCA	290	1.5	58	Raudsepp et al. 2004*	
glucose-6-phosphate dehydrogenase	G6PD	X	F: CCAGAATCTCATGGTGCTGA R: GATGACACAGGCGATGTTGT	199	2.0	65	Raudsepp et al. 2002	AF133202
gamma-aminobutyric acid A receptor, epsilon	GABRE	Xq29	F: CGCCTCTTCATCCATGTCTAC R: GCACCTACAGGTTAAGGCAAA	112	1.5	55	Perrocheau et al. 2005*	AY817470
GDP dissociation inhibitor 1	GDI1	X	F: CTACAGTGGGGCGTAAGAGC R: GTTCCCAGCATCTCTGCTTC	259	1.5	60	Raudsepp et al. 2004	BM735209
gap junction protein, beta 1	GJB1	X	F: CTACGACCACTTTTTCCCCA R: CCCTGAGATGTGGACCTTGT	204	2.0	58	Raudsepp et al. 2004	AJ319909
glycerol kinase	GK	Xp21	F: CTTCTTATGGCTGCTACTTCGTC R: GCAATATGGCATTATTGGTGA	613	4	58		
galactosidase, alpha	GLA	X	F: AATGACCTCCGACACATCAG R: GAAGCAAAACAGTGCCTGTG	~700	1.5	60	Raudsepp et al. 2004	
glycine receptor, alpha 2	GLRA2	Xq17	F: TCCTGGGTAACTGATGG R: TGAAGTGGTTTGTCTCTAAG	296	1.5	58	Milenkovic et al. 2002*; Raudsepp et al. 2004	
glypican 3	GPC3	Xq27	F: CTGACTTCCTAGTGCCCAGCTC R: CCATGTTCTAGAAGCCAAACATAG	273	2.0	58	Lear et al. 2001*	G62152
glycoprotein M6B	GPM6B	Xp22	F: ATGCTGCATCAAGTGTCTGG R: CAAGGCATGGTCACTTGTGT	166	1.5	65	Raudsepp et al. 2004*	BM414631
G protein-coupled receptor 64	GPR64	X	F: TGTTTCATTGTGGTCCTGGTT R: GTAAAAATGTAAGGCCAGCG	114	2.0	55	Raudsepp et al. 2004	
G protein-coupled receptor associated sorting protein 1	GPRASP1 (KIAA0443)	Xq21p ox	F: GGTCAGTCAGGGAAATTCG R: AACTCGGGAGGAGGGATAAT	278	1.5	60	Raudsepp et al. 2004*	
glutamate receptor, ionotropic, AMPA 3	GRIA3	X	F: CCCTTGGCTTATGAAATCTG R: TTCATTTGGAGGATCCGGAG	159	2.0	58	Raudsepp et al. 2004	

glycogenin 2	GYG2	Xp25	F: GGTTATCCTCTCAAGGGTGT R: TGTCTGCATCCAGGAAGAC	170	1.5	54	Raudsepp et al. 2004	
haloacid dehalogenase-like hydrolase domain containing 1A	HDHD1A	Xp24	F: CGGCTGTATTTCAGTGGTGT R: CTTCCACCAGCTCCTCTTTG	160	1.5	55		
hephaestin	HEPH	X	F: TGAAGATGCTGGGCATGCA R: CTTGAAGCTGTCATCCAGG	179	1.5	60	Raudsepp et al. 2004	
hypoxanthine phosphoribosyltransferase 1	HPRT1	X	F: AGTGATTGCTTTTTGTGTCAGTCA R: TACTTGCAAATGGGCCTTCT	112	2.0	58	Chowdhary et al. 2003	AY008794
5-hydroxytryptamine receptor 2C	HTR2C	X	F: ATGTCTGGCCACTACCTAGA R: GAATTGAAACGGCTATGCTC	148	1.5	58	Raudsepp et al. 2004	
HECT, UBA and WWE domain containing 1	HUWE1 (<i>UREB1</i>)	X	F: GATAAGCCCTTTGTGAGAAGC R: CAGATTAGGCCGAGCACTT	171	1.5	62	Raudsepp et al. 2004	BI395210
immunoglobulin superfamily, member 1	IGSF1	Xq27	F: CCCTCATCAATCTCCAGGCAAC R: GTACAGTGAGGAGTTACAGGGGCA	~300	2.0	58	Raudsepp et al. 2002*	NM_001555
insulin receptor substrate 4	IRS4	Xq23	F: AAAACCACAAAAGCCCACAC R: AAATGGCACTCCGAACCTCAA	196	1.5	60	Raudsepp et al. 2004*	
integral membrane protein 2A	ITM2A	Xq14-q15	F: AATCATTGATGTGCCTGTCC R: CATCAGATAGCAGTTCCCCA	368	1.5	60	Raudsepp et al. 2004*	
jumonji, AT rich interactive domain 1C	JARID1C (<i>SMCX</i>)	X	F: GCATCGCTTACCCCTATGAG R: TGTCTTCCTCTGTGGGTTC	~1200	1.5	63	Raudsepp et al. 2004	U52363
Kallmann syndrome 1 sequence	KAL1	Xp24	F: TAAGTGGTCTCGAATTCAATATTTTC R: TGTGGCGTCGTCTTCACTA	100	2	55		
KIAA1166	KIAA1166 (<i>HCA127</i>)	X	F: GAATGACCTAAACAAGCTGC R: ATAGGTCAGGGAGCCTCT	119	1.5	60	Raudsepp et al. 2004	
kelch-like 4 (<i>Drosophila</i>)	KLHL4	X	F: GGCTACATATTGGCACCATG R: TTGACATGGGAGGCATCAC	165	1.5	58	Raudsepp et al. 2004	

kelch-like 13 (Drosophila)	KLHL13 (<i>BKLDH2</i>)	X	F: GAGTCATGATGGCCTCTGC R: GCAGCTTCCAGTGTGTCTTG	300	1.5	63	Raudsepp et al. 2004	
lysosomal-associated membrane protein 2	LAMP2 (<i>HSTX-9</i>)	Xq25-q26	F: CGGTTCTATCTGAAGGAGGTG R: CCTTCACATTGAAAGGCTGA	~600	1.5	58	Raudsepp et al. 2004*	BI961803
leucine zipper, down-regulated in cancer 1	LDOC1	Xq28	F: AGAACAGCCAGCTCATGGAA R: GCCGTCTGCACGATAAACTC	151	1.5	58	Raudsepp et al. 2004*	
microsatellite	LEX003	X	F: ACATCTAACCAGTGCTGAGACT R: GAAGGAAAAAAGGAGGAAGAC	143-164	3.0	58	Coogle et al. 1996	AF075607
microsatellite	LEX010	X	F: TGGGCTAAAATTTAATTTGGG R: ACCAAAACATATGCAAATTAA	198-206	2.0	TD 60	Coogle et al. 1996a	AF075613
microsatellite	LEX013	X	F: TGCTAGAGGAAGGGATAAAGG R: CTCTGCTCTTCCATTTCTTGC	122-128	2.0	58	Coogle et al. 1996a	AF075615
microsatellite	LEX022	X	F: AACATATCCATCGCCTCACA R: TGCAAATTCAGTGAAGTGG	101-113	2.0	TD 60	Coogle et al. 1996b	AF075624
microsatellite	LEX024 (<i>UM001</i>)	X	F: GGGGGTAGAGGGAAAAAGAG R: TTGTTGGCAGATCCCAGG	131-150	2.0	58	Coogle et al. 1996b	AF075626
microsatellite	LEX026	X	F: CAGAGTGAATGGCAAATCC R: CAGCCCTCCAAAGAGTTTAC	231-243	2.0	58	Coogle et al. 1996c	AF075628
microsatellite	LEX027	X	F: ACCACTGGGAAACTGTGTAA R: GCCCAGAATCCGAACC	187-200	2.0	58	Coogle et al. 1996c	AF075629
microsatellite	LEX028	X	F: AACTGGGGATCACAACACAT R: TTGGTACAGGAGCGTCTCTT	268-281	2.0	58	Coogle et al. 1996c	AF075630
LON peptidase N- terminal domain and ring finger 3	LONRF3 (<i>RNF127</i>)	X	F: GAATATGGCTGCATCCTAGAG R: TGTGTTGTAACCATCCCCGC	126	1.5	60		
melanoma antigen family D, 1	MAGED1	X	F: TGCAATAGTCTTTCCCCTGAGT R: GATACCAAACTCGACAGCACA	167	1.5	59		CX598229
melanoma antigen family D, 4	MAGED4	X	F: AGGTACCCTCAAGGCACGTA R: AATGTTTCGTCTGATTCTCGG	455	1.5	58	Raudsepp et al. 2004	BM414656
melanoma antigen family H, 1	MAGEH1	Xp13-p12	F: TTATAAGCCGGTGCCCCGT R: GCACCTGAATTGAGGATAGC	198	1.5	58	Raudsepp et al. 2004*	

monoamine oxidase A	MAOA	X	F: GGATCTGGTCAAGTAAGCGA R: GGCCTCCTTGTAATACATCA	~600	3.0	58	Raudsepp et al. 2004	
monoamine oxidase B	MAOB	X	F: GGGGCAAAGAGTTGGAATG R: TCCCCTACCACATGTTGAG	375	2.0	61	Momozawa et al. 2007	AB178283
mitochondrial carrier triple repeat 6	MCART6 (LOC170242)	X	F: GGAAAGAAAAGCTGGCAC R: GAAGTATTGAGGGCCTTCGT	168	1.5	55	Raudsepp et al. 2004	
midline 1	MID1	X	F: CCCTATTTGTCTGGAGCTC R: GATGATGTTCTGCAGGGTG	220	1.5	58	Raudsepp et al. 2004	
midline 2	MID2	X	F: TTGTGCTCACAGCCTCTGC R: CAGAACTGGCAAGCAATTCTG	294	1.5	53	Raudsepp et al. 2004	
male-specific lethal 3-like 1 (Drosophila)	MSL3L1	X	F: CAATGCAGCCTTTTCAGC R: CTTAATCCATCCACCATCTC	~780	1.5	62	Raudsepp et al. 2004	
moesin	MSN	X	F: AGGATGTGCGGAAGGAAAG R: TCAGGCGGGCAGTAAATATC	157	1.5	50	Raudsepp et al. 2004	
myotubularin 1	MTM1	Xq29	F: GGTCTACCAAATAAGACATCTCAAG R: AGCGTTTACAAAAAGCCAGA	100	1.5	58	Raudsepp et al. 2004*	
matrix-remodelling associated 5	MXRA5 (AdlicanX)	Xp25	F: TTTGCCAATGGGACCCTG R: CGGACTGCATGAAGGAGTT	274	1.5	62	Raudsepp et al. 2004*	
nucleosome assembly protein 1-like 3	NAP1L3	X	F: CCAGATCACAATGATCCCTT R: TGATGCATTAGGAACCACTC	169	1.5	TD 65	Raudsepp et al. 2004	
neuroligin 4, X-linked	NLGN4X	Xp25	F: TTCATGTACACAGACTGGGC R: GTAGAAGTAGGTAGGCGAGC	150	1.5	53 - 57	Raudsepp et al. 2004*	
nuclear receptor subfamily 0, group B, member 1	NR0B1	Xp21 prox	F: GGGCAGCATCCTCTACAACA R: CACCTGGAAGCAGGGTAAGT	201	1.5	62	Raudsepp et al. 2004	AF167158
nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	Xp13	F: CTGTTAGTGAGTAGCAGTCG R: CAATGCTAACCGAATCTTCC	241	1.5	58	Raudsepp et al. 2004*	
microsatellite	NVHEQ075	X	F: ATAACCCTGCTTACCCCTCTGT R: CAGGTGACATATCCCAAGGTGTA	98-112	2.0	58	Bjornstad et al. 2000	AJ245766

odz, odd Oz/ten-m homolog 1 (Drosophila)	ODZ1	Xq26-q27	F: CAGCAACGGAGTCCTGAAAA R: GGTTGTCCAGCCATTTTCGT	115	1.5	58	Raudsepp et al. 2004*	
opsin 1 (cone pigments), medium-wave-sensitive	OPN1MW	X	F: GACCTGGCAGAGACCATCAT R: CAGCTTGGCATCAAATCTCA	~700	1.5	62	Raudsepp et al. 2004	AF132043
ornithine carbamoyltransferase	OTC	Xp16-p15	F: TCAGATCTGCTGATAGCCA R: GTGTGGACAACCACTACAAA	~200	2.0	58	Godard et al. 2000*	ECA000935
purinergic receptor P2Y, G-protein coupled, 10	P2RY10	X	F: AGTGCTGCCATATGGGTC R: TATGATAGGGAGTGAAGCAG	328	1.5	58		
poly(A) binding protein, cytoplasmic 5	PABPC5	X	F: GGAAAACCATTCGCGCTTAT R: TTGAGCCGCACTCCATTCA	172	1.5	55	Raudsepp et al. 2004	
p21 (CDKN1A)-activated kinase 3	PAK3	Xq24-q25	F: TACTCCCTCGGATTATGTAATTTTC R: GGAGGTTTCGAATGCAAGAGGA	238	2.0	58	Raudsepp et al. 2002; Raudsepp et al. 2004*	G62153
pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1	X	F: AATGTGATCTTCACCGGCTG R: GCTTTTAACTCCATTCGGCG	115	1.5	58	Raudsepp et al. 2004	
progesterone receptor membrane component 1	PGRMC1	X	F: GGGCAAACCTGCTGAAGGA R: CTTTCTGGATTTGTGACACAC	293	1.5	60	Raudsepp et al. 2004	
phosphorylase kinase, alpha 1 (muscle)	PHKA1	Xq14	F: GCAGATGATATCATGTTGGC R: ATGGCACAGATGCTGTGG	155	1.5	58	Raudsepp et al. 2004*	
phosphatidylinositol glycan anchor biosynthesis, class A	PIGA	X	F: TGCCTGATTGAAAGAGGGCA R: CAGCATTAGGAATGACGGAC	454	1.5	63	Raudsepp et al. 2004	
praja 1	PJA1	X	F: GTCAAACCAACCAAGAGGAG R: TCCTCCTCACTATCATCTG	202	1.5	58	Raudsepp et al. 2004	
phosphatidylinositol-specific phospholipase C, X	PLCXD1	Xp25	F: ATCTCGGAGTGGCTGGAGAG R: GCCCGAAGATGTTCTCTGAC	121	1.5	58		DN510195

domain containing 1

plastin 3	PLS3	X	F: TGTCAGGGCACACCTGAAAT R: CACTGGGTGGAAAGCAAAAT	198	1.5	62	Raudsepp et al. 2004	AW260928
POU domain, class 3, transcription factor 4	POU3F4	X	F: ATTACTTGCAGGGAGTTCC R: CCAGCCACTTGTTTCAGCA	648	2.0	58	Raudsepp et al. 2004	
protein phosphatase, EF-hand calcium binding domain 1	PPEF1	X	F: CTCATCTCCATGGAAGAATT R: GCTTCCATCTTTGTTTAAGTCC	122	1.5	58	Raudsepp et al. 2004	
peroxiredoxin 4	PRDX4	X	F: GACAAGGGAATCCTAAGAC R: TTCTCCGTGTTTGTTCAGTGT	111	2.0	55	Raudsepp et al. 2004	
protein kinase, X-linked	PRKX	Xp25	F: CGCTTCCTGTACATGCTGATGGAG R: TCTTGGCGAACCCGAAGTCGGTGA	229	1.5	58		
retinoblastoma binding protein 7	RBBP7	X	F: TGCATATTTGGGAACAGCAA R: TACTGCTCCATGAACGCTTG	277	1.5	62	Raudsepp et al. 2004	
RNA binding motif protein 3	RBM3	X	F: ACCTTTTAGAAAGCTCCATGTGTTTT R: ACCAGGGCAGTGATCTTGAGTAA	300	2.0	58	Raudsepp et al. 2002	NM_016809
RNA binding motif protein, X-linked	RBMX	X	F: TTCCCTAAAGGCCACTTCCT R: CATAACCCGACCACCCTCTA	153	1.5	53	Raudsepp et al. 2004	BI961399
ribosomal protein L10	RPL10 (<i>HESTX-8</i>)	X	F: GTACATGGTGAAAAGCTGTGG R: GGGCTTCAATCACATGCTC	755	2.0	58	Raudsepp et al. 2004	BI961947
ribosomal protein L36a	RPL36A (<i>HESTX-10</i>)	X	F: CACAATACAAGAAGGGCAAGG R: CACCATAGCCACTCTGCTTC	269	2.0	58	Raudsepp et al. 2004	BI961599
ribosomal protein S6 kinase, 90kDa, polypeptide 3	RPS6KA3	X	F: GGATATTTGGTACCGTGGTG R: AAGAGACGAAAGCAGGAGCA	144	1.5	58	Raudsepp et al. 2004	
spermidine/spermin e N1-acetyltransferase 1	SAT1 (<i>SAT</i> , <i>HESTX-13</i>)	X	F: GGTAGCAGAATGGAATGAACCATC R: AGCAAGTACTCCTTGTCGATCTTG	111	2.0	65	Raudsepp et al. 2004	BI961507
sex comb on midleg-like 2 (Drosophila)	SCML2	X	F: GTTGGCATGAAGTTGGAAGC R: TTTTCACATGTCCCAACAGG	176	2.0	55	Raudsepp et al. 2004	
serpin peptidase inhibitor, clade A	SERPINA7	X	F: TCAACCTGTACCGGAGGTTC R: TTCCAGCTCCTTCTTTGGAA	230	2.0	55	Raudsepp et al. 2004	

member 7

microsatellite	SGCV31 (<i>UM038</i>)	Xq13- q14	F1: GACAGAACAGAAGAAGACCGG R1: CTTTCAATATGGCTCGCTCCTAC F2: CAAGACAGAACAGAAGAAGAC R2: ATATGGCTCGCTCCTAC	143 113 - 137	3.0 2.0	58	Godard et al. 1997*; George et al. 1998; Raudsepp et al. 2002	U90606 AF195583
SH3 domain binding glutamic acid-rich protein like	SH3BGRL (<i>HESTX-6</i>)	Xq14- q15	F: GAAACAGCAAGATGTACTGGG R: CAGGCACATTTTCTCTCATCC	110	2.0	58	Raudsepp et al. 2004*	BI961868
shroom family member 2	SHROOM2 (<i>APXL</i>)	Xp25	F: TCCAGCAGCACGAGGACGCCAA R: TTTCGGGCTGAAGGCTGTCCAA	225	1.5	62	Raudsepp et al. 2004*	
solute carrier family 25 member 6	SLC25A6	Xp25	F: CTTTCTGGAGGGGACAACCT R: GCCCAGAAAGATCTGCTTGT	102	1.5	55		
solute carrier family 6, member 14	SLC6A14	X	F: CTGATTGACCACTTCTGTGC R: CCACCATAGCCAGAATATCCA	450	1.5	60	Raudsepp et al. 2004	
spermine synthase	SMS	Xp22	F: GACAGATACTGGCCCACTGC R: GCCAAATCACTTTCCGCCAA	867	1.5	62	Raudsepp et al. 2004*	
sprouty homolog 3 (<i>Drosophila</i>)	SPRY3	X	F: AGTGAGCACCTCTTCATC R: CCCTTAACACAGCAGAGACA	158	2.0	55	Raudsepp et al. 2004	
sushi-repeat- containing protein, X-linked	SRPX	X	F: GGAGACCACAAGATCCAGTA R: GTCAGTGGAGCACTTCATGT	838	1.5	58	Raudsepp et al. 2004	
sushi-repeat- containing protein, X-linked 2	SRPX2	X	F: CATGGATCTAGGGACAGGACTC R: GGCTCCTCCAGTGCTATCTAAA	129	1.5	59		CX595244
steroid sulfatase (microsomal), arylsulfatase C, isozyme S	STS (<i>STS-X</i> , <i>ARSCI</i>)	Xp25	F: CTCTTGACAGGGTCTTGGTGT R: GCACCAATGGATGTTTTTCC	200	2.0	TD 50	Raudsepp et al. 2002*	AF133204
synaptobrevin-like 1	SYBL1	X	F: CGCGAGCCTTTAATTTTCTG R: TGCAGCCAAGACACTTGAGA	119	3.0	56	Raudsepp et al. 2004	

TATA box binding protein (TBP)-associated factor	TAF1	X	F: TCTTCGAGGCACCTTTGGA R: ATGTGCTTTAGCAAGGGCTG	314	1.5	58	Raudsepp et al. 2004	
transducin (beta)-like 1X-linked	TBL1X	X	F: AGTAACAAAGACGTCACCTC R: GGCCTTTATGTTGGCCTAAG	~500	1.5	58		
TIMP metalloproteinase inhibitor 1	TIMP1 (<i>HESTX-5</i>)	X	F: CCTCAGAAGTCAACCAGACC R: CTCCGACCTGTGGAAGTATC	345	1.5	58	Raudsepp et al. 2004	
microsatellite	TKY020	Xq29	F: ACAGTGCTCCCTGCTCCGGA R: TCATGCTCAGAGTTTTGGGTG	149	4.0	58	Hirota et al. 2001*	AB009590
microsatellite	TKY038	Xq23	F: TAAGTATTCTCATAAACGGG R: GGAATAATAACAGCATCCTC	134	2.0	55	Hirota et al. 2001*	AB048344
microsatellite	TKY039	Xp21	F: AAGCAGGGATAGTAAAGGAC R: TCTTCCTACCCTTTTTTGGGA	236	2.0	TD 60	Hirota et al. 2001*	AB048345
microsatellite	TKY040	X	F: TATCTCACTTGACCATACCT R: CTGGATTACCATTTGGATTT	153	2.0	58	Hirota et al. 2001	AB048346
microsatellite	TKY270	X	F: CTGCTTTAGAGAAACAACT R: CCATGGTGAGAAAAATGAGA	166-172	1.5	52	Kakoi et al. 2000	AB048312
microsatellite	TKY514	X	F: TCACCCGCTTCGTCAAATG R: ACTTAACCTCTTGCTATCTCG	187	2.0	58		AB103732
microsatellite	TKY519	X	F: CCTCCCTGCTGTCAATCCTA R: TTGCAGGAGAACTACCCAAA	163-183	1.5	58	Tozaki et al. 2004	AB103737
microsatellite	TKY753	X	F: TATTATTGCCGTCGTCGTTG R: TGTGTGTGGTGTTTGGAGCA	175	2.0	58	Tozaki et al. 2004	AB103971
microsatellite	TKY836	X	F: AAGGGCTCGGATTCTTCC R: CTCAGGGAGCCCTCTCTT	251	2.0	58		AB104054
microsatellite	TKY915	X	F: TCCAATGACGCCTGGAAC R: GATGGTTGCACAACAGTGTG	176	2.0	58		AB104133
microsatellite	TKY959	X	F: GATGCCACATCTTACTTTC R: TCAAAGTGTTCCAGCTTTGG	268	2.0	58		AB104177
microsatellite	TKY968	X	F: ATGAGGGAACCATTATCTGC R: TCTGTTTACCTCAGATGGAG	211	2.0	58		AB104186

microsatellite	TKY991	X	F: AGGCCCAGAAAGATAAAGTG R: GTTAAGAGTAAGGAGTAGGC	160	2.0	58		AB104209
microsatellite	TKY1073	X	F: AGAGATGAAGTCAGGCTTTC R: TGAACAGGAATTCCCATCTC	203	2.0	58		AB104291
microsatellite	TKY1084	X	F: CACAGTGTGCTCCCATATG R: CTGCCCTCTTCTGGAATTG	197	2.0	58		AB104302
microsatellite	TKY1103	X	F: AGAGAGGAAACTGCAGCTC R: AACAGCTGAACTCTACACTG	212	2.0	58		AB104321
microsatellite	TKY1105	X	F: GATCAAGGTAATAGAAAAGAGTAT R: GAATGGAGGTGGACTATGG	217	2.0	58		AB104323
microsatellite	TKY1130	X	F: TAGACCACAGTTGAAGCTTG R: ACCTTAGGGAAGCTGGAAG	222	2.0	58		AB104348
microsatellite	TKY1135	X	F: AGCACATTTTCGGGGATATC R: AGCTAAAAAACCAGTTGAC	163	2.0	58		AB104353
microsatellite	TKY1996	X	F: AATAAAGCCTGCATTAGGAG R: ATCCTTGGTCTAAAACACAG	139	1.5	58	Tozaki et al. 2007	AB215939
microsatellite	TKY2732	X	F: GATCAGTTAGATAGTCCATAACTAAG R: TAGTTGGACTAGAGCAGAAC	181	1.5	58	Tozaki et al. 2007	AB216675
microsatellite	TKY3315	X	F: GGGGTAGAGCAGGGAGAA R: TGTGGTGTTAAACCATGCTG	215	1.5	58	Tozaki et al. 2007	AB217258
toll-like receptor 7	TLR7	Xp23- p22	F: GAGGAAAGGGACTGGTTA R: ACACTGCCAGAAGTACGGGT	300	1.5	62	Raudsepp et al. 2004*	
toll-like receptor 8	TLR8	X	F: TAGCCAAGGTAAAAGGCTAC R: TGCATGAGGTTGTCTGATGAT	211	1.5	54	Raudsepp et al. 2004	
transmembrane protein 47	TMEM47	X	F: TAGGATTGTGCGTGTTTATCC R: TTTCTGGCTTGTTCTCAACTG	362	1.5	58		CT974349
transmembrane protein 185A	TMEM185A (<i>FAM11A</i>)	X	F: TGCTGCTGTTCTCTGTGTTG R: ATATTGGGGATTTCGTGCC	185	1.5	58	Raudsepp et al. 2004	
thymosin, beta 4, X- linked	TMSB4X	Xp23- p22	F: ATTCCACAAGCATTGCCTTC R: CCCACTTCTTCCTTCACCAA	210	1.5	58	Raudsepp et al. 2004*	
thymosin-like 8	TMSL8	X	F: AGCAGGAGAAAGAGTGTGT R: AGGTGAGAAGACATCAGAAGA	153	1.5	60	Raudsepp et al. 2004	

tenomodulin	TNMD (<i>CHM1L</i>)	X	F: TCACTTCCCTACCAACGACA R: GGCATGATGACACGACAGAT	550	1.5	65		AB059407
microsatellite	UCDEQ428	X	F: CTTTTCCCCGAACCTCCTAC R: TTGGATGCTCCGAGAAGAGT	125 - 137	3.0	58	Swinburne et al. 2000	U67407
microsatellite	UCDEQ502	X	F: CCTTGGGCTTTAGCAACT R: CCATTGGAACTGAGAGG	155 - 167	3.0	58	Eggleston- Stott et al. 1997	U67420
microsatellite	UM035	X	F: GTGATGGATGACATGAGG R: GCATTTAAAACACTAGAACAC	~200	2.0	58		AF195581
microsatellite	UMNe058	X	F: GATCCAAGACTTGAAGGTTAGC R: TTTCTCACCATCCTCCTTGAC	143 - 165	2.0	58	Roberts et al. 2000	AF191693
microsatellite	UMNe060	X	F: TGTGGCAGGAAAAACACATG R: CCATAATCCATGAGCCTATTCC	146 - 154	2.0	55	Roberts et al. 2000	AF191694
microsatellite	UMNe091	X	F: GCAACAATAAGATACCCAAAGCAG R: GATCTTGGCCAACAACCTCGTC	153	1.5	58	Wagner et al. 2004a	AY391286
microsatellite	UMNe107	X	F: TGCATATGTAGATGTATATAGGACAGG R: TTTCCCTACACTGGGACTGC	143	1.5	55	Mickelson et al. 2003	AF536250
microsatellite	UMNe134	X	F: CACTCTGGCTTATGTTTGTGC R: GAGTTCTGTGGCTAATCCTTG	116	1.5	58		
microsatellite	UMNe148	X	F: GATCAAACACTAGAATGTTTCACAC R: CAGCTGTGAGGCAGAGACTG	110	1.5	65	Mickelson et al. 2003	AF536262
microsatellite	UMNe202	X	F: ATGATTCCAAATGAGGCCTG R: AGCAATCCTTGCAGGCAG	187	2.0	58	Mickelson et al. 2003	AF536285
microsatellite	UMNe266	X	F: TTCCAAAAAACATAACAGGGTG R: CCAATTTGAATGCTTTTCATTG	150	2.0	58	Mickelson et al. 2003	AF536324
microsatellite	UMNe350	X	F: GCAAAATAAAAGGGTCACTTGC R: AGTGCTCCAGGTGCTTATATCC	153	2.0	58	Wagner et al. 2004a	AY391343
microsatellite	UMNe360	X	F: ATCAAGCCATGCTGTAGCG R: ATGCAGCAGTCTACCGCC	169	2.0	62		
microsatellite	UMNe363	X	F: ACTTACCCATCAACAAAATGGG R: TTGGGACTTCTCAGCCTCC	211	2.0	58		

microsatellite	UMNe375	X	F: GGAGCCAGTTCAAAGATTTCC R: ATTCAGTGGGTGTTTTGCC	130	2.0	58	Wagner et al. 2004a	AY391357
microsatellite	UMNe376	X	F: ACGCATATTAAAGTTTGAGAAAGTCC R: CAGACCTACTGAATTGGAATACACC	155	2.0	58	Wagner et al. 2004a	AY391358
microsatellite	UMNe386	X	F: ACTTCCACAATCATGTGAGCC R: CTGTGTGATTTGGGGCAAG	169	2.0	62		
microsatellite	UMNe387	X	F: AACTCATTTCAGACCACTAGGGG R: ATCACTCAGAGAAAAGTGCCTG	144	2.0	58		
microsatellite	UMNe390	X	F: TATGAGACTCTGACATTTGCTGTG R: ATATTCCCTTCCTGAAACAGTCC	195	2.0	62	Wagner et al. 2004b	AY464476
microsatellite	UMNe394	X	F: AGGACACCAGTTTAATCATCGG R: TTCCAAAGCAACAGCAAATG	144	3.0	58		
microsatellite	UMNe397	X	F: TGTGGCTCCATCTCTCCAG R: TTTTCATGTCCCTAGGAAATTC	126	2.0	55	Wagner et al. 2004b	AY464478
microsatellite	UMNe402	X	F: AAGATGTGGCCTGTTTCAGG R: TTGATTCCTGGAGACTGATGG	244	2.0	58	Wagner et al. 2004b	AY464479
microsatellite	UMNe415	X	F: TGGAAACAACCTAAGTGTCGG R: CAGCCTCTCCCTATTTTCCC	287	1.5	60	Wagner et al. 2004b	AY464483
microsatellite	UMNe437	X	F: CACTTCGGGGAATAAGCATC R: CTTCAATTGAAAATCCCTTTTCG	214	1.5	50		
microsatellite	UMNe446	X	F: AGCATCCAGTCCACTGCAG R: GGCAGGTAAGTTTGAGAACCC	378	1.5	58	Wagner et al. 2004c	AY735252
microsatellite	UMNe483	X	F: GTGGAGGTGGGGAGAAGAG R: GCTCTCAGGAGCACAGGC	~200	1.5	60	Wagner et al. 2004b	AY464500
microsatellite	UMNe492	X	F: GATTTGCATTTTGTATTGCTGC R: ATTCTGTGGATGTGTGAAGGC	~400	1.5	60	Wagner et al. 2004b	AY464504
microsatellite	UMNe511	X	F: TTTTCCCACTCCTCAGCC R: TCTGCTCCAATGTTACAGC	349	1.5	58		
microsatellite	UMNe522	X	F: GCAATCCCACATCTGGGTAG R: TCTGACCTCAAGGTCCATCC	~200	1.5	62	Wagner et al. 2004b	AY464516
microsatellite	UMNe594	X	F: CAGTAAATTTTTTCGTGTGG R: TTGCATTGTACACTTTAAATGG	138	1.5	58		

microsatellite	UMNe596	X	F: CCAGCGTTTTCTTGTTTTAAGG R: CAAAGCTCACCCCTTCCC	249	1.5	58		
microsatellite	UMNe597	X	F: ACCTTCAAATGCCCAAAGTG R: TATGCTTGCTTTTGTCTGTC	318	1.5	58		
ubiquitin specific peptidase 11	USP11	X	F: TCATGGATGTAAACTGACAGGC R: GGGACAGGGACAACCATAAATA	280	1.5	59		CX598430
ubiquitin specific peptidase 9, X- linked	USP9X (<i>HESTX-7</i>)	X	F: GCATGGTAGCTCTCTTCAGCA R: GTTCATCTCCAAGCCATTCC	266	2.0	68	Raudsepp et al. 2004	BI961890
microsatellite	VHL81	Xq24- q26	F: CAACTATGTACTTTGGGGAGCT R: GTCCATGAAATTCTAGTTGTTGC	162 - 174	2.0	58	van Haeringen et al. 1998; Raudsepp et al. 2002*	Y08443
WD repeat domain 40B	WDR40B (<i>LOC139170</i>)	X	F: ACCTGTGGGTGAACTACTTC R: GAGGCCTGAAGGGAGAGG	119	1.5	TD 65	Raudsepp et al. 2004	
WD repeat domain 45	WDR45 (<i>JM5</i>)	X	F: GGGTAGAGCCGGAAGAGTC R: TGCTTGGGGTTGGTAG	100	3.0	55	Raudsepp et al. 2004	BI395200
microsatellite	XCA001	X	F: AACTCCTCGTTCTCATGTTGC R: TGCAGACTGCCAGCTGATAC	233	1.5	58		AY820147
Xg blood group	XG	Xp25	F: AGAACGTGTGAGGGCTTCAG R: GCTCATTGATTTCAAGCAGGA	168	1.5	58		CX597271
X (inactive)-specific transcript	XIST	Xq13	F: ACCCATTGAAAACCCATTGA R: GGGGGTGGAGGAAGTAGAAG	200	2.0	TD 60	Shiue et al. 2000* ; Raudsepp et al. 2002	U50911
zinc finger, BED- type containing 1	ZBED1	Xp25	F: AACGAGGTACCCCTCAAGT R: GTTCCTCTTGGCGCTGAC	154	1.5	55		
zinc finger, DHHC- type containing 9	ZDHHC9	Xq26- q27	F: GGACTTTTGATGATGTTTGACC R: TTCTTTCTCACCACCATCAC	150	1.5	58	Raudsepp et al. 2004*	
Zic family member 3 heterotaxy 1 (<i>Drosophila</i>)	ZIC3	X	F: CAGATGGTTGTTTAACTGCG R: CAGGGATGATTAATCCAGC	145	1.5	63	Raudsepp et al. 2004	

zinc finger protein 711	ZNF711 (ZNF6)	X	F: GAGCATATGGGGAACACA R: CATCTTCTCCCGCTGCAT	~1200	1.5	60	Raudsepp et al. 2004
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