

Supplementary Table 1. Information for ECA6p and ECA18 markers^a

Symbol	Name	Human chromosome	Mb	FISH location	Primers 5'-3'	Product size (bp)	MgCl ₂ (mM)	Ta (°C)	Reference Accession No.	RF
MYL1	Myosin, light polypeptide 1, alkali; skeletal, fast	2q34	210.9		F: GACCAGGGCAGCTATGAAGA R: TGGCTAAGACATGACGGAGTT	100	1.5	58	this study, equine skeletal muscle EST library	
CPS1	Carbamoyl-phosphate synthetase 1, mitochondrial	2q34	211.2		F: TCAAATGAGATTCCAAGGGAAG R: TGAGGGACAGTAAAGAGATGAC	242	1.5	64	DQ001083	23
AC092680 (AJ584440)	Human BAC clone	2q34	212.9		F: AGAACCCCTCCCATTGAATC R: GCACATCTTCTCCCTCTTTTG	584	1.5	62	AJ584440	26
SMARCAL1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1	2q35	217.1		F: CGCTGCCTTCCGCAAGTTCG R: GGGTCCACTCCAGAAAGGTCG	132	1.5	60	BM414611	21
RNF25 (HEST2-11)	Ring finger protein 25	2q35	219.3		F: CCTTTGGAACCCGAGTCAAC R: TGGCAGTTCCTGGGTATCAGT	309	2	52	BI961897	
DES	Desmin	2q35	220.1		F: GCAGCCAACAAGAACAATGA R: CCTTGAGGGCGTCGATCT	103	1.5	58	this study, equine skeletal muscle EST library	
INHA*	Inhibin, alpha	2q35	220.2	6p14	F: GCAGCATTGTGCTTGCATC R: GAGAAGTGAAGGAAGAGGG	121	1.5	60	D50327	17
PAX3***	Paired box gene 3 (Waardenburg syndrome 1)	2q36.1	222.9		F: CACACAAGATTATGCGCCC R: CCACCTGATTTCTCACTCTCC	153	1.5	60	AF179634	20
CUL3***	Cullin 3	2q36.2	225.1		F: TGCTGTGTCGTTCTGTTTC R: CTCTTCTATGTTACTGCCATCC	247	1.5	54	DQ001085	18
COL4A4	Collagen, type IV, alpha 4	2q36.3	227.6		F: AGACAGACGGACAGCAGTAG R: TGAGGGAAGGAGAAGTAGTGG	196	1.5	56	DQ001082	18
NCL	Nucleolin	2q37.1	232.1		F: AACAAACAGGAAGGAAAGGAAG R: TGGGAGAGTTAATATGCCAATG	104	1.5	58	DQ001113	22
UGT1A1*	UDP glycosyltransferase 1 family, polypeptide A1	2q37.1	234.4	6p12	F: CATCATGCGCCTCTCCAGCC R: CTGGTACCAGGTGAGGTCGTGGG	~140	1.5	65	Mariat et al. 2001	
ARL7	ADP-ribosylation factor-like 7	2q37.1	235.1		F: AGAACCCAGAGACAGAAGTCC R: ACCAGCCCATTTAGAAATCAG	243	1.5	60	CD470070	23

TKY1090	Microsatellite				F: CATCCCAGGGACAAACATC R: CAGGGACAATCTTAGACAAAC	174	1.5	58	AB104308	
TKY543	Microsatellite				F: AGGAAAGCGGTGTGGTACAG R: CACACAAGACGGACGAATGT	239	1.5	58	AB103761	
UMNe87	Microsatellite				F: CCTCCAAATTCCTTCCCTTTTAG R: GCTCACTTTAGCCATGTCAAGC	146	1.5	62	AF536243	
UMNe195	Microsatellite				F: AGTGAAAACCTCAAAGCACAGG R: TGGCCCCAGAGAAAAATG	~550	1.5	55	AY391318	
UMNe197	Microsatellite				F: CTGGTTGAAGCTTGTCTCTC R: CCGCTTGTCCAGTGACATAG	188	2	58	AF536282	
UMNe203	Microsatellite				F: GTAACAAAGCCCCTAATTGCC R: TGAGCCAACACAACACTTCTG	131	2	62	AF536286	
UMNe233	Microsatellite				F: AGAACAGTACATGCTGTGGTCC R: CTGTGAACCGTCTCATGAGTG	141	2	58	AF536305	
UMNe248	Microsatellite				F: GATAATGCCTCTTGTCTCCC R: AAGATGAAGAGAGGTTAGCCTAGTG	110	2	58	AF536316	
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	2q14.1	118.2	18q15	F: AAATAGGACGTAGGCCAGAG R: TCCAATCACACATCCATCAG	127	1.5	58	DQ001087	21
TUDPEc010	Equine expressed sequence				F: CCCAAATTCACCCGGTTCTAC R: GGAGTAAGCAATGCAGAGGT	242	2	58	BI395085	
EPB41L5 (KIAA1548)	Erythrocyte membrane protein band 4.1 like 5	2q14.2	120.4	18q15	F: CCTCCAGTAATCAGACATAA R: GCATATTTACACAAGCC	144	1.5	58	DQ001101/ DQ001102	14
BIN1	Bridging integrator 1	2q14.3	127.5	18q12-q13	F: TGGAGAGGGAGAGAGGAAC R: GACACAGGCACACTCAGG	305	1.5	60	DQ001077	8.7
UGCGL1 (HUGT1)	UDP-glucose ceramide glucosyltransferase-like 1	2q14.3	128.5		F: TCCTGCTGTTAACTTTGTCC R: GTGTCCACCAAGTCTCATTTT	181	1.5	60	DQ001098	23
MGAT5	Mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	2q21.2	134.8		F: CCTTTCCTCCCTAGCGATAC R: TGTCATAGCCATAGCCCAAAAC	102	1.5	56	DQ001110	21
LRP1B	Low density lipoprotein-related protein 1B	2q22.1	140.8		F: CTTAGCAAGGTCACAAAAGGG R: GCAGAAGGGCAAGAAATCAAC	126	1.5	58	DQ001105	17
KYNU	Kynureninase (L-kynurenine hydrolase)	2q22.2	143.4		F: CATCCCATCAAACACTAAATAC R: CACATCCACACTGCTCAC	155	1.5	58	DQ001103	17
ZFHX1B	Zinc finger homeobox 1b	2q22.3	144.9		F: GAATTCACAGCGGTGAGTAG R: TTGGTAGTACCACAGGTCTC	181	1.5	58	DQ001126/ DQ001127	13
ORC4L	Origin recognition complex,	2q23.1	148.5	18q22	F: CCATACAGCTTTAACTCAGCC	154	1.5	58	DQ001115	14

	subunit 4-like (yeast)				R: GCCAATGCTTTTCAGTAGCAC					
KIF5C	Kinesin family member 5C	2q23.1	149.6		F: CAGCTCAGCAGGAGATAGAG R: GCCTATCCTATCCTTCTTCCTC	93	1.5	58	CD468079	16
TNFAIP6 (HEST2-13)	Tumor necrosis factor, alpha- induced protein 6	2q23.3	152.0		F: CGGTGGCATCTTTACAG R: ACGCTGACCATACTTGAG	112	2	58	BI961885	
FNBP3	Formin-binding protein 3	2q23.3	153.3		F: AAAAACGCACAGCAACTAGAC R: TTGATGTCAAAGGTTACATAGTAATG	349	1.5	56	DQ001090/ DQ001091	13
PSCDBP	Pleckstrin homology, Sec7 and coiled-coil domains, binding protein	2q24.1	158.0		F: TTGCAAGGACATCACCTGGGAG R: TGTGTTGCTGAGGTTTGGGG	118	1.5	60	DQ001118	16
ACVR1	Activin A receptor, type I	2q24.1	158.4		F: GTGAATGACAGTAGTCACAGG R: CAGGTACACAGAGATGGAAAAG	155	1.5	60	DQ001074	23
GCG**	Glucagon	2q24.2	162.8	18q22	F: GGGCATGAAGTTATACAGCTTG R: TGAAAAGCCTGATAGAAACCTG	110	1.5	58	AY008785	18
SSB	Sjogren syndrome antigen B (autoantigen La)	2q31.1	170.4		F: TGGATTATTTTGGAGTGGAAATC R: ATGAAGCCAGGATGTCTCG	123	1.5	58	DQ001122/ DQ001123	14
GAD1	Glutamate decarboxylase 1 (brain, 67kDa)	2q31.1	171.4		F: GAGCCATCTTGTTGTAGTCTTC R: ATGCATATTACTCAGTTGCC	148	1.5	58	DQ001092	17
HOXD10	Homeo box D10	2q31.1	176.8		F: GCAACAAAAGAGCACAAATGAG R: TCACTGGATGAAAGGCAAGG	104	1.5	58	DQ001096	12
COL3A1	Collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	2q32.2	189.6		F: GACAGCCACAAAATGGATGA R: CACCTTTTACTCCAGGCTGC	286	1.5	60	DQ001081	15
MYOB1 AK000160 (AC068056)	Myosin IB	2q32.3	192.0		F: CCTTGAAAAGAATTTCCCTTGC R: AGAAGATGAGCCACAAGACC	127	1.5	56	AK000160	13
AJ577071 (AC006196)*	Equus caballus GSS, BAC clone CH241-101P3	2q32.3	195.3	18q25	F: TCCGTAACATCAAATCGGAAC R: GTGAATATGGAGTGAAGTGGAG	591	1.5	62	AJ577071	12
SF3B1	Splicing factor 3b, subunit 1, 155kDa	2q33.1	198.0		F: CAACTTCTCCCAGACCTTTTTTC R: AACCCATTATGGTAAAGACAGC	102	1.5	62	DQ001120	11
HSPD1	Heat shock 60kDa protein 1 (chaperonin)	2q33.1	198.1		F: TAACAGAGAAGCCACTCCAG R: TGAGAAGATTATGCAGAGTTCC	249	1.5	60	DQ001097	14
BZW1 (BZAP45)	Basic leucine zipper and W2 domains 1	2q33.1	201.5		F: GTGTTTCTTAGCTCCTTGTC R: CAATGTGTTTAGCCCTGATCC	101	1.5	56	DQ001078	17

NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	2q33	206.8	18q26	F: GAGACTTCTTCCAATCTGTTCC R: TGATGTTATTCTCCCAGGCG	~1161	1.5	56	BI395134	18
EEF1B2 (HEST2-17)	Eukaryotic translation elongation factor 1 beta 2	2q33.3	206.8		F: CAGATATGGCAAAGCTGG R: CTCAAAAGCAGTGATCCG	561	2	58	BI961819	
KIAA0971	Homo sapiens KIAA0971 (KIAA0971), mRNA	2q33.3	207.4		F: GGACAATTGCCAAAAGGATG R: GCTTCACCCACAGCATGAAGA	159	1.5	58	this study, equine skeletal muscle EST library	
GRB14†	Growth factor receptor-bound protein 14	2q24.3	165.1	18q23	F: GGCCACAGCACATTGTTTATC R: GCCGACTAACTATGGATTCTGC	213	1.5	60	DQ001094	
AJ584004†	Equus caballus GSS, BAC clone CH241-102B19	2q31.3	180.5	18q24	F: TCACAAAGTGTTAGGCACCAG R: AGATAGCCGCATAGGCAGAG	534	1.5	62	AJ584004	
AHT115	Microsatellite				F: GAACCCAAGAGGAGTCCACA R: ACACACCTCAAGCAAAACACC	124-134	1.5	58	J. Swinburne pers. comm	
AHT127	Microsatellite				F: TGAGTGAGTGCTGGGAAGTC R: CTTCCCCCAAACCAGAACT	176-180	1.5	58	J. Swinburne pers. comm	
HMS75	Microsatellite			18q25	F: CCCTATTGTTCTGGAATCG R: GGAAAGTAACGTTAGAGTTTGGG	150	1.5	58	Mariat et al. 2001	
LEX016	Microsatellite				F: GTGGGGCCGGTATAGTGATTG R: ACCCTAACTGATAACTGATAGA	171 - 185	2	58.0	AF075618; Coogle et al. 1996	
TKY016	Microsatellite			18q26	F: GGTTATGGTTTGGTATCTGTC R: AAAACAATGGCTTCTGGTCA	120	2	58	Kakoi et al. 1999	
TKY019*	Microsatellite			18q13	F: CTTCTGCTGATTCTGAATG R: GGATCTCCTTAAATGGAACA	150	2	58	Kakoi et al. 1999	
TKY101	Microsatellite				F: TCTGAAATACCGTGTGCCT R: TTCTGCCTCCCTCCAACCTT	200	1.5	58	Mashima et al. 1999	
TKY1055	Microsatellite				F: AGAAGGTCATCAAACGATGC R: GCTGTTGAGATATTGACAGC	112	1.5	58	AB104273	
TKY407	Microsatellite				F: TCCTGCTGTGAGTTCATGA R: CATCTTGTGCTGGGGATCTT	214	1.5	58	AB103625	
TKY426	Microsatellite				F: TCCCTCCATGTCTCTTTCCTT R: ATTTGAATTACCGCGGACT	121	1.5	58	AB103644	
TKY449	Microsatellite				F: GAGCCAATTCCTTATAATAC R: TTTAGTCACCTGGACAGATG	182	1.5	58	AB103667	

TKY589	Microsatellite	F: TATCCTGGATTGGGGTCTG R: TGCAGGGAGGTGGAGCCG	115	1.5	58	AB103807
TKY608	Microsatellite	F: AGCAACAGATGTTACCTCAG R: AAACCTTCTCTTTCCCTAC	108	1.5	58	AB103826
TKY770	Microsatellite	F: CCCTGTCATGTATAAAGTAGAAGG R: GGGGCTAAATAAGGTTGTATATGG	219	1.5	58	AB103988
TKY799	Microsatellite	F: GATTCCATCTCCAGTCAGAG R: TGACACGCACTATAAACTCC	109	1.5	58	AB104017
TKY909	Microsatellite	F: GAGTCACACTTCTGGGAAG R: GCTACCAAACAACACTTGGT	188	1.5	58	AB104127
UMNe89	Microsatellite	F: TCCTGTGTCCTTCTGAGATACCC R: ACCAGGGAATCTTGAGAAATG	174	1.5	60	AF536245
UMNe95	Microsatellite	F: TGTCCAAATAAATTTAGTCAAAACAG R: ACCCATGATTCATCACTGC	179	1.5	58	AF536246
UMNe97	Microsatellite	F: TGTCAGGTGGCATTCAAATC R: TAACCAACAATGCCCAAGTC	202	1.5	58	AY391288
UMNe114	Microsatellite	F: AACCCAAAAGCATTGAGAAG R: TCTGCACCAGTTTTGTACGC	129	1.5	58	AY391295
UMNe180	Microsatellite	F: TGGAAAATCCTCACAACTGC R: TATATTTTCCTTTGCGTGTGC	148	2	58	AY391313
UMNe243	Microsatellite	F: TCCATCTATCAGTCTACTTCCAGC R: GAACTAACACACCTCATTTTCCC	151	2	58	AF536313
UMNe263	Microsatellite	F: TCTCTTCCCTTCCCTTC R: ATAATGATATTGGCTGCCTGTG	165	2	60	AF536322
UMNe307	Microsatellite	F: ATTGTCCCTGCTCCATGAAG R: GTCCCATGCTCTCCATG	139	2	58	AY731383
UMNe308	Microsatellite	F: TCTTTGTTAAAACACGTATACCACA R: TATTGTCTTGAAAGAAATCGTTGC	162	2	58	DQ013266
UMNe442	Microsatellite	F: TACAGGTTTTCCCATGAACAC R: ATGGATGGGCTTAGGAGGTC	170	1.5	58	AY464487
UMNe501	Microsatellite	F: CCCATGATTTAATTGTCTGCTG R: TCCAAGTTTTTCCGAAATG	296	1.5	58	AY731404
UMNe505	Microsatellite	F: CCAGAAAGGCTGTGTTCTTACC R: TGCTGCTTTGAGAATTGTGG	243	1.5	58	AY464509

^a Notations are as follows: *old FISH data, new RH data, **new FISH data, old RH data, † markers with FISH data but no RH data, ***previously typed on RH panel, re-typed with new primers as controls. Retention frequency is abbreviated as RF.

Supplementary Table 2. Information for ECA15 markers^a

Symbol	Name	Human chromosome	Mb	FISH location	Primers 5'-3'	Product size (bp)	MgCl ₂ (mM)	Ta (°C)	Reference Accession No.	RF
MYT1L	Myelin transcription factor 1-like	2p25.3	1.7		F: GCCCGACAGAAGTGTAAAGAC R: ATTCAATATACAGCACTTGCCC	143	1.5	60	DQ001112	8.7
AJ542706 (AC068292)	Equus caballus GSS, BAC clone CH241-100A9	2p25.2	3.8		F: AGTGACAAACGCTTTTCCAG R: CTGACAAGGGGGTATTGTG	647	1.5	62	AJ542706	12
RSAD2 (CIG5)	Viperin	2p25.2	6.9	15q27	F: CATCTCCTGTGACAGCTTTG R: TCTGTTCCCTCATATCCTCTTC	179	1.5	58	CD471892	13
ROCK2	Rho-associated protein kinase 2	2p25.1	11.2	15q26	F: TTTATAAGAGCACGTCCCATTC R: ACTTCCGATAGCATAGGTAACC	169	1.5	58	DQ001119	15
DDX1	ATP-dependent helicase DEAD-box protein 1	2p24.3	15.6	15q26	F: GCATTATAAACTAGCCTCACC R: AAACGATGAGTCCATCACTTAC	141	1.5	58	DQ001086	13
ITSN2	Intersectin 2	2p23.3	24.3		F: CAGCATTGGGAACACAGAG R: AGGTAAAATGAGTGACAACAGG	120	1.5	58	DQ001100	11
NRBP	Nuclear receptor binding protein	2p23.3	27.5		F: CAACGTAAGTCCCTTTGGC R: TCCTACGAGTGAAGAATCCC	115	1.5	58	DQ001114	14
PPP1CB	Protein phosphatase 1, catalytic subunit, beta	2p23.2	28.8	15q25	F: CAAAGACGATATTAAGGTCAAG R: AAGGAGTAGAAAAGTCAGCA	215	1.5	58	BM414639	16
XDH	Xanthine dehydrogenase	2p23.1	31.4		F: CAGGGAATCCCTTCCACTAC R: CTGGAGCCAACATCCATGAC	~900	1.5	60	BI961081	21
LTBP1	Latent transforming growth factor beta binding protein 1	2p22.3	33.2	15q24	F: CCTTTTGCTATGTTTTTCTGCC R: GCTGAAGTGTCTTTTGGTCTG	141	1.5	58	DQ001106/ DQ001107	15
CEPBZ (CBF2)	CCAAT/enhancer binding protein zeta	2p22.2	37.3		F: TCTTGGCTCAAACTCAACTC R: TGTATTCAACTATGTGAGGCA	146	1.5	55	DQ001079	14
MAP4K3	Mitogen-activated protein kinase kinase kinase	2p22.1	39.3		F: TGAGGAGAGGAGAAGGAAGG R: GAAAGGAGAAAACAAGGGGC	129	1.5	58	DQ001108	14
EPAS1	Endothelial PAS domain protein 1	2p21	46.4	15q22-q23	F: GACTCATTCTGGCTGTGAGG R: AGGGCAGATGTAGAGGGAAG	182	1.5	60	DQ001089	21
FBXO11 (VIT1)	Vitiligo-associated protein VIT-1	2p16.3	47.9		F: GCTGCAAAAAGTGGCTGAATG R: AATGAACGGCAAGAGCAATG	114	1.5	60	DQ001124	20
LHCGR*	Luteinizing hormone/choriogonadotropin receptor	2p16.3	48.8	15q22-q23	F: CACACTAGAAAGATGGCACAC R: TGGGGAGGCAATACTGAC	170	1.5	60	AY464091	20
ACYP2	Acylphosphatase 2, muscle type	2p16.2	54.2		F: ACACAGAAGATGAGGCTAGG R: TGGAATTGACTTTCTCTTCAGG	114	1.5	60	AW260913	22
SPTBN1*	Spectrin, beta, non-erythrocytic 1	2p16.2	54.6	15q22	F: CGAAGTACTGTGTCGTTGTG R: ACCAAATCCTTCCAAACATCC	290	1.5	60	AY008817	22
EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	2p16.1	56.0		F: AAGACTTCCCATCTGAAC R: AGTCAGGAATCTTCTTAGAG	132	1.5	56	DQ001088	25

VRK2	Vaccinia related kinase 2	2p16.1	58.1	15q22	F: TGTCTCTCTCTCTCTCTAC R: ACACACACATACACAGACATTC	225	1.5	58	DQ001125	18
PAPOLG	Poly(A) polymerase gamma	2p16.1	60.9		F: TGGGGTAAGTAATGGTCAGG R: CGTATTGTGTCTCATGCCATC	160	1.5	60	BM414606	29
PAPOLG (FLJ12972) (HEST2-7)	Hypothetical poly (A) polymerase gamma	2p16.1	60.9		F: AACTGAGCATGCGTTCA R: TGTGTCTCATGCCATCCT	370	2	55	AK023034	
MDH1*	Malate dehydrogenase 1, NAD (soluble)	2p15	63.7	15q21.3	F: AGAAAGAACATAGCCTTAGCAG R: GAAAAAGTCACCTCCACCAG	200	1.5	58	DQ001109	23
SLC1A4	Solute carrier family 1, member 4	2p14	65.1		F: AACACCAATCTCGCCATAAC R: ACTGAAAACCACACAACCC	129	1.5	54	DQ001121	22
PLEK (HEST2-20)	Pleckstrin	2p13.3	68.5		F: CCCCCTGAGGAAAGAAGAGTAGG R: CGAGGAGCAGGAATAGTCTCATGG	104	2	58	BI961655	
GFPT1	Glutamine-fructose-6-phosphate transaminase 1	2p13.3	69.4		F: GCCATAGAACTTGGAGGAAC R: CAGACAATCCCAAACAAGAAC	132	1.5	58	DQ001093	23
TIA1 (HEST2-15)	TIA1 cytotoxic granule- associated RNA binding protein	2p13.3	70.3		F: CCTGCATATGGAATGTATGGC R: GCTGCACTCCGTAATTTGGTC	974	3	50	BI961840	
ADD2	Adducin 2 (beta)	2p13.3	70.8		F: ACAAGGGGAACAGAACAAC R: GCGAGCAAGAAGCAGAAATC	220	1.5	58	DQ001075/ DQ001076	21
CCT7	Chaperonin containing TCP1, subunit 7 (eta)	2p13.2	73.3		F: CCAAAGCACTGATCCTGAC R: AACTCACTCTCTCCCTTGAC	195	1.5	58	DQ001080	21
HK2	Hexokinase 2	2p13	74.9		F: CCAGCAATTCTTGAGTGCC R: ACTCACCCAACCTTCAATTTCC	142	1.5	58	DQ001095	20
CTNNA2	Catenin (cadherin-associated protein), alpha 2	2p12	79.6		F: TCCTTCTGAACACTGAGAACC R: AGGGGCATATTGACCACAC	112	1.5	56	DQ001084	20
CAPG (HEST2-16)	Capping protein (actin filament), gelsolin-like	2p11.2	85.5		F: CATCTCCCGCATGCAGTA R: TTGAAGATGGGACTCTCGC	655	2	58	BI961838	
MAT2A	Methionine adenosyltransferase II, alpha	2p11.2	85.6		F: AAGCAAAACAATCAGCAAGAC R: AGGGACGGAAAAACAAGAAC	170	1.5	56	DQ009808/ DQ009809	21
FLJ13110 (HEST2-8)	Chromosome 2 open reading frame 23	2p11.2	86.3		F: CACATTTCAAAGGCCAGC R: TGTGACTAGGGAGTTGGTTC	397	2	58	this study	
PROM2 (LOC150696)	Prominin 2	2q11.1	95.3		F: GCGACTCCTTTCCAGCCCAC R: TCAGCCCTTCCCCTCAGCTC	95	1.5	60	DQ001104	17
ARID5A (MRF-1) (HEST2-18)	AT rich interactive domain 5A isoform 1; modulator recognition factor I	2q11.2	96.6		F: GGAGGGCACTGTGCAAAGA R: CCCACTGAACTTTGCCAGC	170	2	58	BI961816	
SEMA4C (HEST2-2)	Semaphorin 4C	2q11.2	96.9		F: TAACTGGTACTCGCAGACTGCTGA R: CTCGGCCTACATTCCAGAGAGTGT	~700	3	58	Equine monocyte EST library, this	

									study	
ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	2q11.2	97.7		F: AGGCAGCAGAGGTGTTTTT R: GAAAGTCGACTCCCTCTTGC	619	1.5	58	Equine skeletal muscle EST library, this study	
REV1L (HEST2-10)	REV1-like (yeast)	2q11.2	99.4		F: GGTCCAGTTTTCCAAATC R: GGAGCTGTGGAGTTCAGTAA	440	4	TD60	Equine monocyte EST library, this study	
EIF5B (IF2)	Eukaryotic translation initiation factor 5B	2q11.2	99.4	15q12	F: ACTGTGAAGAGCTGAGAGCC R: AAACATCCCCACCCAAGAAC	101	1.5	58	DQ001099	22
IL18RAP	Interleukin 18 receptor accessory protein	2q11.2	102.4	15q12	F: TGGATGACCAAACACTGAAAC R: TCCACCAATCTCTCTACTCAC	355	1.5	58	CD467478	21
IL1A	Interleukin 1, alpha	2q13	113.2		F: TCATTGGCGTTTGAGTCAGCA R: GTAAACATTTCATTTAGAATTAC	932	1.5	58	Kato et al. 1995	
PAX8	Paired box gene 8	2q13	113.6		F: TTGGGGGAATCATGACAGAG R: AGGATGTGGTGTATGAGGAAG	214	1.5	60	DQ001116/ DQ001117	26
COR042**	Microsatellite			15q26	F: CAAATGTGCTCCATCTCCAAC R: GCCAGCTCCCTTACTCTGTA	153-155	2	58	AF10835	
COR075**	Microsatellite			15q27	F: GCCCTAGTTAGCAACCAACA R: AAGATTGATTCCCTCAGCACG	192-214	2	58	AF142612	
HMB2 (AHT2)	Microsatellite				F: GTGCCACCACCTCTGTGATT R: TGGAGAAGGATCTTGGGCTC	106	2	58	Binns et al. 1995	
HMS01**	Microsatellite			15q27	F: CATCACTCTTCATGTCTGCTTGG R: TTGACATAAATGCTTATCCTATGGC	170-180	2	58	X74630	
HTG06	Microsatellite			15q26-q27	F: CCTGCTTGGAGGCTGTGATAAGAT R: GTTCACTGAATGTCAAATTCTGCT	84-100	2	58	Ellegren et al. 1992; Godard et al. 1998	
TKY1033	Microsatellite				F: AGACATGGATTTAGGGAGTG R: GCAGAGCCATGCTAAAACCTG	146	1.5	58	AB104251	
TKY1091	Microsatellite				F: ACAAGTGGAAAGAAGTGGAG R: CCATCTGCAGAAGTAATCCA	140	1.5	58	AB104309	
TKY1165	Microsatellite				F: AAGACCAACACCGTAAAAATC R: CCTACCAGAGTCCAGATTC	300	1.5	58	AB104383	
TKY433**	Microsatellite			15q26	F: TCCCATCTCCTTTTGTCTGC R: GCCAGAATGAACTAAGACCCTCT	267	1.5	58	AB103651	
TKY531	Microsatellite				F: ACCACTTAAACCGCGCTTC R: GGTCTTTAAGCTCTGCTCG	160	1.5	58	AB103749	

TKY779	Microsatellite		F: GAAATTTGGGGAGCCAAAGG R: TATACAGAAGCCAGTTCCAG	146	1.5	58	AB103997
TKY795	Microsatellite		F: AGAGTAATGTGGTGGAGGAG R: TTTTGTGGCTAGGTTTTGGG	151	1.5	58	AB104013
TKY814	Microsatellite		F: ATGCAAAGTCCAGAAACAGA R: TGGGGAACCTCTAAATAACG	155	1.5	58	AB104032
TKY861	Microsatellite		F: GACTCCAGTGTGTTAGAGG R: CAGGACTGCCACAGCTTC	241	1.5	58	AB104079
TKY885	Microsatellite		F: TCAAAGTGGAGCTTCCTGG R: TGGAAACTCATCCTCTAAGG	230	1.5	58	AB104103
TKY926	Microsatellite		F: GATCATGTACTGGGCACAG R: ATGAGCAACCGGGTGAAG	89	1.5	58	AB104144
UMNe84	Microsatellite	15q27	F: ACAGTTGGATATCCGTGGGAAC R: TCTGTTATGTGTTGCCCTCTGC	216	1.5	58	AY391284
UMNe102	Microsatellite		F: ATGCATGCTCATTGCAGAAC R: GCACAAAGAAATTTCCAACCTCC	191	1.5	58	AY391290
UMNe149	Microsatellite		F: AAATGATTTGATAGCACCAGGG R: TTTCTATGCATAGACAGCAAGG	114	1.5	58	AF536263
UMNe156	Microsatellite		F: AGACTAGCTTCAAATTGCCCC R: TCAATTGCCTATGCTTGAAGG	126	1.5	58	AF536268
UMNe198	Microsatellite		F: CAAGAACTGGCATCAGAATTTTC R: TCTTGGGTCTCACTCACTCTCC	152	2	58	AF536283
UMNe219	Microsatellite		F: GTGTCCACTGAAGGATAAAGGG R: TAGCATAATGGCCCTCAAGG	164	2	58	AF536298
UMNe245	Microsatellite		F: TTGCATAGGGACAATCCTACG R: ACAAACCCTACCACTCGGC	104	2	55	AY391327
UMNe250	Microsatellite		F: ATGTTCAAGTGCCTCACCTCC R: GTCTTCGCATTTTAGCCTGC	202	2	58	AF536318
UMNe373	Microsatellite		F: AGGCCACTCAAGCCACAG R: CACCTCCTCCTCCAAATGAG	265	2	58	AY391355
UMNe388**	Microsatellite	15q27	F: ATCCTAGGGTAGAGCCTGCC R: TGGGCCTTTACTCCACCTC	237	2	58	AY464474
UMNe575	Microsatellite		F: CTTTTGAGGAATCTCCATACCG R: GGACCAGGCTGTTTCTGAAC	265	1.5	58	AY735277

^a Notations are as follows: *old FISH data, new RH data, and **new FISH data, old RH data. Retention frequency is abbreviated as RF.