

Differential Genes					
gene ID	log2Fold Change	pval	padj	Gene_title	Symbol
Cluster-62068.91323	7.9822	6.52E-42	9.39E-37	ankyrin repeat and sterile alpha motif domain containing 1A (ANKS1A)	ANKS1A
Cluster-62068.96708	7.4272	2.01E-33	7.24E-29	laminin, alpha 3 (LAMA3)	LAMA3
Cluster-62068.72330	6.9436	1.04E-27	1.87E-23	paroxysmal nonkinesigenic dyskinesia (PNKD)	PNKD
Cluster-62068.112831	6.4222	6.67E-29	1.60E-24	pyruvate dehydrogenase phosphatase regulatory subunit (PDPR)	PDPR
Cluster-62068.63548	6.3617	4.02E-21	4.83E-17	cleavage and polyadenylation specific factor 3(CPSF3)	CPSF3, YSH1
Cluster-62068.87900	6.3151	6.04E-23	9.65E-19	RIO kinase 3 (RIOK3)	RIOK3
Cluster-62068.75621	6.2389	3.67E-22	4.80E-18	THO complex 1 (THOC1)	THOC1
Cluster-62068.94740	6.1613	4.70E-21	5.20E-17	BAC RP11-489N6	RP11-489N6
Cluster-62068.93350	6.033	3.31E-28	6.80E-24	desmoglein 2 (DSG2)	DSG2
Cluster-62068.104440	6.0189	2.64E-17	1.66E-13	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2)	SLC7A2, ATRC2
Cluster-62068.113897	5.9385	6.62E-18	4.77E-14	asp (abnormal spindle) homolog, microcephaly associated (Drosophila) (ASPM)	ASPM, ASP
Cluster-62068.115994	5.9165	1.29E-18	1.03E-14	immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3 (TCIRG1)	ATPeV0A, ATP6N
Cluster-62068.84799	5.9001	3.30E-19	2.97E-15	ZXD family zinc finger C (ZXDC)	ZXDC
Cluster-62068.95720	5.6566	6.67E-17	3.84E-13	protein disulfide isomerase family A, member 6 (PDIA6)	PDIA6, TXNDC7
Cluster-62068.65928	5.6026	9.71E-15	3.59E-11	sphingomyelin synthase 1 (SGMS1)4	SGMS
Cluster-62068.142479	5.5954	2.38E-15	1.07E-11	family with sequence similarity 124A (FAM124A)	FAM124A
Cluster-62068.101985	5.5944	2.84E-18	2.15E-14	Canis familiaris chromosome 16, clone XX-202C11	--
Cluster-62068.93490	5.5547	2.63E-16	1.35E-12	arginase 2 (ARG2)	rocF, arg
Cluster-62068.113160	5.451	9.67E-15	3.59E-11	transmembrane protein 248 (TMEM248)	TMEM248

Cluster-62068.133873	5.3432	7.27E-15	2.91E-11	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 (DDX11)	DDX11, CHL1, CTF1
Cluster-62068.102207	5.3359	8.09E-15	3.15E-11	nucleoporin 205kDa (NUP205)	NUP205, NUP192
Cluster-62068.130670	5.3067	5.99E-15	2.54E-11	raftlin family member 2 (RFTN2)	RFTN2
Cluster-62068.36514	5.261	3.88E-14	1.21E-10	Ursus maritimus methyltransferase like 25 (METTL25)	METTL25
Cluster-62068.69146	5.2067	1.14E-12	2.46E-09	heat shock 70kDa protein 12A (HSPA12A)	HSPA12A
Cluster-62068.113256	5.1693	1.84E-13	5.11E-10	aminomethyltransferase (AMT)	gcvT, AMT
Cluster-62068.98101	5.1171	8.00E-14	2.35E-10	phospholipase C, delta 1 (PLCD1)	PLCD
Cluster-62068.103189	5.0682	1.88E-13	5.12E-10	v-akt murine thymoma viral oncogene homolog 1 (AKT1)	AKT
Cluster-62068.99389	5.068	9.37E-14	2.70E-10	uncharacterized LOC101684958 (LOC101684958), ncRNA	LOC101684958
Cluster-62068.72605	5.0428	3.03E-13	7.76E-10	forkhead box N2 (FOXN2), transcript variant X4	CSDA, ZONAB
Cluster-62068.118515	4.9965	6.17E-12	1.18E-08	Canis familiaris chromosome 11, clone XX-368E15	--
Cluster-62068.82586	4.9752	9.67E-12	1.70E-08	small G protein signaling modulator 1 (SGSM1)	SGSM1
Cluster-62068.69968	4.9388	1.47E-12	3.03E-09	Odobenus rosmarus divergens protein phosphatase 2(PPP2R3B)	PPP2R3
Cluster-62068.128605	4.9213	9.04E-12	1.63E-08	transcriptional adaptor 2A (TADA2A)	TADA2A
Cluster-62068.25450	4.9142	2.02E-12	4.09E-09	RecQ mediated genome instability 1 (RMI1)	RMI1, BRAP75
Cluster-62068.117061	4.8934	1.58E-11	2.65E-08	Ursus maritimus dedicator of cytokinesis 9 (DOCK9)	DOCK9
Cluster-62068.141855	4.853	7.06E-12	1.30E-08	ELOVL fatty acid elongase 6 (ELOVL6)	ELOVL6
Cluster-62068.109638	4.8509	4.88E-12	9.50E-09	protein kinase N3 (PKN3)	PKN
Cluster-62068.138386	4.8282	2.03E-11	3.25E-08	phosphatidylinositol-4,5-bisphosphate 3-kinase (PIK3CA)	PIK3C
Cluster-62068.116555	4.826	1.58E-11	2.65E-08	Odobenus rosmarus divergens TBC1 domain family(TBC1D19)	TBC1D19
Cluster-62068.50694	4.7736	1.81E-11	2.96E-08	netrin G2 (NTNG2)	NTNG2
Cluster-62068.96445	4.7527	5.31E-16	2.64E-12	Canis familiaris chromosome 16	--
Cluster-62068.113790	4.7304	1.60E-11	2.65E-08	Ursus maritimus family with sequence similarity 49(FAM49A)	FAM49A
Cluster-62068.85901	4.7234	4.82E-11	6.81E-08	dystrophia myotonica-protein kinase (DMPK)	DMPK

Cluster-62068.80031	4.6976	2.69E-11	4.12E-08	UbiA prenyltransferase domain containing 1 (UBIAD1)	UBIAD1
Cluster-62068.105290	4.6567	3.91E-11	5.86E-08	peroxidasin (PXDN)	PXDN
Cluster-62068.134771	4.6379	4.75E-11	6.77E-08	family with sequence similarity 193, member A (FAM193A)4	FAM193A
Cluster-62068.145738	4.6222	2.19E-10	2.55E-07	zinc finger protein 532 (ZNF532)	ZNF532
Cluster-62068.69866	4.6209	1.20E-10	1.54E-07	NOP2/Sun RNA methyltransferase family, member 2 (NSUN2)	NSUN2
Cluster-62068.104641	4.6151	9.04E-10	8.86E-07	neuronal PAS domain protein 1 (NPAS1)	NPAS1_3
Cluster-62068.106879	4.6134	2.40E-13	6.29E-10	minichromosome maintenance complex component 3 associated protein (MCM3AP)	MCM3AP
Cluster-62068.120676	4.6098	1.01E-10	1.33E-07	mitogen-activated protein kinase binding protein 1 (MAPKBP1)	MAPKBP1
Cluster-62068.70905	4.6001	1.07E-10	1.39E-07	RNA pseudouridylate synthase domain containing 4 (RPUSD4)	RPUSD4
Cluster-62068.96447	4.5986	3.95E-14	1.21E-10	Canis familiaris chromosome 16, clone XX-202C11	--
Cluster-62068.94417	4.5846	2.55E-10	2.91E-07	laminin, alpha 5 (LAMA5)	LAMA3_5
Cluster-62068.148302	4.578	1.72E-10	2.12E-07	cell adhesion molecule L1-like (CHL1)	CHL1
Cluster-62068.52575	4.5758	1.38E-10	1.73E-07	coiled-coil domain containing 102A (CCDC102A)	CCDC102A
Cluster-62068.123308	4.5556	2.63E-10	2.96E-07	Odobenus rosmarus divergens very low density lipoprotein receptor (VLDLR)	VLDLR
Cluster-62068.116615	4.5524	1.87E-10	2.24E-07	3 BAC RP11-158G18 (Roswell Park Cancer Institute Human BAC Library) complete sequence	--
Cluster-62068.66814	4.5202	2.01E-10	2.39E-07	tetratricopeptide repeat domain 39A (TTC39A)	TTC39A
Cluster-62068.112364	4.5101	4.16E-10	4.41E-07	nuclear body protein SP140-like protein (LOC101693643)	--
Cluster-62068.104204	4.5031	2.85E-10	3.11E-07	bromodomain containing 4 (BRD4)	BRD4
Cluster-62068.57468	4.4973	3.61E-10	3.88E-07	establishment of sister chromatid cohesion N-acetyltransferase 1 (ESCO1)	ESCO, ECO1
Cluster-62068.82012	4.4859	7.16E-10	7.16E-07	minichromosome maintenance complex component 2 (MCM2)	MCM2
Cluster-62068.54559	4.4588	1.36E-09	1.28E-06	zinc finger, C2HC-type containing 1A (ZC2HC1A)	ZC2HC1A
Cluster-62068.57003	4.445	5.95E-10	6.12E-07	transmembrane protein 161B (TMEM161B)	TMEM161B
Cluster-62068.127919	4.4335	1.76E-09	1.61E-06	3-phosphoinositide dependent protein kinase 1 (PDPK1)	PDPK1

Cluster-62068.28899	4.4247	9.31E-10	9.06E-07	ret proto-oncogene (RET)	RET
Cluster-62068.149994	4.4154	6.85E-10	6.95E-07	von Willebrand factor A domain containing 5B2 (VWA5B2)	VWA5B2
Cluster-62068.116244	4.3756	2.02E-09	1.80E-06	uncharacterized LOC106004386 (LOC106004386)	EEF1D
Cluster-62068.77978	4.3462	2.45E-09	2.14E-06	von Willebrand factor A domain containing 5B2 (VWA5B2)	VWA5B2
Cluster-62068.121428	4.3462	1.70E-09	1.57E-06	Human DNA sequence from clone RP11-500G10 on chromosome 10	--
Cluster-62068.119842	4.3306	3.41E-13	8.46E-10	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2)	SMARCC
Cluster-62068.26933	4.3147	5.30E-09	4.26E-06	transcription termination factor, RNA polymerase II (TTF2)	TTF2
Cluster-62068.152129	4.3057	3.39E-09	2.85E-06	ral guanine nucleotide dissociation stimulator-like 3 (RGL3)	RGL3
Cluster-62068.171727	4.3049	3.17E-09	2.72E-06	Odobenus rosmarus divergens membrane metallo-endopeptidase-like 1 (MMEL1)	MMEL1
Cluster-62068.141788	4.2961	3.82E-09	3.20E-06	RAB36, member RAS oncogene family (RAB36)	RAB36
Cluster-62068.114647	4.2564	5.63E-09	4.40E-06	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein) (HADHB)	HADHB
Cluster-62068.71823	4.2516	5.45E-09	4.33E-06	coiled-coil domain containing 151 (CCDC151)	CCDC151
Cluster-62068.92511	4.2489	2.41E-08	1.48E-05	Canis familiaris chromosome 16	--
Cluster-62068.114552	4.2479	5.59E-09	4.40E-06	cleavage and polyadenylation factor I subunit 1 (CLP1)	CLP1, HERB
Cluster-72532.0	4.2387	5.16E-09	4.17E-06	DTW domain containing 2 (DTWD2)	DTWD2
Cluster-62068.178785	4.2336	4.78E-09	3.91E-06	ferredoxin-fold anticodon binding domain containing 1 (FDXACB1)	FDXACB1
Cluster-62068.75403	4.2264	6.18E-09	4.79E-06	ADAM metallopeptidase with thrombospondin type 1 motif(ADAMTS9)	ADAMTS9
Cluster-62068.90323	4.222	2.39E-08	1.47E-05	mitochondrial calcium uptake 1 (MICU1)	MICU1
Cluster-62068.98794	4.1869	1.88E-08	1.22E-05	spectrin, alpha, non-erythrocytic 1 (SPTAN1)3	SPTAN1
Cluster-62068.119297	4.1514	2.85E-08	1.71E-05	protein regulator of cytokinesis 1 (PRC1)	PRC1
Cluster-62068.182487	4.1471	1.22E-08	8.35E-06	bone morphogenetic protein/retinoic acid inducible neural-specific 3	BRINP3

				(BRINP3)	
Cluster-62068.49400	4.1282	1.77E-08	1.16E-05	protein tyrosine phosphatase, receptor type (PTPRR)	PTPRR
Cluster-62068.93588	4.1216	1.96E-08	1.26E-05	leucine rich repeat containing 45 (LRRC45)	LRRC45
Cluster-62068.117721	4.1115	3.15E-08	1.85E-05	pappalysin 2 (PAPPA2)	PAPPA2
Cluster-62068.132888	4.1025	2.19E-08	1.36E-05	HAUS augmin-like complex (HAUS5)	HAUS5
Cluster-62068.131598	4.0844	2.11E-08	1.33E-05	TNF receptor-associated protein 1 (TRAP1)	TRAP1, HSP75
Cluster-62068.146019	4.0589	4.36E-08	2.46E-05	KRAB-A domain containing 2 (KRBA2)	KRBA2
Cluster-62068.89655	4.0453	6.93E-12	1.30E-08	Leptonychotes weddellii collagen alpha-1(IV) chain-like (LOC102729200)	COL4A
Cluster-62068.49587	4.0388	6.14E-08	3.33E-05	Odobenus rosmarus divergens tyrosylprotein sulfotransferase 1 (TPST1)	TPST
Cluster-62068.159161	4.0344	8.48E-09	6.10E-06	F-box and leucine-rich repeat protein 8 (FBXL8)	FBXL8
Cluster-62068.97581	4.0051	8.06E-08	4.22E-05	myosin VI (MYO6)	MYO6
Cluster-62068.52700	4.0035	4.95E-08	2.76E-05	fibroblast growth factor receptor substrate 3 (FRS3)	FRS3
Cluster-62068.136366	4.0015	1.10E-07	5.64E-05	prolactin receptor (PRLR)	PRLR
Cluster-62068.57912	3.984	7.44E-08	3.97E-05	ankyrin repeat domain 34B (ANKRD34B)	ANKRD34B
Cluster-62068.139592	3.972	6.58E-08	3.53E-05	Ursus maritimus beta-1,4-N-acetyl-galactosaminyl transferase 3 (B4GALNT3)	--
Cluster-62068.48372	3.957	2.08E-07	9.35E-05	12 BAC RP11-285E4	--
Cluster-62068.147726	3.9537	1.11E-07	5.64E-05	notch 4 (NOTCH4)	NOTCH
Cluster-62068.61752	3.9292	2.12E-07	9.49E-05	storkhead box 2 (STOX2)	STOX2
Cluster-62068.130317	3.9229	1.12E-07	5.71E-05	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2)	ROCK2
Cluster-62068.176344	3.9191	1.18E-07	5.88E-05	Ursus maritimus F-box protein 48 (FBXO48)	FBXO48
Cluster-62068.22116	3.9087	1.19E-07	5.90E-05	tachykinin, precursor 1 (TAC1)	TAC1
Cluster-62068.67443	3.907	1.17E-07	5.84E-05	Ovis canadensis canadensis isolate 43U chromosome 25 sequence	--
Cluster-62068.120962	3.9059	1.93E-07	8.83E-05	aldo-keto reductase family 1, member E2 (AKR1E2)	AKR1E2, AKR1CL2

Cluster-62068.177222	3.8988	1.30E-07	6.30E-05	ATP synthase mitochondrial F1 complex assembly factor 2 (ATPAF2), transcript variant X4	ATPeAF2, ATPAF2, ATP12
Cluster-62068.98283	3.8798	1.46E-07	6.92E-05	Ailuropoda melanoleuca zinc finger homeobox 3 (ZFHX3)	ATBF1
Cluster-62068.51442	3.8795	7.54E-08	3.99E-05	Schistosoma curassoni genome assembly S_curassoni_Dakar ,scaffold SCUD_contig0019022	--
Cluster-79064.0	3.8641	2.08E-07	9.35E-05	ankyrin repeat domain 55 (ANKRD55)	ANKRD55
Cluster-62068.154865	3.8415	2.34E-07	0.00010236	leucine rich repeat containing 42 (LRRC42)	LRRC42
Cluster-62068.97881	3.8289	3.01E-07	0.00012608	collagen, type I, alpha 1 (COL1A1)	COL1AS
Cluster-62068.131748	3.8283	2.83E-07	0.00012032	neuronal cell adhesion molecule (NRCAM)2	NRCAM
Cluster-62068.149497	3.8273	2.69E-10	3.00E-07	LanC lantibiotic synthetase component C-like 1 (LANCL1)	LANCL1
Cluster-62068.93964	3.8183	2.89E-07	0.00012154	cryptochrome circadian clock 2 (CRY2)	CRY
Cluster-62068.168311	3.8051	3.56E-07	0.00014334	opioid binding protein/cell adhesion molecule-like (OPCML), transcript variant X4	OPCML
Cluster-62068.22254	3.79	9.64E-07	0.00033484	uteroferrin-associated basic protein 2-like (LOC101674813)	--
Cluster-62068.191461	3.7796	3.70E-07	0.00014858	MACACA MULATTA BAC clone CH250-201N11 from chromosome 12	--
Cluster-62068.92521	3.7784	1.42E-07	6.77E-05	solute carrier family 16, member 14 (SLC16A14)	SLC16A14
Cluster-62068.23008	3.7724	5.41E-07	0.00020905	protein tyrosine phosphatase, receptor type (PTPRC)	PTPRC, CD45
Cluster-62068.99369	3.7714	9.10E-07	0.00031958	prolactin receptor (PRLR)	PRLR
Cluster-62068.92107	3.7533	4.63E-07	0.00018113	angiotensin I converting enzyme 2 (ACE2)	ACEH, ACE2
Cluster-62068.138056	3.752	1.35E-06	0.00043993	coiled-coil domain containing 15 (CCDC15)	CCDC15
Cluster-62068.89353	3.7428	5.38E-09	4.30E-06	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	SLC4A8
Cluster-62068.155377	3.7252	7.04E-07	0.00026059	Felis catus BAC clone FCAB-55H12 from chromosome unknown	--
Cluster-62068.106503	3.7222	6.88E-07	0.00025589	RAS p21 protein activator (GTPase activating protein) 1 (RASA1)	RASA1, RASGAP

Cluster-62068.107771	3.7146	3.94E-07	0.00015486	serpin peptidase inhibitor, clade D (heparin cofactor), member 1 (SERPIND1)	SERPIND1, HCF2
Cluster-62068.137958	3.7054	7.49E-07	0.00027253	regulating synaptic membrane exocytosis 3 (RIMS3)	RIMS3
Cluster-62068.58929	3.7012	1.47E-06	0.00046644	Ursus maritimus solute carrier family 26 (anion exchanger), member 6 (SLC26A6)	SLC26A6
Cluster-62068.83389	3.6788	1.11E-06	0.00038164	sterile alpha motif domain containing 11 (SAMD11)	SAMD11
Cluster-62068.108350	3.6779	1.36E-06	0.00044151	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group) (GCNT2)	GCNT2
Cluster-62068.32243	3.6678	9.39E-07	0.00032829	Canis Familiaris chromosome 5, clone XX-10I19	--
Cluster-62068.133995	3.6626	1.91E-06	0.00057749	cell wall biogenesis 43 C-terminal homolog (CWH43)	--
Cluster-62068.65775	3.6599	1.18E-06	0.00039714	pleckstrin homology domain-containing family A member 7 (LOC101678352)	LOC101678352
Cluster-62068.17365	3.6493	1.16E-06	0.00039261	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.129990	3.6485	1.26E-06	0.00041684	Ursus maritimus kelch domain containing 1 (KLHDC1)	KLHDC1
Cluster-62068.119960	3.6396	7.84E-07	0.00028287	DnaJ (Hsp40) homolog, subfamily C(DNAJC24)	DPH4, DNAJC24
Cluster-62068.33662	3.6311	1.28E-06	0.00041962	MACACA MULATTA BAC clone CH250-364H1 from chromosome 1	--
Cluster-62068.140683	3.6207	1.36E-06	0.00044151	ribosomal protein S6 kinase, 90kDa, polypeptide 1 (RPS6KA1)	RPS6KA, RSK2
Cluster-62068.84625	3.6203	9.14E-11	1.22E-07	growth differentiation factor 3 (GDF3)	GDF3
Cluster-62068.64181	3.6128	1.60E-06	0.00049571	inositol polyphosphate-5-phosphatase(INPP5D)	SHIP1, INPP5D
Cluster-62068.93181	3.6029	2.93E-08	1.74E-05	proteasome (prosome, macropain) (PSMA6)	PSMA6
Cluster-62068.109825	3.5875	2.57E-06	0.0007365	signal transducer and activator of transcription 2 (STAT2)	STAT2
Cluster-62068.69806	3.5765	3.27E-06	0.00090501	Canis familiaris chromosome 16, clone XX-202C11	--
Cluster-62068.75245	3.5737	2.39E-06	0.0006916	required for meiotic nuclear division 1 homolog (RMND1)	--
Cluster-62068.93416	3.5703	1.24E-10	1.58E-07	claudin 8 (CLDN8)	CLDN
Cluster-62068.96362	3.5656	2.67E-06	0.00076031	protein phosphatase 1, regulatory subunit 21 (PPP1R21)	PPP1R21, CCDC128,

					KLRAQ1
Cluster-62068.89888	3.5533	3.52E-06	0.00095769	vertebrae development associated (VRTN)	VRTN
Cluster-62068.59642	3.5488	3.83E-06	0.0010221	transmembrane protein 106A (TMEM106A)	TMEM106A
Cluster-62068.48534	3.5282	4.12E-06	0.0010845	dachsous cadherin-related 1 (DCHS1)	DCHS1_2, PCDH16_23
Cluster-62068.84530	3.5274	3.89E-06	0.0010356	collagen, type XV, alpha 1 (COL15A1)	COL15A1
Cluster-62068.116490	3.5266	3.21E-06	0.00089699	Ailuropoda melanoleuca zinc finger, DHHC-type containing 21 (ZDHHC21)	ZDHHC
Cluster-62068.155803	3.5203	7.88E-07	0.00028367	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	SSX2IP, ADIP
Cluster-62068.105649	3.516	1.24E-07	6.12E-05	ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4)	SIAT4C
Cluster-62068.70969	3.5155	3.03E-06	0.00085293	SIL1 nucleotide exchange factor (SIL1)	SIL1
Cluster-62068.175605	3.5124	5.51E-06	0.0013717	kelch-like family member 41 (KLHL41)	KBTBD5_10
Cluster-62068.155391	3.5098	4.86E-06	0.0012351	family with sequence similarity 101(FAM101B)	--
Cluster-62068.188199	3.5096	3.62E-06	0.00097823	chromosome 17, clone RP11-357H14	RP11-357H14
Cluster-62068.158690	3.5059	1.22E-06	0.00041088	Canis familiaris, clone XX-7D6	--
Cluster-62068.77996	3.5021	7.40E-06	0.0017374	Bos taurus BAC CH240-237H4	--
Cluster-62068.82557	3.4972	6.09E-06	0.0014713	BRF2, RNA polymerase III transcription initiation factor 50 kDa subunit (BRF2)	BRF2
Cluster-62068.172942	3.4946	3.96E-06	0.0010495	Human DNA sequence from clone RP11-330A16 on chromosome 6	--
Cluster-62068.128709	3.4926	4.28E-06	0.0011174	growth regulation by estrogen in breast cancer-like (GREB1L)	GREB1L
Cluster-62068.43445	3.4913	3.74E-06	0.0010033	uncharacterized LOC106005543 (LOC106005543)	--
Cluster-62068.76480	3.4902	5.16E-06	0.0013018	origin recognition complex, subunit 4 (ORC4)2	ORC4
Cluster-62068.105816	3.4736	3.12E-07	0.00012944	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	SLC4A8
Cluster-62068.48989	3.4573	6.03E-06	0.0014647	agmatine ureohydrolase (agmatinase) (AGMAT)	speB
Cluster-62068.46629	3.4489	5.49E-06	0.0013715	RAR-related orphan receptor A (RORA)	NR1F1, RORA

Cluster-62068.146217	3.4406	9.84E-06	0.002164	G protein-coupled receptor 143 (GPR143)	OA1, GPR143
Cluster-62068.45910	3.4395	5.97E-06	0.0014594	zinc finger protein 713 (ZNF713)	KRAB
Cluster-62068.100278	3.4369	8.69E-06	0.0019805	glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM)	GATM
Cluster-62068.185558	3.4319	8.36E-06	0.0019288	chromosome unknown open reading frame, human C5orf28 (LOC101684264), transcript variant X4	--
Cluster-62068.54331	3.4265	7.28E-06	0.0017174	UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), RefSeqGene on chromosome 10	UPF2
Cluster-62068.81731	3.4248	6.34E-06	0.0015301	Panthera tigris altaica alkB, alkylation repair homolog 6 (E. coli) (ALKBH6)	ALKBH6
Cluster-62068.175432	3.4205	7.13E-06	0.0016873	janus kinase and microtubule interacting protein 2 (JAKMIP2), transcript variant X6	JAKMIP2
Cluster-62068.86384	3.4154	1.23E-06	0.00041119	Odobenus rosmarus divergens actin, alpha, cardiac muscle 1 (ACTC1)	ACTC1
Cluster-62068.118145	3.4117	7.41E-07	0.00027153	solute carrier family 26 (anion exchanger), member 4 (SLC26A4)	SLC26A4, PDS
Cluster-62068.74963	3.411	1.57E-06	0.00049438	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.86016	3.4109	2.47E-06	0.00070839	phosphoglucomutase 1 (PGM1)	pgm
Cluster-62068.115828	3.4028	2.23E-09	1.96E-06	Meles meles leucurus isolate TB402b alpha cardiac actin (ACTC) gene, partial cds	ACTA2
Cluster-62068.159964	3.3999	8.17E-06	0.0018906	phosphodiesterase 11A (PDE11A)	PDE11
Cluster-62068.24024	3.3999	9.24E-06	0.0020821	DAZ interacting zinc finger protein 1-like (DZIP1L), transcript variant X6	DZIP1
Cluster-62068.162610	3.393	9.28E-06	0.0020873	Ailuropoda melanoleuca plexin C1 (PLXNC1)	PLXNC
Cluster-62068.65235	3.3898	9.42E-06	0.0021097	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	SLC4A8
Cluster-62068.128533	3.3842	1.09E-05	0.0023374	5'-nucleotidase, cytosolic II (NT5C2)	NT5C2
Cluster-62068.102107	3.3839	8.87E-06	0.0020138	Leptonchotes weddellii protein phosphatase 1, catalytic subunit, gamma isozyme (PPP1CC)	PPP1C

Cluster-62068.89696	3.3804	1.32E-05	0.0027303	Ailurogobius melanoleuca tumor protein p53 inducible protein 11 (TP53I11)	--
Cluster-62068.94291	3.3801	1.13E-06	0.0003861	AT rich interactive domain 5A (MRF1-like) (ARID5A)	ARID5A
Cluster-62068.96463	3.3747	1.21E-09	1.16E-06	Sus scrofa mRNA, clone:AMP010013D11, expressed in alveolar macrophage	SNAPC4
Cluster-62068.24459	3.3718	9.16E-06	0.0020663	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL)	E4.1.3.3, nanA, NPL
Cluster-62068.13533	3.3713	1.05E-05	0.0022714	Odobenus rosmarus divergens chromosome unknown open reading frame, human C9orf172 (LOC101371046)	--
Cluster-62068.57872	3.3672	2.30E-06	0.00066805	low density lipoprotein receptor-related protein 2 (LRP2)	LRP2
Cluster-62068.100249	3.3672	9.63E-06	0.0021363	chromosome unknown open reading frame, human C16orf93 (LOC101684016)	--
Cluster-62068.137392	3.365	3.45E-07	0.00014059	synaptosomal-associated protein, 25kDa (SNAP25)	SNAP25
Cluster-62068.88084	3.3561	4.82E-06	0.001229	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), transcript variant X7	SLC4A8
Cluster-62068.96228	3.3484	2.69E-06	0.00076475	carbonic anhydrase II (CA2)	CA2
Cluster-62068.146738	3.347	1.08E-05	0.0023245	polo-like kinase 3 (PLK3)	PLK3, CNK
Cluster-62068.152244	3.3437	1.45E-05	0.0029447	Rho GTPase activating protein 12 (ARHGAP12), transcript variant X6	ARHGAP12
Cluster-62068.116762	3.3361	2.64E-06	0.00075448	hexokinase domain containing 1 (HKDC1)	HK
Cluster-62068.110850	3.3352	3.65E-06	0.0009833	v-akt murine thymoma viral oncogene homolog 2 (AKT2), transcript variant X4	AGA, aspG
Cluster-62068.145250	3.3329	1.42E-05	0.0029061	zinc finger protein, FOG family member 1 (ZFPM1)	ZFPM1, FOG1
Cluster-62068.92666	3.3172	1.41E-05	0.0028945	Odobenus rosmarus divergens PDZ domain containing 1 (PDZK1)	PDZK1
Cluster-62068.23290	3.3166	1.41E-05	0.0028945	uncharacterized LOC101691309 (LOC101691309), ncRNA	--
Cluster-62068.18506	3.3139	1.49E-05	0.0029949	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma (PIK3C2G), misc_RNA	PIK3C2
Cluster-62068.126321	3.3086	1.46E-05	0.00295	Human DNA sequence from clone RP11-336F23 on chromosome 1	--

Cluster-62068.44617	3.2946	1.69E-05	0.0033154	proprotein convertase subtilisin/kexin type 1 (PCSK1)	PCSK1
Cluster-62068.66463	3.2885	1.87E-05	0.003594	osteoclast associated, immunoglobulin-like receptor (OSCAR)	OSCAR
Cluster-62068.86163	3.2856	4.67E-13	1.14E-09	chromosome unknown open reading frame, human C20orf24 (LOC106003404)	C20orf24
Cluster-62068.61151	3.2622	2.10E-05	0.0039396	RP11-159D12	--
Cluster-62068.81431	3.261	3.10E-05	0.0053737	chromosome unknown open reading frame, human C4orf26 (LOC101671167)	--
Cluster-62068.75299	3.2598	2.85E-07	0.00012069	L-amino-acid oxidase-like (LOC101679701)	IL4I1
Cluster-62068.59171	3.2587	1.94E-05	0.0037049	glycerol kinase 5 (putative) (GK5)	GK5
Cluster-62068.18714	3.2554	1.18E-05	0.0024852	Leptonychotes weddellii tyrosine aminotransferase (TAT)	TAT
Cluster-62068.165119	3.2516	2.39E-05	0.004336	Pan troglodytes BAC clone CH251-15E3 from chromosome 15	--
Cluster-62068.40035	3.2514	2.18E-05	0.004042	Ovis aries musimon uncharacterized LOC105603321 (LOC105603321), transcript variant X7, misc_RNA	--
Cluster-62068.161255	3.2414	2.24E-06	0.0006552	endogenous retrovirus group K member 113 Pol protein-like (LOC106004070)	--
Cluster-29662.0	3.2371	2.66E-05	0.0047212	Canis Familiaris chromosome 37, clone XX-341P11	--
Cluster-62068.69119	3.2361	2.33E-05	0.0042518	proline-rich basic protein 1 (PROB1)	PROB1
Cluster-62068.164708	3.2346	2.62E-05	0.0046806	acetylserotonin O-methyltransferase (ASMT)	ASMT
Cluster-62068.153764	3.2336	3.94E-06	0.0010456	chromosome 15, clone RP11-151H2	PPCDC, coaC
Cluster-62068.77258	3.225	2.43E-05	0.0043915	CTTNBP2 N-terminal like (CTTNBP2NL)	CTTNBP2NL
Cluster-62068.65226	3.2194	3.02E-05	0.005238	E74-like factor 5 (ets domain transcription factor) (ELF5)	ELF5
Cluster-62068.22117	3.2191	3.37E-05	0.0057804	tachykinin, precursor 1 (TAC1)	TAC1
Cluster-68303.0	3.2164	1.38E-05	0.002848	chromosome 16 clone RP11-124K4	--
Cluster-62068.157950	3.1988	3.73E-05	0.0062056	Odobenus rosmarus divergens poly(rC) binding protein 3 (PCBP3), transcript variant X4	PCBP2_3_4
Cluster-62068.109894	3.1943	2.48E-05	0.0044716	Canis familiaris chromosome 16, clone XX-202C11	--

Cluster-62068.73831	3.1865	3.52E-05	0.0059419	ariadne RBR E3 ubiquitin protein ligase 1 (ARIH1)	ARIH1
Cluster-62068.114476	3.1834	4.56E-05	0.00725	cAMP responsive element modulator (CREM)3	CREM
Cluster-62068.63498	3.1796	3.41E-05	0.0058215	phospholipase C, beta 4 (PLCB4), transcript variant X8	PLCB
Cluster-62068.96843	3.1792	4.64E-05	0.007334	collagen, type III, alpha 1 (COL3A1)	COL1A5
Cluster-62068.122679	3.179	8.06E-06	0.0018695	actin, alpha, cardiac muscle 1 (ACTC1)	ACTC1
Cluster-62068.60720	3.1763	3.75E-05	0.0062247	transmembrane protein 39A (TMEM39A)	TMEM39A
Cluster-34356.0	3.1728	3.74E-05	0.0062128	solute carrier family 22 (organic cation/zwitterion transporter), member 4 (SLC22A4), transcript variant X4	SLC22A4_5, OCTN
Cluster-62068.99427	3.15	2.57E-07	0.00011035	Canis Familiaris chromosome 14, clone XX-483F1	--
Cluster-62068.66223	3.143	4.89E-05	0.0076412	alpha-2-macroglobulin-like 1 (A2ML1), transcript variant X4	A2ML1
Cluster-62068.11926	3.1364	4.40E-05	0.0070896	KIAA1211 ortholog (KIAA1211)	KIAA1211
Cluster-62068.26969	3.1346	2.49E-07	0.00010774	Canis lupus familiaris protein tyrosine phosphatase, receptor type, B (PTPRB)	--
Cluster-62068.100687	3.1264	4.93E-07	0.00019244	zyxin (ZYG)	FZD5_8, fz2
Cluster-62068.113766	3.1248	4.28E-05	0.0069244	paralemmin 3 (PALM3)	PALM3
Cluster-62068.147770	3.1219	6.85E-05	0.0099565	sperm associated antigen 5 (SPAG5)	SPAG5
Cluster-62068.62684	3.1208	5.13E-05	0.0079259	chromosome 16 clone RP11-98C8	--
Cluster-62068.78060	3.1178	3.23E-05	0.0055753	cytohesin 1 (CYTH1), transcript variant X4	CYTH
Cluster-62068.84841	3.1141	2.41E-05	0.0043644	glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM)	GATM
Cluster-62068.15859	3.1076	2.41E-05	0.0043645	Ailuropoda melanoleuca uncharacterized LOC105235271 (LOC105235271), ncRNA	--
Cluster-62068.165476	3.1064	2.03E-05	0.0038347	chromosome 17, clone RP11-613C6	--
Cluster-62068.131637	3.1061	6.23E-05	0.0092356	Ovis canadensis canadensis isolate 43U chromosome 2 sequence	--
Cluster-62068.67553	3.1034	5.46E-05	0.0083261	ring finger protein 135 (RNF135)	SQSTM1
Cluster-62068.44616	3.1005	4.54E-05	0.0072387	proprotein convertase subtilisin/kexin type 1 (PCSK1)	PCSK1
Cluster-62068.66513	3.0976	4.85E-05	0.0076141	solute carrier family 26 (anion exchanger), member 4 (SLC26A4)	SLC26A4, PDS

Cluster-62068.47305	3.0963	5.72E-05	0.0086466	sperm flagellar 2 (SPEF2)	SPEF2
Cluster-62068.53740	3.0892	7.17E-05	0.010339	uncharacterized LOC101674124 (LOC101674124), ncRNA	--
Cluster-62068.103295	3.0882	6.87E-05	0.0099711	tafazzin (TAZ)	TAZ
Cluster-62068.151484	3.0882	2.24E-05	0.0041219	enolase superfamily member 1 (ENOSF1)	fucD
Cluster-62068.47949	3.0865	5.98E-05	0.0089243	WD repeat domain 60 (WDR60)	WDR60
Cluster-62068.105181	3.0856	3.46E-05	0.0058883	Felis catus solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15 (SLC25A15)	SLC25A2_15, ORNT
Cluster-62068.94757	3.0854	8.10E-13	1.82E-09	Odobenus rosmarus divergens collagen, type I, (COL1A1)	COL1A1
Cluster-62068.96949	3.0812	3.36E-05	0.0057587	folate receptor 1 (adult) (FOLR1)	FOLR
Cluster-62068.96981	3.0654	2.03E-05	0.0038386	actin, alpha, cardiac muscle 1 (ACTC1)	ACTC1
Cluster-62068.28614	3.0652	7.37E-05	0.010536	acyl-CoA dehydrogenase family, member 10 (ACAD10)	ACAD10
Cluster-62068.113337	3.0636	2.35E-05	0.0042782	laminin, gamma 2 (LAMC2)	LAMC2
Cluster-62068.93965	3.0619	2.12E-08	1.33E-05	thiosulfate sulfurtransferase (rhodanese) (TST)	TST, MPST, sseA
Cluster-62068.131591	3.055	7.30E-05	0.010485	tweety family member 1 (TTYH1)	TTYH1
Cluster-62068.35084	3.0548	8.17E-05	0.011391	zinc finger, DHHC-type containing 3 (ZDHHC3)	ZDHHC3
Cluster-62068.139526	3.0488	8.56E-05	0.011823	chromosome 17, clone CTD-2132N18	--
Cluster-62068.81069	3.0442	7.69E-09	5.68E-06	alpha-2-macroglobulin-like 1 (A2ML1), transcript variant X4	A2ML1
Cluster-62068.128336	3.0378	8.19E-05	0.011394	Bos taurus isolate 9198 myocyte enhancer factor 2B (MEF2B) gene, promoter region	RFXANK
Cluster-62068.24987	3.0313	9.49E-05	0.012761	mal, T-cell differentiation protein-like (MALL)	MALL
Cluster-62068.127386	3.0309	9.01E-05	0.012325	zinc finger, AN1-type domain 4 (ZFAND4)	ANUBL1
Cluster-62068.56654	3.0305	1.08E-05	0.0023245	Canis lupus familiaris tetraspanin 9 (TSPAN9), transcript variant X7	TSPAN9
Cluster-78916.0	3.0298	8.66E-05	0.011934	Ovis canadensis canadensis isolate 43U chromosome 4 sequence	--
Cluster-62068.51047	3.0235	3.46E-05	0.0058883	Ceratotherium simum simum UTX gene, intron 22	--
Cluster-62068.131405	3.0151	0.000103	0.013621	Neovison vison clone Mvi1905 microsatellite sequence	--

Cluster-62068.95239	3.0133	4.96E-05	0.0077126	Odobenus rosmarus divergens collagen alpha-1(II) chain-like (LOC101382725)	--
Cluster-62068.95003	3.0087	9.03E-07	0.0003178	Ovis canadensis canadensis isolate 43U chromosome 2 sequence	--
Cluster-62068.58023	3.0078	0.000115	0.014845	zinc finger protein 319 (ZNF319)	ZNF319
Cluster-62068.146307	3.0057	0.000103	0.013636	Ovis canadensis canadensis isolate 43U chromosome 19 sequence	--
Cluster-62068.18582	3.0009	2.99E-07	0.00012566	GINS complex subunit 4 (Sld5 homolog) (GINS4)	GINS4, SLD5
Cluster-62068.82476	3.0002	2.28E-10	2.62E-07	C1q and tumor necrosis factor related protein 6 (C1QTNF6)	C1QTNF6
Cluster-62068.60605	3	0.000112	0.014543	chromosome unknown open reading frame, human C16orf71 (LOC101691483), transcript variant X7	--
Cluster-62068.22408	2.9981	6.73E-05	0.0098333	syndecan binding protein (syntenin) 2 (SDCBP2)	SDCBP2
Cluster-62068.65719	2.9973	0.000109	0.014207	Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17)	ARHGEF17
Cluster-60388.0	2.9967	5.32E-05	0.0081572	cartilage intermediate layer protein 2 (CILP2)	CILP2
Cluster-62068.121712	2.995	0.000122	0.015546	Leptonychotes weddellii vacuolar protein sorting 33 homolog B (yeast) (VPS33B)	VPS33B
Cluster-62068.27992	2.994	0.000125	0.015794	Ovis canadensis canadensis isolate 43U chromosome 12 sequence	--
Cluster-62068.50702	2.9927	0.000107	0.014003	armadillo repeat containing 6 (ARMC6), transcript variant X4	ARMC6
Cluster-62068.102523	2.9927	8.67E-07	0.00030812	Ursus maritimus archain 1 (ARCN1)	ARCN1
Cluster-62068.36557	2.9873	2.00E-05	0.0038049	phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), transcript variant X4	PDE1
Cluster-62068.79057	2.9869	1.84E-05	0.0035518	SH3-domain GRB2-like 3 (SH3GL3), misc_RNA	SH3GL
Cluster-62068.61558	2.9848	1.77E-05	0.0034578	ATPase, class V, type 10B (ATP10B)	ATP10B
Cluster-62068.30490	2.9843	1.60E-05	0.0031695	Src-like-adaptor (SLA), transcript variant X4	SLA
Cluster-62068.90444	2.9787	4.54E-06	0.0011732	histone H1.2 (LOC101676607)	H1_5
Cluster-62068.46454	2.977	0.000138	0.017053	protein tyrosine phosphatase, receptor type, R (PTPRR)	PTPRR
Cluster-62068.96001	2.9741	0.000142	0.017287	Ailuropoda melanoleuca KIAA1324 ortholog (KIAA1324)	KIAA1324

Cluster-62068.160427	2.9721	7.39E-05	0.010558	TRAF family member-associated NFkB activator (TANK), transcript variant X4	TANK
Cluster-62068.180279	2.9706	0.00015	0.018035	myosin VIIA (MYO7A)	MYO7
Cluster-62068.92429	2.9692	1.17E-05	0.002469	uncharacterized LOC106005866 (LOC106005866), ncRNA	--
Cluster-62068.155733	2.9676	0.000129	0.016258	Canis Familiaris chromosome 17, clone XX-365L15	RP-L33, MRPL33, rpmG
Cluster-62068.155698	2.9629	0.000127	0.016002	chromosome 11, clone RP1-59M18	--
Cluster-62068.72150	2.9626	0.000134	0.016694	solute carrier family 6 (neurotransmitter transporter), member 6 (SLC6A6)	SLC6A6S
Cluster-49238.0	2.9595	0.000147	0.017736	uncharacterized LOC106004415 (LOC106004415), ncRNA	--
Cluster-62068.157105	2.9579	5.78E-05	0.0087039	calcium/calmodulin-dependent protein kinase II gamma (CAMK2G)2	CAMK2
Cluster-62068.92430	2.9552	7.23E-05	0.010399	Canis lupus familiaris uncharacterized LOC102152191 (LOC102152191), misc_RNA	--
Cluster-62068.167148	2.9468	0.000152	0.018216	Ursus maritimus uncharacterized LOC103676250 (LOC103676250), ncRNA	--
Cluster-62068.47350	2.9448	2.30E-05	0.0042272	cholinergic receptor, nicotinic, alpha 3 (neuronal) (CHRNA3)	CHRNA3
Cluster-62068.63411	2.9404	0.000162	0.019213	Odobenus rosmarus divergens dishevelled associated activator of morphogenesis 1 (DAAM1)	DAAM
Cluster-62068.64128	2.94	4.52E-05	0.0072221	vesicle-associated membrane protein 4 (VAMP4)	VAMP4
Cluster-62068.163008	2.9374	0.000134	0.016716	solute carrier family 26 (anion exchanger), member 4 (SLC26A4)	SLC26A4, PDS
Cluster-62068.33359	2.9366	0.00016	0.01909	dihydrouridine synthase 2 (DUS2), transcript variant X6	DUS2
Cluster-62068.38804	2.935	0.000155	0.018476	ATPase type 13A1 (ATP13A1)	ATP13A1
Cluster-22933.0	2.9304	0.000175	0.020272	cholinergic receptor, nicotinic, alpha 3 (neuronal) (CHRNA3)	CHRNA3
Cluster-60834.1	2.9272	0.000136	0.016824	gamma-aminobutyric acid (GABA) A receptor, delta (GABRD)	GABRD
Cluster-62068.107270	2.925	0.000178	0.020567	solute carrier family 6 (neurotransmitter transporter), member 8 (SLC6A8)	SLC6A6S

Cluster-62068.98524	2.9241	3.62E-06	0.00097823	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), transcript variant X8	SEMA5
Cluster-62068.96002	2.9239	5.24E-08	2.89E-05	Ursus maritimus KIAA1324 ortholog (KIAA1324)	KIAA1324
Cluster-62068.192409	2.9229	0.000166	0.019591	Canis lupus familiaris fragile histidine triad (FHIT), transcript variant 1	FHIT
Cluster-62068.29783	2.9221	3.78E-05	0.0062539	E74-like factor 5 (ets domain transcription factor) (ELF5)	ELF5
Cluster-62068.57528	2.92	0.000121	0.015419	uncharacterized LOC106003856 (LOC106003856), ncRNA	--
Cluster-62068.29782	2.9179	0.00013	0.01629	E74-like factor 5 (ets domain transcription factor) (ELF5)	ELF5
Cluster-62068.39319	2.9079	0.000179	0.020648	tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18)	TNFSF18, GITRL
Cluster-62068.95753	2.9032	1.74E-10	2.12E-07	Leptonychotes weddellii collagen alpha-1(I) chain-like (LOC102742903)	--
Cluster-62068.82311	2.8991	0.000154	0.018394	laminin, gamma 2 (LAMC2)	LAMC2
Cluster-62068.113616	2.8984	0.000187	0.021314	intraflagellar transport 57 (IFT57)	ESRRBL1, HIPPI
Cluster-62068.87854	2.8983	0.000201	0.022499	Leptonychotes weddellii transketolase (TKT)	tktA, tktB
Cluster-62068.35051	2.896	0.000117	0.015028	ATPase, class V, type 10B (ATP10B)	ATP10B
Cluster-62068.129382	2.888	0.000198	0.022304	RNA binding motif protein 38 (RBM38)	RBM38
Cluster-62068.109337	2.8867	0.000204	0.022702	Odobenus rosmarus divergens C2 calcium-dependent domain containing 4B (C2CD4B)	C2CD4B
Cluster-62068.61498	2.886	0.000228	0.02467	transient receptor potential cation channel, subfamily M, member 5 (TRPM5), transcript variant X7	TRPM5
Cluster-62068.84995	2.8804	9.57E-06	0.002126	alpha-2-macroglobulin-like 1 (A2ML1), transcript variant X4	A2ML1
Cluster-62068.94496	2.8794	1.58E-06	0.00049438	uncharacterized LOC106006158 (LOC106006158), ncRNA	--
Cluster-62068.150046	2.8729	9.65E-05	0.012905	annexin A3 (ANXA3)	ANXA3
Cluster-62068.130986	2.8719	2.19E-06	0.00064739	Ovis canadensis canadensis isolate 43U chromosome 16 sequence	--
Cluster-62068.87272	2.8687	0.000253	0.026575	leukocyte cell derived chemotaxin 1 (LECT1)	LECT1

Cluster-62068.171459	2.8674	0.000234	0.025112	Leber congenital amaurosis 5-like (LCA5L), transcript variant X6	LCA5L
Cluster-62068.18707	2.8657	0.000226	0.024515	angiopoietin-like 3 (ANGPTL3)	ANGPTL3
Cluster-62068.138577	2.8649	9.65E-05	0.012905	propionyl CoA carboxylase, alpha polypeptide (PCCA)	PCCA, pccA
Cluster-62068.81909	2.8646	0.000259	0.026985	low density lipoprotein receptor-related protein 2 (LRP2)	LRP2
Cluster-62068.68956	2.8638	0.00011	0.014325	solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1)	SLC15A1, PEPT1
Cluster-39470.0	2.8636	0.000248	0.026267	chromosome 17, clone RP11-666A8	--
Cluster-62068.22983	2.8616	1.55E-07	7.29E-05	Ailuropoda melanoleuca coagulation factor II (thrombin) (F2)	F2
Cluster-62068.56013	2.8608	0.000247	0.026201	FYVE, RhoGEF and PH domain containing 3 (FGD3)	FGD3
Cluster-62068.88944	2.8508	0.000272	0.028057	Neovison vison clone LINE	--
Cluster-62068.146840	2.8494	0.000249	0.026366	ABI family, member 3 (ABI3)	ABI3
Cluster-62068.82402	2.846	7.80E-05	0.010995	uncharacterized LOC106003559 (LOC106003559), ncRNA	--
Cluster-62068.116713	2.8443	1.77E-10	2.14E-07	carboxypeptidase Z (CPZ)	CPZ
Cluster-62068.140464	2.8427	0.000104	0.013689	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), RefSeqGene on chromosome 12	SLC4A8
Cluster-62068.139558	2.84	0.000172	0.020131	regulating synaptic membrane exocytosis 3 (RIMS3)	RIMS3
Cluster-62068.8063	2.8397	0.000272	0.028043	genomic DNA, chromosome 11 clone:RP11-775D16	--
Cluster-62068.120348	2.8394	0.000265	0.027487	peptidase D (PEPD), RefSeqGene on chromosome 19	PEPD
Cluster-62068.74882	2.8389	0.00027	0.027875	Odobenus rosmarus divergens protein tyrosine phosphatase type IVA, member 1 (PTP4A1)	PTP4A
Cluster-62068.104318	2.8377	0.00032	0.031402	synaptotagmin IV (SYT4)	SYT4
Cluster-62068.90611	2.8371	1.93E-07	8.83E-05	Mustela vison clone IX3J3s1 genomic sequence	--
Cluster-62068.149110	2.8351	0.00021	0.023187	7-dehydrocholesterol reductase (DHCR7)	DHCR7
Cluster-62068.143453	2.8315	5.95E-05	0.0088883	TBC1 domain family, member 2 (TBC1D2), transcript variant X4	TBC1D2
Cluster-62068.164409	2.8235	0.000288	0.029051	histone deacetylase 3 (HDAC3)	HDAC3

Cluster-62068.96118	2.8233	3.45E-10	3.73E-07	Ailuropoda melanoleuca KIAA1324 ortholog (KIAA1324)	KIAA1324
Cluster-62068.172070	2.8232	0.0002	0.022401	uncharacterized LOC106006908 (LOC106006908), ncRNA	--
Cluster-62068.122367	2.8199	0.000175	0.020275	dedicator of cytokinesis 5 (DOCK5)	DOCK5
Cluster-62068.98388	2.8188	2.28E-05	0.0041866	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5), transcript variant X6	NUDT5
Cluster-62068.102545	2.8185	4.44E-06	0.0011493	solute carrier family 16, member 14 (SLC16A14)	SLC16A14
Cluster-62068.69865	2.8146	0.000351	0.033861	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1)	SRD5A1
Cluster-62068.158265	2.805	0.00014	0.017192	uncharacterized LOC101683862 (LOC101683862)4, ncRNA	--
Cluster-62068.143807	2.7996	1.15E-05	0.0024306	RAS-like, family 11, member B (RASL11B)	RASL11B
Cluster-62068.25078	2.7991	9.10E-09	6.49E-06	pregnancy up-regulated nonubiquitous CaM kinase (PNCK)	PNCK
Cluster-62068.114221	2.7929	3.41E-05	0.0058215	cyclin-dependent kinase-like 2 (CDC2-related kinase) (CDKL2)	CDKL2
Cluster-62068.94340	2.7889	0.000404	0.037512	epidermal growth factor (EGF)	EGF
Cluster-62068.119467	2.7828	9.08E-05	0.012397	signal-induced proliferation-associated 1 like 2 (SIPA1L2)	SIPA1L2, SPAL2
Cluster-67194.0	2.7824	0.000245	0.02609	Ursus maritimus cadherin 18, type 2 (CDH18)	CDH18
Cluster-62068.102660	2.7804	0.000375	0.035554	flotillin 1 (FLOT1)	FLOT
Cluster-62068.76801	2.777	0.000206	0.022906	Ursus maritimus translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae) (TOMM70A)	TOMM70A
Cluster-62068.125506	2.7755	2.63E-05	0.004686	nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant X4	NR4A1, HMR
Cluster-62068.101242	2.7738	3.11E-09	2.68E-06	KIAA1324 ortholog (KIAA1324), transcript variant X4	KIAA1324
Cluster-62068.12536	2.7722	0.000223	0.024225	Fanconi anemia, complementation group M (FANCM)	FANCM
Cluster-62068.157467	2.7663	0.000394	0.036698	Odobenus rosmarus divergens basic proline-rich protein (LOC105757347)	--
Cluster-62068.92973	2.7628	0.000414	0.037995	milk fat globule-EGF factor 8 protein (MFGE8)	MFGE8

Cluster-62068.152657	2.7616	0.000406	0.0376	coagulation factor X (F10)	F10
Cluster-62068.97764	2.7603	0.000448	0.040393	Rap guanine nucleotide exchange factor (GEF) 3 (RAPGEF3)	RAPGEF3, EPAC1
Cluster-62068.135123	2.7542	0.000177	0.020452	target of EGR1, member 1 (nuclear) (TOE1)	TOE1
Cluster-62068.85308	2.7534	0.000424	0.038553	Ailuropoda melanoleuca YTH domain containing 1 (YTHDC1)	YTHDC1
Cluster-62068.98128	2.7516	1.46E-07	6.92E-05	1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9)	GPAT3_4, AGPAT9, AGPAT6
Cluster-62068.19300	2.7491	0.000174	0.020215	Human DNA sequence from clone RP11-31E23 on chromosome 1q31.3-32.1	--
Cluster-61968.0	2.7447	0.000472	0.04184	bora, aurora kinase A activator (BORA)	BORA
Cluster-62068.146379	2.742	0.00012	0.015324	solute carrier family 24 (SLC24A2)	SLC24A2
Cluster-62068.101040	2.733	0.000261	0.027133	chromosome 16 clone RP11-413H22	--
Cluster-62068.79119	2.7283	1.75E-07	8.17E-05	Ovis canadensis canadensis isolate 43U chromosome 20 sequence	--
Cluster-62068.102191	2.7277	4.02E-08	2.32E-05	X-linked Kx blood group (XK)	XK
Cluster-62068.98127	2.7262	1.25E-07	6.12E-05	1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9)	AGPAT9
Cluster-62068.101252	2.726	5.94E-05	0.0088883	TBP-like 1 (TBPL1)	TBPL1
Cluster-62068.177044	2.7234	0.000365	0.034845	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	--
Cluster-62068.175046	2.7151	0.000325	0.031728	troponin I type 1 (skeletal, slow) (TNNI1)	TNNI1
Cluster-62068.164091	2.7149	0.00054	0.046254	suppressor of variegation 3-9 homolog 2 (Drosophila) (SUV39H2)	SUV39H2
Cluster-62068.109663	2.7128	1.38E-05	0.002848	cyclin-dependent kinase-like 2 (CDC2-related kinase) (CDKL2)	CDKL
Cluster-62068.83341	2.7106	5.84E-07	0.00022188	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.101731	2.7085	1.88E-07	8.72E-05	SUN domain containing ossification factor (SUCO), transcript variant X4, misc_RNA	SUCO
Cluster-62068.169218	2.7071	0.000586	0.049108	uncharacterized LOC106006266 (LOC106006266)	--
Cluster-62068.135865	2.7067	0.000587	0.049141	lipocalin 1 (LCN1)	LCN1

Cluster-62068.98833	2.7062	5.60E-07	0.0002141	C1q and tumor necrosis factor related protein 6 (C1QTNF6)	C1QTNF6
Cluster-62068.146922	2.7056	0.00032	0.031402	formin homology 2 domain containing 3 (FHOD3)	FHOD3
Cluster-62068.79104	2.6989	0.000569	0.048098	limb and CNS expressed 1 like (LIX1L)	LIX1L
Cluster-55624.0	2.6967	0.000596	0.049757	Pan troglodytes BAC clone CH251-679I17 from chromosome 15	--
Cluster-40312.0	2.6965	0.000304	0.03028	Canis familiaris chromosome 8, clone XX-152I15	--
Cluster-62068.83975	2.6944	3.67E-06	0.00098671	Ursus maritimus coatmer protein complex, subunit beta 2 (beta prime) (COPB2)	COPB2, SEC27
Cluster-62068.178761	2.6918	0.000161	0.019124	KIAA1614 ortholog (KIAA1614)	KIAA1614
Cluster-62068.15067	2.6901	0.000477	0.04213	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.114400	2.6896	4.08E-05	0.0066692	Rhesus Macaque BAC CH250-276H13	--
Cluster-54352.0	2.6895	0.000152	0.018217	Canis lupus familiaris zinc finger protein 454 (ZNF454)	KRAB
Cluster-62068.139715	2.6869	9.30E-07	0.0003258	Odobenus rosmarus divergens PDZ domain containing 8 (PDZD8)	PDZD8
Cluster-22215.0	2.6849	5.80E-05	0.008723	uncharacterized LOC101686146 (LOC101686146), ncRNA	--
Cluster-26385.0	2.6823	0.000425	0.038672	Cercocebus atys regulator of G-protein signaling 3 (RGS3)	RGS3
Cluster-62068.80525	2.6804	3.09E-07	0.00012844	Canis familiaris, clone XX-228B21	--
Cluster-62068.135412	2.678	0.000317	0.031162	Odobenus rosmarus divergens Rap guanine nucleotide exchange factor (GEF) 4 (RAPGEF4)	RAPGEF4, EPAC2
Cluster-62068.90443	2.6708	0.000488	0.042986	histone H1.2 (LOC101676607)	H1_5
Cluster-62068.14645	2.6666	0.000503	0.043814	Ailuropoda melanoleuca clone gpbaab	--
Cluster-62068.136072	2.6666	0.000597	0.049757	Bos taurus uncharacterized LOC101905583 (LOC101905583), ncRNA	--
Cluster-62068.120539	2.6652	0.000168	0.019787	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	SLC4A8
Cluster-62068.69420	2.6652	4.56E-05	0.00725	solute carrier family 12 (potassium/chloride transporter), member 7 (SLC12A7), transcript variant X4	SLC12A7, KCC4
Cluster-62068.61556	2.6624	0.000382	0.036011	ATPase, class V, type 10B (ATP10B)	ATP10B

Cluster-62068.99363	2.6602	5.37E-06	0.0013462	ornithine aminotransferase (OAT)	rocD, OAT
Cluster-62068.152726	2.6571	0.000226	0.024515	zinc finger protein 469 (ZNF469)	ZNF469
Cluster-62068.96613	2.6523	5.33E-05	0.0081572	Rhesus Macaque BAC CH250-276H13 () complete sequence	SIAT4C
Cluster-62068.82928	2.6496	0.000284	0.028802	Felis catus FLA extended class II, class II, class III, proximal and central class I region genomic sequence	--
Cluster-79398.0	2.649	0.000239	0.025472	cannabinoid receptor 1 (brain) (CNR1)	CNR1
Cluster-62068.30601	2.6489	0.000202	0.022625	Ovis canadensis canadensis isolate 43U chromosome 17 sequence	--
Cluster-62068.86756	2.6414	0.000468	0.04166	transmembrane protein 218 (TMEM218)	SLC37A1_2
Cluster-35572.0	2.6412	0.000215	0.023549	Human DNA sequence from clone RP11-336F23 on chromosome 1	--
Cluster-62068.73385	2.6327	0.000302	0.030139	BAC clone RP11-468A23 from 4	--
Cluster-62068.114799	2.631	5.49E-05	0.0083625	atypical chemokine receptor 4 (ACKR4)	CCRL1, CCR11
Cluster-62068.130037	2.6308	2.86E-07	0.00012069	Ailuropoda melanoleuca fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10)	FUT10
Cluster-62068.161830	2.6289	0.000357	0.034314	Ovis canadensis canadensis isolate 43U chromosome 12 sequence	--
Cluster-62068.168792	2.6264	0.000358	0.034314	neuron navigator 3 (NAV3), transcript variant X4	NAV3
Cluster-62068.97113	2.6247	0.000408	0.03776	FXYP domain containing ion transport regulator 4 (FXYP4), transcript variant X4	FXYP4, CHIF
Cluster-62068.118666	2.6239	0.000352	0.033942	polymerase (RNA) III (DNA directed) polypeptide B (POLR3B)	RPC2, POLR3B
Cluster-62068.148210	2.6158	0.00033	0.032177	opioid binding protein/cell adhesion molecule-like (OPCML), transcript variant X9	OPCML
Cluster-62068.31066	2.6136	0.000175	0.020275	T-cell surface glycoprotein CD1a-like (LOC101689902)	CD1
Cluster-62068.94489	2.602	3.29E-06	0.00090819	antizyme inhibitor 1 (AZIN1), transcript variant 2	AZIN1
Cluster-62068.106988	2.5979	0.000297	0.029762	transmembrane protein 27 (TMEM27)	TMEM27
Cluster-62068.87375	2.597	3.76E-05	0.0062247	PDZ domain containing 1 (PDZK1)	PDZK1
Cluster-62068.80564	2.5931	0.000177	0.020488	Ailuropoda melanoleuca delta-like 1 (Drosophila) (DLL1)	DLL

Cluster-62068.115474	2.5895	0.000101	0.013409	transcription factor CP2-like 1 (TFCP2L1)	TFCP2
Cluster-62068.95848	2.5875	2.39E-05	0.0043406	CD320 molecule (CD320)	CD320
Cluster-62068.151037	2.5843	0.000358	0.034314	Ursus maritimus cysteine conjugate-beta lyase 2 (CCBL2), transcript variant X4	CCBL
Cluster-62068.107255	2.58	0.000221	0.02412	branched chain amino-acid transaminase 1, cytosolic (BCAT1)	E2.6.1.42, ilvE
Cluster-62068.85556	2.5738	5.38E-05	0.008218	transmembrane protein 27 (TMEM27)	TMEM27
Cluster-62068.96013	2.569	3.77E-07	0.00014996	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	--
Cluster-62068.161832	2.5687	0.000544	0.046537	Ailuropoda melanoleuca uncharacterized LOC105239280 (LOC105239280), ncRNA	--
Cluster-62068.110767	2.5665	0.000122	0.01552	coiled-coil domain containing 15 (CCDC15), transcript variant X6	CCDC15
Cluster-62068.77347	2.566	3.91E-05	0.0064187	TBC1 domain family, member 19 (TBC1D19)	TBC1D19
Cluster-62068.126323	2.5642	0.000256	0.026831	Human DNA sequence from clone RP11-336F23 on chromosome 1	--
Cluster-62068.82852	2.5614	0.000307	0.030461	laminin, alpha 1 (LAMA1)	LAMA1_2
Cluster-62068.20827	2.5552	0.00049	0.043086	Pan troglodytes BAC clone CH251-696K14 from chromosome 11	--
Cluster-62068.90194	2.5549	1.45E-12	3.02E-09	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.88240	2.5522	1.95E-05	0.0037219	ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4), transcript variant X6	SIAT4C
Cluster-62068.98468	2.5403	0.000468	0.041665	Canis lupus familiaris serine/arginine-rich splicing factor 4 (SRSF4)	SFRS4_5_6
Cluster-62068.97509	2.5338	0.00019	0.021611	Pig DNA sequence from clone CH242-113D8 on chromosome 7	--
Cluster-62068.68790	2.5311	3.16E-06	0.00088541	regulator of calcineurin 1 (RCAN1)	RCAN1, MCIP1
Cluster-62068.75215	2.5288	0.000374	0.035514	Ovis canadensis canadensis isolate 43U chromosome 6 sequence	--
Cluster-62068.80357	2.5279	4.04E-11	5.88E-08	flavin containing monooxygenase 2 (non-functional) (FMO2)	FMO
Cluster-62068.150670	2.5264	0.000343	0.033169	synaptotagmin-like 3 (SYTL3)	SYTL
Cluster-62068.99755	2.5241	1.24E-05	0.0025878	transcription factor CP2-like 1 (TFCP2L1)	TFCP2L1
Cluster-62068.143551	2.5208	7.92E-05	0.011109	Mandrillus leucophaeus uncharacterized LOC105531271 (LOC105531271),	--

				misc_RNA	
Cluster-62068.91641	2.5098	4.28E-06	0.0011174	1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9)	GPAT3_4, AGPAT9, AGPAT6
Cluster-62068.109550	2.5025	3.38E-05	0.0057908	ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4), transcript variant X6	SIAT4C
Cluster-62068.67899	2.4986	1.94E-07	8.83E-05	major facilitator superfamily domain containing 2A (MFSD2A)	MFSD2A
Cluster-62068.124438	2.4973	2.22E-07	9.82E-05	p21 protein (Cdc42/Rac)-activated kinase 3 (PAK3), RefSeqGene on chromosome X	PAK3
Cluster-62068.123209	2.4942	0.000593	0.049546	vasoactive intestinal peptide receptor 2 (VIPR2)	VIPR2
Cluster-62068.91677	2.4855	8.88E-07	0.00031329	Ursus maritimus flavin containing monooxygenase 2 (non-functional) (FMO2), transcript variant X4	FMO2
Cluster-62068.79054	2.4849	0.000104	0.013748	SH3-domain GRB2-like 3 (SH3GL3), transcript variant X4	SH3GL
Cluster-62068.66058	2.4758	3.72E-07	0.00014871	Odobenus rosmarus divergens solute carrier family 25 (mitochondrial carnitine/acylcarnitine carrier), member 29 (SLC25A29)	SLC25A29
Cluster-62068.88702	2.4736	5.04E-05	0.0078104	solute carrier family 16, member 14 (SLC16A14)	SLC16A14
Cluster-62068.70296	2.472	0.000295	0.029556	Canis familiaris, clone XX-134M17	--
Cluster-62068.67298	2.4694	0.00014	0.01719	NDRG family member 3 (NDRG3)	NDRG3
Cluster-62068.78547	2.4676	6.05E-07	0.00022932	activated leukocyte cell adhesion molecule (ALCAM), transcript variant X4	ALCAM
Cluster-62068.124082	2.4657	5.53E-09	4.38E-06	synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP)	SSX2IP, ADIP
Cluster-62068.119476	2.4651	1.83E-05	0.0035486	SH3-domain GRB2-like 3 (SH3GL3), misc_RNA	SH3GL3
Cluster-62068.98984	2.4633	2.20E-06	0.00064955	flavin containing monooxygenase 2 (non-functional) (FMO2)	FMO
Cluster-62068.97284	2.4607	0.000415	0.038043	megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1)	--
Cluster-62068.113928	2.4593	0.000172	0.020073	fibroblast growth factor receptor 4 (FGFR4)	FGFR4
Cluster-62068.128798	2.4584	1.38E-06	0.00044523	carboxypeptidase Z (CPZ)	CPZ

Cluster-62068.153242	2.4562	0.000418	0.038181	collagen triple helix repeat containing 1 (CTHRC1)	CTHRC1
Cluster-62068.84286	2.4561	5.52E-05	0.0083817	Canis Familiaris chromosome 27, clone XX-53N21	--
Cluster-62068.111614	2.4471	5.78E-05	0.0087039	noggin (NOG)	NOG
Cluster-62068.62540	2.4457	7.57E-07	0.00027461	Ailuropoda melanoleuca transmembrane protease, serine 2 (TMPRSS2)	TMPRSS2
Cluster-62068.106838	2.4427	3.75E-06	0.0010058	KIAA1324 ortholog (KIAA1324), transcript variant X4	KIAA1324
Cluster-74011.0	2.4376	0.000553	0.047	Odobenus rosmarus divergens v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN)	NMYC, MYCN
Cluster-62068.91676	2.4371	4.54E-05	0.0072387	Ursus maritimus flavin containing monooxygenase 2 (non-functional) (FMO2), transcript variant X4	FMO2
Cluster-18608.0	2.4369	0.000459	0.041087	interleukin 1, alpha (IL1A)	IL1A
Cluster-62068.43614	2.4299	0.00015	0.017976	Pig DNA sequence from clone CH242-240D13 on chromosome 1	--
Cluster-62068.118383	2.4218	4.66E-05	0.0073499	SH3-domain GRB2-like 3 (SH3GL3)	SH3GL
Cluster-62068.90993	2.4199	3.40E-05	0.0058172	Ovis canadensis canadensis isolate 43U chromosome 22 sequence	--
Cluster-62068.95030	2.4163	9.05E-05	0.012362	uncharacterized LOC106005866 (LOC106005866), ncRNA	--
Cluster-62068.66886	2.411	2.22E-05	0.004097	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), transcript variant X8	SEMA5
Cluster-62068.84736	2.4106	2.92E-08	1.74E-05	plastin 1 (PLS1)	PLS1
Cluster-62068.81599	2.4105	1.13E-07	5.71E-05	cadherin 4, type 1, R-cadherin (retinal) (CDH4)	CDH4
Cluster-62068.86350	2.4104	0.000337	0.032742	Canis lupus familiaris hydrogen voltage-gated channel 1 (HVCN1)	HVCN1
Cluster-62068.131847	2.407	2.12E-05	0.0039638	serpin peptidase inhibitor, clade B (ovalbumin), member 2 (SERPINB2)	SERPINB
Cluster-62068.131888	2.4057	5.90E-08	3.24E-05	cadherin 4, type 1, R-cadherin (retinal) (CDH4)	CDH4
Cluster-62068.81648	2.4023	6.70E-09	5.08E-06	Odobenus rosmarus divergens ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9)	ADAMTS9
Cluster-62068.180705	2.3976	0.000418	0.038218	Pongo abelii BAC clone CH276-169E9 from chromosome 5	--

Cluster-62068.96975	2.3903	8.13E-05	0.011342	Ursus maritimus KIAA1324 ortholog (KIAA1324)	KIAA1324
Cluster-62068.80428	2.3851	0.000187	0.021314	dishevelled-binding antagonist of beta-catenin 2 (DACT2)	DACT2
Cluster-62068.133033	2.3827	1.87E-06	0.00056555	D-amino-acid oxidase (DAO)	DAO, aao
Cluster-62068.100814	2.3799	0.000245	0.026097	genomic DNA, chromosome 8q23, clone: KB1254G8	--
Cluster-62068.22702	2.3788	3.06E-05	0.0053088	Canis familiaris, clone XX-459P12	--
Cluster-62068.90360	2.3743	9.16E-06	0.0020663	inositol monophosphatase domain containing 1 (IMPAD1)	--
Cluster-62068.107007	2.374	0.000267	0.027645	carboxypeptidase X (M14 family), member 2 (CPXM2)	CPXM2
Cluster-62068.120318	2.3708	9.21E-05	0.012504	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold5468	--
Cluster-62068.76103	2.3693	6.34E-05	0.0093786	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A (MGAT4A)	--
Cluster-62068.106987	2.361	9.74E-05	0.012991	transmembrane protein 27 (TMEM27), transcript variant X4	TMEM27
Cluster-62068.94216	2.3567	0.000108	0.014166	CD320 molecule (CD320)	CD320
Cluster-62068.142158	2.3567	0.000161	0.019171	nascent polypeptide-associated complex subunit alpha, muscle-specific form (LOC101682205)	--
Cluster-62068.124744	2.3566	0.000137	0.016907	cytidine deaminase (CDA)	cdd, CDA
Cluster-62068.20054	2.3427	8.58E-05	0.011843	chromosome 1 clone RP4-771M4	--
Cluster-62068.122412	2.3413	0.000236	0.025261	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A (MGAT4A)	--
Cluster-62068.124668	2.336	0.00017	0.019938	cytidine deaminase (CDA)	cdd, CDA
Cluster-62068.165904	2.3327	0.000338	0.032779	lipopolysaccharide-binding protein-like (LOC101690223)	LBP
Cluster-62068.124081	2.3279	1.07E-22	1.53E-18	synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP)	SSX2IP, ADIP
Cluster-62068.93953	2.3257	2.59E-08	1.57E-05	collagen, type I, alpha 1 (COL1A1)	COL1A5
Cluster-62068.125024	2.3247	9.31E-09	6.54E-06	K(lysine) acetyltransferase 2A (KAT2A)	PCAF, KAT2, GCN5
Cluster-62068.167735	2.3196	0.000361	0.034593	BAC clone RP11-795C1 from 2	--

Cluster-62068.138482	2.3174	0.000405	0.03757	ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9)	ADAMTS9
Cluster-62068.95613	2.313	8.39E-05	0.011618	transcription factor CP2-like 1 (TFCP2L1)	TFCP2
Cluster-62068.71214	2.3093	3.76E-07	0.00014996	FK506 binding protein 5 (FKBP5)	FKBP4_5
Cluster-62068.84885	2.3061	6.56E-06	0.0015762	Ailuropoda melanoleuca KIAA1324 ortholog (KIAA1324)	KIAA1324
Cluster-62068.93665	2.302	0.000109	0.014203	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5), transcript variant X4	NUDT5
Cluster-62068.132097	2.2992	3.62E-05	0.0060774	six transmembrane epithelial antigen of the prostate 1 (STEAP1)	STEAP1
Cluster-62068.105880	2.2957	1.15E-05	0.0024366	TBP-like 1 (TBPL1)	TBP, tbp
Cluster-62068.76470	2.2827	0.000374	0.035514	cAMP responsive element modulator (CREM)	CREM
Cluster-62068.96367	2.2796	6.74E-05	0.0098344	teneurin transmembrane protein 4 (TENM4)	TENM4
Cluster-62068.92725	2.2763	0.000336	0.032634	solute carrier family 6 (amino acid transporter), member 14 (SLC6A14)	SLC6A5S
Cluster-62068.80121	2.2724	0.000377	0.035665	like-glycosyltransferase (LARGE)	LARGE
Cluster-62068.88961	2.2719	1.68E-07	7.89E-05	Canis lupus familiaris plastin 1 (PLS1)	PLS1
Cluster-62068.99314	2.2703	0.000438	0.039603	Microcebus murinus cyclin G1 (CCNG1)	CCNG1
Cluster-62068.106871	2.2697	2.58E-08	1.56E-05	leucine rich repeat containing 3 (LRRC3)	LRRC3
Cluster-62068.146731	2.2688	0.000548	0.046685	Ovis canadensis canadensis isolate 43U chromosome 8 sequence	--
Cluster-62068.93129	2.2616	0.000264	0.027449	solute carrier family 16, member 14 (SLC16A14)	SLC16A14
Cluster-62068.89125	2.2564	1.27E-05	0.002648	methionine adenosyltransferase II, beta (MAT2B)	metK
Cluster-62068.70438	2.2515	2.13E-10	2.49E-07	heparan sulfate 6-O-sulfotransferase 2 (HS6ST2)	HS6ST2
Cluster-62068.92631	2.2504	6.46E-09	4.92E-06	Macaca nemestrina serine/arginine-rich splicing factor 7 (SRSF7), misc_RNA	GEMIN6, SIP2
Cluster-62068.81639	2.2496	4.68E-08	2.62E-05	ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9)	ADAMTS9
Cluster-62068.137277	2.2491	4.31E-05	0.0069572	cell growth regulator with EF-hand domain 1 (CGREF1)	CGREF1
Cluster-62068.87001	2.2454	4.39E-05	0.0070799	Odobenus rosmarus divergens procollagen C-endopeptidase enhancer (PCOLCE)	--
Cluster-62068.129241	2.2437	0.000372	0.035445	uncharacterized LOC106006958 (LOC106006958), ncRNA	--

Cluster-62068.72796	2.2423	1.63E-05	0.0032095	SH3 and cysteine rich domain (STAC)	STAC
Cluster-62068.97641	2.2385	8.34E-05	0.011561	transmembrane protein 161A (TMEM161A)	TMEM161A
Cluster-62068.109051	2.2371	2.06E-09	1.83E-06	insulin-like growth factor 1 (somatomedin C) (IGF1)	IGF1
Cluster-62068.89656	2.2351	0.000169	0.0199	vascular endothelial growth factor A (VEGFA)	VEGFA
Cluster-62068.90765	2.2322	8.55E-06	0.0019633	proline rich membrane anchor 1 (PRIMA1)	SEPT3_9_12
Cluster-62068.91507	2.2229	0.000114	0.014692	Sus scrofa vascular endothelial growth factor A-like (LOC100737169)	VEGFA
Cluster-62068.69015	2.2223	7.88E-05	0.011091	flavin containing monooxygenase 2 (non-functional) (FMO2)	FMO
Cluster-62068.99667	2.2152	2.38E-07	0.00010342	collagen, type I, alpha 1 (COL1A1)	COL1AS
Cluster-62068.50776	2.2127	0.000105	0.013756	Leopardus geoffroyi isolate OGE-136949 SINE Can-SINE	--
Cluster-62068.95562	2.2078	7.12E-09	5.34E-06	collagen, type I, alpha 1 (COL1A1)	COL1AS
Cluster-62068.112734	2.2041	0.000271	0.027975	HNF1 homeobox A (HNF1A)	HNF1A
Cluster-62068.78156	2.2038	0.000571	0.04816	uncharacterized LOC106005866 (LOC106005866), ncRNA	--
Cluster-62068.43929	2.2034	6.56E-05	0.0096318	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.111434	2.2033	3.85E-05	0.0063477	carboxypeptidase X (M14 family), member 1 (CPXM1)	CPXM1
Cluster-62068.107138	2.2003	0.000145	0.017595	V-set and immunoglobulin domain containing 10 (VSIG10)	TCF1, HNF1A
Cluster-62068.46432	2.1888	1.64E-05	0.0032242	msh homeobox 2 (MSX2)	MSX
Cluster-62068.95175	2.187	1.85E-06	0.00056079	1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9)	GPAT3_4, AGPAT9, AGPAT6
Cluster-62068.87339	2.1803	0.000331	0.032229	vascular endothelial growth factor A (VEGFA), RefSeqGene on chromosome 6	VEGFA
Cluster-62068.81524	2.1715	0.000598	0.049811	pyrroline-5-carboxylate reductase 1 (PYCR1)	PYCR1
Cluster-62068.118465	2.1663	6.95E-06	0.0016588	cystathionine gamma-lyase (CTH)	CTH
Cluster-62068.101676	2.1644	0.000423	0.038553	regulator of G-protein signaling 3 (RGS3), transcript variant X7	RGS3
Cluster-62068.92579	2.1617	0.000299	0.02993	transcription factor CP2-like 1 (TFCP2L1)	TFCP2

Cluster-62068.122417	2.1617	0.00026	0.027133	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A (MGAT4A)	MGAT4A_B
Cluster-62068.142126	2.1517	0.000445	0.040123	chromosome 17, clone RP11-314A20	--
Cluster-62068.142160	2.1516	0.000105	0.013766	Ailuropoda melanoleuca uncharacterized LOC100483315 (LOC100483315), ncRNA	--
Cluster-62068.36988	2.1444	0.000122	0.015467	steroid 17-alpha-hydroxylase/17,20 lyase (LOC101671806)	CYP17A
Cluster-62068.110058	2.1405	1.58E-05	0.0031423	Callithrix jacchus uncharacterized LOC103791965 (LOC103791965), ncRNA	--
Cluster-62068.113743	2.1382	1.92E-07	8.83E-05	glutamine-rich 1 (QRICH1)	QRICH1
Cluster-62068.102698	2.1349	2.73E-05	0.0048152	Bos taurus ornithine decarboxylase (ODC) gene, complete cds	ODC1, speC, speF
Cluster-62068.72261	2.1339	0.000308	0.030531	Odobenus rosmarus divergens complement component (3b/4b) receptor 1-like (CR1L)	CD46, MCP
Cluster-61909.0	2.1316	0.000125	0.015865	Ursus maritimus testis expressed 33 (TEX33)	TEX33
Cluster-62068.95616	2.1284	0.000551	0.046853	transcription factor CP2-like 1 (TFCP2L1)	TFCP2
Cluster-62068.99976	2.1271	2.68E-05	0.0047591	sel-1 suppressor of lin-12-like 3 (SEL1L3)	SEL1L3
Cluster-62068.103151	2.1253	0.000412	0.037912	myosin VA (heavy chain 12, myoxin) (MYO5A)	MYO5
Cluster-62068.84994	2.113	1.52E-07	7.20E-05	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.120902	2.1058	2.84E-05	0.0049653	exportin 1 (XPO1)	XPO1
Cluster-62068.93996	2.1048	0.000358	0.034314	transmembrane protein 189 (LOC101670792)	UBE2V
Cluster-62068.61193	2.1029	1.59E-06	0.00049493	Mustela vison clone XI3L13 microsatellite Mvi4068 sequence	--
Cluster-62068.118467	2.1016	0.00045	0.04049	X-linked Kx blood group (XK)	XK
Cluster-62068.89072	2.1008	0.000271	0.027975	Canis lupus familiaris X-linked Kx blood group (McLeod syndrome) (XK)	XK
Cluster-62068.55523	2.1003	0.000132	0.016487	sarcosine dehydrogenase (SARDH)	SARDH
Cluster-62068.84005	2.0984	9.56E-06	0.002126	uncharacterized LOC106007259 (LOC106007259)	--
Cluster-62068.88740	2.0971	8.60E-05	0.011862	dual specificity phosphatase 14 (DUSP14)	K14165
Cluster-62068.92321	2.0957	0.000227	0.02454	polyhomeotic homolog 1 (Drosophila) (PHC1)	PHC1, EDR1

Cluster-62068.165219	2.0938	1.14E-05	0.0024149	vav 2 guanine nucleotide exchange factor (VAV2)	VAV2
Cluster-62068.106345	2.0871	4.11E-05	0.0067038	neuronal cell adhesion molecule (NRCAM)	NRCAM
Cluster-62068.104095	2.0826	0.000589	0.049264	PDX1 C-terminal inhibiting factor 1 (PCIF1)	PCIF1
Cluster-62068.98003	2.0815	1.00E-09	9.70E-07	insulin-like growth factor 1 (somatomedin C) (IGF1)	IGF1
Cluster-62068.150815	2.0785	1.38E-05	0.0028418	ankyrin repeat domain 34B (ANKRD34B)	ANKRD34B
Cluster-62068.75393	2.0748	0.000474	0.041928	Canis lupus familiaris salt-inducible kinase 1 (SIK1)	SIK1
Cluster-62068.92389	2.0743	0.000258	0.026966	serum/glucocorticoid regulated kinase 1 (SGK1)	SGK1
Cluster-62068.82784	2.0714	2.14E-06	0.00063886	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1)	CTNNAL1
Cluster-62068.86084	2.0607	6.24E-05	0.0092356	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1)	--
Cluster-62068.87940	2.0576	1.47E-06	0.00046644	fibromodulin (FMOD)	FMOD
Cluster-62068.102098	2.0572	9.74E-05	0.012991	laminin, alpha 1 (LAMA1)	LAMA1_2
Cluster-62068.62748	2.0562	7.69E-05	0.010851	phosphatase, orphan 2 (PHOSPHO2)	PHOSPHO2
Cluster-62068.50864	2.0561	0.000314	0.030941	KIAA1211 ortholog (KIAA1211)	KIAA1211
Cluster-62068.93024	2.053	0.000478	0.042158	deiodinase, iodothyronine (DIO3)	DIO3
Cluster-62068.118310	2.0529	2.63E-05	0.004686	SRSF protein kinase 2 (SRPK2)	SRPK2
Cluster-62068.89653	2.0483	0.000481	0.0424	Panthera tigris altaica vascular endothelial growth factor A (VEGFA)	VEGFA
Cluster-62068.103530	2.0464	3.20E-05	0.0055275	ornithine decarboxylase 1 (ODC1)	E4.1.1.17, ODC1, speC, speF
Cluster-62068.144780	2.0374	0.000301	0.030037	Ailuropoda melanoleuca WDYHV motif containing 1 (WDYHV1)	WDYHV1
Cluster-62068.131713	2.0358	0.000411	0.037912	PCI domain containing 2 (PCID2)	PCID2
Cluster-62068.86974	2.0344	1.73E-06	0.00052898	cAMP responsive element modulator (CREM)	CREM
Cluster-62068.66789	2.0331	0.000286	0.028913	phosphatase and actin regulator 4 (PHACTR4)	PHACTR4
Cluster-62068.101584	2.0282	1.58E-06	0.00049438	Ailuropoda melanoleuca histone H2B type 2-F (LOC105234948)	--
Cluster-62068.55131	2.0157	0.000496	0.043501	angiotensin I converting enzyme 2 (ACE2)	ACEH, ACE2
Cluster-62068.150902	2.0154	2.15E-05	0.0039976	actin-like 7B (ACTL7B)	ACTL7B

Cluster-62068.52176	2.0121	1.08E-05	0.0023245	cell adhesion molecule L1-like (CHL1)8	CHL1
Cluster-62068.78445	2.0098	0.000546	0.046578	Ursus maritimus tetraspanin 1 (TSPAN1)	TSPAN1
Cluster-62068.57152	2.0095	0.000515	0.044647	transmembrane protein 2 (TMEM2)	TMEM2
Cluster-62068.129189	2.0084	0.000205	0.02278	beaded filament structural protein 1, filensin (BFSP1)	BFSP1
Cluster-62068.97471	2.0049	0.000472	0.04184	uncharacterized LOC106005600 (LOC106005600)	--
Cluster-62068.100793	2.0039	4.04E-05	0.0066163	death effector domain containing 2 (DEDD2)	DEDD2
Cluster-62068.50231	2.0023	4.66E-05	0.0073499	BAC RP11-267D19	--
Cluster-62068.152128	2.0022	1.25E-05	0.0025976	ral guanine nucleotide dissociation stimulator-like 3 (RGL3)	RGL3
Cluster-62068.93630	2.0011	0.000166	0.019591	small nuclear RNA activating complex(SNAPC4)	SNAPC4
Cluster-62068.67908	2.0003	0.000113	0.014574	major facilitator superfamily domain containing 2A (MFSD2A)	MFSD2A
Cluster-62068.129311	1.9988	0.000135	0.01675	uncharacterized LOC101681318 (LOC101681318)	--
Cluster-62068.86988	1.9987	9.98E-06	0.0021878	solute carrier family 18 (vesicular monoamine transporter), member 2 (SLC18A2)	SLC18A1_2, VMAT
Cluster-62068.7808	1.9984	7.58E-05	0.010758	perilipin 5 (PLIN5)	PLIN5
Cluster-62068.172708	1.9911	0.000249	0.02633	Ailuropoda melanoleuca importin 9 (IPO9)	IPO9
Cluster-62068.67905	1.991	7.33E-05	0.010513	major facilitator superfamily domain containing 2A (MFSD2A)	MFSD2A
Cluster-62068.66760	1.9909	1.16E-05	0.0024563	sorbitol dehydrogenase (SORD)	SORD, gutB
Cluster-62068.130560	1.9895	2.32E-05	0.0042359	fatty acid desaturase 1 (FADS1)	FADS1
Cluster-62068.93317	1.9892	0.000137	0.016944	PH domain and leucine rich repeat protein phosphatase 1 (PHLPP1)	PHLPP
Cluster-62068.49033	1.9889	0.000379	0.035812	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	--
Cluster-62068.102064	1.9735	0.000318	0.031225	ornithine decarboxylase 1 (ODC1)	ODC1, speC, speF
Cluster-62068.97183	1.9711	0.000528	0.045482	delta(4)-desaturase, sphingolipid 2 (DEGS2)	DEGS2
Cluster-62068.96130	1.9699	3.32E-06	0.00091267	collagen, type I, alpha 1 (COL1A1)	COL1A1
Cluster-62068.78477	1.9685	7.10E-07	0.00026227	Odobenus rosmarus divergens plastin 1 (PLS1)	PLS1
Cluster-62068.96213	1.9658	8.33E-06	0.001925	uncharacterized LOC106006467 (LOC106006467)	--

Cluster-62068.90488	1.965	0.000555	0.047071	EPH receptor B6 (EPHB6)	EPHB6
Cluster-62068.148149	1.962	7.88E-05	0.011091	BAC clone RP11-707F2 from 4	--
Cluster-62068.116556	1.9562	5.93E-05	0.0088776	TBC1 domain family (TBC1D19)	TBC1D19
Cluster-62068.93541	1.953	1.24E-12	2.62E-09	Ailuropoda melanoleuca laminin (LAMC3)	LAMC3
Cluster-62068.131399	1.952	7.94E-05	0.011117	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB)	CSF2RB, IL3RB
Cluster-62068.94276	1.9462	1.14E-06	0.00038622	laminin, gamma 3 (LAMC3)	LAMC3
Cluster-62068.98385	1.9449	0.000471	0.041825	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5)	NUDT5
Cluster-62068.154153	1.9419	0.000521	0.045088	Human DNA sequence from clone RP11-323H21 on chromosome 9q34.1-34.3	--
Cluster-62068.87156	1.9353	1.91E-07	8.83E-05	Bos taurus ornithine decarboxylase (ODC) gene	ODC
Cluster-62068.71991	1.9349	3.35E-05	0.0057533	TPA: long non-coding RNA OTTHUMT00000473295.1 (RP11-129M16.4 gene)	--
Cluster-62068.132690	1.9312	5.54E-05	0.0084114	WD repeat domain 11 (WDR11)	WDR11
Cluster-62068.90679	1.9296	7.84E-07	0.00028287	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.78324	1.9255	0.000246	0.026112	Canis familiaris chromosome 20	--
Cluster-62068.84337	1.9253	0.000229	0.024693	laminin, alpha 1 (LAMA1)	LAMA1_2
Cluster-62068.94621	1.9248	0.000382	0.036011	Odobenus rosmarus divergens ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4)	ST3GAL4
Cluster-62068.35882	1.9224	0.000238	0.025429	UTP6, small subunit (SSU) processome component(UTP6)	UTP6
Cluster-62068.71296	1.921	0.000362	0.034684	Ovis canadensis canadensis isolate 43U chromosome 2 sequence	--
Cluster-62068.18034	1.9201	5.96E-05	0.0088967	chromosome 19, cosmids R31158, R31874, and R28125	--
Cluster-62068.98373	1.9144	1.07E-05	0.0023126	Mustela vison clone VII6J9 genomic sequence	--
Cluster-62068.86989	1.9142	0.000253	0.026589	solute carrier family 18 (vesicular monoamine transporter), member 2 (SLC18A2)	SLC18A2

Cluster-62068.113705	1.9129	1.48E-05	0.0029916	Sus scrofa mRNA, clone:ITT010099D03, expressed in small intestine	--
Cluster-62068.80991	1.9128	0.000503	0.043814	solute carrier family 23 (ascorbic acid transporter), member 1 (SLC23A1)	SLC23A1_2, SVCT1_2
Cluster-62068.103261	1.9126	0.000138	0.016987	nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5)	NUDT5
Cluster-62068.88788	1.9123	0.000171	0.019968	Ailuropoda melanoleuca cyclin-dependent kinase 12 (CDK12)	CDK12
Cluster-62068.161987	1.911	4.41E-06	0.0011449	cell adhesion molecule L1-like (CHL1)8	CHL1
Cluster-62068.94419	1.909	0.000412	0.037912	Canis familiaris chromosome X, clone XX-146G22	--
Cluster-62068.49806	1.9	0.000376	0.035655	Odobenus rosmarus divergens PARK2 co-regulated (PACRG)	PACRG
Cluster-62068.104170	1.8968	0.000142	0.017274	endogenous retrovirus group PABLB member 1 Env polyprotein-like (LOC106003903)	--
Cluster-62068.122281	1.891	8.81E-05	0.012088	Pig DNA sequence from clone CH242-421P6 on chromosome X	--
Cluster-62068.116216	1.8892	6.01E-06	0.0014647	insulin-like growth factor 1 (IGF1)	IGF1
Cluster-62068.92142	1.8852	0.000528	0.045482	FOSMID clone ABC9-43898400I17 from chromosome 9	--
Cluster-62068.86435	1.8782	5.85E-06	0.0014395	carboxypeptidase N, polypeptide 1 (CPN1)	CPN1
Cluster-62068.96375	1.8764	6.45E-07	0.00024256	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase (MTHFD2)	MTHFD2
Cluster-62068.136646	1.8759	0.000473	0.041904	gamma-glutamyltransferase 1 (GGT1)	GGT1
Cluster-62068.99920	1.8738	0.000391	0.036655	histone H2B type 1 (LOC101671838)	--
Cluster-62068.108356	1.8714	1.32E-10	1.67E-07	Mustela vison clone XI3L13 microsatellite Mvi4068 sequence	--
Cluster-62068.95533	1.8642	2.19E-05	0.00405	secreted protein, acidic, cysteine-rich (osteonectin) (SPARC)	SPARC
Cluster-62068.119801	1.852	0.000385	0.03624	Leptonychotes weddellii lysine (K)-specific demethylase 1A (KDM1A)	KDM1A, AOF2, LSD1
Cluster-62068.67676	1.8502	1.97E-05	0.0037428	phosphoserine phosphatase (PSPH)	PSPH
Cluster-62068.106127	1.8459	8.69E-05	0.01196	C-type lectin domain family 11, member A (CLEC11A)	CLEC11A
Cluster-62068.85626	1.8459	0.000442	0.039935	chondroadherin (CHAD)	CHAD

Cluster-62068.134390	1.8431	4.47E-05	0.007168	flavin containing monooxygenase 2 (non-functional) (FMO2)	FMO
Cluster-62068.83129	1.8401	0.000343	0.033169	Odobenus rosmarus divergens laminin, gamma 3 (LAMC3)	LAMC3
Cluster-62068.98134	1.8387	4.89E-05	0.0076412	frizzled class receptor 1 (FZD1)	FZD1_7, fz
Cluster-62068.78319	1.8362	0.00017	0.019938	MARVEL domain containing 3 (MARVELD3)	MARVELD3
Cluster-62068.140928	1.835	3.33E-07	0.00013662	platelet-activating factor acetylhydrolase 2 (PAFAH2)	PAFAH
Cluster-62068.96824	1.8343	8.75E-06	0.0019901	secreted protein, acidic, cysteine-rich (osteonectin) (SPARC)	--
Cluster-62068.84735	1.8339	3.34E-06	0.00091744	plastin 1 (PLS1)	PLS1
Cluster-62068.124083	1.8251	0.000193	0.021809	synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP)	SSX2IP, ADIP
Cluster-62068.107231	1.8245	2.00E-05	0.0038028	ADP-ribosylation factor-like 2 binding protein (ARL2BP)	ARL2BP, BART
Cluster-62068.140871	1.8183	4.19E-05	0.0068194	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.128641	1.8167	5.51E-06	0.0013717	insulin-like growth factor 1 (IGF1)	IGF1
Cluster-62068.113665	1.8135	7.61E-05	0.010778	uncharacterized LOC101681516	--
Cluster-62068.136774	1.8084	0.000485	0.042734	Canis Familiaris chromosome 31	PSMG1, DSCR2, PAC1
Cluster-62068.70688	1.8048	1.64E-05	0.0032331	xenotropic and polytropic retrovirus receptor 1 (XPR1)	XPR1
Cluster-62068.75151	1.803	0.000347	0.03355	solute carrier family 16(SLC16A6)	SLC16A6
Cluster-62068.107886	1.8009	5.19E-05	0.0079888	potassium channel tetramerization domain containing 12 (KCTD12)	KCTD12
Cluster-62068.88989	1.7965	0.000466	0.041583	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1)	CEACAM
Cluster-62068.105695	1.795	9.71E-05	0.012971	lipase, endothelial (LIPG)	E3.1.1.3
Cluster-62068.89233	1.7926	1.58E-06	0.00049438	Ailurogaster melanoleuca histone H3 (LOC100471070)	H3
Cluster-62068.111169	1.7913	1.28E-09	1.21E-06	collagen, type XII, alpha 1 (COL12A1)	COL12A1
Cluster-62068.128982	1.7888	0.000212	0.023285	solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8)	SLC4A8
Cluster-62068.72006	1.7835	6.04E-05	0.0090092	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1

Cluster-62068.73607	1.776	4.21E-08	2.39E-05	Canis lupus familiaris KIAA1244 ortholog (KIAA1244)	KIAA1244
Cluster-62068.118202	1.7748	1.43E-05	0.0029065	Mustela vison xenotropic and polytropic murine leukemia virus receptor mRNA	--
Cluster-62068.96489	1.7723	2.11E-08	1.33E-05	Ailuropoda melanoleuca uncharacterized LOC105238840	--
Cluster-62068.112609	1.767	7.35E-05	0.010513	Odobenus rosmarus divergens plastin 1 (PLS1)	PLS1
Cluster-62068.105450	1.7641	0.000165	0.019526	patatin-like phospholipase domain containing 6 (PNPLA6)	NTE, NRE
Cluster-62068.96360	1.7618	0.000555	0.047071	uncharacterized LOC106005600 (LOC106005600)	--
Cluster-62068.114846	1.7592	0.000414	0.037995	Ovis canadensis canadensis isolate 43U chromosome 23 sequence	--
Cluster-62068.78502	1.7559	2.34E-05	0.0042666	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 (DHX57), transcript variant X7	--
Cluster-62068.128880	1.7541	9.57E-05	0.012832	RAN binding protein 3 (RANBP3)	RANBP3
Cluster-62068.95585	1.7532	3.00E-05	0.0052248	Equus caballus collagen(COL1A2)	COL1AS
Cluster-62068.83293	1.7523	0.000502	0.043814	shootin 1 (SHTN1)	SHTN1
Cluster-62068.87759	1.7477	0.000234	0.025112	dystonin (DST)6	DST
Cluster-62068.70812	1.7447	0.000536	0.046002	attractin-like 1 (ATRNL1)	ATRNL1
Cluster-62068.86535	1.7434	0.00038	0.035905	farnesyl diphosphate synthase (FDPS)	FDPS
Cluster-62068.73200	1.742	7.07E-05	0.010213	Canis lupus familiaris xenotropic and polytropic retrovirus receptor 1 (XPR1)	--
Cluster-62068.80480	1.7344	1.16E-06	0.00039316	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.117125	1.7296	0.000141	0.017212	ADAM metallopeptidase with thrombospondin type 1 motif, 12 (ADAMTS12)	ADAMTS12
Cluster-62068.93273	1.7206	5.76E-06	0.0014229	ST3 beta-galactoside alpha-2,3-sialyltransferase 2 (ST3GAL2)	SIAT4B
Cluster-62068.71917	1.7171	0.000166	0.019587	guanine nucleotide binding protein (G protein) (GNA14)	GNA14
Cluster-62068.91464	1.7139	0.000382	0.036011	paired box 8 (PAX8)	PAX8
Cluster-62068.137413	1.7087	0.000188	0.021315	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1)	CEACAM

Cluster-62068.96460	1.706	3.43E-05	0.0058501	Pig DNA sequence from clone CH242-206C22 on chromosome X	SNAPC4
Cluster-62068.112755	1.706	0.000339	0.032911	cholinergic receptor, nicotinic, alpha 5 (neuronal) (CHRNA5)	CHRNA5
Cluster-62068.95538	1.7032	1.54E-06	0.00048538	adenosine kinase (ADK)	ADK
Cluster-62068.104101	1.6939	2.81E-05	0.0049224	FIC domain containing (FICD)	FICD
Cluster-62068.95198	1.6915	0.00022	0.024012	solute carrier family 19 (thiamine transporter) (SLC19A2)	SLC19A2_3, THTR
Cluster-62068.93607	1.6901	0.000181	0.020785	procollagen C-endopeptidase enhancer (PCOLCE)	PCOLCE
Cluster-62068.136652	1.6887	0.00038	0.035905	cyclin-dependent kinase 18 (CDK18)	CDK18
Cluster-62068.75270	1.6844	0.000326	0.031816	pleckstrin and Sec7 domain containing 4 (PSD4)	PSD4
Cluster-62068.63050	1.6844	1.12E-05	0.0023968	periostin, osteoblast specific factor (POSTN)	POSTN
Cluster-62068.107357	1.6769	2.45E-06	0.00070447	methyltransferase like 20 (METTL20)	METTL20
Cluster-62068.91424	1.6754	0.000534	0.045874	endogenous retrovirus group PABLB member 1 Env polyprotein-like (LOC106003903)	--
Cluster-62068.105990	1.6741	0.000424	0.038553	ATPase, H ⁺ transporting (ATP6V1A)	ATPeV1A, ATP6A
Cluster-62068.42264	1.6694	0.000363	0.034684	Pig DNA sequence from clone CH242-171I16 on chromosome 6	--
Cluster-62068.70538	1.6684	0.00049	0.043085	myoglobin (MB)	MB
Cluster-62068.97298	1.6656	2.86E-06	0.00080721	Canis familiaris chromosome X, clone XX-35E2	--
Cluster-62068.91270	1.6596	1.08E-05	0.0023245	high mobility group nucleosome binding domain 1 (HMGN1)	HMGN1
Cluster-62068.65418	1.659	3.19E-07	0.00013196	uncharacterized LOC101678065 (LOC101678065), ncRNA	--
Cluster-62068.117258	1.6564	0.000343	0.033185	doublecortin-like kinase 1 (DCLK1)	DCLK1
Cluster-62068.82088	1.6558	4.40E-05	0.00709	myocardin (MYOCD)	MYOCD
Cluster-62068.93284	1.652	0.000419	0.038292	embigin (EMB)	EMB
Cluster-62068.77728	1.6518	0.000571	0.048151	dihydrouridine synthase 4-like (S. cerevisiae) (DUS4L)	DUS4
Cluster-62068.102312	1.6482	2.44E-06	0.0007019	leucine rich repeat containing 3 (LRRC3)	LRRC3

Cluster-62068.95127	1.6418	2.09E-08	1.33E-05	Canis familiaris chromosome 16	--
Cluster-62068.107430	1.6402	0.000401	0.037334	homeobox B2 (HOXB2)	HOX_2
Cluster-62068.89711	1.6351	9.44E-06	0.0021097	solute carrier family 18 (vesicular monoamine transporter), member 2 (SLC18A2)	SLC18A1_2, VMAT
Cluster-62068.67193	1.6348	0.000498	0.043632	WDYHV motif containing 1 (WDYHV1)	WDYHV1
Cluster-62068.67128	1.6323	1.84E-05	0.0035567	trafficking protein particle complex 2 (TRAPPC2)	TRAPPC2
Cluster-62068.111798	1.6321	6.63E-05	0.0097077	ets homologous factor (EHF)	EHF
Cluster-62068.97665	1.6298	6.69E-07	0.00025028	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8 (SLC9A8)	SLC9A8, NHE8
Cluster-62068.71992	1.6269	0.000412	0.037912	solute carrier family 18 (vesicular monoamine transporter), member 2 (SLC18A2)	SLC18A1_2, VMAT
Cluster-62068.117379	1.6249	0.000154	0.018394	Cbl proto-oncogene-like 1, E3 ubiquitin protein ligase (CBLL1)	CBLL1
Cluster-62068.120490	1.6219	0.000377	0.035665	Ailuropoda melanoleuca transcription factor 12 (TCF12)	TCF12
Cluster-62068.57524	1.6205	0.000222	0.024174	transforming acidic coiled-coil-containing protein 2 (LOC101683250)	TACC2
Cluster-62068.103661	1.6168	0.000459	0.041087	Ailuropoda melanoleuca tectonic family member 1 (TCTN1)	TCTN1_3
Cluster-62068.101786	1.6162	0.000395	0.036778	spalt-like transcription factor 1 (SALL1)	SALL1
Cluster-62068.126285	1.6128	0.000301	0.030037	growth differentiation factor 7 (GDF7)	MYO5
Cluster-62068.140962	1.5984	2.70E-05	0.0047677	Odobenus rosmarus divergens peroxisomal trans-2-enoyl-CoA reductase (PECR)	PECR
Cluster-62068.82483	1.5976	2.52E-07	0.00010865	Canis lupus familiaris v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog (MYCL)	MYCL
Cluster-62068.131326	1.5969	7.89E-05	0.011091	Canis familiaris chromosome X	--
Cluster-62068.84267	1.5892	5.42E-07	0.00020905	Ailuropoda melanoleuca autophagy related 4C, cysteine peptidase (ATG4C)	ATG4
Cluster-62068.86748	1.5825	0.000356	0.03421	KIAA0513 ortholog (KIAA0513)	KIAA0513
Cluster-62068.134241	1.58	7.03E-05	0.010178	frizzled class receptor 1 (FZD1)	FZD1_7, fz

Cluster-62068.96643	1.5761	0.000509	0.044186	SECIS binding protein 2 (SECISBP2)	SECISBP2, SBP2
Cluster-62068.119097	1.5733	2.07E-10	2.45E-07	ring finger protein 170 (RNF170)	RNF170
Cluster-62068.95962	1.5701	0.000292	0.029439	ribosomal modification protein rimK-like family member B (RIMKLB), transcript variant X7	RIMKLB, NAAGS-I
Cluster-62068.140341	1.5695	0.000431	0.0391	Leptonychotes weddellii dynamin 3 (DNM3)	DNM
Cluster-62068.57054	1.569	0.000194	0.021952	Bos taurus TBC1 domain family(TBC1D24)	TBC1D24
Cluster-62068.83671	1.5639	2.30E-05	0.0042183	potassium channel tetramerization domain containing 12 (KCTD12)	KCTD12
Cluster-62068.48224	1.5637	7.21E-05	0.010376	solute carrier family 35(SLC35F2)	SLC35F2
Cluster-62068.94853	1.5587	0.000229	0.024729	clone CH237-505N16	--
Cluster-62068.90586	1.5578	0.000275	0.028235	neuronal cell adhesion molecule (NRCAM)6	NRCAM
Cluster-62068.147772	1.5549	0.000432	0.039157	dystrobrevin, alpha (DTNA)9	DTNA
Cluster-62068.90450	1.5532	0.000268	0.027733	Ursus maritimus phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2-like (LOC103677640)	--
Cluster-62068.87546	1.5524	7.62E-05	0.010786	glutamine--fructose-6-phosphate transaminase 1 (GFPT1)	GFPT1
Cluster-62068.67900	1.5493	0.000148	0.017856	Ursus maritimus major facilitator superfamily domain containing 2A (MFSD2A)	MFSD2A
Cluster-62068.74662	1.5493	0.000574	0.048352	leucine-rich pentatricopeptide repeat containing (LRPPRC)	LRPPRC
Cluster-62068.105145	1.5474	0.000541	0.046351	sushi-repeat containing protein (SRPX)	SRPX
Cluster-62068.88791	1.5457	2.16E-06	0.00064086	neuronal cell adhesion molecule (NRCAM)5	NRCAM
Cluster-62068.117878	1.5456	3.49E-05	0.0058958	RNA binding motif (RNP1, RRM) protein 3 (RBM3)	RBM3
Cluster-62068.129670	1.5395	0.000392	0.036655	lipid droplet associated hydrolase (LDAH)	LDAH
Cluster-62068.96484	1.5366	0.00045	0.0405	adenosine kinase (ADK)	ADK
Cluster-62068.87534	1.531	1.01E-05	0.0022084	protein NipSnap homolog 3A (LOC101678130)	--
Cluster-62068.94488	1.5205	0.000276	0.028293	Panthera tigris altaica procollagen C-endopeptidase enhancer (PCOLCE)	--
Cluster-62068.119316	1.5173	0.00013	0.016314	dipeptidase 1 (renal) (DPEP1)	DPEP

Cluster-62068.80042	1.5161	1.48E-06	0.00046806	nidogen 2 (osteonidogen) (NID2)	NID
Cluster-62068.96962	1.5086	0.000145	0.017643	collagen, type I, alpha 2 (COL1A2)	COL1AS
Cluster-62068.82777	1.5083	0.00024	0.025595	Odobenus rosmarus divergens SUN domain containing ossification factor (SUCO)	--
Cluster-62068.96867	1.5065	4.93E-05	0.0076743	uncharacterized LOC101674667 (LOC101674667)	--
Cluster-62068.85565	1.5031	2.08E-05	0.0039129	BAC clone RP11-779O18 from 5	DUSP, MKP
Cluster-62068.110854	1.4985	1.56E-05	0.003111	Felis catus solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15 (SLC25A15)	SLC25A15
Cluster-62068.82776	1.4982	9.35E-05	0.012623	Odobenus rosmarus divergens SUN domain containing ossification factor (SUCO)	SUCO
Cluster-62068.94385	1.4973	0.000565	0.047792	adenylosuccinate lyase (ADSL)	purB, ADSL
Cluster-62068.117653	1.4913	0.000118	0.015122	dihydrolipoamide dehydrogenase (DLD)	DLD, lpd, pdhD
Cluster-62068.124062	1.491	0.000392	0.036655	Ursus maritimus T-cell surface glycoprotein CD1b-like (LOC103672077)	CD1
Cluster-62068.96850	1.4895	5.06E-06	0.001277	ribosomal modification protein rimK-like family member B (RIMKLB)	RIMKLB, NAAGS-I
Cluster-62068.96964	1.4847	6.44E-05	0.0094846	collagen (COL1A2)	COL1AS
Cluster-62068.121967	1.4839	1.27E-07	6.20E-05	teneurin transmembrane protein 4 (TENM4)	TENM4
Cluster-62068.97743	1.4814	0.000391	0.036618	solute carrier family 31 (copper transporter)	SLC31A1
Cluster-62068.97147	1.4801	0.000575	0.048414	CD248 molecule, endosialin (CD248)	CD248, CD164L1
Cluster-62068.111282	1.4793	0.000545	0.046562	solute carrier family 7(SLC7A4)	SLC7A4
Cluster-62068.88381	1.4764	6.05E-06	0.0014658	solute carrier family 41 (magnesium transporter)	SLC41A
Cluster-62068.90115	1.467	1.43E-06	0.00045765	tubulin tyrosine ligase (TTL)	TTL
Cluster-62068.69294	1.4654	0.000285	0.0289	coagulation factor V (proaccelerin, labile factor) (F5)	F5
Cluster-62068.92571	1.4612	2.78E-05	0.0048732	sex hormone-binding globulin (SHBG)	SHBG
Cluster-62068.107646	1.4585	0.000549	0.046732	KIAA0513 ortholog (KIAA0513)	KIAA0513

Cluster-62068.119498	1.4476	3.94E-05	0.0064664	oxysterol binding protein-like 7	OSBPL7
Cluster-62068.83822	1.4427	3.59E-05	0.0060262	calcium/calmodulin-dependent protein kinase ID (CAMK1D)	CAMK1
Cluster-62068.80463	1.4425	0.000179	0.020605	glutathione peroxidase 8 (putative) (GPX8)	GPX8
Cluster-62068.106996	1.4401	0.000226	0.024515	activated leukocyte cell adhesion molecule (ALCAM)	ALCAM
Cluster-62068.99186	1.4395	4.89E-05	0.0076412	biglycan (BGN)	BGN
Cluster-62068.105674	1.439	0.000506	0.044007	neural cell adhesion molecule 1 (NCAM1)	NCAM
Cluster-62068.93147	1.4351	4.04E-06	0.0010656	ribosomal modification protein rimK-like family member B (RIMKLB)	RIMKLB, NAAGS-I
Cluster-62068.102645	1.4342	0.000353	0.034047	signal recognition particle 19kDa (SRP19)	SRP19
Cluster-62068.105166	1.434	3.28E-06	0.00090619	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase (EHHADH)	EHHADH
Cluster-62068.78550	1.4275	0.000102	0.013459	Leptonychotes weddellii activated leukocyte cell adhesion molecule (ALCAM)	--
Cluster-62068.112169	1.4193	0.000319	0.031348	JAZF zinc finger 1 (JAZF1)	JAZF1
Cluster-62068.91247	1.4082	0.000203	0.022702	myosin VC (MYO5C)	MYO5
Cluster-62068.93146	1.4072	4.20E-08	2.39E-05	ribosomal modification protein rimK-like family member B (RIMKLB)	RIMKLB
Cluster-62068.74670	1.4031	4.28E-05	0.0069244	chromosome unknown open reading frame, human C11orf54 (LOC101688598)	--
Cluster-62068.66826	1.4023	4.42E-06	0.0011454	alpha-2-macroglobulin-like 1 (A2ML1)	A2ML1
Cluster-62068.131695	1.4017	1.07E-05	0.002313	zinc finger protein 2 homolog (LOC101685904)	KRAB
Cluster-62068.90904	1.3976	7.28E-06	0.0017174	melanoma cell adhesion molecule (MCAM)	MCAM, CD146
Cluster-62068.90945	1.3795	4.81E-06	0.0012284	ribosomal modification protein rimK-like family member B (RIMKLB)	--
Cluster-62068.103516	1.3775	8.64E-11	1.16E-07	ribosomal modification protein rimK-like family member B (RIMKLB)	RIMKLB
Cluster-62068.97087	1.3746	0.000393	0.036668	cordon-bleu WH2 repeat protein-like 1 (COBLL1)	COBLL1
Cluster-62068.94112	1.3686	9.57E-05	0.012832	neural cell adhesion molecule 1 (NCAM1)	NCAM1
Cluster-62068.67929	1.3643	0.000474	0.041961	biglycan (BGN)	BGN

Cluster-62068.100238	1.3614	0.00029	0.029206	Ras suppressor protein 1 (RSU1)	RSU1
Cluster-62068.112347	1.3605	0.000414	0.037995	superkiller viralicidic activity 2-like (SKIV2L)	SKI2, SKIV2L
Cluster-62068.98125	1.3585	8.51E-08	4.42E-05	testin LIM domain protein (TES)	TES
Cluster-62068.87314	1.357	7.13E-11	9.69E-08	ribosomal modification protein rimK-like family member B (RIMKLB)	RIMKLB
Cluster-62068.60128	1.3567	7.67E-06	0.0017909	nidogen 2 (osteonidogen) (NID2)	NID
Cluster-62068.168191	1.3483	0.000181	0.020713	shugoshin-like 1 (SGOL1)	SGOL1
Cluster-62068.88474	1.3472	9.20E-05	0.012504	NACC family member 2, BEN and BTB (POZ) domain containing (NACC2)	BTBD14
Cluster-62068.95262	1.3469	4.47E-05	0.0071682	collagen, type III, alpha 1 (COL3A1)	COL1AS
Cluster-62068.59018	1.3443	5.79E-05	0.0087105	piggyBac transposable element derived 1 (PGBD1)	PGBD1
Cluster-62068.91748	1.3403	0.000393	0.036655	sorting nexin 18 (SNX18)	SNX9_18_33
Cluster-62068.75115	1.3383	0.000256	0.026821	chromosome unknown open reading frame, human C8orf58 (LOC101672066)	--
Cluster-62068.119757	1.3368	0.00043	0.039002	prolactin receptor (PRLR)	PRLR
Cluster-62068.130202	1.3364	0.000199	0.022316	prolactin receptor (PRLR)	PRLR
Cluster-62068.76244	1.3344	0.000235	0.025194	autophagy related 4C, cysteine peptidase (ATG4C)	ATG4
Cluster-62068.67389	1.3238	0.000398	0.037027	tetraspanin 13 (TSPAN13)	TSPAN13_31
Cluster-62068.103633	1.3224	3.43E-08	2.00E-05	palmitoyl-protein thioesterase 1 (PPT1)	PPT
Cluster-62068.97146	1.3192	0.000313	0.03093	CD248 molecule, endosialin (CD248)	CD248, CD164L1
Cluster-62068.94039	1.3178	0.000462	0.041282	actin, beta (ACTB)	ACTB_G1
Cluster-62068.100232	1.317	2.10E-08	1.33E-05	Ras suppressor protein 1 (RSU1)	RSU1
Cluster-62068.78548	1.3162	0.000393	0.036655	activated leukocyte cell adhesion molecule (ALCAM)	ALCAM
Cluster-62068.42263	1.3095	0.00012	0.015335	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	AUH
Cluster-62068.95741	1.3077	5.21E-05	0.008009	coenzyme Q10B (COQ10B)	COQ10
Cluster-62068.157555	1.3024	0.000276	0.028264	Pig DNA sequence from clone CH242-171I16 on chromosome 6	--
Cluster-62068.94335	1.3013	3.88E-05	0.0063872	collagen, type III, alpha 1 (COL3A1)	COL1AS
Cluster-62068.26866	1.2999	0.000193	0.021867	phosphodiesterase 7B (PDE7B)	PDE7

Cluster-62068.125742	1.2999	1.28E-06	0.00042095	basic, immunoglobulin-like variable motif containing (BIVM)	BIVM
Cluster-62068.130910	1.2945	1.23E-05	0.0025692	mitogen-activated protein kinase kinase kinase 13 (MAP3K13)	MAP3K13
Cluster-62068.92353	1.2896	0.000112	0.01449	collagen, type III, alpha 1 (COL3A1)	COL3A1
Cluster-62068.90647	1.2886	0.000173	0.020145	glutaminase (GLS)	glsA, GLS
Cluster-62068.99528	1.2865	3.07E-06	0.0008614	neuronal regeneration related protein (NREP)	NREP
Cluster-62068.122242	1.2749	0.00041	0.037876	multiple EGF-like-domains 9 (MEGF9)	MEGF9
Cluster-62068.99455	1.2736	4.97E-05	0.0077183	syncytin-1-like (LOC101693826)	--
Cluster-62068.79490	1.2729	2.21E-06	0.00065046	twisted gastrulation BMP signaling modulator 1 (TWSG1)	TWSG1
Cluster-62068.134592	1.2711	5.86E-05	0.0088023	SET binding factor 2 (SBF2)	SBF1_2, MTMR5_13
Cluster-62068.115078	1.2668	4.69E-05	0.0073888	Condylura cristata spalt-like transcription factor 1 (SALL1)	SALL1
Cluster-62068.112583	1.2667	0.00053	0.04561	protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	PACSIN2
Cluster-62068.98411	1.2593	0.000462	0.041282	tetraspanin 1 (TSPAN1)	TSPAN1
Cluster-62068.62872	1.2577	0.000132	0.016487	X-prolyl aminopeptidase (aminopeptidase P)	XPNPEP2
Cluster-62068.127778	1.2547	5.94E-06	0.0014567	sodium channel, voltage gated, type III alpha subunit (SCN3A)	SCN3A
Cluster-62068.127997	1.2518	3.47E-06	0.00094998	cyclin and CBS domain divalent metal cation transport mediator 4 (CNNM4)	CNNM
Cluster-62068.55687	1.2479	7.57E-05	0.010753	Pan troglodytes frizzled class receptor 3 (FZD3)	FZD3
Cluster-62068.108508	1.2465	2.52E-05	0.0045276	chromosome unknown open reading frame, human C14orf80 (LOC101681451)	C14orf80
Cluster-62068.66502	1.2443	4.98E-05	0.007733	lymphocyte cytosolic protein 1 (L-plastin) (LCP1)	LCP1, PLS2
Cluster-62068.94800	1.2369	0.000546	0.046578	transmembrane 9 superfamily member 3 (TM9SF3)	TM9SF3
Cluster-62068.67673	1.2366	0.000111	0.014379	phosphoserine phosphatase (PSPH)	serB, PSPH
Cluster-62068.96716	1.2348	0.000179	0.020627	lumican (LUM)	LUM
Cluster-62068.96206	1.23	0.000282	0.028715	Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130020O11 product:procollagen, type III, alpha 1,	COL1A5

				full insert sequence	
Cluster-62068.104418	1.2286	6.56E-05	0.0096318	squamous cell carcinoma antigen recognized by T cells 3 (SART3)	--
Cluster-62068.70770	1.2285	0.000193	0.021844	basic helix-loop-helix family, member a15 (BHLHA15)	BHLHB8, MIST1
Cluster-62068.147937	1.2279	0.000417	0.038181	dysferlin (DYSF)6	DYSF
Cluster-62068.94234	1.2263	4.24E-06	0.0011109	gem (nuclear organelle) associated protein 6 (GEMIN6)	GEMIN6
Cluster-62068.93617	1.2258	4.59E-05	0.0072919	solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6 (SLC5A6)	SLC5A6, SMVT
Cluster-62068.116420	1.2198	9.14E-05	0.012464	exportin 5 (XPO5)	XPO5
Cluster-62068.92681	1.2198	0.000319	0.031348	transforming growth factor, beta 2 (TGFB2)	TGFB2
Cluster-62068.112622	1.2163	0.000204	0.022705	patatin-like phospholipase domain containing 8 (PNPLA8)	PNPLA8
Cluster-62068.71969	1.2129	0.000108	0.014166	DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9)	DNAJB9
Cluster-62068.135515	1.2115	4.61E-06	0.0011895	bone morphogenetic protein receptor, type IB (BMPRI1B)	BMPRI1B, ALK6
Cluster-62068.83916	1.2048	0.000294	0.029554	transmembrane protein 245 (TMEM245)	TMEM245
Cluster-62068.98172	1.1917	0.000469	0.041688	CDC-like kinase 1 (CLK1)	CLK
Cluster-62068.96889	1.1893	6.98E-06	0.0016626	protein tyrosine phosphatase, receptor type, F (PTPRF), transcript variant X4	PTPRF, LAR
Cluster-62068.90188	1.1882	1.61E-06	0.00049893	Leptonychotes weddellii integrin beta 1 binding protein (melusin) 2 (ITGB1BP2)	NONO, NRB54
Cluster-62068.89639	1.1847	2.90E-05	0.0050673	myosin light chain kinase (MYLK)	MYLK
Cluster-62068.110238	1.1785	0.000289	0.029188	coproporphyrinogen oxidase (CPOX)	CPOX, hemF
Cluster-62068.114833	1.1696	0.000503	0.043831	Canis lupus familiaris DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX46)	DDX46, PRP5
Cluster-62068.133689	1.1692	5.80E-06	0.001429	Canis lupus familiaris nudix (nucleoside diphosphate linked moiety X)-type motif 12 (NUDT12)	NUDT12, nudC
Cluster-62068.65695	1.1661	2.90E-05	0.0050687	chromosome unknown open reading frame, human C9orf72 (LOC101687732)	C9orf72
Cluster-62068.106457	1.1645	0.000494	0.043352	collagen, type V, alpha 2 (COL5A2)	COL1A5

Cluster-62068.104102	1.1587	0.000173	0.020145	FIC domain containing (FICD)	FICD
Cluster-62068.133924	1.1546	7.11E-06	0.0016858	GrpE-like 2, mitochondrial (E. coli) (GRPEL2)	GRPE
Cluster-62068.111438	1.1429	0.000145	0.017573	solute carrier family 39, member 11 (SLC39A11)	SLC39A11, ZIP11
Cluster-62068.129357	1.1418	0.00013	0.01629	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (SEMA4G)	SEMA4
Cluster-62068.87459	1.1394	0.000252	0.026575	heat-responsive protein 12 (HRSP12)	HRSP12
Cluster-62068.106523	1.1367	4.91E-05	0.0076596	sorting nexin 2 (SNX2)	SNX1_2
Cluster-62068.70996	1.1327	4.32E-06	0.0011253	URB2 ribosome biogenesis 2 homolog (S. cerevisiae) (URB2)	URB2
Cluster-62068.123631	1.1324	3.57E-05	0.0060081	zinc finger, DHHC-type containing 13 (ZDHHC13)	ZDHHC
Cluster-62068.119758	1.1278	6.22E-05	0.0092356	prolactin receptor (PRLR)	PRLR
Cluster-62068.78251	1.1269	0.000187	0.021314	nuclear transport factor 2-like export factor 2 (NXT2)	NXT2
Cluster-62068.63278	1.1265	0.000384	0.036108	haloacid dehalogenase-like hydrolase domain containing 2 (HDHD2)	HDHD2
Cluster-62068.96791	1.1244	8.82E-05	0.0121	tropomyosin 1 (alpha) (TPM1)5	TPM1
Cluster-62068.70838	1.1239	3.25E-06	0.00090384	lipase, endothelial (LIPG)	LIPG
Cluster-62068.96255	1.1055	5.61E-06	0.001389	Odobenus rosmarus divergens sphingosine-1-phosphate phosphatase 1 (SGPP1)	SGPP1
Cluster-62068.94920	1.105	0.00054	0.046254	Ursus maritimus galactokinase 2 (GALK2)	GALK2
Cluster-62068.83861	1.0996	0.000115	0.01483	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3 (SLC5A3)	SLC5A3
Cluster-62068.108292	1.0931	6.59E-05	0.0096611	Felis catus glypican 6 (GPC6)	GPC6
Cluster-62068.39780	1.0929	0.000119	0.015252	Leptonychotes weddellii IKBKB interacting protein (IKBIP)	IKBIP
Cluster-62068.88170	1.0903	0.000113	0.014616	rhophilin, Rho GTPase binding protein 2 (RHPN2)	RHPN2
Cluster-62068.86408	1.0885	8.62E-06	0.0019731	Pig DNA sequence from clone CH242-78D20 on chromosome X	--
Cluster-62068.137425	1.0877	0.000253	0.026609	RIO kinase 3 (RIOK3)	RIOK3, SUDD
Cluster-62068.62098	1.0838	3.48E-05	0.0058916	kelch-like family member 18 (KLHL18)	KLHL18

Cluster-62068.72702	1.0832	9.76E-06	0.0021562	FUN14 domain containing 1 (FUNDC1)	FUNDC1
Cluster-62068.82383	1.0789	7.99E-05	0.011169	chromosome unknown open reading frame, human C9orf41 (LOC101692030)	--
Cluster-62068.74030	1.0673	1.50E-05	0.0030116	potassium channel, two pore domain subfamily K, member 6 (KCNK6)	KCNK6
Cluster-62068.121704	1.0529	0.000352	0.03396	solute carrier family 7 (SLC7A1)	SLC7A1
Cluster-62068.96397	1.0517	0.000478	0.042185	tumor suppressor candidate 3 (TUSC3)	OST3, OST6
Cluster-62068.58741	1.0352	0.000246	0.026112	cyclin G2 (CCNG2)	CCNG2
Cluster-62068.92721	1.0289	9.97E-05	0.013248	GTPase activating protein (SH3 domain) binding protein 2 (G3BP2)	G3BP2
Cluster-62068.125021	1.0256	0.000578	0.048665	Odobenus rosmarus divergens rab GTPase-activating protein 1-like, isoform 10 (LOC101363017)	--
Cluster-62068.71703	1.025	4.10E-09	3.39E-06	aconitase 1, soluble (ACO1)	ACO, acnA
Cluster-62068.91157	1.0207	2.94E-05	0.0051305	Ailuropoda melanoleuca spalt-like transcription factor 4 (SALL4)	SALL4
Cluster-62068.92209	1.0202	0.000224	0.024382	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta (YWHAQ)	YWHAB_Q_Z
Cluster-62068.83814	1.0141	0.000207	0.022951	Sus scrofa transitional endoplasmic reticulum ATPase-like (LOC100516776)	VCP, CDC48
Cluster-62068.94099	1.0015	0.000546	0.046588	trafficking protein particle complex 11 (TRAPPC11)	TRAPPC11
Cluster-62068.86649	1.0007	0.00021	0.023223	Canis familiaris, clone XX-237B24	--
Cluster-62068.77803	0.99863	0.000165	0.01955	forkhead box A2 (FOXA2)	FOXA2, HNF3B
Cluster-62068.132943	0.99564	0.000309	0.030624	uncharacterized LOC106005084 (LOC106005084)	--
Cluster-62068.82625	0.99501	0.000527	0.045436	calcineurin-like EF-hand protein 1 (CHP1)	CHP, CHP1
Cluster-62068.103568	0.99025	0.000314	0.030961	3-hydroxy-3-methylglutaryl-CoA reductase (HMGCR)	HMGCR
Cluster-62068.101785	0.98758	4.80E-05	0.007538	Ailuropoda melanoleuca spalt-like transcription factor 1 (SALL1)	SALL1
Cluster-62068.107172	0.97732	9.42E-05	0.01268	acyl-CoA synthetase long-chain family member 4 (ACSL4)	ACSL, fadD
Cluster-62068.84549	0.96456	0.000585	0.049108	translocated promoter region, nuclear basket protein (TPR)	TPR, MLP1, MLP2
Cluster-62068.103711	0.96236	0.00013	0.016289	Ursus maritimus low density lipoprotein receptor-related protein 2 (LRP2)	LRP2

Cluster-62068.131545	0.95801	0.000314	0.030961	helicase, lymphoid-specific (HELLS)	HELLS, DDM1
Cluster-62068.74607	0.94626	0.000366	0.034905	protein NipSnap homolog 3A (LOC101679135)	--
Cluster-62068.99661	0.94349	0.000521	0.045085	pyruvate dehydrogenase kinase, isozyme 1 (PDK1)	PDK1
Cluster-62068.76167	0.93668	0.0001	0.013322	tetratricopeptide repeat domain 39A (TTC39A)	TTC39A
Cluster-62068.109041	0.93027	8.54E-05	0.011808	G protein-coupled receptor kinase interacting ArfGAP 1 (GIT1)	GIT1
Cluster-62068.83847	0.92311	0.000188	0.021388	epithelial splicing regulatory protein 2 (ESRP2)	ESRP1_2
Cluster-62068.65154	0.91807	0.000118	0.015151	Odobenus rosmarus divergens JAZF zinc finger 1 (JAZF1)	JAZF1
Cluster-62068.55983	0.91522	0.00037	0.035257	polymerase (RNA) III (DNA directed) polypeptide E (80kD) (POLR3E)	RPC5, POLR3E
Cluster-62068.104356	0.9131	0.00038	0.035916	pleiotrophin (PTN)	PTN
Cluster-62068.111992	0.90988	0.000508	0.044108	protein tyrosine phosphatase, receptor type, D (PTPRD)3	PTPRD
Cluster-62068.106706	0.88662	1.10E-05	0.0023572	Felis catus RAB GTPase activating protein 1-like (RABGAP1L)	RABGAP1L
Cluster-62068.121796	0.86341	0.000553	0.047	phosphatidylinositol 3-kinase, catalytic subunit type 3 (PIK3C3)	PIK3C3, VPS34
Cluster-62068.89954	0.84741	1.82E-05	0.003528	myosin ID (MYO1D)	MYO1
Cluster-62068.96914	0.82964	0.000503	0.043814	nudE neurodevelopment protein 1 (NDE1)	NDE1, NUDE
Cluster-62068.121618	0.81405	0.000224	0.024382	Leptonychotes weddellii WW domain containing E3 ubiquitin protein ligase 1 (WWP1)	AIP5, WWP1
Cluster-62068.94691	0.80915	0.000407	0.037744	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic (CMPK1)	CMPK1, UMPK
Cluster-62068.70730	0.80084	0.000191	0.021651	staufer double-stranded RNA binding protein 1 (STAU1)	STAU
Cluster-62068.131267	0.79407	0.000201	0.022534	Felis catus cyclin C (CCNC)	CCNC
Cluster-62068.135883	0.79173	0.000109	0.014203	microtubule-associated protein 9 (MAP9)	MAP9
Cluster-62068.109915	0.76564	7.53E-05	0.010717	iron-responsive element binding protein 2 (IREB2)	IREB2
Cluster-62068.114752	0.76092	0.000581	0.048781	acyl-CoA dehydrogenase, C-4 to C-12 straight chain (ACADM)	ACADM, acd
Cluster-62068.68527	0.75139	0.000575	0.048414	Ursus maritimus insulin-degrading enzyme (IDE)	IDE, ide
Cluster-62068.74211	0.73249	8.68E-06	0.0019805	Leptonychotes weddellii cell division cycle 14A (CDC14A)	CDC14
Cluster-62068.72018	0.72973	0.000588	0.049209	zinc finger and SCAN domain containing 29 (ZSCAN29)	KRAB

Cluster-62068.99656	0.6981	0.000412	0.037912	GRAM domain containing 1B (GRAMD1B)	GRAMD1B
Cluster-62068.105471	-0.5629	0.000569	0.048108	signal-regulatory protein alpha (SIRPA)	SIRPA
Cluster-62068.96260	-0.7567	5.13E-05	0.0079259	odd-skipped related transcription factor 2 (OSR2)	OSR, ODD
Cluster-62068.111828	-0.8103	5.36E-05	0.0082006	odd-skipped related transcription factor 2 (OSR2)	OSR, ODD
Cluster-62068.121058	-0.8196	4.65E-05	0.0073499	Leptonychotes weddellii wingleless-type MMTV integration site family, member 5A (WNT5A)	WNT11
Cluster-62068.77697	-0.8322	0.000414	0.037995	transforming growth factor, beta receptor III (TGFB3)	TGFB3
Cluster-62068.96413	-0.8348	0.000461	0.041206	retrotransposon gag domain containing 4 (RGAG4)	RGAG4
Cluster-62068.120738	-0.916	0.000294	0.029554	thrombospondin 2 (THBS2)	THBS2S
Cluster-62068.82287	-0.925	0.00057	0.048151	RNA binding motif protein 23 (RBM23)	RBM23
Cluster-62068.45619	-0.9652	8.21E-05	0.011405	Ursus maritimus plexin domain containing 2 (PLXDC2), misc_RNA	PLXDC2
Cluster-62068.86089	-0.9679	0.000411	0.037912	CD74 molecule, major histocompatibility complex, class II invariant chain (CD74)	CD74, DHLAG
Cluster-62068.109962	-0.99	0.000411	0.037912	desmoglein 2 (DSG2)	DSG2
Cluster-62068.112601	-1.0027	2.43E-06	0.00070011	F-box protein 32 (FBXO32)	FBXO25_32
Cluster-62068.119569	-1.0171	2.48E-05	0.004474	uncharacterized LOC106004563 (LOC106004563)	--
Cluster-62068.29075	-1.0298	1.46E-05	0.0029598	DNA-damage-inducible transcript 4-like (DDIT4L)	DDIT4L
Cluster-62068.59484	-1.0687	0.00013	0.016336	Odobenus rosmarus divergens tumor necrosis factor (ligand) superfamily, member 12 (TNFSF12)	TNFSF12, TWEAK
Cluster-62068.109190	-1.0701	0.000363	0.034747	solute carrier family 7 (amino acid transporter light chain, bo,+ system), member 9 (SLC7A9)	SLC7A9, BAT1
Cluster-62068.67730	-1.0703	4.84E-05	0.0075952	natriuretic peptide receptor 1 (NPR1)	ANPRA, NPR1
Cluster-62068.35410	-1.0744	0.000132	0.016512	Nance-Horan syndrome(NHS)	NHS
Cluster-62068.56604	-1.0768	0.000308	0.030541	Leptonychotes weddellii zinc finger protein 717 (ZNF717)	KRAB
Cluster-62068.116265	-1.0882	0.000321	0.031453	F-box protein 32 (FBXO32)	FBXO25_32

Cluster-62068.131785	-1.1202	0.00029	0.029206	aminomethyltransferase (AMT)	gcvT, AMT
Cluster-62068.108960	-1.1372	0.000278	0.028463	KN motif and ankyrin repeat domains 2 (KANK2)	KANK2
Cluster-62068.46338	-1.1442	8.86E-05	0.012143	histamine receptor H1 (HRH1)	HRH1
Cluster-62068.110053	-1.1758	0.00046	0.041102	lysine (K)-specific methyltransferase 2E (KMT2E)	KMT2E
Cluster-62068.134171	-1.1772	3.84E-06	0.0010236	leucine-rich repeat containing G protein-coupled receptor 5 (LGR5)	LGR5, GPR49
Cluster-62068.98293	-1.1949	0.000118	0.015112	filamin A, alpha (FLNA)	FLNA
Cluster-62068.88738	-1.1979	0.000141	0.017264	trypsin domain containing 1 (TYSND1)	TYSND1
Cluster-62068.163425	-1.1981	5.51E-05	0.0083748	B-cell CLL/lymphoma 2 (BCL2)	BCL2
Cluster-62068.94683	-1.2114	3.58E-06	0.00097064	integrin, beta 4 (ITGB4)	ITGB4
Cluster-62068.92707	-1.2156	0.000247	0.026215	Fanconi anemia, complementation group G (FANCG)	FANCG
Cluster-62068.63929	-1.2279	1.19E-06	0.00039949	transmembrane protein 200C (TMEM200C)	TMEM200C
Cluster-62068.59733	-1.2301	0.000389	0.036452	lipase A, lysosomal acid, cholesterol esterase (LIPA)	LIPA
Cluster-62068.103536	-1.239	0.000464	0.041418	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	ABCC5
Cluster-62068.86742	-1.2607	0.000233	0.025106	HOP homeobox (HOPX)	HOPX
Cluster-62068.130035	-1.2665	0.000211	0.023223	fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10)	FUT10
Cluster-62068.56789	-1.2711	0.000438	0.03961	Canis lupus familiaris mitochondrial ribosome recycling factor (MRRF)	COL4A
Cluster-62068.156657	-1.2926	0.000124	0.015688	solute carrier family 7 (amino acid transporter light chain, bo,+ system), member 9 (SLC7A9)	SLC7A9
Cluster-62068.114313	-1.3021	7.90E-09	5.80E-06	adrenergic, alpha-2C-, receptor (ADRA2C) gene	ADRA2C
Cluster-62068.169907	-1.3046	1.59E-06	0.00049462	phospholipase A2, group IID (PLA2G2D)	PLA2G, SPLA2
Cluster-62068.92330	-1.3082	0.000409	0.037857	integrin, beta 8 (ITGB8), transcript variant X6	ITGB8
Cluster-62068.121404	-1.3195	5.46E-05	0.0083261	progesterone receptor (PGR)	NR3C3, PGR
Cluster-62068.111388	-1.3295	0.000116	0.014953	collagen, type XXVII, alpha 1 (COL27A1)	COL1A5
Cluster-62068.52307	-1.382	1.53E-05	0.0030707	transmembrane protein 200C (TMEM200C)	TMEM200C
Cluster-62068.130666	-1.3837	0.000212	0.023307	dishevelled associated activator of morphogenesis 1 (DAAM1)	DAAM

Cluster-62068.141260	-1.3959	0.000457	0.040926	Ovis canadensis canadensis isolate 43U chromosome 14 sequence	--
Cluster-62068.126402	-1.4167	0.000187	0.021314	Pongo abelii BAC clone CH276-451O22 from chromosome 14	--
Cluster-62068.61596	-1.4324	2.15E-05	0.0039976	insulin-like growth factor binding protein 3 (IGFBP3)	--
Cluster-62068.159147	-1.434	0.000276	0.028264	benzodiazepine receptor (peripheral) associated protein 1 (BZRAP1)1	--
Cluster-62068.100858	-1.4365	2.03E-06	0.00061114	complement component 4A (Rodgers blood group) (C4A)	C4
Cluster-62068.113945	-1.4397	0.000172	0.02014	chromosome unknown open reading frame, human C16orf58 (LOC101670422)	--
Cluster-62068.170910	-1.4433	7.82E-06	0.0018198	calcium/calmodulin-dependent protein kinase IG (CAMK1G)	CAMK1
Cluster-62068.56307	-1.4441	4.56E-05	0.00725	glycerol-3-phosphate dehydrogenase 1 (soluble) (GPD1)	GPD1
Cluster-62068.93829	-1.4472	0.000458	0.041032	HOP homeobox (HOPX)	HOPX
Cluster-62068.141259	-1.4479	0.000579	0.048665	Ovis canadensis canadensis isolate 43U chromosome 14 sequence	--
Cluster-62068.39755	-1.4512	0.000552	0.046917	cap methyltransferase 1 (CMTR1)1	CMTR1, FTSJD2, MTR1
Cluster-62068.139945	-1.4548	8.15E-08	4.25E-05	EGF containing fibulin-like extracellular matrix protein 1 (EFEMP1)	EFEMP1, FBLN3
Cluster-62068.113109	-1.4568	1.48E-05	0.0029874	spectrin repeat containing, nuclear envelope 1 (SYNE1)	SYNE1
Cluster-62068.30092	-1.4673	6.60E-05	0.0096704	glutamate-rich 3 (ERICH3)	ERICH3
Cluster-62068.81105	-1.4808	0.000142	0.017274	signal transducer and activator of transcription 5B (STAT5B)	STAT5A
Cluster-62068.106868	-1.4839	8.13E-05	0.011342	CD44 molecule (Indian blood group) (CD44)5	CD44
Cluster-62068.143608	-1.488	0.000309	0.030624	laminin, alpha 3 (LAMA3)	LAMA3_5
Cluster-62068.10562	-1.5003	0.000281	0.028605	WD repeat domain 90 (WDR90)	WDR90
Cluster-62068.98045	-1.5037	0.000253	0.026575	achalasia, adrenocortical insufficiency, alacrimia (AAAS)	AAAS
Cluster-62068.32574	-1.5047	5.57E-05	0.0084387	ankyrin repeat domain 6 (ANKRD6)	ANKRD6
Cluster-62068.47861	-1.5155	2.33E-06	0.00067763	OTU deubiquitinase 1 (OTUD1)	OTUD1
Cluster-62068.61815	-1.535	0.000491	0.043099	Felis catus clone RP86-117J4	--
Cluster-62068.106867	-1.5521	3.66E-10	3.90E-07	Canis lupus familiaris CD44 molecule (Indian blood group) (CD44)	CD44

Cluster-62068.134116	-1.5584	0.000446	0.040166	protein phosphatase 6, regulatory subunit 1 (PPP6R1)	PPP6R1, SAPS1
Cluster-59433.0	-1.5624	0.000511	0.044355	genomic DNA, chromosome 18 clone:RP11-793A3	--
Cluster-62068.46253	-1.5695	0.000499	0.043678	leucine-rich repeat containing G protein-coupled receptor 5 (LGR5)	LGR5, GPR49
Cluster-62068.103706	-1.5743	7.32E-06	0.0017245	MAS-related GPR, member F (MRGPRF), transcript variant X7	MRGPRF
Cluster-62068.130867	-1.5749	3.41E-07	0.00013944	Felis catus BAC clone FCAB-33H12 from chromosome unknown	--
Cluster-62068.136476	-1.5835	0.000252	0.026575	mucin 16, cell surface associated (MUC16)3	MUC16
Cluster-62068.47860	-1.5996	1.98E-07	8.96E-05	Odobenus rosmarus divergens OTU deubiquitinase 1 (OTUD1)	OTUD1
Cluster-62068.77058	-1.6007	3.73E-05	0.0062056	synaptotagmin X (SYT10)	--
Cluster-62068.108961	-1.6009	0.000276	0.028293	KN motif and ankyrin repeat domains 2 (KANK2)	KANK2
Cluster-62068.138269	-1.6039	0.000166	0.019591	SAP30 binding protein (SAP30BP)	SAP30BP
Cluster-62068.105692	-1.606	0.000539	0.046254	plexin D1 (PLXND1)	PLXND
Cluster-62068.93226	-1.6174	9.70E-06	0.0021443	MAP-kinase activating death domain (MADD)	MADD
Cluster-62068.78941	-1.6303	2.01E-05	0.0038158	tubulin tyrosine ligase-like family member 3 (TTLL3)	TTLL3_8
Cluster-62068.77876	-1.6401	3.00E-05	0.0052248	peptidase domain containing associated with muscle regeneration 1 (PAMR1)	PAMR1
Cluster-62068.123202	-1.6409	0.00056	0.047413	Ailuropoda melanoleuca uncharacterized LOC105236424 (LOC105236424)	--
Cluster-62068.124657	-1.652	2.36E-05	0.0042933	Ursus maritimus plexin domain containing 1 (PLXDC1)	PLXDC1
Cluster-62068.85496	-1.6636	0.000494	0.043352	RAS protein activator like 1 (GAP1 like) (RASAL1)	RASAL1
Cluster-62068.24520	-1.6686	9.21E-05	0.012504	solute carrier family 6 , member 20 (SLC6A20)	SLC6A20
Cluster-62068.134801	-1.6709	0.000514	0.044553	WD repeat domain 66 (WDR66), RefSeqGene on chromosome 12	WDR66
Cluster-62068.64862	-1.6724	0.000216	0.023669	BARX homeobox 2 (BARX2)	BARX
Cluster-62068.106076	-1.6846	7.46E-05	0.010631	integrin, beta 4 (ITGB4), transcript variant X4	ITGB4
Cluster-62068.108579	-1.6851	1.84E-06	0.00055889	Pongo abelii progesterone receptor (PGR)	PGR
Cluster-62068.116157	-1.6929	0.000227	0.024526	leucine-rich repeat containing G protein-coupled receptor 5 (LGR5)	LGR5, GPR49
Cluster-62068.63550	-1.7203	5.44E-06	0.0013633	Ailuropoda melanoleuca zinc finger protein 692 (ZNF692)	ZNF692
Cluster-62068.31434	-1.739	0.000174	0.020215	glutamate-rich 3 (ERICH3)	ERICH3

Cluster-62068.183579	-1.7517	1.82E-06	0.00055331	FAT atypical cadherin 3 (FAT3)	FAT3
Cluster-62068.125025	-1.7562	0.000233	0.025079	K(lysine) acetyltransferase 2A (KAT2A)	PCAF, KAT2, GCN5
Cluster-62068.126277	-1.7753	6.27E-05	0.009281	toll-like receptor 4 (TLR4)	--
Cluster-62068.104135	-1.7779	0.000294	0.029553	TraB domain containing 2B (TRABD2B)	TRABD2B
Cluster-62068.74732	-1.801	1.43E-06	0.00045765	angel homolog 1 (Drosophila) (ANGEL1)	ANGEL
Cluster-62068.13319	-1.8148	0.000274	0.028166	pleckstrin homology domain containing, family S member 1 (PLEKHS1)	PLEKHS1
Cluster-62068.71602	-1.8165	0.000284	0.028802	chromosome unknown open reading frame, human C10orf10 (LOC101689972)	C10orf10
Cluster-62068.61809	-1.8306	9.37E-06	0.0021036	Ailuropoda melanoleuca ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3)	ABCC3
Cluster-62068.57750	-1.8386	0.00023	0.02474	Ovis canadensis canadensis isolate 43U chromosome 15 sequence	--
Cluster-62068.50958	-1.8457	2.50E-05	0.0045057	ceruloplasmin (ferroxidase) (CP)	CP
Cluster-62068.149607	-1.8708	0.000592	0.049468	synaptojanin 2 (SYNJ2)	SYNJ2
Cluster-62068.61200	-1.8791	9.51E-05	0.01277	haplotype 1 alpha2C adrenergic receptor (ADRA2C) gene	ADRA2C
Cluster-62068.85145	-1.8806	6.41E-05	0.0094592	CD44 molecule (Indian blood group) (CD44)	CD44
Cluster-62068.58800	-1.9072	0.000525	0.04529	proline and serine rich 2 (PROSER2)	PROSER2
Cluster-62068.167517	-1.9092	0.000113	0.014574	odd-skipped related 1 (Drosophila) (OSR1) gene	OSR1
Cluster-62068.16781	-1.9105	9.86E-06	0.0021647	glutamate-rich 3 (ERICH3)	--
Cluster-62068.47859	-1.9265	3.64E-05	0.0060805	Human DNA sequence from clone RP11-426A21 on chromosome 10	--
Cluster-62068.51321	-1.9271	2.70E-06	0.00076604	Odobenus rosmarus divergens intraflagellar transport 172 (IFT172)	IFT172
Cluster-62068.63646	-1.9326	0.000113	0.014616	immunoglobulin superfamily, DCC subclass, member 4 (IGDCC4)	IGDCC4
Cluster-62068.146190	-1.9373	2.75E-05	0.0048427	cytochrome P450 4A11 (LOC101674954)	CYP4A11
Cluster-62068.143430	-1.9406	2.02E-06	0.00060713	ADAM metallopeptidase domain 33 (ADAM33)1	ADAM33
Cluster-62068.121033	-1.9428	2.19E-05	0.0040562	FXYP domain containing ion transport regulator 1 (FXYP1)	FXYP1, PLM

Cluster-62068.125195	-1.9449	4.01E-11	5.88E-08	neuronal guanine nucleotide exchange factor (NGEF)	NGEF, EPHEXIN
Cluster-62068.125193	-1.9503	0.000141	0.017264	plexin A2 (PLXNA2)	PLXNA
Cluster-62068.131048	-1.9649	1.31E-05	0.0027109	family with sequence similarity 160, member B1 (FAM160B1)	--
Cluster-62068.17263	-1.9683	0.000183	0.020885	Ovis canadensis canadensis isolate 43U chromosome 19 sequence	--
Cluster-62068.40461	-1.9896	3.12E-05	0.0053979	Odobenus rosmarus divergens neuronal guanine nucleotide exchange factor (NGEF)	NGEF, EPHEXIN
Cluster-62068.45543	-2.0173	5.59E-05	0.0084559	uncharacterized LOC106004170 (LOC106004170)	--
Cluster-62068.73913	-2.0375	4.51E-10	4.72E-07	CD44 molecule (Indian blood group) (CD44)	CD44
Cluster-62068.26807	-2.0528	7.01E-05	0.010153	chromosome unknown open reading frame, human C1orf168 (LOC101670515)	--
Cluster-62068.88810	-2.0538	1.42E-05	0.0028945	CLK4-associating serine/arginine rich protein (CLASRP)	SFRS16
Cluster-62068.125769	-2.0546	4.97E-06	0.0012594	ceruloplasmin (ferroxidase) (CP)	CP
Cluster-62068.155328	-2.0548	0.00018	0.020648	ADAMTS-like 4 (ADAMTSL4)	ADAMTSL4
Cluster-62068.101612	-2.0606	0.000158	0.018826	Sus scrofa CGRP receptor component (CRCP)	CRCP
Cluster-62068.58226	-2.0718	1.16E-07	5.81E-05	Rhinolophus ferrumequinum retrovirus isolate RfRV	--
Cluster-62068.65080	-2.0729	2.23E-09	1.96E-06	MMS19 cytosolic iron-sulfur assembly component (MMS19)	MET18, MMS19
Cluster-62068.125196	-2.0896	3.50E-07	0.00014226	plexin A2 (PLXNA2)	PLXNA2
Cluster-62068.53401	-2.0955	0.000251	0.026502	IKAROS family zinc finger 4 (Eos) (IKZF4)1	IKZF, ZNFN1A
Cluster-62068.77354	-2.1071	9.18E-05	0.012491	complement component 4A (Rodgers blood group) (C4A)	C4
Cluster-62068.34910	-2.1277	1.29E-05	0.0026899	peptidyl arginine deiminase(PADI2)	--
Cluster-62068.86915	-2.1456	0.000417	0.038181	G protein-coupled receptor 161 (GPR161)	GPR161
Cluster-62068.48665	-2.1598	3.52E-06	0.00095769	pleiomorphic adenoma gene-like 1 (PLAGL1)	PLAGL1
Cluster-62068.20770	-2.1695	0.00017	0.019938	Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10)	ARHGEF10
Cluster-62068.112980	-2.1803	0.000324	0.031707	steroid 21-hydroxylase (LOC101689319)	TN
Cluster-62068.57805	-2.1829	0.000555	0.047071	Odobenus rosmarus divergens RAS protein activator like 1 (RASAL1)	RASAL1

Cluster-62068.102115	-2.1922	0.000585	0.049108	lon peptidase 1 (LONP1)	PRSS15, PIM1
Cluster-62068.157520	-2.1931	1.99E-07	8.97E-05	Ailuropoda melanoleuca prokineticin 2 (PROK2)	PROK2
Cluster-62068.61599	-2.2047	3.55E-05	0.0059767	insulin-like growth factor binding protein 3 (IGFBP3)	IGFBP3
Cluster-62068.96059	-2.2147	7.47E-05	0.010634	proline rich membrane anchor 1 (PRIMA1)	SEPT3_9_12
Cluster-62068.116118	-2.2268	1.08E-05	0.0023245	T-cell, immune regulator 1, ATPase, H ⁺ transporting, lysosomal V0 subunit A3 (TCIRG1)	ATPeV0A, ATP6N
Cluster-62068.164291	-2.2268	0.000234	0.025112	uncharacterized LOC101679780 (LOC101679780)	--
Cluster-62068.69758	-2.2294	1.15E-07	5.80E-05	Leptonychotes weddellii insulin-like growth factor-binding protein 3-like (LOC102738536)	--
Cluster-62068.97727	-2.2382	3.82E-05	0.0063015	RIMS binding protein 2 (RIMBP2)	RIMBP2
Cluster-62068.17620	-2.2382	6.45E-05	0.0094903	chromosome unknown open reading frame, human C1orf168 (LOC101670515)	--
Cluster-62068.308	-2.2503	0.000136	0.016866	Canis lupus familiaris uncharacterized LOC102155364 (LOC102155364), misc_RNA	--
Cluster-62068.100587	-2.2541	1.57E-05	0.0031311	uncharacterized LOC101689364 (LOC101689364)	--
Cluster-62068.76123	-2.2545	1.40E-09	1.31E-06	NDRG family member 2 (NDRG2)	NDRG2
Cluster-62068.118731	-2.2753	0.000183	0.020943	actin binding LIM protein family (ABLIM2)4	ABLIM
Cluster-62068.28639	-2.2827	0.000155	0.018479	polypeptide N-acetylgalactosaminyltransferase 15 (GALNT15)	GALNT
Cluster-62068.125194	-2.2856	1.58E-05	0.0031423	neuronal guanine nucleotide exchange factor (NGEF)	NGEF, EPHEXIN
Cluster-62068.121405	-2.2912	2.10E-08	1.33E-05	progesterone receptor (PGR)	NR3C3, PGR
Cluster-62068.34908	-2.294	1.88E-05	0.0036007	peptidyl arginine deiminase(PADI2)	E3.5.3.15
Cluster-62068.67996	-2.3088	0.000308	0.030531	ZPR1 zinc finger (ZPR1)	K06874
Cluster-62068.100650	-2.3173	2.15E-06	0.00063886	hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD)	HPGD
Cluster-62068.161213	-2.3256	3.73E-05	0.0062056	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (WFIKK2)	--

Cluster-62068.86747	-2.3397	8.39E-06	0.0019297	mesoderm development candidate 2 (MESDC2)	MESDC2
Cluster-62068.49578	-2.3615	7.77E-06	0.0018108	thyroglobulin (TG)	TG
Cluster-62068.145374	-2.3828	0.000173	0.020145	glutathione S-transferase theta 2B (GSTT2B)	GST, gst
Cluster-62068.37816	-2.3937	0.000367	0.034966	regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant X6	RFX1_2_3
Cluster-62068.20888	-2.3938	0.000421	0.038382	Ailuropoda melanoleuca uncharacterized LOC105235025 (LOC105235025)	--
Cluster-77665.0	-2.3976	0.000527	0.04543	Fc fragment of IgG binding protein (FCGBP)	FCGBP
Cluster-62068.117447	-2.3981	5.44E-05	0.0082991	BCL2-associated athanogene 5 (BAG5)	BAG5
Cluster-62068.146198	-2.4123	0.000533	0.045829	ATPase type 13A4 (ATP13A4)	ATP13A3_4_5
Cluster-62068.184060	-2.4166	0.000273	0.02807	Canis lupus familiaris solute carrier organic anion transporter family, member 1A2 (SLCO1A2)	SLCO1A2
Cluster-62068.55632	-2.4209	1.49E-08	9.88E-06	histone deacetylase 11 (HDAC11)	HDAC11
Cluster-62068.66595	-2.43	0.000187	0.021286	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1)	ADCYAP1R1
Cluster-62068.106397	-2.4383	3.91E-07	0.00015455	CD44 molecule (CD44)4	CD44
Cluster-62068.67088	-2.4416	6.70E-05	0.0097972	unc-5 netrin receptor B (UNC5B)	UNC5
Cluster-62068.72317	-2.4523	0.00021	0.023187	transportin 3 (TNPO3)	TRPO3, MTR10
Cluster-62068.49238	-2.4542	0.000244	0.025954	calcium-sensing receptor (CASR)	CASR
Cluster-62068.167330	-2.4669	5.45E-07	0.00020941	Odobenus rosmarus divergens H-2 class II histocompatibility antigen, E-S beta chain-like (LOC101379947)	MHC2
Cluster-62068.34909	-2.4752	1.37E-08	9.19E-06	peptidyl arginine deiminase, type II (PADI2)	PADI2
Cluster-62068.192354	-2.4752	0.000305	0.030305	deleted in malignant brain tumors 1 protein (LOC101678849)	DMBT1
Cluster-62068.110999	-2.4768	1.12E-05	0.0023968	Odobenus rosmarus divergens claudin 10 (CLDN10)	CLDN
Cluster-62068.4273	-2.4853	3.53E-07	0.00014276	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	--
Cluster-62068.114551	-2.4993	0.000302	0.030145	peptidase domain containing associated with muscle regeneration 1	PAMR1

				(PAMR1), transcript variant X7	
Cluster-62068.188760	-2.5036	0.00011	0.01436	Ursus maritimus ADP-ribosyltransferase 4 (ART4)	ART4
Cluster-62068.171737	-2.5168	0.000252	0.026575	ADP-ribosyltransferase 4 (ART4)	ART4, DO
Cluster-62068.130575	-2.5209	0.000523	0.045167	Ailuropoda melanoleuca transcription factor CP2 (TFCP2)	TFCP2
Cluster-62068.42468	-2.5315	0.000472	0.04184	arylsulfatase G (ARSG)	ARSG
Cluster-62068.187165	-2.5378	4.22E-06	0.0011067	Ovis canadensis canadensis isolate 43U chromosome 1 sequence	--
Cluster-62068.75398	-2.538	0.000472	0.04184	transmembrane 7 superfamily member 3 (TM7SF3)	TM7SF3
Cluster-62068.159003	-2.5477	0.000207	0.022983	chromosome 3 clone RP11-245G23	--
Cluster-62068.87022	-2.5666	0.000452	0.040591	Ovis canadensis canadensis isolate 43U chromosome 15 sequence	--
Cluster-62068.29469	-2.576	0.000209	0.023143	Ailuropoda melanoleuca collagen alpha-6(VI) chain (LOC100463941)	COL6A
Cluster-62068.105469	-2.5953	0.000374	0.035514	Canis familiaris chromosome 24	SIRPA_B1_G
Cluster-62068.65199	-2.5983	8.71E-05	0.011982	transmembrane protein 214 (TMEM214)	TMEM214
Cluster-62068.80124	-2.6129	8.85E-07	0.0003132	tudor domain containing 12 (TDRD12)	TDRD12
Cluster-62068.148702	-2.6346	0.000263	0.027363	armadillo repeat containing 9 (ARMC9)	ARMC9
Cluster-62068.161897	-2.6378	3.52E-05	0.0059419	Mustela vison clone I210 genomic sequence	--
Cluster-62068.21697	-2.6397	0.000227	0.024526	GATA binding protein 3 (GATA3)	GATA3
Cluster-62068.156680	-2.6405	0.000598	0.049811	Ovis canadensis canadensis isolate 43U chromosome 13 sequence	--
Cluster-62068.113550	-2.6543	0.000294	0.029554	protein tyrosine phosphatase (PTPRR)	PTPRR
Cluster-62068.648	-2.6582	4.24E-05	0.0068896	chromosome 3 clone RP11-543A18	--
Cluster-62068.118710	-2.674	0.000148	0.017869	KIAA0368 ortholog (KIAA0368)	ECM29
Cluster-62068.173547	-2.6746	0.000301	0.030086	UBX domain protein 10 (UBXN10)	UBXN10
Cluster-62068.11264	-2.6865	2.13E-05	0.0039649	glutamate-rich 3 (ERICH3)	ERICH3
Cluster-55981.1	-2.6911	0.000579	0.048665	SH2 domain containing 1B (SH2D1B)	SH2D1B
Cluster-62068.5821	-2.6924	0.000386	0.03625	Ovis canadensis canadensis isolate 43U chromosome 19 sequence	--

Cluster-62068.157005	-2.6957	5.87E-13	1.39E-09	kallikrein 1 (KLK1)	KLK1_2
Cluster-62068.58315	-2.6987	0.000396	0.036879	RPGRIP1-like (RPGRIP1L)	RPGRIP1L
Cluster-62068.40631	-2.7017	0.000544	0.046537	caspase recruitment domain family(CARD10)	CARD10
Cluster-62068.29538	-2.7028	1.57E-05	0.0031366	bone morphogenetic protein 8a (BMP8A)	BMP8
Cluster-62068.50867	-2.7059	0.000549	0.046767	zinc finger protein 496 (ZNF496)	ZNF496
Cluster-45687.0	-2.7099	0.000523	0.045167	WD repeat domain 88 (WDR88)	WDR88
Cluster-62068.157883	-2.7141	7.43E-05	0.010609	catenin (cadherin-associated protein) (CTNNA2)	CTNNA
Cluster-62068.168145	-2.72	0.0005	0.043711	solute carrier family 23 member 2 (LOC101693604)	SLC23A1_2, SVCT1_2
Cluster-62068.179121	-2.7211	0.000496	0.043498	armadillo repeat containing 6 (ARMC6)	ARMC6
Cluster-62068.163899	-2.7212	0.000313	0.03093	Canis lupus familiaris chromosome 7 open reading frame	C7H1orf27
Cluster-62068.7173	-2.725	8.36E-07	0.00029798	sialidase 2 (cytosolic sialidase) (NEU2)	NEU2
Cluster-62068.151925	-2.7301	0.000502	0.043814	Cbl proto-oncogene B, E3 ubiquitin protein ligase (CBLB)	ITGAM
Cluster-11502.0	-2.732	0.000481	0.0424	transmembrane protein 74 (TMEM74)	TMEM74
Cluster-62068.167891	-2.734	0.000103	0.013586	uncharacterized LOC106006249	--
Cluster-62068.148850	-2.7379	0.00014	0.017192	chromosome 5, BAC clone 7g12 (LBNL H126)	CXCL14, SCYB14
Cluster-62068.587	-2.7396	0.000467	0.041624	C-type lectin domain family 4 member G (LOC101689830)	--
Cluster-62068.161180	-2.7522	0.00043	0.039002	calcium responsive transcription factor (CARF)1	CARF
Cluster-62068.131714	-2.7528	0.000442	0.03994	zinc finger, MYM-type 2 (ZMYM2)	ZMYM2
Cluster-51444.0	-2.758	0.000402	0.037398	MACACA MULATTA BAC clone CH250-201N11 from chromosome 12	--
Cluster-62068.26977	-2.7597	0.000423	0.038553	Felis catus BAC clone FCAB-53H12 from chromosome unknown	--
Cluster-62068.178141	-2.7617	6.16E-08	3.34E-05	Sus scrofa clone CH242-189G19 protein kinase AMP-activated alpha 2 catalytic subunit (PRKAA2) gene	PRKAA, AMPK
Cluster-62068.98635	-2.7658	9.40E-05	0.012661	THO complex 1 (THOC1)	THOC1

Cluster-62068.33982	-2.7679	0.000416	0.038127	GTF2I repeat domain containing 1 (GTF2IRD1)	TFII-I, GTF2I
Cluster-46443.0	-2.7754	0.000386	0.036276	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.16434	-2.7775	0.00036	0.03453	Pan troglodytes zinc finger protein 639 (ZNF639)	ZNF639
Cluster-62068.177931	-2.7831	0.000403	0.03741	myosin IIIB (MYO3B)	MYO3, DFNB30
Cluster-62068.38233	-2.7842	1.40E-07	6.74E-05	thyroglobulin (TG)	TG
Cluster-62068.79215	-2.7859	0.000364	0.03476	esterase D (ESD)	frmB, ESD, fghA
Cluster-62068.17157	-2.7886	0.000211	0.023223	Pig DNA sequence from clone CH242-512B14 on chromosome X	--
Cluster-62068.143866	-2.7915	0.000392	0.036655	jumonji domain containing 1C (JMJD1C)	JMJD1C
Cluster-62068.9159	-2.7977	0.000138	0.016987	glutamate-rich 3 (ERICH3)	ERICH3
Cluster-62068.3071	-2.8039	4.46E-05	0.007168	uncharacterized LOC106007422 (LOC106007422)	--
Cluster-62068.83711	-2.8066	1.16E-17	7.93E-14	palmitoyl-protein thioesterase 1 (PPT1)	PPT
Cluster-52261.0	-2.8129	0.000312	0.030824	uncharacterized LOC106005443 (LOC106005443)	--
Cluster-39582.0	-2.8134	8.99E-05	0.012297	SVOP-like (SVOPL)	SVOPL
Cluster-17836.0	-2.8179	0.000299	0.029928	natural cytotoxicity triggering receptor 1 (LOC101670751)	NCR1
Cluster-62068.94474	-2.8205	0.000223	0.024225	Odobenus rosmarus divergens integrin (ITGB4)	ITGB4
Cluster-62068.8779	-2.821	3.76E-06	0.0010059	Ailuropoda melanoleuca collagen alpha-6(VI) chain (LOC100463941)	COL6A
Cluster-62068.152097	-2.8212	0.000113	0.014618	Human DNA sequence from clone RP11-426L16 on chromosome 1	--
Cluster-62068.11471	-2.8233	0.00028	0.028572	glutaminase 2 (liver, mitochondrial) (GLS2)	GLS2
Cluster-62068.46334	-2.8271	0.000283	0.028729	Odobenus rosmarus divergens UV radiation resistance associated (UVRAG)	UVRAG
Cluster-31737.0	-2.829	0.00028	0.028537	Pig DNA sequence from clone CH242-244H5 on chromosome X	--
Cluster-62068.176015	-2.8308	0.000267	0.027655	microtubule-associated protein tau (MAPT)9	MAPT, TAU
Cluster-62068.25250	-2.8309	0.000283	0.028757	meiosis-specific nuclear structural 1 (MNS1)	MNS1
Cluster-62068.45237	-2.8316	0.000272	0.028043	thrombospondin 2 (THBS2)	THBS2S
Cluster-42250.2	-2.8316	0.000272	0.028043	Parascaris equorum genome assembly P_equorum ,scaffold PEQ_scaffold0015810	--

Cluster-62068.190191	-2.8333	0.000261	0.027133	Ursus maritimus NIMA-related kinase 5 (NEK5)	NEK
Cluster-62068.91041	-2.8357	0.000275	0.028203	Odobenus rosmarus divergens ubiquilin 1 (UBQLN1)	UBQLN, DSK2
Cluster-62068.176312	-2.8404	0.000257	0.026856	uridine phosphorylase 1 (UPP1)	udp, UPP
Cluster-62068.186723	-2.8434	0.000273	0.02807	Ovis canadensis canadensis isolate 43U chromosome 15 sequence	--
Cluster-62068.175595	-2.8504	3.92E-07	0.00015455	chromosome 5 clone RP11-158J3	--
Cluster-62068.27776	-2.8533	0.00024	0.025619	WW domain containing E3 ubiquitin protein ligase 2 (WWP2)	WWP2, AIP2
Cluster-62068.19273	-2.8535	0.000238	0.025409	coiled-coil domain containing 93 (CCDC93)	CCDC93
Cluster-62068.58539	-2.8564	0.000257	0.026856	Leptonychotes weddellii uncharacterized LOC102742436, ncRNA	BBC3, PUMA
Cluster-63313.0	-2.8602	2.84E-06	0.0008006	Neovison vison cytochrome P450 family 1 subfamily A polypeptide 1 (CYP1A1)	CYP1A1
Cluster-62068.169472	-2.8612	0.000148	0.017856	Ailuropoda melanoleuca cytochrome P450 4A6-like (LOC100465965)	--
Cluster-62068.190467	-2.8653	0.000261	0.027133	cat eye syndrome chromosome region (CECR1)	CECR1, ADA2
Cluster-62068.14994	-2.8675	0.000214	0.023475	Human DNA sequence from clone RP1-122O8 on chromosome 6q14.2-16.1	--
Cluster-62068.148085	-2.869	0.000212	0.023285	crystallin, lambda 1 (CRYL1)	CRYL1
Cluster-62068.43562	-2.872	0.000211	0.023223	uncharacterized LOC106007064 (LOC106007064)	--
Cluster-62068.21612	-2.8725	0.00022	0.024061	kinesin family member 6 (KIF6)	KIF6_9
Cluster-62068.5536	-2.8761	0.000137	0.016944	Bos taurus uncharacterized LOC101906240 (LOC101906240)8	--
Cluster-62068.105569	-2.882	0.000202	0.022625	A-Raf proto-oncogene, serine/threonine kinase (ARAF)	ARAF, ARAF1
Cluster-55370.0	-2.884	0.000197	0.022218	synaptonemal complex protein 2 (SYCP2)	SYCP2
Cluster-62068.144666	-2.886	0.00021	0.023187	Rhesus Macaque BAC CH250-4H19 complete sequence	UPK1
Cluster-62068.78004	-2.8876	0.000205	0.022796	Odobenus rosmarus divergens sterile alpha motif domain containing 14 (SAMD14)	SAMD14
Cluster-62068.149627	-2.8915	3.91E-05	0.0064187	solute carrier family 16 (SLC16A9)	SLC16A9
Cluster-62068.115377	-2.8915	0.000231	0.024923	glutamic-pyruvate transaminase (GPT)	GPT, ALT
Cluster-62068.32171	-2.8928	0.000193	0.021809	DNA cross-link repair 1A (DCLRE1A)	DCLRE1A,

					SNM1A
Cluster-62068.170868	-2.9016	1.59E-05	0.0031626	metastasis associated 1 family, member 3 (MTA3)	MTA3
Cluster-62068.132697	-2.9037	0.00018	0.020662	COMM domain containing 9 (COMMD9)	COMMD9
Cluster-62068.23491	-2.905	0.000196	0.022121	Ursus maritimus cell adhesion associated, oncogene regulated (CDON)	CDON
Cluster-62068.143543	-2.9075	7.33E-05	0.010513	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ)	NFKBIZ
Cluster-62068.180969	-2.9123	0.000169	0.0199	poly (ADP-ribose) polymerase family, member 3 (PARP3)	PARP
Cluster-62068.190702	-2.9169	0.000165	0.01955	zinc finger, SWIM-type containing 2 (ZSWIM2)	ZSWIM2
Cluster-62068.154653	-2.9181	0.000174	0.020215	alpha-kinase 1 (ALPK1)	ALPK1
Cluster-62068.117848	-2.9221	0.00017	0.019938	uncharacterized LOC101672653 (LOC101672653)	LOC101672653
Cluster-62068.50460	-2.9237	0.000178	0.020561	Odobenus rosmarus divergens myeloid/lymphoid or mixed-lineage leukemia	MLLT1_3, ENL, AF9
Cluster-62068.43915	-2.9267	0.000166	0.019606	BCL2-like 13 (apoptosis facilitator) (BCL2L13)	BCL2L13
Cluster-62068.159087	-2.9273	0.000168	0.019787	zinc finger, CCHC domain containing 6 (ZCCHC6)	TUT
Cluster-62068.140574	-2.9314	0.000149	0.017961	PDZ domain containing 3 (PDZD3)	PDZD3
Cluster-62068.44477	-2.9344	8.75E-05	0.012014	Odobenus rosmarus divergens diacylglycerol O-acyltransferase 2 (DGAT2)	DGAT2
Cluster-62068.135376	-2.9359	8.20E-05	0.011394	integrin(ITGA9)	ITGA9
Cluster-62068.141506	-2.9403	0.000142	0.017287	DLA class II histocompatibility antigen, DR-1 beta chain-like (LOC101670362)	--
Cluster-62068.155611	-2.9448	0.000141	0.017232	Canis lupus familiaris t-SNARE domain containing 1 (TSNARE1)	TSNARE1
Cluster-62068.64643	-2.945	0.000139	0.017135	cyclin D1 (CCND1)	CCND1
Cluster-69151.0	-2.9474	0.000148	0.017837	MACACA MULATTA BAC clone CH250-25B17 from chromosome 1	--
Cluster-62068.168513	-2.9483	0.000146	0.017645	nucleotide-binding oligomerization domain containing 2 (NOD2)	NOD2
Cluster-62068.182040	-2.9528	4.62E-05	0.0073249	carbonic anhydrase III (CA3)	E4.2.1.1
Cluster-62068.63255	-2.9539	2.66E-05	0.0047212	zinc finger, MYND-type containing 15 (ZMYND15)	ZMYND15

Cluster-62068.112123	-2.9561	0.000148	0.017837	Ursus maritimus KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 (KDELR1)	KDELR1
Cluster-62068.131645	-2.962	0.00014	0.017192	neuron navigator 1 (NAV1)	NAV1
Cluster-62068.3706	-2.9662	0.000155	0.018476	cell death-inducing DFFA-like effector c (CIDEc)	CIDEc
Cluster-62068.131109	-2.9674	0.000133	0.016552	inositol polyphosphate-5-phosphatase F (INPP5F)	INPP5F
Cluster-62068.165458	-2.9695	0.000133	0.016577	chromosome 19 clone CTB-60E11	--
Cluster-62068.154308	-2.9974	0.00011	0.014281	UBX domain protein 11 (UBXN11)	UBXN11
Cluster-62068.53754	-2.9986	0.000111	0.014459	period circadian clock 2 (PER2)	PER
Cluster-62068.24977	-2.9991	0.000116	0.014953	arachidonate 5-lipoxygenase (ALOX5)	ALOX5
Cluster-62068.155259	-3.0053	9.65E-05	0.012905	striatin, calmodulin binding protein (STRN)	STRN1_3_4
Cluster-62068.167704	-3.0087	9.92E-05	0.013212	chromosome 17, clone RP11-498C9	--
Cluster-62068.17796	-3.016	9.18E-05	0.012491	immunoglobulin superfamily (IGSF10)	IGSF10
Cluster-62068.84721	-3.0168	4.45E-05	0.0071655	transmembrane protein 214 (TMEM214)	TMEM214
Cluster-62068.87273	-3.02	9.36E-05	0.012627	WD repeat domain 6 (WDR6)	WDR6
Cluster-62068.8154	-3.0213	9.25E-05	0.012539	solute carrier family 35, member F3 (SLC35F3)	SLC35F3_4
Cluster-62068.129475	-3.0227	7.50E-07	0.00027253	chemokine (C-X-C motif) ligand 14 (CXCL14)	CXCL14, SCYB14
Cluster-62068.167826	-3.0331	8.19E-05	0.011394	carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11)	CHST11
Cluster-62068.12630	-3.0435	9.33E-05	0.012607	solute carrier family 35 (UDP-GlcA/UDP-GalNAc transporter)	SLC35D
Cluster-62068.175393	-3.0552	7.34E-05	0.010513	Macaca mulatta BAC CH250-440C19	--
Cluster-24.0	-3.0593	7.66E-05	0.010827	Ovis canadensis canadensis isolate 43U chromosome 10 sequence	--
Cluster-62068.177104	-3.0648	6.75E-05	0.0098377	Ursus maritimus phosphatidylinositol-4-phosphate 5-kinase	PIP5K
Cluster-62068.158732	-3.0648	6.85E-05	0.0099565	Felis catus uncharacterized LOC102900733 (LOC102900733)	--
Cluster-62068.63553	-3.0676	7.57E-05	0.010753	STAM binding protein (STAMPB), RefSeqGene on chromosome 2	STAMPB
Cluster-62068.148552	-3.0716	6.41E-05	0.0094615	Leptonychotes weddellii integral membrane protein 2A (ITM2A)	ITM2A

Cluster-62068.78518	-3.0814	6.16E-05	0.0091658	secretion associated, Ras related GTPase 1B (SAR1B)	SAR1
Cluster-62068.78523	-3.0834	6.88E-05	0.0099711	obscurin-like 1 (OBSL1)	OBSL1
Cluster-62068.187704	-3.0904	6.12E-05	0.0091189	Felis catus FLA extended class II, class II, class III, proximal and central class I region genomic sequence	MHC2
Cluster-1089.0	-3.0988	2.53E-05	0.0045468	chromosome 3 clone CTC-501D11	CTC-501D11
Cluster-62068.98198	-3.1012	2.69E-05	0.0047629	ribosomal protein L3 (RPL3)	RP-L3e, RPL3
Cluster-62068.37541	-3.1061	1.94E-05	0.0037151	Pig DNA sequence from clone CH242-96E20 on chromosome X	--
Cluster-62068.9276	-3.1162	9.50E-06	0.0021217	sialidase 2 (cytosolic sialidase) (NEU2)	NEU2
Cluster-62068.134388	-3.1177	5.09E-05	0.0078748	unc-13 homolog D (C. elegans) (UNC13D)	UNC13D
Cluster-62068.27760	-3.118	5.76E-05	0.0087001	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL)	E4.1.3.3, nanA, NPL
Cluster-62068.98329	-3.1233	5.26E-05	0.0080744	Canis lupus familiaris ecotropic viral integration site 5-like (EVI5L), transcript variant 1	EVI5L
Cluster-62068.52400	-3.1268	4.61E-05	0.0073094	IQ motif and Sec7 domain 2 (IQSEC2)	IQSEC
Cluster-62068.109202	-3.1294	5.18E-05	0.007983	solute carrier family 26 (anion exchanger), member 11 (SLC26A11)	SLC26A11
Cluster-62068.75360	-3.1331	5.66E-05	0.0085585	interferon, gamma-inducible protein 30 (IFI30)	IFI30, GILT
Cluster-62068.171169	-3.1341	4.48E-05	0.0071702	membrane metallo-endopeptidase-like 1 (MMEL1)	MMEL1
Cluster-62068.101885	-3.1405	4.86E-05	0.0076162	Panthera tigris altaica family with sequence similarity 192	FAM192A
Cluster-62068.121690	-3.1503	2.67E-07	0.00011437	chemokine (C-X-C motif) ligand 14 (CXCL14)	CXCL14
Cluster-62068.4980	-3.152	6.60E-06	0.0015845	Heterocephalus glaber 5-hydroxytryptamine (serotonin) receptor 1A, G protein-coupled (Htr1a)	--
Cluster-62068.47597	-3.1535	3.77E-05	0.0062357	Canis lupus familiaris sterile alpha motif and leucine zipper containing kinase AZK (ZAK)	ZAK, MLTK
Cluster-49238.1	-3.1537	1.87E-05	0.003594	uncharacterized LOC106004415 (LOC106004415)	--
Cluster-62068.182041	-3.154	9.83E-06	0.0021633	carbonic anhydrase III (CA3)	E4.2.1.1

Cluster-62068.156839	-3.158	5.32E-06	0.0013366	Ursus americanus clone UA-BM3-P1C09 microsatellite sequence	--
Cluster-62068.6184	-3.1596	4.78E-05	0.0075255	Canis lupus familiaris uncharacterized LOC102155802 (LOC102155802)	--
Cluster-62068.180381	-3.1755	3.33E-05	0.0057229	zinc finger protein 385C (ZNF385C)	ZNF385C
Cluster-62068.37565	-3.1806	3.29E-05	0.0056681	dihydrouridine synthase 2 (DUS2)	DUS2
Cluster-19684.0	-3.1822	3.48E-05	0.0058916	Ovis canadensis canadensis isolate 43U chromosome 19 sequence	--
Cluster-62068.61663	-3.1834	3.48E-05	0.0058916	bromodomain containing 1 (BRD1)	BRD1, BRPF2
Cluster-62068.22390	-3.1839	3.28E-05	0.0056581	ZFP91 zinc finger protein (ZFP91)	ZFP91
Cluster-62068.182451	-3.1891	4.02E-05	0.0065887	Ovis canadensis canadensis isolate 43U chromosome 8 sequence	--
Cluster-62068.133462	-3.1951	3.63E-05	0.0060791	Odobenus rosmarus divergens ubiquitin protein ligase E3B (UBE3B)	UBE3B
Cluster-62068.170901	-3.1998	2.75E-05	0.0048375	dynamamin binding protein (DNMBP)	DNMBP
Cluster-62068.100561	-3.2038	4.16E-05	0.006782	paroxysmal nonkinesigenic dyskinesia (PNKD)	PNKD
Cluster-62068.159278	-3.2322	2.55E-05	0.0045779	ankyrin repeat domain 55 (ANKRD55)	ANKRD55
Cluster-13462.0	-3.2329	2.23E-05	0.0041034	uncharacterized LOC106006270 (LOC106006270)	--
Cluster-62068.173485	-3.2486	2.18E-05	0.0040493	zinc finger with KRAB and SCAN domains 2 (ZKSCAN2)	ZKSCAN
Cluster-62068.185643	-3.2571	2.07E-05	0.003894	Felis catus clone RP86-588L5	--
Cluster-34321.0	-3.2585	2.02E-05	0.0038178	Odobenus rosmarus divergens zinc finger, FYVE domain containing 28 (ZFYVE28)	ZFYVE28
Cluster-62068.123720	-3.2677	1.76E-05	0.0034239	polyamine modulated factor 1 binding protein 1 (PMFBP1)	DHX38, PRP16
Cluster-62068.117313	-3.2705	1.83E-05	0.0035412	Odobenus rosmarus divergens breast cancer metastasis suppressor 1 (BRMS1)	BRMS1
Cluster-62068.11039	-3.2708	1.95E-05	0.0037219	ATP-binding cassette, sub-family A (ABC1)	ABCA8
Cluster-62068.122361	-3.2731	1.69E-05	0.0033046	uncharacterized LOC106006249 (LOC106006249)	--
Cluster-62068.129060	-3.2762	1.81E-05	0.0035128	ATPase type 13A1 (ATP13A1)	ATP13A1
Cluster-62068.140791	-3.2856	7.29E-07	0.00026762	DAZ interacting zinc finger protein 1 (DZIP1)	CLDN
Cluster-62068.173363	-3.2925	3.54E-07	0.00014276	olfactomedin 4 (OLFM4)	OLFM4
Cluster-62068.55650	-3.2961	1.67E-05	0.0032754	cDNA, FLJ18301	--

Cluster-62068.20096	-3.3065	1.45E-05	0.0029447	Macaca mulatta neurogenic locus notch homolog protein 3-like (NOTCH3)	NOTCH3
Cluster-62068.39399	-3.3075	1.61E-05	0.0031874	Odobenus rosmarus divergens neuroblastoma breakpoint family member 6-like protein (LOC101363536)	--
Cluster-62068.3770	-3.3079	1.50E-05	0.0030116	sialic acid binding Ig-like lectin 1, sialoadhesin (SIGLEC1)	SN, SIGLEC1
Cluster-62068.184059	-3.3141	3.31E-07	0.0001363	solute carrier organic anion transporter family(SLCO1A2)	SLCO1A
Cluster-62068.31067	-3.3152	1.86E-05	0.003579	T-cell surface glycoprotein CD1a-like (LOC101690926)	CD1
Cluster-62068.133551	-3.3188	1.44E-05	0.0029263	25-hydroxycholesterol 7-alpha-hydroxylase (LOC101686726)	CYP7B
Cluster-62068.86722	-3.3238	1.25E-06	0.00041595	sialidase 2 (cytosolic sialidase) (NEU2)	NEU2_3_4
Cluster-62068.149222	-3.3241	1.62E-05	0.0031933	sperm flagellar 2 (SPEF2)	SPEF2
Cluster-62068.8785	-3.3254	1.35E-05	0.002798	Pan troglodytes BAC clone RP43-136P16 from chromosome 7	--
Cluster-62068.163163	-3.3288	1.23E-05	0.0025783	nicotinamide N-methyltransferase (NNMT)	NNMT
Cluster-29086.0	-3.3293	1.21E-05	0.0025377	membrane-spanning 4-domains, subfamily A (MS4A7)	MS4A7
Cluster-62068.75957	-3.3295	1.13E-05	0.0023984	Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17)	GEF
Cluster-62068.116984	-3.3357	1.16E-05	0.0024563	Microcebus murinus histone deacetylase 7 (HDAC7)	HDAC7
Cluster-62068.138861	-3.3391	1.14E-05	0.0024284	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B (PLEKHG4B)	PLEKHG4B
Cluster-62068.25115	-3.3408	1.25E-05	0.0025976	SWI5 recombination repair homolog (SWI5)	SWI5
Cluster-62068.133187	-3.3447	1.01E-05	0.0022133	cryptochrome circadian clock 2 (CRY2)	CRY
Cluster-62068.56484	-3.3583	1.01E-05	0.00221	tetratricopeptide repeat domain 39C (TTC39C)	TTC39C
Cluster-62068.16156	-3.3669	1.21E-05	0.0025338	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor (NFKBIZ)	NFKBIZ
Cluster-62068.16078	-3.3767	9.67E-06	0.0021415	MACACA MULATTA BAC clone CH250-58H12 from chromosome unknown	--
Cluster-62068.63823	-3.3776	1.03E-05	0.0022333	polypeptide N-acetylgalactosaminyltransferase 3 (GALNT3)	GALNT
Cluster-62068.106086	-3.3796	1.34E-06	0.00043554	lysosomal-associated membrane protein 2 (LAMP2)	LAMP2

Cluster-62068.69129	-3.3834	1.03E-05	0.0022333	intraflagellar transport 140 (IFT140)	IFT140
Cluster-62068.190003	-3.3843	8.63E-06	0.0019731	Canis familiaris chromosome 31	--
Cluster-62068.168416	-3.3894	9.38E-06	0.0021036	Ursus maritimus F-box protein 48 (FBXO48)	FBXO48
Cluster-62068.167164	-3.3914	9.56E-06	0.002126	KIAA1257 ortholog (KIAA1257)	ACAD9
Cluster-62068.131015	-3.397	9.81E-06	0.0021633	low density lipoprotein receptor-related protein 4 (LRP4)	LRP4
Cluster-62068.72106	-3.3971	8.63E-06	0.0019731	elaC ribonuclease Z 2 (ELAC2)	rnz
Cluster-62068.172726	-3.404	6.95E-06	0.0016588	sorting nexin 18 (SNX18)	SNX18
Cluster-62068.113017	-3.4063	3.95E-07	0.000155	kinesin light chain 2 (KLC2)	KLC2
Cluster-62068.7647	-3.4068	6.90E-06	0.0016534	noncompact myelin associated protein (NCMAP)	NCMAP
Cluster-62068.163671	-3.409	8.11E-07	0.00029132	zinc finger, SWIM-type containing 2 (ZSWIM2)	ZSWIM2
Cluster-62068.118935	-3.411	7.49E-06	0.0017539	chromosome transmission fidelity factor 8 (CHTF8)	UTP4, CIRH1A
Cluster-62068.146257	-3.4151	7.05E-06	0.0016744	coiled-coil domain containing 57 (CCDC57)	CCDC57
Cluster-62068.165297	-3.4154	7.49E-06	0.0017539	Ovis canadensis canadensis isolate 43U chromosome 4 sequence	--
Cluster-62068.167579	-3.4158	7.67E-06	0.0017909	chromosome 3 clone RP11-543A18	--
Cluster-62068.62384	-3.4162	7.33E-06	0.0017245	KIAA0100 ortholog (KIAA0100)	KIAA0100
Cluster-62068.34329	-3.4187	2.82E-06	0.00079711	carbonic anhydrase XII (CA12)	E4.2.1.1
Cluster-62068.150449	-3.4198	8.38E-06	0.0019296	gamma-glutamyltransferase 5 (GGT5)	GGT1_5
Cluster-62068.141324	-3.4255	5.94E-08	3.25E-05	Odobenus rosmarus divergens ankyrin 3, node of Ranvier (ankyrin G) (ANK3)	ANK
Cluster-8064.0	-3.4325	6.07E-06	0.0014687	Ovis canadensis canadensis isolate 43U chromosome 24 sequence	--
Cluster-62068.110942	-3.4411	5.01E-06	0.0012682	protein kinase N2 (PKN2)	PKN
Cluster-62068.17866	-3.4434	6.39E-06	0.0015386	absent in melanoma 1-like (AIM1L)	AIM1L
Cluster-62068.50242	-3.4488	6.02E-06	0.0014647	Odobenus rosmarus divergens CTP synthase 2 (CTPS2)	pyrG, CTPS
Cluster-62068.83805	-3.4608	4.66E-06	0.0012009	ankyrin 1, erythrocytic (ANK1)	ANK
Cluster-62068.121485	-3.4625	5.74E-06	0.0014192	Canis lupus familiaris c-abl oncogene 2, non-receptor tyrosine kinase (ABL2)	ABL2

Cluster-62068.64302	-3.4701	3.23E-06	0.00089963	Balaenoptera acutorostrata scammoni RAS p21 protein activator 4 (RASA4)	RASA4, CAPRI
Cluster-62068.30765	-3.4742	4.69E-06	0.001206	tetratricopeptide repeat domain 23-like (TTC23L)	--
Cluster-62068.108471	-3.4789	5.61E-07	0.0002141	KRI1 homolog (KRI1)	KRI1
Cluster-62068.65739	-3.4799	4.73E-06	0.0012132	intraflagellar transport 27 (IFT27), RefSeqGene on chromosome 22	IFT27
Cluster-55787.0	-3.4864	3.98E-06	0.0010546	solute carrier family 23 member 2 (LOC101693604)	--
Cluster-62068.132728	-3.4989	3.26E-06	0.00090435	leukemia inhibitory factor receptor alpha (LIFR)	LIFR
Cluster-62068.82584	-3.5115	3.44E-06	0.00094258	Leptonychotes weddellii plectin (PLEC)	PLEC
Cluster-62068.185925	-3.539	2.71E-06	0.00076878	lipoma HMGIC fusion partner-like 3 (LHFPL3)	LHFPL3
Cluster-62068.44476	-3.5514	1.04E-06	0.0003573	diacylglycerol O-acyltransferase 2 (DGAT2)	DGAT2
Cluster-62068.66766	-3.5577	2.24E-06	0.0006552	GDNF-inducible zinc finger protein 1 (GZF1)	GZF1
Cluster-62068.142998	-3.5703	2.25E-06	0.00065786	Equus caballus beta-1,4-N-acetyl-galactosaminyl transferase 4 (B4GALNT4)	B4GALNT4
Cluster-62068.147149	-3.5864	1.64E-06	0.00050513	MDM2 proto-oncogene, E3 ubiquitin protein ligase (MDM2)	MDM2
Cluster-45655.0	-3.587	2.14E-06	0.00063886	aldehyde oxidase 4-like (LOC101693479)	AOX
Cluster-62068.28522	-3.5945	1.63E-06	0.0005047	Odobenus rosmarus divergens potassium channel, voltage gated modifier subfamily G, member 3 (KCNG3)	KCNG3
Cluster-62068.81754	-3.5953	5.83E-10	6.04E-07	isoamyl acetate-hydrolyzing esterase 1 homolog (IAH1)	IAH1
Cluster-62068.173980	-3.6033	2.42E-06	0.00070011	MIS18 binding protein 1 (MIS18BP1)	MIS18BP1
Cluster-62068.76362	-3.608	2.26E-06	0.00065798	uncharacterized LOC101694508 (LOC101694508)	--
Cluster-62068.95618	-3.6126	1.64E-06	0.00050513	aryl hydrocarbon receptor nuclear translocator (ARNT)	ARNT
Cluster-62068.157479	-3.6181	2.22E-06	0.00065097	calcium/calmodulin-dependent protein kinase IG (CAMK1G)	CAMK1
Cluster-62068.185158	-3.6231	2.08E-06	0.00062478	Odobenus rosmarus divergens zinc finger protein 704 (ZNF704)	ZNF704
Cluster-62068.122995	-3.6287	1.76E-06	0.00053551	Ursus maritimus kelch domain containing 1 (KLHDC1)	KLHDC1
Cluster-62068.47429	-3.6365	1.23E-06	0.00041119	regucalcin (RGN)	gnl, RGN
Cluster-62068.144284	-3.6449	1.45E-06	0.00046487	Ursus maritimus TM2 domain containing 2 (TM2D2)	TM2D2
Cluster-62068.189136	-3.6476	1.25E-06	0.00041401	deleted in malignant brain tumors 1 protein-like (LOC106004722)	DMBT1

Cluster-62068.33067	-3.6527	1.28E-06	0.00041962	zinc finger, CCHC domain containing 14 (ZCCHC14)	ZCCHC14
Cluster-62068.51610	-3.6529	9.52E-07	0.00033187	Equus przewalskii trinucleotide repeat containing 6C (TNRC6C)	TNRC6, GW182
Cluster-62068.13116	-3.654	1.13E-06	0.00038497	spermatogenesis associated 7 (SPATA7)	SPATA7
Cluster-62068.130404	-3.654	9.88E-07	0.00034198	ankyrin repeat domain 52 (ANKRD52)	ANKRD52
Cluster-62068.24236	-3.661	1.47E-06	0.00046644	neurotrophic tyrosine kinase, receptor (NTRK3)	NTRK3
Cluster-62068.132113	-3.6644	1.26E-06	0.00041641	programmed cell death 5 (PDCD5)	PDCD5, TFAR19
Cluster-62068.83683	-3.6773	1.11E-06	0.00038164	extended synaptotagmin-like protein 1 (ESYT1)	ESYT1
Cluster-62068.32533	-3.6802	1.31E-06	0.0004278	chordin-like 2 (CHRD2)	CHRD2
Cluster-62068.31287	-3.6807	9.65E-07	0.00033484	uncharacterized LOC106007196 (LOC106007196)	--
Cluster-62068.174256	-3.6817	1.31E-06	0.00042712	Human DNA sequence from clone RP11-4K3 on chromosome 1	--
Cluster-62068.154349	-3.6841	8.24E-07	0.00029443	pyruvate dehydrogenase kinase (PDK4)	PDK2_3_4
Cluster-62068.8878	-3.689	1.47E-14	5.05E-11	mucin 13, cell surface associated (MUC13)	MUC13
Cluster-62068.142960	-3.6948	8.81E-07	0.00031232	centrosomal protein 128kDa (CEP128)0	CEP128
Cluster-62068.68626	-3.6957	1.24E-06	0.00041401	Odobenus rosmarus divergens histone deacetylase 5 (HDAC5)	HDAC4_5
Cluster-62068.55392	-3.7137	5.77E-07	0.00021972	SAGA-associated factor 29 homolog (LOC101684788)	--
Cluster-62068.55151	-3.7138	9.97E-07	0.00034437	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 (HSD3B7)	HSD3B7
Cluster-62068.83348	-3.7159	8.18E-07	0.00029304	glycosylated lysosomal membrane protein (GLMP)	GLMP
Cluster-62068.82182	-3.7288	6.07E-07	0.00022935	ADP-ribosylation factor-like 4A (ARL4A)	ARL4
Cluster-62068.149099	-3.7349	7.50E-07	0.00027253	Ailuropoda melanoleuca pogo transposable element with ZNF domain (POGZ)	POGZ
Cluster-62068.104460	-3.7394	6.77E-07	0.00025261	ATPase type 13A2 (ATP13A2)	ATP13A2
Cluster-62068.78889	-3.7423	5.43E-07	0.00020905	katanin p80 (WD repeat containing) subunit B 1 (KATNB1)	KATNB1
Cluster-62068.86727	-3.7552	6.14E-07	0.00023159	histone deacetylase 3 (HDAC3)	HDAC3
Cluster-62068.65240	-3.7801	3.54E-07	0.00014276	structural maintenance of chromosomes 5 (SMC5)	SMC5

Cluster-62068.53985	-3.8384	2.14E-07	9.53E-05	caspase 8, apoptosis-related cysteine peptidase (CASP8)	CASP8
Cluster-62068.134410	-3.8418	1.21E-14	4.34E-11	uncharacterized LOC101694508 (LOC101694508)	LOC101694508
Cluster-62068.39695	-3.8511	2.35E-07	0.00010236	ATP-binding cassette, sub-family A (ABC1) (ABCA5)	ABCA5
Cluster-62068.35375	-3.8512	3.25E-07	0.00013418	Ursus maritimus phosphoinositide kinase, FYVE finger containing (PIKFYVE)	PIKFYVE, FAB1
Cluster-62068.79235	-3.8518	2.35E-07	0.00010236	tripartite motif containing 3 (TRIM3)	TRIM2_3
Cluster-62068.119217	-3.8586	3.81E-07	0.00015097	TBC1 (tre-2/USP6, BUB2, cdc16) domain family(TBC1D1)	TBC1D1
Cluster-62068.86581	-3.8637	2.49E-07	0.00010774	lysyl oxidase-like 2 (LOXL2)	LOXL2_3_4
Cluster-62068.116879	-3.8665	2.68E-07	0.00011446	protein-O-mannosyltransferase 2 (POMT2)	POMT
Cluster-62068.71	-3.8718	2.16E-07	9.61E-05	ELOVL fatty acid elongase 2 (ELOVL2)	ELOVL2
Cluster-62068.152605	-3.8822	1.34E-07	6.48E-05	serine/threonine-protein phosphatase 4 regulatory subunit 1-like (LOC101690113)	PPP4R1
Cluster-62068.44025	-3.8911	1.87E-07	8.71E-05	chromosome unknown open reading frame, human C9orf64 (LOC101670215)	--
Cluster-62068.128949	-3.8984	2.19E-07	9.68E-05	Ailuropoda melanoleuca peptidylprolyl isomerase (cyclophilin)-like 6 (PPIL6)	PPIL6
Cluster-62068.52468	-3.9074	1.12E-08	7.75E-06	transmembrane protein 138 (TMEM138)	TMEM138
Cluster-62068.92742	-3.9264	9.01E-08	4.65E-05	RUN and SH3 domain containing 2 (RUSC2)	RUSC2
Cluster-62068.60160	-3.9322	2.44E-11	3.79E-08	translocase of inner mitochondrial membrane 50 homolog (TIMM50)	TIM50
Cluster-62068.140387	-3.9333	1.53E-07	7.23E-05	Ovis canadensis canadensis isolate 43U chromosome 14 sequence	--
Cluster-62068.173794	-3.9453	1.24E-07	6.12E-05	Rho GTPase activating protein 6 (ARHGAP6)	ARHGAP6
Cluster-62068.74994	-3.9502	1.16E-07	5.81E-05	thrombospondin 1 (THBS1)	THBS1
Cluster-62068.148743	-3.9504	8.54E-08	4.42E-05	zinc finger protein OZF-like (LOC101692271)	KRAB
Cluster-62068.106215	-3.951	8.00E-08	4.21E-05	adenylate cyclase 7 (ADCY7)	ADCY7
Cluster-62068.87324	-3.9633	6.29E-08	3.39E-05	polo-like kinase 2 (PLK2)	PLK2
Cluster-62068.60592	-3.9701	1.38E-07	6.65E-05	double C2-like domain-containing protein gamma (LOC101677986)	NUDT8

Cluster-62068.115391	-3.9754	7.50E-08	3.98E-05	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5)	ITGA5
Cluster-62068.117903	-3.9776	9.15E-08	4.71E-05	abhydrolase domain containing 16A (ABHD16A)	ABHD16A
Cluster-62068.12142	-3.9823	6.79E-08	3.64E-05	WD repeat domain 17 (WDR17)	WDR17
Cluster-62068.108747	-4.0087	5.23E-08	2.89E-05	transmembrane protein 39B (TMEM39B)	TMEM39B
Cluster-35405.0	-4.0159	3.86E-08	2.23E-05	DTW domain containing 2 (DTWD2)	DTWD2
Cluster-62068.121908	-4.0259	6.01E-08	3.28E-05	Aotus nancymae TEA domain family member 2 (TEAD2)	TEAD
Cluster-62068.6499	-4.0276	4.10E-08	2.35E-05	Canis Familiaris chromosome 6	--
Cluster-62068.110872	-4.0525	5.14E-08	2.86E-05	superkiller viralicidic activity 2-like (SKIV2L)	SKI2, SKIV2L
Cluster-62068.7627	-4.0674	2.94E-08	1.74E-05	anoctamin 9 (ANO9)	ANO9, TMEM16J
Cluster-62068.126986	-4.0874	2.21E-08	1.37E-05	RAS p21 protein activator 3 (RASA3)	RASA3
Cluster-62068.34939	-4.0911	2.07E-08	1.33E-05	whirlin (LOC101691120)	--
Cluster-62068.75920	-4.1003	2.80E-08	1.69E-05	PDZ domain containing ring finger 3 (PDZRN3)	PDZRN3_4, LNX3_4
Cluster-62068.191882	-4.1034	1.68E-08	1.11E-05	uncharacterized LOC101688371 (LOC101688371)	--
Cluster-62068.76722	-4.1256	3.71E-08	2.15E-05	ring finger protein 223 (RNF223)	RNF223
Cluster-62068.139898	-4.127	1.45E-08	9.67E-06	double C2-like domain-containing protein gamma (LOC101677986)	NUDT8
Cluster-62068.123130	-4.1312	2.97E-08	1.75E-05	proline-rich transmembrane protein 2 (PRRT2)	PRRT2
Cluster-62068.118430	-4.1324	1.32E-08	8.89E-06	urocortin (UCN)	MPV17
Cluster-62068.161689	-4.1347	2.55E-08	1.55E-05	Ovis canadensis canadensis isolate 43U chromosome 3 sequence	--
Cluster-62068.74231	-4.1484	1.17E-08	8.06E-06	tetratricopeptide repeat domain 19 (TTC19)	TTC19
Cluster-62068.143818	-4.1564	1.11E-09	1.06E-06	choline kinase alpha (CHKA)	CHK
Cluster-62068.36733	-4.1592	1.31E-08	8.89E-06	Ursus maritimus spermatogenesis associated 6-like (SPATA6L)	SPATA6L
Cluster-62068.21842	-4.169	1.21E-08	8.29E-06	chromosome 17, clone RP11-357H14	--
Cluster-62068.103622	-4.1705	1.53E-08	1.01E-05	TBC1 domain family, member 16 (TBC1D16)	TBC1D16

Cluster-62068.74715	-4.172	4.27E-09	3.51E-06	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1)	RCBTB
Cluster-62068.46864	-4.182	7.94E-09	5.81E-06	solute carrier family 38, member 8 (SLC38A8)	SLC38A7_8
Cluster-62068.161438	-4.1864	9.21E-09	6.53E-06	lipin 3 (LPIN3)	LPIN
Cluster-62068.142296	-4.1877	6.78E-09	5.11E-06	leucine-rich repeats and calponin homology (CH) domain containing 3 (LRCH3)	LRCH3
Cluster-62068.93946	-4.1971	1.37E-08	9.19E-06	large tumor suppressor kinase 2 (LATS2)	LATS1_2, Wts
Cluster-62068.179776	-4.2085	7.17E-09	5.35E-06	mitochondrial translational release factor 1 (MTRF1)	prfA, MTRF1, MRF1
Cluster-62068.175538	-4.2116	6.24E-09	4.81E-06	Pan troglodytes BAC clone CH251-696K14 from chromosome 11	--
Cluster-62068.80781	-4.2275	7.49E-09	5.56E-06	histone deacetylase 10 (HDAC10)	HDAC10
Cluster-62068.138194	-4.2355	1.90E-08	1.23E-05	trafficking protein particle complex 9 (TRAPPC9), RefSeqGene on chromosome 8	TRAPPC9
Cluster-62068.66149	-4.2479	5.11E-09	4.16E-06	uncharacterized LOC101683508 (LOC101683508)	--
Cluster-62068.146858	-4.2705	9.11E-09	6.49E-06	growth regulation by estrogen in breast cancer-like (GREB1L)	GREB1L
Cluster-62068.83712	-4.2743	5.82E-09	4.53E-06	mitogen-activated protein kinase kinase kinase 9 (MAP3K9)	MAP3K9
Cluster-62068.90491	-4.2764	8.38E-09	6.09E-06	EPH receptor B6 (EPHB6)	EPHB6
Cluster-62068.75719	-4.2799	3.88E-09	3.23E-06	Leptonychotes weddellii peripheral myelin protein 22 (PMP22)	PMP22
Cluster-62068.124330	-4.2944	9.31E-09	6.54E-06	bleomycin hydrolase (BLMH)	pepC
Cluster-62068.131407	-4.3201	3.31E-09	2.82E-06	Ovis canadensis canadensis isolate 43U chromosome 7 sequence	DHRS4
Cluster-62068.173753	-4.3206	2.50E-09	2.17E-06	WSC domain-containing protein 1-like (LOC101683385)	--
Cluster-62068.86895	-4.3287	3.37E-09	2.85E-06	MON1 secretory trafficking family member B (MON1B)	MON1B
Cluster-62068.153608	-4.3397	1.77E-09	1.62E-06	Ovis canadensis canadensis isolate 43U chromosome 5 sequence	--
Cluster-62068.43297	-4.3507	1.61E-09	1.49E-06	Leptonychotes weddellii zinc finger, DBF-type containing 2 (ZDBF2)	ZDBF2
Cluster-62068.102387	-4.3786	1.92E-09	1.72E-06	mitochondrial translational initiation factor 2 (MTIF2)	infB, MTIF2

Cluster-62068.70627	-4.4052	7.23E-10	7.18E-07	Felis catus ADP-ribosylation factor related protein 1 (ARFRP1)	ARFRP1
Cluster-62068.117871	-4.4384	6.90E-10	6.95E-07	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase (HUWE1)	HUWE1, MULE
Cluster-62068.127344	-4.4816	2.81E-10	3.09E-07	nuclear export mediator factor (NEMF)	NEMF
Cluster-62068.71904	-4.4913	6.68E-10	6.82E-07	forkhead box P1 (FOXP1)	FOXP
Cluster-62068.145686	-4.499	2.60E-10	2.95E-07	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F (MAFF)	MAFF_G_K
Cluster-62068.69045	-4.5071	2.77E-10	3.07E-07	Odobenus rosmarus divergens zinc finger, BED-type containing 3 (ZBED3)	ZBED3
Cluster-62068.134672	-4.5326	4.53E-10	4.72E-07	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2 (SPOCK2)	SPOCK
Cluster-62068.136063	-4.5891	8.53E-10	8.41E-07	aquaporin 10 (AQP10)	AQP10
Cluster-62068.95725	-4.5985	6.82E-11	9.35E-08	flightless I actin binding protein (FLII)	FLII
Cluster-62068.107969	-4.6142	6.10E-11	8.52E-08	ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3)	ENPP1_3
Cluster-62068.103269	-4.6805	1.91E-11	3.09E-08	laminin, alpha 5 (LAMA5)	LAMA3_5
Cluster-62068.100927	-4.6807	6.35E-11	8.80E-08	actin filament associated protein 1 (AFAP1)	AFAP1
Cluster-62068.44460	-4.6868	2.45E-11	3.79E-08	growth regulation by estrogen in breast cancer-like (GREB1L)	GREB1L
Cluster-62068.96424	-4.7362	4.00E-11	5.88E-08	calcium binding protein 39-like (CAB39L)	SETDB2
Cluster-62068.122576	-4.7548	1.42E-10	1.77E-07	ly-6/neurotoxin-like protein 1 (LOC101676258)	--
Cluster-62068.102833	-4.7702	4.51E-11	6.50E-08	sushi domain containing 6 (SUSD6)	SUSD6
Cluster-62068.78683	-4.7948	7.78E-12	1.42E-08	lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR)	TNFRSF3, LTBR
Cluster-62068.153572	-4.8055	6.37E-12	1.21E-08	Ailuropoda melanoleuca uncharacterized LOC105241397 (LOC105241397)	LOC105241397
Cluster-62068.142358	-4.8283	9.69E-12	1.70E-08	Odobenus rosmarus divergens ribonuclease P/MRP 30kDa subunit (RPP30)	RPP1, RPP30
Cluster-62068.117457	-4.8305	2.42E-11	3.79E-08	lon peptidase 2, peroxisomal (LONP2)	lon
Cluster-62068.38701	-4.881	2.28E-12	4.55E-09	zinc finger, MYM-type 6 (ZMYM6)	ZMYM6
Cluster-62068.145617	-4.9079	3.70E-12	7.30E-09	Ailuropoda melanoleuca ER degradation enhancer, mannosidase alpha-like 1 (EDEM1)	EDEM1

Cluster-62068.148818	-4.9324	1.06E-12	2.30E-09	B-cell CLL/lymphoma 9 (BCL9)	BCL9
Cluster-62068.136993	-4.9486	1.17E-11	2.03E-08	jumonji domain containing 6 (JMJD6)	JMJD6
Cluster-62068.79339	-4.953	1.35E-11	2.31E-08	pleckstrin and Sec7 domain containing 3 (PSD3)3	PSD
Cluster-62068.117974	-4.9746	9.97E-13	2.21E-09	acid phosphatase 2, lysosomal (ACP2)	ACP2
Cluster-62068.80034	-5.1559	3.72E-14	1.21E-10	UbiA prenyltransferase domain containing 1 (UBIAD1)	UBIAD1
Cluster-62068.69571	-5.1568	3.87E-14	1.21E-10	trafficking protein particle complex 2 (TRAPPC2)	TRAPPC2
Cluster-62068.90195	-5.1568	6.74E-13	1.57E-09	mitogen-activated protein kinase kinase kinase 1, E3 ubiquitin protein ligase (MAP3K1)	MAP3K1, MEKK1
Cluster-62068.185039	-5.1588	2.19E-13	5.84E-10	5-hydroxytryptamine (serotonin) receptor 1A, G protein-coupled (HTR1A)	HTR1
Cluster-62068.89354	-5.159	3.67E-14	1.21E-10	mediator complex subunit 10 (MED10)	MED10, NUT2
Cluster-62068.149651	-5.1935	4.18E-14	1.25E-10	RAS p21 protein activator 2 (RSA2)	RSA2, GAP1M
Cluster-62068.99877	-5.2119	7.18E-13	1.64E-09	polypyrimidine tract binding protein 1 (PTBP1)	PTBP1, PTB
Cluster-62068.99323	-5.2223	3.76E-15	1.64E-11	ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A (ATP6V1A)	ATPeV1A, ATP6A
Cluster-62068.77187	-5.2425	1.40E-14	4.91E-11	Canis familiaris TCTA gene, AMT gene, NICN1 gene, DAG1 gene and BSN gene	--
Cluster-62068.82680	-5.2523	3.07E-13	7.76E-10	HECT domain containing E3 ubiquitin protein ligase 1 (HECTD1)	HECTD1
Cluster-62068.90540	-5.355	6.36E-15	2.61E-11	WD repeat and FYVE domain containing 2 (WDFY2)	WDFY2
Cluster-62068.85832	-5.4227	2.19E-15	1.05E-11	interleukin 13 receptor, alpha 1 (IL13RA1)	IL13RA1
Cluster-62068.51913	-5.4595	2.31E-15	1.07E-11	tRNA methyltransferase 2 homolog A (TRMT2A)	TRMT2A
Cluster-62068.75652	-5.4893	2.38E-16	1.27E-12	mediator complex subunit 11 (MED11)	MED11
Cluster-62068.60273	-5.5757	1.47E-16	8.13E-13	ras responsive element binding protein 1 (RREB1)	RREB1
Cluster-62068.113249	-5.6508	2.77E-17	1.66E-13	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (AGAP1)	PINK1
Cluster-62068.62596	-5.8227	6.70E-19	5.68E-15	ZXD family zinc finger C (ZXDC)	ZXDC
Cluster-62068.125746	-6.0343	6.47E-20	6.66E-16	immunoglobulin-like variable motif containing (BIVM)	ERCC5, XPG,

					RAD2
Cluster-62068.122018	-6.037	1.99E-19	1.91E-15	uncharacterized LOC101694508 (LOC101694508)	LOC101694508
Cluster-62068.76334	-6.5331	3.17E-34	1.52E-29	NEDD4 binding protein 1 (N4BP1)	N4BP1
Cluster-62068.116422	-7.0783	8.76E-31	2.52E-26	exportin 5 (XPO5)	XPO5
Cluster-62068.77633	-7.7671	3.41E-37	2.46E-32	TEA domain family member 3 (TEAD3)	TEAD

Table S2. Primers used for Q-PCR.

Gene	Primers	PCR product (bp)
EGF	F: CCG TGC TTT GGT TTC CAG TG R: CCA GAT CCA CCA CCC CAA AA	283
HBEGF	F: AGA AGC CCC ACG ATG ACA AG R: CCT CCC AGT GGA AAA TCG CT	105
EGFR	F: ACA CAG TCT TTC GGC TCT GG R: GTT TTC TCT TGC GGT CGT CG	267
ER	F: GCC ATT TGT TCG CTT GCT CA R: ATC TTG GGC TCT CCA ACA CG	206
IGF1	F: CTC GTC CAC AAT GCC TGT CT R: GCT GAA CTG GTG GAT GCT CT	117
LIF	F: CGT CCG GCA TGG AGT GTA AA R: ATC TTC CTT CTC GGT GGT GC	293
FKBP4	F: ACA GTA TCG GTG GAG TTG AAA A R: ATT CCA TGC TGT GGG ACT GG	194
ODC	F: CAG GGT ATT GGG CTG GTG AG R: ATG GTG GTA ATT CTG CGG GG	201

ASMT	F: TCCTGTGCTGTATCCCAACCT R: CCCTATGCTGCCAGAAATCC	119
PDE11	F: CAAAGGGATGCTGTGGACTG R: TGTGAAACTGAAGCCGATGC	217
MCM2	F: TTGCCAGTATTGCTCCTTCC R: TTGATGTCACCTCGCACCTT	121
PMP22	F: TATGGCTTTGCCTACATCCTG R: TGGTATGGTTTGAGTTTGGGTT	210
PIK3C2	F: CCAAGCGGGAACCTCAAGAA R: GAACCTGTAATCATCAGCACCA	219
SLC4A8	F: CCGTGCCAATCCGTTAAG R: AAGAGAGACAAGAAGGGTAGG	107
CD1	F: GCTTGATATTGTTGGCCATAGTAG R: AGGCTTCTGGGTGCTTCTTC	146
GALNT	F: ACCCTTCCAATACCAACGACT R: ATACTTTCTACCTCCATTACCCT	107
VEGFA	F: CAG GAA GAG CGG GGG CT R: GGA GGA GGG ACC TGG GG	101
cmyc	F: AGT GCT TTG GAG TAT CCT TTT CA R: CAT GGT CAC CCC ACC TTA CC	243
PR	F: CTA CCT GTG TGG ACG AAC CC R: CCT AAG GTC TCC CTG ACC GA	121

PRLR	F: TTGCTCTAACCCGAGACTGG R: TTGTTTTGCTGTTAGACTGCGT	128
LAMA3	F: GAAGGACAAGAAGGACGAAGAG R: AACCACAAGTGGCAGGTAAAA	180
GAPDH	F: TAGTGTCCAGGGTGGGTGTT R: CTGTGCTGTTCCGCTGGTTTA	162

PPI network

