10.1071/RD13099_AC

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Supplementary Material

Table S1. Information of reverse transcription qPCR-specific primers of target and housekeeping genes expressed in bovine blastocysts

Gene symbol	Gene name	Accession number	Taqman assay*
ACSL3	acyl-CoA synthetase long-chain family member 3	NM_001205468.1	Bt04282139_m1
ACSL6	acyl-CoA synthetase long-chain family member 6	BC111155.1	Bt03231695_m1
AUH	AU RNA binding protein/enoyl-CoA hydratase	NM_001105436.1	Bt03275798_m1
ELOVL6	ELOVL fatty acid elongase 6	NM_001102155.1	Bt00907566_m1
ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	NM_175796.2	Bt03216728_m1
CAT	catalase	BC103066.1	Bt03228716_m1
GPX4	glutathione peroxidase 4	NM_174770.3	Bt03259613_g1
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	NM_001075148.1	Bt03244880_m1
IFNT2	interferon tau	NM_001015511.3	Bt03210579_g1
PAG2	pregnancy-associated glycoprotein 2	NM_176614.1	Bt03292796_gH
KRT18	keratin 18	NM_001192095.1	Bt00989202_g1
DAD1	defender against cell death 1	NM_001034761.1	Bt03221619_m1

DAP	death-associated protein	BC103332.1	Bt03230650_m1
PRDX2	peroxiredoxin 2	NM_174763.2	Bt03216179_g1
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	AB098979.1	Bt03210913_g1
ACTB	actin, beta	NM_173979.3	Bt03279174_g1
PPIA	peptidylprolyl isomerase A (cyclophilin A)	NM_178320.2	Bt03224614_g1

* Applied Biosystems Taqman Gene Expression Assays Reference.

Table S2. List of differentially expressed transcripts between Simmental and Nellore blastocysts

Representative public ID	Gene title	Gene symbol	Fold change	*P*-value
NM_174133.2	polyubiquitin	*LOC281370*	3.42	0.0107
CK980192	4112256 BARC 9BOV Bos taurus cDNA clone 9BOV41_N23 3-, mRNA sequence	---	2.81	0.0411
BP107621	gastrin-releasing peptide	*GRP*	2.80	0.0131
BE749511	tripartite motif-containing 2	*TRIM2*	2.79	0.0011
NM_174133.2	polyubiquitin	*LOC281370*	2.66	0.0142
CK943278	F11 receptor	*F11R*	2.60	0.0326
CB425639	placenta-specific 8	*PLAC8*	2.59	0.0059
AU278102	CDGSH iron sulfur domain 1	*CISD1*	2.59	0.0331
CK849176	glutamic pyruvate transaminase (alanine aminotransferase) 2	*GPT2*	2.56	0.0116
CK953255	aldehyde dehydrogenase 2 family (mitochondrial)	*ALDH2*	2.55	0.0032
CB420281	desmoglein 2	*DSG2*	2.51	0.0394
CK978263	RAB10, member RAS oncogene family	*RAB10*	2.45	0.0251
CK952849	similar to ribosomal protein S4, X-linked X /// similar to ribosomal protein S4, X-linked X /// similar to ribosomal protein S4, X-linked X /// ribosomal protein S4, X-linked /// ribosomal protein S4, Y-linked 1 /// ribosomal protein S4, Y-linked 2	*LOC781612 /// LOC783463 /// LOC784060 /// RPS4X /// RPS4Y1 /// RPS4Y2*	2.40	0.0235
AY528254.1	COX5A protein	*COX5A*	2.34	0.0307
CK777089	mitochondrial ribosomal protein L22	*MRPL22*	2.33	0.0096
CK959803	chaperonin containing TCP1, subunit 6A (zeta 1)	*CCT6A*	2.29	0.0001
CK848474	myoferlin	*MYOF*	2.29	0.0017
AY342429.1	CD46 molecule, complement regulatory protein	*CD46*	2.20	0.0249
M62428.1	ubiquitin C	*UBC*	2.20	0.0122
CB424390	testis expressed 12	*TEX12*	2.17	0.0055

CB461078	721004 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	2.15	0.0047
CK948740	pyruvate dehydrogenase (lipoamide) alpha 1	*PDHA1*	2.15	0.0202
BP110236	CDC28 protein kinase regulatory subunit 2	*CKS2*	2.13	0.0296
AV618456	pallidin homolog (mouse)	*PLDN*	2.12	0.0003
BI535743	glycogen synthase kinase 3 alpha	*GSK3A*	2.11	0.0298
NM_174025.2	crystallin, zeta (quinone reductase)	*CRYZ*	2.10	0.0104
BP108263	secreted seminal-vesicle Ly-6 protein 1	*SSLP1*	2.09	0.0065
CB533459	succinate-CoA ligase, ADP-forming, beta subunit	*SUCLA2*	2.09	0.0188
CK966474	neuroepithelial cell transforming gene 1	*NET1*	2.09	0.0203
BP105001	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	*PIP4K2A*	2.08	0.0092
NM_174760.2	ribosomal protein L10	*RPL10*	2.06	0.0447
AW656417	eukaryotic translation termination factor 1	*ETF1*	2.05	0.0444
CK848597	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	*ATP5C1*	2.05	0.0145
AV601802	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	*ATP5A1*	2.05	0.0487
CB419743	Transmembrane protein 127	*TMEM127*	2.03	0.0006
CB535261	768672 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	2.03	0.0129
BP102330	ribosomal protein L39	*RPL39*	2.02	0.0325
BM435101	zinc finger protein 36, C3H type-like 1	*ZFP36L1*	2.02	0.0057
NM_174778.1	ribosomal protein S27a	*RPS27A*	1.99	0.0494
AV615649	tetraspanin 6	*TSPAN6*	1.98	0.0297
AV598939	reticulon 3	*RTN3*	1.98	0.0003
NM_175796.2	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	*ATP5B*	1.97	0.0327
CK961717	asparaginyl-tRNA synthetase	*NARS*	1.97	0.0242
CB451598	chaperonin containing TCP1, subunit 4 (delta)	*CCT4*	1.97	0.0368
CB166358	lysosomal-associated membrane protein 2	*LAMP2*	1.97	0.0094
CK848991	prosaposin	*PSAP*	1.95	0.0322

CK959800	synaptosomal-associated protein, 23kDa	*SNAP23*	1.94	0.0043
CB463704	wntless homolog (Drosophila)	*WLS*	1.94	0.0036
NM_174099.2	lactate dehydrogenase A	*LDHA*	1.93	0.0193
CB170586	tumor-associated calcium signal transducer 2	*TACSTD2*	1.92	0.0202
CB424217	COX4 neighbor	*COX4NB*	1.89	0.0225
BE751816	optineurin	*OPTN*	1.88	0.0196
BM435937	polymerase (DNA-directed), epsilon 4 (p12 subunit)	*POLE4*	1.88	0.0122
CK772572	glycerophosphodiester phosphodiesterase 1	*GDE1*	1.87	0.0122
NM_174334.2	hydroxysteroid (17-beta) dehydrogenase 10	*HSD17B10*	1.86	0.0187
AW313986	phosphatidylinositol glycan anchor biosynthesis, class B	*PIGB*	1.84	0.0016
AU232438	heat shock 27kDa protein 1	*HSPB1*	1.84	0.0144
BP107757	ribosomal protein S20	*RPS20*	1.81	0.0103
CB172313	ribosomal protein L7-like 1	*RPL7L1*	1.81	0.0018
CB426729	RNA pseudouridylate synthase domain containing 3	*RPUSD3*	1.81	0.0227
NM_175795.2	cytochrome c oxidase subunit VIIb	*COX7B*	1.81	0.0072
CB533274	tropomyosin 3	*TPM3*	1.80	0.0389
CB433758	non-POU domain containing, octamer-binding	*NONO*	1.79	0.0428
BE681641	tetratricopeptide repeat domain 9C	*TTC9C*	1.79	0.0025
CK775657	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	*LSM7*	1.78	0.0405
CK770115	translocase of inner mitochondrial membrane 8 homolog A (yeast)	*TIMM8A*	1.78	0.0023
BM431714	1Duo26D1.ab1 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA sequence	---	1.78	0.0002
CB531801	signal sequence receptor, delta (translocon-associated protein delta)	*SSR4*	1.77	0.0005
CK960423	cytochrome c, somatic /// similar to cytochrome c-like protein	*CYCS /// LOC100138364*	1.76	0.0310
CK955868	arginine and glutamate rich 1	*ARGLU1*	1.76	0.0234
BE758011	zinc and ring finger 1	*ZNRF1*	1.76	0.0078

CK955677	keratin 19	*KRT19*	1.75	0.0294
BE721168	ubiquitin-conjugating enzyme E2F (putative)	*UBE2F*	1.75	0.0277
CK975252	ubiquinol-cytochrome c reductase complex 7.2 kDa protein	*UQCR10*	1.73	0.0417
CB443641	valosin containing protein (p97)/p47 complex interacting protein 1	*VCPIP1*	1.73	0.0216
CB460291	sorting nexin 6	*SNX6*	1.73	0.0201
CK846588	ribosomal protein L26-like 1	*RPL26L1*	1.73	0.0152
CK848926	protein disulfide isomerase family A, member 6	*PDIA6*	1.72	0.0139
CK772515	claudin 6	*CLDN6*	1.72	0.0214
CK972168	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	*ELOVL6*	1.71	0.0180
CB533579	RAB10, member RAS oncogene family	*RAB10*	1.71	0.0479
BP107394	ribosomal protein L21	*RPL21*	1.71	0.0381
CK848419	cell division cycle associated 8	*CDCA8*	1.71	0.0119
CK773855	eukaryotic translation elongation factor 1 gamma	*EEF1G*	1.71	0.0245
CB170168	SAR1 homolog A (S. cerevisiae)	---	1.70	0.0157
CK771620	similar to G protein-coupled receptor	*LOC782069*	1.70	0.0075
CK772180	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	*ATP6V0D2*	1.70	0.0476
CK778641	mutS homolog 6 (E. coli)	*MSH6*	1.70	0.0233
CK775344	mitochondrial ribosomal protein S15	*MRPS15*	1.69	0.0255
CB421885	proteasome (prosome, macropain) subunit, beta type, 2	*PSMB2*	1.69	0.0407
CB441821	similar to mCG142710	*LOC511229*	1.69	0.0090
CK944937	cytoskeleton associated protein 2	*CKAP2*	1.68	0.0404
CB168209	Influenza virus NS1A binding protein	*IVNS1ABP*	1.67	0.0118
BM256963	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	*DDX19A*	1.67	0.0413
CB425905	basic leucine zipper and W2 domains 1	*BZW1*	1.66	0.0187
BM434841	PREDICTED: PWWP domain-containing protein 2A	*PWWP2A*	1.66	0.0389
BP109396	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	*SLC25A20*	1.66	0.0104
BP102572	CD59 molecule, complement regulatory protein	*CD59*	1.65	0.0490

CK975531	biliverdin reductase A	*BLVRA*	1.65	0.0071
CK971899	CDC5 cell division cycle 5-like (S. pombe)	*CDC5L*	1.65	0.0258
CK848123	ribosomal protein S24; similar to ribosomal protein S24	---	1.64	0.0073
BE682761	181057 MARC 4BOV Bos taurus cDNA 5-, mRNA sequence	---	1.64	0.0027
AU278120	transmembrane protein 209	*TMEM209*	1.63	0.0038
CB433125	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	*DDX3X*	1.63	0.0077
CK951444	transmembrane protein 20	*TMEM20*	1.63	0.0137
CK959397	polymerase (RNA) II (DNA directed) polypeptide F	*POLR2F*	1.62	0.0471
CK772522	karyopherin alpha 3 (importin alpha 4)	*KPNA3*	1.62	0.0076
NM_174212.1	UDP-glucose pyrophosphorylase 2	*UGP2*	1.62	0.0286
CK769700	abhydrolase domain containing 11	*ABHD11*	1.61	0.0081
CK948835	sorbin and SH3 domain-containing protein 1	*SORBS1*	1.61	0.0083
CK950633	kinesin family member 23	*KIF23*	1.61	0.0125
CB461980	heme binding protein 1	*HEBP1*	1.61	0.0009
CB451616	706397 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	1.61	0.0008
CK772462	mitochondrial ribosomal protein L39	*MRPL39*	1.61	0.0027
CK777982	cystatin B (stefin B)	*CSTB*	1.60	0.0426
CB428736	BCL2-associated athanogene 2	*BAG2*	1.60	0.0363
BE236706	galactose mutarotase (aldose 1-epimerase)	*GALM*	1.60	0.0073
NM_175803.2	tubulin folding cofactor A	*TBCA*	1.60	0.0334
CB168605	similar to ribophorin I	*LOC617690*	1.60	0.0325
CB166510	splicing factor 3b, subunit 2, 145kDa	*SF3B2*	1.59	0.0254
BE665193	rabaptin, RAB GTPase binding effector protein 1	*RABEP1*	1.59	0.0193
CB467596	transmembrane protein 167A	*TMEM167A*	1.59	0.0003
NM_174465.2	SEC11 homolog A (S. cerevisiae)	*SEC11A*	1.59	0.0441
AV602127	eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*	1.59	0.0044
NM_175822.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	*NDUFB4*	1.59	0.0060

CK947713	transmembrane protein 49	*TMEM49*	1.58	0.0361
AV607802	nuclear receptor coactivator 1	*NCOA1*	1.57	0.0032
CB451234	ribosomal protein L36a-like	*RPL36AL*	1.57	0.0164
CK775424	ecdysoneless homolog (Drosophila)	*ECD*	1.57	0.0116
CK775235	polymerase (RNA) I polypeptide E, 53kDa	*POLR1E*	1.57	0.0039
CK967668	calpain 2, (m/II) large subunit	*CAPN2*	1.57	0.0180
CK965677	aldolase A, fructose-bisphosphate	*ALDOA*	1.56	0.0058
CK770196	mitochondrial ribosomal protein L16	*MRPL16*	1.56	0.0174
CB461416	TBC1 domain family, member 4	*TBC1D4*	1.55	0.0081
BP109944	solute carrier family 30 (zinc transporter), member 5	*SLC30A5*	1.55	0.0068
CK772666	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	*BUB1B*	1.54	0.0059
CK845911	phospholipase C, gamma 1	---	1.54	0.0469
NM_176613.2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	*ATP5G2*	1.54	0.0370
BM087625	reticulon 4 interacting protein 1	*RTN4IP1*	1.53	0.0088
CB533320	defender against cell death 1	*DAD1*	1.53	0.0355
CK776397	overexpressed breast tumor protein homolog	*TOMM6*	1.52	0.0334
CK771323	chromosome 19 open reading frame 63 ortholog	*C18H19ORF63*	1.52	0.0260
BG937530	TWIST neighbor	*TWISTNB*	1.52	0.0002
CK849084	chromosome 14 open reading frame 147 ortholog	*C21H14orf147*	1.52	0.0061
CK778368	TPX2, microtubule-associated, homolog (Xenopus laevis)	*TPX2*	1.51	0.0206
BF046219	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	*SNRPD2*	1.51	0.0223
CK967463	vacuolar protein sorting 29 homolog (S. cerevisiae)	*VPS29*	1.51	0.0216
BP102272	X (inactive)-specific transcript	*XIST*	1.51	0.0482
CK849726	coiled-coil-helix-coiled-coil-helix domain containing 3	*CHCHD3*	1.50	0.0269
CK965203	AU RNA binding protein/enoyl-CoA hydratase	*AUH*	1.50	0.0145
CK775497	fibrillarin	*FBL*	1.50	0.0251
BE237565	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	*SUGT1*	1.50	0.0262
CK953132	aldo-keto reductase family 1, member A1 (aldehyde	*AKR1A1*	–1.61	0.0053

	reductase)			
BF605641	zinc ribbon domain containing 1	*ZNRD1*	–1.71	0.0062
CB426568	synaptonemal complex protein 3	*SYCP3*	–1.98	0.0190
BP108137	BP108137 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone ORCS116263-, mRNA sequence	---	–1.99	0.0004
CB440375	interleukin 33	*IL33*	–2.01	0.0224
NM_176614.1	pregnancy-associated glycoprotein 2	*PAG2*	–2.28	0.0001

Table S3. List of differentially expressed transcripts between *in vivo*- (MODE) and *in vitro*- (IVP) produced bovine blastocysts

Representative public ID	Gene title	Gene symbol	Fold change	*P*-value
CB427000	Transcribed locus, moderately similar to NP_989434.1 gamma-adducin [Gallus gallus]	---	–4.56	0.0001
BF043546	S100 calcium binding protein A2	*S100A2*	–4.35	0.0001
CB171376	major allergen Equ c 1-like	*LOC783399*	–4.18	0.0020
CK953121	plastin 1	*PLS1*	–4.03	0.0008
BE752516	shisa homolog 2 (Xenopus laevis)	*SHISA2*	–3.92	0.0001
CB166446	nucleobindin 2	*NUCB2*	–3.85	0.0001
M31556.1	interferon tau	*IFNT2*	–3.76	0.0001
CK772448	tubulin, beta 2A	*TUBB2B*	–3.66	0.0003
CK955586	destrin (actin depolymerizing factor)	*DSTN*	–3.53	0.0010
AU278717	P antigen family, member 4 (prostate associated)	*PAGE4*	–3.47	0.0014
CK848316	palladin, cytoskeletal associated protein	*PALLD*	–3.46	0.0007
CK775121	heme binding protein 2	*HEBP2*	–3.42	0.0006
CK976192	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	*HMGCS1*	–3.41	0.0040
CK847756	actin, gamma 1	*ACTG1*	–3.36	0.0114
NM_174431.1	peroxiredoxin 1	*PRDX1*	–3.34	0.0094
CK848418	keratin 18	*KRT18*	–3.31	0.0006
CK950834	cyclin G1	*CCNG1*	–3.30	0.0002
NM_174409.2	osteoclast stimulating factor 1	*OSTF1*	–3.27	0.0025
CK974301	pituitary tumor-transforming 1 interacting protein	*PTTG1IP*	–3.25	0.0015
CK968451	glycyl-tRNA synthetase	*GARS*	–3.19	0.0001

CB170514	ribosomal protein L7	*RPL7*	–3.15	0.0153
CB165272	WD repeat domain 54	*WDR54*	–3.13	0.0016
CB436429	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	*MTHFD2*	–3.12	0.0002
CK961820	cytochrome P450, family 51, subfamily A, polypeptide 1	*CYP51A1*	–3.07	0.0012
NM_174062.2	ferritin, heavy polypeptide 1	*FTH1*	–3.03	0.0068
NM_174099.2	lactate dehydrogenase A	*LDHA*	–3.00	0.0001
CB171187	ATPase, Na+/K+ transporting, beta 3 polypeptide	*ATP1B3*	–2.96	0.0034
NM_174650.1	S100 calcium-binding protein A10	*S100A10*	–2.94	0.0004
CK776082	plasma membrane proteolipid (plasmolipin)	*PLLP*	–2.94	0.0001
CK969361	tumor protein, translationally-controlled 1	*TPT1*	–2.93	0.0051
CB461365	PREDICTED: Bos taurus uncharacterized LOC100850521 (LOC100850521), miscRNA	---	–2.93	0.0092
CK955677	keratin 19	*KRT19*	–2.93	0.0001
CK848695	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	*HSPA5*	–2.92	0.0018
CK780160	ribosomal protein S27-like	*RPS27L*	–2.91	0.0033
BM435101	zinc finger protein 36, C3H type-like 1	*ZFP36L1*	–2.91	0.0001
CK972401	chloride intracellular channel 1	*CLIC1*	–2.90	0.0170
BI680642	clathrin, heavy chain (Hc)	*CLTC*	–2.87	0.0199
CB443595	tumor protein, translationally-controlled 1	*TPT1*	–2.87	0.0186
AV615649	tetraspanin 6	*TSPAN6*	–2.83	0.0008
CB171354	epithelial cell adhesion molecule	*EPCAM*	–2.80	0.0029
CK966964	Protein tyrosine phosphatase type IVA, member 1	*PTP4A1*	–2.79	0.0165
CK948397	eukaryotic translation elongation factor 1 beta 2	*EEF1B*	–2.79	0.0159
CK848320	ornithine aminotransferase	*OAT*	–2.78	0.0185
CB168618	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	*GNB2L1*	–2.78	0.0050
CK849687	lectin, galactoside-binding, soluble, 3	*LGALS3*	–2.76	0.0169
AB032826.1	selenoprotein P, plasma, 1	*SEPP1*	–2.76	0.0017

NM_174149.1	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	*ATP6V0C*	–2.75	0.0058
CK728409	cornichon homolog 4 (Drosophila)	*CNIH4*	–2.74	0.0015
AF013064	ribosomal protein L6	*RPL6*	–2.74	0.0249
BM252020	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	*DEGS1*	–2.73	0.0062
CK969361	tumor protein, translationally-controlled 1	*TPT1*	–2.73	0.0142
NM_174780.2	brain abundant, membrane attached signal protein 1	*BASP1*	–2.72	0.0156
CB172029	ribosomal protein L4	*RPL4*	–2.72	0.0117
X04851.1	clathrin, light chain (Lca)	*CLTA*	–2.71	0.0054
BF889659	RAB5-interacting protein	*RIP5*	–2.70	0.0098
BG358191	golgin A4	*GOLGA4*	–2.69	0.0069
CK969180	ribosomal protein L9	*RPL9*	–2.68	0.0151
CK770477	cysteine and glycine-rich protein 2	*CSRP2*	–2.67	0.0183
NM_173968.2	thioredoxin	*TXN*	–2.67	0.0024
CK977042	testis expressed 2	*TEX2*	–2.67	0.0005
AW315315	12525 MARC 2BOV Bos taurus cDNA 5-, mRNA sequence	---	–2.67	0.0213
NM_174315.2	fatty acid binding protein 5 (psoriasis-associated)	*FABP5*	–2.65	0.0001
BM929161	ribosomal protein L23	*RPL23*	–2.64	0.0109
NM_174689.1	ADP-ribosylation factor 4	*ARF4*	–2.61	0.0001
AB099060.1	ribosomal protein S2	*RPS2*	–2.60	0.0094
NM_173893.1	beta-2-microglobulin	*B2M*	–2.60	0.0078
CB166924	ribosomal protein L5	*RPL5*	–2.60	0.0093
CK948251	sorting nexin 2	*SNX2*	–2.59	0.0146
CK968996	sorbitol dehydrogenase	*SORD*	–2.59	0.0100
CK848675	AHNAK nucleoprotein	*AHNAK*	–2.58	0.0041
CK941764	transmembrane protein 14C	*TMEM14C*	–2.57	0.0074
CB168037	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	*SLC16A1*	–2.57	0.0060
NM_174147.2	plasminogen activator, urokinase	*PLAU*	–2.56	0.0023

CK953000	lactate dehydrogenase B	*LDHB*	–2.56	0.0357
CK952806	similar to ribosomal protein S6-like /// ribosomal protein S6	*LOC787914 /// RPS6*	–2.54	0.0137
CK975591	carboxymethylenebutenolidase homolog (Pseudomonas)	*CMBL*	–2.53	0.0001
BP103379	PREDICTED: Bos taurus uncharacterized LOC100847108 (LOC100847108), miscRNA	---	–2.52	0.0001
CK940634	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	*GNAI3*	–2.50	0.0030
CK778202	phosphatidylinositol transfer protein, alpha	*PITPNA*	–2.48	0.0002
BE750213	claudin 23	*CLDN23*	–2.48	0.0053
NM_174472.2	TIMP metallopeptidase inhibitor 2	*TIMP2*	–2.46	0.0001
CB171483	nucleosome assembly protein 1-like 1	*NAP1L1*	–2.46	0.0097
CK974042	ribosomal protein S3A	*RPS3A*	–2.46	0.0189
CB451042	eukaryotic translation initiation factor 1A, X-linked	*EIF1AX*	–2.45	0.0187
AV602127	eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1	*EEF1A1 /// LOC782989 /// LOC789867*	–2.45	0.0124
BP108852	ribosomal protein S18	*RPS18*	–2.44	0.0211
AW266900	fragile X mental retardation, autosomal homolog 1	*FXR1*	–2.44	0.0110
AW657942	Bos taurus cDNA clone IMAGE:7944277	---	–2.44	0.0350
CK770348	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	*CASK*	–2.44	0.0003
BP108127	ribosomal protein L27	*RPL27*	–2.43	0.0217
CK770030	ribosomal protein L11	*RPL11*	–2.42	0.0239
BM251913	ribosomal protein S14	*RPS14*	–2.42	0.0096
CB420281	desmoglein 2	*DSG2*	–2.42	0.0286
CB423230	CD48 molecule	*CD48*	–2.41	0.0288
CK770847	heme oxygenase (decycling) 1	*HMOX1*	–2.39	0.0009
NM_175784.2	annexin A1	*ANXA1*	–2.39	0.0219

CB425639	placenta-specific 8	*PLAC8*	–2.38	0.0053
NM_174760.2	ribosomal protein L10	*RPL10*	–2.38	0.0119
CB172030	cornichon homolog 4 (Drosophila)	*CNIH4*	–2.38	0.0001
BM483751	golgi reassembly stacking protein 2, 55kDa	*GORASP2*	–2.37	0.0021
CK953606	cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 4	*CYP3A28*	–2.37	0.0426
CK957037	RAB11A, member RAS oncogene family	*RAB11A*	–2.37	0.0257
CK953368	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	*YWHAQ*	–2.37	0.0217
CB166882	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	*NPM1*	–2.36	0.0481
CK771078	gamma-inducible protein 30	*IFI30*	–2.36	0.0001
CB165323	phosphatidylethanolamine binding protein	*PEBP1*	–2.36	0.0269
NM_174806.2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	*GOT2*	–2.36	0.0025
CB165391	actin related protein 2/3 complex, subunit 5, 16kDa	*ARPC5*	–2.36	0.0005
CK848538	heat shock 70kDa protein 4	*HSPA4*	–2.35	0.0304
BP105001	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	*PIP4K2A*	–2.34	0.0020
CK972263	translocation associated membrane protein 1	*TRAM1*	–2.34	0.0065
CK953351	hydroxysteroid (17-beta) dehydrogenase 11	*HSD17B11*	–2.34	0.0398
CA035980	ribosomal protein S23	*RPS23*	–2.34	0.0339
BE682987	core-binding factor, beta subunit	---	–2.34	0.0132
NM_175782.1	lectin, galactoside-binding, soluble, 1	*LGALS1*	–2.33	0.0041
CK941606	ribosomal protein L3	*Rpl3*	–2.33	0.0212
BE756166	quaking homolog, KH domain RNA binding (mouse)	---	–2.32	0.0025
CK848838	CAP, adenylate cyclase-associated protein 1 (yeast)	*CAP1*	–2.32	0.0061
CB424390	testis expressed 12	*TEX12*	–2.31	0.0019
CK945714	Obg-like ATPase 1	*OLA1*	–2.31	0.0196
CK845887	ATPase, H+ transporting, lysosomal V0 subunit a4	*ATP6V0A4*	–2.31	0.0034
CB167946	ribosomal protein S3	*RPS3*	–2.31	0.0108
NM_174241.2	annexin A8	*ANXA8*	–2.31	0.0039

CK978877	heterogeneous nuclear ribonucleoprotein A/B	*HNRNPAB*	–2.30	0.0221
CK956896	keratin 8	*KRT8*	–2.29	0.0017
CK945417	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	*TCEB1*	–2.29	0.0090
CK953517	programmed cell death 6	*PDCD6*	–2.29	0.0088
BP107427	ribosomal protein L26	*RPL26*	–2.29	0.0224
CB537825	PREDICTED: Bos taurus uncharacterized LOC100848375 (LOC100848375), miscRNA	---	–2.28	0.0001
CK979098	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	*NFU1*	–2.28	0.0054
CK770170	Asparaginase like 1	*ASRGL1*	–2.28	0.0212
CB166901	phosphoserine aminotransferase 1	*PSAT1*	–2.28	0.0005
CK941902	oxysterol binding protein-like 1A	*OSBPL1A*	–2.28	0.0241
CB449605	chloride intracellular channel 4	*CLIC4*	–2.28	0.0059
CK775789	transmembrane protein 97	*TMEM97*	–2.28	0.0215
M81190.1	desmocollin 2	*DSC2*	–2.28	0.0066
CB433697	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	*PSMD14*	–2.27	0.0318
CK952849	similar to ribosomal protein S4, X-linked X /// similar to ribosomal protein S4, X-linked X /// similar to ribosomal protein S4, X-linked X /// ribosomal protein S4, X-linked /// ribosomal protein S4, Y-linked 1 /// ribosomal protein S4, Y-linked 2	*LOC781612 /// LOC783463 /// LOC784060 /// RPS4X /// RPS4Y1 /// RPS4Y2*	–2.27	0.0218
BI538866	ADAM metallopeptidase domain 9 (meltrin gamma)	*ADAM9*	–2.27	0.0042
BE751337	acyl-CoA synthetase long-chain family member 3	*ACSL3*	–2.27	0.0075
CK848926	protein disulfide isomerase family A, member 6	*PDIA6*	–2.26	0.0006
CB533161	transmembrane BAX inhibitor motif containing 6	*TMBIM6*	–2.26	0.0041
NM_175813.1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	*EIF2S1*	–2.25	0.0174
CB533458	synaptophysin-like 1	*SYPL1*	–2.25	0.0029
CB169082	ribosomal protein, large, P0	*RPLP0*	–2.25	0.0226

D00467.1	ferredoxin 1	*FDX1*	–2.24	0.0046
CB531064	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	*ST13*	–2.24	0.0376
CK974513	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	*PSMD11*	–2.24	0.0192
NM_176614.1	pregnancy-associated glycoprotein 2	*PAG2*	–2.24	0.0001
CK779560	UMC-bend_0A02-013-e05 Day 8 Uterus bend Bos taurus cDNA 3-, mRNA sequence	---	–2.24	0.0008
AW485507	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	*EIF2S3*	–2.24	0.0298
CK973336	ribosomal protein, large, P0	*RPLP0*	–2.24	0.0019
CK966418	4081208 BARC 9BOV Bos taurus cDNA clone 9BOV1_A09 3-, mRNA sequence	---	–2.23	0.0009
CK972818	Parkinson disease (autosomal recessive, early onset) 7	*PARK7*	–2.23	0.0041
BI539096	KH domain containing, RNA binding, signal transduction associated 1	*KHDRBS1*	–2.22	0.0003
BM366524	family with sequence similarity 32, member A	*FAM32A*	–2.21	0.0188
BE236720	capping protein (actin filament) muscle Z-line, alpha 1	*CAPZA1*	–2.21	0.0167
NM_175780.1	myosin, light chain 6, alkali, smooth muscle and non-muscle	*MYL6*	–2.21	0.0200
CK728106	SUB1 homolog (S. cerevisiae)	*SUB1*	–2.21	0.0078
NM_174049.1	enolase 1, (alpha)	*ENO1*	–2.21	0.0035
CB420617	solute carrier family 13 (sodium/sulfate symporters), member 4	*SLC13A4*	–2.21	0.0006
NM_175814.2	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	*SDHC*	–2.21	0.0157
CK961971	ribosomal protein L17	*RPL17*	–2.21	0.0448
NM_205797.1	similar to 60S ribosomal protein L12 /// ribosomal protein L12	*LOC784762 /// RPL12*	–2.21	0.0308
CK774588	tight junction protein 1 (zona occludens 1)	*TJP1*	–2.20	0.0125
CB165372	similar to MORF-related gene 15	*LOC785568*	–2.20	0.0459

CK948193	integral membrane protein 2B	*ITM2B*	–2.19	0.0104
CK849608	eukaryotic translation elongation factor 2	*EEF2*	–2.19	0.0486
CB464010	mitochondrial carrier homolog 1 (C. elegans)	*MTCH1*	–2.18	0.0176
CK969113	ornithine decarboxylase antizyme 1	*OAZ1*	–2.18	0.0295
BM251691	ribosomal protein L27a	*RPL27A*	–2.18	0.0243
AY528251.1	ribosomal protein S12	*RPS12*	–2.18	0.0342
CB445831	quinone oxidoreductase-like protein 2-like	*LOC100299281*	–2.17	0.0002
CB463704	wntless homolog (Drosophila)	*WLS*	–2.17	0.0009
CB448765	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	*CLN8*	–2.17	0.0003
CB535820	SMAD specific E3 ubiquitin protein ligase 2	*SMURF2*	–2.17	0.0073
CK849793	sequestosome 1	*SQSTM1*	–2.16	0.0456
CK773855	eukaryotic translation elongation factor 1 gamma	*EEF1G*	–2.16	0.0024
CB167065	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	*ITGB1*	–2.16	0.0412
BM255343	myosin, light chain 7, regulatory	*MYL7*	–2.16	0.0001
CK961338	SEC31 homolog A (S. cerevisiae)	*SEC31A*	–2.15	0.0097
CK770475	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	*HIF1A*	–2.15	0.0005
NM_174217.1	ezrin	*EZR*	–2.14	0.0136
CK770613	filamin binding LIM protein 1	*FBLIM1*	–2.14	0.0004
NM_177516.1	glutathione S-transferase pi 1	*GSTP1*	–2.13	0.0014
CK769429	lysosomal-associated membrane protein 1	*LAMP1*	–2.13	0.0010
CK968736	ribosomal protein S8	*RPS8*	–2.13	0.0465
CB530156	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	*CALM1 /// CALM3*	–2.13	0.0028
CB433764	Kruppel-like factor 6	*KLF6*	–2.12	0.0030
CK848693	mesoderm development candidate 2	*MESDC2*	–2.12	0.0046
CK848313	eukaryotic translation initiation factor 4B	*EIF4B*	–2.12	0.0209
CB171490	similar to Coiled-coil-helix-coiled-coil-helix domain	---	–2.12	0.0100

	Transcribed locus, strongly similar to XP_343484.1 PREDICTED: dystroglycan 1 (dystrophin-associated glycoprotein 1) [Rattus norvegicus]			
CB451437	transmembrane 9 superfamily member 2	*TM9SF2*	–2.12	0.0285
CK965736	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	*VAPA*	–2.11	0.0395
CB170586	tumor-associated calcium signal transducer 2	*TACSTD2*	–2.11	0.0080
NM_174281.2	coatomer protein complex, subunit beta 2 (beta prime)	*COPB2*	–2.11	0.0325
CB456571	RAB1A, member RAS oncogene family	*RAB1A*	–2.11	0.0161
BM435937	polymerase (DNA-directed), epsilon 4 (p12 subunit)	*POLE4*	–2.11	0.0038
CK969757	ubiquitin carboxyl-terminal hydrolase L5	*UCHL5*	–2.11	0.0146
CB166320	splicing factor, arginine/serine-rich 3	*SFRS3*	–2.10	0.0419
BE750474	NCK adaptor protein 1	*NCK1*	–2.10	0.0006
NM_174729.2	voltage-dependent anion channel 1 pseudogene 5	*VDAC1P5*	–2.10	0.0025
CK949239	signal peptidase complex subunit 2 homolog (S. cerevisiae)	*SPCS2*	–2.10	0.0209
CK773259	bifunctional apoptosis regulator	*BFAR*	–2.10	0.0341
CK849836	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	*STT3B*	–2.10	0.0001
CB421885	proteasome (prosome, macropain) subunit, beta type, 2	*PSMB2*	–2.09	0.0063
CK848736	peptidase (mitochondrial processing) beta	*PMPCB*	–2.09	0.0135
CB440375	interleukin-33	*IL33*	–2.09	0.0143
CK849088	MHC class I antigen /// MHC Class I JSP.1 /// hypothetical protein 100125016	*BOLA-N /// JSP.1 /// LOC100125916*	–2.09	0.0100
CK948152	similar to Protein-S-isoprenylcysteine O-methyltransferase (Isoprenylcysteine carboxylmethyltransferase) (Prenylcysteine carboxyl methyltransferase) (pcCMT) (Prenylated protein carboxyl methyltransferase) (PPMT)	---	–2.09	0.0002
CB459236	desmoplakin	*DSP*	–2.09	0.0081

NM_174778.1	ribosomal protein S27a	*RPS27A*	–2.08	0.0335
NM_174749.2	peroxiredoxin 5	*PRDX5*	–2.08	0.0023
CB455141	actin related protein 2/3 complex, subunit 2, 34kDa /// similar to actin related protein 2/3 complex subunit 2	*ARPC2 /// LOC785054*	–2.08	0.0324
BE685292	podoplanin	*PDPN*	–2.08	0.0204
CB444452	p21 protein (Cdc42/Rac)-activated kinase 1	*PAK1*	–2.08	0.0003
CK847195	stratifin	*SFN*	–2.08	0.0003
AB099060.1	ribosomal protein S2	*RPS2*	–2.07	0.0226
CK951179	CSE1 chromosome segregation 1-like (yeast)	*CSE1L*	–2.07	0.0124
CB531601	eukaryotic translation initiation factor 1	*EIF1*	–2.07	0.0315
AV601221	ribosomal protein L8	*RPL8*	–2.06	0.0247
CB172782	SFT2 domain containing 1	*SFT2D1*	–2.06	0.0158
CK848915	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	*MLH1*	–2.05	0.0017
CK769520	oligosaccharyltransferase complex subunit	*OSTC*	–2.05	0.0107
AV618700	WW domain-binding protein 2	*WBP2*	–2.05	0.0271
BE478318	Protein FAM177A1	*FAM177A1*	–2.05	0.0193
CK849191	X-box binding protein pseudogene 1	*XBPP1*	–2.05	0.0004
NM_174568.1	poly(A) binding protein, cytoplasmic 1	*PABPC1*	–2.04	0.0214
NM_174455.2	ribosomal protein L24	*RPL24*	–2.04	0.0138
AU276080	ADP-ribosylation factor-like protein 8A	---	–2.04	0.0006
CK967649	zinc finger protein 207	*ZNF207*	–2.04	0.0094
CK849180	translocase of outer mitochondrial membrane 20 homolog (yeast)	*TOMM20*	–2.04	0.0491
AV610198	prolyl 4-hydroxylase, beta polypeptide	*P4HB*	–2.04	0.0236
CK964985	annexin A3	*ANXA3*	–2.04	0.0012
CB168642	chromosome 20 open reading frame 30 ortholog	*C13H20orf30*	–2.04	0.0047
CK948574	beta-2-microglobulin	*B2M*	–2.03	0.0037
BP101535	phosphatidylinositol binding clathrin assembly protein	*PICALM*	–2.03	0.0345
NM_174333.2	protein disulfide isomerase family A, member 3	*PDIA3*	–2.03	0.0050

NM_174711.2	casein kinase 1, alpha 1	*CSNK1A1*	–2.03	0.0045
BP108263	secreted seminal-vesicle Ly-6 protein 1	*SSLP1*	–2.03	0.0075
CB533579	RAB10, member RAS oncogene family	*RAB10*	–2.02	0.0133
BM433128	FK506 binding protein 9, 63 kDa	---	–2.02	0.0027
CK975976	death-associated protein	*DAP*	–2.02	0.0016
AY342429.1	CD46 molecule, complement regulatory protein	*CD46*	–2.01	0.0397
NM_174226.2	ARP3 actin-related protein 3 homolog (yeast)	*ACTR3*	–2.01	0.0350
CK974450	basic transcription factor 3	*BTF3*	–2.01	0.0154
CK776121	NSA2 ribosome biogenesis homolog (S. cerevisiae)	*NSA2*	–2.00	0.0197
CB439434	similar to testis derived transcript /// testis derived transcript (3 LIM domains)	*LOC789240 /// TES*	–2.00	0.0007
CK847310	syntaxin 8	*STX8*	–2.00	0.0072
CB461909	ATX1 antioxidant protein 1 homolog (yeast)	*ATOX1*	–2.00	0.0001
AV618619	presenilin 1	*PSEN1*	–2.00	0.0280
CK948244	malate dehydrogenase 1, NAD (soluble)	*MDH1*	–1.99	0.0361
AV608010	laminin, gamma 1 (formerly LAMB2)	*LAMC1*	–1.99	0.0005
CK774111	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	*PSMD10*	–1.99	0.0012
BM104814	dynein, light chain, Tctex-type 3 /// similar to TCTE1L	*DYNLT3 /// LOC782745*	–1.99	0.0224
CB463753	ribosomal protein S16	*RPS16*	–1.99	0.0449
CB431775	Bos taurus uncharacterized LOC100847427 (LOC100847427), miscRNA	---	–1.99	0.0008
BE722892	F-box protein 7	*FBXO7*	–1.99	0.0181
AU276294	3-hydroxy-3-methylglutaryl-CoA reductase	*HMGCR*	–1.99	0.0479
BP108845	ribosomal protein S21	*RPS21*	–1.98	0.0045
CB165258	sterol-C4-methyl oxidase-like	*SC4MOL*	–1.98	0.0074
CK977244	ribosomal protein L19	*RPL19*	–1.98	0.0100
CK846611	tumor susceptibility gene 101	*TSG101*	–1.98	0.0108
CK847264	lysosomal protein transmembrane 4 alpha	*LAPTM4A*	–1.97	0.0177

AY241933.1	stearoyl-CoA desaturase (delta-9-desaturase)	*SCD*	–1.97	0.0060
CB446456	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1	*TSTD1*	–1.97	0.0285
NM_175803.2	tubulin folding cofactor A	*TBCA*	–1.97	0.0051
CK974463	dynein, cytoplasmic 1, intermediate chain 2	*DYNC1I2*	–1.97	0.0410
CB431074	ribosomal protein S25 /// similar to mCG10725	*RPS25 /// RPS25*	–1.96	0.0361
CK848228	nuclear factor (erythroid-derived 2)-like 2	*NFE2L2*	–1.96	0.0208
CB456714	CTTNBP2 N-terminal-like protein	---	–1.96	0.0296
CB432286	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	*ALG9*	–1.96	0.0003
NM_174343.2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	*HSD3B1*	–1.96	0.0003
BP108713	ribosomal protein L23a	*RPL23A*	–1.95	0.0348
CK848474	myoferlin	*MYOF*	–1.94	0.0068
CK979703	plakophilin 2	*PKP2*	–1.94	0.0357
CB464066	clathrin, heavy chain (Hc)	*CLTC*	–1.94	0.0424
BE684355	protein tyrosine phosphatase, receptor type, K	*PTPRK*	–1.94	0.0014
CK961552	EFR3 homolog A (S. cerevisiae)	*EFR3A*	–1.94	0.0079
CK975718	nuclear receptor coactivator 4	*NCOA4*	–1.93	0.0137
NM_174810.2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	*ATP6V1E1*	–1.93	0.0082
CK981091	signal sequence receptor, alpha	*SSR1*	–1.93	0.0047
AU275302	GLI pathogenesis-related 2	*GLIPR2*	–1.92	0.0302
NM_174340.2	histidine triad nucleotide binding protein 2	*HINT2*	–1.92	0.0062
CK773920	protease, serine, 23	*PRSS23*	–1.92	0.0005
CK963545	endothelial PAS domain protein 1	*EPAS1*	–1.92	0.0119
CK974007	mesencephalic astrocyte-derived neurotrophic factor	*MANF*	–1.92	0.0041
BP108915	dynein, light chain, LC8-type 1	*DYNLL1*	–1.92	0.0093
CK848969	Transcription elongation factor A (SII)-like 8	*TCEAL8*	–1.92	0.0002
AV602184	tubulin, alpha 1a /// tubulin, alpha 1b /// tubulin, alpha 1c	*TUBA1A ///*	–1.91	0.0069

		TUBA1B /// TUBA1C		
BE752394	ribosomal protein L31	*RPL31*	–1.91	0.0472
BE666389	stress-associated endoplasmic reticulum protein 1	*SERP1*	–1.91	0.0013
CK951982	general transcription factor IIE, polypeptide 2, beta 34kDa	*GTF2E2*	–1.91	0.0443
AU275257	ribosomal protein L18	*RPL18*	–1.91	0.0137
CK953663	ribosomal protein SA	*RPSA*	–1.90	0.0065
CB451598	chaperonin containing TCP1, subunit 4 (delta)	*CCT4*	–1.90	0.0492
CB430170	606040 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.90	0.0162
CK960868	thioesterase superfamily member 4	*THEM4*	–1.90	0.0006
CK963094	hypothetical protein MGC127538	*MGC127538*	–1.90	0.0392
AW311862	desmocollin 2	---	–1.90	0.0002
BP106980	aldo-keto reductase family 1, member B1 (aldose reductase)	*AKR1B1*	–1.89	0.0036
BF776610	7-dehydrocholesterol reductase	*DHCR7*	–1.89	0.0144
CB467891	polymerase (RNA) I polypeptide D, 16kDa	*POLR1D*	–1.89	0.0021
BE684608	protease, serine, 8	*PRSS8*	–1.89	0.0021
NM_175800.2	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	*NDUFS4*	–1.89	0.0184
CB166358	lysosomal-associated membrane protein 2	*LAMP2*	–1.89	0.0147
CB450657	transmembrane protein 85	*TMEM85*	–1.88	0.0034
CK777018	choline phosphotransferase 1	*CHPT1*	–1.88	0.0004
BF043332	ras suppressor protein 1	*RSU1*	–1.88	0.0028
CK947713	transmembrane protein 49	*TMEM49*	–1.88	0.0089
NM_177520.2	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	*MGAT4A*	–1.88	0.0028
CK846717	proteasome (prosome, macropain) 26S subunit, ATPase, 6	*PSMC6*	–1.88	0.0383

BP107757	ribosomal protein S20	*RPS20*	–1.88	0.0088
AV610889	glyceraldehyde-3-phosphate dehydrogenase	*GAPDH*	–1.87	0.0030
CK769676	mitochondrial ribosomal protein L45	*MRPL45*	–1.87	0.0009
CK955846	mitochondrial ribosomal protein L3	*MRPL3*	–1.87	0.0136
AV617586	fermitin family homolog 2 (Drosophila)	*FERMT2*	–1.87	0.0374
CK958502	filamin A interacting protein 1-like	*FILIP1L*	–1.87	0.0255
BP103163	BTB (POZ) domain containing 1	*BTBD1*	–1.86	0.0290
CK974428	chromosome 11 open reading frame 73 ortholog	*C29H11orf73*	–1.86	0.0233
CK771035	interferon regulatory factor 5	*IRF5*	–1.86	0.0012
CK848932	fucosidase, alpha-L- 1, tissue	*FUCA1*	–1.85	0.0019
AU098162	AU098162 Cloned bovine fetus cDNA Bos taurus cDNA clone Cln454 3-, mRNA sequence	---	–1.85	0.0129
CK778646	proteasome (prosome, macropain) assembly chaperone 1	*PSMG1*	–1.85	0.0243
CK775998	latrophilin 2	*LPHN2*	–1.85	0.0030
NM_174465.2	SEC11 homolog A (S. cerevisiae)	*SEC11A*	–1.85	0.0140
CB172516	hypothetical LOC513740	*LOC513740*	–1.85	0.0313
CK943646	arsenic (+3 oxidation state) methyltransferase	*AS3MT*	–1.85	0.0004
NM_174445.2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	*PTGS2*	–1.85	0.0046
CK975949	quinoid dihydropteridine reductase	*QDPR*	–1.85	0.0423
CK772180	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	*ATP6V0D2*	–1.84	0.0310
CK952626	adaptor-related protein complex 3, sigma 1 subunit	*AP3S1*	–1.84	0.0153
CB468257	ataxin 2	*ATXN2*	–1.83	0.0408
CK948086	vesicle-associated membrane protein 3 (cellubrevin)	*VAMP3*	–1.83	0.0407
CK950056	deoxyribonuclease I-like 3	*DNASE1L3*	–1.83	0.0431
BF653531	vacuolar protein sorting 41 homolog (S. cerevisiae)	*VPS41*	–1.83	0.0009
NP_776577.1	peptidylprolyl isomerase B (cyclophilin B)	*PPIB*	–1.83	0.0038
CK950519	dehydrogenase E1 and transketolase domain containing 1	*DHTKD1*	–1.82	0.0090
CK847287	ADP-ribosylation factor 4 /// similar to ADP-ribosylation	*ARF4 ///*	–1.82	0.0206

	factor 4	*LOC614581*		
CK977019	mitotic checkpoint component Mad2 /// MAD2 mitotic arrest deficient-like 1 (yeast)	*MAD2 /// MAD2L1*	–1.82	0.0139
BE667214	metadherin	*MTDH*	–1.82	0.0419
CK774104	mitochondrial ribosomal protein L19	*MRPL19*	–1.82	0.0027
CK846906	DnaJ (Hsp40) homolog, subfamily B, member 1	*DNAJB1*	–1.82	0.0033
CK948151	ribophorin II	*RPN2*	–1.81	0.0324
BI541888	hypothetical protein LOC532603	*LOC532603*	–1.81	0.0001
CK960514	eukaryotic translation initiation factor 3, subunit F	*EIF3F*	–1.81	0.0310
AU275462	collagen, type XII, alpha 1	*COL12A1*	–1.81	0.0017
NM_175831.2	cytochrome c oxidase subunit VIIc	*COX7C*	–1.81	0.0152
NM_201527.1	superoxide dismutase 2, mitochondrial	*SOD2*	–1.80	0.0445
CK957676	ARP2 actin-related protein 2 homolog (yeast)	*ACTR2*	–1.80	0.0249
CK948142	chromosome 10 open reading frame 84 ortholog	*C26H10orf84*	–1.79	0.0346
CK772973	dicarbonyl/L-xylulose reductase	*DCXR*	–1.79	0.0346
CB464064	superoxide dismutase 1, soluble	*SOD1*	–1.79	0.0010
BP103554	phosphatase, orphan 2	*PHOSPHO2*	–1.79	0.0216
BP104582	adducin 3 (gamma)	---	–1.78	0.0473
CK954454	3-ketodihydrosphingosine reductase	*KDSR*	–1.78	0.0093
CK980844	beta-carotene oxygenase 2	*BCO2*	–1.78	0.0014
CK951345	PREDICTED: yorkie homolog	---	–1.78	0.0260
CB434763	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	*YWHAG*	–1.78	0.0480
CK973814	solute carrier family 44, member 1	*SLC44A1*	–1.78	0.0011
CB531775	CDV3 homolog (mouse)	*CDV3*	–1.78	0.0376
CB169092	similar to Uncharacterized protein C1orf175 homolog	---	–1.78	0.0229
M13236.1	guanine nucleotide binding protein (G protein), beta polypeptide 1	*GNB1*	–1.78	0.0033
CB172231	IMP (inosine monophosphate) dehydrogenase 2	*IMPDH2*	–1.77	0.0222
CK972144	N-acylsphingosine amidohydrolase (acid ceramidase) 1	*ASAH1*	–1.77	0.0054

CB166154	ralA binding protein 1	*RALBP1*	–1.77	0.0137
CK848295	adaptor-related protein complex 2, beta 1 subunit	*AP2B1*	–1.77	0.0056
CK775888	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	*SPR*	–1.77	0.0051
CB447825	Anillin, actin binding protein	*ANLN*	–1.77	0.0230
CK847914	MPV17 mitochondrial membrane protein-like 2	*MPV17L2*	–1.77	0.0010
CK770918	transcription elongation factor A (SII)-like 4	*TCEAL4*	–1.76	0.0039
CK940683	replication protein A1, 70kDa	*RPA1*	–1.76	0.0003
CF764324	coiled-coil domain containing 90A	*CCDC90A*	–1.76	0.0037
CK980929	N-acetylgalactosaminidase, alpha-	*NAGA*	–1.75	0.0042
BM255214	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	*TAF10*	–1.75	0.0150
CB432337	sorting nexin 4	*SNX4*	–1.75	0.0198
AV607592	actin, beta	*ACTB*	–1.75	0.0107
NM_174080.2	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	*UBE2K*	–1.75	0.0328
CB420377	catenin, beta interacting protein 1	*CTNNBIP1*	–1.74	0.0027
CK948245	mitogen-activated protein kinase 14	*MAPK14*	–1.74	0.0089
BM445534	PREDICTED: Bos taurus uncharacterized LOC100849050 (LOC100849050), miscRNA	---	–1.74	0.0017
CK945640	FAT tumor suppressor homolog 1 (Drosophila)	*FAT1*	–1.74	0.0165
CK849264	phosphoglycerate kinase 1	*PGK1*	–1.74	0.0351
AW447102	grancalcin, EF-hand calcium binding protein	---	–1.74	0.0304
CB424513	ATP-binding cassette, sub-family B (MDR/TAP), member 6	*ABCB6*	–1.74	0.0040
CK946141	hypothetical protein LOC510320	*LOC510320*	–1.74	0.0223
CB170194	trinucleotide repeat containing 6B	*TNRC6B*	–1.73	0.0043
CK849599	YME1-like 1 (S. cerevisiae)	*YME1L1*	–1.73	0.0104
NM_174384.2	lysyl oxidase-like 4	*LOXL4*	–1.73	0.0010
AV593983	similar to Zinc finger protein 330 /// zinc finger protein	*LOC787714 ///*	–1.73	0.0381

	330	*ZNF330*		
CK775309	protein phosphatase 2, catalytic subunit, beta isozyme	*PPP2CB*	–1.73	0.0471
CB461923	histone-lysine N-methyltransferase SETMAR	---	–1.73	0.0124
BE667009	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	*B3GNT2*	–1.73	0.0070
CK950804	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	*KPNA2*	–1.73	0.0360
CK963170	ribosomal protein L7a	*RPL7A*	–1.73	0.0322
CB427169	SH3-domain binding protein 5 (BTK-associated)	*SH3BP5*	–1.73	0.0045
AV610889	glyceraldehyde-3-phosphate dehydrogenase	*GAPDH*	–1.73	0.0048
CK981095	desmocollin 2	---	–1.73	0.0019
CK971474	Ras homolog enriched in brain	*RHEB*	–1.73	0.0224
CB433327	609685 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.72	0.0098
NM_174163.2	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	*RAC1*	–1.72	0.0148
BE681760	kinectin 1 (kinesin receptor)	*KTN1*	–1.72	0.0171
BI849971	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	*LHPP*	–1.72	0.0067
CB535095	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	*SH3YL1*	–1.72	0.0014
NM_174830.1	eukaryotic translation initiation factor 6	*EIF6*	–1.72	0.0248
CB464654	inositol monophosphatase domain containing 1	*IMPAD1*	–1.72	0.0073
CK773530	N-terminal asparagine amidase	*NTAN1*	–1.72	0.0003
AV610144	annexin A2	*ANXA2*	–1.72	0.0105
NM_174792.2	ferritin, light polypeptide	*FTL*	–1.71	0.0003
CK950694	TSC22 domain family, member 1	*TSC22D1*	–1.71	0.0167
CK848754	melanoma antigen family D, 2	*MAGED2*	–1.70	0.0035
CK777001	integrator complex subunit 6	*INTS6*	–1.70	0.0344
BM257007	chromatin modifying protein 5	*CHMP5*	–1.70	0.0096
AV615731	COMM domain containing 8	*COMMD8*	–1.70	0.0119
CK971190	ribosomal protein L10a	*RPL10A*	–1.70	0.0155

NM_174821.2	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	*SERPING1*	–1.70	0.0032
CB420458	ADP-ribosylhydrolase like 2	*ADPRHL2*	–1.70	0.0312
CK958930	spastic paraplegia 20 (Troyer syndrome)	*SPG20*	–1.70	0.0011
CK954398	catalase	*CAT*	–1.70	0.0079
BE757079	CDC42 small effector 2	*CDC42SE2*	–1.69	0.0093
CK772515	claudin 6	*CLDN6*	–1.69	0.0339
CK770196	mitochondrial ribosomal protein L16	*MRPL16*	–1.69	0.0110
CB530449	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	*SLC11A2*	–1.69	0.0317
CK774881	single stranded DNA binding protein 3	*SSBP3*	–1.69	0.0169
NM_173900.2	CD9 molecule	*CD9*	–1.69	0.0309
CK774530	similar to Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-75)	*LOC524974*	–1.69	0.0264
M22559.1	ATPase inhibitory factor 1	*ATPIF1*	–1.69	0.0434
CK948267	KIAA0174	*IST1*	–1.69	0.0041
BE753186	carnosine synthase 1	*CARNS1*	–1.69	0.0484
BE664930	152833 MARC 4BOV Bos taurus cDNA 5-, mRNA sequence	---	–1.69	0.0058
BM252109	LIM domain only 4	*LMO4*	–1.69	0.0003
CB531088	unc-50 homolog (C. elegans)	*UNC50*	–1.69	0.0001
BM251302	growth hormone inducible transmembrane protein	*GHITM*	–1.68	0.0061
CB535077	SH3-domain kinase binding protein 1	*SH3KBP1*	–1.68	0.0062
BM364070	zinc finger, RAN-binding domain containing 2	*ZRANB2*	–1.68	0.0294
CK770852	solute carrier family 35 (CMP-sialic acid transporter), member A1	*SLC35A1*	–1.68	0.0002
AV616294	ribosomal protein L34	*RPL34*	–1.68	0.0215
CK848797	sterol carrier protein 2	*SCP2*	–1.68	0.0019
CK770586	nidogen 2 (osteonidogen)	*NID2*	–1.68	0.0107
CK846622	tumor protein D52	*TPD52*	–1.67	0.0096

AV590436	JNK1/MAPK8-associated membrane protein	*JKAMP*	–1.67	0.0050
BM430362	CD164 molecule, sialomucin	*CD164*	–1.67	0.0063
CK954456	v-ral simian leukemia viral oncogene homolog A (ras related)	*RALA*	–1.67	0.0082
CB460291	sorting nexin 6	*SNX6*	–1.67	0.0398
CK848993	thioredoxin domain containing 5 (endoplasmic reticulum)	*TXNDC5*	–1.67	0.0029
AW356461	major facilitator superfamily domain containing 1	*MFSD1*	–1.67	0.0084
NM_174212.1	UDP-glucose pyrophosphorylase 2	*UGP2*	–1.67	0.0327
CK771210	PDZ and LIM domain 1	*PDLIM1*	–1.66	0.0203
CK974440	amyloid beta (A4) precursor-like protein 2	*APLP2*	–1.66	0.0084
AV597296	phospholipase A2, group XV	*PLA2G15*	–1.66	0.0094
CK848545	insulin-like growth factor binding protein 7	*IGFBP7*	–1.66	0.0008
BE749971	Mannosidase, alpha, class 2A, member 1	*MAN2A1*	–1.66	0.0062
BE668288	Sec61 gamma subunit	*SEC61G*	–1.66	0.0110
NM_174222.2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	*TAP2*	–1.66	0.0009
CB531166	glia maturation factor, beta	---	–1.66	0.0401
BE237565	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	*SUGT1*	–1.66	0.0145
CB443641	valosin containing protein (p97)/p47 complex interacting protein 1	*VCPIP1*	–1.65	0.0481
CK846024	multiple coagulation factor deficiency 2	*MCFD2*	–1.65	0.0004
CK973552	4104251 BARC 9BOV Bos taurus cDNA clone 9BOV28_A10 3-, mRNA sequence	---	–1.65	0.0001
CK973241	amino-terminal enhancer of split	*AES*	–1.65	0.0008
CK778182	similar to Nitric oxide-inducible gene protein	*LOC618360*	–1.65	0.0171
CB169572	proteasome (prosome, macropain) subunit, beta type, 6	*PSMB6*	–1.64	0.0062
CB461755	aspartylglucosaminidase	*AGA*	–1.64	0.0003
CB169181	transportin 1	*TNPO1*	–1.64	0.0367
CK849512	CD63 molecule	*CD63*	–1.64	0.0058
AW656252	108398 MARC 1BOV Bos taurus cDNA 5-, mRNA	---	–1.64	0.0014

	sequence			
NM_174770.2	glutathione peroxidase 4 (phospholipid hydroperoxidase)	*GPX4*	–1.64	0.0001
CK975764	synovial sarcoma translocation, chromosome 18	*SS18*	–1.64	0.0030
CK977771	transgelin 2	*TAGLN2*	–1.63	0.0330
CK774887	transmembrane emp24 protein transport domain containing 4	*TMED4*	–1.63	0.0365
CK983051	PREDICTED: Bos taurus uncharacterized LOC100850521 (LOC100850521), miscRNA	---	–1.63	0.0325
CB170168	SAR1 homolog A (S. cerevisiae)	---	–1.63	0.0366
CK965599	esterase D	*ESD*	–1.63	0.0097
CB433424	609787 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.63	0.0137
BI774070	ubiquitin specific peptidase 9, X-linked	*USP9X*	–1.63	0.0171
AU278311	solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	*SLC16A13*	–1.63	0.0023
CK969061	nuclear casein kinase and cyclin-dependent kinase substrate 1	*NUCKS1*	–1.63	0.0035
CB456402	TBC1 domain family, member 20	*TBC1D20*	–1.62	0.0080
CK777681	KIAA1715	*KIAA1715*	–1.62	0.0292
CK971624	general transcription factor IIB /// similar to Transcription initiation factor IIB (General transcription factor TFIIB) (S300-II)	*GTF2B /// LOC786656*	–1.62	0.0338
BG358861	BOVMS1-002-Q1-E1-E7 Monsanto bovine skeletal muscle cDNA library BOVMS1 Bos taurus cDNA clone BOVMS1-002-Q1-E1-E7 5-, mRNA sequence	---	–1.62	0.0012
CB452134	SLAIN motif family, member 2	*SLAIN2*	–1.62	0.0044
AV594069	ribosomal protein L36	*RPL36*	–1.62	0.0323
CK849138	zinc finger protein 75D	*ZNF75D*	–1.62	0.0117
CK770335	PRELI domain containing 1	*PRELID1*	–1.62	0.0041
CK972445	similar to RNA-binding protein 35A (RNA-binding motif	*LOC788414*	–1.62	0.0273

	protein 35A)			
CK967765	amyloid beta (A4) precursor protein	*APP*	–1.62	0.0109
CK941870	4065282 BARC 10BOV Bos taurus cDNA clone 10BOV12_A19 3-, mRNA sequence	---	–1.62	0.0142
CK975531	biliverdin reductase A	*BLVRA*	–1.61	0.0161
BP109178	SHC (Src homology 2 domain containing) transforming protein 1	*SHC1*	–1.61	0.0177
CK848549	immediate early response 3 interacting protein 1	*IER3IP1*	–1.61	0.0335
NM_174190.2	supervillin	*SVIL*	–1.61	0.0103
CK771661	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	*KDELR3*	–1.61	0.0023
CK959800	synaptosomal-associated protein, 23kDa	*SNAP23*	–1.61	0.0395
CB167910	pelota homolog (Drosophila)	*PELO*	–1.61	0.0009
CK970588	transmembrane protein C10orf57 homolog	*C28H10orf57*	–1.61	0.0076
NM_174152.2	peptidylprolyl isomerase B (cyclophilin B)	*PPIB*	–1.61	0.0007
CK957293	chromosome 11 open reading frame 75 ortholog /// similar to MGC133535 protein	*C29H11orf75 /// LOC786469*	–1.61	0.0029
CB465159	proteasome (prosome, macropain) subunit, alpha type, 5	*PSMA5*	–1.61	0.0224
AV601291	eukaryotic translation initiation factor 3, subunit E	*EIF3E*	–1.61	0.0265
CB166013	acyl-CoA binding domain containing 6	*ACBD6*	–1.60	0.0053
CK846911	acyl-CoA synthetase long-chain family member 6	*ACSL6*	–1.60	0.0139
CK777259	proline/serine-rich coiled-coil 1	*PSRC1*	–1.60	0.0063
CB430119	prefoldin subunit 1	*PFDN1*	–1.60	0.0168
CK771718	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	*DPM1*	–1.60	0.0074
CB166009	iron-sulfur cluster scaffold homolog (E. coli)	*ISCU*	–1.60	0.0157
CK948574	beta-2-microglobulin	*B2M*	–1.60	0.0189
CB426311	UDP-glucose ceramide glucosyltransferase	*UGCG*	–1.59	0.0498
CB168007	reticulocalbin 1, EF-hand calcium binding domain	*RCN1*	–1.59	0.0012
CK959644	MYC induced nuclear antigen	*MINA*	–1.59	0.0012
CK972308	UBX domain protein 4	*UBXN4*	–1.59	0.0418

CK846207	synaptogyrin 1	*SYNGR1*	–1.59	0.0001
CK976524	metadherin	*MTDH*	–1.59	0.0349
CB530355	similar to Nckap1 protein	*LOC510404*	–1.59	0.0098
CK771637	flotillin 1	*FLOT1*	–1.59	0.0003
CK849625	cathepsin H	*CTSH*	–1.59	0.0011
BP102272	X (inactive)-specific transcript	*XIST*	1.50	0.0479
CK726980	UMC-bemiv_0B02-002-d05 Metaphase II stage oocyte bemiv Bos taurus cDNA 3-, mRNA sequence	---	1.52	0.0059
CK943621	4067664 BARC 10BOV Bos taurus cDNA clone 10BOV15_E01 3-, mRNA sequence	---	1.55	0.0118
CK948835	sorbin and SH3 domain-containing protein 1	*SORBS1*	1.56	0.0113
BE665099	forkhead box P4	*FOXP4*	1.60	0.0369
CK774445	similar to Transforming growth factor-beta induced protein IG-H3 precursor (Beta IG-H3) (Kerato-epithelin) (RGD-containing collagen associated protein) (RGD-CAP)	*LOC539596*	1.61	0.0144
BE667577	CKLF-like MARVEL transmembrane domain containing 7	*CMTM7*	1.61	0.0111
CK957215	4097701 BARC 10BOV Bos taurus cDNA clone 10BOV3_P12 3-, mRNA sequence	---	1.62	0.0165
CB424435	nicotinamide nucleotide adenylyltransferase 1	*NMNAT1*	1.66	0.0336
CK776579	similar to NEPH1 protein	*LOC781667*	1.71	0.0004
BF776493	similar to WNK lysine deficient protein kinase 4	---	1.78	0.0155
CB441821	similar to mCG142710	*LOC511229*	1.84	0.0035
CB461078	721004 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	1.93	0.0109
NM_174844.1	glycine cleavage system protein H (aminomethyl carrier)	*GCSH*	1.99	0.0292
AW632179	potassium channel tetramerisation domain containing 1	*KCTD1*	2.92	0.0036
CB535261	768672 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	3.08	0.0007

Table S4. List of differentially expressed transcripts regarding the interaction between subspecies (*B. taurus indicus* – Nellore vs. *B. taurus taurus* - Simmental) and origin (MODE vs IVP)

Representative public ID	Gene title	Gene symbol	Fold change	*P*-value
BP108263	secreted seminal-vesicle Ly-6 protein 1	*SSLP1*	1.67	0.0158
CK955677	keratin 19	*KRT19*	1.57	0.0145
CB166446	nucleobindin 2	*NUCB2*	1.55	0.0353
CK776789	similar to trophoblast Kunitz domain protein 5	*LOC618696*	1.54	0.0449
CK958396	destrin (actin depolymerizing factor)	*DSTN*	–1.59	0.0033
CB424435	nicotinamide nucleotide adenylyltransferase 1	*NMNAT1*	–1.60	0.0381
CK942763	similar to Tropomyosin alpha-1 chain (Tropomyosin-1) (Alpha-tropomyosin) /// tropomyosin 1 (alpha)	*LOC788816 /// TPM1*	–1.60	0.0149
CB172313	ribosomal protein L7-like 1	*RPL7L1*	–1.61	0.0197
CK848123	970838 BARC 5BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.61	0.0105
CK775514	squamous cell carcinoma antigen recognized by T cells 3	*SART3*	–1.61	0.0241
CB171498	ribosomal protein L15	*RPL15*	–1.62	0.0041
CK958448	tropomyosin 3	*TPM3*	–1.63	0.0250
CK849123	eukaryotic translation initiation factor 3, subunit G	*EIF3G*	–1.64	0.0473
BE749511	tripartite motif-containing 2	*TRIM2*	–1.64	0.0472
NM_175795.2	cytochrome c oxidase subunit VIIb	*COX7B*	–1.65	0.0242
CB447648	Carnitine palmitoyltransferase 1A (liver)	*CPT1A*	–1.65	0.0362
CB461923	SET domain and mariner transposase fusion gene	*SETMAR*	–1.66	0.0423
AU276758	phosphodiesterase 4D interacting protein	*PDE4DIP*	–1.66	0.0498
CK775725	BMS1 homolog, ribosome assembly protein (yeast)	*BMS1*	–1.67	0.0113
NM_174313.2	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	*FABP3*	–1.68	0.0249
BP109396	solute carrier family 25 (carnitine/acylcarnitine translocase),	*SLC25A20*	–1.68	0.0147

	member 20			
BI537914	428203 MARC 4BOV Bos taurus cDNA 5-, mRNA sequence	---	–1.68	0.0156
BP102272	X (inactive)-specific transcript	*XIST*	–1.69	0.0136
AV594069	ribosomal protein L36	*RPL36*	–1.70	0.0339
CK847594	hypothetical LOC506494	*MGC159500*	–1.70	0.0460
CK776519	967837 MARC 4BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.71	0.0342
CB531801	signal sequence receptor, delta (translocon-associated protein delta)	*SSR4*	–1.72	0.0023
NM_176614.1	pregnancy-associated glycoprotein 2	*PAG2*	–1.73	0.0047
BM445534	PREDICTED: Bos taurus uncharacterized LOC100849050 (LOC100849050), miscRNA	---	–1.75	0.0040
NM_174844.1	glycine cleavage system protein H (aminomethyl carrier)	*GCSH*	–1.81	0.0337
CB461078	721004 MARC 6BOV Bos taurus cDNA 3-, mRNA sequence	---	–1.82	0.0095
CK778646	proteasome (prosome, macropain) assembly chaperone 1	*PSMG1*	–1.83	0.0491
AU275257	ribosomal protein L18	*RPL18*	–1.85	0.0380
CK948858	selenophosphate synthetase 2	*SEPHS2*	–1.85	0.0272
CK777978	phosphoribosyl pyrophosphate synthetase 1	*PRPS1*	–1.86	0.0010
BE749963	alanyl-tRNA synthetase	*AARS*	–1.90	0.0332
AU233180	Tropomyosin 1 (alpha)	*TPM1*	–1.91	0.0164
NM_174763.2	peroxiredoxin 2	*PRDX2*	–1.92	0.0292
BM435101	zinc finger protein 36, C3H type-like 1	*ZFP36L1*	–1.94	0.0394
NM_174334.2	hydroxysteroid (17-beta) dehydrogenase 10	*HSD17B10*	–1.97	0.0124
CK963170	ribosomal protein L7a	*RPL7A*	–2.03	0.0098
CK971789	ubiquitin-conjugating enzyme E2 variant 1	*UBE2V1*	–2.16	0.0189
CB464010	mitochondrial carrier homolog 1 (C. elegans)	*MTCH1*	–2.16	0.0369
CK963094	hypothetical protein MGC127538	*MGC127538*	–2.17	0.0196
CB464808	Protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	*PRKAR1A*	–2.17	0.0313

CK728409	cornichon homolog 4 (Drosophila)	*CNIH4*	–2.17	0.0416
CK968451	glycyl-tRNA synthetase	*GARS*	–2.21	0.0338
AY192438.1	thymosin beta 4, X-linked	*TMSB4X*	–2.33	0.0326
CK780160	ribosomal protein S27-like	*RPS27L*	–2.39	0.0483
AW485507	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	*EIF2S3*	–2.40	0.0300
CK772180	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	*ATP6V0D2*	–2.42	0.0029
CK846999	glutamyl aminopeptidase (aminopeptidase A)	*ENPEP*	–2.49	0.0175
CK953606	cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 4	*CYP3A28*	–2.51	0.0483