

ProbesetID	log2 fold-change				Public ID	Gene Title	Gene Symbol	Tentative function (UniProtKB)
	LPS vs control	E. coli 444 vs control	E. coli 1000 vs control	E. coli 1048 vs control				
Ssc.19163.1.S1_at	-1.51	-1.42	-1.10	-1.71	BF078930	Transcribed locus	---	
Ssc.19268.2.A1_at	-1.09	-1.09	-1.11	-1.16	CF359637	Transcribed locus, moderately similar to NP_660274.1 chromosome 14 open reading frame 143 (Homo sapiens)	---	Calcium ion binding
AFFX-SSC-28SrRNA_at	-1.16	-1.46	-1.26	-1.20	AFFX-SSC-28SrRNA	Sus scrofa 28S rRNA	---	
Ssc.24007.1.S1_at	2.16	1.04	1.38	1.68	CK450048	paternally expressed 10	PEG10	Nucleic acid binding
Ssc.15937.1.A1_at	1.50	1.54	1.41	1.62	AF248308.1	Transcribed locus, moderately similar to XP_375341.1 similar to Ig heavy chain - human (fragment) (Homo sapiens)	---	
Ssc.19692.1.S1_at	1.34		1.87	1.92	BF078671	chemokine (C-X-C motif) ligand 2	CXCL2	Immune response
Ssc.4871.1.S1_at	1.85		2.21	2.57	NM_001001861.1	chemokine (C-X-C motif) ligand 2	CXCL2	Immune response
Ssc.658.1.S1_at	1.93		2.29	2.18	NM_213867.1	interleukin 8	IL8	Cytokine, inflammatory response, immune response
Ssc.14467.2.S1_a_at	1.99	1.24	1.14		AY028311.1	amphiregulin	AREG	Cytokine, growth factor
Ssc.286.1.S1_s_at	-1.72			-1.84	NM_213817.1	inflammatory response protein 6	IRG6	Antiviral defense, defense response to virus
Ssc.208.1.S1_at	2.22	2.75	1.83		NM_214412.1	cytochrome P450 1A1	CYP1A1	Oxidation reduction
Ssc.113.1.S2_at			1.12	2.16	NM_214029.1	interleukin 1, alpha	IL1A	Cytokine, inflammatory response, immune response
Ssc.113.1.S1_at			1.28	2.58	M86730.1	interleukin 1, alpha	IL1A	Cytokine, inflammatory response, immune response
Ssc.10453.1.S1_at			-1.07	-1.42	BF713714	Transcribed locus, highly similar to NP_000087.1 ceruloplasmin (ferroxidase) (Homo sapiens)	---	Oxidoreductase, transport
Ssc.26317.1.S1_at	1.23			-1.55	AY509877.1	alpha-2-macroglobulin	A2M	Endopeptidase inhibitor activity
Ssc.7090.1.A1_at	1.46			-1.48	NM_214395.1	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	SERPINA1	Protease inhibitor, serine protease inhibitor
Ssc.16053.1.S1_at				-1.08	AF069643.1	matrix metalloproteinase 13 precursor	MMP-13	Hydrolase, protease, metalloprotease
Ssc.4368.3.S1_at	-1.73			-1.19	BP463181	F-box protein 32	FBXO32	Ubl conjugation pathway
Ssc.4368.1.S1_at	-1.59			-1.32	BI817204	F-box protein 32	FBXO32	Ubl conjugation pathway
Ssc.221.1.S1_at	-1.09			-1.55	NM_214061.1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78	MX1	Antiviral defense, reponse to virus
Ssc.21.1.S1_s_at	-1.05			-1.66	AF319661.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	DDX58	Antiviral defense, immune response, innate immunity
Ssc.15888.1.S1_at	-1.22			-1.07	NM_213805.1	oxidized low density lipoprotein (lectin-like) receptor 1	OLR1	Cell adhesion, immune response, inflammatory response
Ssc.16648.1.S1_at	-1.28	-1.35	-2.30	-3.34	CK458095	Thioredoxin interacting protein	TXNIP	Cell cycle, transcription, transcription regulation

Ssc.6097.1.S1_at	1.16				CN166758	Thioredoxin reductase	TRXR1	Oxidoreductase
Ssc.5549.2.S1_at	1.06				CB468944	Fatty acid binding protein 5	FABP5	Transport, lipid binding
Ssc.16470.1.S1_a_at					CO994432	Transcribed locus, moderately similar to NP_002571.1 pancreatitis-associated protein (Homo sapiens)	PAP	Acute phase, inflammatory response
Ssc.604.1.S1_at					BX924285	Liver fatty acid binding protein	FABP1	Transport, lipid binding
Ssc.16525.1.S1_at					CB285696	Transcribed locus, moderately similar to NP_000125.1 fatty acid binding protein 2, intestinal (Homo sapiens)	FABP2	Transport, lipid binding
Ssc.11079.1.A1_at	-1.29		-1.04	-1.58	NM_213936.1	ribonuclease, RNase A family, 4	RNASE4	Endonuclease, hydrolase, nuclease
Ssc.24282.1.S1_at	2.44		1.89	2.55	AJ747030	Transcribed locus, moderately similar to NP_002080.1 chemokine (C-X-C motif) ligand 2 (Homo sapiens)	---	Immune response, inflammatory response
Ssc.11879.1.A1_at	1.37		1.11	1.33	BQ600284	Transcribed locus, moderately similar to NP_001245.1 CDC6 cell division cycle 6 homolog (S. cerevisiae) (Homo sapiens)	---	Cell cycle, cell division, DNA replication, mitosis
Ssc.10686.1.S1_at		-1.13	-1.10	-1.56	AJ656758	Transcribed locus	---	
Ssc.30532.1.A1_at	-1.88		-1.12	-2.04	CO993367	Transcribed locus	---	
Ssc.9238.1.A1_at	-1.44	-1.08		-1.47	BF709956	Transcribed locus	---	
Ssc.6788.1.A1_at	-1.16		-1.03	-1.27	AJ683882	Transcribed locus	---	
Ssc.22530.1.S1_at	-1.14	-1.54		-1.62	CF795706	Transcribed locus	---	
Ssc.6189.1.A1_at	1.94		1.21	1.24	BQ601447	Transcribed locus	---	
Ssc.6550.1.A1_at	-1.29		-1.04	-1.56	CK462428	Transcribed locus	---	
AFFX-Ss_IRP_3_at	-1.71			-1.80	AFFX-r2-TagQ-5	Clone 76H1	---	
Ssc.1257.3.S1_at	-1.24			-1.30	BP460358	similar to phosphoinositide-3-kinase interacting protein 1	LOC100155147	Integral to membrane
AFFX-Ss_IRP_M_at	-1.14			-1.27	AFFX-r2-TagQ-5	Clone 76H1	---	
Ssc.4679.1.S1_at	-1.10			-1.01	CN157788	angiogenin	ANG1	Angiogenesis, differentiation
Ssc.6948.1.A1_at	-1.01			-1.43	BI404568	similar to neuroserpin	LOC100154352	Protease inhibitor, serine protease inhibitor
Ssc.1843.1.S1_at	1.06			1.06	BX925328	similar to v-myb myeloblastosis viral oncogene homolog (avian)-like 2	LOC100157175	
Ssc.1843.2.S1_at	1.07			1.04	AW785539	similar to v-myb myeloblastosis viral oncogene homolog (avian)-like 2	LOC100157175	
Ssc.14243.1.S1_at	1.19			1.03	BX671487	cyclin B	CCNB1	Cell cycle, cell division
Ssc.2753.1.S1_at	1.19			1.04	CN166341	Polo-like kinase 1 (Drosophila)	PLK1	Cell cycle, cell division, mitosis
Ssc.4747.1.S1_at	1.38		1.01		NM_001003662.1	folliculin	FST	
Ssc.13476.1.A1_at	1.73			1.26	CN162607	paternally expressed 10	PEG10	Nucleic acid binding
AFFX-SSC-5SrRNA_at		-1.94		-1.55	AFFX-SSC-5SrRNA		---	
Ssc.24401.1.A1_s_at			-1.23	-1.98	CK457947	Low molecular weight kininogen	KNG	Cysteine-type endopeptidase inhibitor activity
Ssc.13961.2.A1_at			1.13	1.28	CO994537	Eukaryotic translation elongation factor 1 alpha 1	EEF1A1	Elongation factor

Ssc.22068.1.S1_at			1.87	1.49	CN154316	Transcribed locus, highly similar to NP_077016.1 hypothetical protein MGC4504 (Homo sapiens)	---	Apoptosis, unfolded protein response
Ssc.10441.1.S1_at	1.57			-1.01	CN159120	Transcribed locus, moderately similar to NP_001068.1 UDP glycosyltransferase 2 family, polypeptide B17 (Homo sapiens)	---	Glycosyltransferase, transferase
Ssc.1977.1.S1_at	-1.03	-1.29			BF075309	Transcribed locus, moderately similar to NP_035014.1 N-myc downstream regulated gene 1 (Mus musculus)	---	Response to metal ion
Ssc.3391.3.S1_at	1.04			1.29	BF194088	Transcribed locus, moderately similar to NP_005429.1 FOS-like antigen 1 (Homo sapiens)	---	Cellular defense response, response to virus
Ssc.3391.1.S1_at	1.10			1.33	BI400819	Transcribed locus, moderately similar to NP_005429.1 FOS-like antigen 1 (Homo sapiens)	---	Cellular defense response, response to virus
Ssc.2099.1.S1_at	1.11			1.06	CO939739	Transcribed locus, highly similar to NP_004847.2 kinesin family member 23 (Homo sapiens)	---	Cell cycle, cell division, mitosis
Ssc.16603.1.A1_at	1.14			-1.62	BI181630	Transcribed locus, moderately similar to NP_000005.1 alpha-2-macroglobulin (Homo sapiens)	---	Endopeptidase inhibitor activity
Ssc.19346.1.S1_at	1.14			1.05	CK451940	Transcribed locus, moderately similar to NP_071394.2 caspin homolog (Xenopus laevis) (Homo sapiens)	---	Cell cycle, DNA repair, DNA damage
Ssc.19326.1.A1_at	1.15			1.21	CF368489	Transcribed locus, moderately similar to NP_057427.2 centromere protein F, 350400ka (mitosin) (Homo sapiens)	---	Developmental protein
Ssc.4976.1.S1_at	1.19			1.01	CK464589	Transcribed locus, moderately similar to NP_006333.1 transforming, acidic coiled-coil containing protein 3 (Homo sapiens)	---	
Ssc.22370.1.S1_at	1.19			1.07	CF792337	Transcribed locus, highly similar to NP_076999.1 defective in sister chromatid cohesion homolog 1 (S. cerevisiae) (Homo sapiens)	---	Cell cycle, DNA replication
Ssc.27275.1.A1_at	1.19			1.09	CK455395	Transcribed locus, moderately similar to NP_060286.1 hypothetical protein FLJ20425 (Homo sapiens)	---	Protein binding
Ssc.4430.1.S1_at	1.05			1.13	CF788826	Transcribed locus, highly similar to NP_079021.2 SHC SH2-domain binding protein 1 (Homo sapiens)	---	
Ssc.21011.1.S1_at	1.92			1.05	Z99081	Transcribed locus, highly similar to NP_000080.1 collagen, type I, alpha 2 (Homo sapiens)	---	Rho protein signal transduction
Ssc.22564.1.A1_at		-3.36		-2.77	CF795787	Transcribed locus, weakly similar to XP_379739.1 LOC401630 (Homo sapiens)	---	
Ssc.26282.1.S1_a_at		-1.26	-1.09		CF795087	Transcribed locus, weakly similar to NP_690845.1 Saccharomyces cerevisiae TAR1 gene	---	Regulation of cellular respiration
Ssc.4104.1.S1_at		1.18		1.83	CN162948	Transcribed locus, highly similar to NP_061931.1 DNA-damage-inducible transcript 4 (Homo sapiens)	---	Apoptosis, negative regulation of signal transcription
Ssc.10471.1.A1_at			-1.20	-1.26	BF702214	Transcribed locus, moderately similar to XP_128791.2 THUMP domain containing 2 (Mus musculus)	---	
Ssc.9136.1.S1_at			1.02	1.26	BX918559	Transcribed locus, highly similar to NP_036250.2 CCR4 carbon catabolite repression 4-like (S. cerevisiae) (Homo sapiens)	---	Biological rhythms
Ssc.11124.1.A1_at			1.18	1.45	BII84483	Transcribed locus, highly similar to NP_055551.1 KIAA0101 (Homo sapiens)	---	

Ssc.24221.2.A1_at	-1.30			-1.59	BI181166	Transcribed locus, highly similar to NP_035017.1 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Mus musculus)	---	Transport
Ssc.27688.1.S1_at	-1.29			-1.08	BG608619	Transcribed locus	---	
Ssc.30786.1.A1_at	-1.67			-1.14	AJ657499	Transcribed locus	---	
Ssc.30752.1.S1_at	-1.66			-2.15	BX921277	Transcribed locus	---	
Ssc.31140.1.S1_at	-1.51			-2.12	BX922784	Transcribed locus	---	
Ssc.12886.1.A1_at	-1.41	-1.09			CF796076	Transcribed locus	---	
Ssc.18959.1.A1_at	-1.10			-1.30	CF365136	Transcribed locus	---	
Ssc.27195.1.A1_at	-1.36			-1.21	CN165941	Transcribed locus	---	
Ssc.29492.1.A1_at	-1.19			-1.38	CO956576	Transcribed locus	---	
Ssc.30752.2.A1_at	-1.71			-2.67	BI119523	Transcribed locus	---	
Ssc.21169.1.S1_at	-1.08			-1.17	BE032622	Transcribed locus	---	
Ssc.30637.1.A1_at	-1.05			-1.67	CO940830	Transcribed locus	---	
Ssc.25070.1.A1_at	1.06			1.06	CK461396	Transcribed locus	---	
Ssc.7562.1.A1_at	1.11		1.14		BQ599273	Transcribed locus	---	
Ssc.942.1.S1_at	1.27		1.18		CK465005	Transcribed locus	---	
Ssc.5182.1.A1_at	1.28			1.19	BF710924	Transcribed locus	---	
Ssc.25069.1.S1_at	1.29			1.05	CN153765	Transcribed locus	---	
Ssc.7771.1.A1_at	1.43			1.56	CK468060	Transcribed locus	---	
Ssc.3666.1.A1_at	1.86		1.04		CK459289	Transcribed locus	---	
Ssc.25948.1.S1_at	1.92		1.52		BX925423	Transcribed locus	---	
Ssc.12680.1.A1_at		-1.15		-1.30	BI403263	Transcribed locus	---	
Ssc.14230.1.A1_at		-1.05		-1.03	CF789095	Transcribed locus	---	
Ssc.7990.1.A1_at		-1.05		-1.27	CN166387	Transcribed locus	---	
Ssc.4081.1.A1_at		-1.02		-1.10	BQ601662	Transcribed locus	---	
Ssc.18253.1.S1_at			-1.16	-1.20	CF179697	Transcribed locus	---	
Ssc.19089.1.A1_at			-1.15	-1.38	CF367800	Transcribed locus	---	
Ssc.9039.1.A1_at			-1.04	-1.24	CF366256	Transcribed locus	---	
Ssc.5799.1.S1_at			-1.04	-1.78	BF709288	Transcribed locus	---	
Ssc.8893.1.A1_at			1.18	1.15	BF708608	Transcribed locus	---	
Ssc.9376.1.A1_at			1.31	1.08	BF710373	Transcribed locus	---	
Ssc.23778.3.S1_at	-1.49				BP167798	prostate transmembrane protein, androgen induced 1	CR956367.2	Ubl conjugation pathway
Ssc.383.1.S1_at	-1.43				NM_213792.1	odd homeobox 1 protein	OB1	Transcription, transcription regulation

Ssc.23778.2.S1_at	-1.35				BX674651	prostate transmembrane protein, androgen induced 1	CR956367.2	Ubl conjugation pathway
Ssc.3920.1.S1_at	-1.31				CN160546	prostate transmembrane protein, androgen induced 1	CR956367.2	Ubl conjugation pathway
Ssc.23778.1.S1_at	-1.10				BE031847	prostate transmembrane protein, androgen induced 1	CR956367.2	Ubl conjugation pathway
Ssc.14246.1.S1_at	-1.09				BX667508	gelsolin	LOC396874	Cytoplasm, secreted
Ssc.6966.2.S1_a_at	-1.03				AB031957.1	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	CDKN1B	Cell cycle, protein kinase inhibitor
Ssc.15841.1.S1_at	-1.01				AJ316066.1	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	Cell cycle, kinase activity
Ssc.15893.1.S1_at	-1.00				BX676059	sarcolipin	SLN	Regulation of calcium ion transport
Ssc.27187.1.S1_at	1.00				CN160280	similar to spindle and KT associated 1	LOC100157355	
Ssc.15588.1.S1_at	1.01				AF085482.1	insulin-like growth factor binding protein 3	IGFBP3	Regulation of apoptosis, cell growth
Ssc.15824.1.S1_at	1.04				BG382957	karyopherin alpha 2	KPNA2	Binding, protein transporter activity
Ssc.14182.1.A1_at	1.05				CK451027	Cyclin B2	CCNB2	Cell cycle, cell division
Ssc.16341.1.S1_at	1.06				BP447300	prostaglandin-endoperoxide synthase 1	PTGS1	Dioxygenase, oxidoreductase, peroxidase
Ssc.10536.1.S1_at	1.08				CF791997	apoptosis-related protein	PNAS-5	Metal ion binding, protein binding
Ssc.11630.1.S1_at	1.10				CK449997	pituitary tumor-transforming 1	PTTG1	Cell cycle, cell division, mitosis, chromosome partition, DNA repair, DNA damage
Ssc.28124.1.A1_at	1.11				CN162886	Aurora kinase A	CR956640.2	Cell cycle, cell division, mitosis
Ssc.873.1.S1_at	1.12				AJ687786	cell division cycle 2, G1 to S and G2 to M	CDC2	ATP binding, protein kinase activity
Ssc.27540.2.S1_at	1.14				CN166809	similar to ubiquitin-conjugating enzyme E2C	LOC100153133	Ubl conjugation pathway
Ssc.115.1.S1_s_at	1.27				X60677.1	heme oxygenase (decycling) 1	HMOX1	Oxidoreductase
Ssc.1466.1.A1_at	1.27				CN160915	aurora kinase A	CR956640.2	Cell cycle, cell division, mitosis
SscAffx.8.1.S1_s_at	1.32				NM_001005154.1	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	Transcription, transcription regulation
Ssc.3139.1.A1_at		-1.42			CK456262	Regulator of G-protein signaling 2, 24kDa	RGS2	Signal transducer activity
Ssc.7314.1.A1_at			1.03		NM_214321.1	prostaglandin G/H synthase-2	PGHS-2	Oxidation reduction, response to oxidative stress
Ssc.17286.1.A1_at			1.10		CK460825	BTG family, member 2	BTG2	
Ssc.9075.1.A1_at			1.44		NM_213880.1	C-JUN protein	C-JUN	Transcription, transcription regulation
Ssc.10884.1.A1_at				-2.01	BF713431	similar to interferon activated gene 203	LOC100156073	
Ssc.8516.1.A1_at				-1.96	NM_214389.1	glutathione S-transferase	GSTA2	Transferase
Ssc.15926.1.S1_at				-1.66	NM_214148.1	epithelial chloride channel protein	AECC	Calcium transport, ion transport
Ssc.12.1.S1_at				-1.45	NM_213992.1	sulfotransferase family 1E, estrogen-preferring, member 1	SULT1E1	Transferase
Ssc.153.1.S1_at				-1.25	NM_214044.1	dihydropyrimidine dehydrogenase	DPYD	Oxidoreductase
Ssc.5604.1.S1_at				-1.18	CN154806	protein S (alpha)	PROS1	Calcium ion binding
Ssc.11422.1.A1_at				-1.07	BI182449	similar to phospholipase A1 member A	LOC100154368	Lipid degradation, phospholipase A1 activity

Ssc.27786.1.S1_at				1.02	BG384060	Fatty acid binding protein 4, adipocyte	FABP4	Transport, lipid binding
Ssc.10237.1.S1_at				1.05	AJ301200	similar to heat shock 27kDa protein 8	LOC100155338	Stress response
SscAffx.11.1.S1_a_at				1.07	NM_214448.1	involucrin	IVL	Keratinization
Ssc.314.1.S1_at				1.12	NM_214107.1	adrenomedullin	ADM	Hormone activity
Ssc.27786.2.S1_at				1.38	CO994913	CD74 antigen	CD74	MHC class II protein binding, immune response, antigen processing and presentation
Ssc.26709.1.S1_at	-1.72				CN159962	Transcribed locus, moderately similar to XP_224544.2 similar to EBV-induced G protein-coupled receptor 2 (EBI2) (Rattus norvegicus)	---	Adaptive immunity, immunity
Ssc.17780.1.S1_s_at	-1.66				AB087911.1	Transcribed locus, weakly similar to XP_135339.1 similar to RIKEN cDNA A430107P09 gene (Mus musculus)	---	
Ssc.22037.1.S1_at	-1.52				CN160898	Transcribed locus, moderately similar to NP_006753.1 Lysosomal-associated multispinning membrane protein-5 (Homo sapiens)	---	Transport
Ssc.12171.1.A1_at	-1.23				BQ603723	Transcribed locus, highly similar to XP_376328.1 family with sequence similarity 13, member A1 (Homo sapiens)	---	
Ssc.22620.1.S1_at	-1.18				BX666072	Transcribed locus, moderately similar to NP_001538.3 interferon-induced protein with tetratricopeptide repeats 2 (Homo sapiens)	---	Binding
Ssc.28517.2.S1_at	-1.16				BI346421	Transcribed locus, highly similar to NP_071302.2 dual specificity phosphatase 10 (Mus musculus)	---	Hydrolase
Ssc.20515.1.S1_at	-1.14				BG382428	Transcribed locus, highly similar to NP_004096.2 EGF-containing fibulin like extracellular matrix protein 1 (Homo sapiens)	---	Calcium ion binding, protein binding
Ssc.3648.1.S1_a_at	-1.13				F23133	Transcribed locus, moderately similar to NP_060765.1 hypothetical protein FLJ11000 (Homo sapiens)	---	
Ssc.15069.1.S1_at	-1.11				BI345060	Transcribed locus, moderately similar to NP_570952.1 cytochrome P450, family 4, subfamily f, polypeptide 13 (Mus musculus)	---	Monoxygenase, oxidoreductase
Ssc.26224.1.S1_at	-1.10				BX917028	Transcribed locus, highly similar to NP_064567.2 transmembrane, prostate androgen induced RNA (Homo sapiens)	CR956367.2	Ubl conjugation pathway
Ssc.18862.1.A1_at	-1.10				CF368734	Transcribed locus, moderately similar to XP_221535.2 similar to downregulated in ovarian cancer 1 (Rattus norvegicus)	---	
Ssc.24221.1.S1_at	-1.02				CK451013	Transcribed locus, highly similar to NP_035017.1 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Mus musculus)	---	Transport, NADH dehydrogenase activity
Ssc.1313.1.A1_at	1.01				CK464624	Transcribed locus, moderately similar to NP_077001.1 XTP3-transactivated protein A (Homo sapiens)	---	Hydrolase
Ssc.21959.1.S1_at	1.01				CN158067	Transcribed locus, highly similar to NP_644802.1 cysteinyl-tRNA synthetase (Homo sapiens)	---	Protein biosynthesis, ligase
Ssc.23822.1.S1_a_at	1.02				CN161582	Transcribed locus, highly similar to NP_001354.1 dyskeratosis congenita 1, dyskerin (Homo sapiens)	---	Isomerase, ribonucleoprotein

Ssc.5041.1.A1_at	1.03				CN154405	Transcribed locus, moderately similar to NP_006161.1 nucleolar protein 1, 120kDa (Homo sapiens)	---	Methyltransferase, transferase
Ssc.5821.1.S1_at	1.04				CK462319	Transcribed locus, moderately similar to NP_003026.1 TAL1 (SCL) interrupting locus (Homo sapiens)	---	Developmental protein
Ssc.23877.1.S1_at	1.05				BP165838	Transcribed locus, highly similar to NP_001228.1 cyclin A2 (Homo sapiens)	---	Cell cycle, cell division, mitosis
Ssc.24422.1.S1_at	1.06				BE235697	Transcribed locus, highly similar to NP_055316.1 ubiquitin-conjugating enzyme E2S (Homo sapiens)	---	Cell cycle, cell division, Ubl conjugation pathway
Ssc.3994.1.S1_at	1.06				BF713387	Transcribed locus, moderately similar to NP_115722.1 hypothetical protein MGC13096 (Homo sapiens)	---	
Ssc.5401.1.S1_at	1.06				BF190854	Transcribed locus, highly similar to XP_375911.1 KIAA0186 gene product (Homo sapiens)	---	
Ssc.22206.1.S1_at	1.07				CK463608	Transcribed locus, highly similar to NP_055606.1 maternal embryonic leucine zipper kinase (Homo sapiens)	---	Kinase, transferase
Ssc.28512.1.S1_at	1.09				BX672980	Transcribed locus, moderately similar to NP_071741.2 chromosome condensation protein G (Homo sapiens)	---	Cell cycle, cell division, mitosis, DNA condensation
Ssc.7195.1.A1_at	1.09				BQ598156	Transcribed locus, moderately similar to NP_004327.1 BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast) (Homo sapiens)	---	Apoptosis, cell cycle, cell division, mitosis, chromosome partition
Ssc.12475.1.A1_at	1.11				CF364971	Transcribed locus, highly similar to XP_222105.2 similar to expressed sequence AI480570 (Rattus norvegicus)	---	
Ssc.24183.1.S1_at	1.12				CK456980	Transcribed locus, weakly similar to XP_341696.1 similar to RIKEN cDNA 2610510J17 (Rattus norvegicus)	---	
Ssc.14117.1.A1_at	1.12				CK450499	Transcribed locus, moderately similar to NP_631899.1 novel 58.3 KDA protein (Homo sapiens)	---	Intracellular signaling cascade
Ssc.11995.1.A1_at	1.14				CB476520	Transcribed locus, moderately similar to NP_006627.1 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (Homo sapiens)	---	Hydrolase, oxydoreductase
Ssc.26899.1.A1_at	1.15				CN162826	Transcribed locus, weakly similar to NP_060674.2 cytoskeleton associated protein 2 (Homo sapiens)	---	Apoptosis, cell cycle
Ssc.21217.1.A1_at	1.16				CF792040	Transcribed locus, moderately similar to XP_372192.2 Similar to RIKEN cDNA 2700049P18 gene (Homo sapiens)	---	
Ssc.7594.1.A1_at	1.25				CN165502	Transcribed locus, highly similar to NP_060839.1 DEP domain containing 1B (Homo sapiens)	---	Intracellular signaling cascade
Ssc.11108.1.A1_at	1.29				CF792943	Transcribed locus, moderately similar to NP_000295.1 peripheral myelin protein 22 (Homo sapiens)	---	
Ssc.1986.1.S1_at	1.35				CK452098	Transcribed locus, moderately similar to NP_542158.1 prostaglandin-endoperoxide synthase 1 (prostaglandin GH synthase and cyclooxygenase) (Homo sapiens)	---	Dioxygenase, oxidoreductase, peroxidase
Ssc.22545.1.A1_at	1.37				CK449996	Transcribed locus, highly similar to NP_060255.2 hypothetical protein FLJ20364 (Homo sapiens)	---	Cell cycle, cell division, mitosis
Ssc.26568.1.A1_s_at	1.42				CN153199	Transcribed locus, weakly similar to NP_149020.1 cyclin B3 (Homo sapiens)	---	Cell cycle, cell division, meiosis

Ssc.19382.1.A1_at	1.48				CF180618	Transcribed locus, highly similar to NP_004554.1 phosphoenolpyruvate carboxykinase 2 (mitochondrial) (Homo sapiens)	---	Decarboxylase, lyase
Ssc.11609.1.A1_at	1.52				BI182003	Transcribed locus, highly similar to NP_001664.2 asparagine synthetase (Homo sapiens)	---	Ligase
Ssc.18999.1.A1_at			-1.09		CO940748	Transcribed locus, moderately similar to NP_848599.2 hypothetical protein FLJ40427 (Homo sapiens)	---	Ubl conjugation pathway
Ssc.16460.1.S1_at			1.13		CB285513	Transcribed locus, highly similar to NP_001955.1 early growth response 1 (Homo sapiens)	---	Transcription, transcription regulation
Ssc.24986.1.S1_at				-1.64	CK463807	Transcribed locus, highly similar to NP_000680.2 aldehyde dehydrogenase 1 family, member A1 (Homo sapiens)	---	Oxidoreductase
Ssc.17353.1.S1_at				-1.58	CK459510	Transcribed locus, moderately similar to NP_031712.1 complement component factor i (Mus musculus)	---	
Ssc.5453.1.A1_at				-1.49	CK465332	Transcribed locus, moderately similar to NP_036545.1 glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (Homo sapiens)	---	Acyltransferase, transferase
Ssc.5557.1.S1_at				-1.45	CN153429	Transcribed locus, moderately similar to NP_780750.1 RIKEN cDNA 9430086K21 gene (Mus musculus)	---	
Ssc.19980.1.S1_at				-1.35	BX675506	Transcribed locus, weakly similar to NP_055080.1 a disintegrin and metalloproteinase domain 28 (Homo sapiens)	---	Hydrolase, protease, metalloprotease
Ssc.24974.1.S1_at				-1.32	BE234949	Transcribed locus, highly similar to XP_223684.2 similar to Peroxisomal membrane protein PEX13 (Peroxin-13) (Rattus norvegicus)	---	Protein transport, transport
Ssc.6595.1.A1_at				-1.30	BQ599735	Transcribed locus, moderately similar to NP_080498.1 DNA segment, Chr 3, ERATO Doi 789, expressed (Mus musculus)	---	
Ssc.11246.1.A1_at				-1.23	BI181165	Transcribed locus, moderately similar to XP_346818.1 Rattus norvegicus LOC360432 gene	---	
Ssc.25962.1.S1_at				-1.18	BX925692	Transcribed locus, moderately similar to NP_008825.3 flavin containing monooxygenase 3 (Homo sapiens)	---	Monooxygenase, oxidoreductase
Ssc.14318.1.S1_at				-1.14	CK449951	Transcribed locus, highly similar to NP_789794.1 Bardet-Biedl syndrome 7 (Homo sapiens)	---	Protein binding
Ssc.12504.1.A1_at				-1.09	CK465051	Transcribed locus, weakly similar to NP_919043.1 DNA segment, Chr 12, ERATO Doi 647, expressed (Mus musculus)	---	
Ssc.10110.1.A1_at				-1.08	BQ599693	Transcribed locus, highly similar to NP_758527.1 Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (Homo sapiens)	---	Regulation of transcription, DNA dependent
Ssc.11477.3.A1_at				-1.07	CF794867	Transcribed locus, highly similar to NP_115938.1 IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (Homo sapiens)	---	Hydrolase, protease
Ssc.7785.1.S1_at				-1.06	CK456652	Transcribed locus, moderately similar to NP_443164.1 pro-oncosis receptor inducing membrane injury gene (Homo sapiens)	---	Receptor
Ssc.6425.3.A1_at				-1.06	BI399085	Transcribed locus, moderately similar to NP_005679.1 ATP-binding cassette, sub-family C (CFTRMRP), member 5 (Homo sapiens)	---	Transport

Ssc.26864.1.A1_at				-1.02	CN162547	Transcribed locus, weakly similar to XP_150149.1 RIKEN cDNA 9230113P08 gene (Mus musculus)	---	
Ssc.10238.1.A1_at				-1.02	BI400310	Transcribed locus, moderately similar to NP_035519.1 solute carrier family 12, member 1 (Mus musculus)	---	
Ssc.13226.1.A1_at				-1.02	BQ604865	Transcribed locus, moderately similar to NP_113646.1 B aggressive lymphoma gene (Homo sapiens)	---	Transferase
Ssc.27912.1.S1_at				-1.01	CF365868	Transcribed locus, highly similar to XP_114432.2 zinc finger protein 608 (Homo sapiens)	---	Zinc ion binding
Ssc.11164.2.S1_a_at				1.02	CO953604	Transcribed locus, highly similar to NP_445980.1 DNA polymerase gamma (Rattus norvegicus)	---	DNA-directed DNA polymerase, nucleotidyltransferase, transferase
Ssc.8947.1.S1_at				1.03	BX667843	Transcribed locus, moderately similar to NP_003661.1 basic helix-loop-helix domain containing, class B, 2 (Homo sapiens)	---	
Ssc.17230.1.A1_at				1.04	CK460624	Transcribed locus, weakly similar to XP_343961.1 similar to Da1-6 (Rattus norvegicus)	---	Actin binding
Ssc.21184.1.S1_at				1.06	CN155420	Transcribed locus, highly similar to NP_032272.1 hippocampus abundant gene transcript 1 (Mus musculus)	---	Transport
Ssc.25920.1.S1_at				1.08	BX925015	Transcribed locus, highly similar to XP_213765.2 similar to CCT (chaperonin containing TCP-1) zeta subunit (Rattus norvegicus)	---	ATP binding, protein folding
Ssc.11519.2.A1_at				1.10	BII83297	Transcribed locus, moderately similar to NP_075813.1 pellino 1 (Mus musculus)	---	Protein binding, ubiquitin-proteoligase activity
Ssc.11519.1.A1_at				1.16	BII85881	Transcribed locus, moderately similar to NP_075813.1 pellino 1 (Mus musculus)	---	Protein binding, ubiquitin-proteoligase activity
Ssc.5396.1.S1_at				1.23	CF792567	Transcribed locus, highly similar to NP_003197.2 transcription factor 21 (Homo sapiens)	---	Transcription, transcription regulation
Ssc.7524.1.A1_at	-1.30				BQ599075	Transcribed locus	---	
Ssc.27680.1.S1_at	-1.28				AW480248	Transcribed locus	---	
Ssc.7637.2.S1_at	-1.26				BI339207	Transcribed locus	---	
Ssc.29750.1.A1_at	-1.25				CO993759	Transcribed locus	---	
Ssc.4664.1.S1_at	-1.25				BM482000	Transcribed locus	---	
Ssc.2274.1.A1_at	-1.23				BE232665	Transcribed locus	---	
Ssc.27042.1.A1_at	-1.22				CN165949	Transcribed locus	---	
Ssc.30871.1.A1_at	-1.17				BII18962	Transcribed locus	---	
Ssc.18929.1.S1_s_at	-1.14				CF366027	Transcribed locus	---	
Ssc.6382.1.A1_at	-1.13				BI343750	Transcribed locus	---	
Ssc.26680.1.A1_at	-1.10				CN154736	Transcribed locus	---	
Ssc.4272.1.A1_at	-1.10				BQ599843	Transcribed locus	---	
Ssc.17387.1.A1_at	-1.06				CO948677	Transcribed locus	---	
Ssc.10466.1.A1_at	-1.09				BQ602626	Transcribed locus	---	

Ssc.3271.1.A1_at	-1.03				BF703659	Transcribed locus	---	
Ssc.19413.1.A1_at	-1.02				CF360057	Transcribed locus	---	
Ssc.6697.1.S1_at	-1.01				CO954523	Transcribed locus	---	
Ssc.5648.1.A1_at	-1.01				BF702975	Transcribed locus	---	
Ssc.30194.1.A1_at	-1.00				CN162805	Transcribed locus	---	
Ssc.21700.1.A1_at	-1.00				CF792064	Transcribed locus	---	
Ssc.24758.1.A1_at	1.03				CK466750	Transcribed locus	---	
Ssc.18028.1.A1_at	1.03				CF180509	Transcribed locus	---	
Ssc.9504.1.A1_at	1.04				BF710717	Transcribed locus	---	
Ssc.18907.1.A1_at	1.05				CF365630	Transcribed locus	---	
Ssc.13591.1.A1_at	1.07				BQ602801	Transcribed locus	---	
Ssc.3088.1.S1_at	1.07				CN166193	Transcribed locus	---	
Ssc.30351.1.A1_at	1.12				CO990628	Transcribed locus	---	
Ssc.21130.1.S1_at	1.13				CK449422	Transcribed locus	---	
Ssc.7546.1.A1_at	1.14				BQ599193	Transcribed locus	---	
Ssc.5863.1.S1_at	1.14				BII184061	Transcribed locus	---	
Ssc.6097.1.S1_a_at	1.15				BX672990	Transcribed locus	---	
Ssc.30436.1.A1_at	1.16				CO991902	Transcribed locus	---	
Ssc.27421.1.A1_at	1.16				CN160251	Transcribed locus	---	
Ssc.27298.1.A1_at	1.17				CK464598	Transcribed locus	---	
Ssc.24584.1.S1_at	1.18				CK460583	Transcribed locus	---	
Ssc.24459.1.S1_at	1.27				CK457302	Transcribed locus	---	
Ssc.13547.1.A1_at	1.33				BQ602672	Transcribed locus	---	
Ssc.29855.1.A1_at	1.37				CO937870	Transcribed locus	---	
Ssc.31016.1.A1_at	1.43				CO949604	Transcribed locus	---	
Ssc.25317.1.S1_at	1.53				BX914997	Transcribed locus	---	
Ssc.29281.1.A1_at	1.68				CO953055	Transcribed locus	---	
Ssc.9440.1.A1_at	2.30				CN069729	Transcribed locus	---	
Ssc.3509.1.S1_at		-1.35			BE235252	Transcribed locus	---	
Ssc.6294.2.S1_at		-1.25			BI340023	Transcribed locus	---	
Ssc.7834.1.A1_at		-1.02			BQ599559	Transcribed locus	---	
Ssc.21884.1.A1_at		1.10			CF794971	Transcribed locus	---	
Ssc.27410.1.S1_at			-1.22		CN159453	Transcribed locus	---	

Ssc.22608.1.S1_at			-1.14		BX667042	Transcribed locus	---	
Ssc.18307.1.A1_at			-1.08		BQ597547	Transcribed locus	---	
Ssc.22521.1.A1_at			-1.05		CK465789	Transcribed locus	---	
Ssc.19629.2.S1_s_at			1.01		BQ603077	Transcribed locus	---	
Ssc.3411.1.A1_at			1.05		CK461446	Transcribed locus	---	
Ssc.16466.1.A1_at			1.15		CK459813	Transcribed locus	---	
Ssc.13423.1.A1_at			1.19		BI404586	Transcribed locus	---	
Ssc.8436.1.S1_at			1.19		BF710666	Transcribed locus	---	
Ssc.4643.1.A1_at			1.35		BF712417	Transcribed locus	---	
Ssc.22550.1.A1_at			1.37		CO943105	Transcribed locus	---	
Ssc.9607.1.A1_at			1.53		BF711037	Transcribed locus	---	
Ssc.3189.1.A1_at			1.60		BQ600803	Transcribed locus	---	
Ssc.30916.1.A1_at				-1.50	CO947301	Transcribed locus	---	
Ssc.14075.1.A1_at				-1.46	CK459115	Transcribed locus	---	
Ssc.6928.1.A1_at				-1.45	CO989436	Transcribed locus	---	
Ssc.31189.1.S1_at				-1.31	CO952477	Transcribed locus	---	
Ssc.23764.1.S1_at				-1.30	BG895329	Transcribed locus	---	
Ssc.19337.1.A1_at				-1.29	BM190087	Transcribed locus	---	
Ssc.30063.1.A1_at				-1.24	CO951943	Transcribed locus	---	
Ssc.7558.1.A1_at				-1.24	BQ599267	Transcribed locus	---	
Ssc.26005.1.S1_at				-1.24	BX926252	Transcribed locus	---	
Ssc.22362.1.A1_at				-1.23	CF792366	Transcribed locus	---	
Ssc.29231.1.A1_at				-1.21	CO952377	Transcribed locus	---	
Ssc.17861.1.A1_at				-1.20	BI118294	Transcribed locus	---	
Ssc.21026.1.S1_at				-1.19	CD572509	Transcribed locus	---	
Ssc.10673.1.A1_at				-1.16	BI404740	Transcribed locus	---	
Ssc.22377.1.A1_at				-1.15	CF792421	Transcribed locus	---	
Ssc.9039.2.S1_at				-1.15	CF364838	Transcribed locus	---	
Ssc.14415.1.A1_at				-1.15	BQ602223	Transcribed locus	---	
Ssc.5187.1.S1_at				-1.14	BI405042	Transcribed locus	---	
Ssc.8238.1.S1_at				-1.13	BF702474	Transcribed locus	---	
Ssc.25145.1.S1_at				-1.12	CK465844	Transcribed locus	---	
Ssc.7893.1.A1_at				-1.12	BI404005	Transcribed locus	---	

Ssc.23126.1.S1_at				-1.11	BX674432	Transcribed locus	---	
Ssc.7755.1.A1_at				-1.11	CF792275	Transcribed locus	---	
Ssc.24178.1.A1_at				-1.11	CK457006	Transcribed locus	---	
Ssc.23368.1.A1_at				-1.10	BQ599629	Transcribed locus	---	
Ssc.26983.1.A1_at				-1.09	CN164747	Transcribed locus	---	
Ssc.29749.1.A1_at				-1.09	CO942872	Transcribed locus	---	
Ssc.13053.1.A1_at				-1.08	BQ603979	Transcribed locus	---	
Ssc.7907.1.A1_at				-1.08	BI181465	Transcribed locus	---	
Ssc.14352.1.S1_at				-1.06	AJ656944	Transcribed locus	---	
Ssc.28084.1.A1_at				-1.05	CN031521	Transcribed locus	---	
Ssc.26692.1.A1_at				-1.05	CN157023	Transcribed locus	---	
Ssc.17005.1.A1_at				-1.05	CB475105	Transcribed locus	---	
Ssc.10642.1.S1_at				-1.04	CN162548	Transcribed locus	---	
Ssc.13414.1.A1_at				-1.03	BI405191	Transcribed locus	---	
Ssc.25324.1.S1_at				-1.02	CO946796	Transcribed locus	---	
Ssc.4427.1.A1_at				-1.02	BQ598146	Transcribed locus	---	
Ssc.27465.1.S1_at				1.05	CN160638	Transcribed locus	---	
Ssc.30870.1.A1_at				1.37	CF790577	Transcribed locus	---	