

Supplementary Material**Table S1.** Genes up-regulated in the CL of stimulated in relation to control animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene Title	Gene Symbol	fold change	P value
Bt.16350.2.A1_s_at	guanylate binding protein 5	GBP5	4.42	0.002
Bt.2498.2.A1_a_at	fibrinogen gamma chain	FGG	3.81	0.002
Bt.440.1.S1_at	neurotensin	NTS	3.74	0.036
Bt.27760.1.S1_at	major histocompatibility complex, class I, A /// major histocompatibility complex, class I, A	BoLA /// HLA-A	3.56	0.022
Bt.146.1.S1_at	defensin, beta 4A	DEFB4A	3.12	0.002
Bt.7165.1.S1_at	chemokine (C-X-C motif) ligand 5	CXCL5	3.06	0.031
Bt.15731.1.A1_at	V-set and immunoglobulin domain containing 4	VSIG4	3.03	0.047
Bt.22869.1.S2_at	fatty acid binding protein 5 (psoriasis-associated)	FABP5	3.02	0.006
Bt.4604.1.S1_a_at	acyl-CoA synthetase medium-chain family member 1	ACSM1	2.93	0.001
Bt.6406.1.S3_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	2.92	0.011
Bt.19845.2.A1_at	coagulation factor XIII, A1 polypeptide	F13A1	2.83	0.005
Bt.209.3.S1_at	lysozyme (renal amyloidosis)	LYZ	2.77	0.0003
Bt.15908.1.S1_at	methyltransferase like 7A	METTL7A	2.59	0.007
Bt.28383.1.S1_at	granulysin	GNLY	2.58	0.034
Bt.20455.1.S1_at	Microtubule-associated protein tau	MAPT	2.56	0.047
Bt.6556.1.S1_at	regakine 1	LOC504773	2.55	0.011
Bt.11259.1.S1_at	putative ISG12(a) protein	ISG12(A)	2.55	0.037
Bt.28243.1.S1_a_at	vanin 1	VNN1	2.54	0.008
Bt.405.1.S1_at	follistatin	FST	2.52	0.002
Bt.9510.2.A1_a_at	T-cell immunoglobulin and mucin domain containing 4	TIMD4	2.47	0.024
Bt.499.1.S1_a_at	prolactin receptor serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	PRLR	2.44	0.010
Bt.2712.1.S1_at	antiproteinase, antitrypsin, member 5	SERPINA5	2.43	0.00004
Bt.26875.1.A1_at	N-acetylated alpha-linked acidic dipeptidase-like 2	NAALADL2	2.43	0.018
Bt.19620.1.A1_at	interferon-induced protein 44	IFI44	2.41	0.004
Bt.2334.1.S1_at	CD68 molecule	CD68	2.34	0.004
Bt.14005.1.S1_at	CD53 molecule	CD53	2.32	0.005
Bt.15713.1.A1_at	pleckstrin	PLEK	2.31	0.016
Bt.8436.1.S1_at	interferon, alpha-inducible protein 6	IFI6	2.29	0.006
Bt.24012.1.A1_at	similar to guanylate binding protein 1	LOC511531	2.25	0.020
Bt.15731.1.A1_at	V-set and immunoglobulin domain containing 4	VSIG4	2.24	0.039
Bt.18219.1.A1_at	Hypothetical LOC784866	LOC784866	2.24	0.013
Bt.24813.1.A1_at	receptor (chemosensory) transporter protein 4	RTP4	2.22	0.002
Bt.20164.1.S1_at	complement component 1, q subcomponent, B chain	C1QB	2.22	0.006
Bt.28624.1.S1_at	Sterile alpha motif domain containing 9	SAMD9	2.19	0.007
Bt.21950.1.S1_s_at	chemokine (C-C motif) ligand 16	CCL16	2.18	0.007
Bt.4482.1.S1_at	macrophage scavenger receptor 1	MSR1	2.17	0.026
Bt.21576.1.S1_at	complement component 1, q subcomponent, C chain	C1QC	2.17	0.005

Bt.7204.1.S1_at	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	FCGR3	2.17	0.0001
Bt.1458.1.S1_at	phosphoglucosyltransferase 5	PGM5	2.13	0.004
Bt.21759.1.S1_at	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	BBOX1	2.13	0.001
Bt.24467.1.S1_at	radical S-adenosyl methionine domain containing 2	RSAD2	2.12	0.022
Bt.21284.2.S1_at	cysteine rich transmembrane BMP regulator 1 (chordin-like)	CRIM1	2.11	0.003
Bt.2294.1.S1_a_at	ubiquitin-like modifier activating enzyme 7	UBA7	2.10	0.002
Bt.20891.1.S1_at	2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	2.08	0.012
Bt.12694.1.S1_at	tumor necrosis factor receptor superfamily, member 21	TNFRSF21	2.08	0.040
Bt.12304.1.S1_at	ISG15 ubiquitin-like modifier	ISG15	2.07	0.020
Bt.1577.1.S1_at	complement component 1, q subcomponent, A chain	C1QA	2.07	0.019
Bt.50.1.S1_at	CD8a molecule	CD8A	2.06	0.030
Bt.12805.1.S1_at	phospholipase B domain containing 1	PLBD1	2.02	0.010
Bt.10077.1.S2_at	interferon regulatory factor 1	IRF1	2.01	0.0003
Bt.21820.1.S1_at	similar to GTPase, IMAP family member 5	LOC530077	2.01	0.021
Bt.287.1.S1_at	ribonuclease, RNase A family, k6	RNASE6	2.00	0.047
Bt.13293.1.S1_at	CD48 molecule	CD48	1.99	0.005
Bt.26968.1.S1_at	plexin C1	PLXNC1	1.99	0.010
Bt.23278.1.S1_at	allograft inflammatory factor 1	AIF1	1.98	0.001
Bt.20790.1.S1_at	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	1.97	0.019
Bt.1983.1.S1_at	egf-like module containing, mucin-like, hormone receptor-like 1	EMR1	1.97	0.003
Bt.21883.1.S1_at	placenta-specific 8	PLAC8	1.96	0.003
Bt.4675.1.S1_a_at	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1	1.96	0.026
Bt.14853.1.A1_at	RAB3A interacting protein (rabin3)	RAB3IP	1.94	0.001
Bt.18672.1.A1_at	tRNA methyltransferase 12 homolog (S. cerevisiae)	TRMT12	1.94	0.005
Bt.1791.1.A1_at	neural proliferation, differentiation and control, 1	NPDC1	1.93	0.016
Bt.22270.1.S1_at	chromosome 10 open reading frame 38 ortholog	C13H10ORF38	1.92	0.028
Bt.350.1.S1_s_at	MHC class II antigen	BLA-DQB	1.92	0.040
Bt.26666.1.S1_at	ADP-ribosylation factor 5	ARF5	1.92	0.020
Bt.2520.1.S1_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	1.91	0.012
Bt.3414.3.A1_a_at	ArfGAP with FG repeats 1	AGFG1	1.91	0.045
Bt.13315.1.S1_at	acyl-CoA synthetase family member 2	ACSF2	1.89	0.0001
Bt.6936.1.S1_at	chemokine (C-C motif) ligand 14	CCL14	1.89	0.005
Bt.26700.1.S1_at	histamine N-methyltransferase	HNMT	1.87	0.032
Bt.9211.1.S1_at	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	APBB1IP	1.85	0.001
Bt.471.1.S1_at	thrombomodulin	THBD	1.85	0.001
Bt.24238.1.A1_at	macrophage expressed 1	MPEG1	1.85	0.016
Bt.22829.1.A1_at	deoxynucleotidyltransferase, terminal, interacting protein 2 /// glutamate-cysteine ligase, modifier subunit	DNTTIP2 /// GCLM	1.84	0.005
Bt.139.1.A1_at	ADAM metalloproteinase domain 2	ADAM2	1.84	0.004
Bt.9504.1.A1_at	chemokine (C-C motif) ligand 4	CCL4	1.83	0.049
Bt.13127.1.S1_at	angiopoietin 1	ANGPT1	1.83	0.009
Bt.9786.1.S1_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-	ST6GALNAC2	1.83	0.0003

Bt.24707.1.S1_at	CD86 molecule	CD86	1.82	0.019
Bt.6826.1.S1_at	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	LCP2	1.82	0.038
Bt.2942.1.S1_at	similar to KIAA0405	FLRT2	1.82	0.026
Bt.26636.1.S1_at	natural killer cell group 7 sequence	NKG7	1.81	0.004
Bt.23641.1.S1_at	carbonic anhydrase XIII	CA13	1.81	0.003
Bt.4615.1.S1_at	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ITGB2	1.80	0.009
Bt.25107.1.A1_at	FYVE, RhoGEF and PH domain containing 5	FGD5	1.79	0.042
Bt.22465.1.S1_at	similar to EF-hand calcium-binding domain-containing protein 4A	LOC615055	1.79	0.037
Bt.132.1.S1_at	defensin, beta 1	EBD	1.79	0.003
Bt.6151.1.S1_at	colony stimulating factor 1 receptor	CSF1R	1.78	0.034
Bt.9807.1.S1_at	glycoprotein (transmembrane) nmb	GNPMB	1.78	0.012
Bt.9662.1.S1_at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	1.78	0.046
Bt.22491.1.A1_at	similar to Nkp80 NK receptor	LOC618591	1.78	0.028
Bt.9974.1.S1_at	chemokine (C-C motif) ligand 3	CCL3	1.78	0.039
Bt.9215.1.A1_at	WW domain containing oxidoreductase	WVVOX	1.77	0.035
Bt.21224.1.S1_at	dedicator of cytokinesis 10	DOCK10	1.76	0.004
Bt.12196.1.S1_at	protein tyrosine phosphatase, receptor type, C	PTPRC	1.76	0.044
Bt.20918.1.A1_at	phosphoinositide-3-kinase interacting protein 1	PIK3IP1	1.76	0.044
Bt.28439.1.S1_a_at	lymphocyte antigen 9	LY9	1.75	0.005
Bt.21131.1.A1_at	similar to transmembrane protein 166	LOC528994	1.75	0.023
Bt.18566.1.A1_at	similar to hCG27535	LOC539805	1.75	0.017
Bt.12500.2.S1_a_at	lymphocyte cytosolic protein 1 (L-plastin)	LCP1	1.75	0.035
Bt.2858.1.S1_at	abhydrolase domain containing 6	ABHD6	1.75	0.046
Bt.3115.1.A1_at	aspartylglucosaminidase	AGA	1.75	0.005
Bt.5092.2.A1_at	histone deacetylase 6	HDAC6	1.74	0.021
Bt.6963.1.A1_at	ecotropic viral integration site 2B	EVI2B	1.74	0.006
Bt.4147.1.S1_at	phosphodiesterase 6A, cGMP-specific, rod, alpha	PDE6A	1.73	0.025
Bt.22576.1.A1_at	protein phosphatase 1, regulatory (inhibitor) subunit 3D	PPP1R3D	1.72	0.020
Bt.22050.1.S1_at	hemopoietic cell kinase	HCK	1.72	0.010
Bt.23559.1.S1_at	thiamin pyrophosphokinase 1	TPK1	1.72	0.023
Bt.6387.1.A1_at	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	CHST7	1.72	0.007
Bt.2818.2.S1_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 2	NUDT2	1.72	0.003
Bt.6980.1.S1_at	SLAM family member 7	SLAMF7	1.72	0.014
Bt.20054.1.S1_at	interferon regulatory factor 9	IRF9	1.72	0.005
Bt.10001.1.A1_at	solute carrier family 39 (zinc transporter), member 14	SLC39A14	1.71	0.001
Bt.16234.2.S1_at	splicing factor, arginine/serine-rich 18	SFRS18	1.71	0.020
Bt.19521.1.A1_at	alcohol dehydrogenase 4 (class II), pi polypeptide	ADH4	1.71	0.031
Bt.13134.1.S1_at	jun oncogene	JUN	1.71	0.017
Bt.19028.1.A1_at	transient receptor potential cation channel, subfamily C, member 6	TRPC6	1.71	0.042
Bt.5493.1.S1_at	S100 calcium binding protein A4	S100A4	1.70	0.047
Bt.11057.1.S1_at	shisa homolog 3 (<i>Xenopus laevis</i>)	SHISA3	1.70	0.007

Bt.12745.3.S1_at	phospholipase A2, group IB (pancreas)	PLA2G1B	1.70	0.046
Bt.2047.1.S1_at	adrenomedullin	ADM	1.69	0.024
Bt.13428.2.S1_at	fructose-1,6-bisphosphatase 1	FBP1	1.69	0.026
Bt.7214.1.S1_a_at	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	COL4A3BP	1.69	0.00003
Bt.4107.1.S1_at	desmocollin 2	DSC2	1.69	0.036
Bt.7264.1.S1_at	cathepsin F	CTSF	1.68	0.002
Bt.23173.1.S1_at	pancreatic progenitor cell differentiation and proliferation factor	PPDPF	1.68	0.002
Bt.4153.1.S1_at	dual specificity phosphatase 12	DUSP12	1.68	0.0002
Bt.6406.1.S3_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	1.68	0.010
Bt.25039.1.S1_at	hypothetical protein LOC100302527	LOC100302527	1.67	0.023
Bt.1377.1.S1_at	chemokine (C-C motif) receptor 1	CCR1	1.67	0.035
Bt.28288.1.S1_at	DnaJ (Hsp40) homolog, subfamily B, member 1 similar to Interleukin-32 precursor (IL-32) (Natural killer cells protein 4) (Tumor necrosis factor alpha-inducing factor)	DNAJB1	1.67	0.033
Bt.7013.1.S1_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	LOC505800	1.67	0.002
Bt.6009.1.S1_at		SLC7A7	1.67	0.039
Bt.27830.1.A1_at	SP140 nuclear body protein	SP140	1.66	0.0002
Bt.25887.1.A1_at	UDP-glucose ceramide glucosyltransferase	UGCG	1.65	0.016
Bt.17766.1.S1_at	chromosome 3 open reading frame 23 ortholog	C22H3ORF23	1.65	0.007
Bt.1151.1.S1_at	cellular retinoic acid binding protein 2	CRABP2	1.65	0.030
Bt.8939.1.S1_at	TYRO protein tyrosine kinase binding protein	TYROBP	1.65	0.047
Bt.14207.1.S1_at	glycine C-acetyltransferase	GCAT	1.65	0.008
Bt.27073.1.S1_at	acyl-CoA dehydrogenase, long chain	ACADL	1.64	0.017
Bt.24098.1.A1_at	interferon induced with helicase C domain 1	IFIH1	1.64	0.019
Bt.17380.1.S1_at	transmembrane protein 205	TMEM205	1.64	0.029
Bt.7873.1.S1_at	basal cell adhesion molecule (Lutheran blood group) forkhead-associated (FHA) phosphopeptide binding domain 1	BCAM	1.64	0.013
Bt.26654.1.S1_at		FHAD1	1.64	0.011
Bt.5343.1.A1_at	CD300 molecule-like family member g major histocompatibility complex, class II, DM beta-chain, expressed	CD300LG	1.64	0.001
Bt.1007.1.S1_at		BOLA-DMB	1.64	0.012
Bt.6963.1.A1_at	ecotropic viral integration site 2B	EVI2B	1.64	0.008
Bt.3862.1.S1_a_at	peroxisome proliferator-activated receptor gamma	PPARG	1.64	0.015
Bt.21997.2.A1_at	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K	PPM1K	1.63	0.007
Bt.18251.2.A1_at	similar to BMP-2-inducible protein kinase (BIKe)	LOC505766	1.63	0.034
Bt.1607.1.S1_at	unc-51-like kinase 1 (C. elegans)	ULK1	1.63	0.012
Bt.20883.1.S1_at	angiogenin, ribonuclease, RNase A family, 5	ANG	1.63	0.012
Bt.15615.1.S1_at	NLR family, CARD domain containing 5	NLRC5	1.63	0.037
Bt.5326.2.S1_at	BTG family, member 2	BTG2	1.63	0.038
Bt.26426.1.A1_at	RNA binding motif protein 43	RBM43	1.63	0.027
Bt.3046.2.S1_at	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	FCN2	1.63	0.037
Bt.14029.1.S1_at	chondroitin sulfate N-acetylgalactosaminyltransferase 2	CSGALNACT2	1.63	0.021
Bt.16678.1.S1_at	brain expressed X-linked 2	BEX2	1.63	0.022
Bt.9563.1.S1_at	ankyrin repeat, SAM and basic leucine zipper domain containing 1	ASZ1	1.62	0.045

Bt.25537.1.A1_at	UDP-glucuronate decarboxylase 1	UXS1	1.62	0.009
Bt.13198.1.S1_at	signal-regulatory protein alpha	SIRPA	1.61	0.018
Bt.1165.1.S1_at	adenylate cyclase 7	ADCY7	1.61	0.007
Bt.26060.1.A1_at	Bruton agammaglobulinemia tyrosine kinase	BTK	1.61	0.012
Bt.14035.1.S1_at	protein kinase C, beta	PRKCB	1.61	0.013
Bt.8915.1.A1_at	dehydrogenase E1 and transketolase domain containing 1	DHTKD1	1.60	0.029
Bt.27943.1.S1_at	signal transducer and activator of transcription 2, 113kDa	STAT2	1.60	0.015
Bt.28865.1.A1_at	ribosomal protein S8	RPS8	1.60	0.014
Bt.16001.1.S1_at	cytochrome P450, family 27, subfamily A, polypeptide 1	CYP27A1	1.60	0.012
Bt.20091.1.S1_at	transcription factor 20 (AR1)	TCF20	1.60	0.024
Bt.13934.1.S1_at	CD3g molecule, gamma (CD3-TCR complex)	CD3G	1.60	0.049
Bt.28908.1.A1_at	similar to guanylate binding protein 4	LOC507055	1.60	0.050
Bt.6434.1.S1_at	ring finger protein 149	RNF149	1.60	0.011
Bt.28490.1.S1_at	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	IMMP2L	1.59	0.024
Bt.24623.1.A1_at	erythrocyte membrane protein band 4.1 like 4A	EPB41L4A	1.59	0.038
Bt.26983.1.S1_at	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1	1.59	0.007
Bt.25030.1.A1_a_at	transmembrane 9 superfamily member 2	TM9SF2	1.59	0.030
Bt.25111.1.A1_at	Similar to interferon-induced protein 44-like	LOC508347	1.59	0.010
Bt.25039.1.S1_at	hypothetical protein LOC100302527	LOC100302527	1.59	0.018
Bt.21431.1.S1_at	lymphotoxin beta (TNF superfamily, member 3)	LTB	1.59	0.042
Bt.19514.1.A1_at	hypothetical protein LOC100140616	LOC100140616	1.59	0.005
Bt.4049.1.S1_at	armadillo repeat containing, X-linked 6	ARMCX6	1.59	0.009
Bt.5259.1.S1_at	XIAP associated factor 1	XAF1	1.58	0.025
Bt.16068.1.A1_at	Glutamate-cysteine ligase, catalytic subunit	GCLC	1.58	0.033
Bt.16857.1.A1_at	fragile histidine triad gene	FHIT	1.58	0.018
Bt.16632.1.A1_at	hypothetical LOC613276	LOC613276	1.58	0.010
Bt.7632.1.S1_a_at	NCK-associated protein 1-like	NCKAP1L	1.58	0.027
Bt.4293.1.S1_at	intercellular adhesion molecule 3	ICAM3	1.58	0.031
Bt.12964.1.A1_at	Glycoprotein M6B	GPM6B	1.58	0.010
Bt.17571.1.A1_at	spleen focus forming virus (SFFV) proviral integration oncogene spi1	SPI1	1.57	0.032
Bt.2657.1.S1_a_at	fermitin family homolog 3 (Drosophila)	FERMT3	1.57	0.010
Bt.351.1.S1_at	coronin, actin binding protein, 1A	CORO1A	1.57	0.039
Bt.23276.2.S1_at	similar to Absent in melanoma 1 protein	LOC526200	1.57	0.050
Bt.21154.2.S1_at	serine/threonine kinase 4	STK4	1.57	0.010
Bt.9349.1.S1_at	similar to coagulation factor VIII-associated protein	LOC617475	1.57	0.034
Bt.7393.1.S1_at	Nephronectin	NPNT	1.57	0.022
Bt.22179.1.S1_at	similar to basement membrane-induced gene	LOC507126	1.57	0.014
Bt.13769.1.S1_at	Microtubule-associated protein 2	MAP2	1.57	0.034
Bt.12849.2.S1_at	solute carrier organic anion transporter family, member 2B1	SLCO2B1	1.57	0.030
Bt.18203.1.A1_at	junctional adhesion molecule 2	JAM2	1.56	0.001
Bt.143.1.S1_at	neutrophil cytosolic factor 2	NCF2	1.56	0.031

Bt.8803.1.A1_at	complement component 1, r subcomponent	C1R	1.56	0.036
Bt.13493.1.A1_at	Cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	CELSR2	1.56	0.013
Bt.1275.1.S1_at	similar to fractalkine	LOC517354	1.56	0.005
Bt.2726.2.S1_at	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	DACT1	1.56	0.044
Bt.5392.1.S1_at	CD36 molecule (thrombospondin receptor)	CD36	1.56	0.002
Bt.7938.1.S1_at	cathepsin S	CTSS	1.56	0.012
Bt.13113.1.S1_at	L-gulonono-gamma-lactone oxidase	GULO	1.55	0.032
Bt.23233.2.S1_at	ubiquitin specific peptidase 18	USP18	1.55	0.014
Bt.22739.2.S1_at	suppressor of cytokine signaling 4	SOCS4	1.55	0.006
Bt.13959.1.S1_at	protein kinase C, epsilon	PRKCE	1.55	0.044
Bt.21732.1.S1_at	ribonuclease T2	RNASET2	1.55	0.047
Bt.16180.1.S1_at	poly (ADP-ribose) polymerase family, member 11	PARP11	1.55	0.030
Bt.21897.1.S1_at	ring finger protein 217	RNF217	1.55	0.043
Bt.20762.2.S1_at	Chronic lymphocytic leukemia deletion region gene 6 protein homolog	CLLD6	1.55	0.012
Bt.4622.1.S1_at	mannosidase, alpha, class 2B, member 1	MAN2B1	1.54	0.001
Bt.16983.1.S1_at	TRIM6-TRIM34 readthrough	TRIM6-TRIM34	1.54	0.024
Bt.18219.1.A1_at	Hypothetical LOC784866	LOC784866	1.54	0.009
Bt.17110.2.A1_at	flavin containing monooxygenase 5	FMO5	1.54	0.014
Bt.21147.2.S1_a_at	hypothetical protein LOC507810	LOC507810	1.54	0.009
Bt.2905.1.S1_at	NDRG family member 2	NDRG2	1.54	0.001
Bt.23488.1.S1_at	complement factor properdin	CFP	1.54	0.043
Bt.8945.1.S1_at	toll-like receptor 2	TLR2	1.54	0.035
Bt.8804.1.S1_at	NEL-like 2 (chicken)	NELL2	1.53	0.001
Bt.6438.1.A1_at	transforming growth factor, beta 2	TGFB2	1.52	0.032
Bt.196.1.S1_at	8KDa amlexanox-binding protein	S100A13	1.52	0.008
Bt.1616.1.A1_at	superoxide dismutase 3, extracellular	SOD3	1.52	0.039
Bt.9444.1.S1_at	serine/threonine kinase 17a	STK17A	1.52	0.048
Bt.4544.1.S1_at	integrin, alpha 6	ITGA6	1.52	0.040
Bt.24069.1.A1_at	C-type lectin domain family 2, member D	CLEC2D	1.52	0.004
Bt.12743.1.A1_at	ATP-binding cassette, sub-family D (ALD), member 4	ABCD4	1.52	0.011
Bt.27364.1.S1_at	platelet-activating factor receptor	PTAFR	1.52	0.023
Bt.1585.1.A1_at	hypothetical protein LOC534992	C2orf43	1.51	0.006
Bt.4946.1.S1_at	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	RAC2	1.51	0.034
Bt.18440.2.S1_at	similar to guanylate binding protein 4	LOC510382	1.51	0.023
Bt.23174.1.S1_at	CD74 molecule, major histocompatibility complex, class II invariant chain	CD74	1.51	0.020
Bt.14166.2.S1_at	transmembrane protein 150C	TMEM150C	1.51	0.0004
Bt.9350.1.A1_at	ganglioside-induced differentiation-associated protein 1	GDAP1	1.50	0.023
Bt.29873.1.S1_at	mesoderm specific transcript homolog (mouse)	MEST	1.50	0.024
Bt.20600.2.A1_a_at	MYC induced nuclear antigen	MINA	1.50	0.019
Bt.20409.1.S1_at	poly (ADP-ribose) polymerase family, member 9	PARP9	1.50	0.005
Bt.26905.1.A1_at	protein phosphatase 1, regulatory (inhibitor) subunit 3B	PPP1R3B	1.50	0.001
Bt.1539.1.S1_at	GM2 ganglioside activator	GM2A	1.50	0.024

Bt.13486.1.A1_at

glycine dehydrogenase (decarboxylating)

GLDC

1.50

0.040

Table S2. Genes down-regulated in the CL of stimulated in relation to control animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene title	Gene Symbol	Fold Change	P value
Bt.4404.1.A1_at	protease, serine, 2 (trypsin 2)	PRSS2	-11.60	0.0000001
Bt.27140.1.S1_at	similar to mKIAA1077 protein	LOC535166	-5.64	0.0002
Bt.16201.1.S1_at	S100 calcium binding protein A9	S100A9	-4.65	0.0013
Bt.396.2.S1_a_at	cellular retinoic acid binding protein 1	CRABP1	-4.50	0.03
Bt.23042.1.S1_at	metallothionein 1E	MT1A	-4.23	0.01
Bt.3000.2.S1_a_at	microtubule-associated protein 1 light chain 3 gamma	MAP1LC3C	-4.16	0.04
Bt.27963.1.A1_at	neutral cholesterol ester hydrolase 1	NCEH1	-3.93	0.0009
Bt.17990.1.A1_at	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	-3.32	0.01
Bt.9360.1.S1_at	S100 calcium binding protein A8	S100A8	-3.19	0.0042
Bt.27140.1.S1_at	similar to mKIAA1077 protein	LOC535166	-3.15	0.0003
Bt.14200.1.A1_at	metallothionein 1E	MT1E	-3.10	0.02
Bt.22389.1.S1_at	shisa homolog 2 (<i>Xenopus laevis</i>)	SHISA2	-2.47	0.04
Bt.8953.1.S1_at	prostaglandin E synthase	PTGES	-2.40	0.03
Bt.10823.1.A1_s_at	hydroletharus syndrome 1	HYLS1	-2.33	0.0029
Bt.17990.1.A1_at	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	-2.29	0.01
Bt.10144.1.A1_s_at	T-cell lymphoma invasion and metastasis 1	TIAM1	-2.27	0.0004
Bt.4714.1.S1_at	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	MMP9	-2.26	0.00003
Bt.546.1.S1_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	KCNMA1	-2.15	0.01
Bt.25744.1.A1_at	solute carrier family 38, member 11	SLC38A11	-2.09	0.0023
Bt.29009.1.A1_at	ryanodine receptor 3	RYR3	-2.06	0.02
Bt.26100.2.A1_at	glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	-2.02	0.02
Bt.13482.1.S1_at	nephroblastoma overexpressed	NOV	-2.01	0.01
Bt.16201.2.A1_at	S100 calcium binding protein A9	S100A9	-1.99	0.01
Bt.29619.1.A1_at	chromosome 6 open reading frame 141 ortholog	C23H6orf141	-1.99	0.01
Bt.8479.1.A1_at	nitric oxide synthase 2, inducible	NOS2	-1.96	0.01
Bt.28456.1.S1_at	similar to alpha-tubulin	LOC407195	-1.95	0.01
Bt.29009.1.A1_at	ryanodine receptor 3	RYR3	-1.95	0.01
Bt.4224.1.S1_at	adenylate kinase 1	AK1	-1.94	0.01
Bt.21079.1.A1_at	similar to solute carrier family 35, member F2	LOC782215	-1.93	0.02
Bt.11420.1.A1_at	prolyl 4-hydroxylase, alpha polypeptide III	P4HA3	-1.91	0.0017
Bt.27866.1.A1_at	myo-inositol oxygenase	MIOX	-1.89	0.01
Bt.19093.1.S1_at	Aldehyde dehydrogenase 1 family, member A2	ALDH1A2	-1.89	0.03
Bt.9423.1.S1_at	Platelet-derived growth factor receptor, alpha polypeptide	PDGFRA	-1.88	0.05
Bt.23294.1.A1_at	PDZ and LIM domain 3	PDLIM3	-1.86	0.02
Bt.5247.1.S1_at	prostaglandin I2 (prostacyclin) synthase	PTGIS	-1.85	0.0013
Bt.28456.1.S1_at	similar to alpha-tubulin	LOC407195	-1.83	0.01

Bt.9379.1.S1_at	monoamine oxidase A	MAOA	-1.82	0.02
Bt.2568.1.S1_at	perilipin 2	PLIN2	-1.82	0.01
Bt.12297.1.S1_at	lysyl oxidase-like 4	LOXL4	-1.82	0.01
Bt.10398.1.S1_at	pentraxin 3, long phosphatidylinositol glycan anchor biosynthesis, class K	PTX3	-1.81	0.03
Bt.3580.2.S1_at	heme oxygenase (decycling) 2	PIGK	-1.81	0.0004
Bt.3226.1.S1_at	carbonyl reductase 3	HMOX2	-1.78	0.01
Bt.22496.1.S1_at	carbonyl reductase 3	CBR3	-1.77	0.01
Bt.18228.2.S1_a_at	Sec61 alpha 2 subunit (S. cerevisiae)	SEC61A2	-1.77	0.0024
Bt.5268.1.S1_at	follistatin-like 3 (secreted glycoprotein) NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	FSTL3	-1.77	0.0003
Bt.26741.1.S1_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	NIF3L1	-1.77	0.03
Bt.13899.1.A1_at	leucine zipper, down-regulated in cancer 1	ENPP1	-1.76	0.04
Bt.16830.1.S1_at	leucine zipper, down-regulated in cancer 1	LDOC1	-1.76	0.01
Bt.12294.2.A1_at	Adhesion molecule with Ig-like domain 2 transmembrane emp24 protein transport domain containing 6	AMIGO2	-1.75	0.02
Bt.628.1.S1_at	RNA pseudouridylate synthase domain containing 3	TMED6	-1.74	0.0003
Bt.23235.1.S1_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	RPUSD3	-1.73	0.0006
Bt.9267.1.A1_at	unc-13 homolog D (C. elegans)	APOBEC3B	-1.72	0.02
Bt.20343.1.S1_at	unc-13 homolog D (C. elegans)	UNC13D	-1.68	0.03
Bt.8624.1.S1_at	arginase, type II	ARG2	-1.68	0.0036
Bt.26309.1.A1_at	sorting nexin 31	SNX31	-1.67	0.04
Bt.19482.1.A1_at	transferrin receptor (p90, CD71)	TFRC	-1.67	0.02
Bt.8109.2.A1_at	sushi-repeat-containing protein, X-linked 2	SRPX2	-1.67	0.04
Bt.3870.1.S1_at	Tubulin tyrosine ligase-like family, member 3 reticulocalbin 3, EF-hand calcium binding domain	TTLL3	-1.67	0.04
Bt.4078.2.S1_a_at	RAS-like, estrogen-regulated, growth inhibitor	RCN3	-1.67	0.0023
Bt.24842.1.A1_at	RAS-like, estrogen-regulated, growth inhibitor	RERG	-1.66	0.02
Bt.4865.1.S1_at	elastin microfibril interfacier 1 potassium large conductance calcium- activated channel, subfamily M, beta member 4	EMILIN1	-1.66	0.02
Bt.19643.2.S1_at	similar to RIKEN cDNA 4930519N13 /// similar to KIAA0980 protein /// similar to KIAA0980 protein /// similar to RIKEN cDNA 4930519N13	KCNMB4 LOC513940 /// LOC783633 /// LOC785425 /// LOC787322	-1.66	0.02
Bt.27546.1.S1_at	adenosine deaminase-like	LOC513940 /// LOC783633 /// LOC785425 /// LOC787322	-1.66	0.0021
Bt.28556.1.S1_at	adenosine deaminase-like	ADAL	-1.65	0.04
Bt.4510.1.S1_at	polyamine-modulated factor 1	PMF1	-1.65	0.02
Bt.6658.2.A1_at	family with sequence similarity 46, member B general transcription factor I1H, polypeptide 1, 62kDa	FAM46B	-1.64	0.01
Bt.19585.2.S1_at	tumor protein D52-like 1	GTF2H1	-1.63	0.02
Bt.15740.1.A1_at	tumor protein D52-like 1	TPD52L1	-1.63	0.04
Bt.9777.1.S1_at	3-hydroxybutyrate dehydrogenase, type 1 nudix (nucleoside diphosphate linked moiety X)-type motif 10	BDH1	-1.63	0.03
Bt.24396.3.A1_at	NmrA-like family domain containing 1 core 1 synthase, glycoprotein-N- acetylgalactosamine 3-beta- galactosyltransferase, 1	NUDT10	-1.62	0.0007
Bt.20530.1.S1_at	NmrA-like family domain containing 1 core 1 synthase, glycoprotein-N- acetylgalactosamine 3-beta- galactosyltransferase, 1	NMRAL1	-1.62	0.03
Bt.22740.1.A1_at	plasminogen activator, urokinase	C1GALT1	-1.61	0.03
Bt.2519.1.S1_at	plasminogen activator, urokinase	PLAU	-1.61	0.02

Bt.3580.1.A1_at	similar to Phosphatidylinositol glycan anchor biosynthesis, class K	LOC782466	-1.61	0.0007
Bt.19681.1.A1_at	Similar to Uncharacterized protein KIAA0802 phospholipase D1, phosphatidylcholine-specific	LOC538547	-1.61	0.03
Bt.13996.3.A1_at	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	PLD1	-1.60	0.05
Bt.27675.1.A1_at	hydroxyacid oxidase 2 (long chain)	KIT	-1.60	0.03
Bt.23966.1.A1_at	protein tyrosine phosphatase, receptor type, G	HAO2	-1.59	0.01
Bt.24790.1.A1_at	GINS complex subunit 4 (Sld5 homolog)	PTPRG	-1.59	0.02
Bt.1804.1.S1_at	calcium/calmodulin-dependent protein kinase II inhibitor 1	GINS4	-1.59	0.01
Bt.16230.1.S1_at	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	CAMK2N1	-1.59	0.04
Bt.23658.2.S1_at	glutathione S-transferase omega 1	ASF1B	-1.58	0.04
Bt.28194.1.S1_at	transmembrane protein 45A	GSTO1	-1.58	0.0020
Bt.2159.1.S1_at	RAB GTPase activating protein 1-like cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	TMEM45A	-1.57	0.03
Bt.23619.1.S1_a_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	RABGAP1L	-1.57	0.03
Bt.20420.1.S1_at	peptidase inhibitor 16	CDKN2C	-1.57	0.0016
Bt.24504.1.A1_at	myosin, heavy chain 11, smooth muscle	GALNT12	-1.57	0.0044
Bt.4912.1.S1_at	RAB, member RAS oncogene family-like 5	PI16	-1.57	0.04
Bt.12685.1.S1_at	keratin 18	MYH11	-1.57	0.02
Bt.18626.1.A1_at	phosphatidylinositol glycan anchor biosynthesis, class K	RABL5	-1.57	0.02
Bt.1745.1.S1_at	hydroxysteroid (11-beta) dehydrogenase 1	KRT18	-1.56	0.05
Bt.3580.2.S1_at	lipolysis stimulated lipoprotein receptor	PIGK	-1.56	0.0006
Bt.13027.1.A1_at	microtubule-associated protein 1A	HSD11B1	-1.56	0.01
Bt.12462.1.S1_at	similar to tescalcin	LSR	-1.56	0.0015
Bt.1953.1.S1_at	sal-like 2 (Drosophila)	MAP1A	-1.55	0.04
Bt.18080.3.A1_at	TRAF2 and NCK interacting kinase	LOC787094	-1.55	0.04
Bt.2179.1.S1_a_at	centromere protein N	SALL2	-1.54	0.0030
Bt.6803.1.A1_at	pyruvate kinase, muscle	TNIK	-1.54	0.05
Bt.10816.1.S1_s_at	interleukin 33	CENPN	-1.54	0.05
Bt.23399.1.S1_at	adiponectin receptor 2	PKM2	-1.54	0.03
Bt.22094.1.A1_at	retinoblastoma binding protein 8	IL33	-1.54	0.03
Bt.805.1.S1_at	FXFD domain containing ion transport regulator 1	ADIPOR2	-1.54	0.04
Bt.27316.2.A1_at	RAB32, member RAS oncogene family pleckstrin homology-like domain, family A, member 2	RBBP8	-1.54	0.01
Bt.20510.1.S1_at	regulator of G-protein signaling 2, 24kDa nucleolar protein 3 (apoptosis repressor with CARD domain)	FXFD1	-1.53	0.03
Bt.6603.1.A1_at	kinesin light chain 1	RAB32	-1.53	0.05
Bt.1702.1.A1_at	lymphoid enhancer-binding factor 1	PHLDA2	-1.53	0.04
Bt.10855.1.S1_at	multiple EGF-like-domains 10	RGS2	-1.53	0.02
Bt.1185.2.S1_at	uronyl-2-sulfotransferase	NOL3	-1.53	0.01
Bt.5626.3.S1_at		KLC1	-1.52	0.04
Bt.6527.1.S1_at		LEF1	-1.52	0.02
Bt.3996.1.S1_at		MEGF10	-1.52	0.01
Bt.21924.1.A1_at		UST	-1.52	0.01

Bt.12010.2.S1_at	ADAM metallopeptidase with thrombospondin type 1 motif, 1	ADAMTS1	-1.52	0.05
Bt.24801.1.A1_at	similar to Class B basic helix-loop-helix protein 5 (bHLHB5) (Protein BETA3)	LOC525275	-1.52	0.05
Bt.4995.1.A1_at	Anillin, actin binding protein	ANLN	-1.51	0.05
Bt.28582.1.S1_s_at	activating signal cointegrator 1 complex subunit 1	ASCC1	-1.51	0.02
Bt.18101.1.A1_at	olfactomedin 1	OLFM1	-1.51	0.03
Bt.27549.1.A1_at	tudor domain containing 6	TDRD6	-1.51	0.03
Bt.25788.1.S1_at	zinc finger and BTB domain containing 16	ZBTB16	-1.51	0.02
Bt.26343.1.S1_at	microsomal triglyceride transfer protein	MTTP	-1.51	0.03
Bt.26730.1.S1_at	torsin A interacting protein 2	TOR1AIP2	-1.50	0.01
Bt.22545.2.S1_at	fibulin 1	FBLN1	-1.50	0.0038

Table S3. Genes up-regulated in the CL of superovulated in relation to control animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene title	Gene Symbol	Fold Change	P value
Bt.3805.1.S1_at	MHC class I antigen /// MHC Class I JSP.1	BOLA-N	7.06	0.04
Bt.15528.1.S1_at	Macrophage migration inhibitory factor	MIF	6.16	0.04
Bt.12930.1.S1_a_at	Tachykinin, precursor 1	TAC1	5.27	0.03
Bt.7165.1.S1_at	Chemokine (C-X-C motif) ligand 5	CXCL5	4.52	0.04
Bt.440.1.S1_at	Neurotensin	NTS	4.10	0.04
Bt.4594.1.S1_at	MHC class II antigen	BLA-DQB	4.06	0.01
Bt.17599.1.A1_at	Cadherin 8, type 2	CDH8	3.35	0.03
Bt.8967.1.S1_at	Myostatin	MSTN	2.93	0.01
Bt.21131.1.A1_at	Similar to transmembrane protein 166	LOC528994	2.78	0.001
Bt.5273.1.S1_at	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	ITGAV	2.70	0.02
Bt.5935.2.S1_a_at	Lysosomal protein transmembrane 4 alpha	LAPTM4A	2.56	0.002
Bt.13789.1.A1_at	CD14 molecule	CD14	2.56	0.05
Bt.4751.1.S1_a_at	Major histocompatibility complex, class II, DQ alpha 2	BOLA-DQA2	2.53	0.01
Bt.209.3.S1_at	Lysozyme (renal amyloidosis)	LYZ	2.39	0.004
Bt.19845.2.A1_at	Coagulation factor XIII, A1 polypeptide	F13A1	2.36	0.01
Bt.23093.1.S1_at	Chemokine (C-X-C motif) ligand 2	CXCL2	2.36	0.004
Bt.12295.1.S1_at	Podoplanin	PDPN	2.35	0.001
Bt.22045.1.S1_at	Six transmembrane epithelial antigen of the prostate 2	STEAP2	2.34	0.01
Bt.29403.1.S1_at	Trefoil factor 2	TFF2	2.31	0.004
Bt.5494.1.S1_at	CD44 molecule (Indian blood group)	CD44	2.18	0.02
Bt.4679.1.S1_at	Fc fragment of igg, low affinity iib, receptor (CD32)	FCGR2	2.13	0.02
Bt.8945.1.S1_at	Toll-like receptor 2	TLR2	2.12	0.03
Bt.22869.1.S2_at	Fatty acid binding protein 5 (psoriasis-associated)	FABP5	2.05	0.01
Bt.26700.1.S1_at	Histamine N-methyltransferase	HNMT	2.05	0.01
Bt.367.1.S1_at	Survival motor neuron	OLR1	2.05	0.05
Bt.471.1.S1_at	Thrombomodulin	THBD	2.00	0.02
Bt.6406.1.S3_at	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	2.00	0.003
Bt.24592.1.S1_at	Neuritin 1	NRN1	1.94	0.01
Bt.19028.1.A1_at	Transient receptor potential cation channel, subfamily C, member 6	TRPC6	1.93	0.01
Bt.9559.2.S1_at	Amyloid beta (A4) precursor protein	APP	1.93	0.03
Bt.21950.1.S1_at	Chemokine (C-C motif) ligand 16	CCL16	1.93	0.03
Bt.3885.4.S1_x_at	Chloride channel accessory 3 (pseudogene)	CLCA3P	1.92	0.01
Bt.12805.1.S1_at	Phospholipase B domain containing 1	PLBD1	1.91	0.02
Bt.9510.2.A1_a_at	T-cell immunoglobulin and mucin domain containing 4	TIMD4	1.91	0.03
Bt.19514.1.A1_at	Hypothetical protein LOC100140616	LOC100140616	1.88	0.03
Bt.23278.1.S1_at	Allograft inflammatory factor 1	AIF1	1.87	0.002
Bt.3885.4.S1_a_at	Chloride channel accessory 3 (pseudogene) /// similar to calcium-activated chloride channel	CLCA3P /// LOC784768	1.87	0.01
Bt.146.1.S1_at	Defensin, beta 4A	DEFB4A	1.86	0.02

Bt.2334.1.S1_at	CD68 molecule	CD68	1.86	0.02
Bt.20639.1.A1_at	PHD finger protein 3	PHF3	1.84	0.03
Bt.9821.1.S1_at	Amino adipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT	1.83	0.004
Bt.6731.1.S1_at	Chromosome 1 open reading frame 54 ortholog	C3H1orf54	1.82	0.03
Bt.26666.1.S1_at	ADP-ribosylation factor 5	ARF5	1.82	0.05
Bt.9350.1.A1_at	Ganglioside-induced differentiation-associated protein 1	GDAP1	1.78	0.01
Bt.21224.1.S1_at	Dedicator of cytokinesis 10	DOCK10	1.78	0.001
Bt.20248.1.S1_at	Ribonuclease H2, subunit A	RNASEH2A	1.78	0.01
Bt.15808.1.S1_at	Membrane-associated ring finger (C3HC4) 3	MARCH3	1.77	0.02
Bt.13484.1.A1_at	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	PPP1R3C	1.76	0.01
Bt.22512.2.S1_at	Kelch-like 5 (Drosophila)	KLHL5	1.76	0.02
Bt.25537.1.A1_at	UDP-glucuronate decarboxylase 1	UXS1	1.76	0.03
Bt.27339.1.A1_at	Membrane metallo-endopeptidase	MME	1.76	0.02
Bt.27887.1.S1_at	Yippee-like 2 (Drosophila)	YPEL2	1.76	0.04
Bt.15979.1.S1_at	Survival motor neuron	SMN1	1.74	0.01
Bt.9807.1.S1_at	Glycoprotein (transmembrane) nmb	GPNMB	1.70	0.01
Bt.5598.1.S1_at	Chromosome 8 open reading frame 4 ortholog	C27H8orf4	1.70	0.02
Bt.27929.1.S1_at	WD repeat and FYVE domain containing 1	WDFY1	1.70	0.04
Bt.24238.1.A1_at	Macrophage expressed 1	MPEG1	1.69	0.003
Bt.13293.1.S1_at	CD48 molecule	CD48	1.69	0.01
Bt.22081.1.S1_at	LIM domain 7	LMO7	1.68	0.03
Bt.18533.1.S1_at	Activating transcription factor 3	ATF3	1.68	0.001
Bt.8939.1.S1_at	TYRO protein tyrosine kinase binding protein	TYROBP	1.68	0.03
Bt.5858.1.S1_at	P21 protein (Cdc42/Rac)-activated kinase 1	PAK1	1.67	0.01
Bt.6795.1.S1_at	Actin related protein 2/3 complex, subunit 3, 21kda	ARPC3	1.67	0.01
Bt.4110.1.S1_at	Histamine receptor H1	HRH1	1.67	0.003
Bt.4635.1.S1_at	Calponin 2	CNN2	1.65	0.03
Bt.26635.1.S1_at	Frizzled homolog 1 (Drosophila)	FZD1	1.65	0.01
Bt.619.2.A1_at	Similar to 65 kda Yes-associated protein (YAP65) /// Yes-associated protein 1	LOC787360 /// YAP1	1.65	0.02
Bt.9027.1.S1_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	1.64	0.03
Bt.22050.1.S1_at	Hemopoietic cell kinase	HCK	1.64	0.02
Bt.2726.2.S1_at	Dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	DACT1	1.63	0.04
Bt.2629.1.S1_at	Renin binding protein	RENBP	1.63	0.05
Bt.24707.1.S1_at	CD86 molecule	CD86	1.62	0.05
Bt.6208.1.A1_at	Component of oligomeric golgi complex 5	COG5	1.62	0.01
Bt.4989.1.S1_at	Tuftelin 1	TUFT1	1.62	0.002
Bt.24824.1.S1_at	Glycosyltransferase 8 domain containing 2	GLT8D2	1.61	0.04
Bt.685.1.A1_at	Asparaginase like 1	ASRGL1	1.61	0.05
Bt.28288.1.S1_at	Dnaj (Hsp40) homolog, subfamily B, member 1	DNAJB1	1.61	0.05
Bt.25087.3.S1_at	Ras homolog gene family, member Q	RHOQ	1.60	0.01
Bt.16730.1.A1_at	Solute carrier family 41, member 2	SLC41A2	1.60	0.001
Bt.14143.1.S1_at	Carboxypeptidase E	CPE	1.60	0.004

Bt.196.1.S1_at	8kda amlexanox-binding protein	S100A13	1.59	0.03
Bt.22042.1.S1_at	Transmembrane protein 30B	TMEM30B	1.58	0.05
Bt.4279.2.S1_at	SHC (Src homology 2 domain containing) transforming protein 1	SHC1	1.58	0.001
Bt.6387.1.A1_at	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	CHST7	1.58	0.01
Bt.27920.1.A1_at	Hematopoietically expressed homeobox	HHEX	1.57	0.02
Bt.3414.3.A1_a_at	Arfgap with FG repeats 1	AGFG1	1.56	0.02
Bt.11428.1.A1_at	Chromosome 21 open reading frame 7 ortholog	C1H21ORF7	1.56	0.03
Bt.6047.1.S1_at	Cysteine and glycine-rich protein 1	CSRP1	1.56	0.01
Bt.23493.1.S1_at	Thrombospondin 1	THBS1	1.56	0.03
Bt.6057.1.S1_at	Von Willebrand factor A domain containing 1	VWA1	1.56	0.04
Bt.20245.1.S1_at	Pleckstrin homology domain containing, family O member 1	PLEKHO1	1.56	0.03
Bt.28675.1.S1_at	Arachidonate 12-lipoxygenase	ALOX12	1.55	0.002
Bt.28225.1.A1_at	SAM domain, SH3 domain and nuclear localization signals 1	SAMSN1	1.55	0.04
Bt.24841.1.S1_at	Spla/ryanodine receptor domain and SOCS box containing 1	SPSB1	1.55	0.02
Bt.27247.1.A1_at	Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	1.55	0.05
Bt.4342.1.S1_at	Selectin P	SELP	1.55	0.01
Bt.143.1.S1_at	Neutrophil cytosolic factor 2	NCF2	1.54	0.03
Bt.13486.1.A1_at	Glycine dehydrogenase (decarboxylating)	GLDC	1.54	0.003
Bt.5605.3.S1_at	Myristoylated alanine-rich protein kinase C substrate	MARCKS	1.54	0.03
Bt.24335.1.S1_at	Dual adaptor of phosphotyrosine and 3-phosphoinositides	DAPP1	1.54	0.04
Bt.9527.2.S1_at	Kruppel-like factor 10	KLF10	1.54	0.02
Bt.25979.1.S1_a_at	Ectonucleoside triphosphate diphosphohydrolase 4	ENTPD4	1.53	0.01
Bt.3862.1.S1_a_at	Peroxisome proliferator-activated receptor gamma	PPARG	1.53	0.03
Bt.12314.1.S1_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	1.53	0.04
Bt.25948.1.A1_at	Deltex homolog 1 (Drosophila)	DTX1	1.52	0.03
Bt.27073.1.S1_at	Acyl-coa dehydrogenase, long chain	ACADL	1.52	0.01
Bt.26535.1.S1_at	Tuftelin interacting protein 11	TFIP11	1.52	0.04
Bt.17952.1.A1_at	Cyclin-dependent kinase 8	CDK8	1.52	0.03
Bt.4357.1.S1_at	Tetraspanin 7	TSPAN7	1.51	0.05
Bt.4622.1.S1_at	Mannosidase, alpha, class 2B, member 1	MAN2B1	1.51	0.002
Bt.3546.1.S1_at	Receptor tyrosine kinase-like orphan receptor 2	ROR2	1.50	0.05
Bt.2610.1.S1_at	Molybdenum cofactor sulfurase	MOCOS	1.50	0.01
Bt.1537.1.S1_at	N-myc downstream regulated 1	NDRG1	1.50	0.04

Table S4 -Genes down-regulate in the CL of superovulated in relation to control animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene title	Gene Symbol	Fold Change	P -value
Bt.29824.1.S1_s_at	MHC class I heavy chain	BOLA	-13.29	3.6E-07
Bt.9172.1.A1_at	acidic repeat containing	ACRC	-1.90	0.02
Bt.16041.2.S1_at	actin binding LIM protein 1	ABLIM1	-1.97	0.01
Bt.4604.1.S1_a_at	acyl-CoA synthetase medium-chain family member 1	ACSM1	-1.65	0.02
Bt.8933.2.S1_at	adaptor-related protein complex 3, sigma 2 subunit	AP3S2	-1.56	0.004
Bt.19093.1.S1_at	Aldehyde dehydrogenase 1 family, member A2	ALDH1A2	-1.96	0.01
Bt.28278.1.S1_at	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	ACE2	-1.89	0.004
Bt.24853.1.A1_at	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	ASAP2	-1.55	0.01
Bt.10078.1.S1_at	asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase homolog (yeast)	ALG11	-1.60	0.01
Bt.24370.1.A1_at	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	ALG13	-1.82	0.002
Bt.11527.1.A1_at	BCL2-like 2	BCL2L2	-1.54	0.004
Bt.9020.1.S1_at	bladder cancer associated protein	BLCAP	-1.56	0.01
Bt.27440.1.A1_at	bromodomain adjacent to zinc finger domain, 2B	BAZ2B	-1.67	0.01
Bt.20860.3.A1_at	calcyphosine-like	CAPSL	-1.79	0.03
Bt.8508.1.A1_at	cAMP responsive element binding protein 3-like 2	CREB3L2	-1.77	0.01
Bt.13321.1.S1_at	centrosome and spindle pole associated protein 1	CSPP1	-1.88	0.01
Bt.17474.1.A1_at	chromosome 3 open reading frame 63 ortholog	C22H3ORF63	-1.78	0.003
Bt.17474.1.A1_at	chromosome 3 open reading frame 63 ortholog	C22H3ORF63	-1.90	0.01
Bt.8823.2.S1_at	chromosome 9 open reading frame 46 ortholog	C8H9ORF46	-2.27	0.01
Bt.16243.2.A1_at	CKLF-like MARVEL transmembrane domain containing 8	CMTM8	-1.65	0.04
Bt.27498.1.S1_at	coiled-coil domain containing 104	CCDC104	-1.67	0.05
Bt.3946.1.S1_at	coiled-coil domain containing 3	CCDC3	-2.07	0.02
Bt.29725.1.S1_at	collagen, type IV, alpha 4	COL4A4	-1.54	0.01
Bt.23722.1.A1_at	complement component 6	C6	-1.76	0.02
Bt.18557.1.S1_at	complement component 7	C7	-1.69	0.01
Bt.12510.3.S1_at	CREB regulated transcription coactivator 1	CRTC1	-1.52	0.03
Bt.3317.1.A1_at	cubilin (intrinsic factor-cobalamin receptor)	CUBN	-1.51	0.01
Bt.20799.3.A1_at	dedicator of cytokinesis 1	DOCK1	-1.65	0.001
Bt.26495.2.S1_at	DnaJ (Hsp40) homolog, subfamily C, member 19	DNAJC19	-1.57	0.01
Bt.14051.1.S1_at	dual specificity phosphatase 16	DUSP16	-2.01	0.01
Bt.20340.2.S1_at	dystrophia myotonica-protein kinase	DMPK	-1.75	0.0001
Bt.27286.1.S1_a_at	ecdysoneless homolog (Drosophila)	ECD	-1.63	0.02
Bt.3276.2.S1_at	enolase superfamily member 1	ENOSF1	-1.57	0.005
Bt.16212.1.A1_at	Enoyl Coenzyme A hydratase domain containing 3	ECHDC3	-2.54	0.01
Bt.22545.2.S1_at	fibulin 1	FBLN1	-1.53	0.01
Bt.20510.1.S1_at	FXFD domain containing ion transport regulator 1	FXFD1	-1.55	0.01
Bt.13763.1.S1_at	GLE1 RNA export mediator homolog (yeast)	GLE1	-1.56	0.02

Bt.12964.1.A1_at	Glycoprotein M6B	GPM6B	-1.83	0.02
Bt.20852.1.A1_at	GNAS complex locus	GNAS	-2.12	0.01
Bt.26769.1.S1_at	GTPase, IMAP family member 8	GIMAP8	-1.95	0.03
Bt.22058.1.A1_at	Hect domain and RLD 5	HERC5	-1.51	0.02
Bt.24694.1.A1_at	HEG homolog 1 (zebrafish)	HEG1	-1.97	0.01
Bt.18908.1.S1_at	Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	-1.78	0.003
Bt.21688.1.S1_at	hypothetical LOC100196901	LOC100196901 LOC783847 ///	-3.79	0.02
Bt.2578.1.A1_at	hypothetical LOC783847 /// transmembrane protein 150C	TMEM150C	-2.07	0.01
Bt.28461.2.S1_a_at	insulin receptor	INSR	-3.01	0.02
Bt.12186.1.S1_at	insulin-like 3 (Leydig cell)	INSL3	-4.33	0.04
Bt.13285.1.A1_at	La ribonucleoprotein domain family, member 1	LARP1	-1.60	0.04
Bt.16172.1.A1_at	Leucyl-tRNA synthetase 2, mitochondrial	LARS2	-1.96	0.001
Bt.23267.1.S1_at	lymphatic vessel endothelial hyaluronan receptor 1	LYVE1	-1.55	0.03
Bt.6527.1.S1_at	lymphoid enhancer-binding factor 1	LEF1	-1.56	0.01
Bt.4714.1.S1_at	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	MMP9	-1.59	0.001
Bt.13221.1.S1_at	MDN1, midasin homolog (yeast)	MDN1	-1.95	0.01
Bt.25291.1.A1_at	melanoma inhibitory activity family, member 3	MIA3	-1.68	0.01
Bt.1797.1.S1_at	metallophosphoesterase 1	MPPE1	-1.72	0.02
Bt.20102.1.S1_at	MPV17 mitochondrial membrane protein-like 2	MPV17L2	-1.60	0.02
Bt.13707.1.A1_at	myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	-1.51	0.01
Bt.20045.1.A1_at	neutral cholesterol ester hydrolase 1	NCEH1	-1.79	0.002
Bt.20045.1.A1_at	neutral cholesterol ester hydrolase 1	NCEH1	-2.00	0.002
Bt.8479.1.A1_at	nitric oxide synthase 2, inducible	NOS2	-1.53	0.03
Bt.25965.2.S1_at	nuclear receptor co-repressor 1	NCOR1	-1.56	0.01
Bt.24396.3.A1_at	nudix (nucleoside diphosphate linked moiety X)-type motif 10	NUDT10	-1.62	0.002
Bt.17386.1.A1_at	PAN3 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	PAN3	-1.63	0.002
Bt.20518.1.A1_at	paraneoplastic antigen MA2	PNMA2	-1.51	0.03
Bt.16133.2.S1_at	phosphatidylinositol glycan anchor biosynthesis, class H	PIGH	-1.58	0.02
Bt.8518.2.A1_at	Phosphodiesterase 8B	PDE8B	-1.59	0.01
Bt.20038.1.S1_at	pleckstrin homology domain containing, family B (evectins) member 1	PLEKHB1	-1.78	0.01
Bt.1898.1.S1_at	PQ loop repeat containing 2	PQLC2	-1.54	0.02
Bt.18218.1.A1_at	Protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	PPP3CC	-1.67	0.02
Bt.9710.1.S1_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	-1.53	0.01
Bt.16784.1.S1_at	pygopus homolog 1 (Drosophila)	PYGO1	-1.63	0.01
Bt.21039.1.A1_at	RAS, dexamethasone-induced 1	RASD1	-1.93	0.02
Bt.23678.1.A1_at	RCD1 required for cell differentiation1 homolog (S. pombe)	RQCD1	-1.55	0.003
Bt.17026.1.S1_at	Rho GTPase activating protein 17	ARHGAP17	-1.55	0.01
Bt.24442.1.A1_at	Rho guanine nucleotide exchange factor (GEF) 11	ARHGEF11	-1.72	0.02
Bt.24490.2.S1_at	ribonuclease P/MRP 38kDa subunit	RPP38	-1.54	0.005
Bt.13898.2.S1_at	ribosomal protein S27-like	RPS27L	-2.28	0.004
Bt.22359.2.A1_at	RIO kinase 3 (yeast)	RIOK3	-1.51	0.01

Bt.9546.1.S1_at	RNA binding motif protein, X-linked 2-like	LOC613705	-1.90	0.001
Bt.23235.1.S1_at	RNA pseudouridylate synthase domain containing 3	RPUSD3	-1.52	0.003
Bt.4177.3.A1_at	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ROBO2	-1.67	0.02
Bt.4177.3.A1_at	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ROBO2	-1.53	0.02
Bt.29009.1.A1_at	ryanodine receptor 3	RYR3	-1.59	0.03
Bt.24983.1.A1_at	similar to dynein, cytoplasmic 2, heavy chain 1	LOC512287	-1.63	0.01
Bt.16148.2.A1_a_at	similar to hCG2036584	LOC532848	-1.85	0.0004
Bt.9179.2.S1_at	similar to mCG142721	RNF213	-1.93	0.004
Bt.22433.1.A1_at	solute carrier family 22 (organic cation/carnitine transporter), member 5	SLC22A5	-1.69	0.01
Bt.15717.2.S1_at	sorting nexin 7	SNX7	-1.54	0.02
Bt.10565.1.A1_at	spectrin repeat containing, nuclear envelope 1	SYNE1	-1.70	0.01
Bt.13549.2.S1_at	splicing factor, arginine/serine-rich 18	SFRS18	-1.73	0.001
Bt.13249.1.A1_at	stearoyl-CoA desaturase 5	SCD5	-1.52	0.05
Bt.18086.1.S1_at	TBC1 domain family, member 7	TBC1D7	-1.80	0.02
Bt.10144.1.A1_s_at	T-cell lymphoma invasion and metastasis 1	TIAM1	-1.55	0.01
Bt.11240.1.A1_at	tet oncogene family member 2	TET2	-1.94	0.005
Bt.25051.1.A1_at	tetratricopeptide repeat domain 14	TTC14	-1.72	0.00002
Bt.22035.2.S1_at	thioredoxin domain containing 15	TXNDC15	-1.52	0.02
Bt.27903.1.A1_at	THO complex 2	THOC2	-1.63	0.01
Bt.4053.1.S1_at	thromboxane A2 receptor	TBXA2R	-1.86	0.01
Bt.4053.1.S1_at	thromboxane A2 receptor	TBXA2R	-1.96	0.01
Bt.29472.1.A1_at	TIA1 cytotoxic granule-associated RNA binding protein	TIA1	-1.61	0.04
Bt.6803.1.A1_at	TRAF2 and NCK interacting kinase	TNIK	-1.70	0.001
Bt.5336.1.A1_a_at	transferrin	TF	-1.71	0.04
Bt.26669.1.S1_at	transmembrane and coiled-coil domains 7	TMCO7	-1.55	0.02
Bt.11438.1.S1_at	troponin I type 3 (cardiac)	TNNI3	-2.08	0.05
Bt.3741.1.S1_at	tuberous sclerosis 1	TSC1	-1.66	0.004
Bt.754.1.S1_at	tubulin tyrosine ligase-like family, member 3	TTL3	-1.57	0.003
Bt.6851.1.S1_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	B4GALT5	-1.64	0.01
Bt.20434.1.A1_at	UFM1-specific peptidase 2	UFSP2	-1.50	0.002
Bt.4138.2.S1_at	vascular endothelial growth factor A	VEGFA	-1.52	0.01
Bt.24284.1.A1_at	Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	-2.29	0.01
Bt.11847.1.A1_at	X (inactive)-specific transcript	XIST	-1.69	0.05
Bt.24975.2.S1_at	YTH domain containing 2	YTHDC2	-1.69	0.02
Bt.26259.3.A1_at	zinc finger protein 462	ZNF462	-1.54	0.003
Bt.3235.1.A1_at	Zinc finger, MYND-type containing 8	ZMYND8	-1.55	0.03
Bt.7208.1.S1_at	zona pellucida glycoprotein 2 (sperm receptor)	ZP2	-1.53	0.05

Table S5. Genes up-regulated in the CL of stimulated in relation to superovulated animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene title	Gene Symbol	Fold Change	P value
Bt.3805.1.S1_at	MHC class I antigen /// MHC Class I JSP.1	BOLA-N	17.04	0.01
Bt.4404.1.A1_at	protease, serine, 2 (trypsin 2)	PRSS2	15.87	0.000001
Bt.4751.1.S1_a_at	major histocompatibility complex, class II, DQ alpha 2	BOLA-DQA2	7.86	0.05
Bt.22867.2.A1_at	histocompatibility complex, class II, DQ alpha, type 1	BOLA-DQA1	6.72	0.00002
Bt.16201.1.S1_at	S100 calcium binding protein A9	S100A9	5.83	0.0001
Bt.23042.1.S1_at	metallothionein 1E	MT1A	4.22	0.005
Bt.27140.1.S1_at	similar to mKIAA1077 protein	LOC535166	3.73	0.002
Bt.17697.1.A1_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase)	SERPINA11	3.62	0.04
Bt.8967.1.S1_at	myostatin	MSTN	3.35	0.001
Bt.9360.1.S1_at	S100 calcium binding protein A8	S100A8	3.28	0.001
Bt.2560.1.S1_at	microfibrillar associated protein 5	MFAP5	3.26	0.05
Bt.1645.1.S1_at	prostaglandin D2 synthase 21kDa (brain)	PTGDS	3.06	0.01
Bt.14200.1.A1_at	metallothionein 1E	MT1E	3.06	0.004
Bt.28934.1.S1_at	amphiregulin	AREG	2.95	0.03
Bt.12297.1.S1_at	lysyl oxidase-like 4	LOXL4	2.77	0.02
Bt.24354.1.S1_at	cystatin B (stefin B)	CSTB	2.73	0.02
Bt.14949.1.A1_at	similar to Alpha-2-macroglobulin precursor (Pregnancy zone)	LOC506828	2.67	0.03
Bt.367.1.S1_at	oxidized low density lipoprotein (lectin-like) receptor 1	OLR1	2.58	0.01
Bt.12295.1.S1_at	podoplanin	PDPN	2.58	0.002
Bt.22526.1.S1_at	heat shock 22kDa protein 8	HSPB8	2.47	0.03
Bt.357.1.S1_at	S100 calcium binding protein A12 (calgranulin C)	S100A12	2.31	0.04
Bt.22854.1.S1_at	carbonic anhydrase II	CA2	2.29	0.003
Bt.2529.1.S1_at	metallothionein 2A	MT2A	2.28	0.01
Bt.4063.1.S1_at	phospholipase A2, group VII (platelet-activating factor a	PLA2G7	2.26	0.002
Bt.27973.1.S1_at	solute carrier organic anion transporter family, member 3A1	SLCO3A1	2.23	0.03
Bt.25744.1.A1_at	solute carrier family 38, member 11	SLC38A11	2.19	0.05
Bt.11420.1.A1_at	prolyl 4-hydroxylase, alpha polypeptide III	P4HA3	2.17	0.001
Bt.23399.1.S1_at	pyruvate kinase, muscle	PKM2	2.15	0.005
Bt.9779.1.S1_at	similar to TLH29 protein precursor	ISG12(B)	2.11	0.02
Bt.568.1.S1_at	integrin-binding sialoprotein	IBSP	2.10	0.02
Bt.19585.2.S1_at	general transcription factor IIH, polypeptide 1, 62kDa	GTF2H1	2.08	0.01
Bt.9949.2.S1_at	PDZ and LIM domain 7 (enigma)	PDLIM7	2.04	0.01
Bt.23205.1.S1_s_at	similar to Synaptotagmin-1 (Synaptotagmin I) (SytI) (p65)	LOC787239	2.04	0.05
Bt.3226.1.S1_at	heme oxygenase (decycling) 2	HMOX2	2.03	0.002
Bt.20512.2.S1_at	collagen, type XV, alpha 1	COL15A1	1.97	0.004
Bt.5935.2.S1_a_at	lysosomal protein transmembrane 4 alpha	LAPTM4A	1.95	0.02
Bt.22586.1.A1_at	Inositol monophosphatase domain containing 1	IMPAD1	1.94	0.0001
Bt.20096.2.S1_a_at	FXVD domain containing ion transport regulator 5	FXVD5	1.93	0.04

Bt.16029.1.S2_at	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	FUT1	1.93	0.04
Bt.24842.1.A1_at	RAS-like, estrogen-regulated, growth inhibitor	RERG	1.92	0.01
Bt.2159.1.S1_at	transmembrane protein 45A	TMEM45A	1.91	0.01
Bt.17473.2.S1_at	ribulose-5-phosphate-3-epimerase	RPE	1.91	0.04
Bt.3307.1.A1_at	Norrie disease (pseudoglioma)	NDP	1.90	0.01
Bt.9735.2.A1_at	apolipoprotein M	APOM	1.89	0.0001
Bt.27549.1.A1_at	tudor domain containing 6	TDRD6	1.89	0.04
Bt.6510.1.S1_at	inositol 1,3,4-triphosphate 5/6 kinase	ITPK1	1.88	0.04
Bt.9527.2.S1_at	Kruppel-like factor 10	KLF10	1.87	0.003
Bt.12712.1.A1_at	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	ETS1	1.86	0.03
Bt.4357.1.S1_at	tetraspanin 7	TSPAN7	1.85	0.002
Bt.5515.1.S1_at	5'-nucleotidase, ecto (CD73)	NT5E	1.85	0.05
Bt.8624.1.S1_at	arginase, type II	ARG2	1.85	0.0002
Bt.3809.1.S1_at	lactate dehydrogenase A	LDHA	1.85	0.02
Bt.8492.1.A1_at	junctional adhesion molecule 3	JAM3	1.84	0.03
Bt.22279.1.S1_at	reprimin, TP53 dependent G2 arrest mediator candidate	RPRM	1.84	0.05
Bt.15616.1.S1_at	solute carrier family 16, member 3 (monocarboxylic acid)	SLC16A3	1.84	0.02
Bt.9777.1.S1_at	3-hydroxybutyrate dehydrogenase, type 1	BDH1	1.84	0.05
Bt.10980.1.S1_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ABCC9	1.82	0.005
Bt.18228.1.A1_at	Sec61 alpha 2 subunit (S. cerevisiae)	SEC61A2	1.82	0.001
Bt.28687.1.A1_at	similar to ZMYM6 protein	LOC618247	1.81	0.04
Bt.6047.1.S1_at	cysteine and glycine-rich protein 1	CSRP1	1.80	0.002
Bt.5061.1.S1_at	phosphofructokinase, liver	PFKL	1.80	0.002
Bt.16832.1.A1_at	dihydrodipicolinate synthase-like, mitochondrial	DHDPSL	1.79	0.002
Bt.685.1.A1_at	Asparaginase like 1	ASRGL1	1.79	0.02
Bt.27087.1.A1_at	transmembrane protein 156	TMEM156	1.79	0.04
Bt.22740.1.A1_at	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta	C1GALT1	1.76	0.02
Bt.13036.1.S1_at	progesterone receptor	PGR	1.76	0.05
Bt.22054.2.S1_a_at	chromosome 20 open reading frame 7 ortholog	C13H20ORF7	1.76	0.004
Bt.23619.1.S1_a_at	RAB GTPase activating protein 1-like	RABGAP1L	1.75	0.0005
Bt.15528.1.S1_at	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	1.75	0.03
Bt.9714.1.S1_at	actin, gamma 2, smooth muscle, enteric	ACTG2	1.75	0.04
Bt.3551.1.S1_at	solute carrier family 17, member 9	SLC17A9	1.75	0.03
Bt.3885.5.S1_x_at	chloride channel accessory 3 (pseudogene)	CLCA3P	1.75	0.01
Bt.26578.1.S1_at	solute carrier family 13	SLC13A3	1.75	0.02
Bt.15808.1.S1_at	membrane-associated ring finger (C3HC4) 3	MARCH3	1.74	0.01
Bt.5523.1.S1_at	Golgi membrane protein 1	GOLM1	1.74	0.004
Bt.25087.3.S1_at	ras homolog gene family, member Q	RHOQ	1.74	0.01
Bt.23373.1.S1_at	nuclear receptor subfamily 4, group A, member 1	NR4A1	1.73	0.01
Bt.24335.1.S1_at	dual adaptor of phosphotyrosine and 3-phosphoinositides	DAPP1	1.73	0.0003
Bt.12477.2.S1_at	tropomyosin 2 (beta)	TPM2	1.73	0.04
Bt.22400.1.A1_at	slit homolog 3 (Drosophila)	SLIT3	1.72	0.05

Bt.5268.1.S1_at	follistatin-like 3 (secreted glycoprotein)	FSTL3	1.71	0.001
Bt.6685.2.A1_at	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2,	MTHFD2	1.70	0.01
Bt.6603.1.A1_at	RAB32, member RAS oncogene family	RAB32	1.70	0.01
Bt.21470.2.S1_a_at	fatty acid desaturase 3	FADS3	1.70	0.02
Bt.20217.1.S1_at	nicalin homolog (zebrafish)	NCLN	1.70	0.001
Bt.21131.1.A1_at	similar to transmembrane protein 166	LOC528994	1.70	0.002
Bt.19507.1.A1_at	complement component 8, beta polypeptide	C8B	1.69	0.0002
Bt.9821.1.S1_at	Aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl	AASDHPPT	1.69	0.005
Bt.3170.2.S1_at	mitochondrial intermediate peptidase	MIPEP	1.69	0.01
Bt.9999.2.A1_at	transcription factor B1, mitochondrial	TFB1M	1.69	0.04
Bt.1024.2.S1_at	chromosome 8 open reading frame 41 ortholog	C27H8ORF41	1.69	0.004
Bt.19482.1.A1_at	transferrin receptor (p90, CD71)	TFRC	1.68	0.003
Bt.13743.1.A1_at	riboflavin kinase	RFK	1.68	0.02
Bt.22045.1.S1_at	six transmembrane epithelial antigen of the prostate 2	STEAP2	1.68	0.03
Bt.17990.1.A1_at	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	1.68	0.02
Bt.22488.1.A1_at	solute carrier family 30 (zinc transporter), member 6	SLC30A6	1.67	0.004
Bt.21079.1.A1_at	similar to solute carrier family 35, member F2	LOC782215	1.66	0.04
Bt.24206.1.A1_at	BTB (POZ) domain containing 1	BTBD1	1.65	0.04
Bt.16130.1.S1_at	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	APPBP2	1.64	0.0001
Bt.19643.2.S1_at	potassium large conductance calcium-activated channel, member 4	KCNMB4	1.64	0.04
Bt.20793.1.A1_s_at	laminin, gamma 1 (formerly LAMB2)	LAMC1	1.64	0.005
Bt.12551.1.S1_at	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	TSR1	1.64	0.01
Bt.19564.1.A1_at	CREB regulated transcription coactivator 3	CRTC3	1.63	0.02
Bt.3988.1.S1_at	translocator protein (18kDa)	TSPO	1.63	0.01
Bt.4198.1.S1_at	deoxythymidylate kinase (thymidylate kinase)	DTYMK	1.62	0.03
Bt.10387.1.S1_at	ATP-binding cassette, sub-family F (GCN20), member 1	ABCF1	1.62	0.01
Bt.21546.1.S1_at	similar to ATPase, Class II, type 9A	LOC516579	1.61	0.05
Bt.1804.1.S1_at	GINS complex subunit 4 (Sld5 homolog)	GINS4	1.61	0.01
Bt.18484.1.A1_at	5'-nucleotidase domain containing 1	NT5DC1	1.61	0.03
Bt.10144.1.A1_s_at	T-cell lymphoma invasion and metastasis 1	TIAM1	1.61	0.01
Bt.27866.1.A1_at	myo-inositol oxygenase	MIOX	1.61	0.02
Bt.14520.1.A1_at	CD109 molecule	CD109	1.60	0.05
Bt.3980.1.S1_at	scinderin	SCIN	1.60	0.02
Bt.29823.1.S1_at	MHC class I heavy chain	BOLA	1.60	0.003
Bt.3196.1.S1_at	stimulated by retinoic acid gene 6 homolog (mouse)	STRA6	1.60	0.01
Bt.26100.1.S1_at	glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	1.59	0.01
Bt.20637.1.S1_at	Signal sequence receptor, gamma (translocon-associated protein	SSR3	1.58	0.01
Bt.8318.1.S1_at	CD276 molecule	CD276	1.58	0.03
Bt.4224.1.S1_at	adenylate kinase 1	AK1	1.58	0.05
Bt.23026.1.A1_at	Tropomyosin 1 (alpha)	TPM1	1.58	0.03
Bt.3794.1.S1_at	phosphofructokinase, platelet	PFKP	1.58	0.02
Bt.18533.1.S1_at	activating transcription factor 3	ATF3	1.58	0.002

Bt.6964.1.S1_at	tropomodulin 1	TMOD1	1.58	0.03
Bt.22362.1.S1_at	SH3-domain kinase binding protein 1	SH3KBP1	1.57	0.04
Bt.23551.3.S1_at	N(alpha)-acetyltransferase 50, NatE catalytic subunit	NAA50	1.57	0.03
Bt.12645.1.S1_at	RAB15, member RAS oncogene family	RAB15	1.57	0.01
Bt.12614.1.A1_s_at	eukaryotic translation initiation factor 3, subunit B	EIF3B	1.57	0.001
Bt.22586.1.A1_at	Inositol monophosphatase domain containing 1	IMPAD1	1.57	0.0002
Bt.4245.1.S1_at	rhomboid domain containing 2	RHBDD2	1.57	0.004
Bt.21115.2.S1_at	Sec23 homolog A (<i>S. cerevisiae</i>)	SEC23A	1.57	0.02
Bt.5318.1.S1_at	retinol binding protein 4, plasma	RBP4	1.57	0.04
Bt.24841.1.S1_at	splA/ryanodine receptor domain and SOCS box containing 1	SPSB1	1.56	0.03
Bt.26652.1.S1_at	similar to anchor protein	CELSR3	1.56	0.0004
Bt.26730.1.S1_at	torsin A interacting protein 2	TOR1AIP2	1.56	0.02
Bt.17361.1.A1_at	chromosome 12 open reading frame 23 ortholog	C5H12orf23	1.55	0.003
Bt.11176.1.S1_at	transmembrane protein 14A	TMEM14A	1.55	0.003
Bt.24517.2.A1_at	G protein-coupled receptor, family C, group 5, member B	GPRC5B	1.55	0.03
Bt.16730.1.A1_at	solute carrier family 41, member 2	SLC41A2	1.55	0.002
Bt.6657.1.S1_at	transmembrane protein 63B	TMEM63B	1.54	0.04
Bt.13027.1.A1_at	hydroxysteroid (11-beta) dehydrogenase 1	HSD11B1	1.54	0.05
Bt.20530.1.S1_at	NmrA-like family domain containing 1	NMRAL1	1.54	0.01
Bt.3109.1.A1_s_at	suppressor of Ty 4 homolog 1 (<i>S. cerevisiae</i>)	SUPT4H1	1.54	0.02
Bt.17824.1.S1_at	vacuolar protein sorting 36 homolog (<i>S. cerevisiae</i>)	VPS36	1.53	0.01
Bt.8706.1.S1_at	mitogen-activated protein kinase-activated protein kinase 3	MAPKAPK3	1.53	0.01
Bt.10084.1.S1_at	caspase 3, apoptosis-related cysteine peptidase	CASP3	1.53	0.01
Bt.11650.1.A1_at	eukaryotic translation elongation factor 1 alpha	EEF1A1	1.53	0.03
Bt.5829.1.S1_at	phosphatidic acid phosphatase type 2C	PPAP2C	1.52	0.02
Bt.26973.1.S1_at	tolloid-like 2	TLL2	1.52	0.04
Bt.18575.1.A1_at	DTW domain containing 2	DTWD2	1.52	0.01
Bt.11270.2.S1_at	valyl-tRNA synthetase	VAR5	1.52	0.003
Bt.23870.1.S1_at	2-deoxyribose-5-phosphate aldolase homolog (<i>C. elegans</i>)	DERA	1.52	0.04
Bt.4952.2.S1_a_at	ribosomal protein L22-like 1	RPL22L1	1.52	0.01
Bt.8496.1.S1_at	adhesion molecule with Ig-like domain 3	AMIGO3	1.51	0.04
Bt.2568.1.S1_at	perilipin 2	PLIN2	1.51	0.01
Bt.28500.1.S1_at	TBC1 domain family, member 14	TBC1D14	1.51	0.002
Bt.7178.1.S1_at	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	1.50	0.002

Table S6. Genes down-regulated in the CL of stimulated in relation to superovulated animals (1.5 fold, $P \leq 0.05$).

UniGene ID	Gene title	Gene Symbol	Fold Change	P value
Bt.29824.1.S1_s_at	MHC class I heavy chain	BOLA	-7.69	0.04
Bt.4604.1.S1_a_at	acyl-CoA synthetase medium-chain family member 1	ACSM1	-4.84	0.00001
Bt.20891.1.S1_at	2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	-4.53	0.03
Bt.12186.1.S1_at	insulin-like 3 (Leydig cell)	INSL3	-4.17	0.04
Bt.11438.1.S1_at	troponin I type 3 (cardiac)	TNNI3	-3.39	0.01
Bt.28461.2.S1_a_at	insulin receptor	INSR	-3.18	0.02
Bt.21688.1.S1_at	hypothetical LOC100196901	LOC100196901	-3.12	0.03
Bt.499.1.S1_a_at	prolactin receptor	PRLR	-2.88	0.0031
Bt.9659.1.S1_a_at	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	-2.82	0.01
Bt.20455.1.S1_at	Microtubule-associated protein tau	MAPT	-2.75	0.03
Bt.17232.1.A1_at	arginine vasopressin receptor 1A	AVPR1A	-2.68	0.0011
Bt.17729.1.A1_at	interferon-induced protein 44	IFI44	-2.68	0.04
Bt.14035.1.S1_at	protein kinase C, beta	PRKCB	-2.67	0.04
Bt.24284.1.A1_at	Wolf-Hirschhorn syndrome candidate 1-like 1	WHSC1L1	-2.60	0.0050
Bt.139.1.A1_at	ADAM metallopeptidase domain 2	ADAM2	-2.53	0.04
Bt.27123.1.A1_at	MDS1 and EVI1 complex locus	MECOM	-2.53	0.02
Bt.2498.2.A1_a_at	fibrinogen gamma chain	FGG	-2.41	0.01
Bt.4107.1.S1_at	desmocollin 2	DSC2	-2.40	0.0011
Bt.15908.1.S1_at	methyltransferase like 7A	METTL7A	-2.36	0.02
Bt.21773.2.S1_at	guanylate binding protein 5	GBP5	-2.32	0.01
Bt.24694.1.A1_at	HEG homolog 1 (zebrafish)	HEG1	-2.29	0.0019
Bt.16212.1.A1_at	Enoyl Coenzyme A hydratase domain containing 3	ECHDC3	-2.27	0.01
Bt.8436.1.S1_at	interferon, alpha-inducible protein 6	IFI6	-2.25	0.01
Bt.21759.2.A1_at	Butyrobetaine (gamma), 2-oxoglutarate dioxygenase	BBOX1	-2.23	0.0003
Bt.28383.1.S1_at	granulysin	GNLY	-2.21	0.03
Bt.12964.1.A1_at	Glycoprotein M6B	GPM6B	-2.21	0.0013
Bt.1458.1.S1_at	phosphoglucomutase 5	PGM5	-2.21	0.01
Bt.3187.1.A1_s_at	solute carrier family 5 (sodium/glucose cotransporter), member 11	SLC5A11	-2.20	0.02
Bt.25738.1.A1_at	endoplasmic reticulum protein 27	ERP27	-2.18	0.03
Bt.24467.1.S1_at	radical S-adenosyl methionine domain containing 2	RSAD2	-2.17	0.0016
Bt.28744.1.S1_at	guanylate binding protein 4	GBP4	-2.11	0.02
Bt.12634.1.A1_at	hypothetical LOC616371	LOC616371	-2.11	0.03
Bt.13221.1.S1_at	MDN1, midasin homolog (yeast)	MDN1	-2.11	0.02
Bt.9504.1.A1_at	chemokine (C-C motif) ligand 4	CCL4	-2.08	0.03
Bt.13898.2.S1_at	ribosomal protein S27-like	RPS27L	-2.08	0.01

Bt.21126.2.S1_at	synuclein, beta	SNCB	-2.06	0.01
Bt.3560.1.S1_at	WAS/WASL interacting protein family, member 3	WIPF3	-2.03	0.01
Bt.344.1.S1_at	major histocompatibility complex, class II, DM alpha-chain,	BOLA-DMA	-2.02	0.01
Bt.11259.1.S1_at	putative ISG12(a) protein	ISG12(A)	-2.01	0.0029
Bt.11847.1.A1_at	X (inactive)-specific transcript	XIST	-2.01	0.01
Bt.29725.1.S1_at	collagen, type IV, alpha 4	COL4A4	-2.00	0.01
Bt.7204.1.S1_at	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	FCGR3	-2.00	0.0001
Bt.22118.3.S1_at	Usher syndrome 1C binding protein 1	USHBP1	-2.00	0.03
Bt.20164.1.S1_at	complement component 1, q subcomponent, B chain	C1QB	-1.99	0.0044
Bt.24069.1.A1_at	C-type lectin domain family 2, member D	CLEC2D	-1.98	0.01
Bt.20409.1.S1_at	poly (ADP-ribose) polymerase family, member 9	PARP9	-1.98	0.01
Bt.8508.1.A1_at	cAMP responsive element binding protein 3-like 2	CREB3L2	-1.97	0.01
Bt.22430.1.A1_at	cytochrome b-245, beta polypeptide	CYBB	-1.97	0.03
Bt.920.1.S1_at	ring finger protein 181	RNF181	-1.97	0.0004
Bt.16068.1.A1_at	Glutamate-cysteine ligase, catalytic subunit	GCLC	-1.96	0.03
Bt.15912.1.S1_at	placenta-specific 8	PLAC8	-1.94	0.0017
Bt.20852.1.A1_at	GNAS complex locus	GNAS	-1.93	0.05
Bt.16041.1.S1_at	actin binding LIM protein 1	ABLIM1	-1.92	0.0035
Bt.13315.1.S1_at	acyl-CoA synthetase family member 2	ACSF2	-1.92	0.0008
Bt.14122.1.A1_at	Vav 3 guanine nucleotide exchange factor	VAV3	-1.92	0.01
Bt.24813.1.A1_at	receptor (chemosensory) transporter protein 4	RTP4	-1.91	0.0011
Bt.9185.1.A1_at	GRAM domain containing 1C	GRAMD1C	-1.90	0.02
Bt.17368.1.A1_at	purinergic receptor P2Y, G-protein coupled, 14	P2RY14	-1.90	0.03
Bt.13428.2.S1_at	fructose-1,6-bisphosphatase 1	FBP1	-1.89	0.04
Bt.17989.2.S1_at	proteasomal ATPase-associated factor 1	PAAF1	-1.89	0.02
Bt.1069.1.A1_at	protein tyrosine phosphatase, receptor type, R	PTPRR	-1.87	0.01
Bt.13127.1.S1_at	angiotensin II type 1 receptor	ANGPT1	-1.86	0.0027
Bt.26968.1.S1_at	plexin C1	PLXNC1	-1.86	0.02
Bt.9179.2.S1_at	similar to mCG142721	RNF213	-1.86	0.01
Bt.3235.1.A1_at	Zinc finger, MYND-type containing 8	ZMYND8	-1.86	0.04
Bt.2901.1.A1_at	zinc finger protein 192	ZNF192	-1.86	0.0026
Bt.7208.1.S1_at	zona pellucida glycoprotein 2 (sperm receptor)	ZP2	-1.86	0.04
Bt.15511.1.A1_at	fatty acid binding protein 3, muscle and heart (mammary-derived)	FABP3	-1.85	0.04
Bt.28008.1.S1_s_at	potassium intermediate/small conductance calcium-activated	KCNN2	-1.84	0.04
Bt.11057.1.S1_at	shisa homolog 3 (Xenopus laevis)	SHISA3	-1.84	0.0010
Bt.2426.2.S1_at	transmembrane protein 101	TMEM101	-1.83	0.02
Bt.16077.1.S1_at	receptor (G protein-coupled) activity modifying protein 3	RAMP3	-1.82	0.0039
Bt.1007.1.S1_at	major histocompatibility complex, class II, DM beta-chain	BOLA-DMB	-1.81	0.00004
Bt.21147.2.S1_a_at	hypothetical protein LOC507810	LOC507810	-1.81	0.02
Bt.1491.1.S1_at	complement component 1, s subcomponent	C1S	-1.80	0.03
Bt.26654.1.S1_at	forkhead-associated (FHA) phosphopeptide binding domain 1	FHAD1	-1.80	0.01
Bt.21576.1.S1_at	complement component 1, q subcomponent, C chain	C1QC	-1.79	0.01

Bt.11769.2.S1_at	EP300 interacting inhibitor of differentiation 3	EID3	-1.79	0.04
Bt.8905.1.S1_at	itchy E3 ubiquitin protein ligase homolog (mouse)	ITCH	-1.79	0.00003
Bt.11482.1.S1_at	NFKB inhibitor interacting Ras-like 1	NKIRAS1	-1.79	0.0008
Bt.11240.1.A1_at	tet oncogene family member 2	TET2	-1.79	0.04
Bt.17172.1.S1_at	gap junction protein, alpha 5, 40kDa	GJA5	-1.78	0.02
Bt.25039.1.S1_at	hypothetical protein LOC100302527	LOC100302527	-1.78	0.01
Bt.24012.1.A1_at	similar to guanylate binding protein 1	LOC511531	-1.78	0.03
Bt.25965.2.S1_at	nuclear receptor co-repressor 1	NCOR1	-1.78	0.01
Bt.28537.1.S1_at	ankyrin repeat and sterile alpha motif domain containing 4B	ANKS4B	-1.77	0.04
Bt.9974.1.S1_at	chemokine (C-C motif) ligand 3	CCL3	-1.77	0.02
Bt.1787.2.S1_at	transmembrane protein 100	TMEM100	-1.77	0.04
Bt.24370.1.A1_at	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	ALG13	-1.76	0.0014
Bt.350.1.S1_s_at	MHC class II antigen	BLA-DQB	-1.76	0.0013
Bt.6434.1.S1_at	ring finger protein 149	RNF149	-1.76	0.01
Bt.16036.1.S1_at	SH3 domain binding glutamic acid-rich protein like 2	SH3BGRL2	-1.76	0.02
Bt.14040.1.S1_at	prostaglandin reductase 2	PTGR2	-1.75	0.0004
Bt.514.1.S1_at	DnaJ (Hsp40) homolog, subfamily C, member 6	DNAJC6	-1.74	0.02
Bt.8518.2.A1_at	Phosphodiesterase 8B	PDE8B	-1.74	0.01
Bt.27023.1.S1_at	Amylase, alpha 2A (pancreatic)	AMY2A	-1.73	0.05
Bt.5657.1.A1_at	E2F transcription factor 5, p130-binding /// similar to E2F	E2F5 ///	-1.73	0.0040
Bt.27440.1.A1_at	bromodomain adjacent to zinc finger domain, 2B	BAZ2B	-1.72	0.02
Bt.5333.3.S1_a_at	cysteine-rich with EGF-like domains 1	CRELD1	-1.72	0.04
Bt.26629.1.S1_a_at	F-box and WD repeat domain containing 7	FBXW7	-1.72	0.04
Bt.3115.1.A1_at	aspartylglucosaminidase	AGA	-1.71	0.04
Bt.20860.3.A1_at	calcyphosine-like	CAPSL	-1.71	0.01
Bt.23662.2.S1_at	ring finger protein 34	RNF34	-1.71	0.01
Bt.9288.1.S1_at	Actin filament associated protein 1-like 1	AFAP1L1	-1.70	0.01
Bt.5392.1.S1_at	CD36 molecule (thrombospondin receptor)	CD36	-1.70	0.01
Bt.13113.1.S1_at	L-gulon-gamma-lactone oxidase	GULO	-1.70	0.02
Bt.15867.2.S1_at	small EDRK-rich factor 2	SERF2	-1.70	0.02
Bt.20613.1.A1_at	Breast cancer anti-estrogen resistance 3	BCAR3	-1.69	0.01
Bt.27889.1.S1_at	Dihydrolipoamide dehydrogenase	DLD	-1.69	0.05
Bt.17898.1.A1_at	microtubule-associated protein 9	MAP9	-1.69	0.0027
Bt.20340.2.S1_at	dystrophia myotonica-protein kinase	DMPK	-1.68	0.0021
Bt.6389.1.A1_at	similar to 1A6/DRIM (down-regulated in metastasis)	LOC618652	-1.68	0.01
Bt.9710.1.S1_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	-1.68	0.02
Bt.5336.1.A1_a_at	transferrin	TF	-1.68	0.00004
Bt.20095.1.A1_at	Zinc finger protein 142	ZNF142	-1.68	0.04
Bt.146.1.S1_at	defensin, beta 4A	DEFB4A	-1.67	0.01
Bt.13766.2.S1_at	dipeptidyl-peptidase 8	DPP8	-1.67	0.03
Bt.3215.1.S1_at	ephrin-A1	EFNA1	-1.66	0.01
Bt.24537.1.A1_at	Zinc finger, RAN-binding domain containing 2	ZRANB2	-1.66	0.04

Bt.23722.1.A1_at	complement component 6	C6	-1.65	0.01
Bt.13390.2.S1_a_at	2,4-dienoyl CoA reductase 1, mitochondrial	DECR1	-1.65	0.001
Bt.6110.1.S1_at	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	P4HTM	-1.65	0.05
Bt.20790.1.S1_at	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	-1.65	0.01
Bt.12503.1.A1_at	carbonic anhydrase XIII	CA13	-1.64	0.0022
Bt.28562.1.S1_at	syntabulin (syntaxin-interacting)	SYBU	-1.64	0.01
Bt.1602.1.S1_at	zinc finger protein 613	ZNF613	-1.64	0.05
Bt.17474.1.A1_at	chromosome 3 open reading frame 63 ortholog	C22H3ORF63	-1.63	0.02
Bt.14005.1.S1_at	CD53 molecule	CD53	-1.63	0.01
Bt.4360.1.S1_at	cytochrome b-561	CYB561	-1.63	0.01
Bt.26513.1.S1_at	esophageal cancer related gene 4 protein	ECRG4	-1.63	0.05
Bt.28428.1.S1_at	similar to ATPase family AAA domain-containing protein 2B	LOC518785	-1.63	0.01
Bt.19038.1.A1_at	similar to K06A9.1b	LOC616937	-1.63	0.02
Bt.7131.2.S1_at	pallidin homolog (mouse)	PLDN	-1.63	0.03
Bt.28865.1.A1_at	ribosomal protein S8	RPS8	-1.63	0.01
Bt.21154.2.S1_at	serine/threonine kinase 4	STK4	-1.63	0.0033
Bt.20284.1.S1_at	torsin family 3, member A	TOR3A	-1.63	0.0033
Bt.6404.1.S1_at	Kruppel-like factor 15	KLF15	-1.62	0.01
Bt.25111.1.A1_at	Similar to interferon-induced protein 44-like	LOC508347	-1.62	0.01
Bt.488.1.S2_at	phospholipase A2 receptor 1, 180kDa	PLA2R1	-1.62	0.03
Bt.26143.1.A1_at	REST corepressor 3	RCOR3	-1.62	0.0025
Bt.11739.1.S1_a_at	signal transducing adaptor family member 2	STAP2	-1.62	0.0039
Bt.28390.1.S1_at	TSC22 domain family, member 3	TSC22D3	-1.62	0.0047
Bt.20848.1.A1_at	tetratricopeptide repeat domain 36	TTC36	-1.62	0.02
Bt.4049.1.S1_at	armadillo repeat containing, X-linked 6	ARMCX6	-1.61	0.0048
Bt.24651.1.A1_at	Protein FAM149B1	FAM149B1	-1.61	0.04
Bt.21838.2.S1_at	leukocyte receptor cluster (LRC) member 1	LENG1	-1.61	0.03
Bt.13618.1.A1_at	similar to Putative steroid dehydrogenase KIK-1	LOC508455	-1.61	0.01
Bt.15615.1.S1_at	NLR family, CARD domain containing 5	NLRC5	-1.61	0.02
Bt.7393.1.S1_at	Nephronectin	NPNT	-1.61	0.03
Bt.17659.1.S1_at	phosphatidylserine synthase 1	PTDSS1	-1.61	0.02
Bt.15882.3.S1_at	sorcin	SRI	-1.61	0.01
Bt.20883.1.S1_at	angiogenin, ribonuclease, RNase A family, 5	ANG	-1.60	0.01
Bt.24853.1.A1_at	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	ASAP2	-1.60	0.0035
Bt.27434.1.A1_at	Biphenyl hydrolase-like (serine hydrolase)	BPHL	-1.60	0.05
Bt.4321.1.S1_at	cytokine inducible SH2-containing protein	CISH	-1.60	0.04
Bt.10077.1.S3_at	interferon regulatory factor 1	IRF1	-1.60	0.0017
Bt.16148.1.A1_at	similar to hCG2036584	LOC532848	-1.60	0.02
Bt.1742.2.S1_a_at	Similar to LOC496253 protein	LOC784007	-1.60	0.0012
Bt.14676.1.S1_at	poly (ADP-ribose) polymerase family, member 14	PARP14	-1.60	0.04
Bt.28278.1.S1_at	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	ACE2	-1.59	0.0039
Bt.18908.1.S1_at	Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	-1.59	0.01

Bt.20054.1.S1_at	interferon regulatory factor 9	IRF9	-1.59	0.0013
Bt.16172.1.A1_at	Leucyl-tRNA synthetase 2, mitochondrial	LARS2	-1.59	0.0040
Bt.22465.1.S1_at	similar to EF-hand calcium-binding domain-containing protein 4A	LOC615055	-1.59	0.01
Bt.1580.1.S1_at	secretogranin V (7B2 protein)	SCG5	-1.59	0.0036
Bt.29472.1.A1_at	TIA1 cytotoxic granule-associated RNA binding protein	TIA1	-1.59	0.03
Bt.7251.1.S1_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide2	B3GALT2	-1.58	0.02
Bt.13777.2.S1_at	GTPase, IMAP family member 7	GIMAP7	-1.58	0.04
Bt.22058.1.A1_at	Hect domain and RLD 5	HERC5	-1.58	0.01
Bt.18316.1.A1_at	Similar to UPF0474 protein C5orf41	LOC513587	-1.58	0.03
Bt.14061.1.A1_at	hypothetical LOC534389	MGC143209	-1.58	0.05
Bt.5232.2.S1_a_at	NECAP endocytosis associated 2	NECAP2	-1.58	0.02
Bt.27901.1.S1_at	CNKSR family member 3	CNKSR3	-1.57	0.01
Bt.23354.1.S1_at	epoxide hydrolase 1, microsomal (xenobiotic)	EPHX1	-1.57	0.05
Bt.10330.1.S1_at	HMG-box transcription factor 1	HBP1	-1.57	0.0042
Bt.24277.1.S1_at	Membrane-associated ring finger (C3HC4) 6	MARCH6	-1.57	0.01
Bt.13707.1.A1_at	myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	-1.57	0.02
Bt.16326.1.S1_at	transmembrane protein 140	TMEM140	-1.57	0.0029
Bt.26813.1.S1_at	cache domain containing 1	CACHD1	-1.56	0.03
Bt.10543.1.S1_at	Hypothetical protein LOC784675	KIAA1462	-1.56	0.0035
Bt.25992.1.A1_at	membrane protein, palmitoylated 5 (MAGUK p55 member 5)	MPP5	-1.56	0.02
Bt.12211.1.S1_at	peroxisomal D3,D2-enoyl-CoA isomerase	PECI	-1.56	0.01
Bt.26887.1.S1_at	synaptotagmin-like 3	SYTL3	-1.56	0.01
Bt.10044.3.A1_a_at	WD repeat domain 67	WDR67	-1.56	0.02
Bt.20762.2.S1_at	Chronic lymphocytic leukemia deletion region gene 6 protein	CLLD6	-1.55	0.0006
Bt.8795.1.S1_at	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	DYSF	-1.55	0.01
Bt.29874.1.S1_at	eukaryotic translation initiation factor 2C, 3	EIF2C3	-1.55	0.04
Bt.26962.1.S1_at	glycosylphosphatidylinositol anchored high density lipoprotein	GPIHBP1	-1.55	0.05
Bt.24983.1.A1_at	similar to dynein, cytoplasmic 2, heavy chain 1	LOC512287	-1.55	0.02
Bt.17386.1.A1_at	PAN3 poly(A) specific ribonuclease subunit	PAN3	-1.55	0.05
Bt.28577.2.S1_at	SUMO1/sentrin specific peptidase 6	SEN6	-1.55	0.01
Bt.18672.1.A1_at	tRNA methyltransferase 12 homolog (S. cerevisiae)	TRMT12	-1.55	0.0028
Bt.372.1.S1_at	A kinase (PRKA) anchor protein 5	AKAP5	-1.54	0.01
Bt.4351.2.S1_at	brain and reproductive organ-expressed (TNFRSF1A modulator)	BRE	-1.54	0.03
Bt.17012.1.A1_s_at	DnaJ (Hsp40) homolog, subfamily C, member 7	DNAJC7	-1.54	0.05
Bt.27123.1.A1_at	MDS1 and EVI1 complex locus	MECOM	-1.54	0.02
Bt.7136.1.S1_at	Sialidase 3 (membrane sialidase)	NEU3	-1.54	0.02
Bt.17428.1.A1_at	NHL repeat containing 3	NHLRC3	-1.54	0.01
Bt.26495.2.S1_at	DnaJ (Hsp40) homolog, subfamily C, member 19	DNAJC19	-1.53	0.04
Bt.9082.1.S1_at	lectin, galactoside-binding, soluble, 4	LGALS4	-1.53	0.04
Bt.10169.1.S1_at	similar to Uncharacterized protein C8orf42 homolog	LOC614166	-1.53	0.03
Bt.13411.1.S1_at	LPS-responsive vesicle trafficking, beach and anchor containing	LRBA	-1.53	0.01

Bt.16133.2.S1_at	phosphatidylinositol glycan anchor biosynthesis, class H	PIGH	-1.53	0.0022
Bt.10001.1.A1_at	solute carrier family 39 (zinc transporter), member 14	SLC39A14	-1.53	0.0024
Bt.25051.1.A1_at	tetratricopeptide repeat domain 14	TTC14	-1.53	0.02
Bt.2294.1.S1_a_at	ubiquitin-like modifier activating enzyme 7	UBA7	-1.53	0.02
Bt.23233.1.S1_at	ubiquitin specific peptidase 18	USP18	-1.53	0.01
Bt.8608.1.S1_at	zinc finger protein 605	ZNF605	-1.53	0.04
Bt.13357.1.S1_at	biorientation of chromosomes in cell division 1-like	BOD1L	-1.52	0.02
Bt.27381.1.S1_at	coenzyme Q10 homolog A (<i>S. cerevisiae</i>)	COQ10A	-1.52	0.05
Bt.25291.1.A1_at	melanoma inhibitory activity family, member 3	MIA3	-1.52	0.0015
Bt.4439.1.S1_at	phospholipase A2, group IB (pancreas)	PLA2G1B	-1.52	0.02
Bt.14002.2.S1_at	splicing factor, arginine/serine-rich 18	SFRS18	-1.52	0.02
Bt.22433.1.A1_at	solute carrier family 22 (organic cation/carnitine transporter), 5	SLC22A5	-1.52	0.02
Bt.8976.1.S1_at	transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	-1.52	0.0003
Bt.25250.1.S1_at	transmembrane 9 superfamily member 3	TM9SF3	-1.52	0.0039
Bt.25597.1.A1_at	tripartite motif-containing 52	TRIM52	-1.52	0.05
Bt.8117.1.S1_at	unc-51-like kinase 2 (<i>C. elegans</i>)	ULK2	-1.52	0.01
Bt.5259.1.S1_at	XIAP associated factor 1	XAF1	-1.52	0.01
Bt.4762.1.S1_at	MHC class I heavy chain /// MHC class I antigen clone 2 /// non-	BOLA /// BOLA	-1.51	0.04
Bt.5343.1.A1_at	CD300 molecule-like family member g	CD300LG	-1.51	0.0044
Bt.3931.1.S1_at	CGRP receptor component	CRCP	-1.51	0.01
Bt.5134.1.S1_at	CYB5 protein	CYB5A	-1.51	0.0026
Bt.2172.1.S1_at	similar to HEPH	LOC510736	-1.51	0.0027
Bt.12739.1.S1_at	membrane-associated ring finger (C3HC4) 2	MARCH2	-1.51	0.02
Bt.27300.1.A1_at	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	RASGRP1	-1.51	0.04
Bt.9786.1.S1_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3	ST6GALNAC2	-1.51	0.01
Bt.6361.1.S1_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	-1.50	0.0048
Bt.28780.1.A1_at	FYVE, RhoGEF and PH domain containing 4	FGD4	-1.50	0.01
Bt.5560.1.S1_at	IgA regulatory protein	IGIP	-1.50	0.02
Bt.7240.1.S1_at	leucine aminopeptidase 3	LAP3	-1.50	0.0045
Bt.24680.1.A1_at	protein arginine methyltransferase 10 (putative)	PRMT10	-1.50	0.03
Bt.15607.1.S1_at	sorting nexin 16	SNX16	-1.50	0.03