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Supplement 1. List of genes affected by pregnancy in the intercaruncular endometrium on d 17 of the cycle or pregnancy. Genes were selected based on an absolute expression value > 40 and P-value <0.01. Fold effect and regulation columns consider the effects of pregnancy using the cyclic endometrium as the reference. (i.e. Down regulation means the pregnant endometrium has a lower gene expression than cyclic endometrium)

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
similar to C1qR(p)	*LOC539690*	539690	---	5.44E-09	0.19	Down
oxytocin receptor	*OXTR*	281371	0007165 // signal transduction // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 0045777 // positive regulation of blood pressure // inferred from electron	0.00027	0.20	Down
polymeric immunoglobulin receptor	*PIGR*	281401	---	4.75E-07	0.20	Down
Similar to collagen, type XIV, alpha 1	*LOC781493*	781493	---	3.59E-08	0.21	Down
immunoglobulin superfamily, member 10	*IGSF10*	537487	---	3.26E-08	0.23	Down
glutamate receptor, ionotropic, kainate 1	*GRIK1*	533760	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation	4.16E-05	0.23	Down
SH3 domain binding glutamic acid-rich protein	*SH3BGR*	617797	---	1.92E-08	0.24	Down

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
plasmalemma vesicle associated protein	*PLVAP*	524990	---	3.84E-07	0.25	Down
sodium channel, nonvoltage-gated 1 alpha	*SCNN1A*	282348	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation	1.17E-06	0.25	Down
immunoglobulin superfamily containing leucine-rich repeat	*ISLR*	515018	---	1.16E-06	0.26	Down
leucine rich repeat and fibronectin type III domain containing 5	*LRFN5*	539366	---	0.000357	0.27	Down
glycosyltransferase 8 domain containing 2	*GLT8D2*	523294	0016051 // carbohydrate biosynthetic process // inferred from electronic annotation	4.07E-08	0.27	Down
endothelin 3	*EDN3*	513753	0019229 // regulation of vasoconstriction // inferred from electronic annotation	7.11E-05	0.28	Down
Carbonic anhydrase VIII	*CA8*	515918	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	2.33E-07	0.30	Down
carbonic anhydrase VIII	*CA8*	515918	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	7.66E-08	0.31	Down
proline/arginine-rich end leucine-rich	*PRELP*	282000	---	2.12E-08	0.31	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
repeat protein						
H19, imprinted maternally expressed untranslated mRNA	*H19*	100126192	---	0.00275	0.31	Down
solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	*SLC16A2*	535872	0006810 // transport // inferred from electronic annotation	5.02E-09	0.32	Down
sphingosine kinase 2	*SPHK2*	533103	0007205 // activation of protein kinase C activity // inferred from electronic annotation	2.38E-13	0.32	Down
protein phosphatase 1, regulatory (inhibitor) subunit 16B	*PPP1R16B*	282091	---	1.50E-09	0.32	Down
matrix-remodelling associated 8	*MXRA8*	522392	---	3.21E-10	0.32	Down
fibroblast activation protein, alpha	*FAP*	508882	0006508 // proteolysis // inferred from electronic annotation	2.21E-09	0.33	Down
glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	*GPIHBP1*	512826	---	3.00E-07	0.33	Down
myostatin	*MSTN*	281187	0007179 // transforming growth factor beta receptor signaling pathway // inferred from electronic annotation /// 0040007 // growth // inferred from electronic annotation /// 0045941 // positive regulation of transcription // inferred from electronic annot	7.89E-06	0.33	Down
SRY (sex determining region Y)-box 18	*SOX18*	519439	0006355 // regulation of transcription, DNA-dependent // inferred from	5.32E-07	0.33	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			electronic annotation			
Similar to MPIF-1	*LOC508666*	508666	---	5.87E-07	0.34	Down
Tetraspanin 2	*TSPAN2*	539001	---	2.76E-05	0.34	Down
hypothetical protein LOC100125878	*LOC100125878*	100125878	---	8.19E-08	0.34	Down
RAC/CDC42 exchange factor	*GEFT*	506075	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	9.61E-07	0.35	Down
transforming growth factor, beta 2	*TGFB2*	534069	0000902 // cell morphogenesis // inferred from electronic annotation /// 0001501 // skeletal development // inferred from electronic annotation /// 0001568 // blood vessel development // inferred from electronic annotation /// 0001654 // eye development /	8.76E-05	0.36	Down
LIM and cysteine-rich domains 1	*LMCD1*	540474	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation	1.09E-07	0.36	Down
Chromosome 14 open reading frame 37 ortholog	*C10H14orf37*	508562	---	0.000116	0.36	Down
metallophosphoesterase domain containing 2	*MPPED2*	540914	---	7.99E-07	0.36	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
CD300 molecule-like family member g	*CD300LG*	615388	0006955 // immune response // inferred from electronic annotation	3.68E-05	0.36	Down
fatty acid binding protein 7, brain	*FABP7*	777787	0006810 // transport // inferred from electronic annotation	7.99E-06	0.36	Down
platelet/endothelial cell adhesion molecule (CD31 antigen)	*PECAM1*	282303	0007155 // cell adhesion // inferred from electronic annotation	9.44E-08	0.37	Down
potassium large conductance calcium-activated channel, subfamily M, alpha member 1	*KCNMA1*	282573	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006813 // potassium ion transport // inferred from electronic annotation /// 0008152 // metabolic process // inferred from	0.00036	0.37	Down
urocanase domain containing 1	*UROC1*	528246	0006548 // histidine catabolic process // inferred from electronic annotation	3.19E-11	0.37	Down
cAMP responsive element binding protein 3-like 4	*CREB3L4*	529566	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	3.60E-06	0.37	Down
calponin 1, basic, smooth muscle	*CNN1*	534583	0031032 // actomyosin structure organization and biogenesis // inferred from electronic annotation	1.16E-06	0.37	Down
corticotropin releasing hormone binding protein	*CRHBP*	540087	---	0.000229	0.37	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
cadherin 13, H-cadherin (heart)	*CDH13*	512302	0001938 // positive regulation of endothelial cell proliferation // inferred from electronic annotation /// 0001954 // positive regulation of cell-matrix adhesion // inferred from electronic annotation /// 0002040 // sprouting angiogenesis // inferred fro	7.91E-06	0.37	Down
integrin, alpha 7	*ITGA7*	506953	---	0.001001	0.37	Down
leucine rich repeat containing 17	*LRRC17*	777690	---	1.34E-08	0.38	Down
hemicentin 1	*HMCN1*	521326	---	1.05E-07	0.38	Down
cartilage associated protein	*CRTAP*	540924	---	1.29E-08	0.38	Down
V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	*KIT*	280832	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation /// 0007243 // protein kinase cascade // inferred f	0.001176	0.39	Down
reticulocalbin 3, EF-hand calcium binding domain	*RCN3*	522073	---	1.02E-05	0.39	Down
collagen, type XII, alpha 1	*COL12A1*	359712	0006817 // phosphate transport // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation	9.29E-06	0.39	Down

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Transmembrane protease, serine 2	*TMPRSS2*	511037	0006508 // proteolysis // inferred from electronic annotation	0.003658	0.39	Down
similar to nonclathrin coat protein zeta-COP	*LOC616222*	616222	---	5.01E-09	0.40	Down
sideroflexin 3	*SFXN3*	511755	0006812 // cation transport // inferred from electronic annotation	8.22E-09	0.40	Down
butyrylcholinesterase	*BCHE*	534616	---	3.38E-07	0.41	Down
versican	*VCAN*	282662	0007155 // cell adhesion // inferred from electronic annotation /// 0007507 // heart development // inferred from electronic annotation	0.003346	0.41	Down
coiled-coil domain containing 80	*CCDC80*	515235	---	5.28E-08	0.41	Down
junctophilin 4	*JPH4*	781073	---	5.27E-05	0.41	Down
potassium large conductance calcium-activated channel, subfamily M, alpha member 1	*KCNMA1*	282573	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006813 // potassium ion transport // inferred from electronic annotation /// 0008152 // metabolic process // inferred from	1.08E-06	0.41	Down
similar to CMP-N-acetylneuraminic acid hydroxylase	*LOC537017*	537017	---	0.000737	0.41	Down

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Nephronectin	*NPNT*	513362	---	5.10E-09	0.41	Down
zinc finger protein 521	*ZNF521*	538792	0045449 // regulation of transcription // inferred from electronic annotation	6.47E-08	0.41	Down
reticulocalbin 3, EF-hand calcium binding domain	*RCN3*	522073	---	8.85E-09	0.41	Down
LAMA-like protein 1	*LOC317710*	317710	0016042 // lipid catabolic process // inferred from electronic annotation	1.65E-06	0.41	Down
hypothetical LOC515128	*LOC515128*	515128	---	5.07E-07	0.42	Down
C20orf142-like	*LOC518159*	518159	---	4.18E-08	0.42	Down
nephroblastoma overexpressed	*NOV*	505727	0001558 // regulation of cell growth // inferred from electronic annotation	0.009023	0.42	Down
sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	*SEMA5A*	506636	---	0.001504	0.42	Down
fibulin 5	*FBLN5*	535185	0007155 // cell adhesion // inferred from electronic annotation /// 0007596 // blood coagulation // inferred from electronic annotation	8.60E-07	0.42	Down
Similar to KIAA1568 protein	*LOC781194*	781194	---	3.65E-06	0.42	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
microtubule-associated protein 1B	*MAP1B*	514739	0006457 // protein folding // inferred from electronic annotation	0.00506	0.43	Down
similar to nonclathrin coat protein zeta-COP	*LOC616222*	616222	---	1.40E-09	0.43	Down
guanidinoacetate N-methyltransferase	*GAMT*	515270	---	1.95E-12	0.43	Down
nitric oxide synthase 1 (neuronal) adaptor protein	*NOS1AP*	783439	---	5.49E-07	0.43	Down
aquaporin 1 (Colton blood group)	*AQP1*	282653	0006810 // transport // inferred from electronic annotation	0.00163	0.43	Down
GTF2I repeat domain containing 1	*GTF2IRD1*	507792	---	9.41E-06	0.43	Down
hypothetical LOC535165	*LOC535165*	535165	---	5.63E-07	0.43	Down
membrane metallo-endopeptidase	*MME*	536741	---	0.000832	0.44	Down
myocilin, trabecular meshwork inducible glucocorticoid response	*MYOC*	281342	---	8.12E-07	0.44	Down
FK506 binding protein 10, 65 kDa	*FKBP10*	535310	0006457 // protein folding // inferred from electronic annotation	7.88E-06	0.44	Down
speckle-type POZ protein	*SPOP*	530618	0006512 // ubiquitin cycle // inferred from electronic annotation	5.79E-07	0.44	Down
similar to transmembrane and tetratricopeptide repeat containing 2	*LOC781126*	781126	---	2.13E-06	0.44	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
sarcoglycan, epsilon	*Sgce*	407209	---	7.59E-07	0.44	Down
protein tyrosine phosphatase, receptor type, D	*PTPRD*	532751	---	2.19E-07	0.44	Down
G protein-coupled receptor 153	*GPR153*	518906	---	4.57E-07	0.44	Down
transmembrane protein 88	*TMEM88*	507172	---	1.34E-08	0.45	Down
Hypothetical protein LOC784675	*KIAA1462*	784675	---	1.18E-05	0.45	Down
hydrogen voltage-gated channel 1	*HVCN1*	616570	---	1.99E-08	0.45	Down
protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	*PPP2R2B*	509290	0007165 // signal transduction // inferred from electronic annotation	1.37E-07	0.45	Down
WAP four-disulfide core domain 1	*WFDC1*	505366	---	4.28E-06	0.45	Down
TIMP metallopeptidase inhibitor 4	*TIMP4*	317694	---	0.00045	0.46	Down
Collagen, type XI, alpha 1	*COL11A1*	287013	0006817 // phosphate transport // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation	0.00684	0.46	Down
myotubularin related protein 9	*MTMR9*	521746	0046839 // phospholipid dephosphorylation // inferred from electronic annotation	3.04E-07	0.46	Down
lysozyme (renal amyloidosis)	*LYZ*	777776	0008152 // metabolic process // inferred from electronic annotation /// 0016998 // cell wall catabolic process	0.004467	0.46	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			// inferred from electronic annotation /// 0019835 // cytolysis // inferred from electronic annotation /// 0042742 // defense response to bacter			
carboxypeptidase E	*CPE*	280753	0006508 // proteolysis // inferred from electronic annotation /// 0030070 // insulin processing // inferred from electronic annotation	1.39E-05	0.46	Down
similar to polydom	*LOC781282*	781282	0007155 // cell adhesion // inferred from electronic annotation	0.002868	0.46	Down
plexin domain containing 2	*PLXDC2*	515731	0007275 // multicellular organismal development // inferred from electronic annotation	0.001097	0.47	Down
Usher syndrome 1C binding protein 1	*USHBP1*	768083	---	1.93E-07	0.47	Down
protein tyrosine phosphatase, receptor type, D	*PTPRD*	532751	---	1.57E-08	0.47	Down
membrane metallo-endopeptidase	*MME*	536741	---	0.002086	0.47	Down
spleen trypsin inhibitor	*LOC404103*	404103	---	0.00752	0.47	Down
polo-like kinase 2 (Drosophila)	*PLK2*	539449	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	1.72E-09	0.47	Down
Kruppel-like factor 11	*KLF11*	616730	---	0.000104	0.47	Down

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Calcium channel, voltage-dependent, T type, alpha 1G subunit	*CACNA1G*	282411	0006811 // ion transport // inferred from electronic annotation /// 0006816 // calcium ion transport // inferred from electronic annotation	4.11E-05	0.47	Down
tripartite motif-containing 2	*TRIM2*	538617	---	0.001435	0.48	Down
insulin-like growth factor 1 (somatomedin C)	*IGF1*	281239	---	0.002449	0.48	Down
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	*CDKN1C*	510972	0007050 // cell cycle arrest // inferred from electronic annotation	8.06E-08	0.48	Down
phosphoglucomutase 5	*PGM5*	785045	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006508 // proteolysis // inferred from electronic annotation	1.10E-07	0.48	Down
CD59 molecule, complement regulatory protein	*CD59*	505574	---	7.46E-05	0.48	Down
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	*GALNTL1*	526331	---	3.06E-06	0.48	Down
S-adenosylhomocysteine hydrolase-like 2	*AHCYL2*	532836	0006730 // one-carbon compound metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	1.38E-05	0.48	Down
Collagen, type V, alpha 3	*COL5A3*	507881	0007155 // cell adhesion // inferred	1.25E-05	0.49	Down

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			from electronic annotation			
Neurotrophic tyrosine kinase, receptor, type 2	*NTRK2*	505824	---	0.003821	0.49	Down
Chromobox homolog 6	*CBX6*	513830	0006333 // chromatin assembly or disassembly // inferred from electronic annotation	2.41E-09	0.49	Down
collagen, type IV, alpha 5 (Alport syndrome)	*COL4A5*	511602	0006817 // phosphate transport // inferred from electronic annotation	2.20E-06	0.49	Down
interleukin 33	*IL33*	507054	---	0.001472	0.49	Down
neuroligin 3	*NLGN3*	511251	0007155 // cell adhesion // inferred from electronic annotation	3.91E-07	0.49	Down
collagen, type IV, alpha 4	*COL4A4*	407107	0006817 // phosphate transport // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation	0.001911	0.49	Down
nestin	*NES*	522383	0006886 // intracellular protein transport // inferred from electronic annotation /// 0006888 // ER to Golgi vesicle-mediated transport // inferred from electronic annotation	5.02E-06	0.49	Down
phosphofructokinase, muscle	*PFKM*	506544	0006096 // glycolysis // inferred from electronic annotation	7.35E-08	0.49	Down
secretion regulating guanine nucleotide	*SERGEF*	534377	0050709 // negative regulation of protein secretion // inferred from	6.44E-09	0.49	Down

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exchange factor			electronic annotation			
similar to SMAP-2b	*MGC148871*	615490	---	0.000412	0.49	Down
wingless-type MMTV integration site family, member 2B	*WNT2B*	445420	0007223 // Wnt receptor signaling pathway, calcium modulating pathway // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation /// 0016055 // Wnt receptor signaling pathway // inferr	0.002584	0.49	Down
surfactant associated protein G	*SFTPG*	616978	---	0.000106	0.49	Down
S-adenosylhomocysteine hydrolase-like 2	*AHCYL2*	532836	0006730 // one-carbon compound metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	0.000111	0.49	Down
hydroxysteroid (11-beta) dehydrogenase 1-like	*HSD11B1L*	404546	0008152 // metabolic process // inferred from electronic annotation	2.30E-05	0.49	Down
phospholipase C-like 2	*PLCL2*	510408	0006629 // lipid metabolic process // inferred from electronic annotation /// 0007242 // intracellular signaling cascade // inferred from electronic annotation	2.60E-06	0.49	Down
sal-like 2 (Drosophila)	*SALL2*	527574	---	1.71E-06	0.49	Down

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hairy and enhancer of split 1, (Drosophila)	*HES1*	539547	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation /// 0001889 // liver development // inferred from electronic annotation /// 0006350 // transcription // inferred from electronic annotat	1.10E-06	0.49	Down
histone H4-like	*LOC617875*	617875	0006334 // nucleosome assembly // inferred from electronic annotation	5.00E-10	0.50	Down
D component of complement (adipsin)	*DF*	505647	0006508 // proteolysis // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0006957 // complement activation, alternative pathway // inferred from electronic annotation /// 0045087 // innate immu	0.000305	0.50	Down
ADAM-like, decysin 1	*ADAMDEC1*	505890	0006508 // proteolysis // inferred from electronic annotation	0.002581	0.50	Down
similar to type VII collagen	*LOC507133*	507133	0006817 // phosphate transport // inferred from electronic annotation	1.89E-05	0.50	Down
Cysteinyl-tRNA synthetase 2, mitochondrial (putative)	*CARS2*	506598	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006423 // cysteinyl-tRNA aminoacylation // inferred from	0.001262	0.50	Down

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			electronic annotation			
WNT1 inducible signaling pathway protein 2	*WISP2*	534658	0001558 // regulation of cell growth // inferred from electronic annotation	1.99E-05	0.50	Down
actin, alpha 2, smooth muscle, aorta	*ACTA2*	515610	0030240 // muscle thin filament assembly // inferred from sequence or structural similarity /// 0048741 // skeletal muscle fiber development // inferred from sequence or structural similarity	0.003231	0.50	Down
hypothetical LOC615685	*LOC615685*	615685	---	3.37E-09	0.50	Down
MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	*MFNG*	505267	---	5.18E-09	0.50	Down
hypothetical LOC615685	*LOC615685*	615685	---	2.62E-07	0.50	Down
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	*KRT10*	281888	---	1.89E-07	0.50	Down
hypothetical protein LOC783163	*LOC783163*	783163	---	3.36E-08	0.50	Down
pleckstrin homology-like domain, family B, member 2	*PHLDB2*	509784	---	0.000279	0.50	Down
Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	*CTR9*	534265	---	4.36E-07	0.51	Down

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chromobox homolog 6	*CBX6*	513830	0006333 // chromatin assembly or disassembly // inferred from electronic annotation	2.46E-09	0.51	Down
hypothetical LOC538778	*LOC538778*	538778	---	0.005279	0.51	Down
Carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	*CHST9*	525909	---	1.83E-06	0.51	Down
tenascin XB	*TNXB*	282654	0007155 // cell adhesion // inferred from direct assay /// 0007165 // signal transduction // inferred from electronic annotation /// 0030036 // actin cytoskeleton organization and biogenesis // inferred from mutant phenotype /// 0030198 // extracellular m	2.15E-05	0.51	Down
bone morphogenetic protein 2	*BMP2*	615037	0040007 // growth // inferred from electronic annotation	2.31E-07	0.51	Down
microfibrillar-associated protein 4	*MFAP4*	286766	0007155 // cell adhesion // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation	8.07E-05	0.51	Down
dispatched homolog 1 (Drosophila)	*DISP1*	534637	---	3.30E-05	0.51	Down
CXXC finger 5	*CXXC5*	538485	---	1.94E-08	0.51	Down
breast carcinoma amplified sequence 4	*BCAS4*	617710	---	2.48E-08	0.51	Down

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chromosome 12 open reading frame 57 ortholog	*C5H12ORF57*	511545	---	5.84E-09	0.51	Down
hypothetical LOC511765	*MGC137169*	511765	---	5.23E-06	0.52	Down
CAP-GLY domain containing linker protein 3	*CLIP3*	522965	---	1.76E-06	0.52	Down
muscle RAS oncogene homolog	*MRAS*	540803	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	2.05E-10	0.52	Down
pyridoxal (pyridoxine, vitamin B6) phosphatase	*PDXP*	506308	0008152 // metabolic process // inferred from electronic annotation	2.03E-06	0.52	Down
fasciculation and elongation protein zeta 1 (zygin I)	*FEZ1*	511751	---	7.57E-06	0.52	Down
secretogranin V (7B2 protein)	*SCG5*	508224	0007218 // neuropeptide signaling pathway // inferred from electronic annotation	1.64E-05	0.52	Down
thymocyte selection-associated high mobility group box	*TOX*	525888	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	7.99E-05	0.52	Down
melanoma antigen family D, 4-like	*LOC100125231*	100125231	---	3.98E-07	0.52	Down
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like	*LOC614717*	614717	0006486 // protein amino acid glycosylation // inferred from	1.48E-07	0.52	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			electronic annotation			
claudin 10	*CLDN10*	506545	---	0.002208	0.52	Down
Dihydropyrimidinase-like 3	*DPYSL3*	509796	---	4.26E-10	0.52	Down
ionized calcium binding adapter molecule 2	*C9orf58*	617493	---	5.45E-06	0.52	Down
odd-skipped related 2 (Drosophila)	*OSR2*	508692	0008284 // positive regulation of cell proliferation // inferred from electronic annotation /// 0048704 // embryonic skeletal morphogenesis // inferred from electronic annotation	0.00552	0.52	Down
cadherin 2, type 1, N-cadherin (neuronal)	*CDH2*	281062	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion // inferred from electronic annotation /// 0016339 // calcium-dependent cell-cell adhesion // inferred from electronic annotation /// 0016477 // cell m	8.38E-05	0.52	Down
roundabout homolog 4, magic roundabout (Drosophila)	*ROBO4*	783785	---	0.000124	0.53	Down
hypothetical protein LOC788205	*LOC788205*	788205	---	0.000712	0.53	Down
Hypothetical protein LOC781544	*LOC781544*	781544	---	4.27E-08	0.53	Down

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
FXYD domain containing ion transport regulator 1 (phospholemman)	*FXYD1*	616139	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation	1.15E-09	0.53	Down
Intestinal cell (MAK-like) kinase	*ICK*	506286	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.000562	0.53	Down
leprecan-like 1	*LEPREL1*	511799	0019538 // protein metabolic process // inferred from electronic annotation	0.005077	0.53	Down
odd-skipped related 2 (Drosophila)	*OSR2*	508692	0008284 // positive regulation of cell proliferation // inferred from electronic annotation /// 0048704 // embryonic skeletal morphogenesis // inferred from electronic annotation	3.51E-06	0.53	Down
importin 11	*IPO11*	538236	0000059 // protein import into nucleus, docking // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation	3.58E-06	0.53	Down
NFKB inhibitor interacting Ras-like 1	*NKIRAS1*	522875	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation	2.33E-06	0.53	Down
phosphoinositide-3-kinase, regulatory subunit 2 (beta)	*PIK3R2*	282308	0007165 // signal transduction // inferred from electronic annotation ///	1.49E-07	0.53	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			0019987 // negative regulation of anti-apoptosis // inferred from sequence or structural similarity			
Paternally expressed 10	*PEG10*	618138	---	0.00223	0.53	Down
olfactomedin-like 3	*OLFML3*	505318	---	1.70E-07	0.53	Down
von Willebrand factor A domain containing 1	*VWA1*	505917	---	2.78E-06	0.53	Down
heat shock transcription factor 2 binding protein	*HSF2BP*	617142	0006950 // response to stress // inferred from electronic annotation	6.14E-05	0.53	Down
lymphocyte-specific protein tyrosine kinase	*LCK*	508890	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0006882 // cellular zinc ion homeostasis // inferred from sequence or structural similarity /// 0006917 // induction of apoptosis // inferred from sequence or structu	0.000289	0.53	Down
murine retrovirus integration site 1 homolog	*MRVI1*	281918	---	4.49E-05	0.53	Down
methionine sulfoxide reductase B3	*MSRB3*	617849	---	3.54E-07	0.53	Down
1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	*ACCS*	505649	0009058 // biosynthetic process // inferred from electronic annotation	1.91E-05	0.53	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
LIM domain binding 2	*LDB2*	617976	0007275 // multicellular organismal development // inferred from electronic annotation	4.79E-07	0.53	Down
solute carrier family 41, member 3	*SLC41A3*	524085	0006812 // cation transport // inferred from electronic annotation	2.05E-06	0.53	Down
family with sequence similarity 92, member A1	*FAM92A1*	614070	---	1.59E-08	0.53	Down
nidogen 1	*NID1*	534319	0007160 // cell-matrix adhesion // inferred from electronic annotation /// 0008218 // bioluminescence // inferred from electronic annotation /// 0018298 // protein-chromophore linkage // inferred from electronic annotation	5.99E-05	0.53	Down
solute carrier family 22, member 17	*SLC22A17*	539848	0006810 // transport // inferred from electronic annotation	3.87E-05	0.53	Down
Polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	*POLR2A*	282312	0006350 // transcription // inferred from electronic annotation	5.96E-05	0.54	Down
jagged 2	*JAG2*	517405	---	1.61E-05	0.54	Down
filamin A, alpha (actin binding protein 280)	*FLNA*	281165	---	2.29E-07	0.54	Down
hypothetical protein LOC781852	*LOC781852*	781852	---	8.37E-07	0.54	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
potassium channel tetramerisation domain containing 15	*KCTD15*	512578	0006813 // potassium ion transport // inferred from electronic annotation	4.33E-08	0.54	Down
ankylosis, progressive homolog (mouse)	*ANKH*	511800	0006817 // phosphate transport // inferred from electronic annotation	1.94E-05	0.54	Down
zinc finger protein 358	*ZNF358*	505837	---	1.32E-06	0.54	Down
CXXC finger 5	*CXXC5*	538485	---	1.52E-09	0.54	Down
hypothetical LOC614402	*LOC614402*	614402	---	0.009461	0.54	Down
Polymorphic microsatellite locus (AFZ1)	---	---	---	9.70E-08	0.54	Down
similar to FLJ00128 protein	*LOC527362*	527362	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	8.74E-06	0.54	Down
histamine N-methyltransferase	*HNMT*	613413	---	1.94E-06	0.54	Down
GTP binding protein overexpressed in skeletal muscle	*GEM*	538437	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	1.21E-05	0.54	Down
sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	*SEMA5A*	506636	---	3.62E-06	0.54	Down
similar to high-risk human papilloma viruses E6 oncoproteins targeted protein	*LOC534839*	534839	---	3.63E-06	0.54	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
E6TP1 alpha; putative GAP protein alpha						
similar to CMP-N-acetylneuraminic acid hydroxylase	*LOC537017*	537017	---	0.000105	0.54	Down
D site of albumin promoter (albumin D-box) binding protein	*DBP*	503577	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0048511 // rhythmic process // inferred from electronic annotation	3.47E-08	0.54	Down
retinol binding protein 1, cellular	*RBP1*	537379	0006810 // transport // inferred from electronic annotation /// 0042572 // retinol metabolic process // inferred from sequence or structural similarity	1.08E-06	0.55	Down
carbonic anhydrase XI	*CA11*	326334	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	0.000983	0.55	Down
glutathione S-transferase M1	*GSTM1*	327709	0008152 // metabolic process // inferred from electronic annotation	7.11E-05	0.55	Down
Kruppel-like factor 11	*KLF11*	616730	---	7.74E-08	0.55	Down
MAS-related GPR, member F	*MRGPRF*	615886	0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	0.001106	0.55	Down
hypothetical LOC616610	*LOC61661*	616610	0006508 // proteolysis // inferred from electronic annotation /// 0006629 //	1.63E-08	0.55	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
	0		lipid metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation			
septin 4	*SEPT4*	538801	0007049 // cell cycle // inferred from electronic annotation	1.12E-06	0.55	Down
Laminin, alpha 4	*LAMA4*	529670	0030155 // regulation of cell adhesion // inferred from electronic annotation /// 0030334 // regulation of cell migration // inferred from electronic annotation /// 0045995 // regulation of embryonic development // inferred from electronic annotation	2.94E-05	0.55	Down
similar to KIAA1623 protein	*LOC528201*	528201	---	1.91E-07	0.55	Down
Aldehyde dehydrogenase 1 family, member A2	*ALDH1A2*	535075	---	0.009624	0.55	Down
similar to SMAP-2b	*MGC148871*	615490	---	4.00E-07	0.55	Down
filamin C, gamma (actin binding protein 280)	*FLNC*	528415	---	1.69E-05	0.55	Down
dimethylarginine dimethylaminohydrolase 1	*DDAH1*	537391	0006809 // nitric oxide biosynthetic process // inferred from direct assay /// 0017014 // protein amino acid nitrosylation // inferred from direct	5.36E-07	0.55	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			assay			
Tripartite motif-containing 45	*TRIM45*	539091	---	0.001513	0.55	Down
membrane-bound transcription factor peptidase, site 1	*MBTPS1*	511682	0006508 // proteolysis // inferred from electronic annotation	4.62E-15	0.55	Down
Down syndrome critical region protein 3	*DSCR3*	507647	0007034 // vacuolar transport // inferred from electronic annotation	1.45E-07	0.55	Down
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	*SMARCD3*	777769	---	2.37E-05	0.55	Down
adhesion molecule with Ig-like domain 1	*AMIGO1*	524284	---	8.27E-05	0.55	Down
Similar to Hlcs	*LOC534247*	534247	0006464 // protein modification process // inferred from electronic annotation	4.23E-08	0.55	Down
similar to KIAA0793 protein	*LOC514637*	514637	---	0.0001	0.55	Down
ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	*ENPP2*	532663	0006935 // chemotaxis // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation /// 0016042 // lipid catabolic process // inferred from electronic annotation	2.31E-10	0.55	Down
PHD finger protein 10	*PHF10*	507648	---	2.71E-11	0.55	Down

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ephrin-A5	*EFNA5*	616742	---	0.000187	0.55	Down
alcohol dehydrogenase, iron containing, 1	*ADHFE1*	507711	0008152 // metabolic process // inferred from electronic annotation /// 0015993 // molecular hydrogen transport // inferred from sequence or structural similarity	6.59E-07	0.56	Down
mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	*MSH2*	533115	0001701 // in utero embryonic development // inferred from electronic annotation /// 0002204 // somatic recombination of immunoglobulin genes during immune response // inferred from electronic annotation /// 0006119 // oxidative phosphorylation // inferre	1.13E-08	0.56	Down
leukotriene B4 12-hydroxydehydrogenase	*LTB4DH*	513177	0008152 // metabolic process // inferred from electronic annotation	0.00404	0.56	Down
lymphocyte-specific protein tyrosine kinase	*LCK*	508890	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0006882 // cellular zinc ion homeostasis // inferred from sequence or structural similarity /// 0006917 // induction of apoptosis // inferred from sequence or structu	0.000648	0.56	Down
myosin light chain kinase	*MYLK*	338037	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	2.75E-05	0.56	Down

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
similar to SLC2A4 regulator	*LOC511523*	511523	---	2.78E-08	0.56	Down
ephrin-A5	*EFNA5*	616742	---	0.001107	0.56	Down
collagen, type IV, alpha 5 (Alport syndrome)	*COL4A5*	511602	0006817 // phosphate transport // inferred from electronic annotation	2.06E-05	0.56	Down
chromodomain helicase DNA binding protein 3 /// centrobin, centrosomal BRCA2 interacting protein	*CHD3 /// CNTROB*	532673 /// 539106	0006333 // chromatin assembly or disassembly // inferred from electronic annotation /// 0042309 // homoiothermy // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation /// 0050826 // respons	5.83E-09	0.56	Down
Estrogen receptor 1 alpha (ESR1) mRNA, partial sequence	*ESR1*	---	---	5.34E-11	0.56	Down
regulator of calcineurin 2	*RCAN2*	525636	0019722 // calcium-mediated signaling // inferred from electronic annotation	0.000703	0.56	Down
acyl-Coenzyme A oxidase 2, branched chain	*ACOX2*	514969	0006631 // fatty acid metabolic process // inferred from electronic annotation /// 0006635 // fatty acid beta-oxidation // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation /// 0055114 // oxidation	2.24E-06	0.56	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
similar to DBC2	*LOC782546*	782546	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation	6.35E-06	0.56	Down
EH-domain containing 2	*EHD2*	538348	---	8.53E-08	0.56	Down
cell adhesion molecule 3	*CADM3*	531178	---	0.005869	0.56	Down
arylsulfatase family, member K	*ARSK*	533618	0008152 // metabolic process // inferred from electronic annotation	1.61E-07	0.56	Down
SIX homeobox 5	*SIX5*	513676	---	0.000164	0.56	Down
Kinetochore associated 1	*KNTC1*	506353	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.000171	0.56	Down
transcription elongation factor A (SII), 3	*TCEA3*	533803	0006350 // transcription // inferred from electronic annotation /// 0006354 // RNA elongation // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006357 // regulation	0.000151	0.57	Down
thymidylate synthetase	*TYMS*	507631	0006231 // dTMP biosynthetic process // inferred from electronic	1.37E-07	0.57	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			annotation /// 0009165 // nucleotide biosynthetic process // inferred from electronic annotation			
hypothetical protein LOC533126	*LOC533126*	533126	---	7.62E-05	0.57	Down
pleckstrin homology-like domain, family B, member 2	*PHLDB2*	509784	---	8.81E-05	0.57	Down
transcription factor-like 5 (basic helix-loop-helix)	*TCFL5*	513750	0045449 // regulation of transcription // inferred from electronic annotation	5.12E-06	0.57	Down
Coiled-coil-helix-coiled-coil-helix domain containing 6	*CHCHD6*	615934	---	4.93E-05	0.57	Down
ADP-ribosylation factor-like 3	*ARL3*	540040	0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	2.00E-09	0.57	Down
dynamin 1	*DNM1*	508794	0006897 // endocytosis // inferred from electronic annotation	1.22E-06	0.57	Down
Similar to copine III-like related protein	*LOC782388*	782388	---	8.94E-08	0.57	Down
CDNA clone IMAGE:8067330	---	---	---	1.79E-07	0.57	Down
Wilms tumor 1 interacting protein	*WTIP*	505059	---	2.27E-06	0.57	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
Musculoskeletal, embryonic nuclear protein 1	*MUSTN1*	616088	---	1.09E-06	0.57	Down
similar to LOC113230 protein	*LOC539805*	539805	---	0.000277	0.57	Down
POZ (BTB) and AT hook containing zinc finger 1	*PATZ1*	532416	---	3.35E-08	0.57	Down
zinc finger protein 532	*ZNF532*	533847	---	1.40E-06	0.57	Down
ankyrin repeat domain 50	*ANKRD50*	527956	---	1.05E-09	0.57	Down
two pore segment channel 1	*TPCN1*	510830	---	1.94E-05	0.57	Down
heat shock 22kDa protein 8	*HSPB8*	539524	0006950 // response to stress // inferred from electronic annotation	0.003792	0.57	Down
similar to B0432.9	*LOC505636*	505636	---	1.22E-06	0.57	Down
nucleosome assembly protein 1-like 5	*NAP1L5*	508508	0006334 // nucleosome assembly // inferred from electronic annotation	1.46E-09	0.57	Down
osteoglycin	*OGN*	280884	---	0.000721	0.57	Down
sialic acid binding Ig-like lectin 10	*SIGLEC10*	504258	---	2.62E-05	0.57	Down
CD44 molecule (Indian blood group)	*CD44*	281057	0007155 // cell adhesion // inferred from electronic annotation	0.000112	0.57	Down
transmembrane protein 132A	*TMEM132*	540137	---	2.77E-09	0.58	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
	A					
family with sequence similarity 62 (C2 domain containing), member A	*FAM62A*	520669	---	1.31E-09	0.58	Down
heat shock 70kD protein 12B	*HSPA12B*	515590	---	6.26E-09	0.58	Down
cyclin-dependent kinase 5	*CDK5*	281066	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0007160 // cell-matrix adhesion // inferred from electronic annotation /// 0007160 // cell-matrix adh	4.86E-07	0.58	Down
proline-rich cyclin A1-interacting protein	*PROCA1*	510175	---	4.54E-07	0.58	Down
heat shock protein, alpha-crystallin-related, B6	*HSPB6*	534551	0006950 // response to stress // inferred from electronic annotation	0.000752	0.58	Down
cyclin-dependent kinase 2-interacting protein	*CINP*	613767	0006260 // DNA replication // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0051301 // cell division // inferred from electronic annotation	0.002413	0.58	Down
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	*ANP32A*	538427	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006913 //	4.76E-10	0.58	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			nucleocytoplasmic transport // inferred from sequence or structural similarity			
musculoskeletal, embryonic nuclear protein 1	*MUSTN1*	616088	---	2.11E-07	0.58	Down
ephrin-A5	*EFNA5*	616742	---	3.77E-06	0.58	Down
Matrix-remodelling associated 7	*MXRA7*	617087	---	6.87E-11	0.58	Down
Chromosome 9 open reading frame 6 ortholog	*C8H9orf6*	507081	---	1.54E-06	0.58	Down
vascular endothelial growth factor A	*VEGFA*	281572	0001525 // angiogenesis // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation /// 0008283 // cell proliferation // inferred from electronic annotation /// 0030154 // cell differen	3.44E-06	0.58	Down
Coiled-coil and C2 domain containing 2A	*CC2D2A*	517240	---	0.000784	0.58	Down
Similar to myotonic dystrophy kinase	*LOC513675*	513675	---	0.00139	0.58	Down
serum deprivation response (phosphatidylserine binding protein)	*SDPR*	532333	---	0.000173	0.58	Down
EP300 interacting inhibitor of	*EID1*	506056	---	9.38E-07	0.58	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
differentiation 1						
CDC42 effector protein (Rho GTPase binding) 1	*CDC42EP1*	511099	0008360 // regulation of cell shape // inferred from electronic annotation	1.00E-06	0.58	Down
Similar to CMP-N-acetylneuraminic acid hydroxylase	*LOC537017*	537017	---	2.71E-05	0.58	Down
cathepsin F	*CTSF*	509715	0006508 // proteolysis // inferred from electronic annotation	1.59E-09	0.58	Down
Similar to LOC496253 protein	*LOC784007*	784007	---	0.001077	0.58	Down
Notch homolog 4 (Drosophila)	*NOTCH4*	537814	---	4.79E-08	0.58	Down
collagen, type I, alpha 1	*COL1A1*	282187	0006817 // phosphate transport // inferred from electronic annotation	0.000125	0.58	Down
annexin A11	*ANXA11*	282142	---	4.99E-07	0.58	Down
parathyroid hormone receptor 1	*PTHR1*	507783	0001501 // skeletal development // inferred from electronic annotation /// 0001503 // ossification // inferred from electronic annotation /// 0002062 // chondrocyte differentiation // inferred from electronic annotation /// 0002076 // osteoblast developme	3.27E-06	0.58	Down
similar to neuregulin 2	*LOC783452*	783452	---	0.00205	0.58	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
Coiled-coil domain containing 8	*CCDC8*	616838	---	5.72E-09	0.58	Down
sterile alpha motif domain containing 1	*SAMD1*	785246	---	5.12E-07	0.58	Down
hypothetical LOC509875	*LOC509875*	509875	---	0.003552	0.58	Down
zinc finger protein 362	*ZNF362*	508065	---	7.95E-09	0.59	Down
Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	*CHST7*	540357	---	2.73E-06	0.59	Down
ankyrin repeat domain 23	*ANKRD23*	525365	---	8.65E-06	0.59	Down
collagen, type I, alpha 1	*COL1A1*	282187	0006817 // phosphate transport // inferred from electronic annotation	1.65E-05	0.59	Down
Ribosomal protein S8	*RPS8*	404140	---	0.000136	0.59	Down
melanoma inhibitory activity	*MIA*	280857	0007160 // cell-matrix adhesion // inferred from electronic annotation /// 0030198 // extracellular matrix organization and biogenesis // inferred from electronic annotation	1.21E-05	0.59	Down
angiopoietin-like 2	*ANGPTL2*	512019	---	3.93E-06	0.59	Down
jagged 1 (Alagille syndrome)	*JAG1*	783681	---	6.84E-08	0.59	Down
Collagen, type XXVII, alpha 1	*COL27A1*	513668	0006817 // phosphate transport // inferred from electronic annotation /// 0007155 // cell adhesion // inferred	0.000169	0.59	Down

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			from electronic annotation			
ST3 beta-galactoside alpha-2,3-sialyltransferase 6	*ST3GAL6*	444860	0006486 // protein amino acid glycosylation // inferred from electronic annotation	0.000266	0.59	Down
sarcoglycan, epsilon	*Sgce*	407209	---	1.50E-06	0.59	Down
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	*CITED1*	282182	0045449 // regulation of transcription // inferred from electronic annotation	1.97E-05	0.59	Down
phosphomannomutase 1	*PMM1*	537070	0008152 // metabolic process // inferred from electronic annotation /// 0019307 // mannose biosynthetic process // inferred from electronic annotation	1.96E-09	0.59	Down
ATP-binding cassette, sub-family A (ABC1), member 5	*ABCA5*	510497	---	1.04E-06	0.59	Down
Hypoxia-inducible factor prolyl 4-hydroxylase	*PH-4*	538626	0019538 // protein metabolic process // inferred from electronic annotation	4.19E-06	0.59	Down
carnitine palmitoyltransferase 1C	*CPT1C*	513710	---	1.52E-06	0.59	Down
dystonin	*DST*	535297	0007050 // cell cycle arrest // inferred from electronic annotation	5.04E-08	0.59	Down
AHNAK nucleoprotein 2	*AHNAK2*	527701	---	6.67E-08	0.59	Down
Similar to POTE8A	*LOC786977*	786977	---	7.82E-06	0.59	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
Phosphatidylinositol-4-phosphate 5-kinase, type I, beta	*PIP5K1B*	537654	0046488 // phosphatidylinositol metabolic process // inferred from electronic annotation	0.006005	0.59	Down
carbonic anhydrase VB, mitochondrial	*CA5B*	514494	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	0.000146	0.59	Down
iroquois homeobox 3	*IRX3*	540417	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation	0.000367	0.59	Down
casein kinase 1, epsilon	*CSNK1E*	768234	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0016055 // Wnt receptor signaling pathway // inferred from electronic annotation	2.93E-05	0.59	Down
CD302 molecule	*CD302*	100126272	---	2.67E-07	0.59	Down
neurotrophic tyrosine kinase, receptor, type 2	*NTRK2*	505824	---	0.000133	0.59	Down
DNL-type zinc finger	*DNLZ*	514124	0045449 // regulation of transcription // inferred from electronic annotation	1.74E-09	0.59	Down
LIM domain binding 1	*LDB1*	526472	0007275 // multicellular organismal development // inferred from electronic annotation	5.62E-07	0.60	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
Hypothetical protein LOC784675	*KIAA1462*	784675	---	3.57E-07	0.60	Down
hypothetical LOC515954	*LOC515954*	515954	---	3.27E-09	0.60	Down
hypothetical LOC538778	*LOC538778*	538778	---	6.10E-05	0.60	Down
adenylate cyclase 4	*ADCY4*	788151	0006412 // translation // inferred from electronic annotation /// 0007242 // intracellular signaling cascade // inferred from electronic annotation /// 0009190 // cyclic nucleotide biosynthetic process // inferred from electronic annotation	5.08E-05	0.60	Down
protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	*PPP1R1B*	282459	0006350 // transcription // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation /// 0007621 // negative regulation of female receptivity // inferred from electronic annotation	2.79E-05	0.60	Down
KN motif and ankyrin repeat domains 1	*KANK1*	534869	---	0.001115	0.60	Down
collagen, type XIII, alpha 1	*COL13A1*	613849	0006817 // phosphate transport // inferred from electronic annotation	0.00418	0.60	Down
hypothetical LOC514296	*LOC514296*	514296	---	3.93E-05	0.60	Down

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aminoacylase 1 /// similar to aminoacylase-1	*ACY1 /// LOC790609*	768058 /// 790609	0006508 // proteolysis // inferred from electronic annotation /// 0006520 // amino acid metabolic process // inferred from electronic annotation	2.20E-07	0.60	Down
similar to sulfatase 1	*LOC535166*	535166	---	0.000536	0.60	Down
Hypothetical protein LOC787439	*LOC787439*	787439	---	0.000783	0.60	Down
cyclin D1	*CCND1*	524530	0000320 // re-entry into mitotic cell cycle // inferred from electronic annotation /// 0001934 // positive regulation of protein amino acid phosphorylation // inferred from electronic annotation /// 0006468 // protein amino acid phosphorylation // inferre	0.001024	0.60	Down
transforming growth factor beta 1 induced transcript 1	*TGFB1I1*	515834	0016055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 0030154 // cell differentiation // inferred from electronic annotation	6.56E-05	0.60	Down
pleckstrin homology domain containing, family G (with RhoGef domain) member 2	*PLEKHG2*	504530	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	1.71E-05	0.60	Down
snail homolog 2 (Drosophila)	*SNAI2*	520631	0006350 // transcription // inferred from electronic annotation ///	2.45E-05	0.60	Down

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			0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation ///			
Makorin, ring finger protein, 1	*MKRN1*	514986	---	1.26E-09	0.60	Down
prostaglandin D2 synthase 21kDa (brain)	*PTGDS*	286858	0001516 // prostaglandin biosynthetic process // inferred from sequence or structural similarity /// 0001516 // prostaglandin biosynthetic process // inferred from electronic annotation /// 0006629 // lipid metabolic process // inferred from electronic an	2.22E-07	0.60	Down
Ras-related GTP binding D	*RRAGD*	541106	---	6.13E-05	0.60	Down
dihydropyrimidinase-like 2	*DPYSL2*	533746	0007275 // multicellular organismal development // inferred from electronic annotation /// 0007399 // nervous system development // inferred from electronic annotation /// 0030154 // cell differentiation // inferred from electronic annotation	2.49E-05	0.60	Down
trafficking protein, kinesin binding 1	*TRAK1*	531649	---	1.67E-06	0.60	Down
claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	*CLDN5*	617453	---	0.007199	0.60	Down

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membrane-associated ring finger (C3HC4) 9	*MAR9*	540871	---	4.32E-05	0.60	Down
similar to SNHG8 protein	*LOC782900*	782900	---	2.19E-07	0.60	Down
nuclear factor I/A	*NFIA*	615371	0006260 // DNA replication // inferred from electronic annotation /// 0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	6.25E-09	0.61	Down
Hypothetical protein LOC510660	*LOC510660*	510660	---	0.004804	0.61	Down
homeobox B7	*HOXB7*	281820	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation ///	0.002263	0.61	Down
hypothetical LOC523257	*LOC523257*	523257	---	3.63E-06	0.61	Down
synaptogyrin 3	*SYNGR3*	618415	---	0.000865	0.61	Down
transcription elongation factor A (SII), 2	*TCEA2*	507729	0006350 // transcription // inferred	1.40E-06	0.61	Down

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			from electronic annotation /// 0006354 // RNA elongation // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006357 // regulation			
Neurotrophic tyrosine kinase, receptor, type 2	*NTRK2*	505824	---	1.02E-06	0.61	Down
similar to High-mobility group box 3	*LOC532409*	532409	---	4.21E-05	0.61	Down
similar to Chromosome 17 open reading frame 75	*LOC506032*	506032	---	2.18E-05	0.61	Down
CWF19-like 1, cell cycle control (S. pombe)	*CWF19L1*	506212	---	4.88E-07	0.61	Down
coiled-coil domain containing 23	*CCDC23*	614073	---	1.35E-09	0.61	Down
similar to mineralocorticoid receptor	*LOC613833*	613833	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	6.19E-05	0.61	Down
Neurotrophic tyrosine kinase, receptor, type 2	*NTRK2*	505824	---	2.64E-05	0.61	Down
melanoma cell adhesion molecule	*MCAM*	281301	---	0.003342	0.61	Down
Solute carrier family 7, member 6	*SLC7A6OS*	512543	---	0.000453	0.61	Down

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opposite strand						
myosin light chain kinase	*MYLK*	338037	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	9.32E-05	0.61	Down
adenylate kinase 1	*AK1*	280715	0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolic process // inferred from electronic annotation /// 0046034 // ATP metabolic process // inferred from electronic annotation	4.88E-07	0.61	Down
LIM domain binding 1	*LDB1*	526472	0007275 // multicellular organismal development // inferred from electronic annotation	4.18E-08	0.61	Down
similar to dynein cytoplasmic heavy chain 2	*LOC512287*	512287	0007018 // microtubule-based movement // inferred from electronic annotation	0.000145	0.61	Down
anthrax toxin receptor 2	*ANTXR2*	510080	---	0.000839	0.61	Down
sal-like 2 (Drosophila)	*SALL2*	527574	---	0.000289	0.61	Down
dimethylglycine dehydrogenase	*DMGDH*	504453	---	0.000184	0.61	Down
importin 11	*IPO11*	538236	---	1.67E-06	0.61	Down
Kruppel-like factor 11	*KLF11*	616730	---	0.000294	0.61	Down
serpin peptidase inhibitor, clade A (alpha-	*SERPINA5*	338050	0007283 // spermatogenesis //	0.007589	0.62	Down

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1 antiproteinase, antitrypsin), member 5			inferred from electronic annotation			
solute carrier family 6 (neurotransmitter transporter, creatine), member 8	*SLC6A8*	282367	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation /// 0006836 // neurotransmitter transport // inferre	2.92E-06	0.62	Down
potassium large conductance calcium-activated channel, subfamily M, beta member 4	*KCNMB4*	520448	0006813 // potassium ion transport // inferred from electronic annotation	0.002327	0.62	Down
similar to SLIT3	*LOC615883*	615883	0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	0.000389	0.62	Down
cytochrome P450, family 2, subfamily U, polypeptide 1	*CYP2U1*	535227	0055114 // oxidation reduction // inferred from electronic annotation	2.65E-07	0.62	Down
hypothetical protein LOC790454	*LOC790454*	790454	---	0.000419	0.62	Down
G protein-coupled receptor 116	*GPR116*	532674	0007218 // neuropeptide signaling pathway // inferred from electronic annotation /// 0007601 // visual perception // inferred from electronic annotation	3.05E-05	0.62	Down
CXXC finger 5	*CXXC5*	538485	---	1.23E-05	0.62	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
phosphoinositide-3-kinase interacting protein 1	*PIK3IP1*	512082	---	1.32E-05	0.62	Down
similar to protocadherin gamma B6 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily C, 3	*LOC510849 /// PCDHGA8 /// PCDHGB4 /// PCDHGC3*	100125301 /// 510849 /// 521340 /// 532241	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion // inferred from electronic annotation	5.69E-08	0.62	Down
PRA1 domain family, member 2	*PRAF2*	508703	0006810 // transport // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation	1.00E-08	0.62	Down
Zinc finger protein 608	*ZNF608*	509992	---	5.58E-06	0.62	Down
similar to MEGF8	*LOC615688*	615688	---	6.44E-08	0.62	Down
endothelin receptor type A	*EDNRA*	281749	0001569 // patterning of blood vessels // inferred from electronic annotation /// 0001666 // response to hypoxia // inferred from electronic annotation /// 0001701 // in utero embryonic development // inferred from electronic annotation /// 0007165 // sig	0.000912	0.62	Down
tribbles homolog 2 (Drosophila)	*TRIB2*	352960	0006468 // protein amino acid phosphorylation // inferred from	0.000535	0.62	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			sequence or structural similarity /// 0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0043405 // regulation of MAP kinase activity // inferred from seq			
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	*PLOD2*	533642	0019538 // protein metabolic process // inferred from electronic annotation	5.99E-05	0.62	Down
tropomyosin 2 (beta)	*TPM2*	497015	---	0.000128	0.62	Down
RAB34, member RAS oncogene family	*RAB34*	282028	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	1.10E-08	0.62	Down
syntaxin 10	*STX10*	525379	0006886 // intracellular protein transport // inferred from electronic annotation /// 0048193 // Golgi vesicle transport // inferred from electronic annotation	0.000158	0.62	Down
FYN oncogene related to SRC, FGR, YES	*FYN*	527263	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation	3.02E-06	0.62	Down
hypothetical LOC504970	*LOC504970*	504970	---	0.009259	0.62	Down
TGF beta-inducible nuclear protein 1 (L-	*TINP1*	522309	0006364 // rRNA processing // inferred from electronic annotation ///	3.73E-07	0.63	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
name related LNR42)			0042254 // ribosome biogenesis and assembly // inferred from electronic annotation			
myozenin 1	*MYOZ1*	281939	---	0.000712	0.63	Down
similar to RAD21-like 1 (S. pombe)	*LOC512408*	512408	---	1.81E-07	0.63	Down
hypothetical protein FLJ14213	*FLJ14213*	505048	---	0.005893	0.63	Down
Inositol polyphosphate-5-phosphatase, 40kDa	*INPP5A*	615232	---	3.98E-08	0.63	Down
damage-specific DNA binding protein 2, 48kDa	*DDB2*	519357	---	3.84E-07	0.63	Down
tubulin tyrosine ligase-like family, member 3	*TTLL3*	531866	0006464 // protein modification process // inferred from electronic annotation /// 0030041 // actin filament polymerization // inferred from electronic annotation	2.36E-07	0.63	Down
transient receptor potential cation channel, subfamily V, member 2	*TRPV2*	507664	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation	0.001838	0.63	Down
ligand dependent nuclear receptor corepressor	*LCOR*	507668	---	2.49E-07	0.63	Down
odd-skipped related 2 (Drosophila)	*OSR2*	508692	0008284 // positive regulation of cell proliferation // inferred from	9.21E-08	0.63	Down

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			electronic annotation /// 0048704 // embryonic skeletal morphogenesis // inferred from electronic annotation			
Rho GTPase activating protein 24	*ARHGAP24*	539902	0007165 // signal transduction // inferred from electronic annotation	0.00511	0.63	Down
tetraspanin 6	*TSPAN6*	514741	---	7.24E-08	0.63	Down
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	*ANP32A*	538427	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006913 // nucleocytoplasmic transport // inferred from sequence or structural similarity	3.71E-09	0.63	Down
StAR-related lipid transfer (START) domain containing 10	*STARD10*	514624	---	0.007221	0.63	Down
dual specificity phosphatase 7	*DUSP7*	785016	0006470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 0016311 // dephosphorylation // inferred from electronic annotation	1.21E-05	0.63	Down
kelch-like 8 (Drosophila)	*KLHL8*	532960	---	0.000186	0.63	Down
uveal autoantigen with coiled-coil domains and ankyrin repeats	*UACA*	281559	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0008630 // DNA damage response, signal	4.15E-08	0.63	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			transduction resulting in induction of apoptosis // inferred from electronic annotation /// 0008631 // induction of apo			
GDP-mannose 4,6-dehydratase	*GMDS*	617688	0008152 // metabolic process // inferred from electronic annotation /// 0019673 // GDP-mannose metabolic process // inferred from electronic annotation /// 0044237 // cellular metabolic process // inferred from electronic annotation	0.000953	0.63	Down
prenylcysteine oxidase 1	*PCYOX1*	100125835	0008152 // metabolic process // inferred from electronic annotation	5.95E-08	0.63	Down
TYRO3 protein tyrosine kinase	*TYRO3*	788224	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.000108	0.63	Down
pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	*PLEKHH3*	541100	0005975 // carbohydrate metabolic process // inferred from electronic annotation	1.86E-06	0.63	Down
transmembrane protein 98	*TMEM98*	513445	---	6.16E-05	0.63	Down
myeloid leukemia factor 1	*MLF1*	533379	0002318 // myeloid progenitor cell differentiation // inferred from sequence or structural similarity /// 0002318 // myeloid progenitor cell differentiation // inferred from electronic annotation /// 0006350 //	0.008448	0.63	Down

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			transcription // inferred from sequence or s			
sulfite oxidase	*SUOX*	509837	0055114 // oxidation reduction // inferred from electronic annotation	1.22E-09	0.63	Down
limb bud and heart development homolog (mouse)	*LBH*	616148	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation	0.000835	0.63	Down
lysyl oxidase-like 1	*LOXL1*	281903	---	1.52E-05	0.63	Down
coiled-coil domain containing 138	*CCDC138*	507644	---	1.30E-07	0.63	Down
Notch homolog 4 (Drosophila)	*NOTCH4*	537814	---	1.06E-06	0.63	Down
serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	*SERPINE2*	282521	0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	1.48E-06	0.63	Down
collagen, type I, alpha 2	*COL1A2*	282188	0006817 // phosphate transport // inferred from electronic annotation	1.51E-06	0.63	Down
hypothetical protein LOC515282	*CXorf45*	515282	---	5.49E-05	0.63	Down
similar to OB-cadherin-1 /// cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11 /// LOC535363*	535363 /// 785475	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion	3.69E-05	0.63	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			// inferred from electronic annotation			
phospholipid transfer protein	*PLTP*	505640	---	0.000303	0.63	Down
TBC1 domain family, member 24	*TBC1D24*	529002	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation	6.90E-08	0.63	Down
Eukaryotic translation initiation factor 2-alpha kinase 2	*EIF2AK2*	347700	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	4.52E-05	0.64	Down
similar to Pur-gamma B-form	*LOC512941*	512941	---	1.70E-06	0.64	Down
MACRO domain containing 1	*MACROD1*	613568	---	0.006848	0.64	Down
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	*MLLT3*	521962	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	4.47E-06	0.64	Down
RAB30, member RAS oncogene family	*RAB30*	540583	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation	3.82E-07	0.64	Down
similar to tigger transposable element derived 5	*LOC540422*	540422	---	3.44E-07	0.64	Down
CXXC finger 5	*CXXC5*	538485	---	1.08E-06	0.64	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
syntaxin 10	*STX10*	525379	0006886 // intracellular protein transport // inferred from electronic annotation /// 0048193 // Golgi vesicle transport // inferred from electronic annotation	1.72E-08	0.64	Down
WD repeat domain 51B	*WDR51B*	525136	---	1.74E-09	0.64	Down
Heparan sulfate proteoglycan 2	*HSPG2*	444872	0007155 // cell adhesion // inferred from electronic annotation	1.08E-05	0.64	Down
fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	*FGFR2*	404193	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.001821	0.64	Down
armadillo repeat containing, X-linked 6	*ARMCX6*	768308	---	4.99E-05	0.64	Down
trinucleotide repeat containing 6C	*TNRC6C*	504217	---	6.95E-07	0.64	Down
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	*GNAI1*	281790	0007165 // signal transduction // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	2.65E-07	0.64	Down
roundabout, axon guidance receptor, homolog 1 (Drosophila)	*ROBO1*	536815	---	0.001495	0.64	Down
ribonuclease H2, subunit C	*RNASEH2C*	505618	---	5.18E-07	0.64	Down

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cysteine and glycine-rich protein 1	*CSRP1*	615329	---	1.21E-05	0.64	Down
ELK3, ETS-domain protein (SRF accessory protein 2)	*ELK3*	541125	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	7.52E-05	0.64	Down
Regulator of G-protein signaling 5	*RGS5*	540509	0009968 // negative regulation of signal transduction // inferred from electronic annotation	0.00198	0.64	Down
similar to KIAA2038 protein	*LOC783429*	783429	---	0.000171	0.64	Down
hypothetical LOC517668	*LOC517668*	517668	---	1.71E-05	0.64	Down
LATS, large tumor suppressor, homolog 2 (Drosophila)	*LATS2*	508208	---	0.0047	0.64	Down
Meis homeobox 1	*MEIS1*	613877	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation	2.98E-07	0.64	Down
similar to OTTHUMP00000022229	*LOC616324*	616324	---	7.06E-11	0.64	Down
cytochrome P450, family 20, subfamily A, polypeptide 1	*CYP20A1*	532945	0055114 // oxidation reduction // inferred from electronic annotation	2.56E-05	0.64	Down
endomucin	*EMCN*	616367	---	5.71E-05	0.64	Down

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phosphatase, orphan 2	*PHOSPHO 2*	507308	0008152 // metabolic process // inferred from electronic annotation	6.98E-08	0.64	Down
Chromosome 1 open reading frame 21 ortholog	*H16C1ORF 21*	781721	---	2.67E-05	0.64	Down
natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	*NPR2*	281357	0006182 // cGMP biosynthetic process // inferred from electronic annotation /// 0006182 // cGMP biosynthetic process // inferred from sequence or structural similarity /// 0006468 // protein amino acid phosphorylation // inferred from electronic annotatio	6.28E-05	0.64	Down
TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	*TEK*	280939	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007160 // cell-matrix adhesion // inferred from electronic annotation /// 0016337 // cell-cell adhesion // inferred from electronic annotation /// 0030334 // regulat	0.000141	0.64	Down
monocyte to macrophage differentiation-associated	*MMD*	513155	0019835 // cytolysis // inferred from electronic annotation	1.24E-05	0.64	Down
armadillo repeat containing, X-linked 1	*ARMCX1*	504577	---	0.000288	0.64	Down
transcription factor 4	*TCF4*	534935	0045449 // regulation of transcription // inferred from electronic annotation	6.46E-06	0.64	Down

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C-type lectin domain family 14, member A	*CLEC14A*	509367	---	9.21E-07	0.64	Down
Small EDRK-rich factor 2	*SERF2*	527852	---	1.10E-07	0.64	Down
transmembrane protein 119	*TMEM119*	510926	---	2.27E-06	0.65	Down
mannose receptor, C type 2	*MRC2*	529049	---	1.56E-06	0.65	Down
galactose-1-phosphate uridylyltransferase	*GALT*	506997	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006012 // galactose metabolic process // inferred from electronic annotation	3.86E-07	0.65	Down
Doublecortin-like kinase 1	*DCLK1*	613449	0007242 // intracellular signaling cascade // inferred from electronic annotation	1.92E-05	0.65	Down
S-adenosylhomocysteine hydrolase-like 2	*AHCYL2*	532836	0006730 // one-carbon compound metabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	1.62E-05	0.65	Down
EGF-like, fibronectin type III and laminin G domains	*EGFLAM*	534427	---	0.000104	0.65	Down
hypothetical protein LOC788023	*LOC788023*	788023	---	5.84E-07	0.65	Down
casein kinase I beta	*CSNK1B*	785423	0006468 // protein amino acid	0.000153	0.65	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			phosphorylation // inferred from electronic annotation /// 0016055 // Wnt receptor signaling pathway // inferred from electronic annotation			
Aspartate beta-hydroxylase	*ASPH*	286771	0018193 // peptidyl-amino acid modification // inferred from electronic annotation	5.27E-06	0.65	Down
TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	*TAF7*	509327	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation	1.51E-08	0.65	Down
junctional adhesion molecule 2	*JAM2*	538846	---	3.60E-06	0.65	Down
Tubulin, beta	*TUBB*	615087	0007017 // microtubule-based process // inferred from electronic annotation /// 0007018 // microtubule-based movement // inferred from electronic annotation /// 0051258 // protein polymerization // inferred from electronic annotation	2.48E-05	0.65	Down
coenzyme Q10 homolog A (S. cerevisiae)	*COQ10A*	538821	---	0.000449	0.65	Down
DAZ interacting protein 3, zinc finger	*DZIP3*	537349	---	0.00017	0.65	Down
similar to DEAD/H (Asp-Glu-Ala-	*LOC54031*	540312	---	0.000594	0.65	Down

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
Asp/His) box polypeptide 26B	*2*					
outer dense fiber of sperm tails 2-like	*ODF2L*	533508	---	0.001921	0.65	Down
transmembrane protein 117	*TMEM117*	614719	---	3.15E-05	0.65	Down
chondroitin polymerizing factor	*CHPF*	540002	---	3.66E-06	0.65	Down
Coenzyme Q10 homolog A (S. cerevisiae)	*COQ10A*	538821	---	1.14E-05	0.65	Down
coiled-coil domain containing 85B	*CCDC85B*	540332	---	0.000268	0.65	Down
Low density lipoprotein receptor-related protein 4	*LRP4*	504317	---	3.65E-05	0.65	Down
RALBP1 associated Eps domain containing 2	*REPS2*	526887	---	0.000478	0.65	Down
hypothetical LOC613826	*LOC613826*	613826	---	1.52E-06	0.65	Down
MACRO domain containing 1	*MACROD1*	613568	---	0.000157	0.65	Down
insulin-like growth factor binding protein 7	*IGFBP7*	616368	0001558 // regulation of cell growth // inferred from electronic annotation	8.38E-08	0.65	Down
hypothetical protein LOC785375	*LOC785375*	785375	---	5.03E-06	0.65	Down
similar to NAC-beta splice /// NLR family, pyrin domain containing 1	*LOC528166 /// NLRP1*	528166 /// 790698	0006952 // defense response // inferred from electronic annotation	2.91E-07	0.65	Down

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similar to HOXB8	*LOC785855*	785855	---	0.000808	0.65	Down
four and a half LIM domains 1	*FHL1*	509056	---	6.90E-07	0.65	Down
Calcium/calmodulin-dependent protein kinase II inhibitor 1	*CAMK2N1*	616227	---	0.000312	0.65	Down
cysteine-rich secretory protein LCCL domain containing 2 /// translocase of inner mitochondrial membrane 13 homolog (yeast)	*CRISPLD2 /// TIMM13*	505329 /// 516325	0006626 // protein targeting to mitochondrion // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation /// 0045039 // protein import into	1.38E-06	0.65	Down
zinc finger protein 532	*ZNF532*	533847	---	8.23E-07	0.65	Down
damage-specific DNA binding protein 1, 127kDa	*DDB1*	511951	0006512 // ubiquitin cycle // inferred from electronic annotation	1.13E-06	0.65	Down
melanoma antigen family D, 1	*MGC128691*	512562	---	3.09E-07	0.65	Down
microfibrillar-associated protein 2	*MFAP2*	281912	---	0.000216	0.65	Down
spondin 2, extracellular matrix protein	*SPON2*	513844	0007155 // cell adhesion // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation	0.000186	0.65	Down

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
protein tyrosine phosphatase, receptor type, S	*PTPRS*	537480	---	2.36E-05	0.65	Down
transmembrane protein 135	*TMEM135*	523885	---	1.74E-08	0.66	Down
breast cancer metastasis-suppressor 1-like	*BRMS1L*	514432	0001558 // regulation of cell growth // inferred from electronic annotation /// 0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	1.14E-05	0.66	Down
eukaryotic translation initiation factor 2C, 1	*EIF2C1*	522972	---	4.65E-10	0.66	Down
uracil-DNA glycosylase	*UNG*	511381	0006281 // DNA repair // inferred from electronic annotation /// 0006284 // base-excision repair // inferred from electronic annotation /// 0006974 // response to DNA damage stimulus // inferred from electronic annotation /// 0008152 // metabolic process	0.000251	0.66	Down
gamma-glutamyltransferase 1 /// gamma-glutamyltransferase 5	*GGT1 /// GGT5*	615582 /// 787326	---	4.11E-05	0.66	Down
small EDRK-rich factor 2	*SERF2*	527852	---	8.63E-08	0.66	Down
tetraspanin 6	*TSPAN6*	514741	---	2.62E-08	0.66	Down

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hypothetical LOC617871	*LOC617871*	617871	---	0.0005	0.66	Down
spondin 1, extracellular matrix protein	*SPON1*	282866	0007155 // cell adhesion // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation	0.000214	0.66	Down
DNA-damage-inducible transcript 4-like	*DDIT4L*	510906	0009968 // negative regulation of signal transduction // inferred from electronic annotation	0.00851	0.66	Down
Stabilin 1	*STAB1*	505543	0007155 // cell adhesion // inferred from electronic annotation	0.000641	0.66	Down
similar to versican V0 splice-variant	*LOC786374*	786374	---	0.000578	0.66	Down
Tctex1 domain containing 2	*TCTEX1D2*	504554	---	0.001556	0.66	Down
protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	*PPP3CA*	286852	0000082 // G1/S transition of mitotic cell cycle // inferred from electronic annotation /// 0006606 // protein import into nucleus // inferred from electronic annotation /// 0006816 // calcium ion transport // inferred from electronic annotation /// 00069	1.76E-10	0.66	Down
kelch-like 10 (Drosophila)	*KLHL10*	541263	---	1.26E-05	0.66	Down
secreted frizzled-related protein 2	*SFRP2*	510821	0007275 // multicellular organismal	0.000376	0.66	Down

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			development // inferred from electronic annotation /// 0016055 // Wnt receptor signaling pathway // inferred from electronic annotation			
anthrax toxin receptor 2	*ANTXR2*	510080	---	0.006699	0.66	Down
hypothetical LOC614402	*LOC614402*	614402	---	0.000185	0.66	Down
DTW domain containing 1	*DTWD1*	540840	---	9.56E-09	0.66	Down
Development and differentiation enhancing factor-like 1	*DDEFL1*	523797	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0019752 // carboxylic acid metabolic process // inferred from electronic annotation /// 0032312 // regulation of ARF GTPase activity // inferred from electronic annotatio	7.15E-07	0.66	Down
matrix metallopeptidase 11 (stromelysin 3)	*MMP11*	539109	0006508 // proteolysis // inferred from electronic annotation	0.00037	0.66	Down
chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	*CABC1*	536925	---	1.32E-06	0.66	Down
ephrin-A2	*EFNA2*	614453	---	0.000273	0.66	Down
PDZ and LIM domain 4	*PDLIM4*	515410	---	9.91E-11	0.66	Down
GRP1 (general receptor for phosphoinositides 1)-associated scaffold	*GRASP*	507181	---	0.000192	0.66	Down

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protein						
fumarylacetoacetate hydrolase (fumarylacetoacetase)	*FAH*	508724	0006559 // L-phenylalanine catabolic process // inferred from electronic annotation /// 0006572 // tyrosine catabolic process // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation /// 0009072 // aro	0.003537	0.66	Down
EGF-like-domain, multiple 7	*EGFL7*	613671	---	0.000111	0.66	Down
Membrane-associated ring finger (C3HC4) 6	*MAR6*	540371	---	4.81E-10	0.66	Down
SUMO1/sentrin specific peptidase 6	*SENP6*	533853	---	8.82E-05	0.66	Down
collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	*COL3A1*	510833	0006817 // phosphate transport // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	6.87E-08	0.66	Down
Melanoma associated antigen (mutated) 1	*MUM1*	513471	---	4.57E-06	0.66	Down
Hypothetical protein LOC782307	*LOC782307*	782307	---	8.49E-06	0.66	Down
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	*GALNT1*	282241	0006493 // protein amino acid O-linked glycosylation // inferred from electronic annotation	0.002422	0.66	Down

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(GalNAc-T1)						
cytoplasmic linker associated protein 2	*CLASP2*	531418	---	0.000453	0.66	Down
beta-site APP-cleaving enzyme 1	*BACE1*	614333	0006508 // proteolysis // inferred from electronic annotation	0.006438	0.66	Down
tubulin tyrosine ligase-like family, member 3	*TTLL3*	531866	0006464 // protein modification process // inferred from electronic annotation	2.25E-07	0.66	Down
sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	*SIRT3*	614027	0006342 // chromatin silencing // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006476 // protein amino acid deacetylation // inferred from electronic annotation	8.93E-06	0.66	Down
receptor (G protein-coupled) activity modifying protein 2	*RAMP2*	504230	0006886 // intracellular protein transport // inferred from electronic annotation /// 0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	4.22E-06	0.66	Down
hypothetical LOC533774	*LOC533774*	533774	---	7.58E-08	0.66	Down
prostaglandin E receptor 4 (subtype EP4)	*PTGER4*	282331	0007165 // signal transduction // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway //	0.004571	0.66	Down

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			inferred from electronic annotation			
metastasis suppressor 1 /// similar to Metastasis suppressor protein 1 (Missing in metastasis protein) (Metastasis suppressor YGL-1)	*LOC788499 /// MTSS1*	523498 /// 788499	---	7.65E-07	0.66	Down
microtubule-associated protein 1A	*MAP1A*	515593	---	0.00084	0.66	Down
solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	*SLC16A3*	510085	---	0.008446	0.66	Down
similar to OB-cadherin-1 /// cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11 /// LOC535363*	535363 /// 785475	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion // inferred from electronic annotation	0.000103	0.66	Down
McKusick-Kaufman syndrome	*MKKS*	614288	0006457 // protein folding // inferred from electronic annotation	5.53E-05	0.66	Down
platelet endothelial aggregation receptor 1	*PEAR1*	787112	---	0.001594	0.66	Down
galactose-1-phosphate uridylyltransferase	*GALT*	506997	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006012 // galactose metabolic process // inferred from electronic annotation	2.75E-07	0.66	Down
serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	*SERPINF1*	281386	0016525 // negative regulation of angiogenesis // inferred from electronic annotation /// 0050769 // positive regulation of neurogenesis // inferred from sequence or structural	2.40E-05	0.66	Down

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			similarity /// 0050769 // positive regulation of neurogenesis // inferred from			
family with sequence similarity 109, member B	*FAM109B*	506148	---	0.000241	0.66	Down
hypothetical LOC529053	*LOC529053*	529053	---	3.37E-05	0.67	Down
matrix-remodelling associated 7	*MXRA7*	617087	---	2.92E-05	0.67	Down
junctional adhesion molecule 2	*JAM2*	538846	---	0.000222	0.67	Down
similar to BCL-6 corepressor	*LOC541088 /// LOC784529*	541088 /// 784529	---	0.000758	0.67	Down
cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	*CDKN2C*	505691	---	0.000214	0.67	Down
Hypothetical protein LOC784805	*LOC784805*	784805	---	3.08E-06	0.67	Down
abhydrolase domain containing 2	*ABHD2*	508717	0009611 // response to wounding // inferred from sequence or structural similarity /// 0030336 // negative regulation of cell migration // inferred from sequence or structural similarity	2.24E-05	2.00	Up
DnaJ (Hsp40) homolog, subfamily A,	*DNAJA1*	528862	0006457 // protein folding // inferred	1.33E-06	2.00	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
member 1			from electronic annotation			
atlastin 3	*ATL3*	515124	0006955 // immune response // inferred from electronic annotation	1.81E-08	2.00	Up
aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	*ALDH5A1*	532724	0008152 // metabolic process // inferred from electronic annotation	0.007179	2.01	Up
Similar to LFA-3	*LOC782186*	782186	---	3.27E-05	2.01	Up
interferon regulatory factor 8	*IRF8*	614909	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	1.47E-06	2.01	Up
chemokine (C-X-C motif) ligand 2	*CXCL2*	281212	0006954 // inflammatory response // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation	0.008841	2.02	Up
Solute carrier family 25, member 30	*SLC25A30*	507021	0006810 // transport // inferred from electronic annotation /// 0006839 // mitochondrial transport // inferred from electronic annotation	1.29E-09	2.02	Up
3'(2'), 5'-bisphosphate nucleotidase 1	*BPNT1*	521254	---	6.94E-10	2.02	Up
Transmembrane protein 53	*TMEM53*	540738	---	2.31E-06	2.02	Up

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DnaJ (Hsp40) homolog, subfamily C, member 1	*DNAJC1*	510387	---	2.19E-11	2.02	Up
valosin containing protein (p97)/p47 complex interacting protein 1	*VCPIP1*	539643	---	5.00E-11	2.02	Up
protein kinase C, delta	*PRKCD*	505708	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007242 // intracellular signaling cascade // inferred from electronic annotation	2.84E-05	2.02	Up
Similar to RAD21-like 1 (S. pombe)	*LOC512408*	512408	---	0.000922	2.03	Up
deoxyribonuclease II, lysosomal	*DNASE2*	282218	0006259 // DNA metabolic process // inferred from electronic annotation /// 0006308 // DNA catabolic process // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0007275 // multicellular organismal dev	1.88E-07	2.04	Up
Vestigial like 1 (Drosophila)	*VGLL1*	613549	0045449 // regulation of transcription // inferred from electronic annotation	0.006553	2.05	Up
Ras association (RalGDS/AF-6) domain family member 1	*RASSF1*	510276	0007165 // signal transduction // inferred from electronic annotation /// 0007242 // intracellular signaling cascade // inferred from electronic annotation	2.54E-10	2.06	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
cadherin 1, type 1, E-cadherin (epithelial)	*CDH1*	282637	0007155 // cell adhesion // inferred from electronic annotation /// 0007156 // homophilic cell adhesion // inferred from electronic annotation /// 0016337 // cell-cell adhesion // inferred from electronic annotation /// 0019538 // protein metabolic proces	0.004911	2.06	Up
serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	*SERPING1*	281035	0007596 // blood coagulation // inferred from electronic annotation	8.30E-06	2.07	Up
adenylate kinase 2	*AK2*	280716	0006139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolic process // inferred from electronic annotation	1.82E-06	2.08	Up
similar to eyes absent 3	*LOC514364*	514364	0007275 // multicellular organismal development // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	1.07E-05	2.08	Up
interferon regulatory factor 6	*IRF6*	614253	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	7.59E-07	2.08	Up
similar to squamous cell-specific protein	*LOC786490*	786490	---	1.23E-06	2.09	Up

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complement factor properdin	*CFP*	539605	---	7.74E-06	2.09	Up
Nicotinamide phosphoribosyltransferase	*NAMPT*	520472	---	1.58E-07	2.09	Up
eukaryotic translation termination factor 1	*ETF1*	541077	0006412 // translation // inferred from electronic annotation /// 0006415 // translational termination // inferred from electronic annotation	4.93E-07	2.10	Up
brain abundant, membrane attached signal protein 1	*BASP1*	286842	---	8.74E-07	2.10	Up
Tripartite motif-containing 25	*TRIM25*	510923	---	0.000205	2.10	Up
arrestin, beta 1	*ARRB1*	281637	0007165 // signal transduction // inferred from electronic annotation /// 0007600 // sensory perception // inferred from electronic annotation /// 0050896 // response to stimulus // inferred from electronic annotation	3.09E-07	2.10	Up
MIT, microtubule interacting and transport, domain containing 1	*MITD1*	504291	---	1.97E-07	2.10	Up
Hypothetical LOC511953	*LOC511953*	511953	---	3.54E-06	2.10	Up
ubiquitin D	*UBD*	504548	0006464 // protein modification process // inferred from electronic annotation	0.008696	2.11	Up
Hypothetical LOC533333	*MGC13910*	533333	---	3.33E-06	2.11	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
	9					
FYVE, RhoGEF and PH domain containing 2	*FGD2*	512593	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation	1.67E-06	2.11	Up
protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma	*PPP2R3C*	533147	---	1.47E-08	2.12	Up
serine/threonine kinase 17a	*STK17A*	513665	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	3.43E-05	2.12	Up
fibromodulin	*FMOD*	281168	---	6.43E-07	2.12	Up
asparagine-linked glycosylation 14 homolog	*ALG14*	506537	---	3.69E-06	2.13	Up
apoptosis-inducing factor, mitochondrion-associated, 1	*AIFM1*	535714	0045454 // cell redox homeostasis // inferred from electronic annotation	5.20E-11	2.13	Up
interferon regulatory factor 6	*IRF6*	614253	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	3.12E-06	2.13	Up
DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	*DIMT1L*	509725	0000154 // rRNA modification // inferred from electronic annotation /// 0006364 // rRNA processing // inferred from electronic annotation	5.85E-07	2.13	Up

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growth arrest and DNA-damage-inducible, beta	*GADD45B*	618405	0000186 // activation of MAPKK activity // inferred from electronic annotation /// 0006469 // negative regulation of protein kinase activity // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0007275	3.31E-09	2.14	Up
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	*ABCC3*	533151	0006810 // transport // inferred from electronic annotation	4.62E-09	2.14	Up
sestrin 2	*SESN2*	509863	0007050 // cell cycle arrest // inferred from electronic annotation	4.76E-09	2.14	Up
tripartite motif-containing 38	*TRIM38*	531022	0016567 // protein ubiquitination // inferred from electronic annotation	1.68E-12	2.14	Up
Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	*CASP1*	514214	0006508 // proteolysis // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0042981 // regulation of apoptosis // inferred from electronic annotation	8.26E-06	2.15	Up
signal-regulatory protein alpha /// similar to MyD-1 antigen	*LOC782991 /// SIRPA*	327666 /// 782991	---	5.37E-06	2.15	Up
chromosome 3 open reading frame 38 ortholog	*C1H3ORF38*	511707	0006508 // proteolysis // inferred from electronic annotation	1.22E-12	2.15	Up
DEAD (Asp-Glu-Ala-As) box polypeptide	*DDX19B*	517438	---	6.31E-08	2.16	Up

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19B						
interferon induced transmembrane protein 3 (1-8U)	*IFITM3*	282255	0009607 // response to biotic stimulus // inferred from electronic annotation	5.62E-11	2.16	Up
major histocompatibility complex, class II, DM beta-chain, expressed	*BOLA-DMB*	282491	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and present	1.72E-08	2.17	Up
transmembrane protein 79	*TMEM79*	513599	---	3.46E-06	2.17	Up
nuclear receptor subfamily 4, group A, member 1	*NR4A1*	528390	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	0.000153	2.18	Up
karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	*KPNA2*	513592	0006606 // protein import into nucleus // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation	8.54E-08	2.18	Up
hematopoietic cell-specific Lyn substrate 1	*HCLS1*	508445	0008284 // positive regulation of cell proliferation // inferred from sequence or structural similarity /// 0009725 // response to hormone stimulus //	0.00023	2.19	Up

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			inferred from sequence or structural similarity /// 0030218 // erythrocyte differentiation // inferred f			
hexosaminidase B (beta polypeptide)	*HEXB*	618571	0005975 // carbohydrate metabolic process // inferred from electronic annotation	2.31E-05	2.20	Up
adipose differentiation-related protein	*ADFP*	280981	---	1.36E-06	2.20	Up
C-type lectin domain family 2, member D	*CLEC2D*	617565	---	1.53E-05	2.20	Up
sestrin 2	*SESN2*	509863	0007050 // cell cycle arrest // inferred from electronic annotation	2.95E-12	2.21	Up
Synaptotagmin-like 3	*SYTL3*	506884	---	0.003314	2.21	Up
StAR-related lipid transfer (START) domain containing 5	*STARD5*	512369	0006810 // transport // inferred from electronic annotation /// 0006869 // lipid transport // inferred from electronic annotation	2.46E-09	2.21	Up
megakaryocyte-associated tyrosine kinase	*MATK*	504668	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	0.000441	2.21	Up
ADP-ribosylation factor 3	*ARF3*	510994	0006810 // transport // inferred from electronic annotation /// 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0015031 // protein transport // inferred from electronic annotation /// 0016192 //	3.08E-11	2.21	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			vesicle-medi			
hematopoietic cell-specific Lyn substrate 1	*HCLS1*	508445	0008284 // positive regulation of cell proliferation // inferred from sequence or structural similarity /// 0009725 // response to hormone stimulus // inferred from sequence or structural similarity /// 0030218 // erythrocyte differentiation // inferred f	0.000384	2.21	Up
proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	*PSMB9*	510593	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation	6.14E-10	2.22	Up
Collagen, type XVIII, alpha 1	*COL18A1*	508076	0006817 // phosphate transport // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation	3.68E-08	2.22	Up
plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	*PKP1*	281405	0007155 // cell adhesion // inferred from electronic annotation	3.94E-05	2.22	Up
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	*MTHFD2L*	536269	0008152 // metabolic process // inferred from electronic annotation /// 0009396 // folic acid and derivative biosynthetic process // inferred from electronic annotation	2.21E-06	2.23	Up
RanBP-type and C3HC4-type zinc finger containing 1	*RBCK1*	504400	0006464 // protein modification process // inferred from electronic	3.22E-10	2.24	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			annotation			
claudin 16	*CLDN16*	282184	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0016338 // calcium-independent cell-cell adhesion // inferred from sequence or structural similarity	0.000197	2.24	Up
dihydrolipoamide S-acetyltransferase	*DLAT*	512723	---	1.15E-06	2.24	Up
carbonic anhydrase IV	*CA4*	280741	0006730 // one-carbon compound metabolic process // inferred from electronic annotation	0.000182	2.24	Up
Similar to interleukin 32	*LOC505800*	505800	---	8.95E-05	2.24	Up
Boc homolog (mouse)	*BOC*	512018	---	6.99E-08	2.24	Up
ecotropic viral integration site 2B	*EVI2B*	617442	---	6.70E-06	2.25	Up
prolactin regulatory element binding	*PREB*	525256	---	1.70E-09	2.26	Up
ATPase family, AAA domain containing 1	*ATAD1*	506045	---	1.51E-16	2.26	Up
2',3'-cyclic nucleotide 3' phosphodiesterase	*CNP*	280752	0007409 // axonogenesis // inferred from electronic annotation /// 0008344 // adult locomotory behavior // inferred from electronic annotation /// 0009214 // cyclic nucleotide	9.59E-13	2.27	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			catabolic process // inferred from electronic annotation /// 0016070 // RNA met			
SAR1 gene homolog A (S. cerevisiae)	*SAR1A*	517171	0006810 // transport // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation /// 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0015031 /	9.63E-08	2.29	Up
interleukin 18 binding protein	*IL18BP*	617470	---	2.13E-06	2.29	Up
chromosome 10 open reading frame 10 ortholog	*C28H10ORF10*	613715	---	4.25E-05	2.30	Up
small G protein signaling modulator 3	*SGSM3*	767820	0007049 // cell cycle // inferred from electronic annotation /// 0007050 // cell cycle arrest // inferred from electronic annotation /// 0032313 // regulation of Rab GTPase activity // inferred from electronic annotation /// 0032483 // regulation of Rab p	9.62E-07	2.30	Up
similar to WD repeat domain, phosphoinositide interacting 1	*MGC159964*	528410	---	0.000246	2.30	Up
hypothetical LOC539087	*MGC134419*	539087	---	1.14E-08	2.30	Up
protease, serine, 8	*PRSS8*	613506	0006508 // proteolysis // inferred from	4.47E-07	2.30	Up

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			electronic annotation			
serine/threonine kinase 38 like	*STK38L*	514787	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	1.59E-11	2.30	Up
Mov10, Moloney leukemia virus 10, homolog (mouse)	*MOV10*	523206	---	5.53E-12	2.31	Up
solute carrier family 2 (facilitated glucose transporter), member 1	*SLC2A1*	282356	0006810 // transport // inferred from electronic annotation /// 0008643 // carbohydrate transport // inferred from electronic annotation /// 0015758 // glucose transport // inferred from sequence or structural similarity /// 0046323 // glucose import // t	2.26E-10	2.31	Up
dipeptidyl-peptidase 3	*DPP3*	510200	0006508 // proteolysis // inferred from electronic annotation	8.57E-11	2.31	Up
tumor necrosis factor, alpha-induced protein 6	*TNFAIP6*	493710	0007155 // cell adhesion // inferred from electronic annotation	3.05E-10	2.32	Up
phospholipase A1 member A	*PLA1A*	515900	0006629 // lipid metabolic process // inferred from electronic annotation /// 0016042 // lipid catabolic process // inferred from electronic annotation	4.18E-06	2.33	Up
RAS and EF-hand domain containing	*RASEF*	513223	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 0015031 // protein transport // inferred from	8.47E-05	2.33	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			electronic annotation			
membrane-spanning 4-domains, subfamily A, member 8B	*MS4A8B*	415111	0007165 // signal transduction // inferred from electronic annotation	1.35E-10	2.33	Up
claudin 4	*CLDN4*	414921	0016338 // calcium-independent cell-cell adhesion // inferred from sequence or structural similarity	1.72E-07	2.33	Up
hypothetical protein LOC522909	*LOC522909*	522909	---	1.52E-06	2.33	Up
CDKN2A interacting protein	*CDKN2AIP*	513265	---	2.37E-11	2.34	Up
interferon regulatory factor 3	*IRF3*	516979	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0009615 // response to virus // inferred from electronic annotation /// 0031663 // lipopol	3.64E-11	2.34	Up
selenoprotein T	*SELT*	783831	0045454 // cell redox homeostasis // inferred from electronic annotation	3.46E-08	2.34	Up
cysteine rich transmembrane BMP regulator 1 (chordin-like)	*CRIM1*	506264	0001558 // regulation of cell growth // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation /// 0007339 // binding of sperm to zona pellucida // inferred from electronic	2.62E-05	2.35	Up

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			annotation			
MORC family CW-type zinc finger 3	*MORC3*	513807	---	2.21E-12	2.35	Up
tubulointerstitial nephritis antigen-like 1	*TINAGL1*	509642	0006508 // proteolysis // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	1.82E-05	2.36	Up
hypothetical LOC539299	*LOC539299*	539299	---	3.41E-12	2.36	Up
similar to HEPH	*LOC510736*	510736	---	2.31E-07	2.36	Up
DKFZP564O0823 protein	*DKFZP564O0823*	518368	---	0.007523	2.36	Up
carnitine acetyltransferase	*CRAT*	512902	---	1.01E-08	2.36	Up
allograft inflammatory factor 1	*AIF1*	280989	0051017 // actin filament bundle formation // inferred from electronic annotation	5.05E-09	2.36	Up
syndecan 2	*SDC2*	615785	---	2.68E-05	2.37	Up
ring finger protein 19B	*RNF19B*	509774	---	1.51E-09	2.37	Up
mitochondrial tumor suppressor 1	*MTUS1*	515016	0007049 // cell cycle // inferred from electronic annotation	1.76E-05	2.37	Up
similar to FLJ11171 protein	*LOC78191*	781914	---	6.49E-07	2.38	Up

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	4					
HIG1 domain family, member 1A	*HIGD1A*	768057	---	3.21E-10	2.38	Up
similar to C-type lectin domain family 2, member h	*LOC504309*	504309	---	2.14E-12	2.38	Up
annexin A1	*ANXA1*	327662	0007049 // cell cycle // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation /// 0018149 // peptide cross-linking // inferred from electronic annotation /// 0030216 // keratinocyte differentiation	3.97E-15	2.38	Up
nuclear protein 1	*NUPR1*	614673	---	6.89E-07	2.39	Up
similar to Signal peptide peptidase-like 2A	*LOC530325*	530325	---	8.19E-12	2.39	Up
hypothetical LOC508353	*LOC508353*	508353	---	5.69E-05	2.40	Up
Mucin 13, cell surface associated	*MUC13*	511430	---	7.32E-08	2.41	Up
complement component 1, q subcomponent, A chain	*C1QA*	534961	0006817 // phosphate transport // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0006958 // complement activation, classical pathway // inferred from electronic annotation /// 0045087 //	7.57E-08	2.41	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			innat			
BCL2-like 1	*BCL2L1*	282152	0006915 // apoptosis // inferred from electronic annotation /// 0042981 // regulation of apoptosis // inferred from electronic annotation	4.80E-07	2.41	Up
tyrosyl-tRNA synthetase	*YARS*	281581	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006437 // tyrosyl-tRNA aminoacylation // inferred from electronic annotation	1.08E-06	2.41	Up
general transcription factor IIB /// similar to general transciption factor TfIIB	*GTF2B /// LOC786656*	513231 /// 786656	0006350 // transcription // inferred from electronic annotation /// 0006352 // transcription initiation // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006413 //	5.98E-12	2.42	Up
macrophage scavenger receptor 1	*MSR1*	281311	0006817 // phosphate transport // inferred from electronic annotation /// 0006897 // endocytosis // inferred from electronic annotation /// 0006898 // receptor-mediated endocytosis // inferred from electronic annotation	4.56E-07	2.42	Up
similar to C-type lectin domain family 2,	*LOC50430*	504309	---	8.26E-13	2.42	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
member h	*9*					
2,4-dienoyl CoA reductase 2, peroxisomal	*DECR2*	768256	0008152 // metabolic process // inferred from electronic annotation /// 0009239 // enterobactin biosynthetic process // inferred from electronic annotation	6.97E-08	2.42	Up
solute carrier family 27 (fatty acid transporter), member 5	*SLC27A5*	533016	0008152 // metabolic process // inferred from electronic annotation	2.64E-07	2.43	Up
death-associated protein 6	*DAXX*	504336	---	1.11E-10	2.44	Up
transmembrane 4 L six family member 1	*TM4SF1*	533038	---	3.91E-09	2.44	Up
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	*FCER1G*	282226	0001798 // positive regulation of type IIa hypersensitivity // inferred from electronic annotation /// 0001805 // positive regulation of type III hypersensitivity // inferred from electronic annotation /// 0001812 // positive regulation of type I hypersen	1.64E-10	2.46	Up
glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	*GRINA*	510225	---	2.28E-10	2.46	Up
acyl-CoA synthetase short-chain family member 2	*ACSS2*	506459	0008152 // metabolic process // inferred from electronic annotation	5.90E-07	2.46	Up
ubiquitin specific peptidase 25	*USP25*	524531	0006511 // ubiquitin-dependent protein catabolic process // inferred	1.89E-11	2.46	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			from electronic annotation			
PAP associated domain containing 4	*PAPD4*	533862	---	1.12E-11	2.47	Up
interleukin 20 receptor beta	*IL20RB*	534581	---	0.001878	2.48	Up
lysophospholipase I	*LYPLA1*	539992	0006629 // lipid metabolic process // inferred from electronic annotation /// 0006631 // fatty acid metabolic process // inferred from electronic annotation	1.66E-05	2.49	Up
transmembrane protein 106A	*TMEM106A*	508269	---	2.15E-09	2.49	Up
Intercellular adhesion molecule 2	*ICAM2*	506088	0016337 // cell-cell adhesion // inferred from electronic annotation	3.76E-05	2.49	Up
sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	*SOAT1*	504287	---	6.40E-07	2.50	Up
Similar to Probable phospholipid-transporting ATPase VA (P-locus fat-associated ATPase)	*LOC510723*	510723	---	2.37E-07	2.50	Up
Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	*FCGR3A*	281766	---	4.17E-10	2.50	Up
phospholipase D1, phosphatidylcholine-specific	*PLD1*	514554	0007154 // cell communication // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation	4.32E-07	2.51	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
survival motor neuron	*SMN*	281492	0000245 // spliceosome assembly // inferred from electronic annotation /// 0006397 // mRNA processing // inferred from electronic annotation	4.29E-08	2.51	Up
RNA binding motif protein 43	*RBM43*	617625	---	5.77E-10	2.51	Up
Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	*NFATC1*	511224	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	3.24E-07	2.52	Up
WD repeat domain 16	*WDR16*	505885	---	0.000231	2.52	Up
selectin L (lymphocyte adhesion molecule 1)	*SELL*	281485	0007155 // cell adhesion // inferred from electronic annotation /// 0007155 // cell adhesion // non-traceable author statement	1.04E-09	2.53	Up
MAD2 mitotic arrest deficient-like 2 (yeast)	*MAD2L2*	506605	0007067 // mitosis // inferred from electronic annotation	8.49E-14	2.55	Up
Transmembrane protein 127	*TMEM127*	513620	---	0.000548	2.56	Up
CD53 molecule	*CD53*	505040	---	5.13E-09	2.58	Up
regakine 1	*LOC504773*	504773	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // inflammatory response // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation	1.15E-06	2.58	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
optineurin	*OPTN*	534150	---	3.34E-13	2.58	Up
stefin C	*LOC514170*	514170	---	0.002248	2.60	Up
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	*SLC25A5*	282479	0006810 // transport // inferred from electronic annotation	6.14E-09	2.60	Up
peroxidasin homolog (Drosophila)	*PXDN*	515860	0006979 // response to oxidative stress // inferred from electronic annotation	2.56E-06	2.60	Up
agrin	*AGRN*	525795	0007213 // acetylcholine receptor signaling, muscarinic pathway // inferred from electronic annotation /// 0008033 // tRNA processing // inferred from electronic annotation /// 0043113 // receptor clustering // inferred from electronic annotation	2.35E-13	2.61	Up
similar to Chromosome 9 open reading frame 61	*LOC509420*	509420	---	1.14E-07	2.61	Up
nucleoporin 93kDa	*NUP93*	510004	0006810 // transport // inferred from electronic annotation	3.41E-07	2.61	Up
similar to ubiquitin specific proteinase 43	*LOC506996*	506996	---	2.10E-05	2.62	Up
interferon regulatory factor 1	*IRF1*	337917	0006350 // transcription // inferred from electronic annotation ///	1.75E-06	2.62	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0045786 // negative regul			
F-box protein 33	*FBXO33*	539998	---	2.20E-11	2.63	Up
optineurin	*OPTN*	534150	---	6.18E-09	2.64	Up
F-box protein 33	*FBXO33*	539998	---	1.48E-12	2.64	Up
crystallin, mu	*CRYM*	505167	0008152 // metabolic process // inferred from electronic annotation	0.000118	2.64	Up
methionyl-tRNA synthetase 2, mitochondrial	*MARS2*	514726	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006431 // methionyl-tRNA aminoacylation // inferred from electronic annotation	1.24E-07	2.65	Up
transmembrane 4 L six family member 1	*TM4SF1*	533038	---	7.42E-13	2.66	Up
Intercellular adhesion molecule 2	*ICAM2*	506088	0016337 // cell-cell adhesion // inferred from electronic annotation	2.06E-05	2.66	Up
interferon induced transmembrane protein 1 (9-27)	*IFITM1*	353510	0009607 // response to biotic stimulus // inferred from electronic annotation	6.83E-12	2.66	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
creatine kinase, mitochondrial 1 (ubiquitous)	*CKMT1*	281692	---	1.03E-06	2.68	Up
interleukin 1 receptor antagonist	*IL1RN*	281860	0006955 // immune response // inferred from electronic annotation	2.84E-09	2.70	Up
Hypothetical protein LOC509620	*LOC509620*	509620	---	1.55E-10	2.71	Up
interferon regulatory factor 5	*IRF5*	615340	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	3.26E-07	2.71	Up
optineurin	*OPTN*	534150	---	1.06E-07	2.71	Up
survival motor neuron	*SMN*	281492	0000245 // spliceosome assembly // inferred from electronic annotation /// 0006397 // mRNA processing // inferred from electronic annotation	3.20E-08	2.72	Up
ectonucleotide pyrophosphatase/phosphodiesterase 3	*ENPP3*	529405	0008152 // metabolic process // inferred from electronic annotation	0.000464	2.72	Up
MAD2 mitotic arrest deficient-like 2 (yeast)	*MAD2L2*	506605	0007067 // mitosis // inferred from electronic annotation	3.71E-12	2.72	Up
lectin, galactoside-binding, soluble, 3 binding protein	*LGALS3BP*	531137	---	9.05E-13	2.73	Up
glutathione S-transferase M4	*GSTM4*	783879	0008152 // metabolic process //	7.04E-06	2.74	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			inferred from electronic annotation			
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 /// serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11	*SERPINA1 /// SERPINA11*	280699 /// 538280	0009405 // pathogenesis // inferred from electronic annotation	0.000933	2.74	Up
argininosuccinate lyase	*ASL*	512771	0000050 // urea cycle // inferred from electronic annotation /// 0006526 // arginine biosynthetic process // inferred from electronic annotation /// 0008652 // amino acid biosynthetic process // inferred from electronic annotation /// 0042450 // arginine	6.73E-07	2.80	Up
solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	*SLC25A19*	504418	0006810 // transport // inferred from electronic annotation	4.43E-10	2.80	Up
tripartite motif-containing 25	*TRIM25*	510923	---	4.94E-10	2.81	Up
solute carrier family 27 (fatty acid transporter), member 2	*SLC27A2*	535727	0008152 // metabolic process // inferred from electronic annotation	1.29E-06	2.82	Up
tripartite motif-containing 21	*TRIM21*	359715	0016567 // protein ubiquitination // inferred from electronic annotation	1.53E-10	2.82	Up
CASP8 and FADD-like apoptosis regulator	*CFLAR*	497199	0006508 // proteolysis // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0042981 // regulation of apoptosis // inferred from electronic	0.000262	2.82	Up

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			annotation			
oxidative stress induced growth inhibitor 1	*OSGIN1*	768073	---	8.82E-06	2.83	Up
myelin protein zero-like 1	*MPZL1*	539387	---	1.31E-07	2.83	Up
sphingomyelin phosphodiesterase, acid-like 3B	*SMPDL3B*	518699	---	8.05E-07	2.83	Up
tachykinin receptor 3	*TACR3*	404136	0007165 // signal transduction // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	0.000149	2.84	Up
signal transducer and activator of transcription 1, 91kDa	*STAT1*	510814	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation /// 0045449 // regulation of transcription // inferred from electronic annotation	5.29E-14	2.84	Up
similar to glutathione peroxidase 2 /// RAB15, member RAS onocogene family	*LOC533088 /// RAB15*	533088 /// 614507	0006810 // transport // inferred from electronic annotation /// 0006886 // intracellular protein transport // inferred from electronic annotation /// 0006913 // nucleocytoplasmic transport // inferred from electronic annotation /// 0006979 // response to	3.15E-05	2.87	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
transmembrane protein 156	*TMEM156*	533681	---	2.19E-06	2.89	Up
ganglioside induced differentiation associated protein 2	*GDAP2*	508774	---	1.42E-12	2.90	Up
serine palmitoyltransferase, long chain base subunit 2	*SPTLC2*	537972	0009058 // biosynthetic process // inferred from electronic annotation	1.32E-10	2.90	Up
N-myc (and STAT) interactor	*NMI*	511280 /// 784981	---	2.29E-13	2.91	Up
RCD1 required for cell differentiation1 homolog (S. pombe)	*RQCD1*	536537	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	1.65E-08	2.92	Up
solute carrier family 5 (sodium/glucose cotransporter), member 1	*SLC5A1*	282361	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation /// 0006970 // response to osmotic stress // inferre	3.64E-05	2.92	Up
Actin binding LIM protein family, member 3	*ABLIM3*	613794	0007010 // cytoskeleton organization and biogenesis // inferred from electronic annotation	3.51E-07	2.93	Up
complement factor B	*CFB*	514076	0006508 // proteolysis // inferred from electronic annotation /// 0006955 //	7.71E-06	2.94	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			immune response // inferred from electronic annotation /// 0006956 // complement activation // inferred from electronic annotation /// 0006957 // complement activation, alternati			
neural precursor cell expressed, developmentally down-regulated 4-like	*NEDD4L*	510003	0006464 // protein modification process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation	4.67E-12	2.95	Up
similar to aldehyde oxidase 2	*LOC518393*	518393	0006826 // iron ion transport // inferred from electronic annotation /// 0006879 // cellular iron ion homeostasis // inferred from electronic annotation	0.000348	3.00	Up
SERTA domain containing 1	*SERTAD1*	539321	---	1.01E-11	3.01	Up
neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)	*NCF2*	281346	---	2.57E-08	3.02	Up
tryptophanyl-tRNA synthetase	*WARS*	281576	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006436 // tryptophanyl-tRNA aminoacylation // inferred from electronic annotation	7.27E-11	3.03	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
myelin protein zero-like 1	*MPZL1*	539387	---	1.01E-07	3.04	Up
lysozyme 1	*LYZ1*	281287	0008152 // metabolic process // inferred from electronic annotation /// 0016998 // cell wall catabolic process // inferred from electronic annotation /// 0019835 // cytolysis // inferred from electronic annotation /// 0042742 // defense response to bacter	0.002306	3.04	Up
myelin protein zero-like 1	*MPZL1*	539387	---	2.78E-09	3.05	Up
similar to putative polypeptide N-acetylgalactosaminyltransferase	*LOC505622*	505622	---	1.65E-05	3.06	Up
basic leucine zipper and W2 domains 2	*BZW2*	326579	0006446 // regulation of translational initiation // inferred from electronic annotation	3.35E-08	3.06	Up
hypothetical LOC616344	*LOC616344*	616344	---	4.19E-09	3.06	Up
CD40 molecule, TNF receptor superfamily member 5	*CD40*	286849	0002768 // immune response-regulating cell surface receptor signaling pathway // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation ///	4.73E-07	3.08	Up
phosphoenolpyruvate carboxykinase 2	*PCK2*	282856	0006094 // gluconeogenesis //	1.49E-08	3.08	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
(mitochondrial)			inferred from electronic annotation			
lymphocyte antigen 6 complex, locus E	*LY6E*	510977	---	1.02E-12	3.09	Up
solute carrier family 12 (sodium/potassium/chloride transporters), member 2	*SLC12A2*	286845	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation /// 0006821 // chloride transport // inferred from e	8.53E-07	3.09	Up
histone cluster 1, H1c	*HIST1H1C*	513971	0006334 // nucleosome assembly // inferred from electronic annotation	1.82E-06	3.10	Up
aminolevulinate, delta-, synthase 1	*ALAS1*	534286	0009058 // biosynthetic process // inferred from electronic annotation /// 0033014 // tetrapyrrole biosynthetic process // inferred from electronic annotation	1.01E-10	3.12	Up
EH-domain containing 4	*EHD4*	505206	---	5.58E-10	3.12	Up
ATPase family, AAA domain containing 1	*ATAD1*	506045	---	1.54E-07	3.12	Up
ganglioside induced differentiation associated protein 2	*GDAP2*	508774	---	2.11E-15	3.13	Up
Bcl2-like 14 (apoptosis facilitator)	*BCL2L14*	508365	0006915 // apoptosis // inferred from electronic annotation /// 0042981 // regulation of apoptosis // inferred	7.97E-07	3.14	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			from electronic annotation			
synaptogyrin 1	*SYNGR1*	534995	---	6.92E-05	3.16	Up
Protease, serine, 22	*PRSS22*	510394	0006508 // proteolysis // inferred from electronic annotation	4.65E-05	3.16	Up
similar to LFA-3	*LOC782186*	782186	---	2.25E-06	3.17	Up
serine incorporator 2	*SERINC2*	513593	---	4.72E-10	3.19	Up
crystallin, mu	*CRYM*	505167	0008152 // metabolic process // inferred from electronic annotation	3.98E-05	3.21	Up
apoptosis-associated tyrosine kinase	*AATK*	511515	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	1.63E-06	3.22	Up
coiled-coil domain containing 136	*CCDC136*	615922	---	1.30E-09	3.25	Up
5'-nucleotidase, cytosolic III	*NT5C3*	511858	---	3.38E-10	3.27	Up
N-myc (and STAT) interactor	*NMI*	511280	---	1.71E-13	3.29	Up
Oncostatin M receptor	*OSMR*	514720	---	3.27E-07	3.29	Up
hypothetical LOC616344	*LOC616344*	616344	---	2.97E-11	3.30	Up
Hypothetical LOC514701	*LOC514701*	514701	---	1.29E-07	3.33	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	*TAP1*	524959	0006810 // transport // inferred from electronic annotation	2.11E-12	3.34	Up
StAR-related lipid transfer (START) domain containing 5	*STARD5*	512369	0006810 // transport // inferred from electronic annotation /// 0006869 // lipid transport // inferred from electronic annotation	4.70E-08	3.35	Up
lectin, galactoside-binding, soluble, 3 binding protein	*LGALS3BP*	531137	---	6.28E-08	3.37	Up
interferon induced transmembrane protein 1 (9-27)	*IFITM1*	353510	0009607 // response to biotic stimulus // inferred from electronic annotation	2.56E-12	3.38	Up
ribonuclease, RNase A family, k6	*RNASE6*	282341	---	3.23E-12	3.39	Up
neurochondrin	*NCDN*	505994	---	1.26E-05	3.41	Up
Proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	*PSMF1*	617807	---	4.07E-17	3.41	Up
solute carrier family 12 (sodium/potassium/chloride transporters), member 2	*SLC12A2*	286845	0006810 // transport // inferred from electronic annotation /// 0006811 // ion transport // inferred from electronic annotation /// 0006814 // sodium ion transport // inferred from electronic annotation /// 0006821 // chloride transport // inferred from e	9.58E-09	3.42	Up
ubiquitin-conjugating enzyme E2L 6	*UBE2L6*	509471	0006512 // ubiquitin cycle // inferred from electronic annotation /// 0043687 // post-translational protein	7.80E-13	3.44	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			modification // inferred from electronic annotation /// 0051246 // regulation of protein metabolic process // inferred from electronic annotation			
ATPase family, AAA domain containing 1	*ATAD1*	506045	---	3.47E-10	3.45	Up
EH-domain containing 4	*EHD4*	505206	---	1.87E-06	3.51	Up
2',3'-cyclic nucleotide 3' phosphodiesterase	*CNP*	280752	0007409 // axonogenesis // inferred from electronic annotation /// 0008344 // adult locomotory behavior // inferred from electronic annotation /// 0009214 // cyclic nucleotide catabolic process // inferred from electronic annotation /// 0016070 // RNA met	3.36E-06	3.54	Up
CD69 molecule	*CD69*	281058	---	1.33E-09	3.55	Up
similar to NKp80 NK receptor	*LOC618591*	618591	---	3.11E-06	3.57	Up
tumor-associated calcium signal transducer 2	*TACSTD2*	539853	---	4.61E-09	3.57	Up
Major histocompatibility complex, class I	*LOC512672*	512672	0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and presentation // inferred from	1.12E-09	3.57	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			electronic annotation			
PYD and CARD domain containing	*PYCARD*	282846	0006508 // proteolysis // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0042981 // regulation of apoptosis // inferred from electron	1.20E-08	3.58	Up
suppressor of cytokine signaling 1	*SOCS1*	518795	---	4.33E-09	3.62	Up
interferon-induced protein 35	*IFI35*	510697	---	2.86E-15	3.63	Up
ubiquitin-conjugating enzyme E2L 6	*UBE2L6*	509471	0006512 // ubiquitin cycle // inferred from electronic annotation /// 0043687 // post-translational protein modification // inferred from electronic annotation /// 0051246 // regulation of protein metabolic process // inferred from electronic annotation	2.03E-11	3.63	Up
hypothetical LOC510382	*LOC510382*	510382	---	0.000834	3.68	Up
transmembrane protein 45B	*TMEM45B*	510305 /// 784875	---	1.22E-07	3.68	Up
chemokine (C-C motif) ligand 2 /// chemokine (C-C motif) ligand 11	*CCL11 /// CCL2*	281043 ///	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // inflammatory response //	2.33E-06	3.69	Up

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		404072	inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation			
glutathione synthetase	*GSS*	525059	0006750 // glutathione biosynthetic process // inferred from electronic annotation	4.69E-06	3.69	Up
tryptophanyl-tRNA synthetase	*WARS*	281576	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation /// 0006436 // tryptophanyl-tRNA aminoacylation // inferred from electronic annotation	4.43E-11	3.71	Up
complement component 1, q subcomponent, B chain	*C1QB*	617435	0006817 // phosphate transport // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0006958 // complement activation, classical pathway // inferred from electronic annotation /// 0045087 // innat	6.66E-12	3.72	Up
endothelial PAS domain protein 1	*EPAS1*	282711	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0007165 // signal transduction // inferred from electronic annotation /// 0045449 //	1.32E-06	3.72	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			regul			
Spindle assembly 6 homolog (C. elegans)	*SASS6*	504467	---	4.92E-13	3.74	Up
vestigial like 1 (Drosophila)	*VGLL1*	613549	0045449 // regulation of transcription // inferred from electronic annotation	7.56E-05	3.78	Up
SP140 nuclear body protein	*SP140*	510377	---	5.19E-13	3.79	Up
signal transducer and activator of transcription 2, 113kDa	*STAT2*	511023	---	1.05E-15	3.79	Up
lymphocyte antigen 6 complex, locus G6C	*LY6G6C*	505805	---	7.22E-07	3.81	Up
ecotropic viral integration site 2B	*EVI2B*	617442	---	1.57E-07	3.84	Up
carboxypeptidase X (M14 family), member 2	*CPXM2*	534505	---	0.000613	3.85	Up
solute carrier family 38, member 5	*SLC38A5*	512495	---	5.52E-08	3.87	Up
phosphomevalonate kinase	*PMVK*	513533	0006694 // steroid biosynthetic process // inferred from electronic annotation /// 0006695 // cholesterol biosynthetic process // inferred from electronic annotation /// 0008610 // lipid biosynthetic process // inferred from electronic annotation /// 0016	2.74E-08	3.87	Up
chemokine (C-C motif) ligand 2 /// chemokine (C-C motif) ligand 11	*CCL11 /// CCL2*	281043 /// 404072	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // inflammatory response // inferred from electronic annotation ///	2.56E-06	3.88	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			0006955 // immune response // inferred from electronic annotation			
similar to Complement C4-A precursor (Acidic complement C4)	*LOC617696*	617696	0006954 // inflammatory response // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0006956 // complement activation // inferred from electronic annotation /// 0006958 // complement activation,	9.10E-12	3.90	Up
complement component 1, q subcomponent, C chain	*C1QC*	509968	0006817 // phosphate transport // inferred from electronic annotation	2.21E-10	3.95	Up
Dickkopf homolog 1 (Xenopus laevis)	*DKK1*	504445	---	6.43E-08	3.95	Up
lectin, galactoside-binding, soluble, 9 (galectin 9)	*LGALS9*	510813	---	1.09E-11	3.97	Up
Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	*PLEKHA4*	510748	---	2.12E-09	3.99	Up
histocompatibility complex, class II, DQ alpha, type 1	*BOLA-DQA1*	282534	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and present	0.008907	4.01	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
uroplakin 1B	*UPK1B*	282113	0030855 // epithelial cell differentiation // inferred from electronic annotation	0.008398	4.01	Up
arginase, type II	*ARG2*	518752	0000050 // urea cycle // inferred from electronic annotation /// 0006525 // arginine metabolic process // inferred from electronic annotation /// 0006527 // arginine catabolic process // inferred from electronic annotation /// 0006941 // striated muscle c	3.11E-07	4.02	Up
TRIM6-TRIM34	*TRIM6-TRIM34*	539820	---	6.03E-14	4.03	Up
tumor necrosis factor receptor superfamily, member 13B	*TNFRSF13B*	617948	---	2.21E-09	4.03	Up
damage-regulated autophagy modulator	*DRAM*	533992	---	7.60E-13	4.10	Up
oncostatin M receptor	*OSMR*	514720	---	1.21E-05	4.18	Up
cytochrome P450, family 26, subfamily A, polypeptide 1	*CYP26A1*	539047	0055114 // oxidation reduction // inferred from electronic annotation	0.002529	4.22	Up
adenosine deaminase, RNA-specific	*ADAR*	505134	0006396 // RNA processing // inferred from electronic annotation	6.89E-17	4.24	Up
regulator of G-protein signaling 16	*RGS16*	282035	0009968 // negative regulation of signal transduction // inferred from electronic annotation	2.72E-10	4.26	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
hematopoietic SH2 domain containing	*HSH2D*	510693	---	1.41E-06	4.31	Up
similar to hexokinase II	*LOC614107*	614107	0006096 // glycolysis // inferred from electronic annotation	2.43E-16	4.36	Up
similar to Sialic acid binding Ig-like lectin 5	*LOC512863*	512863	---	7.85E-06	4.42	Up
shisa homolog 5 (Xenopus laevis)	*SHISA5*	616861	0006915 // apoptosis // inferred from electronic annotation	1.57E-15	4.42	Up
tudor domain containing 7	*TDRD7*	506702	---	4.56E-16	4.46	Up
histocompatibility complex, class II, DQ alpha, type 1	*BOLA-DQA1*	282534	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and present	0.006714	4.46	Up
Similar to guanylate binding protein 1	*LOC511531*	511531	---	1.21E-06	4.47	Up
CD86 molecule	*CD86*	414345	---	9.26E-09	4.48	Up
transmembrane protein 140	*TMEM140*	515475	---	3.88E-12	4.50	Up
caspase 4, apoptosis-related cysteine peptidase	*CASP4*	338039	0006508 // proteolysis // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic	9.77E-14	4.53	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			annotation /// 0006917 // induction of apoptosis // traceable author statement /// 0042981 // regulation of apoptosis // inferred from elect			
ataxin 3	*ATXN3*	790880	---	1.47E-12	4.55	Up
caspase 4, apoptosis-related cysteine peptidase	*CASP4*	338039	0006508 // proteolysis // inferred from electronic annotation /// 0006915 // apoptosis // inferred from electronic annotation /// 0006917 // induction of apoptosis // traceable author statement /// 0042981 // regulation of apoptosis // inferred from elect	1.01E-15	4.61	Up
meprin A, beta	*MEP1B*	540701	0006508 // proteolysis // inferred from electronic annotation	1.94E-07	4.62	Up
similar to TLH29 protein precursor	*ISG12(B)*	617420	---	6.28E-06	4.67	Up
SP140 nuclear body protein	*SP140*	510377	---	6.41E-16	4.70	Up
tripartite motif-containing 6	*TRIM6*	616948	0016567 // protein ubiquitination // inferred from electronic annotation	1.77E-13	4.71	Up
unc-93 homolog A (C. elegans)	*UNC93A*	613535	---	2.30E-07	4.75	Up
interferon-induced protein with tetratricopeptide repeats 5	*IFIT5*	515091	---	1.78E-14	4.75	Up
CAMP responsive element modulator	*CREM*	540605	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription,	1.27E-10	4.76	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			DNA-dependent // inferred from electronic annotation			
poly (ADP-ribose) polymerase family, member 9	*PARP9*	510532	---	1.35E-16	4.78	Up
dopa decarboxylase (aromatic L-amino acid decarboxylase)	*DDC*	280762	0006519 // amino acid and derivative metabolic process // inferred from electronic annotation /// 0019752 // carboxylic acid metabolic process // inferred from electronic annotation /// 0042423 // catecholamine biosynthetic process // inferred from electr	1.55E-06	4.80	Up
crystallin, alpha B	*CRYAB*	281719	0006916 // anti-apoptosis // inferred from electronic annotation /// 0006916 // anti-apoptosis // inferred from sequence or structural similarity /// 0032387 // negative regulation of intracellular transport // inferred from electronic annotation /// 0032	4.46E-12	4.81	Up
nuclear localized factor 1	*NLF1*	529849	---	1.54E-07	4.87	Up
solute carrier family 15 (oligopeptide transporter), member 1	*SLC15A1*	521181	0006857 // oligopeptide transport // inferred from electronic annotation	1.83E-05	4.94	Up
similar to KIAA0342 protein	*LOC509859*	509859	---	1.22E-13	5.10	Up
pyrophosphatase (inorganic) 1	*PPA1*	280701	0006796 // phosphate metabolic process // inferred from electronic	1.10E-17	5.22	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
			annotation			
poly (ADP-ribose) polymerase family, member 12	*PARP12*	513185	---	4.02E-15	5.23	Up
unc-45 homolog B (C. elegans)	*UNC45B*	535385	---	4.35E-09	5.23	Up
activating transcription factor 3	*ATF3*	515266	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	8.93E-10	5.29	Up
Fc fragment of IgG, high affinity Ia, receptor (CD64)	*FCGR1A*	282227	---	9.36E-14	5.32	Up
BCL2-like 12 (proline rich)	*BCL2L12*	533338	---	9.62E-13	5.36	Up
macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	*MST1R*	525504	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0007275 // multicellular organismal development // inferred from electronic annotation	6.85E-12	5.44	Up
NLR family, CARD domain containing 5	*NLRC5*	782441	---	6.05E-10	5.47	Up
similar to Sialic acid binding Ig-like lectin 5 /// sialic acid binding Ig-like lectin 14	*LOC512863 /// SIGLEC14*	512863 /// 614923	---	2.86E-05	5.47	Up
tryptophanyl-tRNA synthetase /// similar to WARS protein	*LOC790042 /// WARS*	281576 ///	0006412 // translation // inferred from electronic annotation /// 0006418 // tRNA aminoacylation for protein	4.34E-08	5.51	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
		790042	translation // inferred from electronic annotation /// 0006436 // tryptophanyl-tRNA aminoacylation // inferred from electronic annotation			
deoxyribonuclease I-like 3	*DNASE1L3*	512512	0006308 // DNA catabolic process // inferred from electronic annotation	1.98E-07	5.55	Up
dickkopf homolog 1 (Xenopus laevis)	*DKK1*	504445	0007275 // multicellular organismal development // inferred from electronic annotation /// 0030178 // negative regulation of Wnt receptor signaling pathway // inferred from electronic annotation	7.45E-09	5.61	Up
Minichromosome maintenance complex component 10	*MCM10*	527595	---	0.000108	5.67	Up
Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	*PLEKHA4*	510748	---	1.08E-09	5.73	Up
signal transducer and activator of transcription 2, 113kDa	*STAT2*	511023	---	4.20E-17	5.75	Up
hypothetical LOC512949 /// hypothetical protein LOC789693	*LOC512949 /// LOC789693*	512949 /// 789693	---	5.28E-11	5.77	Up
BCL2-like 15	*BCL2L15*	509786	0006915 // apoptosis // inferred from electronic annotation	7.98E-11	5.81	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
similar to putative ISG12(a) protein	*ISG12(A)*	507138	0015992 // proton transport // inferred from electronic annotation	1.50E-10	5.85	Up
Rho GTPase activating protein 15	*ARHGAP15*	616246	0007165 // signal transduction // inferred from electronic annotation	9.90E-08	5.89	Up
chemokine (C-C motif) receptor 7	*CCR7*	510668	0007165 // signal transduction // inferred from electronic annotation /// 0007186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation	1.73E-06	6.05	Up
solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	*SLC16A1*	505775	0006810 // transport // inferred from electronic annotation /// 0015711 // organic anion transport // inferred from electronic annotation	3.55E-09	6.08	Up
pyridoxal (pyridoxine, vitamin B6) kinase	*PDXK*	514168	0008615 // pyridoxine biosynthetic process // inferred from electronic annotation	2.22E-07	6.15	Up
abhydrolase domain containing 1	*ABHD1*	510774	---	4.57E-14	6.22	Up
arachidonate 5-lipoxygenase-activating protein	*ALOX5AP*	613869	0006691 // leukotriene metabolic process // inferred from electronic annotation /// 0019370 // leukotriene biosynthetic process // inferred from electronic annotation	2.73E-10	6.27	Up
Forkhead box S1	*FOXS1*	540142	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription,	5.05E-17	6.36	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
			DNA-dependent // inferred from electronic annotation			
guanylate binding protein 4	*GBP4*	613313	0006955 // immune response // inferred from electronic annotation	1.32E-08	6.45	Up
interferon induced with helicase C domain 1	*IFIH1*	535490	0042981 // regulation of apoptosis // inferred from electronic annotation	6.85E-13	6.56	Up
similar to OTTHUMP00000017061	*LOC616136*	616136	---	2.73E-11	6.61	Up
interferon regulatory factor 9	*IRF9*	509855	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	5.30E-14	6.63	Up
S100 calcium binding protein A12 (calgranulin C)	*S100A12*	282467	---	1.63E-08	6.67	Up
hypothetical LOC510382	*LOC510382*	510382	---	0.000939	6.74	Up
interferon, alpha-inducible protein 6	*IFI6*	512913	0001836 // release of cytochrome c from mitochondria // inferred from sequence or structural similarity /// 0006916 // anti-apoptosis // inferred from sequence or structural similarity /// 0043154 // negative regulation of caspase activity // inferred fro	8.22E-15	6.91	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
guanylate binding protein 5	*GBP5*	516949	0006955 // immune response // inferred from electronic annotation	1.63E-08	6.95	Up
hypothetical LOC506759	*LOC506759*	506759	---	4.31E-17	7.19	Up
glycosylphosphatidylinositol specific phospholipase D1	*GPLD1*	287025	0006507 // GPI anchor release // inferred from electronic annotation	4.18E-06	7.39	Up
interferon induced with helicase C domain 1	*IFIH1*	535490	0042981 // regulation of apoptosis // inferred from electronic annotation	1.01E-08	7.48	Up
similar to Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (HuGBP-1)	*LOC512486*	512486	0006955 // immune response // inferred from electronic annotation	4.01E-11	7.58	Up
polyribonucleotide nucleotidyltransferase 1	*PNPT1*	508877	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006396 // RNA processing // inferred from electronic annotation /// 0006402 // mRNA catabolic process // inferred from electronic annotation	2.12E-19	7.71	Up
Guanylate binding protein 5	*GBP5*	516949	0006955 // immune response // inferred from electronic annotation	3.91E-08	7.73	Up
protein associated with topoisomerase II homolog 1 (yeast)	*PATL1*	537453	---	4.43E-11	7.74	Up
hypothetical protein LOC783855	*MGC14317*	783855	---	1.20E-10	7.79	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
	0					
eukaryotic translation initiation factor 2-alpha kinase 2	*EIF2AK2*	347700	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	1.44E-09	7.84	Up
shisa homolog 2 (Xenopus laevis)	*SHISA2*	617336	0007275 // multicellular organismal development // inferred from electronic annotation	7.54E-06	7.89	Up
zinc finger, NFX1-type containing 1	*ZNFX1*	539807	---	1.21E-15	8.03	Up
tumor necrosis factor (ligand) superfamily, member 13b	*TNFSF13B*	504507	0006955 // immune response // inferred from electronic annotation	3.04E-11	8.20	Up
hypothetical protein LOC787376	*LOC787376*	787376	---	9.63E-15	8.28	Up
pentraxin-related gene, rapidly induced by IL-1 beta	*PTX3*	541148	---	1.44E-09	8.32	Up
placenta-specific 8	*PLAC8*	767910	---	5.55E-14	8.53	Up
trophoblast Kunitz domain protein 1	*TKDP1*	404076	---	0.00918	8.60	Up
tumor necrosis factor (ligand) superfamily, member 13b	*TNFSF13B*	504507	0006955 // immune response // inferred from electronic annotation	3.06E-13	8.61	Up
transmembrane protein 140	*TMEM140*	515475	---	1.61E-10	8.65	Up
poly (ADP-ribose) polymerase family, member 14	*PARP14*	540789	---	4.02E-15	8.76	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	*MX1*	280872	0009615 // response to virus // inferred from electronic annotation	1.77E-11	9.04	Up
hypothetical LOC524159	*LOC524159*	524159	---	1.58E-14	9.06	Up
abhydrolase domain containing 1	*ABHD1*	510774	---	3.52E-10	9.25	Up
XIAP associated factor 1	*XAF1*	509740	0006915 // apoptosis // inferred from electronic annotation /// 0007049 // cell cycle // inferred from electronic annotation /// 0045786 // negative regulation of cell cycle // inferred from electronic annotation	7.70E-16	9.51	Up
poly (ADP-ribose) polymerase family, member 12	*PARP12*	513185	---	5.50E-15	9.58	Up
receptor (chemosensory) transporter protein 4	*RTP4*	532442	---	1.41E-12	9.75	Up
Similar to hook1 protein	*LOC785042*	785042	0000226 // microtubule cytoskeleton organization and biogenesis // inferred from electronic annotation	2.68E-13	9.84	Up
uterine milk protein precursor	*LOC286871*	286871	0007565 // female pregnancy // inferred from electronic annotation	7.19E-07	10.11	Up
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	*PLEKHA4*	510748	---	2.89E-16	10.29	Up

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Poly (ADP-ribose) polymerase family, member 12	*PARP12*	513185	---	3.87E-11	10.31	Up
shisa homolog 3 (Xenopus laevis)	*SHISA3*	781091	---	2.62E-08	10.39	Up
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	*MGAT4A*	282276	0005975 // carbohydrate metabolic process // inferred from electronic annotation	4.77E-11	10.68	Up
RNA helicase LGP2	*LGP2*	508378	---	4.61E-14	10.72	Up
transmembrane protein 40	*TMEM40*	505490	---	6.29E-06	11.01	Up
ring finger protein 213	*RNF213*	509283	---	1.64E-11	11.14	Up
keratin 17	*KRT17*	281889	---	3.50E-09	11.27	Up
arachidonate 12-lipoxygenase	*ALOX12*	407169	0006691 // leukotriene metabolic process // inferred from electronic annotation /// 0006916 // anti-apoptosis // inferred from sequence or structural similarity /// 0008284 // positive regulation of cell proliferation // inferred from sequence or structur	8.58E-12	11.35	Up
trophoblast protein-1 /// similar to interferon tau	*LOC618974 /// LOC782273 /// TP-1*	317698 /// 618974 /// 782273	0006952 // defense response // inferred from electronic annotation /// 0007565 // female pregnancy // inferred from electronic annotation /// 0009615 // response to virus // inferred from electronic annotation	0.003234	11.35	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
chemokine (C-X-C motif) ligand 10	*CXCL10*	615107	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // inflammatory response // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation	3.05E-10	11.55	Up
Hypothetical protein LOC781418	*LOC781418*	781418	---	6.76E-15	11.96	Up
zinc finger, NFX1-type containing 1	*ZNFX1*	539807	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	1.94E-13	12.22	Up
interferon induced transmembrane protein 5	*IFITM5*	526461	0009607 // response to biotic stimulus // inferred from electronic annotation	3.90E-13	13.25	Up
uterine milk protein precursor	*LOC286871*	286871	0007565 // female pregnancy // inferred from electronic annotation	2.29E-07	13.33	Up
guanylate binding protein 5	*GBP5*	516949	0006955 // immune response // inferred from electronic annotation	3.52E-10	13.35	Up
receptor (chemosensory) transporter protein 4	*RTP4*	532442	---	1.08E-11	13.40	Up
three prime repair exonuclease 1	*TREX1*	282099	0006281 // DNA repair // inferred from electronic annotation /// 0006974 // response to DNA damage stimulus // inferred from electronic annotation	1.65E-13	13.63	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
complement component 2	*C2*	515440	0006508 // proteolysis // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0006956 // complement activation // inferred from electronic annotation /// 0006958 // complement activation, classical	4.73E-11	13.79	Up
similar to CG33196-PB /// similar to Extracellular proteinase inhibitor	*LOC515676 /// LOC787253*	515676 /// 787253	---	2.72E-06	13.80	Up
poly (ADP-ribose) polymerase family, member 12	*PARP12*	513185	---	5.04E-10	13.83	Up
major histocompatibility complex, class II, DQ alpha 2	*BOLA-DQA2*	282535	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation /// 0019882 // antigen processing and present	0.008125	13.86	Up
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	*DDX58*	504760	---	2.27E-14	13.89	Up
ring finger protein 213	*RNF213*	509283	---	1.19E-11	13.94	Up
ubiquitin-like modifier activating enzyme	*UBA7*	497204	0006464 // protein modification	1.41E-13	13.96	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
7			process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation /// 0008152 // metabolic process // inferred from electronic annotation			
placenta-specific 8	*PLAC8*	509228	---	3.36E-09	13.98	Up
receptor (chemosensory) transporter protein 4	*RTP4*	532442	---	2.59E-11	14.23	Up
2',5'-oligoadenylate synthetase 1, 40/46kDa	*OAS1*	347699	0006955 // immune response // inferred from electronic annotation	3.03E-13	14.75	Up
crystallin, gamma S	*CRYGS*	281724	0002009 // morphogenesis of an epithelium // inferred from electronic annotation /// 0002088 // lens development in camera-type eye // inferred from electronic annotation	2.07E-08	14.80	Up
mixed lineage kinase domain-like	*MLKL*	790225	0006468 // protein amino acid phosphorylation // inferred from electronic annotation	8.44E-12	15.36	Up
interferon regulatory factor 7	*IRF7*	100125591	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	6.74E-14	15.46	Up

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Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
fructose-1,6-bisphosphatase 1	*FBP1*	513483	0005975 // carbohydrate metabolic process // inferred from electronic annotation /// 0006094 // gluconeogenesis // inferred from electronic annotation	5.64E-06	15.56	Up
Guanylate binding protein 5	*GBP5*	516949	0006955 // immune response // inferred from electronic annotation	1.92E-09	17.20	Up
T-cell immunoglobulin and mucin domain containing 4	*TIMD4*	507549	---	9.89E-13	17.59	Up
fibroblast growth factor-binding protein (FGF-BP) /// similar to fibroblast growth factor-binding protein	*LOC281812 /// LOC783341*	281812 /// 783341	---	7.52E-08	17.83	Up
indoleamine-pyrrole 2,3 dioxygenase	*INDO*	506281	---	1.80E-12	19.73	Up
ubiquitin specific peptidase 18	*USP18*	515202	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	1.64E-14	20.07	Up
Interferon-induced protein 44	*IFI44*	508348	---	1.49E-12	20.38	Up
sterile alpha motif domain containing 9	*SAMD9*	514205	---	5.36E-14	24.15	Up
ubiquitin specific peptidase 18	*USP18*	515202	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	1.62E-13	24.66	Up
interferon-induced protein 44	*IFI44*	508348	---	1.76E-12	25.03	Up

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Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	*FABP3*	281758	0006656 // phosphatidylcholine biosynthetic process // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	3.16E-11	27.47	Up
Similar to lipopolysaccharide binding protein	*LOC514978*	514978	---	1.80E-20	27.62	Up
chemokine (C-C motif) ligand 8	*CCL8*	281044 /// 788169	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // inflammatory response // inferred from electronic annotation /// 0006955 // immune response // inferred from electronic annotation	3.38E-12	28.05	Up
sialic acid binding Ig-like lectin 1, sialoadhesin	*SIGLEC1*	539759	---	4.56E-20	30.09	Up
similar to lipopolysaccharide binding protein	*LOC514978*	514978	---	7.10E-19	31.25	Up
radical S-adenosyl methionine domain containing 2	*RSAD2*	506415	0009615 // response to virus // inferred from electronic annotation /// 0051607 // defense response to virus // inferred from sequence or structural similarity	1.59E-10	31.91	Up
interferon-induced protein 44 /// hypothetical protein LOC790424	*IFI44 /// LOC790424*	508348 /// 790424	---	1.69E-12	33.15	Up

Gene Title	Gene Symbol	Entrez Gene	Putative Function	*P*-value	Fold Effect	Regulation
ISG15 ubiquitin-like modifier	*ISG15*	281871	0006464 // protein modification process // inferred from electronic annotation /// 0006512 // ubiquitin cycle // inferred from electronic annotation /// 0009615 // response to virus // inferred from electronic annotation /// 0019941 // modification-depend	2.32E-11	33.54	Up
Similar to Interferon-induced protein 44-like	*LOC508347*	508347	---	5.60E-14	34.05	Up
interferon regulatory factor 7	*IRF7*	100125591	0006350 // transcription // inferred from electronic annotation /// 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 0006810 // transport // inferred from electronic annotation	2.37E-11	34.49	Up
peroxidasin homolog (Drosophila)	*PXDN*	515860	0006468 // protein amino acid phosphorylation // inferred from electronic annotation /// 0006979 // response to oxidative stress // inferred from electronic annotation /// 0007155 // cell adhesion // inferred from electronic annotation	9.44E-14	44.13	Up
Chromosome 11 open reading frame 34 ortholog	*H15C11ORF34*	505518	---	5.96E-13	44.63	Up
Similar to Bone marrow stromal cell	*LOC50740*	507402	---	2.79E-11	44.82	Up

Gene Title	**Gene Symbol**	**Entrez Gene**	**Putative Function**	***P*-value**	**Fold Effect**	**Regulation**
antigen 2	*2*					
interferon-induced protein 44	*IFI44*	508348	---	4.55E-11	50.01	Up
indoleamine-pyrrole 2,3 dioxygenase	*INDO*	506281	---	7.89E-12	64.46	Up
Similar to Bone marrow stromal cell antigen 2	*LOC507402*	507402	---	1.39E-10	69.36	Up
ubiquitin specific peptidase 18	*USP18*	515202	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	9.18E-12	79.24	Up
interferon-induced protein with tetratricopeptide repeats 2	*IFIT2*	527528	---	9.72E-13	84.14	Up
Ubiquitin specific peptidase 18	*USP18*	515202	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	2.07E-11	94.13	Up
interferon stimulated exonuclease gene 20kDa	*ISG20*	506604	---	2.35E-15	140.99	Up
myxovirus (influenza virus) resistance 2 (mouse)	*MX2*	280873	0009615 // response to virus // inferred from electronic annotation	5.45E-13	224.96	Up
C-type lectin domain family 4, member F	*CLEC4F*	511001	---	5.65E-23	404.60	Up
chromosome 11 open reading frame 34 ortholog	*C15H11ORF34*	505518	---	3.74E-15	417.90	Up