

Table S1: Differentially expressed genes at day 3 of nitrite therapy

Gene Name	Accession#	Ratio	SEM	P Value
Metallothionein 4	NM_008631	6.01	0.03	0.018
Myosin, heavy polypeptide 7, cardiac muscle, beta	NM_080728	5.35	0.003	0.014
RIKEN cDNA 1600029D21 gene	BC022950	4.98	0.016	0.0001
Glutathione S-transferase, alpha 2 (Yc2)	NM_008182	4.38	0.012	0.001
Troponin I, skeletal, slow 1	NM_021467	4.23	0.002	0.017
Troponin T1, skeletal, slow	NM_011618	4.15	0.003	0.035
Four and a half LIM domains 1	BF466856	4.03	0.004	0.004
Metallothionein 3	NM_013603	3.88	0.006	0.026
Prostaglandin reductase 2	BE283373	3.79	0.007	0.002
Myosin, light polypeptide 2, regulatory, cardiac, slow	NM_010861	3.56	0.002	0.047
Troponin C, cardiac/slow skeletal	NM_009393	3.49	0.001	0.038
DIX domain containing 1	BB758432	3.39	0.009	0.004
Flavin containing monooxygenase 5	NM_010232	3.33	0.04	0.005
zinc finger protein 697	BC002224	3.28	0.02	0.012
Park2 co-regulated	AK005771	3.19	0.007	0.001
Kin of IRRE like 3 (Drosophila)	AK005197	3.17	0.055	0.025
Potassium voltage-gated channel, subfamily Q, member 5	AV362204	3.12	0.028	0.001
DnaJ (Hsp40) homolog, subfamily A, member 4	NM_021422	3.05	0.001	0.004
Myomesin family, member 3	AW553161	2.99	0.006	0.006
ATPase, (Na+)/K+ transporting, beta 4 polypeptide	NM_133690	2.89	0.012	0.005
Ankyrin repeat domain 2 (stretch responsive muscle)	NM_020033	2.86	0.0001	0.006
Chemokine (C-X-C motif) receptor 6	AF301018	2.84	0.015	0.028
Cysteine and glycine-rich protein 3	NM_013808	2.82	0.0001	0.007
myosin, heavy polypeptide 2, skeletal muscle, adult	BC008538	2.8	0.0001	0.0001
Troponin T2, cardiac	L47552	2.75	0.004	0.017
Zinc finger protein 64	BF020964	2.7	0.019	0.032
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	AF158746	2.62	0.019	0.007
RIKEN cDNA 2310002L09 gene	AK009097	2.58	0.001	0.0001
Tropomyosin 3, gamma	NM_022314	2.58	0.002	0.035
Myogenin	NM_031189	2.57	0.001	0.004
Prostaglandin-endoperoxide synthase 2	M94967	2.54	0.017	0.011
Myozenin 2	NM_021503	2.53	0.001	0.013
TatD DNase domain containing 1	BB761179	2.53	0.002	0.003
Transcribed locus	BM730637	2.53	0.008	0.001
Transcribed locus	AV231357	2.51	0.001	0.0001
Transcribed locus	AV346607	2.51	0.017	0.01
Cysteine-rich C-terminal 1	AK009010	2.5	0.033	0.009
Glycogen synthase 1, muscle	NM_030678	2.49	0.001	0.0001
Solute carrier family 22 (organic cation transporter), member 4	BC010590	2.49	0.011	0.031
Solute carrier family 16 (monocarboxylic acid transporters), member 3	NM_030696	2.48	0.0001	0.0001
Chloride intracellular channel 5	BB610000	2.47	0.003	0.011
Transmembrane protein 143	AK013719	2.47	0.006	0.01
HECT domain containing 2	AW114007	2.46	0.013	0.034
UEV and lactate/malate dehydrogenase domains	NM_016855	2.46	0.014	0.007
Cyclic AMP-regulated phosphoprotein, 21	NM_033264	2.45	0.005	0.005

Fibroblast growth factor 13	AF020737	2.43	0.004	0.001
RIKEN cDNA 8030451F13 gene	AW743000	2.43	0.001	0.006
Cadherin 5	NM_009868	2.41	0.009	0.013
Mus musculus tumor-associated antigen 1 (Taa1), mRNA.	NM_009310	2.39	0.005	0.026
TEA domain family member 4	D87965	2.38	0.01	0.0001
Transcribed locus	BB322227	2.38	0.001	0.007
Lactate dehydrogenase B	AV219418	2.37	0.002	0.004
LIM and cysteine-rich domains 1	BC019124	2.37	0.0001	0.011
Transcribed locus	BM730637	2.33	0.008	0.0001
Rhomboid, veinlet-like 1 (Drosophila)	BC021549	2.32	0.004	0.002
RIKEN cDNA 4833439L19 gene	NM_029241	2.32	0.002	0.002
Smoothelin-like 1	NM_024230	2.29	0.002	0.013
Target of myb1-like 2 (chicken)	BM226574	2.29	0.01	0.003
Tumor necrosis factor receptor superfamily, member 19	AF167554	2.29	0.019	0.007
Predicted gene, ENSMUSG00000074670	BC002189	2.26	0.015	0.012
Sterile alpha motif domain containing 4	BB626348	2.26	0.012	0.036
Ubiquitin-conjugating enzyme E2G 2	AF296657	2.26	0.002	0.005
Cell growth regulator with EF hand domain 1	BC023116	2.25	0.005	0.005
Heat shock protein family, member 7 (cardiovascular)	BG968304	2.23	0.0001	0.005
Small proline-rich protein 1A	NM_009264	2.23	0.008	0.011
FXFD domain-containing ion transport regulator 6	AB032010	2.22	0.003	0.021
Plasmacytoma variant translocation 1	BI453402	2.2	0.033	0.042
Uridine-cytidine kinase 2	NM_030724	2.2	0.001	0.001
DNA-damage-inducible transcript 4	AK017926	2.19	0.001	0.011
Expressed sequence AU040829	BB079908	2.18	0.003	0.004
Myosin, light polypeptide 4	NM_010858	2.18	0.001	0.01
Popeye domain containing 2	NM_022318	2.18	0.001	0.002
Dynamin 1-like	BC027538	2.14	0.006	0.003
ARP1 actin-related protein 1 homolog B (yeast)	BG801851	2.13	0.001	0.002
Integrin alpha 7	NM_008398	2.13	0.001	0.001
Sodium channel, voltage-gated, type V, alpha	BB516098	2.13	0.004	0.003
SRY-box containing gene 17	NM_011441	2.13	0.003	0.013
Neural cell adhesion molecule 1	NM_010875	2.12	0.005	0.017
Potassium inwardly rectifying channel, subfamily J, member 11	U73626	2.12	0.002	0.0001
Suppressor of cytokine signaling 3	BB241535	2.12	0.001	0.002
Transcribed locus	AK017367	2.12	0.012	0.004
ESTs	BB515192	2.11	0.002	0.018
mitochondrial carrier homolog 2	AV067008	2.11	0.0001	0.016
Purinergic receptor P2Y, G-protein coupled 2	NM_008773	2.11	0.004	0.003
Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	BC019978	2.11	0.001	0.013
Transcribed locus, moderately similar to NP_766184.1 SEC24 related gene family, member C [Mus musculus]	AK018074	2.11	0.018	0.042
EH-domain containing 2	BC027084	2.1	0.004	0.011
Leucine rich repeat protein 1, neuronal	NM_008516	2.1	0.005	0.027
Gene model 129, (NCBI)	BB407125	2.09	0.005	0.004
Transcribed locus	BB766817	2.09	0.01	0.037
Coiled-coil domain containing 109A	AV259428	2.08	0.007	0.004
AHNAK nucleoprotein (desmoyokin)	AK009866	2.07	0.004	0.02
CUB and zona pellucida-like domains 1	NM_008411	2.07	0.016	0.002

Keratin 18	NM_010664	2.07	0.016	0.03
Mus musculus RIKEN cDNA 1110055E19 gene (1110055E19Rik), mRNA.	NM_026839	2.07	0.0001	0.011
Vitronectin	BB251864	2.06	0.013	0.026
Solute carrier family 8 (sodium/calcium exchanger), member 3	NM_080440	2.05	0.006	0.009
ESTs	BB386239	2.04	0.011	0.036
RIKEN cDNA 1700052N19 gene	NM_024261	2.04	0.009	0.003
RIKEN cDNA 2900073G15 gene	NM_026064	2.04	0.001	0.003
Transcribed locus	AW553649	2.04	0.025	0.03
Transcribed locus	BB764453	2.04	0.004	0.002
TBC1 domain family, member 1	BB501891	2.03	0.01	0.014
Calsequestrin 2	NM_009814	2.02	0.002	0.001
Coagulation factor II (thrombin) receptor-like 1	NM_007974	2.02	0.006	0.027
Myosin light chain 2, precursor lymphocyte-specific	NM_021611	2.02	0.012	0.028
EGL nine homolog 3 (<i>C. elegans</i>)	BB284358	2.01	0.001	0.006
CDNA sequence BC048679	AV360837	2	0.016	0.023
Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	BI155184	2	0.01	0.001
Paired-like homeodomain transcription factor 2	U80011	2	0.003	0.034
TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	AV213552	2	0.015	0.002
Claspin homolog (<i>Xenopus laevis</i>)	BG067086	0.5	0.003	0.022
ESTs, Moderately similar to S12207 hypothetical protein (<i>M.musculus</i>)	BM119933	0.5	0.007	0.001
Myosin Va	NM_010864	0.5	0.001	0.003
Transcribed locus	BM213788	0.5	0.009	0.047
Transcribed locus	BG067469	0.5	0.004	0.008
Zinc finger, RAN-binding domain containing 3	BM228797	0.5	0.002	0.006
DnaJ (Hsp40) homolog, subfamily B, member 14	BE952491	0.498	0.003	0.013
ESTs	BB206454	0.498	0.004	0.005
ESTs	BB467915	0.498	0.007	0.009
Glia maturation factor, gamma	NM_022024	0.498	0.001	0.011
RIKEN cDNA B430201A12 gene	BB325849	0.498	0.001	0.0001
Solute carrier family 37 (glycerol-3-phosphate transporter), member 2	BC022752	0.498	0.002	0.017
Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	BI738328	0.498	0.001	0.005
Tousled-like kinase 2 (<i>Arabidopsis</i>)	BM198864	0.498	0.008	0.016
Transcribed locus	AA266723	0.498	0.004	0.025
DNA segment, Chr 8, ERATO Doi 82, expressed	BM195829	0.495	0.003	0.029
RIKEN cDNA 2810417H13 gene	AK017673	0.495	0.0001	0.005
Transcribed locus	BB362579	0.495	0.009	0.019
Transcribed locus	BB192700	0.495	0.004	0.025
Activated leukocyte cell adhesion molecule	AV315205	0.493	0.009	0.007
ESTs	BB499275	0.493	0.008	0.003
F-box protein 5	AK011820	0.493	0.003	0.014
Transmembrane protein 106A	BC022145	0.493	0.001	0.005
EST X83313	BG065719	0.49	0.006	0.018
ESTs	AI604411	0.49	0.006	0.005
ESTs, Weakly similar to NED4 MOUSE NEDD-4 PROTEIN (<i>M.musculus</i>)	AI593288	0.49	0.008	0.003

Jumonji, AT rich interactive domain 1C (Rbp2 like)	BB165753	0.49	0.013	0.033
Rho GTPase activating protein 9	AU043488	0.49	0.007	0.006
Shc SH2-domain binding protein 1	NM_011369	0.49	0.002	0.006
Sterol O-acyltransferase 1	BG064396	0.49	0.001	0.003
Transcribed locus	BB104669	0.49	0.003	0.009
cyclin B1	NM_007629	0.488	0.002	0.016
FERM domain containing 4B	BB009122	0.488	0.001	0.009
Fermitin family homolog 3 (Drosophila)	BG066664	0.488	0.001	0.004
Testis-specific kinase 2	BQ179435	0.488	0.005	0.001
Transcribed locus	BB480970	0.488	0.004	0.007
CAP, adenylate cyclase-associated protein 1 (yeast)	NM_007598	0.485	0.011	0.011
CDNA sequence BC052328	BM224662	0.485	0.001	0.007
DBF4 homolog (S. cerevisiae)	NM_013726	0.485	0.001	0.004
ESTs	BG071091	0.485	0.006	0.007
FYN binding protein	BB157866	0.485	0.001	0.001
Mucolipin 2	AK014467	0.485	0.008	0.036
RIKEN cDNA 4921513D23 gene	BB123487	0.485	0.005	0.005
RIKEN cDNA 9430034F23 gene	AK020456	0.485	0.013	0.036
Transcribed locus	AU020421	0.485	0.006	0.024
Transcribed locus	AW537708	0.485	0.0001	0.003
annexin A6	AK013026	0.483	0.005	0.001
ESTs	BB373572	0.483	0.007	0.015
PR domain containing 1, with ZNF domain	NM_007548	0.483	0.006	0.005
T-box 1	AF326960	0.483	0.002	0.022
Dedicator of cyto-kinesis 2	NM_033374	0.481	0.001	0.021
ESTs	BM199910	0.481	0.003	0.003
Heme oxygenase (decycling) 1	NM_010442	0.481	0.0001	0.006
Interferon, alpha-inducible protein 27	AY090098	0.481	0.001	0.007
Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	U96693	0.481	0.002	0.004
Liver glycogen phosphorylase	NM_133198	0.481	0.001	0.001
RIKEN cDNA 2310045N14 gene	AK009831	0.481	0.002	0.016
RIKEN cDNA A230054D04 gene	BB542960	0.481	0.004	0.039
Transcribed locus	BB235876	0.481	0.004	0.003
Transcribed locus	BM244144	0.481	0.006	0.004
Transcribed locus	BB753814	0.481	0.01	0.012
Transcribed locus, strongly similar to NP_780438.2 serine/arginine repetitive matrix 2 [Mus musculus]	BB821417	0.481	0.003	0.0001
Baculoviral IAP repeat-containing 6	BB527646	0.478	0.007	0.005
Cytoskeleton-associated protein 4	BB312117	0.478	0.001	0.0001
Dynactin 5	NM_011121	0.478	0.003	0.034
Interferon induced transmembrane protein 1	BC027285	0.478	0.002	0.025
Receptor (calcitonin) activity modifying protein 2	AF146523	0.478	0.0001	0.014
Rho GTPase activating protein 17	BB749468	0.478	0.005	0.041
CD300 antigen like family member B	BB230267	0.476	0.002	0.004
Epidermal growth factor receptor pathway substrate 8	NM_007945	0.476	0.001	0.0001
lysosomal-associated protein transmembrane 5	BB218107	0.476	0.0001	0.001
SERTA domain containing 4	BQ174721	0.476	0.002	0.009
Transcribed locus	BG076154	0.476	0.003	0.008
Adipose differentiation related protein	NM_007408	0.474	0.0001	0.003

Chitinase 3-like 3	NM_009892	0.474	0.001	0.038
Collagen, type XII, alpha 1	AW412729	0.474	0.004	0.014
Coronin, actin binding protein 1A	BB740218	0.474	0.001	0.007
ESTs	BG075224	0.474	0.01	0.045
Fc receptor, IgE, high affinity I, gamma polypeptide	NM_010185	0.474	0.0001	0.002
Transcribed locus	BB202321	0.474	0.016	0.032
Transcribed locus	C85455	0.474	0.005	0.015
Tropomyosin 1, alpha	BM232388	0.474	0.001	0.008
ESTs	BB039073	0.472	0.006	0.017
Solute carrier family 25, member 30	BB032012	0.472	0.002	0.001
Transcribed locus	AI606033	0.472	0.005	0.031
Transcribed locus	AV330236	0.472	0.01	0.014
Transcribed locus	BM243379	0.472	0.001	0.001
Twinfilin, actin-binding protein, homolog 1 (Drosophila)	BI662615	0.472	0.003	0.026
Mus musculus, Similar to transgelin 2, clone MGC:6300 IMAGE:2654381, mRNA, complete cds	AV212626	0.469	0.001	0.023
Coiled-coil domain containing 109B	NM_025779	0.467	0.002	0.007
Complement component 3a receptor 1	NM_009779	0.467	0.0001	0.002
Membrane-spanning 4-domains, subfamily A, member 6B	NM_027209	0.467	0.0001	0.002
Regulator of G-protein signaling 18	BB139986	0.467	0.006	0.02
RIKEN cDNA A630042L21 gene	BB233267	0.467	0.006	0.002
Transcribed locus	BF715043	0.467	0.001	0.0001
Transcribed locus	BB051012	0.467	0.011	0.022
Transcribed locus	BG094104	0.467	0.005	0.002
Transcribed locus	BB433596	0.467	0.007	0.023
CD52 antigen	NM_013706	0.465	0.0001	0.005
Deoxycytidine kinase	BB030204	0.465	0.001	0.005
Epidermal growth factor-containing fibulin-like extracellular matrix protein 1	BC023060	0.465	0.001	0.004
expressed sequence AV025504	BB115446	0.465	0.001	0.001
Nuclear transcription factor, X-box binding-like 1	NM_133921	0.465	0.002	0.011
Transcribed locus	BM203526	0.465	0.005	0.021
High mobility group AT-hook 2	BB105328	0.463	0.016	0.001
RAP2B, member of RAS oncogene family	BB390705	0.463	0.003	0.001
Transcribed locus	BG074304	0.463	0.006	0.006
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	BG066773	0.463	0.001	0.001
Bone marrow stromal cell antigen 1	AI647987	0.461	0.005	0.007
Platelet-derived growth factor, C polypeptide	NM_019971	0.461	0.003	0.02
RIKEN cDNA 4930506M07 gene	BB559293	0.461	0.002	0.0001
RIKEN cDNA 4932415G12 gene	AK015136	0.461	0.018	0.039
Signal sequence receptor, gamma	AU022074	0.461	0.0001	0.039
toll-like receptor 13	BI655907	0.461	0.001	0.012
Chemokine (C-C motif) ligand 9	AF128196	0.459	0.0001	0.01
EST	AV084904	0.459	0.0001	0.002
ESTs	BG075606	0.459	0.007	0.013
Sperm associated antigen 5	BM208112	0.459	0.011	0.004
Transcribed locus	BB827631	0.459	0.003	0.003
Transcribed locus	BF165681	0.459	0.002	0.005
ESTs	BB425118	0.457	0.014	0.027

ESTs, Weakly similar to JAK3 MOUSE TYROSINE-PROTEIN KINASE JAK3 (M.musculus)	BG063073	0.457	0.012	0.005
Kinesin family member 2C	NM_134471	0.457	0.005	0.005
Transcribed locus	BE690666	0.457	0.01	0.005
5-hydroxytryptamine (serotonin) receptor 2B	NM_008311	0.455	0.006	0.022
ESTs	AU040352	0.455	0.007	0.003
ESTs	AV369290	0.455	0.009	0.002
RIKEN cDNA 6330500D04 gene	AV329070	0.455	0.006	0.004
Solute carrier family 15, member 3	NM_023044	0.455	0.002	0.05
Asp (abnormal spindle)-like, microcephaly associated (Drosophila)	NM_009791	0.452	0.003	0.001
Deleted in lymphocytic leukemia, 2	AA189481	0.452	0.007	0.009
DNA segment, Chr 10, ERATO Doi 276, expressed	BG066654	0.452	0.008	0.029
ESTs, Weakly similar to GNMSLL retrovirus-related reverse transcriptase homolog - mouse retrotransposon (M.musculus)	AI506532	0.452	0.003	0.012
Phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	AK012196	0.452	0.003	0.001
Protein phosphatase 1H (PP2C domain containing)	AU040848	0.452	0.003	0.001
Structural maintenance of chromosomes 6	BB056038	0.452	0.012	0.001
Z-DNA binding protein 1	AK008179	0.452	0.005	0.019
Zwilch, kinetochore associated, homolog (Drosophila)	BC027435	0.452	0.002	0.023
ESTs	BE980962	0.45	0.007	0.0001
ESTs	BB394466	0.45	0.004	0.003
expressed sequence AU015263	BG070233	0.45	0.003	0.008
Lysosomal acid lipase A	AI596237	0.45	0.001	0.013
Schlafen 2	NM_011408	0.45	0.001	0.011
Transcribed locus	BF225802	0.45	0.0001	0.002
Ect2 oncogene	NM_007900	0.448	0.002	0.003
Topoisomerase (DNA) II alpha	BB749838	0.448	0.006	0.013
Transcribed locus	BF147024	0.448	0.02	0.008
growth arrest specific 1 /FL=gb:NM_008086.1	BB550400	0.446	0.001	0.005
Macrophage scavenger receptor 1	L04274	0.446	0.01	0.02
RIKEN cDNA 2310022G15 gene	BF783360	0.446	0.003	0.015
Transcribed locus	BI685536	0.446	0.001	0.007
Transcribed locus	BB229269	0.446	0.005	0.004
Transcribed locus	AW537708	0.446	0.003	0.025
Fatty acid binding protein 7, brain	NM_021272	0.444	0.007	0.003
Gene model 885, (NCBI)	BE629676	0.444	0.004	0.004
Neurobeachin like 1	BB022773	0.444	0.006	0.009
Six transmembrane epithelial antigen of prostate 2	AK015015	0.444	0.004	0.017
Thrombospondin 2	NM_011581	0.444	0.001	0.006
Transcribed locus, strongly similar to XP_141626.3 PREDICTED: similar to Ubiquitin-conjugating enzyme E2Q (putative) 2 [Mus m	AW550321	0.444	0.006	0.015
Cysteinyl leukotriene receptor 1	BC027102	0.442	0.006	0.018
Fc receptor, IgG, high affinity I	AF143181	0.442	0.001	0.008
Thyroid hormone receptor interactor 13	AK010336	0.442	0.002	0.011
Transcribed locus	BB262899	0.442	0.017	0.047
Cathepsin C	BM237633	0.439	0.004	0.007
CD180 antigen	NM_008533	0.439	0.004	0.004
C-type lectin domain family 5, member a	NM_021364	0.439	0.007	0.005
Epithelial stromal interaction 1 (breast)	BF020640	0.439	0.003	0.019
Expressed sequence C79407	BB540053	0.439	0.005	0.002

Kinesin family member 22	BC003427	0.439	0.006	0.02
Myb-like, SWIRM and MPN domains 1	BB045598	0.439	0.009	0.047
Discs, large (Drosophila) homolog-associated protein 5	BM250919	0.437	0.007	0.046
Hyaluronan mediated motility receptor (RHAMM)	BC021427	0.437	0.003	0.002
Maternal embryonic leucine zipper kinase	NM_010790	0.437	0.003	0.048
Transforming growth factor, beta induced	NM_009369	0.437	0.0001	0.0001
Pleckstrin	AF181829	0.435	0.001	0.004
transforming growth factor, beta induced, 68 kDa	BB533460	0.435	0.0001	0.0001
A disintegrin and metallopeptidase domain 12 (meltrin alpha)	NM_007400	0.433	0.002	0.001
Collagen, type I, alpha 2	BB150460	0.433	0.008	0.009
Transcribed locus	BB490889	0.433	0.01	0.009
Transcribed locus	BB380864	0.433	0.018	0.018
ATPase, class V, type 10A	BM249532	0.431	0.008	0.039
Formin 1	BB164513	0.431	0.009	0.003
Protein tyrosine phosphatase, receptor type, O	AF295638	0.431	0.008	0.009
Transcribed locus	BB538816	0.431	0.006	0.008
Baculoviral IAP repeat-containing 5	BC004702	0.429	0.001	0.002
Mitogen-activated protein kinase kinase kinase kinase 1	BB546619	0.429	0.007	0.014
N-acetylneuraminase pyruvate lyase	BC022734	0.429	0.001	0.017
TAO kinase 1	BM238077	0.429	0.008	0.003
Apolipoprotein B editing complex 1	BC003792	0.427	0.001	0.005
DNA segment, Chr 10, ERATO Doi 709, expressed	BG069224	0.427	0.005	0.004
Paternally expressed 3	AB003040	0.427	0.001	0.002
Transcribed locus	BG067008	0.427	0.006	0.006
Transmembrane protein 97	NM_133706	0.427	0.004	0.005
Cyclin A2	X75483	0.426	0.001	0.002
Hypothetical protein LOC100043636	BE688410	0.426	0.001	0.021
Transcribed locus	AV349116	0.426	0.002	0.01
BCL2-like 11 (apoptosis facilitator)	BB667581	0.424	0.001	0.001
Exonuclease domain containing 1	BB091183	0.424	0.009	0.038
Ribosome binding protein 1	NM_133626	0.424	0.001	0.028
Transcribed locus	BM234702	0.424	0.005	0.032
Transcribed locus	BB070941	0.424	0.007	0.011
Sorting nexin 6	BC025911	0.422	0.003	0.005
Transmembrane protein 100	NM_026433	0.422	0.001	0.046
Tripartite motif-containing 59	NM_025863	0.422	0.003	0.018
Complement factor properdin	BB800282	0.418	0.001	0.005
Fidgetin-like 1	NM_021891	0.418	0.003	0.031
Transcribed locus	BG066234	0.418	0.004	0.006
tripartite motif-containing 34	AF220142	0.418	0.003	0.029
C-type lectin domain family 4, member a3	AK014135	0.417	0.001	0.001
Transcribed locus	BE692425	0.417	0.002	0.003
Disabled homolog 2 (Drosophila)	AK017619	0.415	0.003	0.007
promyelocytic leukemia	BB667149	0.415	0.005	0.022
Versican	BM251152	0.415	0.003	0.002
ESTs	BB735884	0.413	0.009	0.004
Transcribed locus	BB420529	0.413	0.003	0.002
Embigin	BG064842	0.412	0.001	0.005
ESTs	BM123108	0.412	0.017	0.049

Interferon activated gene 204	NM_008329	0.412	0.003	0.022
Transcribed locus	BB367687	0.412	0.007	0.005
Transcribed locus, moderately similar to XP_001477892.1 PREDICTED: hypothetical protein [Mus musculus]	BG862223	0.412	0.003	0.008
UDP glucuronosyltransferase 1 family, polypeptide A6B	D87867	0.412	0.0001	0.001
E1A binding protein p400	BM236717	0.408	0.006	0.007
RIKEN cDNA 5830411K21 gene	BM220939	0.408	0.002	0.007
Transmembrane protein 8 (five membrane-spanning domains)	NM_021793	0.408	0.005	0.018
Coagulation factor XIII, A1 subunit	NM_028784	0.407	0.0001	0.002
ESTs, Weakly similar to TYROSINE-PROTEIN KINASE JAK3 (M.musculus)	BB441213	0.407	0.008	0.007
5-nucleotidase domain containing 2	BC011230	0.405	0.002	0.002
Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 homolog (human)	BM235514	0.405	0.006	0.009
Diaphanous homolog 3 (Drosophila)	NM_019670	0.405	0.01	0.037
ESTs, Weakly similar to phosphatase (Caenorhabditis elegans) (C.elegans)	BG075843	0.405	0.003	0.03
Follistatin	NM_008046	0.405	0.005	0.036
inner centromere protein	BB418702	0.405	0.001	0.002
ROD1 regulator of differentiation 1 (S. pombe)	BB519382	0.405	0.002	0.016
Centromere protein N	BM230253	0.403	0.002	0.012
IKAROS family zinc finger 1	AV317621	0.403	0.002	0.004
Leukocyte specific transcript 1	U72644	0.403	0.002	0.0001
Transcribed locus	BM116703	0.403	0.012	0.027
Membrane-spanning 4-domains, subfamily A, member 8A	NM_022430	0.4	0.01	0.025
Budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	AU045529	0.398	0.003	0.014
Transcribed locus	BG061923	0.397	0.003	0.006
Colony stimulating factor 3 receptor (granulocyte)	NM_007782	0.395	0.002	0.004
C-type lectin domain family 4, member d	NM_010819	0.395	0.001	0.007
RIKEN cDNA E130016E03 gene	AW547464	0.395	0.022	0.032
Schlafen 8	BC024709	0.395	0.006	0.039
RIKEN cDNA 4930428B01 gene	BB167877	0.394	0.008	0.013
Transcribed locus, strongly similar to NP_033509.1 ubiquitously transcribed tetratricopeptide repeat gene, X chromosome [Mus Zinc finger E-box binding homeobox 2	BB306686	0.394	0.014	0.014
RIKEN cDNA 4831429J16 gene	NM_015753	0.394	0.001	0.003
RIKEN cDNA 4831429J16 gene	BB702047	0.392	0.001	0.005
Toll-like receptor 1	AF316985	0.392	0.003	0.004
Mannose receptor, C type 1	NM_008625	0.391	0.0001	0.002
WW domain containing adaptor with coiled-coil	BM240080	0.391	0.003	0.015
Transcribed locus	BB460274	0.389	0.009	0.005
Meteorin, glial cell differentiation regulator-like	BB544962	0.386	0.009	0.015
T-box18	AK012980	0.386	0.004	0.015
Transcribed locus	BB236216	0.386	0.003	0.008
ESTs	BE853428	0.385	0.006	0.004
RIKEN cDNA 0610025L06 gene	AV010467	0.385	0.001	0.0001
CD244 natural killer cell receptor 2B4	NM_018729	0.382	0.007	0.005
Ecotropic viral integration site 2a	A1122415	0.382	0.002	0.001
RNA binding motif protein 47	BB400564	0.382	0.004	0.031
CD5 antigen-like	NM_009690	0.379	0.005	0.003

kit oncogene	X65997	0.379	0.005	0.048
Dermatan sulfate epimerase	BM207218	0.377	0.002	0.002
RIKEN cDNA 6720463M24 gene	AK020138	0.375	0.008	0.016
ESTs	BB462614	0.372	0.009	0.036
Transmembrane protein 176A	AU040201	0.372	0.003	0.008
WNT1 inducible signaling pathway protein 2	NM_016873	0.372	0.002	0.0001
ESTs	A1785329	0.368	0.011	0.023
Transcribed locus	BB455909	0.368	0.004	0.0001
Membrane-spanning 4-domains, subfamily A, member 6D	NM_026835	0.366	0.001	0.002
Signal-regulatory protein beta 1	A1662854	0.365	0.001	0.0001
Structural maintenance of chromosomes 2	B1684556	0.365	0.007	0.0001
Chemokine (C-C motif) receptor 5	D83648	0.364	0.001	0.004
Latent transforming growth factor beta binding protein 2	NM_013589	0.364	0.002	0.001
MARCKS-like 1	NM_010807	0.362	0.002	0.031
Transcribed locus	BB336138	0.362	0.006	0.01
Transcribed locus	BM241342	0.361	0.003	0.021
Vav 1 oncogene	NM_011691	0.361	0.004	0.001
Zinc finger CCCH type containing 12D	BB508669	0.361	0.007	0.004
Transcribed locus	BB468551	0.358	0.005	0.005
ESTs	BM240056	0.357	0.012	0.001
RIKEN cDNA 4930547N16 gene	BM205349	0.357	0.011	0.027
Glucosaminyl (N-acetyl) transferase 1, core 2	AK017462	0.356	0.003	0.0001
ESTs	BB147698	0.351	0.006	0.001
Chemokine (C-X-C motif) ligand 12	BC006640	0.348	0.0001	0.01
C-type lectin domain family 4, member n	AF240358	0.348	0.006	0.011
Mus musculus, clone IMAGE:3492506, mRNA, partial cds	AW763751	0.345	0.004	0.01
Transmembrane and coiled coil domains 1	BB470329	0.342	0.014	0.029
Fc receptor-like S, scavenger receptor	BC016551	0.341	0.001	0.0001
Interferon induced transmembrane protein 6	BB193024	0.341	0.003	0.003
Interleukin 1 receptor, type I	NM_008362	0.34	0.001	0.0001
RIKEN cDNA 8430436C05 gene	AU016566	0.339	0.004	0.005
Similar to SIRP beta 1 cell surface protein	BB224524	0.338	0.002	0.005
C-type lectin domain family 4, member a2	BC006623	0.337	0.001	0.001
Kinesin family member 20B	BB200034	0.337	0.004	0.0001
hematological and neurological expressed sequence 1	AV067695	0.336	0.0001	0.04
ribonuclease L (2, 5-oligoisoadenylate synthetase-dependent)	BF714880	0.333	0.002	0.002
Serine/threonine kinase 17b (apoptosis-inducing)	A1661948	0.333	0.007	0.012
Immunoglobulin superfamily, member 6	NM_030691	0.33	0.002	0.001
ESTs	AW909042	0.329	0.009	0.004
Allograft inflammatory factor 1	NM_019467	0.325	0.001	0.004
Transcribed locus	BM239436	0.325	0.008	0.009
Insulin-like growth factor binding protein 5	NM_010518	0.324	0.001	0.0001
CD163 antigen	NM_053094	0.323	0.001	0.034
Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	BG865910	0.321	0.001	0.012
G-protein coupled receptor 65	NM_008152	0.316	0.003	0.0001
Mus musculus growth arrest specific 1 (Gas1), mRNA.	BB550400	0.312	0.0001	0.005
Chemokine (C-C motif) ligand 12	U50712	0.307	0.003	0.013
ESTs	BB488200	0.306	0.003	0.006
C-type lectin domain family 4, member e	NM_019948	0.304	0.004	0.011

Pro-platelet basic protein	NM_023785	0.303	0.003	0.004
Epstein-Barr virus induced gene 2	BM242490	0.301	0.003	0.003
Chemokine (C-C motif) receptor 2	BB148128	0.299	0.001	0.001
TBC1 domain family, member 9	BE853276	0.294	0.008	0.037
Membrane-spanning 4-domains, subfamily A, member 4C	NM_029499	0.293	0.002	0.003
Placenta-specific 8	AF263458	0.289	0.001	0.003
Transcribed locus	BB183534	0.284	0.003	0.001
ESTs	BB040443	0.281	0.002	0.009
Protein kinase, cAMP dependent regulatory, type II beta	BB216074	0.275	0.005	0.023
Transcribed locus	BE632903	0.275	0.008	0.022
RIKEN cDNA 2900062L11 gene	AK013740	0.273	0.012	0.034
S100 calcium binding protein A8 (calgranulin A)	NM_013650	0.261	0.001	0.001
Collagen and calcium binding EGF domains 1	BB197647	0.258	0.007	0.002
Cytochrome P450, family 1, subfamily b, polypeptide 1	BI251808	0.253	0.002	0.003
Chemokine (C-C motif) ligand 8	NM_021443	0.222	0.001	0.029
Transcribed locus	BB205102	0.206	0.01	0.01
Formyl peptide receptor 2	NM_008039	0.198	0.005	0.0001
Matrix metallopeptidase 9	NM_013599	0.198	0.004	0.001
S100 calcium binding protein A9 (calgranulin B)	NM_009114	0.195	0.001	0.001
Schlafen 4	AF099975	0.195	0.002	0.001
Mus musculus membrane-spanning 4-domains, subfamily A, member 9 (Ms4a9), mRNA.	NM_022429	0.192	0.002	0.001
DEXH (Asp-Glu-X-His) box polypeptide 58	AF316999	0.189	0.013	0.045
hypothetical protein LOC215866	BC002257	0.173	0.004	0.026
Chemokine (C-X-C motif) ligand 5	NM_009141	0.128	0.003	0.01
Secreted frizzled-related protein 2	NM_009144	0.128	0.001	0.0001
ESTs	BB160675	0.083	0.047	0.04
ESTs	AU019852	0.074	0.017	0.0001
Cell adhesion molecule with homology to L1CAM	NM_007697	0.073	0.023	0.002
Transient receptor potential cation channel, subfamily M, member 3	BB377721	0.059	0.032	0.001
Membrane-spanning 4-domains, subfamily A, member 4B	BB199001	0.051	0.033	0.026