Supplement Material

Tissue fixation and immunohistochemical analysis: Following intubation, the chest was opened and the heart was perfusion fixed for 2 minutes at 120 mmHg with 4% paraformaldehyde (Sigma, St. Louis, MO) in phosphate buffered saline (PBS) via left ventricular stab (a right atrial defect provided the egress for blood and fluid). Fixed hearts were immersed in 30% sucrose overnight, embedded into OCT (TissueTek), frozen, and prepared into 10-micron thick frozen sections. Anti-GFP (rabbit polyclonal conjugated to Alexa Fluor 488, Invitrogen) and anti-troponin I or anti-connexin (rabbit polyclonal, Santa Cruz Biotechnology) staining was carried out. Primary antibodies were used at dilutions of 1:200 (anti-GFP) and 1:100 (anti-troponin I and connexin). Secondary biotinylated anti-rabbit (Invitrogen) antibody was used for troponin-I and connexin, and then visualized with streptavidin Alexa Fluor 555 (Invitrogen). Confocal microscopy was performed on a Leica SP5 confocal system (Leica, Wetzlar, Germany).

Bioluminescence imaging of BMMC transplantation: The bioluminescent imaging system consists of a super sensitive, cooled (-90º C) CCD camera mounted onto a light-tight imaging chamber. The CCD chip is 2.7 cm^2, and consists of 2048 x 2048 pixels at 13.5 microns each. The camera is capable of detecting a minimum radiance of 100 photons/second/cm^2/steradian and can achieve a minimal image pixel resolution of 50 microns. The system does not allow for 3-dimensional imaging, hence spatial resolution is limited to a compressed, 2 dimensional image for analysis. Images were acquired using 1-10 minute intervals until peak signal was observed. BLI was quantified by creation of polygonal regions of interest (ROIs) by a technician (blinded to the experimental groups) over the precordium. Cell signal was reported in units of average photons per second per centimeter square per steradian (photons/s/cm^2/sr).

Validation of BLI by PCR analysis of BMMC-injected hearts *ex vivo*: For *ex vivo* validation of BLI, a standard curve was first generated by correlating cycle counts from real-time polymerase chain reaction probing for the male *Sry* gene in female hearts injected with known numbers of male BMMCs. Female animals receiving male BMMCs (n=8), were then imaged at various time points, followed by immediate harvest of the heart-cell complex for DNA extraction and RT-PCR for *Sry*. Cycle count results were then correlated with *in vivo* BLI signal strength by linear regression analysis. Correlation of BLI signal to cell number was achieved by extrapolation from the standard curve analysis of PCR cycle count to the known numbers of injected cells.

Positron emission tomography (PET) analysis: Regions of interest (ROIs) were drawn (by a technician blinded to the treatment groups) over the anterolateral wall (horizontal view). The counts per pixel per minute were converted to counts per milliliter per minute with a calibration constant obtained from scanning a cylindrical phantom. The ROI counts per milliliter per minute were converted to counts per gram per minute (assuming a tissue density of 1 g/mL) and divided by the injected dose to obtain an image ROI-derived [^{18}F]-FDG percentage injected dose per gram of heart (% ID/g) as previously described [1].

Echocardiographic determination of left ventricular contractility: Echocardiography was performed using the General Electric Vivid 7 Dimension imaging system equipped with a 13 MHz linear probe (GE, Milwaukee, MI). Mice receiving BMMC (n=20) or PBS (n=22) following I/R injury were assessed pre-operatively, 2, 4 and 6 weeks post-operatively. Animals were induced with isoflurane, placed supine, and received continuous inhaled anesthetic (1.5-2%) for the duration of the imaging session. Echocardiography was performed by two independent operators (blinded to the animal treatment groups), and M-mode short axis views of the LV were obtained. Analysis of the M-mode images was performed by a blinded technician using built-in GE analysis software.

Flow cytometry analysis: 1×10^6 BMMCs were incubated with 1 μl monoclonal antibody specific for CD31, CD34, CD45, CD11b, sca-1, CD44, CD28, flk-2, Thy1.1, or c-kit (BD, San Jose, CA) in 2% FBS/PBS at 4°C for 30 min and analyzed by FACSCalibur with Cellquest software (BD, San Jose, CA).

Invasive cardiovascular hemodynamics: Animals receiving either BMMC (n=15) or PBS (n=13) following I/R injury were assayed 6-weeks following surgery. Simultaneous measurements of pressure and volume were obtained using a specialized conductance catheter (Millar Instruments, Houston, Texas). Animals were induced and maintained with inhaled isoflurane (1-2%) in 100% oxygen. Mice were intubated and ventilated at a tidal volume of 200 μl at 100 breaths per minute (Harvard Apparatus, Holliston, MA). The internal jugular vein was cannulated with PE-10 tubing and a 10% albumin solution infused at 5 μl/min. The right carotid artery was next cannulated with the pressure-volume catheter which was advanced retrograde across the aortic valve to lie along the long axis of the left ventricle. The temperature of the mice was constantly monitored by a rectal probe and maintained at 37º C by a self-regulating heating pad (Fine Science Tools, San Francisco, CA). After baseline loops were recorded, occlusion parameters were recorded during and after three 5-second manual occlusions of the inferior vena cava (via transabdominal approach).

REFERENCES

1. Toyama H, Ichise M, Liow JS, Vines DC, Seneca NM, Modell KJ, Seidel J, Green MV, Innis RB. Evaluation of anesthesia effects on [18f]fdg uptake in mouse brain and heart using small animal pet. *Nucl Med Biol*. 2004;31:251-256

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure I. Schematic of experimental design. Fluc$^+$/eGFP$^+$ BMMCs were isolated and administered via direct intra-myocardial injection into wild-type (WT) FVB (syngeneic) mice who had undergone acute ischemia-reperfusion injury or sham surgery (no injury). Cell survival was assessed by longitudinal BLI carried out for several weeks. Hearts were explanted from a subset of animals in both groups, digested, and eGFP$^+$ BMMCs were isolated by FACS for whole-genome transcriptional profiling. This provided gene regulation profiles as a function of ischemic myocardial environment following transplant. To assess functional changes after BMMC transplant, I/R mice receiving BMMC were compared longitudinally against mice undergoing I/R injury with injection of PBS alone. This cohort underwent echocardiographic analysis, PET imaging, as well as pressure-volume loop and histological analysis.

Supplemental Figure II. Transplantation of BMMCs into non-ischemic hindlimb **(A)** A representative animal injected with 3 x 10^6 BMMCs into the hindlimb of syngeneic FVB mice shows significant bioluminescence activity at day 7, which decreases progressively over the following 3 weeks. (B) Detailed quantitative analysis of signals from all animals transplanted with BMMCs. Signal activity is expressed as photons/s/cm^2/sr.

Supplemental Figure III. Early BLI imaging predicts cardiac functional improvement. **(A)** Representative animals (n=6 per group) injected with 2 x 10^6 BMMCs show significant variability of BLI signal intensity on day 2 after permanent LAD occlusion. **(B)** Detailed quantitative analysis of signals from all animals transplanted with BMMCs. Signal activity is expressed as photons/s/cm^2/sr. **(C)** Day 2 BLI signal intensity (horizontal axis) correlates robustly with BLI signal at day 35 (vertical axis). **(D)** Day 2 BLI signal intensity (horizontal axis) correlates well with cardiac function assessed by echocardiography at day 42 (vertical axis).

Supplemental Figure IV. Isolation of L2G85-derived, GFP^+ bone marrow mononuclear cells by Langendorf-digestion and FACS sorting after myocardial transplantation. **(A)** FACS analysis of a digested WT heart that received PBS 4 days prior to explantation compared with **(B)** WT heart that received 5×10^6 L2G-dervived bone marrow mononuclear cells reveals a distinct, GFP-expressing group of cells (red box). **(C)** Examination of the sorted cell population by fluorescent microscopy reveals GFP-expressing cells (scale bar=50µm) with a cytosolic pattern of GFP expression and autofluorescence of the multi-lobular nucleus of a typical mononuclear cell (blue-bordered inlay, scale bar=5µm).

SUPPLEMENTAL TABLES

Supplemental Table I. Genes with upregulated expression in BMMCs transplanted into I/R-injured hearts vs. sham-operated hearts.

Gene ID	Gene Name	fold change	q-value
4370	RE1-silencing transcription factor	18.447	0.0190
507	Myeloperoxidase	18.427	0.0190
15302	Low density lipoprotein receptor-related protein 1	16.621	0.0337
2167	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	11.396	0.0299
6386	RIKEN cDNA 2700023B17 gene	11.142	0.0190
21261	RIKEN cDNA 1300012C15 gene	10.153	0.0237
7699	ESTs BG069076	9.323	0.0190
16738	ESTs BG075144	8.386	0.0365
16804	RIKEN cDNA 1810009A16 gene	7.642	0.0297
7296	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	7.277	0.0190
7522	Eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	6.913	0.0264
14155	H3062E05-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3062E05 5', MRNA sequence	6.785	0.0434
22355	Actinin, alpha 1	6.345	0.0190
11400	DNA segment, Chr 4, ERATO Doi 78, expressed	6.264	0.0299
11307	ESTs BM237222	6.235	0.0337
16604	ESTs BM208190	5.892	0.0190
13515	Cholinergic receptor, muscarinic 3, cardiac	5.685	0.0297
7259	BCL2-like 13 (apoptosis facilitator)	5.592	0.0190
13118	Methionine sulfoxide reductase A	5.535	0.0219
9211	Sarcoglycan, delta (dystrophin-associated glycoprotein)	5.405	0.0365
5604	ESTs BM115315	5.240	0.0245
5772	RIKEN cDNA C230081A13 gene	5.140	0.0337
3248	C77241 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone J0027H07 3' similar to Mus musculus Mhc class II A beta polypeptide, partial cds, mRNA, MRNA sequence	5.080	0.0299
9661	SET and MYND domain containing 2	4.900	0.0337
17276	Hypothetical protein 4931417A20	4.887	0.0245
18390	Cysteine conjugate-beta lyase 1	4.753	0.0245
11285	5'-nucleotidase, cytosolic II	4.614	0.0365
7689	Polymerase (DNA directed), eta (RAD 30 related)	4.590	0.0190
10441	Estrogen receptor 1 (alpha)	4.585	0.0190
5680	Peroxisome proliferator activated receptor binding protein	4.543	0.0000
1309	prolactin-like protein A	4.516	0.0299
16987	ESTs BG068989	4.485	0.0245
21804	Transient receptor potential cation channel, subfamily M, member 3	4.480	0.0434
6204	AT rich interactive domain 5B (Mrf1 like)	4.452	0.0237
26	leukocyte receptor cluster (LRC) member 8	4.426	0.0190
3535	CXORF15	4.418	0.0000
21557	Mitogen-activated protein kinase kinase kinase kinase 3	4.404	0.0299
8574	ESTs AW542165	4.370	0.0434
3282	RAR-related orphan receptor alpha	4.345	0.0190
17635	H3039A12-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3039A12 3', MRNA sequence	4.314	0.0434
11968	ESTs AW556287	4.260	0.0458
7245	C0201C10-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus	4.254	0.0299

	cDNA clone NIA:C0201C10 IMAGE:30010689 3', MRNA sequence		
208	RNA binding motif protein, X chromosome	4.239	0.0299
21002	Mus musculus transcribed sequence with moderate similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	4.234	0.0402
608	LIM and SH3 protein 1	4.215	0.0297
21782	Paired box gene 2	4.206	0.0434
7087	CDK5 regulatory subunit associated protein 2	4.192	0.0190
13127	Ryanodine receptor 2, cardiac	4.188	0.0337
13733	Ribonuclease P 25 subunit (human)	4.139	0.0299
6424	Nuclear receptor coactivator 1	4.104	0.0190
5958	ESTs C86523	4.090	0.0299
7674	RIKEN cDNA 6230416A05 gene	4.054	0.0190
7060	RIKEN cDNA 2610304G08 gene	4.051	0.0219
6659	Zinc finger, CSL domain containing 2	4.007	0.0190
11601	RIKEN cDNA F830020C16 gene	4.003	0.0297
3032	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	3.985	0.0299
16347	ESTs BM114250	3.963	0.0365
16769	Neurotrimin	3.961	0.0297
11562	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	3.915	0.0299
5336	Phosphatidylinositol-3-phosphatase associated protein	3.912	0.0237
4349	T-box 19	3.905	0.0434
9023	ESTs BM205822	3.880	0.0245
640	Splicing factor, arginine/serine-rich 2, interacting protein	3.861	0.0297
169	Zinc finger protein 106	3.859	0.0245
18213	Chemokine (C-C motif) receptor 2	3.846	0.0190
13741	Ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	3.815	0.0458
18117	L0502G02-3 NIA Mouse Newborn Heart cDNA Library Mus musculus cDNA clone L0502G02 3', MRNA sequence	3.812	0.0299
8597	Open reading frame 5	3.806	0.0237
3445	ESTs AU016686	3.786	0.0434
5096	CDNA sequence BC027057	3.716	0.0299
4558	ESTs BM220566	3.709	0.0402
1971	ESTs BM115946	3.707	0.0190
7032	ESTs BG065784	3.707	0.0190
22083	RIKEN cDNA E430034C17 gene	3.701	0.0402
681	hematopoietic SH2 protein	3.700	0.0237
8355	RIKEN cDNA 9130001E16 gene	3.690	0.0245
7541	Zinc finger, matrin-like	3.672	0.0365
22333	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	3.667	0.0402
18351	DNA2 DNA replication helicase 2-like (yeast)	3.663	0.0190
21440	EST AU024779	3.639	0.0337
6831	Suppression of tumorigenicity 7-like	3.627	0.0190
4564	ESTs BM234559	3.618	0.0365
908	vacuolar protein sorting 26 (yeast)	3.595	0.0190
2388	ESTs BM120829	3.586	0.0190
9457	PHD finger protein 17	3.576	0.0245
17470	Calsyntenin 2	3.572	0.0299
695	ESTs BM219095	3.556	0.0190
6815	DEAH (Asp-Glu-Ala-His) box polypeptide 35	3.546	0.0245
9006	Exportin 6	3.510	0.0190
54	Cleavage and polyadenylation specific factor 5	3.486	0.0245

3921	Cathepsin B	3.475	0.0299
34	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	3.466	0.0337
16990	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	3.462	0.0337
8354	ESTs BG066588	3.439	0.0458
5126	Phosphoserine/threonine/tyrosine interaction protein	3.435	0.0297
9237	Clathrin, heavy polypeptide (Hc)	3.433	0.0299
12753	H3061G02-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3061G02 3', MRNA sequence	3.431	0.0402
7730	ESTs BG070577	3.421	0.0245
1530	CDNA sequence BC065123	3.414	0.0299
18356	RIKEN cDNA A930015D03 gene	3.398	0.0190
4033	nuclear receptor coactivator 6 interacting protein	3.381	0.0190
11394	DiGeorge syndrome critical region gene 8	3.381	0.0190
12962	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	3.376	0.0190
18	Huntingtin interacting protein 1	3.354	0.0190
4328	Splicing factor, arginine/serine-rich 15	3.345	0.0245
22000	G protein-coupled receptor 172B	3.333	0.0190
8377	UNKNOWN C0302G08	3.325	0.0245
5416	Copine III	3.323	0.0299
4327	Proteasome (prosome, macropain) subunit, beta type 2	3.285	0.0402
6348	Radical fringe gene homolog (Drosophila)	3.278	0.0458
5000	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130006F20 product:unknown EST, full insert sequence	3.261	0.0299
12739	Seizure related 6 homolog (mouse)-like	3.259	0.0190
7158	Matrix metalloproteinase 23	3.245	0.0190
4129	Cell division cycle 37 homolog (S. cerevisiae)	3.241	0.0245
22411	ESTs BG071060	3.240	0.0434
12696	RIKEN cDNA 2600014M03 gene	3.225	0.0190
6176	EST X83328	3.221	0.0337
4341	ESTs BM219738	3.215	0.0190
14545	ESTs BG075148	3.207	0.0245
13725	CXXC finger 5	3.205	0.0365
10192	zinc finger RNA binding protein	3.184	0.0190
13426	BTB (POZ) domain containing 6	3.179	0.0297
10951	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	3.176	0.0434
7022	ESTs BM120426	3.174	0.0299
8118	Laminin B1 subunit 1	3.173	0.0190
7594	purine rich element binding protein B	3.169	0.0434
5542	Prolactin-like protein M	3.163	0.0190
7144	CDNA sequence BC022960	3.159	0.0337
17001	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230004D16 product:unclassifiable, full insert sequence.	3.151	0.0299
9973	ESTs BG068936	3.146	0.0337
19809	Diaphanous homolog 2 (Drosophila)	3.143	0.0434
10567	Olfactory receptor 56	3.129	0.0237
4682	RIKEN cDNA 1110007A13 gene	3.123	0.0237
2333	Nuclear receptor coactivator 2	3.103	0.0190
16830	L0003G04-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA Library Mus musculus cDNA clone L0003G04 3', MRNA sequence	3.096	0.0190
16530	CD53 antigen	3.079	0.0264
5544	ESTs BG068457	3.061	0.0365
8796	RIKEN cDNA 2210020M01 gene	3.057	0.0337
7688	ESTs BG064687	3.057	0.0458

10408	SEC24 related gene family, member A (S. cerevisiae)	3.051	0.0000
15714	B-cell linker	3.051	0.0190
7478	UNKNOWN L0812F11	3.037	0.0299
8579	Nucleoporin 205	3.033	0.0190
3040	Calcium channel, voltage-dependent, L type, alpha 1D subunit	3.033	0.0237
5213	ESTs BM217965	3.030	0.0299
2620	Similar to General transcription factor 3C polypeptide 3 (Transcription factor IIIC-gamma subunit) (TF3C-gamma) (TFIIIC 102 kDa subunit) (TFIIIC102)	3.029	0.0237
6522	homer homolog 3 (Drosophila)	3.019	0.0190
2400	transcribed sequence with moderate similarity to protein prf:1614337A (M.musculus) 1614337A formin [Mus musculus]	3.015	0.0190
5585	ESTs BG075241	3.014	0.0299
10623	Translocated promoter region	3.003	0.0190
4990	Transducin (beta)-like 1X-linked receptor 1	2.988	0.0299
6702	Membrane-spanning 4-domains, subfamily A, member 6B	2.982	0.0297
7281	Cleavage and polyadenylation specific factor 1	2.976	0.0337
5995	Phosphorylase kinase alpha 2	2.969	0.0365
1067	Glutamyl-prolyl-tRNA synthetase	2.966	0.0458
19	RIKEN cDNA E130014J05 gene	2.964	0.0190
21642	ESTs BG067237	2.960	0.0299
3786	Forkhead box J3	2.954	0.0337
5609	L0283C06-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA clone L0283C06 3', MRNA sequence	2.944	0.0237
15306	RIKEN cDNA 1700022C02 gene	2.937	0.0000
17043	RIKEN cDNA 5330417K06 gene	2.924	0.0264
21107	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.922	0.0299
15036	F-box protein 39	2.921	0.0297
7482	hypothetical protein B430319G23	2.915	0.0245
6147	Embryonic large molecule derived from yolk sac	2.894	0.0190
11690	Pleckstrin and Sec7 domain containing 4	2.893	0.0245
8132	Tudor domain containing 3	2.893	0.0365
6627	Myeloid cell nuclear differentiation antigen	2.891	0.0458
473	Ras homolog gene family, member U	2.883	0.0337
4999	Vav 3 oncogene	2.879	0.0190
1115	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.878	0.0190
9574	Trinucleotide repeat containing 6a	2.876	0.0190
18148	ESTs BM236686	2.875	0.0297
8593	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	2.873	0.0245
9460	Ubiquitin-like 1 (sentrin) activating enzyme E1A	2.871	0.0219
11872	RIKEN cDNA 1300018J18 gene	2.870	0.0190
3915	solute carrier family 25 (mitochondrial carrier; ornithine transporter), member 15	2.853	0.0299
7513	Sarcospan	2.843	0.0297
16101	RIKEN cDNA 1110021E09 gene	2.841	0.0237
11635	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	2.839	0.0190
12372	RIKEN cDNA 5730414C17 gene	2.838	0.0402
7459	Inositol polyphosphate multikinase	2.831	0.0190
12685	ESTs BG076236	2.830	0.0264
11842	Mus musculus beta globin mRNA, partial cds	2.828	0.0299
6959	Casein kinase II, alpha 1 polypeptide	2.825	0.0299
1974	ESTs BG084297	2.810	0.0245
14785	tripartite motif protein 16	2.808	0.0264
19605	RIKEN cDNA 2810028N01 gene	2.806	0.0190
9236	Pleckstrin homology domain containing, family G (with RhoGef domain) member 4	2.804	0.0299

5206	ESTs AU041696	2.794	0.0190
8119	Vav2 oncogene	2.790	0.0434
8598	ESTs BQ558545	2.789	0.0337
15060	R3H domain (binds single-stranded nucleic acids)	2.785	0.0190
4911	NOL1/NOP2/Sun domain family 2	2.781	0.0299
4347	transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	2.774	0.0264
9233	RIKEN cDNA 3110002H16 gene	2.772	0.0237
909	Estrogen receptor 2 (beta)	2.771	0.0299
485	F-box and leucine-rich repeat protein 12	2.768	0.0299
12336	CDNA sequence BC002230	2.767	0.0299
602	CWF19-like 2, cell cycle control (S. pombe)	2.765	0.0365
19802	RIKEN cDNA 2210408F21 gene	2.758	0.0299
7030	Glyoxylate reductase/hydroxypyruvate reductase	2.758	0.0299
22094	RIKEN cDNA D930043N17 gene	2.756	0.0000
4910	A kinase (PRKA) anchor protein (yotiao) 9	2.753	0.0299
5875	ESTs C79677	2.752	0.0245
9234	Zinc finger protein 94	2.749	0.0219
7464	RIKEN cDNA 3110001I22 gene	2.749	0.0458
7279	ESTs BM293416	2.742	0.0402
7950	Gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	2.737	0.0365
6875	Peroxiredoxin 3	2.735	0.0365
607	ESTs BG074084	2.734	0.0337
7691	Ligand of numb-protein X 2	2.721	0.0458
7607	ESTs BM239048	2.719	0.0365
8644	ESTs BM241069	2.711	0.0299
14462	RIKEN cDNA 9030624J02 gene	2.707	0.0190
18888	RIKEN cDNA B230120H23 gene	2.701	0.0264
7928	RIKEN cDNA 4933429I20 gene	2.700	0.0402
18589	Fas (TNFRSF6)-associated via death domain	2.698	0.0190
11093	RIKEN cDNA 2410002O22 gene	2.695	0.0000
4957	Expressed sequence C78409	2.691	0.0245
5758	Hyaluronan and proteoglycan link protein 1	2.689	0.0299
8789	ESTs BG070566	2.684	0.0245
178	DnaJ (Hsp40) homolog, subfamily C, member 7	2.682	0.0297
680	Protein kinase C, eta	2.663	0.0190
5989	ESTs BI076718	2.662	0.0434
4905	Expressed sequence AI447904	2.661	0.0337
12922	Possibly intronic in U014579-H3037B07	2.655	0.0245
16592	EST AA407452	2.652	0.0245
4598	Expressed sequence AI848218	2.652	0.0237
9663	Vacuolar protein sorting 16 (yeast)	2.647	0.0264
1533	Ubiquitin specific protease 31	2.644	0.0190
3673	Serine (or cysteine) proteinase inhibitor, clade B, member 9	2.636	0.0237
17457	Transmembrane channel-like gene family 3	2.636	0.0245
21947	Glycerol phosphate dehydrogenase 2, mitochondrial	2.635	0.0000
12917	Latent transforming growth factor beta binding protein 1	2.635	0.0299
51	PAK1 interacting protein 1	2.632	0.0337
4242	Ankyrin repeat domain 25	2.629	0.0297
11361	IQ motif containing GTPase activating protein 1	2.623	0.0190
2251	Calmodulin binding protein 1	2.620	0.0402
11912	Ribosomal protein L28	2.615	0.0402
7664	Aminoacylase 1	2.612	0.0337
12772	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif,	2.609	0.0458

	18		
13406	Transmembrane protein 16F	2.608	0.0190
20424	Ubiquitin specific protease 7	2.604	0.0190
21048	Hephaestin	2.602	0.0190
15950	RIKEN cDNA C530014P21 gene	2.600	0.0365
14223	hypothetical protein 4933427D06	2.599	0.0245
603	Lactation elevated 1	2.599	0.0402
20951	Chondroitin sulfate GalNAcT-2	2.598	0.0337
12164	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	2.595	0.0245
15635	Trans-acting transcription factor 1	2.595	0.0337
18489	RIKEN cDNA E430028B21 gene	2.594	0.0190
6990	ADP-ribosylation factor GTPase activating protein 1	2.579	0.0458
5580	Tensin	2.578	0.0297
3478	Solute carrier family 30 (zinc transporter), member 4	2.578	0.0190
9245	L-threonine dehydrogenase	2.574	0.0434
21797	Annexin A4	2.573	0.0245
16501	Guanylate nucleotide binding protein 2	2.572	0.0245
7287	Zinc metalloproteinase, STE24 homolog (S. cerevisiae)	2.569	0.0337
6635	Teratocarcinoma expressed, serine rich	2.567	0.0245
5061	DNA segment, Chr 2, ERATO Doi 435, expressed	2.562	0.0190
4742	Oxoglutarate dehydrogenase (lipoamide)	2.559	0.0299
11540	Ubiquitin specific protease 3	2.557	0.0245
696	Secretory carrier membrane protein 1	2.557	0.0299
380	Flap structure specific endonuclease 1	2.555	0.0365
13258	RIKEN cDNA 5033428A16 gene	2.552	0.0245
389	Cytoplasmic polyadenylation element binding protein 4	2.551	0.0264
7277	hypothetical protein D430050E18	2.549	0.0337
6453	Hypothetical protein 9530064J02	2.546	0.0190
10075	Candidate tumor suppressor OVCA2	2.542	0.0190
3706	RIKEN cDNA 1810012N01 gene	2.540	0.0337
8365	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330428H05 product:unknown EST, full insert sequence	2.540	0.0402
18967	RIKEN cDNA 4932417H02 gene	2.539	0.0245
7836	RIKEN cDNA 1110032A03 gene	2.538	0.0219
21108	Laminin, alpha 2	2.537	0.0297
13125	XPA binding protein 1	2.535	0.0237
1127	RIKEN cDNA 6720464I07 gene	2.535	0.0264
20254	RIKEN cDNA 3010021M21 gene	2.535	0.0458
9890	Eukaryotic translation initiation factor 5	2.535	0.0299
9447	Polymerase (RNA) III (DNA directed) polypeptide F	2.534	0.0190
16371	RIKEN cDNA 4930579K19 gene	2.534	0.0245
11753	Complement receptor related protein	2.531	0.0245
4562	RIKEN cDNA 2610042O14 gene	2.523	0.0365
19799	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230039L18 product:unknown EST, full insert sequence.	2.518	0.0219
12255	Mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	2.516	0.0190
20432	AU024754 Mouse unfertilized egg cDNA Mus musculus cDNA clone J0460A12 3', MRNA sequence	2.516	0.0264
15013	Chloride channel calcium activated 1	2.515	0.0458
17725	MAP kinase-interacting serine/threonine kinase 1	2.513	0.0297
7052	RIKEN cDNA 5830415L20 gene	2.507	0.0264
2149	G protein-coupled receptor kinase 5	2.505	0.0299
11910	CDC-like kinase 2	2.502	0.0190
17346	5'-nucleotidase, cytosolic II	2.501	0.0190

469	Inner centromere protein	2.500	0.0337
14512	Eyes absent 3 homolog (Drosophila)	2.490	0.0190
12632	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae)	2.489	0.0190
5156	GTL2, imprinted maternally expressed untranslated mRNA	2.482	0.0402
22048	Ets variant gene 4 (E1A enhancer binding protein, E1AF)	2.481	0.0245
20521	CDNA sequence BC037674	2.477	0.0264
12131	clathrin, heavy polypeptide (Hc)	2.474	0.0190
21927	Speckle-type POZ protein	2.471	0.0190
694	casein kinase 1, alpha 1	2.471	0.0365
22433	RIKEN cDNA 4632412E09 gene	2.471	0.0190
6631	Hypothetical protein E030010A14	2.467	0.0434
21955	CDNA sequence BC039282	2.466	0.0190
4550	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430010H01 product:unknown EST, full insert sequence.	2.464	0.0245
7267	Proteasome (prosome, macropain) subunit, alpha type, 8	2.464	0.0402
21517	UDP-glucose pyrophosphorylase 2	2.457	0.0458
5344	DNA segment, Chr 10, Wayne State University 102, expressed	2.452	0.0365
4136	Hydroxysteroid dehydrogenase-4, delta<5>-3-beta	2.441	0.0365
15958	RIKEN cDNA 4930563C04 gene	2.441	0.0245
6661	ESTs BM195572	2.439	0.0337
19319	Pre-B-cell leukemia transcription factor interacting protein 1	2.439	0.0402
8389	Niemann Pick type C2	2.439	0.0190
16603	RIKEN cDNA 1110004P21 gene	2.437	0.0190
8577	Transforming, acidic coiled-coil containing protein 1	2.435	0.0297
8055	CCR4-NOT transcription complex, subunit 6	2.433	0.0190
4243	ESTs C78651	2.431	0.0365
596	ubiquitin specific protease 8	2.423	0.0337
3424	Baculoviral IAP repeat-containing 1b	2.421	0.0190
30	ATP-binding cassette, sub-family G (WHITE), member 2	2.420	0.0190
8003	Solute carrier organic anion transporter family, member 4a1	2.419	0.0365
7518	BAI1-associated protein 1	2.417	0.0299
2187	RIKEN cDNA 6030404K05 gene	2.415	0.0337
12963	Meiotic recombination 11 homolog A (S. cerevisiae)	2.412	0.0190
5072	Protein kinase C binding protein 1	2.410	0.0245
14975	CDK5 regulatory subunit associated protein 1-like 1	2.402	0.0190
4174	CAMP-regulated phosphoprotein 19	2.400	0.0402
7897	DNA segment, Chr 11, ERATO Doi 518, expressed	2.398	0.0458
13993	Retinoic acid induced 17	2.396	0.0190
13100	Transcription factor 19	2.396	0.0245
2613	RIKEN cDNA 3230401M21 gene	2.395	0.0245
7488	Adaptor-related protein complex 3, beta 2 subunit	2.393	0.0337
17889	ESTs AW556563	2.393	0.0299
8092	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.392	0.0434
19606	Laminin, gamma 1	2.388	0.0337
3984	Syntaxin binding protein 1	2.387	0.0402
3812	Ribosomal protein L5	2.383	0.0190
9566	CCR4-NOT transcription complex, subunit 6-like	2.383	0.0190
15819	GTPase, IMAP family member 4	2.380	0.0299
5160	Expressed sequence AI225782	2.374	0.0299
20514	Zinc finger protein 295	2.371	0.0190
8806	Similar to prostaglandin D receptor	2.370	0.0402
17551	RIKEN cDNA 5330440M15 gene	2.367	0.0245

6868	RIKEN cDNA 6720464I07 gene	2.365	0.0458
14813	Interferon alpha responsive gene	2.360	0.0190
8804	Follicle stimulating hormone receptor	2.359	0.0365
52	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.358	0.0434
8567	RIKEN cDNA 2010106G01 gene	2.357	0.0245
2186	CDNA sequence BC024814	2.357	0.0337
7421	RIKEN cDNA 1500032D16 gene	2.355	0.0299
9016	RIKEN cDNA E430023H19 gene	2.353	0.0299
13321	RIKEN cDNA D230046B21 gene	2.351	0.0365
9577	RIKEN cDNA 5830415L20 gene	2.347	0.0000
1758	RIKEN cDNA A230055J12 gene	2.346	0.0434
14030	Optic atrophy 1 homolog (human)	2.345	0.0190
246	Disrupted in renal carcinoma 2 (human)	2.344	0.0434
6420	RIKEN cDNA 6430706D22 gene	2.343	0.0402
5258	RIKEN cDNA 2900060P06 gene	2.341	0.0458
6845	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	2.337	0.0297
17654	TBC1 domain family, member 2	2.336	0.0237
19129	Transducin (beta)-like 1X-linked receptor 1	2.334	0.0245
20061	RIKEN cDNA E030004N02 gene	2.330	0.0299
4615	RIKEN cDNA 4633402D15 gene	2.324	0.0237
7276	Mitogen activated protein kinase kinase 1	2.323	0.0365
475	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	2.322	0.0337
5345	Leucine zipper transcription factor-like 1	2.322	0.0365
15189	Cell division cycle 40 homolog (yeast)	2.320	0.0219
15448	BCS1-like (yeast)	2.320	0.0264
18543	Dystrophin, muscular dystrophy	2.319	0.0299
690	SUMO/sentrin specific protease 3	2.316	0.0402
18592	Bystin-like	2.316	0.0190
3697	RIKEN cDNA 1110012D08 gene	2.315	0.0237
13587	Tripartite motif protein 37	2.312	0.0190
6841	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	2.311	0.0365
5119	Guanine nucleotide binding protein-like 3 (nucleolar)	2.310	0.0402
15245	Synaptojanin 2	2.309	0.0190
10658	Pleiomorphic adenoma gene-like 2	2.308	0.0434
5844	Mitogen-activated protein kinase kinase kinase 14	2.306	0.0190
10076	RIKEN cDNA 1200013B08 gene	2.306	0.0299
6238	Expressed sequence AI462438	2.304	0.0190
7591	Transient receptor potential cation channel, subfamily M, member 7	2.302	0.0297
5584	RIKEN cDNA 4930503E14 gene	2.301	0.0299
21980	Napsin A aspartic peptidase	2.301	0.0402
1667	Expressed sequence C80008	2.296	0.0402
1116	Tumor necrosis factor (ligand) superfamily, member 8	2.296	0.0365
8829	RIKEN cDNA 5430439M09 gene	2.294	0.0190
7037	RIKEN cDNA 2610507L03 gene	2.293	0.0365
8159	ESTs BG068633	2.292	0.0458
8588	Oral cancer overexpressed 1	2.292	0.0337
17938	similar to zinc finger protein 97	2.291	0.0219
18032	RIKEN cDNA 2610304F09 gene	2.288	0.0190
15341	Oxysterol binding protein-like 2	2.287	0.0219
6741	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.285	0.0434
2504	Ribosomal protein L8	2.283	0.0219

19310	Synapse associated protein 1	2.282	0.0190
17641	Fms interacting protein	2.281	0.0190
15269	RIKEN cDNA 2210404D11 gene	2.279	0.0365
2188	Sperm associated antigen 5	2.277	0.0299
12112	Splicing factor, arginine/serine rich 9	2.270	0.0190
13181	Solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	2.269	0.0299
15972	Homer homolog 1 (Drosophila)	2.269	0.0190
7033	ESTs BG069333	2.269	0.0365
3937	Rho GTPase activating protein 18	2.267	0.0190
1752	Transcription factor-like 1	2.266	0.0365
4537	UNKNOWN H3111B03	2.266	0.0402
18321	ESTs AW554592	2.266	0.0365
2809	RIKEN cDNA 1300018J18 gene	2.263	0.0245
6031	Thymoma viral proto-oncogene 3	2.255	0.0237
7297	Neuroblastoma ras oncogene	2.253	0.0264
7156	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	2.251	0.0245
18632	Nucleolar protein family 6 (RNA-associated)	2.242	0.0245
12122	Forkhead box O1	2.242	0.0299
9544	Coenzyme Q6 homolog (yeast)	2.241	0.0299
4639	RIKEN cDNA 2810450G17 gene	2.241	0.0434
1553	Fanconi anemia, complementation group D2	2.241	0.0458
21180	Kinesin family member 4	2.241	0.0190
18222	Interleukin 18 binding protein	2.241	0.0245
11862	RIKEN cDNA 0610037L13 gene	2.241	0.0219
6953	adenomatosis polyposis coli	2.240	0.0402
553	Interleukin-1 receptor-associated kinase 1	2.239	0.0458
16749	Cellular repressor of E1A-stimulated genes 1	2.238	0.0219
7049	Carboxylesterase 2	2.237	0.0245
1549	Lysophospholipase 3	2.237	0.0402
16129	Solute carrier family 22 (organic cation transporter), member 5	2.232	0.0190
9949	aldehyde dehydrogenase 9, subfamily A1	2.232	0.0190
3916	Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430015A10 product:hypothetical Lysine-rich region containing protein, full insert sequence	2.231	0.0365
2593	TBC1 domain family, member 19	2.231	0.0299
7159	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	2.230	0.0237
20976	G1 to S phase transition 1	2.227	0.0237
21081	RIKEN cDNA 9130227C08 gene	2.225	0.0297
12965	RIKEN cDNA 2700008N14 gene	2.224	0.0365
13314	RIKEN cDNA 4833409A17 gene	2.224	0.0402
8692	Suppressor of cytokine signaling 2	2.224	0.0365
21336	CDNA sequence BC030335	2.224	0.0190
5396	Engulfment and cell motility 3, ced-12 homolog (C. elegans)	2.221	0.0245
13103	Mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	2.221	0.0190
18766	RIKEN cDNA 1810055E12 gene	2.219	0.0219
4049	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.219	0.0434
11618	RIKEN cDNA 4933431N12 gene	2.217	0.0337
20998	transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	2.213	0.0365
21362	Glycerol-3-phosphate dehydrogenase 1-like	2.212	0.0190
4130	RIKEN cDNA 2900046H12 gene	2.211	0.0434
20805	Similar to Sorting nexin 23	2.208	0.0237

2608	Ubiquitin specific protease 31	2.208	0.0190
7577	Calreticulin	2.207	0.0297
14055	translocase of outer mitochondrial membrane 20 homolog (yeast)	2.206	0.0297
10437	Solute carrier family 35, member B4	2.206	0.0190
21500	Palmitoyl-protein thioesterase 1	2.204	0.0245
9694	Purine rich element binding protein B	2.198	0.0297
1764	Heat shock protein 8	2.193	0.0237
12966	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	2.190	0.0434
20469	Growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	2.189	0.0190
17953	RIKEN cDNA 4930507D05 gene	2.189	0.0402
4228	Chemokine (C-C motif) ligand 9	2.188	0.0297
5764	RIKEN cDNA 1190002N15 gene	2.188	0.0402
17861	Prolyl endopeptidase	2.187	0.0190
20658	Splicing factor, arginine/serine-rich 2, interacting protein	2.185	0.0190
20822	RIKEN cDNA 9530020G05 gene	2.184	0.0299
8686	SH3 multiple domains 2	2.183	0.0434
8848	Ribosomal protein L15	2.183	0.0190
20310	ATP-binding cassette, sub-family D (ALD), member 4	2.181	0.0219
1112	copper chaperone for superoxide dismutase	2.180	0.0219
236	ESTs BG074720	2.179	0.0434
2813	stearoyl-Coenzyme A desaturase 1	2.177	0.0190
21555	Membrane bound C2 domain containing protein	2.177	0.0237
13140	Pyridoxal (pyridoxine, vitamin B6) kinase	2.174	0.0337
6101	Dipeptidylpeptidase 8	2.174	0.0190
13886	ESTs BG075117	2.173	0.0365
16574	Germ cell-specific gene 2	2.168	0.0299
13949	Malic enzyme 2, NAD(+)-dependent, mitochondrial	2.168	0.0190
13537	RIKEN cDNA 5730409G15 gene	2.168	0.0190
17849	RIKEN cDNA 9130230N09 gene	2.166	0.0365
17293	transcribed sequence with weak similarity to protein sp:P11369 (M.musculus) POL2_MOUSE Retrovirus-related POL polyprotein [Contains: Reverse transcriptase ; Endonuclease]	2.166	0.0190
19075	RIKEN cDNA B830009D23 gene	2.165	0.0299
10391	Cytochrome P450, family 11, subfamily a, polypeptide 1	2.165	0.0458
9266	Forkhead box P2	2.165	0.0402
17645	ESTs BQ556237	2.164	0.0299
10699	Procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	2.163	0.0264
10959	Linker of T-cell receptor pathways	2.163	0.0299
20804	RIKEN cDNA 1200020A08 gene	2.163	0.0190
5802	expressed sequence AI838577	2.161	0.0434
15715	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	2.161	0.0245
22170	N-ethylmaleimide sensitive fusion protein attachment protein alpha	2.160	0.0299
8784	WAP four-disulfide core domain 1	2.160	0.0402
6252	Testis expressed gene 12	2.159	0.0365
15882	Vesicle-associated membrane protein 2	2.158	0.0402
8817	Signaling intermediate in Toll pathway-evolutionarily conserved	2.157	0.0434
4858	Rho/rac guanine nucleotide exchange factor (GEF) 18	2.156	0.0237
13700	Mus musculus, Similar to cytochrome c oxidase III, mitochondrial, clone IMAGE:4500967, mRNA	2.155	0.0297
3732	Zinc finger, DHHC domain containing 16	2.155	0.0299
16978	Glycosyltransferase-like domain containing 1	2.155	0.0434
6944	lectin, galactose binding, soluble 8	2.155	0.0190

14706	Replication protein A1	2.154	0.0190
12892	Transmembrane emp24 protein transport domain containing 5	2.154	0.0190
6838	ESTs AU022566	2.151	0.0402
19039	ESTs AW552788	2.151	0.0190
5120	Protocadherin gamma subfamily C, 3	2.151	0.0402
4512	Similar to bromodomain containing protein 1; BR140-like gene	2.148	0.0434
17082	RIKEN cDNA 4930522P08 gene	2.146	0.0190
2185	Ubiquitin specific protease 22	2.146	0.0365
1159	RIKEN cDNA 1810055G02 gene	2.143	0.0245
18976	RIKEN cDNA 1810063B05 gene	2.143	0.0245
15524	ESTs BM206654	2.141	0.0402
22389	Histone deacetylase 6	2.137	0.0237
22338	RIKEN cDNA 2810428C21 gene	2.136	0.0245
4806	N-ethylmaleimide sensitive fusion protein attachment protein gamma	2.136	0.0434
10071	Valyl-tRNA synthetase 2	2.136	0.0365
2689	Solute carrier family 14 (urea transporter), member 1	2.134	0.0297
19648	Glutamate-cysteine ligase, catalytic subunit	2.134	0.0299
18760	RIKEN cDNA 1110015K06 gene	2.132	0.0337
16575	L0241D06-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA clone L0241D06 3', MRNA sequence	2.132	0.0299
16626	Leucine-rich and death domain containing	2.132	0.0237
18267	RIKEN cDNA 1700064K09 gene	2.131	0.0219
12964	ESTs BM218837	2.131	0.0190
20632	Muscleblind-like 1 (Drosophila)	2.130	0.0245
1476	Cytoplasmic polyadenylation element binding protein 2	2.129	0.0245
7066	RIKEN cDNA A930038C07 gene	2.129	0.0434
19502	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	2.127	0.0245
21916	Serine/arginine-rich protein specific kinase 2	2.127	0.0245
11233	Signal sequence receptor, alpha	2.126	0.0190
1324	PWP2 (periodic tryptophan protein) homolog, yeast	2.126	0.0245
6390	Deleted in polyposis 1	2.126	0.0402
4331	Integral inner nuclear membrane protein MAN1	2.122	0.0190
7742	Splicing factor 3b, subunit 3	2.119	0.0190
21986	RIKEN cDNA 6430548M08 gene	2.119	0.0190
17253	Adaptor-related protein complex 3, beta 1 subunit	2.116	0.0337
9792	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor	2.115	0.0365
12321	ceroid-lipofuscinosis, neuronal 5	2.115	0.0190
18344	Retinoblastoma 1	2.114	0.0402
17026	RIKEN cDNA 2700094F01 gene	2.113	0.0190
13185	Ring finger and WD repeat domain 3	2.113	0.0299
13907	RIKEN cDNA 3830406C13 gene	2.112	0.0190
9071	Sperm associated antigen 5	2.110	0.0365
11901	RIKEN cDNA C330017I15 gene	2.108	0.0219
18296	Prominin 1	2.107	0.0245
17005	THAP domain containing 4	2.107	0.0245
21810	Adaptor-related protein complex AP-4, mu 1	2.106	0.0190
1524	RNA polymerase 1-4	2.106	0.0299
4970	RIKEN cDNA 6230412P20 gene	2.104	0.0264
3875	Eukaryotic translation initiation factor 3, subunit 5 (epsilon)	2.102	0.0434
8658	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	2.099	0.0245
7143	Nuclear receptor co-repressor 2	2.098	0.0245
15767	Opioid growth factor receptor	2.095	0.0299
11636	ATPase, Class V, type 10D	2.093	0.0190
10139	Leucine-zipper-like transcriptional regulator, 1	2.093	0.0190

8026	Mus musculus, Similar to cytochrome c oxidase III, mitochondrial, clone IMAGE:4500967, mRNA	2.092	0.0299
14901	RIKEN cDNA D730044K07 gene	2.092	0.0264
7345	L0271F09-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA clone L0271F09 3', MRNA sequence	2.092	0.0245
5629	Lectin, mannose-binding 2	2.091	0.0297
20202	expressed sequence AW124694	2.091	0.0237
10044	Mitogen activated protein kinase kinase 2	2.090	0.0365
7932	RIKEN cDNA 2410118I19 gene	2.090	0.0299
17703	RIKEN cDNA 3010001F23 gene	2.089	0.0299
10482	Actin related protein 2/3 complex, subunit 4	2.089	0.0190
4760	Fatty acid desaturase 3	2.088	0.0190
19006	Hypothetical A830091E24	2.088	0.0297
6337	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	2.088	0.0365
9224	transcribed sequence with weak similarity to protein pir:S23650 (H.sapiens) S23650 retrovirus-related hypothetical protein II - human retrotransposon LINE-1	2.087	0.0434
19851	Adenomatosis polyposis coli	2.087	0.0297
21525	Glycerol-3-phosphate dehydrogenase 1-like	2.086	0.0264
18459	RIKEN cDNA 5730589K01 gene	2.085	0.0402
16408	Insulin-like growth factor binding protein 3	2.084	0.0365
7238	Testis derived transcript 3	2.083	0.0337
12027	Regulator of G-protein signaling 3	2.080	0.0299
13593	Transmembrane protein 19	2.078	0.0190
1180	RIKEN cDNA 0610037H22 gene	2.078	0.0297
8902	Beta-2 microglobulin	2.077	0.0237
10455	Tumor necrosis factor, alpha-induced protein 1 (endothelial)	2.075	0.0299
13432	RIKEN cDNA D430028G21 gene	2.075	0.0299
14143	DNA methyltransferase 3B	2.074	0.0190
5063	Optic atrophy 1 homolog (human)	2.074	0.0434
21566	Tripartite motif protein 13	2.073	0.0264
22496	Branched chain ketoacid dehydrogenase kinase	2.073	0.0402
55	Integrin binding sialoprotein	2.072	0.0458
7953	Aldo-keto reductase family 1, member A4 (aldehyde reductase)	2.072	0.0458
18842	ESTs C77673	2.071	0.0237
18352	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	2.069	0.0365
8447	DNA segment, Chr 16, ERATO Doi 472, expressed	2.066	0.0219
11170	Ngfi-A binding protein 2	2.066	0.0190
17875	Thioesterase, adipose associated	2.065	0.0245
6675	erythrocyte protein band 4.1	2.065	0.0365
20081	Cyclin-dependent kinase 6	2.065	0.0245
15054	Syndecan 3	2.063	0.0337
6987	Multiple substrate lipid kinase	2.062	0.0299
13431	Expressed sequence C79407	2.062	0.0219
18062	DNA segment, Chr 5, Wayne State University 152, expressed	2.062	0.0190
10754	NMDA receptor-regulated gene 2	2.057	0.0245
1074	transcribed sequence with moderate similarity to protein pir:C21124 (D.melanogaster) C21124 Bkm-like sex-determining region hypothetical protein CS319 - fruit fly (Drosophila melanogaster) (fragment)	2.056	0.0299
2184	Glutamyl-prolyl-tRNA synthetase	2.056	0.0365
16837	Sorbitol dehydrogenase 1	2.055	0.0190
8141	Sorcin	2.054	0.0365
17538	BTB (POZ) domain containing 3	2.054	0.0337
2147	DNA segment, Human S2298E	2.051	0.0245
11142	RIKEN cDNA A630082K20 gene	2.051	0.0365

11874	RIKEN cDNA D230014I24 gene	2.050	0.0245
10636	osmotic stress protein	2.047	0.0190
7502	RIKEN cDNA 2810453L12 gene	2.046	0.0219
8647	Expressed sequence AA415817	2.046	0.0190
16241	RIKEN cDNA 4930403J22 gene	2.045	0.0365
17772	Tissue specific transplantation antigen P35B	2.045	0.0264
5141	Suppressor of cytokine signaling 6	2.043	0.0458
18229	Polymerase (RNA) III (DNA directed) polypeptide E	2.042	0.0299
1120	ESTs BM218892	2.042	0.0402
19047	Ribosomal protein L7-like 1	2.041	0.0219
21685	ADP-ribosyltransferase 3	2.040	0.0299
14059	Eukaryotic translation initiation factor 2, subunit 2 (beta)	2.039	0.0434
3045	Ankyrin repeat and KH domain containing 1	2.039	0.0219
16507	Intersectin 1 (SH3 domain protein 1A)	2.037	0.0299
21930	CDC2-related kinase 7	2.034	0.0297
11940	Troponin I, cardiac	2.033	0.0337
10687	Cystatin C	2.029	0.0299
10140	RIKEN cDNA A430107J06 gene	2.029	0.0219
11367	RIKEN cDNA 1810019A08 gene	2.028	0.0402
18371	RIKEN cDNA 4921521J11 gene	2.027	0.0299
8199	EST BM231793	2.027	0.0299
17492	Eukaryotic translation initiation factor 2 alpha kinase 1	2.026	0.0297
4303	RIKEN cDNA 1110028E10 gene	2.026	0.0402
13104	RIKEN cDNA D230012E17 gene	2.025	0.0264
15921	RIKEN cDNA 2610312E17 gene	2.024	0.0190
10079	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	2.024	0.0365
19505	Chromodomain helicase DNA binding protein 9	2.024	0.0190
18629	Kruppel-like factor 7 (ubiquitous)	2.023	0.0299
19456	RIKEN cDNA 5730509C05 gene	2.022	0.0402
16658	Ceroid-lipofuscinosis, neuronal 2	2.022	0.0237
15912	Ubiquitin-like, containing PHD and RING finger domains 2	2.015	0.0245
664	Tumor necrosis factor superfamily, member 5-induced protein 1	2.012	0.0337
16950	CDC42 small effector 2	2.011	0.0264
18135	RIKEN cDNA 4832441B07 gene	2.006	0.0297
13277	Transforming growth factor beta regulated gene 1	2.004	0.0245
8699	Mus musculus transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	2.003	0.0365
15560	Cell division cycle 6 homolog (S. cerevisiae)	2.002	0.0190
20960	RIKEN cDNA 1300007B12 gene	1.998	0.0190
15842	Diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2	1.998	0.0190
18603	Signal sequence receptor, alpha	1.997	0.0237
16607	TBC1 domain family, member 22a	1.997	0.0297
8186	Zinc finger protein 654	1.996	0.0245
19396	RIKEN cDNA 6530401C20 gene	1.993	0.0299
9007	Mannose-6-phosphate receptor binding protein 1	1.993	0.0299
8253	Expressed sequence AW549877	1.992	0.0190
11434	Zinc finger and BTB domain containing 34	1.990	0.0337
13650	RIKEN cDNA A230065C20 gene	1.988	0.0190
9778	H2-K region expressed gene 6	1.986	0.0402
1323	RIKEN cDNA A630078A22 gene	1.982	0.0190
16668	Eukaryotic translation initiation factor 2B, subunit 5 epsilon	1.981	0.0190
15582	RIKEN cDNA 0610007P08 gene	1.980	0.0264
16578	Immature colon carcinoma transcript 1	1.980	0.0297

8426	Synovial apoptosis inhibitor 1, synoviolin	1.980	0.0245
16584	Trinucleotide repeat containing 15	1.973	0.0245
22336	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	1.973	0.0190
13560	Ribonuclease P/MRP 38 subunit (human)	1.971	0.0402
10381	CDC28 protein kinase 1b	1.970	0.0245
20607	RAB24, member RAS oncogene family	1.970	0.0190
4733	similar to phosphatidylinositol glycan class S (LOC276846), mRNA	1.970	0.0365
3861	TRIF-related adapter molecule TRAM	1.969	0.0402
14659	ELK3, member of ETS oncogene family	1.969	0.0365
10962	Transducin (beta)-like 1 X-linked	1.966	0.0297
18071	CDNA sequence BC054822	1.964	0.0297
8716	Braf transforming gene	1.963	0.0264
5046	SUMO/sentrin specific protease 5	1.963	0.0264
19267	RIKEN cDNA 5031439A09 gene	1.962	0.0190
1099	RIKEN cDNA 2900060B22 gene	1.961	0.0299
3110	Sorting nexin 17	1.961	0.0237
19183	Calcineurin binding protein 1	1.957	0.0245
911	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	1.957	0.0458
21985	DNA segment, Chr X, Immunex 40, expressed	1.957	0.0337
261	ATPase, class V, type 10A	1.957	0.0365
7831	Tissue inhibitor of metalloproteinase 2	1.957	0.0337
12446	Tryptophan rich basic protein	1.956	0.0299
3628	ribosomal protein L6	1.956	0.0365
10398	RIKEN cDNA 2010321M09 gene	1.954	0.0237
8790	CDNA sequence BC020002	1.953	0.0245
3463	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530047H08 product:unknown EST, full insert sequence	1.953	0.0245
17969	spermatid perinuclear RNA binding protein	1.953	0.0299
13376	transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	1.952	0.0365
6690	RIKEN cDNA 1110003F05 gene	1.951	0.0299
22257	SET domain-containing protein 7	1.951	0.0219
3696	Elastin microfibril interfacer 1	1.951	0.0365
1026	RIKEN cDNA 1700022L09 gene	1.947	0.0245
11266	Serine/arginine repetitive matrix 1	1.947	0.0337
11934	Ribosomal protein L7	1.946	0.0337
13223	Ribosomal protein L6	1.945	0.0365
8895	C0620G11-3 NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus musculus cDNA clone C0620G11 3', MRNA sequence	1.943	0.0434
19099	ferritin heavy chain	1.940	0.0365
18757	ATPase, Na+/K+ transporting, alpha 3 polypeptide	1.934	0.0297
12084	Tubulin tyrosine ligase-like family, member 4	1.927	0.0264
11861	RIO kinase 1 (yeast)	1.927	0.0219
5569	Coenzyme Q4 homolog (yeast)	1.927	0.0245
7111	RIKEN cDNA C730036B14 gene	1.925	0.0299
18338	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	1.924	0.0458
10419	RIKEN cDNA 3321401G04 gene	1.924	0.0245
17258	Bicaudal C homolog 1 (Drosophila)	1.921	0.0190
11619	Cullin 4B	1.921	0.0337
20353	Expressed sequence AW547186	1.921	0.0434
13607	RIKEN cDNA D330001F17 gene	1.920	0.0190
8749	SCY1-like 3 (S. cerevisiae)	1.918	0.0237
8974	DNA segment, Chr 14, Abbott 1 expressed	1.917	0.0365

11234	Signal recognition particle 14	1.916	0.0245
22207	Transcribed locus, strongly similar to NP_056099.1 KIAA0467 protein [Homo sapiens]	1.916	0.0299
13199	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.915	0.0299
15743	RIKEN cDNA 2810439F02 gene	1.914	0.0245
22446	Expressed sequence AI462438	1.912	0.0337
13132	Androgen-induced proliferation inhibitor	1.911	0.0190
239	Triosephosphate isomerase 1	1.911	0.0297
404	Expressed sequence AI838661	1.910	0.0190
11120	Guanine nucleotide binding protein, beta 2, related sequence 1	1.910	0.0245
12701	Polymerase (RNA) II (DNA directed) polypeptide I	1.909	0.0434
20492	RIKEN cDNA 4933403F05 gene	1.909	0.0297
13186	Prefoldin 4	1.908	0.0365
8920	Polymerase (DNA directed), epsilon	1.907	0.0219
12384	Ubiquitin specific protease 39	1.906	0.0245
21104	Dynein, cytoplasmic, light intermediate chain 1	1.906	0.0237
16634	B-cell receptor-associated protein 31	1.902	0.0190
13268	CHK2 checkpoint homolog (S. pombe)	1.901	0.0245
16518	Methylmalonic aciduria (cobalamin deficiency) type A	1.900	0.0297
18385	Eukaryotic translation initiation factor 1A, Y-linked	1.900	0.0190
6246	Rho guanine nucleotide exchange factor (GEF) 3	1.899	0.0458
21654	ATP-binding cassette, sub-family A (ABC1), member 1	1.899	0.0245
19027	UNKNOWN L0804D05	1.899	0.0402
10440	Expressed sequence C78859	1.897	0.0365
16883	Vitamin D receptor interacting protein	1.896	0.0434
6203	Acetyl-Coenzyme A acetyltransferase 3	1.894	0.0245
7864	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	1.894	0.0299
3469	Translocase of inner mitochondrial membrane 10 homolog (yeast)	1.893	0.0299
18094	Transmembrane protein 34	1.892	0.0245
7942	CCCTC-binding factor	1.891	0.0434
19436	U5 small nuclear ribonucleoprotein	1.891	0.0299
8308	RIKEN cDNA 2310067E08 gene	1.891	0.0297
18728	Radixin	1.890	0.0245
12266	PREDICTED: Mus musculus similar to RIKEN cDNA 6030426L16 (LOC382713), mRNA	1.890	0.0434
19367	ESTs AU021877	1.889	0.0365
8615	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	1.887	0.0299
13623	Phosphoribosyl pyrophosphate synthetase-associated protein 1	1.884	0.0402
9648	Nucleoporin 43	1.882	0.0337
19867	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1.881	0.0299
7769	H3093B08-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3093B08 3', MRNA sequence	1.881	0.0458
21667	DNA Segment, Chr 15 Massachusetts Institute of Technology 260	1.880	0.0337
9196	RIKEN cDNA E130016I23 gene	1.880	0.0245
2831	RIKEN cDNA 5330439J01 gene	1.878	0.0299
18357	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1.878	0.0264
8760	RIKEN cDNA 1500041J02 gene	1.876	0.0245
18358	ESTs BM219239	1.875	0.0434
17985	F-box only protein 3	1.875	0.0299
11876	RIKEN cDNA 4833418A01 gene	1.873	0.0458
5463	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.868	0.0337
14027	RIKEN cDNA 2810407C02 gene	1.867	0.0434
22318	Adaptor protein complex AP-2, mu1	1.867	0.0264
3525	Bromodomain containing 8	1.864	0.0458
8344	expressed sequence AA409541	1.864	0.0365
20350	Solute carrier family 39 (zinc transporter), member 14	1.864	0.0402

15160	RIKEN cDNA C130061O14 gene	1.863	0.0299
15146	Fanconi anemia, complementation group D2	1.862	0.0299
11586	Zinc finger protein 281	1.861	0.0190
14044	Protocadherin 12	1.860	0.0365
17341	CAMP-regulated phosphoprotein 19	1.860	0.0190
12909	RIKEN cDNA 0610041E09 gene	1.858	0.0219
18104	Ubiquitin-conjugating enzyme E2N	1.856	0.0337
17674	RIKEN cDNA 9430020M11 gene	1.856	0.0237
9310	Mitogen-activated protein kinase 6	1.855	0.0299
11663	Integrin alpha 3	1.855	0.0458
4797	DNA segment, Chr 10, University of California at Los Angeles 1	1.855	0.0402
7837	RIKEN cDNA 6330415G19 gene	1.854	0.0219
9257	nuclear receptor coactivator 6 interacting protein	1.854	0.0337
859	Ribosomal protein L38	1.850	0.0402
11654	Sorbitol dehydrogenase 1	1.848	0.0237
1327	PDZ domain containing 11	1.847	0.0402
21713	Proline synthetase co-transcribed	1.846	0.0297
8526	Transcription factor B2, mitochondrial	1.846	0.0297
18414	Transducin-like enhancer of split 1, homolog of Drosophila E(spl)	1.845	0.0297
14309	Expressed sequence AI315068	1.845	0.0237
5248	Proteasome (prosome, macropain) subunit, beta type 4	1.845	0.0245
8815	Golgi associated PDZ and coiled-coil motif containing	1.844	0.0434
15190	Adaptor protein complex AP-1, sigma 1	1.844	0.0337
5165	Neuraminidase 1	1.843	0.0458
1398	Cyclin E2	1.841	0.0245
19636	ARP3 actin-related protein 3 homolog (yeast)	1.841	0.0402
6298	Karyopherin (importin) alpha 3	1.840	0.0297
19403	RIKEN cDNA 1700047N06 gene	1.840	0.0337
17648	Ubiquitin specific protease 45	1.838	0.0297
9367	Alkylglycerone phosphate synthase	1.835	0.0245
17983	Vacuolar protein sorting 29 (S. pombe)	1.835	0.0365
7271	Gene model 1564, (NCBI)	1.835	0.0458
7208	Dynamin 1-like	1.834	0.0434
22173	Hydroxysteroid (17-beta) dehydrogenase 12	1.834	0.0264
15291	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	1.834	0.0190
11885	DNA segment, Chr 15, ERATO Doi 785, expressed	1.832	0.0337
4355	RIKEN cDNA 0610009E20 gene	1.831	0.0299
13171	Stress-induced phosphoprotein 1	1.830	0.0299
22121	Nuclear receptor coactivator 2	1.830	0.0365
18800	RIKEN cDNA 1110018O08 gene	1.829	0.0297
10338	BPY2 interacting protein 1	1.829	0.0299
21007	Protein phosphatase 4, regulatory subunit 1	1.828	0.0299
20674	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	1.827	0.0402
14464	neuron navigator 1	1.827	0.0190
13201	SA rat hypertension-associated homolog	1.826	0.0299
13543	DEAH (Asp-Glu-Ala-His) box polypeptide 40	1.824	0.0245
21950	Lectin, galactoside-binding, soluble, 3 binding protein	1.824	0.0365
20124	Chromosome condensation 1-like	1.823	0.0337
12140	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	1.821	0.0297
11406	RIKEN cDNA 1200004M23 gene	1.821	0.0245
21431	ESTs BM195385	1.821	0.0245
18020	Gene model 603, (NCBI)	1.820	0.0337
11698	SH3 domain binding glutamic acid-rich protein-like 3	1.820	0.0458

12455	SH3-domain binding protein 4	1.820	0.0365
18829	MAD homolog 4 (Drosophila)	1.815	0.0337
4344	Progesterone receptor membrane component 1	1.815	0.0245
19581	ribosomal protein S17	1.814	0.0190
12399	Zinc finger protein 131	1.813	0.0264
14274	hypothetical protein D430005B17	1.813	0.0219
14973	Thyroid hormone receptor interactor 4	1.811	0.0237
8677	Mitogen activated protein kinase kinase kinase 4	1.810	0.0237
15855	gene trap locus 6	1.810	0.0190
16136	Tumor necrosis factor, alpha-induced protein 2	1.808	0.0365
61	RIKEN cDNA 9430034D17 gene	1.807	0.0458
451	CCR4-NOT transcription complex, subunit 1	1.806	0.0337
21280	RIKEN cDNA 9830160H19 gene	1.805	0.0434
1202	Polo-like kinase 3 (Drosophila)	1.805	0.0337
17287	Kelch-like 6 (Drosophila)	1.802	0.0299
22311	RIKEN cDNA A830007P12 gene	1.800	0.0402
5293	Hypothetical protein E130101M22	1.800	0.0245
16366	Mitogen activated protein kinase 14	1.799	0.0245
10115	RIKEN cDNA 2210409M21 gene	1.796	0.0299
20292	E2F transcription factor 5	1.796	0.0297
14497	RIKEN cDNA D230019N24 gene	1.795	0.0190
18097	RIKEN cDNA E030041M21 gene	1.794	0.0297
6925	RIKEN cDNA 1200014M14 gene	1.794	0.0299
13809	Calcium/calmodulin-dependent protein kinase II gamma	1.793	0.0458
17524	RIKEN cDNA B430108F07 gene	1.793	0.0337
20095	Splicing factor, arginine/serine-rich 11	1.793	0.0190
7387	Zinc finger, RAN-binding domain containing 1	1.791	0.0190
9468	CDNA sequence BC023151	1.790	0.0297
1078	Ets variant gene 3	1.790	0.0365
3247	Coronin 7	1.789	0.0297
19822	similar to TATA element modulatory factor 1 (LOC232286), mRNA	1.789	0.0297
16794	RIKEN cDNA 2010305A19 gene	1.788	0.0458
5398	Hypothetical protein 4930565O14	1.785	0.0299
18141	DNA segment, Chr 5, Wayne State University 178, expressed	1.784	0.0434
20040	Angiotensin II, type I receptor-associated protein	1.784	0.0402
14894	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	1.784	0.0297
7973	cDNA sequence BC011426	1.781	0.0190
6681	RIKEN cDNA 0610040B21 gene	1.781	0.0402
3886	Nucleoporin 54	1.781	0.0237
5816	anti-Mullerian hormone type 2 receptor	1.780	0.0337
20444	Hypothetical protein 6530404F10Rik	1.780	0.0299
4551	Mevalonate kinase	1.779	0.0365
10133	Expressed sequence AU019823	1.778	0.0237
19874	SH3-domain kinase binding protein 1	1.777	0.0337
6225	CDNA sequence BC026744	1.777	0.0434
20063	RIKEN cDNA C730049F20 gene	1.774	0.0365
16480	Vinculin	1.772	0.0337
15946	Fas-associated factor 1	1.770	0.0365
4088	kinesin family member 18A	1.770	0.0297
16505	DNA segment, Chr 5, ERATO Doi 40, expressed	1.769	0.0337
19834	Heme binding protein 1	1.768	0.0299
3701	RIKEN cDNA 4933434E20 gene	1.767	0.0299
17587	Phosphatidylinositol glycan, class A	1.767	0.0299
7847	Polymerase (DNA directed), delta 1, catalytic subunit	1.766	0.0219

9466	RIKEN cDNA 1110008L16 gene	1.765	0.0245
15163	RIKEN cDNA 1300006C19 gene	1.765	0.0237
6319	RIKEN cDNA 1200015A19 gene	1.764	0.0264
7629	Heat shock 70kDa protein 12A	1.762	0.0402
4320	Ubiquitin specific protease 3	1.762	0.0297
6597	MYST histone acetyltransferase 2	1.761	0.0245
1367	Gene model 493, (NCBI)	1.759	0.0434
17697	Tankyrase 1 binding protein 1	1.759	0.0337
16722	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	1.756	0.0299
14279	CDNA sequence AK122525	1.755	0.0299
19544	RIKEN cDNA 6330416G13 gene	1.754	0.0245
8696	DnaJ (Hsp40) homolog, subfamily B, member 10	1.753	0.0297
21743	Nudix (nucleoside diphosphate linked moiety X)-type motif 5	1.753	0.0245
8438	Gem (nuclear organelle) associated protein 5	1.750	0.0434
9437	RIKEN cDNA C130089K02 gene	1.749	0.0365
7167	WD repeat domain 21	1.749	0.0458
22073	RIKEN cDNA 2600010L24 gene	1.748	0.0297
16513	CDNA sequence BC051080	1.747	0.0219
16674	Autophagy 7-like (S. cerevisiae)	1.747	0.0365
9923	Nuclear fragile X mental retardation protein interacting protein	1.747	0.0237
5478	RIKEN cDNA 1200009B18 gene	1.747	0.0337
21017	Ataxin 7-like 4	1.745	0.0337
2142	Nodal modulator 1	1.744	0.0237
7176	RIKEN cDNA 9630045H20 gene	1.744	0.0237
3417	Ring finger protein 141	1.744	0.0299
1954	Ring finger protein 12	1.743	0.0190
18637	PDZ and LIM domain 7	1.743	0.0337
14852	Chemokine-like factor super family 8	1.742	0.0299
7141	RIKEN cDNA 1110021E09 gene	1.741	0.0190
10867	Prostaglandin-endoperoxide synthase 1	1.741	0.0365
13644	RIKEN cDNA F830004D09 gene	1.740	0.0299
20914	Lymphocyte antigen 75	1.738	0.0299
13620	zinc finger protein 386 (Kruppel-like)	1.737	0.0190
4513	RNA, U22 small nucleolar	1.737	0.0299
14798	RIKEN cDNA 1810074P20 gene	1.736	0.0402
21071	RIKEN cDNA 1700029B21 gene	1.736	0.0297
20025	TBC1 domain family, member 13	1.736	0.0365
21776	ESTs C78717	1.736	0.0245
10340	zinc finger protein 198	1.736	0.0434
20920	RIKEN cDNA E130016E03 gene	1.736	0.0245
21718	Inositol 1,3,4-triphosphate 5/6 kinase	1.735	0.0337
6771	Zinc finger protein 482	1.732	0.0237
8852	TAP binding protein-like	1.732	0.0337
20041	McKusick-Kaufman syndrome protein	1.732	0.0402
1943	Cell division cycle associated 2	1.730	0.0337
11192	Isocitrate dehydrogenase 3 (NAD+), gamma	1.729	0.0365
9683	RIKEN cDNA 2810407E01 gene	1.729	0.0434
19063	CDNA sequence BC021438	1.728	0.0434
2172	RIKEN cDNA C330018L13 gene	1.728	0.0299
20410	Uridine monophosphate synthetase	1.727	0.0264
16879	Exocyst complex component 8	1.727	0.0297
6783	Neuropilin 2	1.727	0.0245
12904	Chromatin modifying protein 2B	1.726	0.0245
14969	RIKEN cDNA 0610042C05 gene	1.726	0.0402

15299	RIKEN cDNA 0610025O11 gene	1.725	0.0299
4035	Ribosomal protein L23	1.723	0.0299
630	RIKEN cDNA 8030451K01 gene	1.722	0.0299
18850	tumor necrosis factor receptor superfamily, member 1b	1.720	0.0299
17230	Leukocyte receptor cluster (LRC) member 4	1.719	0.0458
10838	Dynein, cytoplasmic, intermediate chain 2	1.718	0.0299
1284	perlecan (heparan sulfate proteoglycan 2)	1.717	0.0299
2416	RIKEN cDNA 2810037C03 gene	1.717	0.0237
11282	RIKEN cDNA 2310066E14 gene	1.714	0.0297
5684	Pleckstrin homology domain interacting protein	1.713	0.0434
2459	Epidermal growth factor receptor pathway substrate 15, related sequence	1.712	0.0299
16764	Ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	1.712	0.0365
4321	O-acetyltransferase	1.710	0.0190
15825	RIKEN cDNA 2310003L22 gene	1.709	0.0245
19772	Breast cancer 1	1.708	0.0264
12700	RIKEN cDNA 3300001P08 gene	1.708	0.0299
5841	RIKEN cDNA 1810020C19 gene	1.707	0.0402
15076	Protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.706	0.0299
14520	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	1.705	0.0337
16254	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	1.705	0.0297
13841	Iduronate 2-sulfatase	1.705	0.0337
11616	Transcription factor Dp 1	1.704	0.0402
12135	RIKEN cDNA 4632434I11 gene	1.703	0.0264
20995	ESTs AA407555	1.702	0.0402
12828	Sorting nexin 13	1.702	0.0237
18984	Tafazzin	1.702	0.0264
18595	RIKEN cDNA 1300007F04 gene	1.701	0.0297
12648	embryonic epithelial gene 1	1.701	0.0402
13807	RIKEN cDNA B230339H12 gene	1.701	0.0297
18070	RIKEN cDNA 5830472F04 gene	1.701	0.0337
15110	Zinc and ring finger 2	1.701	0.0299
229	Unknown (protein for IMAGE:5696235)	1.701	0.0190
7058	Glycogen synthase 3, brain	1.700	0.0402
22204	RIKEN cDNA 2700019D07 gene	1.700	0.0190
18176	RIKEN cDNA 5730405M06 gene	1.700	0.0299
10545	Kringle containing transmembrane protein 1	1.699	0.0237
12569	Eukaryotic translation initiation factor 2B, subunit 3	1.698	0.0297
10627	Putative homeodomain transcription factor 2	1.697	0.0365
11487	Expressed sequence C78541	1.697	0.0264
11283	RAB interacting factor	1.697	0.0297
16427	DNA segment, Chr 13, Wayne State University 64, expressed	1.696	0.0337
11071	RIKEN cDNA 2810452K22 gene	1.696	0.0299
33	Tubulin, gamma complex associated protein 2	1.695	0.0365
16160	Aldolase 1, A isoform	1.695	0.0458
12377	RIKEN cDNA 4933411K20 gene	1.694	0.0337
9242	RIKEN cDNA 0610012D09 gene	1.693	0.0402
17596	DOM-3 homolog Z (C. elegans)	1.692	0.0264
20852	FLN29 gene product	1.692	0.0264
13600	Colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	1.691	0.0365
18811	RIKEN cDNA 4432411E13 gene	1.689	0.0434
17138	CDNA sequence BC053440	1.687	0.0434
19825	RIKEN cDNA 4921511H13 gene	1.687	0.0299
3648	RIKEN cDNA 5830434P21 gene	1.687	0.0402
18245	RIKEN cDNA 1110056N09 gene	1.687	0.0299

18034	Dynein, cytoplasmic, light intermediate polypeptide 2	1.686	0.0264
6270	Succinate-CoA ligase, GDP-forming, alpha subunit	1.684	0.0337
4095	cyclin A2	1.682	0.0297
1107	Expressed sequence AI429612	1.681	0.0299
5322	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	1.681	0.0297
6813	Thyroid hormone receptor associated protein 3	1.681	0.0237
7608	RIKEN cDNA 9930021J03 gene	1.680	0.0434
15843	F-box protein 42	1.679	0.0402
11838	CCR4-NOT transcription complex, subunit 6	1.679	0.0297
444	RIKEN cDNA 2700059D21 gene	1.679	0.0245
3074	SEC23A (S. cerevisiae)	1.678	0.0299
15496	Spectrin beta 2	1.678	0.0365
13973	Expressed sequence AI256624	1.678	0.0299
4994	similar to mKIAA0185 protein (LOC381227), mRNA	1.677	0.0299
18171	Tumor protein, translationally-controlled 1	1.676	0.0402
746	Zinc finger protein 655	1.676	0.0365
22151	RIKEN cDNA 5730469D23 gene	1.675	0.0297
14495	Regulating synaptic membrane exocytosis 2	1.675	0.0245
15652	Activating signal cointegrator 1 complex subunit 2	1.674	0.0297
8650	similar to 60S ribosomal protein L11 (LOC328825), mRNA	1.669	0.0299
9736	Ubiquitin protein ligase E3A	1.668	0.0237
10369	Ribosomal protein S21	1.666	0.0337
16543	Transmembrane protein 33	1.665	0.0365
14732	RIKEN cDNA 5730403H17 gene	1.665	0.0245
16635	Zinc finger protein 142	1.664	0.0337
3929	RIKEN cDNA 1110057K04 gene	1.662	0.0365
2616	RIKEN cDNA 4930519P11 gene	1.662	0.0365
21939	RIKEN cDNA 9130011E15 gene	1.660	0.0299
15158	Mus musculus hypothetical LOC223827 (LOC223827), mRNA	1.659	0.0264
2313	Janus kinase 2	1.659	0.0299
8747	RIKEN cDNA 4732496O08 gene	1.658	0.0190
12513	Protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2	1.657	0.0434
11855	SEC15-like 1 (S. cerevisiae)	1.656	0.0245
8342	Signal recognition particle 68	1.655	0.0299
15726	Protein kinase D2	1.655	0.0337
10091	RIKEN cDNA 5730410I19 gene	1.654	0.0337
16698	Ngfi-A binding protein 1	1.654	0.0337
11550	RIKEN cDNA 0610039N19 gene	1.654	0.0337
3409	RIKEN cDNA 1110020P09 gene	1.654	0.0297
17640	RIKEN cDNA 1110020G09 gene	1.652	0.0434
20756	Zinc finger protein 85, related sequence 1	1.650	0.0299
9101	serine protease inhibitor, Kunitz type 1	1.650	0.0297
4302	Acetyl-Coenzyme A acetyltransferase 1	1.647	0.0458
21701	Transcription factor 4	1.646	0.0365
16240	Mus musculus transcribed sequence with strong similarity to protein pir:I38346 (H.sapiens) I38346 elastic titin - human (fragment)	1.646	0.0245
4522	Carboxypeptidase X 1 (M14 family)	1.645	0.0299
5860	Pyruvate dehydrogenase complex, component X	1.645	0.0365
9084	RIKEN cDNA 3830405G04 gene	1.644	0.0299
14641	Activating transcription factor 2	1.644	0.0402
15403	Stromal cell derived factor receptor 2	1.644	0.0245
7390	Retinoid X receptor interacting protein 110	1.644	0.0245
17961	Sphingomyelin phosphodiesterase 1, acid lysosomal	1.643	0.0434
5556	Glyoxalase 1	1.643	0.0365

14700	Lin 7 homolog c (C. elegans)	1.643	0.0365
8473	RIKEN cDNA 2610208M17 gene	1.642	0.0299
10110	Breakpoint cluster region homolog	1.642	0.0297
14878	Coiled-coil domain containing 16	1.640	0.0402
20564	RAN binding protein 5	1.638	0.0402
3746	RIKEN cDNA 2510049I19 gene	1.636	0.0299
19485	RIKEN cDNA 2310042M24 gene	1.634	0.0402
10326	Transmembrane channel-like gene family 6	1.634	0.0299
12649	ring finger protein 26	1.633	0.0337
19547	WD repeat domain 36	1.633	0.0402
6080	OCIA domain containing 1	1.632	0.0299
9912	Zinc finger, DHHC domain containing 7	1.630	0.0190
6213	RIKEN cDNA A230054D04 gene	1.627	0.0297
16335	Cofactor required for Sp1 transcriptional activation, subunit 6	1.627	0.0434
15928	Nardilysin, N-arginine dibasic convertase, NRD convertase 1	1.626	0.0434
8872	RIKEN cDNA 5430428G01 gene	1.625	0.0299
16377	SET and MYND domain containing 3	1.624	0.0434
11965	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	1.623	0.0297
16510	5-azacytidine induced gene 2	1.623	0.0337
13784	RIKEN cDNA 5830434P21 gene	1.622	0.0337
22153	RIKEN cDNA 1700123O20 gene	1.621	0.0264
20248	Protein kinase, cAMP dependent, catalytic, beta	1.621	0.0365
13625	Epidermal growth factor	1.620	0.0297
3883	RIKEN cDNA 5730405M06 gene	1.619	0.0402
7291	Casein kinase 1, gamma 1	1.619	0.0337
6388	FUN14 domain containing 2	1.617	0.0458
16255	RIKEN cDNA 2410008K03 gene	1.617	0.0434
8720	Isovaleryl coenzyme A dehydrogenase	1.616	0.0365
14314	THAP domain containing 7	1.615	0.0245
4718	Dual specificity phosphatase 16	1.615	0.0402
12625	Limb-bud and heart	1.615	0.0434
17419	Muscle glycogen phosphorylase	1.613	0.0458
15802	Thioredoxin domain containing 4 (endoplasmic reticulum)	1.612	0.0299
15049	RNA pseudouridylate synthase domain containing 4	1.612	0.0458
6253	PRP31 pre-mRNA processing factor 31 homolog (yeast)	1.610	0.0365
12525	CDNA sequence AK129128	1.610	0.0299
16861	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	1.609	0.0337
6693	CDNA sequence BC026590	1.606	0.0434
7172	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	1.605	0.0297
5583	ADP-ribosylation factor interacting protein 2	1.605	0.0337
15713	golgi SNAP receptor complex member 2	1.604	0.0190
13746	RIKEN cDNA 9030418K01 gene	1.603	0.0365
19958	Methyl-CpG binding domain protein 1	1.602	0.0434
12444	RIKEN cDNA 8030443L12 gene	1.602	0.0434
15503	Sorting nexin family member 27	1.600	0.0337
18397	Expressed sequence AL024069	1.600	0.0299
14524	Casein kinase 1, alpha 1	1.600	0.0245
11836	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1.599	0.0337
5656	RIKEN cDNA 6330583M11 gene	1.599	0.0365
11536	RIKEN cDNA 0610033I05 gene	1.598	0.0264
15395	Lysyl-tRNA synthetase	1.598	0.0337
881	RIKEN cDNA 2310057G13 gene	1.597	0.0458
20029	CDNA sequence BC024806	1.595	0.0337

18786	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	1.594	0.0434
19673	C0194A11-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus musculus cDNA clone C0194A11 3', MRNA sequence	1.593	0.0337
15873	Survival motor neuron domain containing 1	1.592	0.0402
13786	Zinc finger protein 294	1.592	0.0299
7958	CDNA sequence BC024683	1.587	0.0337
17095	RIKEN cDNA 2410043F08 gene	1.584	0.0299
16998	CDNA sequence BC023829	1.584	0.0402
14756	Casitas B-lineage lymphoma-like 1	1.584	0.0245
21770	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	1.581	0.0245
19393	Protein phosphatase 4, regulatory subunit 2	1.581	0.0434
5957	Nucleoporin 88	1.580	0.0402
15457	Expressed sequence AA415817	1.580	0.0297
689	G0120G06-3 NIA Mouse E7.5 Embryonic Portion cDNA Library Mus musculus cDNA clone G0120G06 3', MRNA sequence	1.580	0.0190
13424	Pyrroline-5-carboxylate reductase-like	1.578	0.0337
13867	F-box only protein 8	1.578	0.0299
12790	RIKEN cDNA B930068K11 gene	1.574	0.0365
11116	Mus musculus cDNA clone IMAGE:5689029, partial cds	1.573	0.0337
739	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	1.569	0.0434
11806	Testis expressed gene 264	1.569	0.0299
6190	Eukaryotic translation termination factor 1	1.568	0.0299
19194	EST BM235972	1.566	0.0337
21076	RIKEN cDNA 2700049P18 gene	1.562	0.0434
13182	Chaperonin subunit 4 (delta)	1.560	0.0434
10399	Alanyl-tRNA synthetase	1.560	0.0458
8084	DNA segment, Chr 10, Johns Hopkins University 81 expressed	1.559	0.0402
21504	RAB22A, member RAS oncogene family	1.558	0.0434
18156	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	1.556	0.0458
5876	Shwachman-Bodian-Diamond syndrome homolog (human)	1.556	0.0245
8869	Transcription factor EC	1.554	0.0365
21707	CCNDBP1 interactor	1.553	0.0434
11193	CDNA sequence BC040823	1.553	0.0402
13649	RIKEN cDNA B330012G18 gene	1.551	0.0402
10556	RIKEN cDNA 3110048L19 gene	1.550	0.0245
17669	Leucine rich repeat (in FLII) interacting protein 2	1.550	0.0458
11915	Copine I	1.549	0.0365
15262	ATP synthase mitochondrial F1 complex assembly factor 2	1.548	0.0458
20644	Expressed sequence AA517853	1.548	0.0365
9175	Expressed sequence AI461788	1.546	0.0458
9351	Zinc finger protein 148	1.544	0.0434
16904	Mus musculus cDNA clone MGC:59529 IMAGE:6336581, complete cds	1.544	0.0299
14754	PRP31 pre-mRNA processing factor 31 homolog (yeast)	1.544	0.0434
6437	Nucleosome assembly protein 1-like 4	1.543	0.0365
12343	Eukaryotic translation initiation factor 4, gamma 1	1.543	0.0458
14295	Aurora kinase A	1.542	0.0365
17274	RIKEN cDNA 2900057K09 gene	1.542	0.0434
11201	RIKEN cDNA A830039H10 gene	1.542	0.0337
13788	RIKEN cDNA 1110067M05 gene	1.541	0.0299
14895	Metastasis associated 3	1.539	0.0434
14882	Translin	1.539	0.0402
16476	adenylate kinase 3 alpha-like	1.537	0.0458
10431	Cardiomyopathy associated 1	1.535	0.0299

22175	Testis-specific protein, Y-encoded-like 1	1.531	0.0458
4952	Shc SH2-domain binding protein 1	1.531	0.0434
15143	NADH dehydrogenase (ubiquinone) Fe-S protein 2	1.530	0.0402
10223	Amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.525	0.0434
16828	Protein tyrosine phosphatase, non-receptor type 23	1.525	0.0402
21717	RIKEN cDNA 5830468K18 gene	1.524	0.0299
19848	Actin related protein 2/3 complex, subunit 2	1.524	0.0434
2413	RIKEN cDNA 2810017D21 gene	1.524	0.0337
13617	Adaptor-related protein complex 1, sigma 2 subunit	1.523	0.0402
15564	Transmembrane 6 superfamily member 1	1.523	0.0434
13524	Protein phosphatase 1, regulatory (inhibitor) subunit 7	1.521	0.0434
9046	ubiquitin specific protease 12	1.520	0.0434
15374	CDNA sequence BC010304	1.518	0.0299
12365	Golgi apparatus protein 1	1.517	0.0219
20244	RIKEN cDNA 0610039A15 gene	1.516	0.0337
21230	Parkinson disease (autosomal recessive, early onset) 7	1.514	0.0434
10259	Stress 70 protein chaperone, microsome-associated, human homolog	1.509	0.0365
22252	phosphoglycerate mutase 1	1.507	0.0365
22320	Phosphatidylinositol transfer protein, beta	1.506	0.0297
15289	CDNA sequence BC010584	1.506	0.0434
20451	RIKEN cDNA 1810013D10 gene	1.506	0.0297
4828	Ubiquitin-conjugating enzyme E2N	1.503	0.0402
17047	Ankyrin repeat and SAM domain containing 1	1.502	0.0458
16137	Forkhead box M1	1.501	0.0237
14317	Runt related transcription factor 2	1.501	0.0458
9866	Expressed sequence AI413782	1.498	0.0337
22417	Aldehyde dehydrogenase 3 family, member B1	1.497	0.0458
19248	Lysocardiolipin acyltransferase	1.496	0.0434
19571	AarF domain containing kinase 1	1.494	0.0458
15346	RIKEN cDNA 2700085E05 gene	1.493	0.0458
3331	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	1.493	0.0434
1326	RIKEN cDNA 4933433P14 gene	1.489	0.0219
9915	Host cell factor C1 regulator 1 (XPO1-dependent)	1.488	0.0402
17865	Nuclear cap binding protein subunit 1, 80kDa	1.484	0.0402
13098	M-phase phosphoprotein 1	1.482	0.0365
18780	Muskelin 1, intracellular mediator containing kelch motifs	1.478	0.0365
4531	Retinoic acid induced 12	1.475	0.0402
14491	RIKEN cDNA D930043N17 gene	1.474	0.0434
15433	Polymerase (RNA) II (DNA directed) polypeptide B	1.469	0.0458
15563	CLIP associating protein 1	1.468	0.0402
14446	Glutamate-cysteine ligase , modifier subunit	1.467	0.0337
8758	Peroxisomal membrane protein 3	1.460	0.0365
10844	Glutaminase	1.457	0.0299
6930	Transcription elongation factor B (SIII), polypeptide 3	1.453	0.0434
4314	Transmembrane emp24 protein transport domain containing 5	1.451	0.0299
20977	Myocyte enhancer factor 2B	1.449	0.0365
6508	RIKEN cDNA 5730557L09 gene	1.446	0.0434
8115	G patch domain containing 2	1.445	0.0402
20198	Cornichon homolog (Drosophila)	1.443	0.0299
17206	Cofilin 1, non-muscle	1.438	0.0458
9469	Citrate synthase	1.433	0.0458
10892	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.430	0.0337
21569	Small EDRK-rich factor 2	1.429	0.0402
15319	ESTs BM222786	1.425	0.0365

17913	Golgi SNAP receptor complex member 2	1.422	0.0458
14051	THO complex 4	1.419	0.0458
15657	Splicing factor, arginine/serine-rich 1 (ASF/SF2)	1.412	0.0402
12478	Zinc finger, DHHC domain containing 3	1.412	0.0337
16032	Gem (nuclear organelle) associated protein 5	1.410	0.0434
13318	SLIT-ROBO Rho GTPase activating protein 2	1.373	0.0365
10735	ESTs BM117318	1.360	0.0458

Supplemental Table II. Genes with downregulated expression in BMMCs transplanted into I/R-injured hearts vs. sham-operated hearts.

Gene ID	**Gene Name**	**fold change**	**q-value**
7132	Glutathione peroxidase 1	0.671	0.0365
5109	RIKEN cDNA 2310061K06 gene	0.654	0.0434
16801	RIKEN cDNA B430203M17 gene	0.654	0.0301
5528	RIKEN cDNA D030015G18 gene	0.652	0.0458
14091	Sperm associated antigen 7	0.649	0.0434
11734	RIKEN cDNA 2810003C17 gene	0.641	0.0434
2351	Dehydrogenase/reductase (SDR family) member 1	0.628	0.0458
12188	E1A binding protein p400	0.624	0.0337
7048	SEC14-like 1 (S. cerevisiae)	0.623	0.0365
14345	RIKEN cDNA 3010033P07 gene	0.621	0.0402
7429	CBFA2T1 identified gene homolog (human)	0.611	0.0434
13293	Morf4 family associated protein 1	0.611	0.0402
18092	ribosomal protein L26	0.600	0.0402
15212	ESTs AU021001	0.599	0.0434
9274	Mus musculus transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	0.599	0.0365
11007	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	0.594	0.0297
19523	Glutamate oxaloacetate transaminase 1, soluble	0.594	0.0337
4081	Sec11-like 3 (S. cerevisiae)	0.585	0.0434
20751	EST BG060719	0.584	0.0365
8318	Suppressor of cytokine signaling 7	0.582	0.0301
1878	Heterochromatin protein 1, binding protein 3	0.575	0.0365
4452	Protein tyrosine phosphatase, non-receptor type 12	0.562	0.0434
5652	ESTs AU023291	0.561	0.0301
6988	Homeo box B5	0.561	0.0260
10230	actin, gamma, cytoplasmic	0.559	0.0434
305	Syntaxin 16	0.558	0.0402
16920	ESTs AW541810	0.557	0.0301
8279	Jumonji domain containing 1A	0.554	0.0260
20786	Leucine rich repeat (in FLII) interacting protein 1	0.552	0.0458
17348	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	0.551	0.0260
10855	Ankyrin repeat domain 27 (VPS9 domain)	0.550	0.0365
12614	Mus musculus transcribed sequence with strong similarity to protein sp:P11369 (M.musculus) POL2_MOUSE Retrovirus-related POL polyprotein [Contains: Reverse transcriptase ; Endonuclease]	0.548	0.0402
4471	RIKEN cDNA A830055N07 gene	0.544	0.0402
9270	ESTs AW550992	0.544	0.0402
17231	ribosomal protein L39	0.543	0.0434
8517	Suppressor of variegation 4-20 homolog 1 (Drosophila)	0.541	0.0458
2978	ATPase, H+ transporting, lysosomal accessory protein 2	0.540	0.0402
9389	DNA segment, Chr 11, ERATO Doi 497, expressed	0.539	0.0434
16185	Neural precursor cell expressed, developmentally down-regulated gene 8	0.537	0.0402
14950	Nuclear autoantigenic sperm protein (histone-binding)	0.535	0.0365
346	Activin receptor IIB	0.530	0.0458
1436	L0006D07-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA Library Mus musculus cDNA clone L0006D07 3', MRNA sequence	0.530	0.0458
2343	Scavenger receptor class B, member 2	0.528	0.0434

1874	Toll interacting protein	0.523	0.0402
18227	Recombination activating gene 1	0.521	0.0402
7062	apolipoprotein B editing complex 3	0.520	0.0402
9289	12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6820436J05 product:unknown EST, full insert sequence	0.519	0.0434
3415	Malate dehydrogenase 1, NAD (soluble)	0.519	0.0337
8282	ESTs BE824978	0.515	0.0402
3203	RNA binding motif protein 15	0.511	0.0337
9719	Yippee-like 1 (Drosophila)	0.506	0.0297
3380	RIKEN cDNA 2210412B16 gene	0.505	0.0260
9549	RIKEN cDNA 1110032A13 gene	0.503	0.0434
1184	Wingless-related MMTV integration site 4	0.500	0.0458
6824	SH3-domain binding protein 1	0.500	0.0301
3842	G1 to S phase transition 1	0.495	0.0458
4280	EF hand domain containing 2	0.494	0.0434
3312	ESTs BG068561	0.494	0.0237
4609	ESTs BM224731	0.491	0.0297
13821	ESTs BI792213	0.489	0.0365
3840	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	0.488	0.0301
2695	Solute carrier family 41, member 3	0.486	0.0260
9485	Inactive X specific transcripts	0.486	0.0434
1432	Cytokine inducible SH2-containing protein	0.485	0.0301
18255	H3026G02-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3026G02 3', MRNA sequence	0.485	0.0402
6678	ESTs AW556832	0.480	0.0337
8734	PREDICTED: Mus musculus similar to 1-aminocyclopropane-1-carboxylate synthase (LOC381411), mRNA	0.479	0.0434
528	Zinc finger protein 148	0.478	0.0458
10475	Cadherin EGF LAG seven-pass G-type receptor 2	0.475	0.0434
8507	Hypothetical protein C130092E12	0.473	0.0434
6761	Zinc finger CCCH type domain containing 8	0.471	0.0434
12675	Unc-93 homolog B1 (C. elegans)	0.471	0.0365
5712	Filamin, beta	0.466	0.0297
8940	Ral GEF with PH domain and SH3 binding motif 2	0.463	0.0402
2104	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	0.463	0.0337
3626	Human immunodeficiency virus type I enhancer binding protein 3	0.462	0.0458
10890	Potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	0.461	0.0458
9155	Chromodomain helicase DNA binding protein 4	0.456	0.0365
1397	ELOVL family member 6, elongation of long chain fatty acids (yeast)	0.456	0.0337
9622	RIKEN cDNA 2900037I21 gene	0.455	0.0402
7253	Glycine decarboxylase	0.452	0.0434
8675	Neurotensin	0.448	0.0434
18887	Rap guanine nucleotide exchange factor (GEF) 3	0.446	0.0260
1635	Hypothetical protein 4930565O14	0.444	0.0434
713	Bone morphogenetic protein 5	0.441	0.0365
3311	Nuclear factor I/A	0.440	0.0365
2268	Possibly intronic in U003771-H3150E04	0.439	0.0365
755	RIKEN cDNA 2610507L03 gene	0.437	0.0260
5727	transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	0.435	0.0260
3317	RAD51-like 1 (S. cerevisiae)	0.434	0.0337

828	Aldehyde dehydrogenase 18 family, member A1	0.431	0.0402
1992	C0643G01-3 NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus musculus cDNA clone NIA:C0643G01 IMAGE:30024360 3', MRNA sequence	0.430	0.0402
989	transcribed sequence with weak similarity to protein pir:S60466 (D.melanogaster) S60466 transposase - fruit fly (Drosophila melanogaster) transposon element S	0.423	0.0337
2923	RIKEN cDNA 3110050N22 gene	0.421	0.0337
2373	Poly A binding protein, cytoplasmic 1	0.415	0.0260
18758	SPARC-like 1 (mast9, hevin)	0.414	0.0402
6219	1-acylglycerol-3-phosphate O-acyltransferase 3	0.412	0.0402
2982	RIKEN cDNA 1810063B07 gene	0.409	0.0434
1633	ESTs AU024244	0.409	0.0434
761	ESTs BG074061	0.408	0.0434
2857	Transcription factor 7, T-cell specific	0.406	0.0458
1618	Diaphanous homolog 3 (Drosophila)	0.405	0.0434
1705	Protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	0.405	0.0297
1357	RIKEN cDNA 1700129O19 gene	0.404	0.0434
1062	GATA binding protein 1	0.403	0.0301
5513	Mitochondrial ribosomal protein L15	0.403	0.0402
10348	L0053H05-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA Library Mus musculus cDNA clone L0053H05 3', MRNA sequence	0.403	0.0237
9734	Hypothetical protein D030063E12	0.403	0.0260
525	UNKNOWN C0455C10	0.401	0.0365
1272	Yippee-like 1 (Drosophila)	0.400	0.0402
17461	Retinitis pigmentosa GTPase regulator interacting protein 1	0.398	0.0365
18008	transcription factor 7-like 2, T-cell specific, HMG-box	0.395	0.0237
8074	Prickle-like 2 (Drosophila)	0.394	0.0301
1786	AU021859 Mouse unfertilized egg cDNA Mus musculus cDNA clone J0403C04 3', MRNA sequence	0.394	0.0434
3005	ESTs BM115366	0.392	0.0458
2704	RIKEN cDNA 5330431K02 gene	0.390	0.0402
20586	SET and MYND domain containing 3	0.390	0.0402
8210	SET and MYND domain containing 1	0.389	0.0260
1056	Replication factor C (activator 1) 4	0.388	0.0402
3178	Glucosidase, alpha; neutral C	0.388	0.0365
411	H3062A06-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3062A06 3', MRNA sequence	0.387	0.0301
3552	ESTs BG075092	0.384	0.0434
333	Forkhead box N2	0.384	0.0365
2288	C0902B10-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA Library (Long) Mus musculus cDNA clone NIA:C0902B10 IMAGE:30034773 3', MRNA sequence	0.383	0.0365
2278	ATPase, class VI, type 11A	0.381	0.0365
6451	ESTs BG073007	0.377	0.0264
1134	Protein tyrosine phosphatase, receptor type Z, polypeptide 1	0.373	0.0365
802	Glypican 6	0.372	0.0297
1604	Protein kinase, DNA activated, catalytic polypeptide	0.370	0.0260
4638	RIKEN cDNA 9130005N14 gene	0.370	0.0337
3427	ESTs AU018515	0.368	0.0434
2334	WW domain-containing oxidoreductase	0.366	0.0458
1399	RIKEN cDNA A830025P08 gene	0.363	0.0365
3126	Excision repair cross-complementing rodent repair deficiency, complementation group 5	0.363	0.0297

539	Hypothetical protein D230050A05	0.361	0.0402
540	Melanoma antigen, family L, 2	0.361	0.0365
999	ESTs BM219361	0.359	0.0260
1808	ESTs BM220406	0.357	0.0402
1852	Nuclear cap binding protein subunit 2	0.357	0.0402
1423	RIKEN cDNA A230083H22 gene	0.357	0.0402
1053	Methyl-CpG binding domain protein 4	0.355	0.0434
1182	Zinc finger, CSL domain containing 2	0.351	0.0365
1461	PEST-containing nuclear protein	0.347	0.0237
209	Brain and reproductive organ-expressed protein	0.347	0.0402
414	Guanine nucleotide binding protein (G protein), gamma 2 subunit	0.346	0.0402
349	Expressed sequence AW121567	0.346	0.0402
1452	UNKNOWN: Similar to Mus musculus hypothetical gene supported by NM_009444 (LOC232090), mRNA	0.346	0.0365
2561	Transmembrane protein 30B	0.345	0.0402
4668	Myocyte enhancer factor 2C	0.344	0.0402
4621	UNKNOWN L0858B11	0.342	0.0365
541	Cadherin 8	0.341	0.0458
3838	Tripartite motif-containing 35	0.340	0.0434
3089	Ca<2+>dependent activator protein for secretion	0.339	0.0434
2132	RIKEN cDNA 2810423E13 gene	0.339	0.0402
573	ESTs AU024201	0.339	0.0434
1156	RIKEN cDNA 2410198H06 gene	0.338	0.0337
1428	ESTs AW554277	0.336	0.0402
843	Butyrylcholinesterase	0.335	0.0402
837	RIKEN cDNA 9530010C24 gene	0.331	0.0402
1454	Neural precursor cell expressed, developmentally down-regulted gene 4	0.330	0.0190
3054	EST01205 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus musculus cDNA clone C0007A11 3', MRNA sequence	0.329	0.0264
3076	Deafness, autosomal dominant 5 homolog (human)	0.329	0.0434
6756	LUC7-like 2 (S. cerevisiae)	0.328	0.0237
2903	L0052A03-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA Library Mus musculus cDNA clone L0052A03 3', MRNA sequence	0.327	0.0301
2102	Formin binding protein 1	0.327	0.0365
2294	DNA segment, Chr 18, ERATO Doi 653, expressed	0.325	0.0402
18660	Solute carrier family 38, member 4	0.325	0.0365
2262	ESTs AU021139	0.324	0.0301
774	Transcription elongation factor B (SIII), polypeptide 2	0.323	0.0402
1194	RIKEN cDNA 4933426M11 gene	0.322	0.0237
970	Mitochondrial transcription termination factor 1	0.321	0.0434
1261	DNA segment, Chr 8, ERATO Doi 738, expressed	0.320	0.0434
961	ESTs BG069001	0.318	0.0434
1440	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	0.318	0.0365
20231	RIKEN cDNA 4932435O22 gene	0.317	0.0402
1043	RIKEN cDNA 1110037F02 gene	0.317	0.0237
729	Twisted gastrulation homolog 1 (Drosophila)	0.317	0.0402
2505	Fibroblast growth factor 9	0.317	0.0337
1060	RIKEN cDNA E430034C17 gene	0.314	0.0365
1880	CDNA sequence BC016226	0.310	0.0402
134	hydroxysteroid (17-beta) dehydrogenase 7	0.309	0.0365
836	Apoptosis antagonizing transcription factor	0.308	0.0260
5031	Mitofusin 1	0.307	0.0434
1185	RIKEN cDNA E430026A01 gene	0.306	0.0301
348	K0439F11-5N NIA Mouse Mesenchymal Stem Cell cDNA Library (Long) Mus	0.305	0.0434

	musculus cDNA clone NIA:K0439F11 IMAGE:30062854 5', MRNA sequence		
799	Mus musculus transcribed sequence with weak similarity to protein ref:NP_083693.1 (M.musculus) RIKEN cDNA 9030605E16 [Mus musculus]	0.304	0.0402
757	Glutamate receptor, ionotropic, AMPA1 (alpha 1)	0.304	0.0301
1359	RIKEN cDNA 3110001I22 gene	0.302	0.0365
1481	Metastasis associated 3	0.300	0.0402
2323	Aspartate-beta-hydroxylase	0.297	0.0365
317	Protein tyrosine phosphatase, non-receptor type 3	0.297	0.0301
1869	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	0.296	0.0402
7852	RIKEN cDNA 5830411K21 gene	0.296	0.0301
1166	Cleavage and polyadenylation specific factor 5	0.296	0.0458
1013	ESTs BG074637	0.295	0.0402
8296	RIKEN cDNA G430041M01 gene	0.294	0.0402
2775	RIKEN cDNA 1700023F20 gene	0.293	0.0402
1198	Ras-related GTP binding D	0.292	0.0402
626	Transducin-like enhancer of split 6, homolog of Drosophila E(spl)	0.290	0.0297
2078	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0.290	0.0337
1636	Early B-cell factor 1	0.290	0.0402
1782	Zinc finger protein 238	0.289	0.0365
1163	ESTs BM239152	0.288	0.0260
1675	Expressed sequence AA408296	0.287	0.0297
2049	Chaperonin subunit 3 (gamma)	0.285	0.0297
143	Mus musculus transcribed sequence with weak similarity to protein ref:NP_079268.1 (H.sapiens) hypothetical protein FLJ12547 [Homo sapiens]	0.281	0.0297
1154	Carbonic anyhydrase 12	0.280	0.0365
4193	Mitochondrial ribosomal protein S25	0.279	0.0402
308	EH-domain containing 4	0.276	0.0402
1243	Transmembrane protein 45a	0.274	0.0337
2286	transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus) RIKEN cDNA 5730493B19 [Mus musculus]	0.271	0.0402
1129	Empty spiracles homolog 2 (Drosophila)	0.271	0.0434
3855	Expressed sequence AA536749	0.268	0.0337
1770	RIKEN cDNA 4833405L11 gene	0.265	0.0301
2210	Homeo box B1	0.265	0.0365
763	RIKEN cDNA C030032C09 gene	0.264	0.0337
758	LPS-responsive beige-like anchor	0.263	0.0237
5106	Cytochrome P450, family 51	0.257	0.0337
3376	PRP18 pre-mRNA processing factor 18 homolog (yeast)	0.256	0.0365
4599	DNA methyltransferase 3B	0.254	0.0260
7215	Bone morphogenetic protein receptor, type 1A	0.251	0.0337
2571	Guanine nucleotide binding protein, alpha inhibiting 1	0.249	0.0402
13724	MAD homolog 2 (Drosophila)	0.247	0.0297
2081	expressed sequence AI504298	0.246	0.0365
5497	Carbonic anyhydrase 12	0.246	0.0337
279	Spindlin-like	0.244	0.0458
1819	DNA fragmentation factor, beta subunit	0.243	0.0260
3541	RIKEN cDNA 6430511E19 gene	0.236	0.0337
742	ESTs BM117069	0.234	0.0365
2771	RIKEN cDNA C130002M15 gene	0.232	0.0458
1271	KH domain containing, RNA binding, signal transduction associated 2	0.231	0.0237
4933	SRY-box containing gene 2	0.231	0.0337
2441	miRNA containing gene	0.227	0.0337
416	Expressed sequence AI427122	0.227	0.0402

286	ESTs BG069306	0.227	0.0402
300	Similar to Cpo protein	0.225	0.0402
1862	V-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	0.224	0.0264
1877	RIKEN cDNA 2610528E23 gene	0.223	0.0402
2697	RIKEN cDNA 0610008C08 gene	0.223	0.0301
3187	Autism susceptibility candidate 2	0.220	0.0402
1228	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530045K13 product:unknown EST, full insert sequence.	0.218	0.0260
1687	Calcium channel, voltage-dependent, alpha2/delta subunit 3	0.216	0.0301
1784	cytochrome c oxidase subunit VIb, testes-specific	0.214	0.0365
1812	C0258F06-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone C0258F06 3', MRNA sequence	0.212	0.0337
3943	Expressed sequence AU017263	0.209	0.0260
292	RIKEN cDNA 1300013J15 gene	0.209	0.0402
4040	RIKEN cDNA 4930447C04 gene	0.209	0.0260
2257	similar to RIKEN cDNA 1700001E04 (LOC380911), mRNA	0.206	0.0260
74	RIKEN cDNA 1810042K04 gene	0.202	0.0402
1351	Sal-like 1 (Drosophila)	0.200	0.0337
4496	Insulin-like growth factor 2 receptor	0.198	0.0434
726	Peroxisome proliferator activated receptor gamma	0.193	0.0434
13198	Solute carrier family 8 (sodium/calcium exchanger), member 1	0.193	0.0402
2958	Zinc finger protein 96	0.192	0.0260
2731	MYST histone acetyltransferase 1	0.188	0.0301
613	RIKEN cDNA 0610007N19 gene	0.186	0.0301
2059	ESTs BG073657	0.185	0.0434
724	RIKEN cDNA 1700020C11 gene	0.184	0.0458
3210	Sestrin 3	0.181	0.0260
2277	CDNA sequence BC048546	0.181	0.0260
1430	Glutamate receptor, metabotropic 7	0.179	0.0260
1487	Transmembrane protein 5	0.171	0.0365
534	Sorting nexin 2	0.167	0.0260
310	DNA segment, Chr 18, ERATO Doi 653, expressed	0.158	0.0260
1269	Transmembrane emp24 protein transport domain containing 9	0.158	0.0260
2693	RIKEN cDNA A730042J05 gene	0.157	0.0365
1240	Paired box gene 6	0.156	0.0337
4679	PR domain containing 16	0.154	0.0402
1779	RIKEN cDNA D430039N05 gene	0.154	0.0337
2751	Anaphase promoting complex subunit 4	0.152	0.0237
116	protocadherin 7	0.150	0.0264
620	Ubiquitin specific protease 1	0.150	0.0402
1645	Nuclear factor of activated T-cells 5	0.147	0.0260
7003	DNA segment, Chr 11, ERATO Doi 686, expressed	0.144	0.0301
2307	Hypothetical protein A730046J16	0.140	0.0260
1478	Chemokine-like factor super family 4	0.137	0.0402
2335	Mus musculus transcribed sequence with strong similarity to protein pir:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	0.137	0.0365
3850	Transcribed locus, weakly similar to NP_523817.1 CG9888-PA [Drosophila melanogaster]	0.130	0.0365
1021	L0009G02-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA Library Mus musculus cDNA clone L0009G02 3', MRNA sequence	0.124	0.0301
1486	Pleckstrin homology-like domain, family B, member 2	0.071	0.0260

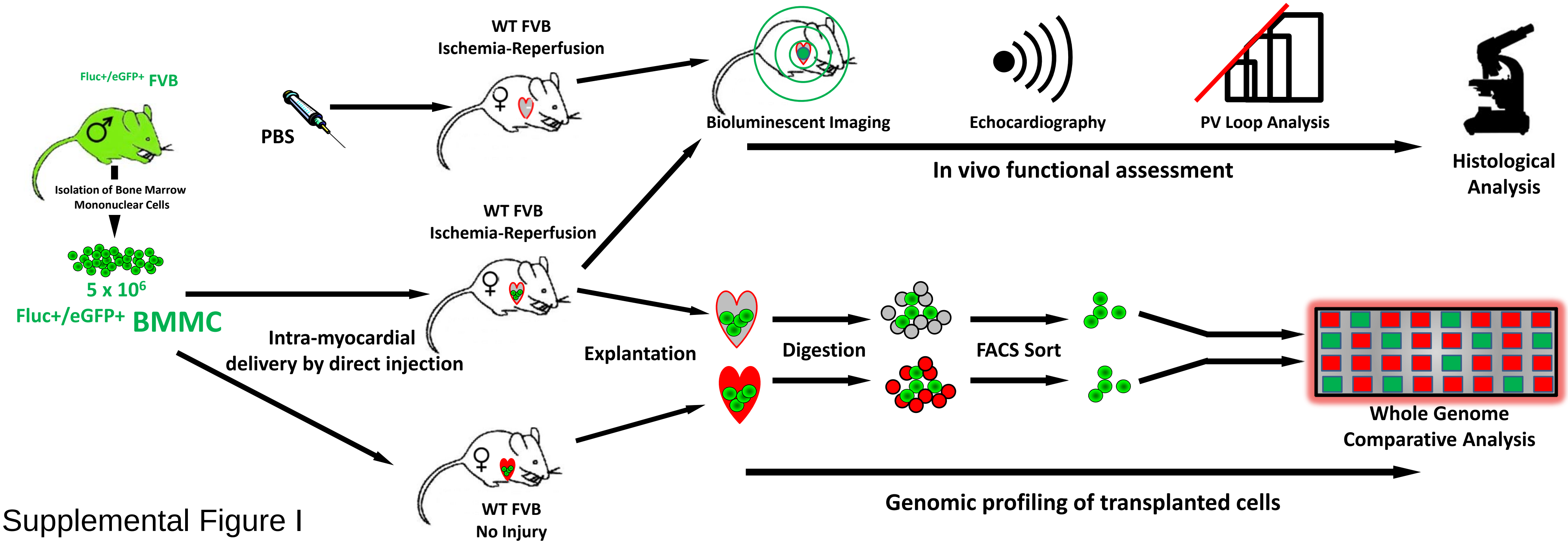
Supplemental Table III. Functional analysis of transcriptional profiling data.

Upregulated

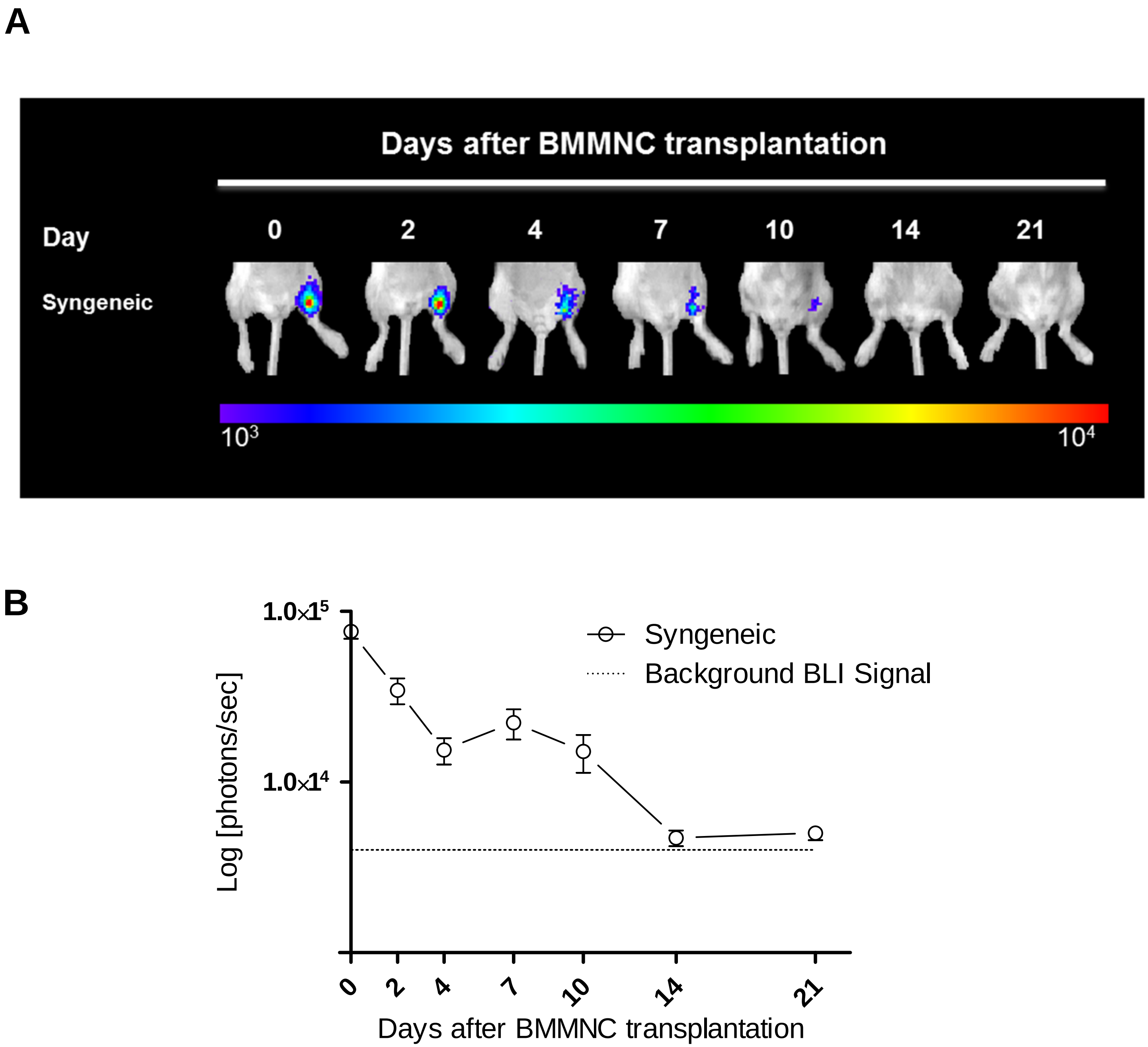
Functional Category	**# of genes**	**p-value**
establishment of localization	173	0.00000
nucleotide binding	141	0.00002
transferase activity	125	0.00002
RNA metabolism	39	0.00021
macromolecule biosynthesis	50	0.00042
translation regulator activity	16	0.00055
vesicle-mediated transport	39	0.00091
cell cycle	23	0.00112
WD-40 repeat	30	0.00115
nucleocytoplasmic transport	13	0.00200
ATPase activity	22	0.00282
HELICc	15	0.00282
protein complex assembly	14	0.00537
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	37	0.00676
ligase activity	34	0.00724
ubiquitin cycle	31	0.00724
transit peptide	21	0.00813
proteolysis	34	0.01023
Pleckstrin homology-type	25	0.01047
enzyme regulator activity	34	0.01047
cytoskeletal protein binding	25	0.02291
transferase activity, transferring acyl groups	16	0.03162
nuclease activity	15	0.03236
lipoprotein metabolism	7	0.03981

Downregulated

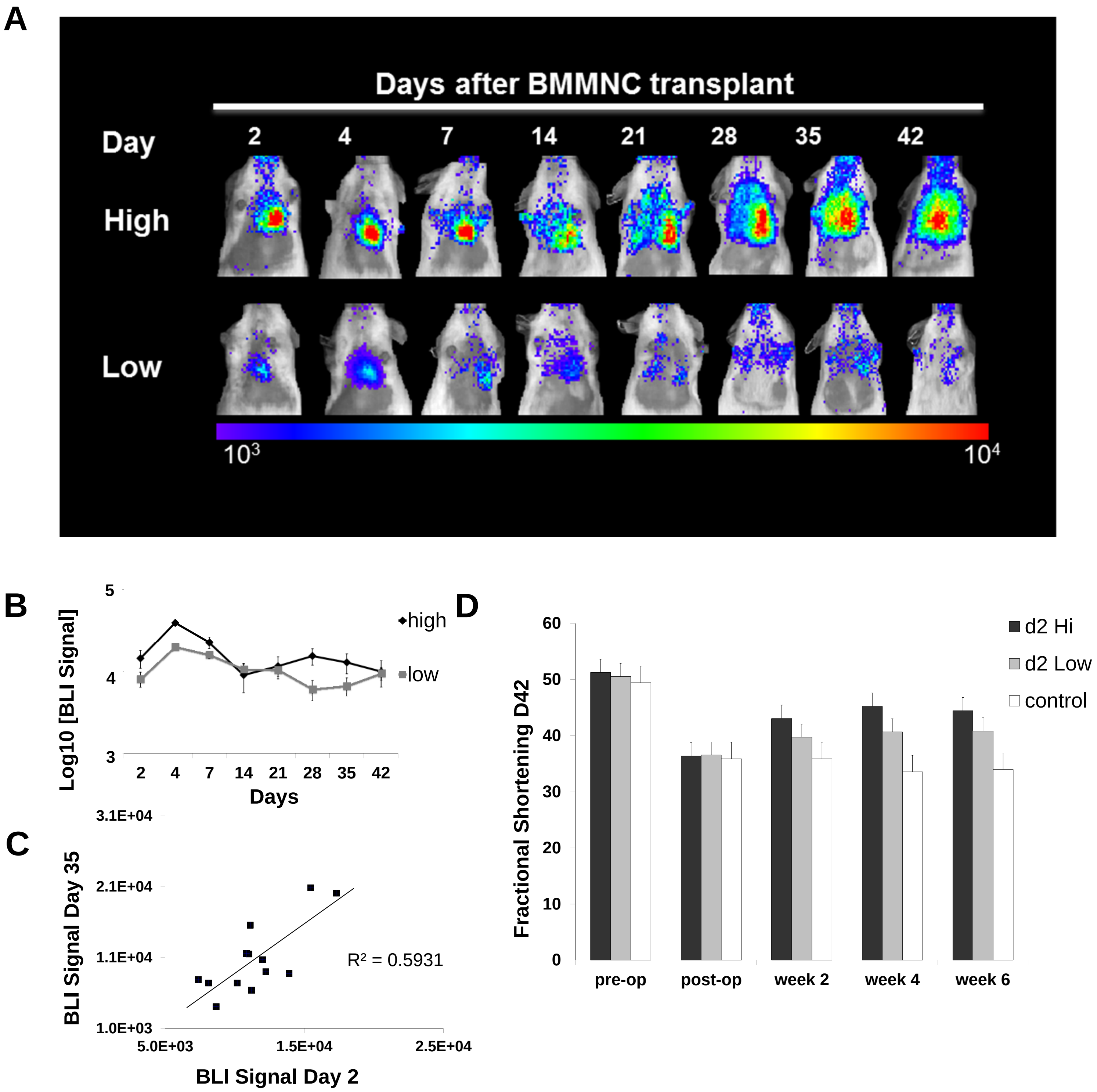
Functional Category	**# of genes**	**p-value**
development	37	0.01479
cell differentiation	19	0.01479
pattern specification	9	0.03715
TGF-BETA SIGNALING PATHWAY	4	0.03715
cell fate commitment	6	0.03715
WNT SIGNALING PATHWAY	6	0.04786



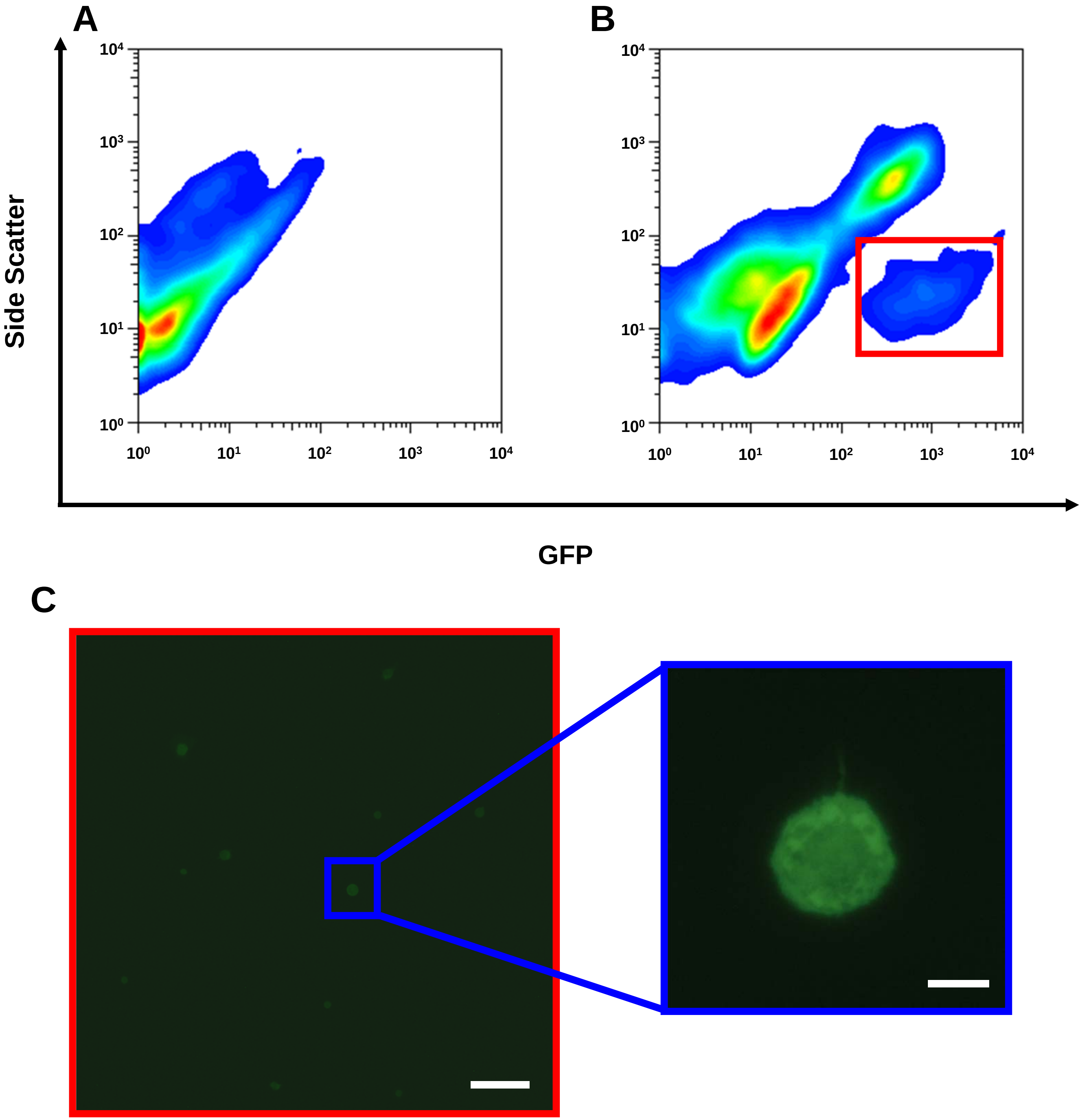
Supplemental Figure I



Supplemental Figure II



Supplemental Figure III



Supplemental Figure IV