# ONLINE APPENDIX – SUPPLEMENTAL DATA

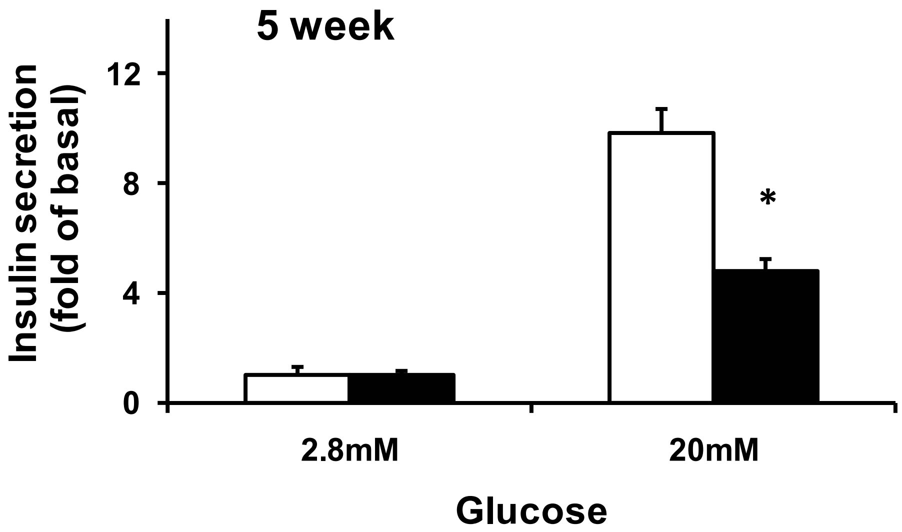

**Figure S1.** Islets from 5-week-old MKR and WT mice were exposed to 2.8 (basal) or 20 mM glucose and insulin secretion measured during 1h. (n = 4 mice per genotype). Data are the mean ± SEM. *, *p* < 0.05 compared to WT.

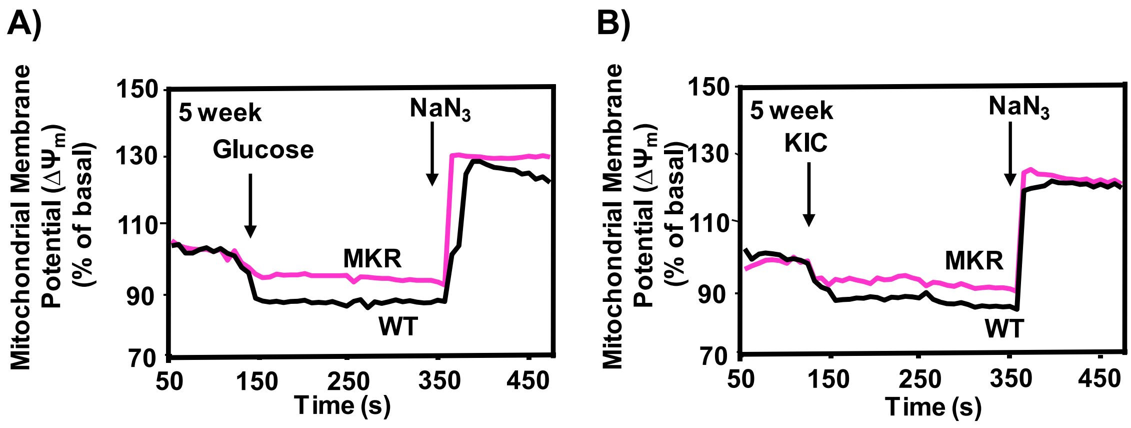

**Figure S2. Decreased mitochondrial membrane potential ($\Delta\Psi_m$) in 5-week-old MKR β-cells**. Mitochondrial membrane potential was measured using Rh123 in dispersed islet cells from 5-week-old MKR and WT mice. Mitochondrial membrane potential was estimated by the difference in Rh123 fluorescent signals between hyperpolarized (glucose, 11 mM (**A**) or KIC, 10 mM (**B**) and fully depolarized (sodium azide, 1 mM) states. Representative kinetic traces of the fluorescent signal from a single β cell are shown. The quatification is shown in Figure 2 (**C** & **F**)

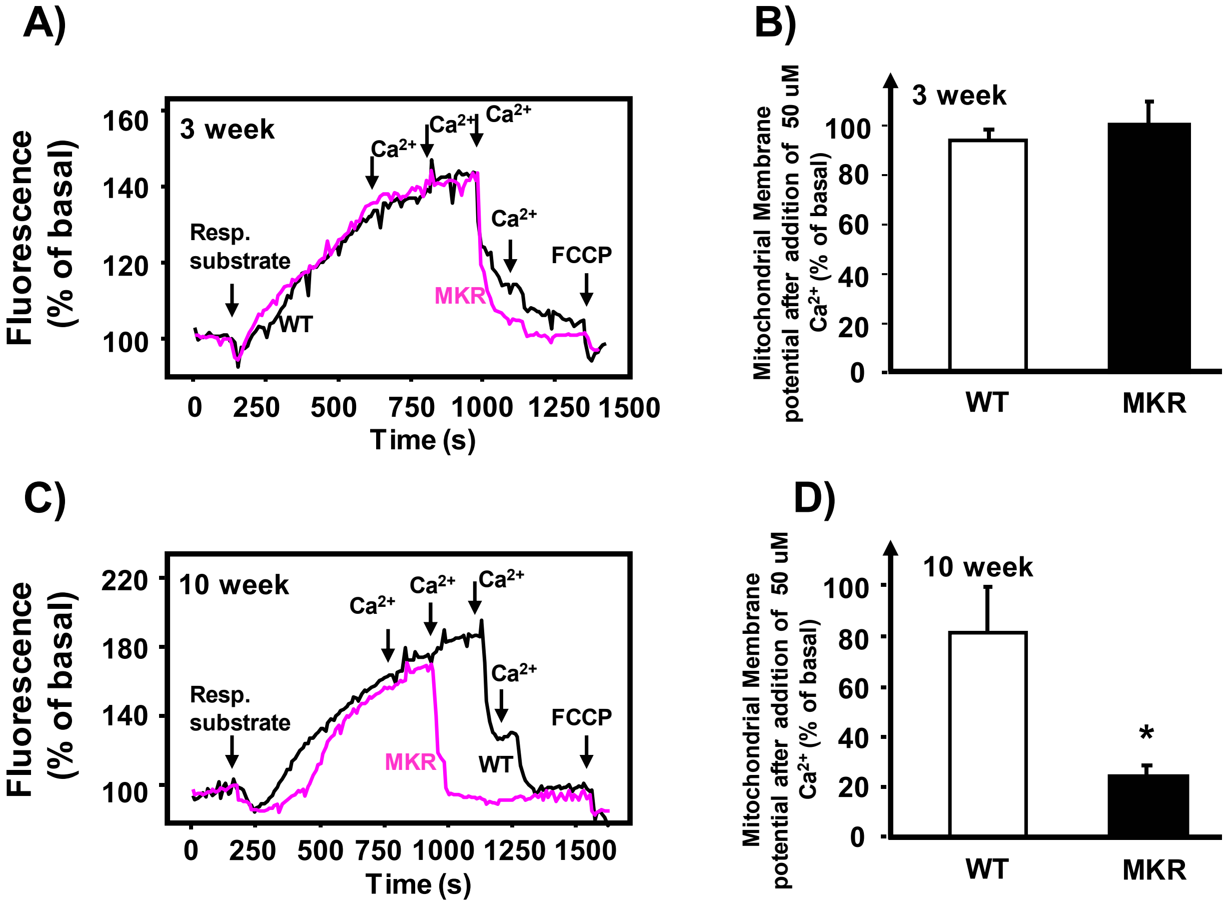

**Figure S3. Mitochondrial $Ca^{2+}$ loading capacity (an indicator of mitochondrial functional state) is decreased in MKR islets.** Mitochondrial $Ca^{2+}$ capacity in permeabilized dispersed islet cells was determined from sustained $Ca^{2+}$-induced dissipation of mitochondrial membrane potential ($\Delta\Psi_{m,}$ driving force for $Ca^{2+}$ uptake), which was monitored with the membrane potential-sensitive dye Rh123 (0.1 μM). The cells were permeabilized with a titrated concentration of saponin determined from the respiration experiment. Formation of $\Delta\Psi_m$ in permeabilized cells supplemented with respiratory substrate caused an increase in fluorescence due to accumulation of Rh123 in the mitochondrial matrix. Subsequent incremental additions of 25 μM $Ca^{2+}$ led to mitochondrial $Ca^{2+}$ sequestration until the mitochondrial $Ca^{2+}$ capacity was exceeded, which caused partial sustained mitochondrial depolarization. Finally, complete depolarization was caused by addition of the chemical uncoupler FCCP. For quantitative comparison between different cell preparations $\Delta\Psi_m$ at 50μM $Ca^{2+}$ was used. (**A** & **C**): Representative kinetic traces of the fluorescent signal from a single β cell. (**B** & **D**): Summary of fluorescent signal changes. (n = 3-5 independent experiments. Measurements were recorded in 30-50 cells from 3 mice per genotype in each experiment). *, $p < 0.05$.

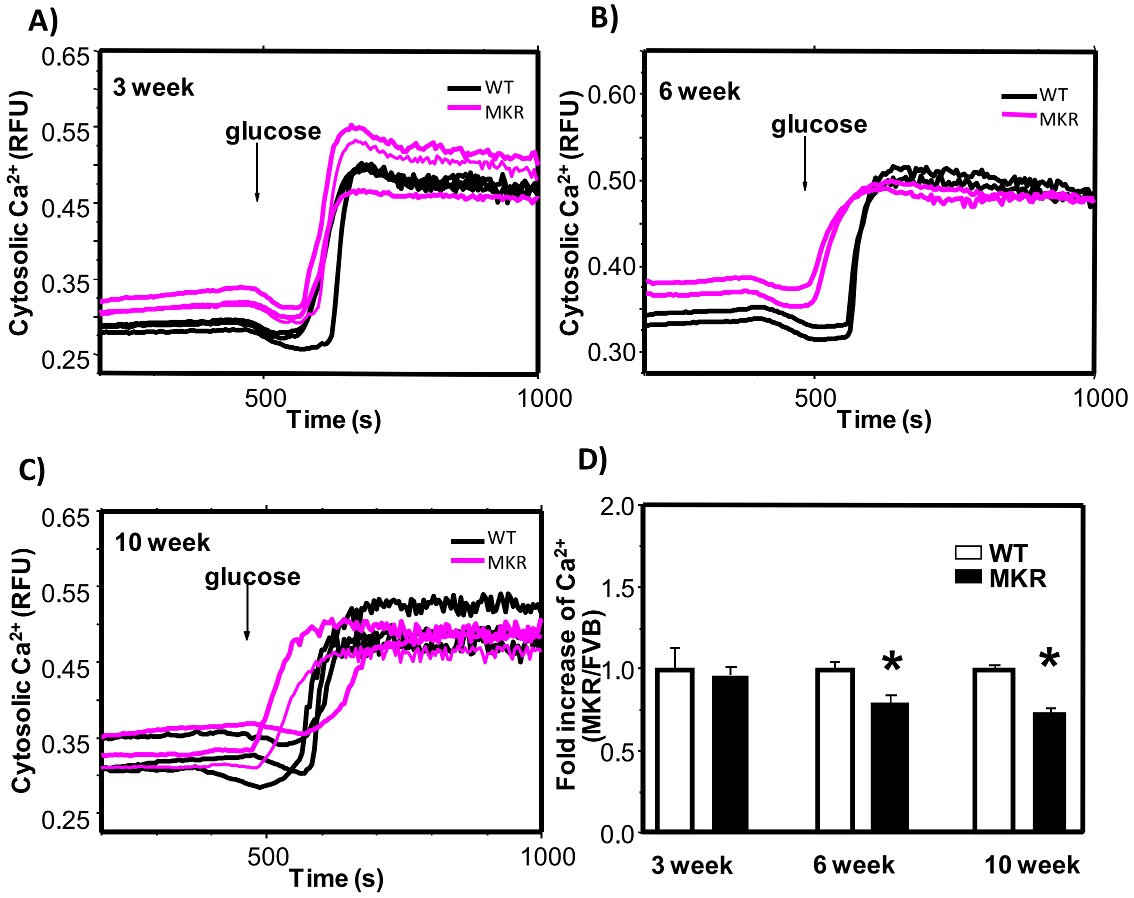

**Figure S4. Islet Cytosolic Ca$^{2+}$ is decreased in 6 and 10-week old MKR islets.** Cytosolic Ca$^{2+}$ was measured in whole islets isolated from 3, 6 and 10 week old WT and MKR mice. The islets were loaded with Fura2 (3 µM) for 45 min at 37°C. The loaded cells were incubated in a perfused chamber on the thermo platform of an Olympus fluorescent BX51W1 microscope. Cells were excited by dual excitation at 340/380 nm, and emission was detected by a 510-nm band pass filter using 415 nm beam splitter. (**A**, **B** & **C**): Representative kinetic traces of the fluorescent ratiometric signal (340/380 nm) from single islets are shown. (**D**): Summary of fluorescent signal changes comparing basal (1 mM glucose) to maximal response in the presense of 11 mM glucose (addition shown by arrow). (n = 3-5 independent experiments. Measurements were recorded in 5-7 islets from 3 mice per genotype in each experiment). *, $p < 0.05$

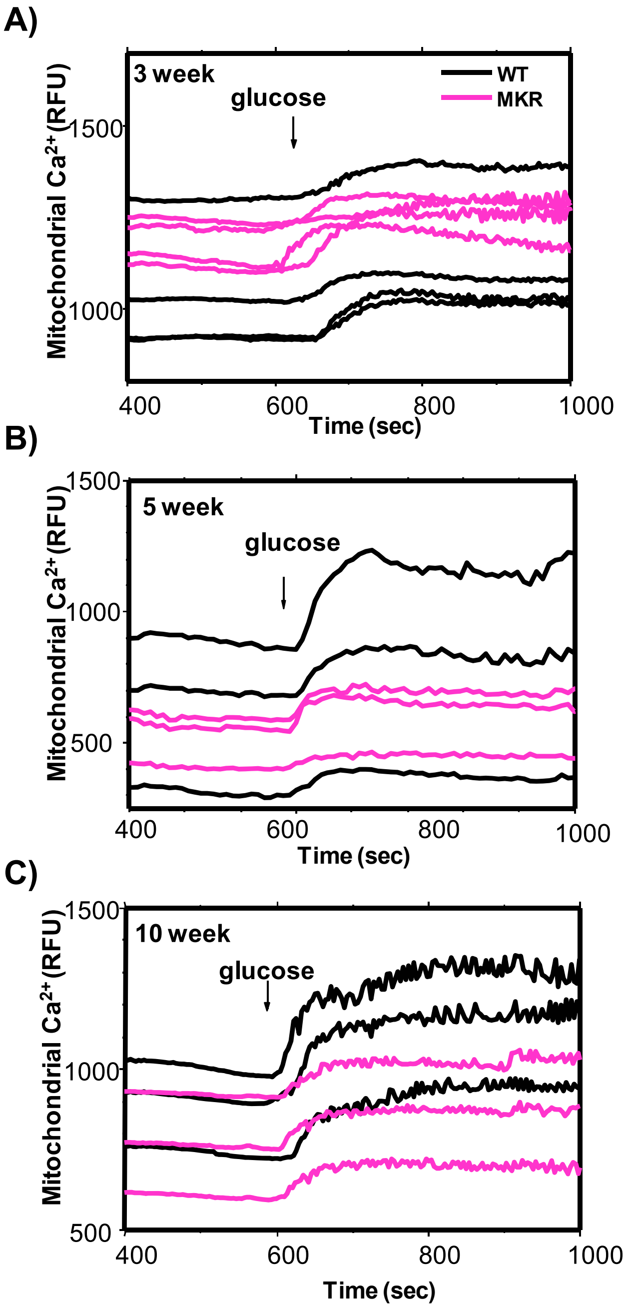

**Figure S5. Reduced mitochondrial Ca$^{2+}$ accumulation in MKR islets: family of traces.** Islets from 3-week-old (**A**), 5-week-old (**B**) and 10-week-old mice **(C)** were loaded with Rhod-2 and photon emission monitored in a chamber perifused with KRB containing basal (1 mM) and 11 mM glucose (addition shown by arrow). Representative kinetic traces from 3-4 islets/genotype are shown. (n = 3-5 independent experiments, each experiment contains 9 islets from 3 mice per genotype).

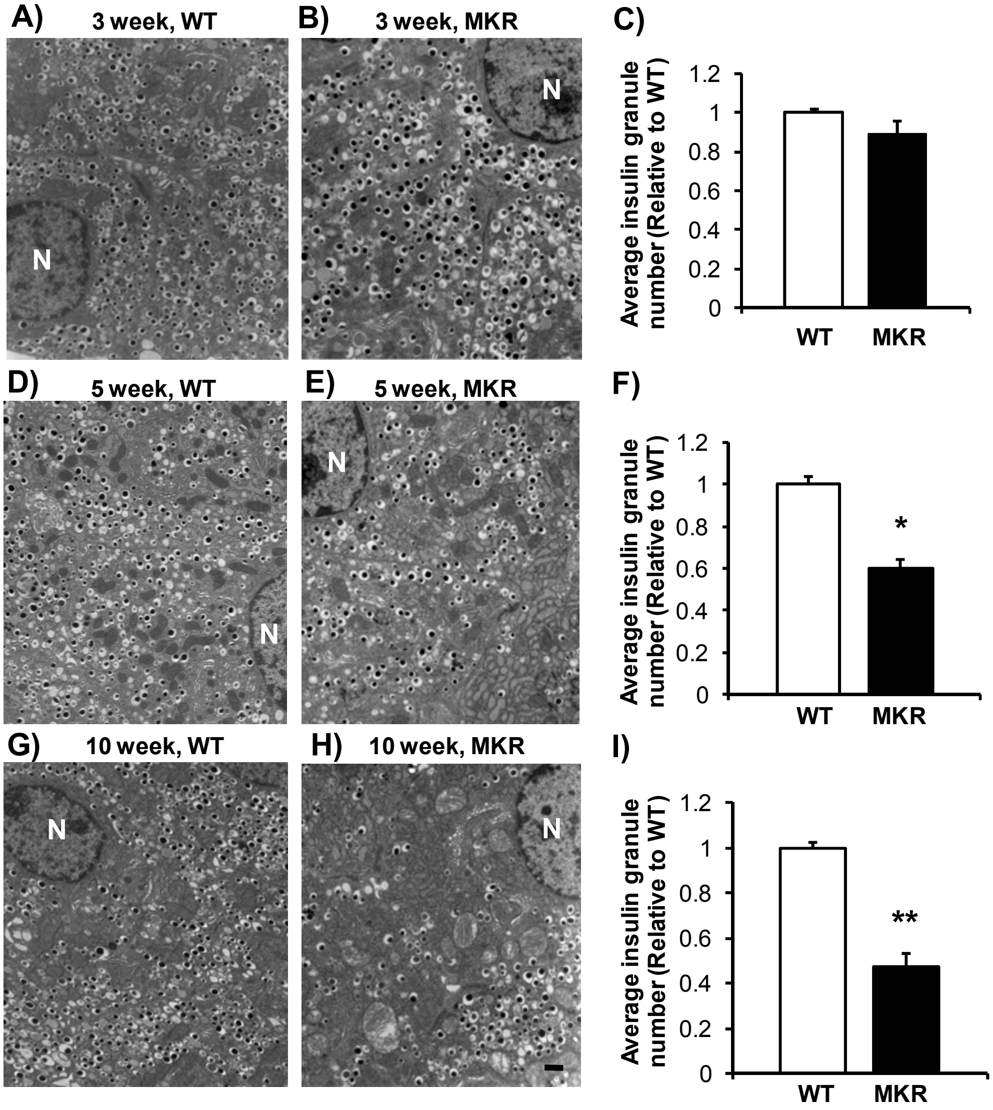

**Figure S6. β-cell dense insulin granule number is reduced in 5 – and 10-week-old MKR islets.** Electron micrographs of ultra-thin sections of islets from 3-week-old, 5-week-old and 10-week-old WT and MKR mice were analyzed and representative images are shown (**A, B, D, E, G, H**). Quantitation of dense insulin granule number was determined using the threshold setting and particle analysis function in Image J software (**C, F, I**). 30 sections were analyzed per age with 3-4 mice per genotype. The black scale bar in the bottom right corner of panel H equals 500nm. The nucleus is labeled with N. *, $p < 0.05$; **, $p < 0.01$ compared to age-matched WT

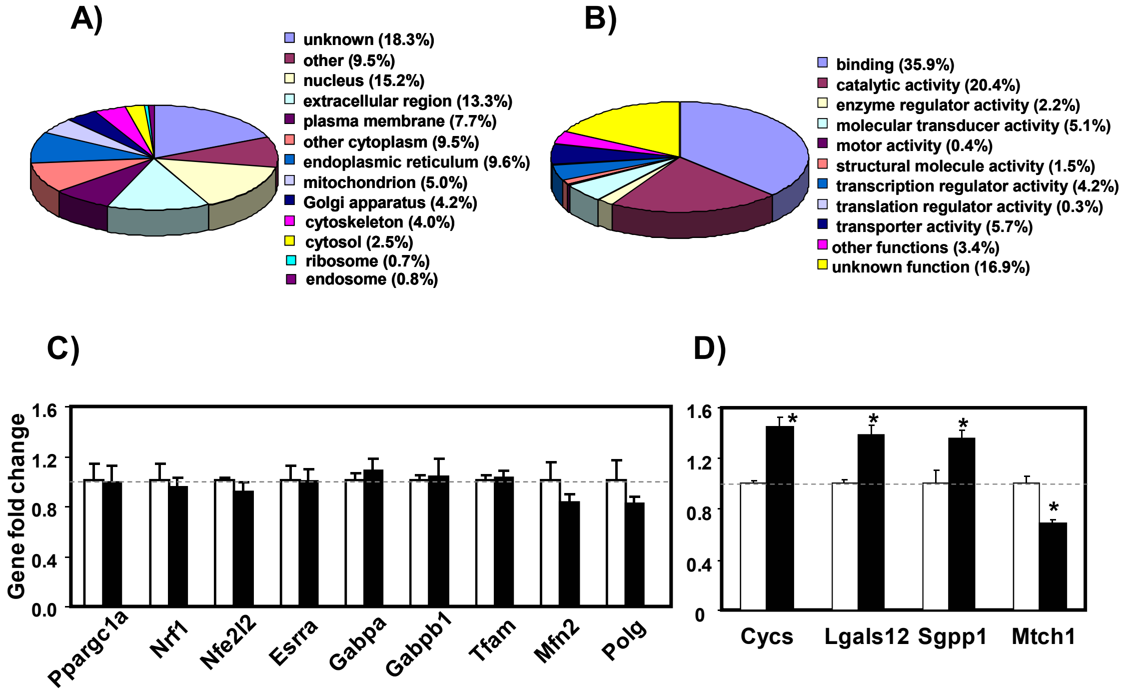

**Figure S7. Functional categorization and fold change of differentially expressed genes in MKR islets.** A total of 849 genes/ESTs were identified to be differentially expressed in MKR diabetic versus WT islets, which were sorted into subcellular location **(A)** and functional categories **(B)**. Relative changes in the levels of genes in MKR islets related to mitochondrial biogenesis **(C)**, and apoptosis **(D)**. * $P < 0.05$

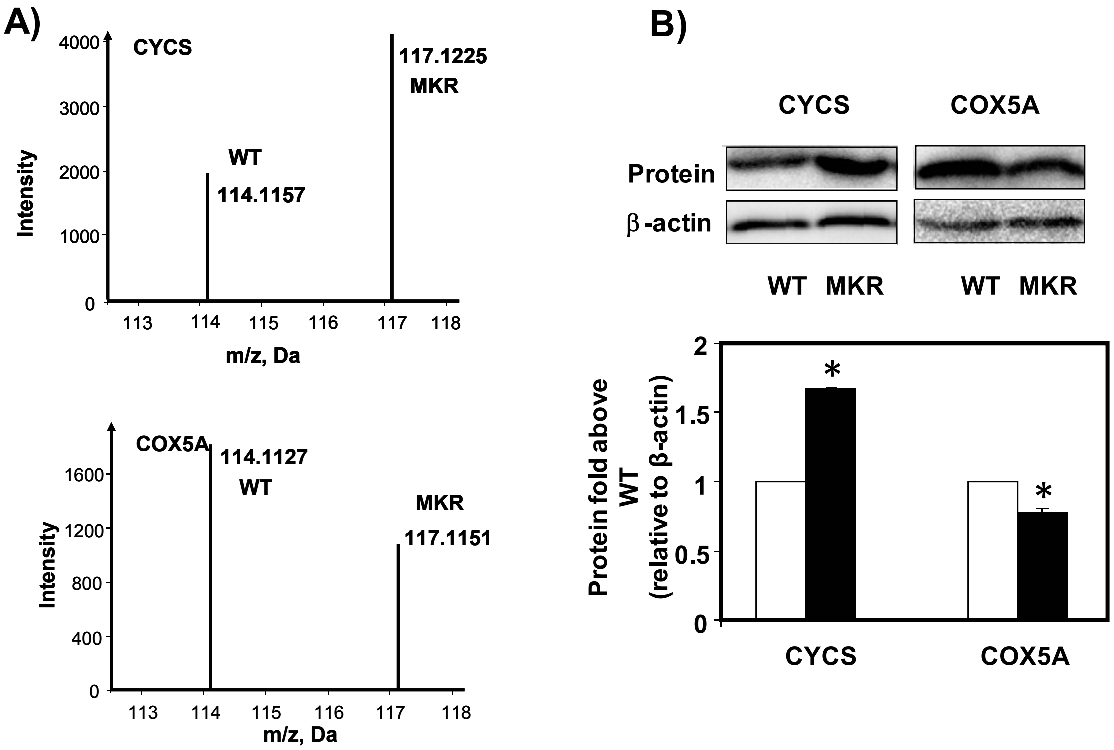

**Figure S8.** **Comparison of protein ratios measured by iTRAQ / Western blotting.** A): iTRAQ mass spectrometry traces of CYCS and COX5A as examples. B) Western blots with analysis showing good correlation between the two methods of measuring protein expression. * $P < 0.05$.

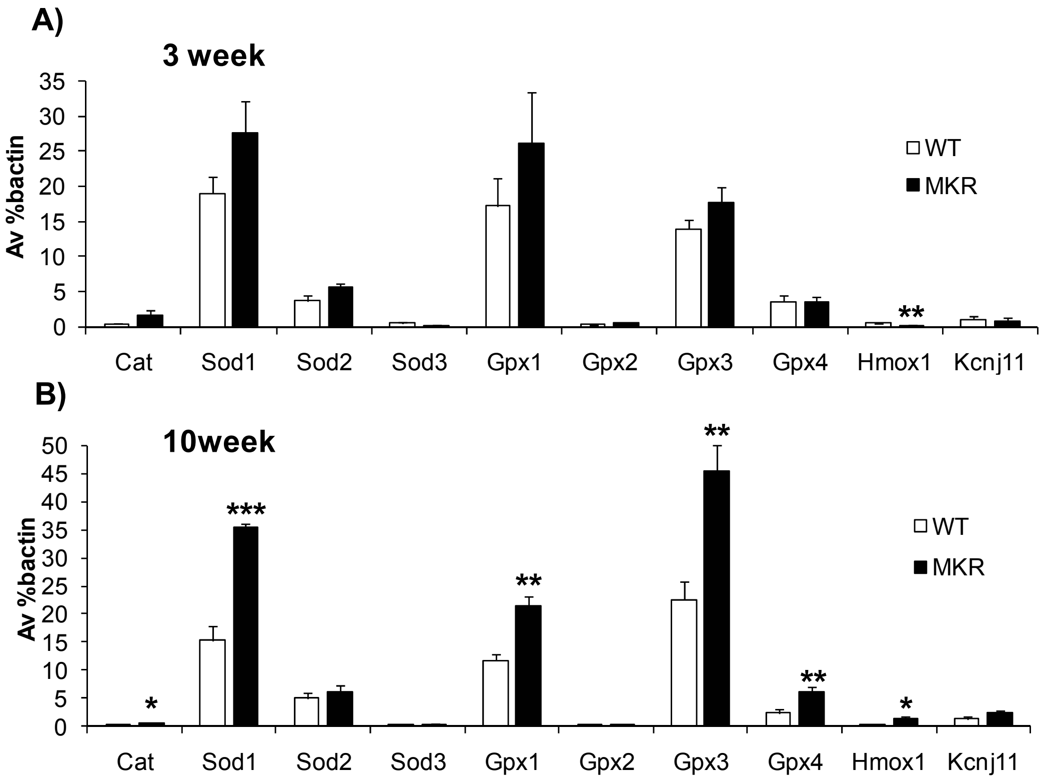

**Figure S9. The expression of anti-oxidant genes is increased in 10-week-old MKR islets.** Islets were isolated, and mRNA was extracted, reversed to cDNA and then the expression of multiple antioxidant genes determined by qRT-PCR and normalized to levels of β-actin (n = 3-5 for each genotype at each age). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ vs. WT. Cat, catalase; Sod, superoxide dismutase; Gpx, glutathione peroxidase; Hmox1, Heme oxygenase 1; Kcnj11, Islet $K_{ATP}$ channel.

## Table S1 Summary of the differentially expressed genes in 10-week-old diabetic islets

| Acce. No. | Gene Symbol | Gene Name | Fold (MKR/WT) | S.E. |
|---|---|---|---|---|
| 1415696_at | Sara1 | SAR1a gene homolog 1 (S. cerevisiae) | 1.29 | 0.03 |
| 1415698_at | Golph2 | golgi phosphoprotein 2 | 1.52 | 0.10 |
| 1415741_at | Tparl | TPA regulated locus | 1.45 | 0.09 |
| 1415749_a_at | Rragc | Ras-related GTP binding C | 0.78 | 0.04 |
| 1415775_at | Rbbp7 | retinoblastoma binding protein 7 | 0.79 | 0.02 |
| 1415822_at | Scd2 | stearoyl-Coenzyme A desaturase 2 | 0.64 | 0.06 |
| 1415827_a_at | D3Ucla1 | DNA segment, Chr 3 | 1.23 | 0.00 |
| 1415889_a_at | Tra1 | tumor rejection antigen gp96 | 1.56 | 0.10 |
| 1415899_at | Junb | Jun-B oncogene | 0.54 | 0.12 |
| 1415904_at | Lpl | lipoprotein lipase | 0.20 | 0.00 |
| 1415911_at | Impact | imprinted and ancient | 0.74 | 0.02 |
| 1415917_at | Mthfd1 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), | 0.66 | 0.03 |
| 1415919_at | Npdc1 | neural proliferation, differentiation and control gene 1 | 1.42 | 0.11 |
| 1415952_at | Mark2 | MAP/microtubule affinity-regulating kinase 2 | 0.68 | 0.05 |
| 1415954_at | Try4 /// Trygn16 | trypsin 4 /// trypsinogen 16 | 1.86 | 0.40 |
| 1415961_at | Itm2c | integral membrane protein 2C | 1.48 | 0.07 |
| 1415975_at | Carhsp1 | calcium regulated heat stable protein 1 | 1.52 | 0.06 |
| 1415987_at | Hdlbp | high density lipoprotein (HDL) binding protein | 1.67 | 0.08 |
| 1415996_at | Txnip | thioredoxin interacting protein | 2.92 | 0.30 |
| 1416029_at | Klf10 | Kruppel-like factor 10 | 2.75 | 0.37 |
| 1416044_at | Fliih | flightless I homolog (Drosophila) | 0.75 | 0.06 |
| 1416060_at | Tbc1d15 | TBC1 domain family, member 15 | 1.38 | 0.03 |
| 1416069_at | Pfkp | phosphofructokinase, platelet | 0.65 | 0.04 |
| 1416108_a_at | Tmed3 | transmembrane emp24 domain containing 3 | 1.59 | 0.10 |
| 1416114_at | Sparcl1 | SPARC-like 1 (mast9, hevin) | 1.71 | 0.15 |
| 1416119_at | Txn1 | thioredoxin 1 | 1.39 | 0.08 |
| 1416167_at | Prdx4 | peroxiredoxin 4 | 1.39 | 0.12 |
| 1416234_at | AA959742 | expressed sequence AA959742 | 1.38 | 0.03 |
| 1416266_at | Pdyn | prodynorphin | 3.34 | 0.21 |
| 1416330_at | Cd81 | CD 81 antigen | 0.68 | 0.02 |
| 1416339_a_at | Prkcsh | protein kinase C substrate 80K-H | 1.45 | 0.03 |
| 1416347_at | Men1 | multiple endocrine neoplasia 1 | 1.35 | 0.03 |
| 1416401_at | Kai1 | kangai 1 (suppression of tumorigenicity 6, prostate) | 1.36 | 0.08 |
| 1416411_at | Gstm2 | glutathione S-transferase, mu 2 | 0.60 | 0.04 |
| 1416414_at | Emilin1 | elastin microfibril interfacer 1 | 1.75 | 0.12 |
| 1416416_x_at | Gstm1 | glutathione S-transferase, mu 1 | 0.52 | 0.04 |
| 1416431_at | Tubb6 | tubulin, beta 6 | 3.46 | 0.73 |
| 1416480_a_at | MGI:1930666 | hypoxia induced gene 1 | 0.51 | 0.07 |

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|---|---|---|---|---|
| 1416484_at | Ttc3 | tetratricopeptide repeat domain 3 | 0.72 | 0.02 |
| 1416497_at | Pdia4 | protein disulfide isomerase associated 4 | 1.91 | 0.09 |
| 1416509_at | MGI:1914262 | SM-11044 binding protein | 1.38 | 0.03 |
| 1416528_at | Sh3bgrl3 | SH3 domain binding glutamic acid-rich protein-like 3 | 0.57 | 0.07 |
| 1416548_at | Slc35b4 | solute carrier family 35, member B4 | 0.63 | 0.05 |
| 1416562_at | Gad1 | glutamic acid decarboxylase 1 | 0.26 | 0.05 |
| 1416588_at | Ptprn | protein tyrosine phosphatase, receptor type, N | 1.45 | 0.09 |
| 1416655_at | C1galt1c1 | C1GALT1-specific chaperone 1 | 1.52 | 0.06 |
| 1416667_at | Ebp | phenylalkylamine Ca2+ antagonist binding protein | 1.36 | 0.13 |
| 1416698_a_at | Cks1b | CDC28 protein kinase 1b | 1.49 | 0.09 |
| 1416699_at | 1110008F13Rik | RIKEN cDNA 1110008F13 gene | 1.29 | 0.03 |
| 1416755_at | Dnajb1 | DnaJ (Hsp40) homolog, subfamily B, member 1 | 0.64 | 0.06 |
| 1416766_at | Mosc2 | MOCO sulphurase C-terminal domain containing 2 | 1.71 | 0.08 |
| 1416768_at | 1110003E01Rik | RIKEN cDNA 1110003E01 gene | 1.38 | 0.03 |
| 1416866_at | Bet1 | blocked early in transport 1 homolog (S. cerevisiae) | 1.68 | 0.17 |
| 1416903_at | Nucb1 | nucleobindin 1 | 1.71 | 0.10 |
| 1416924_at | Bri3 | brain protein I3 | 0.65 | 0.03 |
| 1416939_at | Pyp | pyrophosphatase | 1.55 | 0.07 |
| 1416968_a_at | Hsd3b7 | hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 | 2.05 | 0.09 |
| 1417024_at | Hars | histidyl-tRNA synthetase | 1.38 | 0.07 |
| 1417030_at | 2310028N02Rik | RIKEN cDNA 2310028N02 gene | 0.52 | 0.01 |
| 1417045_at | Bid | BH3 interacting domain death agonist | 0.33 | 0.03 |
| 1417049_at | Rhced | Rhesus blood group CE and D | 2.27 | 0.41 |
| 1417056_at | Psme1 | proteasome (prosome, macropain) 28 subunit, alpha | 0.65 | 0.01 |
| 1417057_a_at | Ppid /// Lamp3 | peptidylprolyl isomerase D (cyclophilin D) /// lysosomal-associated membrane protein 3 | 0.76 | 0.00 |
| 1417059_at | Krtcap2 | keratinocyte associated protein 2 | 1.45 | 0.03 |
| 1417065_at | Egr1 | early growth response 1 | 0.25 | 0.04 |
| 1417070_at | Cyp4v3 | cytochrome P450, family 4, subfamily v, polypeptide 3 | 0.71 | 0.03 |
| 1417083_at | Sec61b | Sec61 beta subunit | 1.23 | 0.05 |
| 1417111_at | Man1a | mannosidase 1, alpha | 1.80 | 0.18 |
| 1417149_at | P4ha2 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide | 1.88 | 0.15 |
| 1417160_s_at | Expi | extracellular proteinase inhibitor | 2.62 | 0.50 |
| 1417179_at | Tspan5 | tetraspanin 5 | 0.76 | 0.03 |
| 1417191_at | Dnajb9 | DnaJ (Hsp40) homolog, subfamily B, member 9 | 1.32 | 0.00 |
| 1417205_at | Kdelr2 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 | 1.50 | 0.19 |
| 1417216_at | Pim2 | proviral integration site 2 | 0.66 | 0.04 |
| 1417245_at | E130016I23Rik | RIKEN cDNA E130016I23 gene | 1.60 | 0.14 |
| 1417267_s_at | Fkbp11 | FK506 binding protein 11 | 2.30 | 0.09 |
| 1417272_at | 9130005N14Rik | RIKEN cDNA 9130005N14 gene | 1.55 | 0.04 |
| 1417273_at | Pdk4 | pyruvate dehydrogenase kinase, isoenzyme 4 | 0.35 | 0.08 |
| 1417287_at | H13 | histocompatibility 13 | 1.75 | 0.14 |
| 1417316_at | Them2 | thioesterase superfamily member 2 | 0.63 | 0.04 |
| 1417336_a_at | Sytl4 | synaptotagmin-like 4 | 0.61 | 0.06 |

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|---|---|---|---|---|
| 1417339_a_at | Dnclc1 | dynein, cytoplasmic, light chain 1 | 1.52 | 0.06 |
| 1417344_at | 2900064A13Rik | RIKEN cDNA 2900064A13 gene | 1.23 | 0.05 |
| 1417354_at | Sil1 | endoplasmic reticulum chaperone SIL1 homolog | 1.41 | 0.00 |
| 1417381_at | C1qa | complement component 1, q subcomponent, alpha polypeptide | 1.97 | 0.17 |
| 1417408_at | F3 | coagulation factor III | 0.57 | 0.10 |
| 1417501_at | Fbxo6b | F-box only protein 6b | 0.59 | 0.05 |
| 1417504_at | Calb1 | calbindin-28K | 0.64 | 0.09 |
| 1417507_at | Cyb561 | cytochrome b-561 | 1.38 | 0.03 |
| 1417600_at | Slc15a2 | solute carrier family 15 (H+/peptide transporter), member 2 | 0.69 | 0.02 |
| 1417660_s_at | Vps29 | vacuolar protein sorting 29 (S. pombe) | 0.78 | 0.02 |
| 1417665_a_at | Cpsf1 | cleavage and polyadenylation specific factor 1 | 0.72 | 0.02 |
| 1417672_at | Slc4a10 | solute carrier family 4, sodium bicarbonate cotransporter-like, member 10 | 2.10 | 0.10 |
| 1417686_at | Lgals12 | lectin, galactose binding, soluble 12 | 1.38 | 0.07 |
| 1417714_x_at | Hba-a1 | hemoglobin alpha, adult chain 1 | 1.23 | 0.05 |
| 1417763_at | Ssr1 | signal sequence receptor, alpha | 1.33 | 0.09 |
| 1417773_at | Nans | N-acetylneuraminic acid synthase (sialic acid synthase) | 1.67 | 0.10 |
| 1417815_a_at | Tde1 | tumor differentially expressed 1 | 1.29 | 0.03 |
| 1417823_at | Gcat | glycine C-acetyltransferase | 0.54 | 0.04 |
| 1417827_at | Ngly1 | N-glycanase 1 | 1.63 | 0.11 |
| 1417864_at | LOC433594 | similar to Pgk1 protein | 1.29 | 0.03 |
| 1417900_a_at | Vldlr | very low density lipoprotein receptor | 0.63 | 0.01 |
| 1417923_at | Pak3 | p21 (CDKN1A)-activated kinase 3 | 1.53 | 0.17 |
| 1417953_at | D6Wsu176e | DNA segment, Chr 6, Wayne State University 176, expressed | 1.38 | 0.03 |
| 1417954_at | Sst | somatostatin | 0.59 | 0.03 |
| 1417965_at | Plekha1 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 | 1.35 | 0.03 |
| 1417991_at | Dio1 | deiodinase, iodothyronine, type I | 2.49 | 0.25 |
| 1418004_a_at | 1810009M01Rik | RIKEN cDNA 1810009M01 gene | 1.23 | 0.00 |
| 1418057_at | Tiam1 | T-cell lymphoma invasion and metastasis 1 | 3.11 | 0.19 |
| 1418093_a_at | Egf | epidermal growth factor | 2.41 | 0.14 |
| 1418097_a_at | Tslpr | thymic stromal-derived lymphopoietin, receptor | 1.45 | 0.07 |
| 1418137_at | Mrp63 | mitochondrial ribosomal protein 63 | 1.39 | 0.08 |
| 1418139_at | Dcx | doublecortin | 1.45 | 0.03 |
| 1418144_a_at | Pip5k1b | phosphatidylinositol-4-phosphate 5-kinase, type 1 beta | 0.76 | 0.03 |
| 1418161_at | Jph3 | junctophilin 3 | 0.46 | 0.05 |
| 1418174_at | Dbp | D site albumin promoter binding protein | 0.52 | 0.13 |
| 1418186_at | Gstt1 | glutathione S-transferase, theta 1 | 0.58 | 0.04 |
| 1418191_at | Usp18 | ubiquitin specific protease 18 | 1.67 | 0.10 |
| 1418206_at | Sdf2l1 | stromal cell-derived factor 2-like 1 | 2.49 | 0.63 |
| 1418223_at | Sec11l1 | Sec11-like 1 (S. cerevisiae) | 1.33 | 0.09 |
| 1418238_at | Ivd | isovaleryl coenzyme A dehydrogenase | 0.57 | 0.07 |
| 1418248_at | Gla | galactosidase, alpha | 1.79 | 0.08 |
| 1418319_at | 1810047C23Rik | RIKEN cDNA 1810047C23 gene | 1.32 | 0.05 |
| 1418324_at | Fem1b | feminization 1 homolog b (C. elegans) | 0.76 | 0.03 |

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|---|---|---|---|---|
| 1418344_at | Tmem8 | transmembrane protein 8 | 0.72 | 0.02 |
| 1418355_at | Nucb2 | nucleobindin 2 | 2.47 | 0.17 |
| 1418364_a_at | Ftl1 | ferritin light chain 1 | 0.76 | 0.03 |
| 1418374_at | Fxyd3 | FXYD domain-containing ion transport regulator 3 | 1.63 | 0.07 |
| 1418389_at | 2810453I06Rik | RIKEN cDNA 2810453I06 gene | 1.35 | 0.03 |
| 1418406_at | Pde8a | phosphodiesterase 8A | 0.74 | 0.04 |
| 1418455_at | Copz2 | coatomer protein complex, subunit zeta 2 | 2.25 | 0.05 |
| 1418478_at | Lmo1 | LIM domain only 1 | 1.77 | 0.21 |
| 1418528_a_at | Dad1 | defender against cell death 1 | 1.32 | 0.05 |
| 1418538_at | Kdelr3 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | 5.80 | 0.26 |
| 1418566_s_at | Nudcd2 | NudC domain containing 2 | 1.60 | 0.14 |
| 1418587_at | Traf3 | Tnf receptor-associated factor 3 | 1.35 | 0.03 |
| 1418594_a_at | Ncoa1 | nuclear receptor coactivator 1 | 0.69 | 0.04 |
| 1418643_at | Tspan13 | tetraspanin 13 | 1.26 | 0.03 |
| 1418701_at | Comt | catechol-O-methyltransferase | 0.79 | 0.02 |
| 1418778_at | 9030408N13Rik | RIKEN cDNA 9030408N13 gene | 0.32 | 0.02 |
| 1418783_at | Trpm5 | transient receptor potential cation channel, subfamily M, member 5 | 0.68 | 0.05 |
| 1418812_a_at | Barhl1 | BarH-like 1 (Drosophila) | 1.67 | 0.13 |
| 1418829_a_at | Eno2 | enolase 2, gamma neuronal | 0.76 | 0.03 |
| 1418888_a_at | Sepx1 | selenoprotein X 1 | 1.42 | 0.06 |
| 1418891_a_at | Rab3d | RAB3D, member RAS oncogene family | 1.92 | 0.12 |
| 1418896_a_at | Rpn2 | ribophorin II | 1.33 | 0.09 |
| 1418899_at | Ufm1 | ubiquitin-fold modifier 1 | 1.42 | 0.06 |
| 1418967_a_at | St7 | Suppression of tumorigenicity 7 | 2.18 | 0.28 |
| 1418979_at | 9030611N15Rik | RIKEN cDNA 9030611N15 gene | 1.32 | 0.05 |
| 1419022_a_at | Eno1 /// LOC433182 | enolase 1, alpha non-neuron /// similar to enolase 1, alpha non-neuron | 1.36 | 0.14 |
| 1419062_at | Epb4.1l3 | erythrocyte protein band 4.1-like 3 | 0.62 | 0.00 |
| 1419077_at | Mpp3 | membrane protein, palmitoylated 3 | 0.58 | 0.06 |
| 1419127_at | Npy | neuropeptide Y | 0.11 | 0.01 |
| 1419177_at | D8Ertd531e | DNA segment, Chr 8, ERATO Doi 531, expressed | 0.74 | 0.04 |
| 1419260_a_at | Snrpb | small nuclear ribonucleoprotein B | 0.79 | 0.02 |
| 1419280_at | Pip5k2a | phosphatidylinositol-4-phosphate 5-kinase, type II, alpha | 1.52 | 0.06 |
| 1419287_at | MGI:1913570 | HSPC171 protein | 1.35 | 0.03 |
| 1419382_a_at | Dhrs4 | dehydrogenase/reductase (SDR family) member 4 | 0.68 | 0.04 |
| 1419392_at | Pclo | piccolo (presynaptic cytomatrix protein) | 0.76 | 0.05 |
| 1419441_at | Arbp | acidic ribosomal phosphoprotein P0 | 1.29 | 0.06 |
| 1419449_a_at | Gnai2 | guanine nucleotide binding protein, alpha inhibiting 2 | 0.55 | 0.01 |
| 1419459_a_at | 2610529C04Rik | RIKEN cDNA 2610529C04 gene | 1.44 | 0.21 |
| 1419496_at | Slco1a6 | solute carrier organic anion transporter family, member 1a6 | 2.71 | 0.12 |
| 1419509_a_at | Nagk | N-acetylglucosamine kinase | 0.81 | 0.00 |
| 1419532_at | Il1r2 | interleukin 1 receptor, type II | 2.25 | 0.05 |
| 1419549_at | Arg1 | arginase 1, liver | 0.34 | 0.05 |

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|---|---|---|---|---|
| 1419569_a_at | Isg20 | interferon-stimulated protein | 1.76 | 0.19 |
| 1419573_a_at | Lgals1 | lectin, galactose binding, soluble 1 | 1.56 | 0.13 |
| 1419595_a_at | Ggh | gamma-glutamyl hydrolase | 1.32 | 0.00 |
| 1419700_a_at | Prom1 | prominin 1 | 2.43 | 0.21 |
| 1419735_at | Csnk | casein kappa | 8.70 | 1.04 |
| 1419979_s_at | Creb3 | cAMP responsive element binding protein 3 | 1.20 | 0.03 |
| 1419994_s_at | D10Ertd641e | DNA segment, Chr 10, ERATO Doi 641, expressed | 1.36 | 0.08 |
| 1420124_s_at | Tcta | T-cell leukemia translocation altered gene | 1.42 | 0.06 |
| 1420127_s_at | Ccpg1 | cell cycle progression 1 | 1.42 | 0.06 |
| 1420411_a_at | Pi4k2b | phosphatidylinositol 4-kinase type 2 beta | 1.56 | 0.10 |
| 1420440_at | Ppy | pancreatic polypeptide | 0.53 | 0.05 |
| 1420477_at | Nap1l1 | nucleosome assembly protein 1-like 1 | 0.78 | 0.02 |
| 1420499_at | Gch1 | GTP cyclohydrolase 1 | 0.72 | 0.02 |
| 1420500_at | Dnajc1 | DnaJ (Hsp40) homolog, subfamily C, member 1 | 1.42 | 0.06 |
| 1420638_at | Prps2 | phosphoribosyl pyrophosphate synthetase 2 | 0.62 | 0.02 |
| 1420646_at | D10Ertd438e | DNA segment, Chr 10, ERATO Doi 438, expressed | 1.55 | 0.23 |
| 1420760_s_at | Ndrl | N-myc downstream regulated-like | 0.53 | 0.05 |
| 1420822_s_at | Sgpp1 | sphingosine-1-phosphate phosphatase 1 | 1.35 | 0.03 |
| 1420843_at | Ptprf | protein tyrosine phosphatase, receptor type, F | 0.65 | 0.06 |
| 1420890_at | Hccs | holocytochrome c synthetase | 0.46 | 0.01 |
| 1421074_at | Cyp7b1 | cytochrome P450, family 7, subfamily b, polypeptide 1 | 1.79 | 0.11 |
| 1421137_a_at | Pkib | protein kinase inhibitor beta, cAMP dependent, testis specific | 1.38 | 0.07 |
| 1421145_at | Slc26a2 | solute carrier family 26 (sulfate transporter), member 2 | 1.71 | 0.08 |
| 1421205_at | Atm | ataxia telangiectasia mutated homolog (human) | 0.72 | 0.08 |
| 1421260_a_at | Srm | spermidine synthase | 1.45 | 0.03 |
| 1421425_a_at | Dscr1l1 | Down syndrome critical region gene 1-like 1 | 0.74 | 0.04 |
| 1421558_at | T2 | brachyury 2 | 0.21 | 0.06 |
| 1421947_at | Gng12 | guanine nucleotide binding protein, gamma 12 | 1.42 | 0.06 |
| 1422052_at | Cdh8 | cadherin 8 | 0.65 | 0.04 |
| 1422101_at | Tnfrsf23 | tumor necrosis factor receptor superfamily, member 23 | 1.96 | 0.04 |
| 1422134_at | Fosb | FBJ osteosarcoma oncogene B | 0.16 | 0.08 |
| 1422216_at | Mid2 | midline 2 | 1.70 | 0.04 |
| 1422241_a_at | Ndufa1 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.45 | 0.07 |
| 1422474_at | Pde4b | phosphodiesterase 4B, cAMP specific | 0.64 | 0.08 |
| 1422489_at | Gcs1 | glucosidase 1 | 1.70 | 0.04 |
| 1422492_at | Cpox | coproporphyrinogen oxidase | 1.50 | 0.15 |
| 1422557_s_at | Mt1 | metallothionein 1 | 0.19 | 0.02 |
| 1422583_at | Rab3b | RAB3B, member RAS oncogene family | 0.60 | 0.03 |
| 1422593_at | Ap3s1 | adaptor-related protein complex 3, sigma 1 subunit | 1.45 | 0.07 |
| 1422601_at | Serpinb9 | serine (or cysteine) proteinase inhibitor, clade B, member 9 | 0.61 | 0.05 |
| 1422605_at | Ppp1r1a | protein phosphatase 1, regulatory (inhibitor) subunit 1A | 0.66 | 0.05 |
| 1422644_at | Sh3bgr | SH3-binding domain glutamic acid-rich protein | 1.74 | 0.07 |
| 1422720_at | Isl1 | ISL1 transcription factor, LIM/homeodomain (islet 1) | 0.68 | 0.05 |

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|---|---|---|---|---|
| 1422728_at | Inha | inhibin alpha | 1.45 | 0.07 |
| 1422809_at | Rims2 | regulating synaptic membrane exocytosis 2 | 0.68 | 0.03 |
| 1422824_s_at | Eps8 | epidermal growth factor receptor pathway substrate 8 | 0.63 | 0.01 |
| 1422833_at | Foxa2 | forkhead box A2 | 0.81 | 0.00 |
| 1422907_at | Gnat2 | guanine nucleotide binding protein, alpha transducing 2 | 1.71 | 0.08 |
| 1422962_a_at | Psmb8 | proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7) | 0.54 | 0.06 |
| 1423052_at | Arf4 | ADP-ribosylation factor 4 | 1.29 | 0.06 |
| 1423082_at | Derl1 | Der1-like domain family, member 1 | 1.45 | 0.07 |
| 1423100_at | Fos | FBJ osteosarcoma oncogene | 0.10 | 0.01 |
| 1423127_at | Impa1 | inositol (myo)-1(or 4)-monophosphatase 1 | 0.79 | 0.02 |
| 1423151_at | Dnajb11 | DnaJ (Hsp40) homolog, subfamily B, member 11 | 1.80 | 0.18 |
| 1423202_a_at | Ncor1 | nuclear receptor co-repressor 1 | 0.78 | 0.02 |
| 1423211_at | Nola3 | nucleolar protein family A, member 3 | 1.32 | 0.05 |
| 1423225_at | MGI:1931466 | selenoprotein K | 1.33 | 0.09 |
| 1423239_at | Impdh1 | inosine 5'-phosphate dehydrogenase 1 | 1.59 | 0.04 |
| 1423247_at | Txndc4 | thioredoxin domain containing 4 (endoplasmic reticulum) | 1.39 | 0.08 |
| 1423263_at | H3f3a | H3 histone, family 3A | 0.81 | 0.00 |
| 1423274_at | Ddx26 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 | 0.83 | 0.04 |
| 1423290_at | Hyou1 | hypoxia up-regulated 1 | 1.80 | 0.33 |
| 1423319_at | Hhex | hematopoietically expressed homeobox | 0.45 | 0.05 |
| 1423332_at | Sdcbp | syndecan binding protein | 1.29 | 0.03 |
| 1423334_at | 1200007D18Rik | RIKEN cDNA 1200007D18 gene | 1.67 | 0.08 |
| 1423478_at | Prkcb1 | protein kinase C, beta 1 | 0.49 | 0.02 |
| 1423490_at | Fbxo3 | F-box only protein 3 | 0.68 | 0.04 |
| 1423505_at | Tagln | transgelin | 3.35 | 0.97 |
| 1423506_a_at | Nnat | neuronatin | 0.26 | 0.08 |
| 1423523_at | Aass | aminoadipate-semialdehyde synthase | 6.10 | 0.49 |
| 1423547_at | Lyzs | lysozyme | 2.00 | 0.08 |
| 1423621_a_at | Slc33a1 | solute carrier family 33 (acetyl-CoA transporter), member 1 | 1.50 | 0.15 |
| 1423626_at | Dst | dystonin | 0.78 | 0.02 |
| 1423645_a_at | Ddx5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 | 0.71 | 0.06 |
| 1423648_at | Pdia6 | protein disulfide isomerase associated 6 | 1.63 | 0.07 |
| 1423663_at | Flcn | folliculin | 0.71 | 0.05 |
| 1423670_a_at | Srpr | signal recognition particle receptor ('docking protein') | 1.42 | 0.06 |
| 1423687_a_at | Man2c1 | mannosidase, alpha, class 2C, member 1 | 0.74 | 0.04 |
| 1423691_x_at | Krt2-8 | keratin complex 2, basic, gene 8 | 1.26 | 0.03 |
| 1423695_at | 9530090G24Rik | RIKEN cDNA 9530090G24 gene | 1.71 | 0.08 |
| 1423718_at | Ak3 | adenylate kinase 3 | 1.38 | 0.03 |
| 1423722_at | Tmem49 | transmembrane protein 49 | 1.59 | 0.10 |
| 1423730_at | C130052I12Rik | RIKEN cDNA C130052I12 gene | 1.96 | 0.12 |
| 1423732_at | Tram1 | translocating chain-associating membrane protein 1 | 1.35 | 0.03 |
| 1423783_at | Tor2a | torsin family 2, member A | 1.42 | 0.06 |
| 1423914_at | C630004H02Rik | RIKEN cDNA C630004H02 gene | 1.45 | 0.07 |

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|---|---|---|---|---|
| 1423940_at | Yif1 | Yip1 interacting factor homolog (S. cerevisiae) | 1.26 | 0.03 |
| 1423954_at | C3 | complement component 3 | 3.61 | 0.39 |
| 1424024_at | Mcfd2 | multiple coagulation factor deficiency 2 | 1.50 | 0.18 |
| 1424039_at | 1810045K07Rik | RIKEN cDNA 1810045K07 gene | 1.29 | 0.03 |
| 1424065_at | Edem1 | ER degradation enhancer, mannosidase alpha-like 1 | 2.65 | 0.18 |
| 1424072_at | 2010107G23Rik | RIKEN cDNA 2010107G23 gene | 0.69 | 0.03 |
| 1424160_at | Alg5 | asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase) | 1.89 | 0.19 |
| 1424188_at | Rabgap1 | RAB GTPase activating protein 1 | 0.76 | 0.00 |
| 1424208_at | Ptger4 | prostaglandin E receptor 4 (subtype EP4) | 3.78 | 0.42 |
| 1424240_at | Arfip2 | ADP-ribosylation factor interacting protein 2 | 1.45 | 0.07 |
| 1424274_at | MGI:1929095 | vesicle docking protein | 1.42 | 0.06 |
| 1424283_at | Jtb | jumping translocation breakpoint | 1.42 | 0.06 |
| 1424318_at | 1110067D22Rik | RIKEN cDNA 1110067D22 gene | 1.43 | 0.17 |
| 1424356_a_at | Metrnl | meteorin, glial cell differentiation regulator-like | 2.22 | 0.24 |
| 1424369_at | Psmf1 | proteasome (prosome, macropain) inhibitor subunit 1 | 0.71 | 0.03 |
| 1424373_at | Armcx3 | armadillo repeat containing, X-linked 3 | 1.63 | 0.07 |
| 1424394_at | MGI:2149786 | selenoprotein M | 1.33 | 0.11 |
| 1424410_at | Ttc8 | tetratricopeptide repeat domain 8 | 0.71 | 0.03 |
| 1424455_at | Gprasp1 | G protein-coupled receptor associated sorting protein 1 | 0.66 | 0.05 |
| 1424529_s_at | Cgref1 | cell growth regulator with EF hand domain 1 | 3.03 | 0.49 |
| 1424556_at | Pycr1 | pyrroline-5-carboxylate reductase 1 | 2.98 | 0.26 |
| 1424568_at | Tspan2 | tetraspan 2 | 0.66 | 0.03 |
| 1424572_a_at | H2afy | H2A histone family, member Y | 0.81 | 0.00 |
| 1424574_at | Tmed5 | transmembrane emp24 protein transport domain containing 5 | 1.43 | 0.16 |
| 1424612_at | 9330161F08Rik | RIKEN cDNA 9330161F08 gene | 1.70 | 0.04 |
| 1424649_a_at | Tspan8 | tetraspanin 8 | 0.37 | 0.02 |
| 1424650_at | Pdia5 | protein disulfide isomerase associated 5 | 1.39 | 0.12 |
| 1424670_s_at | Zfyve21 | zinc finger, FYVE domain containing 21 | 0.71 | 0.05 |
| 1424693_at | 4933407N01Rik | RIKEN cDNA 4933407N01 gene | 1.38 | 0.03 |
| 1424696_at | Gpr89 | G protein-coupled receptor 89 | 1.48 | 0.03 |
| 1424698_s_at | Gca | grancalcin | 1.53 | 0.17 |
| 1424708_at | 1110014C03Rik | RIKEN cDNA 1110014C03 gene | 1.29 | 0.03 |
| 1424710_a_at | Gorasp2 | golgi reassembly stacking protein 2 | 1.29 | 0.03 |
| 1424734_at | Rasgrf1 | RAS protein-specific guanine nucleotide-releasing factor 1 | 0.59 | 0.04 |
| 1424737_at | Thrsp | thyroid hormone responsive SPOT14 homolog (Rattus) | 1.48 | 0.07 |
| 1424769_s_at | Cald1 | caldesmon 1 | 1.39 | 0.08 |
| 1424806_s_at | 1110039B18Rik | RIKEN cDNA 1110039B18 gene | 1.42 | 0.06 |
| 1424812_at | BC017158 | cDNA sequence BC017158 | 1.62 | 0.00 |
| 1424865_at | Pyy | peptide YY | 0.38 | 0.03 |
| 1424905_a_at | Slc39a11 | solute carrier family 39 (metal ion transporter), member 11 | 1.78 | 0.04 |
| 1424926_at | Sec63 | SEC63-like (S. cerevisiae) | 1.53 | 0.17 |
| 1425018_at | Mcts1 | malignant T cell amplified sequence 1 | 1.32 | 0.05 |

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|---|---|---|---|---|
| 1425029_a_at | Oact2 | O-acyltransferase (membrane bound) domain containing 2 | 1.42 | 0.06 |
| 1425102_a_at | Ace2 | angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 | 0.49 | 0.02 |
| 1425114_at | Rbbp6 | retinoblastoma binding protein 6 | 0.73 | 0.05 |
| 1425250_a_at | Slc14a2 | solute carrier family 14 (urea transporter), member 2 | 0.52 | 0.07 |
| 1425348_a_at | Srprb | signal recognition particle receptor, B subunit | 1.59 | 0.08 |
| 1425458_a_at | Grb10 | growth factor receptor bound protein 10 | 0.48 | 0.01 |
| 1425519_a_at | Ii | Ia-associated invariant chain | 0.68 | 0.07 |
| 1425520_a_at | Dhdds | dehydrodolichyl diphosphate synthase | 1.38 | 0.07 |
| 1425542_a_at | Ppp2r5c | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | 1.42 | 0.06 |
| 1425603_at | 0610011I04Rik | RIKEN cDNA 0610011I04 gene | 1.29 | 0.03 |
| 1425705_a_at | Ero1lb | ERO1-like beta (S. cerevisiae) | 1.38 | 0.03 |
| 1425745_a_at | Tacc2 | transforming, acidic coiled-coil containing protein 2 | 1.55 | 0.07 |
| 1425811_a_at | Csrp1 | cysteine and glycine-rich protein 1 | 1.63 | 0.07 |
| 1425828_at | Nkx6-1 | NK6 transcription factor related, locus 1 (Drosophila) | 0.68 | 0.02 |
| 1425886_at | Fev | FEV (ETS oncogene family) | 0.47 | 0.03 |
| 1425950_at | BC019537 | cDNA sequence BC019537 | 2.11 | 0.18 |
| 1426015_s_at | Asph | aspartate-beta-hydroxylase | 1.63 | 0.11 |
| 1426078_a_at | Gpr108 | G protein-coupled receptor 108 | 1.45 | 0.03 |
| 1426089_a_at | BC003331 | cDNA sequence BC003331 | 1.32 | 0.05 |
| 1426187_a_at | Hax1 | HCLS1 associated X-1 | 1.38 | 0.07 |
| 1426208_x_at | Plagl1 | pleiomorphic adenoma gene-like 1 | 0.74 | 0.04 |
| 1426216_at | Cog6 | component of oligomeric golgi complex 6 | 1.56 | 0.10 |
| 1426225_at | Rbp4 | retinol binding protein 4, plasma | 0.28 | 0.03 |
| 1426235_a_at | Glul | glutamate-ammonia ligase (glutamine synthase) | 0.68 | 0.02 |
| 1426306_a_at | Maged2 | melanoma antigen, family D, 2 | 1.63 | 0.07 |
| 1426309_at | Asb9 | ankyrin repeat and SOCS box-containing protein 9 | 3.13 | 0.70 |
| 1426322_a_at | Kcnmb2 | potassium large conductance calcium-activated channel, subfamily M, beta member 2 | 0.73 | 0.06 |
| 1426342_at | 1300006C19Rik | RIKEN cDNA 1300006C19 gene | 1.26 | 0.03 |
| 1426393_a_at | Sdf4 | stromal cell derived factor 4 | 1.29 | 0.06 |
| 1426413_at | Neurod1 | neurogenic differentiation 1 | 0.78 | 0.02 |
| 1426440_at | Dhrs7 | dehydrogenase/reductase (SDR family) member 7 | 1.79 | 0.14 |
| 1426445_at | Mgea6 | meningioma expressed antigen 6 | 1.39 | 0.12 |
| 1426453_at | Pitrm1 | pitrilysin metalloprotease 1 | 0.76 | 0.03 |
| 1426459_s_at | AW549877 | expressed sequence AW549877 | 0.74 | 0.02 |
| 1426519_at | P4ha1 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide | 1.45 | 0.09 |
| 1426531_at | Zmynd11 | zinc finger, MYND domain containing 11 | 0.79 | 0.02 |
| 1426539_at | Usp11 | ubiquitin specific protease 11 | 0.59 | 0.06 |
| 1426547_at | Gc | group specific component | 2.92 | 0.30 |
| 1426569_a_at | Frk | fyn-related kinase | 1.71 | 0.15 |
| 1426617_a_at | Ttyh1 | tweety homolog 1 (Drosophila) | 1.93 | 0.19 |
| 1426622_a_at | Qpct | glutaminyl-peptide cyclotransferase (glutaminyl cyclase) | 0.37 | 0.07 |
| 1426628_at | Tmem34 | transmembrane protein 34 | 1.42 | 0.10 |
| 1426658_x_at | Phgdh | 3-phosphoglycerate dehydrogenase | 2.25 | 0.11 |

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|---|---|---|---|---|
| 1426662_at | Cmas | cytidine monophospho-N-acetylneuraminic acid synthetase | 2.01 | 0.13 |
| 1426670_at | Agrn | agrin | 1.42 | 0.10 |
| 1426690_a_at | Srebf1 | sterol regulatory element binding factor 1 | 0.74 | 0.02 |
| 1426715_s_at | D11Ertd18e | DNA segment, Chr 11, ERATO Doi 18, expressed | 1.83 | 0.09 |
| 1426721_s_at | Tiparp | TCDD-inducible poly(ADP-ribose) polymerase | 1.42 | 0.06 |
| 1426758_s_at | Gtl2 | GTL2, imprinted maternally expressed untranslated mRNA | 1.29 | 0.06 |
| 1426864_a_at | Ncam1 | neural cell adhesion molecule 1 | 0.58 | 0.06 |
| 1426818_at | Arrdc4 | Expressed sequence AV216361 | 3.68 | 0.36 |
| 1426834_s_at | D930015E06Rik | RIKEN cDNA D930015E06 gene | 0.65 | 0.06 |
| 1426887_at | Nudt11 | nudix (nucleoside diphosphate linked moiety X)-type motif 11 | 0.63 | 0.01 |
| 1426911_at | Dsc2 | desmocollin 2 | 1.42 | 0.09 |
| 1426915_at | Dapk1 | death associated protein kinase 1 | 0.63 | 0.09 |
| 1426950_at | Parp16 | poly (ADP-ribose) polymerase family, member 16 | 1.53 | 0.12 |
| 1426961_at | 6820402O20Rik | RIKEN cDNA 6820402O20 gene | 0.78 | 0.04 |
| 1426972_at | Sec24d | SEC24 related gene family, member D (S. cerevisiae) | 1.35 | 0.03 |
| 1426981_at | Pcsk6 | proprotein convertase subtilisin/kexin type 6 | 0.58 | 0.10 |
| 1427021_s_at | Fth1 /// Dpep2 | ferritin heavy chain 1 /// dipeptidase 2 | 0.76 | 0.03 |
| 1427231_at | Robo1 | roundabout homolog 1 (Drosophila) | 0.58 | 0.02 |
| 1427233_at | Sdccag33 | serologically defined colon cancer antigen 33 | 0.65 | 0.01 |
| 1427236_a_at | Mll5 | myeloid/lymphoid or mixed-lineage leukemia 5 | 0.78 | 0.02 |
| 1427245_at | Arfgap1 | ADP-ribosylation factor GTPase activating protein 1 | 1.32 | 0.05 |
| 1427398_at | Muc4 | mucin 4 | 1.73 | 0.21 |
| 1427442_a_at | App | amyloid beta (A4) precursor protein | 0.59 | 0.03 |
| 1427464_s_at | Hspa5 | heat shock 70kD protein 5 (glucose-regulated protein) | 1.53 | 0.15 |
| 1427472_a_at | C8b | complement component 8, beta subunit | 2.30 | 0.34 |
| 1428050_a_at | 0610007H07Rik | RIKEN cDNA 0610007H07 gene | 1.52 | 0.06 |
| 1428070_at | Syvn1 | synovial apoptosis inhibitor 1, synoviolin | 1.74 | 0.07 |
| 1428109_at | Vps11 | vacuolar protein sorting 11 (yeast) | 0.69 | 0.04 |
| 1428112_at | Armet | arginine-rich, mutated in early stage tumors | 1.46 | 0.12 |
| 1428134_at | 2310005O14Rik | RIKEN cDNA 2310005O14 gene | 1.29 | 0.03 |
| 1428154_s_at | Ppapdc1 | phosphatidic acid phosphatase type 2 domain containing 1 | 1.83 | 0.11 |
| 1428163_at | Sara2 | SAR1a gene homolog 2 (S. cerevisiae) | 1.32 | 0.05 |
| 1428240_at | Nrxn1 | neurexin I | 0.66 | 0.03 |
| 1428269_a_at | Glt8d1 | glycosyltransferase 8 domain containing 1 | 1.48 | 0.03 |
| 1428308_at | Pdrg1 | p53 and DNA damage regulated 1 | 1.62 | 0.00 |
| 1428280_at | Fip1l1 | FIP1 like 1 (S. cerevisiae) | 0.74 | 0.02 |
| 1428323_at | Gpd2 | glycerol phosphate dehydrogenase 2, mitochondrial | 0.66 | 0.05 |
| 1428434_at | Zcchc12 | zinc finger, CCHC domain containing 12 | 3.35 | 0.62 |
| 1428443_a_at | Rap1ga1 | Rap1, GTPase-activating protein 1 | 0.73 | 0.06 |
| 1428445_at | Yif1b | Yip1 interacting factor homolog B (S. cerevisiae) | 1.49 | 0.13 |
| 1428471_at | Sorbs1 | sorbin and SH3 domain containing 1 | 1.78 | 0.27 |
| 1428544_at | 0610007L01Rik | RIKEN cDNA 0610007L01 gene | 1.59 | 0.04 |
| 1428604_at | 2610305D13Rik | RIKEN cDNA 2610305D13 gene | 2.13 | 0.45 |

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|---|---|---|---|---|
| 1428662_a_at | MGI:1916782 | homeobox only domain | 1.49 | 0.13 |
| 1428682_at | Zc3h6 | zinc finger CCCH type containing 6 | 0.68 | 0.02 |
| 1428804_at | Mfap3l | microfibrillar-associated protein 3-like | 2.67 | 0.29 |
| 1428854_at | Tmed8 | transmembrane emp24 domain containing 8 | 0.68 | 0.03 |
| 1428942_at | Mt2 | metallothionein 2 | 0.21 | 0.02 |
| 1429065_at | 1200009F10Rik | RIKEN cDNA 1200009F10 gene | 1.71 | 0.10 |
| 1429071_at | Me3 | malic enzyme 3, NADP(+)-dependent, mitochondrial | 0.30 | 0.09 |
| 1429155_at | 4933411K20Rik | RIKEN cDNA 4933411K20 gene | 0.78 | 0.02 |
| 1429234_s_at | Sept11 | septin 11 | 1.45 | 0.07 |
| 1429244_at | 2610524H06Rik | RIKEN cDNA 2610524H06 gene | 1.72 | 0.15 |
| 1429348_at | Sema3c | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C | 3.42 | 0.21 |
| 1429415_at | Prkcbp1 | protein kinase C binding protein 1 | 0.72 | 0.02 |
| 1429737_a_at | 0610009I22Rik | RIKEN cDNA 0610009I22 gene | 1.49 | 0.13 |
| 1429870_at | C630040K21Rik | RIKEN cDNA C630040K21 gene | 0.60 | 0.01 |
| 1429913_at | Kcnk16 | potassium channel, subfamily K, member 16 | 1.56 | 0.10 |
| 1430309_at | Nipbl | Nipped-B homolog (Drosophila) | 0.74 | 0.04 |
| 1430404_at | 4833416J08Rik | RIKEN cDNA 4833416J08 gene | 0.69 | 0.03 |
| 1430820_a_at | Bbx | bobby sox homolog (Drosophila) | 0.66 | 0.05 |
| 1430856_at | Pex11c | peroxisomal biogenesis factor 11c | 1.52 | 0.06 |
| 1430977_at | A930021C24Rik | RIKEN cDNA A930021C24 gene | 0.50 | 0.06 |
| 1430985_at | 1810027O10Rik | RIKEN cDNA 1810027O10 gene | 0.63 | 0.03 |
| 1431057_a_at | Prss23 | protease, serine, 23 | 4.93 | 0.20 |
| 1431302_a_at | Nudt7 | nudix -type motif 7 | 0.73 | 0.07 |
| 1432023_a_at | 1700019H03Rik | RIKEN cDNA 1700019H03 gene | 2.59 | 0.16 |
| 1432034_at | Neurog3 | neurogenin 3 | 0.50 | 0.13 |
| 1432579_at | Rshl2 | radial spokehead-like 2 | 2.00 | 0.32 |
| 1433488_x_at | Gns | glucosamine (N-acetyl)-6-sulfatase | 1.23 | 0.05 |
| 1433501_at | Ctso | cathepsin O | 0.71 | 0.00 |
| 1433519_at | Nucks1 | nuclear casein kinase and cyclin-dependent kinase substrate 1 | 0.78 | 0.04 |
| 1433529_at | E430002G05Rik | RIKEN cDNA E430002G05 gene | 1.87 | 0.07 |
| 1433551_at | AI427515 | expressed sequence AI427515 | 0.63 | 0.05 |
| 1433558_at | Dab2ip | disabled homolog 2 (Drosophila) interacting protein | 0.62 | 0.05 |
| 1433562_s_at | Atp5f1 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | 1.23 | 0.05 |
| 1433579_at | Tmem30b | transmembrane protein 30B | 0.72 | 0.02 |
| 1433643_at | Cacna2d1 | calcium channel, voltage-dependent, alpha2/delta subunit 1 | 0.81 | 0.00 |
| 1433672_at | 4732479N06Rik | RIKEN cDNA 4732479N06 gene | 0.74 | 0.02 |
| 1433707_at | Gabra4 | Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4 | 8.08 | 2.58 |
| 1433750_at | Slc31a1 | solute carrier family 31, member 1 | 1.62 | 0.00 |
| 1433770_at | Dpysl2 | dihydropyrimidinase-like 2 | 0.68 | 0.05 |
| 1433772_at | Stch | stress 70 protein chaperone, microsome-associated, human homolog | 1.33 | 0.09 |
| 1433784_at | AI265322 | expressed sequence AI265322 | 0.73 | 0.05 |
| 1433791_at | Rab9b | RAB9B, member RAS oncogene family | 1.59 | 0.04 |
| 1433805_at | Jak1 | Janus kinase 1 | 0.69 | 0.02 |

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|---|---|---|---|---|
| 1433806_x_at | Calr | calreticulin | 1.26 | 0.03 |
| 1433855_at | Abat | 4-aminobutyrate aminotransferase | 0.73 | 0.03 |
| 1433857_at | Fath | fat tumor suppressor homolog (Drosophila) | 0.57 | 0.05 |
| 1433887_at | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 | 1.56 | 0.10 |
| 1433897_at | AI597468 | expressed sequence AI597468 | 1.38 | 0.03 |
| 1433916_at | Vamp3 | vesicle-associated membrane protein 3 | 0.79 | 0.02 |
| 1433930_at | Hpse | Heparanase | 0.16 | 0.07 |
| 1433965_at | Atp8a1 | ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 | 0.68 | 0.03 |
| 1433972_at | Camta1 | calmodulin binding transcription activator 1 | 0.43 | 0.04 |
| 1434015_at | Slc2a6 | solute carrier family 2 (facilitated glucose transporter), member 6 | 4.14 | 1.01 |
| 1434028_at | Arnt2 | aryl hydrocarbon receptor nuclear translocator 2 | 0.59 | 0.03 |
| 1434034_at | Cerk | ceramide kinase | 0.69 | 0.03 |
| 1434036_at | Mtss1 | metastasis suppressor 1 | 0.68 | 0.02 |
| 1434073_at | Gprasp2 | G protein-coupled receptor associated sorting protein 2 | 0.70 | 0.06 |
| 1434103_at | AA408278 | expressed sequence AA408278 | 1.38 | 0.03 |
| 1434132_at | E430025E21Rik | RIKEN cDNA E430025E21 gene | 0.78 | 0.04 |
| 1434154_at | Kctd13 | potassium channel tetramerisation domain containing 13 | 0.71 | 0.03 |
| 1434158_at | Gmds | GDP-mannose 4, 6-dehydratase | 2.15 | 0.09 |
| 1434178_at | Mll3 | myeloid/lymphoid or mixed-lineage leukemia 3 | 0.78 | 0.04 |
| 1434194_at | Mtap2 | microtubule-associated protein 2 | 0.78 | 0.02 |
| 1434202_a_at | BC055107 | cDNA sequence BC055107 | 1.49 | 0.09 |
| 1434224_at | Tbl2 | transducin (beta)-like 2 | 1.38 | 0.03 |
| 1434265_s_at | Ank2 | ankyrin 2, brain | 0.46 | 0.03 |
| 1434354_at | Maob | monoamine oxidase B | 0.71 | 0.00 |
| 1434386_at | Atp2c1 | ATPase, Ca++-sequestering | 0.63 | 0.05 |
| 1434437_x_at | Rrm2 | ribonucleotide reductase M2 | 2.40 | 0.71 |
| 1434449_at | Aqp4 | aquaporin 4 | 7.77 | 3.13 |
| 1434498_at | Gm1673 | gene model 1673, (NCBI) | 0.47 | 0.17 |
| 1434503_s_at | Lamp2 | lysosomal membrane glycoprotein 2 | 0.73 | 0.06 |
| 1434526_at | Abhd7 | abhydrolase domain containing 7 | 1.75 | 0.14 |
| 1434555_at | Anp32a | acidic (leucine-rich) nuclear phosphoprotein 32 family, member A | 0.74 | 0.04 |
| 1434593_at | Eif5a2 | eukaryotic translation initiation factor 5A2 | 0.59 | 0.06 |
| 1434642_at | Dhrs8 | dehydrogenase/reductase (SDR family) member 8 | 1.39 | 0.08 |
| 1434662_at | Atg4al | autophagy-related 4A-like (yeast) | 1.41 | 0.00 |
| 1434665_at | Aga | aspartylglucosaminidase | 1.55 | 0.07 |
| 1434702_at | 2600009E05Rik | RIKEN cDNA 2600009E05 gene | 1.48 | 0.03 |
| 1434709_at | C130076O07Rik | RIKEN cDNA C130076O07 gene | 0.70 | 0.06 |
| 1434728_at | Gria3 | RIKEN cDNA E430013K19 gene | 0.41 | 0.08 |
| 1434731_x_at | Prdx1 | peroxiredoxin 1 | 1.29 | 0.06 |
| 1434743_x_at | Rusc1 | RUN and SH3 domain containing 1 | 1.26 | 0.03 |
| 1434775_at | Pard3 | par-3 (partitioning defective 3) homolog (C. elegans) | 0.65 | 0.06 |
| 1434881_s_at | Kctd12 | potassium channel tetramerisation domain containing 12 | 1.99 | 0.43 |
| 1434909_at | Rragd | Ras-related GTP binding D | 0.71 | 0.00 |

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|---|---|---|---|---|
| 1434943_at | BC023055 | cDNA sequence BC023055 | 0.69 | 0.04 |
| 1434989_at | A030001O10Rik | RIKEN cDNA A030001O10 gene | 0.73 | 0.03 |
| 1435009_at | Slc9a6 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 | 1.71 | 0.08 |
| 1435089_at | 2010111I01Rik | RIKEN cDNA 2010111I01 gene | 0.69 | 0.03 |
| 1435176_a_at | Id2 | inhibitor of DNA binding 2 | 0.71 | 0.03 |
| 1435196_at | Ntrk2 | neurotrophic tyrosine kinase, receptor, type 2 | 1.26 | 0.06 |
| 1435222_at | Foxp1 | forkhead box P1 | 0.70 | 0.09 |
| 1435247_at | Ube1dc1 | ubiquitin-activating enzyme E1-domain containing 1 | 1.60 | 0.14 |
| 1435272_at | Itpkb | inositol 1,4,5-trisphosphate 3-kinase B | 0.65 | 0.08 |
| 1435342_at | Kcnk6 | potassium inwardly-rectifying channel, subfamily K, member 6 | 4.44 | 1.51 |
| 1435343_at | Dock10 | dedicator of cytokinesis 10 | 0.58 | 0.13 |
| 1435429_x_at | Rps27l | ribosomal protein S27-like | 1.79 | 0.14 |
| 1435440_at | Pdzk8 | PDZ domain containing 8 | 0.79 | 0.02 |
| 1435456_at | AI428795 | expressed sequence AI428795 | 0.55 | 0.06 |
| 1435468_at | C76566 | expressed sequence C76566 | 0.69 | 0.02 |
| 1435480_at | Braf | Braf transforming gene | 0.71 | 0.03 |
| 1435559_at | Myo6 | myosin VI | 0.65 | 0.06 |
| 1435581_at | Bace2 | beta-site APP-cleaving enzyme 2 | 0.58 | 0.02 |
| 1435626_a_at | Herpud1 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 | 1.45 | 0.03 |
| 1435616_at | Cyp20a1 | cytochrome P450, family 20, subfamily A, polypeptide 1 | 1.38 | 0.03 |
| 1435650_at | Hapln4 | hyaluronan and proteoglycan link protein 4 | 2.37 | 0.19 |
| 1435680_a_at | Dpp7 | dipeptidylpeptidase 7 | 0.52 | 0.07 |
| 1435738_x_at | Serf2 | small EDRK-rich factor 2 | 1.32 | 0.00 |
| 1435787_at | Ppm1l | protein phosphatase 1 (formerly 2C)-like | 0.66 | 0.04 |
| 1435800_a_at | Csda | cold shock domain protein A | 1.60 | 0.14 |
| 1435834_at | Gas2 | Growth arrest specific 2 | 0.69 | 0.04 |
| 1435836_at | Pdk1 | Pyruvate dehydrogenase kinase, isoenzyme 1 | 1.97 | 0.17 |
| 1435956_at | A930004K21Rik | RIKEN cDNA A930004K21 gene | 1.87 | 0.07 |
| 1436010_at | BC036313 | cDNA sequence BC036313 | 0.50 | 0.04 |
| 1436075_at | Sfrp5 | secreted frizzled-related sequence protein 5 | 0.49 | 0.03 |
| 1436076_at | Dlgap1 | discs, large (Drosophila) homolog-associated protein 1 | 0.45 | 0.04 |
| 1436087_at | Dpp10 | dipeptidylpeptidase 10 | 0.46 | 0.10 |
| 1436119_at | Aldh1l2 | aldehyde dehydrogenase 1 family, member L2 | 1.52 | 0.10 |
| 1436141_at | 2610510L01Rik | RIKEN cDNA 2610510L01 gene | 0.46 | 0.10 |
| 1436143_at | 4933425L03Rik | RIKEN cDNA 4933425L03 gene | 1.42 | 0.06 |
| 1436164_at | Slc30a1 | solute carrier family 30 (zinc transporter), member 1 | 0.66 | 0.04 |
| 1436370_at | Gucy2c | guanylate cyclase 2c | 6.25 | 0.50 |
| 1436451_a_at | 1110032D12Rik | RIKEN cDNA 1110032D12 gene | 1.29 | 0.08 |
| 1436493_at | BB181834 | expressed sequence BB181834 | 0.54 | 0.05 |
| 1436501_at | Mtus1 | mitochondrial tumor suppressor 1 | 0.63 | 0.04 |
| 1436509_at | 2410014A08Rik | RIKEN cDNA 2410014A08 gene | 1.63 | 0.07 |
| 1436528_at | Kazald1 | Kazal-type serine protease inhibitor domain 1 | 2.00 | 0.08 |

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|---|---|---|---|---|
| 1436600_at | Tnrc9 | trinucleotide repeat containing 9 | 0.71 | 0.00 |
| 1436616_at | R74740 | expressed sequence R74740 | 0.74 | 0.02 |
| 1436623_at | Entpd7 | ectonucleoside triphosphate diphosphohydrolase 7 | 1.56 | 0.10 |
| 1436746_at | Prkwnk1 | protein kinase, lysine deficient 1 | 0.75 | 0.07 |
| 1436774_at | Sel1h | Sel1 (suppressor of lin-12) 1 homolog (C. elegans) | 1.45 | 0.03 |
| 1436797_a_at | Surf4 | surfeit gene 4 | 1.42 | 0.06 |
| 1436804_s_at | Scyl1 | SCY1-like 1 (S. cerevisiae) | 1.42 | 0.06 |
| 1436809_a_at | Spin | spindlin | 0.70 | 0.08 |
| 1436821_at | Plcxd3 | phosphatidylinositol-specific phospholipase C, X domain containing 3 | 0.48 | 0.01 |
| 1436890_at | Uap1l1 | UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 | 0.59 | 0.01 |
| 1436996_x_at | Lzp-s | P lysozyme structural | 2.07 | 0.21 |
| 1437052_s_at | Slc2a3 | solute carrier family 2, member 3 | 0.37 | 0.05 |
| 1437056_x_at | Crispld2 | cysteine-rich secretory protein LCCL domain containing2 | 4.84 | 1.59 |
| 1437062_s_at | Phyhipl | phytanoyl-CoA hydroxylase interacting protein-like | 0.65 | 0.01 |
| 1437164_x_at | Atp5o | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit | 1.43 | 0.16 |
| 1437192_x_at | Vdac1 | voltage-dependent anion channel 1 | 0.76 | 0.03 |
| 1437197_at | 9430041O17Rik | RIKEN cDNA 9430041O17 gene | 1.23 | 0.00 |
| 1437211_x_at | Elovl5 | ELOVL family member 5, elongation of long chain fatty acids (yeast) | 0.78 | 0.02 |
| 1437249_at | Scap1 | src family associated phosphoprotein 1 | 0.54 | 0.02 |
| 1437250_at | MGI:2151839 | whn-dependent transcript 2 | 0.38 | 0.10 |
| 1437252_at | Gats | opposite strand transcription unit to Stag3 | 0.65 | 0.03 |
| 1437268_at | Lancl3 | LanC lantibiotic synthetase component C-like 3 | 0.50 | 0.03 |
| 1437303_at | Il6st | interleukin 6 signal transducer | 0.76 | 0.00 |
| 1437325_x_at | Aldh18a1 | aldehyde dehydrogenase 18 family, member A1 | 1.45 | 0.03 |
| 1437334_x_at | Parn | poly(A)-specific ribonuclease (deadenylation nuclease) | 1.55 | 0.07 |
| 1437390_x_at | Stx1a | syntaxin 1A (brain) | 0.51 | 0.05 |
| 1437395_at | Zcchc11 | zinc finger, CCHC domain containing 11 | 0.76 | 0.03 |
| 1437465_a_at | P4hb | prolyl 4-hydroxylase, beta polypeptide | 1.36 | 0.11 |
| 1437508_at | Sp4 | trans-acting transcription factor 4 | 0.46 | 0.05 |
| 1437626_at | Zfp36l2 | zinc finger protein 36, C3H type-like 2 | 0.65 | 0.04 |
| 1437667_a_at | Bach2 | BTB and CNC homology 2 | 2.27 | 0.22 |
| 1437709_x_at | Ttc13 | tetratricopeptide repeat domain 13 | 1.38 | 0.03 |
| 1437711_x_at | Odc1 | ornithine decarboxylase, structural 1 | 1.49 | 0.09 |
| 1437782_at | Cntnap2 | contactin associated protein-like 2 | 0.43 | 0.06 |
| 1437838_x_at | Grsf1 | G-rich RNA sequence binding factor 1 | 1.32 | 0.05 |
| 1437874_s_at | Hexb | hexosaminidase B | 0.71 | 0.03 |
| 1437868_at | BC023892 | cDNA sequence BC023892 | 1.84 | 0.16 |
| 1438001_x_at | Dp1 | deleted in polyposis 1 | 1.45 | 0.09 |
| 1438116_x_at | Slc9a3r1 | solute carrier family 9, isoform 3 regulator 1 | 0.68 | 0.04 |
| 1438206_a_at | 2610042O14Rik | RIKEN cDNA 2610042O14 gene | 1.32 | 0.05 |
| 1438232_at | Foxp2 | forkhead box P2 | 2.05 | 0.13 |
| 1438322_x_at | Fdft1 | farnesyl diphosphate farnesyl transferase 1 | 1.23 | 0.05 |
| 1438370_x_at | Dos | downstream of Stk11 | 0.63 | 0.01 |

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|---|---|---|---|---|
| 1438407_at | 9330132E09Rik | RIKEN cDNA 9330132E09 gene | 1.91 | 0.09 |
| 1438480_a_at | MGI:1925112 | thymocyte protein thy28 | 1.43 | 0.16 |
| 1438557_x_at | Dnpep | aspartyl aminopeptidase | 1.38 | 0.03 |
| 1438610_a_at | Cryz | Crystallin, zeta | 0.63 | 0.05 |
| 1438677_at | Pkp4 | plakophilin 4 | 0.68 | 0.04 |
| 1438680_at | Auts2 | autism susceptibility candidate 2 | 0.68 | 0.07 |
| 1438739_at | Cnbp1 | Cellular nucleic acid binding protein 1 | 0.69 | 0.04 |
| 1439007_at | Alg6 | asparagine-linked glycosylation 6 homolog | 1.59 | 0.08 |
| 1439015_at | Gfra1 | glial cell line derived neurotrophic factor family receptor alpha 1 | 1.80 | 0.34 |
| 1439096_at | 5330420D20Rik | RIKEN cDNA 5330420D20 gene | 1.70 | 0.04 |
| 1439148_a_at | Pfkl | phosphofructokinase, liver, B-type | 0.69 | 0.02 |
| 1439189_at | D630023B12Rik | RIKEN cDNA D630023B12 gene | 0.69 | 0.02 |
| 1439266_a_at | Polr3k | polymerase (RNA) III (DNA directed) polypeptide K | 1.36 | 0.08 |
| 1439388_s_at | Bcar1 | breast cancer anti-estrogen resistance 1 | 0.78 | 0.02 |
| 1439433_a_at | Slc35a2 | solute carrier family 35 (UDP-galactose transporter), member 2 | 1.59 | 0.10 |
| 1439435_x_at | Pgk1 | phosphoglycerate kinase 1 | 1.35 | 0.06 |
| 1439560_x_at | LOC432995 | hypothetical gene supported by BC047216 | 0.80 | 0.05 |
| 1439833_at | Sept3 | septin 3 | 0.23 | 0.05 |
| 1440167_s_at | Lpp | LIM domain containing preferred translocation partner in lipoma | 0.69 | 0.02 |
| 1440506_at | Slc7a2 | Solute carrier family 7, member 2 | 0.68 | 0.02 |
| 1440739_at | Vegfc | vascular endothelial growth factor C | 2.00 | 0.00 |
| 1440799_s_at | Farp2 | FERM, RhoGEF and pleckstrin domain protein 2 | 1.42 | 0.06 |
| 1440834_at | Slc5a10 | solute carrier family 5, member 10 | 12.59 | 7.77 |
| 1440884_s_at | A530047J11Rik | RIKEN cDNA A530047J11 gene | 2.37 | 0.23 |
| 1440977_at | Akap13 | A kinase (PRKA) anchor protein 13 | 0.74 | 0.02 |
| 1441214_at | MGI:2443248 | synaptotagmin-like homologue lacking C2 domains b | 0.69 | 0.02 |
| 1441317_x_at | MGI:1923321 | gamma-aminobutyric acid (GABA-B) receptor binding protein | 0.63 | 0.03 |
| 1441439_at | Ucn3 | urocortin 3 | 0.59 | 0.03 |
| 1442018_at | AI426953 | expressed sequence AI426953 | 0.43 | 0.15 |
| 1442113_at | 5330417C22Rik | RIKEN cDNA 5330417C22 gene | 1.45 | 0.09 |
| 1442590_at | Tnfrsf22 | Tumor necrosis factor receptor superfamily, member 22 | 2.17 | 0.24 |
| 1443471_at | Zbtb20 | zinc finger and BTB domain containing 20 | 0.76 | 0.03 |
| 1443870_at | Abcc4 | ATP-binding cassette, sub-family C, member 4 | 0.66 | 0.03 |
| 1444451_at | Pappa2 | pappalysin 2 | 2.83 | 0.11 |
| 1444488_at | Cadps | Ca<2+>dependent activator protein for secretion | 0.76 | 0.03 |
| 1444765_at | Rbpms | RNA binding protein gene with multiple splicing | 0.68 | 0.03 |
| 1445546_at | AI844685 | expressed sequence AI844685 | 7.22 | 2.65 |
| 1446181_at | C85699 | expressed sequence C85699 | 17.24 | 7.64 |
| 1446421_at | Schip1 | Schwannomin interacting protein 1 | 0.64 | 0.06 |
| 1447053_x_at | Ssr3 | signal sequence receptor, gamma | 1.52 | 0.10 |
| 1447090_s_at | Arl1 | ADP-ribosylation factor-like 1 | 1.29 | 0.03 |
| 1447112_s_at | Cryl1 | crystallin, lamda 1 | 0.54 | 0.06 |
| 1447174_at | Dach1 | Dachshund 1 (Drosophila) | 0.70 | 0.06 |

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|---|---|---|---|---|
| 1447624_s_at | Stox2 | storkhead box 2 | 1.26 | 0.03 |
| 1447693_s_at | Neo1 | neogenin | 0.70 | 0.07 |
| 1447725_at | C030034E14Rik | RIKEN cDNA C030034E14 gene | 1.32 | 0.00 |
| 1447854_s_at | Hist2h2be | histone 2, H2be | 0.74 | 0.02 |
| 1447909_s_at | MGI:1931466 | selenoprotein K | 1.43 | 0.16 |
| 1447922_at | Stxbp5l | Syntaxin binding protein 5-like | 0.45 | 0.05 |
| 1448101_s_at | Trim27 | tripartite motif protein 27 | 1.35 | 0.03 |
| 1448108_at | Tde2 | tumor differentially expressed 2 | 1.32 | 0.05 |
| 1448136_at | Enpp2 | ectonucleotide pyrophosphatase/phosphodiesterase 2 | 0.52 | 0.10 |
| 1448169_at | Krt1-18 | keratin complex 1, acidic, gene 18 | 1.26 | 0.03 |
| 1448172_at | Mdh1 | malate dehydrogenase 1, NAD (soluble) | 1.38 | 0.03 |
| 1448190_at | Mrpl33 | mitochondrial ribosomal protein L33 | 1.26 | 0.06 |
| 1448210_at | Rab1 | RAB1, member RAS oncogene family | 1.36 | 0.08 |
| 1448242_at | Sec61a1 | Sec61 alpha 1 subunit (S. cerevisiae) | 1.23 | 0.00 |
| 1448246_at | Hdac1 | histone deacetylase 1 | 0.74 | 0.04 |
| 1448258_a_at | Spcs1 | signal peptidase complex subunit 1 homolog | 1.45 | 0.03 |
| 1448260_at | Uchl1 | ubiquitin carboxy-terminal hydrolase L1 | 0.55 | 0.01 |
| 1448269_a_at | Klhl13 | kelch-like 13 (Drosophila) | 0.37 | 0.05 |
| 1448272_at | Btg2 | B-cell translocation gene 2, anti-proliferative | 0.74 | 0.04 |
| 1448280_at | Syp | synaptophysin | 1.32 | 0.05 |
| 1448333_at | Adprh | ADP-ribosylarginine hydrolase | 1.29 | 0.08 |
| 1448343_a_at | Nbr1 | neighbor of Brca1 gene 1 | 1.21 | 0.06 |
| 1448351_at | Coro1b | coronin, actin binding protein 1B | 0.71 | 0.03 |
| 1448372_a_at | Tmem4 | transmembrane protein 4 | 1.45 | 0.09 |
| 1448393_at | Cldn7 | claudin 7 | 0.56 | 0.03 |
| 1448405_a_at | Cri1 | CREBBP/EP300 inhibitory protein 1 | 1.42 | 0.06 |
| 1448416_at | Mgp | matrix Gla protein | 1.46 | 0.12 |
| 1448424_at | Frzb | frizzled-related protein | 0.69 | 0.03 |
| 1448443_at | Serpini1 | serine proteinase inhibitor, clade I, member 1 | 1.52 | 0.06 |
| 1448513_a_at | Npc2 | Niemann Pick type C2 | 0.78 | 0.02 |
| 1448524_s_at | Ssr4 | signal sequence receptor, delta | 1.52 | 0.06 |
| 1448549_a_at | Dpagt1 | dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 | 1.52 | 0.00 |
| 1448562_at | Upp1 | uridine phosphorylase 1 | 0.45 | 0.04 |
| 1448563_at | Phb | prohibitin | 0.85 | 0.05 |
| 1448569_at | Cd8b1 | CD8 antigen, beta chain 1 | 1.49 | 0.09 |
| 1448595_a_at | Rex3 | reduced expression 3 | 0.71 | 0.06 |
| 1448619_at | Dhcr7 | 7-dehydrocholesterol reductase | 1.45 | 0.07 |
| 1448645_at | Msl31 | male-specific lethal-3 homolog 1 (Drosophila) | 0.51 | 0.02 |
| 1448690_at | Kcnk1 | potassium channel, subfamily K, member 1 | 1.79 | 0.11 |
| 1448694_at | Jun | Jun oncogene | 0.47 | 0.05 |
| 1448702_at | Ier3ip1 | immediate early response 3 interacting protein 1 | 1.45 | 0.07 |
| 1448704_s_at | H47 | histocompatibility 47 | 1.26 | 0.08 |
| 1448753_at | Srp9 | signal recognition particle 9 | 1.33 | 0.09 |

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|---|---|---|---|---|
| 1448758_at | Nrbf2 | nuclear receptor binding factor 2 | 1.39 | 0.12 |
| 1448769_at | Slc35b1 | solute carrier family 35, member B1 | 1.42 | 0.06 |
| 1448788_at | Cd200 | Cd200 antigen | 1.63 | 0.07 |
| 1448789_at | Aldh1a3 | aldehyde dehydrogenase family 1, subfamily A3 | 6.39 | 0.55 |
| 1448808_a_at | Nme2 | expressed in non-metastatic cells 2, protein | 1.29 | 0.06 |
| 1448809_at | Cse1l | chromosome segregation 1-like (S. cerevisiae) | 0.69 | 0.04 |
| 1448824_at | Ube2j1 | ubiquitin-conjugating enzyme E2, J1 | 1.49 | 0.13 |
| 1448829_at | Smc6l1 | SMC6 structural maintenance of chromosomes 6-like 1 | 0.78 | 0.04 |
| 1448830_at | Dusp1 | dual specificity phosphatase 1 | 0.39 | 0.08 |
| 1448867_at | 2310004K06Rik | RIKEN cDNA 2310004K06 gene | 0.71 | 0.06 |
| 1448887_x_at | Fxc1 | fractured callus expressed transcript 1 | 1.42 | 0.10 |
| 1448889_at | Slc38a4 | solute carrier family 38, member 4 | 1.63 | 0.07 |
| 1448910_at | Pecr | peroxisomal trans-2-enoyl-CoA reductase | 2.37 | 0.19 |
| 1448928_at | Hdac6 | histone deacetylase 6 | 0.69 | 0.03 |
| 1448929_at | F13a1 | coagulation factor XIII, A1 subunit | 3.46 | 0.42 |
| 1448948_at | Rga | recombination activating gene 1 gene activation | 1.59 | 0.10 |
| 1448952_at | A030009H04Rik | RIKEN cDNA A030009H04 gene | 0.66 | 0.05 |
| 1448968_at | D7Wsu128e | DNA segment, Chr 7, Wayne State University 128, expressed | 1.71 | 0.10 |
| 1448991_a_at | Ina | internexin neuronal intermediate filament protein, alpha | 1.35 | 0.03 |
| 1449009_at | Tgtp | T-cell specific GTPase | 0.57 | 0.13 |
| 1449011_at | Slc12a7 | solute carrier family 12, member 7 | 0.34 | 0.08 |
| 1449033_at | Tnfrsf11b | tumor necrosis factor receptor superfamily, member 11b | 2.71 | 0.12 |
| 1449063_at | Sec22l1 | SEC22 vesicle trafficking protein-like 1 (S. cerevisiae) | 1.32 | 0.00 |
| 1449067_at | Slc2a2 | solute carrier family 2, member 2 | 0.76 | 0.00 |
| 1449106_at | Gpx3 | glutathione peroxidase 3 | 1.54 | 0.18 |
| 1449139_at | 2310008M10Rik | RIKEN cDNA 2310008M10 gene | 1.38 | 0.07 |
| 1449151_at | Pctk3 | PCTAIRE-motif protein kinase 3 | 1.84 | 0.16 |
| 1449167_at | Epb4.1l4a | erythrocyte protein band 4.1-like 4a | 0.39 | 0.04 |
| 1449203_at | Slco1a5 | solute carrier organic anion transporter family, member 1a5 | 3.28 | 0.33 |
| 1449233_at | Bhlhb8 | basic helix-loop-helix domain containing, class B, 8 | 1.49 | 0.13 |
| 1449254_at | Spp1 | secreted phosphoprotein 1 | 2.85 | 0.23 |
| 1449267_at | 3110023E09Rik | RIKEN cDNA 3110023E09 gene | 1.63 | 0.07 |
| 1449303_at | Sesn3 | sestrin 3 | 0.72 | 0.02 |
| 1449368_at | Dcn | decorin | 0.54 | 0.14 |
| 1449409_at | Sult1c2 | sulfotransferase family, cytosolic, 1C, member 2 | 0.41 | 0.04 |
| 1449465_at | Reln | reelin | 0.27 | 0.07 |
| 1449708_s_at | Chek1 | checkpoint kinase 1 homolog (S. pombe) | 1.94 | 0.26 |
| 1449815_a_at | Ssbp2 | single-stranded DNA binding protein 2 | 0.69 | 0.02 |
| 1449896_at | Mlph | melanophilin | 0.45 | 0.01 |
| 1449930_a_at | Ssr2 | signal sequence receptor, beta | 1.45 | 0.09 |
| 1449967_at | Sim1 | single-minded homolog 1 (Drosophila) | 0.58 | 0.09 |
| 1450017_at | Ccng1 | cyclin G1 | 1.63 | 0.07 |
| 1450042_at | Arx | aristaless related homeobox gene (Drosophila) | 0.30 | 0.01 |

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|---|---|---|---|---|
| 1450048_a_at | Idh2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 0.76 | 0.03 |
| 1450055_at | Vsnl1 | visinin-like 1 | 0.54 | 0.04 |
| 1450117_at | Tcf3 | transcription factor 3 | 2.04 | 0.26 |
| 1450135_at | Fzd3 | frizzled homolog 3 (Drosophila) | 1.38 | 0.03 |
| 1450167_at | Rab37 | RAB37, member of RAS oncogene family | 0.44 | 0.03 |
| 1450240_a_at | Sytl1 | synaptotagmin-like 1 | 1.63 | 0.26 |
| 1450344_a_at | Ptger3 | prostaglandin E receptor 3 (subtype EP3) | 90.04 | 74.65 |
| 1450394_at | Golph3 | golgi phosphoprotein 3 | 1.52 | 0.06 |
| 1450650_at | Myo10 | myosin X | 0.57 | 0.07 |
| 1450684_at | Etv1 | ets variant gene 1 | 1.55 | 0.04 |
| 1450696_at | Psmb9 | proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) | 0.50 | 0.02 |
| 1450685_at | Arpp19 | cAMP-regulated phosphoprotein 19 | 0.73 | 0.03 |
| 1450696_at | Psmb9 | proteosome (prosome, macropain) subunit, beta type 9 | 0.50 | 0.02 |
| 1450697_at | Slc30a7 | solute carrier family 30 (zinc transporter), member 7 | 1.84 | 0.16 |
| 1450734_at | Lztr2 | leucine zipper transcription regulator 2 | 1.67 | 0.10 |
| 1450744_at | Ell2 | elongation factor RNA polymerase II 2 | 1.91 | 0.04 |
| 1450849_at | Hnrpu | heterogeneous nuclear ribonucleoprotein U | 0.62 | 0.07 |
| 1450866_a_at | Mrpl17 | mitochondrial ribosomal protein L17 | 1.39 | 0.08 |
| 1450871_a_at | Bcat1 | branched chain aminotransferase 1, cytosolic | 11.78 | 4.74 |
| 1450891_at | Srp19 | signal recognition particle 19 | 1.46 | 0.14 |
| 1450907_at | Spcs2 | signal peptidase complex subunit 2 homolog | 1.39 | 0.12 |
| 1450911_at | Ppib | peptidylprolyl isomerase B | 1.52 | 0.06 |
| 1450976_at | Ndrg1 | N-myc downstream regulated gene 1 | 0.58 | 0.02 |
| 1451018_at | Leprotl1 | leptin receptor overlapping transcript-like 1 | 0.79 | 0.02 |
| 1451091_at | Txndc5 | thioredoxin domain containing 5 | 1.29 | 0.08 |
| 1451125_at | BC017133 | cDNA sequence BC017133 | 1.56 | 0.10 |
| 1451132_at | Pbxip1 | pre-B-cell leukemia transcription factor interacting protein 1 | 0.62 | 0.07 |
| 1451175_at | Spcs3 | signal peptidase complex subunit 3 homolog | 1.26 | 0.06 |
| 1451214_at | Kbtbd2 | kelch repeat and BTB (POZ) domain containing 2 | 0.76 | 0.00 |
| 1451216_at | Zfp330 | zinc finger protein 330 | 1.39 | 0.12 |
| 1451244_a_at | Zfp422 | zinc finger protein 422 | 0.68 | 0.04 |
| 1451259_at | Smfn | small fragment nuclease | 1.63 | 0.07 |
| 1451263_a_at | Fabp4 | fatty acid binding protein 4, adipocyte | 1.56 | 0.10 |
| 1451277_at | Zadh2 | zinc binding alcohol dehydrogenase, domain containing2 | 0.76 | 0.03 |
| 1451389_at | Zcsl3 | zinc finger, CSL-type containing 3 | 0.60 | 0.06 |
| 1451407_at | Jam4 | junction adhesion molecule 4 | 2.11 | 0.18 |
| 1451411_at | Gprc5b | G protein-coupled receptor, family C, group 5, member B | 2.96 | 0.07 |
| 1451412_a_at | 0610009H04Rik | RIKEN cDNA 0610009H04 gene | 1.66 | 0.24 |
| 1451421_a_at | MGI:1913299 | leucine zipper domain protein | 0.79 | 0.02 |
| 1451452_a_at | Rgs16 | regulator of G-protein signaling 16 | 2.81 | 0.34 |
| 1451461_a_at | Aldoc | aldolase 3, C isoform | 0.47 | 0.02 |
| 1451470_s_at | Eif5a | eukaryotic translation initiation factor 5A | 1.23 | 0.05 |
| 1451478_at | Frap1 | FK506 binding protein 12-rapamycin associated protein1 | 1.70 | 0.04 |

| | | | | |
|---|---|---|---|---|
| 1451534_at | Scgn | secretagogin, EF-hand calcium binding protein | 0.78 | 0.05 |
| 1451580_a_at | Ttr | transthyretin | 1.33 | 0.09 |
| 1451667_at | C530043G21Rik | RIKEN cDNA C530043G21 gene | 0.69 | 0.02 |
| 1451716_at | Mafb | v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian) | 0.30 | 0.06 |
| 1451791_at | Tfpi | tissue factor pathway inhibitor | 0.65 | 0.04 |
| 1451979_at | Kras | v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog | 1.35 | 0.03 |
| 1452036_a_at | Tmpo | thymopoietin | 0.78 | 0.05 |
| 1452052_s_at | Eif3s1 | eukaryotic translation initiation factor 3, subunit 1 alpha | 1.39 | 0.12 |
| 1452059_at | Slc35f5 | solute carrier family 35, member F5 | 1.46 | 0.15 |
| 1452181_at | Ckap4 | cytoskeleton-associated protein 4 | 1.59 | 0.04 |
| 1452211_at | Psme4 | proteasome (prosome, macropain) activator subunit 4 | 1.32 | 0.00 |
| 1452227_at | 2310045A20Rik | RIKEN cDNA 2310045A20 gene | 2.71 | 0.12 |
| 1452257_at | Bdh | 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) | 0.68 | 0.03 |
| 1452263_at | Slc35f4 | solute carrier family 35, member F4 | 14.47 | 6.71 |
| 1452318_a_at | Hspa1b | heat shock protein 1B | 0.23 | 0.03 |
| 1452357_at | Gp1bb /// Sept5 | glycoprotein Ib, beta polypeptide /// septin 5 | 1.33 | 0.09 |
| 1452388_at | Hspa1a | heat shock protein 1A | 0.18 | 0.03 |
| 1452392_a_at | D11Ertd498e | DNA segment, Chr 11, ERATO Doi 498, expressed | 1.59 | 0.04 |
| 1452428_a_at | B2m | beta-2 microglobulin | 0.62 | 0.11 |
| 1452483_a_at | Cd44 | CD44 antigen | 2.68 | 0.53 |
| 1452626_a_at | 1810014F10Rik | RIKEN cDNA 1810014F10 gene | 1.42 | 0.06 |
| 1452657_at | Ap1s2 | adaptor-related protein complex 1, sigma 2 subunit | 0.59 | 0.08 |
| 1452671_s_at | Lman1 | lectin, mannose-binding, 1 | 1.35 | 0.03 |
| 1452740_at | Myh10 | myosin, heavy polypeptide 10, non-muscle | 0.65 | 0.06 |
| 1452754_at | 5730592L21Rik | RIKEN cDNA 5730592L21 gene | 2.71 | 0.17 |
| 1452765_at | Slc39a9 | solute carrier family 39 (zinc transporter), member 9 | 1.38 | 0.03 |
| 1452767_at | Rrbp1 | ribosome binding protein 1 | 1.49 | 0.09 |
| 1452768_at | Tex261 | testis expressed gene 261 | 1.32 | 0.05 |
| 1452770_at | Vkorc1 | vitamin K epoxide reductase complex, subunit 1 | 1.55 | 0.07 |
| 1452783_at | Fndc3b | fibronectin type III domain containing 3B | 1.49 | 0.09 |
| 1452790_x_at | Ndufa3 | NADH dehydrogenase 1 alpha subcomplex, 3 | 1.20 | 0.03 |
| 1452885_at | Sfrs2ip | splicing factor, arginine/serine-rich 2, interacting protein | 0.69 | 0.04 |
| 1452953_at | 1810036I24Rik | RIKEN cDNA 1810036I24 gene | 1.26 | 0.03 |
| 1452968_at | Cthrc1 | collagen triple helix repeat containing 1 | 6.50 | 1.04 |
| 1452982_at | A330103N21Rik | RIKEN cDNA A330103N21 gene | 0.71 | 0.03 |
| 1453003_at | Sorl1 | sortilin-related receptor, LDLR class A repeats-containing | 0.73 | 0.03 |
| 1453008_at | 2300002D11Rik | RIKEN cDNA 2300002D11 gene | 0.71 | 0.03 |
| 1453009_at | Cpm | carboxypeptidase M | 0.60 | 0.07 |
| 1453140_at | 9030612M13Rik | RIKEN cDNA 9030612M13 gene | 0.67 | 0.07 |
| 1453196_a_at | Oasl2 | 2'-5' oligoadenylate synthetase-like 2 | 0.54 | 0.05 |
| 1453222_at | Gse1 | genetic suppressor element 1 | 0.74 | 0.04 |
| 1453246_at | Rab39b | RAB39B, member RAS oncogene family | 1.52 | 0.11 |
| 1453677_a_at | Derl3 | Der1-like domain family, member 3 | 4.00 | 0.00 |

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|---|---|---|---|---|
| 1453708_a_at | Gsto2 | glutathione S-transferase omega 2 | 2.86 | 0.57 |
| 1453796_a_at | 1200009B18Rik | RIKEN cDNA 1200009B18 gene | 1.58 | 0.21 |
| 1453915_a_at | Slc37a3 | solute carrier family 37, member 3 | 1.55 | 0.04 |
| 1454023_a_at | D1Bwg1363e | DNA segment, Chr 1, Brigham & Women's Genetics 1363 expressed | 1.46 | 0.12 |
| 1454632_at | 6330442E10Rik | RIKEN cDNA 6330442E10 gene | 0.69 | 0.04 |
| 1454647_at | 5730439E10Rik | RIKEN cDNA 5730439E10 gene | 1.29 | 0.06 |
| 1454650_at | Trim35 | tripartite motif-containing 35 | 0.63 | 0.01 |
| 1454674_at | Fez1 | fasciculation and elongation protein zeta 1 (zygin I) | 2.25 | 0.14 |
| 1454675_at | Thra | thyroid hormone receptor alpha | 0.34 | 0.32 |
| 1454735_at | Odf2 | outer dense fiber of sperm tails 2 | 0.79 | 0.02 |
| 1454736_at | 4921515A04Rik | RIKEN cDNA 4921515A04 gene | 0.69 | 0.04 |
| 1454832_at | Phactr1 | phosphatase and actin regulator 1 | 0.64 | 0.07 |
| 1454862_at | Phldb2 | pleckstrin homology-like domain, family B, member 2 | 0.65 | 0.01 |
| 1454959_s_at | Gnai1 | guanine nucleotide binding protein, alpha inhibiting 1 | 0.61 | 0.07 |
| 1454937_at | B630005N14Rik | RIKEN cDNA B630005N14 gene | 0.71 | 0.03 |
| 1454961_at | Synj1 | synaptojanin 1 | 0.73 | 0.03 |
| 1455011_at | Stard4 | StAR-related lipid transfer (START) domain containing 4 | 0.67 | 0.07 |
| 1455012_s_at | Trim37 | tripartite motif protein 37 | 0.68 | 0.03 |
| 1455028_at | Mapt | microtubule-associated protein tau | 2.36 | 0.15 |
| 1455029_at | Kif21a | kinesin family member 21A | 0.69 | 0.02 |
| 1455034_at | Nr4a2 | Nuclear receptor subfamily 4, group A, member 2 | 2.05 | 0.09 |
| 1455057_at | Gmps | guanine monphosphate synthetase | 0.66 | 0.00 |
| 1455065_x_at | LOC231914 | similar to mKIAA0060 protein | 0.69 | 0.03 |
| 1455070_at | AL118268 | expressed sequence AL118268 | 0.73 | 0.05 |
| 1455092_at | Zfp207 | zinc finger protein 207 | 1.45 | 0.07 |
| 1455111_at | A430107J06Rik | RIKEN cDNA A430107J06 gene | 1.36 | 0.13 |
| 1455126_x_at | 2310028O11Rik | RIKEN cDNA 2310028O11 gene | 1.26 | 0.03 |
| 1455137_at | Rapgef5 | Rap guanine nucleotide exchange factor (GEF) 5 | 2.51 | 0.37 |
| 1455143_at | Nlgn2 | neuroligin 2 | 0.66 | 0.05 |
| 1455162_at | 4922503N01Rik | RIKEN cDNA 4922503N01 gene | 1.41 | 0.00 |
| 1455213_at | 4930488E11Rik | RIKEN cDNA 4930488E11 gene | 0.56 | 0.08 |
| 1455225_at | Syne1 | synaptic nuclear envelope 1 | 0.68 | 0.04 |
| 1455316_x_at | Ccrn4l | CCR4 carbon catabolite repression 4-like (S. cerevisiae) | 1.39 | 0.08 |
| 1455345_at | Phf15 | PHD finger protein 15 | 0.58 | 0.07 |
| 1455391_at | Rad23a | RAD23a homolog (S. cerevisiae) | 0.79 | 0.02 |
| 1455492_at | B330016D10Rik | RIKEN cDNA B330016D10 gene | 0.64 | 0.09 |
| 1455577_at | Ccl28 | Chemokine (C-C motif) ligand 28 | 1.62 | 0.00 |
| 1455582_at | C1qtnf1 | C1q and tumor necrosis factor related protein 1 | 6.71 | 2.71 |
| 1455795_at | Sart2 | squamous cell carcinoma antigen recognized by T cells 2 | 2.06 | 0.17 |
| 1455804_x_at | Oxct1 | 3-oxoacid CoA transferase 1 | 0.71 | 0.05 |
| 1455839_at | Ugcgl1 | UDP-glucose ceramide glucosyltransferase-like 1 | 1.32 | 0.00 |
| 1455875_x_at | Tm9sf2 | transmembrane 9 superfamily member 2 | 1.29 | 0.03 |
| 1455886_at | Cbl | Casitas B-lineage lymphoma | 0.69 | 0.02 |

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|---|---|---|---|---|
| 1455939_x_at | Srp14 | signal recognition particle 14 | 1.26 | 0.03 |
| 1455940_x_at | Wdr6 | WD repeat domain 6 | 0.69 | 0.04 |
| 1456037_x_at | Preb | prolactin regulatory element binding | 1.35 | 0.06 |
| 1456056_a_at | D6Wsu116e | DNA segment, Chr 6, Wayne State University 116, expressed | 0.74 | 0.04 |
| 1456071_a_at | Cycs | cytochrome c, somatic | 1.45 | 0.07 |
| 1456387_at | Nol4 | nucleolar protein 4 | 0.68 | 0.03 |
| 1456438_x_at | Rpn1 | ribophorin I | 1.32 | 0.05 |
| 1456471_x_at | Phgdh | 3-phosphoglycerate dehydrogenase | 2.26 | 0.19 |
| 1456606_a_at | Chst11 /// Phactr1 | carbohydrate sulfotransferase 11 /// phosphatase and actin regulator 1 | 0.60 | 0.01 |
| 1456739_x_at | Armcx2 | armadillo repeat containing, X-linked 2 | 1.26 | 0.03 |
| 1456743_x_at | Morf4l2 | mortality factor 4 like 2 | 1.23 | 0.05 |
| 1456938_at | Smarcb1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 | 6.05 | 1.95 |
| 1457264_at | Phf20l1 | PHD finger protein 20-like 1 | 0.71 | 0.06 |
| 1457266_at | AW322671 | expressed sequence AW322671 | 1.60 | 0.14 |
| 1457273_at | Odz2 | Odd Oz/ten-m homolog 2 (Drosophila) | 0.56 | 0.08 |
| 1457279_at | Sirt7 | Sirtuin 7 | 0.76 | 0.03 |
| 1457294_at | B130008E12Rik | RIKEN cDNA B130008E12 gene | 1.52 | 0.06 |
| 1457401_at | Dnahc9 | dynein, axonemal, heavy chain 9 | 2.43 | 0.57 |
| 1457424_at | Eya1 | eyes absent 1 homolog (Drosophila) | 0.45 | 0.02 |
| 1457632_s_at | Mrg1 | myeloid ecotropic viral integration site-related gene 1 | 0.76 | 0.00 |
| 1458499_at | Pde10a | phosphodiesterase 10A | 0.62 | 0.05 |
| 1458866_at | A930001M12Rik | RIKEN cDNA A930001M12 gene | 0.64 | 0.08 |
| 1458947_at | Fancc | Fanconi anemia, complementation group C | 0.60 | 0.08 |
| 1459293_at | C030038J10Rik | RIKEN cDNA C030038J10 gene | 2.48 | 0.20 |
| 1459723_at | Gm262 | gene model 262, (NCBI) | 3.79 | 0.45 |
| 1460184_at | Hadhsc | L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain | 0.81 | 0.03 |
| 1460189_at | Wdr23 | WD repeat domain 23 | 0.74 | 0.02 |
| 1459860_x_at | Trim2 | tripartite motif protein 2 | 1.37 | 0.19 |
| 1460041_at | D630040I23Rik | RIKEN cDNA D630040I23 gene | 0.42 | 0.08 |
| 1460203_at | Itpr1 | inositol 1,4,5-triphosphate receptor 1 | 0.36 | 0.06 |
| 1460211_a_at | Kdelr1 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 | 1.60 | 0.16 |
| 1460235_at | Scarb2 | scavenger receptor class B, member 2 | 1.38 | 0.03 |
| 1460238_at | Msln | mesothelin | 0.32 | 0.11 |
| 1460292_a_at | Smarca1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 | 0.54 | 0.05 |
| 1460359_at | LOC434247 | similar to ALEX3 protein | 1.59 | 0.08 |
| 1460424_at | 1810008O21Rik | RIKEN cDNA 1810008O21 gene | 1.71 | 0.08 |
| 1460436_at | Ndst1 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 | 1.38 | 0.03 |
| 1460551_at | Ran | RAN, member RAS oncogene family | 0.65 | 0.04 |
| 1460552_at | Ascc3l1 | activating signal cointegrator 1 complex subunit 3-like 1 | 0.69 | 0.04 |
| 1460561_x_at | Sepw1 | selenoprotein W, muscle 1 | 0.48 | 0.04 |

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|---|---|---|---|---|
| 1460583_at | Golt1b | golgi transport 1 homolog B (S. cerevisiae) | 1.52 | 0.00 |
| 1460649_at | Irak1 | interleukin-1 receptor-associated kinase 1 | 1.23 | 0.05 |
| 1460692_at | Ehmt2 | euchromatic histone lysine N-methyltransferase 2 | 0.76 | 0.03 |
| 1460698_a_at | Sec11l3 | Sec11-like 3 (S. cerevisiae) | 2.11 | 0.19 |
| 1460718_s_at | Mtch1 | mitochondrial carrier homolog 1 (C. elegans) | 0.69 | 0.04 |
| AFFX-PyruCarbMur/L09192_3_at | Pcx | pyruvate carboxylase | 0.59 | 0.05 |

## Table S2 Summary of the differentially expressed genes located in mitochondria in 10-week-old diabetic islets

| Acce. No. | Gene Symbol | Gene Name | Fold (MKR/WT) | S.E. |
|---|---|---|---|---|
| 1415917_at | Mthfd1 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) | 0.661 | 0.026 |
| 1416060_at | Tbc1d15 | TBC1 domain family, member 15 | 1.383 | 0.032 |
| 1416119_at | Txn1 | thioredoxin 1 | 1.387 | 0.083 |
| 1416167_at | Prdx4 | peroxiredoxin 4 | 1.392 | 0.119 |
| 1416562_at | Gad1 | glutamic acid decarboxylase 1 | 0.257 | 0.053 |
| 1416766_at | Mosc2 | MOCO sulphurase C-terminal domain containing 2 | 1.705 | 0.081 |
| 1417273_at | Pdk4 | pyruvate dehydrogenase kinase, isoenzyme 4 | 0.354 | 0.084 |
| 1417316_at | Them2 | thioesterase superfamily member 2 | 0.632 | 0.039 |
| 1417686_at | Lgals12 | lectin, galactose binding, soluble 12 | 1.385 | 0.065 |
| 1417823_at | Gcat | glycine C-acetyltransferase | 0.538 | 0.036 |
| 1418137_at | Mrp63 | mitochondrial ribosomal protein 63 | 1.387 | 0.083 |
| 1418238_at | Ivd | isovaleryl coenzyme A dehydrogenase | 0.570 | 0.069 |
| 1419382_a_at | Dhrs4 | dehydrogenase/reductase (SDR family) member 4 | 0.678 | 0.042 |
| 1420822_s_at | Sgpp1 | sphingosine-1-phosphate phosphatase 1 | 1.351 | 0.032 |
| 1420890_at | Hccs | holocytochrome c synthetase | 0.456 | 0.010 |
| 1422241_a_at | Ndufa1 | NADH dehydrogenase 1 alpha subcomplex, 1 | 1.450 | 0.065 |
| 1422492_at | Cpox | coproporphyrinogen oxidase | 1.496 | 0.148 |
| 1423523_at | Aass | aminoadipate-semialdehyde synthase | 6.102 | 0.487 |
| 1423718_at | Ak3 | adenylate kinase 3 | 1.383 | 0.032 |
| 1424556_at | Pycr1 | pyrroline-5-carboxylate reductase 1 | 2.983 | 0.255 |
| 1426187_a_at | Hax1 | HCLS1 associated X-1 | 1.385 | 0.065 |
| 1426235_a_at | Glul | glutamate-ammonia ligase (glutamine synthase) | 0.676 | 0.016 |
| 1426453_at | Pitrm1 | pitrilysin metalloprotease 1 | 0.759 | 0.030 |
| 1428323_at | Gpd2 | glycerol phosphate dehydrogenase 2, mitochondrial | 0.663 | 0.047 |
| 1429071_at | Me3 | malic enzyme 3, NADP(+)-dependent, mitochondrial | 0.297 | 0.091 |
| 1430985_at | 1810027O10Rik | RIKEN cDNA 1810027O10 gene | 0.631 | 0.028 |
| 1433770_at | Dpysl2 | dihydropyrimidinase-like 2 | 0.680 | 0.055 |
| 1433562_s_at | Atp5f1 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | 1.23 | 0.05 |
| 1433855_at | Abat | 4-aminobutyrate aminotransferase | 0.73 | 0.03 |
| 1434354_at | Maob | monoamine oxidase B | 0.71 | 0.00 |
| 1435009_at | Slc9a6 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 | 1.71 | 0.08 |
| 1435836_at | Pdk1 | Pyruvate dehydrogenase kinase, isoenzyme 1 | 1.97 | 0.17 |
| 1436501_at | Mtus1 | mitochondrial tumor suppressor 1 | 0.63 | 0.04 |
| 1437164_x_at | Atp5o | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit | 1.43 | 0.16 |
| 1437192_x_at | Vdac1 | voltage-dependent anion channel 1 | 0.76 | 0.03 |
| 1437325_x_at | Aldh18a1 | aldehyde dehydrogenase 18 family, member A1 | 1.45 | 0.03 |
| 1448190_at | Mrpl33 | mitochondrial ribosomal protein L33 | 1.26 | 0.06 |

| | | | | |
|---|---|---|---|---|
| 1448563_at | Phb | prohibitin | 0.85 | 0.05 |
| 1448808_a_at | Nme2 | expressed in non-metastatic cells 2, protein | 1.29 | 0.06 |
| 1448887_x_at | Fxc1 | fractured callus expressed transcript 1 | 1.42 | 0.10 |
| 1448910_at | Pecr | peroxisomal trans-2-enoyl-CoA reductase | 2.37 | 0.19 |
| 1450048_a_at | Idh2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 0.76 | 0.03 |
| 1450866_a_at | Mrpl17 | mitochondrial ribosomal protein L17 | 1.39 | 0.08 |
| 1451461_a_at | Aldoc | aldolase 3, C isoform | 0.47 | 0.02 |
| 1452257_at | Bdh | 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) | 0.68 | 0.03 |
| 1452790_x_at | Ndufa3 | NADH dehydrogenase 1 alpha subcomplex, 3 | 1.20 | 0.03 |
| 1455011_at | Stard4 | StAR-related lipid transfer (START) domain containing 4 | 0.67 | 0.07 |
| 1455804_x_at | Oxct1 | 3-oxoacid CoA transferase 1 | 0.71 | 0.05 |
| 1456071_a_at | Cycs | cytochrome c, somatic | 1.45 | 0.07 |
| 1460184_at | Hadhsc | L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain | 0.81 | 0.03 |
| 1460718_s_at | Mtch1 | mitochondrial carrier homolog 1 (C. elegans) | 0.69 | 0.04 |
| AFFX-PyruCarbMur/L09192_3_at | Pcx | pyruvate carboxylase | 0.59 | 0.05 |

Differentially expressed mitochondrial genes identified by microarray in 10-week-old MKR diabetic islets. Categorical analysis was based on biological process functions in Gene Ontology by GoMiner

# Table S3 Summary of the mitochondrial proteins quantitatively identified with 95% confidence in the iTRAQ study

| Unused score | %Cov | Peptide No | Accession No | SWISS Prot ID | Protein name | Fold (MKR/WT) | S.D. |
|---|---|---|---|---|---|---|---|
| 15.96 | 30.59 | 10 | DPYL2_MOUSE | O08553 | Dihydropyrimidinase-related protein 2 | 0.73 | 0.17 |
| 10.37 | 43.75 | 7 | PRDX6_MOUSE | O08709 | Peroxiredoxin-6 | 1.17 | 0.14 |
| 8 | 14.54 | 5 | DLDH_MOUSE | O08749 | Dihydrolipoyl dehydrogenase, mitochondrial precursor | 0.81 | 0.03 |
| 4 | 13.22 | 2 | COX2_MOUSE | P00405 | Cytochrome c oxidase subunit 2 | 0.66 | 0.15 |
| 9.65 | 88.44 | 11 | HBB1_MOUSE | P02088 | Hemoglobin subunit beta-1 | 0.89 | 0.22 |
| 6.47 | 17.91 | 5 | AATM_MOUSE | P05202 | Aspartate aminotransferase, mitochondrial precursor | 0.69 | 0.08 |
| 4 | 17.53 | 2 | SODC_MOUSE | P08228 | Superoxide dismutase [Cu-Zn] | 0.88 | 0.49 |
| 21.64 | 49.41 | 12 | MDHM_MOUSE | P08249 | Malate dehydrogenase, mitochondrial precursor | 0.89 | 0.27 |
| 2.81 | 25.23 | 4 | SODM_MOUSE | P09671 | Superoxide dismutase [Mn], mitochondrial precursor | 0.75 | 0.13 |
| 2.67 | 42.86 | 5 | THIO_MOUSE | P10639 | Thioredoxin | 1.53 | 0.28 |
| 2.04 | 35.86 | 4 | COX5A_MOUSE | P12787 | Cytochrome c oxidase subunit 5A, mitochondrial precursor | 0.69 | 0.22 |
| 16.83 | 49.55 | 12 | G3P_MOUSE | P16858 | Glyceraldehyde-3-phosphate dehydrogenase | 1.72 | 0.68 |
| 2.96 | 15.98 | 2 | COX41_MOUSE | P19783 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor | 0.7 | 0.27 |
| 3.72 | 19.11 | 5 | RS2_MOUSE | P25444 | 40S ribosomal protein S2 | 1.38 | 0.1 |
| 6.96 | 10.22 | 4 | DHE3_MOUSE | P26443 | Glutamate dehydrogenase 1, mitochondrial precursor | 0.58 | 0.17 |
| 5.1 | 75.86 | 5 | ACBP_MOUSE | P31786 | Acyl-CoA-binding protein (ACBP) | 0.89 | 0.06 |
| 14.55 | 18.26 | 10 | GRP75_MOUSE | P38647 | Stress-70 protein, mitochondrial precursor | 1 | 0.13 |
| 4.01 | 15.77 | 4 | ADT1_MOUSE | P48962 | ADP/ATP translocase 1 | 0.63 | 0.12 |
| 8.11 | 23.01 | 10 | VATA1_MOUSE | P50516 | Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform | 0.79 | 0.18 |
| 4.02 | 22.81 | 4 | VATE_MOUSE | P50518 | Vacuolar ATP synthase subunit E | 0.89 | 0.05 |
| 10.72 | 25.19 | 11 | IDHP_MOUSE | P54071 | Isocitrate dehydrogenase [NADP], mitochondrial precursor | 0.64 | 0.1 |
| 2 | 46.59 | 2 | ATPK_MOUSE | P56135 | ATP synthase f chain, mitochondrial | 0.75 | 0.09 |
| 31.34 | 60.49 | 23 | ATPB_MOUSE | P56480 | ATP synthase subunit beta, mitochondrial precursor | 0.82 | 0.07 |
| 9.67 | 57.14 | 5 | CYC_MOUSE | P62897 | Cytochrome c, somatic | 1.35 | 0.03 |
| 30.23 | 52.01 | 19 | CH60_MOUSE | P63038 | 60 kDa heat shock protein, mitochondrial precursor | 0.9 | 0.14 |
| 9.29 | 35.51 | 7 | 1433Z_MOUSE | P63101 | 14-3-3 protein zeta/delta | 0.91 | 0.22 |
| 2.3 | 11.76 | 2 | PHB_MOUSE | P67778 | Prohibitin | 0.54 | 0.08 |
| 9.64 | 21.3 | 7 | FUMH_MOUSE | P97807 | Fumarate hydratase, mitochondrial precursor | 1.46 | 0.39 |
| 2 | 49.44 | 2 | UCRH_MOUSE | P99028 | Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor | 0.66 | 0.12 |
| 6.34 | 24.29 | 5 | PRDX5_MOUSE | P99029 | Peroxiredoxin-5, mitochondrial precursor | 0.99 | 0.04 |
| 16.02 | 70.39 | 9 | NDKB_MOUSE | Q01768 | Nucleoside diphosphate kinase B | 1.33 | 0.38 |
| 23.8 | 39.06 | 18 | ATPA_MOUSE | Q03265 | ATP synthase subunit alpha, mitochondrial precursor | 1.24 | 0.58 |
| 16.96 | 61.94 | 13 | KCRB_MOUSE | Q04447 | Creatine kinase B-type | 0.55 | 0.18 |
| 8.68 | 10.7 | 8 | PYC_MOUSE | Q05920 | Pyruvate carboxylase, mitochondrial precursor | 0.43 | 0.15 |
| 6.25 | 14.13 | 9 | ODO1_MOUSE | Q60597 | 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor | 0.73 | 0.08 |
| 6 | 7.18 | 3 | SAP_MOUSE | Q61207 | Sulfated glycoprotein 1 precursor | 0.85 | 0.44 |
| 16.2 | 43.63 | 10 | HCDH_MOUSE | Q61425 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor | 0.63 | 0.09 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2.91 | 33.33 | 4 | CH10_MOUSE | Q64433 | 10 kDa heat shock protein, mitochondrial | 0.79 | 0.25 |
| 4 | 5.09 | 3 | GPDM_MOUSE | Q64521 | Glycerol-3-phosphate dehydrogenase, mitochondrial precursor | 0.7 | 0.05 |
| 22.26 | 17.73 | 20 | CLH_MOUSE | Q68FD5 | Clathrin heavy chain | 1.48 | 0.71 |
| 10 | 17.28 | 7 | CMC1_MOUSE | Q8BH59 | Calcium-binding mitochondrial carrier protein Aralar1 | 0.6 | 0.09 |
| 4 | 9.19 | 3 | DHSA_MOUSE | Q8K2B3 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor | 0.96 | 0.36 |
| 6.34 | 16.91 | 7 | IMMT_MOUSE | Q8CAQ8 | Mitochondrial inner membrane protein | 0.61 | 0.16 |
| 8.05 | 25.94 | 7 | THIL_MOUSE | Q8QZT1 | Acetyl-CoA acetyltransferase, mitochondrial precursor | 0.86 | 0.07 |
| 3.52 | 6.44 | 2 | MPCP_MOUSE | Q8VEM8 | Phosphate carrier protein, mitochondrial precursor (PTP) | 0.7 | 0.06 |
| 4 | 7.7 | 4 | NDUS1_MOUSE | Q91VD9 | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor | 0.94 | 0.04 |
| 2.34 | 16.63 | 5 | ECHB_MOUSE | Q99JY0 | Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) | 0.62 | 0.04 |
| 16.4 | 33.08 | 19 | ACON_MOUSE | Q99KI0 | Aconitate hydratase, mitochondrial precursor | 0.91 | 0.12 |
| 2 | 9.91 | 2 | ETFA_MOUSE | Q99LC5 | Electron transfer flavoprotein subunit alpha, mitochondrial precursor (Alpha-ETF) | 0.57 | 0.06 |
| 1.54 | 19.23 | 3 | ACPM_MOUSE | Q9CR21 | Acyl carrier protein, mitochondrial precursor (ACP) | 0.9 | 0.13 |
| 4 | 17.92 | 3 | UQCR1_MOUSE | Q9CZ13 | Ubiquinol-cytochrome-c reductase complex core protein 1, mitochondrial precursor | 0.78 | 0.21 |
| 4.02 | 14.44 | 4 | CISY_MOUSE | Q9CZU6 | Citrate synthase, mitochondrial precursor | 0.64 | 0.06 |
| 11.79 | 22.2 | 7 | RL4_MOUSE | Q9D8E6 | 60S ribosomal protein L4 | 1.74 | 1.09 |
| 4 | 14.85 | 4 | NDUA9_MOUSE | Q9DC69 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor | 0.54 | 0.05 |
| 4.04 | 16.35 | 3 | NDUS3_MOUSE | Q9DCT2 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor | 0.91 | 0.05 |
| 2.46 | 27.06 | 4 | ETFB_MOUSE | Q9DCW4 | Electron transfer flavoprotein subunit beta | 0.66 | 0.05 |
| 6 | 37.27 | 4 | ATP5H_MOUSE | Q9DCX2 | ATP synthase D chain, mitochondrial | 0.76 | 0.19 |
| 2 | 14.35 | 2 | MAAI_MOUSE | Q9WVL0 | Maleylacetoacetate isomerase | 1.49 | 0.17 |
| 4 | 4.15 | 2 | P5CS_MOUSE | Q9Z110 | Delta 1-pyrroline-5-carboxylate synthetase (P5CS) | 0.87 | 0.13 |
| 2.8 | 6.41 | 4 | SYV_MOUSE | Q9Z1Q9 | Valyl-tRNA synthetase | 0.74 | 0.03 |
| 6.02 | 16.44 | 5 | ADT2_MOUSE | P51881 | ADP/ATP translocase 2 | 0.75 | 0.14 |
| 26.04 | 45.39 | 16 | KPYM_MOUSE | P52480 | Pyruvate kinase isozyme M2 | 1.24 | 0.25 |
| 5.28 | 14.81 | 5 | AOFB_MOUSE | Q8BW75 | Amine oxidase [flavin-containing] B | 0.33 | 0.07 |

Differentially expressed mitochondrial proteins identified by iTRAQ proteomics scan of 10 week old MKR diabetic islets. All proteins were identified with 95% confidence and containing at least two unique peptides across two of three independent iTRAQ experiments, including the 159 differentially expressed proteins listed in Table 2. “%Cov” represents the number of amino acids matching at least one identified peptide divided by the total number of amino acids in the protein sequence. “Peptide No.” represents the total number of unique peptides assigned to the protein. “Unused score” represents the protein confidence for a detected protein, as calculated by the peptide confidence for peptides not already ‘used’ by higher scoring proteins, and 1.3 is 95% confidence defined by the software. Categorical analysis was based on biological process functions in Gene Ontology by GoMiner.

## Table S4 Primer sequences used in qPCR

| Gene symbol | Accession Number | Forward primer (5'-3') | Reverse primer (5'-3') |
|---|---|---|---|
| Cox1 | YP_001686700 | CGGAAGTATTTTTCTTTGCAGGAT | CAGCAGCCTCCTAGATCATGTG |
| Cox2 | YP_001686701 | TCTCCCCTCTCTACGCATTCTATATAT | ATCATTGGTGCCCTATGGTTTT |
| Cox3 | YP_001686704 | GTGCTAGCCGCAGGCATT | TCCTCCAGCGGGATCAAAG |
| Cat | NM_00984 | GTGCGGACATTCTACACAAAGG | GAACATTGCCGGCCACC |
| Sod1 | NM_011434 | GTGATTGGGATTGCGCAGTA | ACTCATCTGCTACCCTCAAACCA |
| Sod2 | NM_013671 | TTAACGCGCAGATCATGCA | TGAACAATCTCAACGCCACC |
| Sod3 | NM_014435 | CAGCCATGTTGGCCTTCTTGTTCT | ACAGGCTTGACCTGGTTGAGAAGA |
| Gpx1 | NM_008160 | GCATTGGCTTGGTGATTACTGGCT | TCCCGATGCCTTTCCACCTAATGA |
| Gpx2 | NM_030677 | GCATGGCTTACATTGCCAAGTCGT | TTCAATACGTTCAGAGGCAGGGCT |
| Gpx3 | NM_008161 | ACAATTGTCCCAGTGTGTGCAT | GAAACCCAGGGATGGTCCA |
| Gpx4 | NM_008162 | CCCGATATGCTGAGTGTGGTT | AACCAGTTTGGGAGGCAGG |
| Hmox1 | NM_010442 | CCTCACTGGCAGGAAATCATC | TATGTAAAGCGTCTCCACGAGG |
| Kcnj11 | NM_010602 | GACATCCCCATGGAGAATGG | CTCATCACTACCACGTATCGA |
| B-actin | NM_007393 | CTGAATGGCCCAGGTCTGA | GTGTTGAGGCAGCCAGGG |

**Abbreviations**: Cox, cytochrome oxidase; Cat, catalase; Sod, superoxide dismutase; Gpx, glutathione peroxidase; Hmox, heme-oxidase; Kcnj11, Islet $K_{ATP}$ channel.