

Supplemental Figure 1 : Cellular and molecular functions altered by type II diabetes mellitus and Rosiglitazone treatment. Microarray data were analysed by IPA. *Dark blue bars*, db/+ vs. db/db; *medium-blue bars*, db/db mice treated with 10 mg/kg RSG vs. db/db; *bright-blue bars*, db/db mice treated with 30 mg/kg RSG vs. db/db, *black bars*, db/db mice treated with 100 mg/kg RSG vs. db/db; *bold line*, threshold p -value <0.05 , Fisher test and Benjamini-Hochberg correction. * The diabetes effect was given as reciprocal (db/+ vs. db/db) to facilitate direct comparisons with normalizing effect of RSG.

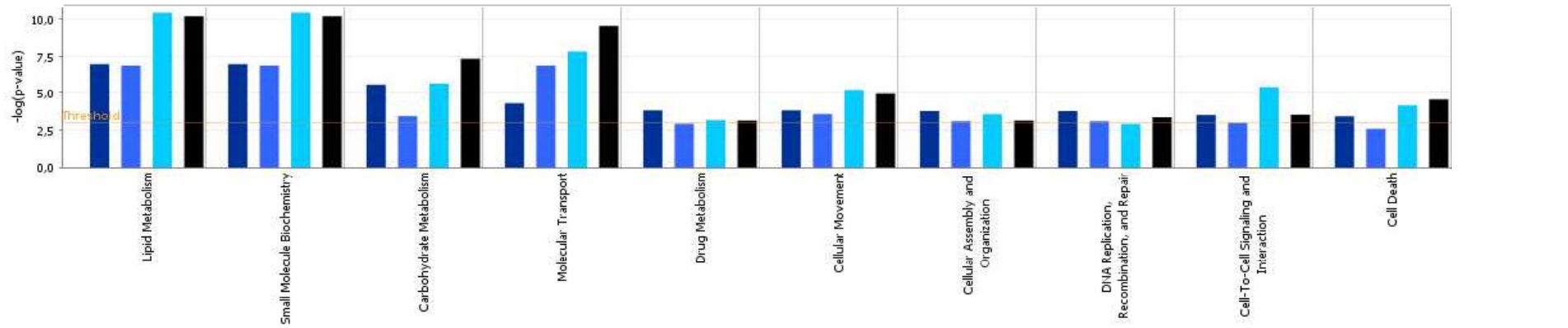
Supplemental Figure 2: Two dimensional representation of differentially expressed genes involved in liver carbohydrates metabolism (A) and in liver FA and TG metabolisms (B). The input consisted of db/+ or RSG-treated db/db vs. untreated db/db reference group. Each gene is represented by a column of coloured boxes and each group by a single row. Each coloured box represent the gene expression value in one group, with expression values ranging from bright green (lowest) to bright red (highest). Missing value are in grey when p -value ≥ 0.001 .

Supplemental Figure 3: Two dimensional representation of differentially expressed genes involved in IAT FFA and TG metabolisms. Same overall format as in Supplemental Figure 2. Missing value are in grey when p -value ≥ 0.001 .

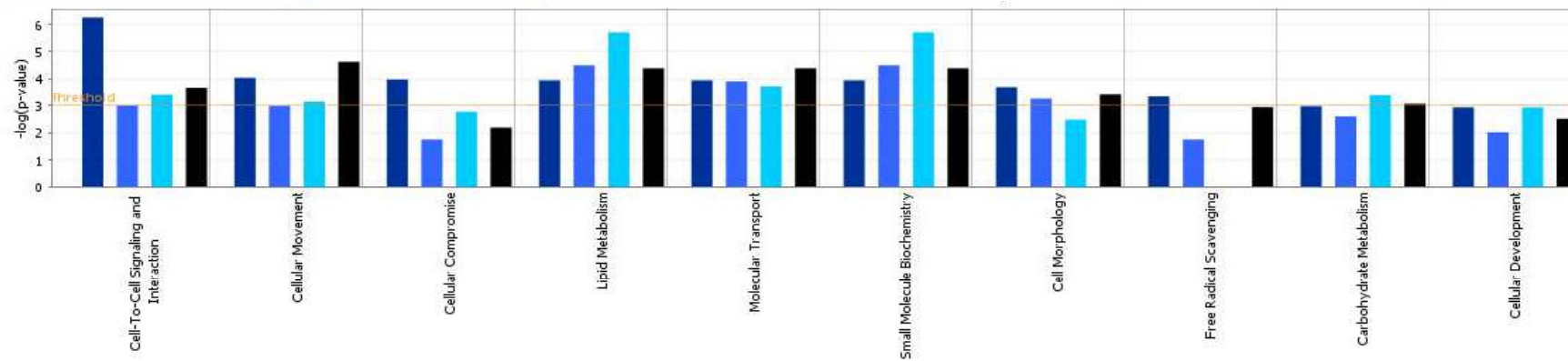
Supplemental Figure 4: Two dimensional representation of differentially expressed genes involved in Soleus muscle lipid and carbohydrate metabolisms. Same overall format as in Supplemental Fig. 2. Genes involved in glucose, FA, and TG metabolisms were studied. Missing value are in grey when p -value ≥ 0.001 .

Supplemental Fig.1

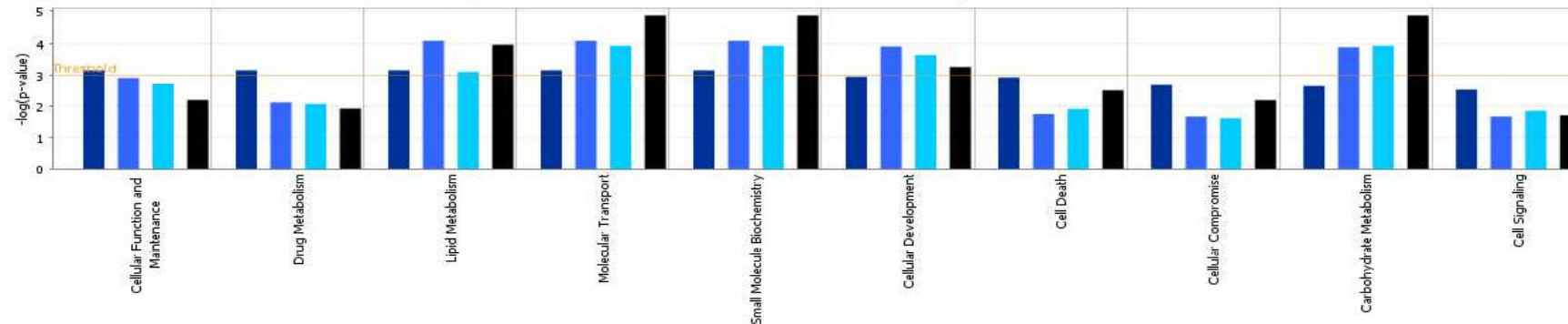
A Liver



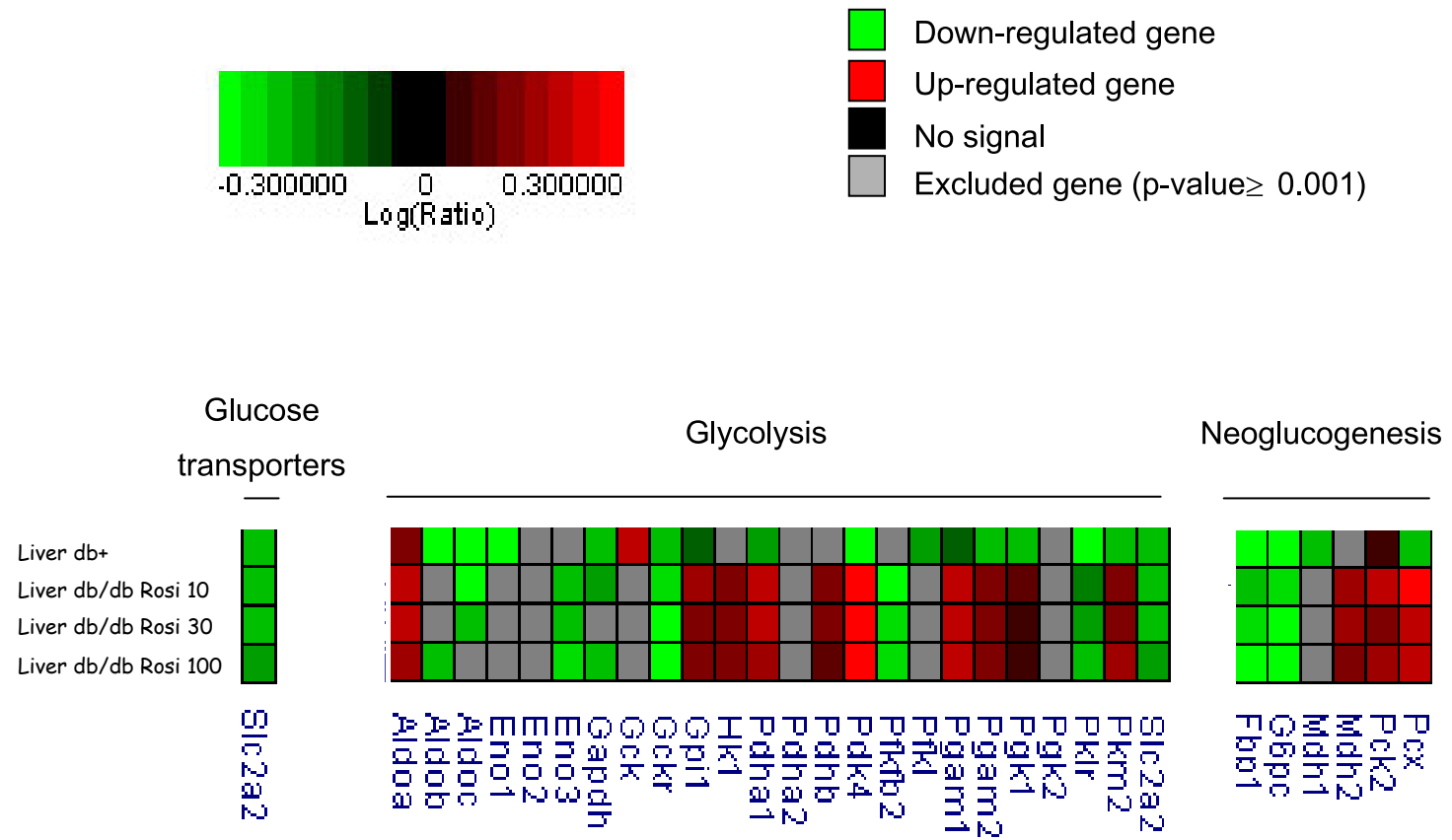
B Adipose Tissue



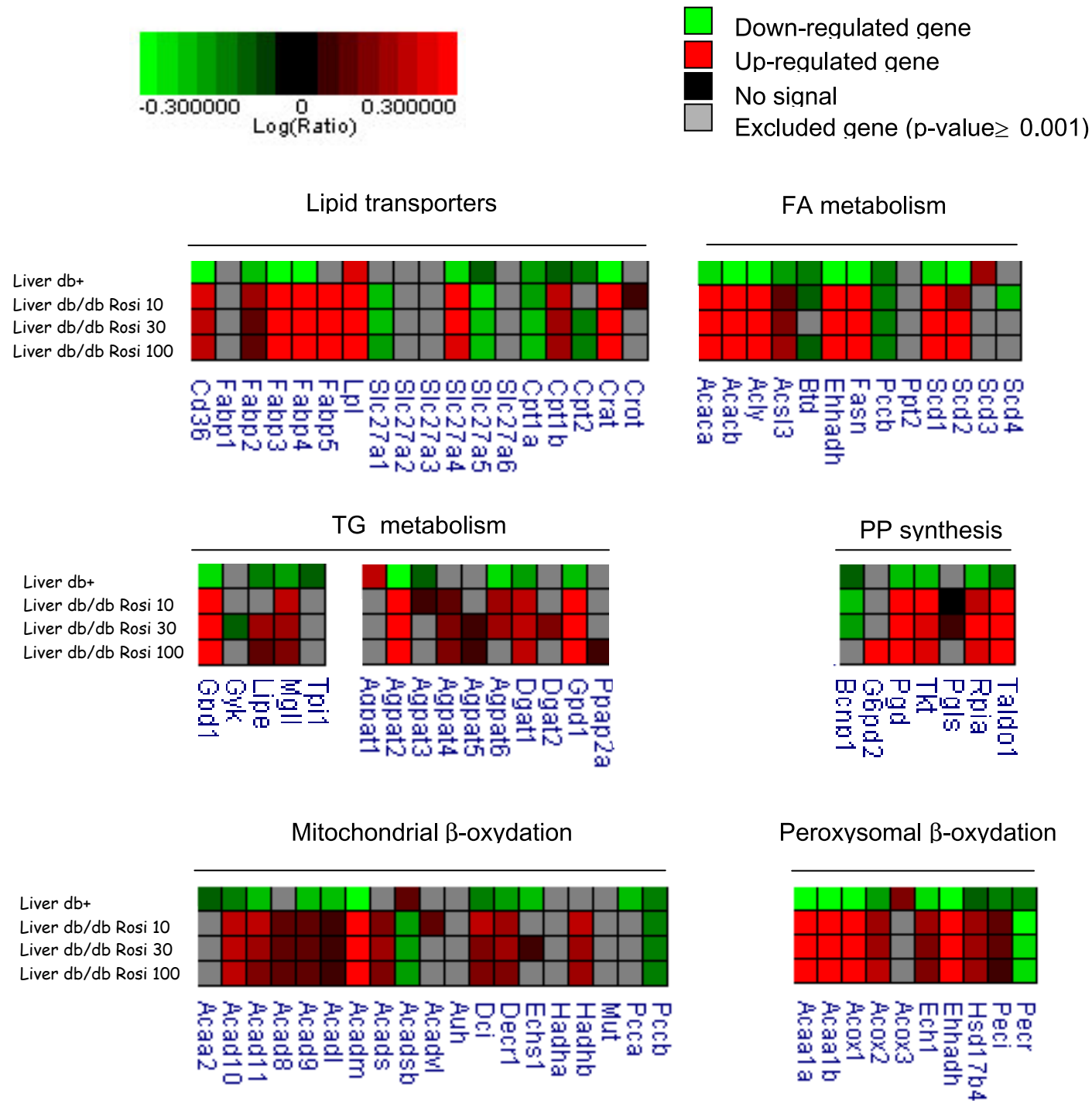
C Soleus muscle



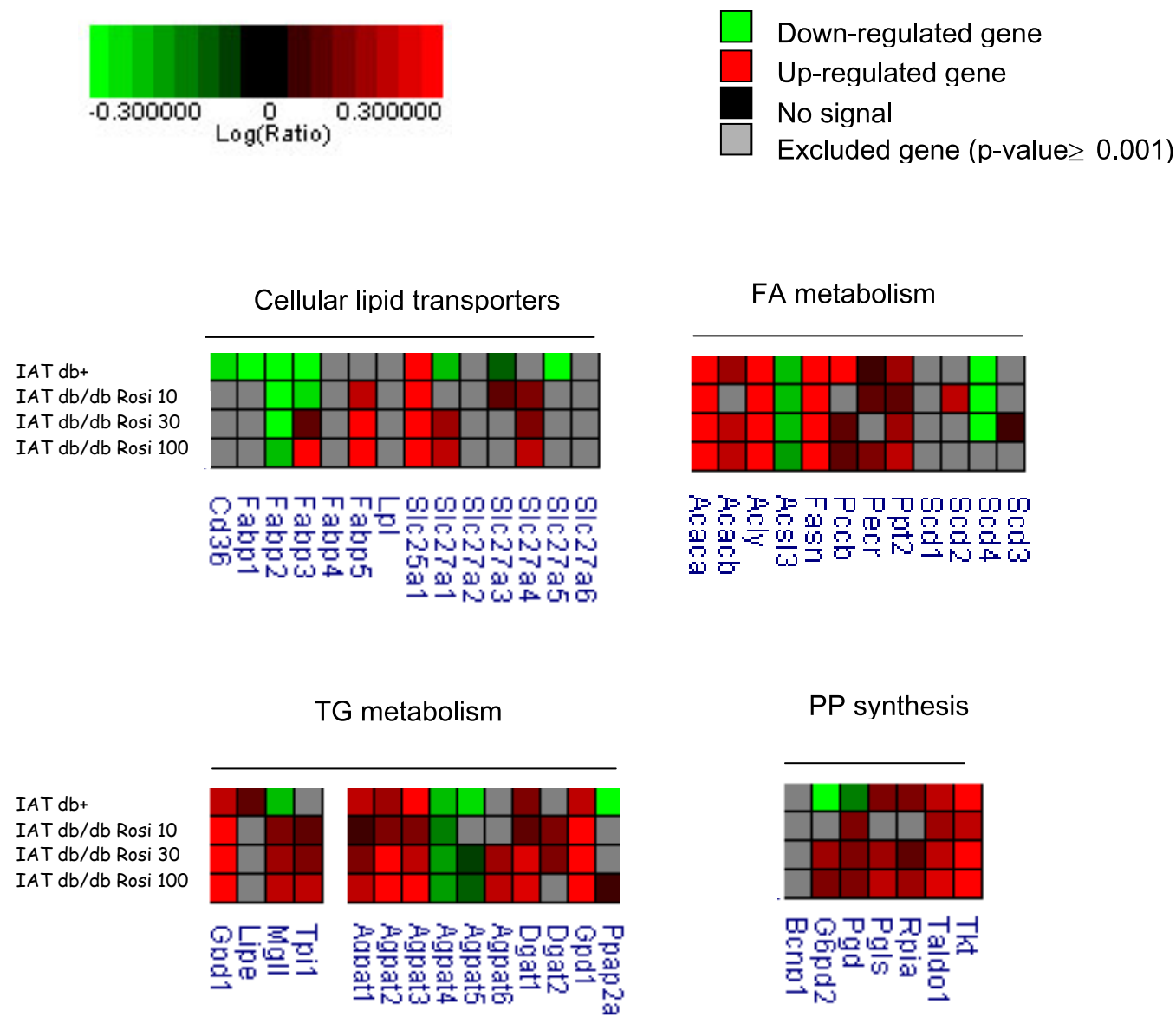
Supplemental Fig. 2A



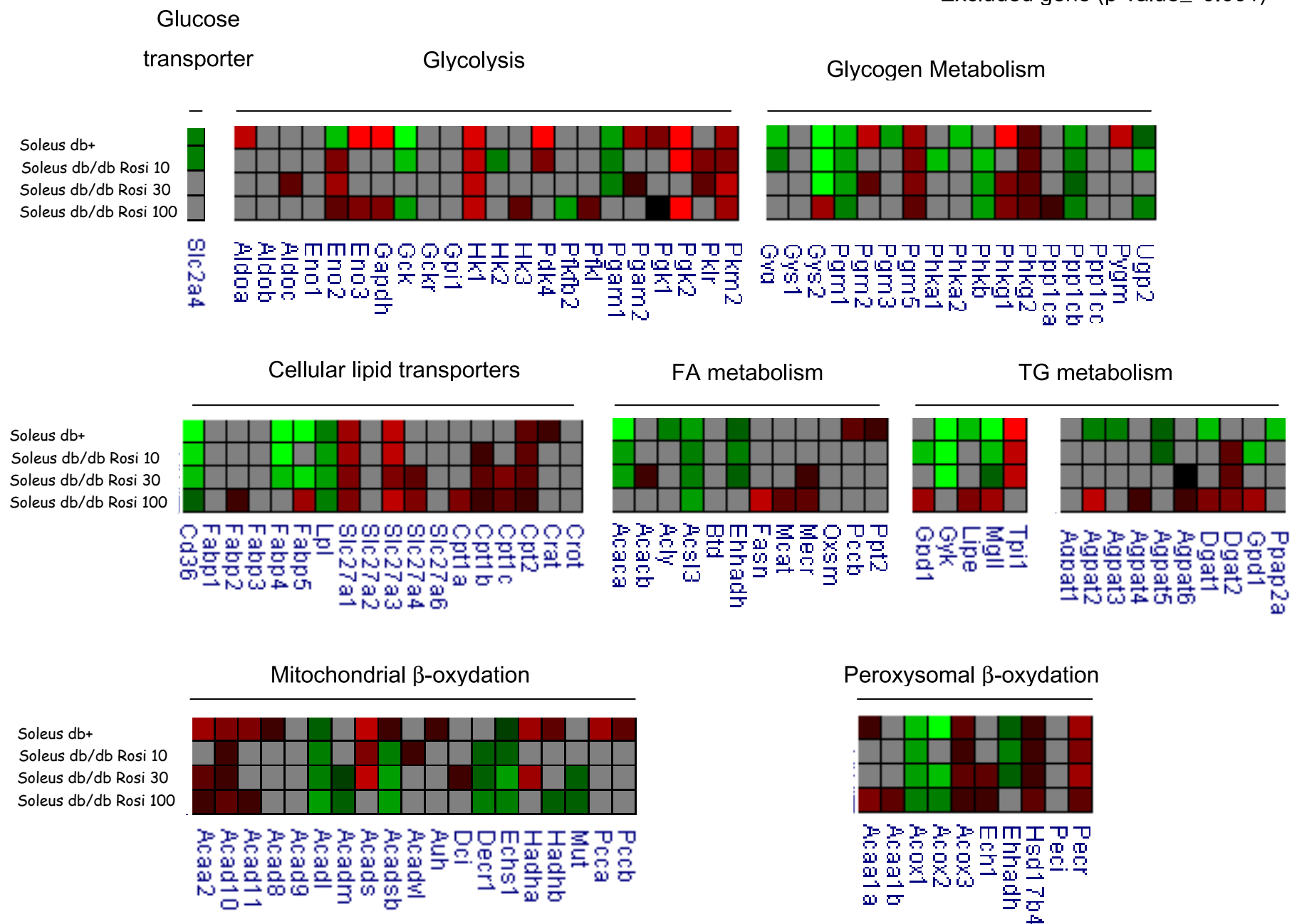
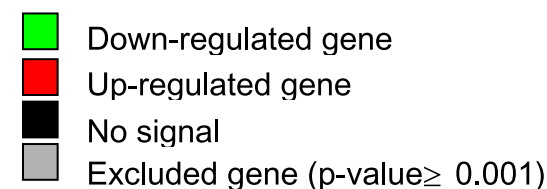
Supplemental Fig. 2B



Supplemental Fig. 3



Supplemental Fig. 4



Supplemental Table 1

Overview of the number of sequences up- and down-regulated in db/+ and RSG-treated samples compared to db/db

| <i>Treatment vs db/db</i> | Liver | | | Inguinal Adipose Tissue | | | Soleus | | |
|----------------------------------|--------------|----------------|-------|--------------------------------|----------------|-------|---------------|----------------|-------|
| | Up-regulated | Down-regulated | Total | Up-regulated | Down-regulated | Total | Up-regulated | Down-regulated | Total |
| db/+* | 3317 | 3222 | 6539 | 7249 | 5958 | 13207 | 3817 | 4078 | 7895 |
| db/db Rosi 10 mg/kg | 2795 | 2772 | 5567 | 3146 | 2564 | 5710 | 1393 | 2020 | 3413 |
| db/db Rosi 30 mg/kg | 2385 | 2403 | 4788 | 5080 | 3925 | 9005 | 1641 | 2003 | 3644 |
| db/db Rosi 100 mg/kg | 2401 | 2148 | 4549 | 5766 | 4569 | 10335 | 1417 | 2203 | 3620 |

Number of sequences with differential expression of at least ± 1.3 -fold and with p-value $p < 0.001$.

Supplemental Table 2: Differentially expressed genes (506 sequences probes) involved in lipid and carbohydrate metabolism. * Resolver unweighted average and microarray probes selected in Fig. 1, 4, 6. When several probes exist for the same gene, selection was based on quality control (signal intensity and spot quality). In grey : sequences that do not pass the statistic and /or fold change thresholds (see Material and Methods). F.C. Fold Change; *p*-value = 0 corresponds to *p*-value < 1E-45.

| Tissue | Sequence Name | Sequence Code | Accession # | Sequence description | db+ | | RSG 10MK | | RSG 30MK | | RSG 100MK | |
|--------|---------------|---------------|-------------|---|-------|----------|----------|----------|----------|----------|-----------|----------|
| | | | | | ratio | P-value | ratio | P-value | ratio | P-value | ratio | P-value |
| Liver | Acaa1a | A_51_P327075 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 0.75 | 1.74E-08 | 1.94 | 8.88E-23 | 1.97 | 7.62E-22 | 1.86 | 1.68E-19 |
| | Acaa1a | A_52_P155990 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 0.60 | 9.07E-10 | 3.26 | 0 | 3.14 | 0 | 2.80 | 0 |
| | Acaa1a | A_52_P423183 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 0.54 | 7.85E-44 | 3.76 | 0 | 3.85 | 0 | 3.62 | 0 |
| | Acaa1b | A_52_P423174 | NM_146230 | acetyl-Coenzyme A acyltransferase 1B | 0.57 | 0 | 3.51 | 4.22E-34 | 3.42 | 0 | 3.05 | 0 |
| | Acaca | A_51_P439426 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.81 | 0.037202 | 3.74 | 1.40E-45 | 3.22 | 1.75E-18 | 3.41 | 0 |
| | Acaca | A_52_P132591 | AF374167 | acetyl-Coenzyme A carboxylase alpha | 0.67 | 0.000031 | 2.14 | 1.22E-19 | 2.16 | 1.86E-15 | 2.03 | 1.21E-12 |
| | Acaca | A_52_P23177 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.97 | 0.194564 | 1.75 | 6.47E-15 | 1.98 | 0 | 1.68 | 8.13E-37 |
| | Acaca | A_52_P318040 | AK132628 | acetyl-Coenzyme A carboxylase alpha | 0.63 | 1.60E-21 | 3.49 | 4.16E-43 | 3.43 | 7.43E-27 | 3.32 | 0 |
| | *Acaca | A_52_P595124 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.89 | 0.074292 | 1.87 | 5.47E-24 | 2.22 | 0 | 1.74 | 3.58E-23 |
| | Acacb | A_51_P239236 | BC022940 | acetyl-Coenzyme A carboxylase beta | 0.58 | 1.73E-30 | 2.40 | 0 | 2.49 | 0 | 2.55 | 0 |
| | *Acacb | A_52_P340167 | NM_133904 | acetyl-Coenzyme A carboxylase beta | 0.75 | 0.000015 | 1.94 | 0 | 2.32 | 2.35E-08 | 1.71 | 4.27E-15 |
| | Acad10 | A_51_P187507 | NM_028037 | acyl-Coenzyme A dehydrogenase family, member 10 | 0.84 | 2.26E-15 | 1.46 | 0 | 1.51 | 0 | 1.49 | 0 |
| | Acad11 | A_52_P85152 | NM_175324 | acyl-Coenzyme A dehydrogenase family, member 11 | 0.75 | 1.03E-28 | 1.47 | 0 | 1.39 | 2.19E-28 | 1.30 | 5.16E-19 |
| | Acad9 | A_51_P341379 | NM_172678 | acyl-Coenzyme A dehydrogenase family, member 9 | 0.65 | 0 | 1.20 | 6.77E-26 | 1.16 | 1.97E-08 | 1.13 | 6.78E-07 |
| | Acadl | A_51_P149455 | NM_007381 | acyl-Coenzyme A dehydrogenase, long-chain | 0.69 | 2.80E-45 | 1.13 | 2.09E-07 | 1.09 | 1.61E-11 | 1.09 | 1.13E-08 |
| | Acadm | A_51_P319879 | NM_007382 | acyl-Coenzyme A dehydrogenase, medium chain | 0.56 | 0 | 1.95 | 0 | 1.82 | 0 | 1.72 | 0 |
| | Acads | A_52_P367745 | NM_007383 | acyl-Coenzyme A dehydrogenase, short chain | 0.84 | 0.024186 | 1.31 | 6.11E-06 | 1.35 | 7.24E-07 | 1.34 | 2.43E-06 |
| | Acat1 | A_51_P319449 | NM_144784 | acetyl-Coenzyme A acetyltransferase 1 | 0.68 | 1.36E-27 | 1.08 | 0.053153 | 1.00 | 0.9906 | 1.05 | 0.348222 |
| | Acat3 | A_51_P139745 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 0.96 | 0.049656 | 0.84 | 6.41E-07 | 0.77 | 1.11E-37 | 0.77 | 0 |
| | Acat3 | A_52_P11959 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 0.86 | 0.010657 | 0.82 | 0.000034 | 0.76 | 1.42E-08 | 0.73 | 2.78E-09 |
| | *Acly | A_51_P261718 | NM_134037 | ATP citrate lyase | 0.55 | 0 | 2.24 | 1.54E-14 | 2.20 | 1.86E-35 | 2.01 | 1.26E-22 |
| | Acly | A_52_P373556 | AK043466 | ATP citrate lyase | 0.82 | 0.282286 | 1.80 | 3.81E-22 | 1.64 | 0.00013 | 1.72 | 5.91E-08 |
| | Aco2 | A_52_P200359 | NM_080633 | aconitase 2, mitochondrial | 0.83 | 2.41E-11 | 1.41 | 2.75E-26 | 1.37 | 5.17E-23 | 1.16 | 0.000202 |

| | | | | | | | | | | | |
|----------|--------------|-----------|---|-------|----------|------|----------|------|----------|------|----------|
| Acox1 | A_51_P366704 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 0.59 | 7.02E-15 | 2.12 | 5.14E-11 | 2.04 | 1.82E-09 | 2.16 | 5.79E-12 |
| Acox1 | A_52_P615096 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 0.59 | 2.27E-16 | 2.29 | 5.47E-43 | 2.22 | 0 | 2.26 | 0 |
| Acox2 | A_51_P206708 | NM_053115 | acyl-Coenzyme A oxidase 2, branched chain | 0.76 | 3.60E-08 | 1.38 | 0 | 1.37 | 5.64E-25 | 1.40 | 2.77E-35 |
| Acsl1 | A_51_P463452 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 1.25 | 8.55E-17 | 2.48 | 0 | 2.69 | 0 | 2.15 | 0 |
| Acsl1 | A_51_P496432 | BC006692 | acyl-CoA synthetase long-chain family member 1 | 1.19 | 2.18E-16 | 2.36 | 0 | 2.51 | 0 | 2.14 | 0 |
| Acsl1 | A_52_P597618 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 1.17 | 2.65E-13 | 2.42 | 0 | 2.63 | 0 | 2.15 | 0 |
| Acsl3 | A_51_P511560 | NM_028817 | acyl-CoA synthetase long-chain family member 3 | 0.75 | 9.90E-07 | 1.22 | 6.74E-07 | 1.25 | 0.000285 | 1.32 | 1.37E-10 |
| Acsl4 | A_51_P268154 | NM_019477 | acyl-CoA synthetase long-chain family member 4 | 1.43 | 5.20E-22 | 1.88 | 4.13E-43 | 1.95 | 0 | 2.11 | 2.80E-45 |
| Acsl4 | A_52_P78203 | NM_207625 | acyl-CoA synthetase long-chain family member 4 | 1.04 | 0.179276 | 1.55 | 0 | 1.60 | 0 | 1.69 | 0 |
| Acsl5 | A_52_P593037 | NM_027976 | acyl-CoA synthetase long-chain family member 5 | 0.68 | 3.91E-32 | 1.81 | 0 | 1.80 | 0 | 1.79 | 0 |
| Acsl6 | A_51_P380699 | NM_144823 | acyl-CoA synthetase long-chain family member 6 | 3.08 | 2.24E-10 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Adcy1 | A_52_P240164 | NM_009622 | adenylate cyclase 1 | 1.39 | 9.03E-09 | 0.91 | 0.422411 | 0.89 | 0.152402 | 0.93 | 0.187814 |
| Adcy1 | A_52_P240170 | BC050125 | adenylate cyclase 1 | 1.33 | 1.40E-45 | 0.72 | 4.40E-18 | 0.68 | 2.23E-27 | 0.75 | 8.99E-28 |
| Adcy4 | A_51_P229911 | NM_080435 | adenylate cyclase 4 | 0.95 | 0.073846 | 1.12 | 0.00004 | 1.32 | 7.03E-07 | 1.14 | 8.44E-07 |
| Adcy9 | A_51_P501538 | NM_009624 | adenylate cyclase 9 | 1.23 | 7.23E-13 | 0.64 | 2.98E-43 | 0.76 | 1.25E-13 | 0.73 | 7.16E-12 |
| Adh1 | A_52_P629895 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.91 | 0.152117 | 1.18 | 0.011872 | 1.22 | 0.004316 | 1.19 | 0.00505 |
| Adh4 | A_51_P189442 | NM_011996 | alcohol dehydrogenase 4 (class II), pi polypeptide | 1.35 | 1.21E-10 | 0.48 | 7.43E-44 | 0.45 | 0 | 0.53 | 1.32E-32 |
| Adh6-ps1 | A_51_P120027 | AK004863 | alcohol dehydrogenase 6 (class V), pseudogene 1 | 24.38 | 0 | 1.00 | 1 | 1.00 | 1 | 1.03 | 0.77865 |
| Adh7 | A_51_P233797 | NM_009626 | alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide | 0.83 | 0.002635 | 1.51 | 5.03E-12 | 1.51 | 3.60E-17 | 1.51 | 1.18E-41 |
| Agpat1 | A_51_P322612 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 1.45 | 1.28E-41 | 1.00 | 0.871515 | 1.02 | 0.547802 | 0.99 | 0.802776 |
| Agpat2 | A_51_P238563 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 0.57 | 2.72E-11 | 2.09 | 0 | 2.04 | 0 | 1.98 | 0 |
| *Agpat2 | A_51_P238565 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 0.60 | 6.53E-13 | 1.99 | 0 | 2.09 | 0 | 1.80 | 0 |
| Agpat5 | A_51_P361286 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 1.31 | 3.40E-07 | 1.01 | 0.877538 | 1.11 | 0.140076 | 1.05 | 0.36821 |
| *Agpat6 | A_51_P335710 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.58 | 4.12E-06 | 1.44 | 0.000494 | 1.45 | 0.000525 | 1.28 | 0.240079 |
| Agpat6 | A_51_P335716 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.66 | 2.80E-10 | 1.44 | 4.63E-09 | 1.41 | 1.58E-08 | 1.21 | 0.007527 |
| Agpat6 | A_52_P24986 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.58 | 0 | 1.23 | 1.45E-19 | 1.42 | 0 | 1.19 | 6.93E-14 |
| Aldh1a1 | A_51_P334942 | NM_013467 | aldehyde dehydrogenase family 1, subfamily A1 | 0.55 | 1.35E-13 | 0.81 | 0.012059 | 0.81 | 0.000799 | 0.76 | 0.000033 |
| Aldh1a3 | A_52_P87843 | NM_053080 | aldehyde dehydrogenase family 1, subfamily A3 | 0.37 | 0 | 0.59 | 4.73E-19 | 0.59 | 8.51E-17 | 0.62 | 5.20E-39 |
| Aldh1a7 | A_51_P383399 | NM_011921 | aldehyde dehydrogenase family 1, subfamily A7 | 0.61 | 0 | 1.36 | 4.01E-23 | 1.21 | 4.30E-22 | 1.27 | 0 |
| Aldh1b1 | A_51_P510418 | NM_028270 | aldehyde dehydrogenase 1 family, member B1 | 0.52 | 0 | 1.31 | 2.60E-09 | 1.24 | 1.54E-13 | 1.17 | 6.97E-08 |
| Aldh2 | A_52_P13109 | AK163452 | aldehyde dehydrogenase 2, mitochondrial | 0.57 | 0 | 0.64 | 1.52E-24 | 0.64 | 3.70E-25 | 0.64 | 0 |
| Aldh3a2 | A_51_P464175 | NM_007437 | aldehyde dehydrogenase family 3, subfamily A2 | 0.34 | 0 | 2.12 | 0 | 1.95 | 0 | 1.71 | 0 |

| | | | | | | | | | | | |
|---------|---------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Aldh4a1 | A_51_P337918 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 0.75 | 1.61E-27 | 0.95 | 0.16603 | 1.04 | 0.071561 | 1.04 | 0.154621 |
| Aldh7a1 | A_51_P470414 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 0.78 | 1.55E-13 | 0.76 | 5.31E-13 | 0.87 | 0.002202 | 0.70 | 1.12E-29 |
| Aldh9a1 | A_51_P106211 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 0.77 | 6.44E-13 | 1.10 | 0.000079 | 1.09 | 0.001279 | 1.06 | 0.032171 |
| Aldh9a1 | A_52_P265877 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 0.70 | 0 | 0.96 | 0.34659 | 1.01 | 0.723912 | 1.03 | 0.321975 |
| Aldoa | A_51_P216905 | NM_007438 | aldolase 1, A isoform | 1.33 | 1.29E-12 | 1.54 | 4.15E-40 | 1.54 | 4.20E-45 | 1.45 | 2.80E-31 |
| *Aldoa | A_52_P98387 | NM_007438 | aldolase 1, A isoform | 1.32 | 3.78E-17 | 1.53 | 0 | 1.56 | 0 | 1.40 | 0 |
| *Aldob | A_51_P337269 | NM_144903 | aldolase 2, B isoform | 0.53 | 6.33E-13 | 0.98 | 0.813021 | 0.80 | 0.002103 | 0.69 | 9.81E-11 |
| Aldob | A_52_P450038 | NM_144903 | aldolase 2, B isoform | 0.57 | 0 | 0.98 | 0.501143 | 0.79 | 3.75E-19 | 0.71 | 3.61E-27 |
| Aldob | A_52_P468023 | NM_144903 | aldolase 2, B isoform | 0.53 | 0 | 0.92 | 0.004378 | 0.78 | 8.51E-26 | 0.70 | 1.80E-31 |
| Aldoc | A_51_P220681 | NM_009657 | aldolase 3, C isoform | 0.59 | 2.74E-28 | 0.53 | 0 | 0.66 | 2.73E-23 | 0.85 | 0.032285 |
| Aldoc | A_51_P425284 | AK039267 | aldolase 3, C isoform | 0.35 | 1.53E-17 | 0.50 | 1.57E-23 | 0.69 | 9.15E-09 | 0.78 | 0.001372 |
| Apoa1 | A_51_P408082 | NM_009692 | apolipoprotein A-I | 4.85 | 0 | 1.84 | 6.15E-35 | 1.93 | 4.42E-36 | 2.69 | 0 |
| Apoa4 | A_51_P327491 | NM_007468 | apolipoprotein A-IV | 0.24 | 0 | 1.32 | 0.003995 | 0.64 | 1.73E-13 | 0.61 | 2.79E-13 |
| Apoa4 | A_51_P327496 | NM_007468 | apolipoprotein A-IV | 0.28 | 0 | 1.22 | 0.048667 | 0.58 | 3.54E-14 | 0.57 | 1.06E-06 |
| Apoa5 | A_51_P259930 | NM_080434 | apolipoprotein A-V | 0.69 | 3.83E-08 | 0.46 | 0 | 0.40 | 0 | 0.46 | 0 |
| Apoa5 | A_52_P292404 | NM_080434 | apolipoprotein A-V | 0.69 | 3.38E-13 | 0.53 | 0 | 0.49 | 0 | 0.56 | 7.50E-42 |
| Apoc2 | A_51_P334979 | NM_009695 | apolipoprotein C-II | 0.76 | 4.35E-15 | 1.24 | 4.78E-17 | 1.04 | 0.041548 | 0.96 | 0.079965 |
| *Apoc3 | A_51_P310629 | NM_023114 | apolipoprotein C-III | 0.83 | 5.90E-18 | 0.72 | 9.30E-27 | 0.70 | 3.21E-35 | 0.70 | 0 |
| Apoc3 | A_52_P574306 | NM_023114 | apolipoprotein C-III | 0.85 | 2.42E-22 | 0.74 | 1.31E-30 | 0.72 | 9.39E-43 | 0.71 | 0 |
| Atp12a | A_52_P329398 | NM_138652 | ATPase, H+/K+ transporting, nongastric, alpha polypeptide | 7.65 | 0 | 1.10 | 0.157139 | 1.21 | 0.001529 | 1.18 | 0.000915 |
| Atp6v1h | A_51_P105604 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.81 | 1.17E-13 | 1.20 | 5.02E-21 | 1.20 | 2.00E-08 | 1.64 | 1.16E-06 |
| Auh | A_52_P107290 | AK003929 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.05 | 0.295136 | 1.35 | 1.96E-09 | 1.65 | 0 | 1.36 | 1.08E-09 |
| Bcnp1 | A_52_P1053160 | AK158308 | BCNP1 homolog | 0.88 | 0.000934 | 0.73 | 8.08E-07 | 0.80 | 0.000151 | 0.84 | 0.000814 |
| Bdh2 | A_51_P470935 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.09 | 0.034396 | 0.62 | 0 | 0.59 | 3.12E-36 | 0.68 | 1.50E-22 |
| Bdh2 | A_52_P195809 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.03 | 0.352063 | 0.61 | 0 | 0.64 | 9.90E-28 | 0.67 | 1.04E-30 |
| Cd36 | A_51_P375138 | L23108 | CD36 antigen | 0.09 | 0 | 1.80 | 0 | 1.76 | 0 | 1.82 | 0 |
| *Cd36 | A_51_P375146 | NM_007643 | CD36 antigen | 0.08 | 0 | 1.62 | 0 | 1.69 | 0 | 1.60 | 1.09E-14 |
| Cox6b2 | A_51_P300506 | NM_183405 | cytochrome c oxidase subunit VIb polypeptide 2 | 1.00 | 0.989976 | 1.34 | 3.97E-19 | 1.27 | 2.59E-16 | 1.23 | 6.70E-13 |
| Cox7a1 | A_51_P148612 | NM_009944 | cytochrome c oxidase, subunit VIIa 1 | 1.25 | 7.57E-10 | 2.57 | 0 | 2.27 | 0 | 2.30 | 0 |
| Cpt1a | A_51_P427674 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 0.85 | 0.002288 | 0.79 | 9.77E-06 | 0.72 | 4.91E-23 | 0.73 | 1.42E-24 |
| Cpt1a | A_52_P219753 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 0.78 | 4.06E-07 | 0.79 | 0.000028 | 0.67 | 1.66E-27 | 0.69 | 2.75E-22 |
| Cpt1b | A_51_P232913 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 0.90 | 0.000156 | 1.55 | 2.84E-13 | 1.37 | 2.25E-24 | 1.39 | 6.61E-19 |
| Cpt1b | A_52_P625508 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 0.55 | 2.96E-08 | 2.04 | 3.23E-28 | 1.55 | 8.90E-09 | 2.05 | 1.84E-42 |
| Cpt1c | A_51_P177562 | NM_153679 | carnitine palmitoyltransferase 1c | 1.00 | 1 | 1.00 | 1 | 0.93 | 0.561109 | 1.00 | 1 |
| Crat | A_51_P440807 | NM_007760 | carnitine acetyltransferase | 0.43 | 0 | 2.66 | 0 | 2.53 | 0 | 2.22 | 0 |

| | | | | | | | | | | | |
|---------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|
| Cs | A_51_P390260 | NM_026444 | citrate synthase | 1.24 | 2.36E-08 | 1.50 | 4.20E-43 | 1.39 | 7.41E-18 | 1.44 | 1.12E-15 |
| Cs | A_52_P182659 | NM_026444 | citrate synthase | 0.96 | 0.118852 | 1.47 | 3.24E-28 | 1.40 | 1.36E-20 | 1.33 | 1.92E-34 |
| Cyp1a1 | A_51_P279693 | NM_009992 | cytochrome P450, family 1, subfamily a, polypeptide 1 | 0.68 | 0.000011 | 0.83 | 0.134841 | 1.00 | 0.990557 | 0.91 | 0.262586 |
| Cyp1a2 | A_51_P450140 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 2.42 | 0 | 0.37 | 0 | 0.42 | 0 | 0.58 | 5.78E-23 |
| Cyp1a2 | A_52_P595871 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 2.46 | 0 | 0.34 | 0 | 0.41 | 0 | 0.58 | 0 |
| Cyp1b1 | A_51_P255456 | NM_009994 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 0.59 | 0.000425 | 1.13 | 0.321098 | 1.13 | 0.600004 | 0.95 | 0.684035 |
| Cyp2a12 | A_51_P206736 | NM_133657 | cytochrome P450, family 2, subfamily a, polypeptide 12 | 0.81 | 2.21E-08 | 0.72 | 7.20E-18 | 0.67 | 5.62E-22 | 0.72 | 8.30E-15 |
| Cyp2a5 | A_52_P246252 | NM_007812 | cytochrome P450, family 2, subfamily a, polypeptide 5 | 0.48 | 1.97E-08 | 0.20 | 0 | 0.25 | 0 | 0.35 | 1.82E-09 |
| Cyp2b10 | A_52_P472486 | NM_009999 | cytochrome P450, family 2, subfamily b, polypeptide 10 | 0.04 | 0 | 0.60 | 4.00E-15 | 0.62 | 1.26E-37 | 0.66 | 4.76E-11 |
| Cyp2b13 | A_51_P492339 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 0.07 | 0 | 0.83 | 2.77E-08 | 0.83 | 0.000075 | 0.79 | 1.99E-06 |
| Cyp2b13 | A_52_P289091 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 0.06 | 0 | 0.51 | 8.94E-12 | 0.45 | 1.74E-30 | 0.49 | 1.51E-19 |
| Cyp2c29 | A_51_P103706 | NM_007815 | cytochrome P450, family 2, subfamily c, polypeptide 29 | 0.96 | 0.072755 | 0.30 | 0 | 0.37 | 0 | 0.46 | 7.98E-23 |
| Cyp2c37 | A_51_P498882 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 0.69 | 2.30E-20 | 0.23 | 0 | 0.32 | 0 | 0.39 | 4.71E-28 |
| Cyp2c37 | A_52_P625249 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 0.65 | 8.30E-30 | 0.22 | 0 | 0.30 | 0 | 0.37 | 8.70E-34 |
| Cyp2c38 | A_51_P342206 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 0.15 | 0 | 0.86 | 2.74E-07 | 0.82 | 2.15E-10 | 0.80 | 9.63E-08 |
| Cyp2c38 | A_52_P468564 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 0.12 | 0 | 0.72 | 7.49E-26 | 0.70 | 1.28E-20 | 0.64 | 0 |
| Cyp2c39 | A_51_P304109 | NM_010003 | cytochrome P450, family 2, subfamily c, polypeptide 39 | 0.73 | 5.65E-16 | 0.34 | 0 | 0.40 | 0 | 0.47 | 1.38E-35 |
| Cyp2c44 | A_51_P209782 | NM_001001446 | cytochrome P450, family 2, subfamily c, polypeptide 44 | 1.55 | 6.48E-37 | 0.45 | 0 | 0.52 | 1.58E-26 | 0.65 | 1.24E-14 |
| Cyp2c54 | A_52_P154580 | NM_206537 | cytochrome P450, family 2, subfamily c, polypeptide 54 | 0.58 | 3.52E-29 | 0.19 | 0 | 0.28 | 0 | 0.36 | 1.26E-32 |
| Cyp2c55 | A_51_P447785 | NM_028089 | cytochrome P450, family 2, subfamily c, polypeptide 55 | 1.05 | 0.327253 | 3.20 | 0 | 3.21 | 0 | 4.19 | 0 |
| Cyp2c70 | A_51_P134142 | NM_145499 | cytochrome P450, family 2, subfamily c, polypeptide 70 | 4.53 | 0 | 0.62 | 8.27E-30 | 1.08 | 0.183788 | 1.22 | 0.000753 |
| Cyp2d10 | A_51_P111192 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 1.19 | 2.69E-21 | 0.72 | 0 | 0.74 | 0 | 0.74 | 0 |
| Cyp2d10 | A_52_P527775 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 1.28 | 8.83E-17 | 0.63 | 0 | 0.62 | 0 | 0.61 | 0 |
| Cyp2d13 | A_52_P372062 | NM_133695 | cytochrome P450, family 2, subfamily d, polypeptide 13 | 1.78 | 0 | 0.53 | 0 | 0.56 | 0 | 0.55 | 0 |
| Cyp2d22 | A_52_P478420 | AK086555 | (Cyp2d13) on chromosome 15. | 0.94 | 0.159817 | 0.64 | 0 | 0.68 | 1.35E-14 | 0.69 | 2.53E-31 |
| Cyp2d22 | A_52_P49391 | AK090296 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 0.76 | 5.32E-30 | 0.68 | 0 | 0.68 | 0 | 0.73 | 3.36E-29 |
| Cyp2d9 | A_51_P124133 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 1.47 | 1.13E-22 | 0.73 | 7.26E-11 | 0.75 | 4.53E-17 | 0.78 | 4.80E-10 |
| Cyp2d9 | A_51_P478303 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 1.60 | 9.81E-45 | 0.75 | 3.13E-13 | 0.77 | 5.65E-06 | 0.77 | 1.89E-11 |
| Cyp2f2 | A_51_P453909 | NM_007817 | cytochrome P450, family 2, subfamily f, polypeptide 2 | 1.45 | 9.69E-16 | 0.93 | 0.074673 | 0.92 | 0.032242 | 1.01 | 0.65503 |
| Cyp2g1 | A_51_P137452 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 0.86 | 0.052464 | 0.23 | 0 | 0.25 | 1.16E-42 | 0.28 | 1.99E-22 |
| Cyp2j6 | A_51_P506328 | NM_010008 | cytochrome P450, family 2, subfamily j, polypeptide 6 | 1.17 | 7.20E-14 | 1.41 | 3.62E-21 | 1.36 | 5.73E-14 | 1.31 | 3.75E-10 |
| Cyp2j9 | A_51_P330044 | NM_028979 | cytochrome P450, family 2, subfamily j, polypeptide 9 | 0.63 | 0 | 0.48 | 2.40E-36 | 0.57 | 1.44E-15 | 0.53 | 0 |
| Cyp3a13 | A_51_P114941 | NM_007819 | cytochrome P450, family 3, subfamily a, polypeptide 13 | 0.49 | 0 | 0.56 | 1.03E-41 | 0.64 | 6.41E-37 | 0.67 | 5.69E-30 |
| Cyp3a25 | A_51_P489367 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 0.75 | 3.44E-09 | 0.45 | 0 | 0.51 | 0 | 0.50 | 0 |

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|----------|--------------|-----------|---|------|----------|------|----------|-------|----------|------|----------|
| Cyp3a44 | A_52_P366803 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 0.56 | 9.81E-23 | 0.61 | 1.34E-17 | 0.70 | 3.18E-22 | 0.83 | 0.000068 |
| Cyp4a10 | A_52_P257774 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.23 | 0 | 0.83 | 0.000044 | 0.92 | 0.113012 | 1.07 | 0.227687 |
| Cyp4a10 | A_52_P340136 | X71478 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.35 | 0 | 0.99 | 0.849133 | 1.01 | 0.946687 | 1.08 | 0.326539 |
| Cyp4a10 | A_52_P6588 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.11 | 0 | 0.89 | 0.171495 | 0.94 | 0.546311 | 1.12 | 0.246269 |
| Cyp4a12a | A_51_P433360 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 0.38 | 0 | 1.16 | 2.65E-08 | 1.18 | 0.000523 | 1.25 | 1.90E-10 |
| Cyp4a12a | A_52_P44914 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 0.91 | 0.030951 | 1.41 | 3.16E-13 | 1.26 | 0.004666 | 1.34 | 2.30E-09 |
| Cyp4a14 | A_51_P238576 | NM_007822 | cytochrome P450, family 4, subfamily a, polypeptide 14 | 0.03 | 0 | 1.13 | 0.122563 | 1.22 | 0.009042 | 1.39 | 2.67E-06 |
| Cyp4b1 | A_51_P118704 | NM_007823 | cytochrome P450, family 4, subfamily b, polypeptide 1 | 0.95 | 0.566855 | 1.20 | 5.75E-08 | 1.28 | 1.16E-09 | 1.25 | 2.98E-06 |
| Cyp4f14 | A_51_P452768 | NM_022434 | cytochrome P450, family 4, subfamily f, polypeptide 14 | 1.64 | 6.22E-33 | 0.29 | 0 | 0.39 | 0 | 0.36 | 0 |
| Cyp4f15 | A_51_P136303 | NM_134127 | cytochrome P450, family 4, subfamily f, polypeptide 15 | 0.90 | 0.000799 | 0.67 | 0 | 0.75 | 0 | 0.79 | 3.21E-29 |
| Cyp51 | A_51_P485791 | NM_020010 | cytochrome P450, family 51 | 0.72 | 0.005145 | 0.95 | 0.4062 | 1.05 | 0.494765 | 1.34 | 1.47E-10 |
| Cyp51 | A_52_P164161 | NM_020010 | cytochrome P450, family 51 | 0.65 | 0.0007 | 1.00 | 0.999137 | 1.03 | 0.669876 | 1.30 | 2.20E-11 |
| Dci | A_51_P105589 | NM_010023 | dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) | 0.83 | 2.16E-18 | 1.45 | 0 | 1.30 | 4.43E-35 | 1.29 | 1.03E-27 |
| Decr1 | A_51_P208555 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 0.82 | 8.62E-19 | 1.39 | 2.04E-30 | 1.27 | 8.78E-29 | 1.26 | 9.98E-12 |
| Decr1 | A_52_P335907 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 0.75 | 4.92E-23 | 1.43 | 0 | 1.35 | 4.42E-19 | 1.27 | 1.38E-08 |
| Dgat1 | A_51_P510059 | NM_010046 | diacylglycerol O-acyltransferase 1 | 0.81 | 6.90E-07 | 1.58 | 2.43E-20 | 1.64 | 9.08E-16 | 1.40 | 3.07E-10 |
| Dgat1 | A_52_P456134 | NM_010046 | diacylglycerol O-acyltransferase 1 | 0.80 | 2.10E-44 | 1.51 | 0 | 1.51 | 4.55E-26 | 1.40 | 3.38E-43 |
| Dgat2 | A_52_P592909 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.88 | 0.005614 | 1.11 | 0.001209 | 1.31 | 3.25E-12 | 1.06 | 0.011493 |
| Dlat | A_51_P265106 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 0.88 | 0.000033 | 1.92 | 0 | 1.91 | 0 | 1.75 | 0 |
| Dlat | A_52_P374642 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 0.89 | 0.000354 | 1.83 | 1.78E-36 | 1.93 | 0 | 1.80 | 3.10E-39 |
| Dld | A_51_P184284 | NM_007861 | dihydrolipoamide dehydrogenase | 0.97 | 0.406823 | 1.32 | 2.94E-25 | 1.25 | 7.94E-17 | 1.24 | 6.08E-09 |
| Dlst | A_51_P290139 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 0.84 | 1.78E-06 | 1.37 | 6.53E-22 | 1.37 | 2.55E-38 | 1.24 | 2.10E-08 |
| Dlst | A_52_P140072 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 0.82 | 0.009767 | 1.40 | 4.54E-07 | 1.38 | 0.000013 | 1.29 | 0.006086 |
| Ech1 | A_51_P421846 | NM_016772 | enoyl coenzyme A hydratase 1, peroxisomal | 0.61 | 0 | 1.35 | 3.52E-27 | 1.32 | 2.28E-20 | 1.28 | 6.85E-13 |
| Echs1 | A_51_P409039 | NM_053119 | enoyl Coenzyme A hydratase, short chain, 1, mitochondrial | 0.74 | 0 | 1.08 | 0.002361 | 1.10 | 6.03E-13 | 1.08 | 0.000037 |
| Ehhadh | A_51_P462918 | NM_023737 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase | 0.59 | 0 | 2.36 | 0 | 2.59 | 0 | 3.17 | 0 |
| Eno1 | A_52_P349939 | NM_023119 | enolase 1, alpha non-neuron | 0.60 | 1.86E-09 | 1.23 | 0.008352 | 1.08 | 0.411163 | 0.97 | 0.780398 |
| Eno3 | A_51_P328539 | NM_007933 | enolase 3, beta muscle | 0.96 | 0.243778 | 0.67 | 9.70E-27 | 0.68 | 3.95E-17 | 0.64 | 1.01E-24 |
| Fabp2 | A_51_P313581 | NM_007980 | fatty acid binding protein 2, intestinal | 0.65 | 0 | 1.38 | 2.27E-15 | 1.19 | 0.000048 | 1.13 | 0.013179 |
| Fabp2 | A_52_P453013 | NM_007980 | fatty acid binding protein 2, intestinal | 0.57 | 0 | 1.30 | 5.72E-20 | 1.16 | 9.70E-08 | 1.10 | 0.055047 |
| Fabp3 | A_51_P167535 | NM_010174 | fatty acid binding protein 3, muscle and heart | 0.56 | 1.14E-33 | 2.71 | 0 | 2.38 | 8.80E-24 | 1.82 | 2.40E-07 |
| Fabp4 | A_51_P336830 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.52 | 3.56E-26 | 8.96 | 0 | 10.73 | 0 | 9.87 | 3.98E-34 |

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|--------|---------------|-----------|---|------|----------|-------|----------|-------|----------|-------|----------|
| *Fabp4 | A_51_P336833 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.53 | 0 | 9.70 | 0 | 13.46 | 0 | 12.13 | 4.09E-32 |
| Fabp4 | A_52_P564544 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.33 | 8.34E-30 | 10.50 | 0 | 12.57 | 0 | 14.53 | 0 |
| Fabp5 | A_51_P387764 | NM_010634 | fatty acid binding protein 5, epidermal | 2.34 | 0.001486 | 14.61 | 0 | 7.69 | 0 | 16.17 | 0 |
| Fasn | A_51_P321126 | NM_007988 | fatty acid synthase | 0.38 | 1.09E-41 | 3.24 | 1.40E-45 | 4.22 | 1.25E-31 | 4.11 | 0 |
| *Fasn | A_52_P100252 | NM_007988 | fatty acid synthase | 0.37 | 2.88E-41 | 3.70 | 0 | 4.19 | 0 | 3.55 | 0 |
| *Fbp1 | A_51_P474701 | NM_019395 | fructose biphosphatase 1 | 0.50 | 6.45E-18 | 0.71 | 0.000066 | 0.63 | 7.07E-10 | 0.51 | 3.16E-18 |
| Fdft1 | A_51_P485946 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 0.54 | 1.41E-32 | 0.79 | 7.02E-14 | 0.86 | 0.006478 | 1.02 | 0.619059 |
| Fdps | A_51_P379798 | NM_134469 | farnesyl diphosphate synthetase | 0.68 | 6.93E-06 | 1.21 | 0.001048 | 1.52 | 3.11E-17 | 1.64 | 9.14E-14 |
| Fdps | A_52_P593965 | AK077979 | farnesyl diphosphate synthetase | 0.49 | 2.66E-16 | 1.39 | 6.62E-07 | 2.07 | 1.93E-17 | 2.04 | 0 |
| Fh1 | A_51_P359333 | NM_010209 | fumarate hydratase 1 | 0.76 | 3.03E-16 | 0.94 | 0.005397 | 0.92 | 0.002433 | 0.88 | 1.30E-17 |
| Fntb | A_51_P517680 | NM_145927 | farnesyltransferase, CAAX box, beta | 1.17 | 0.040671 | 1.45 | 1.85E-15 | 1.16 | 0.222952 | 1.02 | 0.748158 |
| *G6pc | A_51_P462385 | NM_008061 | glucose-6-phosphatase, catalytic | 0.46 | 0.000013 | 0.62 | 2.73E-23 | 0.59 | 1.48E-35 | 0.40 | 8.40E-39 |
| G6pd2 | A_51_P353735 | NM_019468 | glucose-6-phosphate dehydrogenase 2 | 1.00 | 1 | 1.53 | 0.178323 | 1.37 | 0.174128 | 2.96 | 9.02E-08 |
| G6pdx | A_51_P187082 | NM_008062 | glucose-6-phosphate dehydrogenase X-linked | 0.99 | 0.828139 | 2.64 | 0 | 4.05 | 0 | 3.72 | 0 |
| *Gapdh | A_52_P589321 | AK169742 | glyceraldehyde-3-phosphate dehydrogenase | 0.61 | 1.33E-07 | 0.77 | 0.000011 | 0.83 | 0.162769 | 0.72 | 9.59E-14 |
| Gck | A_52_P66580 | BC011139 | glucokinase | 1.49 | 6.85E-23 | 0.97 | 0.427453 | 0.87 | 0.001911 | 0.99 | 0.658739 |
| Gckr | A_51_P198694 | NM_144909 | glucokinase regulatory protein | 0.74 | 6.07E-14 | 0.61 | 3.32E-26 | 0.59 | 1.59E-26 | 0.55 | 2.43E-27 |
| *Gpd1 | A_51_P293853 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 0.71 | 5.06E-15 | 2.59 | 0 | 2.39 | 0 | 1.97 | 8.59E-19 |
| Gpd1 | A_52_P16419 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 0.64 | 3.11E-24 | 2.95 | 0 | 2.58 | 0 | 2.31 | 1.04E-32 |
| Gpi1 | A_51_P426886 | NM_008155 | glucose phosphate isomerase 1 | 0.91 | 4.96E-09 | 1.43 | 0 | 1.33 | 4.02E-25 | 1.26 | 4.93E-30 |
| Gpt2 | A_51_P493886 | NM_173866 | glutamic pyruvate transaminase (alanine aminotransferase) 2 | 0.43 | 0 | 0.93 | 0.02 | 0.90 | 0.00059 | 0.87 | 2.58E-06 |
| Gyg | A_51_P240019 | NM_013755 | glycogenin | 0.86 | 0.000102 | 1.25 | 4.40E-13 | 1.31 | 2.82E-11 | 1.29 | 8.31E-13 |
| Gyk | A_52_P1020291 | AK037633 | glycerol kinase | 1.00 | 0.997854 | 0.81 | 0.009583 | 0.75 | 0.001213 | 0.69 | 8.37E-07 |
| Gyk | A_52_P379205 | AK086200 | Mus musculus 16 days neonate thymus cDNA | 1.00 | 1 | 1.03 | 0.724656 | 1.00 | 1 | 1.03 | 0.799772 |
| Gys2 | A_51_P440315 | NM_145572 | glycogen synthase 2 | 1.12 | 0.022211 | 1.31 | 0 | 1.25 | 3.60E-42 | 1.21 | 1.36E-14 |
| Hadhb | A_51_P217990 | NM_145558 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase beta subunit | 0.94 | 0.03782 | 1.53 | 0 | 1.39 | 2.69E-31 | 1.32 | 2.82E-11 |
| Hk1 | A_52_P102773 | BC072628 | hexokinase 1 | 0.94 | 0.190425 | 1.27 | 2.14E-18 | 1.30 | 1.95E-15 | 1.25 | 1.40E-12 |
| Hk1 | A_52_P9337 | NM_010438 | hexokinase 1 | 1.49 | 6.69E-08 | 1.15 | 0.548976 | 0.91 | 0.508841 | 1.09 | 0.531832 |
| Hmgcl | A_51_P308961 | NM_008254 | 3-hydroxy-3-methylglutaryl-Coenzyme A lyase | 0.78 | 6.91E-09 | 1.97 | 0 | 2.00 | 0 | 1.88 | 4.20E-45 |
| Hmgcr | A_51_P507410 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.52 | 5.89E-44 | 0.66 | 3.67E-09 | 0.92 | 0.386439 | 1.20 | 0.000061 |
| Hmgcr | A_52_P137371 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.48 | 0 | 0.67 | 3.48E-06 | 0.90 | 0.355384 | 1.34 | 2.75E-08 |
| Hmgcr | A_52_P232287 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.52 | 0 | 0.66 | 2.16E-11 | 0.95 | 0.601767 | 1.20 | 0.000469 |
| Hmgcr | A_52_P578922 | AK159899 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.43 | 4.09E-37 | 0.68 | 5.73E-06 | 0.94 | 0.580606 | 1.43 | 7.16E-13 |
| Hmgcr | A_52_P770765 | AK033165 | Mus musculus 15 days embryo male testis cDNA, RIKEN | 0.68 | 4.60E-07 | 0.67 | 2.93E-06 | 1.09 | 0.431686 | 1.57 | 9.55E-13 |

full-length enriched library, clone:8030450I20

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|---------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Hmgcs1 | A_51_P146941 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.35 | 6.00E-16 | 1.27 | 1.18E-07 | 1.45 | 0.000065 | 1.91 | 2.44E-37 |
| Hmgcs1 | A_52_P119039 | AK078743 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.39 | 3.28E-13 | 2.85 | 1.10E-10 | 1.17 | 0.398813 | 2.66 | 3.51E-14 |
| Hmgcs1 | A_52_P388072 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.40 | 2.20E-23 | 1.30 | 7.51E-09 | 1.44 | 3.22E-08 | 1.67 | 0 |
| Hmgcs2 | A_51_P116039 | NM_008256 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 | 0.76 | 5.87E-06 | 0.91 | 0.109208 | 0.78 | 6.29E-06 | 0.73 | 5.20E-06 |
| Hsd17b4 | A_51_P445662 | NM_008292 | hydroxysteroid (17-beta) dehydrogenase 4 | 0.89 | 4.48E-10 | 1.43 | 0 | 1.44 | 0 | 1.35 | 0 |
| ldh2 | A_51_P331507 | NM_173011 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 0.59 | 0 | 1.25 | 7.74E-13 | 1.23 | 2.82E-14 | 1.13 | 1.81E-06 |
| ldi1 | A_51_P329711 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.62 | 0.000572 | 0.94 | 0.282964 | 1.01 | 0.864314 | 1.40 | 2.78E-23 |
| ldi1 | A_52_P441634 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.64 | 4.74E-12 | 0.86 | 0.040286 | 1.03 | 0.693076 | 1.38 | 8.77E-20 |
| Ldha | A_51_P364140 | NM_010699 | lactate dehydrogenase A | 0.65 | 1.90E-11 | 1.06 | 0.489608 | 0.91 | 0.183186 | 0.87 | 0.01318 |
| Ldha | A_51_P364146 | NM_010699 | lactate dehydrogenase A | 0.70 | 2.12E-09 | 1.12 | 0.000081 | 0.98 | 0.432887 | 0.95 | 0.178837 |
| Ldhb | A_51_P409173 | NM_008492 | lactate dehydrogenase B | 1.13 | 5.39E-06 | 1.60 | 2.05E-41 | 1.62 | 8.44E-32 | 1.67 | 0 |
| Lipe | A_51_P435363 | NM_010719 | lipase, hormone sensitive | 0.82 | 0.000756 | 1.20 | 0.005894 | 1.34 | 1.13E-16 | 1.25 | 1.77E-07 |
| *Lipe | A_51_P435366 | NM_010719 | lipase, hormone sensitive | 0.84 | 6.30E-08 | 1.22 | 0.059524 | 1.40 | 1.39E-12 | 1.24 | 9.41E-13 |
| Lpl | A_51_P259296 | NM_008509 | lipoprotein lipase | 1.76 | 1.81E-24 | 4.19 | 0 | 5.63 | 0 | 6.89 | 0 |
| *Lpl | A_52_P257812 | NM_008509 | lipoprotein lipase | 1.66 | 1.34E-24 | 3.24 | 0 | 4.41 | 0 | 4.56 | 0 |
| Mdh1 | A_52_P407796 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 0.75 | 1.21E-11 | 1.01 | 0.808442 | 1.09 | 0.072866 | 0.99 | 0.909665 |
| Mdh2 | A_51_P384879 | NM_008617 | malate dehydrogenase 2, NAD (mitochondrial) | 0.94 | 0.038595 | 1.43 | 0 | 1.34 | 3.39E-30 | 1.33 | 2.66E-41 |
| Mgll | A_51_P139920 | NM_011844 | monoglyceride lipase | 0.80 | 1.08E-29 | 1.49 | 0 | 1.35 | 1.26E-44 | 1.23 | 5.04E-07 |
| *Mgll | A_52_P568977 | AK006949 | monoglyceride lipase | 0.77 | 0.000274 | 0.90 | 0.232786 | 0.88 | 0.255047 | 0.66 | 0.000346 |
| Mgll | A_52_P609778 | NM_011844 | monoglyceride lipase | 0.84 | 3.57E-12 | 1.59 | 0 | 1.41 | 0 | 1.29 | 3.28E-08 |
| Mvd | A_51_P355943 | NM_138656 | mevalonate (diphospho) decarboxylase | 0.40 | 1.36E-43 | 1.29 | 0.000837 | 1.35 | 0.000156 | 1.62 | 1.17E-18 |
| Mvk | A_51_P169527 | NM_023556 | mevalonate kinase | 0.93 | 0.253595 | 0.77 | 0.000037 | 0.77 | 0.000305 | 0.93 | 0.225421 |
| Mvk | A_52_P569067 | NM_023556 | mevalonate kinase | 0.82 | 0.001071 | 0.73 | 1.51E-12 | 0.80 | 0.000418 | 0.93 | 0.00352 |
| Oxct1 | A_51_P107321 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.30 | 7.23E-10 | 1.38 | 1.86E-11 | 1.29 | 2.77E-14 | 1.40 | 7.08E-11 |
| Oxct1 | A_51_P107326 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.35 | 0 | 1.28 | 2.20E-17 | 1.24 | 8.59E-11 | 1.44 | 1.76E-33 |
| Oxct1 | A_52_P430058 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.19 | 0.000017 | 1.33 | 1.70E-08 | 1.37 | 2.19E-07 | 1.50 | 1.73E-06 |
| Pcca | A_51_P484254 | NM_144844 | propionyl-Coenzyme A carboxylase, alpha polypeptide | 0.73 | 2.61E-26 | 1.04 | 0.200605 | 1.03 | 0.33632 | 1.00 | 0.936793 |
| Pck2 | A_52_P21659 | NM_028994 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | 1.11 | 0.000025 | 1.45 | 0 | 1.26 | 5.82E-09 | 1.35 | 2.13E-13 |
| Pcx | A_51_P480578 | NM_008797 | pyruvate carboxylase | 0.74 | 7.36E-10 | 1.81 | 4.88E-24 | 1.62 | 2.03E-21 | 1.63 | 8.96E-17 |
| Pdha1 | A_51_P321391 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 0.95 | 0.022316 | 1.35 | 0 | 1.37 | 0 | 1.29 | 0 |
| Pdha1 | A_52_P581435 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 0.80 | 4.68E-15 | 1.45 | 0 | 1.46 | 0 | 1.39 | 0 |
| *Pdk4 | A_51_P350453 | NM_013743 | pyruvate dehydrogenase kinase, isoenzyme 4 | 0.25 | 1.85E-37 | 3.37 | 0 | 2.22 | 0 | 2.05 | 0 |
| Pecr | A_51_P291749 | NM_023523 | peroxisomal trans-2-enoyl-CoA reductase | 0.82 | 9.44E-31 | 0.57 | 0 | 0.62 | 0 | 0.64 | 1.14E-36 |
| Pfkfb2 | A_51_P184849 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 0.86 | 0.031749 | 0.58 | 0 | 0.63 | 6.43E-24 | 0.64 | 1.40E-45 |

| | | | | | | | | | | | |
|----------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Pfkfb2 | A_52_P142912 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 0.85 | 0.06141 | 0.57 | 2.05E-17 | 0.69 | 3.58E-06 | 0.67 | 4.04E-09 |
| Pfkl | A_51_P310896 | NM_008826 | phosphofructokinase, liver, B-type | 0.76 | 2.77E-06 | 1.01 | 0.902909 | 1.01 | 0.829962 | 0.91 | 0.152082 |
| Pgam1 | A_51_P342669 | NM_023418 | phosphoglycerate mutase 1 | 0.87 | 7.17E-12 | 1.56 | 0 | 1.59 | 0 | 1.49 | 0 |
| Pgam2 | A_51_P264495 | NM_018870 | phosphoglycerate mutase 2 | 0.71 | 4.07E-12 | 1.30 | 0.000013 | 1.34 | 4.56E-09 | 1.33 | 6.16E-11 |
| Pgd | A_51_P391996 | BC011329 | phosphogluconate dehydrogenase | 0.69 | 1.56E-10 | 1.93 | 0 | 1.82 | 2.35E-28 | 1.82 | 4.84E-30 |
| *Pgd | A_52_P84096 | BC011329 | phosphogluconate dehydrogenase | 0.67 | 3.17E-40 | 2.17 | 0 | 2.16 | 0 | 1.92 | 0 |
| Pgk1 | A_51_P182828 | NM_008828 | phosphoglycerate kinase 1 | 0.73 | 0 | 1.21 | 0 | 1.16 | 8.26E-21 | 1.09 | 4.40E-12 |
| Pgk1 | A_52_P600398 | NM_008828 | phosphoglycerate kinase 1 | 0.73 | 3.74E-36 | 1.19 | 3.80E-26 | 1.14 | 5.21E-12 | 1.10 | 1.43E-07 |
| Pgm1 | A_51_P427530 | NM_025700 | phosphoglucomutase 1 | 0.76 | 5.53E-13 | 1.02 | 0.427022 | 1.12 | 0.013984 | 1.16 | 4.47E-07 |
| Pgm3 | A_51_P208987 | NM_028352 | phosphoglucomutase 3 | 3.16 | 0 | 1.12 | 0.014164 | 1.05 | 0.182808 | 1.07 | 0.085847 |
| Pgm3 | A_52_P341449 | NM_028352 | phosphoglucomutase 3 | 0.96 | 0.402342 | 1.37 | 9.63E-20 | 1.45 | 2.67E-13 | 1.35 | 2.05E-18 |
| Pgm5 | A_52_P229924 | NM_175013 | phosphoglucomutase 5 | 0.81 | 0.00044 | 1.67 | 1.86E-12 | 1.40 | 0.001732 | 1.25 | 0.000377 |
| Phkb | A_51_P307624 | NM_199446 | phosphorylase kinase beta | 1.10 | 0.000013 | 1.35 | 9.18E-34 | 1.34 | 1.97E-17 | 1.30 | 5.20E-15 |
| Phkb | A_52_P513347 | NM_199446 | phosphorylase kinase beta | 1.07 | 0.140703 | 1.45 | 5.61E-45 | 1.47 | 1.77E-25 | 1.38 | 2.37E-19 |
| Phkg2 | A_51_P235909 | NM_026888 | phosphorylase kinase, gamma 2 (testis) | 1.05 | 0.207425 | 0.75 | 4.23E-18 | 0.77 | 2.50E-14 | 0.79 | 5.19E-13 |
| Phkg2 | A_52_P19446 | AK089062 | phosphorylase kinase, gamma 2 (testis) | 1.07 | 0.354708 | 0.61 | 9.04E-06 | 0.68 | 1.24E-09 | 0.49 | 0.002143 |
| *Pklr | A_51_P176042 | NM_013631 | pyruvate kinase liver and red blood cell | 0.49 | 0 | 0.83 | 1.13E-09 | 0.76 | 6.83E-18 | 0.67 | 1.41E-11 |
| Pkm2 | A_51_P428913 | D38379 | pyruvate kinase, muscle | 0.68 | 8.81E-11 | 1.29 | 1.07E-14 | 1.27 | 2.33E-10 | 1.31 | 5.43E-08 |
| Pkm2 | A_52_P150212 | NM_011099 | pyruvate kinase, muscle | 0.66 | 1.55E-12 | 1.25 | 9.24E-06 | 1.33 | 1.15E-07 | 1.25 | 0.000367 |
| Pkm2 | A_52_P328249 | AK083076 | pyruvate kinase, muscle | 0.82 | 0.002 | 1.28 | 0.000395 | 1.05 | 0.601695 | 1.29 | 6.97E-06 |
| Pmvk | A_51_P492408 | NM_026784 | phosphomevalonate kinase | 0.66 | 1.97E-12 | 1.33 | 1.22E-11 | 1.59 | 1.72E-26 | 1.68 | 0 |
| Pmvk | A_51_P492410 | NM_026784 | phosphomevalonate kinase | 0.66 | 4.92E-10 | 1.36 | 5.92E-10 | 1.60 | 1.19E-28 | 1.71 | 0 |
| Pparg | A_51_P106799 | NM_011146 | peroxisome proliferator activated receptor gamma | 0.41 | 0 | 1.28 | 8.17E-20 | 1.36 | 7.05E-32 | 1.23 | 2.11E-29 |
| Ppargc1a | A_51_P279038 | NM_008904 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 0.76 | 1.34E-06 | 0.65 | 7.51E-19 | 0.62 | 0 | 0.63 | 1.39E-19 |
| Ppargc1a | A_52_P5945 | AK032149 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 0.61 | 8.10E-20 | 0.59 | 5.19E-24 | 0.57 | 2.51E-28 | 0.57 | 0 |
| Ppargc1b | A_52_P526724 | NM_133249 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.06 | 0.377187 | 0.72 | 1.20E-21 | 0.67 | 8.78E-30 | 0.80 | 5.72E-14 |
| Pygb | A_51_P485810 | NM_153781 | brain glycogen phosphorylase | 0.62 | 0.006731 | 1.24 | 0.022984 | 1.17 | 0.242466 | 1.48 | 0.001698 |
| Pygb | A_52_P350664 | NM_153781 | brain glycogen phosphorylase | 0.86 | 0.039899 | 1.35 | 0.000021 | 1.20 | 0.007881 | 1.39 | 0.00035 |
| *Scd1 | A_52_P682382 | NM_009127 | stearoyl-Coenzyme A desaturase 1 | 0.55 | 1.29E-25 | 5.55 | 0 | 5.84 | 0 | 4.87 | 0 |
| Scd2 | A_51_P129464 | NM_009128 | stearoyl-Coenzyme A desaturase 2 | 0.56 | 0 | 1.43 | 1.03E-08 | 2.07 | 7.01E-45 | 2.51 | 0 |
| Scd3 | A_51_P446045 | NM_024450 | stearoyl-coenzyme A desaturase 3 | 1.35 | 1.26E-15 | 1.04 | 0.508828 | 1.05 | 0.624767 | 1.11 | 0.031111 |
| Scd4 | A_52_P374877 | NM_183216 | stearoyl-coenzyme A desaturase 4 | 1.09 | 0.319806 | 0.69 | 0.00002 | 0.72 | 0.069299 | 0.76 | 0.002199 |
| Slc27a1 | A_51_P117477 | NM_011977 | solute carrier family 27 (fatty acid transporter), member 1 | 0.93 | 0.023386 | 0.67 | 0 | 0.70 | 4.98E-22 | 0.76 | 1.63E-17 |
| Slc27a1 | A_52_P199905 | CB588406 | AGENCOURT_12600125 NIH_MGC_136 Mus musculus | 0.57 | 0 | 0.78 | 2.87E-11 | 0.96 | 0.296208 | 1.02 | 0.703983 |

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|---------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|--|--|
| | | | cDNA clone IMAGE:30290747 5', mRNA sequence. | | | | | | | | | | |
| Slc27a4 | A_51_P408609 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 0.60 | 3.38E-07 | 1.87 | 8.61E-14 | 2.16 | 3.07E-15 | 1.62 | 8.40E-17 | | |
| Slc27a4 | A_52_P61854 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 0.63 | 2.49E-16 | 2.01 | 0 | 2.07 | 0 | 1.79 | 1.30E-18 | | |
| Slc27a5 | A_51_P289742 | NM_009512 | solute carrier family 27 (fatty acid transporter), member 5 | 0.87 | 6.64E-14 | 0.61 | 0 | 0.69 | 0 | 0.73 | 5.80E-11 | | |
| *Slc2a2 | A_51_P185693 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 0.73 | 2.28E-17 | 0.73 | 1.40E-45 | 0.68 | 0 | 0.75 | 3.67E-35 | | |
| Slc2a2 | A_52_P409988 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 0.74 | 5.71E-16 | 0.78 | 2.50E-26 | 0.70 | 0 | 0.75 | 4.88E-22 | | |
| Slc2a4 | A_51_P217498 | NM_009204 | solute carrier family 2 (facilitated glucose transporter), member 4 | 0.23 | 0 | 0.49 | 1.75E-33 | 0.60 | 0 | 0.54 | 1.18E-23 | | |
| Sqle | A_51_P450487 | NM_009270 | squalene epoxidase | 0.43 | 4.39E-07 | 1.00 | 0.997371 | 1.12 | 0.06438 | 1.45 | 1.38E-08 | | |
| Suc1g1 | A_51_P491227 | NM_019879 | succinate-CoA ligase, GDP-forming, alpha subunit | 0.87 | 0.000817 | 1.48 | 0 | 1.44 | 0 | 1.34 | 5.36E-11 | | |
| Suc1g2 | A_51_P478672 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 0.67 | 1.22E-16 | 1.43 | 7.93E-21 | 1.37 | 6.10E-11 | 1.21 | 2.88E-06 | | |
| Suc1g2 | A_52_P58181 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 0.64 | 0 | 1.23 | 0 | 1.21 | 2.80E-45 | 1.19 | 6.71E-19 | | |
| *Taldo1 | A_51_P401958 | NM_011528 | transaldolase 1 | 0.86 | 0.000032 | 2.20 | 0 | 2.06 | 0 | 1.80 | 4.91E-32 | | |
| *Tkt | A_51_P394515 | NM_009388 | transketolase | 0.73 | 0 | 1.73 | 0 | 1.72 | 5.61E-45 | 1.52 | 1.62E-32 | | |
| Tkt | A_52_P624447 | NM_009388 | transketolase | 0.43 | 6.35E-39 | 1.88 | 2.82E-34 | 2.25 | 0 | 1.65 | 0 | | |
| Ucp2 | A_51_P297105 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.66 | 1.96E-19 | 1.96 | 1.06E-32 | 1.80 | 7.75E-39 | 1.72 | 5.56E-22 | | |
| Ucp2 | A_52_P90265 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.47 | 0.000083 | 2.21 | 2.15E-27 | 1.80 | 0.000043 | 1.76 | 8.45E-09 | | |
| Ugp2 | A_51_P475580 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 0.89 | 3.23E-12 | 0.72 | 3.72E-30 | 0.74 | 1.40E-45 | 0.68 | 0 | | |
| Ugp2 | A_52_P42242 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 0.94 | 0.083301 | 0.67 | 0 | 0.68 | 0 | 0.63 | 0 | | |
| Uqcrc2 | A_51_P128648 | NM_025899 | ubiquinol cytochrome c reductase core protein 2 | 1.04 | 0.035657 | 1.3 | 0 | 1.25 | 9.97E-24 | 1.27 | 1.31E-36 | | |
| Acaa2 | A_51_P125260 | NM_177470 | acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) | 0.88 | 0.00002 | 0.98 | 0.366542 | 0.92 | 0.004398 | 0.92 | 0.000624 | | |
| Acad11 | A_51_P299260 | AK041180 | acyl-Coenzyme A dehydrogenase family, member 11 | 1.04 | 0.428559 | 1.10 | 0.095141 | 1.05 | 0.525505 | 1.11 | 0.003956 | | |
| Acad8 | A_51_P244052 | NM_025862 | acyl-Coenzyme A dehydrogenase family, member 8 | 0.96 | 0.265814 | 1.22 | 2.17E-07 | 1.21 | 5.13E-09 | 1.18 | 0.000025 | | |
| Acad9 | A_52_P73208 | AK049931 | acyl-Coenzyme A dehydrogenase family, member 9 | 0.74 | 0.008099 | 0.82 | 0.001363 | 0.90 | 0.393173 | 0.75 | 0.010289 | | |
| Acad5b | A_51_P435068 | NM_025826 | acyl-Coenzyme A dehydrogenase, short/branched chain | 1.17 | 0.000014 | 0.78 | 1.58E-27 | 0.79 | 3.19E-10 | 0.78 | 3.71E-21 | | |
| Acad1l | A_51_P518340 | NM_017366 | acyl-Coenzyme A dehydrogenase, very long chain | 0.97 | 0.599988 | 1.18 | 0.000415 | 1.11 | 0.055613 | 1.11 | 0.047656 | | |
| Acat2 | A_51_P139748 | NM_009338 | acetyl-Coenzyme A acetyltransferase 2 | 0.92 | 0.000014 | 0.86 | 2.21E-07 | 0.78 | 3.15E-31 | 0.80 | 1.59E-22 | | |
| Aco1 | A_51_P391082 | NM_007386 | aconitase 1 | 0.88 | 4.04E-18 | 1.07 | 0.000019 | 1.05 | 0.068426 | 1.05 | 0.002156 | | |
| Aco1 | A_52_P299115 | NM_007386 | aconitase 1 | 0.87 | 8.09E-07 | 1.16 | 3.84E-06 | 1.12 | 0.000097 | 1.07 | 0.042343 | | |
| Aco2 | A_52_P899263 | AK029122 | Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732494K09 | 1.76 | 0.047728 | 0.61 | 0.172401 | 0.87 | 0.302033 | 0.92 | 0.638024 | | |
| Acox3 | A_52_P745 | NM_030721 | acyl-Coenzyme A oxidase 3, pristanoyl | 1.26 | 4.54E-14 | 1.02 | 0.456749 | 0.99 | 0.618229 | 0.96 | 0.116135 | | |
| Acs16 | A_51_P518823 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | | |
| Acs16 | A_52_P204459 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 1.00 | 1 | 0.98 | 0.814953 | 1.00 | 1 | 1.00 | 1 | | |
| Acs16 | A_52_P352187 | NM_001033599 | acyl-CoA synthetase long-chain family member 6 | 1.17 | 0.499166 | 0.99 | 0.971515 | 0.82 | 0.42818 | 1.14 | 0.346036 | | |

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|---------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|
| Adcy1 | A_51_P196718 | NM_009622 | adenylate cyclase 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Adcy1 | A_51_P409900 | NM_009622 | adenylate cyclase 1 | 0.73 | 0.003189 | 1.06 | 0.759762 | 0.88 | 0.638585 | 1.16 | 0.476661 |
| Adcy2 | A_51_P337523 | NM_153534 | adenylate cyclase 2 | 0.97 | 0.83704 | 0.93 | 0.665948 | 1.00 | 1 | 0.71 | 0.195467 |
| Adcy2 | A_52_P165610 | NM_153534 | adenylate cyclase 2 | 1.00 | 1 | 1.00 | 1 | 0.96 | 0.773957 | 1.00 | 1 |
| Adcy3 | A_51_P484671 | NM_138305 | adenylate cyclase 3 | 0.89 | 0.55499 | 1.19 | 0.44025 | 0.85 | 0.481756 | 1.20 | 0.331218 |
| Adcy3 | A_52_P216525 | NM_138305 | adenylate cyclase 3 | 1.04 | 0.908022 | 1.12 | 0.577074 | 1.01 | 0.969592 | 1.19 | 0.518511 |
| Adcy5 | A_51_P199041 | NM_001012765 | adenylate cyclase 5 | 0.99 | 0.922111 | 1.15 | 0.210692 | 1.23 | 0.003304 | 1.14 | 0.221374 |
| Adcy5 | A_52_P449208 | NM_001012765 | adenylate cyclase 5 | 0.99 | 0.910976 | 1.42 | 0.170767 | 1.28 | 0.228457 | 0.80 | 0.354012 |
| Adcy6 | A_51_P243134 | NM_007405 | adenylate cyclase 6 | 0.95 | 0.174433 | 1.27 | 3.16E-32 | 1.26 | 1.47E-27 | 1.25 | 6.57E-16 |
| Adcy7 | A_51_P441622 | NM_007406 | adenylate cyclase 7 | 0.82 | 0.067813 | 1.22 | 0.038712 | 1.26 | 0.025238 | 1.18 | 0.185388 |
| Adcy7 | A_52_P291 | AK012436 | adenylate cyclase 7 | 0.74 | 0.029114 | 1.09 | 0.607726 | 1.74 | 0.012668 | 1.22 | 0.340609 |
| Adcy7 | A_52_P586141 | NM_001037724 | Mus musculus 11 days embryo whole body cDNA, RIKEN library, clone:2700055K03 product:adenylate cyclase 7 | 0.85 | 0.000634 | 1.14 | 5.97E-06 | 1.14 | 0.017144 | 1.18 | 0.014898 |
| Adcy8 | A_51_P303061 | NM_009623 | adenylate cyclase 8 | 0.99 | 0.935242 | 1.00 | 1 | 1.00 | 1 | 0.91 | 0.640409 |
| Adh1 | A_51_P428555 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.96 | 0.096899 | 1.21 | 9.43E-10 | 1.18 | 2.67E-06 | 1.25 | 3.63E-18 |
| Adh1 | A_52_P835985 | AK082149 | alcohol dehydrogenase 1 (class I) | 0.91 | 0.69527 | 1.30 | 0.111469 | 1.06 | 0.808921 | 1.54 | 0.004892 |
| Adh5 | A_51_P404275 | NM_007410 | alcohol dehydrogenase 5 (class III), chi polypeptide | 0.89 | 0.000063 | 0.90 | 0.000247 | 0.90 | 7.30E-07 | 0.95 | 0.091475 |
| Adh6a | A_51_P299608 | AK028114 | alcohol dehydrogenase 6A (class V) | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Adh6a | A_52_P276348 | AK007397 | alcohol dehydrogenase 6A (class V) | 1.00 | 0.997735 | 1.16 | 0.535519 | 1.00 | 1 | 1.14 | 0.499748 |
| Agpat1 | A_52_P200465 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 0.80 | 0.000143 | 0.96 | 0.076962 | 0.98 | 0.33829 | 1.01 | 0.796498 |
| Agpat3 | A_51_P425490 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 0.90 | 0.000062 | 1.11 | 0.000046 | 1.01 | 0.844256 | 1.06 | 0.029224 |
| Agpat3 | A_52_P523569 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 0.86 | 2.27E-10 | 0.99 | 0.766537 | 0.92 | 5.45E-06 | 0.91 | 0.000878 |
| Agpat4 | A_51_P346165 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 0.99 | 0.705586 | 1.17 | 4.87E-11 | 1.26 | 4.45E-19 | 1.25 | 1.13E-11 |
| Agpat4 | A_52_P3029 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 0.99 | 0.607444 | 1.17 | 1.20E-08 | 1.26 | 1.90E-12 | 1.26 | 1.98E-15 |
| Agpat5 | A_52_P572447 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 1.00 | 0.996347 | 1.04 | 0.108555 | 1.09 | 8.78E-06 | 1.10 | 6.51E-15 |
| Alb | A_51_P160713 | NM_009654 | albumin | 0.82 | 0.063363 | 1.09 | 0.343172 | 1.01 | 0.949874 | 1.21 | 0.048001 |
| Aldh1a2 | A_52_P58145 | NM_009022 | aldehyde dehydrogenase family 1, subfamily A2 | 0.90 | 0.239352 | 0.82 | 0.011334 | 0.95 | 0.410671 | 0.98 | 0.753457 |
| Aldh1a3 | A_52_P113518 | AK086764 | aldehyde dehydrogenase family 1, subfamily A3 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Aldh2 | A_52_P116134 | NM_009656 | aldehyde dehydrogenase 2, mitochondrial | 1.01 | 0.773145 | 0.80 | 3.20E-07 | 0.82 | 3.08E-06 | 0.82 | 0.000027 |
| Aldh3a1 | A_51_P310594 | NM_007436 | aldehyde dehydrogenase family 3, subfamily A1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 0.99 | 0.833108 |
| Aldh4a1 | A_52_P123230 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 0.74 | 0.015549 | 1.02 | 0.846919 | 0.91 | 0.393784 | 1.12 | 0.328169 |
| Aldh5a1 | A_51_P491504 | NM_172532 | aldehyde dehydrogenase family 5, subfamily A1 | 1.01 | 0.689756 | 1.21 | 5.56E-22 | 1.25 | 1.27E-29 | 1.26 | 1.30E-29 |
| Aldh5a1 | A_52_P30273 | AK051603 | aldehyde dehydrogenase family 5, subfamily A1 | 0.84 | 0.253295 | 1.31 | 0.204899 | 1.08 | 0.692244 | 1.11 | 0.554028 |
| Aldh7a1 | A_52_P503071 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 0.76 | 0.00726 | 0.92 | 0.387891 | 0.91 | 0.364665 | 0.88 | 0.26421 |

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|----------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Apob | A_51_P380650 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 1.21 | 7.90E-06 | 1.12 | 0.004106 | 0.98 | 0.503855 | 1.10 | 0.050494 |
| Apob | A_51_P413088 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 1.22 | 4.20E-08 | 1.10 | 0.032571 | 1.09 | 0.024028 | 1.19 | 2.69E-06 |
| Apob | A_51_P436690 | BC028880 | Mus musculus apolipoprotein B (Apob), mRNA. | 1.28 | 3.06E-13 | 1.13 | 0.001723 | 1.09 | 0.002936 | 1.17 | 5.80E-09 |
| Apob | A_51_P470542 | XM_137955 | apolipoprotein B | 1.03 | 0.384535 | 0.90 | 0.000306 | 0.86 | 0.000043 | 0.81 | 9.83E-10 |
| Apob | A_52_P441070 | NM_009693 | apolipoprotein B | 1.01 | 0.788954 | 0.95 | 0.009214 | 0.87 | 3.52E-15 | 0.82 | 1.92E-14 |
| Apoc1 | A_51_P164504 | NM_007469 | apolipoprotein C-I | 1.04 | 0.792442 | 0.98 | 0.898478 | 1.00 | 0.97685 | 0.95 | 0.693941 |
| Apoe | A_51_P171999 | NM_009696 | apolipoprotein E | 1.02 | 0.896869 | 1.19 | 0.211645 | 1.26 | 0.098964 | 1.15 | 0.312869 |
| Atp5a1 | A_52_P674489 | NM_007505 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 | 0.9 | 0.012 | 1.02 | 0.633544 | 1.14 | 0.000845 | 1.03 | 0.490052 |
| Atp5b | A_51_P207636 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 0.98 | 0.356308 | 1.23 | 3.62E-22 | 1.22 | 0 | 1.16 | 2.30E-26 |
| Atp5b | A_52_P328078 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 0.95 | 0.40001 | 1.17 | 0.022786 | 1.19 | 0.012458 | 1.08 | 0.275166 |
| Atp5b | A_52_P553841 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 0.97 | 0.605303 | 1.21 | 0.000013 | 1.16 | 0.005251 | 1.16 | 0.003521 |
| Atp5c1 | A_51_P378087 | NM_020615 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | 1.04 | 0.059963 | 1.15 | 0.000036 | 1.18 | 5.42E-13 | 1.15 | 1.69E-08 |
| Atp5e | A_51_P362054 | NM_025983 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit | 1.04 | 0.049145 | 1.01 | 0.655265 | 1.03 | 0.10105 | 0.99 | 0.605945 |
| Atp5h | A_51_P264186 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 0.99 | 0.671692 | 1.04 | 0.008003 | 1.07 | 0.000445 | 1.05 | 0.001581 |
| Atp5h | A_52_P640355 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 0.97 | 0.090714 | 1.03 | 0.27143 | 1.04 | 0.024492 | 1.03 | 0.215367 |
| Atp5k | A_51_P301289 | NM_007507 | ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e | 1.07 | 0.048024 | 1.13 | 0.000039 | 1.16 | 6.70E-07 | 1.08 | 0.02929 |
| Atp6ap1 | A_51_P447988 | NM_018794 | ATPase, H+ transporting, lysosomal accessory protein 1 | 1.00 | 0.996873 | 0.95 | 0.14633 | 0.92 | 0.008952 | 0.93 | 0.033918 |
| Atp6v0a1 | A_51_P142089 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.90 | 4.70E-11 | 0.88 | 2.54E-07 | 0.87 | 2.13E-08 | 0.89 | 1.04E-13 |
| Atp6v0a1 | A_52_P399998 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.88 | 0.017629 | 0.97 | 0.597649 | 0.91 | 0.265117 | 1.09 | 0.351065 |
| Atp6v0a1 | A_52_P515336 | AK045877 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 1.04 | 0.337179 | 0.89 | 0.000272 | 0.90 | 0.186745 | 0.97 | 0.336444 |
| Atp6v1b2 | A_51_P190845 | NM_007509 | ATPase, H+ transporting, lysosomal V1 subunit B2 | 0.86 | 0.024953 | 1.05 | 0.43546 | 1.00 | 0.979399 | 1.05 | 0.547874 |
| Atp6v1c2 | A_51_P518600 | NM_133699 | ATPase, H+ transporting, lysosomal V1 subunit C2 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.10 | 0.643168 |
| Atp6v1e1 | A_51_P166434 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 0.97 | 0.470883 | 1.22 | 9.40E-08 | 1.11 | 0.017259 | 1.18 | 0.002743 |
| Atp6v1e1 | A_52_P303388 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 1.02 | 0.738669 | 1.24 | 7.49E-06 | 1.13 | 0.015844 | 1.17 | 0.001813 |
| Atp6v1g1 | A_51_P140171 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 1.03 | 0.219316 | 1.05 | 0.085816 | 1.06 | 0.004339 | 1.11 | 0.000964 |
| Atp6v1g1 | A_52_P349738 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 0.98 | 0.195864 | 1.06 | 0.003334 | 1.09 | 0.000012 | 1.15 | 1.43E-13 |
| Atp6v1h | A_52_P112888 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.83 | 0.000342 | 1.19 | 1.09E-11 | 1.15 | 6.08E-09 | 1.68 | 4.31E-09 |
| Atp6v1h | A_52_P403420 | AK081492 | ATPase, H+ transporting, lysosomal V1 subunit H | 1.22 | 0.033537 | 1.11 | 0.169795 | 0.81 | 0.062047 | 1.22 | 0.075106 |
| Atp7a | A_51_P312497 | NM_009726 | ATPase, Cu++ transporting, alpha polypeptide | 1.13 | 6.03E-08 | 1.20 | 9.59E-31 | 1.29 | 2.30E-23 | 1.22 | 6.06E-15 |
| Atp7a | A_51_P473179 | AK033254 | ATPase, Cu++ transporting, alpha polypeptide | 0.98 | 0.861463 | 0.90 | 0.401433 | 0.85 | 0.303032 | 0.98 | 0.81128 |
| Auh | A_51_P372473 | NM_016709 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.05 | 0.027074 | 1.04 | 0.216899 | 1.05 | 0.034515 | 1.05 | 0.018087 |

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|---------|--------------|--------------|--|------|----------|------|----------|-------|----------|------|----------|
| Auh | A_52_P4095 | AK169661 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.19 | 0.039658 | 1.04 | 0.654592 | 1.29 | 0.029953 | 1.11 | 0.051057 |
| Bdh1 | A_51_P163106 | NM_175177 | 3-hydroxybutyrate dehydrogenase, type 1 | 0.96 | 0.231285 | 1.09 | 0.003551 | 0.95 | 0.162229 | 0.94 | 0.032961 |
| Bdh1 | A_52_P468343 | AK146962 | 3-hydroxybutyrate dehydrogenase, type 1 | 1.10 | 1.14E-06 | 0.86 | 4.27E-07 | 0.80 | 5.58E-24 | 0.82 | 1.61E-16 |
| Btd | A_51_P196158 | NM_025295 | biotinidase | 0.81 | 1.79E-21 | 0.93 | 0.000532 | 0.94 | 0.001048 | 0.94 | 0.000016 |
| Cat | A_52_P679769 | NM_009804 | catalase | 1.14 | 0.000204 | 0.97 | 0.216827 | 0.92 | 0.00555 | 0.93 | 0.042432 |
| Coq2 | A_51_P447752 | NM_027978 | coenzyme Q2 homolog, prenyltransferase (yeast) | 0.92 | 0.008449 | 1.29 | 9.84E-24 | 1.25 | 1.29E-13 | 1.20 | 1.79E-07 |
| Cox1 | A_51_P315595 | X57780 | M.musculus mRNA for mitochondrial gene for subunit I of cytochrome c oxidase. | 0.98 | 0.603027 | 1.06 | 0.0029 | 1.049 | 0.051597 | 1.07 | 0.012453 |
| Cox4i1 | A_51_P165435 | NM_009941 | cytochrome c oxidase subunit IV isoform 1 | 1.19 | 0.000175 | 1.20 | 0.003221 | 1.24 | 0.000139 | 1.17 | 0.004552 |
| Cox6a1 | A_51_P311540 | NM_007748 | cytochrome c oxidase, subunit VI a, polypeptide 1 | 1.04 | 0.429623 | 1.21 | 0.000472 | 1.22 | 0.000632 | 1.12 | 0.020661 |
| Cox6b1 | A_51_P448032 | NM_025628 | cytochrome c oxidase, subunit VIb polypeptide 1 | 0.95 | 0.048421 | 1.19 | 4.31E-24 | 1.18 | 1.16E-13 | 1.12 | 0.000056 |
| Cox7b | A_51_P160664 | NM_025379 | cytochrome c oxidase subunit VIIb | 1.03 | 0.497297 | 1.15 | 5.77E-07 | 1.16 | 6.16E-06 | 1.16 | 0.000016 |
| Cpt1c | A_52_P269942 | NM_153679 | carnitine palmitoyltransferase 1c | 0.66 | 0.057013 | 1.52 | 0.124214 | 0.83 | 0.334891 | 0.97 | 0.905843 |
| Cpt2 | A_51_P403388 | NM_009949 | carnitine palmitoyltransferase 2 | 0.84 | 0.000014 | 0.99 | 0.88152 | 0.85 | 0.000213 | 0.76 | 6.33E-18 |
| Crot | A_51_P489153 | NM_023733 | carnitine O-octanoyltransferase | 0.92 | 0.280595 | 1.08 | 2.66E-06 | 0.98 | 0.466252 | 1.00 | 0.949289 |
| Crot | A_52_P656336 | NM_023733 | carnitine O-octanoyltransferase | 0.86 | 0.087561 | 1.13 | 0.001593 | 0.97 | 0.522182 | 0.94 | 0.104907 |
| Cyp19a1 | A_51_P474551 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.45 | 0.164478 | 0.93 | 0.64475 | 1.00 | 0.970276 | 1.15 | 0.561799 |
| Cyp19a1 | A_52_P591961 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp1b1 | A_52_P297822 | AK016699 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 0.95 | 0.733546 | 1.00 | 1 | 0.99 | 0.895876 | 1.16 | 0.432126 |
| Cyp2b10 | A_51_P182362 | NM_009998 | Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 10 (Cyp2b10), transcript variant 2, mRNA. | 0.09 | 0 | 1.03 | 0.227611 | 1.00 | 0.940862 | 0.96 | 0.186907 |
| Cyp2b19 | A_51_P352763 | NM_007814 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 1.04 | 0.415928 | 1.08 | 0.180674 | 0.91 | 0.104567 | 1.01 | 0.905298 |
| Cyp2b19 | A_52_P421626 | AK029227 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 1.00 | 1 | 1.00 | 1 | 1.08 | 0.585023 | 1.00 | 1 |
| Cyp2c65 | A_52_P652059 | AK008688 | cytochrome P450, family 2, subfamily c, polypeptide 65 | 1.00 | 0.981529 | 1.18 | 0.233766 | 1.17 | 0.392156 | 1.06 | 0.449655 |
| Cyp2c66 | A_51_P471126 | NM_001011707 | cytochrome P450, family 2, subfamily c, polypeptide 66 | 0.97 | 0.72599 | 0.82 | 0.172389 | 1.11 | 0.536281 | 0.94 | 0.461801 |
| Cyp2d22 | A_51_P124126 | NM_019823 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 1.22 | 1.23E-10 | 0.78 | 4.11E-28 | 0.78 | 1.66E-21 | 0.82 | 1.82E-14 |
| Cyp2e1 | A_51_P283456 | NM_021282 | cytochrome P450, family 2, subfamily e, polypeptide 1 | 1.11 | 0.04857 | 0.84 | 0.000209 | 0.88 | 0.002312 | 0.99 | 0.758209 |
| Cyp2g1 | A_52_P481346 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 1.00 | 1 | 1.05 | 0.744023 | 1.17 | 0.42863 | 1.03 | 0.799866 |
| Cyp2j5 | A_51_P307872 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 1.01 | 0.830123 | 1.02 | 0.640288 | 1.05 | 0.048849 | 1.06 | 0.153443 |
| Cyp2j5 | A_52_P315766 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 1.04 | 0.083529 | 1.03 | 0.068206 | 1.05 | 0.002326 | 1.04 | 0.18742 |
| Cyp2s1 | A_51_P180091 | NM_028775 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 1.05 | 0.538386 | 0.97 | 0.548061 | 1.01 | 0.823561 | 1.02 | 0.61247 |
| Cyp2s1 | A_52_P456837 | AK054324 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.01 | 0.930048 | 1.00 | 1 |
| Cyp3a11 | A_51_P355301 | NM_007818 | cytochrome P450, family 3, subfamily a, polypeptide 11 | 0.86 | 0.000177 | 0.96 | 0.324168 | 0.90 | 0.00769 | 1.08 | 0.001683 |
| Cyp3a16 | A_51_P482051 | NM_007820 | cytochrome P450, family 3, subfamily a, polypeptide 16 | 0.87 | 0.002525 | 1.00 | 0.965319 | 0.98 | 0.707491 | 1.11 | 5.97E-06 |
| Cyp3a25 | A_52_P380314 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 0.71 | 5.38E-11 | 0.41 | 0 | 0.41 | 0 | 0.45 | 0 |
| Cyp3a44 | A_52_P571006 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 0.90 | 0.012206 | 1.04 | 0.291366 | 0.99 | 0.763606 | 1.13 | 8.65E-10 |

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|-------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Cyp51 | A_52_P636752 | NM_020010 | cytochrome P450, family 51 | 0.79 | 0.051095 | 0.94 | 0.360558 | 1.01 | 0.923296 | 1.30 | 2.28E-09 |
| Cyp51 | A_52_P778750 | AK035338 | Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530019F09 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Dgat2 | A_51_P396003 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.89 | 0.008861 | 1.14 | 0.00044 | 1.27 | 1.74E-08 | 1.06 | 0.157726 |
| Dgat2 | A_52_P359739 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.88 | 0.051346 | 1.14 | 0.016177 | 1.28 | 0.000038 | 1.10 | 0.10071 |
| Dld | A_51_P184282 | U73445 | dihydrolipoamide dehydrogenase | 0.90 | 0.001636 | 1.27 | 3.40E-14 | 1.22 | 2.96E-11 | 1.23 | 2.81E-10 |
| Dld | A_52_P536646 | NM_007861 | dihydrolipoamide dehydrogenase | 0.80 | 5.69E-09 | 1.15 | 7.99E-08 | 1.11 | 1.46E-06 | 1.14 | 0.000644 |
| Dlst | A_52_P3383 | AK171100 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 0.85 | 0.006272 | 0.93 | 0.006719 | 0.98 | 0.678665 | 0.94 | 0.036806 |
| Eno2 | A_51_P130028 | NM_013509 | enolase 2, gamma neuronal | 1.34 | 0.271552 | 1.15 | 0.343749 | 1.00 | 1 | 0.98 | 0.912722 |
| Eno2 | A_52_P748882 | NM_013509 | enolase 2, gamma neuronal | 0.99 | 0.903121 | 0.98 | 0.761328 | 1.00 | 1 | 0.96 | 0.744186 |
| Fabp1 | A_51_P487818 | NM_017399 | fatty acid binding protein 1, liver | 1.26 | 0.060944 | 1.53 | 0.001301 | 1.31 | 0.068549 | 1.20 | 0.139975 |
| Fdft1 | A_52_P136138 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 0.60 | 0.017103 | 0.83 | 0.00426 | 0.80 | 0.189778 | 1.24 | 0.122908 |
| Fnta | A_51_P112116 | NM_008033 | farnesyltransferase, CAAX box, alpha | 0.97 | 0.24712 | 1.03 | 0.173159 | 1.02 | 0.437387 | 0.97 | 0.040183 |
| Fntb | A_52_P235241 | NM_145927 | farnesyltransferase, CAAX box, beta | 0.80 | 0.040606 | 0.97 | 0.861701 | 0.93 | 0.608578 | 1.08 | 0.481478 |
| Gck | A_51_P106294 | NM_010292 | glucokinase | 0.97 | 0.476887 | 1.09 | 0.011222 | 0.93 | 0.125807 | 0.99 | 0.865216 |
| Gck | A_52_P259537 | NM_010292 | glucokinase | 1.06 | 0.254595 | 1.28 | 3.19E-08 | 1.17 | 0.013355 | 1.19 | 2.51E-07 |
| Ggps1 | A_51_P179604 | NM_010282 | PREDICTED: Mus musculus geranylgeranyl diphosphate synthase 1, transcript variant 4 (Ggps1), mRNA. | 1.04 | 0.472344 | 1.12 | 0.003896 | 1.15 | 0.007875 | 1.11 | 0.000026 |
| Ggps1 | A_51_P469902 | XM_977926 | geranylgeranyl diphosphate synthase 1 | 1.28 | 5.77E-12 | 0.89 | 0.00143 | 0.94 | 0.079858 | 0.95 | 0.170639 |
| Ggps1 | A_52_P228247 | NM_010282 | geranylgeranyl diphosphate synthase 1 | 0.90 | 0.008867 | 1.14 | 0.000093 | 1.04 | 0.160856 | 1.04 | 0.215054 |
| Gpi1 | A_52_P347412 | L09104 | glucose phosphate isomerase 1 | 1.29 | 0.000019 | 1.01 | 0.809703 | 0.97 | 0.570334 | 1.01 | 0.782621 |
| Gyk | A_51_P297671 | NM_008194 | glycerol kinase | 0.98 | 0.570454 | 1.01 | 0.791418 | 0.88 | 0.000016 | 0.89 | 0.000473 |
| Gyk | A_52_P120066 | NM_212444 | glycerol kinase | 1.04 | 0.040844 | 0.99 | 0.766235 | 0.85 | 0.000011 | 0.91 | 0.000024 |
| Gyk | A_52_P453517 | NM_008194 | glycerol kinase | 0.94 | 0.069562 | 0.91 | 5.49E-06 | 0.79 | 1.01E-06 | 0.81 | 1.15E-08 |
| Gys1 | A_52_P228932 | NM_030678 | glycogen synthase 1, muscle | 0.86 | 0.047964 | 0.93 | 0.605257 | 0.84 | 0.204287 | 0.97 | 0.901676 |
| Hadha | A_52_P193029 | NM_178878 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 0.89 | 0.005546 | 1.14 | 0.006069 | 1.07 | 0.099692 | 1.03 | 0.55424 |
| Hadha | A_52_P338459 | AK035316 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.20 | 0.360011 | 1.07 | 0.719102 | 1.00 | 1 | 1.02 | 0.909089 |
| Hadha | A_52_P658044 | AK050856 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.15 | 0.096182 | 0.85 | 0.006564 | 0.85 | 0.007326 | 0.87 | 0.004653 |
| Hk1 | A_51_P249024 | NM_010438 | hexokinase 1 | 1.18 | 7.57E-07 | 1.05 | 0.335763 | 1.09 | 0.03018 | 1.03 | 0.384791 |
| Hk1 | A_52_P479599 | NM_010438 | hexokinase 1 | 0.87 | 0.522476 | 1.03 | 0.869145 | 1.06 | 0.757768 | 1.07 | 0.652623 |
| Hk1 | A_52_P674530 | NM_010438 | hexokinase 1 | 0.85 | 0.0145 | 1.12 | 0.012129 | 1.05 | 0.273689 | 1.01 | 0.794436 |
| Hk1 | A_52_P87141 | NM_010438 | hexokinase 1 | 0.98 | 0.81715 | 1.00 | 1 | 1.00 | 1 | 1.10 | 0.559198 |

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|--------|--------------|--------------|---|------|----------|------|----------|------|----------|------|----------|
| Hmgcl1 | A_52_P197722 | NM_173731 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 | 1.09 | 0.777923 | 0.77 | 0.218857 | 0.95 | 0.76741 | 1.22 | 0.208341 |
| ldh1 | A_51_P132978 | NM_010497 | isocitrate dehydrogenase 1 (NADP+), soluble | 0.78 | 1.59E-06 | 1.21 | 0.000172 | 1.14 | 0.038305 | 1.22 | 0.001804 |
| ldh3a | A_51_P268559 | NM_029573 | isocitrate dehydrogenase 3 (NAD+) alpha | 1.11 | 0.028306 | 1.10 | 0.024044 | 1.10 | 0.057854 | 1.10 | 0.081078 |
| ldh3b | A_51_P130110 | NM_130884 | isocitrate dehydrogenase 3 (NAD+) beta | 1.03 | 0.033662 | 1.19 | 2.29E-25 | 1.19 | 3.43E-20 | 1.13 | 1.31E-14 |
| ldh3g | A_51_P136729 | NM_008323 | isocitrate dehydrogenase 3 (NAD+), gamma | 1.03 | 0.119279 | 1.17 | 9.42E-10 | 1.12 | 1.59E-06 | 1.07 | 0.025146 |
| Ldhc | A_51_P242403 | NM_013580 | lactate dehydrogenase C | 1.00 | 1 | 1.07 | 0.562345 | 1.00 | 1 | 1.00 | 1 |
| Mcat | A_51_P314855 | NM_001030014 | malonyl CoA:ACP acyltransferase (mitochondrial) | 1.04 | 0.277141 | 1.09 | 0.001639 | 1.18 | 3.41E-08 | 1.17 | 7.36E-10 |
| Mdh1 | A_51_P218179 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 0.84 | 6.43E-16 | 1.13 | 4.33E-14 | 1.15 | 2.95E-17 | 1.11 | 2.40E-06 |
| Mdh1 | A_52_P470451 | AK077724 | malate dehydrogenase 1, NAD (soluble) | 0.82 | 0.001691 | 0.89 | 0.003858 | 0.87 | 0.026208 | 0.88 | 0.028825 |
| Mecr | A_51_P386080 | NM_025297 | mitochondrial trans-2-enoyl-CoA reductase | 1.08 | 0.000028 | 1.18 | 3.33E-24 | 1.20 | 2.09E-24 | 1.11 | 0.000106 |
| Mgll | A_51_P352549 | AK079089 | Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330168D17 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Mut | A_51_P193935 | NM_008650 | methylmalonyl-Coenzyme A mutase | 0.97 | 0.068371 | 1.02 | 0.257427 | 1.05 | 0.014557 | 1.05 | 0.005997 |
| Mut | A_52_P362959 | AK051851 | methylmalonyl-Coenzyme A mutase | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Mut | A_52_P633163 | NM_008650 | methylmalonyl-Coenzyme A mutase | 0.96 | 0.034159 | 0.99 | 0.638194 | 1.05 | 0.035929 | 1.05 | 0.049613 |
| Ndufa1 | A_51_P472405 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.24 | 4.76E-07 | 1.12 | 0.000217 | 1.14 | 0.002727 | 1.15 | 1.53E-06 |
| Ndufa1 | A_52_P139747 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.21 | 1.49E-28 | 1.13 | 2.70E-13 | 1.12 | 5.40E-10 | 1.10 | 0.000048 |
| Ndufa5 | A_51_P170156 | NM_026614 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 | 0.99 | 0.882298 | 1.18 | 2.06E-30 | 1.18 | 1.26E-13 | 1.16 | 6.42E-22 |
| Ogdh | A_51_P122825 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.15 | 3.64E-09 | 1.15 | 8.42E-15 | 1.11 | 0.000541 | 1.03 | 0.161107 |
| Ogdh | A_52_P369310 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.18 | 0.003134 | 1.18 | 1.36E-07 | 1.16 | 0.000016 | 1.11 | 0.000404 |
| Oxct2a | A_51_P125056 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.00 | 1 | 1.16 | 0.515849 | 1.00 | 1 | 1.04 | 0.854468 |
| Oxct2a | A_51_P125062 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.13 | 0.164532 | 1.02 | 0.868195 | 0.90 | 0.446154 | 0.84 | 0.018639 |
| Oxsm | A_51_P312748 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 0.79 | 3.76E-16 | 1.08 | 0.017127 | 1.05 | 0.096452 | 1.01 | 0.629888 |
| Oxsm | A_52_P231635 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 0.79 | 9.32E-21 | 0.93 | 0.001567 | 0.94 | 0.000237 | 0.87 | 4.34E-11 |
| Pccb | A_51_P418259 | NM_025835 | propionyl Coenzyme A carboxylase, beta polypeptide | 0.83 | 0.00004 | 0.82 | 1.48E-16 | 0.81 | 2.82E-10 | 0.84 | 3.26E-10 |
| Pdha2 | A_51_P519857 | NM_008811 | pyruvate dehydrogenase E1 alpha 2 | 1.00 | 1 | 1.16 | 0.509431 | 1.00 | 1 | 1.00 | 1 |
| Pdhb | A_51_P321921 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 1.06 | 0.003688 | 1.27 | 3.32E-18 | 1.21 | 3.33E-10 | 1.19 | 2.46E-09 |
| Pdhb | A_52_P568792 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 1.07 | 0.00361 | 1.30 | 6.01E-25 | 1.29 | 8.97E-25 | 1.24 | 4.77E-19 |
| Peci | A_51_P394665 | NM_011868 | peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase | 0.82 | 3.43E-09 | 1.18 | 9.97E-22 | 1.17 | 3.97E-14 | 1.13 | 9.04E-07 |
| Pfkfb2 | A_51_P335251 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 0.96 | 0.216859 | 0.84 | 9.89E-12 | 0.86 | 0.000024 | 0.99 | 0.77072 |
| Pfkfb2 | A_52_P31125 | BC018418 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 0.94 | 0.610521 | 0.86 | 0.356 | 1.08 | 0.594667 | 0.70 | 0.016372 |
| Pgk2 | A_51_P125487 | NM_031190 | phosphoglycerate kinase 2 | 1.05 | 0.784724 | 1.03 | 0.697266 | 1.00 | 1 | 1.00 | 1 |
| Pgls | A_51_P321794 | NM_025396 | 6-phosphogluconolactonase | 1.03 | 0.291577 | 1.06 | 0.000076 | 1.11 | 2.74E-09 | 1.04 | 0.002036 |
| Pgm2 | A_51_P368074 | NM_028132 | phosphoglucomutase 2 | 0.82 | 3.56E-10 | 0.85 | 5.77E-20 | 0.87 | 4.76E-11 | 0.90 | 0.000429 |
| Pgm5 | A_51_P451052 | NM_175013 | phosphoglucomutase 5 | 0.98 | 0.671143 | 1.08 | 0.075133 | 1.05 | 0.084715 | 1.22 | 1.44E-07 |

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|----------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Pgm5 | A_52_P860000 | NM_175013 | phosphoglucomutase 5 | 1.00 | 1 | 0.98 | 0.818372 | 1.00 | 1 | 1.00 | 1 |
| Phka1 | A_52_P196825 | AK078633 | Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:7330411B16 | 0.88 | 0.480679 | 0.62 | 0.014898 | 0.78 | 0.195584 | 1.08 | 0.648633 |
| Phka1 | A_52_P278311 | NM_008832 | phosphorylase kinase alpha 1 | 0.85 | 0.158018 | 0.78 | 0.11666 | 0.98 | 0.907624 | 0.86 | 0.090491 |
| Phka2 | A_51_P239970 | AK051899 | phosphorylase kinase alpha 2 | 1.00 | 1 | 1.15 | 0.545352 | 1.10 | 0.50509 | 1.04 | 0.686166 |
| Phka2 | A_51_P368950 | AK018208 | Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230017A12 | 0.88 | 0.307474 | 0.93 | 0.702429 | 0.90 | 0.55921 | 0.94 | 0.674615 |
| Phka2 | A_52_P187217 | NM_172783 | phosphorylase kinase alpha 2 | 0.88 | 0.034853 | 0.90 | 0.423898 | 1.18 | 0.215217 | 1.03 | 0.869927 |
| Phka2 | A_52_P657963 | AK045618 | phosphorylase kinase alpha 2 | 1.16 | 0.001022 | 0.93 | 0.022303 | 0.92 | 0.119792 | 1.09 | 0.084881 |
| Phka2 | A_52_P671916 | NM_172783 | phosphorylase kinase alpha 2 | 0.93 | 0.004873 | 0.99 | 0.811022 | 0.96 | 0.088716 | 0.97 | 0.151425 |
| Phkb | A_51_P270725 | AK089493 | phosphorylase kinase beta | 1.14 | 0.000124 | 1.01 | 0.887567 | 0.94 | 0.05564 | 0.90 | 0.00001 |
| Phkb | A_52_P342907 | BC051503 | phosphorylase kinase beta | 1.00 | 1 | 1.01 | 0.953081 | 1.04 | 0.676405 | 1.00 | 1 |
| Phkg1 | A_51_P280890 | NM_011079 | phosphorylase kinase gamma 1 | 1.10 | 0.730057 | 1.03 | 0.892804 | 0.98 | 0.897851 | 0.78 | 0.296068 |
| Ppap2a | A_51_P189104 | NM_008903 | phosphatidic acid phosphatase 2a | 0.83 | 0.079681 | 1.04 | 0.286229 | 1.05 | 0.156363 | 1.15 | 3.81E-14 |
| Ppap2a | A_51_P189105 | AK077275 | phosphatidic acid phosphatase 2a | 0.83 | 0.056563 | 1.02 | 0.467365 | 1.03 | 0.348762 | 1.18 | 1.08E-09 |
| Ppap2a | A_52_P7937 | NM_008903 | phosphatidic acid phosphatase 2a | 0.72 | 0.016261 | 0.96 | 0.171748 | 0.98 | 0.615491 | 1.10 | 1.85E-06 |
| Ppara | A_51_P348334 | NM_011144 | peroxisome proliferator activated receptor alpha | 0.98 | 0.788081 | 1.17 | 8.26E-07 | 1.11 | 0.000408 | 1.27 | 1.26E-13 |
| Ppard | A_51_P271556 | NM_011145 | peroxisome proliferator activator receptor delta | 1.04 | 0.642773 | 0.73 | 0.150016 | 0.63 | 0.208207 | 1.02 | 0.878302 |
| Ppargc1b | A_51_P294891 | NM_133249 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.29 | 0.000013 | 0.81 | 1.75E-07 | 0.78 | 5.26E-15 | 0.89 | 0.000557 |
| Ppargc1b | A_52_P293222 | AK042378 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.25 | 0.003137 | 0.85 | 7.08E-07 | 0.78 | 0.000461 | 0.97 | 0.377482 |
| Ppargc1b | A_52_P883463 | AK045690 | Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230304K20 | 1.15 | 0.158027 | 0.92 | 0.238098 | 0.82 | 0.031244 | 0.78 | 6.90E-06 |
| Ppp1ca | A_51_P509389 | NM_031868 | protein phosphatase 1, catalytic subunit, alpha isoform | 0.80 | 3.22E-14 | 1.06 | 0.033849 | 1.04 | 0.111977 | 1.05 | 0.085473 |
| Ppp1cb | A_51_P342716 | NM_172707 | protein phosphatase 1, catalytic subunit, beta isoform | 0.90 | 0.011973 | 0.97 | 0.410774 | 0.97 | 0.386287 | 0.94 | 0.177457 |
| Ppp1cc | A_52_P519508 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 0.81 | 5.63E-32 | 0.77 | 0 | 0.78 | 0 | 0.78 | 0 |
| Ppp1cc | A_52_P540434 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 0.80 | 6.94E-24 | 0.88 | 6.23E-13 | 0.88 | 1.82E-12 | 0.88 | 1.01E-15 |
| Ppt2 | A_52_P238816 | NM_019441 | palmitoyl-protein thioesterase 2 | 1.03 | 0.383235 | 0.95 | 0.096642 | 0.99 | 0.782912 | 0.96 | 0.270241 |
| Pygl | A_51_P452779 | NM_133198 | liver glycogen phosphorylase | 0.92 | 0.087105 | 1.18 | 0.000045 | 1.06 | 0.218167 | 1.10 | 0.044664 |
| Pygl | A_52_P320181 | AK083075 | liver glycogen phosphorylase | 0.76 | 0.004919 | 1.08 | 0.320657 | 1.03 | 0.694414 | 1.10 | 0.23566 |
| Pygm | A_51_P458973 | NM_011224 | muscle glycogen phosphorylase | 1.00 | 1 | 0.97 | 0.837067 | 1.00 | 1 | 0.98 | 0.863715 |
| Scd4 | A_52_P603237 | BC038322 | stearoyl-coenzyme A desaturase 4 | 1.00 | 1 | 1.07 | 0.666933 | 1.00 | 1 | 0.85 | 0.069816 |
| Sdha | A_51_P410823 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 0.88 | 0.00022 | 1.10 | 1.53E-07 | 1.13 | 4.52E-10 | 1.08 | 0.001453 |
| Sdha | A_52_P109503 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 0.93 | 0.04729 | 1.19 | 7.95E-07 | 1.16 | 0.000027 | 1.11 | 0.000756 |
| Sdhb | A_51_P234853 | NM_023374 | succinate dehydrogenase complex, subunit B, iron sulfur (Ip) | 0.84 | 7.31E-13 | 0.99 | 0.5721 | 1.03 | 0.066127 | 0.97 | 0.08288 |
| Sdhc | A_51_P106373 | NM_025321 | succinate dehydrogenase complex, subunit C, integral | 0.83 | 2.25E-15 | 0.96 | 0.090978 | 0.97 | 0.21256 | 0.95 | 0.058894 |

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|-----|---------|---------------|-----------|--|------|----------|-------|----------|------|----------|------|----------|
| | Sdhc | A_52_P875481 | AK031343 | membrane protein Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030410A06 | 1.08 | 0.644243 | 0.98 | 0.902773 | 1.00 | 0.970829 | 1.00 | 1 |
| | Sdhd | A_51_P260871 | NM_025848 | succinate dehydrogenase complex, subunit D, integral membrane protein | 1.01 | 0.756305 | 1.14 | 0.001428 | 1.10 | 0.043605 | 1.11 | 0.014283 |
| | Slc25a1 | A_51_P350922 | NM_153150 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 0.88 | 2.65E-06 | 1.23 | 2.18E-15 | 1.30 | 2.60E-23 | 1.27 | 3.12E-15 |
| | Slc27a2 | A_51_P484551 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 0.94 | 0.00213 | 0.93 | 0.002681 | 0.97 | 0.231198 | 0.95 | 0.070287 |
| | Slc27a2 | A_52_P1083677 | AK038847 | solute carrier family 27 (fatty acid transporter), member 2 | 0.73 | 0.103408 | 1.14 | 0.607967 | 0.79 | 0.399642 | 0.99 | 0.952548 |
| | Slc27a2 | A_52_P154971 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 0.99 | 0.631588 | 0.94 | 0.001587 | 1.02 | 0.302126 | 0.98 | 0.183616 |
| | Slc27a3 | A_51_P133252 | NM_011988 | solute carrier family 27 (fatty acid transporter), member 3 | 0.87 | 0.255597 | 0.95 | 0.300019 | 0.93 | 0.448725 | 1.00 | 0.992485 |
| | Slc27a6 | A_51_P211616 | AK028699 | solute carrier family 27 (fatty acid transporter), member 6 | 0.99 | 0.890495 | 1.00 | 1 | 1.00 | 1 | 1.07 | 0.578975 |
| | Sucla2 | A_51_P111554 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 0.96 | 0.08897 | 0.97 | 0.289304 | 0.98 | 0.535233 | 0.90 | 0.000028 |
| | Sucla2 | A_52_P533792 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 0.96 | 0.360955 | 1.12 | 0.000544 | 1.14 | 0.000179 | 1.12 | 0.000097 |
| | Sucla2 | A_52_P762514 | AK016060 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 0.88 | 0.421099 | 0.87 | 0.590173 | 0.96 | 0.87672 | 0.89 | 0.412321 |
| | Tkt | A_52_P631197 | AK050793 | transketolase | 0.78 | 0.241876 | 1.48 | 0.186559 | 0.85 | 0.590191 | 1.53 | 0.174647 |
| | Tpi1 | A_51_P433824 | NM_009415 | triosephosphate isomerase 1 | 0.88 | 0.000041 | 1.00 | 0.969896 | 0.98 | 0.678977 | 0.90 | 0.008627 |
| | Tpi1 | A_52_P116102 | AK053780 | Mus musculus 0 day neonate eyeball cDNA, RIKEN library, clone:E130308D14 product:triosephosphate isomerase | 0.97 | 0.812806 | 0.97 | 0.568244 | 0.93 | 0.459585 | 1.05 | 0.53092 |
| | Ucp1 | A_51_P426353 | NM_009463 | uncoupling protein 1 (mitochondrial, proton carrier) | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| | Ucp2 | A_52_P499675 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 1.00 | 1 | 1.01 | 0.960441 | 1.02 | 0.865651 | 1.08 | 0.64936 |
| | Uqcrb | A_51_P472671 | NM_026219 | ubiquinol-cytochrome c reductase binding protein | 1.04 | 0.434255 | 1.05 | 0.055891 | 1.12 | 0.010651 | 1.15 | 1.56E-06 |
| | Uqcrc1 | A_51_P109835 | NM_025407 | ubiquinol-cytochrome c reductase core protein 1 | 0.96 | 0.014244 | 1.09 | 6.31E-07 | 1.12 | 0.000044 | 1.16 | 9.23E-13 |
| | Uqcrcf1 | A_51_P361951 | NM_025710 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 | 0.86 | 7.50E-37 | 1.13 | 2.30E-12 | 1.12 | 7.75E-17 | 1.08 | 0.001294 |
| | Uqcrh | A_51_P431852 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.21 | 1.04E-08 | 1.08 | 0.002795 | 1.06 | 0.00994 | 1.09 | 0.005119 |
| | Uqcrh | A_52_P541875 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.22 | 6.72E-07 | 1.07 | 0.043535 | 1.14 | 2.54E-06 | 1.06 | 0.035047 |
| | Uqcrcq | A_52_P370484 | NM_025352 | ubiquinol-cytochrome c reductase, complex III subunit VII | 1.04 | 0.036 | 1.301 | 0 | 1.25 | 9.97E-24 | 1.27 | 1.31E-36 |
| IAT | Acaa1a | A_51_P327075 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.10 | 0.000167 | 1.26 | 3.60E-15 | 1.41 | 4.04E-28 | 1.59 | 1.68E-27 |
| | Acaa1a | A_52_P155990 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.16 | 0.002963 | 1.39 | 2.29E-09 | 1.92 | 2.15E-33 | 2.32 | 1.40E-45 |
| | *Acaa1a | A_52_P423183 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.26 | 1.05E-14 | 1.50 | 1.15E-27 | 2.07 | 0 | 2.54 | 0 |
| | *Acaa1b | A_52_P423174 | NM_146230 | acetyl-Coenzyme A acyltransferase 1B | 1.35 | 5.22E-28 | 1.50 | 0 | 2.07 | 0 | 2.52 | 0 |
| | *Acaa2 | A_51_P125260 | NM_177470 | acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) | 1.21 | 0.024048 | 1.16 | 6.32E-12 | 1.81 | 2.80E-45 | 2.35 | 0 |
| | Acaca | A_51_P439426 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 7.02 | 0 | 2.04 | 5.09E-27 | 2.81 | 0 | 3.00 | 0 |
| | Acaca | A_52_P132591 | AF374167 | acetyl-Coenzyme A carboxylase alpha | 4.60 | 4.32E-40 | 1.80 | 5.95E-07 | 3.31 | 0 | 3.36 | 5.68E-23 |
| | Acaca | A_52_P23177 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 2.68 | 0 | 1.53 | 1.58E-21 | 1.78 | 0 | 2.07 | 0 |

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|---------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Acaca | A_52_P318040 | AK132628 | acetyl-Coenzyme A carboxylase alpha | 5.28 | 0 | 1.82 | 1.73E-25 | 2.50 | 0 | 2.80 | 0 |
| *Acaca | A_52_P595124 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 5.55 | 0 | 1.61 | 1.91E-17 | 2.64 | 0 | 2.70 | 4.36E-37 |
| Acacb | A_51_P239236 | BC022940 | acetyl-Coenzyme A carboxylase beta | 1.29 | 0.000146 | 1.03 | 0.398657 | 1.33 | 2.02E-08 | 1.44 | 4.24E-26 |
| *Acacb | A_52_P340167 | NM_133904 | acetyl-Coenzyme A carboxylase beta | 1.54 | 5.67E-11 | 1.20 | 0.001612 | 1.67 | 2.29E-12 | 1.56 | 2.35E-23 |
| Acad10 | A_51_P187507 | NM_028037 | acyl-Coenzyme A dehydrogenase family, member 10 | 1.38 | 0 | 1.11 | 0.00006 | 1.15 | 1.93E-20 | 1.23 | 5.76E-31 |
| Acad11 | A_51_P299260 | AK041180 | acyl-Coenzyme A dehydrogenase family, member 11 | 1.70 | 7.46E-18 | 1.17 | 0.056592 | 1.22 | 0.001247 | 1.31 | 5.06E-08 |
| Acad11 | A_52_P85152 | NM_175324 | acyl-Coenzyme A dehydrogenase family, member 11 | 1.06 | 0.014579 | 1.00 | 0.963039 | 1.34 | 7.19E-08 | 1.53 | 1.43E-22 |
| Acad8 | A_51_P244052 | NM_025862 | acyl-Coenzyme A dehydrogenase family, member 8 | 1.36 | 1.55E-21 | 1.05 | 0.264035 | 1.28 | 1.62E-11 | 1.33 | 2.93E-16 |
| Acad9 | A_51_P341379 | NM_172678 | acyl-Coenzyme A dehydrogenase family, member 9 | 1.11 | 1.95E-07 | 1.39 | 1.15E-43 | 1.50 | 0 | 1.77 | 0 |
| Acad9 | A_52_P73208 | AK049931 | acyl-Coenzyme A dehydrogenase family, member 9 | 1.84 | 2.64E-20 | 1.64 | 3.64E-26 | 1.70 | 4.45E-10 | 2.22 | 0 |
| *Acadl | A_51_P149455 | NM_007381 | acyl-Coenzyme A dehydrogenase, long-chain | 1.59 | 1.65E-28 | 1.21 | 9.13E-08 | 1.72 | 0 | 2.00 | 0 |
| *Acadm | A_51_P319879 | NM_007382 | acyl-Coenzyme A dehydrogenase, medium chain | 0.98 | 0.054679 | 1.23 | 2.24E-08 | 1.92 | 0 | 2.26 | 0 |
| *Acads | A_52_P367745 | NM_007383 | acyl-Coenzyme A dehydrogenase, short chain | 1.35 | 0.000141 | 1.34 | 7.62E-10 | 1.88 | 1.09E-35 | 2.08 | 1.15E-43 |
| Acadsb | A_51_P435068 | NM_025826 | acyl-Coenzyme A dehydrogenase, short/branched chain | 1.49 | 2.98E-32 | 0.97 | 0.33264 | 1.01 | 0.525237 | 0.97 | 0.356789 |
| *Acadvl | A_51_P518340 | NM_017366 | acyl-Coenzyme A dehydrogenase, very long chain | 1.79 | 8.97E-14 | 1.46 | 1.53E-17 | 2.37 | 0 | 3.00 | 0 |
| Acat1 | A_51_P319449 | NM_144784 | acetyl-Coenzyme A acetyltransferase 1 | 1.42 | 2.03E-17 | 1.13 | 0.0013 | 1.30 | 1.00E-10 | 1.45 | 7.33E-17 |
| Acat2 | A_51_P139748 | NM_009338 | acetyl-Coenzyme A acetyltransferase 2 | 1.70 | 1.97E-26 | 1.36 | 3.78E-16 | 1.53 | 0 | 1.77 | 0 |
| Acat3 | A_51_P139745 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 1.64 | 2.47E-28 | 1.32 | 1.26E-14 | 1.56 | 4.48E-44 | 1.74 | 0 |
| Acat3 | A_52_P11959 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 1.84 | 2.54E-23 | 1.47 | 3.04E-14 | 1.78 | 1.13E-27 | 1.93 | 2.07E-26 |
| *Acly | A_51_P261718 | NM_134037 | ATP citrate lyase | 7.28 | 0 | 2.11 | 1.72E-41 | 2.91 | 0 | 2.90 | 0 |
| Acly | A_52_P373556 | AK043466 | ATP citrate lyase | 3.42 | 7.18E-08 | 2.17 | 8.59E-28 | 2.49 | 1.63E-34 | 2.88 | 8.98E-13 |
| Aco1 | A_51_P391082 | NM_007386 | aconitase 1 | 1.77 | 0 | 1.37 | 8.08E-25 | 1.70 | 0 | 1.94 | 0 |
| Aco1 | A_52_P299115 | NM_007386 | aconitase 1 | 1.95 | 0 | 1.17 | 0.00943 | 1.53 | 0 | 1.83 | 0 |
| Aco2 | A_52_P200359 | NM_080633 | aconitase 2, mitochondrial | 1.38 | 6.50E-21 | 1.18 | 5.86E-15 | 1.66 | 0 | 1.98 | 0 |
| Aco2 | A_52_P899263 | AK029122 | Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732494K09 | 1.75 | 0.000022 | 0.82 | 0.065118 | 0.49 | 2.11E-12 | 0.60 | 1.69E-06 |
| *Acox1 | A_51_P366704 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 1.38 | 7.60E-19 | 1.37 | 5.14E-30 | 2.06 | 0 | 2.37 | 0 |
| Acox1 | A_52_P615096 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 1.08 | 0.246566 | 1.52 | 3.67E-15 | 2.58 | 1.30E-35 | 2.95 | 0 |
| Acox2 | A_51_P206708 | NM_053115 | acyl-Coenzyme A oxidase 2, branched chain | 1.06 | 0.266203 | 0.93 | 0.525244 | 0.66 | 5.21E-10 | 1.26 | 0.001981 |
| Acs1 | A_51_P463452 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 0.81 | 2.01E-09 | 1.63 | 7.23E-39 | 2.28 | 0 | 2.47 | 0 |
| Acs1 | A_51_P496432 | BC006692 | acyl-CoA synthetase long-chain family member 1 | 0.72 | 2.51E-07 | 1.46 | 1.06E-06 | 1.80 | 8.04E-10 | 1.95 | 2.62E-16 |
| Acs1 | A_52_P597618 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 0.84 | 2.39E-06 | 1.66 | 1.02E-30 | 2.37 | 0 | 2.51 | 0 |
| Acs3 | A_51_P511560 | NM_028817 | acyl-CoA synthetase long-chain family member 3 | 0.72 | 2.25E-17 | 0.71 | 1.03E-33 | 0.73 | 6.14E-25 | 0.75 | 0 |
| Acs4 | A_51_P268154 | NM_019477 | acyl-CoA synthetase long-chain family member 4 | 0.71 | 0 | 1.09 | 0.012564 | 0.96 | 0.087098 | 1.04 | 0.324966 |
| Acs4 | A_52_P78203 | NM_207625 | acyl-CoA synthetase long-chain family member 4 | 0.73 | 7.22E-43 | 0.91 | 1.94E-07 | 0.80 | 1.02E-22 | 0.91 | 0.20608 |

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|---------|--------------|--------------|---|------|----------|------|----------|------|----------|------|----------|
| Acs16 | A_51_P380699 | NM_144823 | acyl-CoA synthetase long-chain family member 6 | 0.76 | 0.004716 | 0.48 | 5.03E-25 | 0.69 | 0.073547 | 0.54 | 0.002169 |
| Acs16 | A_51_P518823 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 0.77 | 0.045444 | 0.40 | 1.30E-09 | 0.54 | 0.015007 | 0.45 | 6.85E-08 |
| Acs16 | A_52_P204459 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 0.71 | 0.184327 | 0.30 | 1.08E-16 | 0.58 | 0.040114 | 0.75 | 0.372019 |
| Adcy1 | A_51_P196718 | NM_009622 | adenylate cyclase 1 | 0.78 | 0.094192 | 0.73 | 0.019699 | 0.61 | 1.87E-06 | 0.56 | 0.004519 |
| Adcy2 | A_51_P337523 | NM_153534 | adenylate cyclase 2 | 0.99 | 0.805389 | 0.67 | 5.12E-08 | 0.80 | 0.343954 | 0.74 | 0.025816 |
| Adcy2 | A_52_P165610 | NM_153534 | adenylate cyclase 2 | 0.91 | 0.109069 | 0.64 | 2.28E-09 | 0.90 | 0.630131 | 0.62 | 0.010218 |
| Adcy3 | A_51_P484671 | NM_138305 | adenylate cyclase 3 | 0.75 | 6.13E-11 | 0.90 | 0.00195 | 1.02 | 0.64436 | 0.99 | 0.729287 |
| Adcy3 | A_52_P216525 | NM_138305 | adenylate cyclase 3 | 0.71 | 1.37E-12 | 0.93 | 0.040575 | 1.04 | 0.342114 | 0.95 | 0.234465 |
| Adcy5 | A_51_P199041 | NM_001012765 | adenylate cyclase 5 | 0.71 | 1.18E-07 | 1.27 | 1.80E-06 | 1.65 | 2.13E-16 | 1.85 | 5.32E-44 |
| Adcy5 | A_52_P449208 | NM_001012765 | adenylate cyclase 5 | 0.72 | 7.82E-08 | 1.26 | 8.07E-08 | 1.64 | 2.31E-43 | 1.79 | 7.41E-41 |
| Adcy7 | A_51_P441622 | NM_007406 | adenylate cyclase 7 | 0.58 | 2.18E-35 | 0.93 | 0.000528 | 0.87 | 0.00061 | 0.77 | 0.000061 |
| Adcy7 | A_52_P291 | AK012436 | adenylate cyclase 7 | 0.54 | 0 | 0.77 | 6.60E-09 | 0.72 | 0 | 0.60 | 2.69E-26 |
| Adcy7 | A_52_P586141 | NM_001037724 | Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library | 0.51 | 0 | 0.90 | 0.006749 | 0.78 | 1.00E-07 | 0.64 | 1.51E-15 |
| Adh1 | A_51_P428555 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.53 | 0 | 0.52 | 1.75E-13 | 0.41 | 0 | 0.62 | 1.18E-06 |
| Adh1 | A_52_P629895 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.49 | 7.03E-40 | 0.52 | 1.86E-11 | 0.40 | 0 | 0.61 | 2.08E-08 |
| Adh4 | A_51_P189442 | NM_011996 | alcohol dehydrogenase 4 (class II), pi polypeptide | 0.43 | 1.13E-12 | 1.11 | 0.007753 | 1.09 | 0.116031 | 1.14 | 0.136515 |
| Adh6a | A_52_P276348 | AK007397 | alcohol dehydrogenase 6A (class V) | 0.54 | 0.009564 | 1.40 | 0.42977 | 1.93 | 4.29E-08 | 0.86 | 0.189521 |
| Adh7 | A_51_P233797 | NM_009626 | alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide | 0.87 | 0.022823 | 1.06 | 0.758067 | 0.74 | 0.000032 | 1.45 | 0.000151 |
| Agpat1 | A_51_P322612 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 1.45 | 2.53E-37 | 1.10 | 0.001214 | 1.30 | 0 | 1.38 | 0 |
| Agpat1 | A_52_P200465 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 1.65 | 1.63E-33 | 1.15 | 4.13E-07 | 1.33 | 0 | 1.52 | 0 |
| Agpat2 | A_51_P238563 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 1.40 | 1.35E-10 | 1.33 | 8.95E-10 | 1.83 | 4.65E-38 | 2.09 | 0 |
| Agpat2 | A_51_P238565 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 1.40 | 1.07E-10 | 1.29 | 1.90E-08 | 1.82 | 0 | 2.07 | 0 |
| *Agpat3 | A_51_P425490 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 1.85 | 0 | 1.33 | 5.29E-40 | 1.65 | 0 | 2.11 | 0 |
| Agpat3 | A_52_P523569 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 1.28 | 2.20E-19 | 1.15 | 3.85E-13 | 1.35 | 1.40E-45 | 1.78 | 0 |
| Agpat4 | A_51_P346165 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 0.66 | 0 | 0.86 | 0.000154 | 0.80 | 3.11E-24 | 0.76 | 2.25E-16 |
| Agpat4 | A_52_P3029 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 0.67 | 0 | 0.89 | 0.000019 | 0.80 | 1.72E-38 | 0.76 | 1.06E-23 |
| Agpat5 | A_51_P361286 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 1.40 | 6.42E-32 | 1.05 | 0.442446 | 1.07 | 0.146953 | 0.84 | 0.000326 |
| Agpat5 | A_52_P572447 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 0.62 | 0 | 1.00 | 0.933406 | 0.95 | 0.000053 | 0.87 | 1.04E-15 |
| *Agpat6 | A_51_P335710 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 1.14 | 0.053586 | 1.06 | 0.279785 | 1.34 | 0.001626 | 1.51 | 2.13E-07 |
| Agpat6 | A_51_P335716 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 1.14 | 0.011291 | 1.02 | 0.706273 | 1.38 | 1.09E-11 | 1.50 | 7.17E-17 |

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|---------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Agpat6 | A_52_P24986 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 1.25 | 1.16E-15 | 1.02 | 0.274867 | 1.19 | 8.99E-12 | 1.31 | 0 |
| Alb | A_51_P160713 | NM_009654 | albumin | 1.61 | 2.50E-20 | 0.91 | 0.259407 | 0.87 | 0.103915 | 1.13 | 0.422462 |
| Aldh1a1 | A_51_P334942 | NM_013467 | aldehyde dehydrogenase family 1, subfamily A1 | 0.59 | 1.36E-24 | 0.68 | 3.30E-19 | 0.63 | 0 | 0.52 | 1.60E-21 |
| Aldh1a2 | A_52_P58145 | NM_009022 | aldehyde dehydrogenase family 1, subfamily A2 | 0.92 | 0.357816 | 1.36 | 0.004352 | 1.30 | 1.89E-08 | 1.39 | 0.00009 |
| Aldh1a3 | A_52_P113518 | AK086764 | aldehyde dehydrogenase family 1, subfamily A3 | 0.88 | 0.126252 | 1.15 | 0.052183 | 1.23 | 0.001185 | 1.33 | 0.000159 |
| Aldh1a3 | A_52_P87843 | NM_053080 | aldehyde dehydrogenase family 1, subfamily A3 | 0.57 | 1.27E-12 | 1.15 | 0.000687 | 1.08 | 0.198151 | 1.14 | 0.009559 |
| Aldh1a7 | A_51_P383399 | NM_011921 | aldehyde dehydrogenase family 1, subfamily A7 | 1.48 | 0 | 1.41 | 8.19E-10 | 1.85 | 0 | 1.93 | 3.62E-40 |
| Aldh1b1 | A_51_P510418 | NM_028270 | aldehyde dehydrogenase 1 family, member B1 | 0.26 | 0 | 0.37 | 0 | 0.41 | 0 | 0.38 | 0 |
| Aldh3a1 | A_51_P310594 | NM_007436 | aldehyde dehydrogenase family 3, subfamily A1 | 0.95 | 0.594929 | 5.03 | 0.000023 | 0.88 | 0.403377 | 4.62 | 6.22E-07 |
| Aldh3a2 | A_51_P464175 | NM_007437 | aldehyde dehydrogenase family 3, subfamily A2 | 0.95 | 0.012784 | 1.23 | 0.004191 | 1.02 | 0.479465 | 1.65 | 1.07E-07 |
| Aldh4a1 | A_51_P337918 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 2.20 | 0 | 1.32 | 5.93E-36 | 1.45 | 0 | 1.45 | 0 |
| Aldh4a1 | A_52_P123230 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 1.48 | 0.001831 | 1.25 | 0.014334 | 1.53 | 3.93E-06 | 1.26 | 0.031732 |
| Aldh5a1 | A_51_P491504 | NM_172532 | aldehyde dehydrogenase family 5, subfamily A1 | 1.60 | 0 | 1.33 | 8.38E-16 | 1.65 | 0 | 1.69 | 0 |
| Aldh5a1 | A_52_P30273 | AK051603 | aldehyde dehydrogenase family 5, subfamily A1 | 2.50 | 6.94E-08 | 2.28 | 0.000092 | 1.36 | 0.13654 | 3.13 | 0.00007 |
| Aldh7a1 | A_52_P503071 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 1.30 | 0.010972 | 1.12 | 0.147386 | 1.45 | 0.000201 | 1.43 | 0.000019 |
| Aldh9a1 | A_51_P106211 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 1.03 | 0.440354 | 1.09 | 0.014949 | 1.34 | 6.55E-24 | 1.24 | 9.79E-10 |
| Aldob | A_51_P337269 | NM_144903 | aldolase 2, B isoform | 0.08 | 0 | 0.54 | 1.68E-19 | 0.46 | 2.46E-07 | 0.74 | 0.062678 |
| Aldob | A_52_P450038 | NM_144903 | aldolase 2, B isoform | 0.09 | 0 | 0.55 | 7.84E-20 | 0.45 | 4.84E-07 | 0.87 | 0.50957 |
| Aldob | A_52_P468023 | NM_144903 | aldolase 2, B isoform | 0.17 | 2.65E-25 | 0.51 | 8.07E-12 | 0.35 | 1.70E-07 | 0.79 | 0.103289 |
| Aldoc | A_51_P220681 | NM_009657 | aldolase 3, C isoform | 0.29 | 0 | 0.50 | 2.70E-12 | 0.40 | 0 | 0.64 | 0.00002 |
| Aldoc | A_51_P425284 | AK039267 | aldolase 3, C isoform | 0.16 | 0 | 0.56 | 4.90E-07 | 0.41 | 3.29E-29 | 0.74 | 0.00161 |
| Apoa4 | A_51_P327491 | NM_007468 | apolipoprotein A-IV | 1.06 | 0.217866 | 1.33 | 5.98E-06 | 1.72 | 3.13E-28 | 1.59 | 1.84E-10 |
| Apoa4 | A_51_P327496 | NM_007468 | apolipoprotein A-IV | 1.52 | 7.60E-08 | 0.77 | 0.000032 | 0.57 | 1.50E-29 | 0.63 | 2.57E-25 |
| Apoa5 | A_51_P259930 | NM_080434 | apolipoprotein A-V | 0.65 | 1.27E-22 | 0.89 | 0.076361 | 0.81 | 0.001705 | 0.95 | 0.482612 |
| Apoa5 | A_52_P292404 | NM_080434 | apolipoprotein A-V | 0.64 | 0.003239 | 0.80 | 0.170864 | 0.63 | 0.000396 | 1.20 | 0.461572 |
| Apob | A_51_P413088 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 0.59 | 0.000456 | 1.00 | 0.984225 | 0.78 | 0.005972 | 1.56 | 0.146049 |
| Apob | A_51_P470542 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 0.16 | 7.44E-38 | 0.57 | 0.003561 | 0.46 | 4.88E-09 | 0.82 | 0.325462 |
| Apob | A_52_P441070 | NM_009693 | apolipoprotein B | 0.13 | 1.82E-22 | 0.45 | 1.78E-14 | 0.53 | 0.000031 | 1.06 | 0.75443 |
| Apoc1 | A_51_P164504 | NM_007469 | apolipoprotein C-I | 3.30 | 0 | 1.78 | 0 | 1.84 | 0 | 2.20 | 0 |
| Apoc2 | A_51_P334979 | NM_009695 | apolipoprotein C-II | 0.54 | 0 | 1.24 | 0.000312 | 1.42 | 7.54E-34 | 1.27 | 4.09E-10 |
| Apoc3 | A_51_P310629 | NM_023114 | apolipoprotein C-III | 2.63 | 3.46E-28 | 1.14 | 0.131834 | 1.34 | 1.70E-07 | 1.29 | 0.026807 |
| Apoc3 | A_52_P574306 | NM_023114 | apolipoprotein C-III | 2.72 | 1.62E-17 | 1.27 | 0.001241 | 1.56 | 2.79E-09 | 1.39 | 0.014807 |
| Apoe | A_51_P171999 | NM_009696 | apolipoprotein E | 1.76 | 6.24E-18 | 1.10 | 0.074183 | 0.84 | 2.63E-06 | 0.87 | 0.000276 |
| Atp12a | A_52_P329398 | NM_138652 | ATPase, H+/K+ transporting, nongastric, alpha polypeptide | 0.11 | 0 | 0.29 | 0.002277 | 0.14 | 0 | 0.47 | 5.75E-10 |

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|----------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| *Atp5a1 | A_52_P674489 | NM_007505 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 | 0.99 | 0.466908 | 1.06 | 0.171404 | 1.34 | 0.000012 | 1.45 | 0.000024 |
| Atp5b | A_52_P328078 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.11 | 0.356843 | 0.95 | 0.580589 | 1.33 | 0.037383 | 1.54 | 0.000785 |
| *Atp5b | A_52_P553841 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.38 | 1.13E-08 | 1.19 | 0.000225 | 1.62 | 1.65E-19 | 1.75 | 2.15E-40 |
| Atp5c1 | A_51_P378087 | NM_020615 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | 1.52 | 2.87E-14 | 1.06 | 0.142672 | 1.31 | 1.99E-10 | 1.36 | 2.09E-10 |
| Atp5e | A_51_P362054 | NM_025983 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit | 1.47 | 7.85E-30 | 0.98 | 0.214906 | 1.13 | 1.36E-07 | 1.19 | 2.63E-40 |
| Atp5h | A_51_P264186 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 1.21 | 2.26E-30 | 1.07 | 0.000193 | 1.26 | 2.80E-45 | 1.41 | 2.65E-40 |
| Atp5h | A_52_P640355 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 1.23 | 3.53E-32 | 1.06 | 0.003234 | 1.26 | 1.37E-24 | 1.47 | 0 |
| Atp5k | A_51_P301289 | NM_007507 | ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e | 2.08 | 0 | 1.25 | 1.54E-13 | 1.68 | 0 | 1.89 | 0 |
| Atp6v0a1 | A_51_P142089 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.50 | 0 | 1.00 | 0.941876 | 1.16 | 7.49E-31 | 1.32 | 9.59E-19 |
| Atp6v0a1 | A_52_P399998 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.35 | 0 | 1.05 | 0.176223 | 1.08 | 0.039803 | 1.19 | 3.75E-11 |
| Atp6v0a1 | A_52_P515336 | AK045877 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.69 | 3.83E-15 | 0.84 | 0.000012 | 0.80 | 1.26E-07 | 0.87 | 0.00159 |
| Atp6v1b2 | A_51_P190845 | NM_007509 | ATPase, H+ transporting, lysosomal V1 subunit B2 | 0.59 | 3.09E-32 | 1.13 | 0.006734 | 1.10 | 0.029943 | 1.10 | 0.071469 |
| Atp6v1c2 | A_51_P518600 | NM_133699 | ATPase, H+ transporting, lysosomal V1 subunit C2 | 0.56 | 1.03E-22 | 1.05 | 0.583413 | 0.96 | 0.395648 | 1.88 | 0.004793 |
| Atp6v1e1 | A_51_P166434 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 0.86 | 0.000917 | 1.11 | 0.01802 | 1.25 | 0.000013 | 1.36 | 1.93E-11 |
| Atp6v1e1 | A_52_P303388 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 0.87 | 0.006562 | 1.11 | 0.01675 | 1.24 | 2.90E-07 | 1.34 | 1.04E-09 |
| Atp6v1h | A_52_P403420 | AK081492 | ATPase, H+ transporting, lysosomal V1 subunit H | 1.54 | 5.30E-25 | 1.47 | 1.31E-13 | 1.46 | 1.65E-15 | 1.45 | 1.39E-10 |
| Auh | A_51_P372473 | NM_016709 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.52 | 1.49E-35 | 1.10 | 0.002853 | 1.14 | 2.10E-07 | 1.14 | 0.00002 |
| Auh | A_52_P107290 | AK003929 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.39 | 1.84E-09 | 1.15 | 0.012556 | 1.38 | 4.36E-13 | 1.26 | 9.30E-08 |
| Auh | A_52_P4095 | AK169661 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.35 | 7.61E-23 | 1.02 | 0.563088 | 1.19 | 2.40E-08 | 1.08 | 0.038711 |
| Bdh1 | A_51_P163106 | NM_175177 | 3-hydroxybutyrate dehydrogenase, type 1 | 0.27 | 3.76E-25 | 0.22 | 0 | 0.24 | 4.39E-26 | 0.38 | 1.54E-13 |
| Bdh1 | A_52_P468343 | AK146962 | 3-hydroxybutyrate dehydrogenase, type 1 | 0.55 | 1.66E-09 | 0.48 | 2.53E-36 | 0.45 | 7.38E-43 | 0.54 | 1.29E-23 |
| Bdh2 | A_51_P470935 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.69 | 9.17E-16 | 1.08 | 0.046784 | 0.98 | 0.445862 | 0.83 | 0.000161 |
| Bdh2 | A_52_P195809 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.50 | 2.08E-08 | 1.17 | 1.94E-08 | 1.11 | 0.001263 | 0.92 | 0.102139 |
| Btd | A_51_P196158 | NM_025295 | biotinidase | 1.08 | 0.005504 | 1.17 | 1.89E-09 | 1.29 | 8.06E-38 | 1.33 | 7.00E-32 |
| Cat | A_52_P679769 | NM_009804 | catalase | 1.23 | 1.09E-06 | 1.28 | 2.06E-06 | 1.80 | 6.59E-43 | 1.77 | 0 |
| Cd36 | A_51_P375138 | L23108 | CD36 antigen | 0.64 | 0 | 1.09 | 0.001594 | 1.00 | 0.844402 | 1.02 | 0.529989 |
| *Cd36 | A_51_P375146 | NM_007643 | CD36 antigen | 0.62 | 1.40E-45 | 0.96 | 0.88613 | 0.97 | 0.300512 | 0.96 | 0.150383 |
| *Cox1 | A_51_P315595 | X57780 | M.musculus mRNA for mitochondrial gene for subunit I of cytochrome c oxidase. | 1.42 | 3.18E-06 | 1.14 | 8.75E-08 | 1.75 | 6.46E-22 | 1.92 | 5.67E-15 |
| Cox4i1 | A_51_P165435 | NM_009941 | cytochrome c oxidase subunit IV isoform 1 | 1.20 | 1.66E-06 | 1.07 | 0.118701 | 1.40 | 2.31E-19 | 1.64 | 0 |
| Cox6a1 | A_51_P311540 | NM_007748 | cytochrome c oxidase, subunit VI a, polypeptide 1 | 0.95 | 0.558589 | 1.19 | 0.010689 | 1.35 | 0.008191 | 1.36 | 0.000064 |
| Cox6b1 | A_51_P448032 | NM_025628 | cytochrome c oxidase, subunit VIb polypeptide 1 | 1.54 | 2.99E-34 | 1.39 | 5.96E-24 | 1.82 | 0 | 2.16 | 0 |

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|---------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|
| Cox6b2 | A_51_P300506 | NM_183405 | cytochrome c oxidase subunit VIb polypeptide 2 | 1.35 | 0 | 1.08 | 0.012779 | 1.37 | 0 | 1.59 | 0 |
| Cox7a1 | A_51_P148612 | NM_009944 | cytochrome c oxidase, subunit VIIa 1 | 1.37 | 4.83E-06 | 0.66 | 1.82E-29 | 1.45 | 7.69E-18 | 1.98 | 0 |
| Cox7b | A_51_P160664 | NM_025379 | cytochrome c oxidase subunit VIIb | 1.96 | 5.42E-32 | 1.33 | 5.47E-16 | 1.87 | 2.94E-44 | 2.15 | 0 |
| Cpt1a | A_51_P427674 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 0.55 | 0 | 1.00 | 0.984125 | 0.99 | 0.702855 | 1.00 | 0.878462 |
| Cpt1a | A_52_P219753 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 0.52 | 0 | 1.13 | 0.002937 | 1.11 | 0.001723 | 1.19 | 6.08E-06 |
| Cpt1b | A_51_P232913 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 0.93 | 0.31128 | 1.12 | 0.001497 | 2.06 | 0 | 3.07 | 0 |
| Cpt1b | A_52_P625508 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 0.92 | 0.198682 | 1.32 | 3.57E-18 | 2.31 | 0 | 3.25 | 0 |
| *Cpt2 | A_51_P403388 | NM_009949 | carnitine palmitoyltransferase 2 | 1.76 | 4.81E-27 | 1.36 | 7.84E-16 | 1.77 | 3.53E-31 | 1.95 | 2.80E-45 |
| *Crat | A_51_P440807 | NM_007760 | carnitine acetyltransferase | 1.17 | 0.00104 | 1.08 | 0.025608 | 1.27 | 6.84E-12 | 1.37 | 0 |
| *Cs | A_51_P390260 | NM_026444 | citrate synthase | 1.96 | 7.01E-45 | 1.58 | 3.38E-27 | 2.28 | 0 | 2.52 | 0 |
| Cs | A_52_P182659 | NM_026444 | citrate synthase | 1.02 | 0.610386 | 1.30 | 1.55E-10 | 1.74 | 3.18E-13 | 1.78 | 6.44E-15 |
| Cyp1a1 | A_51_P279693 | NM_009992 | cytochrome P450, family 1, subfamily a, polypeptide 1 | 2.38 | 4.47E-29 | 0.74 | 0.002613 | 0.52 | 3.19E-34 | 1.01 | 0.944742 |
| Cyp2a12 | A_51_P206736 | NM_133657 | cytochrome P450, family 2, subfamily a, polypeptide 12 | 0.73 | 0.196501 | 1.02 | 0.951948 | 0.66 | 0.05122 | 2.50 | 0.008273 |
| Cyp2a5 | A_52_P246252 | NM_007812 | cytochrome P450, family 2, subfamily a, polypeptide 5 | 0.17 | 0.000019 | 0.51 | 0.000013 | 0.35 | 1.53E-14 | 1.04 | 0.810724 |
| Cyp2b10 | A_51_P182362 | NM_009998 | Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 10 (Cyp2b10), transcript variant 2, mRNA. | 0.53 | 2.61E-10 | 0.96 | 0.362713 | 1.03 | 0.555584 | 0.99 | 0.842969 |
| Cyp2b10 | A_52_P472486 | NM_009999 | cytochrome P450, family 2, subfamily b, polypeptide 10 | 0.34 | 1.20E-18 | 0.81 | 0.000066 | 0.98 | 0.764697 | 0.94 | 0.320957 |
| Cyp2b13 | A_51_P492339 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 0.21 | 0 | 0.97 | 0.688834 | 1.08 | 0.160102 | 1.37 | 1.24E-22 |
| Cyp2b13 | A_52_P289091 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 0.84 | 2.38E-07 | 1.13 | 0.00404 | 1.36 | 2.94E-11 | 1.41 | 2.65E-15 |
| Cyp2b19 | A_51_P352763 | NM_007814 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 0.94 | 0.054748 | 1.41 | 0.008078 | 1.14 | 0.000045 | 2.55 | 9.21E-06 |
| Cyp2c29 | A_51_P103706 | NM_007815 | cytochrome P450, family 2, subfamily c, polypeptide 29 | 0.08 | 0 | 0.18 | 0 | 0.17 | 0 | 0.27 | 0 |
| Cyp2c39 | A_51_P304109 | NM_010003 | cytochrome P450, family 2, subfamily c, polypeptide 39 | 0.09 | 0 | 0.12 | 0 | 0.12 | 0 | 0.15 | 0 |
| Cyp2c44 | A_51_P209782 | NM_001001446 | cytochrome P450, family 2, subfamily c, polypeptide 44 | 0.49 | 4.45E-16 | 1.34 | 5.96E-10 | 1.14 | 0.015473 | 0.83 | 0.001953 |
| Cyp2c54 | A_52_P154580 | NM_206537 | cytochrome P450, family 2, subfamily c, polypeptide 54 | 0.76 | 0.165844 | 0.62 | 0.036596 | 0.43 | 1.19E-08 | 0.86 | 0.639185 |
| Cyp2c55 | A_51_P447785 | NM_028089 | cytochrome P450, family 2, subfamily c, polypeptide 55 | 0.21 | 0 | 0.19 | 0 | 0.17 | 0 | 0.15 | 0 |
| Cyp2c65 | A_52_P652059 | AK008688 | cytochrome P450, family 2, subfamily c, polypeptide 65 | 0.14 | 0 | 0.14 | 0 | 0.11 | 0 | 0.11 | 0 |
| Cyp2c66 | A_51_P471126 | NM_001011707 | cytochrome P450, family 2, subfamily c, polypeptide 66 | 0.33 | 0 | 0.33 | 0 | 0.30 | 0 | 0.23 | 0 |
| Cyp2c70 | A_51_P134142 | NM_145499 | cytochrome P450, family 2, subfamily c, polypeptide 70 | 0.78 | 4.50E-15 | 1.27 | 1.97E-08 | 1.45 | 1.68E-33 | 1.60 | 2.48E-35 |
| Cyp2d10 | A_51_P111192 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 0.46 | 0 | 0.57 | 0 | 0.54 | 0 | 0.60 | 2.88E-33 |
| Cyp2d10 | A_52_P527775 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 0.52 | 0 | 0.53 | 0 | 0.66 | 4.20E-44 | 0.61 | 6.25E-21 |
| Cyp2d13 | A_52_P372062 | NM_133695 | Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13) on chromosome 15. | 0.57 | 8.95E-19 | 0.62 | 7.66E-18 | 0.61 | 0 | 0.64 | 5.20E-17 |
| Cyp2d22 | A_51_P124126 | NM_019823 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 0.59 | 0 | 0.82 | 1.45E-06 | 0.84 | 1.18E-06 | 0.81 | 2.48E-09 |
| Cyp2d22 | A_52_P478420 | AK086555 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 1.00 | 0.910578 | 0.94 | 0.143409 | 0.77 | 8.50E-10 | 0.69 | 4.07E-28 |
| Cyp2d22 | A_52_P49391 | AK090296 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 0.60 | 0 | 0.80 | 5.03E-13 | 0.79 | 6.37E-09 | 0.70 | 2.70E-43 |
| Cyp2d9 | A_51_P124133 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 0.43 | 0 | 0.52 | 0 | 0.49 | 0 | 0.50 | 0 |

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|----------|--------------|-----------|---|------|----------|-------|----------|------|----------|------|----------|
| Cyp2d9 | A_51_P478303 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 0.58 | 0 | 0.64 | 8.64E-41 | 0.62 | 1.12E-44 | 0.64 | 0 |
| Cyp2e1 | A_51_P283456 | NM_021282 | cytochrome P450, family 2, subfamily e, polypeptide 1 | 8.01 | 0 | 0.95 | 0.577506 | 1.69 | 9.36E-08 | 1.53 | 2.80E-22 |
| Cyp2f2 | A_51_P453909 | NM_007817 | cytochrome P450, family 2, subfamily f, polypeptide 2 | 1.00 | 0.99556 | 0.32 | 0.00813 | 0.08 | 0 | 0.48 | 1.37E-13 |
| Cyp2j5 | A_51_P307872 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 0.37 | 1.09E-09 | 0.98 | 0.917797 | 0.74 | 0.123239 | 1.54 | 0.100907 |
| Cyp2j5 | A_52_P315766 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 0.28 | 3.93E-17 | 1.06 | 0.725807 | 0.63 | 0.052138 | 2.09 | 0.042897 |
| Cyp2j6 | A_51_P506328 | NM_010008 | cytochrome P450, family 2, subfamily j, polypeptide 6 | 0.56 | 0 | 0.85 | 3.16E-16 | 0.80 | 9.22E-20 | 0.78 | 7.32E-30 |
| Cyp2j9 | A_51_P330044 | NM_028979 | cytochrome P450, family 2, subfamily j, polypeptide 9 | 0.83 | 4.22E-11 | 0.81 | 0.00009 | 0.76 | 7.59E-23 | 0.71 | 3.96E-17 |
| Cyp2s1 | A_51_P180091 | NM_028775 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 0.06 | 0 | 0.25 | 7.71E-23 | 0.18 | 0 | 0.31 | 4.99E-26 |
| Cyp3a11 | A_51_P355301 | NM_007818 | cytochrome P450, family 3, subfamily a, polypeptide 11 | 0.63 | 3.83E-34 | 0.92 | 0.118121 | 0.99 | 0.880588 | 1.27 | 0.025105 |
| Cyp3a13 | A_51_P114941 | NM_007819 | cytochrome P450, family 3, subfamily a, polypeptide 13 | 0.06 | 0 | 0.08 | 0 | 0.05 | 0 | 0.08 | 0 |
| Cyp3a16 | A_51_P482051 | NM_007820 | cytochrome P450, family 3, subfamily a, polypeptide 16 | 0.69 | 0.009302 | 1.07 | 0.515747 | 1.34 | 0.001489 | 1.85 | 0.000115 |
| Cyp3a25 | A_51_P489367 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 0.13 | 0 | 0.92 | 0.658534 | 0.73 | 0.011648 | 1.39 | 2.37E-06 |
| Cyp3a44 | A_52_P571006 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 0.32 | 1.43E-11 | 1.02 | 0.900719 | 1.34 | 0.063993 | 2.44 | 2.58E-11 |
| Cyp4a10 | A_52_P257774 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.64 | 0.000127 | 1.11 | 0.613712 | 1.32 | 0.023382 | 1.99 | 4.79E-14 |
| Cyp4a10 | A_52_P340136 | X71478 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.64 | 0 | 0.99 | 0.662613 | 1.20 | 0.000048 | 1.32 | 1.12E-12 |
| Cyp4a12a | A_51_P433360 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 0.53 | 0.000028 | 1.03 | 0.822771 | 1.37 | 0.028421 | 3.72 | 1.32E-13 |
| Cyp4a12a | A_52_P44914 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 0.96 | 0.470709 | 1.18 | 0.020545 | 1.13 | 0.001775 | 1.54 | 5.97E-06 |
| Cyp4a14 | A_51_P238576 | NM_007822 | cytochrome P450, family 4, subfamily a, polypeptide 14 | 0.43 | 2.66E-44 | 1.12 | 0.250461 | 1.22 | 0.024474 | 1.80 | 0.000437 |
| Cyp4b1 | A_51_P118704 | NM_007823 | cytochrome P450, family 4, subfamily b, polypeptide 1 | 0.52 | 0 | 1.06 | 0.164935 | 1.37 | 2.52E-12 | 1.76 | 0 |
| Cyp4f14 | A_51_P452768 | NM_022434 | cytochrome P450, family 4, subfamily f, polypeptide 14 | 0.32 | 0 | 0.17 | 0 | 0.14 | 0 | 0.14 | 0 |
| Cyp4f15 | A_51_P136303 | NM_134127 | cytochrome P450, family 4, subfamily f, polypeptide 15 | 0.96 | 0.727041 | 13.53 | 2.29E-07 | 1.82 | 0.060869 | 9.24 | 8.58E-20 |
| Cyp51 | A_51_P485791 | NM_020010 | cytochrome P450, family 51 | 0.52 | 0 | 1.36 | 4.60E-20 | 1.35 | 4.60E-14 | 1.37 | 1.66E-13 |
| Cyp51 | A_52_P164161 | NM_020010 | cytochrome P450, family 51 | 0.59 | 1.07E-22 | 1.16 | 0.003806 | 1.12 | 0.006027 | 1.17 | 0.00003 |
| Cyp51 | A_52_P636752 | NM_020010 | cytochrome P450, family 51 | 0.50 | 0 | 1.32 | 2.89E-14 | 1.25 | 3.79E-09 | 1.26 | 8.85E-14 |
| *Dci | A_51_P105589 | NM_010023 | dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) | 1.68 | 7.62E-29 | 1.26 | 3.86E-14 | 1.68 | 0 | 1.88 | 0 |
| Decr1 | A_51_P208555 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 1.32 | 2.48E-10 | 1.49 | 4.97E-13 | 2.14 | 0 | 2.25 | 0 |
| Decr1 | A_52_P335907 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 1.32 | 1.83E-12 | 1.55 | 4.02E-16 | 2.49 | 0 | 2.56 | 0 |
| *Dgat1 | A_51_P510059 | NM_010046 | diacylglycerol O-acyltransferase 1 | 1.28 | 0.000018 | 1.24 | 4.08E-16 | 1.70 | 7.27E-21 | 1.78 | 4.01E-27 |
| Dgat1 | A_52_P456134 | NM_010046 | diacylglycerol O-acyltransferase 1 | 1.43 | 0 | 1.29 | 0 | 1.57 | 0 | 1.75 | 0 |
| Dgat2 | A_51_P396003 | NM_026384 | diacylglycerol O-acyltransferase 2 | 1.05 | 0.106841 | 1.32 | 1.76E-06 | 1.25 | 7.51E-11 | 1.09 | 0.032628 |
| Dlat | A_51_P265106 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 1.77 | 9.44E-27 | 1.49 | 2.80E-45 | 2.10 | 0 | 2.72 | 0 |
| Dlat | A_52_P374642 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 1.46 | 1.05E-18 | 1.72 | 0 | 2.75 | 0 | 3.41 | 0 |
| Dld | A_51_P184282 | U73445 | dihydrolipoamide dehydrogenase | 1.42 | 2.52E-28 | 1.30 | 3.29E-12 | 1.88 | 0 | 2.11 | 0 |
| Dld | A_51_P184284 | NM_007861 | dihydrolipoamide dehydrogenase | 1.36 | 3.35E-31 | 1.33 | 1.66E-14 | 1.88 | 0 | 2.07 | 0 |

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|---------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Dld | A_52_P536646 | NM_007861 | dihydrolipoamide dehydrogenase | 1.06 | 0.478605 | 1.19 | 0.002094 | 1.83 | 0 | 2.09 | 0 |
| Dlst | A_51_P290139 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.43 | 2.30E-20 | 1.16 | 0.000016 | 1.63 | 3.19E-43 | 1.83 | 2.03E-31 |
| Dlst | A_52_P140072 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.34 | 4.97E-07 | 1.21 | 0.000484 | 1.72 | 2.91E-25 | 1.94 | 1.71E-30 |
| Dlst | A_52_P3383 | AK171100 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.34 | 2.40E-14 | 0.86 | 0.000415 | 0.92 | 0.000487 | 1.00 | 0.98328 |
| Ech1 | A_51_P421846 | NM_016772 | enoyl coenzyme A hydratase 1, peroxisomal | 1.01 | 0.687831 | 1.09 | 0.000067 | 1.30 | 3.22E-22 | 1.40 | 8.18E-32 |
| *Echs1 | A_51_P409039 | NM_053119 | enoyl Coenzyme A hydratase, short chain, 1, mitochondrial | 1.84 | 0 | 1.22 | 1.77E-22 | 1.47 | 0 | 1.59 | 0 |
| *Ehhadh | A_51_P462918 | NM_023737 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase | 1.61 | 0 | 1.45 | 7.20E-24 | 2.75 | 0 | 3.66 | 0 |
| Eno2 | A_51_P130028 | NM_013509 | enolase 2, gamma neuronal | 0.75 | 3.76E-15 | 0.84 | 0.000113 | 0.78 | 1.81E-08 | 0.69 | 1.15E-14 |
| Eno2 | A_52_P748882 | NM_013509 | enolase 2, gamma neuronal | 0.67 | 5.96E-25 | 0.86 | 0.005395 | 0.79 | 7.89E-06 | 0.64 | 6.37E-12 |
| Eno3 | A_51_P328539 | NM_007933 | enolase 3, beta muscle | 1.58 | 0.000042 | 0.41 | 1.63E-11 | 0.54 | 0.052807 | 0.62 | 0.02941 |
| Fabp1 | A_51_P487818 | NM_017399 | fatty acid binding protein 1, liver | 0.14 | 3.83E-09 | 1.13 | 0.228753 | 0.99 | 0.905421 | 1.54 | 0.140999 |
| Fabp2 | A_51_P313581 | NM_007980 | fatty acid binding protein 2, intestinal | 0.52 | 0 | 0.57 | 9.77E-16 | 0.58 | 0 | 0.68 | 1.55E-08 |
| Fabp2 | A_52_P453013 | NM_007980 | fatty acid binding protein 2, intestinal | 0.64 | 0.01274 | 0.45 | 0.021387 | 0.34 | 7.56E-34 | 0.37 | 1.09E-14 |
| Fabp3 | A_51_P167535 | NM_010174 | fatty acid binding protein 3, muscle and heart | 0.60 | 2.79E-06 | 0.62 | 5.97E-15 | 1.20 | 0.000045 | 1.82 | 1.39E-39 |
| Fabp5 | A_51_P387764 | NM_010634 | fatty acid binding protein 5, epidermal | 0.91 | 0.109156 | 1.59 | 9.96E-25 | 2.05 | 0 | 2.15 | 0 |
| Fasn | A_51_P321126 | NM_007988 | fatty acid synthase | 6.27 | 0 | 2.20 | 1.03E-09 | 3.50 | 0 | 2.92 | 0 |
| *Fasn | A_52_P100252 | NM_007988 | fatty acid synthase | 7.73 | 0 | 2.57 | 1.21E-43 | 3.40 | 0 | 3.16 | 0 |
| Fbp1 | A_51_P474701 | NM_019395 | fructose biphosphatase 1 | 0.19 | 0 | 0.62 | 2.04E-21 | 0.50 | 5.25E-13 | 0.81 | 0.000476 |
| Fdft1 | A_51_P485946 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 1.15 | 7.56E-07 | 0.82 | 5.37E-14 | 0.78 | 2.79E-12 | 0.74 | 0 |
| Fdft1 | A_52_P136138 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 0.74 | 0.000017 | 1.03 | 0.615007 | 0.92 | 0.391482 | 0.95 | 0.44805 |
| Fdps | A_51_P379798 | NM_134469 | farnesyl diphosphate synthetase | 0.71 | 5.02E-16 | 1.10 | 0.089033 | 1.09 | 0.009047 | 1.13 | 0.017302 |
| Fdps | A_52_P593965 | AK077979 | farnesyl diphosphate synthetase | 0.89 | 0.195482 | 0.84 | 0.000392 | 0.75 | 1.85E-13 | 1.08 | 0.104434 |
| *Fh1 | A_51_P359333 | NM_010209 | fumarate hydratase 1 | 1.67 | 0 | 1.24 | 1.54E-44 | 1.62 | 0 | 1.79 | 0 |
| Fnta | A_51_P112116 | NM_008033 | farnesyltransferase, CAAX box, alpha | 1.36 | 0 | 1.14 | 2.02E-08 | 1.24 | 2.76E-30 | 1.28 | 3.45E-40 |
| Fntb | A_51_P517680 | NM_145927 | farnesyltransferase, CAAX box, beta | 1.48 | 3.00E-38 | 1.43 | 7.61E-17 | 1.55 | 6.82E-13 | 1.49 | 1.25E-23 |
| G6pd2 | A_51_P353735 | NM_019468 | glucose-6-phosphate dehydrogenase 2 | 0.52 | 2.95E-36 | 1.04 | 0.490293 | 1.34 | 1.26E-09 | 1.26 | 3.30E-06 |
| G6pdx | A_51_P187082 | NM_008062 | glucose-6-phosphate dehydrogenase X-linked | 0.56 | 1.64E-43 | 0.95 | 0.227074 | 1.16 | 0.004811 | 1.21 | 3.10E-06 |
| Gapdh | A_52_P589321 | AK169742 | glyceraldehyde-3-phosphate dehydrogenase | 1.06 | 0.352271 | 0.97 | 0.425108 | 1.20 | 0.000285 | 1.40 | 9.75E-07 |
| Gck | A_51_P106294 | NM_010292 | glucokinase | 1.93 | 6.19E-07 | 0.97 | 0.793299 | 1.15 | 0.185138 | 1.07 | 0.592539 |
| Gck | A_52_P259537 | NM_010292 | glucokinase | 1.85 | 1.04E-14 | 1.10 | 0.256474 | 1.14 | 0.335489 | 1.22 | 0.000102 |
| Ggps1 | A_52_P228247 | NM_010282 | geranylgeranyl diphosphate synthase 1 | 0.76 | 2.37E-21 | 1.27 | 1.64E-14 | 1.21 | 2.22E-11 | 1.16 | 3.02E-09 |
| *Gpd1 | A_51_P293853 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 2.30 | 7.61E-43 | 2.37 | 4.74E-39 | 4.02 | 0 | 4.35 | 0 |
| Gpd1 | A_52_P16419 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 1.58 | 0.000013 | 1.96 | 1.28E-09 | 3.39 | 3.52E-33 | 3.50 | 2.31E-23 |

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|---------|---------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Gpt2 | A_51_P493886 | NM_173866 | glutamic pyruvate transaminase (alanine aminotransferase) 2 | 2.35 | 0 | 0.83 | 6.61E-08 | 0.94 | 0.006933 | 0.78 | 1.57E-18 |
| Gyg | A_51_P240019 | NM_013755 | glycogenin | 1.03 | 0.405407 | 1.36 | 9.99E-16 | 1.56 | 0 | 1.52 | 3.27E-36 |
| Gyk | A_51_P297671 | NM_008194 | glycerol kinase | 0.53 | 0 | 2.32 | 0 | 3.93 | 0 | 5.33 | 0 |
| Gyk | A_52_P1020291 | AK037633 | Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130030N17 | 0.64 | 2.50E-13 | 0.99 | 0.916818 | 1.24 | 0.001514 | 1.82 | 9.84E-36 |
| Gyk | A_52_P120066 | NM_212444 | glycerol kinase | 0.46 | 0 | 2.00 | 8.33E-36 | 3.28 | 0 | 4.27 | 0 |
| Gyk | A_52_P453517 | NM_008194 | glycerol kinase | 0.38 | 9.99E-11 | 2.03 | 1.96E-10 | 3.34 | 0 | 4.10 | 0 |
| Gys1 | A_52_P228932 | NM_030678 | glycogen synthase 1, muscle | 1.67 | 8.06E-34 | 1.09 | 0.041643 | 1.23 | 0.000097 | 1.38 | 1.56E-14 |
| Gys2 | A_51_P440315 | NM_145572 | glycogen synthase 2 | 4.32 | 0 | 4.01 | 0 | 7.11 | 0 | 9.53 | 0 |
| Hadha | A_52_P193029 | NM_178878 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.27 | 0.000044 | 1.44 | 1.66E-11 | 1.93 | 6.98E-42 | 2.43 | 0 |
| Hadha | A_52_P338459 | AK035316 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.74 | 0.003632 | 1.64 | 0.00065 | 1.29 | 0.029932 | 2.21 | 7.03E-21 |
| Hadha | A_52_P658044 | AK050856 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.18 | 0.047648 | 0.84 | 0.011521 | 1.04 | 0.481568 | 1.40 | 2.37E-09 |
| *Hadhb | A_51_P217990 | NM_145558 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit | 1.43 | 0.000205 | 1.38 | 1.08E-20 | 2.01 | 0 | 2.34 | 0 |
| Hk1 | A_52_P102773 | BC072628 | hexokinase 1 | 0.73 | 2.51E-40 | 0.76 | 2.21E-41 | 0.69 | 0 | 0.78 | 7.17E-24 |
| Hk1 | A_52_P479599 | NM_010438 | hexokinase 1 | 0.67 | 1.84E-07 | 0.79 | 0.000047 | 0.82 | 0.000066 | 0.90 | 0.00309 |
| Hk1 | A_52_P674530 | NM_010438 | hexokinase 1 | 0.72 | 1.45E-11 | 0.83 | 4.61E-25 | 0.81 | 2.47E-36 | 0.83 | 5.85E-14 |
| Hk1 | A_52_P87141 | NM_010438 | hexokinase 1 | 1.05 | 0.896584 | 2.14 | 0.000741 | 1.15 | 0.574305 | 1.44 | 0.024512 |
| Hk1 | A_52_P9337 | NM_010438 | hexokinase 1 | 1.14 | 0.083664 | 1.13 | 0.048549 | 1.36 | 9.13E-06 | 1.20 | 0.023784 |
| Hmgcr | A_51_P507410 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.26 | 0 | 1.07 | 0.384694 | 0.91 | 0.071765 | 1.25 | 0.042226 |
| Hmgcr | A_52_P137371 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.36 | 0 | 1.09 | 0.307084 | 0.83 | 2.82E-08 | 1.46 | 0.009554 |
| Hmgcr | A_52_P232287 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.33 | 0 | 1.11 | 0.103932 | 0.96 | 0.237023 | 1.39 | 0.002 |
| Hmgcr | A_52_P578922 | AK159899 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.57 | 0 | 1.20 | 0.028011 | 0.77 | 7.64E-09 | 1.53 | 0.008988 |
| Hmgcr | A_52_P770765 | AK033165 | Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030450I20 | 0.57 | 0 | 1.09 | 0.291929 | 0.79 | 0.000077 | 1.25 | 0.024748 |
| Hmgcs1 | A_51_P146941 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.65 | 2.59E-24 | 1.27 | 4.00E-20 | 1.34 | 6.68E-27 | 1.63 | 0 |
| Hmgcs1 | A_52_P119039 | AK078743 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 1.28 | 0.000061 | 1.38 | 2.66E-18 | 1.22 | 6.36E-09 | 1.91 | 0 |
| Hmgcs1 | A_52_P388072 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.68 | 5.30E-09 | 1.24 | 7.66E-18 | 1.52 | 0 | 1.75 | 1.24E-29 |
| Hmgcs2 | A_51_P116039 | NM_008256 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 | 0.70 | 6.16E-15 | 0.51 | 2.45E-16 | 0.44 | 0 | 0.56 | 1.44E-17 |
| Hsd17b4 | A_51_P445662 | NM_008292 | hydroxysteroid (17-beta) dehydrogenase 4 | 0.87 | 3.91E-15 | 1.23 | 1.14E-23 | 1.45 | 1.30E-35 | 1.51 | 5.72E-39 |
| ldh1 | A_51_P132978 | NM_010497 | isocitrate dehydrogenase 1 (NADP+), soluble | 1.30 | 2.94E-06 | 1.20 | 0.000123 | 1.44 | 9.30E-10 | 1.59 | 1.67E-16 |
| ldh3a | A_51_P268559 | NM_029573 | isocitrate dehydrogenase 3 (NAD+) alpha | 1.05 | 0.404739 | 1.42 | 8.26E-10 | 1.98 | 1.41E-22 | 2.32 | 0 |

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|--------|--------------|--------------|---|------|----------|------|----------|------|----------|-------|----------|
| ldh3b | A_51_P130110 | NM_130884 | isocitrate dehydrogenase 3 (NAD+) beta | 1.49 | 3.50E-38 | 1.18 | 3.05E-06 | 1.73 | 0 | 1.91 | 0 |
| ldh3g | A_51_P136729 | NM_008323 | isocitrate dehydrogenase 3 (NAD+), gamma | 1.67 | 0 | 1.18 | 7.65E-08 | 1.59 | 0 | 1.91 | 0 |
| ldi1 | A_52_P441634 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.66 | 7.58E-26 | 1.34 | 0.017993 | 1.18 | 0.000134 | 2.59 | 0.000029 |
| Ldha | A_51_P364146 | NM_010699 | lactate dehydrogenase A | 1.32 | 9.85E-43 | 1.01 | 0.72351 | 1.07 | 0.009341 | 1.07 | 1.24E-07 |
| Ldhb | A_51_P409173 | NM_008492 | lactate dehydrogenase B | 1.76 | 0 | 1.07 | 0.070957 | 1.36 | 2.59E-23 | 1.81 | 0 |
| Ldhc | A_51_P242403 | NM_013580 | lactate dehydrogenase C | 1.00 | 1 | 0.99 | 0.900343 | 9.87 | 5.24E-27 | 36.24 | 1.00E-18 |
| Mcat | A_51_P314855 | NM_001030014 | malonyl CoA:ACP acyltransferase (mitochondrial) | 1.57 | 4.07E-34 | 1.29 | 3.84E-19 | 1.54 | 0 | 1.66 | 0 |
| Mdh1 | A_51_P218179 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 1.52 | 0 | 1.40 | 3.88E-23 | 1.96 | 0 | 2.30 | 0 |
| Mdh1 | A_52_P407796 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 1.63 | 1.06E-16 | 1.44 | 2.93E-14 | 2.01 | 5.33E-21 | 2.17 | 7.81E-29 |
| Mdh1 | A_52_P470451 | AK077724 | malate dehydrogenase 1, NAD (soluble) | 1.93 | 1.70E-43 | 1.17 | 0.003558 | 1.91 | 0 | 1.95 | 0 |
| *Mdh2 | A_51_P384879 | NM_008617 | malate dehydrogenase 2, NAD (mitochondrial) | 1.17 | 0.016985 | 1.21 | 0.000345 | 1.67 | 1.71E-11 | 1.89 | 1.12E-14 |
| Mecr | A_51_P386080 | NM_025297 | mitochondrial trans-2-enoyl-CoA reductase | 1.20 | 7.13E-16 | 1.21 | 7.43E-06 | 1.61 | 0 | 1.70 | 2.08E-29 |
| Mgll | A_51_P139920 | NM_011844 | monoglyceride lipase | 0.65 | 4.29E-21 | 1.19 | 0.000015 | 1.42 | 2.76E-06 | 1.50 | 5.83E-12 |
| Mgll | A_52_P568977 | AK006949 | monoglyceride lipase | 1.68 | 3.89E-22 | 1.48 | 1.57E-17 | 1.75 | 1.12E-21 | 2.28 | 0 |
| *Mgll | A_52_P609778 | NM_011844 | monoglyceride lipase | 1.57 | 2.82E-41 | 1.47 | 2.31E-17 | 1.95 | 4.21E-13 | 2.25 | 9.44E-19 |
| Mut | A_51_P193935 | NM_008650 | methylmalonyl-Coenzyme A mutase | 1.83 | 0 | 1.19 | 3.68E-06 | 1.30 | 3.21E-31 | 1.32 | 7.73E-17 |
| Mut | A_52_P633163 | NM_008650 | methylmalonyl-Coenzyme A mutase | 2.08 | 0 | 1.23 | 1.43E-14 | 1.36 | 0 | 1.41 | 2.79E-43 |
| Mvd | A_51_P355943 | NM_138656 | mevalonate (diphospho) decarboxylase | 0.74 | 2.46E-11 | 1.37 | 1.74E-10 | 1.28 | 3.91E-09 | 1.48 | 1.56E-30 |
| Ndufa1 | A_51_P472405 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.44 | 1.67E-12 | 1.13 | 0.004442 | 1.42 | 2.92E-13 | 1.52 | 2.27E-20 |
| Ndufa1 | A_52_P139747 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.35 | 9.93E-16 | 1.09 | 2.80E-06 | 1.31 | 3.39E-19 | 1.46 | 2.23E-29 |
| Ndufa5 | A_51_P170156 | NM_026614 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 | 1.43 | 3.05E-24 | 0.97 | 0.195335 | 1.15 | 1.92E-10 | 1.31 | 5.32E-32 |
| Ogdh | A_51_P122825 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.22 | 3.45E-21 | 1.01 | 0.593564 | 1.27 | 2.43E-37 | 1.41 | 4.55E-28 |
| Ogdh | A_52_P369310 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.26 | 3.66E-12 | 1.04 | 0.188474 | 1.28 | 4.41E-19 | 1.41 | 3.85E-23 |
| Oxct1 | A_51_P107321 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.47 | 3.80E-12 | 1.29 | 2.32E-07 | 1.25 | 1.72E-07 | 1.12 | 0.02451 |
| Oxct1 | A_51_P107326 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.31 | 2.18E-34 | 1.25 | 5.09E-14 | 1.18 | 1.10E-11 | 1.08 | 0.006906 |
| Oxct1 | A_52_P430058 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.41 | 6.46E-10 | 1.29 | 1.37E-09 | 1.25 | 5.79E-08 | 1.16 | 0.001094 |
| Oxct2a | A_51_P125056 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.13 | 0.433155 | 1.27 | 0.074115 | 1.80 | 0.00009 | 2.33 | 0.006431 |
| Oxsm | A_51_P312748 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 1.37 | 1.91E-26 | 1.40 | 8.27E-08 | 1.75 | 0 | 2.17 | 0 |
| Oxsm | A_52_P231635 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 1.17 | 6.10E-07 | 1.47 | 3.69E-15 | 2.15 | 0 | 2.62 | 0 |
| Pcca | A_51_P484254 | NM_144844 | propionyl-Coenzyme A carboxylase, alpha polypeptide | 2.34 | 0 | 1.41 | 2.14E-12 | 1.78 | 0 | 1.72 | 4.74E-27 |
| Pccb | A_51_P418259 | NM_025835 | propionyl Coenzyme A carboxylase, beta polypeptide | 1.80 | 0 | 1.04 | 0.10855 | 1.16 | 4.03E-08 | 1.21 | 2.18E-09 |
| Pcx | A_51_P480578 | NM_008797 | pyruvate carboxylase | 2.53 | 0 | 1.67 | 8.92E-28 | 1.95 | 2.69E-38 | 2.20 | 0 |
| Pdha1 | A_51_P321391 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 2.92 | 0 | 1.46 | 0 | 2.15 | 0 | 2.54 | 0 |
| Pdha1 | A_52_P581435 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 2.30 | 0 | 1.28 | 1.39E-28 | 1.67 | 0 | 1.88 | 0 |
| Pdhb | A_51_P321921 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 2.04 | 0 | 1.65 | 0 | 2.32 | 0 | 2.82 | 0 |

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|--------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Pdhb | A_52_P568792 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 2.19 | 0 | 1.69 | 0 | 2.49 | 0 | 3.05 | 0 |
| *Pdk4 | A_51_P350453 | NM_013743 | pyruvate dehydrogenase kinase, isoenzyme 4 | 1.08 | 5.25E-07 | 0.67 | 8.05E-06 | 0.73 | 2.17E-07 | 1.31 | 0.037345 |
| Peci | A_51_P394665 | NM_011868 | peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase | 1.03 | 0.293581 | 1.06 | 0.092592 | 1.24 | 8.88E-12 | 1.43 | 0 |
| Pecr | A_51_P291749 | NM_023523 | peroxisomal trans-2-enoyl-CoA reductase | 1.10 | 0.000388 | 1.19 | 0.00003 | 1.06 | 0.009964 | 1.32 | 3.40E-07 |
| Pfkfb2 | A_51_P184849 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.59 | 0 | 0.92 | 0.031929 | 0.86 | 2.12E-08 | 0.84 | 0.0002 |
| Pfkfb2 | A_51_P335251 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.54 | 1.11E-37 | 1.20 | 0.001143 | 0.96 | 0.699468 | 1.25 | 0.000217 |
| Pfkfb2 | A_52_P142912 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.60 | 5.09E-13 | 0.91 | 0.124836 | 0.90 | 0.1106 | 0.81 | 6.64E-06 |
| Pgam1 | A_51_P342669 | NM_023418 | phosphoglycerate mutase 1 | 1.10 | 0.000529 | 1.38 | 8.25E-25 | 1.73 | 0 | 2.03 | 0 |
| Pgam2 | A_51_P264495 | NM_018870 | phosphoglycerate mutase 2 | 1.99 | 1.48E-11 | 0.53 | 1.52E-11 | 0.58 | 0.056025 | 0.69 | 0.027313 |
| *Pgk1 | A_52_P84096 | BC011329 | phosphogluconate dehydrogenase | 0.81 | 5.75E-12 | 1.21 | 1.33E-12 | 1.31 | 7.47E-39 | 1.19 | 2.69E-19 |
| Pgk1 | A_51_P182828 | NM_008828 | phosphoglycerate kinase 1 | 1.32 | 9.26E-40 | 0.97 | 0.274628 | 1.20 | 1.79E-20 | 1.34 | 0 |
| Pgk1 | A_52_P600398 | NM_008828 | phosphoglycerate kinase 1 | 1.31 | 1.12E-17 | 1.00 | 0.956624 | 1.17 | 4.03E-11 | 1.39 | 0 |
| Pgk2 | A_51_P125487 | NM_031190 | phosphoglycerate kinase 2 | 1.57 | 7.19E-06 | 0.68 | 0.000755 | 0.49 | 2.48E-12 | 0.77 | 0.254138 |
| Pglis | A_51_P321794 | NM_025396 | 6-phosphogluconolactonase | 1.28 | 2.95E-24 | 1.07 | 0.001801 | 1.38 | 6.77E-27 | 1.66 | 0 |
| Pgm1 | A_51_P427530 | NM_025700 | phosphoglucomutase 1 | 0.61 | 2.09E-43 | 0.80 | 2.96E-22 | 0.75 | 3.81E-40 | 0.68 | 0 |
| Pgm2 | A_51_P368074 | NM_028132 | phosphoglucomutase 2 | 1.43 | 1.01E-18 | 0.87 | 0.000045 | 0.93 | 0.051034 | 0.98 | 0.350838 |
| Pgm5 | A_51_P451052 | NM_175013 | phosphoglucomutase 5 | 0.37 | 0 | 0.43 | 0 | 0.35 | 1.62E-29 | 0.33 | 1.52E-26 |
| Pgm5 | A_52_P860000 | NM_175013 | phosphoglucomutase 5 | 0.28 | 1.90E-20 | 0.31 | 3.02E-15 | 0.39 | 0.000886 | 0.32 | 0.000022 |
| Phka1 | A_52_P196825 | AK078633 | Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:7330411B16 | 1.49 | 8.91E-08 | 0.76 | 6.55E-11 | 0.70 | 0.000159 | 0.71 | 8.41E-07 |
| Phka1 | A_52_P278311 | NM_008832 | phosphorylase kinase alpha 1 | 1.47 | 5.17E-08 | 0.52 | 1.55E-09 | 0.49 | 0.000101 | 0.60 | 8.37E-07 |
| Phka2 | A_51_P239970 | AK051899 | phosphorylase kinase alpha 2 | 2.56 | 0.000086 | 1.80 | 0.000915 | 1.82 | 0.000945 | 0.93 | 0.75141 |
| Phka2 | A_51_P368950 | AK018208 | Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230017A12 | 3.01 | 0 | 1.38 | 2.80E-06 | 1.27 | 0.000957 | 1.25 | 0.00109 |
| Phka2 | A_52_P187217 | NM_172783 | phosphorylase kinase alpha 2 | 1.93 | 3.77E-12 | 1.11 | 0.264477 | 1.28 | 0.006506 | 1.14 | 0.156832 |
| Phka2 | A_52_P657963 | AK045618 | phosphorylase kinase alpha 2 | 2.55 | 0 | 1.35 | 1.54E-06 | 1.34 | 5.29E-16 | 1.26 | 0.008224 |
| Phka2 | A_52_P671916 | NM_172783 | phosphorylase kinase alpha 2 | 1.61 | 1.19E-38 | 0.93 | 0.019065 | 0.92 | 0.004802 | 0.94 | 0.074785 |
| Phkb | A_51_P270725 | AK089493 | phosphorylase kinase beta | 1.42 | 0 | 0.99 | 0.82274 | 1.02 | 0.252887 | 0.86 | 0.000272 |
| Phkb | A_51_P307624 | NM_199446 | phosphorylase kinase beta | 1.66 | 6.81E-36 | 0.99 | 0.721901 | 1.02 | 0.651257 | 1.02 | 0.725821 |
| Phkb | A_52_P513347 | NM_199446 | phosphorylase kinase beta | 1.77 | 1.52E-27 | 0.94 | 0.134205 | 1.01 | 0.684222 | 0.96 | 0.353904 |
| Phkg1 | A_51_P280890 | NM_011079 | phosphorylase kinase gamma 1 | 1.80 | 4.52E-13 | 0.42 | 4.54E-15 | 0.16 | 0 | 0.47 | 5.20E-10 |
| Pmvk | A_51_P492408 | NM_026784 | phosphomevalonate kinase | 1.21 | 2.96E-10 | 1.39 | 1.06E-19 | 1.53 | 2.40E-31 | 1.65 | 5.42E-31 |
| Pmvk | A_51_P492410 | NM_026784 | phosphomevalonate kinase | 1.22 | 5.67E-12 | 1.43 | 1.03E-22 | 1.61 | 5.96E-31 | 1.68 | 3.29E-31 |
| Ppap2a | A_51_P189104 | NM_008903 | phosphatidic acid phosphatase 2a | 0.58 | 0 | 0.95 | 0.304266 | 1.04 | 0.203503 | 1.09 | 0.000674 |
| Ppap2a | A_51_P189105 | AK077275 | phosphatidic acid phosphatase 2a | 0.62 | 1.66E-39 | 1.06 | 0.081349 | 1.15 | 4.39E-08 | 1.22 | 5.26E-13 |
| Ppap2a | A_52_P7937 | NM_008903 | phosphatidic acid phosphatase 2a | 0.52 | 0 | 1.09 | 0.062953 | 1.18 | 7.25E-15 | 1.24 | 7.56E-12 |

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|----------|--------------|-----------|---|------|----------|-------|----------|------|----------|------|----------|
| Ppara | A_51_P348334 | NM_011144 | peroxisome proliferator activated receptor alpha | 2.40 | 0 | 1.60 | 0 | 2.16 | 0 | 3.17 | 0 |
| Pparg | A_51_P106799 | NM_011146 | peroxisome proliferator activated receptor gamma | 1.31 | 0 | 1.12 | 5.73E-07 | 1.10 | 4.63E-06 | 1.06 | 0.13698 |
| Ppargc1a | A_51_P279038 | NM_008904 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 2.61 | 0 | 0.80 | 1.24E-10 | 1.13 | 0.000617 | 1.65 | 0 |
| Ppargc1a | A_52_P5945 | AK032149 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 1.98 | 0 | 0.77 | 6.40E-11 | 1.04 | 0.202626 | 1.34 | 4.12E-27 |
| Ppargc1b | A_51_P294891 | NM_133249 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.63 | 4.13E-17 | 0.95 | 0.011936 | 1.37 | 6.41E-23 | 1.83 | 0 |
| Ppargc1b | A_52_P293222 | AK042378 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 2.11 | 7.29E-34 | 1.10 | 0.00366 | 1.67 | 2.97E-14 | 2.33 | 1.54E-44 |
| Ppargc1b | A_52_P526724 | NM_133249 | Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230304K20 | 1.41 | 3.72E-14 | 0.91 | 0.000335 | 1.30 | 6.50E-14 | 1.80 | 0 |
| Ppargc1b | A_52_P883463 | AK045690 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.84 | 0 | 0.83 | 7.91E-07 | 1.21 | 9.04E-13 | 1.50 | 3.25E-26 |
| Ppp1cb | A_51_P342716 | NM_172707 | protein phosphatase 1, catalytic subunit, beta isoform | 0.62 | 0 | 0.78 | 3.30E-21 | 0.79 | 5.03E-30 | 0.77 | 1.00E-18 |
| Ppp1cc | A_52_P519508 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 0.85 | 1.36E-09 | 0.84 | 4.87E-17 | 0.76 | 7.39E-33 | 0.72 | 3.44E-33 |
| Ppt2 | A_52_P238816 | NM_019441 | palmitoyl-protein thioesterase 2 | 1.43 | 8.38E-15 | 1.19 | 0.000216 | 1.41 | 7.11E-40 | 1.54 | 1.23E-39 |
| Pygb | A_52_P350664 | NM_153781 | brain glycogen phosphorylase | 1.41 | 6.87E-11 | 0.91 | 0.019785 | 0.90 | 0.006818 | 0.85 | 0.000025 |
| Pygl | A_51_P452779 | NM_133198 | liver glycogen phosphorylase | 2.46 | 0 | 1.23 | 0.002814 | 1.42 | 5.72E-14 | 1.46 | 1.33E-16 |
| Pygl | A_52_P320181 | AK083075 | liver glycogen phosphorylase | 4.86 | 0 | 2.33 | 9.14E-24 | 2.76 | 0 | 2.32 | 2.37E-15 |
| Pygm | A_51_P458973 | NM_011224 | muscle glycogen phosphorylase | 1.51 | 3.50E-08 | 0.46 | 6.02E-13 | 0.46 | 0.0064 | 0.49 | 5.45E-06 |
| Scd2 | A_51_P129464 | NM_009128 | stearoyl-Coenzyme A desaturase 2 | 1.00 | 0.987206 | 1.48 | 1.01E-06 | 1.23 | 0.001449 | 0.90 | 0.079231 |
| Scd4 | A_52_P374877 | NM_183216 | stearoyl-coenzyme A desaturase 4 | 0.26 | 1.95E-17 | 0.36 | 7.46E-09 | 0.28 | 9.81E-45 | 0.90 | 0.515866 |
| *Sdha | A_51_P410823 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 1.86 | 1.47E-43 | 1.02 | 0.568497 | 1.42 | 6.81E-32 | 1.58 | 0 |
| Sdha | A_52_P109503 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 1.65 | 8.95E-43 | 1.23 | 3.71E-13 | 1.66 | 0 | 1.84 | 0 |
| *Sdhb | A_51_P234853 | NM_023374 | succinate dehydrogenase complex, subunit B, iron sulfur (lp) | 1.76 | 0 | 1.20 | 8.27E-09 | 1.71 | 0 | 1.96 | 0 |
| Sdhc | A_51_P106373 | NM_025321 | succinate dehydrogenase complex, subunit C, integral membrane protein | 1.32 | 1.27E-21 | 1.10 | 4.33E-06 | 1.35 | 6.47E-37 | 1.48 | 1.90E-35 |
| Sdhc | A_52_P875481 | AK031343 | Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030410A06 | 1.83 | 0.000105 | 1.01 | 0.957342 | 0.78 | 0.236953 | 1.16 | 0.361315 |
| Sdhd | A_51_P260871 | NM_025848 | succinate dehydrogenase complex, subunit D, integral membrane protein | 1.29 | 1.13E-10 | 1.11 | 0.001444 | 1.57 | 3.53E-27 | 1.90 | 0 |
| Slc25a1 | A_51_P350922 | NM_153150 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 2.20 | 0 | 2.02 | 0 | 2.79 | 0 | 2.92 | 0 |
| *Slc27a1 | A_51_P117477 | NM_011977 | solute carrier family 27 (fatty acid transporter), member 1 | 0.75 | 0 | 99.00 | 0.256111 | 1.39 | 4.66E-33 | 1.56 | 0 |
| Slc27a1 | A_52_P199905 | CB588406 | AGENCOURT_12600125 NIH_MGC_136 Mus musculus cDNA clone IMAGE:30290747 5', mRNA sequence. | 0.84 | 3.58E-13 | 1.10 | 0.063034 | 1.60 | 1.01E-23 | 1.95 | 0 |
| Slc27a2 | A_52_P154971 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 0.66 | 0.08825 | 0.95 | 0.352499 | 1.05 | 0.478478 | 2.65 | 3.86E-11 |
| Slc27a4 | A_51_P408609 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 0.96 | 0.385821 | 1.25 | 0.000383 | 1.31 | 2.76E-06 | 1.49 | 7.09E-19 |
| Slc27a4 | A_52_P61854 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 0.83 | 0.000053 | 1.20 | 0.000044 | 1.43 | 1.85E-21 | 1.67 | 1.00E-34 |

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|----------|--------------|--------------|--|------|----------|------|----------|------|----------|-------|----------|
| Slc27a5 | A_51_P289742 | NM_009512 | solute carrier family 27 (fatty acid transporter), member 5 | 0.40 | 3.57E-13 | 0.78 | 0.028052 | 0.79 | 0.004282 | 1.53 | 0.005496 |
| Slc2a2 | A_51_P185693 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 0.30 | 9.17E-09 | 0.96 | 0.735134 | 0.65 | 0.020819 | 0.98 | 0.910207 |
| *Slc2a4 | A_51_P217498 | NM_009204 | solute carrier family 2 (facilitated glucose transporter), member 4 | 2.14 | 0 | 1.06 | 0.125701 | 1.45 | 8.00E-26 | 1.58 | 0 |
| Sqle | A_51_P450487 | NM_009270 | squalene epoxidase | 0.51 | 6.70E-42 | 0.87 | 0.015337 | 0.75 | 3.28E-08 | 0.73 | 4.16E-14 |
| Sucla2 | A_51_P111554 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 1.15 | 5.07E-06 | 1.32 | 4.54E-24 | 1.88 | 0 | 2.07 | 0 |
| *Sucla2 | A_52_P533792 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 1.50 | 2.87E-19 | 1.46 | 2.92E-38 | 2.33 | 1.15E-42 | 2.89 | 0 |
| Sucla2 | A_52_P762514 | AK016060 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 0.76 | 0.035691 | 0.73 | 0.121576 | 0.70 | 0.000017 | 0.80 | 0.029037 |
| Sucg1 | A_51_P491227 | NM_019879 | succinate-CoA ligase, GDP-forming, alpha subunit | 1.21 | 6.74E-18 | 1.13 | 1.75E-11 | 1.58 | 0 | 1.98 | 0 |
| *Taldo1 | A_51_P401958 | NM_011528 | transaldolase 1 | 1.60 | 3.91E-38 | 1.33 | 6.41E-12 | 1.61 | 0 | 1.62 | 0 |
| *Tkt | A_51_P394515 | NM_009388 | transketolase | 4.05 | 0 | 1.51 | 6.24E-13 | 1.86 | 0 | 2.04 | 0 |
| Tkt | A_52_P624447 | NM_009388 | transketolase | 2.70 | 1.16E-43 | 1.66 | 2.07E-12 | 1.99 | 0 | 1.96 | 0 |
| Tkt | A_52_P631197 | AK050793 | transketolase | 4.56 | 1.32E-28 | 2.61 | 1.49E-21 | 2.13 | 6.89E-12 | 2.11 | 4.33E-08 |
| Tpi1 | A_51_P433824 | NM_009415 | triosephosphate isomerase 1 | 1.00 | 0.899227 | 1.23 | 8.20E-16 | 1.34 | 4.50E-28 | 1.49 | 0 |
| Tpi1 | A_52_P116102 | AK053780 | Mus musculus 0 day neonate eyeball cDNA, RIKEN library, clone:E130308D14 product:triosephosphate isomerase | 1.40 | 3.38E-11 | 1.17 | 0.000215 | 1.01 | 0.784684 | 1.29 | 2.62E-11 |
| Ucp1 | A_51_P426353 | NM_009463 | uncoupling protein 1 (mitochondrial, proton carrier) | 0.42 | 0.000062 | 3.13 | 0 | 6.79 | 0 | 10.46 | 0 |
| Ucp2 | A_51_P297105 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.37 | 0 | 0.96 | 0.124993 | 0.97 | 0.202268 | 0.93 | 0.020408 |
| Ucp2 | A_52_P499675 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.64 | 0.003502 | 1.54 | 6.23E-12 | 1.82 | 1.02E-08 | 1.40 | 0.000568 |
| Ucp2 | A_52_P90265 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.25 | 0 | 0.99 | 0.904595 | 1.02 | 0.48046 | 0.90 | 0.18525 |
| Ugp2 | A_51_P475580 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 1.24 | 5.26E-25 | 0.79 | 7.29E-33 | 0.75 | 0 | 0.81 | 2.22E-13 |
| Uqcrcb | A_51_P472671 | NM_026219 | ubiquinol-cytochrome c reductase binding protein | 1.81 | 0 | 1.40 | 1.77E-34 | 1.82 | 0 | 2.14 | 0 |
| *Uqcrc1 | A_51_P109835 | NM_025407 | ubiquinol-cytochrome c reductase core protein 1 | 1.41 | 1.47E-19 | 0.99 | 0.49 | 1.35 | 2.17E-31 | 1.54 | 1.43E-32 |
| *Uqcrc2 | A_51_P128648 | NM_025899 | ubiquinol cytochrome c reductase core protein 2 | 1.77 | 1.98E-36 | 1.25 | 0 | 1.79 | 0 | 2.1 | 0 |
| *Uqcrcs1 | A_51_P361951 | NM_025710 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 | 1.70 | 1.02E-39 | 1.28 | 4.81E-26 | 1.89 | 0 | 2.23 | 0 |
| Uqcrcb | A_51_P431852 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.65 | 7.97E-10 | 1.28 | 1.05E-07 | 1.57 | 6.97E-12 | 1.83 | 1.44E-16 |
| Uqcrcb | A_52_P541875 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.89 | 7.02E-22 | 1.43 | 4.96E-20 | 1.81 | 6.82E-33 | 1.97 | 0 |
| *Uqcrcq | A_52_P370484 | NM_025352 | ubiquinol-cytochrome c reductase, complex III subunit VII | 1.35 | 3.90E-07 | 1.18 | 3.94E-08 | 1.60 | 1.50E-14 | 1.80 | 4.07E-18 |
| Acox3 | A_52_P745 | NM_030721 | acyl-Coenzyme A oxidase 3, pristanoyl | 1.07 | 0.012963 | 1.01 | 0.591271 | 0.99 | 0.691992 | 1.08 | 0.006656 |
| Acs15 | A_52_P593037 | NM_027976 | acyl-CoA synthetase long-chain family member 5 | 1.02 | 0.355204 | 0.97 | 0.454445 | 0.81 | 2.28E-19 | 1.11 | 0.077691 |
| Acs16 | A_52_P352187 | NM_001033599 | acyl-CoA synthetase long-chain family member 6 | 0.89 | 0.347724 | 0.78 | 0.063197 | 0.87 | 0.230061 | 1.00 | 0.989916 |
| Adcy1 | A_51_P409900 | NM_009622 | adenylate cyclase 1 | 1.20 | 0.182849 | 0.84 | 0.152138 | 1.03 | 0.757305 | 0.92 | 0.402893 |
| Adcy1 | A_52_P240164 | NM_009622 | adenylate cyclase 1 | 1.23 | 0.001905 | 0.99 | 0.773788 | 1.26 | 2.54E-08 | 1.27 | 6.90E-08 |
| Adcy1 | A_52_P240170 | BC050125 | adenylate cyclase 1 | 1.29 | 3.33E-22 | 1.10 | 0.010514 | 1.14 | 0.000899 | 1.13 | 0.004864 |
| Adcy4 | A_51_P229911 | NM_080435 | adenylate cyclase 4 | 1.05 | 0.028168 | 1.10 | 0.000121 | 1.00 | 0.862828 | 1.12 | 7.65E-07 |

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|----------|---------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Adcy6 | A_51_P243134 | NM_007405 | adenylate cyclase 6 | 0.87 | 0.000478 | 1.03 | 0.50625 | 1.15 | 0.000063 | 1.24 | 4.61E-10 |
| Adcy8 | A_51_P303061 | NM_009623 | adenylate cyclase 8 | 0.95 | 0.684212 | 0.77 | 0.243998 | 0.91 | 0.536823 | 2.65 | 0.00169 |
| Adcy9 | A_51_P501538 | NM_009624 | adenylate cyclase 9 | 1.19 | 2.12E-09 | 0.92 | 0.038269 | 0.89 | 0.000108 | 0.90 | 0.005309 |
| Adh1 | A_52_P835985 | AK082149 | alcohol dehydrogenase 1 (class I) | 0.99 | 0.876288 | 0.77 | 0.381341 | 1.07 | 0.669994 | 0.95 | 0.734211 |
| Adh5 | A_51_P404275 | NM_007410 | alcohol dehydrogenase 5 (class III), chi polypeptide | 0.92 | 0.000204 | 0.96 | 0.248971 | 0.97 | 0.043223 | 0.96 | 0.086322 |
| Adh6a | A_51_P299608 | AK028114 | alcohol dehydrogenase 6A (class V) | 1.00 | 1 | 0.98 | 0.820767 | 1.00 | 1 | 0.95 | 0.678137 |
| Adh6-ps1 | A_51_P120027 | AK004863 | alcohol dehydrogenase 6 (class V), pseudogene 1 | 1.00 | 1 | 1.10 | 0.595158 | 1.00 | 1 | 1.00 | 1 |
| Aldh2 | A_52_P116134 | NM_009656 | aldehyde dehydrogenase 2, mitochondrial | 1.14 | 0.000701 | 0.87 | 0.000112 | 0.79 | 9.73E-08 | 0.84 | 0.000233 |
| Aldh2 | A_52_P13109 | AK163452 | aldehyde dehydrogenase 2, mitochondrial | 0.85 | 0.000098 | 1.10 | 0.00041 | 1.07 | 0.010617 | 0.96 | 0.3178 |
| Aldh7a1 | A_51_P470414 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 1.36 | 0.02373 | 1.23 | 0.009783 | 1.28 | 0.012894 | 1.52 | 0.034321 |
| Aldh9a1 | A_52_P265877 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 1.04 | 0.418261 | 0.86 | 9.77E-06 | 1.02 | 0.478382 | 1.01 | 0.782009 |
| Aldoa | A_51_P216905 | NM_007438 | aldolase 1, A isoform | 0.86 | 0.058289 | 0.93 | 0.131511 | 1.00 | 0.975145 | 1.02 | 0.794427 |
| Aldoa | A_52_P98387 | NM_007438 | aldolase 1, A isoform | 0.88 | 0.101458 | 0.92 | 0.032198 | 1.02 | 0.746366 | 1.03 | 0.545286 |
| Apoa1 | A_51_P408082 | NM_009692 | apolipoprotein A-I | 0.83 | 0.019394 | 1.02 | 0.776411 | 1.17 | 0.005719 | 1.72 | 0.00998 |
| Apob | A_51_P380650 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 1.39 | 0.231049 | 0.99 | 0.95816 | 1.20 | 0.449147 | 0.94 | 0.743505 |
| Apob | A_51_P436690 | BC028880 | apolipoprotein B | 1.00 | 1 | 0.81 | 0.408211 | 0.96 | 0.656631 | 1.29 | 0.211563 |
| Atp5b | A_51_P207636 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.14 | 0.000011 | 1.21 | 0.000014 | 1.53 | 0 | 1.65 | 5.10E-27 |
| Atp6ap1 | A_51_P447988 | NM_018794 | ATPase, H+ transporting, lysosomal accessory protein 1 | 0.93 | 0.018787 | 0.96 | 0.188751 | 0.95 | 0.031868 | 0.86 | 1.23E-06 |
| Atp6v1g1 | A_51_P140171 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 1.21 | 1.51E-11 | 0.99 | 0.678773 | 1.00 | 0.881593 | 1.03 | 0.211064 |
| Atp6v1g1 | A_52_P349738 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 0.96 | 0.06312 | 0.89 | 4.54E-06 | 0.91 | 1.20E-12 | 0.90 | 0.000475 |
| Atp6v1h | A_51_P105604 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.95 | 0.002579 | 1.13 | 0.000013 | 1.25 | 2.42E-19 | 1.30 | 2.80E-18 |
| Atp6v1h | A_52_P112888 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.87 | 1.95E-06 | 1.03 | 0.474404 | 1.26 | 2.45E-17 | 1.24 | 9.44E-13 |
| Atp7a | A_51_P312497 | NM_009726 | ATPase, Cu++ transporting, alpha polypeptide | 0.84 | 2.37E-26 | 0.94 | 0.025972 | 0.82 | 1.50E-14 | 0.84 | 1.29E-09 |
| Atp7a | A_51_P473179 | AK033254 | ATPase, Cu++ transporting, alpha polypeptide | 1.24 | 3.32E-13 | 1.09 | 0.02678 | 0.88 | 0.000192 | 0.90 | 0.07406 |
| Bcnp1 | A_52_P1053160 | AK158308 | BCNP1 homolog | 1.14 | 0.023369 | 0.95 | 0.137616 | 0.95 | 0.312075 | 1.11 | 0.005399 |
| Coq2 | A_51_P447752 | NM_027978 | coenzyme Q2 homolog, prenyltransferase (yeast) | 1.24 | 3.56E-14 | 1.07 | 0.005512 | 1.13 | 0.000575 | 1.19 | 1.37E-15 |
| Cpt1c | A_51_P177562 | NM_153679 | carnitine palmitoyltransferase 1c | 1.09 | 0.428115 | 0.96 | 0.669906 | 0.87 | 0.101224 | 0.80 | 0.04668 |
| Cpt1c | A_52_P269942 | NM_153679 | carnitine palmitoyltransferase 1c | 1.12 | 0.007636 | 1.00 | 0.977338 | 0.88 | 1.20E-06 | 0.81 | 1.06E-10 |
| Crot | A_51_P489153 | NM_023733 | carnitine O-octanoyltransferase | 1.21 | 5.39E-32 | 1.00 | 0.901364 | 1.02 | 0.394437 | 1.02 | 0.411174 |
| Crot | A_52_P656336 | NM_023733 | carnitine O-octanoyltransferase | 1.02 | 0.714633 | 1.05 | 0.106651 | 1.26 | 8.64E-16 | 1.16 | 0.002621 |
| Cyp19a1 | A_51_P474551 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.50 | 0.043947 | 1.12 | 0.457929 | 0.99 | 0.923294 | 1.11 | 0.495814 |
| Cyp19a1 | A_52_P591961 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp1a2 | A_51_P450140 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 1.24 | 0.31197 | 0.97 | 0.874319 | 0.86 | 0.227157 | 0.82 | 0.195549 |
| Cyp1a2 | A_52_P595871 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 1.00 | 1 | 0.79 | 0.19904 | 1.00 | 0.924017 | 1.02 | 0.814531 |

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|---------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Cyp1b1 | A_51_P255456 | NM_009994 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 0.86 | 0.040205 | 0.92 | 0.218161 | 0.83 | 0.000799 | 0.80 | 0.000028 |
| Cyp1b1 | A_52_P297822 | AK016699 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 0.59 | 0.001119 | 0.90 | 0.194968 | 1.01 | 0.955016 | 0.85 | 0.269662 |
| Cyp2b19 | A_52_P421626 | AK029227 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 1.00 | 1 | 1.30 | 0.331601 | 1.00 | 1 | 1.97 | 0.071727 |
| Cyp2c37 | A_51_P498882 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 1.02 | 0.709079 | 0.93 | 0.048272 | 0.99 | 0.740926 | 1.05 | 0.514247 |
| Cyp2c37 | A_52_P625249 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 1.07 | 0.095917 | 0.95 | 0.27194 | 1.07 | 0.00042 | 1.15 | 0.00029 |
| Cyp2c38 | A_51_P342206 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2c38 | A_52_P468564 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2g1 | A_51_P137452 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 1.04 | 0.850515 | 1.05 | 0.644875 | 1.24 | 0.122211 | 1.09 | 0.501205 |
| Cyp2g1 | A_52_P481346 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 0.97 | 0.721233 |
| Cyp2s1 | A_52_P456837 | AK054324 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp3a25 | A_52_P380314 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 1.02 | 0.780025 | 0.67 | 0.158943 | 1.03 | 0.881445 | 1.12 | 0.536849 |
| Cyp3a44 | A_52_P366803 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp4a10 | A_52_P6588 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.81 | 0.217329 | 1.01 | 0.94825 | 1.38 | 0.011993 | 1.25 | 0.266291 |
| Cyp51 | A_52_P778750 | AK035338 | Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530019F09 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Dgat2 | A_52_P359739 | NM_026384 | diacylglycerol O-acyltransferase 2 | 1.16 | 0.029512 | 1.26 | 0.005157 | 1.24 | 0.000893 | 1.16 | 0.02989 |
| Dgat2 | A_52_P592909 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.78 | 0.009147 | 1.16 | 0.121883 | 1.11 | 0.304754 | 0.92 | 0.448932 |
| Eno1 | A_52_P349939 | NM_023119 | enolase 1, alpha non-neuron | 0.95 | 0.550728 | 1.00 | 0.981093 | 1.11 | 0.24385 | 1.10 | 0.259116 |
| Fabp4 | A_51_P336830 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.82 | 0.214911 | 0.97 | 0.808568 | 1.32 | 0.065254 | 1.04 | 0.833539 |
| Fabp4 | A_51_P336833 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.79 | 0.017142 | 1.00 | 0.943548 | 1.12 | 0.175331 | 1.06 | 0.490436 |
| Fabp4 | A_52_P564544 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.82 | 1.01E-08 | 1.00 | 0.949544 | 1.09 | 0.040001 | 1.19 | 4.98E-10 |
| Fntb | A_52_P235241 | NM_145927 | farnesyltransferase, CAAX box, beta | 0.87 | 1.23E-07 | 1.23 | 2.03E-10 | 1.29 | 1.26E-15 | 1.11 | 0.000075 |
| G6pc | A_51_P462385 | NM_008061 | glucose-6-phosphatase, catalytic | 1.06 | 0.088893 | 0.90 | 1.59E-10 | 0.87 | 0.000101 | 1.00 | 0.958128 |
| Gck | A_52_P66580 | BC011139 | glucokinase | 1.14 | 0.000029 | 1.01 | 0.815681 | 1.08 | 0.01196 | 1.08 | 0.017214 |
| Gckr | A_51_P198694 | NM_144909 | glucokinase regulatory protein | 1.28 | 0.0001 | 0.96 | 0.479682 | 0.87 | 0.023119 | 1.18 | 0.113194 |
| Ggps1 | A_51_P179604 | NM_010282 | PREDICTED: Mus musculus geranylgeranyl diphosphate synthase 1, transcript variant 4 (Ggps1), mRNA. | 0.87 | 0.000012 | 1.09 | 0.030017 | 1.12 | 0.000841 | 1.06 | 0.111861 |
| Ggps1 | A_51_P469902 | XM_977926 | geranylgeranyl diphosphate synthase 1 | 1.21 | 7.18E-32 | 1.03 | 0.328169 | 1.05 | 0.003303 | 1.06 | 0.103975 |
| Gpi1 | A_51_P426886 | NM_008155 | glucose phosphate isomerase 1 | 0.94 | 0.014148 | 0.94 | 0.001549 | 1.04 | 0.009042 | 1.10 | 1.02E-09 |
| Gpi1 | A_52_P347412 | L09104 | glucose phosphate isomerase 1 | 1.18 | 2.34E-08 | 0.99 | 0.800149 | 1.05 | 0.419632 | 1.01 | 0.825067 |
| Gyk | A_52_P379205 | AK086200 | glycerol kinase | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Hk1 | A_51_P249024 | NM_010438 | hexokinase 1 | 1.10 | 0.0013 | 0.97 | 0.117679 | 1.04 | 0.225444 | 1.02 | 0.386539 |
| Hmgcl | A_51_P308961 | NM_008254 | 3-hydroxy-3-methylglutaryl-Coenzyme A lyase | 1.27 | 2.34E-11 | 0.94 | 0.019789 | 0.99 | 0.859586 | 1.05 | 0.066699 |
| Hmgcll1 | A_52_P197722 | NM_173731 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 | 0.93 | 0.597122 | 0.95 | 0.589395 | 0.65 | 0.001177 | 0.66 | 0.014421 |
| Idh2 | A_51_P331507 | NM_173011 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 1.09 | 0.002825 | 0.92 | 0.016238 | 1.03 | 0.499745 | 1.01 | 0.574054 |
| Idi1 | A_51_P329711 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.77 | 1.17E-09 | 1.26 | 0.064896 | 0.98 | 0.666972 | 2.07 | 0.004069 |

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|---------|---------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Ldha | A_51_P364140 | NM_010699 | lactate dehydrogenase A | 1.24 | 0.050787 | 1.00 | 0.969275 | 1.19 | 0.071834 | 0.93 | 0.4733 |
| Lipe | A_51_P435363 | NM_010719 | lipase, hormone sensitive | 1.24 | 0.000579 | 0.89 | 0.032418 | 0.98 | 0.77148 | 1.07 | 0.269167 |
| Lipe | A_51_P435366 | NM_010719 | lipase, hormone sensitive | 1.29 | 1.52E-12 | 0.89 | 0.010097 | 1.04 | 0.365704 | 1.05 | 0.165093 |
| Lpl | A_51_P259296 | NM_008509 | lipoprotein lipase | 0.86 | 0.219408 | 1.10 | 0.133678 | 1.04 | 0.723662 | 0.89 | 0.230061 |
| Lpl | A_52_P257812 | NM_008509 | lipoprotein lipase | 0.79 | 0.000038 | 1.00 | 0.978509 | 0.97 | 0.484361 | 0.96 | 0.502204 |
| Mgll | A_51_P352549 | AK079089 | Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330168D17 | 1.04 | 0.799752 | 1.59 | 0.029078 | 1.29 | 0.217801 | 1.34 | 0.238741 |
| Mut | A_52_P362959 | AK051851 | methylmalonyl-Coenzyme A mutase | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Mvk | A_51_P169527 | NM_023556 | mevalonate kinase | 0.98 | 0.716153 | 1.14 | 0.002949 | 1.03 | 0.364409 | 1.14 | 0.014182 |
| Mvk | A_52_P569067 | NM_023556 | mevalonate kinase | 0.89 | 4.62E-08 | 1.10 | 0.001679 | 0.97 | 0.391819 | 1.11 | 0.005468 |
| Oxct2a | A_51_P125062 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.11 | 0.128763 | 1.02 | 0.841826 | 1.04 | 0.659152 | 1.16 | 0.138178 |
| Pck2 | A_52_P21659 | NM_028994 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | 0.95 | 0.106455 | 0.93 | 0.000957 | 0.81 | 1.76E-15 | 0.83 | 4.53E-15 |
| Pdha2 | A_51_P519857 | NM_008811 | pyruvate dehydrogenase E1 alpha 2 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.04 | 0.673396 |
| Pfkfb2 | A_52_P31125 | BC018418 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.17 | 0.15459 | 1.27 | 1.75E-07 | 1.19 | 0.042557 | 1.07 | 0.387925 |
| Pfkl | A_51_P310896 | NM_008826 | phosphofructokinase, liver, B-type | 0.95 | 0.456149 | 0.96 | 0.512786 | 0.98 | 0.737186 | 1.03 | 0.578316 |
| Pgd | A_51_P391996 | BC011329 | phosphogluconate dehydrogenase | 0.81 | 0.000035 | 1.23 | 0.000035 | 1.29 | 2.07E-06 | 1.30 | 6.00E-07 |
| Pgm3 | A_51_P208987 | NM_028352 | phosphoglucomutase 3 | 1.22 | 0.000028 | 0.99 | 0.705489 | 1.12 | 0.021804 | 1.11 | 0.033879 |
| Pgm3 | A_52_P341449 | NM_028352 | phosphoglucomutase 3 | 0.88 | 0.000056 | 0.87 | 0.00035 | 0.94 | 0.186558 | 0.90 | 0.001835 |
| Pgm5 | A_52_P229924 | NM_175013 | phosphoglucomutase 5 | 0.83 | 0.000092 | 0.82 | 0.005585 | 0.89 | 0.007757 | 0.86 | 0.000302 |
| Phkb | A_52_P342907 | BC051503 | phosphorylase kinase beta | 1.00 | 1 | 1.01 | 0.908122 | 1.10 | 0.56797 | 0.95 | 0.71096 |
| Phkg2 | A_51_P235909 | NM_026888 | phosphorylase kinase, gamma 2 (testis) | 1.09 | 0.01052 | 0.91 | 0.008279 | 0.92 | 0.031081 | 0.95 | 0.134684 |
| Phkg2 | A_52_P19446 | AK089062 | phosphorylase kinase, gamma 2 (testis) | 1.07 | 0.260054 | 0.93 | 0.277702 | 0.87 | 0.022259 | 0.94 | 0.415741 |
| Pklr | A_51_P176042 | NM_013631 | pyruvate kinase liver and red blood cell | 0.88 | 0.0008 | 0.86 | 0.00399 | 0.85 | 0.000051 | 0.92 | 0.276819 |
| Pkm2 | A_51_P428913 | D38379 | pyruvate kinase, muscle | 1.28 | 5.22E-08 | 0.81 | 3.81E-10 | 0.82 | 6.03E-06 | 0.85 | 1.66E-09 |
| Pkm2 | A_52_P150212 | NM_011099 | pyruvate kinase, muscle | 1.22 | 9.00E-06 | 0.87 | 0.003785 | 0.86 | 0.002962 | 0.88 | 0.004118 |
| Pkm2 | A_52_P328249 | AK083076 | pyruvate kinase, muscle | 1.01 | 0.819911 | 1.11 | 0.007559 | 1.14 | 0.000067 | 1.19 | 0.000051 |
| Ppard | A_51_P271556 | NM_011145 | peroxisome proliferator activator receptor delta | 0.87 | 0.049211 | 1.05 | 0.529051 | 1.07 | 0.180561 | 1.17 | 0.031455 |
| Ppp1ca | A_51_P509389 | NM_031868 | protein phosphatase 1, catalytic subunit, alpha isoform | 1.01 | 0.704571 | 1.01 | 0.68392 | 1.08 | 0.000249 | 1.11 | 2.42E-07 |
| Ppp1cc | A_52_P540434 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 0.85 | 1.18E-19 | 0.90 | 2.66E-08 | 0.84 | 4.49E-14 | 0.83 | 2.44E-30 |
| Pygb | A_51_P485810 | NM_153781 | brain glycogen phosphorylase | 1.25 | 0.010486 | 0.96 | 0.679262 | 0.88 | 0.18676 | 0.91 | 0.345052 |
| Scd1 | A_52_P682382 | NM_009127 | stearoyl-Coenzyme A desaturase 1 | 0.98 | 0.870532 | 0.82 | 0.041844 | 0.89 | 0.340263 | 0.65 | 0.001507 |
| Scd3 | A_51_P446045 | NM_024450 | stearoyl-coenzyme A desaturase 3 | 0.95 | 0.143426 | 1.00 | 0.943486 | 1.14 | 1.08E-07 | 1.08 | 0.085823 |
| Scd4 | A_52_P603237 | BC038322 | stearoyl-coenzyme A desaturase 4 | 0.91 | 0.501782 | 0.61 | 0.060544 | 0.95 | 0.626895 | 0.99 | 0.96248 |
| Slc27a2 | A_51_P484551 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 1.53 | 0.31249 | 0.89 | 0.600611 | 1.00 | 1 | 1.76 | 0.001391 |
| Slc27a2 | A_52_P1083677 | AK038847 | solute carrier family 27 (fatty acid transporter), member 2 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |

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|--------|---------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|
| | Slc27a3 | A_51_P133252 | NM_011988 | solute carrier family 27 (fatty acid transporter), member 3 | 0.92 | 0.000292 | 1.17 | 5.27E-10 | 1.02 | 0.386599 | 0.93 | 0.028266 |
| | Slc27a6 | A_51_P211616 | AK028699 | solute carrier family 27 (fatty acid transporter), member 6 | 0.75 | 0.377984 | 1.07 | 0.739109 | 1.06 | 0.743573 | 1.11 | 0.581475 |
| | Slc2a2 | A_52_P409988 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 1.18 | 4.74E-09 | 1.06 | 0.094112 | 1.17 | 0.000185 | 1.25 | 1.30E-07 |
| | Suc1g2 | A_51_P478672 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 1.30 | 5.77E-08 | 0.99 | 0.742431 | 1.05 | 0.241363 | 1.09 | 0.053324 |
| | Suc1g2 | A_52_P58181 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 1.18 | 8.07E-13 | 0.89 | 1.03E-09 | 0.99 | 0.77572 | 1.01 | 0.51572 |
| | Ugp2 | A_52_P42242 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 1.24 | 2.28E-15 | 0.80 | 2.67E-22 | 0.80 | 8.70E-10 | 0.80 | 5.89E-44 |
| Soleus | Acaa1a | A_52_P155990 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.32 | 1.17E-11 | 1.14 | 0.028427 | 1.22 | 0.0002 | 1.20 | 0.000123 |
| | Acaa2 | A_51_P125260 | NM_177470 | acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) | 1.37 | 3.94E-36 | 1.14 | 0.010651 | 1.19 | 1.59E-09 | 1.09 | 0.000115 |
| | *Acaca | A_51_P439426 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.57 | 2.15E-08 | 0.75 | 0.004111 | 0.60 | 1.07E-21 | 0.84 | 0.001293 |
| | Acaca | A_52_P132591 | AF374167 | acetyl-Coenzyme A carboxylase alpha | 0.80 | 0.150741 | 0.73 | 0.000566 | 0.88 | 0.12172 | 0.70 | 0.002174 |
| | Acaca | A_52_P318040 | AK132628 | acetyl-Coenzyme A carboxylase alpha | 0.56 | 5.10E-26 | 0.76 | 3.88E-10 | 0.80 | 9.13E-09 | 0.90 | 0.007875 |
| | Acaca | A_52_P595124 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.74 | 3.08E-14 | 0.81 | 0.000278 | 0.98 | 0.798377 | 0.82 | 1.03E-10 |
| | Acads | A_52_P367745 | NM_007383 | acyl-Coenzyme A dehydrogenase, short chain | 1.62 | 1.55E-10 | 1.26 | 0.000114 | 1.59 | 7.86E-16 | 1.20 | 0.009755 |
| | Acadsb | A_51_P435068 | NM_025826 | acyl-Coenzyme A dehydrogenase, short/branched chain | 1.13 | 0.000142 | 0.81 | 3.79E-07 | 0.78 | 1.70E-13 | 0.77 | 2.11E-39 |
| | Acat2 | A_51_P139748 | NM_009338 | acetyl-Coenzyme A acetyltransferase 2 | 1.06 | 0.043541 | 1.39 | 2.92E-13 | 1.30 | 1.10E-16 | 1.39 | 1.19E-11 |
| | Aco1 | A_52_P299115 | NM_007386 | aconitase 1 | 1.59 | 5.22E-15 | 1.34 | 1.01E-06 | 1.14 | 0.062715 | 1.42 | 9.39E-07 |
| | Aco2 | A_52_P200359 | NM_080633 | aconitase 2, mitochondrial | 1.37 | 0 | 1.23 | 9.73E-12 | 1.19 | 1.83E-10 | 1.22 | 2.64E-08 |
| | Aco2 | A_52_P899263 | AK029122 | Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732494K09 | 2.49 | 1.19E-08 | 1.65 | 0.001998 | 0.89 | 0.242534 | 1.14 | 0.163357 |
| | Acox1 | A_51_P366704 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 0.68 | 0 | 0.79 | 2.67E-15 | 0.79 | 6.65E-19 | 0.86 | 8.37E-23 |
| | Acox1 | A_52_P615096 | NM_015729 | acyl-Coenzyme A oxidase 1, palmitoyl | 0.53 | 6.75E-09 | 0.66 | 0.000472 | 0.78 | 0.022822 | 0.74 | 0.004115 |
| | Acox2 | A_51_P206708 | NM_053115 | acyl-Coenzyme A oxidase 2, branched chain | 0.32 | 0 | 0.79 | 0.010544 | 0.73 | 1.88E-22 | 0.85 | 0.000097 |
| | Acs1 | A_52_P597618 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 0.79 | 5.11E-07 | 0.76 | 1.41E-11 | 0.81 | 9.22E-09 | 0.90 | 0.000112 |
| | Acs16 | A_52_P204459 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 1.03 | 0.497727 | 0.78 | 0.00034 | 0.76 | 5.34E-07 | 0.81 | 0.000027 |
| | Acs16 | A_52_P352187 | NM_001033599 | acyl-CoA synthetase long-chain family member 6 | 1.12 | 0.002862 | 1.31 | 0.004379 | 1.32 | 2.41E-08 | 1.25 | 0.000024 |
| | Adcy4 | A_51_P229911 | NM_080435 | adenylate cyclase 4 | 1.43 | 1.45E-09 | 1.22 | 8.53E-10 | 1.29 | 2.03E-10 | 1.42 | 1.39E-16 |
| | Adcy5 | A_51_P199041 | NM_001012765 | adenylate cyclase 5 | 0.30 | 0 | 0.67 | 0.000117 | 0.66 | 0.000034 | 1.36 | 0.000068 |
| | Adcy5 | A_52_P449208 | NM_001012765 | adenylate cyclase 5 | 0.23 | 0 | 0.55 | 1.28E-07 | 0.66 | 9.41E-09 | 1.57 | 3.94E-12 |
| | Agpat2 | A_51_P238563 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 0.90 | 0.072554 | 1.03 | 0.746427 | 1.01 | 0.83659 | 1.53 | 4.39E-14 |
| | Agpat2 | A_51_P238565 | NM_026212 | 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) | 0.84 | 0.000521 | 1.01 | 0.902578 | 1.00 | 0.970781 | 1.51 | 3.48E-18 |
| | Aldh1a1 | A_51_P334942 | NM_013467 | aldehyde dehydrogenase family 1, subfamily A1 | 0.73 | 1.62E-09 | 0.96 | 0.399181 | 0.95 | 0.236953 | 0.94 | 0.090587 |
| | Aldh1a2 | A_52_P58145 | NM_009022 | aldehyde dehydrogenase family 1, subfamily A2 | 1.91 | 0 | 1.43 | 0.000013 | 1.25 | 1.17E-08 | 1.32 | 4.81E-20 |
| | Aldh1a7 | A_51_P383399 | NM_011921 | aldehyde dehydrogenase family 1, subfamily A7 | 0.32 | 0 | 0.63 | 0.000012 | 0.73 | 3.13E-10 | 1.39 | 9.64E-18 |

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|----------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Aldh1b1 | A_51_P510418 | NM_028270 | aldehyde dehydrogenase 1 family, member B1 | 1.18 | 0.000068 | 1.45 | 0.000602 | 1.64 | 0 | 1.44 | 2.31E-14 |
| Aldh2 | A_52_P116134 | NM_009656 | aldehyde dehydrogenase 2, mitochondrial | 1.33 | 0.000015 | 1.13 | 0.119625 | 1.17 | 0.054956 | 1.18 | 0.017117 |
| Aldh2 | A_52_P13109 | AK163452 | aldehyde dehydrogenase 2, mitochondrial | 1.54 | 9.23E-20 | 1.08 | 0.060114 | 1.17 | 0.018255 | 1.23 | 3.55E-07 |
| Aldh5a1 | A_51_P491504 | NM_172532 | aldehyde dehydrogenase family 5, subfamily A1 | 1.47 | 0 | 1.02 | 0.543144 | 1.04 | 0.14417 | 1.10 | 7.47E-08 |
| Aldh5a1 | A_52_P30273 | AK051603 | aldehyde dehydrogenase family 5, subfamily A1 | 3.04 | 3.67E-09 | 1.81 | 0.000602 | 1.72 | 0.022997 | 1.00 | 0.979372 |
| Aldh9a1 | A_51_P106211 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 1.09 | 0.033176 | 1.17 | 0.002505 | 1.23 | 6.19E-09 | 1.31 | 3.05E-08 |
| Aldoa | A_51_P216905 | NM_007438 | aldolase 1, A isoform | 1.56 | 9.30E-10 | 0.90 | 0.191273 | 0.86 | 0.007786 | 1.01 | 0.940985 |
| *Aldoa | A_52_P98387 | NM_007438 | aldolase 1, A isoform | 1.58 | 3.62E-06 | 1.23 | 0.790626 | 0.98 | 0.636253 | 0.99 | 0.380557 |
| Apoa4 | A_51_P327496 | NM_007468 | apolipoprotein A-IV | 1.48 | 0.000172 | 1.48 | 3.75E-06 | 1.13 | 0.005237 | 1.20 | 0.005083 |
| Apoc1 | A_51_P164504 | NM_007469 | apolipoprotein C-I | 0.83 | 1.40E-06 | 0.99 | 0.913887 | 0.92 | 0.16719 | 1.36 | 2.26E-18 |
| Apoc2 | A_51_P334979 | NM_009695 | apolipoprotein C-II | 0.72 | 1.94E-12 | 0.90 | 0.020195 | 0.89 | 0.000016 | 1.07 | 0.027594 |
| Atp5e | A_51_P362054 | NM_025983 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit | 1.48 | 3.79E-39 | 1.04 | 0.1607 | 1.06 | 0.04033 | 1.01 | 0.735085 |
| Atp5k | A_51_P301289 | NM_007507 | ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e | 1.67 | 3.35E-30 | 1.30 | 1.87E-09 | 1.30 | 1.07E-11 | 1.35 | 4.00E-19 |
| Atp6v0a1 | A_52_P399998 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.51 | 9.39E-23 | 0.75 | 4.78E-10 | 0.77 | 1.61E-07 | 0.97 | 0.659058 |
| Atp6v0a1 | A_52_P515336 | AK045877 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.77 | 1.35E-07 | 0.89 | 0.080552 | 1.01 | 0.905102 | 1.00 | 0.981941 |
| Atp6v1c2 | A_51_P518600 | NM_133699 | ATPase, H+ transporting, lysosomal V1 subunit C2 | 0.85 | 0.569534 | 1.39 | 0.050871 | 0.88 | 0.419675 | 1.86 | 0.00001 |
| Atp6v1g1 | A_52_P349738 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 0.76 | 1.58E-36 | 0.92 | 0.003571 | 0.91 | 8.52E-07 | 0.88 | 4.56E-12 |
| Atp6v1h | A_51_P105604 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.36 | 0 | 0.63 | 1.02E-23 | 0.66 | 6.21E-36 | 0.68 | 2.22E-08 |
| Atp6v1h | A_52_P112888 | NM_133826 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.35 | 0 | 0.62 | 0 | 0.63 | 1.29E-35 | 0.68 | 3.34E-14 |
| Atp6v1h | A_52_P403420 | AK081492 | ATPase, H+ transporting, lysosomal V1 subunit H | 0.45 | 5.26E-36 | 0.46 | 1.01E-35 | 0.46 | 5.40E-31 | 0.41 | 2.37E-43 |
| Bdh2 | A_51_P470935 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.39 | 3.07E-08 | 1.26 | 9.11E-12 | 1.19 | 0.000063 | 1.10 | 0.011388 |
| Cd36 | A_51_P375138 | L23108 | CD36 antigen | 0.51 | 0 | 0.66 | 0 | 0.77 | 1.82E-22 | 0.91 | 3.60E-06 |
| *Cd36 | A_51_P375146 | NM_007643 | CD36 antigen | 0.51 | 0 | 0.58 | 3.82E-37 | 0.70 | 9.42E-13 | 0.89 | 0.000299 |
| Cox4i1 | A_51_P165435 | NM_009941 | cytochrome c oxidase subunit IV isoform 1 | 1.39 | 3.12E-23 | 1.08 | 0.01417 | 1.04 | 0.040811 | 1.03 | 0.396332 |
| Cox6b1 | A_51_P448032 | NM_025628 | cytochrome c oxidase, subunit VIb polypeptide 1 | 1.51 | 0 | 1.26 | 9.80E-17 | 1.28 | 8.13E-44 | 1.23 | 2.04E-32 |
| Cox7a1 | A_51_P148612 | NM_009944 | cytochrome c oxidase, subunit VIIa 1 | 2.45 | 0 | 1.29 | 0.000072 | 1.28 | 6.75E-22 | 1.29 | 3.31E-15 |
| Cox7b | A_51_P160664 | NM_025379 | cytochrome c oxidase subunit VIIb | 1.31 | 0.000086 | 1.04 | 0.499824 | 1.15 | 0.007799 | 1.07 | 0.219412 |
| Cpt1a | A_52_P219753 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 1.20 | 0.010108 | 1.11 | 0.112697 | 1.02 | 0.640973 | 1.33 | 2.67E-13 |
| Cs | A_51_P390260 | NM_026444 | citrate synthase | 1.31 | 0.000192 | 1.13 | 0.058684 | 1.09 | 0.1476 | 1.03 | 0.612688 |
| Cyp1a1 | A_51_P279693 | NM_009992 | cytochrome P450, family 1, subfamily a, polypeptide 1 | 0.44 | 6.62E-23 | 0.68 | 7.93E-11 | 1.27 | 0.019932 | 0.95 | 0.502448 |
| Cyp1b1 | A_51_P255456 | NM_009994 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 0.40 | 5.26E-11 | 0.62 | 4.99E-07 | 0.62 | 0.000034 | 0.64 | 2.90E-06 |
| Cyp2c37 | A_51_P498882 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 1.19 | 2.42E-07 | 1.01 | 0.898496 | 1.31 | 0.000091 | 1.19 | 9.95E-08 |
| Cyp2c37 | A_52_P625249 | NM_010001 | cytochrome P450, family 2, subfamily c, polypeptide 37 | 1.31 | 1.34E-20 | 1.18 | 0.001686 | 1.26 | 8.70E-23 | 1.18 | 2.80E-21 |
| Cyp2e1 | A_51_P283456 | NM_021282 | cytochrome P450, family 2, subfamily e, polypeptide 1 | 0.91 | 0.305965 | 0.42 | 3.08E-09 | 0.82 | 0.005241 | 1.07 | 0.473579 |

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|----------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Cyp2f2 | A_51_P453909 | NM_007817 | cytochrome P450, family 2, subfamily f, polypeptide 2 | 8.13 | 5.18E-23 | 1.59 | 0.000064 | 1.40 | 0.061488 | 1.57 | 0.000442 |
| Cyp2j6 | A_51_P506328 | NM_010008 | cytochrome P450, family 2, subfamily j, polypeptide 6 | 0.54 | 0 | 0.95 | 0.324548 | 0.88 | 1.67E-13 | 0.85 | 6.97E-06 |
| Cyp2s1 | A_51_P180091 | NM_028775 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 1.40 | 3.83E-09 | 1.50 | 1.30E-10 | 1.34 | 3.01E-14 | 1.45 | 2.08E-18 |
| Cyp2s1 | A_52_P456837 | AK054324 | cytochrome P450, family 2, subfamily s, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp3a11 | A_51_P355301 | NM_007818 | cytochrome P450, family 3, subfamily a, polypeptide 11 | 1.18 | 0.007357 | 1.32 | 1.41E-11 | 1.15 | 0.002934 | 1.15 | 0.000234 |
| Cyp4a12a | A_52_P44914 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 1.25 | 3.45E-09 | 1.27 | 0.004302 | 1.46 | 2.06E-07 | 1.31 | 3.01E-06 |
| Cyp4b1 | A_51_P118704 | NM_007823 | cytochrome P450, family 4, subfamily b, polypeptide 1 | 0.64 | 7.57E-21 | 0.51 | 8.41E-45 | 0.74 | 2.28E-07 | 1.60 | 7.73E-14 |
| Cyp51 | A_52_P164161 | NM_020010 | cytochrome P450, family 51 | 0.73 | 1.02E-15 | 0.90 | 0.082314 | 0.92 | 0.03594 | 0.92 | 0.024694 |
| Cyp51 | A_52_P636752 | NM_020010 | cytochrome P450, family 51 | 0.65 | 2.95E-14 | 0.88 | 0.054461 | 0.97 | 0.484686 | 1.03 | 0.48922 |
| Dgat1 | A_51_P510059 | NM_010046 | diacylglycerol O-acyltransferase 1 | 0.72 | 1.52E-06 | 1.00 | 0.974134 | 1.07 | 0.231587 | 1.32 | 0.000047 |
| Dgat1 | A_52_P456134 | NM_010046 | diacylglycerol O-acyltransferase 1 | 0.82 | 5.48E-11 | 1.06 | 0.040049 | 1.10 | 4.43E-07 | 1.41 | 6.39E-36 |
| *Dgat2 | A_52_P359739 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.98 | 0.76263 | 1.12 | 0.000396 | 1.24 | 0.000945 | 1.36 | 1.46E-07 |
| Dlat | A_51_P265106 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 1.71 | 0 | 0.97 | 0.516877 | 1.02 | 0.335563 | 1.08 | 0.000154 |
| Dld | A_51_P184284 | NM_007861 | dihydrolipoamide dehydrogenase | 0.92 | 0.026784 | 0.74 | 1.09E-21 | 0.79 | 2.34E-11 | 0.83 | 2.01E-25 |
| Dlst | A_51_P290139 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.34 | 1.39E-11 | 1.05 | 0.28849 | 1.16 | 0.000591 | 1.17 | 0.000112 |
| Eno2 | A_51_P130028 | NM_013509 | enolase 2, gamma neuronal | 0.69 | 0 | 1.26 | 2.69E-07 | 1.38 | 1.16E-13 | 1.18 | 1.17E-08 |
| Eno2 | A_52_P748882 | NM_013509 | enolase 2, gamma neuronal | 0.69 | 2.54E-08 | 1.06 | 0.402799 | 1.36 | 6.02E-12 | 1.11 | 0.005316 |
| *Eno3 | A_51_P328539 | NM_007933 | enolase 3, beta muscle | 2.83 | 0 | 1.72 | 0.646717 | 1.18 | 0.260241 | 1.24 | 1.30E-09 |
| Fabp4 | A_51_P336830 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.33 | 1.40E-37 | 0.48 | 3.38E-10 | 0.63 | 3.48E-11 | 1.20 | 0.033423 |
| *Fabp4 | A_51_P336833 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.30 | 0 | 0.40 | 2.42E-22 | 0.65 | 1.62E-15 | 1.30 | 0.010388 |
| Fabp4 | A_52_P564544 | NM_024406 | fatty acid binding protein 4, adipocyte | 0.37 | 0 | 0.47 | 9.21E-39 | 0.71 | 3.42E-36 | 1.39 | 7.62E-36 |
| Fabp5 | A_51_P387764 | NM_010634 | fatty acid binding protein 5, epidermal | 0.50 | 1.45E-06 | 0.62 | 0.026251 | 0.62 | 0.00005 | 1.36 | 0.000192 |
| *Fasn | A_51_P321126 | NM_007988 | fatty acid synthase | 0.84 | 0.067219 | 1.06 | 0.388131 | 1.14 | 0.84722 | 1.63 | 3.19E-10 |
| Fasn | A_52_P100252 | NM_007988 | fatty acid synthase | 0.92 | 0.475208 | 1.27 | 0.052164 | 1.16 | 0.128215 | 1.73 | 1.55E-29 |
| Fh1 | A_51_P359333 | NM_010209 | fumarate hydratase 1 | 1.36 | 0 | 1.00 | 0.888022 | 1.06 | 0.007412 | 1.04 | 0.020558 |
| G6pd2 | A_51_P353735 | NM_019468 | glucose-6-phosphate dehydrogenase 2 | 0.33 | 6.69E-12 | 0.39 | 3.95E-08 | 0.56 | 0.00062 | 0.99 | 0.861014 |
| G6pdx | A_51_P187082 | NM_008062 | glucose-6-phosphate dehydrogenase X-linked | 0.35 | 0 | 0.67 | 1.84E-10 | 0.63 | 7.44E-27 | 1.23 | 3.84E-13 |
| Gapdh | A_52_P589321 | AK169742 | glyceraldehyde-3-phosphate dehydrogenase | 1.82 | 4.67E-23 | 0.90 | 0.129224 | 1.10 | 0.253773 | 1.28 | 0.000291 |
| Gck | A_51_P106294 | NM_010292 | glucokinase | 0.58 | 5.42E-08 | 0.72 | 3.63E-06 | 0.82 | 0.004276 | 0.77 | 0.000195 |
| Gck | A_52_P259537 | NM_010292 | glucokinase | 0.47 | 1.16E-26 | 0.82 | 0.079532 | 0.71 | 2.90E-13 | 0.70 | 2.35E-19 |
| Ggps1 | A_52_P228247 | NM_010282 | geranylgeranyl diphosphate synthase 1 | 0.66 | 0 | 0.83 | 0.000969 | 0.85 | 2.90E-12 | 0.80 | 6.77E-07 |
| *Gpd1 | A_51_P293853 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 1.10 | 0.772727 | 1.10 | 0.000046 | 0.88 | 0.954744 | 1.42 | 0.000212 |
| Gpd1 | A_52_P16419 | NM_010271 | glycerol-3-phosphate dehydrogenase 1 (soluble) | 1.10 | 0.00167 | 1.09 | 0.000216 | 0.90 | 0.20562 | 1.39 | 0.000145 |
| Gpt2 | A_51_P493886 | NM_173866 | glutamic pyruvate transaminase (alanine aminotransferase) 2 | 1.45 | 7.26E-12 | 0.58 | 3.40E-13 | 0.56 | 0 | 0.61 | 0 |

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|--------|---------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Gyg | A_51_P240019 | NM_013755 | glycogenin | 0.65 | 1.92E-17 | 0.84 | 0.000634 | 0.88 | 0.00568 | 0.85 | 0.002792 |
| Gyk | A_51_P297671 | NM_008194 | glycerol kinase | 0.52 | 2.93E-39 | 0.71 | 1.29E-07 | 0.79 | 0.000013 | 0.90 | 0.022782 |
| Gyk | A_52_P1020291 | AK037633 | Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130030N17 | 0.74 | 0.136567 | 0.69 | 0.02115 | 1.04 | 0.77475 | 0.68 | 0.001291 |
| Gyk | A_52_P120066 | NM_212444 | glycerol kinase | 0.40 | 0 | 0.51 | 3.93E-18 | 0.50 | 1.70E-22 | 0.82 | 0.015727 |
| Gys2 | A_51_P440315 | NM_145572 | glycogen synthase 2 | 0.09 | 0 | 0.43 | 1.81E-07 | 0.55 | 8.26E-09 | 1.39 | 4.68E-10 |
| Hadha | A_52_P193029 | NM_178878 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.39 | 2.84E-07 | 1.25 | 0.001498 | 1.37 | 5.44E-14 | 1.17 | 0.005489 |
| *Hk1 | A_51_P249024 | NM_010438 | hexokinase 1 | 1.80 | 0 | 1.57 | 4.03E-27 | 1.60 | 0 | 1.69 | 0 |
| Hk1 | A_52_P9337 | NM_010438 | hexokinase 1 | 1.49 | 0.000363 | 1.26 | 0.119948 | 1.29 | 0.002023 | 1.62 | 1.06E-17 |
| Hmgcr | A_51_P507410 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.69 | 8.62E-22 | 0.79 | 0.00002 | 0.81 | 9.64E-09 | 0.92 | 0.072297 |
| Hmgcr | A_52_P137371 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.61 | 4.59E-28 | 0.65 | 1.27E-27 | 0.65 | 2.60E-35 | 0.74 | 3.04E-10 |
| Hmgcr | A_52_P232287 | NM_008255 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.71 | 5.93E-14 | 0.88 | 0.011546 | 0.82 | 0.000098 | 0.95 | 0.239244 |
| Hmgcs1 | A_51_P146941 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.71 | 7.01E-44 | 0.82 | 0.000584 | 0.80 | 2.23E-10 | 1.09 | 0.008677 |
| Hmgcs1 | A_52_P388072 | NM_145942 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.67 | 0.000032 | 0.82 | 0.001709 | 0.83 | 0.010221 | 0.97 | 0.769464 |
| ldh1 | A_51_P132978 | NM_010497 | isocitrate dehydrogenase 1 (NADP+), soluble | 0.68 | 0.000084 | 0.77 | 0.000016 | 0.77 | 7.27E-09 | 0.92 | 0.166721 |
| ldh2 | A_51_P331507 | NM_173011 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 0.71 | 8.96E-08 | 0.86 | 0.002463 | 0.90 | 0.002773 | 0.86 | 0.000441 |
| ldh3b | A_51_P130110 | NM_130884 | isocitrate dehydrogenase 3 (NAD+) beta | 1.45 | 4.63E-35 | 1.17 | 8.78E-07 | 1.15 | 5.38E-08 | 1.12 | 1.18E-06 |
| ldh3g | A_51_P136729 | NM_008323 | isocitrate dehydrogenase 3 (NAD+), gamma | 1.54 | 0 | 1.12 | 0.000573 | 1.08 | 8.06E-09 | 1.06 | 0.038974 |
| ldi1 | A_52_P441634 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.69 | 0.00434 | 0.92 | 0.53265 | 0.86 | 0.042166 | 0.76 | 0.000139 |
| Ldha | A_51_P364140 | NM_010699 | lactate dehydrogenase A | 1.54 | 1.39E-09 | 1.12 | 0.158779 | 1.21 | 0.003578 | 1.19 | 0.01037 |
| Ldha | A_51_P364146 | NM_010699 | lactate dehydrogenase A | 1.69 | 1.96E-21 | 1.27 | 0.000064 | 1.43 | 1.69E-12 | 1.35 | 2.58E-18 |
| Ldhb | A_51_P409173 | NM_008492 | lactate dehydrogenase B | 1.21 | 0.012288 | 1.20 | 0.000219 | 1.31 | 4.82E-08 | 1.15 | 0.035811 |
| *Lipe | A_51_P435363 | NM_010719 | lipase, hormone sensitive | 0.73 | 1.22E-06 | 0.91 | 0.286523 | 0.93 | 0.125576 | 1.33 | 3.06E-07 |
| *Lpl | A_52_P257812 | NM_008509 | lipoprotein lipase | 0.86 | 1.68E-07 | 0.72 | 2.81E-08 | 0.81 | 2.94E-12 | 0.80 | 2.98E-07 |
| *Mgll | A_51_P139920 | NM_011844 | monoglyceride lipase | 0.46 | 0 | 0.69 | 7.58E-11 | 0.86 | 4.92E-06 | 1.33 | 3.15E-41 |
| Mgll | A_52_P568977 | AK006949 | monoglyceride lipase | 0.31 | 5.72E-15 | 0.82 | 0.109462 | 0.79 | 0.015795 | 1.56 | 7.16E-06 |
| Mgll | A_52_P609778 | NM_011844 | monoglyceride lipase | 0.61 | 0 | 0.86 | 0.002675 | 0.96 | 0.209898 | 1.39 | 2.33E-43 |
| Mvd | A_51_P355943 | NM_138656 | mevalonate (diphospho) decarboxylase | 0.66 | 1.42E-13 | 1.09 | 0.042214 | 1.04 | 0.240567 | 0.90 | 0.000196 |
| Mvk | A_51_P169527 | NM_023556 | mevalonate kinase | 1.07 | 0.291723 | 1.24 | 0.00019 | 1.36 | 1.77E-06 | 1.27 | 0.000043 |
| Mvk | A_52_P569067 | NM_023556 | mevalonate kinase | 1.14 | 1.26E-06 | 1.29 | 7.39E-13 | 1.29 | 1.43E-18 | 1.34 | 8.97E-44 |
| Ndufa1 | A_51_P472405 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.45 | 1.01E-10 | 1.14 | 0.019957 | 1.11 | 0.02005 | 1.14 | 0.000319 |
| Ndufa1 | A_52_P139747 | NM_019443 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 | 1.48 | 2.10E-27 | 1.09 | 0.004168 | 1.09 | 0.000408 | 1.07 | 0.004441 |
| Ndufa5 | A_51_P170156 | NM_026614 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 | 1.38 | 1.64E-10 | 1.07 | 0.078265 | 1.04 | 0.226138 | 1.05 | 0.061121 |
| Oxct1 | A_51_P107321 | NM_024188 | 3-oxoacid CoA transferase 1 | 1.88 | 2.42E-32 | 0.97 | 0.644723 | 1.01 | 0.762601 | 1.05 | 0.272572 |

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|----------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Oxct1 | A_51_P107326 | NM_024188 | 3-oxoacid CoA transferase 1 | 2.00 | 0 | 1.04 | 0.596856 | 1.11 | 0.000891 | 1.05 | 0.018299 |
| Oxct1 | A_52_P430058 | NM_024188 | 3-oxoacid CoA transferase 1 | 2.06 | 1.75E-26 | 1.02 | 0.768714 | 1.08 | 0.049389 | 1.08 | 0.17035 |
| Oxct2a | A_51_P125062 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.40 | 0.018547 | 1.40 | 0.110332 | 0.98 | 0.906874 | 1.71 | 0.000074 |
| Pcca | A_51_P484254 | NM_144844 | propionyl-Coenzyme A carboxylase, alpha polypeptide | 1.40 | 2.47E-29 | 1.08 | 0.018049 | 1.15 | 0.001581 | 1.11 | 0.003675 |
| Pdk4 | A_51_P350453 | NM_013743 | pyruvate dehydrogenase kinase, isoenzyme 4 | 2.44 | 0 | 1.28 | 0.000148 | 1.21 | 0.025135 | 1.03 | 0.760499 |
| Pecr | A_51_P291749 | NM_023523 | peroxisomal trans-2-enoyl-CoA reductase | 1.42 | 2.54E-14 | 1.28 | 3.28E-08 | 1.34 | 4.14E-12 | 1.16 | 0.000148 |
| Pgam2 | A_51_P264495 | NM_018870 | phosphoglycerate mutase 2 | 1.43 | 0 | 1.07 | 0.067581 | 1.12 | 0.000358 | 1.10 | 0.001147 |
| Pgd | A_51_P391996 | BC011329 | phosphogluconate dehydrogenase | 0.66 | 1.57E-16 | 0.99 | 0.806217 | 1.00 | 0.997956 | 1.18 | 0.000767 |
| Pgd | A_52_P84096 | BC011329 | phosphogluconate dehydrogenase | 0.64 | 0 | 0.95 | 0.139419 | 0.90 | 0.012729 | 1.15 | 1.16E-11 |
| Pgk2 | A_51_P125487 | NM_031190 | phosphoglycerate kinase 2 | 3.73 | 1.01E-06 | 2.34 | 0.000835 | 0.95 | 0.710556 | 2.31 | 0.000036 |
| Pgm1 | A_51_P427530 | NM_025700 | phosphoglucomutase 1 | 0.67 | 3.59E-07 | 0.79 | 3.61E-12 | 0.78 | 2.57E-08 | 0.85 | 0.00018 |
| *Pgm2 | A_51_P368074 | NM_028132 | phosphoglucomutase 2 | 1.60 | 4.32E-21 | 1.41 | 0.002642 | 1.21 | 0.000066 | 1.13 | 0.001763 |
| Pgm5 | A_51_P451052 | NM_175013 | phosphoglucomutase 5 | 1.39 | 4.44E-24 | 1.30 | 4.10E-12 | 1.26 | 7.24E-24 | 1.21 | 7.10E-09 |
| Phka1 | A_52_P196825 | AK078633 | Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:7330411B16 | 0.57 | 1.33E-15 | 0.84 | 0.036055 | 0.96 | 0.496911 | 1.04 | 0.621088 |
| Phka1 | A_52_P278311 | NM_008832 | phosphorylase kinase alpha 1 | 0.75 | 0.005421 | 0.70 | 3.55E-06 | 0.89 | 0.15683 | 0.79 | 0.003431 |
| Phka2 | A_52_P187217 | NM_172783 | phosphorylase kinase alpha 2 | 0.54 | 2.62E-06 | 1.01 | 0.937226 | 1.07 | 0.663911 | 0.96 | 0.766446 |
| Phka2 | A_52_P671916 | NM_172783 | phosphorylase kinase alpha 2 | 0.71 | 8.95E-10 | 0.95 | 0.154461 | 0.95 | 0.248076 | 1.03 | 0.481344 |
| Phkb | A_51_P307624 | NM_199446 | phosphorylase kinase beta | 1.13 | 0.031243 | 0.73 | 6.54E-08 | 0.83 | 0.000019 | 0.79 | 8.19E-15 |
| Phkg1 | A_51_P280890 | NM_011079 | phosphorylase kinase gamma 1 | 3.45 | 0 | 1.12 | 0.274725 | 1.29 | 7.44E-08 | 1.30 | 0.000027 |
| Pklr | A_51_P176042 | NM_013631 | pyruvate kinase liver and red blood cell | 1.08 | 0.115087 | 1.33 | 1.17E-06 | 1.22 | 0.000106 | 1.23 | 0.009216 |
| Pkm2 | A_51_P428913 | D38379 | pyruvate kinase, muscle | 1.54 | 1.53E-28 | 1.33 | 2.62E-06 | 1.45 | 3.18E-26 | 1.44 | 1.30E-24 |
| *Pkm2 | A_52_P150212 | NM_011099 | pyruvate kinase, muscle | 1.46 | 5.65E-07 | 1.44 | 0.000023 | 1.45 | 5.86E-14 | 1.42 | 4.25E-11 |
| Pmvk | A_51_P492408 | NM_026784 | phosphomevalonate kinase | 1.36 | 1.33E-35 | 1.06 | 0.145874 | 1.10 | 0.008097 | 1.31 | 7.49E-23 |
| Pmvk | A_51_P492410 | NM_026784 | phosphomevalonate kinase | 1.37 | 1.24E-39 | 1.10 | 0.00535 | 1.07 | 0.0029 | 1.28 | 1.21E-22 |
| Ppap2a | A_51_P189104 | NM_008903 | phosphatidic acid phosphatase 2a | 0.76 | 3.18E-10 | 1.06 | 0.045156 | 1.04 | 0.313021 | 1.16 | 4.41E-12 |
| Ppap2a | A_51_P189105 | AK077275 | phosphatidic acid phosphatase 2a | 0.62 | 4.63E-32 | 0.91 | 0.073834 | 0.88 | 0.000138 | 0.93 | 0.043749 |
| Ppap2a | A_52_P7937 | NM_008903 | phosphatidic acid phosphatase 2a | 0.65 | 2.09E-21 | 0.96 | 0.174077 | 0.95 | 0.124923 | 1.01 | 0.633173 |
| Pparg | A_51_P106799 | NM_011146 | peroxisome proliferator activated receptor gamma | 0.99 | 0.550338 | 0.97 | 0.492418 | 1.04 | 0.011986 | 1.39 | 4.02E-34 |
| Ppargc1a | A_51_P279038 | NM_008904 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 1.38 | 4.71E-16 | 0.89 | 0.025043 | 0.86 | 0.000178 | 0.79 | 0.008952 |
| Ppargc1a | A_52_P5945 | AK032149 | peroxisome proliferative activated receptor, gamma, coactivator 1 alpha | 0.98 | 0.547165 | 0.73 | 8.04E-09 | 0.81 | 1.30E-08 | 0.94 | 0.373556 |
| Ppargc1b | A_51_P294891 | NM_133249 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 1.95 | 0 | 1.32 | 1.40E-44 | 1.15 | 0.000013 | 1.23 | 0.000371 |
| Ppargc1b | A_52_P293222 | AK042378 | peroxisome proliferative activated receptor, gamma, coactivator 1 beta | 2.07 | 0 | 1.17 | 0.012676 | 1.12 | 0.054584 | 1.05 | 0.337101 |
| Ppargc1b | A_52_P526724 | NM_133249 | peroxisome proliferative activated receptor, gamma, | 1.72 | 0 | 1.25 | 2.02E-13 | 1.09 | 0.007647 | 1.16 | 0.001458 |

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|---------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| | | | coactivator 1 beta | | | | | | | | |
| Ppp1cb | A_51_P342716 | NM_172707 | protein phosphatase 1, catalytic subunit, beta isoform | 0.76 | 0 | 0.83 | 9.55E-08 | 0.89 | 4.49E-06 | 0.86 | 7.01E-11 |
| Pygb | A_52_P350664 | NM_153781 | brain glycogen phosphorylase | 0.88 | 0.102715 | 1.23 | 0.020399 | 1.36 | 6.83E-08 | 1.22 | 0.000313 |
| Pygl | A_51_P452779 | NM_133198 | liver glycogen phosphorylase | 0.68 | 0.000168 | 0.95 | 0.510055 | 0.95 | 0.51978 | 1.41 | 2.89E-11 |
| *Pygm | A_51_P458973 | NM_011224 | muscle glycogen phosphorylase | 1.66 | 2.82E-31 | 1.26 | 0.271705 | 1.05 | 0.524452 | 0.99 | 0.232421 |
| Scd1 | A_52_P682382 | NM_009127 | stearoyl-Coenzyme A desaturase 1 | 0.42 | 3.25E-26 | 0.87 | 0.263589 | 0.97 | 0.685961 | 1.12 | 0.016046 |
| Scd2 | A_51_P129464 | NM_009128 | stearoyl-Coenzyme A desaturase 2 | 0.55 | 2.56E-34 | 0.98 | 0.823701 | 0.86 | 0.000119 | 0.91 | 0.011277 |
| Sdha | A_51_P410823 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 1.33 | 4.71E-25 | 0.92 | 0.024253 | 0.93 | 0.039836 | 0.93 | 0.005933 |
| Sdhc | A_52_P875481 | AK031343 | Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030410A06 | 0.77 | 0.164235 | 0.47 | 0.000076 | 0.47 | 5.50E-06 | 0.57 | 0.005292 |
| Slc25a1 | A_51_P350922 | NM_153150 | solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 | 0.44 | 2.25E-35 | 0.73 | 0.000243 | 0.66 | 2.68E-07 | 1.46 | 8.98E-29 |
| Slc27a1 | A_51_P117477 | NM_011977 | solute carrier family 27 (fatty acid transporter), member 1 | 1.37 | 2.49E-10 | 1.40 | 6.09E-08 | 1.29 | 0.000279 | 1.33 | 5.86E-08 |
| Slc27a3 | A_51_P133252 | NM_011988 | solute carrier family 27 (fatty acid transporter), member 3 | 1.63 | 7.89E-09 | 1.49 | 1.21E-07 | 1.33 | 5.71E-08 | 1.44 | 2.42E-07 |
| SucLa2 | A_51_P111554 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 1.50 | 2.69E-29 | 0.81 | 0.000049 | 0.91 | 0.047026 | 0.88 | 0.000016 |
| SucLa2 | A_52_P762514 | AK016060 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 0.66 | 0.028146 | 0.86 | 0.564567 | 0.62 | 0.000271 | 0.70 | 0.204455 |
| SucLg1 | A_51_P491227 | NM_019879 | succinate-CoA ligase, GDP-forming, alpha subunit | 1.49 | 1.40E-45 | 1.03 | 0.451148 | 1.06 | 0.010828 | 1.06 | 0.005051 |
| Taldo1 | A_51_P401958 | NM_011528 | transaldolase 1 | 0.75 | 1.11E-11 | 0.95 | 0.300857 | 0.91 | 0.054578 | 0.96 | 0.481772 |
| Tkt | A_51_P394515 | NM_009388 | transketolase | 1.02 | 0.752069 | 0.94 | 0.128476 | 0.88 | 0.001529 | 1.39 | 4.17E-15 |
| Tkt | A_52_P624447 | NM_009388 | transketolase | 0.61 | 0.016841 | 1.03 | 0.902915 | 0.69 | 0.01895 | 1.80 | 0.000054 |
| Tpi1 | A_51_P433824 | NM_009415 | triosephosphate isomerase 1 | 1.54 | 1.07E-35 | 1.05 | 0.414226 | 1.14 | 1.07E-06 | 1.23 | 5.77E-15 |
| Tpi1 | A_52_P116102 | AK053780 | Mus musculus 0 day neonate eyeball cDNA, RIKEN library, clone:E130308D14 product:triosephosphate isomerase | 2.78 | 0 | 1.49 | 5.21E-06 | 1.56 | 1.19E-09 | 1.33 | 0.004216 |
| Ucp1 | A_51_P426353 | NM_009463 | uncoupling protein 1 (mitochondrial, proton carrier) | 0.04 | 0 | 0.07 | 0 | 0.19 | 3.23E-14 | 0.65 | 0.000095 |
| Ucp2 | A_51_P297105 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.44 | 0 | 0.82 | 0.00721 | 1.09 | 0.069029 | 1.14 | 4.35E-08 |
| Ucp2 | A_52_P90265 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 0.33 | 4.67E-26 | 0.71 | 0.001089 | 0.99 | 0.930012 | 0.98 | 0.737949 |
| Ugp2 | A_52_P42242 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 0.90 | 0.000077 | 0.70 | 1.54E-32 | 0.87 | 0.018978 | 0.83 | 8.34E-17 |
| Uqcrb | A_51_P472671 | NM_026219 | ubiquinol-cytochrome c reductase binding protein | 1.39 | 3.25E-20 | 1.14 | 0.00007 | 1.12 | 1.43E-06 | 1.09 | 1.22E-07 |
| Uqcrc1 | A_51_P109835 | NM_025407 | ubiquinol-cytochrome c reductase core protein 1 | 1.95 | 0 | 1.48 | 3.51E-10 | 1.71 | 0 | 1.49 | 2.49E-19 |
| Uqcrh | A_51_P431852 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.33 | 0.000849 | 1.06 | 0.420679 | 1.01 | 0.935693 | 1.08 | 0.433436 |
| Acaa1a | A_51_P327075 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.19 | 4.48E-16 | 1.06 | 0.124979 | 1.04 | 0.04893 | 1.13 | 1.93E-07 |
| Acaa1a | A_52_P423183 | NM_130864 | acetyl-Coenzyme A acyltransferase 1A | 1.14 | 0.000125 | 1.06 | 0.132409 | 1.11 | 0.015277 | 1.29 | 1.20E-17 |
| Acaa1b | A_52_P423174 | NM_146230 | acetyl-Coenzyme A acyltransferase 1B | 1.05 | 0.022239 | 0.96 | 0.322991 | 1.01 | 0.822135 | 1.23 | 2.65E-13 |
| Acaca | A_52_P23177 | NM_133360 | acetyl-Coenzyme A carboxylase alpha | 0.98 | 0.700773 | 1.04 | 0.367526 | 1.04 | 0.381595 | 1.07 | 0.048241 |
| Acacb | A_51_P239236 | BC022940 | acetyl-Coenzyme A carboxylase beta | 0.85 | 0.004376 | 0.92 | 0.067161 | 1.02 | 0.691765 | 0.96 | 0.488229 |
| Acacb | A_52_P340167 | NM_133904 | acetyl-Coenzyme A carboxylase beta | 0.98 | 0.667489 | 1.04 | 0.246585 | 1.14 | 7.58E-06 | 1.10 | 0.003934 |

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|--------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Acad10 | A_51_P187507 | NM_028037 | acyl-Coenzyme A dehydrogenase family, member 10 | 1.25 | 1.67E-20 | 1.11 | 0.000559 | 1.14 | 1.01E-08 | 1.21 | 2.58E-25 |
| Acad11 | A_51_P299260 | AK041180 | acyl-Coenzyme A dehydrogenase family, member 11 | 1.24 | 0.144892 | 1.39 | 0.092842 | 0.91 | 0.549948 | 0.95 | 0.498038 |
| Acad11 | A_52_P85152 | NM_175324 | acyl-Coenzyme A dehydrogenase family, member 11 | 1.28 | 2.41E-10 | 0.95 | 0.231552 | 1.06 | 0.114712 | 1.08 | 0.000169 |
| Acad8 | A_51_P244052 | NM_025862 | acyl-Coenzyme A dehydrogenase family, member 8 | 1.15 | 0.000204 | 1.06 | 0.028879 | 1.08 | 0.003063 | 1.03 | 0.283401 |
| Acad9 | A_51_P341379 | NM_172678 | acyl-Coenzyme A dehydrogenase family, member 9 | 1.08 | 0.009483 | 0.97 | 0.213639 | 0.95 | 0.004397 | 0.99 | 0.582952 |
| Acad9 | A_52_P73208 | AK049931 | acyl-Coenzyme A dehydrogenase family, member 9 | 0.87 | 0.117121 | 0.91 | 0.307918 | 0.94 | 0.317526 | 0.90 | 0.063788 |
| Acadl | A_51_P149455 | NM_007381 | acyl-Coenzyme A dehydrogenase, long-chain | 0.87 | 9.52E-10 | 0.83 | 9.03E-13 | 0.82 | 1.81E-15 | 0.79 | 1.10E-28 |
| Acadm | A_51_P319879 | NM_007382 | acyl-Coenzyme A dehydrogenase, medium chain | 0.97 | 0.179736 | 0.90 | 0.004395 | 0.94 | 0.000947 | 0.88 | 0.000507 |
| Acadvl | A_51_P518340 | NM_017366 | acyl-Coenzyme A dehydrogenase, very long chain | 1.10 | 0.033193 | 1.15 | 0.000501 | 1.13 | 0.003419 | 1.05 | 0.382295 |
| Acat1 | A_51_P319449 | NM_144784 | acetyl-Coenzyme A acetyltransferase 1 | 0.99 | 0.778864 | 0.94 | 0.132995 | 0.97 | 0.360534 | 0.90 | 0.009468 |
| Acat3 | A_51_P139745 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 1.02 | 0.641872 | 1.21 | 0.000011 | 1.16 | 1.99E-06 | 1.27 | 1.75E-07 |
| Acat3 | A_52_P11959 | NM_153151 | acetyl-Coenzyme A acetyltransferase 3 | 0.72 | 0.006707 | 0.74 | 0.010481 | 0.97 | 0.80882 | 1.02 | 0.781088 |
| Acly | A_51_P261718 | NM_134037 | ATP citrate lyase | 0.81 | 2.59E-06 | 0.91 | 0.021868 | 0.92 | 0.052358 | 0.96 | 0.287573 |
| Acly | A_52_P373556 | AK043466 | ATP citrate lyase | 1.06 | 0.520694 | 1.12 | 0.619508 | 1.54 | 0.003309 | 0.87 | 0.138099 |
| Aco1 | A_51_P391082 | NM_007386 | aconitase 1 | 0.93 | 0.000178 | 1.01 | 0.530912 | 1.04 | 0.089094 | 1.18 | 2.32E-16 |
| Acox3 | A_52_P745 | NM_030721 | acyl-Coenzyme A oxidase 3, pristanoyl | 1.17 | 1.45E-23 | 1.10 | 0.00069 | 1.18 | 2.96E-12 | 1.15 | 1.49E-12 |
| Acs1 | A_51_P463452 | NM_007981 | acyl-CoA synthetase long-chain family member 1 | 0.84 | 2.77E-06 | 0.77 | 3.30E-09 | 0.83 | 8.62E-06 | 0.89 | 8.05E-08 |
| Acs1 | A_51_P496432 | BC006692 | acyl-CoA synthetase long-chain family member 1 | 0.78 | 2.20E-09 | 0.80 | 1.52E-11 | 0.80 | 2.71E-09 | 0.83 | 1.17E-20 |
| Acs3 | A_51_P511560 | NM_028817 | acyl-CoA synthetase long-chain family member 3 | 0.80 | 1.77E-09 | 0.81 | 3.16E-16 | 0.83 | 2.50E-07 | 0.80 | 1.95E-07 |
| Acs4 | A_51_P268154 | NM_019477 | acyl-CoA synthetase long-chain family member 4 | 1.04 | 0.096446 | 1.01 | 0.818853 | 0.96 | 0.093896 | 0.94 | 0.011828 |
| Acs4 | A_52_P78203 | NM_207625 | acyl-CoA synthetase long-chain family member 4 | 1.06 | 0.002837 | 0.94 | 0.02299 | 0.87 | 3.36E-26 | 0.89 | 1.28E-12 |
| Acs5 | A_52_P593037 | NM_027976 | acyl-CoA synthetase long-chain family member 5 | 1.15 | 4.36E-06 | 1.13 | 0.000777 | 1.08 | 0.00297 | 1.23 | 1.01E-24 |
| Acs6 | A_51_P380699 | NM_144823 | acyl-CoA synthetase long-chain family member 6 | 1.04 | 0.249149 | 1.07 | 0.308739 | 0.99 | 0.786668 | 0.99 | 0.897006 |
| Acs6 | A_51_P518823 | AK147421 | acyl-CoA synthetase long-chain family member 6 | 1.27 | 0.000011 | 0.98 | 0.707002 | 1.00 | 0.936123 | 1.02 | 0.650641 |
| Adcy1 | A_51_P196718 | NM_009622 | adenylate cyclase 1 | 0.80 | 2.99E-06 | 0.83 | 0.000024 | 1.05 | 0.531828 | 0.95 | 0.329481 |
| Adcy1 | A_51_P409900 | NM_009622 | adenylate cyclase 1 | 0.98 | 0.83287 | 0.84 | 0.365628 | 1.20 | 0.221148 | 0.91 | 0.177997 |
| Adcy1 | A_52_P240164 | NM_009622 | adenylate cyclase 1 | 1.03 | 0.465751 | 1.07 | 0.251423 | 1.01 | 0.808106 | 1.09 | 0.058635 |
| Adcy1 | A_52_P240170 | BC050125 | adenylate cyclase 1 | 1.20 | 0.000011 | 1.11 | 0.134943 | 1.02 | 0.577492 | 1.04 | 0.337451 |
| Adcy2 | A_51_P337523 | NM_153534 | adenylate cyclase 2 | 1.02 | 0.290852 | 0.95 | 0.183087 | 1.02 | 0.488724 | 1.01 | 0.857267 |
| Adcy2 | A_52_P165610 | NM_153534 | adenylate cyclase 2 | 0.96 | 0.470969 | 0.97 | 0.530995 | 1.02 | 0.656706 | 1.00 | 0.982121 |
| Adcy3 | A_51_P484671 | NM_138305 | adenylate cyclase 3 | 0.75 | 0.04966 | 0.83 | 0.040127 | 0.86 | 0.003016 | 1.12 | 0.315755 |
| Adcy3 | A_52_P216525 | NM_138305 | adenylate cyclase 3 | 0.85 | 0.101386 | 0.84 | 0.068027 | 0.97 | 0.808796 | 0.88 | 0.2514 |
| Adcy6 | A_51_P243134 | NM_007405 | adenylate cyclase 6 | 1.05 | 0.340208 | 1.10 | 0.037898 | 1.16 | 0.00061 | 1.12 | 0.016211 |
| Adcy7 | A_51_P441622 | NM_007406 | adenylate cyclase 7 | 0.98 | 0.792695 | 1.15 | 0.068732 | 1.14 | 0.001941 | 1.08 | 0.06989 |
| Adcy7 | A_52_P291 | AK012436 | adenylate cyclase 7 | 1.22 | 0.000405 | 1.12 | 0.192001 | 1.24 | 4.64E-06 | 1.17 | 0.016065 |

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|----------|--------------|--------------|--|------|----------|------|----------|------|----------|------|----------|
| Adcy7 | A_52_P586141 | NM_001037724 | Mus musculus 11 days embryo whole body cDNA, RIKEN library, clone:2700055K03 product:adenylate cyclase 7 | 1.05 | 0.289626 | 1.08 | 0.237832 | 1.08 | 0.085512 | 1.09 | 0.031379 |
| Adcy8 | A_51_P303061 | NM_009623 | adenylate cyclase 8 | 1.05 | 0.712023 | 0.99 | 0.963571 | 1.06 | 0.668835 | 1.02 | 0.78393 |
| Adcy9 | A_51_P501538 | NM_009624 | adenylate cyclase 9 | 1.12 | 0.106816 | 0.89 | 0.02162 | 0.91 | 0.116732 | 0.94 | 0.169668 |
| Adh1 | A_51_P428555 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.79 | 0.037549 | 1.11 | 0.003409 | 0.81 | 2.98E-06 | 0.87 | 0.008729 |
| Adh1 | A_52_P629895 | NM_007409 | alcohol dehydrogenase 1 (class I) | 0.84 | 0.140847 | 1.21 | 6.49E-07 | 0.90 | 0.016049 | 0.92 | 0.064815 |
| Adh1 | A_52_P835985 | AK082149 | alcohol dehydrogenase 1 (class I) | 0.67 | 0.119992 | 1.08 | 0.607756 | 1.08 | 0.647858 | 0.98 | 0.893785 |
| Adh4 | A_51_P189442 | NM_011996 | alcohol dehydrogenase 4 (class II), pi polypeptide | 0.98 | 0.905575 | 0.92 | 0.72232 | 1.27 | 0.31604 | 1.04 | 0.817235 |
| Adh5 | A_51_P404275 | NM_007410 | alcohol dehydrogenase 5 (class III), chi polypeptide | 0.94 | 0.003139 | 0.93 | 0.00977 | 0.97 | 0.307343 | 0.91 | 7.09E-12 |
| Adh6a | A_51_P299608 | AK028114 | alcohol dehydrogenase 6A (class V) | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Adh6a | A_52_P276348 | AK007397 | alcohol dehydrogenase 6A (class V) | 0.99 | 0.971309 | 0.94 | 0.701672 | 0.96 | 0.707833 | 1.22 | 0.367623 |
| Adh6-ps1 | A_51_P120027 | AK004863 | alcohol dehydrogenase 6 (class V), pseudogene 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Adh7 | A_51_P233797 | NM_009626 | alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide | 1.00 | 1 | 0.85 | 0.521454 | 1.00 | 1 | 0.99 | 0.872715 |
| Agpat1 | A_51_P322612 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 1.15 | 1.63E-08 | 1.08 | 0.014635 | 1.07 | 0.000684 | 1.09 | 3.10E-10 |
| Agpat1 | A_52_P200465 | NM_018862 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 0.95 | 0.035511 | 0.94 | 0.148671 | 0.90 | 0.003636 | 0.96 | 0.247308 |
| Agpat3 | A_51_P425490 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 0.83 | 2.69E-10 | 1.01 | 0.774893 | 0.98 | 0.634009 | 0.98 | 0.4885 |
| Agpat3 | A_52_P523569 | NM_053014 | 1-acylglycerol-3-phosphate O-acyltransferase 3 | 0.87 | 7.08E-11 | 0.97 | 0.362706 | 0.92 | 0.00007 | 0.97 | 0.109094 |
| Agpat4 | A_51_P346165 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 1.04 | 0.066346 | 1.12 | 0.001252 | 1.06 | 0.075331 | 1.11 | 3.92E-07 |
| Agpat4 | A_52_P3029 | NM_026644 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 1.07 | 0.003171 | 1.09 | 0.009373 | 1.05 | 0.201351 | 1.12 | 1.09E-09 |
| Agpat5 | A_51_P361286 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 1.20 | 0.000231 | 0.89 | 0.023252 | 0.87 | 0.002017 | 0.90 | 0.002004 |
| Agpat5 | A_52_P572447 | NM_026792 | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) | 0.88 | 0.000267 | 0.88 | 0.000424 | 0.91 | 0.004933 | 0.94 | 0.049811 |
| Agpat6 | A_51_P335710 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.84 | 0.117017 | 0.90 | 0.266944 | 0.98 | 0.890974 | 1.04 | 0.674377 |
| Agpat6 | A_51_P335716 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.87 | 0.110022 | 0.99 | 0.83477 | 1.07 | 0.323694 | 1.08 | 0.221706 |
| Agpat6 | A_52_P24986 | NM_018743 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0.96 | 0.013561 | 1.02 | 0.506785 | 1.07 | 2.42E-07 | 1.15 | 1.52E-26 |
| Alb | A_51_P160713 | NM_009654 | albumin | 1.18 | 0.364614 | 1.45 | 0.021919 | 1.13 | 0.542957 | 1.75 | 0.046628 |
| Aldh1a3 | A_52_P113518 | AK086764 | aldehyde dehydrogenase family 1, subfamily A3 | 1.10 | 0.509334 | 1.57 | 0.04757 | 1.07 | 0.748608 | 1.24 | 0.290435 |
| Aldh1a3 | A_52_P87843 | NM_053080 | aldehyde dehydrogenase family 1, subfamily A3 | 1.03 | 0.743357 | 1.13 | 0.083279 | 1.14 | 0.000788 | 1.16 | 0.000516 |
| Aldh3a1 | A_51_P310594 | NM_007436 | aldehyde dehydrogenase family 3, subfamily A1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.06 | 0.640629 |
| Aldh3a2 | A_51_P464175 | NM_007437 | aldehyde dehydrogenase family 3, subfamily A2 | 0.90 | 0.013501 | 0.92 | 0.009309 | 0.95 | 0.198421 | 0.94 | 0.094363 |
| Aldh4a1 | A_51_P337918 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 1.26 | 4.27E-21 | 0.97 | 0.167397 | 1.00 | 0.964569 | 1.06 | 0.00895 |
| Aldh4a1 | A_52_P123230 | NM_175438 | aldehyde dehydrogenase 4 family, member A1 | 1.01 | 0.891926 | 0.98 | 0.884763 | 1.13 | 0.431356 | 0.95 | 0.471991 |
| Aldh7a1 | A_51_P470414 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 1.00 | 0.972001 | 0.84 | 0.434428 | 1.16 | 0.547829 | 1.29 | 0.283871 |

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|----------|--------------|-----------|---|------|----------|------|----------|-------|----------|------|----------|
| Aldh7a1 | A_52_P503071 | NM_138600 | aldehyde dehydrogenase family 7, member A1 | 1.06 | 0.681393 | 1.13 | 0.336483 | 1.06 | 0.67815 | 1.09 | 0.516753 |
| Aldh9a1 | A_52_P265877 | NM_019993 | aldehyde dehydrogenase 9, subfamily A1 | 0.91 | 0.05481 | 0.98 | 0.750604 | 0.94 | 0.393878 | 1.08 | 0.273649 |
| Aldob | A_51_P337269 | NM_144903 | aldolase 2, B isoform | 0.79 | 0.128264 | 0.63 | 0.08003 | 1.25 | 0.522415 | 1.04 | 0.803962 |
| Aldob | A_52_P450038 | NM_144903 | aldolase 2, B isoform | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Aldob | A_52_P468023 | NM_144903 | aldolase 2, B isoform | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.04 | 0.699964 |
| Aldoc | A_51_P220681 | NM_009657 | aldolase 3, C isoform | 1.01 | 0.914675 | 1.09 | 0.045509 | 1.19 | 6.52E-06 | 1.01 | 0.868568 |
| Aldoc | A_51_P425284 | AK039267 | aldolase 3, C isoform | 0.96 | 0.689349 | 0.90 | 0.479271 | 1.15 | 0.373789 | 1.95 | 0.004851 |
| Apoa1 | A_51_P408082 | NM_009692 | apolipoprotein A-I | 1.17 | 0.008365 | 1.13 | 0.109316 | 1.08 | 0.363485 | 1.04 | 0.498525 |
| Apoa4 | A_51_P327491 | NM_007468 | apolipoprotein A-IV | 1.13 | 0.111229 | 1.39 | 0.116943 | 1.11 | 0.451716 | 1.43 | 0.006038 |
| Apoa5 | A_51_P259930 | NM_080434 | apolipoprotein A-V | 1.04 | 0.530319 | 1.02 | 0.697154 | 1.06 | 0.459395 | 1.07 | 0.365893 |
| Apoa5 | A_52_P292404 | NM_080434 | apolipoprotein A-V | 1.00 | 1 | 1.02 | 0.876394 | 1.06 | 0.578807 | 1.03 | 0.765289 |
| Apob | A_51_P380650 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 0.86 | 0.401579 | 1.18 | 0.470212 | 0.91 | 0.60581 | 1.05 | 0.82701 |
| Apob | A_51_P413088 | XM_137955 | Mus musculus apolipoprotein B (Apob), mRNA. | 0.90 | 0.661632 | 1.06 | 0.756031 | 0.91 | 0.557853 | 0.86 | 0.571067 |
| Apob | A_51_P436690 | BC028880 | Mus musculus apolipoprotein B (Apob), mRNA. | 0.98 | 0.853085 | 1.20 | 0.401549 | 1.00 | 1 | 1.00 | 1 |
| Apob | A_51_P470542 | XM_137955 | apolipoprotein B | 1.17 | 0.461651 | 0.93 | 0.666246 | 1.24 | 0.392811 | 0.95 | 0.797845 |
| Apob | A_52_P441070 | NM_009693 | apolipoprotein B | 1.02 | 0.800112 | 0.98 | 0.774689 | 1.00 | 1 | 1.04 | 0.728297 |
| Apoc3 | A_51_P310629 | NM_023114 | apolipoprotein C-III | 0.75 | 0.125071 | 0.70 | 0.027229 | 0.80 | 0.33056 | 1.12 | 0.588091 |
| Apoc3 | A_52_P574306 | NM_023114 | apolipoprotein C-III | 1.00 | 1 | 1.04 | 0.724699 | 1.00 | 1 | 1.00 | 1 |
| Apoe | A_51_P171999 | NM_009696 | apolipoprotein E | 0.83 | 0.000102 | 0.99 | 0.77505 | 0.98 | 0.682914 | 1.01 | 0.778489 |
| Atp12a | A_52_P329398 | NM_138652 | ATPase, H+/K+ transporting, nongastric, alpha polypeptide | 1.07 | 0.18906 | 1.22 | 0.013612 | 1.06 | 0.168039 | 1.07 | 0.092125 |
| Atp5a1 | A_52_P674489 | NM_007505 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 | 1.13 | 0.195469 | 1 | 0.94 | 1.016 | 0.804455 | 0.99 | 0.95 |
| Atp5b | A_51_P207636 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.21 | 3.70E-08 | 1.03 | 0.081285 | 1.10 | 0.003466 | 1.11 | 0.000014 |
| Atp5b | A_52_P328078 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.04 | 0.682844 | 0.98 | 0.866268 | 1.00 | 0.981293 | 1.14 | 0.333119 |
| Atp5b | A_52_P553841 | NM_016774 | ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit | 1.15 | 0.058434 | 1.01 | 0.836146 | 0.97 | 0.676376 | 0.97 | 0.67955 |
| Atp5c1 | A_51_P378087 | NM_020615 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | 0.99 | 0.894279 | 1.03 | 0.669621 | 0.81 | 0.023186 | 0.90 | 0.312507 |
| Atp5h | A_51_P264186 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 1.09 | 0.111437 | 0.90 | 0.003453 | 0.92 | 0.012271 | 0.91 | 0.016054 |
| Atp5h | A_52_P640355 | NM_027862 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | 1.19 | 2.02E-15 | 1.01 | 0.695467 | 1.02 | 0.220206 | 1.02 | 0.500562 |
| Atp6ap1 | A_51_P447988 | NM_018794 | ATPase, H+ transporting, lysosomal accessory protein 1 | 0.87 | 0.008409 | 0.95 | 0.204446 | 0.94 | 0.0464 | 0.96 | 0.160106 |
| Atp6v0a1 | A_51_P142089 | NM_016920 | ATPase, H+ transporting, lysosomal V0 subunit A1 | 0.80 | 3.47E-31 | 1.04 | 0.115276 | 1.06 | 0.000244 | 1.14 | 2.33E-07 |
| Atp6v1b2 | A_51_P190845 | NM_007509 | ATPase, H+ transporting, lysosomal V1 subunit B2 | 0.95 | 0.385013 | 0.97 | 0.64691 | 0.95 | 0.404868 | 0.98 | 0.70339 |
| Atp6v1e1 | A_51_P166434 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 0.87 | 0.000149 | 0.86 | 4.56E-07 | 0.86 | 4.05E-09 | 0.90 | 0.000157 |
| Atp6v1e1 | A_52_P303388 | NM_007510 | VATPase, H+ transporting, lysosomal V1 subunit E1 | 0.90 | 0.002498 | 0.91 | 0.016895 | 0.89 | 0.001121 | 0.90 | 0.007861 |

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|----------|---------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Atp6v1g1 | A_51_P140171 | NM_024173 | ATPase, H+ transporting, lysosomal V1 subunit G1 | 0.89 | 3.16E-12 | 0.92 | 0.000067 | 0.93 | 0.000174 | 0.96 | 0.032797 |
| Atp7a | A_51_P312497 | NM_009726 | ATPase, Cu++ transporting, alpha polypeptide | 1.00 | 0.929925 | 0.94 | 0.017379 | 0.94 | 0.00008 | 0.96 | 0.040515 |
| Atp7a | A_51_P473179 | AK033254 | ATPase, Cu++ transporting, alpha polypeptide | 1.24 | 0.149263 | 0.88 | 0.064741 | 0.98 | 0.891809 | 0.95 | 0.524953 |
| Auh | A_51_P372473 | NM_016709 | AU RNA binding protein/enoyl-coenzyme A hydratase | 1.10 | 0.000293 | 1.01 | 0.799326 | 1.06 | 0.009388 | 1.05 | 0.017079 |
| Auh | A_52_P107290 | AK003929 | AU RNA binding protein/enoyl-coenzyme A hydratase | 0.56 | 1.87E-23 | 0.99 | 0.908521 | 0.93 | 0.198815 | 1.16 | 0.020361 |
| Auh | A_52_P4095 | AK169661 | AU RNA binding protein/enoyl-coenzyme A hydratase | 0.89 | 0.187684 | 1.05 | 0.616422 | 1.02 | 0.855085 | 1.04 | 0.487423 |
| Bcnp1 | A_52_P1053160 | AK158308 | BCNP1 homolog | 0.91 | 0.060879 | 0.88 | 0.003021 | 0.92 | 0.035934 | 1.06 | 0.144708 |
| Bdh1 | A_51_P163106 | NM_175177 | 3-hydroxybutyrate dehydrogenase, type 1 | 1.01 | 0.789445 | 1.00 | 0.96248 | 0.91 | 0.125171 | 1.03 | 0.46998 |
| Bdh1 | A_52_P468343 | AK146962 | 3-hydroxybutyrate dehydrogenase, type 1 | 1.11 | 3.58E-08 | 0.96 | 0.250564 | 1.07 | 0.007208 | 1.11 | 0.000014 |
| Bdh2 | A_52_P195809 | NM_027208 | 3-hydroxybutyrate dehydrogenase, type 2 | 1.29 | 7.84E-07 | 1.21 | 0.000109 | 1.01 | 0.843347 | 0.99 | 0.865289 |
| Btd | A_51_P196158 | NM_025295 | biotinidase | 0.92 | 0.005392 | 1.01 | 0.750581 | 1.01 | 0.674532 | 1.09 | 0.001397 |
| Cat | A_52_P679769 | NM_009804 | catalase | 0.77 | 2.17E-07 | 0.95 | 0.277851 | 0.91 | 0.00025 | 0.91 | 0.016005 |
| Coq2 | A_51_P447752 | NM_027978 | coenzyme Q2 homolog, prenyltransferase (yeast) | 1.23 | 1.08E-14 | 1.12 | 0.00002 | 1.11 | 9.31E-08 | 1.14 | 1.63E-09 |
| Cox1 | A_51_P315595 | X57780 | M.musculus mRNA for mitochondrial gene for subunit I of cytochrome c oxidase. | 1.35 | 0.004183 | 0.9 | 0.300792 | 0.81 | 0.048438 | 0.94 | 0.501250 |
| Cox6a1 | A_51_P311540 | NM_007748 | cytochrome c oxidase, subunit VI a, polypeptide 1 | 0.92 | 0.00068 | 0.90 | 0.027116 | 0.93 | 0.028754 | 1.11 | 0.000188 |
| Cox6b2 | A_51_P300506 | NM_183405 | cytochrome c oxidase subunit VIb polypeptide 2 | 1.22 | 8.67E-35 | 1.12 | 0.000074 | 1.15 | 1.23E-17 | 1.12 | 1.34E-07 |
| Cpt1a | A_51_P427674 | NM_013495 | carnitine palmitoyltransferase 1a, liver | 1.10 | 0.037464 | 0.79 | 0.001022 | 0.82 | 0.004255 | 1.27 | 2.30E-07 |
| Cpt1b | A_51_P232913 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 0.93 | 0.182985 | 0.97 | 0.501011 | 1.13 | 0.005288 | 0.95 | 0.124335 |
| Cpt1b | A_52_P625508 | NM_009948 | carnitine palmitoyltransferase 1b, muscle | 1.05 | 0.21845 | 1.10 | 0.000836 | 1.17 | 5.44E-12 | 1.13 | 3.20E-06 |
| Cpt1c | A_51_P177562 | NM_153679 | carnitine palmitoyltransferase 1c | 0.99 | 0.921547 | 1.00 | 0.994404 | 1.06 | 0.510973 | 1.10 | 0.432697 |
| Cpt1c | A_52_P269942 | NM_153679 | carnitine palmitoyltransferase 1c | 1.15 | 0.036602 | 1.07 | 0.198124 | 1.26 | 4.53E-25 | 1.25 | 8.10E-07 |
| Cpt2 | A_51_P403388 | NM_009949 | carnitine palmitoyltransferase 2 | 1.22 | 4.59E-06 | 1.17 | 0.000793 | 1.20 | 6.34E-07 | 1.13 | 0.000924 |
| Crat | A_51_P440807 | NM_007760 | carnitine acetyltransferase | 1.08 | 0.000211 | 1.03 | 0.254661 | 1.00 | 0.813586 | 0.98 | 0.254275 |
| Crot | A_51_P489153 | NM_023733 | carnitine O-octanoyltransferase | 0.97 | 0.480869 | 0.90 | 0.004802 | 0.92 | 0.009612 | 0.93 | 0.024226 |
| Crot | A_52_P656336 | NM_023733 | carnitine O-octanoyltransferase | 0.75 | 0.011302 | 0.90 | 0.233425 | 0.83 | 0.047341 | 0.89 | 0.16889 |
| Cs | A_52_P182659 | NM_026444 | citrate synthase | 1.04 | 0.471665 | 0.89 | 0.006963 | 0.99 | 0.864901 | 0.98 | 0.707034 |
| Cyp19a1 | A_51_P474551 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.10 | 0.384145 | 1.39 | 0.019697 | 1.24 | 0.116454 | 1.33 | 0.005912 |
| Cyp19a1 | A_52_P591961 | NM_007810 | cytochrome P450, family 19, subfamily a, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp1a2 | A_51_P450140 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 1.31 | 0.137706 | 0.82 | 0.162217 | 1.38 | 0.287854 | 1.12 | 0.397882 |
| Cyp1a2 | A_52_P595871 | NM_009993 | cytochrome P450, family 1, subfamily a, polypeptide 2 | 0.99 | 0.890036 | 0.95 | 0.712519 | 1.00 | 1 | 0.95 | 0.777477 |
| Cyp1b1 | A_52_P297822 | AK016699 | cytochrome P450, family 1, subfamily b, polypeptide 1 | 1.00 | 0.984492 | 1.30 | 0.277073 | 1.00 | 0.976492 | 1.36 | 0.273099 |
| Cyp2a12 | A_51_P206736 | NM_133657 | cytochrome P450, family 2, subfamily a, polypeptide 12 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2a5 | A_52_P246252 | NM_007812 | cytochrome P450, family 2, subfamily a, polypeptide 5 | 1.10 | 0.543826 | 1.06 | 0.773843 | 0.95 | 0.758716 | 0.79 | 0.518717 |
| Cyp2b10 | A_51_P182362 | NM_009998 | Mus musculus cytochrome P450, family 2, subfamily b, polypeptide 10 (Cyp2b10), transcript variant 2, mRNA. | 0.89 | 0.347002 | 1.19 | 0.287759 | 1.19 | 0.351252 | 1.36 | 0.001351 |

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|---------|--------------|--------------|---|------|----------|------|----------|------|----------|------|----------|
| Cyp2b10 | A_52_P472486 | NM_009999 | cytochrome P450, family 2, subfamily b, polypeptide 10 | 0.98 | 0.84385 | 0.98 | 0.879554 | 1.07 | 0.561755 | 1.01 | 0.923178 |
| Cyp2b13 | A_51_P492339 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 0.94 | 0.798648 | 0.94 | 0.613588 | 0.98 | 0.917 | 0.80 | 0.256791 |
| Cyp2b13 | A_52_P289091 | NM_007813 | cytochrome P450, family 2, subfamily b, polypeptide 13 | 1.20 | 0.023833 | 1.03 | 0.660369 | 0.90 | 0.23214 | 1.03 | 0.612147 |
| Cyp2b19 | A_51_P352763 | NM_007814 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 1.18 | 2.23E-06 | 1.15 | 0.013364 | 1.11 | 0.010258 | 1.15 | 0.000106 |
| Cyp2b19 | A_52_P421626 | AK029227 | cytochrome P450, family 2, subfamily b, polypeptide 19 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2c29 | A_51_P103706 | NM_007815 | cytochrome P450, family 2, subfamily c, polypeptide 29 | 1.04 | 0.738679 | 0.94 | 0.503851 | 1.03 | 0.908494 | 1.33 | 0.033906 |
| Cyp2c38 | A_51_P342206 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2c38 | A_52_P468564 | NM_010002 | cytochrome P450, family 2, subfamily c, polypeptide 38 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.05 | 0.62758 |
| Cyp2c39 | A_51_P304109 | NM_010003 | cytochrome P450, family 2, subfamily c, polypeptide 39 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp2c44 | A_51_P209782 | NM_001001446 | cytochrome P450, family 2, subfamily c, polypeptide 44 | 0.77 | 0.207521 | 1.14 | 0.52184 | 1.07 | 0.807855 | 1.15 | 0.373625 |
| Cyp2c54 | A_52_P154580 | NM_206537 | cytochrome P450, family 2, subfamily c, polypeptide 54 | 0.95 | 0.558826 | 1.11 | 0.527632 | 1.10 | 0.4169 | 1.08 | 0.676863 |
| Cyp2c55 | A_51_P447785 | NM_028089 | cytochrome P450, family 2, subfamily c, polypeptide 55 | 0.95 | 0.324697 | 0.87 | 0.001004 | 0.88 | 0.010709 | 0.94 | 0.023592 |
| Cyp2c65 | A_52_P652059 | AK008688 | cytochrome P450, family 2, subfamily c, polypeptide 65 | 0.85 | 0.010483 | 1.04 | 0.63575 | 1.11 | 0.040806 | 0.99 | 0.866459 |
| Cyp2c66 | A_51_P471126 | NM_001011707 | cytochrome P450, family 2, subfamily c, polypeptide 66 | 1.12 | 0.3592 | 1.43 | 0.00157 | 1.09 | 0.467904 | 1.28 | 0.023425 |
| Cyp2c70 | A_51_P134142 | NM_145499 | cytochrome P450, family 2, subfamily c, polypeptide 70 | 1.01 | 0.696792 | 0.95 | 0.146067 | 0.94 | 0.038226 | 0.97 | 0.183637 |
| Cyp2d10 | A_51_P111192 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 1.03 | 0.40488 | 1.12 | 3.64E-06 | 1.03 | 0.41001 | 0.99 | 0.79725 |
| Cyp2d10 | A_52_P527775 | NM_010005 | cytochrome P450, family 2, subfamily d, polypeptide 10 | 1.06 | 0.112615 | 1.02 | 0.580152 | 1.08 | 0.121467 | 1.07 | 0.128513 |
| Cyp2d13 | A_52_P372062 | NM_133695 | Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13) on chromosome 15. | 0.99 | 0.963699 | 0.93 | 0.768373 | 0.99 | 0.960795 | 1.24 | 0.363521 |
| Cyp2d22 | A_51_P124126 | NM_019823 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 0.95 | 0.412927 | 1.08 | 0.028459 | 0.94 | 0.436326 | 0.93 | 0.191909 |
| Cyp2d22 | A_52_P478420 | AK086555 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 1.07 | 0.125863 | 1.15 | 0.00285 | 1.06 | 0.18605 | 0.90 | 0.028834 |
| Cyp2d22 | A_52_P49391 | AK090296 | cytochrome P450, family 2, subfamily d, polypeptide 22 | 0.84 | 0.000546 | 0.87 | 0.000756 | 0.90 | 0.040986 | 0.84 | 0.000016 |
| Cyp2d9 | A_51_P124133 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 1.00 | 0.965657 | 1.03 | 0.176462 | 1.06 | 0.036487 | 1.00 | 0.994884 |
| Cyp2d9 | A_51_P478303 | NM_010006 | cytochrome P450, family 2, subfamily d, polypeptide 9 | 1.25 | 1.19E-12 | 1.18 | 1.69E-10 | 1.14 | 2.90E-13 | 1.09 | 2.15E-06 |
| Cyp2g1 | A_51_P137452 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 1.24 | 0.233244 | 1.10 | 0.678732 | 1.01 | 0.968408 | 1.07 | 0.605405 |
| Cyp2g1 | A_52_P481346 | NM_013809 | cytochrome P450, family 2, subfamily g, polypeptide 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.10 | 0.469839 |
| Cyp2j5 | A_51_P307872 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 0.99 | 0.922366 | 1.12 | 0.641582 | 1.00 | 1 | 1.00 | 1 |
| Cyp2j5 | A_52_P315766 | NM_010007 | cytochrome P450, family 2, subfamily j, polypeptide 5 | 1.07 | 0.577594 | 1.02 | 0.869785 | 1.00 | 1 | 1.00 | 1 |
| Cyp2j9 | A_51_P330044 | NM_028979 | cytochrome P450, family 2, subfamily j, polypeptide 9 | 0.96 | 0.147853 | 0.92 | 0.060985 | 0.88 | 0.000999 | 0.96 | 0.292933 |
| Cyp3a13 | A_51_P114941 | NM_007819 | cytochrome P450, family 3, subfamily a, polypeptide 13 | 0.84 | 0.275835 | 0.84 | 0.379511 | 0.62 | 0.013203 | 0.84 | 0.23384 |
| Cyp3a16 | A_51_P482051 | NM_007820 | cytochrome P450, family 3, subfamily a, polypeptide 16 | 0.93 | 0.754141 | 1.49 | 0.232588 | 1.06 | 0.777923 | 0.89 | 0.494197 |
| Cyp3a25 | A_51_P489367 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 0.97 | 0.7486 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp3a25 | A_52_P380314 | NM_019792 | cytochrome P450, family 3, subfamily a, polypeptide 25 | 1.00 | 1 | 1.00 | 1 | 1.03 | 0.650984 | 1.00 | 1 |
| Cyp3a44 | A_52_P366803 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp3a44 | A_52_P571006 | NM_177380 | cytochrome P450, family 3, subfamily a, polypeptide 44 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |

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|----------|--------------|-----------|--|------|----------|------|----------|------|----------|------|----------|
| Cyp4a10 | A_52_P257774 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 1.04 | 0.818078 | 1.00 | 1 | 1.00 | 1 | 0.90 | 0.448251 |
| Cyp4a10 | A_52_P340136 | X71478 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.90 | 0.197337 | 1.19 | 0.117584 | 1.11 | 0.047816 | 1.15 | 0.016387 |
| Cyp4a10 | A_52_P6588 | NM_010011 | cytochrome P450, family 4, subfamily a, polypeptide 10 | 0.94 | 0.503 | 1.19 | 0.335823 | 1.21 | 0.450878 | 0.84 | 0.590592 |
| Cyp4a12a | A_51_P433360 | NM_177406 | cytochrome P450, family 4, subfamily a, polypeptide 12a | 0.91 | 0.58028 | 1.18 | 0.642361 | 1.21 | 0.335134 | 1.27 | 0.309903 |
| Cyp4a14 | A_51_P238576 | NM_007822 | cytochrome P450, family 4, subfamily a, polypeptide 14 | 1.04 | 0.380304 | 0.99 | 0.844162 | 1.05 | 0.669173 | 1.04 | 0.256985 |
| Cyp4f14 | A_51_P452768 | NM_022434 | cytochrome P450, family 4, subfamily f, polypeptide 14 | 1.11 | 0.496822 | 0.89 | 0.641397 | 1.26 | 0.305074 | 1.01 | 0.926879 |
| Cyp4f15 | A_51_P136303 | NM_134127 | cytochrome P450, family 4, subfamily f, polypeptide 15 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Cyp51 | A_51_P485791 | NM_020010 | cytochrome P450, family 51 | 0.76 | 0.014647 | 0.93 | 0.30741 | 0.95 | 0.531057 | 1.13 | 0.088029 |
| Cyp51 | A_52_P778750 | AK035338 | Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530019F09 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Dci | A_51_P105589 | NM_010023 | dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) | 1.01 | 0.749644 | 1.18 | 0.001632 | 1.10 | 0.000564 | 0.96 | 0.129832 |
| Decr1 | A_51_P208555 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 0.92 | 0.136953 | 0.86 | 0.004363 | 0.83 | 0.002527 | 0.78 | 4.49E-06 |
| Decr1 | A_52_P335907 | NM_026172 | 2,4-dienoyl CoA reductase 1, mitochondrial | 0.93 | 0.07435 | 0.88 | 0.000706 | 0.87 | 3.50E-06 | 0.83 | 1.20E-21 |
| Dgat2 | A_51_P396003 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.96 | 0.551136 | 1.21 | 0.000067 | 1.17 | 0.000962 | 1.28 | 6.42E-10 |
| Dgat2 | A_52_P592909 | NM_026384 | diacylglycerol O-acyltransferase 2 | 0.94 | 0.309034 | 1.12 | 0.007574 | 1.09 | 0.014086 | 1.24 | 4.21E-15 |
| Dlat | A_52_P374642 | NM_145614 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | 1.08 | 0.002847 | 0.90 | 0.000011 | 0.97 | 0.2901 | 0.96 | 0.094663 |
| Dld | A_51_P184282 | U73445 | dihydrolipoamide dehydrogenase | 1.07 | 0.014602 | 0.88 | 0.000048 | 0.91 | 0.000495 | 0.94 | 0.00069 |
| Dld | A_52_P536646 | NM_007861 | dihydrolipoamide dehydrogenase | 0.92 | 0.141547 | 0.79 | 0.011496 | 0.84 | 0.014865 | 0.86 | 0.01186 |
| Dlst | A_52_P140072 | NM_030225 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.17 | 0.028261 | 1.07 | 0.360744 | 1.09 | 0.198018 | 1.15 | 0.042536 |
| Dlst | A_52_P3383 | AK171100 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) | 1.07 | 0.028959 | 0.86 | 0.000755 | 0.85 | 0.000194 | 1.05 | 0.156966 |
| Ech1 | A_51_P421846 | NM_016772 | enoyl coenzyme A hydratase 1, peroxisomal | 0.97 | 0.452515 | 1.21 | 0.001107 | 1.22 | 2.82E-15 | 1.09 | 0.000419 |
| Echs1 | A_51_P409039 | NM_053119 | enoyl Coenzyme A hydratase, short chain, 1, mitochondrial | 0.93 | 0.000959 | 0.87 | 7.62E-07 | 0.80 | 1.13E-35 | 0.84 | 9.23E-26 |
| Ehhadh | A_51_P462918 | NM_023737 | enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase | 0.89 | 0.000136 | 0.84 | 3.02E-06 | 0.86 | 0.000055 | 1.12 | 0.001829 |
| Eno1 | A_52_P349939 | NM_023119 | enolase 1, alpha non-neuron | 1.14 | 0.146494 | 1.00 | 0.97817 | 1.11 | 0.148264 | 1.10 | 0.223193 |
| Fabp1 | A_51_P487818 | NM_017399 | fatty acid binding protein 1, liver | 0.88 | 0.281956 | 0.74 | 0.090117 | 0.83 | 0.303685 | 0.88 | 0.264696 |
| Fabp2 | A_51_P313581 | NM_007980 | fatty acid binding protein 2, intestinal | 1.12 | 0.002604 | 1.08 | 0.148284 | 1.04 | 0.437777 | 1.13 | 0.000022 |
| Fabp2 | A_52_P453013 | NM_007980 | fatty acid binding protein 2, intestinal | 0.66 | 0.008903 | 1.15 | 0.690694 | 1.08 | 0.621853 | 1.15 | 0.311106 |
| Fabp3 | A_51_P167535 | NM_010174 | fatty acid binding protein 3, muscle and heart | 0.85 | 0.303578 | 1.11 | 0.488699 | 1.09 | 0.557694 | 0.91 | 0.583787 |
| Fbp1 | A_51_P474701 | NM_019395 | fructose bisphosphatase 1 | 0.92 | 0.684408 | 0.96 | 0.805518 | 0.95 | 0.799475 | 0.75 | 0.045375 |
| Fdft1 | A_51_P485946 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 1.15 | 2.36E-11 | 1.17 | 8.16E-11 | 1.11 | 8.22E-08 | 1.15 | 9.09E-09 |
| Fdft1 | A_52_P136138 | NM_010191 | farnesyl diphosphate farnesyl transferase 1 | 1.23 | 0.003257 | 0.91 | 0.480531 | 1.17 | 0.282651 | 1.16 | 0.210927 |
| Fdps | A_51_P379798 | NM_134469 | farnesyl diphosphate synthetase | 0.83 | 9.31E-15 | 1.10 | 0.018792 | 1.16 | 8.87E-06 | 1.17 | 5.14E-09 |
| Fdps | A_52_P593965 | AK077979 | farnesyl diphosphate synthetase | 0.89 | 0.003054 | 0.97 | 0.50233 | 0.94 | 0.283164 | 1.13 | 0.0768 |

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|---------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Fnta | A_51_P112116 | NM_008033 | farnesyltransferase, CAAX box, alpha | 1.08 | 0.000385 | 1.02 | 0.228188 | 1.12 | 0.000031 | 1.10 | 0.000018 |
| Fntb | A_51_P517680 | NM_145927 | farnesyltransferase, CAAX box, beta | 0.97 | 0.365488 | 1.00 | 0.986099 | 1.03 | 0.547523 | 1.06 | 0.09753 |
| Fntb | A_52_P235241 | NM_145927 | farnesyltransferase, CAAX box, beta | 0.84 | 7.06E-09 | 0.97 | 0.463486 | 1.00 | 0.985179 | 1.00 | 0.930817 |
| G6pc | A_51_P462385 | NM_008061 | glucose-6-phosphatase, catalytic | 1.14 | 0.000183 | 1.21 | 0.001319 | 1.08 | 0.106185 | 1.14 | 0.000322 |
| Gck | A_52_P66580 | BC011139 | glucokinase | 1.10 | 0.061698 | 0.97 | 0.42253 | 1.11 | 0.029489 | 1.11 | 0.000289 |
| Gckr | A_51_P198694 | NM_144909 | glucokinase regulatory protein | 0.96 | 0.760948 | 1.05 | 0.774406 | 1.17 | 0.297766 | 1.47 | 0.001433 |
| Ggps1 | A_51_P179604 | NM_010282 | PREDICTED: Mus musculus geranylgeranyl diphosphate synthase 1, transcript variant 4 (Ggps1), mRNA. | 0.89 | 0.010082 | 0.93 | 0.12768 | 0.85 | 0.000595 | 0.90 | 0.012398 |
| Ggps1 | A_51_P469902 | XM_977926 | geranylgeranyl diphosphate synthase 1 | 1.04 | 0.198474 | 0.89 | 0.002363 | 0.88 | 0.000012 | 0.87 | 9.86E-10 |
| Gpi1 | A_51_P426886 | NM_008155 | glucose phosphate isomerase 1 | 0.96 | 0.065756 | 1.00 | 0.959669 | 1.03 | 0.047054 | 1.06 | 0.017767 |
| Gpi1 | A_52_P347412 | L09104 | glucose phosphate isomerase 1 | 1.01 | 0.705449 | 1.07 | 0.085853 | 1.10 | 0.061533 | 1.07 | 0.105344 |
| Gyk | A_52_P379205 | AK086200 | glycerol kinase | 1.12 | 0.522919 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Gyk | A_52_P453517 | NM_008194 | glycerol kinase | 1.00 | 0.974152 | 1.21 | 0.486486 | 1.14 | 0.64433 | 0.97 | 0.823924 |
| Gys1 | A_52_P228932 | NM_030678 | glycogen synthase 1, muscle | 0.95 | 0.292576 | 0.98 | 0.65637 | 1.01 | 0.815913 | 0.99 | 0.875561 |
| Hadha | A_52_P338459 | AK035316 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 1.64 | 0.03785 | 1.25 | 0.250483 | 0.94 | 0.597202 | 1.04 | 0.792 |
| Hadha | A_52_P658044 | AK050856 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit | 0.81 | 0.144005 | 0.85 | 0.129918 | 0.84 | 0.091232 | 0.85 | 0.124467 |
| Hadhb | A_51_P217990 | NM_145558 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit | 1.23 | 3.30E-11 | 1.11 | 0.030362 | 1.08 | 0.01388 | 0.92 | 0.000161 |
| Hk1 | A_52_P102773 | BC072628 | hexokinase 1 | 1.04 | 0.301878 | 1.20 | 2.73E-12 | 1.16 | 2.51E-11 | 1.19 | 2.62E-18 |
| Hk1 | A_52_P479599 | NM_010438 | hexokinase 1 | 0.79 | 0.039717 | 0.94 | 0.507839 | 0.97 | 0.799103 | 1.05 | 0.437709 |
| Hk1 | A_52_P674530 | NM_010438 | hexokinase 1 | 0.93 | 0.042922 | 1.07 | 0.20426 | 1.11 | 0.000139 | 1.16 | 1.85E-07 |
| Hk1 | A_52_P87141 | NM_010438 | hexokinase 1 | 1.38 | 0.176002 | 1.10 | 0.662841 | 0.94 | 0.653176 | 1.10 | 0.544626 |
| Hmgcl | A_51_P308961 | NM_008254 | 3-hydroxy-3-methylglutaryl-Coenzyme A lyase | 1.20 | 9.99E-12 | 1.13 | 7.85E-06 | 1.16 | 9.01E-13 | 1.08 | 0.00259 |
| Hmgcll1 | A_52_P197722 | NM_173731 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 | 1.26 | 0.025439 | 1.02 | 0.880237 | 0.95 | 0.572675 | 0.85 | 0.094914 |
| Hmgcr | A_52_P578922 | AK159899 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 0.92 | 0.029724 | 0.91 | 4.99E-07 | 0.92 | 0.000074 | 0.98 | 0.356645 |
| Hmgcr | A_52_P770765 | AK033165 | Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030450I20 | 0.77 | 0.071924 | 0.84 | 0.433231 | 0.89 | 0.365471 | 0.90 | 0.318843 |
| Hmgcs1 | A_52_P119039 | AK078743 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | 0.81 | 0.260819 | 0.90 | 0.614731 | 0.89 | 0.438221 | 0.78 | 0.029329 |
| Hmgcs2 | A_51_P116039 | NM_008256 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 | 1.03 | 0.900147 | 0.99 | 0.980713 | 0.96 | 0.807873 | 0.91 | 0.694633 |
| Hsd17b4 | A_51_P445662 | NM_008292 | hydroxysteroid (17-beta) dehydrogenase 4 | 1.11 | 3.30E-07 | 1.08 | 0.000519 | 1.10 | 1.93E-10 | 1.20 | 1.58E-20 |
| Idh3a | A_51_P268559 | NM_029573 | isocitrate dehydrogenase 3 (NAD+) alpha | 1.20 | 0.000315 | 0.78 | 2.56E-06 | 0.89 | 0.03488 | 0.98 | 0.635659 |
| Idi1 | A_51_P329711 | NM_177960 | isopentenyl-diphosphate delta isomerase | 0.87 | 0.00062 | 1.10 | 0.110183 | 0.92 | 0.010864 | 0.92 | 0.010283 |
| Ldhc | A_51_P242403 | NM_013580 | lactate dehydrogenase C | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Lipe | A_51_P435366 | NM_010719 | lipase, hormone sensitive | 0.90 | 0.005121 | 0.96 | 0.182903 | 0.92 | 0.004157 | 1.17 | 3.60E-06 |

| | | | | | | | | | | | |
|--------|--------------|--------------|---|------|----------|------|----------|------|----------|------|----------|
| Lpl | A_51_P259296 | NM_008509 | lipoprotein lipase | 0.90 | 0.342969 | 0.88 | 0.303114 | 0.79 | 0.075399 | 0.94 | 0.664394 |
| Mcat | A_51_P314855 | NM_001030014 | malonyl CoA:ACP acyltransferase (mitochondrial) | 1.06 | 0.130558 | 1.07 | 0.060024 | 1.11 | 0.010059 | 1.17 | 0.000041 |
| Mdh1 | A_51_P218179 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 1.18 | 7.06E-15 | 1.12 | 0.000283 | 1.24 | 5.14E-15 | 1.24 | 2.18E-18 |
| Mdh1 | A_52_P407796 | NM_008618 | malate dehydrogenase 1, NAD (soluble) | 1.13 | 0.038715 | 0.96 | 0.585048 | 1.03 | 0.571308 | 1.07 | 0.355067 |
| Mdh1 | A_52_P470451 | AK077724 | malate dehydrogenase 1, NAD (soluble) | 1.12 | 0.026756 | 0.79 | 0.000021 | 0.79 | 2.19E-11 | 0.79 | 6.68E-10 |
| Mdh2 | A_51_P384879 | NM_008617 | malate dehydrogenase 2, NAD (mitochondrial) | 1.25 | 0.029863 | 0.91 | 0.342023 | 1.03 | 0.74713 | 1.07 | 0.378048 |
| Mecr | A_51_P386080 | NM_025297 | mitochondrial trans-2-enoyl-CoA reductase | 1.06 | 0.03343 | 1.10 | 0.015291 | 1.12 | 5.45E-06 | 1.21 | 1.37E-13 |
| Mgll | A_51_P352549 | AK079089 | Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330168D17 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Mut | A_51_P193935 | NM_008650 | methylmalonyl-Coenzyme A mutase | 1.10 | 0.026066 | 0.90 | 0.028543 | 0.85 | 0.008602 | 0.87 | 0.012252 |
| Mut | A_52_P362959 | AK051851 | methylmalonyl-Coenzyme A mutase | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Mut | A_52_P633163 | NM_008650 | methylmalonyl-Coenzyme A mutase | 1.07 | 0.008433 | 0.90 | 0.002526 | 0.87 | 2.52E-06 | 0.90 | 0.000023 |
| Ogdh | A_51_P122825 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.16 | 0.000015 | 1.05 | 0.102776 | 1.11 | 0.006447 | 1.05 | 0.109291 |
| Ogdh | A_52_P369310 | NM_010956 | oxoglutarate dehydrogenase (lipoamide) | 1.10 | 0.05833 | 1.03 | 0.502506 | 1.05 | 0.242531 | 1.02 | 0.688472 |
| Oxct2a | A_51_P125056 | NM_022033 | 3-oxoacid CoA transferase 2A | 1.36 | 0.217335 | 1.08 | 0.506497 | 1.03 | 0.815404 | 1.38 | 0.126361 |
| Oxsm | A_51_P312748 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 0.99 | 0.866235 | 0.89 | 0.090421 | 0.90 | 0.044034 | 0.93 | 0.184463 |
| Oxsm | A_52_P231635 | NM_027695 | 3-oxoacyl-ACP synthase, mitochondrial | 1.21 | 3.92E-08 | 1.06 | 0.081873 | 1.17 | 8.55E-07 | 1.22 | 8.86E-23 |
| Pccb | A_51_P418259 | NM_025835 | propionyl Coenzyme A carboxylase, beta polypeptide | 1.16 | 0.000048 | 0.92 | 0.044418 | 0.98 | 0.484509 | 0.98 | 0.485443 |
| Pck2 | A_52_P21659 | NM_028994 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | 1.02 | 0.518626 | 1.17 | 0.000433 | 1.11 | 3.68E-06 | 1.21 | 1.72E-20 |
| Pcx | A_51_P480578 | NM_008797 | pyruvate carboxylase | 1.03 | 0.430291 | 0.99 | 0.826808 | 0.97 | 0.24447 | 1.16 | 0.000265 |
| Pdha1 | A_51_P321391 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 1.06 | 0.33274 | 0.89 | 0.017833 | 0.92 | 0.033921 | 0.93 | 0.087083 |
| Pdha1 | A_52_P581435 | NM_008810 | pyruvate dehydrogenase E1 alpha 1 | 0.99 | 0.783287 | 0.83 | 9.88E-14 | 0.84 | 6.61E-07 | 0.85 | 1.78E-21 |
| Pdha2 | A_51_P519857 | NM_008811 | pyruvate dehydrogenase E1 alpha 2 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |
| Pdha2 | A_51_P321921 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 1.07 | 0.006053 | 1.01 | 0.554244 | 1.10 | 0.000206 | 1.12 | 3.63E-13 |
| Pdha2 | A_52_P568792 | NM_024221 | pyruvate dehydrogenase (lipoamide) beta | 0.95 | 0.066615 | 0.85 | 4.11E-10 | 0.94 | 0.053274 | 0.99 | 0.577593 |
| Peci | A_51_P394665 | NM_011868 | peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase | 0.94 | 0.005073 | 1.04 | 0.081897 | 1.02 | 0.170276 | 1.01 | 0.629259 |
| Pfkfb2 | A_51_P184849 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.16 | 8.95E-07 | 0.97 | 0.461637 | 1.03 | 0.186533 | 0.99 | 0.851213 |
| Pfkfb2 | A_51_P335251 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.05 | 0.458276 | 0.90 | 0.040198 | 0.95 | 0.251436 | 0.80 | 0.000621 |
| Pfkfb2 | A_52_P142912 | NM_008825 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.11 | 0.004998 | 0.80 | 0.000813 | 0.95 | 0.319062 | 0.91 | 0.138245 |
| Pfkfb2 | A_52_P31125 | BC018418 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 | 1.35 | 0.001507 | 1.41 | 0.013794 | 1.21 | 0.291739 | 1.11 | 0.342817 |
| Pfkl | A_51_P310896 | NM_008826 | phosphofructokinase, liver, B-type | 0.98 | 0.734219 | 1.18 | 0.009374 | 1.26 | 0.001513 | 1.23 | 0.000943 |
| Pgam1 | A_51_P342669 | NM_023418 | phosphoglycerate mutase 1 | 0.80 | 2.23E-07 | 0.84 | 2.43E-06 | 0.83 | 0.000017 | 1.02 | 0.612479 |
| Pgk1 | A_51_P182828 | NM_008828 | phosphoglycerate kinase 1 | 1.28 | 6.20E-15 | 1.02 | 0.526348 | 1.03 | 0.193371 | 1.07 | 0.000067 |
| Pgk1 | A_52_P600398 | NM_008828 | phosphoglycerate kinase 1 | 1.25 | 3.55E-08 | 0.98 | 0.580435 | 1.03 | 0.372264 | 1.07 | 0.003277 |
| Pgl3 | A_51_P321794 | NM_025396 | 6-phosphogluconolactonase | 1.15 | 3.38E-08 | 1.20 | 1.33E-12 | 1.20 | 1.45E-23 | 1.21 | 1.10E-42 |

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|----------|---------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Pgm3 | A_51_P208987 | NM_028352 | phosphoglucomutase 3 | 1.07 | 0.278793 | 0.87 | 0.058821 | 0.96 | 0.592948 | 1.01 | 0.806057 |
| Pgm3 | A_52_P341449 | NM_028352 | phosphoglucomutase 3 | 0.79 | 4.84E-09 | 0.99 | 0.827123 | 0.89 | 0.022728 | 0.93 | 0.059139 |
| Pgm5 | A_52_P229924 | NM_175013 | phosphoglucomutase 5 | 1.20 | 0.028011 | 1.17 | 0.037112 | 1.14 | 0.064824 | 1.25 | 0.004129 |
| Pgm5 | A_52_P860000 | NM_175013 | phosphoglucomutase 5 | 1.14 | 0.614435 | 1.10 | 0.258207 | 1.25 | 0.256178 | 0.98 | 0.93904 |
| Phka2 | A_51_P239970 | AK051899 | phosphorylase kinase alpha 2 | 1.00 | 1 | 1.05 | 0.748184 | 1.00 | 1 | 1.00 | 1 |
| Phka2 | A_51_P368950 | AK018208 | Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230017A12 | 0.82 | 0.155074 | 0.89 | 0.522746 | 1.11 | 0.64997 | 0.87 | 0.136028 |
| Phka2 | A_52_P657963 | AK045618 | phosphorylase kinase alpha 2 | 0.87 | 0.014459 | 1.11 | 0.046053 | 0.93 | 0.103166 | 0.82 | 1.50E-13 |
| Phkb | A_51_P270725 | AK089493 | phosphorylase kinase beta | 1.18 | 0.001757 | 0.91 | 0.018839 | 0.99 | 0.64281 | 0.94 | 0.03896 |
| Phkb | A_52_P342907 | BC051503 | phosphorylase kinase beta | 1.10 | 0.528878 | 0.92 | 0.562882 | 1.00 | 1 | 1.04 | 0.718673 |
| Phkb | A_52_P513347 | NM_199446 | phosphorylase kinase beta | 1.16 | 0.015466 | 0.69 | 1.18E-07 | 0.80 | 0.000062 | 0.77 | 5.98E-14 |
| Phkg2 | A_51_P235909 | NM_026888 | phosphorylase kinase, gamma 2 (testis) | 1.17 | 0.000016 | 1.18 | 0.000019 | 1.19 | 1.08E-07 | 1.17 | 7.02E-06 |
| Phkg2 | A_52_P19446 | AK089062 | phosphorylase kinase, gamma 2 (testis) | 0.76 | 0.242253 | 0.92 | 0.60291 | 0.92 | 0.602133 | 0.89 | 0.385471 |
| Pkm2 | A_52_P328249 | AK083076 | pyruvate kinase, muscle | 1.10 | 0.004928 | 1.03 | 0.408358 | 1.14 | 0.001676 | 1.02 | 0.539087 |
| Ppara | A_51_P348334 | NM_011144 | peroxisome proliferator activated receptor alpha | 0.98 | 0.489239 | 0.99 | 0.899554 | 1.00 | 0.891679 | 0.96 | 0.098172 |
| Ppard | A_51_P271556 | NM_011145 | peroxisome proliferator activator receptor delta | 0.94 | 0.291546 | 1.15 | 0.005179 | 1.13 | 0.136575 | 1.05 | 0.434841 |
| Ppargc1b | A_52_P883463 | AK045690 | Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230304K20 | 0.81 | 0.000431 | 0.78 | 2.36E-14 | 0.78 | 1.35E-31 | 0.81 | 7.63E-09 |
| Ppp1ca | A_51_P509389 | NM_031868 | protein phosphatase 1, catalytic subunit, alpha isoform | 0.95 | 0.114105 | 1.07 | 0.117592 | 1.06 | 0.034744 | 1.10 | 0.000596 |
| Ppp1cc | A_52_P519508 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 1.05 | 0.114533 | 0.92 | 0.037383 | 0.96 | 0.174804 | 0.95 | 0.045847 |
| Ppp1cc | A_52_P540434 | NM_013636 | protein phosphatase 1, catalytic subunit, gamma isoform | 1.08 | 0.021697 | 0.94 | 0.013063 | 0.94 | 0.049344 | 0.96 | 0.059605 |
| Ppt2 | A_52_P238816 | NM_019441 | palmitoyl-protein thioesterase 2 | 1.09 | 0.000535 | 1.07 | 0.036481 | 1.05 | 0.006852 | 1.03 | 0.128012 |
| Pygb | A_51_P485810 | NM_153781 | brain glycogen phosphorylase | 0.80 | 0.095792 | 1.16 | 0.227436 | 1.29 | 0.016167 | 1.30 | 0.008205 |
| Pygl | A_52_P320181 | AK083075 | liver glycogen phosphorylase | 1.00 | 1 | 1.00 | 1 | 0.98 | 0.871164 | 1.00 | 1 |
| Scd3 | A_51_P446045 | NM_024450 | stearoyl-coenzyme A desaturase 3 | 1.01 | 0.886387 | 1.16 | 0.000094 | 1.06 | 0.16702 | 1.09 | 0.06064 |
| Scd4 | A_52_P374877 | NM_183216 | stearoyl-coenzyme A desaturase 4 | 1.00 | 1 | 1.00 | 1 | 1.02 | 0.907247 | 1.16 | 0.44379 |
| Scd4 | A_52_P603237 | BC038322 | stearoyl-coenzyme A desaturase 4 | 1.00 | 1 | 0.96 | 0.764418 | 0.97 | 0.702267 | 1.26 | 0.127393 |
| Sdha | A_52_P109503 | NM_023281 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | 1.10 | 0.089656 | 0.97 | 0.580809 | 0.95 | 0.250442 | 0.94 | 0.218484 |
| Sdhb | A_51_P234853 | NM_023374 | succinate dehydrogenase complex, subunit B, iron sulfur (lp) | 1.29 | 5.32E-20 | 1.01 | 0.828356 | 1.04 | 0.265271 | 1.02 | 0.502067 |
| Sdhc | A_51_P106373 | NM_025321 | succinate dehydrogenase complex, subunit C, integral membrane protein | 1.26 | 3.07E-06 | 1.17 | 0.009143 | 1.15 | 0.005156 | 1.04 | 0.393295 |
| Sdhd | A_51_P260871 | NM_025848 | succinate dehydrogenase complex, subunit D, integral membrane protein | 1.19 | 0.000011 | 1.04 | 0.27651 | 1.06 | 0.156084 | 1.02 | 0.661669 |
| Slc27a1 | A_52_P199905 | CB588406 | AGENCOURT_12600125 NIH_MGC_136 Mus musculus cDNA clone IMAGE:30290747 5', mRNA sequence. | 1.02 | 0.500223 | 0.87 | 0.011824 | 0.93 | 0.216123 | 1.18 | 9.55E-10 |
| Slc27a2 | A_51_P484551 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 1.02 | 0.858915 | 1.02 | 0.792639 | 1.00 | 0.969122 | 0.86 | 0.497094 |
| Slc27a2 | A_52_P1083677 | AK038847 | solute carrier family 27 (fatty acid transporter), member 2 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 | 1.00 | 1 |

| | | | | | | | | | | | |
|---------|--------------|-----------|---|------|----------|------|----------|------|----------|------|----------|
| Slc27a2 | A_52_P154971 | NM_011978 | solute carrier family 27 (fatty acid transporter), member 2 | 1.19 | 0.085735 | 1.09 | 0.687762 | 0.81 | 0.327119 | 1.24 | 0.279449 |
| Slc27a4 | A_51_P408609 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 1.00 | 0.991729 | 0.81 | 0.010115 | 1.00 | 0.97244 | 1.22 | 0.048962 |
| Slc27a4 | A_52_P61854 | NM_011989 | solute carrier family 27 (fatty acid transporter), member 4 | 1.05 | 0.32337 | 1.14 | 0.010642 | 1.22 | 0.000104 | 1.27 | 0.000109 |
| Slc27a5 | A_51_P289742 | NM_009512 | solute carrier family 27 (fatty acid transporter), member 5 | 0.92 | 0.352201 | 0.99 | 0.930106 | 1.20 | 0.137374 | 0.99 | 0.937775 |
| Slc27a6 | A_51_P211616 | AK028699 | solute carrier family 27 (fatty acid transporter), member 6 | 1.12 | 0.468952 | 1.00 | 1 | 1.00 | 1 | 1.42 | 0.152761 |
| Slc2a2 | A_51_P185693 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 1.00 | 1 | 1.06 | 0.660862 | 1.00 | 1 | 1.19 | 0.474252 |
| Slc2a2 | A_52_P409988 | NM_031197 | solute carrier family 2 (facilitated glucose transporter), member 2 | 1.18 | 0.006788 | 0.95 | 0.521785 | 1.16 | 0.014602 | 1.11 | 0.027911 |
| Slc2a4 | A_51_P217498 | NM_009204 | solute carrier family 2 (facilitated glucose transporter), member 4 | 0.86 | 1.21E-15 | 0.85 | 1.42E-07 | 0.96 | 0.003481 | 0.98 | 0.245546 |
| Sqle | A_51_P450487 | NM_009270 | squalene epoxidase | 0.89 | 0.043316 | 1.35 | 0.020212 | 1.13 | 0.031236 | 1.20 | 0.001692 |
| Sucla2 | A_52_P533792 | NM_011506 | succinate-Coenzyme A ligase, ADP-forming, beta subunit | 1.28 | 1.24E-16 | 0.93 | 0.009098 | 1.05 | 0.170076 | 1.01 | 0.892332 |
| Sucig2 | A_51_P478672 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 1.15 | 0.000285 | 0.98 | 0.75009 | 1.02 | 0.767559 | 0.81 | 0.001085 |
| Sucig2 | A_52_P58181 | NM_011507 | succinate-Coenzyme A ligase, GDP-forming, beta subunit | 1.01 | 0.758032 | 0.90 | 0.000253 | 0.94 | 0.002485 | 0.92 | 1.80E-07 |
| Tkt | A_52_P631197 | AK050793 | transketolase | 1.04 | 0.846415 | 1.08 | 0.73405 | 0.80 | 0.320987 | 1.19 | 0.416033 |
| Ucp2 | A_52_P499675 | NM_011671 | uncoupling protein 2 (mitochondrial, proton carrier) | 1.60 | 0.234356 | 1.97 | 0.003958 | 1.31 | 0.475073 | 1.39 | 0.325886 |
| Ugp2 | A_51_P475580 | NM_139297 | UDP-glucose pyrophosphorylase 2 | 1.08 | 0.002661 | 0.89 | 0.009003 | 0.98 | 0.678936 | 0.97 | 0.201846 |
| Uqcrc2 | A_51_P128648 | NM_025899 | ubiquinol cytochrome c reductase core protein 2 | 1.25 | 1.64E-31 | 1.11 | 0.000045 | 1.12 | 6.12E-06 | 1.07 | 4.80E-06 |
| Uqcrcs1 | A_51_P361951 | NM_025710 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 | 1.27 | 0 | 0.97 | 0.303646 | 0.99 | 0.806039 | 0.98 | 0.162563 |
| Uqcrh | A_52_P541875 | NM_025641 | ubiquinol-cytochrome c reductase hinge protein | 1.29 | 0.000072 | 1.03 | 0.604336 | 1.00 | 0.937126 | 0.95 | 0.328395 |
| Uqcrcq | A_52_P370484 | NM_025352 | ubiquinol-cytochrome c reductase, complex III subunit VII | 1.28 | 0.008964 | 1.05 | 0.553213 | 1 | 0.93704 | 0.99 | 0.927733 |

Supplemental Table 3: Liver and IAT real-time PCR data analysis and comparison with corresponding microarrays results. Data are presented as ratio of db/⁺ or RSG-treated mice versus db/db mice.

| Sample | qPCR Ratio vs. db/db | | | | | | Microarrays Ratio vs. db/db | | | | | |
|---------------|----------------------|------|------|------|------|-------|-----------------------------|------|------|------|------|-------|
| | Assay ID | Pool | db+ | RSG | RSG | RSG | Sequence | Pool | db+ | RSG | RSG | RSG |
| LIVER | | dbdb | | 10MK | 30MK | 100MK | code | dbdb | | 10MK | 30MK | 100MK |
| Acaa1a | Mm00728460_s1 | 1 | 0.71 | 1.99 | 1.90 | 1.79 | A_52_P423183 | 1 | 0.54 | 3.76 | 3.85 | 3.62 |
| Acaa1b | Mm00728805_s1 | 1 | 0.44 | 4.05 | 3.68 | 3.45 | A_52_P423174 | 1 | 0.57 | 3.51 | 3.42 | 3.05 |
| Acaca | Mm01304285_m1 | 1 | 0.63 | 3.74 | 3.53 | 2.74 | A_52_P595124 | 1 | 0.88 | 1.76 | 2.55 | 1.90 |
| Acacb | Mm01204683_m1 | 1 | 0.46 | 2.28 | 2.22 | 2.01 | A_52_P340167 | 1 | 0.72 | 2.05 | 2.27 | 1.77 |
| Acad10 | Mm00660975_m1 | 1 | 0.70 | 1.45 | 1.54 | 1.42 | A_51_P187507 | 1 | 0.84 | 1.46 | 1.51 | 1.49 |
| Acad11 | Mm00614545_m1 | 1 | 0.77 | 1.64 | 1.55 | 1.37 | A_52_P85152 | 1 | 0.75 | 1.47 | 1.39 | 1.30 |
| Acadm | Mm00431611_m1 | 1 | 0.46 | 1.83 | 1.66 | 1.55 | A_51_P319879 | 1 | 0.56 | 1.95 | 1.82 | 1.72 |
| Acads | Mm00431617_m1 | 1 | 0.67 | 1.18 | 1.12 | 1.05 | A_52_P367745 | 1 | 0.84 | 1.31 | 1.35 | 1.34 |
| Acly | Mm00652520_m1 | 1 | 0.67 | 2.61 | 2.71 | 2.45 | A_51_P261718 | 1 | 0.53 | 1.97 | 2.38 | 2.22 |
| Aco1 | Mm00801417_m1 | 1 | 0.80 | 1.17 | 1.12 | 1.08 | A_51_P391082 | 1 | 0.87 | 1.16 | 1.12 | 1.09 |
| Aco2 | Mm00475673_g1 | 1 | 0.70 | 1.44 | 1.35 | 1.18 | A_52_P200359 | 1 | 0.83 | 1.41 | 1.37 | 1.16 |
| Acox1 | Mm00443579_m1 | 1 | 0.53 | 2.31 | 2.35 | 2.25 | A_51_P366704 | 1 | 0.59 | 2.12 | 2.04 | 2.16 |
| Acox2 | Mm00446408_m1 | 1 | 0.69 | 1.31 | 1.28 | 1.29 | A_51_P206708 | 1 | 0.76 | 1.38 | 1.37 | 1.40 |
| AcsI5 | Mm01261084_g1 | 1 | 0.52 | 1.71 | 1.64 | 1.58 | A_52_P593037 | 1 | 0.68 | 1.81 | 1.80 | 1.79 |
| Adh4 | Mm00478838_m1 | 1 | 1.22 | 0.47 | 0.43 | 0.47 | A_51_P189442 | 1 | 1.35 | 0.48 | 0.45 | 0.53 |
| Adh7 | Mm00507750_m1 | 1 | 0.78 | 2.10 | 1.90 | 1.83 | A_51_P233797 | 1 | 0.83 | 1.51 | 1.51 | 1.51 |
| Agpat2 | Mm00458880_m1 | 1 | 0.46 | 2.32 | 2.22 | 1.87 | A_51_P238565 | 1 | 0.58 | 2.07 | 1.99 | 1.98 |
| Agpat6 | Mm00497622_m1 | 1 | 0.62 | 1.43 | 1.46 | 1.26 | A_51_P335710 | 1 | 0.62 | 1.44 | 1.39 | 1.11 |
| Aldh1a1 | Mm00657317_m1 | 1 | 0.54 | 0.90 | 0.82 | 0.78 | A_51_P334942 | 1 | 0.55 | 0.81 | 0.81 | 0.76 |
| Aldh1a3 | Mm00474049_m1 | 1 | ND | ND | ND | ND | A_52_P87843 | 1 | 0.37 | 0.59 | 0.59 | 0.62 |
| Aldh1a7 | Mm00496380_m1 | 1 | 0.55 | 1.37 | 1.29 | 1.21 | A_51_P383399 | 1 | 0.61 | 1.36 | 1.21 | 1.27 |
| Aldh1b1 | Mm00728303_s1 | 1 | 0.46 | 1.19 | 1.20 | 0.98 | A_51_P510418 | 1 | 0.52 | 1.31 | 1.24 | 1.17 |
| Aldh2 | Mm00477463_m1 | 1 | 0.90 | 0.82 | 0.79 | 0.79 | A_52_P13109 | 1 | 0.57 | 0.64 | 0.64 | 0.64 |
| Aldh3a2 | Mm00839320_m1 | 1 | 0.34 | 2.20 | 1.93 | 1.59 | A_51_P464175 | 1 | 0.34 | 2.12 | 1.95 | 1.71 |
| Aldoa | Mm00833172_g1 | 1 | 1.12 | 1.66 | 1.72 | 1.57 | A_52_P98387 | 1 | 1.30 | 1.54 | 1.49 | 1.43 |
| Aldob | Mm00523296_m1 | 1 | 0.47 | 0.90 | 0.75 | 0.64 | A_51_P337269 | 1 | 0.59 | 0.98 | 0.83 | 0.69 |
| Aldoc | Mm01298116_g1 | 1 | 0.57 | 0.56 | 0.65 | 0.85 | A_51_P220681 | 1 | 0.59 | 0.53 | 0.66 | 0.85 |
| Apoa1 | Mm00437569_m1 | 1 | 4.75 | 1.88 | 2.03 | 2.77 | A_51_P408082 | 1 | 4.85 | 1.84 | 1.93 | 2.69 |
| Apoa5 | Mm00475480_m1 | 1 | 0.60 | 0.49 | 0.40 | 0.51 | A_52_P292404 | 1 | 0.69 | 0.53 | 0.49 | 0.56 |
| Cd36 | Mm01135198_m1 | 1 | 0.07 | 1.83 | 1.76 | 1.58 | A_51_P375146 | 1 | 0.08 | 1.70 | 1.67 | 1.61 |
| Cpt1b | Mm00487200_m1 | 1 | 0.54 | 2.96 | 2.62 | 2.61 | A_52_P625508 | 1 | 0.55 | 2.04 | 1.55 | 2.05 |
| Crat | Mm00483985_m1 | 1 | 0.29 | 2.86 | 2.60 | 2.14 | A_51_P440807 | 1 | 0.43 | 2.66 | 2.53 | 2.22 |
| Cs | Mm00466043_m1 | 1 | 0.96 | 1.55 | 1.43 | 1.27 | A_51_P390260 | 1 | 1.24 | 1.50 | 1.39 | 1.44 |
| Cyp2a4;Cyp2a5 | Mm00487248_g1 | 1 | 0.54 | 0.24 | 0.27 | 0.42 | A_52_P246252 | 1 | 0.48 | 0.20 | 0.25 | 0.35 |
| Cyp2b10 | Mm00456588_mH | 1 | 0.13 | 1.02 | 1.07 | 1.11 | A_52_P472486 | 1 | 0.04 | 0.60 | 0.62 | 0.66 |
| Cyp2b13 | Mm00771172_g1 | 1 | ND | 0.41 | 0.42 | 0.48 | A_52_P289091 | 1 | 0.06 | 0.51 | 0.45 | 0.49 |
| Cyp2c37 | Mm00833845_m1 | 1 | 0.53 | 0.14 | 0.15 | 0.32 | A_51_P498882 | 1 | 0.69 | 0.23 | 0.32 | 0.39 |
| Cyp2c38 | Mm00658527_m1 | 1 | 0.13 | 0.88 | 0.86 | 0.76 | A_52_P468564 | 1 | 0.12 | 0.72 | 0.70 | 0.64 |
| Cyp2c39 | Mm00656110_gH | 1 | 0.06 | 0.74 | 0.71 | 0.72 | A_51_P304109 | 1 | 0.73 | 0.34 | 0.40 | 0.47 |
| Cyp2d22 | Mm00530542_m1 | 1 | 0.82 | 0.78 | 0.79 | 0.86 | A_52_P49391 | 1 | 0.76 | 0.68 | 0.68 | 0.73 |
| Cyp2j9 | Mm00466426_m1 | 1 | 0.55 | 0.47 | 0.48 | 0.55 | A_51_P330044 | 1 | 0.63 | 0.48 | 0.57 | 0.53 |
| Cyp3a13 | Mm00484110_m1 | 1 | 0.43 | 0.49 | 0.60 | 0.61 | A_51_P114941 | 1 | 0.49 | 0.56 | 0.64 | 0.67 |
| Dci | Mm00494452_m1 | 1 | 0.68 | 1.37 | 1.24 | 1.13 | A_51_P105589 | 1 | 0.83 | 1.45 | 1.30 | 1.29 |

| | | | | | | | | | | | | |
|----------|---------------|---|------|-------|------|------|--------------|---|------|-------|-------|-------|
| Decr1 | Mm00470689_m1 | 1 | 0.61 | 1.45 | 1.32 | 1.21 | A_51_P208555 | 1 | 0.82 | 1.39 | 1.27 | 1.26 |
| Dgat1 | Mm01197412_g1 | 1 | 0.66 | 1.57 | 1.63 | 1.42 | A_51_P510059 | 1 | 0.81 | 1.58 | 1.64 | 1.40 |
| Dlat | Mm00455160_m1 | 1 | 0.85 | 1.91 | 1.84 | 1.68 | A_51_P265106 | 1 | 0.88 | 1.92 | 1.91 | 1.75 |
| Dlst | Mm00513470_m1 | 1 | 0.75 | 1.50 | 1.43 | 1.31 | A_51_P290139 | 1 | 0.84 | 1.37 | 1.37 | 1.24 |
| Ech1 | Mm00469322_m1 | 1 | 0.56 | 1.31 | 1.22 | 1.12 | A_51_P421846 | 1 | 0.61 | 1.35 | 1.32 | 1.28 |
| Fabp2 | Mm00433188_m1 | 1 | 0.54 | 1.44 | 1.13 | 1.03 | A_51_P313581 | 1 | 0.65 | 1.38 | 1.19 | 1.13 |
| Fabp3 | Mm02342495_m1 | 1 | 0.83 | 2.14 | 2.60 | 1.68 | A_51_P167535 | 1 | 0.56 | 2.71 | 2.38 | 1.82 |
| Fabp4 | Mm00445880_m1 | 1 | 0.43 | 12.58 | ND | ND | A_51_P336830 | 1 | 0.52 | 8.96 | 10.73 | 9.87 |
| Fabp5 | Mm00783731_s1 | 1 | ND | 10.88 | ND | ND | A_51_P387764 | 1 | 2.34 | 14.61 | 7.69 | 16.17 |
| Fasn | Mm00662322_g1 | 1 | 0.32 | 3.54 | 3.48 | 3.05 | A_52_P100252 | 1 | 0.33 | 2.59 | 2.99 | 2.89 |
| Fbp1 | Mm00490181_m1 | 1 | 0.56 | 0.73 | 0.66 | 0.50 | A_51_P474701 | 1 | 0.50 | 0.73 | 0.64 | 0.52 |
| Fdps | Mm00836315_g1 | 1 | 0.71 | 1.42 | 1.57 | 1.87 | A_51_P379798 | 1 | 0.68 | 1.21 | 1.52 | 1.64 |
| G6pc | Mm00839363_m1 | 1 | 0.37 | 0.61 | 0.55 | 0.36 | A_51_P462385 | 1 | 0.48 | 0.64 | 0.59 | 0.44 |
| Gck | Mm00439129_m1 | 1 | 0.97 | 1.27 | 1.09 | 1.17 | A_52_P259537 | 1 | 1.06 | 1.28 | 1.17 | 1.19 |
| Gckr | Mm00523328_m1 | 1 | 0.71 | 0.63 | 0.59 | 0.55 | A_51_P198694 | 1 | 0.74 | 0.61 | 0.59 | 0.55 |
| Gpd1 | Mm00515846_m1 | 1 | 0.61 | 3.19 | 2.69 | 2.18 | A_51_P293853 | 1 | 0.73 | 2.61 | 2.34 | 1.93 |
| Gyk | Mm00433896_m1 | 1 | 0.91 | 0.92 | 0.80 | 0.79 | A_51_P297671 | 1 | 0.98 | 1.01 | 0.88 | 0.89 |
| Hadhb | Mm00523880_g1 | 1 | 0.82 | 1.32 | 1.27 | 1.09 | A_51_P217990 | 1 | 0.94 | 1.53 | 1.39 | 1.32 |
| Hmgcr | Mm01282499_m1 | 1 | 0.41 | 0.74 | 0.93 | 1.46 | A_52_P578922 | 1 | 0.43 | 0.68 | 0.94 | 1.43 |
| Hmgcs2 | Mm00550050_m1 | 1 | 0.64 | 1.21 | 1.07 | 0.93 | A_51_P116039 | 1 | 0.76 | 0.91 | 0.78 | 2.66 |
| Hsd17b4 | Mm00500443_m1 | 1 | 0.64 | 1.67 | 1.53 | 1.36 | A_51_P445662 | 1 | 0.89 | 1.43 | 1.44 | 1.35 |
| Idi1 | Mm00836417_g1 | 1 | 0.89 | 0.88 | 0.96 | 1.24 | A_52_P441634 | 1 | 0.64 | 0.86 | 1.03 | 1.38 |
| Ldhb | Mm00493146_m1 | 1 | 1.26 | 1.82 | 1.88 | 1.80 | A_51_P409173 | 1 | 1.13 | 1.60 | 1.62 | 1.67 |
| Lipe | Mm00495359_m1 | 1 | 0.80 | 1.44 | 1.50 | 1.31 | A_51_P435366 | 1 | 0.82 | 1.10 | 1.40 | 1.26 |
| Lpl | Mm00434770_m1 | 1 | 1.75 | 4.25 | 6.00 | 6.70 | A_52_P257812 | 1 | 1.62 | 3.33 | 4.22 | 4.97 |
| Mdh2 | Mm00725890_s1 | 1 | 0.85 | 1.51 | 1.38 | 1.28 | A_51_P384879 | 1 | 0.94 | 1.43 | 1.34 | 1.33 |
| Mgl1 | Mm00449274_m1 | 1 | 0.76 | 1.60 | 1.37 | 1.20 | A_52_P568977 | 1 | 0.44 | 1.29 | 0.81 | 0.61 |
| Mvd | Mm00507014_m1 | 1 | 0.40 | 1.36 | 1.24 | 1.55 | A_51_P355943 | 1 | 0.40 | 1.29 | 1.35 | 1.62 |
| Oxct1 | Mm00499303_m1 | 1 | 1.29 | 1.49 | 1.38 | 1.32 | A_51_P107321 | 1 | 1.30 | 1.38 | 1.29 | 1.40 |
| Pdha1 | Mm00468675_m1 | 1 | 0.75 | 1.45 | 1.39 | 1.24 | A_51_P321391 | 1 | 0.95 | 1.35 | 1.37 | 1.29 |
| Pdk4 | Mm00443325_m1 | 1 | 0.31 | 4.26 | 2.92 | 2.50 | A_51_P350453 | 1 | 0.27 | 3.16 | 2.21 | 2.21 |
| Pecr | Mm00502709_m1 | 1 | 0.68 | 0.57 | 0.57 | 0.60 | A_51_P291749 | 1 | 0.82 | 0.57 | 0.62 | 0.64 |
| Pgd | Mm00503037_m1 | 1 | 0.65 | 2.79 | 2.55 | 2.22 | A_52_P84096 | 1 | 0.67 | 2.16 | 2.21 | 2.10 |
| Pgm3 | Mm00459270_m1 | 1 | 0.97 | 1.81 | 1.74 | 1.56 | A_52_P341449 | 1 | 0.96 | 1.37 | 1.45 | 1.35 |
| Pklr | Mm00443090_m1 | 1 | 0.43 | 0.71 | 0.64 | 0.56 | A_51_P176042 | 1 | 0.53 | 0.83 | 0.78 | 0.74 |
| Pmvk | Mm00503429_m1 | 1 | 0.70 | 1.65 | 1.62 | 1.73 | A_51_P492408 | 1 | 0.66 | 1.33 | 1.59 | 1.68 |
| Ppara | Mm00440939_m1 | 1 | 0.69 | 0.99 | 0.91 | 0.99 | A_51_P348334 | 1 | 0.98 | 1.17 | 1.11 | 1.27 |
| Ppard | Mm00803186_g1 | 1 | 1.11 | 1.09 | 1.01 | 1.02 | A_51_P271556 | 1 | 1.04 | 0.73 | 0.63 | 1.02 |
| Pparg | Mm01258518_m1 | 1 | 0.25 | 1.42 | 1.59 | 1.29 | A_51_P106799 | 1 | 0.41 | 1.28 | 1.36 | 1.23 |
| Ppargc1a | Mm00440945_m1 | 1 | 0.55 | 0.51 | 0.51 | 0.53 | A_51_P279038 | 1 | 0.76 | 0.65 | 0.62 | 0.63 |
| Ppargc1b | Mm01208832_m1 | 1 | 1.24 | 0.74 | 0.66 | 0.75 | A_51_P294891 | 1 | 1.29 | 0.81 | 0.78 | 0.89 |
| Scd1 | Mm00772290_m1 | 1 | 0.48 | 5.73 | 5.60 | 4.71 | A_52_P682382 | 1 | 0.60 | 5.00 | 5.27 | 5.77 |
| Scd2 | Mm01208542_m1 | 1 | 0.44 | 1.32 | 1.51 | 1.60 | A_51_P129464 | 1 | 0.56 | 1.43 | 2.07 | 2.51 |
| Slc2a2 | Mm00446224_m1 | 1 | 0.78 | 0.78 | 0.70 | 0.74 | A_51_P185693 | 1 | 0.72 | 0.74 | 0.70 | 0.75 |
| Sqle | Mm00436772_m1 | 1 | 0.60 | 0.93 | 1.02 | 1.34 | A_51_P450487 | 1 | 0.43 | 1.00 | 1.12 | 1.45 |
| Taldo1 | Mm00807080_g1 | 1 | 0.74 | 2.28 | 2.13 | 1.80 | A_51_P401958 | 1 | 0.84 | 2.28 | 2.02 | 1.92 |
| Tkt | Mm00447559_m1 | 1 | 0.63 | 1.81 | 1.66 | 1.45 | A_51_P394515 | 1 | 0.73 | 1.80 | 1.71 | 1.61 |
| Ugp2 | Mm00454826_m1 | 1 | 0.86 | 0.72 | 0.68 | 0.60 | A_51_P475580 | 1 | 0.89 | 0.72 | 0.74 | 0.68 |

| | qPCR Ratio vs. db/db | | | | | | Microarrays Ratio vs. db/db | | | | | |
|----------|----------------------|------|------|------|------|-------|-----------------------------|------|------|------|------|-------|
| Sample | Assay ID | Pool | db+ | RSG | RSG | RSG | Sequence | Pool | db+ | RSG | RSG | RSG |
| IAT | | dbdb | | 10MK | 30MK | 100MK | code | dbdb | | 10MK | 30MK | 100MK |
| Acaa1a | Mm00728460_s1 | 1 | 0.83 | 0.96 | 0.99 | 1.18 | A_52_P423183 | 1 | 1.27 | 1.45 | 2.03 | 2.64 |
| Acaa1b | Mm00728805_s1 | 1 | 0.86 | 1.50 | 2.57 | 3.44 | A_52_P423174 | 1 | 1.31 | 1.45 | 2.04 | 2.47 |
| Acaa2 | Mm00624282_m1 | 1 | 0.84 | 0.91 | 1.36 | 1.83 | A_51_P125260 | 1 | 1.05 | 1.17 | 1.75 | 2.37 |
| Acaca | Mm01304285_m1 | 1 | 5.10 | 1.96 | 2.92 | 3.11 | A_52_P595124 | 1 | 5.02 | 1.58 | 2.45 | 2.76 |
| Acacb | Mm01204683_m1 | 1 | 1.12 | 1.09 | 1.52 | 1.55 | A_52_P340167 | 1 | 1.35 | 1.11 | 1.54 | 1.53 |
| Acad11 | Mm00614545_m1 | 1 | 0.69 | 0.84 | 0.89 | 1.04 | A_52_P85152 | 1 | 1.06 | 1.00 | 1.34 | 1.53 |
| Acad8 | Mm00482266_m1 | 1 | 0.92 | 0.73 | 0.80 | 0.82 | A_51_P244052 | 1 | 1.36 | 1.05 | 1.28 | 1.33 |
| Acad9 | Mm00554429_m1 | 1 | 0.68 | 1.07 | 0.99 | 1.24 | A_51_P341379 | 1 | 1.11 | 1.39 | 1.50 | 1.77 |
| Acadl | Mm00599660_m1 | 1 | 0.84 | 0.98 | 1.42 | 1.63 | A_51_P149455 | 1 | 1.40 | 1.17 | 1.71 | 1.95 |
| Acads | Mm00431617_m1 | 1 | 0.90 | 1.07 | 1.38 | 1.54 | A_52_P367745 | 1 | 1.23 | 1.33 | 1.86 | 2.12 |
| Acadvi | Mm00444296_m1 | 1 | 1.50 | 1.33 | 2.28 | 2.85 | A_51_P518340 | 1 | 1.52 | 1.46 | 2.41 | 3.09 |
| Acat1 | Mm00507463_m1 | 1 | 0.95 | 0.92 | 1.07 | 1.19 | A_51_P319449 | 1 | 1.42 | 1.13 | 1.30 | 1.45 |
| Acat2 | Mm00782408_s1 | 1 | 1.05 | 1.00 | 1.15 | 1.27 | A_51_P139748 | 1 | 1.70 | 1.36 | 1.53 | 1.77 |
| Acat3 | Mm00462484_m1 | 1 | 6.64 | 1.16 | 0.80 | 1.25 | A_51_P139745 | 1 | 1.64 | 1.32 | 1.56 | 1.74 |
| Acly- | Mm00652520_m1 | 1 | 2.28 | 0.86 | 1.42 | 1.48 | A_51_P261718 | 1 | 6.23 | 2.07 | 2.90 | 3.13 |
| Aco1 | Mm00801417_m1 | 1 | 1.28 | 1.17 | 1.40 | 1.61 | A_52_P299115 | 1 | 1.95 | 1.17 | 1.53 | 1.83 |
| Aco2 | Mm00475673_g1 | 1 | 1.19 | 0.99 | 1.58 | 1.92 | A_52_P200359 | 1 | 1.38 | 1.18 | 1.66 | 1.98 |
| Acox1 | Mm00443579_m1 | 1 | 0.90 | 1.13 | 1.67 | 1.98 | A_51_P366704 | 1 | 1.31 | 1.44 | 2.06 | 2.29 |
| Acsl1 | Mm00484217_m1 | 1 | 0.71 | 1.45 | 2.13 | 2.25 | A_51_P496432 | 1 | 0.72 | 1.46 | 1.80 | 1.95 |
| Acsl6 | Mm00522786_m1 | 1 | 0.48 | 0.64 | 0.60 | 0.66 | A_51_P380699 | 1 | 0.76 | 0.48 | 0.69 | 0.54 |
| Adh1 | Mm00507711_m1 | 1 | 0.30 | 0.42 | 0.26 | 0.41 | A_52_P629895 | 1 | 0.49 | 0.52 | 0.40 | 0.61 |
| Agpat1 | Mm00479700_m1 | 1 | 0.89 | 1.09 | 1.38 | 1.46 | A_52_P200465 | 1 | 1.65 | 1.15 | 1.33 | 1.52 |
| Agpat2 | Mm00458880_m1 | 1 | 1.11 | 1.43 | 2.27 | 2.33 | A_51_P238565 | 1 | 1.40 | 1.29 | 1.82 | 2.07 |
| Agpat3 | Mm00474003_m1 | 1 | 1.12 | 1.22 | 1.51 | 2.01 | A_51_P425490 | 1 | 1.81 | 1.31 | 1.65 | 2.07 |
| Agpat4 | Mm00509776_m1 | 1 | 0.48 | 0.80 | 0.79 | 0.68 | A_51_P346165 | 1 | 0.66 | 0.86 | 0.80 | 0.76 |
| Agpat6 | Mm00497622_m1 | 1 | 1.09 | 1.15 | 1.43 | 1.68 | A_51_P335710 | 1 | 1.16 | 1.07 | 1.31 | 1.50 |
| Aldh1a1 | Mm00657317_m1 | 1 | 0.28 | 0.46 | 0.40 | 0.39 | A_51_P334942 | 1 | 0.59 | 0.68 | 0.63 | 0.52 |
| Aldh1a7 | Mm00496380_m1 | 1 | 1.02 | 1.25 | 1.67 | 1.72 | A_51_P383399 | 1 | 1.48 | 1.41 | 1.85 | 1.93 |
| Aldh1b1 | Mm00728303_s1 | 1 | 0.09 | 0.23 | 0.19 | 0.18 | A_51_P510418 | 1 | 0.26 | 0.37 | 0.41 | 0.38 |
| Aldh4a1 | Mm00615268_m1 | 1 | 1.52 | 1.14 | 1.23 | 1.18 | A_51_P337918 | 1 | 2.20 | 1.32 | 1.45 | 1.45 |
| Aldh5a1 | Mm00553115_m1 | 1 | 1.07 | 1.03 | 1.12 | 1.10 | A_51_P491504 | 1 | 1.60 | 1.33 | 1.65 | 1.69 |
| Aldh7a1 | Mm00519645_m1 | 1 | 0.89 | 0.82 | 0.83 | 0.76 | A_51_P470414 | 1 | 1.36 | 1.23 | 1.28 | 1.52 |
| Aldob | Mm00523296_m1 | 1 | 0.10 | 0.62 | 0.33 | 0.94 | A_51_P337269 | 1 | 0.08 | 0.54 | 0.46 | 0.74 |
| Aldoc | Mm01298116_g1 | 1 | 0.06 | 0.53 | 0.16 | 0.44 | A_51_P220681 | 1 | 0.29 | 0.50 | 0.40 | 0.64 |
| Apob | Mm01545156_m1 | 1 | 0.32 | 0.57 | 0.50 | 1.36 | A_51_P470542 | 1 | 0.16 | 0.57 | 0.46 | 0.82 |
| Apoc1 | Mm00431816_m1 | 1 | 2.51 | 1.80 | 2.05 | 2.33 | A_51_P164504 | 1 | 3.30 | 1.78 | 1.84 | 2.20 |
| Atp12a | Mm00446786_m1 | 1 | 0.00 | 0.18 | 0.09 | 0.26 | A_52_P329398 | 1 | 0.11 | 0.29 | 0.14 | 0.47 |
| Atp5b | Mm00443967_g1 | 1 | 0.97 | 0.88 | 1.15 | 1.25 | A_52_P553841 | 1 | 1.31 | 1.21 | 1.62 | 1.81 |
| Atp5c1 | Mm00662408_m1 | 1 | 1.20 | 0.85 | 1.03 | 1.11 | A_51_P378087 | 1 | 1.52 | 1.06 | 1.31 | 1.36 |
| Atp5k | Mm00833200_g1 | 1 | 1.35 | 0.99 | 1.37 | 1.41 | A_51_P301289 | 1 | 2.08 | 1.25 | 1.68 | 1.89 |
| Atp6v0a1 | Mm00444210_m1 | 1 | 0.30 | 1.09 | 1.26 | 1.33 | A_51_P142089 | 1 | 0.50 | 1.00 | 1.16 | 1.32 |
| Atp6v1c2 | Mm00505047_m1 | 1 | 0.31 | 3.33 | 0.93 | 3.04 | A_51_P518600 | 1 | 0.56 | 1.05 | 0.96 | 1.88 |
| Atp6v1h | Mm00505548_m1 | 1 | 0.54 | 0.83 | 0.84 | 0.82 | A_51_P105604 | 1 | 0.95 | 1.13 | 1.25 | 1.30 |
| Bdh1 | Mm00558330_m1 | 1 | 0.18 | 0.28 | 0.12 | 0.30 | A_51_P163106 | 1 | 0.27 | 0.22 | 0.24 | 0.38 |

| | | | | | | | | | | | | |
|---------------|---------------|---|------|------|------|------|--------------|---|------|------|------|------|
| Cox6b1 | Mm00824357_m1 | 1 | 1.10 | 1.11 | 1.51 | 1.62 | A_51_P448032 | 1 | 1.54 | 1.39 | 1.82 | 2.16 |
| Cox6b2 | Mm00839225_g1 | 1 | ND | ND | ND | ND | A_51_P300506 | 1 | 1.35 | 1.08 | 1.37 | 1.59 |
| Cox7a1 | Mm00438296_m1 | 1 | 1.04 | 0.66 | 1.33 | 1.84 | A_51_P148612 | 1 | 1.37 | 0.66 | 1.45 | 1.98 |
| Cox7b | Mm00835076_g1 | 1 | 0.99 | 0.92 | 1.31 | 1.47 | A_51_P160664 | 1 | 1.96 | 1.33 | 1.87 | 2.15 |
| Cpt1b | Mm00487200_m1 | 1 | 0.71 | 1.47 | 3.20 | 4.58 | A_52_P625508 | 1 | 0.92 | 1.32 | 2.31 | 3.25 |
| Cpt2 | Mm00487202_m1 | 1 | 1.40 | 1.39 | 1.93 | 2.21 | A_51_P403388 | 1 | 1.66 | 1.42 | 1.66 | 2.02 |
| Cs | Mm00466043_m1 | 1 | 1.02 | 1.12 | 1.59 | 1.69 | A_51_P390260 | 1 | 1.81 | 1.65 | 2.21 | 2.67 |
| Cyp2a12 | Mm00504878_m1 | 1 | 0.24 | 0.67 | 0.28 | 1.14 | A_51_P206736 | 1 | 0.73 | 1.02 | 0.66 | 2.50 |
| Cyp2a4;Cyp2a5 | Mm00487248_g1 | 1 | 0.14 | 0.76 | 0.21 | 0.75 | A_52_P246252 | 1 | 0.17 | 0.51 | 0.35 | 1.04 |
| Cyp2c29 | Mm00725580_s1 | 1 | 0.36 | 0.36 | 0.12 | 0.37 | A_51_P103706 | 1 | 0.08 | 0.18 | 0.17 | 0.27 |
| Cyp2c39 | Mm00656110_gH | 1 | 0.20 | 3.26 | 1.24 | 2.56 | A_51_P304109 | 1 | 0.09 | 0.12 | 0.12 | 0.15 |
| Cyp2c55 | Mm00472168_m1 | 1 | ND | ND | ND | ND | A_51_P447785 | 1 | 0.21 | 0.19 | 0.17 | 0.15 |
| Cyp2d10 | Mm00731648_m1 | 1 | 0.04 | 0.08 | 0.07 | 0.19 | A_51_P111192 | 1 | 0.46 | 0.57 | 0.54 | 0.60 |
| Cyp2d9 | Mm00651731_m1 | 1 | 0.24 | 0.17 | 0.08 | 0.27 | A_51_P124133 | 1 | 0.43 | 0.52 | 0.49 | 0.50 |
| Cyp2e1 | Mm00491127_m1 | 1 | 6.88 | 0.68 | 1.83 | 1.36 | A_51_P283456 | 1 | 8.01 | 0.95 | 1.69 | 1.53 |
| Cyp2j5 | Mm00487292_m1 | 1 | 0.11 | 1.23 | 0.54 | 2.11 | A_52_P315766 | 1 | 0.28 | 1.06 | 0.63 | 2.09 |
| Cyp2s1 | Mm00512037_m1 | 1 | 0.03 | 0.25 | 0.08 | 0.15 | A_51_P180091 | 1 | 0.06 | 0.25 | 0.18 | 0.31 |
| Cyp3a13 | Mm00484110_m1 | 1 | 0.04 | 0.11 | 0.02 | 0.04 | A_51_P114941 | 1 | 0.06 | 0.08 | 0.05 | 0.08 |
| Cyp3a16 | Mm00655824_m1 | 1 | ND | ND | ND | ND | A_51_P482051 | 1 | 0.69 | 1.07 | 1.34 | 1.85 |
| Cyp4a10 | Mm02601690_gH | 1 | 0.03 | 0.93 | 0.61 | 1.65 | A_52_P257774 | 1 | 0.64 | 1.11 | 1.32 | 1.99 |
| Cyp4a12a | Mm00514494_m1 | 1 | 0.13 | 1.53 | 1.04 | 9.16 | A_51_P433360 | 1 | 0.53 | 1.03 | 1.37 | 3.72 |
| Cyp4a14 | Mm00484132_m1 | 1 | 0.02 | 1.05 | 0.76 | 2.24 | A_51_P238576 | 1 | 0.43 | 1.12 | 1.22 | 1.80 |
| Cyp4b1 | Mm00484138_m1 | 1 | 0.30 | 0.76 | 0.95 | 1.31 | A_51_P118704 | 1 | 0.52 | 1.06 | 1.37 | 1.76 |
| Cyp4f14 | Mm00491623_m1 | 1 | 0.19 | 0.06 | 0.06 | 0.03 | A_51_P452768 | 1 | 0.32 | 0.17 | 0.14 | 0.14 |
| Cyp51 | Mm00490968_m1 | 1 | 0.29 | 0.87 | 0.81 | 0.74 | A_52_P636752 | 1 | 0.50 | 1.32 | 1.25 | 1.26 |
| Dci | Mm00494452_m1 | 1 | 1.02 | 0.95 | 1.21 | 1.38 | A_51_P105589 | 1 | 1.51 | 1.28 | 1.68 | 1.85 |
| Decr1 | Mm00470689_m1 | 1 | 0.93 | 1.18 | 1.67 | 1.88 | A_51_P208555 | 1 | 1.32 | 1.49 | 2.14 | 2.25 |
| Dgat1 | Mm01197412_g1 | 1 | 0.95 | 1.28 | 1.87 | 2.01 | A_51_P510059 | 1 | 1.31 | 1.18 | 1.69 | 1.77 |
| Dlat | Mm00455160_m1 | 1 | 0.97 | 1.24 | 1.85 | 2.22 | A_51_P265106 | 1 | 1.77 | 1.49 | 2.10 | 2.72 |
| Dld | Mm00432831_m1 | 1 | 1.04 | 1.06 | 1.43 | 1.60 | A_51_P184284 | 1 | 1.36 | 1.33 | 1.88 | 2.07 |
| Dlst | Mm00513470_m1 | 1 | 0.98 | 0.97 | 1.36 | 1.54 | A_51_P290139 | 1 | 1.43 | 1.16 | 1.63 | 1.83 |
| Echs1 | Mm00659670_g1 | 1 | 1.15 | 0.95 | 1.12 | 1.23 | A_51_P409039 | 1 | 1.75 | 1.20 | 1.43 | 1.61 |
| Eno2 | Mm00469062_m1 | 1 | 0.43 | 0.64 | 0.45 | 0.40 | A_52_P748882 | 1 | 0.67 | 0.86 | 0.79 | 0.64 |
| Eno3 | Mm00468267_m1 | 1 | 0.99 | 0.38 | 0.34 | 0.37 | A_51_P328539 | 1 | 1.58 | 0.41 | 0.54 | 0.62 |
| Fabp2 | Mm00433188_m1 | 1 | 0.02 | 0.12 | 0.07 | 0.60 | A_51_P313581 | 1 | 0.52 | 0.57 | 0.58 | 0.68 |
| Fabp3 | Mm02342495_m1 | 1 | 0.32 | 0.63 | 1.10 | 1.97 | A_51_P167535 | 1 | 0.60 | 0.62 | 1.20 | 1.82 |
| Fabp4 | Mm00445880_m1 | 1 | 0.70 | 0.97 | 1.25 | 1.33 | A_51_P336830 | 1 | 0.82 | 0.97 | 1.32 | 1.04 |
| Fasn | Mm00662322_g1 | 1 | 9.15 | 2.94 | 4.30 | 4.17 | A_52_P100252 | 1 | 7.31 | 2.49 | 3.18 | 3.55 |
| Fbp1 | Mm00490181_m1 | 1 | 0.34 | 0.51 | 0.24 | 0.60 | A_51_P474701 | 1 | 0.19 | 0.62 | 0.50 | 0.81 |
| Fh1 | Mm00802588_m1 | 1 | 0.85 | 0.88 | 1.06 | 1.15 | A_51_P359333 | 1 | 1.56 | 1.28 | 1.63 | 1.87 |
| Fntb | Mm00521491_m1 | 1 | 0.38 | 0.81 | 0.78 | 0.65 | A_51_P517680 | 1 | 1.48 | 1.43 | 1.55 | 1.49 |
| G6pd2 | Mm00658204_s1 | 1 | 0.29 | 0.37 | 0.08 | 0.24 | A_51_P353735 | 1 | 0.52 | 1.04 | 1.34 | 1.26 |
| Gpd1 | Mm00515846_m1 | 1 | 2.09 | 2.89 | 5.40 | 6.36 | A_51_P293853 | 1 | 2.11 | 2.37 | 4.02 | 4.86 |
| Gyk | Mm00433896_m1 | 1 | 0.43 | 1.73 | 3.30 | 4.43 | A_51_P297671 | 1 | 0.53 | 2.32 | 3.93 | 5.33 |
| Gys1 | Mm00472712_m1 | 1 | 1.17 | 0.93 | 1.20 | 1.24 | A_52_P228932 | 1 | 1.67 | 1.09 | 1.23 | 1.38 |
| Gys2 | Mm00523953_m1 | 1 | 2.92 | 4.16 | 8.08 | 9.97 | A_51_P440315 | 1 | 4.32 | 4.01 | 7.11 | 9.53 |
| Hadha | Mm00805228_m1 | 1 | 0.89 | 1.13 | 1.75 | 2.10 | A_52_P193029 | 1 | 1.27 | 1.44 | 1.93 | 2.43 |
| Hadhb | Mm00523880_g1 | 1 | 1.05 | 1.32 | 2.03 | 2.37 | A_51_P217990 | 1 | 1.19 | 1.38 | 1.99 | 2.41 |
| Hk1 | Mm00439344_m1 | 1 | 0.37 | 0.56 | 0.44 | 0.47 | A_51_P249024 | 1 | 1.10 | 0.97 | 1.04 | 1.02 |
| Hmgcr | Mm01282499_m1 | 1 | 0.20 | 1.20 | 0.53 | 1.28 | A_52_P578922 | 1 | 0.57 | 1.20 | 0.77 | 1.53 |
| Hmgcs1 | Mm00524111_m1 | 1 | 0.54 | 0.96 | 1.04 | 1.14 | A_51_P146941 | 1 | 0.65 | 1.27 | 1.34 | 1.63 |

| | | | | | | | | | | | | |
|----------|---------------|---|------|------|------|------|--------------|---|------|------|------|------|
| Hmgcs2 | Mm00550050_m1 | 1 | 0.21 | 0.42 | 0.22 | 0.45 | A_51_P116039 | 1 | 0.70 | 0.51 | 0.44 | 0.56 |
| Hsd17b4 | Mm00500443_m1 | 1 | 1.06 | 1.36 | 2.07 | 2.13 | A_51_P445662 | 1 | 0.87 | 1.23 | 1.45 | 1.51 |
| Idh1 | Mm00516030_m1 | 1 | 0.68 | 0.92 | 1.00 | 1.06 | A_51_P132978 | 1 | 1.30 | 1.20 | 1.44 | 1.59 |
| Idh3b | Mm00504589_m1 | 1 | 1.10 | 1.00 | 1.48 | 1.74 | A_51_P130110 | 1 | 1.49 | 1.18 | 1.73 | 1.91 |
| Idh3g | Mm00599689_m1 | 1 | 1.15 | 0.90 | 1.18 | 1.35 | A_51_P136729 | 1 | 1.67 | 1.18 | 1.59 | 1.91 |
| Idi1 | Mm00836417_g1 | 1 | 0.35 | 2.11 | 0.65 | 2.47 | A_52_P441634 | 1 | 0.66 | 1.34 | 1.18 | 2.59 |
| Ldhb | Mm00493146_m1 | 1 | 1.01 | 0.77 | 1.02 | 1.41 | A_51_P409173 | 1 | 1.76 | 1.07 | 1.36 | 1.81 |
| Mdh1 | Mm00485106_m1 | 1 | 1.11 | 1.11 | 1.54 | 1.78 | A_51_P218179 | 1 | 1.52 | 1.40 | 1.96 | 2.30 |
| Mgll | Mm00449274_m1 | 1 | 0.51 | 1.28 | 1.68 | 1.91 | A_52_P568977 | 1 | 0.71 | 1.48 | 1.75 | 2.28 |
| Mut | Mm00485312_m1 | 1 | 1.13 | 0.90 | 1.03 | 0.99 | A_52_P633163 | 1 | 2.08 | 1.23 | 1.36 | 1.41 |
| Mvd | Mm00507014_m1 | 1 | 0.60 | 1.07 | 0.97 | 1.14 | A_51_P355943 | 1 | 0.74 | 1.37 | 1.28 | 1.48 |
| Ndufa1 | Mm00444593_m1 | 1 | 0.88 | 0.82 | 0.99 | 1.07 | A_51_P472405 | 1 | 1.44 | 1.13 | 1.42 | 1.52 |
| Pcca | Mm00454899_m1 | 1 | 1.37 | 0.96 | 1.11 | 1.06 | A_51_P484254 | 1 | 2.34 | 1.41 | 1.78 | 1.72 |
| Pcx | Mm00500992_m1 | 1 | 1.97 | 1.26 | 1.58 | 1.53 | A_51_P480578 | 1 | 2.53 | 1.67 | 1.95 | 2.20 |
| Pdha1 | Mm00468675_m1 | 1 | 1.65 | 0.92 | 1.18 | 1.33 | A_51_P321391 | 1 | 2.92 | 1.46 | 2.15 | 2.54 |
| Pdhb | Mm00499323_m1 | 1 | 1.80 | 1.44 | 2.28 | 2.71 | A_52_P568792 | 1 | 2.19 | 1.69 | 2.49 | 3.05 |
| Pdk4 | Mm00443325_m1 | 1 | 0.65 | 0.54 | 0.58 | 0.98 | A_51_P350453 | 1 | 0.72 | 0.49 | 0.67 | 0.86 |
| Pgam2 | Mm00450782_g1 | 1 | 1.09 | 0.44 | 0.42 | 0.40 | A_51_P264495 | 1 | 1.99 | 0.53 | 0.58 | 0.69 |
| Pgk1 | Mm01225301_m1 | 1 | 0.79 | 0.74 | 0.84 | 0.96 | A_51_P182828 | 1 | 1.32 | 0.97 | 1.20 | 1.34 |
| Pgk2 | Mm00446208_s1 | 1 | 0.51 | 0.46 | 0.22 | 1.46 | A_51_P125487 | 1 | 1.57 | 0.68 | 0.49 | 0.77 |
| Pgm1 | Mm00804141_m1 | 1 | 0.51 | 0.77 | 0.72 | 0.69 | A_51_P427530 | 1 | 0.61 | 0.80 | 0.75 | 0.68 |
| Pgm5 | Mm00723432_m1 | 1 | 0.30 | 0.44 | 0.37 | 0.35 | A_52_P860000 | 1 | 0.28 | 0.31 | 0.39 | 0.32 |
| Pmvk | Mm00503429_m1 | 1 | 0.83 | 1.51 | 1.66 | 1.89 | A_51_P492408 | 1 | 1.21 | 1.39 | 1.53 | 1.65 |
| Ppara | Mm00440939_m1 | 1 | 1.50 | 1.26 | 1.84 | 2.77 | A_51_P348334 | 1 | 2.40 | 1.60 | 2.16 | 3.17 |
| Ppard | Mm00803186_g1 | 1 | 0.79 | 0.97 | 0.84 | 0.73 | A_51_P271556 | 1 | 0.87 | 1.05 | 1.07 | 1.17 |
| Pparg | Mm00440945_m1 | 1 | 0.85 | 1.08 | 1.15 | 1.17 | A_51_P106799 | 1 | 1.31 | 1.12 | 1.10 | 1.06 |
| Ppargc1a | Mm01208832_m1 | 1 | 1.25 | 0.56 | 0.94 | 1.34 | A_51_P279038 | 1 | 2.61 | 0.80 | 1.13 | 1.65 |
| Ppargc1b | Mm01258518_m1 | 1 | 3.89 | 0.75 | 1.12 | 1.59 | A_51_P294891 | 1 | 1.63 | 0.95 | 1.37 | 1.83 |
| Ppt2 | Mm00450833_m1 | 1 | 0.97 | 1.15 | 1.36 | 1.48 | A_52_P238816 | 1 | 1.43 | 1.19 | 1.41 | 1.54 |
| Pygl | Mm00500078_m1 | 1 | 2.14 | 1.30 | 1.54 | 1.49 | A_51_P452779 | 1 | 2.46 | 1.23 | 1.42 | 1.46 |
| Pygm | Mm00478582_m1 | 1 | 0.99 | 0.49 | 0.48 | 0.51 | A_51_P458973 | 1 | 1.51 | 0.46 | 0.46 | 0.49 |
| Sdha | Mm01352360_m1 | 1 | 1.16 | 0.83 | 1.05 | 1.19 | A_51_P410823 | 1 | 1.68 | 1.02 | 1.42 | 1.56 |
| Sdhb | Mm00458268_m1 | 1 | 1.15 | 0.90 | 1.27 | 1.48 | A_51_P234853 | 1 | 1.60 | 1.21 | 1.67 | 1.97 |
| Sdhc | Mm00481172_m1 | 1 | 0.84 | 0.85 | 1.02 | 1.06 | A_51_P106373 | 1 | 1.32 | 1.10 | 1.35 | 1.48 |
| Slc27a1 | Mm00449511_m1 | 1 | 0.50 | 1.21 | 1.99 | 2.33 | A_51_P117477 | 1 | 0.75 | 1.04 | 1.39 | 1.58 |
| Slc27a2 | Mm00449517_m1 | 1 | 0.96 | 1.24 | 1.17 | 4.26 | A_51_P484551 | 1 | 1.53 | 0.89 | 1.00 | 1.76 |
| Slc27a4 | Mm01327414_g1 | 1 | 0.72 | 1.41 | 1.46 | 1.84 | A_52_P61854 | 1 | 0.83 | 1.20 | 1.43 | 1.67 |
| Slc2a2 | Mm00446224_m1 | 1 | 0.24 | 0.63 | 0.47 | 0.74 | A_51_P185693 | 1 | 0.30 | 0.96 | 0.65 | 0.98 |
| Slc2a4 | Mm00436615_m1 | 1 | 1.46 | 0.82 | 1.05 | 1.10 | A_51_P217498 | 1 | 2.17 | 1.08 | 1.41 | 1.53 |
| Sqle | Mm00436772_m1 | 1 | 0.38 | 1.00 | 0.83 | 0.84 | A_51_P450487 | 1 | 0.51 | 0.87 | 0.75 | 0.73 |
| Taldo1 | Mm00807080_g1 | 1 | 1.53 | 1.42 | 1.91 | 2.03 | A_51_P401958 | 1 | 1.53 | 1.36 | 1.61 | 1.72 |
| Tkt | Mm00447559_m1 | 1 | 4.12 | 1.57 | 2.05 | 2.05 | A_51_P394515 | 1 | 4.05 | 1.51 | 1.86 | 2.04 |
| Uqcrb | Mm00835346_gH | 1 | 0.77 | 0.75 | 1.02 | 1.13 | A_51_P472671 | 1 | 1.81 | 1.40 | 1.82 | 2.14 |
| Uqcrrf1 | Mm00481849_m1 | 1 | 1.27 | 1.00 | 1.44 | 1.67 | A_51_P361951 | 1 | 1.57 | 1.24 | 1.87 | 2.25 |
| Uqcrrh | Mm00835199_g1 | 1 | 0.99 | 0.97 | 1.29 | 1.47 | A_52_P541875 | 1 | 1.89 | 1.43 | 1.81 | 1.97 |

Supplemental Table 4: Common sequence predictors for liver trioleate concentrations and weight, determined using PLS analysis. Removing redundancy among the 20 predictors led to 16 genes from which 13 displayed PPRE in their proximal promoters as determined by MatInspector from Genomatix suit. Publication-based PPRE are indicated in Bibliography PMID column: PubMed identification number; F.C. Fold Change; p -value= 0 correspond to p -value<1E-45.

| Sequence name | Sequence code | Sequence description | Predicted PPRE | Bibliography PMID | db/+ Foie | db/+ Foie | RGZ 10MK | RGZ 10MK | RGZ 30MK | RGZ 30MK | RGZ 100MK | RGZ 100MK |
|---------------|---------------|--|----------------|--------------------|-----------|-----------|----------|----------|----------|----------|-----------|-----------|
| | | | | | F. C. | P-Value | F. C. | P-Value | F. C. | P-Value | F. C. | P-Value |
| Aldob | A_51_P337269 | aldolase 2, B isoform | X | 15226431 | -1.70 | 6.33E-13 | -1.02 | 0.813021 | -1.20 | 0.002103 | -1.45 | 9.81E-11 |
| Cyp2a5 | A_52_P246252 | cytochrome P450, family 2, subfamily a, polypeptide 5 | | 10454501 | -2.1 | 1.97E-08 | -5.00 | 0 | -4.00 | 0 | -2.85 | 1.82E-09 |
| Cyp2c29 | A_51_P103706 | cytochrome P450, family 2, subfamily c, polypeptide 29 | X | 12130701, 10454501 | -1.04 | 0.072755 | -3.30 | 0 | -2.7 | 0 | -2.17 | 7.98E-23 |
| Cyp2c37 | A_52_P625249 | cytochrome P450, family 2, subfamily c, polypeptide 37 | X | | -1.53 | 8.30E-30 | -4.50 | 0 | -3.33 | 0 | -2.70 | 8.70E-34 |
| Cyp2c37 | A_51_P498882 | cytochrome P450, family 2, subfamily c, polypeptide 37 | | | -1.45 | 2.30E-20 | -4.34 | 0 | -3.12 | 0 | -2.56 | 4.71E-28 |
| Cyp2c39 | A_51_P304109 | cytochrome P450, family 2, subfamily c, polypeptide 39 | X | | -1.37 | 5.65E-16 | -2.94 | 0 | -2.5 | 0 | -2.12 | 1.38E-35 |
| Cyp2c54 | A_52_P154580 | cytochrome P450, family 2, subfamily c, polypeptide 54 | X | | -1.72 | 3.52E-29 | -5.26 | 0 | -3.57 | 0 | -2.78 | 1.26E-32 |
| Cyp2j6 | A_51_P506328 | cytochrome P450, family 2, subfamily j, polypeptide 6 | X | | 1.17 | 7.20E-14 | 1.41 | 3.60E-21 | 1.36 | 5.73E-14 | 1.31 | 3.75E-10 |
| Fabp3 | A_51_P167535 | fatty acid binding protein 3, muscle and heart | X | 15491498, 15130092 | -1.79 | 1.14E-33 | 2.71 | 0 | 2.38 | 8.80E-24 | 1.82 | 2.40E-07 |
| Fb p1 | A_51_P474701 | fructose biphosphatase 1 | X | 15226431, 12072378 | -1.99 | 6.44E-18 | -1.36 | 0.000066 | -1.56 | 7.07E-10 | -1.92 | 3.16E-18 |
| Fh1 | A_51_P359333 | fumarate hydratase 1 | X | | -1.31 | 3.03E-16 | -1.06 | 0.005397 | -1.08 | 0.002433 | -1.14 | 1.30E-17 |
| Gpi1 | A_51_P426886 | glucose phosphate isomerase 1 | X | | -1.09 | 4.96E-09 | 1.43 | 0 | 1.33 | 4.02E-25 | 1.26 | 4.93E-30 |
| Hadhb | A_51_P217990 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit | | 19300518, 11181544 | -1.06 | 0.03782 | 1.53 | 0 | 1.39 | 2.69E-31 | 1.32 | 2.82E-11 |
| Oxct1 | A_52_P430058 | 3-oxoacid CoA transferase 1 | X | | 1.19 | 0.000017 | 1.33 | 1.70E-08 | 1.37 | 2.19E-07 | 1.50 | 1.73E-06 |
| Oxct1 | A_51_P107321 | 3-oxoacid CoA transferase 1 | | | 1.30 | 7.23E-10 | 1.38 | 1.86E-11 | 1.29 | 2.77E-14 | 1.40 | 7.08E-11 |
| Phkb | A_52_P513347 | phosphorylase kinase beta | X | | 1.07 | 0.140703 | 1.45 | 5.61E-45 | 1.47 | 1.77E-25 | 1.38 | 2.37E-19 |

