**SUPPLEMENTAL FILES**

**Supplemental Table 1.** Blast2GO table with BLASTX hits from *M. musculus*, *R. rattus*, and *C griseus* and top three supported Gene Ontology terms for outlier genes from Bayescan and SweeD

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Bayescan |  |  |  |  |  |  |  |
| Seq. Name | Seq. Description | Seq. Length | #Hits | min. eValue | mean Similarity | #GOs | GOs |
| 27887-125 | 26s proteasome non-atpase regulatory subunit 9 | 572 | 5 | 1.02E-43 | 92.80% | 1 | C:proteasome complex |
| 17974-242 | 40s ribosomal protein s15a-like protein | 243 | 5 | 4.92E-08 | 59.20% | 9 | F:L-serine transmembrane transporter activity; C:integral to membrane; P:phosphatidylserine metabolic process; |
| 36491-37 | 5-oxoprolinase isoform x1 | 3504 | 5 | 0 | 96.60% | 2 | P:metabolic process; F:hydrolase activity |
| 26257-147 | PREDICTED: uncharacterized protein C1orf167 homolog | 1635 | 4 | 1.29E-09 | 81.00% | 0 | - |
| 2260-821 | a kinase anchor protein isoform cra\_a | 1645 | 5 | 1.01E-150 | 90.20% | 13 | C:nuclear matrix; F:double-stranded DNA binding; F:zinc ion binding; |
| 40819-1 | adaptin ear-binding coat-associated protein 1 | 1043 | 5 | 3.68E-09 | 94.80% | 5 | C:coated pit; C:clathrin vesicle coat; C:plasma membrane; |
| 20787-217 | adp-ribosylation factor-like protein 1  166 | 1599 | 5 | 2.02E-112 | 100.00% | 15 | C:trans-Golgi network; C:Golgi membrane; P:protein localization to Golgi apparatus; |
| 25795-154 | af478441\_1farnesoid-x-receptor alpha splice variant 1 | 1289 | 5 | 3.09E-160 | 96.20% | 25 | F:retinoid X receptor binding; F:RNA polymerase II distal enhancer sequence-specific DNA binding; P:response to glucose stimulus |
| 902-1236 | alkyldihydroxyacetonephosphate peroxisomal | 1579 | 5 | 4.57E-140 | 99.80% | 5 | F:flavin adenine dinucleotide binding; F:UDP-N-acetylmuramate dehydrogenase activity; P:lipid biosynthetic process; |
| 26183-148 | atp-binding cassette sub-family c member 8-like | 366 | 5 | 6.87E-59 | 99.40% | 13 | F:sulfonylurea receptor activity; F:ATPase activity, coupled to transmembrane movement of substances; P:potassium ion import; |
| 27707-127 | autophagy-related protein 2 homolog a isoform x2 | 704 | 5 | 2.89E-129 | 96.00% | 3 | C:lipid particle; C:membrane; P:autophagy |
| 7690-428 | casp8-associated protein 2 | 501 | 5 | 5.87E-51 | 90.80% | 14 | P:Fas signaling pathway; P:cell cycle; C:mitochondrion; |
| 19-4220 | cytoplasmic dynein 1 heavy chain 1 | 7920 | 5 | 0 | 99.00% | 13 | F:microtubule motor activity; P:transport; C:dynein complex; |
| 3567-665 | gram domain-containing protein 3 | 1397 | 5 | 0 | 93.80% | 1 | C:cytoplasmic microtubule |
| 36706-36 | hermansky-pudlak syndrome 1 protein homolog | 575 | 5 | 5.92E-71 | 95.40% | 9 | P:organelle organization; P:melanocyte differentiation; C:cytoplasmic membrane-bounded vesicle; |
| 35973-42 | isoform cra\_a | 225 | 5 | 8.85E-12 | 80.80% | 5 | C:nucleosome; F:DNA binding; P:nucleosome assembly; |
| 36701-36 | isoform cra\_b | 300 | 5 | 8.59E-54 | 91.60% | 4 | F:nucleic acid binding; C:cytoplasm; F:NAD+ ADP-ribosyltransferase activity; C:plasma membrane |
| 36437-38 | jnk sapk-inhibitory isoform cra\_a  167 | 1184 | 5 | 0 | 97.80% | 9 | P:positive regulation of JUN kinase activity; P:G2 DNA damage checkpoint; P:negative regulation of JNK cascade |
| 23896-185 | low molecular weight phosphotyrosine protein phosphatase-like | 1386 | 5 | 7.90E-111 | 96.00% | 9 | C:cytoplasm; F:non-membrane spanning protein tyrosine phosphatase activity; F:acid phosphatase activity |
| 7750-426 | lysine-specific demethylase 8 | 427 | 5 | 8.93E-91 | 95.20% | 0 | - |
| 11279-335 | mitochondrial ribosomal protein l37 | 1481 | 5 | 0 | 94.20% | 3 | C:mitochondrial ribosome; F:structural constituent of ribosome; P:translation |
| 7975-418 | myosin light chain smooth muscle | 1342 | 5 | 0 | 90.00% | 3 | P:protein phosphorylation; F:ATP binding; F:protein serine/threonine kinase activity |
| 29218-108 | n-alpha-acetyltransferase 50 isoform x1 | 915 | 5 | 9.57E-124 | 99.40% | 4 | C:cytoplasm; F:N-acetyltransferase activity; F:protein binding= |
| 5754-511 | otu domain-containing protein 3 | 512 | 5 | 7.42E-67 | 86.20% | 0 | - |
| 1396-1029 | proteasome activator complex subunit 1 | 1030 | 5 | 1.22E-154 | 96.80% | 5 | F:endopeptidase activator activity; P:positive regulation of endopeptidase activity |
| 2482-790 | protein diaphanous homolog 1 isoform x1 | 2618 | 5 | 0 | 98.80% | 3 | F:actin binding; P:actin filament polymerization; F:Rho GTPase binding |
| 38691-21 | protein mdm4  168 | 490 | 4 | 4.28E-21 | 81.25% | 15 | P:G0 to G1 transition; P:negative regulation of apoptotic process; P:protein stabilization |
| 27691-127 | retroviral nucleocapsid protein gag containing protein | 1224 | 5 | 2.99E-31 | 60.20% | 3 | F:nucleic acid binding; P:viral process; F:zinc ion binding |
| 1371-1036 | signal recognition particle 9 kda protein | 1381 | 5 | 4.23E-51 | 99.60% | 4 | C:signal recognition particle, endoplasmic reticulum targeting; P:negative regulation of translational elongation; F:7S RNA binding |
| 37967-26 | sorbin and sh3 domain-containing protein 2 isoform x3 | 1472 | 5 | 0 | 96.80% | 10 | C:Z disc; F:structural constituent of cytoskeleton; F:structural constituent of muscle |
| 14102-290 | succinate dehydrogenase | 1293 | 5 | 1.95E-94 | 94.20% | 9 | F:metal ion binding; F:succinate dehydrogenase activity; F:heme binding |
| 3135-709 | transmembrane 9 superfamily member 1 isoform 2 | 1250 | 5 | 0 | 98.20% | 6 | C:autophagic vacuole membrane; C:lysosomal membrane; C:integral to membrane |
| 31201-85 | transmembrane protein 115 | 688 | 5 | 2.73E-47 | 97.00% | 4 | C:integral to membrane; P:replicative cell aging; C:Golgi apparatus |
| 22365-204 | transmembrane protein 19 isoform x1 | 2106 | 5 | 8.76E-169 | 96.20% | 1 | C:integral to membrane |
| 37015-34 | tubulin folding cofactor e-like isoform x6 | 954 | 5 | 0 | 99.00% | 2 | C:cytoskeleton; C:cytoplasm |
| 1749-927 | utrophin isoform x2 | 1303 | 5 | 0 | 98.60% | 26 | F:integrin binding; C:membrane raft; F:zinc ion binding |
| SweeD |  |  |  |  |  |  |  |
| Seq. Name | Seq. Description  169 | Seq. Length | #Hits | min. eValue | mean Similarity | #GOs | GOs |
| 42-3615 | 2-oxoglutarate dehydrogenase | 4431 | 5 | 0 | 98.20% | 12 | F:heat shock protein binding; F:thiamine pyrophosphate binding; F:oxoglutarate dehydrogenase (NAD+) activity |
| 537-1509 | 26s proteasome non-atpase regulatory subunit 5 | 1510 | 5 | 0 | 97.80% | 2 | F:protein binding involved in protein folding; C:proteasome regulatory particle, base subcomplex |
| 27546-129 | 6- liver type | 2171 | 5 | 0 | 99.00% | 16 | P:response to glucose stimulus; F:fructose binding; F:kinase binding; F:metal ion binding |
| 37202-32 | PREDICTED: poly | 2091 | 5 | 0 | 88.80% | 4 | F:nucleic acid binding; C:cytoplasm; F:NAD+ ADP-ribosyltransferase activity |
| 10636-348 | aflatoxin b1 aldehyde reductase member 2 | 1643 | 5 | 0 | 95.00% | 7 | P:daunorubicin metabolic process; C:Golgi apparatus; F:alditol:NADP+ 1-oxidoreductase activity |
| 39-3749 | alpha-aminoadipic semialdehyde mitochondrial | 3750 | 5 | 0 | 97.40% | 6 | P:L-lysine catabolic process; F:saccharopine dehydrogenase (NADP+, L-lysine-forming) activity; C:mitochondrion |
| 35790-44 | apolipoprotein b- partial | 13706 | 5 | 0 | 82.40% | 0 | - |
| 2034-860 | dehydrogenase reductase (sdr family) member 3 | 1448 | 5 | 0 | 99.00% | 3 | P:oxidation-reduction process; C:integral to membrane; F:NADP-retinol dehydrogenase activity |
| 408-1655 | disintegrin and metalloproteinase domain-containing protein 9 isoform x1  170 | 2049 | 5 | 0 | 94.80% | 29 | F:integrin binding; P:response to manganese ion; P:monocyte activation |
| 4818-563 | exportin-t isoform x1 | 4119 | 5 | 0 | 98.60% | 7 | F:Ran GTPase binding; C:nuclear pore; P:tRNA export from nucleus |
| 342-1776 | fatty acid desaturase 1 | 3406 | 5 | 0 | 97.00% | 17 | P:arachidonic acid metabolic process; P:transport; P:electron transport chain |
| 533-1512 | fructose- -bisphosphatase 1 | 1513 | 5 | 0 | 95.80% | 0 | - |
| 3964-627 | heat shock protein alpha class a member 1 | 2834 | 5 | 0 | 96.00% | 43 | C:cell surface; C:brush border membrane; F:GTP binding |
| 8960-388 | hepatocyte growth factor activator | 1001 | 5 | 0 | 95.20% | 3 | C:extracellular space; P:proteolysis; F:serine-type endopeptidase activity |
| 1583-971 | isoform cra\_a | 1704 | 5 | 0 | 95.60% | 33 | P:chaperone-mediated protein folding; P:response to virus; P:response to misfolded protein |
| 951-1212 | lysosomal-associated transmembrane protein 4a | 1402 | 5 | 1.83E-164 | 96.00% | 5 | C:endomembrane system; C:integral to membrane; C:Golgi apparatus |
| 26488-144 | pentatricopeptide repeat domain-containing protein mitochondrial isoform x2 | 1179 | 5 | 3.70E-124 | 94.00% | 0 | - |
| 8466-403 | rcc1 and btb domain-containing protein 2 isoform x1 | 1110 | 5 | 2.45E-81 | 84.20% | 0 | - |
| 28127-122 | sarcosine mitochondrial | 2726 | 5 | 0 | 95.80% | 8 | F:aminomethyltransferase activity; P:oxidation-reduction process; F:folic acid binding |
| 17856-243 | serine protease inhibitor a3c-like | 3172 | 5 | 0 | 86.80% | 0 | - |
| 1596-968 | small ubiquitin-related modifier 2 isoform 2 | 1075 | 5 | 3.66E-73 | 91.80% | 4 | P:protein sumoylation; P:positive regulation of transcription from RNA polymerase II promoter; F:SUMO ligase activity |
| 14528-283 | solute carrier family 22 (organic anion transporter) member 7 | 2144 | 5 | 0 | 90.60% | 6 | C:integral to plasma membrane; C:basolateral plasma membrane; P:ion transmembrane transport |
| 1782-919 | solute carrier family 39 (zinc transporter) member 1 | 1615 | 5 | 7.37E-170 | 98.00% | 5 | C:plasma membrane; P:zinc ion transmembrane transport; F:receptor binding |
| 243-1951 | solute carrier family member 13 | 2914 | 5 | 0 | 98.00% | 12 | P:gluconeogenesis; P:response to calcium ion; F:calcium ion binding |
| 6315-484 | udp-glucuronosyltransferase 3a1-like isoform x1 | 2572 | 5 | 0 | 83.80% | 4 | F:glucuronosyltransferase activity; P:cellular response to genistein; C:integral to membrane |

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