### Male Liver Top 10 GO Biological Process Gene Sets Ranked by Potency of Perturbation (Sorted by BMD Median)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Category Name** | Input Genes/Platform Genes in Gene Set | % Gene Set Coverage | Active Genes | BMD1std Median of Gene Set Transcripts (mg/kg) | Median BMDL1Std-BMDU1Std (mg/kg) | Genes with Changed Direction Up | Genes with Changed Direction Down |
| **GO:0009165**  nucleotide biosynthetic process | 3/55 | 5% | rrm2b; gcdh; aldoa | 5.235 | 2.666-10.897 | 3 | 0 |
| **GO:0015850**  organic hydroxy compound transport | 3/50 | 6% | aqp9; apoa1; abcc3 | 5.978 | 3.303-16.491 | 1 | 2 |
| **GO:0051496**  positive regulation of stress fiber assembly | 3/21 | 14% | rhoc; pak1; apoa1 | 6.710 | 2.595-19.237 | 2 | 1 |
| **GO:0042908**  xenobiotic transport | 4/11 | 36% | slc17a3; abcg2; abcc4; abcc3 | 6.716 | 3.394-26.223 | 4 | 0 |
| **GO:0032273**  positive regulation of protein polymerization | 3/30 | 10% | pak1; icam1; hspa1a | 7.304 | 2.595-23.878 | 3 | 0 |
| **GO:0032535**  regulation of cellular component size | 3/60 | 5% | sptan1; icam1; anxa7 | 7.304 | 2.970-23.878 | 3 | 0 |
| **GO:1903426**  regulation of reactive oxygen species biosynthetic process | 5/48 | 10% | rgn; ptgs2; icam1; hspd1; foxo3 | 7.304 | 3.587-23.878 | 3 | 2 |
| **GO:2000351**  regulation of endothelial cell apoptotic process | 3/28 | 11% | icam1; foxo3; ccl2 | 7.304 | 2.250-23.878 | 2 | 1 |
| **GO:0070741**  response to interleukin-6 | 3/14 | 21% | pck1; icam1; ccl2 | 7.304 | 2.250-23.878 | 2 | 1 |
| **GO:1903428**  positive regulation of reactive oxygen species biosynthetic process | 3/33 | 9% | ptgs2; icam1; foxo3 | 7.304 | 2.250-23.878 | 2 | 1 |

Official gene symbols from the Rat Genome Database are shown in the “Active Genes” column. Definitions of Gene Ontology terms were provided by the Gene Ontology Resource (http://geneontology.org/).

**GO process description version:** https://cebs.niehs.nih.gov/cebs/study/002-00600-0002-000-0 V04132020

**GO:0009165 nucleotide biosynthetic process:** The chemical reactions and pathways resulting in the formation of nucleotides, any nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the glycose moiety; may be mono-, di- or triphosphate; this definition includes cyclic-nucleotides (nucleoside cyclic phosphates).

**GO:0015850 organic hydroxy compound transport:** The directed movement of an organic hydroxy compound (organic alcohol) into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore. An organic hydroxy compound is an organic compound having at least one hydroxy group attached to a carbon atom.

**GO:0051496 positive regulation of stress fiber assembly:** Any process that activates or increases the frequency, rate or extent of the assembly of a stress fiber, a bundle of microfilaments and other proteins found in fibroblasts.

**GO:0042908 xenobiotic transport:** The directed movement of a xenobiotic, a compound foreign to living organisms, into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore.

**GO:0032273 positive regulation of protein polymerization:** Any process that activates or increases the frequency, rate or extent of the process of creating protein polymers.

**GO:0032535 regulation of cellular component size:** A process that modulates the size of a cellular component.

**GO:1903426 regulation of reactive oxygen species biosynthetic process:** Any process that modulates the frequency, rate or extent of reactive oxygen species biosynthetic process.

**GO:2000351 regulation of endothelial cell apoptotic process:** Any process that modulates the frequency, rate or extent of endothelial cell apoptotic process.

**GO:0070741 response to interleukin-6:** Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an interleukin-6 stimulus.

**GO:1903428 positive regulation of reactive oxygen species biosynthetic process:** Any process that activates or increases the frequency, rate or extent of reactive oxygen species biosynthetic process.

### Female Liver Top 10 GO Biological Process Gene Sets Ranked by Potency of Perturbation (Sorted by BMD Median)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Category Name** | Input Genes/Platform Genes in Gene Set | % Gene Set Coverage | Active Genes | BMD1std Median of Gene Set Transcripts (mg/kg) | Median BMDL1Std-BMDU1Std (mg/kg) | Genes with Changed Direction Up | Genes with Changed Direction Down |
| **GO:0006475**  internal protein amino acid acetylation | 3/15 | 20% | pck1; ncoa1; ehhadh | 5.355 | 3.108-9.861 | 3 | 0 |
| **GO:0009064**  glutamine family amino acid metabolic process | 3/24 | 13% | gclm; gclc; dao | 8.071 | 3.552-26.141 | 3 | 0 |
| **GO:0046700**  heterocycle catabolic process | 4/63 | 6% | hmox1; dao; aldh1l1; akr7a3 | 8.437 | 2.875-33.533 | 4 | 0 |
| **GO:1901361**  organic cyclic compound catabolic process | 5/89 | 6% | hmox1; dao; cyp1a2; aldh1l1; akr7a3 | 8.803 | 3.082-26.141 | 4 | 1 |
| **GO:0009069**  serine family amino acid metabolic process | 4/13 | 31% | txnrd1; gclm; gclc; dao | 9.286 | 4.360-24.515 | 4 | 0 |
| **GO:0055093**  response to hyperoxia | 3/24 | 13% | txnrd1; cdkn1a; cav1 | 10.500 | 5.321-22.888 | 2 | 1 |
| **GO:1901605**  alpha-amino acid metabolic process | 5/72 | 7% | txnrd1; plod2; gclm; gclc; dao | 10.500 | 5.167-26.141 | 5 | 0 |
| **GO:0007093**  mitotic cell cycle checkpoint | 3/38 | 8% | zwint; kntc1; cdkn1a | 11.920 | 4.772-41.705 | 2 | 1 |
| **GO:0010823**  negative regulation of mitochondrion organization | 3/22 | 14% | hgf; gclc; acaa2 | 11.956 | 5.167-23.735 | 2 | 1 |
| **GO:0035729**  cellular response to hepatocyte growth factor stimulus | 3/14 | 21% | hgf; gclm; gclc | 11.956 | 5.167-23.735 | 2 | 1 |

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**GO:0006475 internal protein amino acid acetylation:** The addition of an acetyl group to a non-terminal amino acid in a protein.

**GO:0009064 glutamine family amino acid metabolic process:** The chemical reactions and pathways involving amino acids of the glutamine family, comprising arginine, glutamate, glutamine and proline.

**GO:0046700 heterocycle catabolic process:** The chemical reactions and pathways resulting in the breakdown of heterocyclic compounds, those with a cyclic molecular structure and at least two different atoms in the ring (or rings).

**GO:1901361 organic cyclic compound catabolic process:** The chemical reactions and pathways resulting in the breakdown of organic cyclic compound.

**GO:0009069 serine family amino acid metabolic process:** The chemical reactions and pathways involving amino acids of the serine family, comprising cysteine, glycine, homoserine, selenocysteine and serine.

**GO:0055093 response to hyperoxia:** Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus indicating increased oxygen tension.

**GO:1901605 alpha-amino acid metabolic process:** The chemical reactions and pathways involving an alpha-amino acid.

**GO:0007093 mitotic cell cycle checkpoint:** A cell cycle checkpoint that ensures accurate chromosome replication and segregation by preventing progression through a mitotic cell cycle until conditions are suitable for the cell to proceed to the next stage.

**GO:0010823 negative regulation of mitochondrion organization:** Any process that decreases the frequency, rate or extent of a process involved in the formation, arrangement of constituent parts, or disassembly of a mitochondrion.

**GO:0035729 cellular response to hepatocyte growth factor stimulus:** Any process that results in a change in state or activity of a cell (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a hepatocyte growth factor stimulus.