**Male Kidney 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:0045444**  fat cell differentiation | 3/34 | 9% | srebf1; pex11a; cebpd | 8.745 | 5.224-15.487 | 1 | 2 |
| **GO:0006984**  ER-nucleus signaling pathway | 3/12 | 25% | srebf1; insig1; bcl2l11 | 8.745 | 5.589-15.487 | 2 | 1 |
| **GO:0019217**  regulation of fatty acid metabolic process | 4/45 | 9% | srebf1; ppard; insig1; acadl | 9.340 | 5.671-17.150 | 4 | 0 |
| **GO:0050796**  regulation of insulin secretion | 3/50 | 6% | srebf1; ppard; hadh | 9.934 | 5.754-18.814 | 3 | 0 |
| **GO:0051301**  cell division | 4/79 | 5% | top2a; cenpw; cdca3; cdc20 | 10.989 | 7.802-19.064 | 4 | 0 |
| **GO:0034329**  cell junction assembly | 3/41 | 7% | lama3; fgf13; ect2 | 11.880 | 8.320-21.047 | 2 | 1 |
| **GO:0033157**  regulation of intracellular protein transport | 6/73 | 8% | srebf1; plk3; kif20b; insig1; ect2; c2cd5 | 12.192 | 8.490-21.873 | 4 | 2 |
| **GO:0002244**  hematopoietic progenitor cell differentiation | 3/31 | 10% | top2a; herc6; cebpd | 12.299 | 8.517-22.796 | 2 | 1 |
| **GO:0007059**  chromosome segregation | 3/37 | 8% | top2a; cenpw; cenpf | 12.299 | 8.517-22.796 | 3 | 0 |
| **GO:0032465**  regulation of cytokinesis | 3/28 | 11% | plk3; kif20b; ect2 | 12.504 | 8.661-22.699 | 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:0045444 fat cell differentiation:** The process in which a relatively unspecialized cell acquires specialized features of an adipocyte, an animal connective tissue cell specialized for the synthesis and storage of fat.

**GO:0006984 ER-nucleus signaling pathway:** Any series of molecular signals that conveys information from the endoplasmic reticulum to the nucleus, usually resulting in a change in transcriptional regulation.

**GO:0019217 regulation of fatty acid metabolic process:** Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving fatty acids.

**GO:0050796 regulation of insulin secretion:** Any process that modulates the frequency, rate or extent of the regulated release of insulin.

**GO:0051301 cell division:** The process resulting in division and partitioning of components of a cell to form more cells; may or may not be accompanied by the physical separation of a cell into distinct, individually membrane-bounded daughter cells.

**GO:0034329 cell junction assembly:** A cellular process that results in the aggregation, arrangement and bonding together of a set of components to form a cell junction.

**GO:0033157 regulation of intracellular protein transport:** Any process that modulates the frequency, rate or extent of the directed movement of proteins within cells.

**GO:0002244 hematopoietic progenitor cell differentiation:** The process in which precursor cell type acquires the specialized features of a hematopoietic progenitor cell, a class of cell types including myeloid progenitor cells and lymphoid progenitor cells.

**GO:0007059 chromosome segregation:** The process in which genetic material, in the form of chromosomes, is organized into specific structures and then physically separated and apportioned to two or more sets. In eukaryotes, chromosome segregation begins with the condensation of chromosomes, includes chromosome separation, and ends when chromosomes have completed movement to the spindle poles.

**GO:0032465 regulation of cytokinesis:** Any process that modulates the frequency, rate or extent of the division of the cytoplasm of a cell and its separation into two daughter cells.

### Female Kidney 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:0051302**  regulation of cell division | 3/51 | 6% | kif18b; ect2; aspm | 10.324 | 7.461-16.862 | 3 | 0 |
| **GO:0007059**  chromosome segregation | 3/37 | 8% | top2a; ska1; kif18b | 11.921 | 8.348-21.048 | 3 | 0 |
| **GO:0051301**  cell division | 7/79 | 9% | top2a; ska1; kif18b; cks2; cdca3; ccnd1; aspm | 11.921 | 8.348-21.048 | 7 | 0 |
| **GO:0070507**  regulation of microtubule cytoskeleton organization | 3/53 | 6% | ska1; ckap2; atf5 | 12.122 | 8.470-21.380 | 2 | 1 |
| **GO:0022402**  cell cycle process | 10/191 | 5% | top2a; kntc1; kif22; kif18b; ect2; cks2; ckap2; cdkn1a; ccnd1; aspm | 13.539 | 9.169-26.565 | 9 | 1 |
| **GO:1903047**  mitotic cell cycle process | 9/146 | 6% | top2a; kntc1; kif22; kif18b; ect2; cks2; ckap2; cdkn1a; ccnd1 | 13.839 | 9.316-27.695 | 8 | 1 |
| **GO:1903046**  meiotic cell cycle process | 3/29 | 10% | top2a; cks2; aspm | 13.839 | 9.316-27.695 | 3 | 0 |
| **GO:0048285**  organelle fission | 3/20 | 15% | top2a; mx2; cks2 | 14.420 | 9.624-29.096 | 2 | 1 |
| **GO:0033762**  response to glucagon | 4/18 | 22% | srebf1; pck1; hmgcs2; cry1 | 20.917 | 13.412-40.119 | 3 | 1 |
| **GO:0032869**  cellular response to insulin stimulus | 4/62 | 6% | srebf1; pck1; hmgcs2; ccl2 | 20.917 | 14.761-40.119 | 3 | 1 |

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

**GO:0051302 regulation of cell division:** Any process that modulates the frequency, rate or extent of the physical partitioning and separation of a cell into daughter cells.

**GO:0007059 chromosome segregation:** The process in which genetic material, in the form of chromosomes, is organized into specific structures and then physically separated and apportioned to two or more sets. In eukaryotes, chromosome segregation begins with the condensation of chromosomes, includes chromosome separation, and ends when chromosomes have completed movement to the spindle poles.

**GO:0051301 cell division:** The process resulting in division and partitioning of components of a cell to form more cells; may or may not be accompanied by the physical separation of a cell into distinct, individually membrane-bounded daughter cells.

**GO:0070507 regulation of microtubule cytoskeleton organization:** Any process that modulates the frequency, rate or extent of the formation, arrangement of constituent parts, or disassembly of cytoskeletal structures comprising microtubules and their associated proteins.

**GO:0022402 cell cycle process:** The cellular process that ensures successive accurate and complete genome replication and chromosome segregation.

**GO:1903047 mitotic cell cycle process:** A process that is part of the mitotic cell cycle.

**GO:1903046 meiotic cell cycle process:** A process that is part of the meiotic cell cycle.

**GO:0048285 organelle fission:** The creation of two or more organelles by division of one organelle.

**GO:0033762 response to glucagon:** 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 glucagon stimulus.

**GO:0032869 cellular response to insulin 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 an insulin stimulus. Insulin is a polypeptide hormone produced by the islets of Langerhans of the pancreas in mammals, and by the homologous organs of other organisms.