### 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:0002886**  regulation of myeloid leukocyte mediated immunity | 3/28 | 11% | rt1-s3; hmox1; c3 | 144.319 | 57.694-153.260 | 2 | 1 |
| **GO:0032570**  response to progesterone | 3/40 | 8% | srebf1; map2; c3 | 145.437 | 104.718-237.081 | 2 | 1 |
| **GO:0002703**  regulation of leukocyte mediated immunity | 4/79 | 5% | rt1-s3; il1b; hmox1; c3 | 149.155 | 83.579-205.964 | 3 | 1 |
| **GO:0002675**  positive regulation of acute inflammatory response | 3/17 | 18% | rt1-s3; il1b; c3 | 153.991 | 109.464-258.668 | 2 | 1 |
| **GO:0072347**  response to anesthetic | 3/44 | 7% | slc6a1; il1b; grin1 | 153.991 | 109.464-258.668 | 3 | 0 |
| **GO:1903531**  negative regulation of secretion by cell | 3/60 | 5% | srebf1; il1b; hmox1 | 153.991 | 109.464-258.668 | 2 | 1 |
| **GO:0009408**  response to heat | 3/59 | 5% | il1b; hmox1; cxcl10 | 153.991 | 109.464-258.668 | 2 | 1 |
| **GO:0050766**  positive regulation of phagocytosis | 3/35 | 9% | il1b; clec7a; c3 | 153.991 | 109.464-258.668 | 3 | 0 |
| **GO:0002718**  regulation of cytokine production involved in immune response | 3/36 | 8% | rt1-s3; il1b; hmox1 | 153.991 | 109.464-258.668 | 2 | 1 |
| **GO:0045665**  negative regulation of neuron differentiation | 3/54 | 6% | map2; il1b; fgf13 | 153.991 | 109.464-258.668 | 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:0002886 regulation of myeloid leukocyte mediated immunity:** Any process that modulates the frequency, rate, or extent of myeloid leukocyte mediated immunity.

**GO:0032570 response to progesterone:** 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 progesterone stimulus.

**GO:0002703 regulation of leukocyte mediated immunity:** Any process that modulates the frequency, rate, or extent of leukocyte mediated immunity.

**GO:0002675 positive regulation of acute inflammatory response:** Any process that activates or increases the frequency, rate, or extent of an acute inflammatory response.

**GO:0072347 response to anesthetic:** 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 anesthetic stimulus. An anesthetic is a substance that causes loss of feeling, awareness, or sensation.

**GO:1903531 negative regulation of secretion by cell:** Any process that stops, prevents or reduces the frequency, rate or extent of secretion by cell.

**GO:0009408 response to heat:** 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 heat stimulus, a temperature stimulus above the optimal temperature for that organism.

**GO:0050766 positive regulation of phagocytosis:** Any process that activates or increases the frequency, rate or extent of phagocytosis.

**GO:0002718 regulation of cytokine production involved in immune response:** Any process that modulates the frequency, rate, or extent of cytokine production that contributes to an immune response.

**GO:0045665 negative regulation of neuron differentiation:** Any process that stops, prevents, or reduces the frequency, rate or extent of neuron differentiation.

### 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:0045087**  innate immune response | 5/87 | 6% | vnn1; fcer1g; col12a1; clec4a; c3 | 57.313 | 37.882-112.773 | 4 | 1 |
| **GO:0002253**  activation of immune response | 4/69 | 6% | fyb1; fcer1g; col12a1; c3 | 78.645 | 45.596-480.937 | 3 | 1 |
| **GO:0002250**  adaptive immune response | 3/57 | 5% | fcer1g; adgre1; clec4a | 82.466 | 47.872-265.955 | 3 | 0 |
| **GO:0050729**  positive regulation of inflammatory response | 3/52 | 6% | tslp; fcer1g; c3 | 99.976 | 53.311-818.733 | 2 | 1 |
| **GO:0006690**  icosanoid metabolic process | 3/48 | 6% | gstp1; ephx1; cyp4a2 | 147.888 | 112.384-215.342 | 3 | 0 |
| **GO:0071385**  cellular response to glucocorticoid stimulus | 3/51 | 6% | hmgcs2; gstp1; ephx1 | 147.888 | 112.384-215.342 | 3 | 0 |
| **GO:1901568**  fatty acid derivative metabolic process | 4/57 | 7% | hmgcs2; gstp1; ephx1; cyp4a2 | 220.130 | 150.351-433.756 | 4 | 0 |
| **GO:0046165**  alcohol biosynthetic process | 3/41 | 7% | hmgcs2; ephx1; cyp26b1 | 238.250 | 181.323-370.243 | 3 | 0 |
| **GO:0045580**  regulation of T cell differentiation | 3/47 | 6% | vnn1; lilrb4; cyp26b1 | 238.250 | 181.323-370.243 | 3 | 0 |
| **GO:0021700**  developmental maturation | 3/51 | 6% | sez6; fgg; c3 | 251.984 | 163.812-471.307 | 2 | 1 |

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**GO:0045087 innate immune response:** Innate immune responses are defense responses mediated by germline encoded components that directly recognize components of potential pathogens.

**GO:0002253 activation of immune response:** Any process that initiates an immune response.

**GO:0002250 adaptive immune response:** An immune response mediated by cells expressing specific receptors for antigen produced through a somatic diversification process, and allowing for an enhanced secondary response to subsequent exposures to the same antigen (immunological memory).

**GO:0050729 positive regulation of inflammatory response:** Any process that activates or increases the frequency, rate or extent of the inflammatory response.

**GO:0006690 icosanoid metabolic process:** The chemical reactions and pathways involving icosanoids, any of a group of C20 polyunsaturated fatty acids.

**GO:0071385 cellular response to glucocorticoid 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 glucocorticoid stimulus. Glucocorticoids are hormonal C21 corticosteroids synthesized from cholesterol with the ability to bind with the cortisol receptor and trigger similar effects. Glucocorticoids act primarily on carbohydrate and protein metabolism, and have anti-inflammatory effects.

**GO:1901568 fatty acid derivative metabolic process:** The chemical reactions and pathways involving fatty acid derivative.

**GO:0046165 alcohol biosynthetic process:** The chemical reactions and pathways resulting in the formation of alcohols, any of a class of compounds containing one or more hydroxyl groups attached to a saturated carbon atom.

**GO:0045580 regulation of T cell differentiation:** Any process that modulates the frequency, rate or extent of T cell differentiation.

**GO:0021700 developmental maturation:** A developmental process, independent of morphogenetic (shape) change, that is required for an anatomical structure, cell or cellular component to attain its fully functional state.