**Table S5.** Gene Ontology pathways (biological processes) that were significantly enriched (*P*<0.05 after permutation) among the transcripts down-regulated after sleep restriction. *Total no. of genes in pathway* represents the number of genes that are annotated to the pathway. *Top no. of genes in pathway* represents the number of genes that were found in the study setting and contributed to the significance of the pathway.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene Ontology ID**  | **Pathway** | **Opt. *P* value** | **Permuted *P* value** | **Total no. of genes in pathway** | **Gene rank** | **Top no. of genes in pathway** |
| GO:0032365 | intracellular lipid transport  | 1.71E-05 | 0.001 | 9 | 124 | 4 |
| GO:0015833 | peptide transport  | 1.48E-04 | 0.003 | 20 | 88 | 4 |
| GO:0015918 | sterol transport  | 1.79E-04 | 0.001 | 8 | 95 | 3 |
| GO:0055092 | sterol homeostasis  | 1.79E-04 | 0.001 | 8 | 95 | 3 |
| GO:0030301 | cholesterol transport  | 1.79E-04 | 0.001 | 8 | 95 | 3 |
| GO:0042632 | cholesterol homeostasis  | 1.79E-04 | 0.001 | 8 | 95 | 3 |
| GO:0045736 | negative regulation of cyclin-dependent protein kinase activity  | 2.91E-04 | 0.003 | 9 | 495 | 5 |
| GO:0006869 | lipid transport  | 3.71E-04 | 0.006 | 49 | 124 | 6 |
| GO:0055088 | lipid homeostasis  | 3.75E-04 | 0.002 | 10 | 95 | 3 |
| GO:0005548 | phospholipid transporter activity  | 3.91E-04 | 0.006 | 14 | 67 | 3 |
| GO:0005319 | lipid transporter activity  | 4.91E-04 | 0.004 | 25 | 95 | 4 |
| GO:0015909 | long-chain fatty acid transport  | 5.82E-04 | 0.005 | 9 | 124 | 3 |
| GO:0008299 | isoprenoid biosynthetic process  | 7.30E-04 | 0.004 | 7 | 2235 | 7 |
| GO:0032393 | MHC class I receptor activity  | 7.52E-04 | 0.005 | 7 | 1418 | 6 |
| GO:0006635 | fatty acid beta-oxidation  | 8.20E-04 | 0.01 | 10 | 124 | 3 |
| GO:0004715 | non-membrane spanning protein tyrosine kinase activity  | 8.23E-04 | 0.011 | 16 | 1756 | 11 |
| GO:0050680 | negative regulation of epithelial cell proliferation  | 1.04E-03 | 0.012 | 15 | 87 | 3 |
| GO:0015908 | fatty acid transport  | 1.11E-03 | 0.007 | 11 | 124 | 3 |
| GO:0009062 | fatty acid catabolic process  | 1.11E-03 | 0.008 | 11 | 124 | 3 |
| GO:0004860 | protein kinase inhibitor activity  | 1.17E-03 | 0.018 | 19 | 279 | 5 |
| GO:0016538 | cyclin-dependent protein kinase regulator activity  | 1.26E-03 | 0.009 | 11 | 529 | 5 |
| GO:0048286 | alveolus development  | 1.28E-03 | 0.01 | 7 | 514 | 4 |
| GO:0030509 | BMP signaling pathway  | 1.29E-03 | 0.011 | 13 | 109 | 3 |
| GO:0007623 | circadian rhythm  | 1.45E-03 | 0.015 | 14 | 2720 | 12 |
| GO:0046395 | carboxylic acid catabolic process  | 1.46E-03 | 0.006 | 12 | 124 | 3 |
| GO:0016054 | organic acid catabolic process  | 1.46E-03 | 0.007 | 12 | 124 | 3 |
| GO:0019210 | kinase inhibitor activity  | 1.51E-03 | 0.018 | 20 | 279 | 5 |
| GO:0000122 | negative regulation of transcription from RNA polymerase II promoter  | 1.53E-03 | 0.043 | 92 | 186 | 9 |
| GO:0045047 | protein targeting to ER  | 1.58E-03 | 0.011 | 13 | 977 | 7 |
| GO:0051180 | vitamin transport  | 1.75E-03 | 0.014 | 7 | 241 | 3 |
| GO:0016197 | endosome transport  | 1.89E-03 | 0.028 | 34 | 99 | 4 |
| GO:0006790 | sulfur metabolic process  | 2.01E-03 | 0.019 | 34 | 47 | 3 |
| GO:0050678 | regulation of epithelial cell proliferation  | 2.13E-03 | 0.017 | 19 | 87 | 3 |
| GO:0050673 | epithelial cell proliferation  | 2.13E-03 | 0.017 | 19 | 87 | 3 |
| GO:0042476 | odontogenesis  | 2.31E-03 | 0.015 | 9 | 1707 | 7 |
| GO:0046486 | glycerolipid metabolic process  | 2.39E-03 | 0.01 | 7 | 1086 | 5 |
| GO:0051181 | cofactor transport  | 2.73E-03 | 0.019 | 8 | 241 | 3 |
| GO:0004896 | hematopoietin/interferon-class (D200-domain) cytokine receptor activity  | 2.80E-03 | 0.028 | 23 | 1936 | 14 |
| GO:0048511 | rhythmic process  | 2.97E-03 | 0.035 | 23 | 2720 | 17 |
| GO:0045639 | positive regulation of myeloid cell differentiation  | 3.33E-03 | 0.04 | 16 | 861 | 7 |
| GO:0004861 | cyclin-dependent protein kinase inhibitor activity  | 3.52E-03 | 0.024 | 9 | 495 | 4 |
| GO:0050663 | cytokine secretion  | 4.04E-03 | 0.035 | 12 | 177 | 3 |
| GO:0034703 | cation channel complex  | 4.07E-03 | 0.032 | 21 | 1983 | 13 |
| GO:0030324 | lung development  | 4.23E-03 | 0.048 | 20 | 514 | 6 |
| GO:0004908 | interleukin-1 receptor activity  | 4.46E-03 | 0.024 | 7 | 1936 | 6 |
| GO:0019966 | interleukin-1 binding  | 4.46E-03 | 0.028 | 7 | 1936 | 6 |
| GO:0019965 | interleukin binding  | 4.59E-03 | 0.036 | 15 | 1936 | 10 |
| GO:0004907 | interleukin receptor activity  | 4.59E-03 | 0.039 | 15 | 1936 | 10 |
| GO:0001709 | cell fate determination  | 4.70E-03 | 0.04 | 12 | 944 | 6 |
| GO:0007034 | vacuolar transport  | 4.82E-03 | 0.023 | 11 | 207 | 3 |
| GO:0006662 | glycerol ether metabolic process  | 5.47E-03 | 0.032 | 8 | 1086 | 5 |
| GO:0050918 | positive chemotaxis  | 5.49E-03 | 0.036 | 9 | 3516 | 9 |
| GO:0001763 | morphogenesis of a branching structure  | 6.18E-03 | 0.045 | 13 | 1590 | 8 |
| GO:0006720 | isoprenoid metabolic process  | 6.24E-03 | 0.037 | 12 | 683 | 5 |
| GO:0042446 | hormone biosynthetic process  | 7.14E-03 | 0.033 | 9 | 2041 | 7 |
| GO:0005112 | Notch binding  | 7.45E-03 | 0.031 | 7 | 400 | 3 |
| GO:0050927 | positive regulation of positive chemotaxis  | 9.79E-03 | 0.047 | 8 | 3516 | 8 |
| GO:0060113 | inner ear receptor cell differentiation  | 1.14E-02 | 0.038 | 8 | 400 | 3 |
| GO:0016601 | Rac protein signal transduction  | 1.25E-02 | 0.049 | 7 | 2327 | 6 |