**Supplementary Tables 2**

S-Table 2A: RNA seq pathways determined from the comparison between SD vs. SD +PFOS and clustered by DAVID.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster 1 | Enrichment Score: 1.38 | |  |  |  |  |  |
| Category | Term | Count | PValue | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_MF\_DIRECT | GO:0005516~calmodulin binding | 6 | 2E-03 | 6.34 | 4E-01 | 3E-01 | 3E-01 |
| KEGG\_PATHWAY | mmu04020:Calcium signaling pathway | 5 | 3E-02 | 4.08 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 2 | Enrichment Score: 1.09 | |  |  |  |  |  |
| KEGG\_PATHWAY | mmu04010:MAPK signaling pathway | 7 | 3E-03 | 4.66 | 4E-01 | 5E-01 | 5E-01 |
| KEGG\_PATHWAY | mmu04014:Ras signaling pathway | 3 | 3E-01 | 2.5 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 3 | Enrichment Score: 0.98 | |  |  |  |  |  |
| GOTERM\_BP\_DIRECT | GO:0035725~sodium ion transmembrane transport | 3 | 7E-02 | 7.05 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006814~sodium ion transport | 3 | 1E-01 | 4.92 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006811~ion transport | 6 | 1E-01 | 2.16 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 4 | Enrichment Score: 0.92 | |  |  |  |  |  |
| GOTERM\_MF\_DIRECT | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding | 13 | 8E-03 | 2.34 | 9E-01 | 6E-01 | 6E-01 |
| GOTERM\_MF\_DIRECT | GO:0043565~sequence-specific DNA binding | 7 | 3E-02 | 2.98 | 1E+00 | 7E-01 | 7E-01 |
| GOTERM\_MF\_DIRECT | GO:0003700~transcription factor activity, sequence-specific DNA binding | 8 | 3E-02 | 2.59 | 1E+00 | 8E-01 | 8E-01 |
| GOTERM\_MF\_DIRECT | GO:1990837~sequence-specific double-stranded DNA binding | 7 | 5E-02 | 2.68 | 1E+00 | 8E-01 | 8E-01 |
| GOTERM\_BP\_DIRECT | GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 11 | 6E-02 | 1.92 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding | 10 | 8E-02 | 1.87 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding | 6 | 1E-01 | 2.37 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0003690~double-stranded DNA binding | 3 | 2E-01 | 3.67 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006355~regulation of transcription, DNA-templated | 9 | 2E-01 | 1.55 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006366~transcription from RNA polymerase II promoter | 3 | 3E-01 | 2.69 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0003677~DNA binding | 11 | 4E-01 | 1.26 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_CC\_DIRECT | GO:0005667~transcription factor complex | 3 | 4E-01 | 2.24 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 5 | Enrichment Score: 0.85 | |  |  |  |  |  |
| GOTERM\_MF\_DIRECT | GO:0005244~voltage-gated ion channel activity | 3 | 1E-01 | 4.56 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0034765~regulation of ion transmembrane transport | 3 | 1E-01 | 4.51 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006811~ion transport | 6 | 1E-01 | 2.16 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 6 | Enrichment Score: 0.33 | |  |  |  |  |  |
| GOTERM\_BP\_DIRECT | GO:0016310~phosphorylation | 5 | 3E-01 | 1.73 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0016301~kinase activity | 5 | 4E-01 | 1.6 | 1E+00 | 1E+00 | 1E+00 |

S-Table 2B: RNA seq pathways determined from the comparison between SD vs. HFD + PFOS and clustered by DAVID .

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster 1 | Enrichment Score: 2.81 | |  |  |  |  |  |
| Category | Term | Count | PValue | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_BP\_DIRECT | GO:0030335~positive regulation of cell migration | 8 | 2E-05 | 9.38 | 1E-02 | 1E-02 | 1E-02 |
| GOTERM\_BP\_DIRECT | GO:0048843~negative regulation of axon extension involved in axon guidance | 4 | 8E-05 | 46.57 | 6E-02 | 3E-02 | 3E-02 |
| GOTERM\_BP\_DIRECT | GO:0071526~semaphorin-plexin signaling pathway | 4 | 2E-04 | 33.09 | 2E-01 | 6E-02 | 6E-02 |
| GOTERM\_BP\_DIRECT | GO:0007411~axon guidance | 6 | 3E-04 | 9.93 | 2E-01 | 6E-02 | 6E-02 |
| GOTERM\_BP\_DIRECT | GO:0007399~nervous system development | 8 | 5E-04 | 5.61 | 3E-01 | 7E-02 | 7E-02 |
| GOTERM\_BP\_DIRECT | GO:0001755~neural crest cell migration | 4 | 6E-04 | 24.18 | 4E-01 | 7E-02 | 7E-02 |
| GOTERM\_MF\_DIRECT | GO:0030215~semaphorin receptor binding | 3 | 2E-03 | 42.99 | 3E-01 | 2E-01 | 2E-01 |
| GOTERM\_MF\_DIRECT | GO:0045499~chemorepellent activity | 3 | 4E-03 | 32.61 | 5E-01 | 2E-01 | 2E-01 |
| KEGG\_PATHWAY | mmu04360:Axon guidance | 5 | 4E-03 | 7.32 | 2E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP\_DIRECT | GO:0007275~multicellular organism development | 10 | 7E-03 | 2.86 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_BP\_DIRECT | GO:0048675~axon extension | 3 | 8E-03 | 21.43 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_BP\_DIRECT | GO:0030154~cell differentiation | 8 | 6E-02 | 2.27 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0001764~neuron migration | 3 | 8E-02 | 6.08 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 2 | Enrichment Score: 1.9 | |  |  |  |  |  |
| GOTERM\_CC\_DIRECT | GO:0034663~endoplasmic reticulum chaperone complex | 3 | 6E-04 | 79.91 | 1E-01 | 1E-01 | 1E-01 |
| GOTERM\_CC\_DIRECT | GO:0042470~melanosome | 4 | 4E-03 | 12.78 | 5E-01 | 2E-01 | 2E-01 |
| GOTERM\_CC\_DIRECT | GO:0005790~smooth endoplasmic reticulum | 3 | 5E-03 | 29.06 | 5E-01 | 2E-01 | 2E-01 |
| GOTERM\_CC\_DIRECT | GO:0005788~endoplasmic reticulum lumen | 4 | 6E-03 | 10.83 | 6E-01 | 2E-01 | 2E-01 |
| KEGG\_PATHWAY | mmu04141:Protein processing in endoplasmic reticulum | 4 | 2E-02 | 6.16 | 8E-01 | 8E-01 | 8E-01 |
| GOTERM\_CC\_DIRECT | GO:0005793~endoplasmic reticulum-Golgi intermediate compartment | 3 | 3E-02 | 10.9 | 1E+00 | 5E-01 | 5E-01 |
| GOTERM\_BP\_DIRECT | GO:0034976~response to endoplasmic reticulum stress | 3 | 3E-02 | 10.48 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 3 | Enrichment Score: 1.76 | |  |  |  |  |  |
| GOTERM\_BP\_DIRECT | GO:0071805~potassium ion transmembrane transport | 4 | 7E-03 | 10.22 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_BP\_DIRECT | GO:1990573~potassium ion import across plasma membrane | 3 | 8E-03 | 21.43 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_BP\_DIRECT | GO:0006813~potassium ion transport | 4 | 9E-03 | 9.18 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_MF\_DIRECT | GO:0005244~voltage-gated ion channel activity | 4 | 9E-03 | 9.07 | 8E-01 | 4E-01 | 4E-01 |
| GOTERM\_BP\_DIRECT | GO:0034765~regulation of ion transmembrane transport | 4 | 1E-02 | 8.73 | 1E+00 | 6E-01 | 6E-01 |
| GOTERM\_MF\_DIRECT | GO:0005267~potassium channel activity | 3 | 3E-02 | 11.53 | 1E+00 | 9E-01 | 9E-01 |
| GOTERM\_BP\_DIRECT | GO:0055085~transmembrane transport | 5 | 5E-02 | 3.47 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006811~ion transport | 5 | 1E-01 | 2.62 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 4 | Enrichment Score: 0.59 | |  |  |  |  |  |
| KEGG\_PATHWAY | mmu04151:PI3K-Akt signaling pathway | 4 | 1E-01 | 2.95 | 1E+00 | 1E+00 | 1E+00 |
| KEGG\_PATHWAY | mmu04014:Ras signaling pathway | 3 | 2E-01 | 3.38 | 1E+00 | 1E+00 | 1E+00 |
| KEGG\_PATHWAY | mmu04010:MAPK signaling pathway | 3 | 3E-01 | 2.7 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 5 | Enrichment Score: 0.54 | |  |  |  |  |  |
| GOTERM\_MF\_DIRECT | GO:0004712~protein serine/threonine/tyrosine kinase activity | 4 | 2E-01 | 2.82 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0005524~ATP binding | 8 | 2E-01 | 1.65 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0004672~protein kinase activity | 4 | 2E-01 | 2.43 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0016310~phosphorylation | 4 | 3E-01 | 2.01 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0006468~protein phosphorylation | 4 | 3E-01 | 1.93 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_MF\_DIRECT | GO:0016301~kinase activity | 4 | 3E-01 | 1.91 | 1E+00 | 1E+00 | 1E+00 |
| Cluster 6 | Enrichment Score: 0.16 | |  |  |  |  |  |
| GOTERM\_MF\_DIRECT | GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding | 3 | 5E-01 | 1.77 | 1E+00 | 1E+00 | 1E+00 |