Supplementary Tables 3

Table 3A: Differential expression proteins from Olink analysis

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| SD vs. SD + PFOS |  |  |  |  |
| Proteins | t.stat | p.value | -log10(p) | FDR |
| Ntf3 | -4.25 | 1.70E-03 | 2.77 | 1.56E-01 |
| Il17f | -2.76 | 2.01E-02 | 1.70 | 4.38E-01 |
| Il5 | -2.69 | 2.28E-02 | 1.64 | 4.38E-01 |
| Mia | -2.68 | 2.32E-02 | 1.63 | 4.38E-01 |
| Lpl | -2.66 | 2.38E-02 | 1.62 | 4.38E-01 |
| SD vs. HFD + PFOS |  |  |  |  |
| Ntf3 | -5.74 | 5.07E-05 | 4.29 | 4.67E-03 |
| Ccl3 | -3.87 | 1.69E-03 | 2.77 | 7.75E-02 |
| Matn2 | -3.40 | 4.35E-03 | 2.36 | 1.33E-01 |
| Rgma | -3.05 | 8.59E-03 | 2.07 | 1.35E-01 |
| Plxna4 | -3.03 | 8.95E-03 | 2.05 | 1.35E-01 |
| Fas | -3.03 | 9.02E-03 | 2.04 | 1.35E-01 |
| Gfra1 | -2.96 | 1.03E-02 | 1.99 | 1.35E-01 |
| Cxcl1 | -2.59 | 2.16E-02 | 1.67 | 2.24E-01 |
| Ccl2 | -2.58 | 2.19E-02 | 1.66 | 2.24E-01 |
| Pdgfb | -2.51 | 2.50E-02 | 1.60 | 2.30E-01 |
| Erbb4 | -2.39 | 3.16E-02 | 1.50 | 2.62E-01 |
| Ppp1r2 | -2.35 | 3.42E-02 | 1.47 | 2.62E-01 |
| Tnfrsf11b | 2.24 | 4.22E-02 | 1.38 | 2.93E-01 |
| Lpl | -2.21 | 4.46E-02 | 1.35 | 2.93E-01 |
| SD vs. HFD |  |  |  |  |
| Fli1 | 3.36 | 3.98E-03 | 2.40 | 1.96E-01 |
| Dlk1 | -3.33 | 4.27E-03 | 2.37 | 1.96E-01 |
| Wisp1 | 3.06 | 7.51E-03 | 2.12 | 2.30E-01 |
| Ccl5 | -2.60 | 1.95E-02 | 1.71 | 3.88E-01 |
| Il17a | -2.55 | 2.15E-02 | 1.67 | 3.88E-01 |
| Lpl | -2.47 | 2.53E-02 | 1.60 | 3.88E-01 |
| Rgma | -2.26 | 3.79E-02 | 1.42 | 4.60E-01 |
| Gcg | -2.21 | 4.17E-02 | 1.38 | 4.60E-01 |
| Il23r | -2.17 | 4.58E-02 | 1.34 | 4.60E-01 |
| Csf2 | -2.12 | 5.00E-02 | 1.30 | 4.60E-01 |
| HFD vs. HFD + PFOS |  |  |  |  |
| Il23r | 3.51 | 2.91E-03 | 2.54 | 2.68E-01 |
| Csf2 | 2.82 | 1.23E-02 | 1.91 | 3.90E-01 |
| Clmp | -2.55 | 2.12E-02 | 1.67 | 3.90E-01 |
| Matn2 | -2.49 | 2.44E-02 | 1.61 | 3.90E-01 |
| Vsig2 | 2.36 | 3.13E-02 | 1.51 | 3.90E-01 |
| Fas | -2.35 | 3.21E-02 | 1.49 | 3.90E-01 |
| Wisp1 | -2.22 | 4.16E-02 | 1.38 | 3.90E-01 |
| Plxna4 | -2.21 | 4.19E-02 | 1.38 | 3.90E-01 |
| Igsf3 | -2.18 | 4.41E-02 | 1.36 | 3.90E-01 |

Table 3B : Pathways determined from DEPs of OLINK analysis of SD\_PFOS comparison.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GOTERM\_BP | |  |  |  |  | |  |  |
| Category | Term | Count | PValue | Fold Enrichment | | Bonferroni | Benjamini | FDR |
| GOTERM\_BP\_DIRECT | GO:0032755~positive regulation of interleukin-6 production | 2 | 0.02 | 72.50 | | 0.88 | 1.00 | 1.00 |
| GOTERM\_BP\_DIRECT | GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation | 2 | 0.02 | 69.38 | | 0.89 | 1.00 | 1.00 |
| GOTERM\_BP\_DIRECT | GO:0006954~inflammatory response | 2 | 0.08 | 20.07 | | 1.00 | 1.00 | 1.00 |
| KEGG\_PATHWAY | |  |  |  | |  |  |  |
| KEGG\_PATHWAY | mmu05321:Inflammatory bowel disease | 2 | 0.02 | 72.67 | | 0.37 | 0.34 | 0.34 |
| KEGG\_PATHWAY | mmu04657:IL-17 signaling pathway | 2 | 0.03 | 48.45 | | 0.50 | 0.34 | 0.34 |
| KEGG\_PATHWAY | mmu04060:Cytokine-cytokine receptor interaction | 2 | 0.09 | 15.43 | | 0.89 | 0.69 | 0.69 |

Table 3C: Pathways determined from DEPs of OLINK analysis of SD\_HFD+PFOS comparison.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Annotation Cluster 1 | Enrichment Score: 2.744168522437947 | | | |  | |  | |  | |  | |
| Category | Term | Count | PValue | Fold Enrichment | | Bonferroni | | Benjamini | | FDR | |
| GOTERM\_BP\_DIRECT | GO:0002548~monocyte chemotaxis | 3 | 3E-04 | 1E+02 | | 1E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0070374~positive regulation of ERK1 and ERK2 cascade | 4 | 4E-04 | 2E+01 | | 1E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0010628~positive regulation of gene expression | 3 | 6E-02 | 7E+00 | | 1E+00 | | 5E-01 | | 5E-01 | |
| Annotation Cluster 2 | Enrichment Score: 2.6013773518144854 | | | |  | |  | |  | |  | |
| GOTERM\_BP\_DIRECT | GO:0070374~positive regulation of ERK1 and ERK2 cascade | 4 | 4E-04 | 2E+01 | | 1E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0030335~positive regulation of cell migration | 4 | 6E-04 | 2E+01 | | 2E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0006468~protein phosphorylation | 3 | 6E-02 | 7E+00 | | 1E+00 | | 5E-01 | | 5E-01 | |
| Annotation Cluster 3 | Enrichment Score: 2.4303989308198437 | | | |  | |  | |  | |  | |
| KEGG\_PATHWAY | mmu04060:Cytokine-cytokine receptor interaction | 5 | 2E-04 | 1E+01 | | 1E-02 | | 1E-02 | | 1E-02 | |
| GOTERM\_BP\_DIRECT | GO:0070098~chemokine-mediated signaling pathway | 3 | 5E-04 | 8E+01 | | 2E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0030593~neutrophil chemotaxis | 3 | 1E-03 | 5E+01 | | 4E-01 | | 1E-01 | | 1E-01 | |
| KEGG\_PATHWAY | mmu05417:Lipid and atherosclerosis | 4 | 1E-03 | 2E+01 | | 1E-01 | | 5E-02 | | 5E-02 | |
| GOTERM\_BP\_DIRECT | GO:0006935~chemotaxis | 3 | 3E-03 | 3E+01 | | 7E-01 | | 1E-01 | | 1E-01 | |
| KEGG\_PATHWAY | mmu05323:Rheumatoid arthritis | 3 | 4E-03 | 3E+01 | | 2E-01 | | 6E-02 | | 6E-02 | |
| GOTERM\_BP\_DIRECT | GO:0006955~immune response | 4 | 4E-03 | 1E+01 | | 8E-01 | | 1E-01 | | 1E-01 | |
| KEGG\_PATHWAY | mmu04061:Viral protein interaction with cytokine and cytokine receptor | 3 | 5E-03 | 3E+01 | | 3E-01 | | 6E-02 | | 6E-02 | |
| KEGG\_PATHWAY | mmu05142:Chagas disease | 3 | 5E-03 | 2E+01 | | 3E-01 | | 6E-02 | | 6E-02 | |
| KEGG\_PATHWAY | mmu04668:TNF signaling pathway | 3 | 7E-03 | 2E+01 | | 4E-01 | | 7E-02 | | 6E-02 | |
| KEGG\_PATHWAY | mmu04062:Chemokine signaling pathway | 3 | 2E-02 | 1E+01 | | 7E-01 | | 2E-01 | | 1E-01 | |
| GOTERM\_BP\_DIRECT | GO:0006954~inflammatory response | 3 | 3E-02 | 1E+01 | | 1E+00 | | 3E-01 | | 3E-01 | |
| KEGG\_PATHWAY | mmu05163:Human cytomegalovirus infection | 3 | 3E-02 | 1E+01 | | 9E-01 | | 2E-01 | | 2E-01 | |
| Annotation Cluster 4 | Enrichment Score: 2.0308520590107917 | | | |  | |  | |  | |  | |
| GOTERM\_BP\_DIRECT | GO:0030335~positive regulation of cell migration | 4 | 6E-04 | 2E+01 | | 2E-01 | | 6E-02 | | 6E-02 | |
| KEGG\_PATHWAY | mmu04010:MAPK signaling pathway | 4 | 3E-03 | 1E+01 | | 2E-01 | | 6E-02 | | 6E-02 | |
| KEGG\_PATHWAY | mmu04151:PI3K-Akt signaling pathway | 3 | 6E-02 | 7E+00 | | 1E+00 | | 4E-01 | | 3E-01 | |
| GOTERM\_BP\_DIRECT | GO:0008284~positive regulation of cell proliferation | 3 | 6E-02 | 7E+00 | | 1E+00 | | 5E-01 | | 5E-01 | |

Table 3D: Pathways determined from DEPs of OLINK analysis of SD\_HFD comparison.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GOTERM\_BP |  |  |  |  |  |  |  |
| Category | Term | Count | PValue | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_BP | GO:0045672~positive regulation of osteoclast differentiation | 3 | 8E-05 | 2E+02 | 2E-02 | 2E-02 | 2E-02 |
| GOTERM\_BP | GO:0032747~positive regulation of interleukin-23 production | 2 | 3E-03 | 6E+02 | 4E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:2000343~positive regulation of chemokine (C-X-C motif) ligand 2 production | 2 | 6E-03 | 3E+02 | 7E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0010744~positive regulation of macrophage derived foam cell differentiation | 2 | 6E-03 | 3E+02 | 7E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0006954~inflammatory response | 3 | 1E-02 | 2E+01 | 9E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0002230~positive regulation of defense response to virus by host | 2 | 1E-02 | 1E+02 | 9E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0034341~response to interferon-gamma | 2 | 1E-02 | 1E+02 | 9E-01 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0007259~JAK-STAT cascade | 2 | 2E-02 | 1E+02 | 1E+00 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0050796~regulation of insulin secretion | 2 | 2E-02 | 1E+02 | 1E+00 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0006955~immune response | 3 | 2E-02 | 1E+01 | 1E+00 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0032735~positive regulation of interleukin-12 production | 2 | 2E-02 | 1E+02 | 1E+00 | 3E-01 | 3E-01 |
| GOTERM\_BP | GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein | 2 | 2E-02 | 8E+01 | 1E+00 | 4E-01 | 4E-01 |
| GOTERM\_BP | GO:0032731~positive regulation of interleukin-1 beta production | 2 | 3E-02 | 6E+01 | 1E+00 | 4E-01 | 4E-01 |
| GOTERM\_BP | GO:0042102~positive regulation of T cell proliferation | 2 | 3E-02 | 6E+01 | 1E+00 | 4E-01 | 4E-01 |
| GOTERM\_BP | GO:0071347~cellular response to interleukin-1 | 2 | 3E-02 | 5E+01 | 1E+00 | 4E-01 | 4E-01 |
| GOTERM\_BP | GO:0032755~positive regulation of interleukin-6 production | 2 | 4E-02 | 4E+01 | 1E+00 | 5E-01 | 5E-01 |
| GOTERM\_BP | GO:0032760~positive regulation of tumor necrosis factor production | 2 | 4E-02 | 4E+01 | 1E+00 | 5E-01 | 5E-01 |
| GOTERM\_BP | GO:0043547~positive regulation of GTPase activity | 2 | 7E-02 | 2E+01 | 1E+00 | 8E-01 | 8E-01 |
| GOTERM\_BP | GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 3 | 8E-02 | 5E+00 | 1E+00 | 9E-01 | 9E-01 |
| GOTERM\_BP | GO:0070374~positive regulation of ERK1 and ERK2 cascade | 2 | 9E-02 | 2E+01 | 1E+00 | 9E-01 | 9E-01 |
| KEGG\_PATHWAY |  |  |  |  |  |  |  |
| KEGG\_PATHWAY | mmu04060:Cytokine-cytokine receptor interaction | 4 | 1E-03 | 2E+01 | 4E-02 | 4E-02 | 4E-02 |
| KEGG\_PATHWAY | mmu05323:Rheumatoid arthritis | 3 | 2E-03 | 4E+01 | 7E-02 | 4E-02 | 4E-02 |
| KEGG\_PATHWAY | mmu05321:Inflammatory bowel disease | 2 | 5E-02 | 4E+01 | 9E-01 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu04657:IL-17 signaling pathway | 2 | 7E-02 | 2E+01 | 9E-01 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu04659:Th17 cell differentiation | 2 | 8E-02 | 2E+01 | 1E+00 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu04668:TNF signaling pathway | 2 | 8E-02 | 2E+01 | 1E+00 | 6E-01 | 6E-01 |

Table 3E: Pathways determined from DEPs of OLINK analysis of HFD\_HFDPFOS comparison.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GOTERM\_BP | |  |  |  |  |  |  |  |
| Category | Term | Count | PValue | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_BP\_DIRECT | GO:0031104~dendrite regeneration | 2 | 9E-04 | 20119 | 2E+03 | 1E-01 | 1E-01 | 1E-01 |
| GOTERM\_BP\_DIRECT | GO:0006955~immune response | 3 | 9E-03 | 20119 | 2E+01 | 7E-01 | 5E-01 | 5E-01 |
| GOTERM\_BP\_DIRECT | GO:0007259~JAK-STAT cascade | 2 | 1E-02 | 20119 | 1E+02 | 8E-01 | 5E-01 | 5E-01 |
| GOTERM\_BP\_DIRECT | GO:0007411~axon guidance | 2 | 6E-02 | 20119 | 3E+01 | 1E+00 | 1E+00 | 1E+00 |
| GOTERM\_BP\_DIRECT | GO:0042127~regulation of cell proliferation | 2 | 6E-02 | 20119 | 3E+01 | 1E+00 | 1E+00 | 1E+00 |
| KEGG\_PATHWAY | |  |  |  |  |  |  |  |
| KEGG\_PATHWAY | mmu04060:Cytokine-cytokine receptor interaction | 3 | 3E-03 | 9011 | 2E+01 | 1E-01 | 1E-01 | 1E-01 |
| KEGG\_PATHWAY | mmu04668:TNF signaling pathway | 2 | 4E-02 | 9011 | 4E+01 | 8E-01 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu04650:Natural killer cell mediated cytotoxicity | 2 | 4E-02 | 9011 | 4E+01 | 8E-01 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu04630:JAK-STAT signaling pathway | 2 | 6E-02 | 9011 | 3E+01 | 9E-01 | 6E-01 | 6E-01 |
| KEGG\_PATHWAY | mmu05167:Kaposi sarcoma-associated herpesvirus infection | 2 | 7E-02 | 9011 | 2E+01 | 1E+00 | 7E-01 | 7E-01 |