|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| ID | Name | Observed gene count | Background gene count | Strength | FDR |
| GO:0007399 | Nervous system development | 28 | 2358 | 0.41 | 0.0137 |
| GO:0007610 | Behavior | 14 | 680 | 0.65 | 0.0137 |
| GO:0009987 | Cellular process | 83 | 13330 | 0.13 | 0.0137 |
| GO:0022008 | Neurogenesis | 24 | 1784 | 0.46 | 0.0137 |
| GO:0048699 | Generation of neurons | 23 | 1660 | 0.48 | 0.0137 |
| GO:0050794 | Regulation of cellular process | 67 | 9541 | 0.18 | 0.0137 |
| GO:0050804 | Modulation of chemical synaptic transmission | 13 | 521 | 0.73 | 0.0137 |
| GO:0065007 | Biological regulation | 72 | 10591 | 0.17 | 0.0137 |
| GO:0065009 | Regulation of molecular function | 40 | 4379 | 0.3 | 0.0137 |
| GO:0098693 | Regulation of synaptic vesicle cycle | 7 | 150 | 1 | 0.0137 |
| GO:0007611 | Learning or memory | 9 | 304 | 0.81 | 0.0156 |
| GO:0045664 | Regulation of neuron differentiation | 14 | 774 | 0.59 | 0.0156 |
| GO:0099536 | Synaptic signaling | 10 | 390 | 0.74 | 0.0156 |
| GO:0007612 | Learning | 7 | 173 | 0.94 | 0.0173 |
| GO:0010975 | Regulation of neuron projection development | 12 | 607 | 0.63 | 0.0212 |
| GO:0007268 | Chemical synaptic transmission | 9 | 335 | 0.76 | 0.0213 |
| GO:0017157 | Regulation of exocytosis | 8 | 255 | 0.83 | 0.0213 |
| GO:0048731 | System development | 38 | 4350 | 0.28 | 0.0213 |
| GO:0050767 | Regulation of neurogenesis | 15 | 948 | 0.53 | 0.0213 |
| GO:0051960 | Regulation of nervous system development | 16 | 1071 | 0.51 | 0.0213 |
| GO:0060284 | Regulation of cell development | 16 | 1086 | 0.5 | 0.0219 |
| GO:0032501 | Multicellular organismal process | 48 | 6272 | 0.22 | 0.0256 |
| GO:0017156 | Calcium-ion regulated exocytosis | 4 | 45 | 1.28 | 0.0329 |
| GO:0065008 | Regulation of biological quality | 34 | 3822 | 0.28 | 0.0329 |
| GO:1901214 | Regulation of neuron death | 9 | 375 | 0.71 | 0.0329 |
| GO:0048167 | Regulation of synaptic plasticity | 7 | 221 | 0.84 | 0.0374 |
| GO:0060627 | Regulation of vesicle-mediated transport | 11 | 600 | 0.6 | 0.0476 |
| GO:1903530 | Regulation of secretion by cell | 12 | 713 | 0.56 | 0.0493 |

Supplementary Tables 1

S-Table 1A Biological Process (Gene Ontology) RNA seq pathways determined from the comparison between SD vs. SD +\_PFOS by String software.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| ID | term description | Observed gene count | Background gene count | Strength | FDR |
| GO:0043005 | Neuron projection | 26 | 1583 | 0.55 | 1.95E-05 |
| GO:0036477 | Somatodendritic compartment | 20 | 1080 | 0.6 | 0.0001 |
| GO:0043025 | Neuronal cell body | 16 | 743 | 0.67 | 0.00017 |
| GO:0045202 | Synapse | 23 | 1492 | 0.52 | 0.00017 |
| GO:0042995 | Cell projection | 30 | 2472 | 0.42 | 0.00018 |
| GO:0120025 | Plasma membrane bounded cell projection | 29 | 2387 | 0.42 | 0.00024 |
| GO:0030054 | Cell junction | 26 | 2050 | 0.44 | 0.00041 |
| GO:0030425 | Dendrite | 14 | 753 | 0.6 | 0.0021 |
| GO:0097060 | Synaptic membrane | 11 | 464 | 0.71 | 0.0021 |
| GO:0043204 | Perikaryon | 7 | 208 | 0.86 | 0.0088 |
| GO:0030424 | Axon | 13 | 791 | 0.55 | 0.0107 |
| GO:0098793 | Presynapse | 11 | 636 | 0.57 | 0.0236 |
| GO:0098794 | Postsynapse | 12 | 761 | 0.53 | 0.0258 |
| GO:0098590 | Plasma membrane region | 16 | 1310 | 0.42 | 0.0379 |

S-Table 1B: RNA seq pathways Cellular Component (Gene Ontology)determined from the comparison between SD vs. SD +\_PFOS by String software.

S-Table 1C: RNA seq pathways Cellular Component (Gene Ontology) determined from the comparison between SD vs. SD +\_HFD+PFOS by String software.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| #term ID | term description | observed gene count | background gene count | strength | false discovery rate |
| GO:0042995 | Cell projection | 24 | 2723 | 0.48 | 0.00068 |
| GO:0120025 | Plasma membrane bounded cell projection | 23 | 2622 | 0.48 | 0.00073 |
| GO:0034663 | Endoplasmic reticulum chaperone complex | 3 | 12 | 1.93 | 0.0072 |
| GO:0043005 | Neuron projection | 16 | 1721 | 0.5 | 0.0147 |
| GO:0005737 | Cytoplasm | 50 | 11788 | 0.16 | 0.0214 |
| GO:0030054 | Cell junction | 18 | 2232 | 0.44 | 0.0214 |
| GO:0097449 | Astrocyte projection | 3 | 22 | 1.67 | 0.0214 |

S-Table 1D: Biological Process (Gene Ontology) determined from the comparison between SD vs. SD +\_HFD+PFOS by String software.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| #term ID | term description | | observed gene count | background gene count | strength | false discovery rate |
| GO:0032501 | | Multicellular organismal process | 41 | 6272 | 0.35 | 3.18E-05 |
| GO:0050794 | | Regulation of cellular process | 51 | 9541 | 0.27 | 3.18E-05 |
| GO:0065007 | | Biological regulation | 53 | 10591 | 0.24 | 3.18E-05 |
| GO:0065008 | | Regulation of biological quality | 32 | 3822 | 0.46 | 3.18E-05 |
| GO:0010769 | | Regulation of cell morphogenesis involved in differentiation | 10 | 343 | 1 | 0.00014 |
| GO:0030154 | | Cell differentiation | 29 | 3674 | 0.43 | 0.00016 |
| GO:0031175 | | Neuron projection development | 13 | 697 | 0.81 | 0.00016 |
| GO:0032879 | | Regulation of localization | 25 | 2806 | 0.49 | 0.00016 |
| GO:0007399 | | Nervous system development | 22 | 2358 | 0.51 | 0.00048 |
| GO:0022008 | | Neurogenesis | 19 | 1784 | 0.56 | 0.00048 |
| GO:0022603 | | Regulation of anatomical structure morphogenesis | 15 | 1090 | 0.68 | 0.00048 |
| GO:0030335 | | Positive regulation of cell migration | 11 | 567 | 0.82 | 0.00069 |
| GO:0000902 | | Cell morphogenesis | 12 | 739 | 0.75 | 0.001 |
| GO:0009987 | | Cellular process | 56 | 13330 | 0.16 | 0.001 |
| GO:0030182 | | Neuron differentiation | 14 | 1056 | 0.66 | 0.001 |
| GO:0048468 | | Cell development | 18 | 1730 | 0.55 | 0.001 |
| GO:0048812 | | Neuron projection morphogenesis | 10 | 479 | 0.86 | 0.001 |
| GO:0048843 | | Negative regulation of axon extension involved in axon guidance | 4 | 27 | 1.71 | 0.001 |
| GO:0050771 | | Negative regulation of axonogenesis | 5 | 67 | 1.41 | 0.001 |
| GO:0051239 | | Regulation of multicellular organismal process | 25 | 3205 | 0.43 | 0.001 |
| GO:0061564 | | Axon development | 9 | 386 | 0.9 | 0.001 |
| GO:0120036 | | Plasma membrane bounded cell projection organization | 14 | 1072 | 0.65 | 0.001 |
| GO:0048522 | | Positive regulation of cellular process | 33 | 5407 | 0.32 | 0.0011 |
| GO:0120035 | | Regulation of plasma membrane bounded cell projection organization | 12 | 788 | 0.72 | 0.0011 |
| GO:0048699 | | Generation of neurons | 17 | 1660 | 0.55 | 0.0012 |
| GO:0048731 | | System development | 29 | 4350 | 0.36 | 0.0012 |
| GO:0007275 | | Multicellular organism development | 31 | 4921 | 0.34 | 0.0013 |
| GO:0007610 | | Behavior | 11 | 680 | 0.75 | 0.0013 |
| GO:0000904 | | Cell morphogenesis involved in differentiation | 10 | 575 | 0.78 | 0.0019 |
| GO:0048518 | | Positive regulation of biological process | 34 | 5869 | 0.3 | 0.0019 |
| GO:0050890 | | Cognition | 8 | 339 | 0.91 | 0.002 |
| GO:0071526 | | Semaphorin-plexin signaling pathway | 4 | 39 | 1.55 | 0.002 |
| GO:0006928 | | Movement of cell or subcellular component | 15 | 1382 | 0.57 | 0.0022 |
| GO:0060548 | | Negative regulation of cell death | 13 | 1046 | 0.63 | 0.0023 |
| GO:0007409 | | Axonogenesis | 8 | 351 | 0.89 | 0.0024 |
| GO:0010975 | | Regulation of neuron projection development | 10 | 607 | 0.75 | 0.0027 |
| GO:0030334 | | Regulation of cell migration | 12 | 915 | 0.65 | 0.0029 |
| GO:0007612 | | Learning | 6 | 173 | 1.08 | 0.0031 |
| GO:0008038 | | Neuron recognition | 4 | 51 | 1.43 | 0.0043 |
| GO:0010770 | | Positive regulation of cell morphogenesis involved in differentiation | 6 | 189 | 1.04 | 0.0045 |
| GO:0042221 | | Response to chemical | 25 | 3720 | 0.36 | 0.0045 |
| GO:0030516 | | Regulation of axon extension | 5 | 112 | 1.19 | 0.0047 |
| GO:0032502 | | Developmental process | 32 | 5629 | 0.29 | 0.0049 |
| GO:0007417 | | Central nervous system development | 12 | 984 | 0.62 | 0.005 |
| GO:0035272 | | Exocrine system development | 4 | 56 | 1.39 | 0.0055 |
| GO:0007611 | | Learning or memory | 7 | 304 | 0.9 | 0.0061 |
| GO:0050770 | | Regulation of axonogenesis | 6 | 203 | 1.01 | 0.0061 |
| GO:0008361 | | Regulation of cell size | 6 | 212 | 0.99 | 0.0073 |
| GO:0051179 | | Localization | 28 | 4646 | 0.32 | 0.0073 |
| GO:0048523 | | Negative regulation of cellular process | 28 | 4672 | 0.31 | 0.0077 |
| GO:0008037 | | Cell recognition | 5 | 131 | 1.12 | 0.0079 |
| GO:0051129 | | Negative regulation of cellular component organization | 10 | 733 | 0.67 | 0.0085 |
| GO:0050877 | | Nervous system process | 12 | 1066 | 0.59 | 0.0088 |
| GO:0043066 | | Negative regulation of apoptotic process | 11 | 913 | 0.62 | 0.0102 |
| GO:0060284 | | Regulation of cell development | 12 | 1086 | 0.58 | 0.0102 |
| GO:0007411 | | Axon guidance | 6 | 234 | 0.95 | 0.0107 |
| GO:0007420 | | Brain development | 10 | 759 | 0.66 | 0.0107 |
| GO:0010941 | | Regulation of cell death | 15 | 1661 | 0.49 | 0.0107 |
| GO:0045595 | | Regulation of cell differentiation | 16 | 1868 | 0.47 | 0.0107 |
| GO:0042981 | | Regulation of apoptotic process | 14 | 1486 | 0.51 | 0.0117 |
| GO:0048519 | | Negative regulation of biological process | 29 | 5108 | 0.29 | 0.0118 |
| GO:0050896 | | Response to stimulus | 35 | 6908 | 0.24 | 0.0134 |
| GO:2000026 | | Regulation of multicellular organismal development | 17 | 2150 | 0.44 | 0.0145 |
| GO:0051094 | | Positive regulation of developmental process | 14 | 1533 | 0.5 | 0.0153 |
| GO:0010720 | | Positive regulation of cell development | 9 | 661 | 0.67 | 0.0172 |
| GO:0040011 | | Locomotion | 12 | 1183 | 0.54 | 0.0187 |
| GO:0048638 | | Regulation of developmental growth | 7 | 388 | 0.79 | 0.0187 |
| GO:0050804 | | Modulation of chemical synaptic transmission | 8 | 521 | 0.72 | 0.0187 |
| GO:0050793 | | Regulation of developmental process | 19 | 2669 | 0.39 | 0.0188 |
| GO:0051128 | | Regulation of cellular component organization | 18 | 2438 | 0.41 | 0.0188 |
| GO:0003008 | | System process | 14 | 1578 | 0.49 | 0.0189 |
| GO:0016477 | | Cell migration | 10 | 845 | 0.61 | 0.0202 |
| GO:0030534 | | Adult behavior | 5 | 174 | 1 | 0.0211 |
| GO:0032535 | | Regulation of cellular component size | 7 | 402 | 0.78 | 0.0217 |
| GO:0048675 | | Axon extension | 3 | 35 | 1.47 | 0.0221 |
| GO:0021954 | | Central nervous system neuron development | 4 | 94 | 1.17 | 0.0224 |
| GO:0040008 | | Regulation of growth | 9 | 701 | 0.65 | 0.0232 |
| GO:0030155 | | Regulation of cell adhesion | 9 | 705 | 0.64 | 0.0239 |
| GO:0045766 | | Positive regulation of angiogenesis | 5 | 181 | 0.98 | 0.0239 |
| GO:0048513 | | Animal organ development | 21 | 3230 | 0.35 | 0.0241 |
| GO:0098739 | | Import across plasma membrane | 4 | 102 | 1.13 | 0.029 |
| GO:0001558 | | Regulation of cell growth | 7 | 429 | 0.75 | 0.0294 |
| GO:1900026 | | Positive regulation of substrate adhesion-dependent cell spreading | 3 | 40 | 1.41 | 0.0295 |
| GO:0045927 | | Positive regulation of growth | 6 | 304 | 0.83 | 0.0304 |
| GO:1990573 | | Potassium ion import across plasma membrane | 3 | 41 | 1.4 | 0.031 |
| GO:0008306 | | Associative learning | 4 | 106 | 1.11 | 0.032 |
| GO:0015800 | | Acidic amino acid transport | 3 | 42 | 1.39 | 0.032 |
| GO:0030900 | | Forebrain development | 7 | 438 | 0.74 | 0.032 |
| GO:0032808 | | Lacrimal gland development | 2 | 7 | 1.99 | 0.032 |
| GO:0048842 | | Positive regulation of axon extension involved in axon guidance | 2 | 7 | 1.99 | 0.032 |
| GO:0034109 | | Homotypic cell-cell adhesion | 3 | 43 | 1.38 | 0.0335 |
| GO:0045765 | | Regulation of angiogenesis | 6 | 313 | 0.82 | 0.0335 |
| GO:0014070 | | Response to organic cyclic compound | 10 | 930 | 0.57 | 0.0354 |
| GO:0071840 | | Cellular component organization or biogenesis | 27 | 4954 | 0.27 | 0.0354 |
| GO:0098712 | | L-glutamate import across plasma membrane | 2 | 8 | 1.94 | 0.0368 |
| GO:0098915 | | Membrane repolarization during ventricular cardiac muscle cell action potential | 2 | 8 | 1.94 | 0.0368 |
| GO:0048589 | | Developmental growth | 7 | 458 | 0.72 | 0.0378 |
| GO:0048639 | | Positive regulation of developmental growth | 5 | 214 | 0.91 | 0.0412 |
| GO:0050768 | | Negative regulation of neurogenesis | 6 | 336 | 0.79 | 0.0431 |
| GO:0031346 | | Positive regulation of cell projection organization | 7 | 474 | 0.71 | 0.0436 |
| GO:0016043 | | Cellular component organization | 26 | 4769 | 0.27 | 0.0443 |
| GO:0061013 | | Regulation of mRNA catabolic process | 4 | 122 | 1.05 | 0.0443 |
| GO:0055067 | | Monovalent inorganic cation homeostasis | 4 | 125 | 1.04 | 0.048 |
| GO:0030168 | | Platelet activation | 3 | 52 | 1.3 | 0.0484 |
| GO:0050920 | | Regulation of chemotaxis | 5 | 226 | 0.88 | 0.0484 |
| GO:0061077 | | Chaperone-mediated protein folding | 3 | 52 | 1.3 | 0.0484 |
| GO:0010646 | | Regulation of cell communication | 20 | 3215 | 0.33 | 0.049 |