Down-regulated genes overlapped with De-Rubeis et al. (FDR<0.1)

## Network Stats

number of nodes:
8
number of edges:
2
average node degree:
0.5
avg. local clustering coefficient:
0.5
expected number of edges:
0
PPI enrichment $p$-value:
0.0263

## Functional enrichments in your network

| Biological Process (GO) |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0008306 |
| associative learning |
| 3 |
| 0.0295 |

Down-regulated genes overlapped with De-Rubeis et al. (FDR<0.3)

## Network Stats

number of nodes:
17
number of edges:
5
average node degree:
0.588
avg. local clustering coefficient:
0.412
expected number of edges:
1
PPI enrichment $p$-value:
0.00647

| pathway ID |
| :---: |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0007399 |
| nervous system development |
| 9 |
| 0.0132 |
| GO:0048731 |
| system development |
| 11 |
| 0.0206 |
| GO:0007275 |
| multicellular organismal development |
| 11 |
| 0.0231 |
| GO:0022603 |
| regulation of anatomical structure morphogenesis |
| 6 |
| 0.0231 |
| GO:0022604 |
| regulation of cell morphogenesis |
| 5 |
| 0.0231 |
| GO:0030182 |
| neuron differentiation |
| 6 |
| 0.0231 |
| GO:0048699 |
| generation of neurons |
| 7 |
| 0.0231 |
| GO:0031175 |
| neuron projection development |
| 5 |
| 0.0232 |
| GO:0008306 |
| associative learning |
| 3 |
| 0.0318 |
| GO:0007409 |
| axonogenesis |
| 4 |
| 0.0354 |
| GO:0061564 |

axon development

| 4 |
| :---: |
| 0.0416 |
| GO:0007420 |
| brain development |
| 5 |
| 0.05 |
| GO:0010975 |
| regulation of neuron projection development |
| 4 |
| 0.05 |
| GO:0016043 |
| cellular component organization |
| 10 |
| 0.05 |
| GO:0030154 |
| cell differentiation |
| 9 |
| 0.05 |
| GO:0048666 |
| neuron development |
| 5 |
| 0.05 |
| GO:0048667 |
| cell morphogenesis involved in neuron differentiation |
| 4 |
| 0.05 |
| GO:0060322 |
| head development |
| 5 |
| 0.05 |

Down-regulated genes overlapped with SFARI-GENE dataset

## Network Stats

number of nodes:
125
number of edges:
176
average node degree:
2.82
avg. local clustering coefficient:
0.336
expected number of edges:

PPI enrichment p-value:

| unctional enrichments in your network |
| :---: |
| Biological Process (GO) |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0007399 |
| nervous system development |
| 44 |
| $5.84 \mathrm{E}-15$ |
| GO:0007610 |
| behavior |
| 25 |
| 2.14E-13 |
| GO:0044700 |
| single organism signaling |
| 56 |
| $6.24 \mathrm{E}-13$ |
| GO:0050794 |
| regulation of cellular process |
| 84 |
| $1.24 \mathrm{E}-12$ |
| GO:0007154 |
| cell communication |
| 56 |
| 1.99E-12 |
| GO:0022008 |
| neurogenesis |
| 34 |
| 2.99E-12 |
| GO:0044708 |
| single-organism behavior |
| 21 |
| 4.09E-12 |
| GO:0065007 |
| biological regulation |
| 87 |
| $4.74 \mathrm{E}-12$ |
| GO:0007268 |
| synaptic transmission |
| 19 |


| 5.03E-12 |
| :---: |
| GO:0044707 |
| single-multicellular organism process |
| 64 |
| $1.59 \mathrm{E}-11$ |
| GO:0050789 |
| regulation of biological process |
| 84 |
| $1.59 \mathrm{E}-11$ |
| GO:0051960 |
| regulation of nervous system development |
| 25 |
| $1.66 \mathrm{E}-11$ |
| GO:0044763 |
| single-organism cellular process |
| 87 |
| 4.82E-11 |
| GO:0048699 |
| generation of neurons |
| 31 |
| 5.69E-11 |
| GO:0007275 |
| multicellular organismal development |
| 56 |
| 1.03E-10 |
| GO:0048731 |
| system development |
| 52 |
| 1.03E-10 |
| GO:0034765 |
| regulation of ion transmembrane transport |
| 18 |
| $1.58 \mathrm{E}-10$ |
| GO:0050803 |
| regulation of synapse structure or activity |
| 15 |
| $2.05 \mathrm{E}-10$ |
| GO:0044699 |
| single-organism process |
| 90 |
| 2.27E-10 |
| GO:0048856 |
| anatomical structure development |
| 56 |
| 2.27E-10 |


| GO:0043269 |
| :---: |
| regulation of ion transport |
| 21 |
| 3.43E-10 |
| GO:0030182 |
| neuron differentiation |
| 25 |
| 3.58E-10 |
| GO:0051128 |
| regulation of cellular component organization |
| 38 |
| 3.80E-10 |
| GO:0007215 |
| glutamate receptor signaling pathway |
| 9 |
| 4.05E-10 |
| GO:0050877 |
| neurological system process |
| 25 |
| 4.05E-10 |
| GO:0050804 |
| modulation of synaptic transmission |
| 15 |
| 1.33E-09 |
| GO:0007267 |
| cell-cell signaling |
| 20 |
| 1.56E-09 |
| GO:0007612 |
| learning |
| 12 |
| 1.86E-09 |
| GO:0048518 |
| positive regulation of biological process |
| 58 |
| 1.86E-09 |
| GO:0007417 |
| central nervous system development |
| 24 |
| 1.93E-09 |
| GO:0007611 |
| learning or memory |
| 14 |
| 2.44E-09 |
| GO:0065008 |

regulation of biological quality


| $5.15 \mathrm{E}-08$ |  |
| :---: | :---: |
| GO:0030154 |  |
| cell differentiation |  |
| 43 |  |
| $8.57 \mathrm{E}-08$ |  |
| GO:0048468 |  |
| cell development |  |
| 29 |  |
| $1.00 \mathrm{E}-07$ |  |
| GO:0060322 |  |
| head development |  |
| 20 |  |
| $1.11 \mathrm{E}-07$ |  |
| GO:0051962 |  |
| positive regulation of nervous system development |  |
| 16 |  |
| 1.19E-07 |  |
| GO:0051239 |  |
| regulation of multicellular organismal process |  |
| 36 |  |
| $1.20 \mathrm{E}-07$ |  |
| GO:0048522 |  |
| positive regulation of cellular process |  |
| 50 |  |
| $1.28 \mathrm{E}-07$ |  |
| GO:0048869 |  |
| cellular developmental process |  |
| 44 |  |
| $1.28 \mathrm{E}-07$ |  |
| GO:0031175 |  |
| neuron projection development |  |
| 17 |  |
| $1.57 \mathrm{E}-07$ |  |
| GO:0051130 |  |
| positive regulation of cellular component organization |  |
| 24 |  |
| 2.89E-07 |  |
| GO:0048667 |  |
| cell morphogenesis involved in neuron differentiation |  |
| 14 |  |
| 3.17E-07 |  |
| GO:0007626 |  |
| locomotory behavior |  |
| 12 |  |

4.11E-07

| GO:0050767 |
| :---: |
| regulation of neurogenesis |
| $4.31 \mathrm{E}-07$ |
| GO:1902578 |
| single-organism localization |
| 37 |
| GO:0007416-07 |
| synapse assembly |
| 7 |
| $4.46 \mathrm{E}-07$ |
| GO:0009893 |
| positive regulation of metabolic process |
| 42 |
| $5.00 \mathrm{E}-07$ |
| GO:2000026 |
| regulation of multicellular organismal development |

28

| GO:0035-07 |
| :---: |
| social behavior |
| 7 |
| $7.05 \mathrm{E}-07$ |
| GO:0061564 |
| axon development |
| 13 |
| $7.05 \mathrm{E}-07$ |
| GO:0009987 |
| cellular process |

88

| $8.98 \mathrm{E}-07$ |
| :---: |
| $\mathrm{GO}: 0050807$ |

regulation of synapse organization
9

| $1.30 \mathrm{E}-06$ |
| :---: |
| GO:0030534 |
| adult behavior |
| 10 |
| $1.31 \mathrm{E}-06$ |
| $\mathrm{GO}: 0019222$ |

regulation of metabolic process
57
$1.34 \mathrm{E}-06$

GO:0050793

| GO:0050793 |
| :---: |
| regulation of developmental process |
| 32 |
| $1.54 \mathrm{E}-06$ |
| GO:0051963 |
| regulation of synapse assembly |
| 8 |
| $1.54 \mathrm{E}-06$ |
| GO:0044093 |
| positive regulation of molecular function |
| 26 |
| $1.55 \mathrm{E}-06$ |
| GO:0050808 |
| synapse organization |
| 9 |
| 1.55E-06 |
| GO:0051179 |
| localization |
| 46 |
| $1.75 \mathrm{E}-06$ |
| GO:0008038 |
| neuron recognition |
| 6 |
| $1.84 \mathrm{E}-06$ |
| GO:0007166 |
| cell surface receptor signaling pathway |
| 26 |
| 1.97E-06 |
| GO:0048167 |
| regulation of synaptic plasticity |
| 9 |
| 2.18E-06 |
| GO:0023051 |
| regulation of signaling |
| 34 |
| 2.25E-06 |
| GO:0007409 |
| axonogenesis |
| 12 |
| $2.50 \mathrm{E}-06$ |
| GO:0048513 |
| organ development |
| 37 |
| $2.74 \mathrm{E}-06$ |
| GO:0051705 |

multi-organism behavior

| 8 |
| :---: |
| $2.77 \mathrm{E}-06$ |
| GO:0000904 |
| cell morphogenesis involved in differentiation |
| 15 |
| 4.04E-06 |
| GO:0051716 |
| cellular response to stimulus |
| 49 |
| 4.45E-06 |
| GO:0048858 |
| cell projection morphogenesis |
| 16 |
| 4.52E-06 |
| GO:0048812 |
| neuron projection morphogenesis |
| 13 |
| 5.26E-06 |
| GO:0051965 |
| positive regulation of synapse assembly |
| 7 |
| 5.32E-06 |
| GO:0065009 |
| regulation of molecular function |
| 33 |
| 5.63E-06 |
| GO:0051049 |
| regulation of transport |
| 26 |
| 8.37E-06 |
| GO:0030900 |
| forebrain development |
| 13 |
| 8.99E-06 |
| GO:0046903 |
| secretion |
| 14 |
| 1.11E-05 |
| GO:0048583 |
| regulation of response to stimulus |
| 36 |
| 1.28E-05 |
| GO:0031344 |
| regulation of cell projection organization |


| 1.30E-05 |
| :---: |
| GO:0000902 |
| cell morphogenesis |
| 18 |
| 1.51E-05 |
| GO:0051234 |
| establishment of localization |
| 38 |
| 1.67E-05 |
| GO:0006810 |
| transport |
| 37 |
| $1.89 \mathrm{E}-05$ |
| GO:0035235 |
| ionotropic glutamate receptor signaling pathway |
| 5 |
| 1.95E-05 |
| GO:0010646 |
| regulation of cell communication |
| 33 |
| $2.21 \mathrm{E}-05$ |
| GO:0010975 |
| regulation of neuron projection development |
| 12 |
| 2.21E-05 |
| GO:0044765 |
| single-organism transport |
| 32 |
| $2.21 \mathrm{E}-05$ |
| GO:0045664 |
| regulation of neuron differentiation |
| 14 |
| $2.55 \mathrm{E}-05$ |
| GO:0007411 |
| axon guidance |
| 9 |
| 2.56E-05 |
| GO:0051094 |
| positive regulation of developmental process |
| 21 |
| 2.77E-05 |
| GO:0008306 |
| associative learning |
| 7 |



GO:0010468

| GO:0010468 |
| :---: |
| regulation of gene expression |
| 38 |
| 0.000125 |
| GO:2000310 |
| regulation of N -methyl-D-aspartate selective glutamate receptor activity |
| 4 |
| 0.000126 |
| GO:0051173 |
| positive regulation of nitrogen compound metabolic process |
| 25 |
| 0.000129 |
| GO:0010648 |
| negative regulation of cell communication |
| 19 |
| 0.000136 |
| GO:0009653 |
| anatomical structure morphogenesis |
| 28 |
| 0.000141 |
| GO:0051641 |
| cellular localization |
| 25 |
| 0.000148 |
| GO:0032412 |
| regulation of ion transmembrane transporter activity |
| 8 |
| 0.000152 |
| GO:0044089 |
| positive regulation of cellular component biogenesis |
| 11 |
| 0.000157 |
| GO:1902474 |
| positive regulation of protein localization to synapse |
| 3 |
| 0.000166 |
| GO:0043085 |
| positive regulation of catalytic activity |
| 20 |
| 0.000167 |
| GO:0007270 |
| neuron-neuron synaptic transmission |
| 6 |
| 0.000174 |
| GO:0010769 |


| 10 |
| :---: |
| 0.000177 |
| GO:0019219 |
| regulation of nucleobase-containing compound metabolic process |
| 36 |
| 0.000179 |
| GO:0040007 |
| growth |
| 12 |
| 0.000179 |
| GO:0048585 |
| negative regulation of response to stimulus |
| 20 |
| 0.000179 |
| GO:0048589 |
| developmental growth |
| 11 |
| 0.000186 |
| GO:0045893 |
| positive regulation of transcription, DNA-templated |
| 22 |
| $0.000195$ |
| GO:0031325 |
| positive regulation of cellular metabolic process |
| 32 |
| $0.000201$ |
| GO:0032940 |
| secretion by cell |
| 11 |
| $0.000202$ |
| GO:0050769 |
| positive regulation of neurogenesis |
| 11 |
| 0.000207 |
| GO:0050790 |
| regulation of catalytic activity |
| 26 |
| 0.000207 |
| GO:0009605 |
| response to external stimulus |
| 23 |
| 0.00021 |
| GO:0098609 |
| cell-cell adhesion |


| $0.00021$ |
| :---: |
| GO:0010628 |
| positive regulation of gene expression |
| 24 |
| 0.000215 |
| GO:0019233 |
| sensory perception of pain |
| 6 |
| 0.000215 |
| GO:0031323 |
| regulation of cellular metabolic process |
| 47 |
| 0.000215 |
| GO:0071805 |
| potassium ion transmembrane transport |
| 7 |
| 0.000215 |
| GO:0035249 |
| synaptic transmission, glutamatergic |
| 5 |
| $0.000231$ |
| GO:0030001 |
| metal ion transport |
| 13 |
| $0.000256$ |
| GO:0051240 |
| positive regulation of multicellular organismal process |
| 21 |
| 0.000258 |
| GO:0050919 |
| negative chemotaxis |
| 4 |
| 0.000271 |
| GO:2000463 |
| positive regulation of excitatory postsynaptic potential |
| 4 |
| 0.000271 |
| GO:0048170 |
| positive regulation of long-term neuronal synaptic plasticity |
| 3 |
| 0.000272 |
| GO:0010557 |
| positive regulation of macromolecule biosynthetic process |


| 0.00029 |
| :---: |
| GO:0048168 |
| regulation of neuronal synaptic plasticity |
| 5 |
| 0.000316 |
| GO:0044087 |
| regulation of cellular component biogenesis |
| 14 |
| 0.00034 |
| GO:0006935 |
| chemotaxis |
| 11 |
| 0.000366 |
| GO:0021953 |
| central nervous system neuron differentiation |
| 8 |
| 0.000367 |
| GO:0023057 |
| negative regulation of signaling |
| 18 |
| 0.000381 |
| GO:0007600 |
| sensory perception |
| 13 |
| 0.000393 |
| GO:0009790 |
| embryo development |
| 18 |
| 0.00042 |
| GO:0010604 |
| positive regulation of macromolecule metabolic process |
| 30 |
| 0.00042 |
| GO:0042221 |
| response to chemical |
| 31 |
| 0.000488 |
| GO:0045935 |
| positive regulation of nucleobase-containing compound metabolic process |
| 23 |
| 0.000488 |
| GO:0007193 |
| adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway |
| 5 |
| 0.000515 |


| GO:0050805 |
| :---: |
| negative regulation of synaptic transmission |
| 5 |
| 0.000515 |
| GO:0008542 |
| visual learning |
| 5 |
| 0.000628 |
| GO:0048169 |
| regulation of long-term neuronal synaptic plasticity |
| 4 |
| 0.000653 |
| GO:0043412 |
| macromolecule modification |
| 29 |
| 0.000672 |
| GO:0022607 |
| cellular component assembly |
| 22 |
| 0.000675 |
| GO:0051481 |
| negative regulation of cytosolic calcium ion concentration |
| 3 |
| 0.000675 |
| GO:0006468 |
| protein phosphorylation |
| 15 |
| 0.000782 |
| GO:0048646 |
| anatomical structure formation involved in morphogenesis |
| 17 |
| $0.000854$ |
| GO:0031346 |
| positive regulation of cell projection organization |
| 9 |
| $0.000924$ |
| GO:0009966 |
| regulation of signal transduction |
| 26 |
| $0.000941$ |
| GO:0060255 |
| regulation of macromolecule metabolic process |
| 44 |
| 0.00102 |
| GO:0007200 |



3

| 0.00175 |
| :---: |
| GO:0050905 |
| neuromuscular process |
| 6 |
| 0.00181 |
| GO:0006464 |
| cellular protein modification process |
| 27 |
| 0.00184 |
| GO:0043933 |
| macromolecular complex subunit organization |
| 22 |
| 0.00195 |
| GO:0007206 |
| phospholipase C-activating G-protein coupled glutamate receptor signaling pathway |
| 2 |
| 0.00197 |
| GO:0019220 |
| regulation of phosphate metabolic process |
| 20 |
| 0.00214 |
| GO:0021537 |
| telencephalon development |
| 8 |
| 0.00214 |
| GO:0008150 |
| biological_process |
| 83 |
| 0.00229 |
| GO:0048511 |
| rhythmic process |
| 9 |
| 0.00229 |
| GO:0031399 |
| regulation of protein modification process |
| 20 |
| 0.00246 |
| GO:0051252 |
| regulation of RNA metabolic process |
| 31 |
| 0.00263 |
| GO:0001505 |
| regulation of neurotransmitter levels |
| 6 |


| 0.00283 |
| :---: |
| GO:1900271 |
| regulation of long-term synaptic potentiation |
| 3 |
| 0.00283 |
| GO:0044085 |
| cellular component biogenesis |
| 22 |
| 0.00289 |
| GO:0007156 |
| homophilic cell adhesion via plasma membrane adhesion molecules |
| 5 |
| 0.00325 |
| GO:0006355 |
| regulation of transcription, DNA-templated |
| 30 |
| 0.00331 |
| GO:0098742 |
| cell-cell adhesion via plasma-membrane adhesion molecules |
| 6 |
| 0.00336 |
| GO:2000112 |
| regulation of cellular macromolecule biosynthetic process |
| 32 |
| 0.00337 |
| GO:0060359 |
| response to ammonium ion |
| 5 |
| 0.0034 |
| GO:0098660 |
| inorganic ion transmembrane transport |
| 11 |
| 0.00355 |
| GO:0045944 |
| positive regulation of transcription from RNA polymerase II promoter |
| 16 |
| 0.0036 |
| GO:0006811 |
| ion transport |
| 16 |
| 0.00367 |
| GO:0009887 |
| organ morphogenesis |
| 15 |
| 0.00376 |


| GO:0072657 |
| :---: |
| protein localization to membrane |
| 8 |
| 0.00379 |
| GO:0098662 |
| inorganic cation transmembrane transport |
| 10 |
| 0.00398 |
| GO:0008361 |
| regulation of cell size |
| 6 |
| 0.00401 |
| GO:0034220 |
| ion transmembrane transport |
| 13 |
| 0.0042 |
| GO:0006357 |
| regulation of transcription from RNA polymerase II promoter |
| 21 |
| 0.00433 |
| GO:0007188 |
| adenylate cyclase-modulating G-protein coupled receptor signaling pathway |
| 6 |
| 0.00433 |
| GO:1903309 |
| negative regulation of chromatin modification |
| 4 |
| 0.00439 |
| GO:0032101 |
| regulation of response to external stimulus |
| 13 |
| 0.00495 |
| GO:0010976 |
| positive regulation of neuron projection development |
| 7 |
| 0.00501 |
| GO:0032880 |
| regulation of protein localization |
| 14 |
| 0.00501 |
| GO:0035385 |
| Roundabout signaling pathway |
| 2 |
| 0.00501 |
| GO:1901315 |

negative regulation of histone H2A K63-linked ubiquitination

| 2 |
| :---: |
| 0.00501 |
| GO:0010647 |
| positive regulation of cell communication |
| 19 |
| 0.00519 |
| GO:0023056 |
| positive regulation of signaling |
| 18 |
| 0.0054 |
| GO:0016358 |
| dendrite development |
| 5 |
| 0.00559 |
| GO:0050795 |
| regulation of behavior |
| 7 |
| 0.00559 |
| GO:0051968 |
| positive regulation of synaptic transmission, glutamatergic |
| 3 |
| 0.00566 |
| GO:1902667 |
| regulation of axon guidance |
| 3 |
| 0.00566 |
| GO:0022603 |
| regulation of anatomical structure morphogenesis |
| 14 |
| 0.00596 |
| GO:0016570 |
| histone modification |
| 8 |
| 0.00605 |
| GO:0060341 |
| regulation of cellular localization |
| 16 |
| 0.00605 |
| GO:0008344 |
| adult locomotory behavior |
| 5 |
| 0.00607 |
| GO:0030902 |
| hindbrain development |



| 0.0095 |
| :---: |
| GO:0048588 |
| developmental cell growth |
| 4 |
| 0.00965 |
| GO:0040008 |
| regulation of growth |
| 11 |
| 0.00991 |
| GO:0072661 |
| protein targeting to plasma membrane |
| 3 |
| 0.00998 |
| GO:0043009 |
| chordate embryonic development |
| 12 |
| 0.0104 |
| GO:0016049 |
| cell growth |
| 5 |
| 0.0109 |
| GO:0043576 |
| regulation of respiratory gaseous exchange |
| 3 |
| 0.0113 |
| GO:0009968 |
| negative regulation of signal transduction |
| 14 |
| 0.0115 |
| GO:0006812 |
| cation transport |
| 12 |
| 0.0119 |
| GO:0006875 |
| cellular metal ion homeostasis |
| 8 |
| 0.0124 |
| GO:1902589 |
| single-organism organelle organization |
| 21 |
| 0.0125 |
| GO:0060560 |
| developmental growth involved in morphogenesis |
| 5 |
| 0.0128 |


| GO:0006874 |
| :---: |
| cellular calcium ion homeostasis |
| 7 |
| 0.0135 |
| GO:0016199 |
| axon midline choice point recognition |
| 2 |
| 0.0139 |
| GO:0044802 |
| single-organism membrane organization |
| 10 |
| 0.0139 |
| GO:0070100 |
| negative regulation of chemokine-mediated signaling pathway |
| 2 |
| 0.0139 |
| GO:0097107 |
| postsynaptic density assembly |
| 2 |
| 0.0139 |
| GO:0097119 |
| postsynaptic density protein 95 clustering |
| 2 |
| 0.0139 |
| GO:2000809 |
| positive regulation of synaptic vesicle clustering |
| 2 |
| 0.0139 |
| GO:0001941 |
| postsynaptic membrane organization |
| 3 |
| 0.0141 |
| GO:0021987 |
| cerebral cortex development |
| 5 |
| 0.0141 |
| GO:0018205 |
| peptidyl-lysine modification |
| 6 |
| 0.0143 |
| GO:0001701 |
| in utero embryonic development |
| 9 |
| 0.0145 |
| GO:0050885 |

neuromuscular process controlling balance

| 4 |
| :---: |
| 0.0145 |
| GO:0043547 |
| positive regulation of GTPase activity |
| 9 |
| 0.0153 |
| GO:0042692 |
| muscle cell differentiation |
| 7 |
| 0.0155 |
| GO:0021602 |
| cranial nerve morphogenesis |
| 3 |
| 0.0156 |
| GO:0048593 |
| camera-type eye morphogenesis |
| 5 |
| 0.0163 |
| GO:0042592 |
| homeostatic process |
| 16 |
| 0.0168 |
| GO:0048729 |
| tissue morphogenesis |
| 11 |
| 0.0169 |
| GO:0001832 |
| blastocyst growth |
| 3 |
| 0.017 |
| GO:0001964 |
| startle response |
| 3 |
| 0.017 |
| GO:0007616 |
| long-term memory |
| 3 |
| 0.017 |
| GO:0033143 |
| regulation of intracellular steroid hormone receptor signaling pathway |
| 4 |
| 0.017 |
| GO:0042325 |
| regulation of phosphorylation |


| GO:0001661 |
| :---: |
| conditioned taste aversion |
| GO:0021825 |
| substrate-dependent cerebral cortex tangential migration |
| 2 |
| GO:0043278 |
| response to morphine |
| 3 |
| GO:0046541 |
| saliva secretion |
| 2 |
| 0.0187 |
| GO:0048675 |
| axon extension |
| 3 |

semaphorin-plexin signaling pathway involved in neuron projection guidance
2
0.0187

GO:1902531
regulation of intracellular signal transduction

| regulation of intracellular signal transduction |
| :---: |
| 16 |
| GO:0044267 |
| cellular protein metabolic process |
| 28 |
| 0.0191 |
| GO:0043266 |
| regulation of potassium ion transport |
| 4 |
| 0.0192 |
| GO:1902580 |
| single-organism cellular localization |


| 0.0198 |
| :---: |
| GO:0006836 |
| neurotransmitter transport |
| 5 |
| 0.02 |
| GO:0048814 |
| regulation of dendrite morphogenesis |
| 4 |
| 0.0201 |
| GO:0006796 |
| phosphate-containing compound metabolic process |
| 19 |
| 0.0202 |
| GO:0090596 |
| sensory organ morphogenesis |
| 7 |
| 0.0202 |
| GO:0009888 |
| tissue development |
| 19 |
| 0.0205 |
| GO:0045471 |
| response to ethanol |
| 5 |
| 0.0205 |
| GO:0001932 |
| regulation of protein phosphorylation |
| 15 |
| 0.021 |
| GO:0032535 |
| regulation of cellular component size |
| 7 |
| 0.0215 |
| GO:0006417 |
| regulation of translation |
| 7 |
| 0.0219 |
| GO:0001508 |
| action potential |
| 4 |
| 0.023 |
| GO:0048878 |
| chemical homeostasis |
| 12 |
| 0.023 |


| GO:0002318 |
| :---: |
| myeloid progenitor cell differentiation |
| 2 |
| 0.0242 |
| GO:0007196 |
| adenylate cyclase-inhibiting G-protein coupled glutamate receptor signaling pathway |
| 2 |
| 0.0242 |
| GO:0048638 |
| regulation of developmental growth |
| 7 |
| 0.0242 |
| GO:0048846 |
| axon extension involved in axon guidance |
| 2 |
| 0.0242 |
| GO:0097104 |
| postsynaptic membrane assembly |
| 2 |
| 0.0242 |
| GO:1900273 |
| positive regulation of long-term synaptic potentiation |
| 2 |
| 0.0242 |
| GO:0055082 |
| cellular chemical homeostasis |
| 9 |
| 0.0246 |
| GO:0016573 |
| histone acetylation |
| 4 |
| 0.0249 |
| GO:1903308 |
| regulation of chromatin modification |
| 5 |
| 0.025 |
| GO:0032228 |
| regulation of synaptic transmission, GABAergic |
| 3 |
| 0.0251 |
| GO:0098900 |
| regulation of action potential |
| 3 |
| 0.0251 |
| GO:0051259 |

protein oligomerization

| 8 |
| :---: |
| 0.0254 |
| GO:0035637 |
| multicellular organismal signaling |
| 4 |
| 0.0256 |
| GO:0072659 |
| protein localization to plasma membrane |
| 5 |
| 0.0256 |
| GO:0032270 |
| positive regulation of cellular protein metabolic process |
| 15 |
| 0.0266 |
| GO:0033144 |
| negative regulation of intracellular steroid hormone receptor signaling pathway |
| 3 |
| 0.0269 |
| GO:0007507 |
| heart development |
| 9 |
| 0.0276 |
| GO:0010959 |
| regulation of metal ion transport |
| 7 |
| 0.0276 |
| GO:0033043 |
| regulation of organelle organization |
| 14 |
| 0.0279 |
| GO:0006887 |
| exocytosis |
| 6 |
| 0.0284 |
| GO:0021954 |
| central nervous system neuron development |
| 4 |
| 0.0288 |
| GO:0048013 |
| ephrin receptor signaling pathway |
| 3 |
| 0.0288 |
| GO:0007158 |
| neuron cell-cell adhesion |



| 0.0354 |
| :---: |
| GO:0009892 |
| negative regulation of metabolic process |
| 23 |
| 0.0356 |
| GO:0030007 |
| cellular potassium ion homeostasis |
| 2 |
| 0.0356 |
| GO:0033036 |
| macromolecule localization |
| 19 |
| 0.0356 |
| GO:0042136 |
| neurotransmitter biosynthetic process |
| 2 |
| 0.0356 |
| GO:0042670 |
| retinal cone cell differentiation |
| 2 |
| 0.0356 |
| GO:0046549 |
| retinal cone cell development |
| 2 |
| 0.0356 |
| GO:0051339 |
| regulation of lyase activity |
| 4 |
| 0.0356 |
| GO:0071822 |
| protein complex subunit organization |
| 14 |
| 0.0356 |
| GO:2000780 |
| negative regulation of double-strand break repair |
| 2 |
| 0.0356 |
| GO:0080134 |
| regulation of response to stress |
| 14 |
| 0.0359 |
| GO:0045859 |
| regulation of protein kinase activity |
| 10 |
| 0.0375 |


| GO:0051336 |
| :---: |
| regulation of hydrolase activity |
| 14 |
| 0.0388 |
| GO:0008104 |
| protein localization |
| 17 |
| 0.0389 |
| GO:0043967 |
| histone H 4 acetylation |
| 3 |
| 0.0427 |
| GO:0002327 |
| immature B cell differentiation |
| 2 |
| 0.0428 |
| GO:0021612 |
| facial nerve structural organization |
| 2 |
| 0.0428 |
| GO:0045792 |
| negative regulation of cell size |
| 2 |
| 0.0428 |
| GO:0048149 |
| behavioral response to ethanol |
| 2 |
| 0.0428 |
| GO:0051129 |
| negative regulation of cellular component organization |
| 9 |
| 0.0428 |
| GO:0071428 |
| rRNA-containing ribonucleoprotein complex export from nucleus |
| 2 |
| 0.0428 |
| GO:0097305 |
| response to alcohol |
| 7 |
| 0.0445 |
| GO:0045665 |
| negative regulation of neuron differentiation |
| 5 |
| 0.0448 |
| GO:0051172 |

negative regulation of nitrogen compound metabolic process

| 16 |
| :---: |
| 0.0456 |
| GO:0019538 |
| protein metabolic process |
| 30 |
| 0.0476 |
| GO:0042220 |
| response to cocaine |
| 3 |
| 0.0478 |
| GO:0051276 |
| chromosome organization |
| 11 |
| 0.0478 |
| GO:0098655 |
| cation transmembrane transport |
| 9 |
| $0.0478$ |
| GO:0018108 |
| peptidyl-tyrosine phosphorylation |
| 5 |
| 0.0483 |
| GO:0007613 |
| memory |
| 4 |
| $0.0493$ |
| GO:0007623 |
| circadian rhythm |
| 5 |
| $0.0493$ |
| GO:0021543 |
| pallium development |
| 5 |
| 0.0493 |
| GO:0006809 |
| nitric oxide biosynthetic process |
| 2 |
| 0.0498 |
| GO:0007169 |
| transmembrane receptor protein tyrosine kinase signaling pathway |
| 7 |
| $0.0498$ |
| GO:0021561 |
| facial nerve development |


| 0.0498 |
| :---: |
| GO:0021610 |
| facial nerve morphogenesis |
| 2 |
| 0.0498 |
| GO:0043966 |
| histone H3 acetylation |
| 3 |
| 0.0498 |
| GO:0090129 |
| positive regulation of synapse maturation |
| 2 |
| 0.0498 |
| (less ...) |


| Molecular Function (GO) |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0008066 |
| glutamate receptor activity |
| 7 |
| $3.20 \mathrm{E}-07$ |
| GO:0022843 |
| voltage-gated cation channel activity |
| 10 |
| $3.80 \mathrm{E}-06$ |
| GO:0022836 |
| gated channel activity |
| 13 |
| $4.60 \mathrm{E}-06$ |
| GO:0005216 |
| ion channel activity |
| 13 |
| \begin{tabular}{ll\|}
\hline
\end{tabular} |
| $1.73 \mathrm{E}-05$ |
| GO:0005515 |
| protein binding |
| 51 |
| $1.73 \mathrm{E}-05$ |
| GO:0005488 |



| 0.00223 |
| :---: |
| GO:0042043 |
| neurexin family protein binding |
| 3 |
| 0.00287 |
| GO:0005230 |
| extracellular ligand-gated ion channel activity |
| 5 |
| 0.00371 |
| GO:0004714 |
| transmembrane receptor protein tyrosine kinase activity |
| 5 |
| 0.00374 |
| GO:0001639 |
| PLC activating G-protein coupled glutamate receptor activity |
| 2 |
| 0.00394 |
| GO:0005003 |
| ephrin receptor activity |
| 3 |
| 0.00661 |
| GO:0017075 |
| syntaxin-1 binding |
| 3 |
| 0.00661 |
| GO:0042393 |
| histone binding |
| 6 |
| 0.00661 |
| GO:0005102 |
| receptor binding |
| 16 |
| 0.0118 |
| GO:0022892 |
| substrate-specific transporter activity |
| 14 |
| 0.0118 |
| GO:0097159 |
| organic cyclic compound binding |
| 43 |
| 0.0125 |
| GO:0043169 |
| cation binding |
| 34 |


| 0.0167 |
| :---: |
| GO:1901363 |
| heterocyclic compound binding |
| 42 |
| 0.0194 |
| GO:0008013 |
| beta-catenin binding |
| 4 |
| 0.0228 |
| GO:0002039 |
| p53 binding |
| 4 |
| 0.0239 |
| GO:0001640 |
| adenylate cyclase inhibiting G-protein coupled glutamate receptor activity |
| 2 |
| 0.0485 |
| GO:0004439 |
| phosphatidylinositol-4,5-bisphosphate 5 -phosphatase activity |
| 2 |
| 0.0485 |
| GO:0005251 |
| delayed rectifier potassium channel activity |
| 3 |
| 0.0485 |
| GO:0015271 |
| outward rectifier potassium channel activity |
| 2 |
| 0.0485 |
| GO:0046872 |
| metal ion binding |
| 32 |
| 0.0485 |
| (less ...) |


| Cellular Component (GO) |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0097458 |
| neuron part |



| $1.61 \mathrm{E}-12$ |
| :---: |
| GO:0030424 |
| axon |
| 19 |
| 4.35E-12 |
| GO:0036477 |
| somatodendritic compartment |
| 23 |
| 4.35E-12 |
| GO:0031226 |
| intrinsic component of plasma membrane |
| 28 |
| $7.45 \mathrm{E}-12$ |
| GO:0005887 |
| integral component of plasma membrane |
| 27 |
| $1.45 \mathrm{E}-11$ |
| GO:0098589 |
| membrane region |
| 28 |
| $1.99 \mathrm{E}-11$ |
| GO:0044459 |
| plasma membrane part |
| 37 |
| $4.04 \mathrm{E}-11$ |
| GO:0034702 |
| ion channel complex |
| 15 |
| $1.41 \mathrm{E}-10$ |
| GO:0033267 |
| axon part |
| 13 |
| $3.73 \mathrm{E}-10$ |
| GO:0098805 |
| whole membrane |
| 31 |
| 4.55E-08 |
| GO:0008076 |
| voltage-gated potassium channel complex |
| 8 |
| $1.04 \mathrm{E}-07$ |
| GO:0098590 |
| plasma membrane region |
| 21 |
| $1.04 \mathrm{E}-07$ |

GO:0031224



| 0.00212 |  |
| :---: | :---: |
| GO:0060077 |  |
| inhibitory synapse |  |
| 3 |  |
| 0.00212 |  |
| GO:0016023 |  |
| cytoplasmic membrane-bounded vesicle |  |
| 15 |  |
| 0.00234 |  |
| GO:0008328 |  |
| ionotropic glutamate receptor complex |  |
| 4 |  |
| 0.00317 |  |
| GO:0098802 |  |
| plasma membrane receptor complex |  |
| 6 |  |
| 0.00361 |  |
| GO:0042383 |  |
| sarcolemma |  |
| 5 |  |
| 0.00552 |  |
| GO:0060076 |  |
| excitatory synapse |  |
| 3 |  |
| 0.00552 |  |
| GO:0042734 |  |
| presynaptic membrane |  |
| 4 |  |
| 0.00561 |  |
| GO:0032590 |  |
| dendrite membrane |  |
| 3 |  |
| 0.00615 |  |
| GO:0005737 |  |
| cytoplasm |  |
| 67 |  |
| 0.00696 |  |
| GO:0030426 |  |
| growth cone |  |
| 5 |  |
| 0.0101 |  |
| GO:0009986 |  |
| cell surface |  |
| 12 |  |


| 0.011 |
| :---: |
| GO:0045121 |
| membrane raft |
| 7 |
| 0.011 |
| GO:0043194 |
| axon initial segment |
| 2 |
| 0.0149 |
| GO:0043235 |
| receptor complex |
| 7 |
| 0.015 |
| GO:0030315 |
| T-tubule |
| 3 |
| 0.0153 |
| GO:0005938 |
| cell cortex |
| 6 |
| 0.0164 |
| GO:0043198 |
| dendritic shaft |
| 3 |
| 0.0195 |
| GO:0043234 |
| protein complex |
| 32 |
| 0.0281 |
| GO:0044424 |
| intracellular part |
| 75 |
| 0.0313 |
| GO:0031253 |
| cell projection membrane |
| 6 |
| 0.0364 |
| GO:0005622 |
| intracellular |
| 76 |
| 0.0373 |
| GO:0031252 |
| cell leading edge |
| 7 |
| 0.0373 |


| GO:0043229 |
| :---: | :---: |
| intracellular organelle |
| 68 |
| GO:0030673 |
| axolemma |
| 2 |
| GO:0033268 <br> node of Ranvier <br> 2 <br> 0.0458 <br> GO:0012505 <br> endomembrane system <br> 28 <br> 0.0472 <br> (less ...) |




## Up-regulated genes overlapped with SFARI-GENE dataset

## Network Stats

number of nodes:
44
number of edges:
14
average node degree:
0.636
avg. local clustering coefficient:
expected number of edges:
6
PPI enrichment p-value:
0.00559

Functional enrichments in your network

| Biological Process (GO) |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0060997 |
| dendritic spine morphogenesis |
| 3 |
| $0.00162$ |
| GO:0098815 |
| modulation of excitatory postsynaptic potential |
| 4 |
| $0.00162$ |
| GO:0071625 |
| vocalization behavior |
| 3 |
| $0.00505$ |
| GO:0044710 |
| single-organism metabolic process |
| 19 |
| 0.00579 |
| GO:0003008 |
| system process |
| 11 |
| 0.0088 |
| GO:0019725 |
| cellular homeostasis |
| 8 |
| 0.0088 |
| GO:0060996 |
| dendritic spine development |
| 3 |
| 0.0088 |
| GO:0065008 |
| regulation of biological quality |
| 16 |
| 0.0088 |
| GO:2000463 |


| 3 |
| :---: |
| 0.0088 |
| GO:0032412 |
| regulation of ion transmembrane transporter activity |
| 5 |
| 0.0106 |
| GO:1901564 |
| organonitrogen compound metabolic process |
| 11 |
| 0.0106 |
| GO:0044237 |
| cellular metabolic process |
| 26 |
| 0.0133 |
| GO:0055114 |
| oxidation-reduction process |
| 9 |
| 0.0157 |
| GO:1900449 |
| regulation of glutamate receptor signaling pathway |
| 3 |
| 0.0214 |
| GO:0010647 |
| positive regulation of cell communication |
| 11 |
| 0.0215 |
| GO:0006167 |
| AMP biosynthetic process |
| 2 |
| $0.0227$ |
| GO:0097113 |
| AMPA glutamate receptor clustering |
| 2 |
| $0.0227$ |
| GO:2000821 |
| regulation of grooming behavior |
| 2 |
| 0.0227 |
| GO:0006749 |
| glutathione metabolic process |
| 3 |
| 0.0351 |
| GO:0006790 |
| sulfur compound metabolic process |

5

| 0.0372 |
| :---: |
| GO:0023056 |
| positive regulation of signaling |
| 10 |
| 0.0388 |
| GO:0035176 |
| social behavior |
| 3 |
| 0.0388 |
| GO:0051823 |
| regulation of synapse structural plasticity |
| 2 |
| 0.0388 |
| GO:0044281 |
| small molecule metabolic process |
| 10 |
| 0.0419 |
| GO:0048813 |
| dendrite morphogenesis |
| 3 |
| 0.0419 |
| GO:0008015 |
| blood circulation |
| 5 |
| 0.0452 |
| (less ...) |


| Molecular Function (GO) |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| GO:0035255 |
| ionotropic glutamate receptor binding |
| 4 |
| $1.63 \mathrm{E}-05$ |
| GO:0043168 |
| anion binding |
| 19 |
| 3.92E-05 |
| GO:0004658 |




| 5 |
| :---: |
| 0.0244 |
| GO:0044444 |
| cytoplasmic part |
| 23 |
| 0.0244 |
| GO:0032839 |
| dendrite cytoplasm |
| 2 |
| 0.0345 |
| GO:0044456 |
| synapse part |
| 6 |
| $0.0398$ |
| GO:0097481 |
| neuronal postsynaptic density |
| 3 |
| $0.0398$ |
| GO:0014069 |
| postsynaptic density |
| 4 |
| $0.0425$ |
| GO:0098794 |
| postsynapse |
| 5 |
| 0.0425 |
| (less ...) |


| KEGG Pathways |
| :---: |
| pathway ID |
| pathway description |
| count in gene set |
| false discovery rate |
| 1100 |
| Metabolic pathways |
| 10 |
| 0.0125 |
| 4724 |
| Glutamatergic synapse |
| 4 |
| 0.0125 |

5016
Huntington s disease

| Huntington s disease |
| :---: | :---: |
| 4 |
| 0.0347 |
| 4146 |
| Peroxisome |
| 3 |
| 0.0372 |

