# group 8

## Global Summary

%DE = 0.52

# genes with fdr < 0.2 = 18295 ( 7864 + / 10431 −)

# genes with fdr < 0.1 = 13972 ( 6597 + / 7375 −)

# genes with fdr < 0.05 = 10658 ( 5607 + / 5051 −)

# genes with fdr < 0.01 = 6308 ( 4070 + / 2238 −)

# genes in genesets = 16360

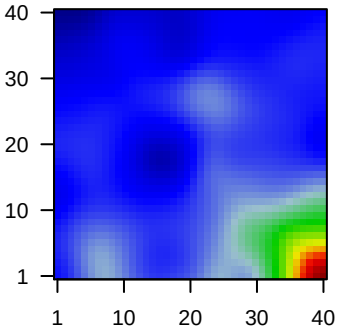
<FC> = 0

<t−score> = −0.15

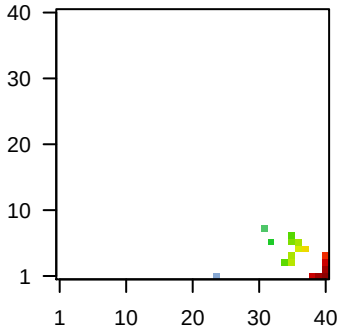
<p−value> = 0

<fdr> = 0.48

**Portrait**




**Top 100 DE genes**




## Global Genelist

| Rank | ID | log(FC) | fdr p−value | | Description Metagene | |
|---|---|---|---|---|---|---|
| 1 | 205551_at | 1.07 | 0e+00 | 1e−12 | 40 x 1 | synaptic vesicle glycoprotein 2B [Source:HGNC Symbol;Acc:I |
| 2 | 214945_at | 0.97 | 0e+00 | 1e−12 | 40 x 1 | novel transcript |
| 3 | 219659_at | 0.83 | 0e+00 | 1e−12 | 39 x 1 | ATPase phospholipid transporting 8A2 [Source:HGNC Symbc |
| 4 | 231489_x_at | 0.99 | 0e+00 | 1e−12 | 40 x 1 | cellular repressor of E1A stimulated genes 2 [Source:HGNC S |
| 5 | 235781_at | 0.83 | 0e+00 | 1e−12 | 40 x 1 | calcium voltage−gated channel subunit alpha1 B [Source:HG |
| 6 | 236081_at | 0.9 | 0e+00 | 1e−12 | 40 x 1 | synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138] |
| 7 | 239765_at | 1.03 | 0e+00 | 1e−12 | 40 x 1 | cytoplasmic polyadenylation element binding protein 3 [Sourc |
| 8 | 206456_at | 1.12 | 2e−16 | 1e−12 | 40 x 1 | gamma−aminobutyric acid type A receptor alpha5 subunit [Sc |
| 9 | 230303_at | 0.96 | 2e−16 | 1e−12 | 40 x 1 | synaptoporin [Source:HGNC Symbol;Acc:HGNC:16507] |
| 10 | 204229_at | 0.87 | 4e−16 | 3e−12 | 40 x 1 | solute carrier family 17 member 7 [Source:HGNC Symbol;Acc |
| 11 | 205113_at | 1.1 | 4e−16 | 3e−12 | 40 x 1 | neurofilament medium [Source:HGNC Symbol;Acc:HGNC:77 |
| 12 | 213558_at | 0.93 | 4e−16 | 3e−12 | 40 x 1 | piccolo presynaptic cytomatrix protein [Source:HGNC Symbo |
| 13 | 229039_at | 0.82 | 4e−16 | 3e−12 | 40 x 1 | synapsin II [Source:HGNC Symbol;Acc:HGNC:11495] |
| 14 | 237250_at | 0.97 | 4e−16 | 3e−12 | 40 x 1 | novel transcript, overlapping GABRA2 |
| 15 | 244118_at | 1.06 | 4e−16 | 3e−12 | 40 x 1 | gamma−aminobutyric acid type A receptor alpha1 subunit [Sc |
| 16 | 224209_s_at | 1.14 | 7e−16 | 3e−12 | 40 x 1 | guanine deaminase [Source:HGNC Symbol;Acc:HGNC:4212 |
| 17 | 221217_s_at | 0.8 | 9e−16 | 3e−12 | 40 x 1 | RNA binding fox−1 homolog 1 [Source:HGNC Symbol;Acc:H |
| 18 | 221805_at | 1.08 | 9e−16 | 3e−12 | 40 x 1 | neurofilament light [Source:HGNC Symbol;Acc:HGNC:7739] |
| 19 | 226086_at | 0.78 | 1e−15 | 3e−12 | 40 x 1 | synaptotagmin 13 [Source:HGNC Symbol;Acc:HGNC:14962] |
| 20 | 203999_at | 0.82 | 1e−15 | 3e−12 | 40 x 1 | synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509] |

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 23.47 | NULL | 574 | BP | synapse |
| 2 | 22.64 | NULL | 7387 | BP | membrane |
| 3 | 20.5 | NULL | 4278 | BP | plasma membrane |
| 4 | 18.64 | NULL | 236 | BP | chemical synaptic transmission |
| 5 | 16.72 | NULL | 240 | BP | postsynaptic membrane |
| 6 | 14 | NULL | 505 | BP | nervous system development |
| 7 | 12.48 | NULL | 627 | BP | ion transport |
| 8 | 11.74 | NULL | 119 | BP | postsynapse |
| 9 | 11.61 | NULL | 28 | BP | synaptic vesicle exocytosis |
| 10 | 11.23 | NULL | 131 | BP | presynapse |
| 11 | 11.1 | NULL | 27 | BP | glutamate secretion |
| 12 | 10.94 | NULL | 6202 | BP | cytoplasm |
| 13 | 10.86 | NULL | 51 | BP | neurotransmitter secretion |
| 14 | 10.14 | NULL | 149 | BP | regulation of ion transmembrane transport |
| 15 | 9.72 | NULL | 131 | BP | potassium ion transport |
| 16 | 9.68 | NULL | 27 | BP | gamma−aminobutyric acid signaling pathway |
| 17 | 9.63 | NULL | 33 | BP | regulation of exocytosis |
| 18 | 9.58 | NULL | 118 | BP | exocytosis |
| 19 | 9.36 | NULL | 13 | BP | synaptic transmission, GABAergic |
| 20 | 9.35 | NULL | 122 | BP | potassium ion transmembrane transport |
| *Underexpressed* | | | | | |
| 1 | −8.03 | NULL | 158 | BP | DNA replication |
| 2 | −7.79 | NULL | 366 | BP | DNA repair |
| 3 | −7.44 | NULL | 1416 | BP | DNA−binding transcription factor activity, RNA polymerase II−speci |
| 4 | −7.29 | NULL | 1387 | BP | regulation of transcription, DNA−templated |
| 5 | −7.03 | NULL | 484 | BP | cellular response to DNA damage stimulus |
| 6 | −6.73 | NULL | 229 | BP | mRNA splicing, via spliceosome |
| 7 | −6.68 | NULL | 152 | BP | rRNA processing |
| 8 | −6.55 | NULL | 1145 | BP | regulation of transcription by RNA polymerase II |
| 9 | −5.88 | NULL | 630 | BP | cell cycle |
| 10 | −5.77 | NULL | 564 | BP | immune system process |
| 11 | −5.64 | NULL | 93 | BP | ribosome biogenesis |
| 12 | −5.46 | NULL | 90 | BP | viral transcription |
| 13 | −5.38 | NULL | 97 | BP | DNA recombination |
| 14 | −5.34 | NULL | 400 | BP | chromatin binding |
| 15 | −5.33 | NULL | 843 | BP | DNA−binding transcription factor activity |
| 16 | −5.3 | NULL | 81 | BP | double−strand break repair via homologous recombination |
| 17 | −5.2 | NULL | 39 | BP | CENP−A containing nucleosome assembly |
| 18 | −5.16 | NULL | 394 | BP | cell division |
| 19 | −5.09 | NULL | 279 | BP | RNA splicing |
| 20 | −4.97 | NULL | 85 | BP | chromosome segregation |

**p−values**