21117A

Global Summary

%DE = 0.1

genes with fdr < 0.2 = 3230 (2370 + / 860 −)

genes with fdr < 0.1 = 2650 (2038 + / 612 −)

genes with fdr < 0.05 = 2157 (1740 + / 417 −)

genes with fdr < 0.01 = 1573 (1316 + / 257 −)

genes in genesets = 16360

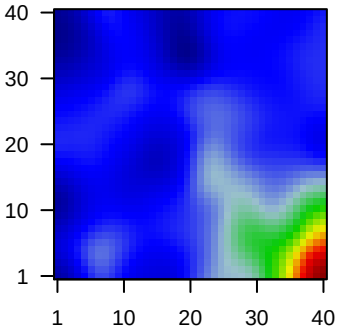
<FC> = 0

<t−score> = 0

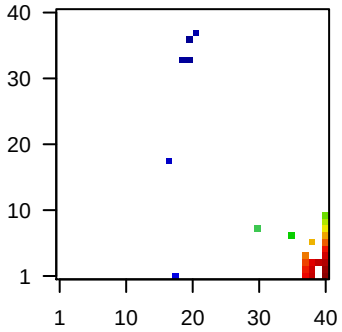
<p−value> = 0.17

<fdr> = 0.9

Portrait



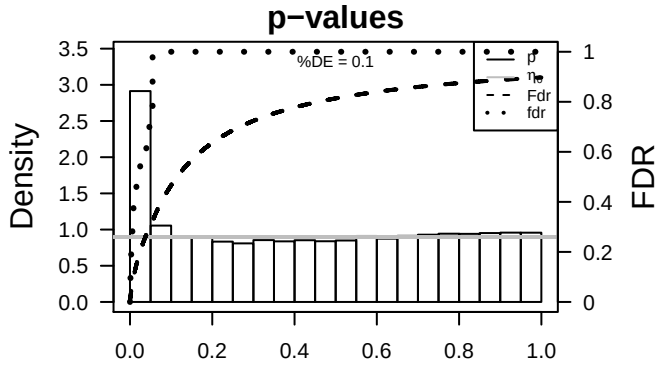
Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1554012_at	1.74	2e−16	2e−13	40 x 2	R−spondin 2 [Source:HGNC Symbol;Acc:HGNC:28583]
2	1554299_at	2.94	2e−16	2e−13	40 x 9	neuronal PAS domain protein 4 [Source:HGNC Symbol;Acc:H
3	1554997_a_at	1.8	2e−16	2e−13	30 x 8	prostaglandin−endoperoxide synthase 2 [Source:HGNC Symb
4	1555800_at	1.98	2e−16	2e−13	40 x 1	zinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:2
5	1557475_at	1.77	2e−16	2e−13	40 x 2	long intergenic non−protein coding RNA 507 [Source:HGNC S
6	1557721_at	1.82	2e−16	2e−13	40 x 5	novel transcript
7	1567628_at	−1.31	2e−16	2e−13	20 x 33	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
8	201340_s_at	1.36	2e−16	2e−13	40 x 1	ectodermal−neural cortex 1 [Source:HGNC Symbol;Acc:HGN
9	201341_at	1.11	2e−16	2e−13	40 x 3	ectodermal−neural cortex 1 [Source:HGNC Symbol;Acc:HGN
10	201909_at	−1.62	2e−16	2e−13	18 x 1	ribosomal protein S4 Y−linked 1 [Source:HGNC Symbol;Acc:R
11	202507_s_at	0.92	2e−16	2e−13	38 x 1	synaptosome associated protein 25 [Source:HGNC Symbol;A
12	203000_at	1	2e−16	2e−13	37 x 1	stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
13	203001_s_at	0.98	2e−16	2e−13	38 x 1	stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
14	203413_at	1.03	2e−16	2e−13	40 x 3	neural EGFL like 2 [Source:HGNC Symbol;Acc:HGNC:7751]
15	203498_at	0.99	2e−16	2e−13	37 x 4	regulator of calcineurin 2 [Source:HGNC Symbol;Acc:HGNC:
16	203510_at	1.85	2e−16	2e−13	40 x 3	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
17	203797_at	1.36	2e−16	2e−13	40 x 1	visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
18	203798_s_at	1.57	2e−16	2e−13	40 x 1	visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
19	203999_at	1.14	2e−16	2e−13	40 x 1	synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509]
20	204081_at	1.28	2e−16	2e−13	40 x 1	neurogranin [Source:HGNC Symbol;Acc:HGNC:8000]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.94	NULL	574	BP	synapse
2	18.72	NULL	236	BP	chemical synaptic transmission
3	15.24	NULL	240	BP	postsynaptic membrane
4	14.18	NULL	4278	BP	plasma membrane
5	13.92	NULL	7387	BP	membrane
6	12.1	NULL	505	BP	nervous system development
7	12.01	NULL	627	BP	ion transport
8	11.25	NULL	119	BP	postsynapse
9	10.48	NULL	28	BP	synaptic vesicle exocytosis
10	10.4	NULL	51	BP	neurotransmitter secretion
11	10.02	NULL	51	BP	regulation of synaptic plasticity
12	9.97	NULL	149	BP	regulation of ion transmembrane transport
13	9.81	NULL	65	BP	learning
14	9.78	NULL	79	BP	memory
15	9.7	NULL	27	BP	glutamate secretion
16	9.46	NULL	33	BP	regulation of exocytosis
17	9.31	NULL	131	BP	potassium ion transport
18	9.09	NULL	30	BP	associative learning
19	9.03	NULL	31	BP	regulation of NMDA receptor activity
20	8.99	NULL	131	BP	presynapse
Underexpressed					
1	−12.32	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
2	−11.58	NULL	564	BP	immune system process
3	−9.92	NULL	43	BP	antigen processing and presentation
4	−8.62	NULL	388	BP	immune response
5	−8.37	NULL	1387	BP	regulation of transcription, DNA−templated
6	−8.12	NULL	417	BP	innate immune response
7	−7.82	NULL	1416	BP	DNA−binding transcription factor activity, RNA polymerase II−speci
8	−7.46	NULL	184	BP	defense response to virus
9	−7.14	NULL	90	BP	viral transcription
10	−6.86	NULL	459	BP	viral process
11	−6.82	NULL	1145	BP	regulation of transcription by RNA polymerase II
12	−6.78	NULL	155	BP	regulation of immune response
13	−6.76	NULL	69	BP	SRP−dependent cotranslational protein targeting to membrane
14	−6.49	NULL	366	BP	DNA repair
15	−6.37	NULL	158	BP	DNA replication
16	−6.04	NULL	484	BP	cellular response to DNA damage stimulus
17	−5.87	NULL	98	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
18	−5.82	NULL	120	BP	translational initiation
19	−5.75	NULL	229	BP	mRNA splicing, via spliceosome
20	−5.13	NULL	843	BP	DNA−binding transcription factor activity