41105N

Global Summary

%DE = 0.07

genes with fdr < 0.2 = 2311 (1535 + / 776 −)

genes with fdr < 0.1 = 1659 (1196 + / 463 −)

genes with fdr < 0.05 = 1331 (990 + / 341 −)

genes with fdr < 0.01 = 871 (665 + / 206 −)

genes in genesets = 16360

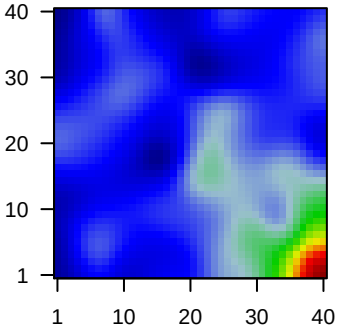
<FC> = 0

<t−score> = 0.06

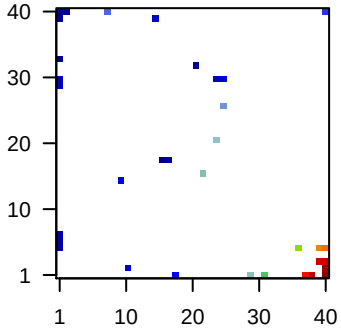
<p−value> = 0.22

<fdr> = 0.93

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201340_s_at	1.08	2e−16	7e−13	40 x 1	ectodermal−neural cortex 1 [Source:HGNC Symbol;Acc:HGN
2	201416_at	−1.05	2e−16	7e−13	1 x 6	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
3	201417_at	−0.89	2e−16	7e−13	1 x 6	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
4	201418_s_at	−0.88	2e−16	7e−13	1 x 30	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
5	203797_at	1.17	2e−16	7e−13	40 x 1	visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
6	203999_at	1.14	2e−16	7e−13	40 x 1	synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509]
7	204081_at	0.93	2e−16	7e−13	40 x 1	neurogranin [Source:HGNC Symbol;Acc:HGNC:8000]
8	204914_s_at	−0.88	2e−16	7e−13	1 x 7	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
9	206565_x_at	−1.5	2e−16	7e−13	1 x 33	
10	208712_at	−1.04	2e−16	7e−13	1 x 30	cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
11	215043_s_at	−1.8	2e−16	7e−13	1 x 33	
12	221916_at	1.1	2e−16	7e−13	40 x 1	neurofilament light [Source:HGNC Symbol;Acc:HGNC:7739]
13	229613_at	−1.16	2e−16	7e−13	1 x 30	NKD1, WNT signaling pathway inhibitor [Source:HGNC Symt
14	232333_at	−0.91	2e−16	7e−13	1 x 39	
15	242405_at	−1.09	2e−16	7e−13	1 x 40	
16	243189_at	−1.5	2e−16	7e−13	15 x 39	nuclear respiratory factor 1 [Source:HGNC Symbol;Acc:HGN
17	202507_s_at	0.9	7e−16	7e−11	38 x 1	synaptosome associated protein 25 [Source:HGNC Symbol;A
18	213004_at	−1.06	7e−16	7e−11	1 x 5	angiopoietin like 2 [Source:HGNC Symbol;Acc:HGNC:490]
19	229039_at	1.09	7e−16	7e−11	40 x 1	synapsin II [Source:HGNC Symbol;Acc:HGNC:11495]
20	215116_s_at	0.88	3e−15	7e−11	40 x 3	dynamin 1 [Source:HGNC Symbol;Acc:HGNC:2972]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.88	NULL	574	BP	synapse
2	16.55	NULL	236	BP	chemical synaptic transmission
3	13.41	NULL	7387	BP	membrane
4	13.09	NULL	4278	BP	plasma membrane
5	12.46	NULL	240	BP	postsynaptic membrane
6	9.48	NULL	51	BP	neurotransmitter secretion
7	9.21	NULL	28	BP	synaptic vesicle exocytosis
8	9.18	NULL	627	BP	ion transport
9	9.15	NULL	27	BP	glutamate secretion
10	8.92	NULL	13	BP	synaptic transmission, GABAergic
11	8.64	NULL	505	BP	nervous system development
12	8.36	NULL	89	BP	neuropeptide signaling pathway
13	8.17	NULL	657	BP	calcium ion binding
14	7.98	NULL	119	BP	postsynapse
15	7.93	NULL	33	BP	regulation of exocytosis
16	7.84	NULL	1435	BP	mitochondrion
17	7.42	NULL	131	BP	presynapse
18	7.37	NULL	16	BP	positive regulation of calcium ion−dependent exocytosis
19	7.35	NULL	15	BP	synaptic vesicle priming
20	7.32	NULL	30	BP	associative learning
Underexpressed					
1	−11.57	NULL	1416	BP	DNA−binding transcription factor activity, RNA polymerase II−speci
2	−10.92	NULL	1387	BP	regulation of transcription, DNA−templated
3	−9.85	NULL	1145	BP	regulation of transcription by RNA polymerase II
4	−8.58	NULL	400	BP	chromatin binding
5	−8.08	NULL	843	BP	DNA−binding transcription factor activity
6	−7.86	NULL	158	BP	DNA replication
7	−7.84	NULL	1086	BP	positive regulation of transcription by RNA polymerase II
8	−7.57	NULL	630	BP	cell cycle
9	−7.25	NULL	394	BP	cell division
10	−6.98	NULL	342	BP	chromatin organization
11	−6.92	NULL	783	BP	negative regulation of transcription by RNA polymerase II
12	−6.77	NULL	613	BP	positive regulation of transcription, DNA−templated
13	−6.68	NULL	484	BP	cellular response to DNA damage stimulus
14	−6.65	NULL	366	BP	DNA repair
15	−6.35	NULL	564	BP	immune system process
16	−5.81	NULL	541	BP	negative regulation of transcription, DNA−templated
17	−5.74	NULL	229	BP	mRNA splicing, via spliceosome
18	−5.49	NULL	90	BP	viral transcription
19	−5.34	NULL	11	BP	neural tube formation
20	−5.33	NULL	10	BP	positive regulation of osteoblast proliferation

p−values