

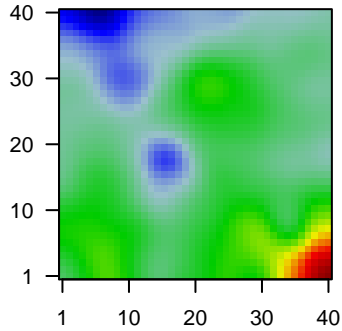
22721L

Global Summary

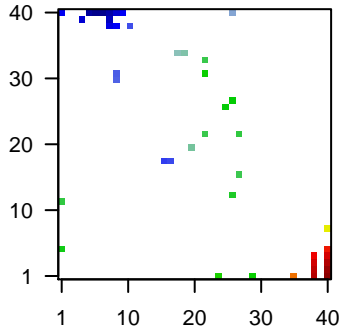
%DE = 0.08
 # genes with fdr < 0.2 = 2845 (1697 + / 1148 -)
 # genes with fdr < 0.1 = 2066 (1283 + / 783 -)
 # genes with fdr < 0.05 = 1600 (998 + / 602 -)
 # genes with fdr < 0.01 = 1120 (710 + / 410 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.06
 <p-value> = 0.2
 <fdr> = 0.92

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1557465_at	1.93	2e-16 3e-13	27 x 16 transmembrane protein 272 [Source:HGNC Symbol;Acc:HGNC:1557465]
2	1558678_s_at	-0.87	2e-16 3e-13	7 x 40 metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC:1558678]
3	201291_s_at	-2.11	2e-16 3e-13	16 x 18 DNA topoisomerase II alpha [Source:HGNC Symbol;Acc:HGNC:201291]
4	201341_at	1.07	2e-16 3e-13	40 x 3 ectodermal-neural cortex 1 [Source:HGNC Symbol;Acc:HGNC:201341]
5	202376_at	1.04	2e-16 3e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:202376]
6	203999_at	1.03	2e-16 3e-13	40 x 1 synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509]
7	204563_at	-1.2	2e-16 3e-13	26 x 27 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
8	205967_at	-1.38	2e-16 3e-13	6 x 40 histone cluster 1 H4 family member c [Source:HGNC Symbol;Acc:HGNC:205967]
9	206084_at	1.95	2e-16 3e-13	40 x 1 protein tyrosine phosphatase, receptor type R [Source:HGNC Symbol;Acc:HGNC:206084]
10	206803_at	1.93	2e-16 3e-13	40 x 1 prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
11	207307_at	2.06	2e-16 3e-13	38 x 3 5-hydroxytryptamine receptor 2C [Source:HGNC Symbol;Acc:HGNC:207307]
12	207553_at	2.01	2e-16 3e-13	40 x 4 opioid receptor kappa 1 [Source:HGNC Symbol;Acc:HGNC:8820]
13	208711_s_at	-1.39	2e-16 3e-13	6 x 40 cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
14	209047_at	0.86	2e-16 3e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:209047]
15	209254_at	-1.4	2e-16 3e-13	7 x 40 kelch domain containing 10 [Source:HGNC Symbol;Acc:HGNC:209254]
16	213004_at	-1.12	2e-16 3e-13	1 x 5 angiotensin II type 2 receptor [Source:HGNC Symbol;Acc:HGNC:490]
17	213850_s_at	-0.92	2e-16 3e-13	8 x 40 SR-related CTD associated factor 11 [Source:HGNC Symbol;Acc:HGNC:213850]
18	214317_x_at	-0.86	2e-16 3e-13	9 x 30 ribosomal protein S9 [Source:HGNC Symbol;Acc:HGNC:1044]
19	214464_at	-1.5	2e-16 3e-13	7 x 40 CDC42 binding protein kinase alpha [Source:HGNC Symbol;Acc:HGNC:214464]
20	215606_s_at	-1.37	2e-16 3e-13	11 x 38 ELKS/RAB6-interacting/CAST family member 1 [Source:HGNC Symbol;Acc:HGNC:215606]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.62	NULL	574	BP synapse
2	16.24	NULL	236	BP chemical synaptic transmission
3	15.37	NULL	4278	BP plasma membrane
4	13.17	NULL	240	BP postsynaptic membrane
5	12.9	NULL	7387	BP membrane
6	10.32	NULL	505	BP nervous system development
7	9.78	NULL	627	BP ion transport
8	8.93	NULL	27	BP glutamate secretion
9	8.86	NULL	119	BP postsynapse
10	8.73	NULL	51	BP neurotransmitter secretion
11	8.51	NULL	131	BP presynapse
12	8.27	NULL	1500	BP signal transduction
13	8.26	NULL	149	BP regulation of ion transmembrane transport
14	7.89	NULL	92	BP axonogenesis
15	7.68	NULL	28	BP synaptic vesicle exocytosis
16	7.65	NULL	275	BP ion transmembrane transport
17	7.59	NULL	122	BP potassium ion transmembrane transport
18	7.37	NULL	33	BP regulation of exocytosis
19	7.33	NULL	36	BP synaptic vesicle endocytosis
20	7.26	NULL	131	BP potassium ion transport
<i>Underexpressed</i>				
1	-9.11	NULL	276	BP translation
2	-8.77	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
3	-8.68	NULL	83	BP mitochondrial translational elongation
4	-8.58	NULL	85	BP mitochondrial translational termination
5	-7.73	NULL	90	BP viral transcription
6	-7.09	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
7	-7.08	NULL	394	BP cell division
8	-6.92	NULL	120	BP translational initiation
9	-6.73	NULL	43	BP mitochondrial electron transport, NADH to ubiquinone
10	-6.53	NULL	59	BP mitochondrial respiratory chain complex I assembly
11	-6.06	NULL	630	BP cell cycle
12	-6	NULL	158	BP DNA replication
13	-5.89	NULL	1435	BP mitochondrion
14	-5.73	NULL	229	BP mRNA splicing, via spliceosome
15	-5.68	NULL	78	BP anaphase-promoting complex-dependent catabolic process
16	-5.66	NULL	85	BP chromosome segregation
17	-5.62	NULL	366	BP DNA repair
18	-5.57	NULL	152	BP rRNA processing
19	-5.29	NULL	484	BP cellular response to DNA damage stimulus
20	-5.1	NULL	29	BP cytoplasmic translation

p-values

