

8276H

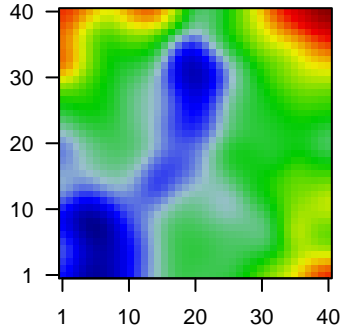
Global Summary

%DE = 0.07
 # genes with fdr < 0.2 = 1039 (197 + / 842 -)
 # genes with fdr < 0.1 = 507 (57 + / 450 -)
 # genes with fdr < 0.05 = 330 (27 + / 303 -)
 # genes with fdr < 0.01 = 142 (6 + / 136 -)

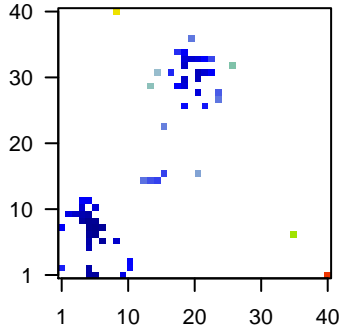
 # genes in genesets = 16360

 <FC> = 0
 <t-score> = -0.21
 <p-value> = 0.27
 <fdr> = 0.93

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	213859_x_at	-2.54	2e-16	6e-12 5 x 2 SWI/SNF related, matrix associated, actin dependent regulat
2	216834_at	-2.52	2e-16	6e-12 21 x 31 regulator of G protein signaling 1 [Source:HGNC Symbol;Acc
3	229259_at	-1.44	6e-15	2e-09 20 x 36 glial fibrillary acidic protein [Source:HGNC Symbol;Acc:HGNC
4	201325_s_at	-1.92	4e-14	8e-09 21 x 30 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:HC
5	201012_at	-2.14	4e-13	8e-09 19 x 33 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
6	208451_s_at	-1.34	4e-13	1e-07 22 x 33 complement C4B (Chido blood group) [Source:HGNC Symbo
7	210982_s_at	-1.4	5e-12	1e-07 20 x 33 major histocompatibility complex, class II, DR alpha [Source:t
8	216591_s_at	-2.14	6e-12	1e-07 11 x 3 succinate dehydrogenase complex, subunit C, integral memb
9	202376_at	-1.49	7e-12	1e-07 19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
10	203868_s_at	-1.77	1e-11	5e-07 23 x 31 vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
11	226875_at	-1.88	3e-11	5e-07 6 x 9 dedicator of cytokinesis 11 [Source:HGNC Symbol;Acc:HGNC
12	223528_s_at	-1.78	4e-11	5e-07 4 x 10 methyltransferase like 17 [Source:HGNC Symbol;Acc:HGNC:
13	212672_at	-1.36	5e-11	5e-07 4 x 9 ATM serine/threonine kinase [Source:HGNC Symbol;Acc:HGI
14	210095_s_at	-1.67	5e-11	5e-07 21 x 16 insulin like growth factor binding protein 3 [Source:HGNC Syr
15	210425_x_at	-1.28	6e-11	1e-06 4 x 9 golgin A8 family member A [Source:HGNC Symbol;Acc:HGNC
16	208747_s_at	-1.66	8e-11	1e-06 18 x 34 complement C1s [Source:HGNC Symbol;Acc:HGNC:1247]
17	36711_at	-1.4	1e-10	4e-06 15 x 31 MAF bZIP transcription factor F [Source:HGNC Symbol;Acc:t
18	225107_at	-1.41	3e-10	4e-06 4 x 9 heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGNC
19	218801_at	-1.76	5e-10	4e-06 4 x 9 UDP-glucose glycoprotein glucosyltransferase 2 [Source:HG
20	212179_at	-1.15	5e-10	4e-06 5 x 8 PNN interacting serine and arginine rich protein [Source:HGNC

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.99	NULL	236	BP chemical synaptic transmission
2	8.36	NULL	574	BP synapse
3	6.32	NULL	240	BP postsynaptic membrane
4	6.03	NULL	627	BP ion transport
5	5.74	NULL	25	BP regulation of dopamine secretion
6	5.73	NULL	505	BP nervous system development
7	5.65	NULL	51	BP regulation of synaptic vesicle exocytosis
8	5.42	NULL	28	BP synaptic vesicle exocytosis
9	5.38	NULL	16	BP regulation of calcium ion-dependent exocytosis
10	5.35	NULL	15	BP calcium ion-regulated exocytosis of neurotransmitter
11	5.33	NULL	115	BP keratinization
12	5.27	NULL	149	BP regulation of ion transmembrane transport
13	5.21	NULL	24	BP G protein-coupled serotonin receptor signaling pathway
14	5.15	NULL	131	BP presynapse
15	5.09	NULL	33	BP regulation of exocytosis
16	5.05	NULL	29	BP calcium ion regulated exocytosis
17	4.81	NULL	48	BP cardiac conduction
18	4.76	NULL	27	BP gamma-aminobutyric acid signaling pathway
19	4.71	NULL	777	BP G protein-coupled receptor signaling pathway
20	4.66	NULL	51	BP neurotransmitter secretion
<i>Underexpressed</i>				
1	-11.61	NULL	4740	BP cytosol
2	-11.53	NULL	6202	BP cytoplasm
3	-9.57	NULL	366	BP DNA repair
4	-8.72	NULL	484	BP cellular response to DNA damage stimulus
5	-8.56	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
6	-8.43	NULL	630	BP cell cycle
7	-7.28	NULL	173	BP cilium assembly
8	-6.92	NULL	180	BP cell projection organization
9	-6.88	NULL	1435	BP mitochondrion
10	-6.83	NULL	394	BP cell division
11	-6.81	NULL	84	BP tRNA processing
12	-6.79	NULL	43	BP antigen processing and presentation
13	-6.78	NULL	564	BP immune system process
14	-6.49	NULL	45	BP non-motile cilium assembly
15	-6.4	NULL	460	BP neutrophil degranulation
16	-6.32	NULL	1145	BP regulation of transcription by RNA polymerase II
17	-6.13	NULL	358	BP mRNA processing
18	-6.03	NULL	229	BP mRNA splicing, via spliceosome
19	-6.02	NULL	99	BP mRNA export from nucleus
20	-5.84	NULL	192	BP methylation

p-values

