

21714E

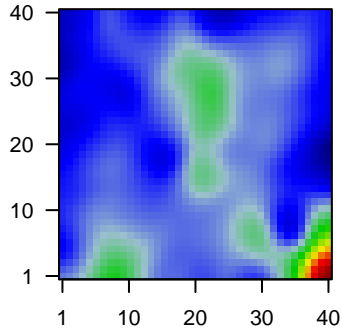
Global Summary

%DE = 0.06
 # genes with $fdr < 0.2$ = 2078 (1425 + / 653 -)
 # genes with $fdr < 0.1$ = 1620 (1143 + / 477 -)
 # genes with $fdr < 0.05$ = 1332 (958 + / 374 -)
 # genes with $fdr < 0.01$ = 831 (626 + / 205 -)

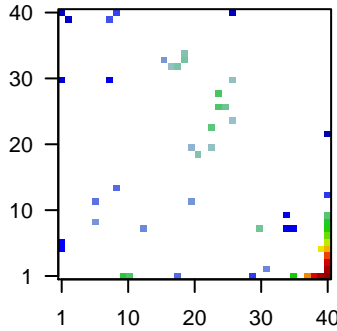
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.1
 <p-value> = 0.23
 <fdr> = 0.94

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	202376_at	1.04	2e-16	4e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
2	203000_at	0.98	2e-16	4e-13	37 x 1 stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
3	203510_at	1.94	2e-16	4e-13	40 x 3 MET proto-oncogene, receptor tyrosine kinase [Source:HGN
4	203999_at	0.88	2e-16	4e-13	40 x 1 synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509]
5	204035_at	1.08	2e-16	4e-13	31 x 2 secretogranin II [Source:HGNC Symbol;Acc:HGNC:10575]
6	204041_at	1.05	2e-16	4e-13	23 x 20 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
7	204712_at	1.61	2e-16	4e-13	40 x 1 WNT inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC:1f
8	204913_s_at	-1.13	2e-16	4e-13	1 x 40 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
9	204963_at	1.05	2e-16	4e-13	26 x 24 sarcospan [Source:HGNC Symbol;Acc:HGNC:11322]
10	205630_at	1.94	2e-16	4e-13	40 x 2 corticotropin releasing hormone [Source:HGNC Symbol;Acc:l
11	205825_at	1.97	2e-16	4e-13	40 x 1 proprotein convertase subtilisin/kexin type 1 [Source:HGNC 3
12	205828_at	2.38	2e-16	4e-13	20 x 12 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC
13	205901_at	2.71	2e-16	4e-13	40 x 1 prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
14	205984_at	1.78	2e-16	4e-13	39 x 5 corticotropin releasing hormone binding protein [Source:HGN
15	206382_s_at	2.85	2e-16	4e-13	40 x 5 brain derived neurotrophic factor [Source:HGNC Symbol;Acc:
16	206552_s_at	2.4	2e-16	4e-13	40 x 1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11:
17	206803_at	3.04	2e-16	4e-13	40 x 1 prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
18	209395_at	1.08	2e-16	4e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
19	211599_x_at	1.87	2e-16	4e-13	40 x 6 MET proto-oncogene, receptor tyrosine kinase [Source:HGN
20	213479_at	1.93	2e-16	4e-13	40 x 1 neuronal pentraxin 2 [Source:HGNC Symbol;Acc:HGNC:795:

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.69	NULL	236	BP chemical synaptic transmission
2	11.46	NULL	574	BP synapse
3	11.32	NULL	4278	BP plasma membrane
4	10.16	NULL	7387	BP membrane
5	8.96	NULL	13	BP synaptic transmission, GABAergic
6	8.51	NULL	240	BP postsynaptic membrane
7	8.37	NULL	27	BP gamma-aminobutyric acid signaling pathway
8	7.27	NULL	627	BP ion transport
9	7.15	NULL	27	BP glutamate secretion
10	7.1	NULL	51	BP neurotransmitter secretion
11	6.73	NULL	43	BP neurotransmitter transport
12	6.67	NULL	777	BP G protein-coupled receptor signaling pathway
13	6.38	NULL	131	BP potassium ion transport
14	6.37	NULL	28	BP synaptic vesicle exocytosis
15	6.36	NULL	79	BP memory
16	6.34	NULL	29	BP calcium ion regulated exocytosis
17	6.18	NULL	119	BP postsynapse
18	6.16	NULL	1500	BP signal transduction
19	6.12	NULL	231	BP extracellular matrix organization
20	5.88	NULL	50	BP nervous system process
<i>Underexpressed</i>				
1	-4.39	NULL	26	BP oligodendrocyte development
2	-4.37	NULL	229	BP mRNA splicing, via spliceosome
3	-4.34	NULL	1435	BP mitochondrion
4	-4.15	NULL	276	BP translation
5	-4.14	NULL	630	BP cell cycle
6	-4.14	NULL	30	BP oligodendrocyte differentiation
7	-4.11	NULL	83	BP mitochondrial translational elongation
8	-4.1	NULL	152	BP rRNA processing
9	-4.09	NULL	85	BP mitochondrial translational termination
10	-4.09	NULL	484	BP cellular response to DNA damage stimulus
11	-4.05	NULL	366	BP DNA repair
12	-3.87	NULL	56	BP DNA damage response, signal transduction by p53 class mediator
13	-3.67	NULL	84	BP tRNA processing
14	-3.58	NULL	158	BP DNA replication
15	-3.58	NULL	21	BP tissue regeneration
16	-3.26	NULL	93	BP ribosome biogenesis
17	-3.24	NULL	77	BP cholesterol homeostasis
18	-3.23	NULL	59	BP mitochondrial respiratory chain complex I assembly
19	-3.1	NULL	119	BP nucleic acid phosphodiester bond hydrolysis
20	-3.04	NULL	358	BP mRNA processing

p-values

