

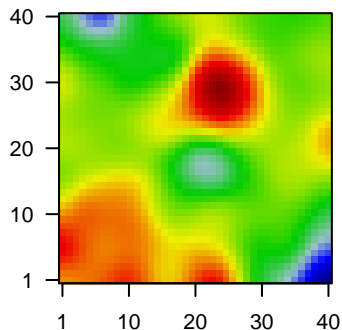
# group 5

## Global Summary

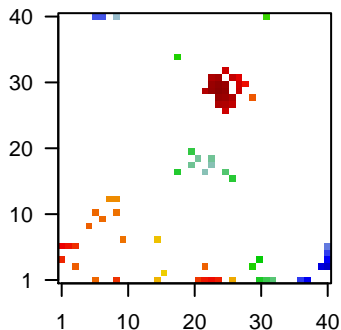
%DE = 0.55  
 # genes with fdr < 0.2 = 20730 ( 11373 + / 9357 -)  
 # genes with fdr < 0.1 = 16652 ( 9346 + / 7306 -)  
 # genes with fdr < 0.05 = 13797 ( 7872 + / 5925 -)  
 # genes with fdr < 0.01 = 8702 ( 5189 + / 3513 -)  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0.2  
 <p-value> = 0.03  
 <fdr> = 0.45

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	244340_x_at	-0.63	4e-16 3e-11	18 x 17
2	226652_at	0.36	2e-15 3e-11	27 x 29 ubiquitin specific peptidase 3 [Source:NCBI gene;Acc:9960]
3	231110_at	0.39	3e-15 3e-11	26 x 28
4	213413_at	0.64	4e-15 6e-11	25 x 29 stonin 1 [Source:HGNC Symbol;Acc:HGNC:17003]
5	214265_at	-0.6	8e-15 6e-11	9 x 40 integrin subunit alpha 8 [Source:HGNC Symbol;Acc:HGNC:6
6	236536_at	0.47	1e-14 6e-11	24 x 1 polypeptide N-acetylgalactosaminyltransferase 13 [Source:H
7	204866_at	0.4	1e-14 6e-11	22 x 1 jade family PHD finger 3 [Source:HGNC Symbol;Acc:HGNC:2
8	210135_s_at	-0.57	1e-14 8e-11	20 x 20 short stature homeobox 2 [Source:HGNC Symbol;Acc:HGNC
9	224976_at	0.33	2e-14 8e-11	24 x 29 nuclear factor I A [Source:HGNC Symbol;Acc:HGNC:7784]
10	1558101_at	0.65	2e-14 8e-11	24 x 29 nuclear factor I A [Source:HGNC Symbol;Acc:HGNC:7784]
11	244117_at	-0.62	3e-14 8e-11	31 x 1
12	223737_x_at	0.8	3e-14 8e-11	24 x 30 carbohydrate sulfotransferase 9 [Source:HGNC Symbol;Acc:3
13	224975_at	0.29	3e-14 8e-11	25 x 30 nuclear factor I A [Source:HGNC Symbol;Acc:HGNC:7784]
14	215046_at	0.48	3e-14 9e-11	23 x 30 KAT8 regulatory NSL complex subunit 1 like [Source:HGNC 3
15	224400_s_at	0.78	4e-14 3e-10	24 x 30 carbohydrate sulfotransferase 9 [Source:HGNC Symbol;Acc:3
16	229348_at	0.23	5e-14 1e-09	27 x 31 UbiA prenyltransferase domain containing 1 [Source:HGNC 3
17	205317_s_at	0.61	1e-13 1e-09	24 x 27 solute carrier family 15 member 2 [Source:HGNC Symbol;Acc
18	230682_x_at	-0.5	2e-13 1e-09	18 x 34 ATP binding cassette subfamily C member 3 [Source:HGNC 3
19	210815_s_at	0.79	2e-13 1e-09	1 x 4 calcitonin receptor like receptor [Source:HGNC Symbol;Acc:3
20	238955_at	0.37	2e-13 2e-09	21 x 1 raflin family member 2 [Source:HGNC Symbol;Acc:HGNC:26

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.67	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-spect
2	13.48	NULL	1145	BP regulation of transcription by RNA polymerase II
3	11.76	NULL	1387	BP regulation of transcription, DNA-templated
4	10.35	NULL	4740	BP cytosol
5	9.03	NULL	358	BP mRNA processing
6	9.02	NULL	783	BP negative regulation of transcription by RNA polymerase II
7	8.99	NULL	229	BP mRNA splicing, via spliceosome
8	8.77	NULL	342	BP chromatin organization
9	8.76	NULL	6202	BP cytoplasm
10	7.8	NULL	843	BP DNA-binding transcription factor activity
11	7.77	NULL	613	BP positive regulation of transcription, DNA-templated
12	7.64	NULL	541	BP negative regulation of transcription, DNA-templated
13	7.49	NULL	279	BP RNA splicing
14	7.47	NULL	1086	BP positive regulation of transcription by RNA polymerase II
15	7.32	NULL	400	BP chromatin binding
16	6.2	NULL	545	BP protein ubiquitination
17	6.18	NULL	56	BP mRNA 3'-end processing
18	6.12	NULL	366	BP DNA repair
19	5.77	NULL	99	BP mRNA export from nucleus
20	5.46	NULL	484	BP cellular response to DNA damage stimulus
<i>Underexpressed</i>				
1	-11.16	NULL	236	BP chemical synaptic transmission
2	-8.69	NULL	627	BP ion transport
3	-7.96	NULL	574	BP synapse
4	-7.96	NULL	4278	BP plasma membrane
5	-7.27	NULL	240	BP postsynaptic membrane
6	-6.9	NULL	149	BP regulation of ion transmembrane transport
7	-6.22	NULL	13	BP synaptic transmission, GABAergic
8	-6.21	NULL	51	BP regulation of synaptic vesicle exocytosis
9	-6.19	NULL	51	BP neurotransmitter secretion
10	-6.03	NULL	43	BP mitochondrial electron transport, NADH to ubiquinone
11	-5.75	NULL	131	BP potassium ion transport
12	-5.65	NULL	275	BP ion transmembrane transport
13	-5.62	NULL	89	BP neuropeptide signaling pathway
14	-5.41	NULL	43	BP neurotransmitter transport
15	-5.41	NULL	122	BP potassium ion transmembrane transport
16	-5.37	NULL	64	BP complement activation, classical pathway
17	-5.34	NULL	657	BP calcium ion binding
18	-5.33	NULL	777	BP G protein-coupled receptor signaling pathway
19	-5.23	NULL	59	BP mitochondrial respiratory chain complex I assembly
20	-5.07	NULL	28	BP synaptic vesicle exocytosis

p-values

