

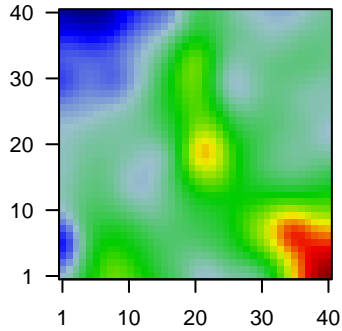
# 22919M

## Global Summary

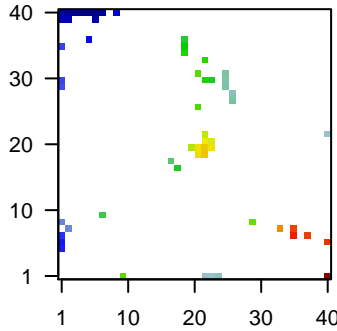
%DE = 0.11  
 # genes with fdr < 0.2 = 3950 ( 2321 + / 1629 - )  
 # genes with fdr < 0.1 = 3147 ( 1859 + / 1288 - )  
 # genes with fdr < 0.05 = 2531 ( 1514 + / 1017 - )  
 # genes with fdr < 0.01 = 1612 ( 984 + / 628 - )  
  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0  
 <p-value> = 0.16  
 <fdr> = 0.89

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1554281_at	-1.57	2e-16 1e-13	1 x 5 novel transcript
2	1558678_s_at	-0.82	2e-16 1e-13	7 x 40 metastasis associated lung adenocarcinoma transcript 1 [So
3	1568780_at	-0.98	2e-16 1e-13	1 x 40 RNA binding protein, fox-1 homolog (C. elegans) 1 (RBF
4	1569110_x_at	-1.55	2e-16 1e-13	7 x 10 programmed cell death 6 (PDCD6) pseudogene
5	201416_at	-1.28	2e-16 1e-13	1 x 6 SRY-box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
6	201761_at	-0.87	2e-16 1e-13	22 x 1 methylenetetrahydrofolate dehydrogenase (NADP+ depend
7	202018_s_at	2.68	2e-16 1e-13	19 x 35 lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
8	202376_at	1.34	2e-16 1e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
9	203548_s_at	-1.64	2e-16 1e-13	26 x 28 lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
10	203549_s_at	-1.12	2e-16 1e-13	26 x 28 lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
11	203797_at	1.07	2e-16 1e-13	40 x 1 visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
12	203999_at	0.98	2e-16 1e-13	40 x 1 synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509]
13	204041_at	1.33	2e-16 1e-13	23 x 20 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
14	204081_at	1.02	2e-16 1e-13	40 x 1 neurogranin [Source:HGNC Symbol;Acc:HGNC:8000]
15	204103_at	-1.47	2e-16 1e-13	22 x 30 C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:H
16	204121_at	-1.53	2e-16 1e-13	1 x 7 growth arrest and DNA damage inducible gamma [Source:HC
17	204913_s_at	-0.97	2e-16 1e-13	1 x 40 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
18	205114_s_at	-1.56	2e-16 1e-13	23 x 30 C-C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:H
19	205289_at	-0.98	2e-16 1e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:H
20	205290_s_at	-2.07	2e-16 1e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:H

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.98	NULL	7387	BP membrane
2	22.82	NULL	4278	BP plasma membrane
3	13.99	NULL	574	BP synapse
4	12.86	NULL	236	BP chemical synaptic transmission
5	11.11	NULL	1242	BP Golgi apparatus
6	10.46	NULL	1500	BP signal transduction
7	10.46	NULL	627	BP ion transport
8	10.04	NULL	657	BP calcium ion binding
9	8.54	NULL	6202	BP cytoplasm
10	8.53	NULL	460	BP neutrophil degranulation
11	8.3	NULL	240	BP postsynaptic membrane
12	8.02	NULL	615	BP transmembrane transport
13	7.94	NULL	33	BP regulation of exocytosis
14	7.86	NULL	133	BP protein localization to plasma membrane
15	7.84	NULL	119	BP postsynapse
16	7.6	NULL	28	BP synaptic vesicle exocytosis
17	7.59	NULL	27	BP glutamate secretion
18	7.57	NULL	505	BP nervous system development
19	7.33	NULL	275	BP ion transmembrane transport
20	7.28	NULL	122	BP potassium ion transmembrane transport
<i>Underexpressed</i>				
1	-8.58	NULL	276	BP translation
2	-8.27	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
3	-8.04	NULL	120	BP translational initiation
4	-7.64	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
5	-7.6	NULL	90	BP viral transcription
6	-7.5	NULL	152	BP rRNA processing
7	-6.72	NULL	229	BP mRNA splicing, via spliceosome
8	-6.69	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-speci
9	-6.39	NULL	1145	BP regulation of transcription by RNA polymerase II
10	-6.35	NULL	400	BP chromatin binding
11	-6.33	NULL	1387	BP regulation of transcription, DNA-templated
12	-6.24	NULL	366	BP DNA repair
13	-6.05	NULL	279	BP RNA splicing
14	-5.97	NULL	358	BP mRNA processing
15	-5.96	NULL	1086	BP positive regulation of transcription by RNA polymerase II
16	-5.76	NULL	484	BP cellular response to DNA damage stimulus
17	-5.66	NULL	843	BP DNA-binding transcription factor activity
18	-5.62	NULL	342	BP chromatin organization
19	-5.45	NULL	93	BP ribosome biogenesis
20	-5.34	NULL	29	BP cytoplasmic translation

p-values

