

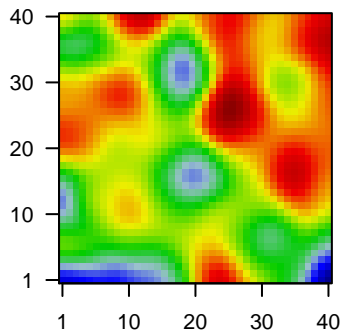
# 3712N

## Global Summary

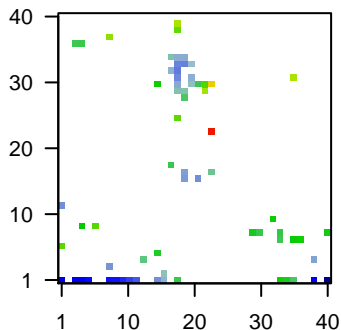
%DE = 0.06  
 # genes with fdr < 0.2 = 1517 ( 356 + / 1161 - )  
 # genes with fdr < 0.1 = 976 ( 198 + / 778 - )  
 # genes with fdr < 0.05 = 658 ( 116 + / 542 - )  
 # genes with fdr < 0.01 = 369 ( 63 + / 306 - )  
  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0.05  
 <p-value> = 0.26  
 <fdr> = 0.94

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	201012_at	-1.84	2e-16	1e-12	19 x 33 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	201295_s_at	-1.31	2e-16	1e-12	4 x 1 WD repeat and SOCS box containing 1 [Source:HGNC Symb
3	201909_at	-1.84	2e-16	1e-12	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:!
4	202376_at	-2.59	2e-16	1e-12	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
5	204103_at	-1.82	2e-16	1e-12	22 x 30 C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:Hi
6	209189_at	-1.31	2e-16	1e-12	20 x 30 Fos proto-oncogene, AP-1 transcription factor subunit [Sour
7	210982_s_at	-1.42	2e-16	1e-12	20 x 33 major histocompatibility complex, class II, DR alpha [Source:t
8	211991_s_at	-1.2	2e-16	1e-12	19 x 33 major histocompatibility complex, class II, DP alpha 1 [Source
9	227260_at	-1.47	2e-16	1e-12	4 x 9
10	229256_at	-1.35	2e-16	1e-12	30 x 8 phosphoglucosyltransferase 2 like 1 [Source:HGNC Symbol;Acc:HG
11	222484_s_at	-1.69	4e-15	1e-10	40 x 1 C-X-C motif chemokine ligand 14 [Source:HGNC Symbol;Ac
12	239432_at	-1.43	5e-15	1e-10	1 x 12 PSMA3 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
13	224588_at	2.11	8e-15	4e-10	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC
14	205579_at	-1.99	2e-14	4e-10	19 x 29 histamine receptor H1 [Source:HGNC Symbol;Acc:HGNC:511
15	219882_at	-1.67	2e-14	4e-09	33 x 7 tubulin tyrosine ligase like 7 [Source:HGNC Symbol;Acc:HGNC
16	201141_at	-1.83	1e-13	7e-09	18 x 32 glycoprotein nmb [Source:HGNC Symbol;Acc:HGNC:4462]
17	223842_s_at	-1.54	2e-13	9e-09	16 x 2 scavenger receptor class A member 3 [Source:HGNC Symb
18	235526_at	-1.44	4e-13	1e-08	4 x 36
19	242344_at	-1.68	1e-12	1e-08	40 x 1 gamma-aminobutyric acid type A receptor beta2 subunit [So
20	213920_at	-1.55	1e-12	1e-08	34 x 1 cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	4.17	NULL	229	BP mRNA splicing, via spliceosome
2	3.88	NULL	19	BP cardiac myofibril assembly
3	3.84	NULL	152	BP rRNA processing
4	3.57	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-speci
5	3.41	NULL	11	BP skeletal muscle myosin thick filament assembly
6	3.31	NULL	14	BP skeletal muscle thin filament assembly
7	3.25	NULL	83	BP mitochondrial translational elongation
8	3.21	NULL	93	BP ribosome biogenesis
9	3.12	NULL	20	BP cardiac muscle tissue morphogenesis
10	3.01	NULL	85	BP mitochondrial translational termination
11	2.91	NULL	279	BP RNA splicing
12	2.89	NULL	10	BP cellular aldehyde metabolic process
13	2.82	NULL	13	BP negative regulation of megakaryocyte differentiation
14	2.79	NULL	59	BP mitochondrial respiratory chain complex I assembly
15	2.72	NULL	358	BP mRNA processing
16	2.7	NULL	26	BP chromatin silencing at rDNA
17	2.67	NULL	23	BP hydrogen peroxide catabolic process
18	2.65	NULL	12	BP negative regulation of glycolytic process
19	2.63	NULL	1435	BP mitochondrion
20	2.58	NULL	40	BP sarcomere organization
<i>Underexpressed</i>				
1	-22.46	NULL	7387	BP membrane
2	-18.06	NULL	4278	BP plasma membrane
3	-11.08	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
4	-10.49	NULL	594	BP cell adhesion
5	-10.43	NULL	1242	BP Golgi apparatus
6	-9.67	NULL	627	BP ion transport
7	-9.44	NULL	236	BP chemical synaptic transmission
8	-9.1	NULL	43	BP antigen processing and presentation
9	-8.81	NULL	615	BP transmembrane transport
10	-8.17	NULL	364	BP inflammatory response
11	-7.9	NULL	460	BP neutrophil degranulation
12	-7.85	NULL	118	BP platelet degranulation
13	-7.63	NULL	388	BP immune response
14	-7.51	NULL	574	BP synapse
15	-7.48	NULL	657	BP calcium ion binding
16	-7.38	NULL	1500	BP signal transduction
17	-7.36	NULL	275	BP ion transmembrane transport
18	-7.08	NULL	254	BP angiogenesis
19	-6.96	NULL	564	BP immune system process
20	-6.82	NULL	170	BP protein glycosylation

p-values

