

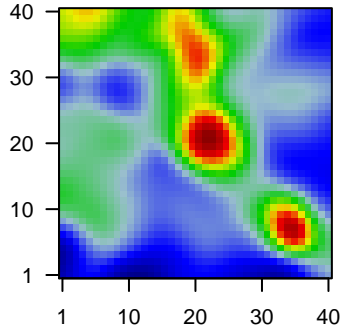
# 2577N

## Global Summary

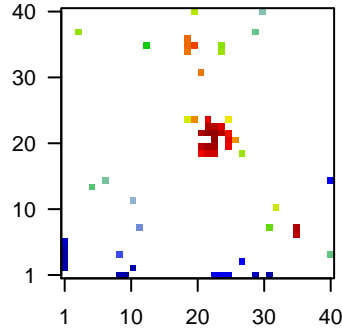
%DE = 0.09  
 # genes with fdr < 0.2 = 2880 ( 1980 + / 900 - )  
 # genes with fdr < 0.1 = 2106 ( 1494 + / 612 - )  
 # genes with fdr < 0.05 = 1789 ( 1280 + / 509 - )  
 # genes with fdr < 0.01 = 1122 ( 826 + / 296 - )  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = -0.05  
 <p-value> = 0.19  
 <fdr> = 0.91

### Portrait



### Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1553635_s_at	2.25	2e-16 2e-13	22 x 20 Tctex1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1553635]
2	1555804_a_at	2.45	2e-16 2e-13	22 x 23 mitogen-activated protein kinase kinase kinase 19 [Source:HGNC Symbol;Acc:HGNC:1555804]
3	1556711_at	2.18	2e-16 2e-13	30 x 40 family with sequence similarity 216 member B [Source:HGNC Symbol;Acc:HGNC:1556711]
4	1557636_a_at	2.43	2e-16 2e-13	21 x 22 chromosome 7 open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:1557636]
5	1558010_s_at	-1.24	2e-16 2e-13	10 x 1 solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:HGNC:1558010]
6	1562371_s_at	2.33	2e-16 2e-13	24 x 23 von Willebrand factor A domain containing 3B [Source:HGNC Symbol;Acc:HGNC:1562371]
7	1563830_a_at	2.3	2e-16 2e-13	25 x 21 forkhead associated phosphopeptide binding domain 1 [Source:HGNC Symbol;Acc:HGNC:1563830]
8	202018_s_at	2.88	2e-16 2e-13	19 x 35 lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
9	204041_at	1.2	2e-16 2e-13	23 x 20 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:6820]
10	205289_at	-1.46	2e-16 2e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:205289]
11	205290_s_at	-1.56	2e-16 2e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:205290]
12	206501_x_at	-1.51	2e-16 2e-13	1 x 2 ETS variant 1 [Source:HGNC Symbol;Acc:HGNC:3490]
13	207659_s_at	1.44	2e-16 2e-13	35 x 7 myelin-associated oligodendrocyte basic protein [Source:HGNC Symbol;Acc:HGNC:207659]
14	208650_s_at	1.89	2e-16 2e-13	1 x 5 CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:208650]
15	208651_x_at	1.71	2e-16 2e-13	1 x 6 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
16	209047_at	1.13	2e-16 2e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:209047]
17	209395_at	1.75	2e-16 2e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
18	209396_s_at	1.97	2e-16 2e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
19	209771_x_at	1.63	2e-16 2e-13	1 x 6 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
20	209772_s_at	2.33	2e-16 2e-13	1 x 5 CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:209772]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.98	NULL	32	BP cilium movement
2	10.94	NULL	180	BP cell projection organization
3	8.71	NULL	11	BP axonemal dynein complex assembly
4	8.67	NULL	14	BP inner dynein arm assembly
5	8.67	NULL	17	BP epithelial cilium movement
6	8.1	NULL	17	BP cilium-dependent cell motility
7	7.98	NULL	173	BP cilium assembly
8	7.9	NULL	21	BP motile cilium assembly
9	6.95	NULL	61	BP flagellated sperm motility
10	6.75	NULL	460	BP neutrophil degranulation
11	6.72	NULL	10	BP epithelial cilium movement involved in determination of left/right asymmetry
12	6.68	NULL	17	BP outer dynein arm assembly
13	6.44	NULL	11	BP cilium movement involved in cell motility
14	6.17	NULL	79	BP microtubule-based movement
15	6.05	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigens on MHC class II
16	5.94	NULL	19	BP axoneme assembly
17	5.34	NULL	26	BP ATP-dependent microtubule motor activity, plus-end-directed
18	5.17	NULL	112	BP motor activity
19	5.01	NULL	43	BP antigen processing and presentation
20	4.96	NULL	71	BP determination of left/right symmetry
<i>Underexpressed</i>				
1	-10.1	NULL	1435	BP mitochondrion
2	-7.55	NULL	574	BP synapse
3	-7.53	NULL	276	BP translation
4	-6.61	NULL	236	BP chemical synaptic transmission
5	-6.57	NULL	240	BP postsynaptic membrane
6	-6.11	NULL	61	BP positive regulation of synapse assembly
7	-5.41	NULL	83	BP mitochondrial translational elongation
8	-5.39	NULL	229	BP mRNA splicing, via spliceosome
9	-5.38	NULL	152	BP rRNA processing
10	-5.35	NULL	85	BP mitochondrial translational termination
11	-4.81	NULL	505	BP nervous system development
12	-4.75	NULL	545	BP protein ubiquitination
13	-4.67	NULL	28	BP telencephalon development
14	-4.66	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
15	-4.65	NULL	120	BP translational initiation
16	-4.65	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
17	-4.57	NULL	59	BP mitochondrial respiratory chain complex I assembly
18	-4.54	NULL	1145	BP regulation of transcription by RNA polymerase II
19	-4.53	NULL	541	BP negative regulation of transcription, DNA-templated
20	-4.42	NULL	400	BP chromatin binding

### p-values

