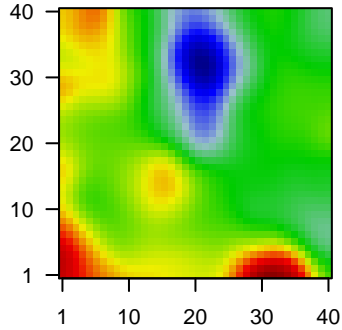


# group 7

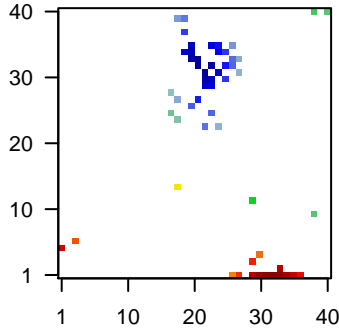
## Global Summary

%DE = 0.59  
 # genes with fdr < 0.2 = 22385 ( 11397 + / 10988 -)  
 # genes with fdr < 0.1 = 17785 ( 9012 + / 8773 -)  
 # genes with fdr < 0.05 = 14495 ( 7319 + / 7176 -)  
 # genes with fdr < 0.01 = 9281 ( 4508 + / 4773 -)  
  
 # genes in genesets = 16360  
  
 <FC> = 0  
 <t-score> = -0.02  
 <p-value> = 0  
 <fdr> = 0.41

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1554141_s_at	-0.49	0e+00	3e-12	22 x 23 WD repeat domain 78 [Source:HGNC Symbol;Acc:HGNC:26;
2	1554791_a_at	-0.53	0e+00	3e-12	23 x 30 KAT8 regulatory NSL complex subunit 1 like [Source:HGNC S
3	204850_s_at	0.67	0e+00	3e-12	1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
4	204851_s_at	0.61	0e+00	3e-12	1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
5	227522_at	0.41	0e+00	3e-12	29 x 1 carboxymethylglutamate decarboxylase homolog [Source:HGNC Sym
6	227830_at	0.63	0e+00	3e-12	34 x 1 gamma-aminobutyric acid type A receptor beta3 subunit [So
7	228504_at	-0.84	0e+00	3e-12	22 x 31 sodium voltage-gated channel alpha subunit 7 [Source:HGNC
8	229313_at	0.45	0e+00	3e-12	34 x 1 anoctamin 5 [Source:HGNC Symbol;Acc:HGNC:27337]
9	231044_at	-0.82	0e+00	3e-12	24 x 35 chromosome 1 open reading frame 194 [Source:HGNC Synt
10	239984_at	-0.43	0e+00	3e-12	23 x 32 sodium voltage-gated channel alpha subunit 7 [Source:HGNC
11	219890_at	-0.64	2e-16	3e-12	20 x 35 C-type lectin domain containing 5A [Source:HGNC Symbol;A
12	229550_at	0.67	2e-16	3e-12	32 x 1 unc-79 homolog, NALCN channel complex subunit [Source:†
13	208860_s_at	0.33	4e-16	3e-12	29 x 3 ATRX, chromatin remodeler [Source:HGNC Symbol;Acc:HGNC
14	211894_x_at	0.69	7e-16	4e-12	31 x 1 seizure related 6 homolog like [Source:HGNC Symbol;Acc:H
15	238808_at	-0.25	7e-16	4e-12	25 x 32 homeobox A13 [Source:HGNC Symbol;Acc:HGNC:5102]
16	230869_at	0.5	9e-16	4e-12	32 x 1 family with sequence similarity 155 member A [Source:HGNC
17	231650_s_at	0.57	1e-15	4e-12	31 x 1
18	207873_x_at	0.79	1e-15	1e-11	31 x 1 seizure related 6 homolog like [Source:HGNC Symbol;Acc:H
19	230561_s_at	-0.76	1e-15	1e-11	22 x 30 KAT8 regulatory NSL complex subunit 1 like [Source:HGNC S
20	213609_s_at	0.61	2e-15	2e-11	31 x 1 seizure related 6 homolog like [Source:HGNC Symbol;Acc:H

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.46	NULL	276	BP translation
2	8.13	NULL	1435	BP mitochondrion
3	7.22	NULL	358	BP mRNA processing
4	7.07	NULL	279	BP RNA splicing
5	6.84	NULL	366	BP DNA repair
6	6.53	NULL	229	BP mRNA splicing, via spliceosome
7	6.35	NULL	484	BP cellular response to DNA damage stimulus
8	5.95	NULL	85	BP mitochondrial translational termination
9	5.85	NULL	83	BP mitochondrial translational elongation
10	5.79	NULL	120	BP translational initiation
11	5.75	NULL	505	BP nervous system development
12	5.47	NULL	630	BP protein transport
13	5.42	NULL	574	BP synapse
14	5.16	NULL	93	BP ribosome biogenesis
15	5.07	NULL	630	BP cell cycle
16	5.04	NULL	90	BP viral transcription
17	5.03	NULL	29	BP cytoplasmic translation
18	4.98	NULL	48	BP synapse organization
19	4.91	NULL	158	BP DNA replication
20	4.61	NULL	240	BP postsynaptic membrane
<i>Underexpressed</i>				
1	-12.77	NULL	564	BP immune system process
2	-12.57	NULL	388	BP immune response
3	-10.92	NULL	364	BP inflammatory response
4	-9.81	NULL	417	BP innate immune response
5	-9.53	NULL	289	BP cytokine-mediated signaling pathway
6	-9.46	NULL	460	BP neutrophil degranulation
7	-8.98	NULL	1500	BP signal transduction
8	-8.71	NULL	155	BP regulation of immune response
9	-8.34	NULL	4278	BP plasma membrane
10	-8.04	NULL	222	BP adaptive immune response
11	-7.04	NULL	151	BP defense response to bacterium
12	-6.87	NULL	151	BP cellular response to lipopolysaccharide
13	-6.75	NULL	56	BP B cell receptor signaling pathway
14	-6.68	NULL	777	BP G protein-coupled receptor signaling pathway
15	-6.61	NULL	148	BP chemotaxis
16	-6.45	NULL	159	BP response to lipopolysaccharide
17	-6.38	NULL	152	BP leukocyte migration
18	-6.35	NULL	89	BP Fc-gamma receptor signaling pathway involved in phagocytosis
19	-6.25	NULL	59	BP positive regulation of T cell proliferation
20	-5.92	NULL	74	BP neutrophil chemotaxis

p-values

