

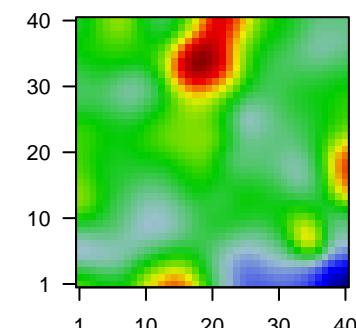
# 2592H

## Global Summary

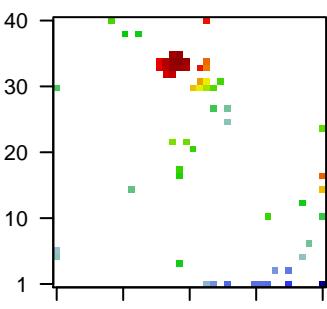
%DE = 0.09  
 # genes with fdr < 0.2 = 3102 ( 1822 + / 1280 - )  
 # genes with fdr < 0.1 = 2329 ( 1384 + / 945 - )  
 # genes with fdr < 0.05 = 1823 ( 1101 + / 722 - )  
 # genes with fdr < 0.01 = 1091 ( 671 + / 420 - )  
 # genes in genesets = 16360

$\langle FC \rangle = 0$   
 $\langle t\text{-score} \rangle = -0.04$   
 $\langle p\text{-value} \rangle = 0.19$   
 $\langle fdr \rangle = 0.91$

## Portrait



## Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description	Metagene
<b>Overexpressed</b>					
1	1554663_a_a'	2.13	2e-16	nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC:1247]	32 x 11
2	1555229_a_a'	2.25	2e-16	complement C1s [Source:HGNC Symbol;Acc:HGNC:1247]	18 x 32
3	1556069_s_at	-1.91	2e-16	hypoxia inducible factor 3 subunit alpha [Source:HGNC Symbol;Acc:HGNC:1697]	26 x 25
4	1558170_at	-1.1	2e-16	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]	32 x 1
5	1567628_at	1.44	2e-16	major histocompatibility complex, class II, DP beta 1 [Source:HGNC Symbol;Acc:HGNC:1697]	20 x 33
6	201137_s_at	1.23	2e-16	serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:1697]	19 x 34
7	202376_at	1.54	2e-16	serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:1697]	19 x 34
8	203290_at	2.37	2e-16	major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:1697]	19 x 34
9	204103_at	-1.55	2e-16	C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:HGNC:1697]	22 x 30
10	204537_s_at	2.12	2e-16	gamma-aminobutyric acid type A receptor epsilon subunit [Source:HGNC Symbol;Acc:HGNC:1697]	18 x 33
11	204575_s_at	2.56	2e-16	matrix metallopeptidase 19 [Source:HGNC Symbol;Acc:HGNC:1697]	17 x 33
12	204614_at	2.08	2e-16	serpin family B member 2 [Source:HGNC Symbol;Acc:HGNC:1697]	16 x 33
13	204684_at	-1.46	2e-16	neuronal pentraxin 1 [Source:NCBI gene;Acc:4884]	40 x 1
14	205114_s_at	-1.89	2e-16	C-C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:HGNC:1697]	23 x 30
15	205374_at	2.44	2e-16	sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]	19 x 33
16	205495_s_at	2.14	2e-16	granulysin [Source:HGNC Symbol;Acc:HGNC:4414]	17 x 33
17	205700_at	-1.97	2e-16	hydroxysteroid 17-beta dehydrogenase 6 [Source:HGNC Symbol;Acc:HGNC:1697]	38 x 7
18	205858_at	2.31	2e-16	nerve growth factor receptor [Source:HGNC Symbol;Acc:HGNC:1697]	19 x 18
19	206012_at	2.11	2e-16	left-right determination factor 2 [Source:HGNC Symbol;Acc:HGNC:1697]	20 x 34
20	206190_at	-2	2e-16	G protein-coupled receptor 17 [Source:HGNC Symbol;Acc:HGNC:1697]	31 x 1

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<b>Overexpressed</b>				
1	15.36	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
2	13.14	NULL	43	BP antigen processing and presentation
3	12.2	NULL	564	immune system process
4	10.36	NULL	388	immune response
5	9.98	NULL	155	regulation of immune response
6	9.39	NULL	4278	plasma membrane
7	8.65	NULL	460	neutrophil degranulation
8	8.59	NULL	7387	membrane
9	8.43	NULL	1242	BP Golgi apparatus
10	8.06	NULL	93	antigen processing and presentation of exogenous peptide antigen
11	7.78	NULL	160	T cell receptor signaling pathway
12	7.77	NULL	6202	cytoplasm
13	7.68	NULL	594	cell adhesion
14	7.64	NULL	417	innate immune response
15	7.15	NULL	64	complement activation, classical pathway
16	7.08	NULL	64	regulation of complement activation
17	6.73	NULL	364	inflammatory response
18	6.61	NULL	289	cytokine-mediated signaling pathway
19	6.55	NULL	36	semaphorin–plexin signaling pathway
20	6.2	NULL	118	platelet degranulation
<b>Underexpressed</b>				
1	-8.35	NULL	1435	mitochondrion
2	-6.26	NULL	276	translation
3	-5.91	NULL	12	regulation of postsynaptic neurotransmitter receptor activity
4	-5.45	NULL	236	chemical synaptic transmission
5	-4.89	NULL	120	translational initiation
6	-4.75	NULL	28	synaptic vesicle exocytosis
7	-4.73	NULL	25	regulation of dopamine secretion
8	-4.58	NULL	15	calcium ion-regulated exocytosis of neurotransmitter
9	-4.48	NULL	21	positive regulation of dendrite extension
10	-4.48	NULL	16	regulation of calcium ion-dependent exocytosis
11	-4.26	NULL	16	positive regulation of calcium ion-dependent exocytosis
12	-4.16	NULL	83	mitochondrial translational elongation
13	-4.15	NULL	59	mitochondrial respiratory chain complex I assembly
14	-4.02	NULL	69	SRP-dependent cotranslational protein targeting to membrane
15	-3.98	NULL	93	ribosome biogenesis
16	-3.97	NULL	85	mitochondrial translational termination
17	-3.92	NULL	30	associative learning
18	-3.87	NULL	43	mitochondrial electron transport, NADH to ubiquinone
19	-3.85	NULL	152	rRNA processing
20	-3.85	NULL	30	sterol biosynthetic process

