

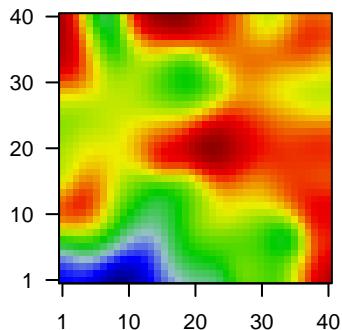
# 21621K

## Global Summary

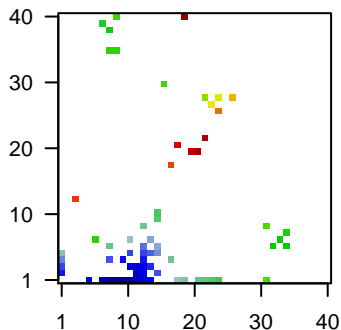
%DE = 0.1  
 # genes with fdr < 0.2 = 3166 ( 1061 + / 2105 - )  
 # genes with fdr < 0.1 = 2282 ( 687 + / 1595 - )  
 # genes with fdr < 0.05 = 1671 ( 448 + / 1223 - )  
 # genes with fdr < 0.01 = 1003 ( 235 + / 768 - )  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = -0.32  
 <p-value> = 0.19  
 <fdr> = 0.9

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1552978_a_at	-2.05	2e-16	2e-13	12 x 1 secretory carrier membrane protein 1 [Source:HGNC Symbol]
2	1554747_a_at	-1.45	2e-16	2e-13	12 x 2 septin 2 [Source:HGNC Symbol;Acc:HGNC:7729]
3	1554784_at	-1.46	2e-16	2e-13	24 x 1 contactin 1 [Source:HGNC Symbol;Acc:HGNC:2171]
4	1557910_at	-1.97	2e-16	2e-13	11 x 1 heat shock protein 90 alpha family class B member 1 [Source:HGNC Symbol;Acc:HGNC:1000]
5	1558009_at	-1.93	2e-16	2e-13	9 x 1 solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:HGNC:1000]
6	1558010_s_at	-2	2e-16	2e-13	10 x 1 solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:HGNC:1000]
7	1558093_s_at	-1.77	2e-16	2e-13	9 x 1 matrin 3 [Source:NCBI gene;Acc:9782]
8	200900_s_at	-1.67	2e-16	2e-13	15 x 5 mannose-6-phosphate receptor, cation dependent [Source:HGNC Symbol;Acc:HGNC:1000]
9	202170_s_at	-1.4	2e-16	2e-13	9 x 35 aminoacidate-sialdehyde dehydrogenase-phosphopantetate [Source:HGNC Symbol;Acc:HGNC:1000]
10	203242_s_at	-1.57	2e-16	2e-13	14 x 3 PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1000]
11	203548_s_at	-1.51	2e-16	2e-13	26 x 28 lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
12	204160_s_at	-1.68	2e-16	2e-13	32 x 6 ectonucleotide pyrophosphatase/phosphodiesterase 4 [Source:HGNC Symbol;Acc:HGNC:1000]
13	204529_s_at	-1.55	2e-16	2e-13	23 x 1 thymocyte selection associated high mobility group box [Source:HGNC Symbol;Acc:HGNC:1000]
14	205289_at	-1.67	2e-16	2e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:1000]
15	205290_s_at	-1.58	2e-16	2e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:1000]
16	206113_s_at	-1.59	2e-16	2e-13	11 x 1 RAB5A, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:1000]
17	206190_at	-1.49	2e-16	2e-13	31 x 1 G protein-coupled receptor 17 [Source:HGNC Symbol;Acc:HGNC:1000]
18	206243_at	-2.52	2e-16	2e-13	15 x 11 TIMP metalloproteinase inhibitor 4 [Source:HGNC Symbol;Acc:HGNC:1000]
19	206331_at	-2.32	2e-16	2e-13	1 x 4 calcitonin receptor like receptor [Source:HGNC Symbol;Acc:HGNC:1000]
20	206501_x_at	-1.87	2e-16	2e-13	1 x 2 ETS variant 1 [Source:HGNC Symbol;Acc:HGNC:3490]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	4.19	NULL	23	BP proximal/distal pattern formation
2	3.93	NULL	15	BP water transport
3	3.92	NULL	43	BP neurotransmitter transport
4	3.85	NULL	12	BP regulation of postsynaptic neurotransmitter receptor activity
5	3.78	NULL	22	BP drug metabolic process
6	3.64	NULL	21	BP cellular response to copper ion
7	3.6	NULL	95	BP anterior/posterior pattern specification
8	3.51	NULL	17	BP cellular response to zinc ion
9	3.35	NULL	1080	BP multicellular organism development
10	3.28	NULL	83	BP xenobiotic metabolic process
11	3.22	NULL	20	BP execution phase of apoptosis
12	3.16	NULL	40	BP embryonic skeletal system development
13	3.1	NULL	51	BP neurotransmitter secretion
14	3.09	NULL	25	BP calmodulin-dependent protein kinase activity
15	3.03	NULL	16	BP negative regulation of growth
16	2.98	NULL	32	BP embryonic forelimb morphogenesis
17	2.97	NULL	30	BP associative learning
18	2.96	NULL	23	BP dopaminergic neuron differentiation
19	2.87	NULL	28	BP synaptic vesicle exocytosis
20	2.86	NULL	159	BP actin cytoskeleton organization
<i>Underexpressed</i>				
1	-9.79	NULL	4740	BP cytosol
2	-8.82	NULL	7387	BP membrane
3	-8.59	NULL	630	BP protein transport
4	-6.71	NULL	358	BP mRNA processing
5	-6.53	NULL	279	BP RNA splicing
6	-6.42	NULL	459	BP viral process
7	-6.36	NULL	276	BP translation
8	-6.06	NULL	6202	BP cytoplasm
9	-6.05	NULL	149	BP protein folding
10	-5.92	NULL	1435	BP mitochondrion
11	-5.78	NULL	229	BP mRNA splicing, via spliceosome
12	-5.65	NULL	43	BP protein destabilization
13	-5.65	NULL	460	BP neutrophil degranulation
14	-5.52	NULL	129	BP rhythmic process
15	-5.47	NULL	80	BP response to endoplasmic reticulum stress
16	-5.47	NULL	1242	BP Golgi apparatus
17	-5.41	NULL	545	BP protein ubiquitination
18	-5.28	NULL	14	BP collagen metabolic process
19	-5.21	NULL	43	BP sphingolipid metabolic process
20	-5.03	NULL	10	BP cardiac left ventricle morphogenesis

p-values

