

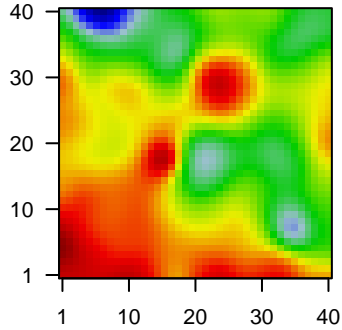
# 9029P

## Global Summary

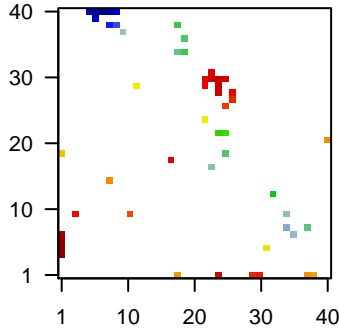
%DE = 0.05  
 # genes with fdr < 0.2 = 1519 ( 661 + / 858 - )  
 # genes with fdr < 0.1 = 919 ( 383 + / 536 - )  
 # genes with fdr < 0.05 = 790 ( 327 + / 463 - )  
 # genes with fdr < 0.01 = 445 ( 177 + / 268 - )  
  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0.14  
 <p-value> = 0.27  
 <fdr> = 0.95

Portrait



Top 100 DE genes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1558678_s_at	-0.82	2e-16	5e-13	7 x 40 metastasis associated lung adenocarcinoma transcript 1 [Sou
2	1569607_s_at	-1.13	2e-16	5e-13	6 x 39 ankyrin repeat domain 20 family member A3 [Source:HGNC ;
3	201909_at	-1.49	2e-16	5e-13	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:Hi
4	202376_at	-1.75	2e-16	5e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
5	203001_s_at	1	2e-16	5e-13	38 x 1 stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
6	203849_s_at	-1.16	2e-16	5e-13	7 x 40 kinesin family member 1A [Source:HGNC Symbol;Acc:HGNC
7	204103_at	1.42	2e-16	5e-13	22 x 30 C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:Hi
8	205114_s_at	1.2	2e-16	5e-13	23 x 30 C-C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:Hi
9	208859_s_at	-1.08	2e-16	5e-13	7 x 40 ATRX, chromatin remodeler [Source:HGNC Symbol;Acc:HGNC
10	213592_at	-1.33	2e-16	5e-13	19 x 36 apelin receptor [Source:HGNC Symbol;Acc:HGNC:339]
11	214218_s_at	2.27	2e-16	5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC
12	214464_at	-1.25	2e-16	5e-13	7 x 40 CDC42 binding protein kinase alpha [Source:HGNC Symbol;A
13	221728_x_at	2	2e-16	5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC
14	223940_x_at	-0.94	2e-16	5e-13	6 x 40 metastasis associated lung adenocarcinoma transcript 1 [Sou
15	224568_x_at	-1.03	2e-16	5e-13	6 x 40 metastasis associated lung adenocarcinoma transcript 1 [Sou
16	224588_at	2.47	2e-16	5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC
17	224590_at	1.84	2e-16	5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC
18	224840_at	-1.15	2e-16	5e-13	22 x 24 FKBP prolyl isomerase 5 [Source:HGNC Symbol;Acc:HGNC:
19	227062_at	-1.17	2e-16	5e-13	18 x 38 nuclear paraspeckle assembly transcript 1 [Source:HGNC Sy
20	227671_at	2.27	2e-16	5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.5	NULL	630	BP cell cycle
2	9.35	NULL	394	BP cell division
3	6.53	NULL	85	BP chromosome segregation
4	6.07	NULL	229	BP mRNA splicing, via spliceosome
5	6.02	NULL	158	BP DNA replication
6	5.88	NULL	164	BP mitotic cell cycle
7	5.83	NULL	366	BP DNA repair
8	5.59	NULL	13	BP microtubule depolymerization
9	5.5	NULL	358	BP mRNA processing
10	5.33	NULL	1145	BP regulation of transcription by RNA polymerase II
11	5.22	NULL	4740	BP cytosol
12	5.19	NULL	11	BP metaphase plate congression
13	5.17	NULL	18	BP eosinophil chemotaxis
14	5.13	NULL	31	BP mitotic sister chromatid segregation
15	5.03	NULL	16	BP positive regulation of calcium-mediated signaling
16	4.94	NULL	24	BP negative regulation of neurogenesis
17	4.89	NULL	279	BP RNA splicing
18	4.75	NULL	26	BP lymphocyte chemotaxis
19	4.72	NULL	783	BP negative regulation of transcription by RNA polymerase II
20	4.7	NULL	22	BP mitotic spindle assembly checkpoint
<i>Underexpressed</i>				
1	-5.9	NULL	21	BP cellular response to copper ion
2	-5.76	NULL	16	BP negative regulation of growth
3	-5.54	NULL	4278	BP plasma membrane
4	-5.19	NULL	118	BP platelet degranulation
5	-5	NULL	21	BP fibrinolysis
6	-4.9	NULL	34	BP acute-phase response
7	-4.81	NULL	128	BP negative regulation of endopeptidase activity
8	-4.8	NULL	64	BP regulation of complement activation
9	-4.77	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
10	-4.68	NULL	47	BP complement activation
11	-4.64	NULL	43	BP antigen processing and presentation
12	-4.61	NULL	64	BP complement activation, classical pathway
13	-4.6	NULL	155	BP regulation of immune response
14	-4.56	NULL	110	BP negative regulation of peptidase activity
15	-4.56	NULL	17	BP cellular response to zinc ion
16	-4.48	NULL	564	BP immune system process
17	-4.43	NULL	25	BP positive regulation of focal adhesion assembly
18	-4.42	NULL	14	BP positive regulation of myelination
19	-4.33	NULL	24	BP regulation of glucose metabolic process
20	-4.27	NULL	52	BP hemostasis

p-values

