

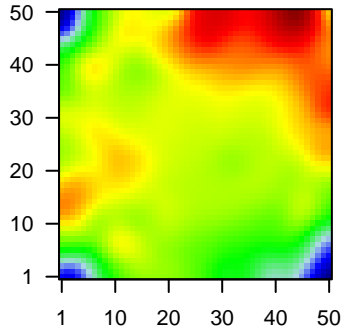
GW_308

Global Summary

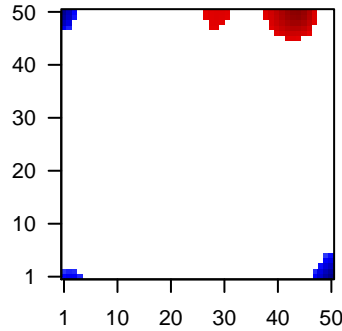
%DE = 0.13
 # genes with fdr < 0.2 = 1706 (746 + / 960 -)
 # genes with fdr < 0.1 = 1222 (483 + / 739 -)
 # genes with fdr < 0.05 = 896 (303 + / 593 -)
 # genes with fdr < 0.01 = 631 (177 + / 454 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.13
 <fdr> = 0.87

Profile



Regulated Spots



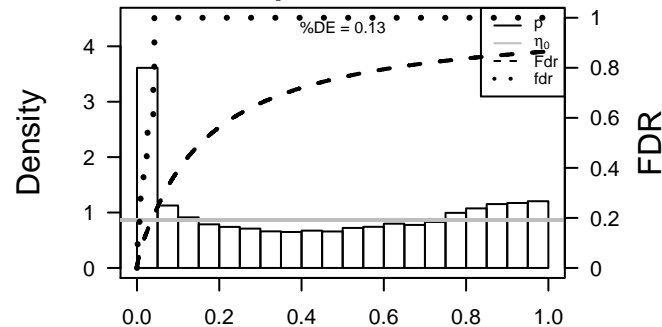
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.69	2e-16	6e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	220	2.24	2e-16	6e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC]
3	218	2.1	2e-16	6e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
4	633	-2.52	2e-16	6e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
5	810	-2.52	2e-16	6e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
6	100133941	-2	2e-16	6e-14	3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
7	4680	-2.34	2e-16	6e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (I)
8	1056	2.37	2e-16	6e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
9	22802	-2	2e-16	6e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20197]
10	1277	-2.56	2e-16	6e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
11	1278	-2.58	2e-16	6e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
12	1281	-2.66	2e-16	6e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
13	1289	-2.14	2e-16	6e-14	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
14	1290	-2.39	2e-16	6e-14	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
15	1293	-2.33	2e-16	6e-14	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
16	1396	-2.08	2e-16	6e-14	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:1396]
17	49860	-2.07	2e-16	6e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	92196	-2.18	2e-16	6e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2196]
19	1672	-2.03	2e-16	6e-14	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
20	1673	-2.05	2e-16	6e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.23	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	12.23	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	11.46	NULL	1318	CC mitochondrion
4	10.91	NULL	370	BP mitotic cell cycle
5	10.59	NULL	949	CC nucleoplasm
6	10.1	NULL	1233	TF KIM_MYC targets
7	9.48	NULL	4640	CC nucleus
8	9.29	NULL	595	MF RNA binding
9	9.2	NULL	649	BP gene expression
10	9.11	NULL	232	BP mitosis
11	8.09	NULL	298	BP DNA repair
12	7.73	NULL	519	Chr Chr 14
13	7.21	NULL	313	Glio wilscher_GBM_Verhaak-CL_expression_D_up
14	7.21	NULL	313	Glio wilscher_GBM_Verhaak-MES_expression_D_down
15	7.21	NULL	313	Glio wilscher_GBM_Verhaak-PNwt_expression_D_up
16	7.01	NULL	436	miRNA target sites
17	6.82	NULL	336	miRNA target sites
18	6.74	NULL	66	CC condensed chromosome kinetochore
19	6.72	NULL	229	BP RNA splicing
20	6.62	NULL	163	BP mRNA splicing, via spliceosome
<i>Underexpressed</i>				
1	-24.61	NULL	553	Cancer Lembecke_Colonc Inflammation
2	-20.94	NULL	1182	CC extracellular region
3	-19.98	NULL	135	H.Tiss WIRTH_Mucosa
4	-17.51	NULL	250	Lymphoma ENZ_Stromal signature 1
5	-17.15	NULL	190	CC extracellular matrix
6	-16.95	NULL	683	CC extracellular space
7	-14.96	NULL	312	BP immune response
8	-14.91	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
9	-14.91	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
10	-14.91	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
11	-14.91	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
12	-14.47	NULL	242	BP extracellular matrix organization
13	-13.91	NULL	69	BP extracellular matrix disassembly
14	-13.55	NULL	21	CC cornified envelope
15	-13.19	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
16	-12.95	NULL	572	Disease GUDJ_psooriasis up
17	-12.67	NULL	64	BP collagen catabolic process
18	-12.36	NULL	403	BP cell adhesion
19	-12.1	NULL	16	MMML C6SCIEJ_MMML 1
20	-11.93	NULL	42	BP keratinization

p-values



GW_308

Local Summary

%DE = 0.75
 # metagenes = 47
 # genes = 599
 # genes in genesets = 592

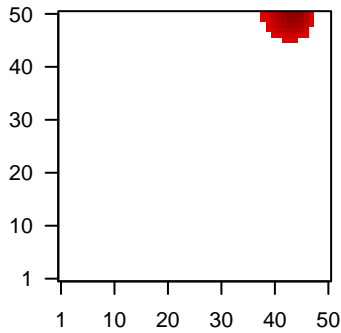
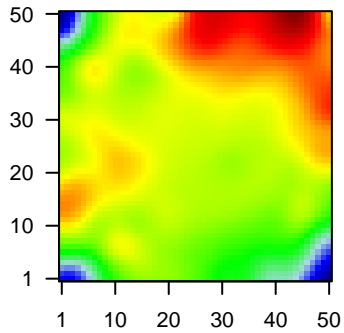
genes with $fdr < 0.1$ = 339 (335 + / 4 -)
 # genes with $fdr < 0.05$ = 205 (203 + / 2 -)
 # genes with $fdr < 0.01$ = 70 (69 + / 1 -)

<r> metagenes = 0.9
 <r> genes = 0.32

<FC> = 0.44
 <shrinkage-t> = 15.3
 <p-value> = 0.03
 <fdr> = 0.67

Profile

Spot



Local Genelist

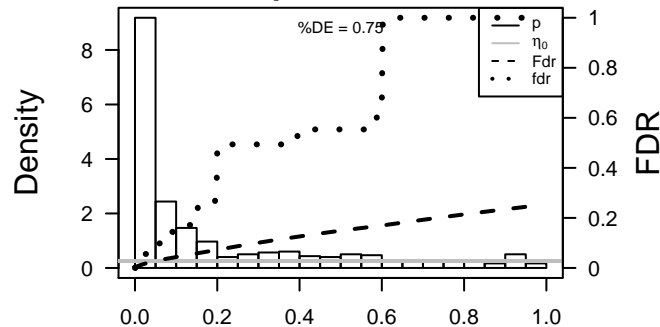
Rank	ID	log(FC)	fdr	p-value	Description
1	8500	1.93	2e-15	3e-06	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (PT
2	134147	1.36	2e-08	8e-06	40 x 48 carboxymethylglutamate decarboxylase homolog (Pseudomonas) [So
3	3945	1.31	7e-08	4e-05	40 x 50 lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
4	3992	1.23	4e-07	4e-05	45 x 50 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
5	3015	1.11	5e-07	4e-05	45 x 48 H2A histone family, member Z [Source:HGNC Symbol;Acc:47
6	4904	1.1	8e-07	6e-05	41 x 49 Y box binding protein 1 [Source:HGNC Symbol;Acc:8014]
7	90390	1.16	2e-06	6e-05	44 x 50 mediator complex subunit 30 [Source:HGNC Symbol;Acc:230
8	708	1.15	2e-06	6e-05	41 x 50 complement component 1, q subcomponent binding protein [
9	6611	1.14	2e-06	6e-05	42 x 50 spermine synthase [Source:HGNC Symbol;Acc:11123]
10	26872	-1.14	3e-06	6e-05	40 x 50 six transmembrane epithelial antigen of the prostate 1 [Sourc
11	3251	1.13	3e-06	6e-05	42 x 50 hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
12	29028	1.13	3e-06	6e-05	44 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Sym
13	7019	1.12	4e-06	6e-05	43 x 45 transcription factor A, mitochondrial [Source:HGNC Symbol;A
14	7083	1.12	4e-06	3e-04	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
15	6627	1.1	6e-06	4e-04	43 x 46 small nuclear ribonucleoprotein polypeptide A' [Source:HGNC
16	7443	1.08	8e-06	5e-04	43 x 50 vaccinia related kinase 1 [Source:HGNC Symbol;Acc:12718]
17	64105	1.03	2e-05	5e-04	45 x 48 centromere protein K [Source:HGNC Symbol;Acc:29479]
18	50810	1.03	2e-05	5e-04	46 x 50 Hepatoma-derived growth factor-related protein 3 [Source:L
19	55635	1.01	3e-05	5e-04	44 x 50 DEP domain containing 1 [Source:HGNC Symbol;Acc:22949]
20	51218	1.01	3e-05	5e-04	41 x 46 glutaredoxin 5 [Source:HGNC Symbol;Acc:20134]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	42.12	NULL	100 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	42.12	NULL	100 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	24.28	NULL	118 / 370	BP mitotic cell cycle
4	21.79	NULL	15 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	20.33	NULL	14 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
6	19.76	NULL	114 / 530	Cancer Lembecke_Normal vs Adenoma
7	19.51	NULL	64 / 232	BP mitosis
8	19.09	NULL	13 / 14	MMML C2SCIEJ_MMML_4
9	18.93	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
10	18.77	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	18.75	NULL	12 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
12	18.6	NULL	16 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
13	18.54	NULL	9 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
14	17.68	NULL	24 / 57	Glio developing astrocytes
15	17.32	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
16	17.01	NULL	13 / 18	BP spindle organization
17	15.73	NULL	11 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
18	15.26	NULL	11 / 15	GSEA C2CHANG_CYCLING_GENES
19	15.21	NULL	10 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
20	15.21	NULL	12 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
21	14.73	NULL	11 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
22	14.57	NULL	11 / 16	Cancer WOLFER_overlap genes
23	14.47	NULL	9 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
24	14.24	NULL	12 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
25	14.21	NULL	11 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
26	14.2	NULL	138 / 949	CC nucleoplasm
27	14.19	NULL	9 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
28	14.02	NULL	15 / 35	BP mitotic nuclear envelope disassembly
29	13.99	NULL	24 / 66	CC condensed chromosome kinetochore
30	13.93	NULL	50 / 149	BP DNA replication
31	13.69	NULL	25 / 56	CC chromosome, centromeric region
32	13.68	NULL	12 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
33	13.45	NULL	8 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
34	13.44	NULL	73 / 572	Disease GUDJ_poriasis up
35	13.16	NULL	22 / 83	CC spindle pole
36	12.69	NULL	22 / 109	CC spindle
37	12.64	NULL	10 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
38	12.57	NULL	4 / 6	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_DN
39	12.56	NULL	10 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
40	12.47	NULL	8 / 15	GSEA C2REACTOME_CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2

p-values



GW_308

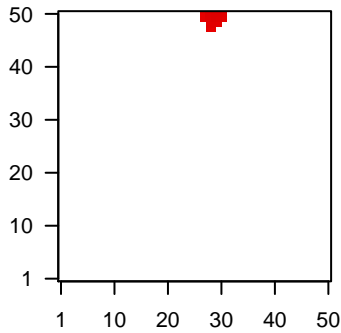
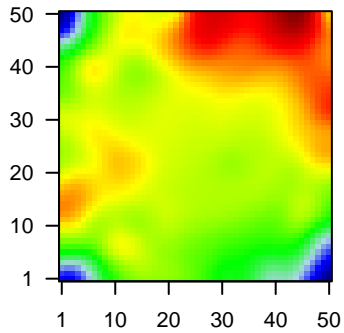
Local Summary

%DE = 0.5
 # metagenes = 15
 # genes = 221
 # genes in genesets = 218
 # genes with $fdr < 0.1$ = 68 (64 + / 4 -)
 # genes with $fdr < 0.05$ = 45 (44 + / 1 -)
 # genes with $fdr < 0.01$ = 12 (12 + / 0 -)

$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.31
 $\langle FC \rangle$ = 0.34
 $\langle \text{shrinkage-t} \rangle$ = 11.8
 $\langle p\text{-value} \rangle$ = 0.06
 $\langle fdr \rangle$ = 0.73

Profile

Spot



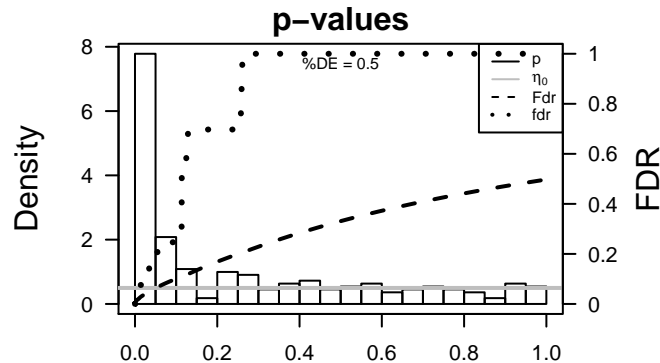
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	55848	1.21	6e-07	3e-04	31 x 50 plasminogen receptor, C-terminal lysine transmembrane prot
2	6175	1.13	3e-06	3e-04	31 x 50 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:1037
3	10935	1.1	5e-06	4e-04	29 x 50 peroxiredoxin 3 [Source:HGNC Symbol;Acc:9354]
4	23443	1.07	9e-06	4e-04	27 x 50 solute carrier family 35 (UDP-N-acetylglucosamine (UDP-G
5	6392	1.06	1e-05	1e-03	31 x 50 succinate dehydrogenase complex, subunit D, integral membi
6	51397	1.02	2e-05	2e-03	29 x 50 COMM domain containing 10 [Source:HGNC Symbol;Acc:30;
7	1738	1	4e-05	4e-03	28 x 50 dihydroipoamide dehydrogenase [Source:HGNC Symbol;Acc
8	51144	0.93	1e-04	4e-03	28 x 50 hydroxysteroid (17-beta) dehydrogenase 12 [Source:HGNC ;
9	653238	0.91	2e-04	4e-03	28 x 47 general transcription factor IIH, polypeptide 2B (pseudogene)
10	10175	0.91	2e-04	4e-03	28 x 50 cornichon family AMPA receptor auxiliary protein 1 [Source:H
11	10959	0.9	2e-04	6e-03	27 x 50 transmembrane emp24 domain trafficking protein 2 [Source:I
12	113402	0.88	3e-04	6e-03	29 x 49 SFT2 domain containing 1 [Source:HGNC Symbol;Acc:21102
13	8065	0.88	3e-04	2e-02	30 x 48 cullin 5 [Source:HGNC Symbol;Acc:2556]
14	79717	0.83	6e-04	2e-02	31 x 50 phosphopantothenoylecysteine synthetase [Source:HGNC Syr
15	8669	0.78	1e-03	2e-02	27 x 50 eukaryotic translation initiation factor 3, subunit J [Source:HG
16	5962	0.78	1e-03	2e-02	27 x 50 radixin [Source:HGNC Symbol;Acc:9944]
17	8050	0.78	1e-03	2e-02	29 x 50 pyruvate dehydrogenase complex, component X [Source:HGI
18	25842	0.78	1e-03	2e-02	29 x 50 anti-silencing function 1A histone chaperone [Source:HGNC
19	1737	0.77	1e-03	2e-02	29 x 50 dihydroipoamide S-acetyltransferase [Source:HGNC Symbol
20	83941	0.77	1e-03	2e-02	29 x 47 TM2 domain containing 1 [Source:HGNC Symbol;Acc:24142]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.38	NULL	4 / 11	MMML C6SCIEJ_MMML 49
2	13.26	NULL	3 / 12	BP regulation of acetyl-CoA biosynthetic process from pyruvate
3	13.26	NULL	3 / 12	GSEA C2REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENAS
4	12.42	NULL	3 / 16	GSEA C2REACTOME_CITRIC_ACID_CYCLE
5	11.83	NULL	4 / 28	BP tricarboxylic acid cycle
6	11.72	NULL	3 / 12	GSEA C2HAZARD_RESPONSE_TO_UV_SCC_UP
7	11.46	NULL	2 / 10	BP maternal placenta development
8	11.36	NULL	3 / 16	GSEA C2REACTOME_PYRUVATE_METABOLISM
9	11.28	NULL	2 / 5	MMML C6SCIEJ_MMML 28
10	10.37	NULL	6 / 62	Glio Stuehler_Proteins_up_in_STS
11	10.34	NULL	1 / 2	miRNA target-mir-659
12	10.29	NULL	3 / 13	GSEA C2SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
13	9.58	NULL	10 / 152	BP cellular metabolic process
14	9.55	NULL	2 / 9	GSEA C2SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP
15	8.91	NULL	3 / 25	BP pyruvate metabolic process
16	8.6	NULL	2 / 15	GSEA C2MATTIOLI_MGUS_VS_PCL
17	8.46	NULL	2 / 10	BP pantothenate metabolic process
18	8.46	NULL	2 / 10	GSEA C2REACTOME_VITAMIN_B5_(PANTOTHENATE)_METABOLISM
19	8.39	NULL	4 / 54	miRNA target-mir-334
20	8.13	NULL	2 / 15	GSEA C2SMOOTH_TCA
21	8.1	NULL	2 / 16	GSEA C2KEGG_CITRATE_CYCLE_TCA_CYCLE
22	7.95	NULL	8 / 86	Lymphon10SOLOWSKI_red total
23	7.86	NULL	2 / 15	GSEA C2LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
24	7.23	NULL	2 / 13	BP COPI coating of Golgi vesicle
25	7.07	NULL	6 / 83	BP respiratory electron transport chain
26	7.05	NULL	3 / 15	MMML C6SCIEJ_MMML 22
27	7.03	NULL	3 / 16	Glio willscher_GBM_STSwt_proteomics-O_UP
28	6.66	NULL	8 / 98	miRNA target-mir-330
29	6.45	NULL	2 / 16	GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
30	6.21	NULL	2 / 12	BP oxidative phosphorylation
31	6.18	NULL	1 / 10	CC IkappaB kinase complex
32	6.18	NULL	1 / 10	GSEA C2TAKAO_RESPONSE_TO_UVB_RADIATION_UP
33	6.16	NULL	15 / 269	miRNA target-mir-3134
34	6.03	NULL	2 / 15	BP actin filament capping
35	5.97	NULL	2 / 16	GSEA C2HORIUCHI_WTAP_TARGETS_DN
36	5.9	NULL	11 / 184	miRNA target-mir-336
37	5.86	NULL	1 / 11	GSEA C2OSMAN_BLADDER_CANCER_DN
38	5.86	NULL	1 / 11	GSEA C2DANG_MYC_TARGETS_UP
39	5.79	NULL	5 / 75	miRNA target-mir-332
40	5.72	NULL	2 / 15	GSEA C2SCHLOSSER_SERUM_RESPONSE_DN



GW_308

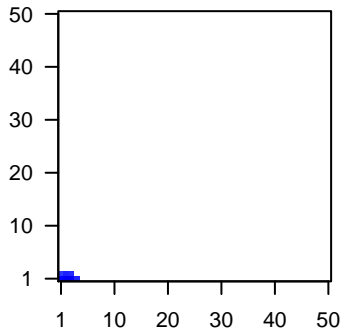
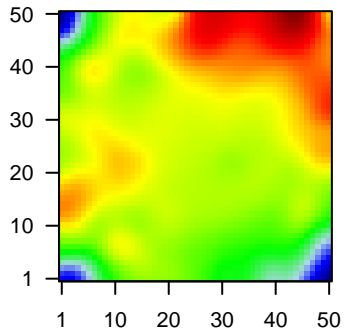
Local Summary

%DE = 0.85
 # metagenes = 7
 # genes = 141
 # genes in genesets = 141
 # genes with $fdr < 0.1 = 112$ (6 + / 106 -)
 # genes with $fdr < 0.05 = 108$ (6 + / 102 -)
 # genes with $fdr < 0.01 = 93$ (5 + / 88 -)

<r> metagenes = 0.99
 <r> genes = 0.48
 <FC> = -0.9
 <shrinkage-t> = -31.66
 <p-value> = 0
 <fdr> = 0.26

Profile

Spot



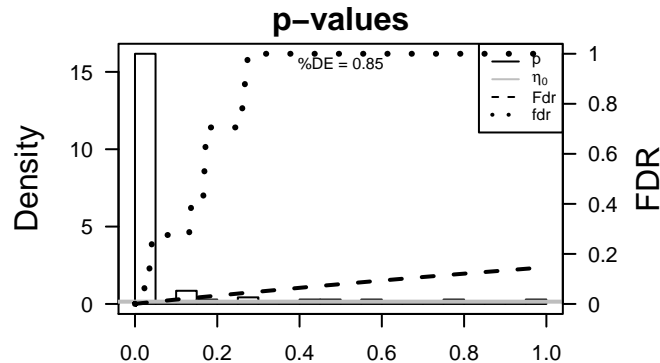
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	633	-2.52	2e-16	4e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
2	1277	-2.56	2e-16	4e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	-2.58	2e-16	4e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	-2.66	2e-16	4e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1289	-2.14	2e-16	4e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1290	-2.39	2e-16	4e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1293	-2.33	2e-16	4e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	3040	-2.45	2e-16	4e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	4060	-2.11	2e-16	4e-16	2 x 1 lumican [Source:HGNC Symbol;Acc:6724]
10	7058	-2.09	2e-16	4e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
11	7431	-1.98	2e-16	4e-16	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]
12	25878	-1.95	9e-16	1e-14	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:25878]
13	7045	-1.77	2e-15	1e-13	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:7045]
14	4314	-1.88	8e-15	3e-13	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:4314]
15	6678	-1.85	2e-14	1e-12	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:6678]
16	165	-1.81	7e-14	3e-12	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
17	4318	-1.78	2e-13	8e-12	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9: [Source:HGNC Symbol;Acc:4318]
18	4973	1.73	1e-12	8e-12	1 x 1 oxidized low density lipoprotein (lectin-like) receptor 1 [Source:HGNC Symbol;Acc:4973]
19	1291	-1.72	1e-12	8e-12	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
20	5159	-1.71	2e-12	8e-12	3 x 1 platelet-derived growth factor receptor, beta polypeptide [Source:HGNC Symbol;Acc:5159]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-52.09	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
2	-50.35	NULL	14 / 16	MMML C6ACIEJ_MMML_1
3	-47.4	NULL	7 / 11	MF platelet-derived growth factor binding
4	-42.84	NULL	50 / 190	CC extracellular matrix
5	-41.61	NULL	28 / 69	BP extracellular matrix disassembly
6	-41.04	NULL	25 / 64	BP collagen catabolic process
7	-40.74	NULL	8 / 12	miRNA target-29c
8	-34.42	NULL	49 / 242	BP extracellular matrix organization
9	-33.42	NULL	18 / 57	MF extracellular matrix structural constituent
10	-33.06	NULL	51 / 250	Lymphocyte ENZ_Stromal signature 1
11	-32.06	NULL	13 / 37	BP collagen fibril organization
12	-30.06	NULL	11 / 19	MF extracellular matrix binding
13	-27.36	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
14	-27.34	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_CARCINOMA
15	-27.11	NULL	10 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
16	-25.98	NULL	8 / 40	BP cellular response to amino acid stimulus
17	-25.74	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_CARCINOMA
18	-24.84	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
19	-24.55	NULL	4 / 10	BP protein heterotrimerization
20	-24.07	NULL	6 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
21	-24.04	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
22	-23.45	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
23	-22.52	NULL	13 / 68	CC collagen
24	-22.18	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
25	-21.92	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
26	-20.85	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
27	-20.46	NULL	5 / 16	GSEA C2URS_ADIPOCYTE_DIFFERENTIATION_DN
28	-19.8	NULL	20 / 119	Lymphocyte ROSOLOWSKI_green total
29	-19.58	NULL	26 / 183	CC proteinaceous extracellular matrix
30	-19.31	NULL	19 / 153	CC endoplasmic reticulum lumen
31	-18.93	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
32	-18.9	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
33	-18.87	NULL	3 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
34	-18.68	NULL	5 / 15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
35	-18.31	NULL	4 / 15	GSEA C2REACTOME_NCAM1_INTERACTIONS
36	-18.25	NULL	10 / 35	Glio Colman_survival_associated
37	-18.24	NULL	7 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
38	-18.2	NULL	5 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
39	-18.13	NULL	16 / 83	CC basement membrane
40	-18.09	NULL	69 / 1182	CC extracellular region



GW_308

Local Summary

%DE = 0.94
 # metagenes = 15
 # genes = 268
 # genes in genesets = 266

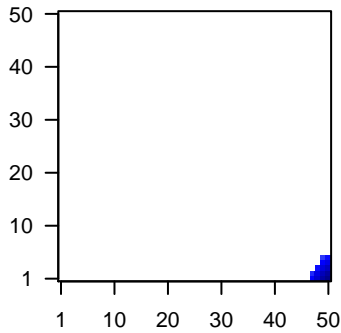
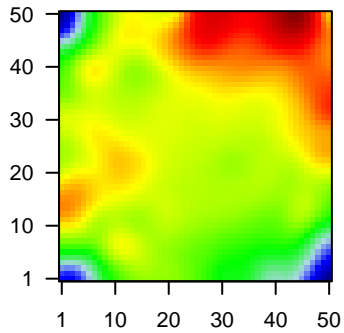
genes with $fdr < 0.1$ = 237 (6 + / 231 -)
 # genes with $fdr < 0.05$ = 237 (6 + / 231 -)
 # genes with $fdr < 0.01$ = 183 (1 + / 182 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.57

$\langle FC \rangle = -0.8$
 $\langle \text{shrinkage-t} \rangle = -27.9$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.32$

Profile

Spot



Local Genelist

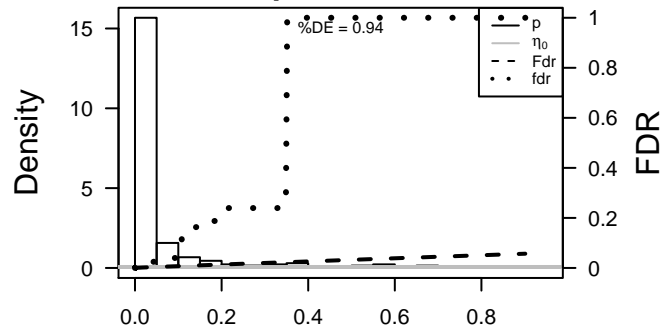
Rank	ID	log(FC)	fdr	p-value	Description
1	1396	-2.08	2e-16	9e-16	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:30278]
2	3113	-2.13	2e-16	9e-16	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:30278]
3	3122	-2.1	2e-16	9e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:30278]
4	3543	-3.22	2e-16	9e-16	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:30278]
5	3512	-1.97	4e-16	8e-14	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
6	5552	-1.88	1e-14	8e-14	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
7	713	-1.87	1e-14	1e-13	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:30278]
8	972	-1.86	2e-14	1e-12	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
9	4283	-1.8	1e-13	1e-12	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:30278]
10	3109	-1.79	2e-13	3e-12	50 x 1 major histocompatibility complex, class II, DM beta [Source:HGNC Symbol;Acc:30278]
11	5996	-1.76	4e-13	3e-12	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:30278]
12	2	-1.75	6e-13	1e-11	50 x 5 alpha-2-macroglobulin [Source:HGNC Symbol;Acc:7]
13	23180	-1.72	1e-12	1e-11	50 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
14	241	-1.7	2e-12	6e-11	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:30278]
15	3128	-1.67	6e-12	6e-11	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene)
16	57172	-1.65	1e-11	1e-10	49 x 1 calcium/calmodulin-dependent protein kinase I gamma [Source:HGNC Symbol;Acc:30278]
17	6347	-1.63	2e-11	1e-10	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:30278]
18	10365	-1.61	3e-11	1e-10	50 x 3 Kruppel-like factor 2 [Source:HGNC Symbol;Acc:6347]
19	3002	-1.61	3e-11	1e-09	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated protein 10)
20	348	-1.54	2e-10	1e-09	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-35.19	NULL	12 / 15	CC MHC class II protein complex
2	-23.72	NULL	86 / 417	H.Tiss WIRTH_Immune system
3	-23.67	NULL	49 / 312	BP immune response
4	-22.22	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
5	-20.71	NULL	15 / 47	BP antigen processing and presentation
6	-20.33	NULL	86 / 553	Cancer Lembecke_Colonic Inflammation
7	-19.06	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
8	-19	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
9	-18.12	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
10	-17.82	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
11	-17.7	NULL	6 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
12	-17.5	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
13	-17.16	NULL	39 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
14	-17.16	NULL	39 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
15	-17.16	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
16	-17.16	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
17	-17.01	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
18	-16.84	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
19	-16.82	NULL	13 / 60	BP T cell costimulation
20	-16.68	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
21	-16.4	NULL	9 / 35	CC trans-Golgi network membrane
22	-16.23	NULL	7 / 28	CC transport vesicle membrane
23	-15.99	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
24	-15.43	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
25	-15.43	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
26	-15.27	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
27	-15.05	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
28	-15.05	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
29	-14.97	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
30	-14.92	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENTATION
31	-14.82	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
32	-14.78	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
33	-14.22	NULL	5 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
34	-14.17	NULL	2 / 5	GSEA C2WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
35	-13.87	NULL	13 / 87	BP antigen processing and presentation of exogenous peptide antigen
36	-13.87	NULL	9 / 46	CC endocytic vesicle membrane
37	-13.8	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
38	-13.53	NULL	17 / 74	BP regulation of immune response
39	-13.14	NULL	1 / 6	H.Tiss WIRTH_Bone marrow
40	-13	NULL	5 / 12	BP immunoglobulin mediated immune response

p-values



GW_308

Local Summary

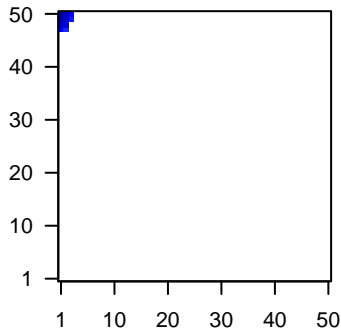
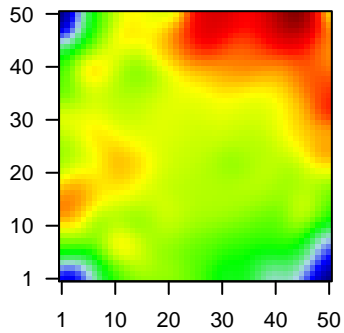
%DE = 0.91
 # metagenes = 10
 # genes = 161
 # genes in genesets = 156

genes with $fdr < 0.1 = 133$ (6 + / 127 -)
 # genes with $fdr < 0.05 = 133$ (6 + / 127 -)
 # genes with $fdr < 0.01 = 124$ (6 + / 118 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.5
 $\langle FC \rangle = -1.07$
 $\langle \text{shrinkage-t} \rangle = -38.02$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.2$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.69	2e-16	1e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	2.1	2e-16	1e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
3	810	-2.52	2e-16	1e-16	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
4	100133941	-2	2e-16	1e-16	3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
5	4680	-2.34	2e-16	1e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (I)
6	22802	-2	2e-16	1e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20193]
7	49860	-2.07	2e-16	1e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
8	92196	-2.18	2e-16	1e-16	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:20193]
9	1672	-2.03	2e-16	1e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
10	1673	-2.05	2e-16	1e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	163351	-2.02	2e-16	1e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC Symbol;Acc:20193]
12	2706	-2.08	2e-16	1e-16	1 x 47 gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;Acc:20193]
13	10804	-2.28	2e-16	1e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;Acc:20193]
14	286887	-3	2e-16	1e-16	1 x 47 keratin 6C [Source:HGNC Symbol;Acc:20406]
15	388533	-2.41	2e-16	1e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC Symbol;Acc:20193]
16	4118	-2.25	2e-16	1e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc:20193]
17	5266	-2.31	2e-16	1e-16	1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Acc:20193]
18	6278	-2.15	2e-16	1e-16	1 x 49 S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:20193]
19	374897	-2.33	2e-16	1e-16	1 x 49 suprabasin [Source:HGNC Symbol;Acc:24950]
20	6698	-2.4	2e-16	1e-16	1 x 50 small proline-rich protein 1A [Source:HGNC Symbol;Acc:112]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-48.26	NULL	69 / 135	H.Tiss WIRTH_Mucosa
2	-43.27	NULL	16 / 21	CC cornified envelope
3	-36.26	NULL	19 / 42	BP keratinization
4	-34.72	NULL	21 / 53	BP keratinocyte differentiation
5	-26.35	NULL	9 / 19	BP peptide cross-linking
6	-25.91	NULL	75 / 572	Disease GUDJ_poriasis up
7	-23.7	NULL	18 / 76	BP epidermis development
8	-19.83	NULL	6 / 16	GSEA C2WNDER_CDH1_TARGETS_3_DN
9	-18.38	NULL	4 / 10	MF RAGE receptor binding
10	-17.52	NULL	6 / 13	BP negative regulation of peptidase activity
11	-14.94	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
12	-14.43	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
13	-13.88	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	-13.75	NULL	3 / 10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING
15	-12.7	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
16	-12.29	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
17	-11.77	NULL	18 / 186	MF structural molecule activity
18	-11.57	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
19	-11.39	NULL	4 / 15	MF retinol dehydrogenase activity
20	-11.08	NULL	4 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
21	-10.89	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
22	-10.65	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
23	-10.53	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
24	-10.37	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
25	-10.36	NULL	8 / 52	BP negative regulation of endopeptidase activity
26	-10.31	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
27	-10.14	NULL	4 / 23	MF peptidase inhibitor activity
28	-10.14	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
29	-10.12	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
30	-10.04	NULL	2 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
31	-9.94	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
32	-9.8	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
33	-9.72	NULL	2 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
34	-9.67	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
35	-9.51	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
36	-9.36	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_1
37	-9.36	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
38	-9.28	NULL	45 / 1182	CC extracellular region
39	-9.23	NULL	2 / 15	CC connexon complex
40	-8.98	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN

p-values

