

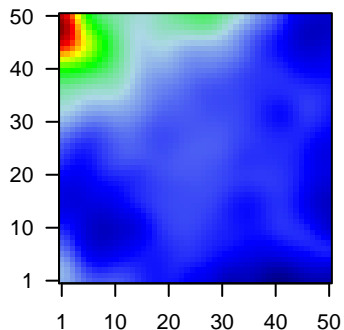
GW_303

Global Summary

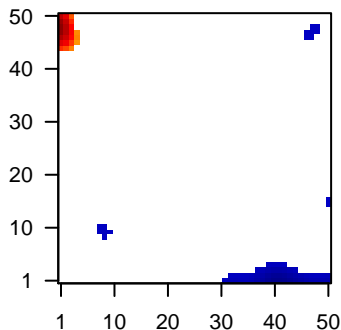
%DE = 0.15
 # genes with $fdr < 0.2$ = 1844 (1057 + / 787 -)
 # genes with $fdr < 0.1$ = 1484 (892 + / 592 -)
 # genes with $fdr < 0.05$ = 1261 (785 + / 476 -)
 # genes with $fdr < 0.01$ = 819 (560 + / 259 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.85

Profile



Regulated Spots



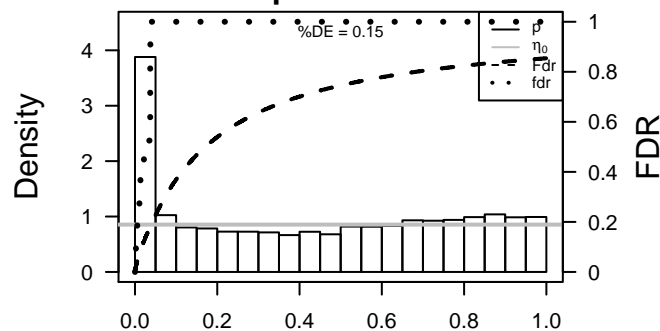
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.58	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
2	441282	1.45	2e-16	3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	222	1.32	2e-16	3e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC]
4	242	1.78	2e-16	3e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Synr]
5	144193	1.41	2e-16	3e-14	15 x 50 amidohydrolase domain containing 1 [Source:HGNC Symbol;]
6	401138	3.21	2e-16	3e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
7	383	1.37	2e-16	3e-14	7 x 45 arginase 1 [Source:HGNC Symbol;Acc:663]
8	91947	1.67	2e-16	3e-14	4 x 43 arrestin domain containing 4 [Source:HGNC Symbol;Acc:280]
9	151516	2.48	2e-16	3e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A]
10	387695	2.39	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt]
11	260436	-1.32	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc]
12	760	2.04	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	51806	1.32	2e-16	3e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
14	57172	1.36	2e-16	3e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG]
15	84290	1.61	2e-16	3e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	948	2.17	2e-16	3e-14	6 x 44 CD36 molecule (thrombospondin receptor) [Source:HGNC S]
17	1041	2.83	2e-16	3e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
18	84518	1.99	2e-16	3e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
19	54544	1.67	2e-16	3e-14	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
20	1466	1.46	2e-16	3e-14	5 x 43 cysteine and glycine-rich protein 2 [Source:HGNC Symbol;A]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	23.56	NULL	42	BP keratinization
2	22.95	NULL	135	H.Tiss WIRTH_Mucosa
3	21.2	NULL	21	CC cornified envelope
4	20.27	NULL	572	Disease GUDDJ_poriasis up
5	17.1	NULL	53	BP keratinocyte differentiation
6	15.95	NULL	76	BP epidermis development
7	10.56	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	10.05	NULL	19	BP peptide cross-linking
9	9.41	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	8.88	NULL	82	CC intermediate filament
11	8.34	NULL	16	GSEA C2JAEGER_METASTASIS_DN
12	8.24	NULL	79	MF serine-type endopeptidase inhibitor activity
13	8.04	NULL	504	Chr Chr 15
14	7.67	NULL	186	MF structural molecule activity
15	7.66	NULL	21	CC desmosome
16	7.29	NULL	44	CC keratin filament
17	7.09	NULL	10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
18	6.93	NULL	16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
19	6.85	NULL	1182	CC extracellular region
20	6.39	NULL	16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
<i>Underexpressed</i>				
1	-7.98	NULL	417	H.Tiss WIRTH_Immune system
2	-7.93	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	-7.72	NULL	51	BP type I interferon signaling pathway
4	-7.71	NULL	633	Chr Chr 9
5	-7.56	NULL	595	MF RNA binding
6	-7.14	NULL	649	BP gene expression
7	-6.9	NULL	949	CC nucleoplasm
8	-6.86	NULL	1749	MF DNA binding
9	-6.64	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	-6.44	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
11	-6.4	NULL	92	BP viral life cycle
12	-6.37	NULL	4640	CC nucleus
13	-6.19	NULL	204	BP cytokine-mediated signaling pathway
14	-6.16	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
15	-6.14	NULL	123	BP defense response to virus
16	-6.13	NULL	1135	Chr Chr 19
17	-6.09	NULL	92	BP translational elongation
18	-6.07	NULL	81	BP viral transcription
19	-5.94	NULL	87	BP translational termination
20	-5.73	NULL	11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN

p-values



GW_303

Local Summary

%DE = 0.96
 # metagenes = 24
 # genes = 304
 # genes in genesets = 296

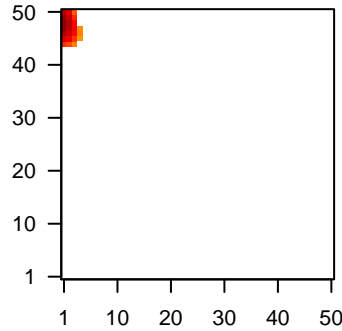
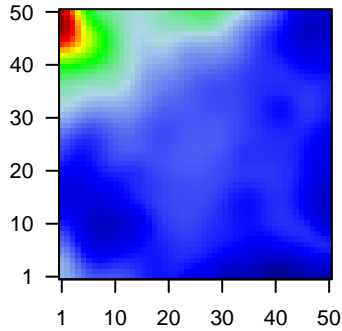
genes with $fdr < 0.1 = 279$ (267 + / 12 -)
 # genes with $fdr < 0.05 = 272$ (263 + / 9 -)
 # genes with $fdr < 0.01 = 244$ (240 + / 4 -)

<r> metagenes = 0.92
 <r> genes = 0.41

<FC> = 0.95
 <shrinkage-t> = 33.55
 <p-value> = 0
 <fdr> = 0.16

Profile

Spot



Local Genelist

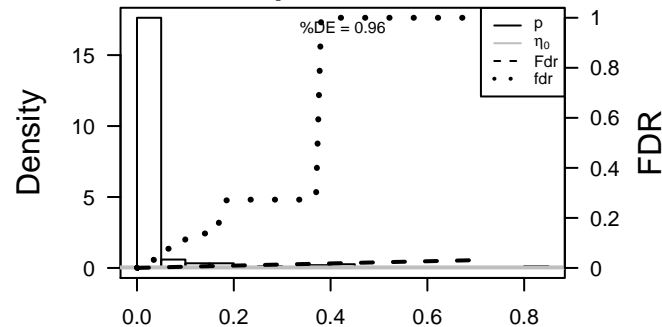
Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.58	2e-16	3e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
2	441282	1.45	2e-16	3e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
3	222	1.32	2e-16	3e-17	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	242	1.78	2e-16	3e-17	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syn
5	151516	2.48	2e-16	3e-17	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
6	387695	2.39	2e-16	3e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	760	2.04	2e-16	3e-17	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	84290	1.61	2e-16	3e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	1041	2.83	2e-16	3e-17	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
10	84518	1.99	2e-16	3e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
11	54544	1.67	2e-16	3e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
12	1474	1.89	2e-16	3e-17	1 x 47 cystatin E/M [Source:HGNC Symbol;Acc:2478]
13	1475	1.53	2e-16	3e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
14	9547	2.05	2e-16	3e-17	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
15	126410	1.33	2e-16	3e-17	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
16	27065	2.1	2e-16	3e-17	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1)
17	55894	2.29	2e-16	3e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
18	414325	2.69	2e-16	3e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	1673	2.86	2e-16	3e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	93099	1.38	2e-16	3e-17	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	43.39	NULL	18 / 21	CC cornified envelope
2	41.22	NULL	90 / 135	H.Tiss WIRTH_Mucosa
3	31.4	NULL	25 / 53	BP keratinocyte differentiation
4	30.83	NULL	19 / 42	BP keratinization
5	28.03	NULL	111 / 572	Disease GUDJ_psooriasis up
6	25.27	NULL	26 / 76	BP epidermis development
7	19.85	NULL	11 / 19	BP peptide cross-linking
8	18.42	NULL	12 / 21	CC desmosome
9	16.61	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	15.23	NULL	19 / 82	CC intermediate filament
11	14.51	NULL	28 / 186	MF structural molecule activity
12	13.58	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
13	12.68	NULL	3 / 8	GSEA C2LIJ_CDX2_TARGETS_DN
14	12.55	NULL	5 / 10	MF RAGE receptor binding
15	12.28	NULL	12 / 44	CC keratin filament
16	12.05	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
17	11.82	NULL	8 / 16	GSEA C2XONDER_CDH1_TARGETS_3_DN
18	11.78	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	11.46	NULL	6 / 13	BP negative regulation of peptidase activity
20	11.22	NULL	8 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
21	11.17	NULL	7 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
22	11.11	NULL	6 / 16	GSEA C2JAEGER_METASTASIS_DN
23	10.96	NULL	7 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
24	10.57	NULL	13 / 79	MF serine-type endopeptidase inhibitor activity
25	10.18	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
26	9.67	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
27	9.66	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
28	9.63	NULL	64 / 1182	CC extracellular region
29	9.47	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
30	9.45	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
31	9.35	NULL	7 / 29	BP regulation of proteolysis
32	9.19	NULL	10 / 52	BP negative regulation of endopeptidase activity
33	8.97	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
34	8.91	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
35	8.88	NULL	4 / 21	CC gap junction
36	8.4	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
37	8.3	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
38	8.29	NULL	4 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
39	8.22	NULL	6 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
40	7.97	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP

p-values



GW_303

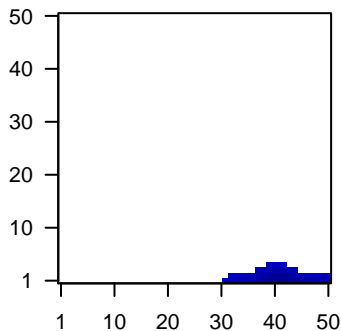
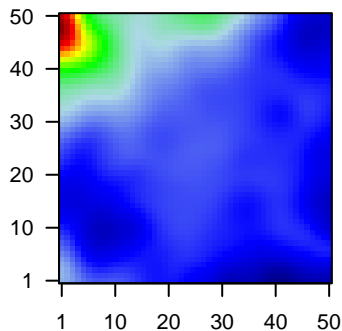
Local Summary

%DE = 0.71
 # metagenes = 51
 # genes = 733
 # genes in genesets = 700
 # genes with $fdr < 0.1$ = 316 (25 + / 291 -)
 # genes with $fdr < 0.05$ = 245 (21 + / 224 -)
 # genes with $fdr < 0.01$ = 141 (14 + / 127 -)

$\langle r \rangle$ metagenes = 0.77
 $\langle r \rangle$ genes = 0.3
 $\langle FC \rangle$ = -0.26
 $\langle \text{shrinkage-t} \rangle$ = -9.3
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.65

Profile

Spot



Local Genelist

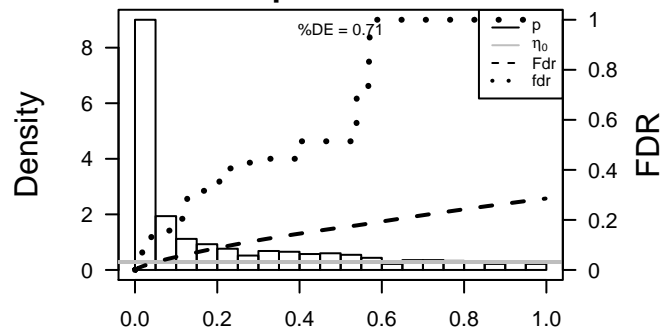
Rank	ID	log(FC)	fdr	p-value	Description
1	260436	-1.32	2e-16	8e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
2	57172	1.36	2e-16	8e-15	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
3	3123	-1.34	2e-16	8e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
4	10561	-1.46	2e-16	8e-15	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16:
5	10964	-1.54	2e-16	8e-15	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
6	3512	2.07	2e-16	8e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglo
7	10410	-1.18	7e-16	7e-14	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC S
8	9636	-1.28	9e-16	8e-13	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:40E
9	51755	1.25	5e-15	2e-12	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
10	4061	-1.23	2e-14	1e-10	32 x 1 lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
11	400818	-1.15	7e-13	4e-10	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
12	10537	-1.12	3e-12	2e-09	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	94240	-1.08	1e-11	2e-09	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc
14	5880	-1.07	2e-11	3e-08	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small C
15	100132406	-1.01	3e-10	3e-08	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
16	3543	0.92	4e-10	3e-08	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
17	54855	0.99	5e-10	1e-07	49 x 1 family with sequence similarity 46, member C [Source:HGNC
18	115361	-0.98	1e-09	3e-07	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
19	10563	-0.94	3e-09	3e-07	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
20	341	-0.94	4e-09	3e-07	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-28.34	NULL	13 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
2	-25.63	NULL	36 / 51	BP type I interferon signaling pathway
3	-24.19	NULL	10 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
4	-23.14	NULL	14 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
5	-20.47	NULL	11 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
6	-20.21	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
7	-20.11	NULL	12 / 16	GSEA C2MOSELERE_IFNA_RESPONSE
8	-19.44	NULL	43 / 123	BP defense response to virus
9	-19.36	NULL	17 / 31	BP negative regulation of viral genome replication
10	-19.2	NULL	13 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	-19.13	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	-18.84	NULL	14 / 15	CC MHC class II protein complex
13	-18.08	NULL	14 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
14	-18.02	NULL	57 / 204	BP cytokine-mediated signaling pathway
15	-17.45	NULL	88 / 312	BP immune response
16	-17.1	NULL	114 / 417	H.Tiss WIRTH_Immune system
17	-16.49	NULL	34 / 109	BP response to virus
18	-16.09	NULL	9 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
19	-15.68	NULL	30 / 60	BP interferon-gamma-mediated signaling pathway
20	-15.02	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
21	-14.87	NULL	25 / 47	BP antigen processing and presentation
22	-14.84	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
23	-14.83	NULL	7 / 16	GSEA C2KU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
24	-14.7	NULL	5 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
25	-14.31	NULL	14 / 23	CC integral to luminal side of endoplasmic reticulum membrane
26	-13.16	NULL	3 / 3	MMML C2SCIEJ_MMML 7
27	-13.07	NULL	3 / 4	MMML C2SCIEJ_MMML 47
28	-12.84	NULL	47 / 274	Lymphonot SPANG_IL21 DN
29	-12.38	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
30	-12.37	NULL	21 / 60	BP T cell costimulation
31	-12.25	NULL	5 / 12	GSEA C2ZHU_CMV_8_HR_UP
32	-12.13	NULL	7 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
33	-12.06	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
34	-12.06	NULL	8 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
35	-11.52	NULL	30 / 74	BP regulation of immune response
36	-11.42	NULL	7 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
37	-11.28	NULL	15 / 32	CC ER to Golgi transport vesicle membrane
38	-11.23	NULL	12 / 43	MF chemokine activity
39	-11.04	NULL	7 / 12	GSEA C2TSAL_DNAJB4_TARGETS_UP
40	-10.59	NULL	6 / 14	GSEA C2KU_AKT1_TARGETS_6HR

p-values



GW_303

Local Summary

%DE = 0.55
 # metagenes = 6
 # genes = 91
 # genes in genesets = 91

 # genes with $fdr < 0.1 = 32$ (1 + / 31 -)
 # genes with $fdr < 0.05 = 23$ (1 + / 22 -)
 # genes with $fdr < 0.01 = 9$ (0 + / 9 -)

 $\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.34

 $\langle FC \rangle = -0.25$
 $\langle \text{shrinkage-t} \rangle = -8.86$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.68$

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	6621	-0.79	9e-07	9e-05	8 x 11 small nuclear RNA activating complex, polypeptide 4, 190kDa
2	2026	-0.75	3e-06	1e-03	10 x 10 enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
3	5442	-0.64	5e-05	1e-03	8 x 11 polymerase (RNA) mitochondrial (DNA directed) [Source:HGI
4	23344	-0.64	6e-05	2e-03	8 x 10 extended synaptotagmin-like protein 1 [Source:HGNC Symb
5	55653	-0.61	1e-04	2e-03	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Symb
6	11165	-0.6	2e-04	3e-03	9 x 11 nudix (nucleoside diphosphate linked moiety X)-type motif 3]
7	147841	-0.58	3e-04	3e-03	8 x 11 SPC24, NDC80 kinetochore complex component [Source:HG
8	2794	-0.56	4e-04	3e-03	9 x 10 guanine nucleotide binding protein-like 1 [Source:HGNC Syr
9	83862	-0.56	5e-04	3e-03	9 x 9 transmembrane protein 120A [Source:HGNC Symbol;Acc:21f
10	51545	-0.56	5e-04	1e-02	8 x 10 zinc finger protein 581 [Source:HGNC Symbol;Acc:25017]
11	22913	-0.53	8e-04	1e-02	8 x 11 RALY heterogeneous nuclear ribonucleoprotein [Source:HGN
12	64710	-0.51	1e-03	1e-02	9 x 11 nuclear casein kinase and cyclin-dependent kinase substrate
13	140465	-0.5	2e-03	1e-02	9 x 9 myosin, light chain 6B, alkali, smooth muscle and non-muscl
14	27161	-0.5	2e-03	1e-02	8 x 10 argonaute RISC catalytic component 2 [Source:HGNC Symb
15	128710	-0.49	2e-03	1e-02	8 x 11 SLX4 interacting protein [Source:HGNC Symbol;Acc:16225]
16	8189	-0.49	2e-03	2e-02	8 x 11 symplekin [Source:HGNC Symbol;Acc:22935]
17	51477	-0.48	3e-03	2e-02	10 x 10 inositol-3-phosphate synthase 1 [Source:HGNC Symbol;Acc
18	27043	-0.47	3e-03	2e-02	9 x 11 proline, glutamate and leucine rich protein 1 [Source:HGNC S
19	11284	-0.47	3e-03	2e-02	8 x 10 polynucleotide kinase 3'-phosphatase [Source:HGNC Symbc
20	10953	-0.46	4e-03	2e-02	9 x 9 translocase of outer mitochondrial membrane 34 [Source:HGI

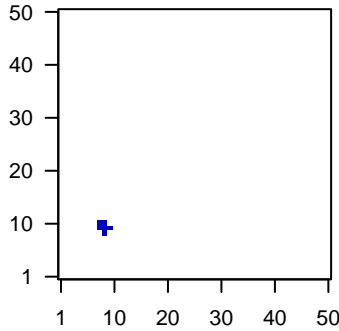
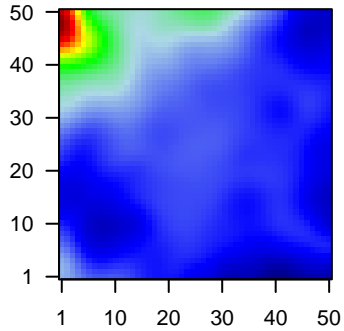
Local Geneset Analysis

Underexpression

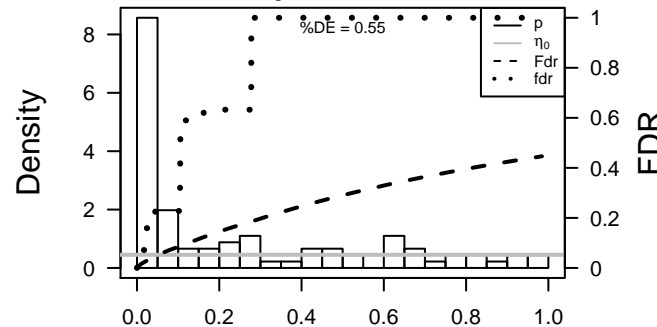
Rank	GSZ	p-value	#in/all	Geneset
1	-10.68	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
2	-10.68	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION
3	-10.68	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION
4	-10.37	NULL	1 / 9	GSEA C2REACTOME_RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL
5	-9.8	NULL	1 / 10	GSEA C2REACTOME_TRANSCRIPTION
6	-8.37	NULL	2 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
7	-8.07	NULL	1 / 13	GSEA C2REACTOME_GLYCOLYSIS
8	-7.76	NULL	1 / 14	GSEA C2TOMIDA_METASTASIS_DN
9	-7.47	NULL	1 / 15	GSEA C2MOOHA_GLYCOLYSIS
10	-7.47	NULL	1 / 15	GSEA C2REACTOME_GLYCONEOGENESIS
11	-7.22	NULL	1 / 16	CC photoreceptor inner segment
12	-7.22	NULL	1 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
13	-7.22	NULL	1 / 16	GSEA C2MOOHA_GLYCONEOGENESIS
14	-7.22	NULL	1 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
15	-7.09	NULL	2 / 24	miRNA target network
16	-6.62	NULL	1 / 10	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G5
17	-6.48	NULL	1 / 9	miRNA target network
18	-6.39	NULL	1 / 6	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
19	-6.37	NULL	1 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	-6.27	NULL	2 / 40	BP transcription from RNA polymerase III promoter
21	-6.24	NULL	2 / 42	BP inositol phosphate metabolic process
22	-6.21	NULL	1 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
23	-6.12	NULL	1 / 10	MF miRNA binding
24	-6.12	NULL	1 / 10	BP negative regulation of translational initiation
25	-6.12	NULL	1 / 10	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G6_DN
26	-6.11	NULL	1 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
27	-6.06	NULL	1 / 9	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
28	-5.81	NULL	1 / 10	GSEA C2SHIRAIHI_PLZF_TARGETS_UP
29	-5.81	NULL	1 / 11	CC mRNA cap binding complex
30	-5.78	NULL	1 / 11	BP positive regulation of protein dephosphorylation
31	-5.72	NULL	1 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
32	-5.71	NULL	1 / 5	GSEA C2NAGY_PCAF_COMPONENTS_HUMAN
33	-5.52	NULL	1 / 9	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
34	-5.48	NULL	1 / 13	GSEA C2ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
35	-5.48	NULL	1 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
36	-5.43	NULL	1 / 11	GSEA C2SMITH_TERT_TARGETS_UP
37	-5.42	NULL	1 / 8	GSEA C2BIOCARTA_STRESS_PATHWAY
38	-5.42	NULL	2 / 12	BP mRNA cleavage
39	-5.33	NULL	1 / 13	CC muscle myosin complex
40	-5.33	NULL	1 / 13	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION

Profile

Spot



p-values



GW_303

Local Summary

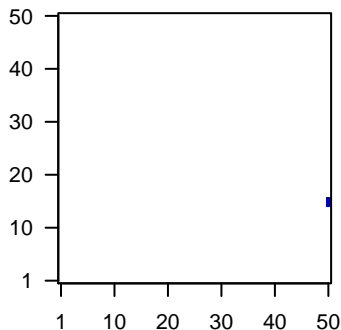
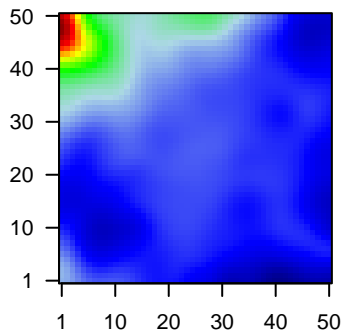
%DE = 0.81
 # metagenes = 2
 # genes = 48
 # genes in genesets = 48
 # genes with $fdr < 0.1 = 24$ (2 + / 22 -)
 # genes with $fdr < 0.05 = 24$ (2 + / 22 -)
 # genes with $fdr < 0.01 = 11$ (0 + / 11 -)

<r> metagenes = 0.99
 <r> genes = 0.39

<FC> = -0.31
 <shrinkage-t> = -10.88
 <p-value> = 0.01
 <fdr> = 0.58

Profile

Spot



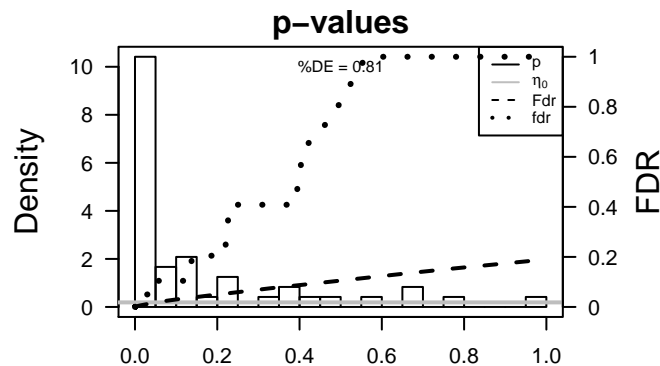
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	6542	-0.74	4e-06	5e-05	50 x 16 solute carrier family 7 (cationic amino acid transporter, y+ sys
2	8543	-0.71	9e-06	1e-04	50 x 15 LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
3	221061	-0.67	3e-05	1e-04	50 x 16 family with sequence similarity 171, member A1 [Source:HGNC
4	85315	-0.66	3e-05	2e-04	50 x 15 progesterin and adipoQ receptor family member VIII [Source:HG
5	4602	-0.63	7e-05	2e-04	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source
6	26018	-0.63	8e-05	2e-04	50 x 16 leucine-rich repeats and immunoglobulin-like domains 1 [So
7	51768	-0.63	8e-05	3e-04	50 x 16 transmembrane 7 superfamily member 3 [Source:HGNC Sym
8	56994	-0.61	1e-04	7e-04	50 x 16 choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
9	9847	-0.58	3e-04	7e-04	50 x 16 C2 calcium-dependent domain containing 5 [Source:HGNC S
10	55320	-0.58	3e-04	5e-03	50 x 16 MIS18 binding protein 1 [Source:HGNC Symbol;Acc:20190]
11	7716	-0.53	1e-03	5e-03	50 x 16 vascular endothelial zinc finger 1 [Source:HGNC Symbol;Acc
12	56997	-0.51	1e-03	1e-02	50 x 16 aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
13	79191	-0.46	4e-03	1e-02	50 x 15 iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
14	909	-0.45	5e-03	1e-02	50 x 16 CD1a molecule [Source:HGNC Symbol;Acc:1634]
15	217	0.44	6e-03	1e-02	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HC
16	23412	0.43	7e-03	1e-02	50 x 15 COMM domain containing 3 [Source:HGNC Symbol;Acc:233
17	1365	-0.43	7e-03	2e-02	50 x 15 claudin 3 [Source:HGNC Symbol;Acc:2045]
18	59084	-0.41	1e-02	2e-02	50 x 15 ectonucleotide pyrophosphatase/phosphodiesterase 5 (putati
19	399948	-0.39	1e-02	2e-02	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
20	79762	-0.39	1e-02	3e-02	50 x 15 chromosome 1 open reading frame 115 [Source:HGNC Symt

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.51	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY
2	-14.02	NULL	1 / 2	TF MYC_Cell cycle DOWN
3	-11.41	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
4	-10.91	NULL	2 / 34	BP thymus development
5	-10.67	NULL	1 / 9	GSEA C2BASSO_CD40_SIGNALING_UP
6	-10.67	NULL	1 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
7	-10.65	NULL	1 / 11	MF enhancer sequence-specific DNA binding
8	-10.56	NULL	1 / 12	BP nitric oxide biosynthetic process
9	-10.05	NULL	1 / 10	BP positive regulation of histone H3-K4 methylation
10	-9.72	NULL	1 / 10	MF diacylglycerol binding
11	-9.69	NULL	1 / 13	BP negative regulation of protein complex assembly
12	-9.69	NULL	1 / 13	GSEA C2BENPORATH_ES_CORE_NINE_CORRELATED
13	-9.69	NULL	1 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
14	-9.52	NULL	1 / 11	BP homeostasis of number of cells
15	-9.52	NULL	1 / 11	Pathw AcBENTINK_e213.2
16	-9.52	NULL	1 / 11	GSEA C2DOANE_BREAST_CANCER_ESR1_UP
17	-9.52	NULL	1 / 11	GSEA C2TURJANSKI_MAPK1_AND_MAPK2_TARGETS
18	-9.06	NULL	1 / 12	GSEA C2PROVENZANI_METASTASIS_UP
19	-9.06	NULL	1 / 12	GSEA C2DING_LUNG_CANCER_BY_MUTATION_RATE
20	-8.94	NULL	1 / 15	GSEA C2DOANE_BREAST_CANCER_CLASSES_DN
21	-8.94	NULL	1 / 15	GSEA C2PUJANA_BREAST_CANCER_LIT_INT_NETWORK
22	-8.94	NULL	1 / 15	GSEA C2SUNG_METASTASIS_STROMA_UP
23	-8.94	NULL	1 / 15	GSEA C2FAELT_B_CLL_WITH_VH3_21_DN
24	-8.94	NULL	1 / 15	GSEA C2MMS_MOUSE_LYMPH_HIGH_4HRS_UP
25	-8.74	NULL	1 / 11	BP positive regulation of protein targeting to membrane
26	-8.69	NULL	1 / 17	MF amino acid transmembrane transporter activity
27	-8.66	NULL	1 / 13	GSEA C2OSADA_ASCL1_TARGETS_UP
28	-8.66	NULL	1 / 13	GSEA C2ALONSO_METASTASIS_UP
29	-8.66	NULL	1 / 13	GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
30	-8.63	NULL	1 / 16	BP ventricular septum development
31	-8.63	NULL	1 / 16	GSEA C2QUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMF
32	-8.63	NULL	1 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXP1_FUSION_UP
33	-8.47	NULL	2 / 41	TF Tissue/AQUERIZAS_Thymus
34	-8.31	NULL	2 / 39	miRNA target starBase
35	-8.3	NULL	1 / 14	GSEA C2ONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
36	-8.3	NULL	1 / 14	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
37	-8.3	NULL	1 / 14	GSEA C2GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
38	-8.3	NULL	1 / 14	GSEA C2TENEDINI_MEGAKARYOCYTE_MARKERS
39	-8.3	NULL	1 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
40	-8.3	NULL	1 / 14	GSEA C2VANTVEER_BREAST_CANCER_ESR1_UP



GW_303

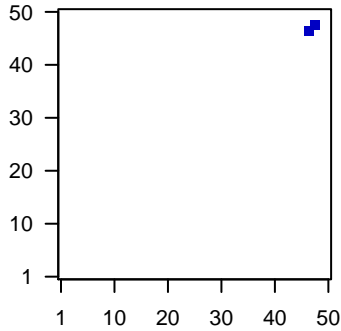
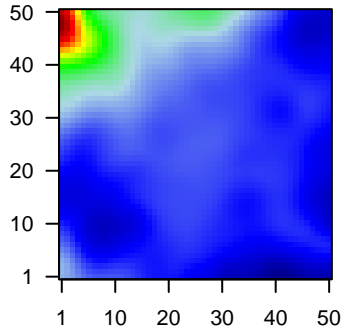
Local Summary

%DE = 0.7
 # metagenes = 7
 # genes = 58
 # genes in genesets = 58
 # genes with $fdr < 0.1$ = 28 (2 + / 26 -)
 # genes with $fdr < 0.05$ = 26 (1 + / 25 -)
 # genes with $fdr < 0.01$ = 11 (0 + / 11 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.38
 $\langle FC \rangle = -0.29$
 $\langle \text{shrinkage-t} \rangle = -10.25$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.63$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	8364	-1.06	4e-13	7e-12	47 x 46 histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
2	84223	-1.14	8e-13	1e-07	47 x 46 IQ motif containing G [Source:HGNC Symbol;Acc:25251]
3	91057	-0.92	8e-09	4e-04	46 x 47 coiled-coil domain containing 34 [Source:HGNC Symbol;Acc:1773]
4	1019	-0.67	2e-05	6e-04	46 x 47 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:1773]
5	3148	-0.64	6e-05	1e-03	46 x 46 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
6	11073	-0.6	2e-04	1e-03	47 x 48 topoisomerase (DNA) II binding protein 1 [Source:HGNC Symbol;Acc:1773]
7	4172	-0.59	2e-04	1e-03	46 x 47 minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:1773]
8	4174	-0.58	3e-04	8e-03	46 x 46 minichromosome maintenance complex component 5 [Source:HGNC Symbol;Acc:1773]
9	55723	-0.52	1e-03	8e-03	46 x 47 anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:1773]
10	4175	-0.5	2e-03	8e-03	46 x 47 minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:1773]
11	142	-0.5	2e-03	8e-03	47 x 46 poly (ADP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:1773]
12	116028	-0.49	2e-03	1e-02	46 x 47 RecQ mediated genome instability 2 [Source:HGNC Symbol;Acc:1773]
13	25804	-0.48	3e-03	3e-02	47 x 47 LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:HGNC Symbol;Acc:1773]
14	3184	-0.39	7e-03	3e-02	46 x 46 heterogeneous nuclear ribonucleoprotein D (AU-rich element) [Source:HGNC Symbol;Acc:1773]
15	9355	-0.43	8e-03	3e-02	47 x 47 LIM homeobox 2 [Source:HGNC Symbol;Acc:6594]
16	2956	-0.42	8e-03	3e-02	47 x 48 mutS homolog 6 [Source:HGNC Symbol;Acc:7329]
17	51087	0.41	1e-02	3e-02	47 x 46 Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
18	1371	-0.41	1e-02	3e-02	48 x 48 coproporphyrinogen oxidase [Source:HGNC Symbol;Acc:232]
19	653659	-0.4	1e-02	4e-02	48 x 48 transmembrane protein 183A [Source:HGNC Symbol;Acc:20179]
20	78995	-0.37	2e-02	4e-02	46 x 46 chromosome 17 open reading frame 53 [Source:HGNC Symbol;Acc:1773]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-23.72	NULL	3 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
2	-21	NULL	3 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
3	-20.64	NULL	1 / 7	GSEA C2NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
4	-16.31	NULL	3 / 22	BP DNA replication initiation
5	-15.57	NULL	3 / 24	MF DNA helicase activity
6	-15.17	NULL	2 / 11	BP response to lead ion
7	-14.3	NULL	2 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
8	-14.02	NULL	2 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
9	-13.81	NULL	3 / 30	BP DNA strand elongation involved in DNA replication
10	-13.59	NULL	1 / 15	GSEA C2BAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN
11	-13.53	NULL	2 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
12	-13.46	NULL	2 / 16	GSEA C2HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2
13	-13.19	NULL	1 / 6	GSEA C2MYLYKANGAS_AMPLIFICATION_HOT_SPOT_21
14	-13.19	NULL	1 / 6	GSEA C2HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER
15	-13.11	NULL	2 / 16	GSEA C2Y_AGING_PREMATURITY_DN
16	-11.23	NULL	1 / 8	TF MYC_Cell cycle UP
17	-11.23	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLIFIED_IN_SOFT_TISSUE_CANCER
18	-10.88	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER
19	-10.88	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER_MARKERS
20	-10.52	NULL	1 / 9	miRNA target-24
21	-10.48	NULL	1 / 4	miRNA target-220
22	-10.35	NULL	3 / 16	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
23	-9.47	NULL	1 / 10	MF RAGE receptor binding
24	-9.47	NULL	1 / 10	GSEA C2BIOCARTA_DNAFRAGMENT_PATHWAY
25	-9.26	NULL	2 / 15	GSEA C2PRAMOONJAGO_SOX4_TARGETS_DN
26	-9.22	NULL	1 / 5	GSEA C2CHOI_ATL_ACUTE_STAGE
27	-8.98	NULL	1 / 11	GSEA C2BIOCARTA_SET_PATHWAY
28	-8.97	NULL	1 / 12	BP response to hyperoxia
29	-8.97	NULL	1 / 12	GSEA C2HEDENFALK_BREAST_CANCER_HEREDITARY_VS_SPORADIC
30	-8.95	NULL	6 / 149	BP DNA replication
31	-8.81	NULL	2 / 31	BP DNA metabolic process
32	-8.75	NULL	11 / 370	BP mitotic cell cycle
33	-8.68	NULL	1 / 4	MMML C2SCIEJ_MMML 41
34	-8.67	NULL	2 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
35	-8.58	NULL	1 / 13	GSEA C2BIOCARTA_RB_PATHWAY
36	-8.58	NULL	1 / 13	GSEA C2SA_REG_CASCADE_OF_CYCLIN_EXPR
37	-8.5	NULL	2 / 11	GSEA C2LIANG_SILENCED_BY_METHYLATION_DN
38	-8.47	NULL	2 / 33	Cancer KUIPER_MM good survival
39	-8.33	NULL	2 / 14	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
40	-8.31	NULL	1 / 8	GSEA C2FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK

