

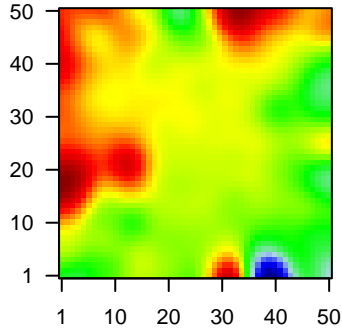
GW_168

Global Summary

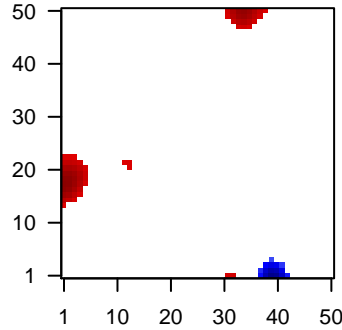
%DE = 0.14
 # genes with fdr < 0.2 = 1732 (932 + / 800 -)
 # genes with fdr < 0.1 = 1245 (685 + / 560 -)
 # genes with fdr < 0.05 = 951 (526 + / 425 -)
 # genes with fdr < 0.01 = 687 (378 + / 309 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.86

Profile



Regulated Spots



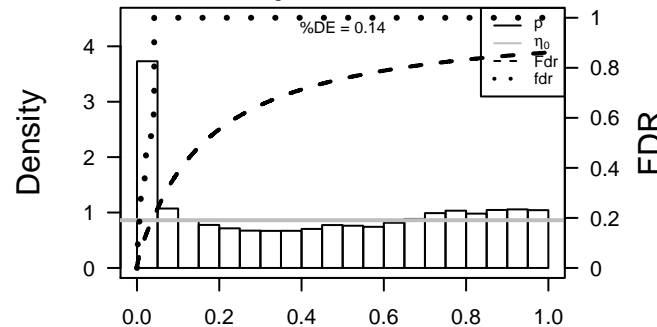
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	79852	1.74	2e-16 7e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	8644	1.87	2e-16 7e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
3	401138	1.72	2e-16 7e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
4	151516	2.83	2e-16 7e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
5	445	1.82	2e-16 7e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
6	344905	1.87	2e-16 7e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
7	10974	1.77	2e-16 7e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
8	760	1.85	2e-16 7e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	51806	1.61	2e-16 7e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
10	1056	1.66	2e-16 7e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
11	1359	2.14	2e-16 7e-14	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
12	49860	-2.08	2e-16 7e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	1511	1.88	2e-16 7e-14	50 x 7 cathepsin G [Source:HGNC Symbol;Acc:2532]
14	9547	1.71	2e-16 7e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
15	1843	-2.27	2e-16 7e-14	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3
16	1958	-2.02	2e-16 7e-14	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
17	641737	-1.79	2e-16 7e-14	40 x 1
18	2353	-2.51	2e-16 7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:+
19	2354	-2.32	2e-16 7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source
20	2877	2.24	2e-16 7e-14	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.68	NULL	1318	CC mitochondrion
2	11.16	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
3	11.04	NULL	83	BP respiratory electron transport chain
4	10.54	NULL	153	MF structural constituent of ribosome
5	10.03	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
6	9.88	NULL	304	CC mitochondrial inner membrane
7	9.33	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	9.24	NULL	572	Disease GUDJ_poriasis up
9	8.96	NULL	51	BP type I interferon signaling pathway
10	8.68	NULL	167	CC ribosome
11	8.38	NULL	152	BP cellular metabolic process
12	8.22	NULL	31	BP negative regulation of viral genome replication
13	8.15	NULL	253	BP translation
14	7.87	NULL	1253	BP small molecule metabolic process
15	7.8	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
16	7.76	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMQUIMOD
17	7.64	NULL	957	Chr Chr 11
18	7.62	NULL	36	CC mitochondrial respiratory chain complex I
19	7.44	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
20	7.31	NULL	34	MF NADH dehydrogenase (ubiquinone) activity
<i>Underexpressed</i>				
1	-11.39	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-9.98	NULL	280	Chr Chr 13
3	-9.65	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
4	-9.59	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
5	-9.49	NULL	391	miRNA target-mir-181A--181B--181C--181D
6	-9.46	NULL	16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
7	-9.03	NULL	699	Chr Chr 5
8	-8.42	NULL	39	TF Tissue/AQUERIZAS_Thyroid
9	-8.17	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
10	-8.11	NULL	171	miRNA target-mir-369-3p
11	-8.11	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
12	-8.1	NULL	436	miRNA target-mir-34b
13	-8.04	NULL	269	miRNA target-mir-324
14	-7.88	NULL	9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
15	-7.87	NULL	271	miRNA target-mir-34b
16	-7.87	NULL	155	miRNA target-mir-300b
17	-7.86	NULL	368	miRNA target-mir-34a
18	-7.84	NULL	467	miRNA target-mir-30A--5P--30C--30D--30E--5P
19	-7.82	NULL	246	miRNA target-mir-554-5p
20	-7.8	NULL	267	miRNA target-mir-34b

p-values



GW_168

Local Summary

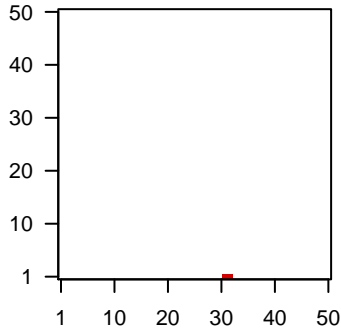
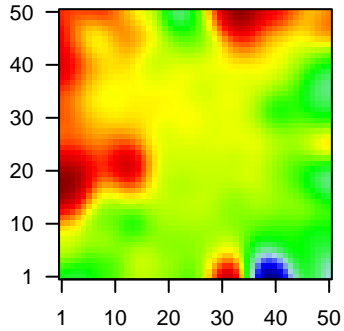
%DE = 0.79
 # metagenes = 2
 # genes = 100
 # genes in genesets = 98
 # genes with $fdr < 0.1$ = 68 (64 + / 4 -)
 # genes with $fdr < 0.05$ = 62 (59 + / 3 -)
 # genes with $fdr < 0.01$ = 52 (49 + / 3 -)

<r> metagenes = 1
 <r> genes = 0.51

<FC> = 0.56
 <shrinkage-t> = 19.78
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



Local Genelist

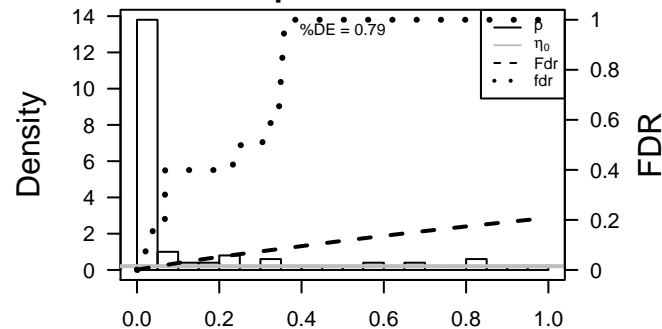
Rank	ID	log(FC)	fdr	p-value	Description
1	55008	1.96	2e-16	2e-15	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
2	9636	1.98	2e-16	2e-15	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:406
3	4600	1.72	2e-16	2e-15	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
4	3433	1.56	2e-15	1e-12	32 x 1 interferon-induced protein with tetratricopeptide repeats 2 [S
5	8519	1.48	5e-14	3e-11	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC S
6	4061	1.39	2e-12	3e-11	32 x 1 lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
7	2537	1.37	3e-12	5e-11	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;f
8	3804	1.35	7e-12	5e-11	32 x 1 killer cell immunoglobulin-like receptor, two domains, long cy
9	3434	1.35	8e-12	5e-10	32 x 1 interferon-induced protein with tetratricopeptide repeats 1 [S
10	629	1.3	3e-11	6e-10	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
11	51191	1.28	8e-11	6e-10	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
12	8638	1.27	9e-11	3e-09	32 x 1 2'-5'-oligoadenylate synthetase-like [Source:HGNC Symbol;
13	55601	1.24	3e-10	5e-09	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC
14	91543	1.22	5e-10	8e-09	32 x 1 radical S-adenosyl methionine domain containing 2 [Source:l
15	64108	1.21	9e-10	4e-08	32 x 1 receptor (chemosensory) transporter protein 4 [Source:HGNC
16	3627	-1.16	4e-09	4e-08	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
17	10410	1.05	6e-09	4e-08	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC S
18	10578	1.14	7e-09	1e-07	32 x 1 granulysin [Source:HGNC Symbol;Acc:4414]
19	4599	1.02	2e-08	1e-07	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible
20	3430	1.11	2e-08	1e-06	32 x 1 interferon-induced protein 35 [Source:HGNC Symbol;Acc:53

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	56.75	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
2	54.14	NULL	28 / 51	BP type I interferon signaling pathway
3	52.92	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
4	52.44	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
5	46.71	NULL	7 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
6	44.3	NULL	10 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	43.16	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
8	40.67	NULL	13 / 31	BP negative regulation of viral genome replication
9	37.1	NULL	10 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
10	33.76	NULL	26 / 109	BP response to virus
11	33.76	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
12	33.2	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
13	33.15	NULL	12 / 16	GSEA C2MOSELERLE_IFNA_RESPONSE
14	32.7	NULL	3 / 4	MMML C2SCIEJ_MMML_47
15	32.34	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
16	31.84	NULL	30 / 123	BP defense response to virus
17	31.5	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
18	30.5	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
19	29.63	NULL	2 / 2	MMML C2SCIEJ_MMML_27
20	27.86	NULL	33 / 204	BP cytokine-mediated signaling pathway
21	25.8	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
22	24.03	NULL	3 / 5	GSEA C2BROWNE_INTERFERON_RESPONSIVE_GENES
23	23.61	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
24	23.5	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
25	23.5	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
26	22.67	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
27	21.9	NULL	30 / 274	Lymphom SPANG_IL21 DN
28	21.22	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
29	20.76	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
30	20.76	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
31	20.42	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
32	19.44	NULL	6 / 32	BP negative regulation of type I interferon production
33	18.55	NULL	46 / 572	Disease GUDJ_psooriasis up
34	17.95	NULL	5 / 18	BP response to interferon-gamma
35	16.93	NULL	2 / 12	GSEA C2BROWNE_HCMV_INFECTION_4HR_UP
36	16.57	NULL	9 / 51	MF double-stranded RNA binding
37	16.15	NULL	3 / 16	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
38	15.94	NULL	3 / 16	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
39	15.9	NULL	4 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_UP
40	15.04	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_

p-values



GW_168

Local Summary

%DE = 0.64
 # metagenes = 39
 # genes = 425
 # genes in genesets = 420

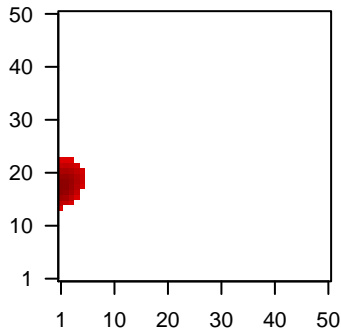
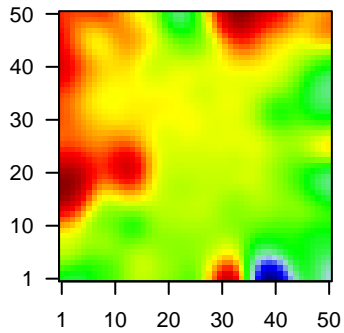
genes with $fdr < 0.1 = 148$ (139 + / 9 -)
 # genes with $fdr < 0.05 = 123$ (115 + / 8 -)
 # genes with $fdr < 0.01 = 37$ (36 + / 1 -)

<r> metagenes = 0.93
 <r> genes = 0.26

<FC> = 0.3
 <shrinkage-t> = 10.61
 <p-value> = 0.03
 <fdr> = 0.71

Profile

Spot



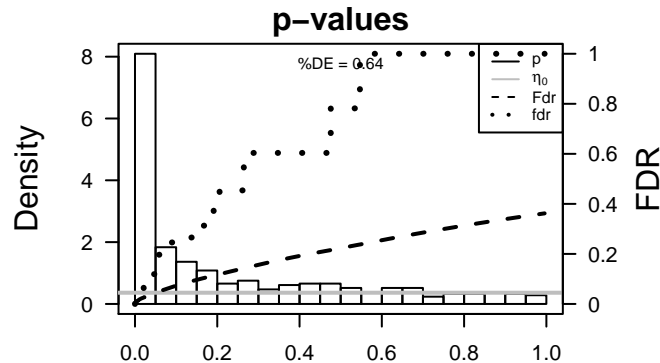
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4495	1.81	2e-16	2e-14	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
2	51702	2.07	2e-16	2e-14	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;A
3	283869	1.44	3e-13	7e-11	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
4	51083	1.41	9e-13	7e-11	1 x 15 galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
5	1152	1.4	1e-12	2e-09	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
6	51337	1.33	1e-11	2e-09	3 x 21 thioesterase superfamily member 6 [Source:HGNC Symbol;A
7	131076	1.32	2e-11	4e-07	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
8	116238	1.15	5e-09	4e-07	4 x 19 TLC domain containing 1 [Source:HGNC Symbol;Acc:25177]
9	51373	1.14	6e-09	4e-07	1 x 16 28S ribosomal protein S17, mitochondrial; HCG1984214, isof
10	388581	1.14	8e-09	1e-05	1 x 15 family with sequence similarity 132, member A [Source:HGNC
11	64979	1.05	1e-07	5e-04	1 x 16 mitochondrial ribosomal protein L36 [Source:HGNC Symbol;f
12	4715	0.88	7e-06	5e-04	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
13	85359	0.88	8e-06	5e-04	2 x 20 DiGeorge syndrome critical region gene 6-like [Source:HGNC
14	55290	0.87	1e-05	8e-04	1 x 16 BRF2, RNA polymerase III transcription initiation factor 50 kD
15	58477	0.84	2e-05	8e-04	2 x 21 signal recognition particle receptor, B subunit [Source:HGNC
16	51081	0.84	2e-05	8e-04	3 x 19 mitochondrial ribosomal protein S7 [Source:HGNC Symbol;A
17	64951	0.82	3e-05	8e-04	2 x 18 mitochondrial ribosomal protein S24 [Source:HGNC Symbol;f
18	1537	0.81	4e-05	8e-04	2 x 18 cytochrome c-1 [Source:HGNC Symbol;Acc:2579]
19	6227	0.81	4e-05	8e-04	1 x 17 ribosomal protein S21 [Source:HGNC Symbol;Acc:10409]
20	7965	0.8	5e-05	8e-04	1 x 15 aminoacyl tRNA synthetase complex-interacting multifunc

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.87	NULL	25 / 153	MF structural constituent of ribosome
2	12.16	NULL	6 / 19	CC mitochondrial small ribosomal subunit
3	11.09	NULL	29 / 253	BP translation
4	10.23	NULL	21 / 167	CC ribosome
5	10.01	NULL	94 / 1318	CC mitochondrion
6	9.98	NULL	5 / 15	CC mitochondrial large ribosomal subunit
7	9.71	NULL	1 / 7	MMML C2G3CIEJ_MMML_13
8	8.74	NULL	4 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
9	8.69	NULL	4 / 13	BP ribosomal small subunit biogenesis
10	8.66	NULL	18 / 96	BP rRNA processing
11	8.54	NULL	4 / 10	MF NADH dehydrogenase activity
12	8.53	NULL	3 / 13	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
13	8.42	NULL	2 / 21	BP feeding behavior
14	8.33	NULL	2 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
15	8.16	NULL	6 / 34	MF NADH dehydrogenase (ubiquinone) activity
16	8.15	NULL	1 / 6	GSEA C2REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
17	8.15	NULL	1 / 6	GSEA C2REACTOME_GPCR_LIGAND_BINDING
18	7.97	NULL	1 / 10	BP cellular response to zinc ion
19	7.89	NULL	6 / 36	CC mitochondrial respiratory chain complex I
20	7.84	NULL	3 / 10	MF monosaccharide binding
21	7.81	NULL	2 / 8	GSEA C2REACTOME_G_ALPHA_I_SIGNALING_EVENTS
22	7.48	NULL	1 / 7	GSEA C2REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
23	7.43	NULL	2 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
24	7.17	NULL	3 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
25	7.11	NULL	4 / 13	GSEA C2REACTOME_GLYCOLYSIS
26	6.94	NULL	1 / 8	GSEA C2SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
27	6.93	NULL	2 / 16	BP monocyte differentiation
28	6.87	NULL	1 / 13	BP cellular response to cadmium ion
29	6.85	NULL	3 / 17	CC proteasome core complex
30	6.78	NULL	12 / 83	BP respiratory electron transport chain
31	6.69	NULL	2 / 10	BP creatine metabolic process
32	6.63	NULL	3 / 18	MF threonine-type endopeptidase activity
33	6.62	NULL	4 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
34	6.53	NULL	5 / 35	BP mitochondrial electron transport, NADH to ubiquinone
35	6.5	NULL	2 / 10	GSEA C2ZHU_CMV_24_HR_UP
36	6.5	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP
37	6.46	NULL	2 / 11	GSEA C2SCIBETTA_KDMSB_TARGETS_DN
38	6.46	NULL	26 / 304	CC mitochondrial inner membrane
39	6.44	NULL	1 / 9	GSEA C2SOUYER_TUMOR_INVASIVENESS
40	6.34	NULL	9 / 55	CC proteasome complex



GW_168

Local Summary

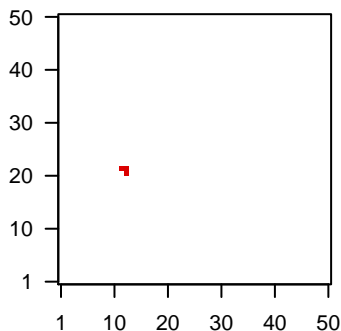
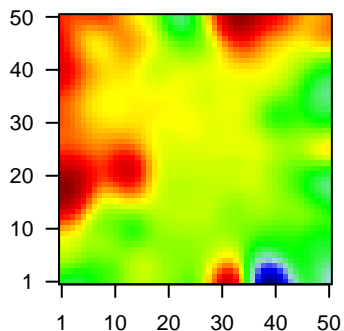
%DE = 0.75
 # metagenes = 3
 # genes = 30
 # genes in genesets = 29
 # genes with $fdr < 0.1 = 18$ (18 + / 0 -)
 # genes with $fdr < 0.05 = 11$ (11 + / 0 -)
 # genes with $fdr < 0.01 = 3$ (3 + / 0 -)

<r> metagenes = 1
 <r> genes = 0.28

<FC> = 0.38
 <shrinkage-t> = 13.28
 <p-value> = 0.03
 <fdr> = 0.64

Profile

Spot



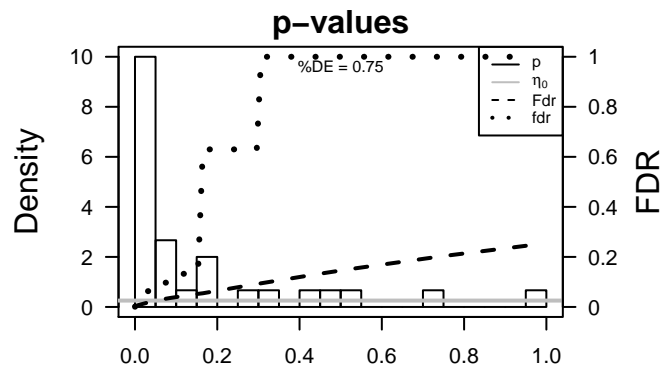
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	10430	0.92	3e-06	8e-04	13 x 22 transmembrane protein 147 [Source:HGNC Symbol;Acc:3041
2	64963	0.76	1e-04	1e-03	13 x 21 mitochondrial ribosomal protein S11 [Source:HGNC Symbol;Acc:3041
3	22977	0.72	3e-04	6e-03	13 x 21 aldo-keto reductase family 7, member A3 (aflatoxin aldehyde
4	6834	0.64	1e-03	1e-02	13 x 21 surfeit 1 [Source:HGNC Symbol;Acc:11474]
5	5018	0.6	2e-03	1e-02	13 x 22 oxidase (cytochrome c) assembly 1-like [Source:HGNC Syml
6	5436	0.57	4e-03	1e-02	13 x 21 polymerase (RNA) II (DNA directed) polypeptide G [Source:H
7	54958	0.52	8e-03	1e-02	13 x 21 transmembrane protein 160 [Source:HGNC Symbol;Acc:2604
8	374395	0.51	9e-03	1e-02	12 x 22 transmembrane protein 179B [Source:HGNC Symbol;Acc:33;
9	11257	0.51	9e-03	2e-02	13 x 22 TP53 target 1 (non-protein coding) [Source:HGNC Symbol;A
10	8574	0.5	1e-02	3e-02	13 x 21 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde
11	9526	0.48	2e-02	3e-02	12 x 22 mannose-P-dolichol utilization defect 1 [Source:HGNC Syml
12	8402	0.46	2e-02	6e-02	13 x 21 solute carrier family 25 (mitochondrial carrier; oxoglutarate ca
13	4201	0.42	3e-02	6e-02	13 x 21 male-enhanced antigen 1 [Source:HGNC Symbol;Acc:6986]
14	374659	0.41	4e-02	6e-02	13 x 21 HD domain containing 3 [Source:HGNC Symbol;Acc:30522]
15	6827	0.4	4e-02	1e-01	12 x 22 suppressor of Ty 4 homolog 1 (S. cerevisiae) [Source:HGNC
16	7923	0.36	7e-02	1e-01	13 x 22 hydroxysteroid (17-beta) dehydrogenase 8 [Source:HGNC S;
17	10456	0.35	7e-02	1e-01	13 x 22 HCLS1 associated protein X-1 [Source:HGNC Symbol;Acc:1
18	54460	0.34	9e-02	1e-01	13 x 22 mitochondrial ribosomal protein S21 [Source:HGNC Symbol;A
19	30834	0.33	1e-01	1e-01	13 x 22 zinc ribbon domain containing 1 [Source:HGNC Symbol;Acc:
20	22818	0.3	1e-01	1e-01	13 x 22 coatomer protein complex, subunit zeta 1 [Source:HGNC Syn

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	20.89	NULL	2 / 12	BP cellular aldehyde metabolic process
2	20.37	NULL	2 / 13	CC mitochondrial respiratory chain
3	18.22	NULL	2 / 9	GSEA C2KEGG_RNA_POLYMERASE
4	15.93	NULL	2 / 20	BP aerobic respiration
5	14.46	NULL	2 / 19	CC mitochondrial small ribosomal subunit
6	14.43	NULL	1 / 14	Glio VERHAAK_CL subtype
7	12.35	NULL	1 / 8	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
8	12.35	NULL	1 / 8	GSEA C2REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
9	11.5	NULL	1 / 9	GSEA C2REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_CO
10	11.5	NULL	1 / 9	GSEA C2REACTOME_HIV1_TRANSCRIPTION_ELONGATION
11	11.5	NULL	1 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
12	11.5	NULL	1 / 9	GSEA C2REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE
13	11.5	NULL	1 / 9	GSEA C2REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME
14	11.21	NULL	1 / 14	Glio VERHAAK_NL subtype
15	11	NULL	1 / 12	BP oxidative phosphorylation
16	10.8	NULL	1 / 10	GSEA C2KEGG_HUNTINGTONS_DISEASE
17	10.8	NULL	1 / 10	GSEA C2REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
18	10.8	NULL	1 / 10	GSEA C2REACTOME_HIV_LIFE_CYCLE
19	10.8	NULL	1 / 10	GSEA C2REACTOME_HIV1_TRANSCRIPTION_INITIATION
20	10.8	NULL	1 / 10	GSEA C2REACTOME_MRNA_PROCESSING
21	10.8	NULL	1 / 10	GSEA C2REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INT
22	10.8	NULL	1 / 10	GSEA C2REACTOME_TRANSCRIPTION
23	10.2	NULL	1 / 11	GSEA C2REACTOME_HIV_INFECTION
24	10.2	NULL	1 / 11	GSEA C2REACTOME_TRANSCRIPTION_COUPLED_NER
25	10.03	NULL	2 / 11	Cancer GENTLES_modul5
26	9.69	NULL	1 / 12	GSEA C2TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
27	9.69	NULL	1 / 12	GSEA C2KEGG_PURINE_METABOLISM
28	9.69	NULL	1 / 12	GSEA C2KEGG_PYRIMIDINE_METABOLISM
29	9.69	NULL	1 / 12	GSEA C2REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIP
30	9.69	NULL	1 / 12	GSEA C2REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED
31	9.69	NULL	1 / 12	GSEA C2REACTOME_NUCLEOTIDE_EXCISION_REPAIR
32	9.25	NULL	1 / 13	GSEA C2REACTOME_FORMATION_AND_MATURATION_OF_MRNA_TRA
33	9.25	NULL	1 / 13	GSEA C2REACTOME_TAT_MEDIATED_HIV1_ELONGATION_ARREST_AN
34	9.07	NULL	3 / 38	MF DNA-directed RNA polymerase activity
35	8.85	NULL	1 / 14	GSEA C2REACTOME_DNA_REPAIR
36	8.85	NULL	1 / 14	GSEA C2REACTOME_MRNA_SPLICING
37	8.85	NULL	1 / 14	GSEA C2REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAININ
38	8.85	NULL	1 / 14	GSEA C2REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS
39	8.62	NULL	1 / 16	BP mitochondrial respiratory chain complex I assembly
40	8.62	NULL	1 / 16	GSEA C2KEGG_PROTEIN_EXPORT



GW_168

Local Summary

%DE = 0.67
 # metagenes = 23
 # genes = 314
 # genes in genesets = 303

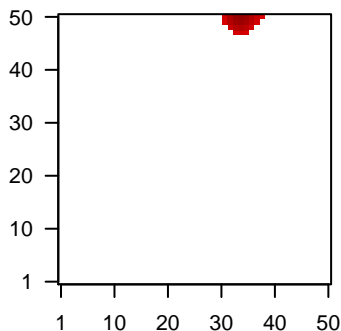
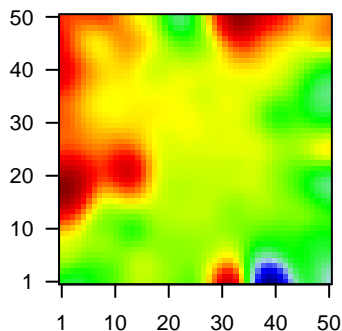
genes with $fdr < 0.1 = 127$ (127 + / 0 -)
 # genes with $fdr < 0.05 = 113$ (113 + / 0 -)
 # genes with $fdr < 0.01 = 50$ (50 + / 0 -)

<r> metagenes = 0.93
 <r> genes = 0.25

<FC> = 0.36
 <shrinkage-t> = 12.49
 <p-value> = 0.03
 <fdr> = 0.65

Profile

Spot



Local Genelist

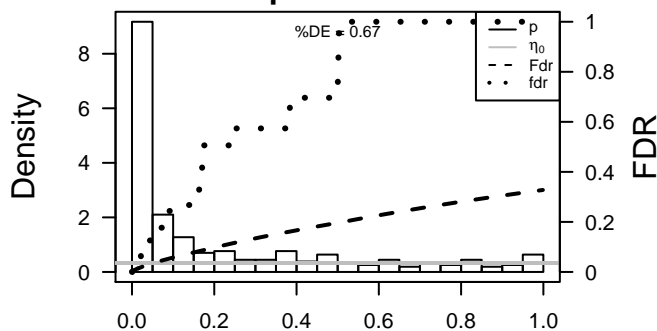
Rank	ID	log(FC)	fdr	p-value	Description
1	5321	1.1	2e-08	2e-05	35 x 50 phospholipase A2, group IVA (cytosolic, calcium-dependent)
2	509	1.01	3e-07	2e-05	31 x 50 ATP synthase, H+ transporting, mitochondrial F1 complex, ga
3	55505	0.97	6e-07	2e-05	34 x 50 NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:14378]
4	27257	0.97	9e-07	2e-05	34 x 50 LSM1 homolog, U6 small nuclear RNA associated (S. cerevis
5	6147	0.95	1e-06	2e-05	33 x 49 ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
6	1207	0.95	1e-06	2e-05	31 x 49 chloride channel, nucleotide-sensitive, 1A [Source:HGNC Sy
7	6175	0.95	1e-06	8e-05	31 x 50 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:1037
8	55856	0.93	2e-06	3e-04	34 x 50 acyl-CoA thioesterase 13 [Source:HGNC Symbol;Acc:20999
9	132946	0.9	5e-06	9e-04	36 x 48 ADP-ribosylation factor-like 9 [Source:HGNC Symbol;Acc:2
10	11164	0.83	2e-05	9e-04	36 x 50 nudix (nucleoside diphosphate linked moiety X)-type motif 5
11	539	0.81	4e-05	9e-04	32 x 50 ATP synthase, H+ transporting, mitochondrial F1 complex, O
12	26175	0.81	4e-05	9e-04	37 x 50 transmembrane protein 251 [Source:HGNC Symbol;Acc:2021
13	84833	0.8	5e-05	9e-04	33 x 50 up-regulated during skeletal muscle growth 5 homolog (mous
14	7386	0.8	5e-05	9e-04	34 x 50 ubiquinol-cytochrome c reductase, Rieske iron-sulfur polype
15	51023	0.79	6e-05	9e-04	32 x 50 mitochondrial ribosomal protein S18C [Source:HGNC Symbo
16	51020	0.78	7e-05	9e-04	34 x 50 HD domain containing 2 [Source:HGNC Symbol;Acc:21078]
17	80273	0.77	9e-05	9e-04	35 x 50 GrpE-like 1, mitochondrial (E. coli) [Source:HGNC Symbol;A
18	388722	0.77	9e-05	9e-04	36 x 50 chromosome 1 open reading frame 53 [Source:HGNC Symbc
19	1349	0.77	1e-04	9e-04	33 x 50 cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;Ac
20	64976	0.76	1e-04	9e-04	34 x 50 mitochondrial ribosomal protein L40 [Source:HGNC Symbol;f

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	27.7	NULL	29 / 83	BP respiratory electron transport chain
2	21.11	NULL	36 / 153	MF structural constituent of ribosome
3	20.67	NULL	45 / 304	CC mitochondrial inner membrane
4	20.23	NULL	30 / 152	BP cellular metabolic process
5	19.92	NULL	8 / 19	CC mitochondrial proton-transporting ATP synthase complex
6	18.79	NULL	32 / 167	CC ribosome
7	17.64	NULL	7 / 10	CC large ribosomal subunit
8	17.52	NULL	21 / 87	BP translational termination
9	17.42	NULL	5 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
10	16.91	NULL	20 / 81	BP viral transcription
11	16.84	NULL	6 / 15	BP ATP synthesis coupled proton transport
12	16.74	NULL	5 / 14	BP mitochondrial ATP synthesis coupled proton transport
13	16.56	NULL	41 / 253	BP translation
14	16.49	NULL	21 / 92	BP translational elongation
15	16.37	NULL	13 / 36	CC mitochondrial respiratory chain complex I
16	15.78	NULL	6 / 11	Cancer GENTLES_modul5
17	15.73	NULL	20 / 92	BP viral life cycle
18	15.71	NULL	12 / 34	MF NADH dehydrogenase (ubiquinone) activity
19	15.66	NULL	14 / 51	CC cytosolic large ribosomal subunit
20	15.54	NULL	103 / 1318	CC mitochondrion
21	14.59	NULL	12 / 35	BP mitochondrial electron transport, NADH to ubiquinone
22	14.5	NULL	8 / 26	MF cytochrome-c oxidase activity
23	14.3	NULL	23 / 128	BP translational initiation
24	14.11	NULL	22 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
25	14.05	NULL	21 / 109	BP SRP-dependent cotranslational protein targeting to membrane
26	13.04	NULL	28 / 242	BP RNA metabolic process
27	13.03	NULL	8 / 23	CC mitochondrial ribosome
28	12.2	NULL	26 / 219	BP mRNA metabolic process
29	11.65	NULL	5 / 12	BP oxidative phosphorylation
30	9.98	NULL	26 / 287	BP viral process
31	9.69	NULL	3 / 11	GSEA C2BIOCARTA_ETC_PATHWAY
32	9.62	NULL	4 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
33	9.4	NULL	3 / 13	GSEA C2BROWNE_HCMV_INFECTION_48HR_DN
34	9.07	NULL	5 / 18	MF 2 iron, 2 sulfur cluster binding
35	9.01	NULL	4 / 9	GSEA C2KEGG_RIBOSOME
36	9.01	NULL	4 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
37	9.01	NULL	4 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
38	9.01	NULL	4 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
39	9.01	NULL	4 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
40	9.01	NULL	4 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT

p-values



GW_168

Local Summary

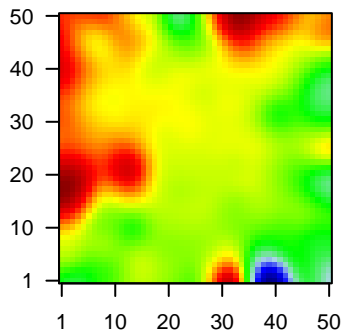
%DE = 0.86
 # metagenes = 16
 # genes = 255
 # genes in genesets = 229

genes with $fdr < 0.1$ = 195 (0 + / 195 -)
 # genes with $fdr < 0.05$ = 195 (0 + / 195 -)
 # genes with $fdr < 0.01$ = 149 (0 + / 149 -)

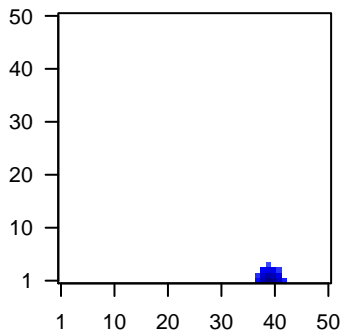
<r> metagenes = 0.98
 <r> genes = 0.48

<FC> = -0.66
 <shrinkage-t> = -23.4
 <p-value> = 0
 <fdr> = 0.31

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	641737	-1.79	2e-16	4e-15	40 x 1
2	126205	-1.63	2e-16	4e-15	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbol]
3	25862	-1.56	2e-15	7e-14	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20202]
4	399900	-1.41	5e-15	7e-14	39 x 1
5	100132406	-1.53	6e-15	7e-14	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC Symbol;Acc:28880]
6	84061	-1.53	8e-15	1e-12	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
7	90586	-1.49	4e-14	2e-12	39 x 1 amine oxidase, copper containing 4, pseudogene [Source:HGNC Symbol;Acc:28880]
8	3586	-1.37	8e-14	3e-12	40 x 1 interleukin 10 [Source:HGNC Symbol;Acc:5962]
9	91368	-1.33	2e-13	7e-12	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC Symbol;Acc:28880]
10	84278	-1.42	5e-13	7e-12	39 x 1
11	255031	-1.42	5e-13	3e-11	40 x 1 long intergenic non-protein coding RNA 957 [Source:HGNC Symbol;Acc:28880]
12	400818	-1.39	1e-12	5e-11	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProtKB/TrEMBL;Acc:E7I10]
13	51478	-1.37	4e-12	5e-11	39 x 1 hydroxysteroid (17-beta) dehydrogenase 7 [Source:HGNC Symbol;Acc:28880]
14	9747	-1.24	6e-12	5e-11	39 x 1 family with sequence similarity 115, member A [Source:HGNC Symbol;Acc:28880]
15	729603	-1.24	7e-12	5e-11	40 x 1
16	57835	-1.34	9e-12	5e-11	40 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7I10]
17	440157	-1.34	1e-11	5e-11	39 x 1
18	5143	-1.23	1e-11	8e-11	39 x 1 phosphodiesterase 4C, cAMP-specific [Source:HGNC Symbol;Acc:28880]
19	7766	-1.33	1e-11	3e-10	40 x 1 Zinc finger protein 223 [Source:UniProtKB/TrEMBL;Acc:K7EI10]
20	55142	-1.32	2e-11	3e-10	40 x 1 HAU5 augmin-like complex, subunit 2 [Source:HGNC Symbol;Acc:28880]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-15.6	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-12.72	NULL	3 / 14	MMML C6S/CIEJ_MMML 8
3	-8.77	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
4	-8.6	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
5	-8.26	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
6	-7.4	NULL	2 / 14	BP cellular response to estradiol stimulus
7	-7.39	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
8	-7.39	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
9	-7.14	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
10	-6.34	NULL	2 / 14	BP mitochondrion morphogenesis
11	-6.25	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
12	-6.21	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
13	-6.03	NULL	3 / 24	BP negative regulation of T cell proliferation
14	-5.9	NULL	1 / 4	MMML C6S/CIEJ_MMML 44
15	-5.85	NULL	2 / 16	BP cognition
16	-5.66	NULL	1 / 10	CC oligosaccharyltransferase complex
17	-5.42	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process
18	-5.42	NULL	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
19	-5.42	NULL	2 / 15	BP female gamete generation
20	-5.11	NULL	1 / 11	BP negative regulation of interleukin-12 production
21	-5.11	NULL	1 / 11	GSEA C2SU_PANCREAS
22	-5.05	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
23	-5.03	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOLESTEROL
24	-4.97	NULL	2 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
25	-4.95	NULL	2 / 15	GSEA C2THUM_SYSTOLIC_HEART_FAILURE_DN
26	-4.93	NULL	1 / 9	GSEA C2BROWNE_HCMV_INFECTION_1HR_DN
27	-4.86	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
28	-4.84	NULL	1 / 12	BP negative regulation of growth of symbiont in host
29	-4.84	NULL	1 / 14	Cancer LIU_COMMON_CANCER_GENES
30	-4.81	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
31	-4.77	NULL	2 / 22	BP negative regulation of interferon-gamma production
32	-4.75	NULL	3 / 19	BP sprouting angiogenesis
33	-4.66	NULL	2 / 23	BP protein N-linked glycosylation
34	-4.63	NULL	3 / 15	GSEA C2WANG_CLIM2_TARGETS_UP
35	-4.61	NULL	1 / 13	BP negative regulation of B cell proliferation
36	-4.61	NULL	1 / 13	GSEA C2NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
37	-4.61	NULL	1 / 13	GSEA C2KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
38	-4.61	NULL	1 / 13	GSEA C2BIOCARTA_DC_PATHWAY
39	-4.59	NULL	1 / 14	BP magnesium ion transport
40	-4.57	NULL	1 / 7	GSEA C2LIU_CMYB_TARGETS_DN

p-values

