

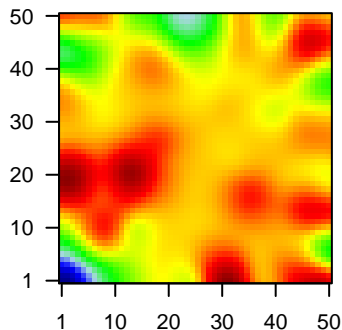
GW_033

Global Summary

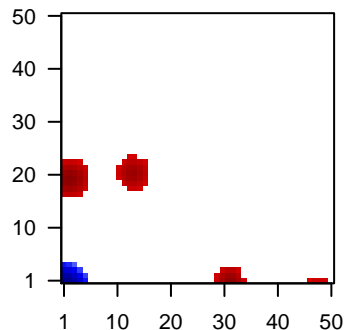
%DE = 0.13
 # genes with fdr < 0.2 = 1564 (783 + / 781 -)
 # genes with fdr < 0.1 = 1081 (524 + / 557 -)
 # genes with fdr < 0.05 = 887 (417 + / 470 -)
 # genes with fdr < 0.01 = 572 (259 + / 313 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.14
 <fdr> = 0.87

Profile



Regulated Spots



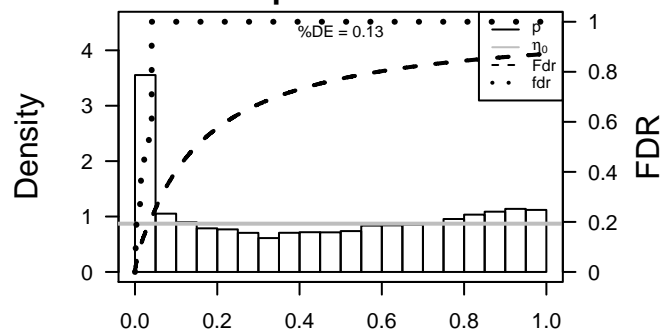
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	-2.01	2e-16	6e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	633	-2.33	2e-16	6e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	760	-2	2e-16	6e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
4	1308	-2.29	2e-16	6e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
5	1277	-2.61	2e-16	6e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
6	1278	-3.03	2e-16	6e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
7	1281	-3.02	2e-16	6e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
8	1282	-2.18	2e-16	6e-14	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
9	1289	-2.05	2e-16	6e-14	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
10	1291	-2.25	2e-16	6e-14	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
11	1293	-2.42	2e-16	6e-14	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	1298	1.93	2e-16	6e-14	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
13	1475	1.97	2e-16	6e-14	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
14	1513	-1.95	2e-16	6e-14	4 x 1 cathepsin K [Source:HGNC Symbol;Acc:2536]
15	3627	2.75	2e-16	6e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;]
16	4283	2.29	2e-16	6e-14	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac]
17	1809	-2.18	2e-16	6e-14	6 x 1 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:3015]
18	1843	-1.89	2e-16	6e-14	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30]
19	1948	-1.93	2e-16	6e-14	1 x 5 ephrin-B2 [Source:HGNC Symbol;Acc:3227]
20	1958	-2.12	2e-16	6e-14	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.65	NULL	52	Chr Chr HSCHR6_MHC_QBL
2	10.15	NULL	15	CC MHC class II protein complex
3	9.63	NULL	1135	Chr Chr 19
4	8.33	NULL	47	BP antigen processing and presentation
5	7.77	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
6	7.53	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
7	7.32	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
8	7.21	NULL	10	BP cellular response to zinc ion
9	7.19	NULL	717	Chr Chr 16
10	7.09	NULL	1318	CC mitochondrion
11	7.07	NULL	51	BP type I interferon signaling pathway
12	6.99	NULL	304	CC mitochondrial inner membrane
13	6.96	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
14	6.96	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
15	6.88	NULL	7	MMML C6SCIEJ_MMML 13
16	6.76	NULL	83	BP respiratory electron transport chain
17	6.7	NULL	13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
18	6.56	NULL	135	H.Tiss WIRTH_Mucosa
19	6.35	NULL	60	BP interferon-gamma-mediated signaling pathway
20	6.31	NULL	74	BP regulation of immune response
<i>Underexpressed</i>				
1	-20.32	NULL	250	LymphomaENZ_Stromal signature 1
2	-18.64	NULL	190	CC extracellular matrix
3	-17.14	NULL	242	BP extracellular matrix organization
4	-14.65	NULL	16	MMML C6SCIEJ_MMML 1
5	-14.29	NULL	11	MF platelet-derived growth factor binding
6	-14.24	NULL	69	BP extracellular matrix disassembly
7	-14.01	NULL	64	BP collagen catabolic process
8	-13.51	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
9	-12.44	NULL	15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
10	-11.56	NULL	12	miRNA target-29c
11	-11.43	NULL	403	BP cell adhesion
12	-11.38	NULL	57	MF extracellular matrix structural constituent
13	-10.94	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
14	-10.84	NULL	83	CC basement membrane
15	-10.56	NULL	183	CC proteinaceous extracellular matrix
16	-10.39	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
17	-10.34	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
18	-10.29	NULL	683	CC extracellular space
19	-10.22	NULL	37	BP collagen fibril organization
20	-10.2	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP

p-values



GW_033

Local Summary

%DE = 0.7
 # metagenes = 15
 # genes = 162
 # genes in genesets = 159

 # genes with $fdr < 0.1 = 90$ (87 + / 3 -)
 # genes with $fdr < 0.05 = 76$ (75 + / 1 -)
 # genes with $fdr < 0.01 = 60$ (60 + / 0 -)

 $\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.37

 $\langle FC \rangle = 0.53$
 $\langle \text{shrinkage-t} \rangle = 18.48$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.51$

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3627	2.75	2e-16	5e-15	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:10513]
2	8519	1.93	2e-16	5e-15	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC Symbol;Acc:10513]
3	6890	1.63	4e-12	1e-09	32 x 1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
4	10866	1.55	4e-11	1e-09	32 x 1 HLA complex P5 (non-protein coding) [Source:HGNC Symbol;Acc:10513]
5	7453	1.55	5e-11	2e-09	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:10513]
6	6288	1.53	8e-11	1e-08	31 x 1 serum amyloid A1 [Source:HGNC Symbol;Acc:10513]
7	10581	1.34	6e-10	1e-08	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:10513]
8	629	1.45	7e-10	1e-08	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
9	51191	1.44	1e-09	3e-07	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
10	10410	1.26	6e-09	3e-07	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC Symbol;Acc:10513]
11	54922	1.32	2e-08	3e-07	30 x 1 Ras interacting protein 1 [Source:HGNC Symbol;Acc:24716]
12	3134	1.32	2e-08	3e-07	32 x 1 major histocompatibility complex, class I, F [Source:HGNC Symbol;Acc:10513]
13	9997	1.32	2e-08	9e-07	32 x 1 SCO2 cytochrome c oxidase assembly protein [Source:HGNC Symbol;Acc:10513]
14	4277	1.28	6e-08	9e-07	32 x 1 MHC class I polypeptide-related sequence B [Source:HGNC Symbol;Acc:10513]
15	3804	1.27	7e-08	9e-07	32 x 1 killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail
16	3135	1.27	8e-08	4e-05	32 x 1 major histocompatibility complex, class I, G [Source:HGNC Symbol;Acc:10513]
17	257101	1.14	1e-06	4e-05	32 x 2 zinc finger protein 683 [Source:HGNC Symbol;Acc:28495]
18	5699	1.12	2e-06	4e-05	32 x 1 proteasome (prosome, macropain) subunit, beta type, 10 [Source:HGNC Symbol;Acc:10513]
19	51296	1.1	3e-06	4e-05	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3 [Source:HGNC Symbol;Acc:10513]
20	54739	1.09	4e-06	6e-05	32 x 1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]

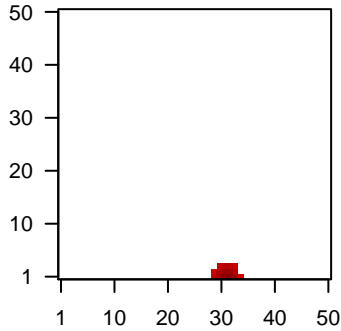
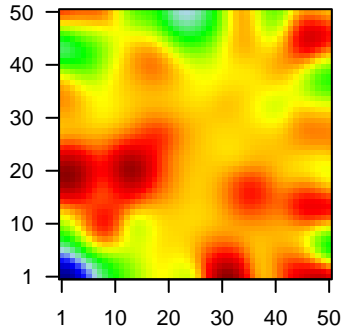
Local Geneset Analysis

Overexpression

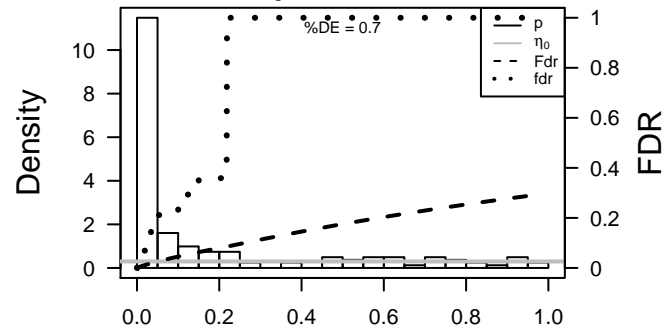
Rank	GSZ	p-value	#in/all	Geneset
1	34.49	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
2	34.27	NULL	29 / 51	BP type I interferon signaling pathway
3	33.63	NULL	6 / 6	Lymphocyte activation-induced chemokine (Lymphocyte activation-induced chemokine)
4	31.62	NULL	2 / 2	MMML C6SCIEJ_MMML_27
5	29.61	NULL	11 / 16	GSEA C2ROSEVIC_RESPONSE_TO_IMIQUMOD
6	26.98	NULL	7 / 10	CC MHC class I protein complex
7	26.58	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
8	25.23	NULL	7 / 18	MF peptide antigen binding
9	24.79	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
10	24.74	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
11	23.19	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
12	23.03	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
13	22.71	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
14	21.69	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
15	20.99	NULL	6 / 14	GSEA C2RADEVA_RESPONSE_TO_IFNA1_UP
16	19.92	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
17	19.91	NULL	34 / 204	BP cytokine-mediated signaling pathway
18	19.14	NULL	13 / 70	BP antigen processing and presentation of exogenous peptide antigen
19	18.9	NULL	27 / 109	BP response to virus
20	18.56	NULL	13 / 74	BP antigen processing and presentation of exogenous peptide antigen
21	18.5	NULL	31 / 123	BP defense response to virus
22	18.33	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
23	18.18	NULL	11 / 74	BP regulation of immune response
24	18.02	NULL	9 / 52	Chr HSCR6_MHC_QBL
25	17.68	NULL	2 / 10	BP positive regulation of cAMP-mediated signaling
26	17.42	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
27	16.88	NULL	29 / 312	BP immune response
28	16.79	NULL	14 / 31	BP negative regulation of viral genome replication
29	16.78	NULL	5 / 18	BP response to interferon-gamma
30	16.56	NULL	13 / 91	BP antigen processing and presentation of peptide antigen via MHC class II
31	16.47	NULL	13 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
32	16.39	NULL	9 / 47	BP antigen processing and presentation
33	15.95	NULL	2 / 12	BP positive regulation of leukocyte chemotaxis
34	15.64	NULL	5 / 23	CC integral to luminal side of endoplasmic reticulum membrane
35	15.58	NULL	1 / 2	miRNA target-152
36	15.01	NULL	3 / 9	GSEA C2FURUKAWA_DUSP6_TARGETS_PCI35_UP
37	14.85	NULL	50 / 572	Disease GUDJ_poriasis up
38	14.34	NULL	3 / 8	GSEA C2KEGG_PRIMARY_IMMUNODEFICIENCY
39	14.03	NULL	33 / 274	Lymphocyte activation-induced chemokine (Lymphocyte activation-induced chemokine)
40	14.01	NULL	6 / 32	CC ER to Golgi transport vesicle membrane

Profile

Spot



p-values



GW_033

Local Summary

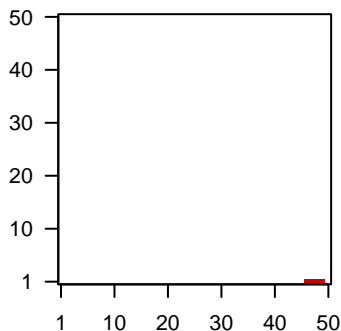
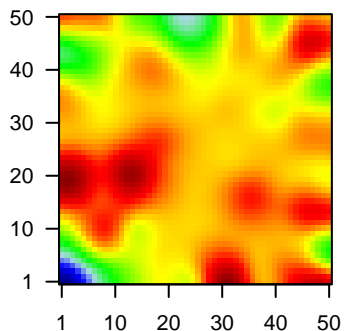
%DE = 0.57
 # metagenes = 4
 # genes = 94
 # genes in genesets = 93
 # genes with $fdr < 0.1$ = 38 (38 + / 0 -)
 # genes with $fdr < 0.05$ = 27 (27 + / 0 -)
 # genes with $fdr < 0.01$ = 25 (25 + / 0 -)

<r> metagenes = 1
 <r> genes = 0.63

<FC> = 0.5
 <shrinkage-t> = 17.38
 <p-value> = 0
 <fdr> = 0.61

Profile

Spot



Local Genelist

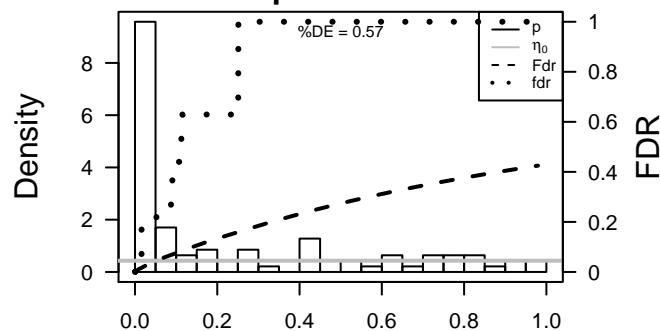
Rank	ID	log(FC)	fdr	p-value	Description
1	4283	2.29	2e-16	4e-15	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:10548]
2	3620	2.63	2e-16	4e-15	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:10548]
3	5790	1.57	3e-11	1e-09	49 x 1 protein tyrosine phosphatase, receptor type, C-associated pr
4	3119	1.55	5e-11	3e-08	49 x 1 major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:10548]
5	7318	1.46	7e-10	7e-07	48 x 1 ubiquitin-like modifier activating enzyme 7 [Source:HGNC Sy
6	115361	1.32	2e-08	7e-07	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048]
7	4818	1.3	4e-08	8e-07	49 x 1 natural killer cell group 7 sequence [Source:HGNC Symbol;A
8	915	1.27	7e-08	8e-07	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC S
9	2634	1.27	7e-08	5e-06	47 x 1 guanylate binding protein 2, interferon-inducible [Source:HG
10	6352	1.22	2e-07	5e-06	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:10548]
11	3120	1.19	5e-07	5e-06	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:HGNC Symbol;Acc:10548]
12	10437	1.19	5e-07	5e-06	46 x 1 interferon, gamma-inducible protein 30 [Source:HGNC Symb
13	3543	1.08	6e-07	5e-06	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
14	3669	1.17	7e-07	5e-05	48 x 1 interferon stimulated exonuclease gene 20kDa [Source:HGNC
15	393	1.12	2e-06	5e-05	49 x 1 Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:10548]
16	2999	1.1	3e-06	1e-04	47 x 1 granzyme H (cathepsin G-like 2, protein h-CCPX) [Source:H
17	5920	1.06	7e-06	3e-04	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Sour
18	10628	1	2e-05	3e-04	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
19	3001	1	2e-05	4e-04	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
20	3695	0.98	3e-05	6e-03	47 x 1 integrin, beta 7 [Source:HGNC Symbol;Acc:6162]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	23.82	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
2	23.61	NULL	3 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
3	22.83	NULL	2 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
4	20.51	NULL	4 / 15	CC MHC class II protein complex
5	20.48	NULL	3 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
6	19.64	NULL	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
7	16.77	NULL	4 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
8	16.64	NULL	1 / 10	BP tryptophan catabolic process
9	15.82	NULL	42 / 417	H.Tiss WIRTH_Immune system
10	15.74	NULL	1 / 11	GSEA C2NAKAJIMA_EOSINOPHIL
11	15.46	NULL	3 / 15	GSEA C2HAHTOLA_SEZARY_SYNDROM_DN
12	15.42	NULL	2 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
13	14.57	NULL	6 / 47	BP antigen processing and presentation
14	14.44	NULL	1 / 10	BP positive regulation of cAMP-mediated signaling
15	14.44	NULL	1 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
16	14.18	NULL	21 / 312	BP immune response
17	13.62	NULL	2 / 11	GSEA C2FUJII_YBX1_TARGETS_UP
18	13	NULL	3 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
19	12.98	NULL	1 / 12	GSEA C2KONUMA_COLON_CANCER_MSL_DN
20	12.84	NULL	3 / 16	BP cytolysis
21	12.72	NULL	3 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
22	12.39	NULL	1 / 13	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
23	11.88	NULL	3 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
24	11.82	NULL	3 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
25	11.81	NULL	2 / 32	Glio Donson-Misc immune function-associated with LTS in HGA
26	11.77	NULL	2 / 12	CC T cell receptor complex
27	11.73	NULL	1 / 4	MMML C2SCIEJ_MMML_2
28	11.69	NULL	2 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
29	11.49	NULL	5 / 13	Cancer GENTLES_modul18
30	11.38	NULL	2 / 15	GSEA C2SHIPP_DLCL_VS_FOLLICULAR_LYMPHOMA_DN
31	11.38	NULL	2 / 15	GSEA C2KENNY_CTNNB1_TARGETS_DN
32	11.33	NULL	2 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
33	10.99	NULL	1 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
34	10.99	NULL	1 / 16	GSEA C2WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN
35	10.99	NULL	1 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
36	10.83	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
37	10.61	NULL	1 / 17	BP positive regulation of release of sequestered calcium ion into cytosol
38	10.56	NULL	1 / 22	BP positive regulation of interleukin-12 production
39	10.5	NULL	1 / 2	GSEA C2SUTIERREZ_MULTIPLE_MYELOMA_UP
40	10.4	NULL	1 / 6	GSEA C2RAY_ALZHEIMERS_DISEASE

p-values



GW_033

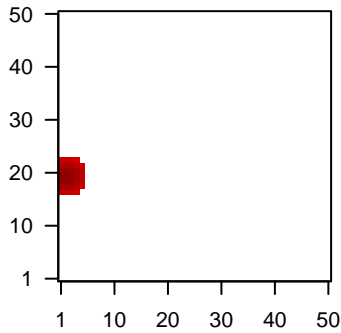
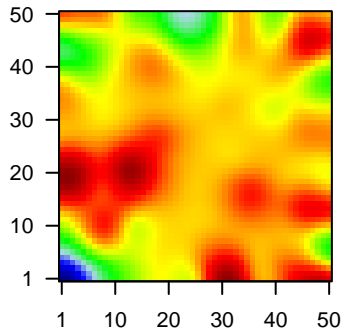
Local Summary

%DE = 0.6
 # metagenes = 33
 # genes = 329
 # genes in genesets = 324
 # genes with $fdr < 0.1$ = 146 (145 + / 1 -)
 # genes with $fdr < 0.05$ = 97 (96 + / 1 -)
 # genes with $fdr < 0.01$ = 34 (34 + / 0 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.28
 $\langle FC \rangle = 0.42$
 $\langle \text{shrinkage-t} \rangle = 14.57$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.66$

Profile

Spot



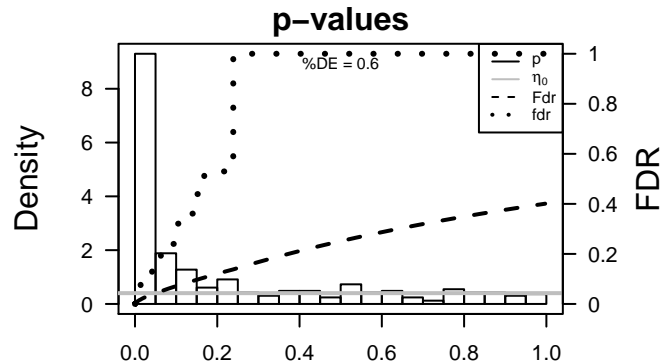
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	728489	1.24	2e-07	1e-05	1 x 19 DNL-type zinc finger [Source:HGNC Symbol;Acc:33879]
2	51337	1.23	2e-07	3e-05	3 x 21 thioesterase superfamily member 6 [Source:HGNC Symbol;A
3	8045	1.18	6e-07	3e-05	2 x 22 Ras association (RalGDS/AF-6) domain family (N-terminal) i
4	84300	1.17	7e-07	1e-04	2 x 18 ubiquinol-cytochrome c reductase complex assembly factor 2
5	55168	1.13	2e-06	3e-04	2 x 20 mitochondrial ribosomal protein S18A [Source:HGNC Symbo
6	85359	1.05	8e-06	3e-04	2 x 20 DiGeorge syndrome critical region gene 6-like [Source:HGNC
7	389541	1.05	8e-06	3e-04	3 x 19 late endosomal/lysosomal adaptor, MAPK and MTOR activat
8	374291	1.04	1e-05	3e-04	3 x 21 NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (†
9	7936	1.04	1e-05	3e-04	1 x 19 negative elongation factor complex member E [Source:HGNC
10	51069	1.02	1e-05	3e-04	2 x 18 mitochondrial ribosomal protein L2 [Source:HGNC Symbol;Ar
11	54939	1.01	2e-05	3e-04	3 x 19 COMM domain containing 4 [Source:HGNC Symbol;Acc:260;
12	5652	1.01	2e-05	3e-04	1 x 22 protease, serine, 8 [Source:HGNC Symbol;Acc:9491]
13	29988	1	2e-05	3e-04	2 x 21 solute carrier family 2 (facilitated glucose transporter), memb
14	353	1	2e-05	8e-04	1 x 21 adenine phosphoribosyltransferase [Source:HGNC Symbol;A
15	79095	0.98	3e-05	8e-04	4 x 23 chromosome 9 open reading frame 16 [Source:HGNC Symbc
16	79897	0.97	4e-05	8e-04	3 x 19 ribonuclease P/MRP 21kDa subunit [Source:HGNC Symbol;#
17	25886	0.97	4e-05	1e-03	3 x 17 POC1 centriolar protein A [Source:HGNC Symbol;Acc:24488
18	51079	0.94	7e-05	1e-03	2 x 21 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, [3]
19	57407	0.94	7e-05	1e-03	1 x 20 NmrA-like family domain containing 1 [Source:HGNC Symbo
20	3006	0.92	9e-05	1e-03	5 x 20 histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	14.88	NULL	4 / 10	MF NADH dehydrogenase activity
2	11.4	NULL	86 / 1318	CC mitochondrion
3	10.3	NULL	28 / 304	CC mitochondrial inner membrane
4	9.77	NULL	6 / 34	MF NADH dehydrogenase (ubiquinone) activity
5	9.72	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
6	9.45	NULL	6 / 36	CC mitochondrial respiratory chain complex I
7	9.33	NULL	4 / 13	GSEA C2MOOTHA_VOXPPOS
8	9.06	NULL	12 / 83	BP respiratory electron transport chain
9	8.84	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
10	8.81	NULL	21 / 153	MF structural constituent of ribosome
11	8.48	NULL	4 / 16	GSEA C2BIOCARTA_PTDINS_PATHWAY
12	8.19	NULL	4 / 16	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
13	8	NULL	3 / 11	MMML C6SCIEJ_MMML 15
14	7.51	NULL	16 / 152	BP cellular metabolic process
15	7.39	NULL	5 / 35	BP mitochondrial electron transport, NADH to ubiquinone
16	7.19	NULL	5 / 19	CC mitochondrial small ribosomal subunit
17	7.18	NULL	2 / 7	GSEA C2REACTOME_SIGNALING_BY_WNT
18	7.13	NULL	3 / 12	BP apoptotic nuclear changes
19	7.03	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
20	6.88	NULL	2 / 13	CC mitochondrial respiratory chain
21	6.86	NULL	4 / 16	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
22	6.86	NULL	4 / 16	GSEA C2MOOTHA_MITOCHONDRIA
23	6.85	NULL	23 / 253	BP translation
24	6.79	NULL	4 / 16	GSEA C2NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
25	6.52	NULL	17 / 167	CC ribosome
26	6.47	NULL	3 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
27	6.27	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
28	6.27	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF
29	6.27	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
30	6.27	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
31	6.25	NULL	3 / 14	GSEA C2STEIN_ESRRA_TARGETS_UP
32	6.25	NULL	1 / 5	GSEA C2ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
33	6.17	NULL	38 / 717	Chr Chr 16
34	6.14	NULL	2 / 13	GSEA C2ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
35	6.07	NULL	4 / 49	CC mitochondrial intermembrane space
36	6.06	NULL	4 / 13	BP ribosomal small subunit biogenesis
37	5.97	NULL	3 / 15	CC DNA-directed RNA polymerase III complex
38	5.95	NULL	1 / 3	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
39	5.95	NULL	1 / 3	GSEA C2KEGG_PARKINSONS_DISEASE
40	5.83	NULL	2 / 15	Cancer GENTLES_modul1



GW_033

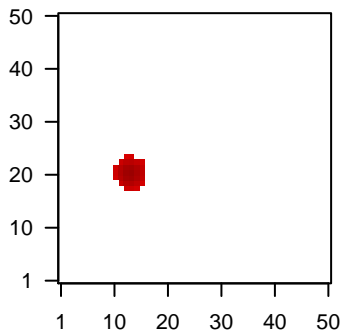
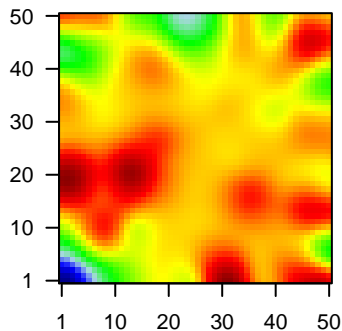
Local Summary

%DE = 0.76
 # metagenes = 33
 # genes = 282
 # genes in genesets = 275
 # genes with fdr < 0.1 = 138 (137 + / 1 -)
 # genes with fdr < 0.05 = 84 (83 + / 1 -)
 # genes with fdr < 0.01 = 38 (38 + / 0 -)

<r> metagenes = 0.94
 <r> genes = 0.21
 <FC> = 0.41
 <shrinkage-t> = 14.43
 <p-value> = 0.04
 <fdr> = 0.71

Profile

Spot



Local Genelist

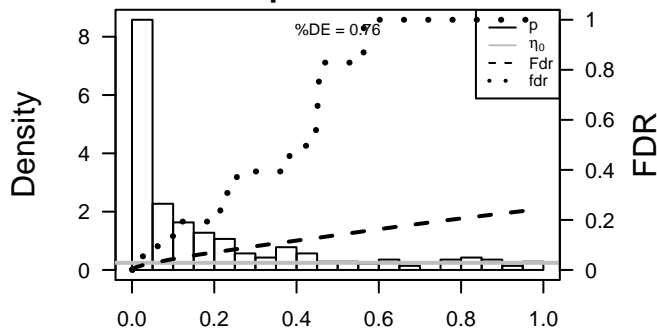
Rank	ID	log(FC)	fdr	p-value	Description
1	10591	1.1	3e-06	1e-04	13 x 20 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 [Source:HGNC]
2	51471	1.09	4e-06	4e-04	14 x 18 N-acetyltransferase 8 (GCN5-related, putative) [Source:HGNC]
3	84681	1.03	1e-05	4e-04	14 x 21 histidine triad nucleotide binding protein 2 [Source:HGNC Symbol]
4	7923	1.01	2e-05	4e-04	13 x 22 hydroxysteroid (17-beta) dehydrogenase 8 [Source:HGNC Symbol]
5	4201	0.99	3e-05	4e-04	13 x 21 male-enhanced antigen 1 [Source:HGNC Symbol;Acc:6986]
6	4713	0.98	3e-05	4e-04	14 x 21 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 11 kDa subunit [Source:HGNC Symbol;Acc:10000]
7	10217	0.98	3e-05	9e-04	15 x 21 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide 2) [Source:HGNC Symbol;Acc:10000]
8	9296	0.96	5e-05	1e-03	14 x 21 ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F [Source:HGNC Symbol;Acc:10000]
9	10245	0.94	6e-05	1e-03	13 x 20 translocase of inner mitochondrial membrane 17 homolog B (human) [Source:HGNC Symbol;Acc:10000]
10	8673	0.92	1e-04	1e-03	14 x 21 vesicle-associated membrane protein 8 [Source:HGNC Symbol;Acc:10000]
11	51647	0.92	1e-04	1e-03	14 x 22 family with sequence similarity 96, member B [Source:HGNC Symbol;Acc:10000]
12	84316	0.91	1e-04	3e-03	14 x 21 LSM domain containing 1 [Source:HGNC Symbol;Acc:28212]
13	84987	0.89	2e-04	3e-03	14 x 21 cytochrome c oxidase assembly homolog 14 (S. cerevisiae) [Source:HGNC Symbol;Acc:10000]
14	29099	0.88	2e-04	5e-03	14 x 22 COMM domain containing 9 [Source:HGNC Symbol;Acc:25000]
15	54344	0.85	3e-04	5e-03	14 x 21 dolichyl-phosphate mannosyltransferase polypeptide 3 [Source:HGNC Symbol;Acc:10000]
16	51307	0.82	5e-04	5e-03	15 x 19 family with sequence similarity 53, member C [Source:HGNC Symbol;Acc:10000]
17	26001	0.81	6e-04	5e-03	13 x 20 ring finger protein 167 [Source:HGNC Symbol;Acc:24544]
18	154467	0.81	6e-04	5e-03	14 x 21 coiled-coil domain containing 167 [Source:HGNC Symbol;Acc:10000]
19	126003	0.81	6e-04	5e-03	14 x 22 trafficking protein particle complex 5 [Source:HGNC Symbol;Acc:10000]
20	140823	0.81	6e-04	5e-03	14 x 22 reactive oxygen species modulator 1 [Source:HGNC Symbol;Acc:10000]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	9.75	NULL	67 / 1318	CC mitochondrion
2	9.74	NULL	3 / 10	MF NADH dehydrogenase activity
3	8.86	NULL	1 / 4	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G5_UP
4	8.69	NULL	3 / 9	GSEA C2KEGG_RNA_POLYMERASE
5	7.21	NULL	9 / 83	BP respiratory electron transport chain
6	7.08	NULL	3 / 11	BP positive regulation of protein targeting to membrane
7	6.95	NULL	18 / 304	CC mitochondrial inner membrane
8	6.94	NULL	2 / 7	MMML C6SCIEJ_MMML 48
9	6.93	NULL	3 / 12	GSEA C2REACTOME_NUCLEOTIDE_EXCISION_REPAIR
10	6.91	NULL	4 / 20	Lymphoma OSOLOWSKI_red UP
11	6.9	NULL	54 / 1233	TF KIM_MYC targets
12	6.49	NULL	4 / 36	CC mitochondrial respiratory chain complex I
13	6.31	NULL	3 / 15	GSEA C2REACTOME_MRNA_SPLICING_MINOR_PATHWAY
14	6.19	NULL	12 / 152	BP cellular metabolic process
15	6.12	NULL	2 / 11	Cancer GENTLES_modul5
16	6.06	NULL	4 / 34	MF NADH dehydrogenase (ubiquinone) activity
17	5.93	NULL	3 / 25	MF hydrogen ion transmembrane transporter activity
18	5.92	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
19	5.72	NULL	2 / 9	GSEA C2REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX
20	5.72	NULL	2 / 9	GSEA C2REACTOME_HIV1_TRANSCRIPTION_ELONGATION
21	5.7	NULL	2 / 8	GSEA C2REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS
22	5.68	NULL	6 / 38	MF DNA-directed RNA polymerase activity
23	5.67	NULL	2 / 6	MMML C6SCIEJ_MMML 29
24	5.48	NULL	1 / 8	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIAL
25	5.38	NULL	2 / 10	GSEA C2REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
26	5.38	NULL	2 / 10	GSEA C2REACTOME_HIV1_TRANSCRIPTION_INITIATION
27	5.38	NULL	2 / 10	GSEA C2REACTOME_MRNA_PROCESSING
28	5.38	NULL	2 / 10	GSEA C2REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INTERRUPTED_TRANSCRIPTION
29	5.27	NULL	3 / 15	CC mitochondrial large ribosomal subunit
30	5.16	NULL	5 / 47	BP protein targeting to mitochondrion
31	5.12	NULL	1 / 9	GSEA C2DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
32	5.12	NULL	1 / 9	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
33	5.09	NULL	2 / 11	GSEA C2REACTOME_TRANSCRIPTION_COUPLED_NER
34	5.03	NULL	2 / 17	CC mitochondrial envelope
35	5.02	NULL	41 / 1135	Chr Chr 19
36	4.98	NULL	3 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
37	4.93	NULL	2 / 10	BP peroxisome fission
38	4.83	NULL	2 / 12	GSEA C2KEGG_PYRIMIDINE_METABOLISM
39	4.83	NULL	2 / 12	GSEA C2REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPTION
40	4.81	NULL	1 / 10	GSEA C2BASSO_CD40_SIGNALING_DN

p-values



GW_033

Local Summary

%DE = 0.92
 # metagenes = 17
 # genes = 263
 # genes in genesets = 262

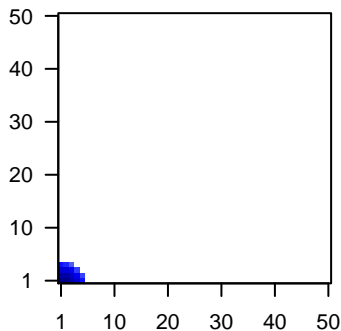
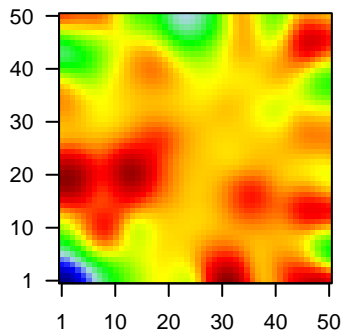
genes with $fdr < 0.1 = 224$ (5 + / 219 -)
 # genes with $fdr < 0.05 = 218$ (5 + / 213 -)
 # genes with $fdr < 0.01 = 192$ (5 + / 187 -)

<r> metagenes = 0.96
 <r> genes = 0.4

<FC> = -0.93
 <shrinkage-t> = -32.57
 <p-value> = 0
 <fdr> = 0.24

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	-2.01	2e-16	2e-16	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	633	-2.33	2e-16	2e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	1277	-2.61	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	-3.03	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	-3.02	2e-16	2e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1282	-2.18	2e-16	2e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
7	1289	-2.05	2e-16	2e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1291	-2.25	2e-16	2e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
9	1293	-2.42	2e-16	2e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	1513	-1.95	2e-16	2e-16	4 x 1 cathepsin K [Source:HGNC Symbol;Acc:2536]
11	3040	2.37	2e-16	2e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
12	3043	1.96	2e-16	2e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
13	4060	-2.5	2e-16	2e-16	2 x 1 lumican [Source:HGNC Symbol;Acc:6724]
14	4312	-2.39	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi]
15	4314	-2.34	2e-16	2e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
16	5270	-2.17	2e-16	2e-16	1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	6678	-2.02	2e-16	2e-16	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:t
18	7058	-2.01	2e-16	2e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
19	7070	-2.11	2e-16	2e-16	4 x 1 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:11801]
20	7431	-2.14	2e-16	2e-16	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-41.4	NULL	63 / 190	CC extracellular matrix
2	-41.31	NULL	8 / 11	MF platelet-derived growth factor binding
3	-41.08	NULL	15 / 16	MMML1 C6C1EJ_MMML1
4	-39.4	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
5	-36.83	NULL	72 / 250	LymphomaENZ_Stromal signature 1
6	-34.87	NULL	31 / 69	BP extracellular matrix disassembly
7	-34.3	NULL	8 / 12	miRNA target-29c
8	-33.77	NULL	28 / 64	BP collagen catabolic process
9	-33.54	NULL	67 / 242	BP extracellular matrix organization
10	-27.47	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
11	-27.37	NULL	20 / 57	MF extracellular matrix structural constituent
12	-26.75	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
13	-26.23	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
14	-24.65	NULL	15 / 37	BP collagen fibril organization
15	-23.86	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
16	-23.6	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
17	-23.53	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
18	-23.37	NULL	12 / 40	BP cellular response to amino acid stimulus
19	-23.3	NULL	11 / 19	MF extracellular matrix binding
20	-21.68	NULL	37 / 183	CC proteinaceous extracellular matrix
21	-21.43	NULL	7 / 16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
22	-21.35	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
23	-21.14	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
24	-21.07	NULL	76 / 683	CC extracellular space
25	-20.78	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
26	-20.71	NULL	6 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
27	-20.35	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
28	-20.35	NULL	4 / 10	BP protein heterotrimerization
29	-20.23	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
30	-20.15	NULL	12 / 35	Glio Colman_survival_associated
31	-20.04	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
32	-19.94	NULL	23 / 119	LymphomaBOSOLOWSKI_green total
33	-19.59	NULL	62 / 553	Cancer Lembcke_Colonc Inflammation
34	-19.41	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
35	-19	NULL	6 / 13	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
36	-18.99	NULL	5 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
37	-18.87	NULL	18 / 68	CC collagen
38	-18.59	NULL	103 / 1182CC	extracellular region
39	-18.54	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
40	-18.15	NULL	22 / 83	CC basement membrane

p-values

