

GW_107

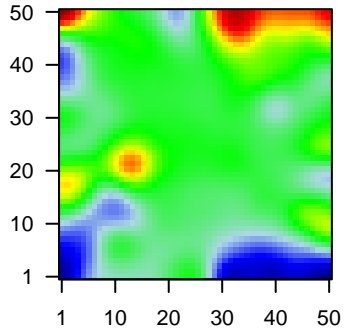
Global Summary

%DE = 0.17
 # genes with fdr < 0.2 = 2049 (1138 + / 911 -)
 # genes with fdr < 0.1 = 1581 (898 + / 683 -)
 # genes with fdr < 0.05 = 1276 (741 + / 535 -)
 # genes with fdr < 0.01 = 763 (457 + / 306 -)

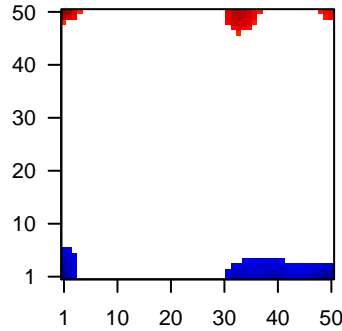
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.83

Profile



Regulated Spots



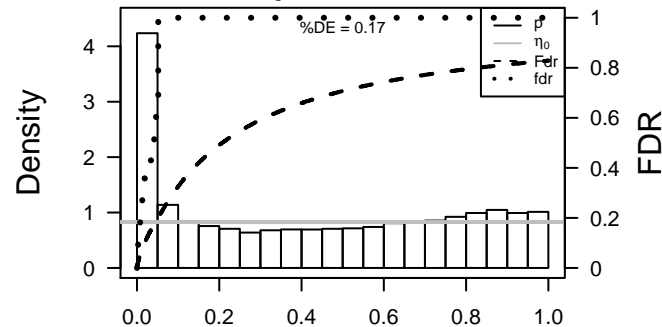
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	58	2.35	2e-16 7e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	131	2.13	2e-16 7e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	2.15	2e-16 7e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	2.04	2e-16 7e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy
5	216	2.7	2e-16 7e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	29113	1.79	2e-16 7e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
7	84290	1.81	2e-16 7e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
8	6364	-2.01	2e-16 7e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
9	49860	3.03	2e-16 7e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
10	1469	2.41	2e-16 7e-14	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
11	83888	2.7	2e-16 7e-14	50 x 50 fibroblast growth factor binding protein 2 [Source:HGNC Sym
12	2312	2.18	2e-16 7e-14	1 x 49 filaggrin [Source:HGNC Symbol;Acc:3748]
13	100288413	1.84	2e-16 7e-14	14 x 50 endogenous retrovirus group MER34, member 1 [Source:HGI
14	2877	2.27	2e-16 7e-14	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
15	2938	2.37	2e-16 7e-14	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Ac
16	119391	1.94	2e-16 7e-14	5 x 48 glutathione S-transferase omega 2 [Source:HGNC Symbol;A
17	43849	1.83	2e-16 7e-14	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6:
18	3851	2.92	2e-16 7e-14	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
19	196374	2.31	2e-16 7e-14	1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926]
20	643479	1.87	2e-16 7e-14	1 x 49

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.8	NULL	153	MF structural constituent of ribosome
2	15.2	NULL	167	CC ribosome
3	14.57	NULL	253	BP translation
4	13.73	NULL	1318	CC mitochondrion
5	13.1	NULL	81	BP viral transcription
6	12.98	NULL	87	BP translational termination
7	12.92	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
8	12.7	NULL	92	BP translational elongation
9	12.14	NULL	92	BP viral life cycle
10	11.46	NULL	128	BP translational initiation
11	10.44	NULL	135	H.Tiss WIRTH_Mucosa
12	10.37	NULL	51	CC cytosolic large ribosomal subunit
13	10.29	NULL	242	BP RNA metabolic process
14	10.15	NULL	287	BP viral process
15	10.14	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
16	10.1	NULL	83	BP respiratory electron transport chain
17	9.48	NULL	304	CC mitochondrial inner membrane
18	9.42	NULL	219	BP mRNA metabolic process
19	9.01	NULL	152	BP cellular metabolic process
20	8.8	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
<i>Underexpressed</i>				
1	-16.09	NULL	553	Cancer Lembecke_Colonc Inflammation
2	-13.56	NULL	8023	MF protein binding
3	-12.38	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
4	-12.38	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
5	-12.38	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
6	-12.38	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
7	-11.65	NULL	2659	CC plasma membrane
8	-11.65	NULL	417	H.Tiss WIRTH_Immune system
9	-11.5	NULL	312	BP immune response
10	-11.47	NULL	1167	BP signal transduction
11	-11.22	NULL	316	Cancer SPANG_BCL6-index2
12	-10.65	NULL	274	Lymphoma SPANG_IL21 DN
13	-10.21	NULL	269	BP inflammatory response
14	-10.19	NULL	51	BP type I interferon signaling pathway
15	-10	NULL	386	Chr Chr 22
16	-9.97	NULL	242	BP extracellular matrix organization
17	-9.73	NULL	250	Lymphoma IENZ_Stromal signature 1
18	-9.08	NULL	1720	Chr Chr 1
19	-8.9	NULL	530	BP innate immune response
20	-8.87	NULL	204	BP cytokine-mediated signaling pathway

p-values



GW_107

Local Summary

%DE = 0.97
 # metagenes = 24
 # genes = 301
 # genes in genesets = 291

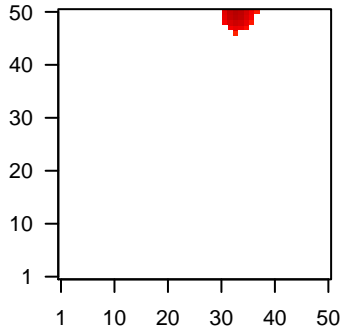
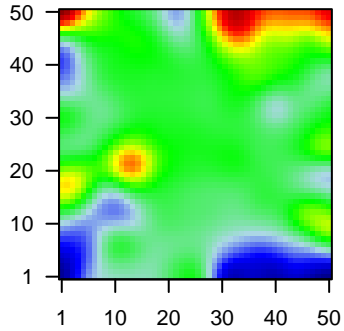
 # genes with $fdr < 0.1 = 282$ (280 + / 2 -)
 # genes with $fdr < 0.05 = 282$ (280 + / 2 -)
 # genes with $fdr < 0.01 = 209$ (209 + / 0 -)

<r> metagenes = 0.94
 <r> genes = 0.26

 <FC> = 0.57
 <shrinkage-t> = 19.87
 <p-value> = 0
 <fdr> = 0.4

Profile

Spot



Local Genelist

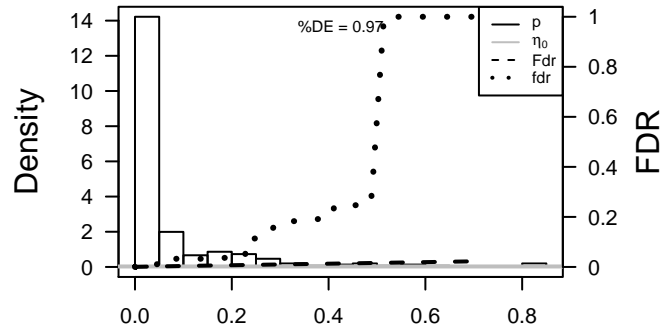
Rank	ID	log(FC)	fdr	p-value	Description
1	401505	1.36	2e-10	9e-08	33 x 50 translocase of outer mitochondrial membrane 5 homolog (yea
2	6154	1.21	2e-08	9e-08	32 x 49 ribosomal protein L26 [Source:HGNC Symbol;Acc:10327]
3	6160	1.2	2e-08	2e-07	32 x 49 ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]
4	4712	1.17	5e-08	4e-07	33 x 49 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17
5	6175	1.14	1e-07	5e-07	31 x 50 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:1037
6	132946	1.12	2e-07	5e-07	36 x 48 ADP-ribosylation factor-like 9 [Source:HGNC Symbol;Acc:25
7	64776	1.11	2e-07	1e-06	32 x 49 chromosome 11 open reading frame 1 [Source:HGNC Symbc
8	83955	1.09	4e-07	1e-06	32 x 49 nascent-polypeptide-associated complex alpha polypeptide I
9	81853	1.07	7e-07	1e-06	32 x 50 transmembrane protein 14B [Source:HGNC Symbol;Acc:2138
10	10455	1.07	7e-07	1e-06	32 x 48 enoyl-CoA delta isomerase 2 [Source:HGNC Symbol;Acc:14
11	9556	1.06	8e-07	1e-06	35 x 50 chromosome 14 open reading frame 2 [Source:HGNC Symbc
12	6392	1.06	9e-07	2e-06	31 x 50 succinate dehydrogenase complex, subunit D, integral membr
13	6165	1.05	1e-06	6e-06	33 x 49 ribosomal protein L35a [Source:HGNC Symbol;Acc:10345]
14	6147	1.03	2e-06	7e-06	33 x 49 ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
15	6164	1	4e-06	7e-06	32 x 50 ribosomal protein L34 [Source:HGNC Symbol;Acc:10340]
16	10799	0.99	4e-06	7e-06	34 x 50 ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;#
17	84233	0.98	5e-06	7e-06	31 x 49 transmembrane protein 126A [Source:HGNC Symbol;Acc:25
18	653702	0.98	6e-06	7e-06	33 x 48
19	6144	0.97	7e-06	7e-06	32 x 48 ribosomal protein L21 [Source:HGNC Symbol;Acc:10313]
20	7341	0.96	8e-06	7e-06	35 x 50 small ubiquitin-like modifier 1 [Source:HGNC Symbol;Acc:12

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	26.05	NULL	42 / 153	MF structural constituent of ribosome
2	24.79	NULL	29 / 83	BP respiratory electron transport chain
3	23.14	NULL	23 / 81	BP viral transcription
4	23.13	NULL	24 / 87	BP translational termination
5	22.66	NULL	24 / 92	BP translational elongation
6	21.56	NULL	15 / 51	CC cytosolic large ribosomal subunit
7	21.55	NULL	23 / 92	BP viral life cycle
8	21.44	NULL	46 / 253	BP translation
9	21.3	NULL	37 / 167	CC ribosome
10	20.31	NULL	24 / 109	BP SRP-dependent cotranslational protein targeting to membrane
11	19.77	NULL	26 / 128	BP translational initiation
12	19.27	NULL	24 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
13	18.13	NULL	44 / 304	CC mitochondrial inner membrane
14	17.8	NULL	30 / 152	BP cellular metabolic process
15	17.62	NULL	13 / 36	CC mitochondrial respiratory chain complex I
16	17.26	NULL	12 / 34	MF NADH dehydrogenase (ubiquinone) activity
17	16.8	NULL	7 / 10	CC large ribosomal subunit
18	16.49	NULL	103 / 1318	CC mitochondrion
19	15.96	NULL	12 / 35	BP mitochondrial electron transport, NADH to ubiquinone
20	15.3	NULL	6 / 11	Cancer GENTLES_modul5
21	14.59	NULL	29 / 242	BP RNA metabolic process
22	14.41	NULL	8 / 19	CC mitochondrial proton-transporting ATP synthase complex
23	14.28	NULL	27 / 219	BP mRNA metabolic process
24	13.82	NULL	4 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
25	12.93	NULL	4 / 9	GSEA C2KEGG_RIBOSOME
26	12.93	NULL	4 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
27	12.93	NULL	4 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
28	12.93	NULL	4 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
29	12.93	NULL	4 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
30	12.93	NULL	4 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
31	12.93	NULL	4 / 9	GSEA C2REACTOME_VIRAL_MRNA_TRANSLATION
32	12.65	NULL	4 / 11	BP ribosomal large subunit biogenesis
33	12.37	NULL	7 / 26	MF cytochrome-c oxidase activity
34	12.35	NULL	29 / 287	BP viral process
35	12.19	NULL	4 / 10	GSEA C2REACTOME_TRANSLATION
36	11.28	NULL	35 / 482	BP cellular protein metabolic process
37	10.47	NULL	44 / 649	BP gene expression
38	10.42	NULL	6 / 15	BP ATP synthesis coupled proton transport
39	9.85	NULL	9 / 23	CC mitochondrial ribosome
40	9.7	NULL	5 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU

p-values



GW_107

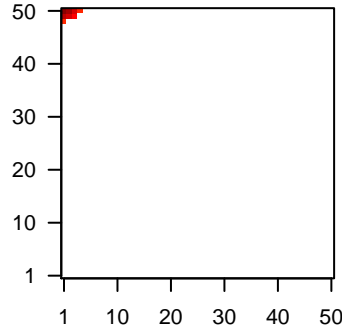
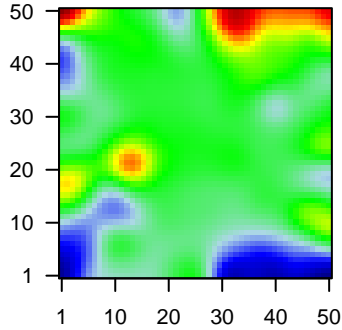
Local Summary

%DE = 0.83
 # metagenes = 8
 # genes = 154
 # genes in genesets = 151
 # genes with $fdr < 0.1 = 103$ (98 + / 5 -)
 # genes with $fdr < 0.05 = 99$ (94 + / 5 -)
 # genes with $fdr < 0.01 = 91$ (88 + / 3 -)

<r> metagenes = 0.99
 <r> genes = 0.5
 <FC> = 0.8
 <shrinkage-t> = 28.24
 <p-value> = 0
 <fdr> = 0.34

Profile

Spot



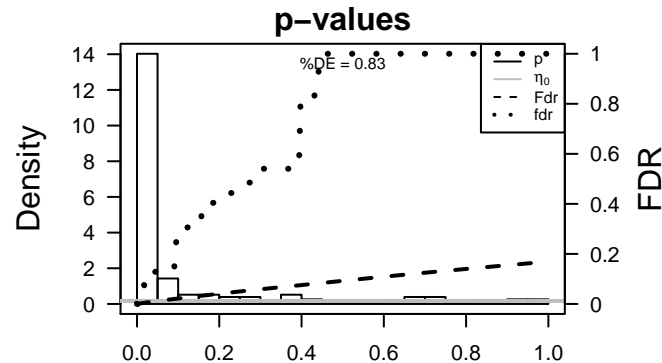
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	2.13	2e-16	3e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	2.15	2e-16	3e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
3	84290	1.81	2e-16	3e-16	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
4	49860	3.03	2e-16	3e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
5	2312	2.18	2e-16	3e-16	1 x 49 filaggrin [Source:HGNC Symbol;Acc:3748]
6	2877	2.27	2e-16	3e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
7	43849	1.83	2e-16	3e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6:
8	3851	2.92	2e-16	3e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
9	196374	2.31	2e-16	3e-16	1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926]
10	643479	1.87	2e-16	3e-16	1 x 49
11	4118	2.54	2e-16	3e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
12	5507	1.83	2e-16	3e-16	3 x 50 protein phosphatase 1, regulatory subunit 3C [Source:HGNC
13	83886	1.76	2e-16	3e-16	1 x 50 protease, serine 27 [Source:HGNC Symbol;Acc:15475]
14	51458	1.84	2e-16	3e-16	1 x 50 Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
15	8796	1.8	2e-16	3e-16	1 x 50 sciellin [Source:HGNC Symbol;Acc:10573]
16	57152	1.85	2e-16	3e-16	1 x 50 secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
17	11005	1.76	2e-16	3e-16	1 x 50 serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
18	84651	3.01	2e-16	3e-16	1 x 50 serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
19	6707	1.67	2e-16	3e-16	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126
20	7053	1.89	2e-16	3e-16	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	40.97	NULL	66 / 135	H.Tiss WIRTH_Mucosa
2	21.99	NULL	17 / 53	BP keratinocyte differentiation
3	19.98	NULL	6 / 13	BP negative regulation of peptidase activity
4	18.76	NULL	13 / 21	CC cornified envelope
5	17.71	NULL	69 / 572	Disease GUDJ_psooriasis up
6	15.47	NULL	6 / 38	BP epithelial cell differentiation
7	15.03	NULL	4 / 15	MF retinol dehydrogenase activity
8	14.93	NULL	7 / 19	BP peptide cross-linking
9	14.33	NULL	15 / 42	BP keratinization
10	12.21	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
11	11.16	NULL	44 / 1182	CC extracellular region
12	10.69	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
13	10.3	NULL	3 / 16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
14	9.94	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
15	9.9	NULL	6 / 82	CC intermediate filament
16	9.67	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
17	9.6	NULL	12 / 186	MF structural molecule activity
18	9.5	NULL	4 / 39	BP retinoid metabolic process
19	9.48	NULL	4 / 44	CC keratin filament
20	9.47	NULL	18 / 76	BP epidermis development
21	9.38	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
22	9.32	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
23	9.23	NULL	3 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
24	9.1	NULL	10 / 122	MF serine-type endopeptidase activity
25	9.02	NULL	8 / 52	BP negative regulation of endopeptidase activity
26	9.02	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
27	8.96	NULL	6 / 16	GSEA C2ROMER_TUMORIGENESIS_DN
28	8.52	NULL	2 / 16	BP negative regulation of proteolysis
29	8.42	NULL	4 / 23	MF peptidase inhibitor activity
30	8.38	NULL	3 / 18	BP retinol metabolic process
31	8.17	NULL	4 / 27	BP response to bacterium
32	8.14	NULL	1 / 10	MF monosaccharide binding
33	8.1	NULL	5 / 29	BP regulation of proteolysis
34	8	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
35	7.79	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
36	7.75	NULL	1 / 11	Glio VERHAAK_Brain
37	7.59	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
38	7.36	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
39	7.35	NULL	1 / 12	MF channel activity
40	7.31	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION



GW_107

Local Summary

%DE = 0.78
 # metagenes = 5
 # genes = 130
 # genes in genesets = 129

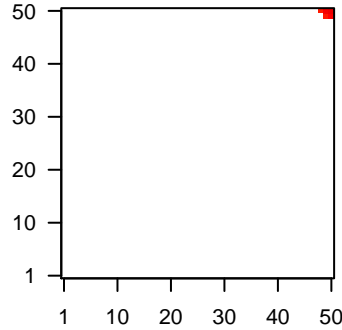
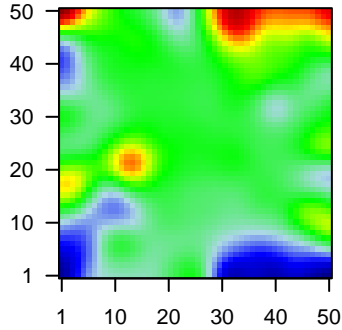
 # genes with $fdr < 0.1$ = 75 (69 + / 6 -)
 # genes with $fdr < 0.05$ = 68 (64 + / 4 -)
 # genes with $fdr < 0.01$ = 60 (58 + / 2 -)

 $\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.31

 $\langle FC \rangle = 0.56$
 $\langle \text{shrinkage-t} \rangle = 19.61$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.44$

Profile

Spot



Local Genelist

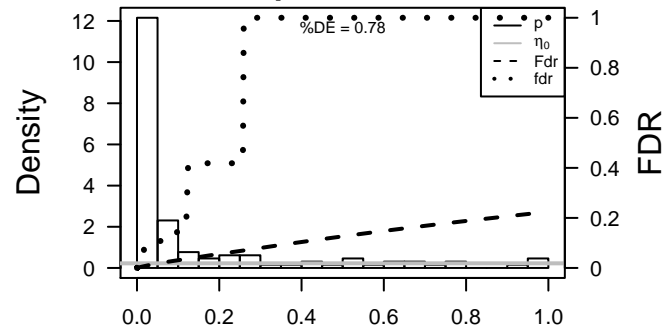
Rank	ID	log(FC)	fdr	p-value	Description
1	216	2.7	2e-16	2e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	83888	2.7	2e-16	2e-15	50 x 50 fibroblast growth factor binding protein 2 [Source:HGNC Sym
3	2938	2.37	2e-16	2e-15	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc
4	4922	2.72	2e-16	2e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
5	26047	1.74	7e-16	2e-13	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
6	139728	1.68	6e-15	4e-13	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l
7	3880	1.65	2e-14	3e-11	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
8	57291	1.53	1e-12	3e-11	50 x 50 differentiation antagonizing non-protein coding RNA [Source:
9	200634	1.51	2e-12	1e-10	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
10	4072	1.48	6e-12	2e-10	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
11	5096	1.46	1e-11	2e-09	49 x 50 propionyl CoA carboxylase, beta polypeptide [Source:HGNC :
12	255758	1.39	9e-11	7e-09	50 x 50 Tctex1 domain containing 2 [Source:HGNC Symbol;Acc:284E
13	26256	1.35	4e-10	7e-09	50 x 50 calcium binding tyrosine-(Y)-phosphorylation regulated [Sou
14	159371	1.33	6e-10	2e-08	49 x 50 solute carrier family 35, member G1 [Source:HGNC Symbol;/
15	1780	1.31	1e-09	6e-08	50 x 50 dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
16	205428	1.27	3e-09	8e-08	50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbc
17	349565	1.24	9e-09	8e-08	50 x 50 nicotinamide nucleotide adenyltransferase 3 [Source:HGNC
18	54575	1.24	9e-09	4e-06	50 x 50 UDP glucuronosyltransferase 1 family, polypeptide A10 [Sour
19	112609	1.12	2e-07	4e-06	50 x 50 melanocortin 2 receptor accessory protein 2 [Source:HGNC S
20	4953	1.08	6e-07	4e-06	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	21.3	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	16.98	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
3	16.98	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
4	16.4	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
5	13.39	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
6	13.32	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
7	13.32	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
8	13.14	NULL	2 / 12	BP cellular aldehyde metabolic process
9	12.93	NULL	3 / 13	BP regulation of blood vessel size
10	12.51	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
11	12.51	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
12	11.96	NULL	1 / 11	Glio neurons_glio
13	11.87	NULL	1 / 11	GSEA C2YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP
14	11.25	NULL	1 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
15	10.44	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
16	10.4	NULL	2 / 18	MF acyl-CoA dehydrogenase activity
17	10.28	NULL	1 / 14	MF Ras GTPase activator activity
18	10.28	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
19	10.28	NULL	1 / 14	GSEA C2MAHADEVAN_IMATINIB_RESISTANCE_UP
20	10.23	NULL	3 / 16	GSEA C2BOYALULT_LIVER_CANCER_SUBCLASS_G1_DN
21	10.04	NULL	4 / 15	GSEA C2REACTOME_GlutATHIONE_CONJUGATION
22	9.99	NULL	1 / 15	MF neuropeptide hormone activity
23	9.88	NULL	1 / 15	GSEA C2DORSAM_HOXA9_TARGETS_UP
24	9.86	NULL	2 / 10	BP biotin metabolic process
25	9.29	NULL	5 / 20	MF glutathione transferase activity
26	9.09	NULL	3 / 15	BP lipid glycosylation
27	8.99	NULL	1 / 18	BP positive regulation of Ras GTPase activity
28	8.89	NULL	1 / 18	BP retinol metabolic process
29	8.61	NULL	8 / 34	BP glutathione metabolic process
30	8.59	NULL	2 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
31	8.37	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
32	8.3	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
33	7.9	NULL	11 / 119	BP xenobiotic metabolic process
34	7.81	NULL	2 / 15	MF glucuronosyltransferase activity
35	7.57	NULL	1 / 11	CC axolemma
36	7.56	NULL	1 / 10	GSEA C2YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
37	7.5	NULL	2 / 16	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
38	7.48	NULL	2 / 16	GSEA C2KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
39	7.33	NULL	5 / 79	BP vitamin metabolic process
40	7.21	NULL	1 / 26	MF growth factor binding

p-values



GW_107

Local Summary

%DE = 0.75
 # metagenes = 17
 # genes = 259
 # genes in genesets = 257

genes with $fdr < 0.1$ = 166 (10 + / 156 -)
 # genes with $fdr < 0.05$ = 147 (8 + / 139 -)
 # genes with $fdr < 0.01$ = 101 (6 + / 95 -)

<r> metagenes = 0.96

<r> genes = 0.36

<FC> = -0.48

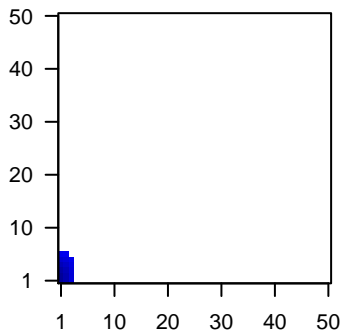
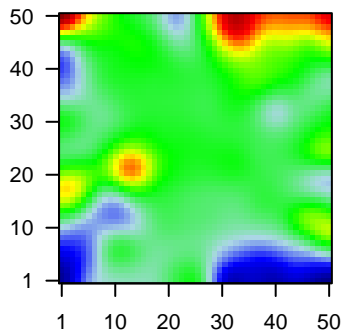
<shrinkage-t> = -16.85

<p-value> = 0

<fdr> = 0.46

Profile

Spot



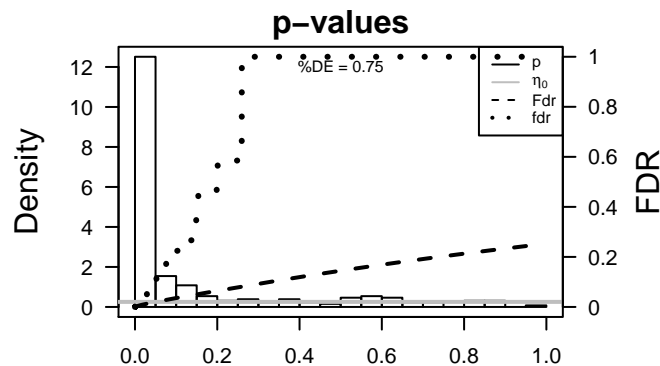
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	7045	-1.64	2e-16	1e-14	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:5318]
2	3371	-1.75	4e-16	5e-11	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
3	12	-1.52	2e-12	5e-11	1 x 1
4	3576	-1.52	2e-12	3e-10	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
5	5054	-1.48	7e-12	8e-09	1 x 2 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
6	54206	-1.37	2e-10	8e-09	1 x 4 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;A
7	7128	-1.36	3e-10	8e-09	1 x 1 tumor necrosis factor, alpha-induced protein 3 [Source:HGNC
8	4627	-1.23	5e-10	8e-09	1 x 6 myosin, heavy chain 9, non-muscle [Source:HGNC Symbol;A
9	1307	-1.33	6e-10	8e-09	1 x 2 collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
10	1294	-1.33	7e-10	8e-09	1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
11	7057	-1.32	8e-10	9e-09	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
12	23213	-1.32	9e-10	2e-08	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
13	83716	-1.31	1e-09	2e-08	2 x 1 cysteine-rich secretory protein LCCL domain containing 2 [S
14	5743	-1.3	1e-09	3e-08	1 x 1 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H s
15	6624	-1.19	2e-09	5e-08	1 x 6 fascin homolog 1, actin-bundling protein (Strongylocentrotus
16	595	-1.2	2e-09	5e-08	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
17	3918	-1.27	3e-09	7e-08	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
18	633	-1.17	4e-09	1e-07	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
19	1051	-1.15	6e-09	1e-07	1 x 4 CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC
20	414062	-1.24	8e-09	1e-07	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-30.95	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
2	-28.69	NULL	57 / 242	BP extracellular matrix organization
3	-26.46	NULL	46 / 190	CC extracellular matrix
4	-25.58	NULL	24 / 64	BP collagen catabolic process
5	-24.71	NULL	25 / 69	BP extracellular matrix disassembly
6	-22.86	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
7	-21.17	NULL	7 / 11	MF platelet-derived growth factor binding
8	-20.93	NULL	14 / 16	MMLL C2SCIEJ_MMLL_1
9	-20.86	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
10	-20.73	NULL	8 / 19	MF extracellular matrix binding
11	-20.16	NULL	58 / 250	LymphomaL1ENZ_Stromal signature 1
12	-20.14	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
13	-19.99	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
14	-18.31	NULL	6 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
15	-17.97	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
16	-17.94	NULL	68 / 683	CC extracellular space
17	-17.88	NULL	6 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
18	-17.87	NULL	3 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
19	-17.65	NULL	51 / 403	BP cell adhesion
20	-17.45	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
21	-17.41	NULL	56 / 553	Cancer Lembecke_Colonic Inflammation
22	-17.25	NULL	6 / 15	GSEA C2ASU_IL6_SIGNALING_SCAR_DN
23	-17.23	NULL	12 / 35	Glio Colman_survival_associated
24	-17.1	NULL	5 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXP01_FUSION_DN
25	-16.81	NULL	3 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
26	-16.77	NULL	92 / 1182	CC extracellular region
27	-16.62	NULL	6 / 16	GSEA C2AMIT_SERUM_RESPONSE_60_MCF10A
28	-16.23	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
29	-16.02	NULL	7 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
30	-15.96	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
31	-15.83	NULL	5 / 16	GSEA C2JRS_ADIPOCYTE_DIFFERENTIATION_DN
32	-15.41	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
33	-15.38	NULL	32 / 183	CC proteinaceous extracellular matrix
34	-15.23	NULL	5 / 14	GSEA C2SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
35	-15.22	NULL	10 / 40	BP cellular response to amino acid stimulus
36	-15.16	NULL	4 / 13	GSEA C2CHIN_BREAST_CANCER_COPY_NUMBER_UP
37	-15.08	NULL	18 / 83	CC basement membrane
38	-15.03	NULL	38 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
39	-15.03	NULL	38 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
40	-15.03	NULL	38 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down



GW_107

Local Summary

%DE = 0.79
 # metagenes = 67
 # genes = 862
 # genes in genesets = 828

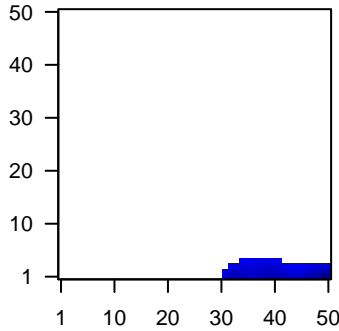
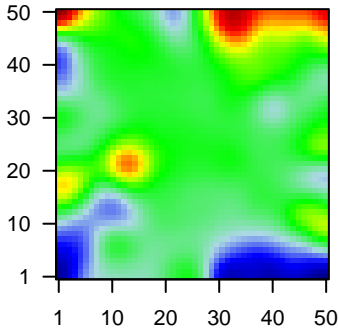
 # genes with $fdr < 0.1$ = 466 (19 + / 447 -)
 # genes with $fdr < 0.05$ = 383 (13 + / 370 -)
 # genes with $fdr < 0.01$ = 257 (10 + / 247 -)

 $\langle r \rangle$ metagenes = 0.76
 $\langle r \rangle$ genes = 0.3

 $\langle FC \rangle = -0.44$
 $\langle \text{shrinkage-t} \rangle = -15.51$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.55$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	6364	-2.01	2e-16	4e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:1037]
2	10964	-1.68	7e-15	1e-11	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Acc:1037]
3	629	-1.62	6e-14	3e-11	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
4	115362	-1.57	3e-13	3e-11	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989]
5	3106	-1.44	4e-13	6e-10	32 x 1 major histocompatibility complex, class I, B [Source:HGNC Symbol;Acc:1037]
6	684	-1.49	4e-12	6e-10	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1037]
7	3936	-1.47	7e-12	7e-10	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:1037]
8	9651	-1.46	1e-11	1e-09	35 x 2 phospholipase C, eta 2 [Source:HGNC Symbol;Acc:29037]
9	10561	-1.45	2e-11	4e-09	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:1616]
10	51296	-1.42	4e-11	1e-07	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3 [Source:HGNC Symbol;Acc:1037]
11	85441	-1.31	1e-09	1e-07	32 x 1 helicase with zinc finger 2, transcriptional coactivator [Source:HGNC Symbol;Acc:1037]
12	972	-1.29	2e-09	1e-07	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:1037]
13	4283	-1.29	2e-09	1e-07	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:1037]
14	5341	-1.27	3e-09	1e-07	50 x 1 plectstrin [Source:HGNC Symbol;Acc:9070]
15	94240	-1.27	4e-09	2e-07	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbol;Acc:1037]
16	3128	-1.26	5e-09	2e-07	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo) [Source:HGNC Symbol;Acc:1037]
17	440353	-1.25	6e-09	2e-07	40 x 1 [Source:HGNC Symbol;Acc:1037]
18	3689	-1.25	7e-09	4e-07	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4) [Source:HGNC Symbol;Acc:1037]
19	5880	-1.24	9e-09	4e-07	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP-binding protein) [Source:HGNC Symbol;Acc:1037]
20	3659	-1.23	1e-08	6e-07	32 x 1 interferon regulatory factor 1 [Source:HGNC Symbol;Acc:6116]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-22.92	NULL	35 / 51	BP type I interferon signaling pathway
2	-21.94	NULL	130 / 417	H.Tiss WIRTH_Immune system
3	-20.53	NULL	13 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
4	-20.12	NULL	96 / 312	BP immune response
5	-19.3	NULL	14 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
6	-19.11	NULL	45 / 123	BP defense response to virus
7	-19.02	NULL	10 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
8	-18.62	NULL	14 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
9	-18.14	NULL	14 / 15	CC MHC class II protein complex
10	-16.86	NULL	14 / 16	GSEA C2JROSEVIC_RESPONSE_TO_JMIQUIMOD
11	-16.65	NULL	120 / 553	Cancer Lembcke_Coloniac Inflammation
12	-16.28	NULL	58 / 204	BP cytokine-mediated signaling pathway
13	-16.27	NULL	14 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
14	-15.92	NULL	26 / 47	BP antigen processing and presentation
15	-15.58	NULL	11 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
16	-15.28	NULL	30 / 60	BP interferon-gamma-mediated signaling pathway
17	-15.16	NULL	18 / 31	BP negative regulation of viral genome replication
18	-15.03	NULL	34 / 109	BP response to virus
19	-14.97	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
20	-13.87	NULL	15 / 23	CC integral to lumenal side of endoplasmic reticulum membrane
21	-13.71	NULL	60 / 274	Lymphoma SPANG_IL21 DN
22	-13.27	NULL	9 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
23	-12.99	NULL	31 / 74	BP regulation of immune response
24	-12.83	NULL	5 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
25	-12.82	NULL	61 / 316	Cancer SPANG_BCL6-index2
26	-12.52	NULL	9 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
27	-12.1	NULL	74 / 572	Disease GUDJ_pсориазis up
28	-11.89	NULL	11 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
29	-11.8	NULL	6 / 6	Lymphoma BAVE_MHCII BL DN
30	-11.73	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
31	-11.34	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
32	-11.33	NULL	15 / 32	CC ER to Golgi transport vesicle membrane
33	-11.14	NULL	5 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION
34	-10.97	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
35	-10.96	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
36	-10.92	NULL	9 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
37	-10.77	NULL	18 / 52	Chr Chr HSCHR6_MHC_QBL
38	-10.77	NULL	5 / 12	GSEA C2ZHU_CMV_8_HR_UP
39	-10.42	NULL	10 / 22	Lymphoma BAVE_NFkB BL DN
40	-10.42	NULL	73 / 530	BP innate immune response

p-values

