GW_118

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1963 (1064 + / 899 −)

genes with fdr < 0.1 = 1658 (887 + / 771 −)

genes with fdr < 0.05 = 1271 (673 + / 598 −)

genes with fdr < 0.01 = 829 (436 + / 393 −)

genes in genesets = 16332

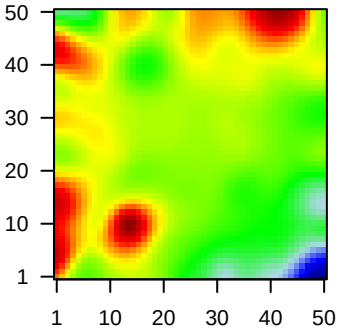
<FC> = 0

<shrinkage−t> = 0

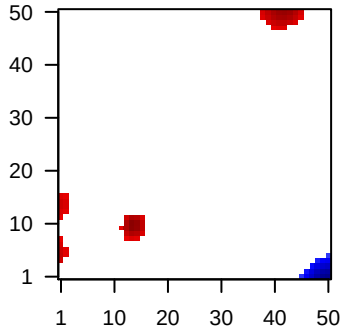
<p−value> = 0.1

<fdr> = 0.85

Profile



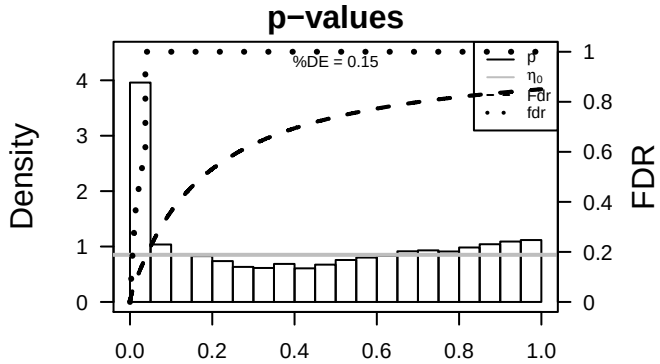
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.92	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
2	222	1.93	2e−16	5e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	55107	1.82	2e−16	5e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
4	10409	1.63	2e−16	5e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
5	92747	2.45	2e−16	5e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
6	375791	−1.61	2e−16	5e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symt
7	768	2.36	2e−16	5e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
8	919	−1.5	2e−16	5e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
9	22802	−1.85	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	49860	−1.91	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	131566	1.67	2e−16	5e−14	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
12	1717	1.68	2e−16	5e−14	13 x 50	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
13	10202	2.48	2e−16	5e−14	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
14	2167	2.66	2e−16	5e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
15	2201	1.54	2e−16	5e−14	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
16	2354	−1.74	2e−16	5e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
17	729428	3.05	2e−16	5e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
18	729422	3.05	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	100132399	1.54	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
20	100008586	3.04	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.34	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	11.34	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	9.94	NULL	957	Chr	Chr 11
4	8.66	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	8.25	NULL	370	BP	mitotic cell cycle
6	7.43	NULL	519	Chr	Chr 14
7	7.17	NULL	39	BP	glycolysis
8	6.89	NULL	12	BP	hemidesmosome assembly
9	6.61	NULL	20	TF	MYC_Metabolism UP
10	6.55	NULL	63	TF	MYC_Targets UP
11	5.97	NULL	13	GSEA C2	REACTOME_GLYCOLYSIS
12	5.8	NULL	1233	TF	KIM_MYC targets
13	5.8	NULL	34	Chr	Chr Y
14	5.78	NULL	232	BP	mitosis
15	5.74	NULL	15	GSEA C2	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
16	5.73	NULL	16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	5.71	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
18	5.68	NULL	35	Glio	Colman_survival_associated
19	5.67	NULL	16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
20	5.59	NULL	150	BP	protein folding
Underexpressed					
1	−12.9	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−12.77	NULL	312	BP	immune response
3	−12.54	NULL	417	H.Tiss	WIRTH_Immune system
4	−10.17	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	−9.7	NULL	274	Lymphoma	SPANG_IL21 DN
6	−9.41	NULL	15	CC	MHC class II protein complex
7	−9.14	NULL	633	Chr	Chr 9
8	−8.9	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
9	−8.69	NULL	51	BP	type I interferon signaling pathway
10	−8.45	NULL	316	Cancer	SPANG_BCL6−index2
11	−8.19	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−7.88	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	−7.88	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	−7.88	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	−7.88	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	−7.85	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
17	−7.31	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
18	−7.28	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
19	−7.17	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
20	−6.95	NULL	530	BP	innate immune response

GW_118

Local Summary

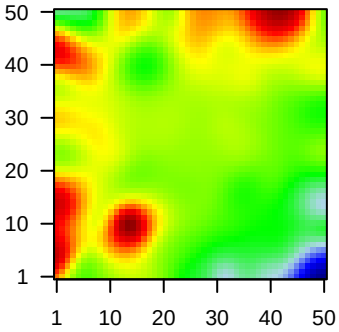
%DE = 0.71
metagenes = 7
genes = 172
genes in genesets = 170

genes with fdr < 0.1 = 94 (93 + / 1 −)
genes with fdr < 0.05 = 87 (86 + / 1 −)
genes with fdr < 0.01 = 73 (72 + / 1 −)

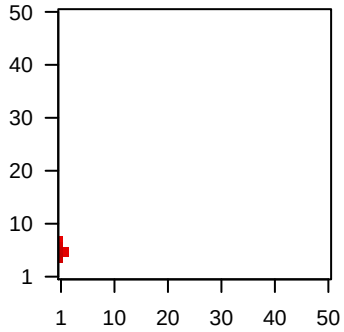
<r> metagenes = 0.98
<r> genes = 0.33

<FC> = 0.48
<shrinkage−t> = 16.89
<p−value> = 0
<fdr> = 0.47

Profile



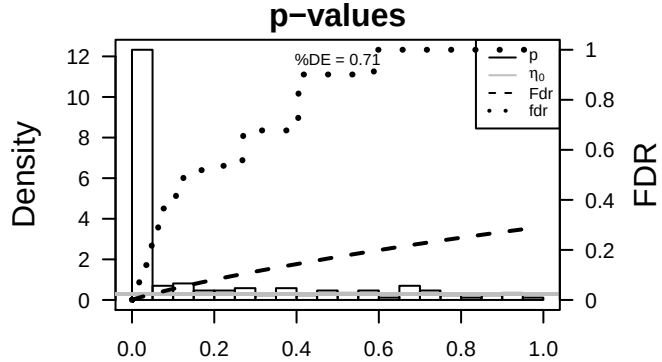
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	1.82	2e−16	3e−15	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	768	2.36	2e−16	3e−15	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	131566	1.67	2e−16	3e−15	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
4	2201	1.54	2e−16	3e−15	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
5	3909	1.46	1e−15	4e−13	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
6	6591	1.41	1e−14	6e−13	1 x 4	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
7	5210	1.39	2e−14	3e−12	1 x 5	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 4 [S
8	79783	1.36	9e−14	3e−12	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
9	10272	1.34	2e−13	3e−12	1 x 4	follistatin−like 3 (secreted glycoprotein) [Source:HGNC Symb
10	595	1.25	2e−13	3e−12	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
11	196527	1.34	2e−13	8e−10	1 x 5	anoctamin 6 [Source:HGNC Symbol;Acc:25240]
12	3667	1.22	2e−11	8e−10	1 x 5	insulin receptor substrate 1 [Source:HGNC Symbol;Acc:6125
13	6624	1.11	3e−11	8e−09	1 x 6	fascin homolog 1, actin−bundling protein (Strongylocentrotus
14	51330	1.16	2e−10	8e−09	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
15	84058	1.14	4e−10	9e−09	1 x 7	WD repeat domain 54 [Source:HGNC Symbol;Acc:25770]
16	4651	1.13	5e−10	7e−08	1 x 6	myosin X [Source:HGNC Symbol;Acc:7593]
17	56034	1.1	2e−09	8e−08	1 x 4	platelet derived growth factor C [Source:HGNC Symbol;Acc:8
18	11014	1.07	4e−09	8e−08	1 x 6	KDEL (Lys−Asp−Glu−Leu) endoplasmic reticulum protein rete
19	8727	1.07	5e−09	2e−07	1 x 5	catenin (cadherin−associated protein), alpha−like 1 [Source:H
20	25914	1.05	9e−09	1e−06	1 x 8	rotatin [Source:HGNC Symbol;Acc:18654]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.11	NULL	2 / 4	miRNA target	hsa−195
2	17.79	NULL	3 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
3	17.71	NULL	1 / 2	miRNA target	hsa−16−1
4	16.93	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNwt_expression_N_down
5	16.93	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNmut_expression_N_up
6	15.85	NULL	4 / 12	BP	hemidesmosome assembly
7	14.86	NULL	4 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
8	14.28	NULL	3 / 15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
9	14.2	NULL	2 / 6	miRNA target	hsa−7b
10	13.75	NULL	3 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
11	13.58	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
12	12.64	NULL	3 / 11	MF	actin−dependent ATPase activity
13	12.61	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
14	12.43	NULL	2 / 10	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_DN
15	12.36	NULL	2 / 5	miRNA 3UTR	hsa−213
16	12.33	NULL	3 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
17	12.15	NULL	5 / 16	MF	fibronectin binding
18	11.69	NULL	7 / 27	CC	integrin complex
19	11.34	NULL	1 / 4	miRNA target	hsa−20a
20	11.22	NULL	4 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
21	10.89	NULL	28 / 403	BP	cell adhesion
22	10.66	NULL	3 / 15	BP	negative regulation of anoikis
23	10.34	NULL	1 / 2	miRNA target	hsa−124a
24	10.34	NULL	4 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
25	10.33	NULL	3 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_32HR_DN
26	10.33	NULL	3 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_48HR_DN
27	10.17	NULL	4 / 16	GSEA C2	SWEET_KRAS_TARGETS_UP
28	10.15	NULL	2 / 14	BP	positive regulation of cell−cell adhesion
29	9.98	NULL	4 / 16	GSEA C2	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
30	9.97	NULL	2 / 11	miRNA target	hsa−16
31	9.9	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
32	9.9	NULL	1 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
33	9.9	NULL	1 / 5	miRNA target	hsa−15a
34	9.87	NULL	2 / 16	Glio	VERHAAK_MES subtype
35	9.49	NULL	2 / 12	MF	activin binding
36	9.44	NULL	2 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
37	9.39	NULL	4 / 12	BP	heparan sulfate proteoglycan biosynthetic process
38	9.37	NULL	1 / 6	GSEA C2	TSAI_DNAJB4_TARGETS_DN
39	9.26	NULL	1 / 2	TF	MYC_ECM cell adhesion DOWN
40	9.2	NULL	2 / 17	BP	morphogenesis of an epithelium

GW_118

Local Summary

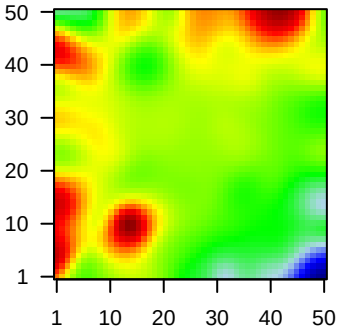
%DE = 0.96
metagenes = 20
genes = 98
genes in genesets = 74

genes with fdr < 0.1 = 83 (75 + / 8 −)
genes with fdr < 0.05 = 65 (65 + / 0 −)
genes with fdr < 0.01 = 58 (58 + / 0 −)

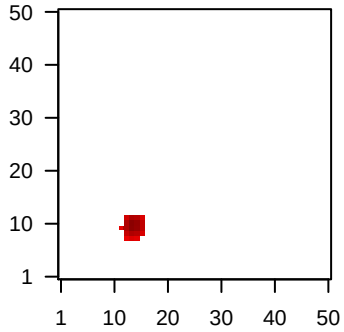
<r> metagenes = 0.97
<r> genes = 0.29

<FC> = 0.87
<shrinkage−t> = 30.61
<p−value> = 0
<fdr> = 0.39

Profile



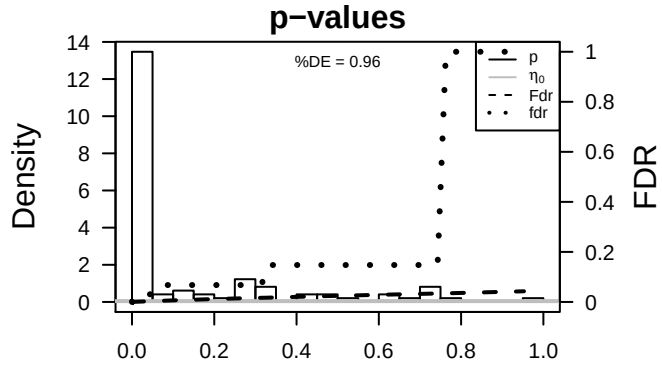
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	3.05	2e−16	5e−17	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	3.05	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100132399	1.54	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	3.04	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	3.11	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.06	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	2.77	2e−16	5e−17	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	2.62	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.57	2e−16	5e−17	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	3.45	2e−16	5e−17	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.53	2e−16	5e−17	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	3.28	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	3.04	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2578	1.64	2e−16	5e−17	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	1.51	2e−16	5e−17	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	100101629	2.12	2e−16	5e−17	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	121355	2.38	2e−16	5e−17	14 x 11	gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265(
18	4100	2.2	2e−16	5e−17	14 x 11	melanoma antigen family A, 1 (directs expression of antigen M
19	4109	2.35	2e−16	5e−17	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
20	64591	1.98	2e−16	5e−17	15 x 11	testis specific protein, Y−linked 2 [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	14.73	NULL	31 / 630	Chr	Chr X
2	11.88	NULL	1 / 11	GSEA C2	SU_PLACENTA
3	10.62	NULL	1 / 10	GSEA C2	CONRAD_GERMLINE_STEM_CELL
4	10.22	NULL	1 / 14	GSEA C2	NIELSEN_GIST
5	10.22	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
6	9.8	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
7	9.66	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
8	9.46	NULL	1 / 12	GSEA C2	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
9	9.25	NULL	1 / 2	miRNA target	mir−107
10	9.16	NULL	3 / 23	BP	calcium−dependent cell−cell adhesion
11	8.84	NULL	2 / 34	Chr	Chr Y
12	8.12	NULL	9 / 120	H.Tiss	WIRTH_Testis
13	7.94	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
14	7.78	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
15	7.56	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
16	7.47	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
17	7.03	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
18	6.91	NULL	3 / 37	BP	synapse assembly
19	6.67	NULL	1 / 11	Glio	willscher_GBM_Verhaak−CL_expression_M_down
20	6.67	NULL	1 / 11	Glio	willscher_GBM_Verhaak−MES_expression_M_down
21	6.67	NULL	1 / 11	Glio	willscher_GBM_Verhaak−PNmut_expression_M_up
22	6.26	NULL	1 / 10	GSEA C2	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1
23	6.26	NULL	1 / 10	GSEA C2	CONRAD_STEM_CELL
24	5.89	NULL	1 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
25	5.67	NULL	2 / 22	BP	male meiosis
26	5.26	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_UP
27	5.19	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
28	5.13	NULL	1 / 10	GSEA C2	WEBER_METHYLATED_HCP_IN_SPERM_DN
29	5.09	NULL	2 / 86	BP	nucleosome assembly
30	4.83	NULL	1 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
31	4.83	NULL	1 / 15	miRNA 3UTR	GTTRT−379
32	4.82	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
33	4.82	NULL	1 / 11	GSEA C2	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN
34	4.66	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
35	4.35	NULL	1 / 12	GSEA C2	KEGG_LYSINE_DEGRADATION
36	4.32	NULL	1 / 13	GSEA C2	SU_TESTIS
37	4.09	NULL	9 / 481	BP	biological_process
38	4.08	NULL	3 / 99	BP	homophilic cell adhesion
39	4.05	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
40	4.02	NULL	1 / 5	miRNA target	mir−181a

GW_118

Local Summary

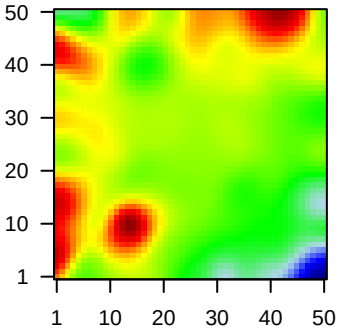
%DE = 0.63
metagenes = 9
genes = 136
genes in genesets = 136

genes with fdr < 0.1 = 60 (60 + / 0 −)
genes with fdr < 0.05 = 60 (60 + / 0 −)
genes with fdr < 0.01 = 39 (39 + / 0 −)

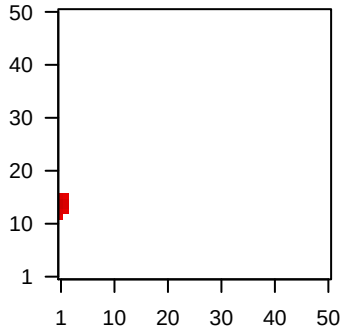
<r> metagenes = 0.97
<r> genes = 0.29

<FC> = 0.42
<shrinkage−t> = 14.62
<p−value> = 0
<fdr> = 0.57

Profile



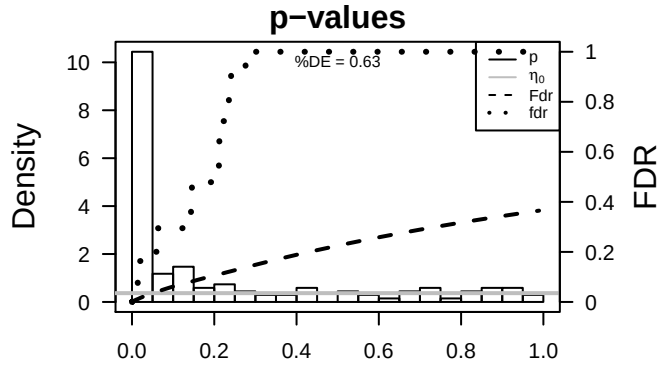
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10202	2.48	2e−16	6e−15	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
2	51083	2.11	2e−16	6e−15	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
3	8772	1.47	7e−16	5e−13	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
4	131076	1.41	1e−14	2e−09	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
5	81037	1.21	3e−11	2e−07	1 x 14	CLPTM1−like [Source:HGNC Symbol;Acc:24308]
6	64979	1.07	5e−09	4e−07	1 x 16	mitochondrial ribosomal protein L36 [Source:HGNC Symbol;A
7	51373	1.04	1e−08	4e−07	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
8	5214	1.02	2e−08	1e−06	1 x 13	phosphofructokinase, platelet [Source:HGNC Symbol;Acc:88
9	10963	1	4e−08	2e−06	1 x 16	stress−induced−phosphoprotein 1 [Source:HGNC Symbol;Ac
10	219927	0.98	8e−08	3e−06	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;A
11	79080	0.96	2e−07	3e−06	1 x 14	coiled−coil domain containing 86 [Source:HGNC Symbol;Acc
12	27294	0.94	2e−07	3e−06	1 x 16	dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;
13	991	0.94	2e−07	4e−06	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
14	220064	0.93	3e−07	6e−05	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
15	116447	0.88	1e−06	6e−05	1 x 15	topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbo
16	25902	0.86	3e−06	1e−04	1 x 13	methylenetetrahydrofolate dehydrogenase (NADP+ dependen
17	7965	0.84	5e−06	2e−04	1 x 15	aminoacyl tRNA synthetase complex−interacting multifunctior
18	3217	0.81	8e−06	3e−04	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
19	6389	0.79	1e−05	3e−04	1 x 12	succinate dehydrogenase complex, subunit A, flavoprotein (F
20	10598	0.78	2e−05	9e−04	1 x 14	AHA1, activator of heat shock 90kDa protein ATPase homolo

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	20.22	NULL	2 / 10	GSEA C2ZHU_CMV_24_HR_UP
2	20.22	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP
3	18.34	NULL	1 / 6	GSEA C2REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
4	18.34	NULL	1 / 6	GSEA C2REACTOME_GPCR_LIGAND_BINDING
5	16.77	NULL	1 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
6	16.77	NULL	1 / 7	GSEA C2REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
7	16.75	NULL	2 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
8	15.52	NULL	1 / 8	GSEA C2SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
9	15.52	NULL	1 / 8	GSEA C2REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
10	13.66	NULL	1 / 10	GSEA C2WELCSH_BRCA1_TARGETS_1_DN
11	13.66	NULL	1 / 10	GSEA C2TAKAO_RESPONSE_TO_UVB_RADIATION_UP
12	13.32	NULL	2 / 13	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_C
13	12.93	NULL	1 / 11	GSEA C2SCIBETTA_KDM5B_TARGETS_DN
14	12.93	NULL	1 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
15	12.93	NULL	1 / 11	GSEA C2PARK_APL_PATHOGENESIS_DN
16	12.9	NULL	2 / 18	BP smooth muscle contraction
17	12.76	NULL	1 / 15	BP myeloid dendritic cell differentiation
18	12.76	NULL	1 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_7
19	12.7	NULL	1 / 6	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_DN
20	12.31	NULL	1 / 12	GSEA C2BHATTACHARYA_EMBRYONIC_STEM_CELL
21	12.3	NULL	1 / 16	GSEA C2TING_SILENCED_BY_DICER
22	12.21	NULL	2 / 13	GSEA C2NADERI_BREAST_CANCER_PROGNOSIS_UP
23	11.76	NULL	1 / 13	GSEA C2KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
24	11.28	NULL	1 / 14	GSEA C2FARMER_BREAST_CANCER_BASAL_VS_LULMINAL
25	11.28	NULL	1 / 14	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP
26	11.28	NULL	1 / 14	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_DN
27	10.84	NULL	1 / 15	MF neuropeptide hormone activity
28	10.84	NULL	1 / 15	GSEA C2NAGASHIMA_NRG1_SIGNALING_UP
29	10.84	NULL	1 / 15	GSEA C2FERNANDEZ_BOUND_BY_MYC
30	10.45	NULL	1 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
31	10.45	NULL	1 / 16	GSEA C2TAVOR_CEBPA_TARGETS_DN
32	10.45	NULL	1 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
33	10.45	NULL	1 / 16	GSEA C2BROWNE_HCMV_INFECTION_24HR_UP
34	10.1	NULL	1 / 17	Disease BCHETNIA_EBM up
35	10.02	NULL	1 / 9	GSEA C2BIOCARTA_RELA_PATHWAY
36	10.02	NULL	1 / 9	GSEA C2BIOCARTA_NFKB_PATHWAY
37	10.02	NULL	1 / 9	GSEA C2BIOCARTA_SODD_PATHWAY
38	10.02	NULL	1 / 9	GSEA C2REACTOME_DEATH_RECEPTOR_SIGNALLING
39	9.65	NULL	3 / 14	BP regulation of protein catabolic process
40	9.56	NULL	1 / 25	BP cellular response to oxidative stress

GW_118

Local Summary

%DE = 0.77
metagenes = 25
genes = 381
genes in genesets = 378

genes with fdr < 0.1 = 235 (235 + / 0 −)
genes with fdr < 0.05 = 180 (180 + / 0 −)
genes with fdr < 0.01 = 127 (127 + / 0 −)

<r> metagenes = 0.95
<r> genes = 0.35

<FC> = 0.43
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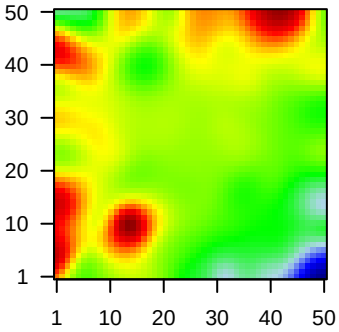
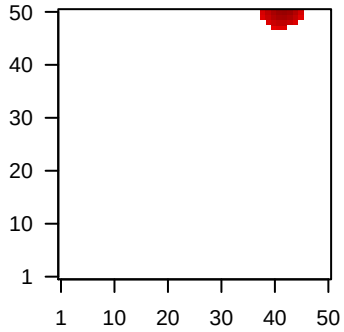
<p−value> = 0.01
<fdr> = 0.53

Profile



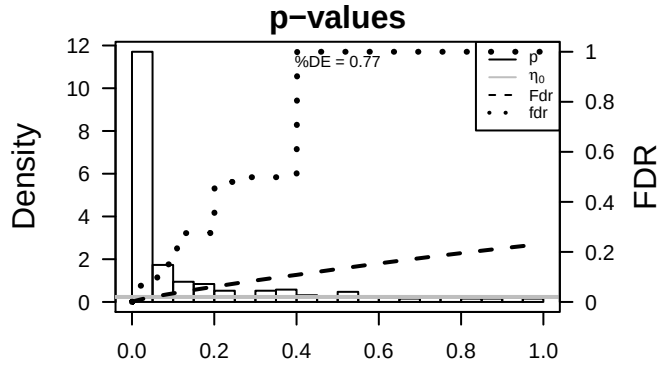
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8500	1.65	2e−16	7e−15	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
2	23480	1.66	2e−16	7e−15	39 x 50	Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
3	9319	1.58	2e−16	7e−15	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbc
4	55915	1.39	3e−14	3e−10	38 x 50	LanC lantibiotic synthetase component C−like 2 (bacterial) [S
5	6611	1.27	3e−12	6e−10	42 x 50	spermine synthase [Source:HGNC Symbol;Acc:11123]
6	79657	1.24	1e−11	2e−08	41 x 49	RNA polymerase II associated protein 3 [Source:HGNC Syml
7	220042	1.13	6e−10	2e−08	42 x 50	chromosome 11 open reading frame 82 [Source:HGNC Symt
8	113130	1.13	6e−10	2e−08	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
9	7153	1.12	8e−10	8e−08	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
10	136	1.1	2e−09	2e−07	41 x 50	adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
11	3992	1.07	4e−09	4e−07	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
12	134147	1.05	9e−09	2e−06	40 x 48	carboxymethylenebutenolidase homolog (Pseudomonas) [So
13	29028	1.01	3e−08	2e−06	44 x 50	ATPase family, AAA domain containing 2 [Source:HGNC Sym
14	51504	0.99	5e−08	9e−06	38 x 50	tRNA methyltransferase 11−2 homolog (S. cerevisiae) [Sourc
15	10606	0.96	2e−07	9e−06	43 x 50	phosphoribosylaminoimidazole carboxylase, phosphoribosyla
16	3945	0.93	3e−07	9e−06	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
17	55353	0.92	4e−07	9e−06	42 x 50	lysosomal protein transmembrane 4 beta [Source:HGNC Sym
18	137392	0.92	5e−07	9e−06	40 x 50	family with sequence similarity 92, member A1 [Source:HGN(
19	10576	0.91	6e−07	9e−06	41 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
20	4173	0.91	6e−07	2e−05	44 x 50	minichromosome maintenance complex component 4 [Source

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.2	NULL	67 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	33.2	NULL	67 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	20.81	NULL	11 / 14	MMML C6	MACIEJ_MMML 4
4	19.43	NULL	10 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
5	18.27	NULL	72 / 370	BP	mitotic cell cycle
6	17.14	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	16.77	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
8	16.22	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
9	16.01	NULL	72 / 530	Cancer	Lembcke_Normal vs Adenoma
10	15.57	NULL	19 / 57	Glio	developing astrocytes
11	15.47	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
12	14.79	NULL	11 / 18	BP	spindle organization
13	14.45	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
14	14.07	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
15	13.75	NULL	41 / 232	BP	mitosis
16	13.41	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
17	13.15	NULL	8 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
18	12.92	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
19	12.87	NULL	9 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	12.79	NULL	5 / 15	GSEA C2	FERRANDO_HOX11_NEIGHBORS
21	12.73	NULL	5 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY
22	12.65	NULL	18 / 56	CC	chromosome, centromeric region
23	12.46	NULL	6 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
24	12.18	NULL	8 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
25	11.92	NULL	62 / 572	Disease	GUDJ_psoriasis up
26	11.89	NULL	27 / 148	BP	G1/S transition of mitotic cell cycle
27	11.7	NULL	8 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
28	11.66	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
29	11.52	NULL	6 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
30	11.35	NULL	9 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
31	11.3	NULL	4 / 11	GSEA C2	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_
32	11.1	NULL	6 / 16	Cancer	WOLFER_overlap genes
33	11.1	NULL	3 / 4	MMML C6	MACIEJ_MMML 41
34	11.08	NULL	4 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
35	10.9	NULL	5 / 14	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
36	10.9	NULL	7 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
37	10.84	NULL	8 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
38	10.77	NULL	6 / 15	GSEA C2	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
39	10.77	NULL	3 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
40	10.48	NULL	6 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP

GW_118

Local Summary

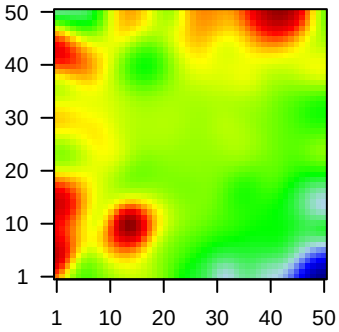
%DE = 0.92
metagenes = 19
genes = 308
genes in genesets = 305

genes with fdr < 0.1 = 257 (6 + / 251 −)
genes with fdr < 0.05 = 257 (6 + / 251 −)
genes with fdr < 0.01 = 221 (5 + / 216 −)

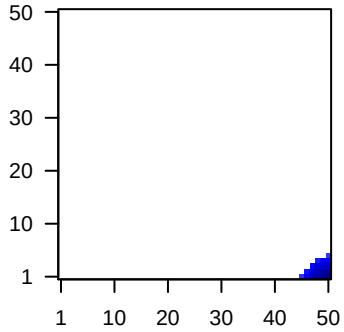
<r> metagenes = 0.98
<r> genes = 0.55

<FC> = −0.63
<shrinkage−t> = −22.06
<p−value> = 0
<fdr> = 0.24

Profile



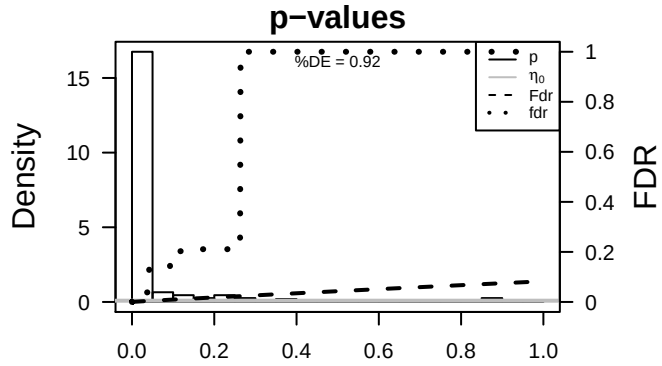
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	919	−1.5	2e−16	1e−15	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
2	3113	−1.51	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
3	3122	−1.49	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
4	3543	−1.62	2e−16	1e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
5	9806	−1.54	2e−16	1e−15	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
6	3128	−1.49	4e−16	1e−14	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
7	3108	−1.46	1e−15	1e−14	50 x 1	major histocompatibility complex, class II, DM alpha [Source:H
8	54855	−1.45	2e−15	1e−14	49 x 1	family with sequence similarity 46, member C [Source:HGNC
9	3109	−1.45	2e−15	2e−14	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
10	57172	−1.44	4e−15	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
11	2634	−1.43	4e−15	1e−13	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HGI
12	10628	−1.39	8e−15	2e−13	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
13	241	−1.39	2e−14	2e−13	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
14	3669	−1.39	2e−14	3e−13	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGNC
15	10365	−1.38	3e−14	9e−12	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
16	3059	1.31	7e−13	9e−12	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
17	7454	−1.31	7e−13	5e−11	50 x 1	Wiskott−Aldrich syndrome [Source:HGNC Symbol;Acc:12731
18	3120	−1.26	4e−12	5e−11	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
19	972	−1.26	4e−12	5e−11	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
20	4067	−1.25	6e−12	1e−10	46 x 2	v−yes−1 Yamaguchi sarcoma viral related oncogene homolog

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.96	NULL	13 / 15	CC	MHC class II protein complex
2	−26.82	NULL	93 / 417	H.Tiss	WIRTH_Immune system
3	−22.43	NULL	55 / 312	BP	immune response
4	−21.94	NULL	97 / 553	Cancer	Lembcke_Colonic Inflammation
5	−20.5	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
6	−20.32	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
7	−18.74	NULL	18 / 60	BP	T cell costimulation
8	−18.73	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
9	−18.69	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
10	−17.87	NULL	16 / 47	BP	antigen processing and presentation
11	−17.46	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
12	−17.25	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	−17.25	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	−17.25	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	−17.25	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	−16.63	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
17	−15.75	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
18	−15.27	NULL	18 / 84	BP	T cell receptor signaling pathway
19	−15.15	NULL	18 / 74	BP	regulation of immune response
20	−14.97	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
21	−14.96	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
22	−14.76	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
23	−14.67	NULL	7 / 13	Cancer	GENTLES_modul18
24	−14.49	NULL	5 / 12	BP	immunoglobulin mediated immune response
25	−14.33	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
26	−14.02	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
27	−14	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
28	−13.51	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
29	−13.39	NULL	8 / 28	CC	transport vesicle membrane
30	−13.36	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
31	−13.3	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
32	−13.24	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
33	−13.09	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
34	−12.83	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
35	−12.68	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
36	−12.58	NULL	10 / 35	CC	trans−Golgi network membrane
37	−12.48	NULL	25 / 162	CC	external side of plasma membrane
38	−12.43	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
39	−12.4	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
40	−12.37	NULL	4 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY