GW_223

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1842 (946 + / 896 −)

genes with fdr < 0.1 = 1411 (707 + / 704 −)

genes with fdr < 0.05 = 1217 (608 + / 609 −)

genes with fdr < 0.01 = 790 (397 + / 393 −)

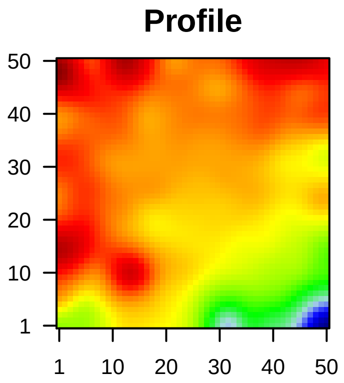
genes in genesets = 16332

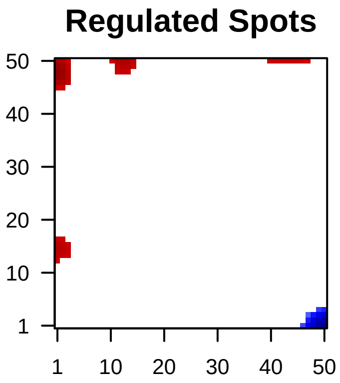
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

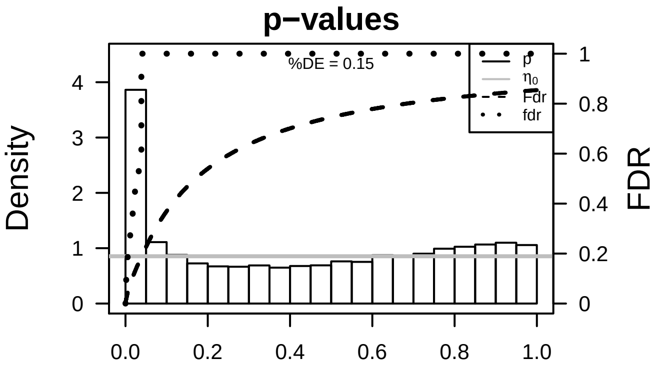
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	1.76	2e−16	4e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
2	57016	−1.65	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
3	222	2.25	2e−16	4e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
4	151516	2.7	2e−16	4e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;
5	23120	1.77	2e−16	4e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
6	479	1.71	2e−16	4e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
7	84707	2.04	2e−16	4e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
8	684	−2.06	2e−16	4e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
9	713	−1.62	2e−16	4e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
10	260436	−1.66	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	29113	3.29	2e−16	4e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
12	771	−1.69	2e−16	4e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
13	972	−1.91	2e−16	4e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
14	1041	2.61	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
15	1152	1.62	2e−16	4e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
16	22802	−3	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	49860	−3.06	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	3627	−2.3	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
19	9547	−1.98	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
20	4283	−1.74	2e−16	4e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.13	NULL	21	CC	cornified envelope
2	13.96	NULL	42	BP	keratinization
3	12.48	NULL	53	BP	keratinocyte differentiation
4	8.91	NULL	135	H.Tiss	WIRTH_Mucosa
5	8.41	NULL	19	BP	peptide cross−linking
6	7.64	NULL	21	CC	desmosome
7	6.24	NULL	714	Chr	Chr 6
8	5.97	NULL	76	BP	epidermis development
9	5.71	NULL	21	CC	gap junction
10	5.53	NULL	370	BP	mitotic cell cycle
11	5.52	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
12	5.52	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
13	5.43	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
14	5.38	NULL	1720	Chr	Chr 1
15	4.89	NULL	23	Chr	Chr HSCHR6_MHC_DBB
16	4.88	NULL	186	MF	structural molecule activity
17	4.82	NULL	717	Chr	Chr 16
18	4.8	NULL	44	BP	skin development
19	4.77	NULL	4640	CC	nucleus
20	4.62	NULL	10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
Underexpressed					
1	−18.41	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−17.56	NULL	312	BP	immune response
3	−15.01	NULL	417	H.Tiss	WIRTH_Immune system
4	−13.78	NULL	51	BP	type I interferon signaling pathway
5	−12.49	NULL	15	CC	MHC class II protein complex
6	−12.38	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
7	−11.56	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
8	−11.46	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	−11.46	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	−11.46	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	−11.46	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	−11.15	NULL	60	BP	interferon−gamma−mediated signaling pathway
13	−11	NULL	47	BP	antigen processing and presentation
14	−10.64	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
15	−10.47	NULL	204	BP	cytokine−mediated signaling pathway
16	−10.36	NULL	316	Cancer	SPANG_BCL6−index2
17	−10.23	NULL	123	BP	defense response to virus
18	−10.05	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
19	−10	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
20	−9.8	NULL	162	CC	external side of plasma membrane

GW_223

Local Summary

%DE = 0.68

metagenes = 12

genes = 154

genes in genesets = 154

genes with fdr < 0.1 = 78 (74 + / 4 −)

genes with fdr < 0.05 = 60 (57 + / 3 −)

genes with fdr < 0.01 = 39 (38 + / 1 −)

<r> metagenes = 0.98

<r> genes = 0.3

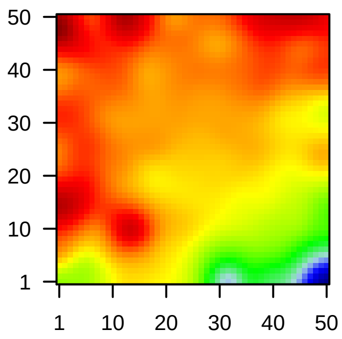
<FC> = 0.38

<shrinkage−t> = 13.34

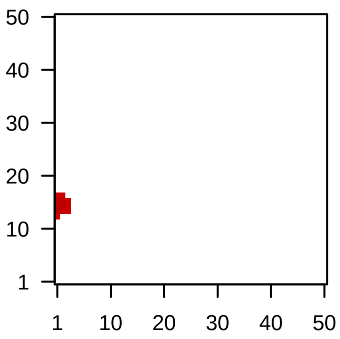
<p−value> = 0.01

<fdr> = 0.57

Profile



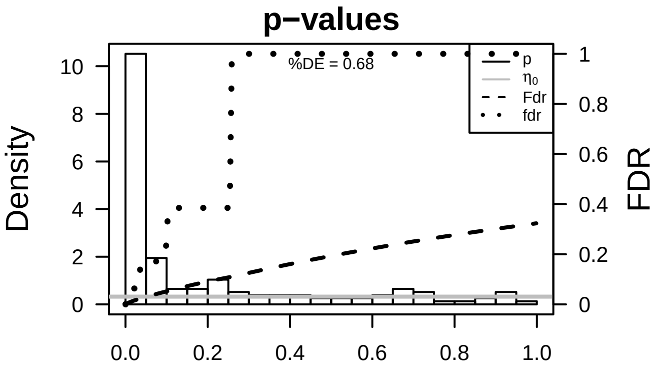
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1152	1.62	2e−16	1e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
2	220064	1.54	3e−15	3e−12	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
3	51083	1.46	7e−14	2e−10	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
4	8772	1.35	5e−12	9e−10	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
5	6535	1.31	2e−11	7e−09	1 x 16	solute carrier family 6 (neurotransmitter transporter), member
6	4495	−1.25	2e−10	2e−08	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
7	93273	1.21	5e−10	6e−07	2 x 15	LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
8	142678	1.11	1e−08	7e−06	1 x 17	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symb
9	2017	1.03	1e−07	2e−05	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]
10	4728	0.97	7e−07	2e−05	2 x 17	NADH dehydrogenase (ubiquinone) Fe−S protein 8, 23kDa (
11	219931	0.95	1e−06	6e−05	1 x 14	two pore segment channel 2 [Source:HGNC Symbol;Acc:208
12	3237	0.92	2e−06	6e−05	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
13	65003	0.9	4e−06	6e−05	2 x 17	mitochondrial ribosomal protein L11 [Source:HGNC Symbol;
14	3217	0.89	5e−06	9e−05	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
15	80028	0.88	7e−06	9e−05	1 x 14	F−box and leucine−rich repeat protein 18 [Source:HGNC Sy
16	4282	0.8	8e−06	3e−04	2 x 15	macrophage migration inhibitory factor (glycosylation−inhibiti
17	283869	0.83	2e−05	3e−04	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
18	230	0.81	3e−05	3e−04	2 x 17	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A
19	5499	0.81	3e−05	3e−04	1 x 13	protein phosphatase 1, catalytic subunit, alpha isozyme [Sou
20	25902	0.81	3e−05	3e−04	1 x 13	methylenetetrahydrofolate dehydrogenase (NADP+ depender

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	18.21	NULL	2 / 10	BP creatine metabolic process
2	14.93	NULL	1 / 3	GSEA C2 WEBER_METHYLATED_LCP_IN_SPERM_DN
3	13.21	NULL	2 / 7	GSEA C2 CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
4	12	NULL	1 / 6	GSEA C2 REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
5	12	NULL	1 / 6	GSEA C2 REACTOME_GPCR_LIGAND_BINDING
6	11.88	NULL	1 / 3	GSEA C2 KEGG_OXIDATIVE_PHOSPHORYLATION
7	11.88	NULL	1 / 3	GSEA C2 KEGG_PARKINSONS_DISEASE
8	11.63	NULL	3 / 14	GSEA C2 STEIN_ESRRA_TARGETS_UP
9	11.56	NULL	2 / 10	GSEA C2 STEIN_ESRRA_TARGETS
10	11.31	NULL	3 / 14	GSEA C2 LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
11	11.21	NULL	2 / 13	GSEA C2 NADERI_BREAST_CANCER_PROGNOSIS_UP
12	11.18	NULL	4 / 16	GSEA C2 WONG_EMBRYONIC_STEM_CELL_CORE
13	11.08	NULL	1 / 6	GSEA C2 GALI_TP53_TARGETS_APOPTOTIC_DN
14	11.05	NULL	1 / 5	GSEA C2 WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN
15	10.99	NULL	1 / 7	GSEA C2 REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
16	10.81	NULL	2 / 18	BP smooth muscle contraction
17	10.79	NULL	3 / 16	GSEA C2 WONG_MITOCHONDRIA_GENE_MODULE
18	10.79	NULL	3 / 16	GSEA C2 MOOTHA_HUMAN_MITODB_6_2002
19	10.6	NULL	1 / 9	GSEA C2 GOUYER_TUMOR_INVASIVENESS
20	10.23	NULL	2 / 11	GSEA C2 SCIBETTA_KDM5B_TARGETS_DN
21	10.19	NULL	1 / 8	GSEA C2 SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
22	10.19	NULL	1 / 8	GSEA C2 REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
23	10.01	NULL	1 / 4	GSEA C2 REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETI
24	10.01	NULL	1 / 4	GSEA C2 REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
25	10.01	NULL	1 / 4	GSEA C2 REACTOME_REGULATION_OF_INSULIN_SECRETION
26	9.98	NULL	4 / 18	MF ribonucleoprotein complex binding
27	9.87	NULL	2 / 13	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_C
28	9.74	NULL	2 / 12	GSEA C2 BHATTACHARYA_EMBRYONIC_STEM_CELL
29	9.39	NULL	2 / 21	BP feeding behavior
30	8.99	NULL	2 / 10	GSEA C2 KEGG_HUNTINGTONS_DISEASE
31	8.97	NULL	1 / 10	GSEA C2 WELCSH_BRCA1_TARGETS_1_DN
32	8.97	NULL	1 / 10	GSEA C2 TAKAO_RESPONSE_TO_UVB_RADIATION_UP
33	8.88	NULL	2 / 16	GSEA C2 MOOTHA_MITOCHONDRIA
34	8.8	NULL	2 / 14	GSEA C2 KRASNOSELSKAYA_ILF3_TARGETS_DN
35	8.79	NULL	1 / 9	GSEA C2 BIOCARTA_RELA_PATHWAY
36	8.79	NULL	1 / 9	GSEA C2 BIOCARTA_NFKB_PATHWAY
37	8.79	NULL	1 / 9	GSEA C2 BIOCARTA_SODD_PATHWAY
38	8.79	NULL	1 / 9	GSEA C2 REACTOME_DEATH_RECEPTOR_SIGNALLING
39	8.79	NULL	1 / 5	GSEA C2 REACTOME_ELECTRON_TRANSPORT_CHAIN
40	8.74	NULL	2 / 15	GSEA C2 CHOW_RASSF1_TARGETS_DN

GW_223

Local Summary

%DE = 0.86

metagenes = 17

genes = 233

genes in genesets = 227

genes with fdr < 0.1 = 174 (125 + / 49 −)

genes with fdr < 0.05 = 155 (115 + / 40 −)

genes with fdr < 0.01 = 128 (96 + / 32 −)

<r> metagenes = 0.95

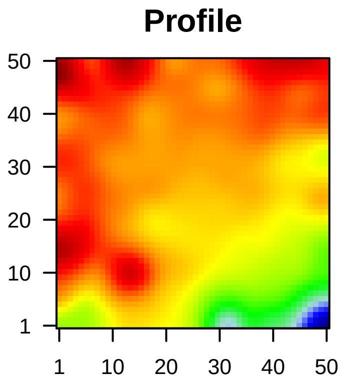
<r> genes = 0.44

<FC> = 0.38

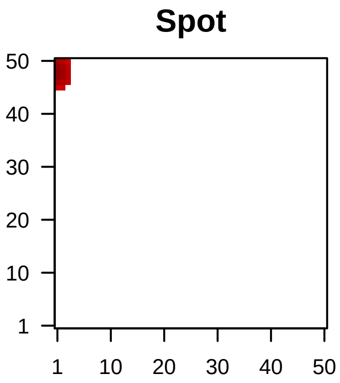
<shrinkage−t> = 13.56

<p−value> = 0

<fdr> = 0.35



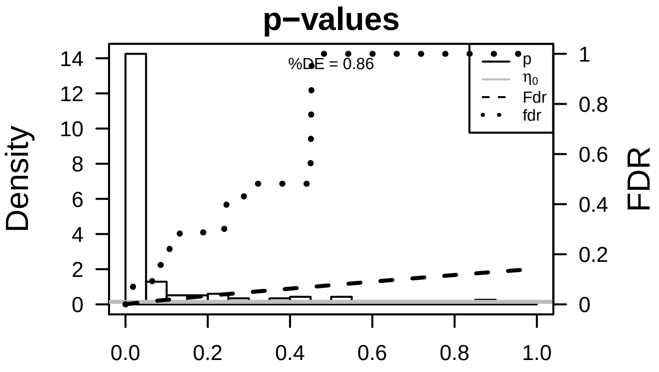
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−1.65	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	222	2.25	2e−16	2e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	151516	2.7	2e−16	2e−16	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
4	23120	1.77	2e−16	2e−16	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
5	29113	3.29	2e−16	2e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
6	1041	2.61	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
7	22802	−3	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	49860	−3.06	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	9547	−1.98	2e−16	2e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
10	1672	−2.61	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	1823	1.77	2e−16	2e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
12	1828	1.75	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	2012	−1.7	2e−16	2e−16	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
14	10804	2.15	2e−16	2e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	3848	1.94	2e−16	2e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
16	3860	−2.8	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
17	3868	1.69	2e−16	2e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
18	388533	2.5	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
19	84648	2.74	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
20	653499	1.61	2e−16	2e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	41.67	NULL	18 / 21	CC	cornified envelope
2	34.37	NULL	19 / 42	BP	keratinization
3	33.94	NULL	24 / 53	BP	keratinocyte differentiation
4	22.52	NULL	10 / 19	BP	peptide cross−linking
5	21.98	NULL	12 / 21	CC	desmosome
6	18.01	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
7	17.92	NULL	23 / 76	BP	epidermis development
8	13.57	NULL	97 / 572	Disease	GUDJ_psoriasis up
9	10.52	NULL	5 / 10	MF	RAGE receptor binding
10	10.13	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	10.07	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	10	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
13	9.85	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
14	9.52	NULL	2 / 23	Chr	Chr HSCHR6_MHC_DBB
15	9.31	NULL	7 / 51	MF	protein binding, bridging
16	9.21	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
17	9.2	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
18	9.04	NULL	3 / 21	CC	gap junction
19	8.94	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
20	8.55	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
21	8.21	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
22	8.15	NULL	23 / 186	MF	structural molecule activity
23	7.85	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
24	7.56	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
25	7.32	NULL	5 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
26	7.24	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
27	7.23	NULL	2 / 15	CC	connexon complex
28	7.19	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
29	7.01	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	6.72	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
31	6.72	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
32	6.72	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
33	6.66	NULL	1 / 15	CC	interstitial matrix
34	6.44	NULL	8 / 82	MF	structural constituent of cytoskeleton
35	6.42	NULL	1 / 16	MF	fibronectin binding
36	6.05	NULL	1 / 9	GSEA C2	SCHLOSSER_SERUM_RESPONSE_UP
37	5.86	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
38	5.82	NULL	1 / 19	MF	hyaluronic acid binding
39	5.78	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
40	5.75	NULL	3 / 13	BP	intermediate filament cytoskeleton organization

GW_223

Local Summary

%DE = 0.74

metagenes = 12

genes = 149

genes in genesets = 148

genes with fdr < 0.1 = 72 (66 + / 6 −)

genes with fdr < 0.05 = 54 (50 + / 4 −)

genes with fdr < 0.01 = 31 (29 + / 2 −)

<r> metagenes = 0.98

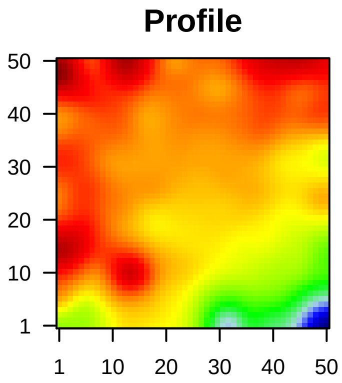
<r> genes = 0.27

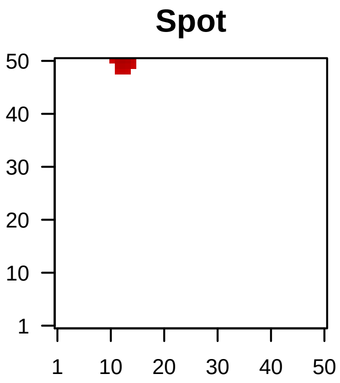
<FC> = 0.38

<shrinkage−t> = 13.17

<p−value> = 0

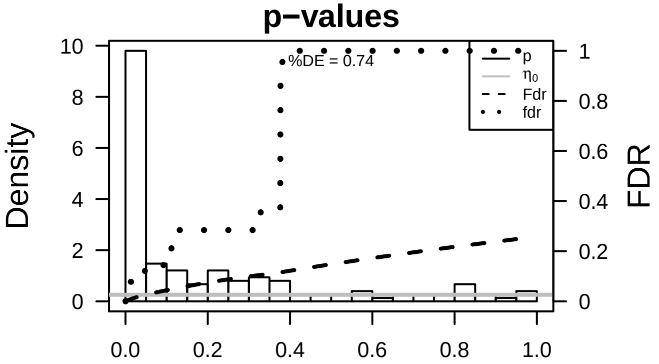
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1717	1.9	2e−16	3e−15	13 x 50	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
2	1749	2.04	2e−16	3e−15	13 x 50	distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918]
3	5217	1.9	2e−16	3e−15	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]
4	4741	1.55	2e−15	3e−12	15 x 50	neurofilament, medium polypeptide [Source:HGNC Symbol;A
5	63928	1.46	8e−14	1e−10	13 x 50	calcineurin−like EF−hand protein 2 [Source:HGNC Symbol;A
6	1109	1.35	4e−12	1e−09	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	1399	1.3	3e−11	2e−08	14 x 50	v−crk avian sarcoma virus CT10 oncogene homolog−like [So
8	140809	1.21	6e−10	2e−08	13 x 50	sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
9	406988	1.2	8e−10	4e−07	12 x 50	MIR205 host gene (non−protein coding) [Source:HGNC Sym
10	2564	1.11	1e−08	5e−07	13 x 50	gamma−aminobutyric acid (GABA) A receptor, epsilon [Sourc
11	55971	1.09	2e−08	8e−07	13 x 50	BAI1−associated protein 2−like 1 [Source:HGNC Symbol;Acc
12	1646	1.07	5e−08	8e−07	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
13	2539	1.05	7e−08	1e−06	13 x 50	glucose−6−phosphate dehydrogenase [Source:HGNC Symbo
14	4828	1.04	1e−07	3e−06	13 x 50	neuromedin B [Source:HGNC Symbol;Acc:7842]
15	57568	1.01	2e−07	3e−06	11 x 50	signal−induced proliferation−associated 1 like 2 [Source:HGN
16	4854	1	3e−07	3e−06	13 x 50	notch 3 [Source:HGNC Symbol;Acc:7883]
17	2817	1	3e−07	4e−06	14 x 50	glypican 1 [Source:HGNC Symbol;Acc:4449]
18	386757	0.98	5e−07	4e−06	14 x 50	solute carrier family 6 (neurotransmitter transporter), member
19	285987	0.98	5e−07	2e−05	15 x 49	DLX6 antisense RNA 1 [Source:HGNC Symbol;Acc:37151]
20	2950	0.88	1e−06	2e−05	12 x 50	glutathione S−transferase pi 1 [Source:HGNC Symbol;Acc:46



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	16.04	NULL	1 / 6	GSEA C2	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS
2	16.04	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
3	13.92	NULL	3 / 15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
4	13.66	NULL	2 / 15	GSEA C2	JEON_SMAD6_TARGETS_DN
5	11.94	NULL	2 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_DN
6	11.47	NULL	2 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
7	11.35	NULL	1 / 11	BP	ear development
8	11.35	NULL	1 / 11	GSEA C2	SU_PLACENTA
9	10.74	NULL	3 / 31	BP	positive regulation of actin filament polymerization
10	10.58	NULL	1 / 11	BP	sterol biosynthetic process
11	10.44	NULL	2 / 12	BP	head development
12	10.33	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
13	9.91	NULL	1 / 14	GSEA C2	ENK_UV_RESPONSE_EPIDERMIS_UP
14	9.89	NULL	1 / 4	miRNA target	miR−206
15	9.88	NULL	2 / 12	BP	positive regulation of protein import into nucleus
16	9.76	NULL	2 / 15	miRNA target−starBase	hsa−miR−220a
17	9.63	NULL	1 / 13	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
18	9.53	NULL	1 / 15	BP	cellular response to BMP stimulus
19	9.53	NULL	1 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
20	9.19	NULL	1 / 16	MF	HMG box domain binding
21	9.17	NULL	3 / 56	miRNA target−starBase	hsa−miR−151−3p
22	9.13	NULL	3 / 33	BP	cholesterol biosynthetic process
23	9.12	NULL	2 / 15	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
24	8.95	NULL	2 / 10	H.Tiss	WIRTH_B−cells
25	8.79	NULL	2 / 16	GSEA C2	KEGG_STEROID_BIOSYNTHESIS
26	8.56	NULL	1 / 16	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_U
27	8.35	NULL	3 / 15	GSEA C2	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
28	8.27	NULL	1 / 5	GSEA C2	OHM_EMBRYONIC_CARCINOMA_UP
29	8.04	NULL	4 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
30	7.88	NULL	1 / 21	BP	bone morphogenesis
31	7.82	NULL	2 / 14	GSEA C2	REACTOME_ACTIVATION_OF_RAC
32	7.78	NULL	1 / 13	BP	intermediate filament cytoskeleton organization
33	7.77	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
34	7.71	NULL	2 / 15	BP	pentose−phosphate shunt
35	7.19	NULL	2 / 41	miRNA target−starBase	hsa−miR−525−3p
36	7.17	NULL	1 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
37	7.14	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
38	7.14	NULL	1 / 22	CC	nuclear outer membrane
39	7.11	NULL	1 / 12	BP	androgen metabolic process
40	7.1	NULL	1 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN

GW_223

Local Summary

%DE = 0.68

metagenes = 8

genes = 223

genes in genesets = 222

genes with fdr < 0.1 = 88 (85 + / 3 −)

genes with fdr < 0.05 = 73 (71 + / 2 −)

genes with fdr < 0.01 = 50 (50 + / 0 −)

<r> metagenes = 0.93

<r> genes = 0.37

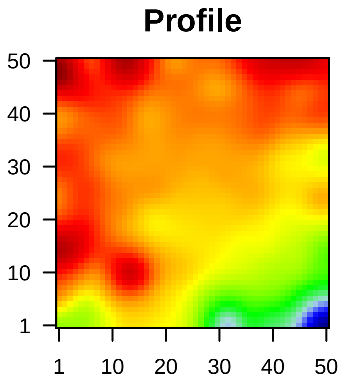
<FC> = 0.31

<shrinkage−t> = 10.94

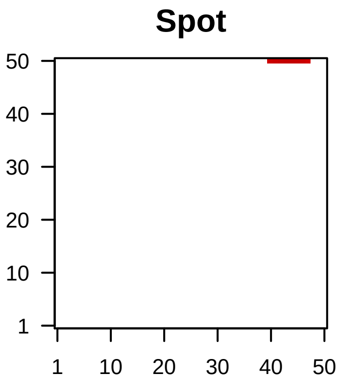
<p−value> = 0.02

<fdr> = 0.64

Profile



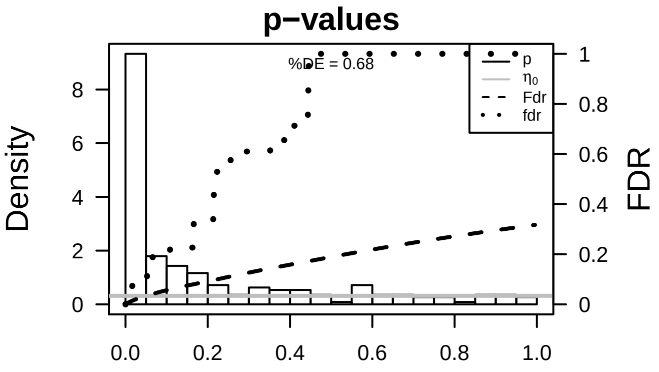
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8500	1.38	2e−12	9e−07	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
2	5902	1.11	1e−08	3e−06	43 x 50	RAN binding protein 1 [Source:HGNC Symbol;Acc:9847]
3	51678	1.06	5e−08	1e−05	40 x 50	membrane protein, palmitoylated 6 (MAGUK p55 subfamily m
4	8833	1.02	2e−07	9e−05	45 x 50	guanine monphosphate synthase [Source:HGNC Symbol;Acc
5	10165	0.93	2e−06	9e−05	40 x 50	solute carrier family 25 (aspartate/glutamate carrier), member
6	23350	0.92	3e−06	2e−04	45 x 50	U2 snRNP−associated SURP domain containing [Source:HG
7	10857	0.88	6e−06	2e−04	47 x 50	progesterone receptor membrane component 1 [Source:HGN
8	51319	0.87	9e−06	2e−04	43 x 50	arginine/serine−rich coiled−coil 1 [Source:HGNC Symbol;Acc
9	152559	0.86	1e−05	2e−04	40 x 50	progestin and adipoQ receptor family member III [Source:HG
10	170506	0.85	1e−05	3e−04	41 x 50	DEAH (Asp−Glu−Ala−His) box polypeptide 36 [Source:HGNC
11	55699	0.84	2e−05	3e−04	40 x 50	isoleucyl−tRNA synthetase 2, mitochondrial [Source:HGNC S
12	116832	0.83	2e−05	3e−04	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
13	54517	0.83	2e−05	7e−04	41 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:
14	79017	0.81	3e−05	8e−04	41 x 50	gamma−glutamylcyclotransferase [Source:HGNC Symbol;Ac
15	128061	0.8	4e−05	1e−03	41 x 50	chromosome 1 open reading frame 131 [Source:HGNC Sym
16	1163	0.77	8e−05	1e−03	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
17	51122	0.76	1e−04	1e−03	42 x 50	COMM domain containing 2 [Source:HGNC Symbol;Acc:249
18	7991	0.74	2e−04	1e−03	46 x 50	tumor suppressor candidate 3 [Source:HGNC Symbol;Acc:30
19	51659	0.72	2e−04	1e−03	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
20	54443	0.72	2e−04	1e−03	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.4	NULL	37 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	17.4	NULL	37 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	11.47	NULL	8 / 18	BP	spindle organization
4	11.4	NULL	4 / 16	GSEA C2	MOOTHA_MITOCHONDRIA
5	10.73	NULL	4 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY
6	10.53	NULL	5 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
7	10.49	NULL	35 / 370	BP	mitotic cell cycle
8	10.02	NULL	4 / 15	GSEA C2	TIEN_INTESTINE_PROBIOTICS_24HR_UP
9	9.96	NULL	3 / 16	GSEA C2	LY_AGING_PREMATURE_DN
10	9.95	NULL	43 / 530	Cancer	Lembcke_Normal vs Adenoma
11	9.94	NULL	9 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
12	9.83	NULL	4 / 14	BP	purine nucleotide biosynthetic process
13	9.7	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
14	9.53	NULL	11 / 56	CC	chromosome, centromeric region
15	8.88	NULL	5 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
16	8.75	NULL	8 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
17	8.71	NULL	38 / 914	Chr	Chr 3
18	8.64	NULL	2 / 14	GSEA C2	DAIRKEE_CANCER_PRONE_RESPONSE_BPA
19	8.41	NULL	3 / 17	CC	proteasome accessory complex
20	8.41	NULL	2 / 9	GSEA C2	BROWNE_HCMV_INFECTION_18HR_UP
21	8.21	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G1
22	7.9	NULL	12 / 140	Lymphoma	DAVE_BL−vs−DLBCL
23	7.84	NULL	6 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
24	7.79	NULL	6 / 16	Cancer	WOLFER_overlap genes
25	7.76	NULL	4 / 14	MMML CGS	MACIEJ_MMML 4
26	7.52	NULL	2 / 16	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
27	7.51	NULL	2 / 16	GSEA C2	GALE_APL_WITH_FLT3_MUTATED_UP
28	7.43	NULL	2 / 13	GSEA C2	BIOCARTA_P27_PATHWAY
29	7.41	NULL	9 / 67	BP	chromosome segregation
30	7.41	NULL	2 / 13	MF	magnesium ion transmembrane transporter activity
31	7.35	NULL	2 / 12	GSEA C2	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
32	7.34	NULL	8 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−c
33	7.26	NULL	10 / 68	Cancer	SHAUGHNESSY_MM high risk
34	7.11	NULL	2 / 14	BP	magnesium ion transport
35	7.1	NULL	3 / 16	GSEA C2	REACTOME_REV_MEDIATED_NUCLEAR_EXPORT_OF_HIV1_F
36	7.1	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
37	7.09	NULL	2 / 12	GSEA C2	OSMAN_BLADDER_CANCER_UP
38	6.96	NULL	5 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
39	6.93	NULL	21 / 232	BP	mitosis
40	6.87	NULL	12 / 148	BP	G1/S transition of mitotic cell cycle

GW_223

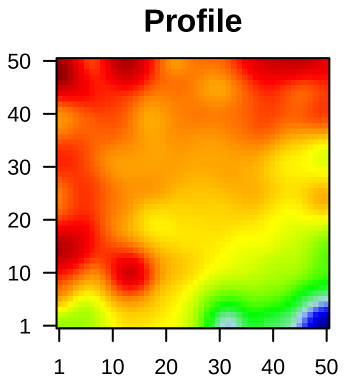
Local Summary

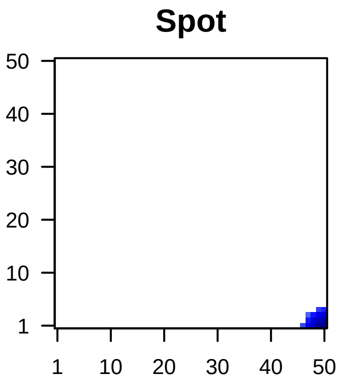
%DE = 0.98
metagenes = 15
genes = 264
genes in genesets = 262

genes with fdr < 0.1 = 252 (4 + / 248 −)
genes with fdr < 0.05 = 252 (4 + / 248 −)
genes with fdr < 0.01 = 229 (2 + / 227 −)

<r> metagenes = 0.99
<r> genes = 0.6

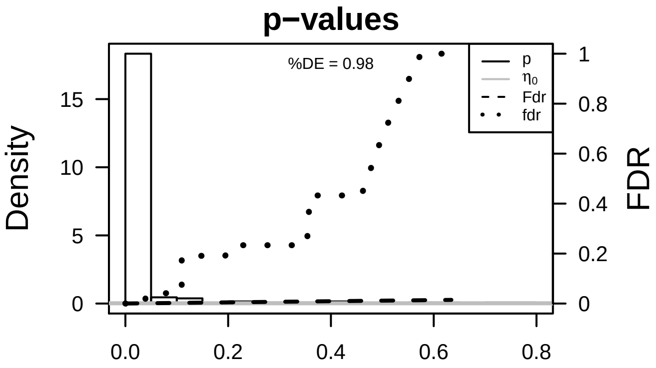
<FC> = −0.85
<shrinkage−t> = −29.74
<p−value> = 0
<fdr> = 0.15





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	713	−1.62	2e−16	6e−17	50 x 1	complement component 1, q subcomponent, B chain [Source
2	260436	−1.66	2e−16	6e−17	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
3	972	−1.91	2e−16	6e−17	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
4	4283	−1.74	2e−16	6e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
5	54855	−1.63	2e−16	6e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
6	3108	−2.1	2e−16	6e−17	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
7	3109	−1.93	2e−16	6e−17	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
8	3113	−2.24	2e−16	6e−17	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
9	3122	−2.3	2e−16	6e−17	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
10	3128	−1.8	2e−16	6e−17	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
11	3512	−2.14	2e−16	6e−17	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	3543	−1.51	2e−16	6e−17	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
13	3936	−1.71	2e−16	6e−17	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
14	5341	−1.74	2e−16	6e−17	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
15	5920	−2	2e−16	6e−17	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
16	5996	−1.79	2e−16	6e−17	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
17	5552	−1.88	2e−16	6e−17	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
18	10537	−1.76	2e−16	6e−17	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
19	3059	−1.54	3e−15	1e−14	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
20	962	−1.53	4e−15	1e−14	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.41	NULL	12 / 15	CC	MHC class II protein complex
2	−29.79	NULL	90 / 417	H.Tiss	WIRTH_Immune system
3	−25.05	NULL	94 / 553	Cancer	Lembcke_Colonic Inflammation
4	−23.8	NULL	52 / 312	BP	immune response
5	−23.62	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−23.54	NULL	15 / 47	BP	antigen processing and presentation
7	−22.82	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
8	−20.07	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
9	−18.78	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
10	−18.76	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
11	−18.21	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
12	−17.85	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
13	−17.84	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−17.84	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−17.84	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−17.84	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−17.71	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
18	−17.19	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
19	−17.14	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	−16.83	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
21	−16.74	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
22	−16.16	NULL	14 / 60	BP	T cell costimulation
23	−16.05	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
24	−15.97	NULL	7 / 28	CC	transport vesicle membrane
25	−15.33	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
26	−15.23	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
27	−15.17	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
28	−15.17	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
29	−15.17	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
30	−15.12	NULL	5 / 12	BP	immunoglobulin mediated immune response
31	−15	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
32	−14.81	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
33	−14.78	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
34	−14.59	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
35	−14.56	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
36	−14.52	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
37	−14.46	NULL	15 / 84	BP	T cell receptor signaling pathway
38	−14.28	NULL	8 / 35	CC	trans−Golgi network membrane
39	−14.24	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
40	−13.82	NULL	17 / 74	BP	regulation of immune response