GW_307

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1874 (1086 + / 788 −)

genes with fdr < 0.1 = 1449 (893 + / 556 −)

genes with fdr < 0.05 = 1235 (802 + / 433 −)

genes with fdr < 0.01 = 833 (585 + / 248 −)

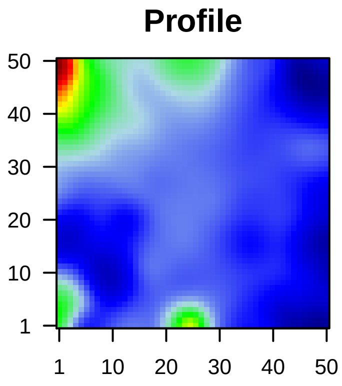
genes in genesets = 16332

<FC> = 0

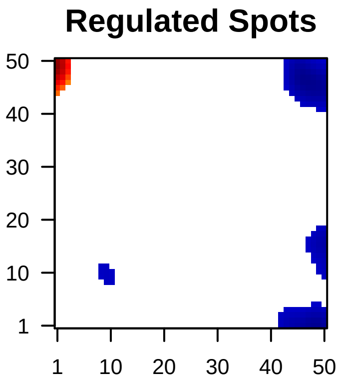
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.86



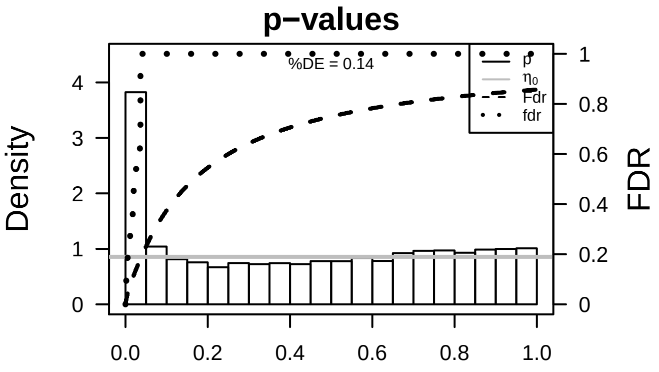
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.11	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.28	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	1.54	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	56895	1.43	2e−16	3e−14	2 x 5	1−acylglycerol−3−phosphate O−acyltransferase 4 [Source:HC
5	57016	1.36	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	242	1.66	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
7	445328	−2.16	2e−16	3e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
8	140458	1.4	2e−16	3e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
9	650	1.37	2e−16	3e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10
10	387695	1.85	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
11	148304	1.6	2e−16	3e−14	1 x 41	chromosome 1 open reading frame 74 [Source:HGNC Symbo
12	260436	1.94	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
13	375791	1.78	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
14	51806	1.78	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
15	845	1.35	2e−16	3e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
16	978	1.7	2e−16	3e−14	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
17	1158	2.84	2e−16	3e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
18	202333	1.41	2e−16	3e−14	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:143
19	84518	1.49	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
20	49860	2.61	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	29.04	NULL	135	H.Tiss	WIRTH_Mucosa
2	19.89	NULL	572	Disease	GUDJ_psoriasis up
3	18.6	NULL	127	H.Tiss	WIRTH_Muscle
4	17.69	NULL	36	BP	muscle filament sliding
5	17.05	NULL	21	CC	cornified envelope
6	16.21	NULL	42	BP	keratinization
7	15.86	NULL	53	BP	keratinocyte differentiation
8	15.72	NULL	76	BP	epidermis development
9	15.54	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
10	15.06	NULL	16	H.Tiss	WIRTH_Hippocampus
11	12.75	NULL	44	MF	structural constituent of muscle
12	11.93	NULL	19	BP	peptide cross−linking
13	11.29	NULL	12	CC	myosin filament
14	10.89	NULL	37	CC	sarcomere
15	10.51	NULL	14	CC	contractile fiber
16	9.52	NULL	84	BP	muscle contraction
17	9.37	NULL	88	CC	Z disc
18	8.91	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	8.82	NULL	1182	CC	extracellular region
20	8.75	NULL	13	CC	muscle myosin complex
Underexpressed					
1	−11.88	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−11.88	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−7.58	NULL	1749	MF	DNA binding
4	−7.28	NULL	149	BP	DNA replication
5	−7.27	NULL	940	MF	nucleic acid binding
6	−7.16	NULL	743	Chr	Chr 7
7	−6.57	NULL	949	CC	nucleoplasm
8	−6.49	NULL	370	BP	mitotic cell cycle
9	−6.3	NULL	1574	BP	transcription, DNA−templated
10	−6.24	NULL	417	H.Tiss	WIRTH_Immune system
11	−6.19	NULL	649	BP	gene expression
12	−6.16	NULL	755	Lymphoma	SPANG_BCR UP
13	−6.09	NULL	30	BP	DNA strand elongation involved in DNA replication
14	−6.08	NULL	4640	CC	nucleus
15	−6.02	NULL	1581	BP	regulation of transcription, DNA−dependent
16	−5.84	NULL	595	MF	RNA binding
17	−5.8	NULL	298	BP	DNA repair
18	−5.73	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
19	−5.71	NULL	386	Chr	Chr 22
20	−5.7	NULL	1318	CC	mitochondrion

GW_307

Local Summary

%DE = 0.89

metagenes = 18

genes = 260

genes in genesets = 254

genes with fdr < 0.1 = 226 (221 + / 5 −)

genes with fdr < 0.05 = 222 (217 + / 5 −)

genes with fdr < 0.01 = 197 (195 + / 2 −)

<r> metagenes = 0.93

<r> genes = 0.42

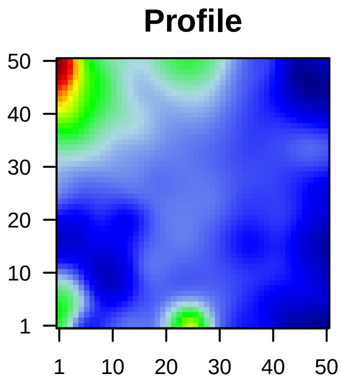
<FC> = 0.89

<shrinkage−t> = 31.26

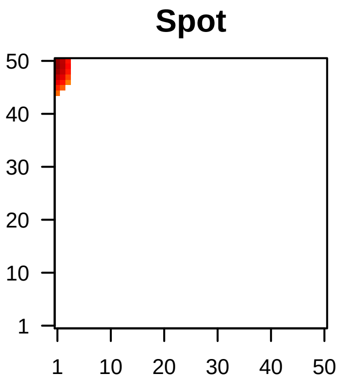
<p−value> = 0

<fdr> = 0.18

Profile



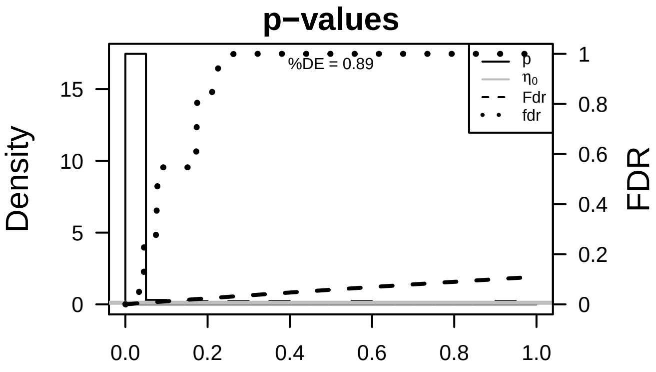
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.54	2e−16	1e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.36	2e−16	1e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	242	1.66	2e−16	1e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
4	387695	1.85	2e−16	1e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
5	375791	1.78	2e−16	1e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
6	978	1.7	2e−16	1e−16	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
7	84518	1.49	2e−16	1e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	49860	2.61	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	1475	1.38	2e−16	1e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
10	55894	2.08	2e−16	1e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	2.44	2e−16	1e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	1.96	2e−16	1e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1824	1.33	2e−16	1e−16	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
14	1828	2.16	2e−16	1e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	1830	1.37	2e−16	1e−16	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
16	2167	2.46	2e−16	1e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	10804	1.59	2e−16	1e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
18	26525	1.61	2e−16	1e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
19	56300	1.75	2e−16	1e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
20	43849	1.53	2e−16	1e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	54.82	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
2	39.85	NULL	18 / 21	CC	cornified envelope
3	34.88	NULL	19 / 42	BP	keratinization
4	33.27	NULL	24 / 53	BP	keratinocyte differentiation
5	31.24	NULL	102 / 572	Disease	GUDJ_psoriasis up
6	25.91	NULL	24 / 76	BP	epidermis development
7	24.44	NULL	10 / 19	BP	peptide cross−linking
8	16.35	NULL	12 / 21	CC	desmosome
9	15.18	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
10	14.99	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	14.18	NULL	6 / 13	BP	negative regulation of peptidase activity
12	13.4	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	13.33	NULL	12 / 44	CC	keratin filament
14	12.83	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
15	12.51	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	12.39	NULL	26 / 186	MF	structural molecule activity
17	11.94	NULL	5 / 10	MF	RAGE receptor binding
18	11.92	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
19	11.87	NULL	7 / 29	BP	regulation of proteolysis
20	11.76	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
21	11.56	NULL	10 / 52	BP	negative regulation of endopeptidase activity
22	11.47	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
23	11.46	NULL	19 / 82	CC	intermediate filament
24	11.28	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
25	11.16	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
26	11.09	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
27	10.86	NULL	61 / 1182	CC	extracellular region
28	10.69	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
29	10.26	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
30	10.12	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
31	9.83	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
32	9.35	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
33	9.06	NULL	13 / 122	MF	serine−type endopeptidase activity
34	8.93	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
35	8.86	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
36	8.75	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
37	8.54	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
38	8.04	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
39	7.94	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
40	7.78	NULL	4 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24

GW_307

Local Summary

%DE = 0.73

metagenes = 37

genes = 480

genes in genesets = 475

genes with fdr < 0.1 = 248 (15 + / 233 −)

genes with fdr < 0.05 = 153 (11 + / 142 −)

genes with fdr < 0.01 = 87 (9 + / 78 −)

<r> metagenes = 0.94

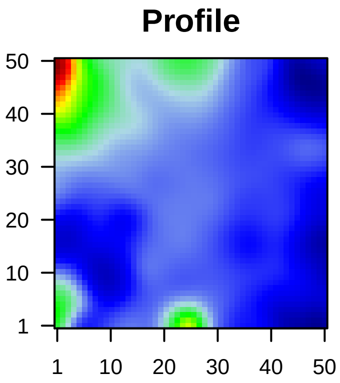
<r> genes = 0.49

<FC> = −0.26

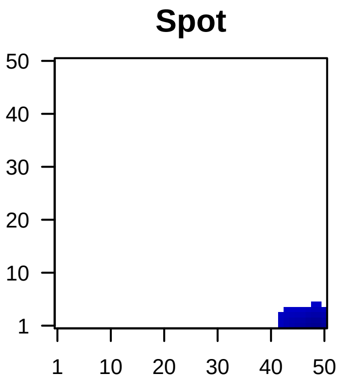
<shrinkage−t> = −9.13

<p−value> = 0.02

<fdr> = 0.68



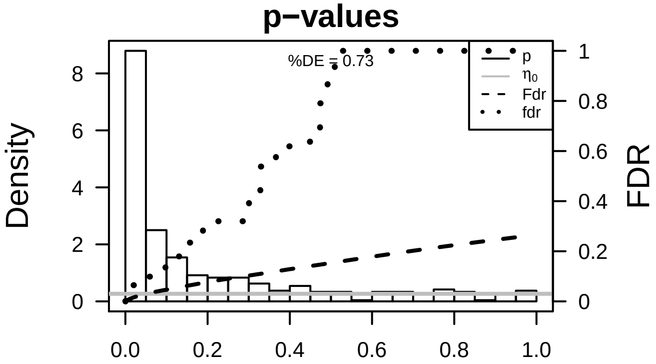
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	1.94	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
2	10628	−1.27	4e−16	2e−11	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
3	9404	1.17	2e−13	8e−11	50 x 1	leupaxin [Source:HGNC Symbol;Acc:14061]
4	23231	−1.14	8e−13	2e−10	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGN
5	57172	−1.12	2e−12	4e−09	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
6	81618	−1.05	4e−11	4e−09	48 x 5	integral membrane protein 2C [Source:HGNC Symbol;Acc:61
7	1116	1.04	7e−11	7e−09	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
8	84446	−1.03	1e−10	5e−08	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
9	1117	0.99	6e−10	5e−08	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]
10	91607	−0.96	1e−09	5e−08	48 x 4	schlafen family member 11 [Source:HGNC Symbol;Acc:2663
11	54855	−0.96	2e−09	5e−08	49 x 1	family with sequence similarity 46, member C [Source:HGNC
12	51755	−0.96	2e−09	1e−07	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
13	3120	0.94	3e−09	1e−07	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
14	3512	−0.94	4e−09	1e−07	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
15	6363	−0.93	5e−09	2e−06	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
16	3543	−0.82	2e−08	4e−06	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
17	3123	0.87	5e−08	1e−05	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
18	374882	−0.82	2e−07	1e−05	42 x 1	transmembrane protein 205 [Source:HGNC Symbol;Acc:296
19	11040	−0.81	3e−07	1e−05	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
20	91353	−0.81	4e−07	2e−05	48 x 1	



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.61	NULL	124 / 417	H.Tiss	WIRTH_Immune system
2	−14.79	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	−14.45	NULL	124 / 553	Cancer	Lembcke_Colonic Inflammation
4	−13.47	NULL	73 / 312	BP	immune response
5	−12.49	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−12.02	NULL	8 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
7	−11.58	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
8	−10.84	NULL	9 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
9	−10.61	NULL	14 / 28	BP	B cell receptor signaling pathway
10	−10.52	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
11	−10.13	NULL	5 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
12	−9.98	NULL	7 / 13	MMML CGS	MACIEJ_MMML 6
13	−9.98	NULL	31 / 162	CC	external side of plasma membrane
14	−9.6	NULL	5 / 12	BP	dendritic cell chemotaxis
15	−9.59	NULL	41 / 327	Lymphoma	SPANG_CD40 6hrs UP
16	−9.56	NULL	19 / 74	BP	regulation of immune response
17	−9.45	NULL	5 / 12	BP	immunoglobulin mediated immune response
18	−9.38	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
19	−9.3	NULL	10 / 13	Cancer	GENTLES_modul18
20	−8.6	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP
21	−8.58	NULL	7 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
22	−8.53	NULL	24 / 60	BP	T cell costimulation
23	−8.45	NULL	4 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
24	−8.39	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
25	−8.21	NULL	7 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
26	−8.13	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
27	−8.04	NULL	6 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
28	−8.01	NULL	11 / 43	BP	positive regulation of T cell proliferation
29	−8.01	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
30	−8.01	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	−7.98	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
32	−7.97	NULL	9 / 16	GSEA C2	SU_THYMUS
33	−7.96	NULL	5 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
34	−7.81	NULL	13 / 45	BP	T cell activation
35	−7.76	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
36	−7.67	NULL	57 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
37	−7.67	NULL	57 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
38	−7.67	NULL	57 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
39	−7.67	NULL	57 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
40	−7.64	NULL	4 / 11	GSEA C2	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN

GW_307

Local Summary

%DE = 0.66

metagenes = 10

genes = 87

genes in genesets = 86

genes with fdr < 0.1 = 42 (0 + / 42 −)

genes with fdr < 0.05 = 36 (0 + / 36 −)

genes with fdr < 0.01 = 11 (0 + / 11 −)

<r> metagenes = 0.97

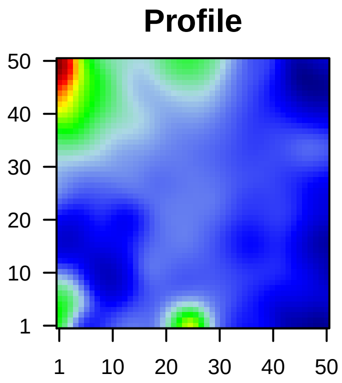
<r> genes = 0.31

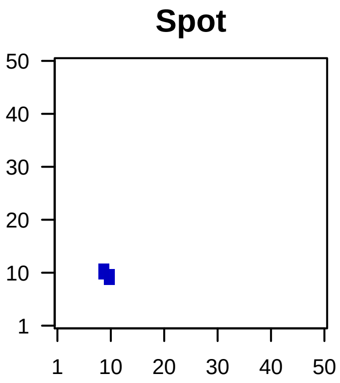
<FC> = −0.29

<shrinkage−t> = −9.99

<p−value> = 0.03

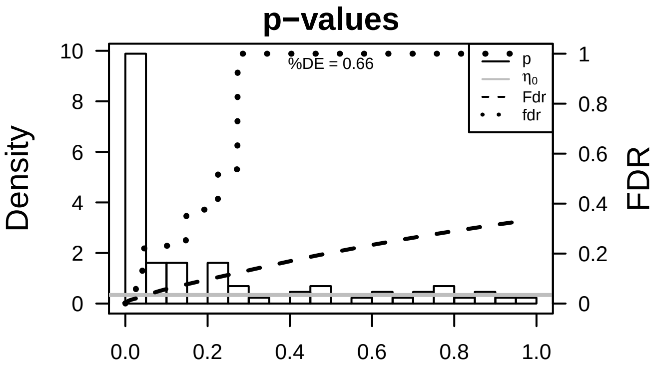
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51477	−0.81	4e−07	2e−04	10 x 10	inositol−3−phosphate synthase 1 [Source:HGNC Symbol;Acc
2	100101267	−0.7	1e−05	2e−04	11 x 11	POM121 transmembrane nucleoporin C [Source:HGNC Syml
3	51593	−0.69	1e−05	2e−04	10 x 12	serrate RNA effector molecule homolog (Arabidopsis) [Source
4	57414	−0.68	2e−05	3e−03	9 x 10	rhomboid domain containing 2 [Source:HGNC Symbol;Acc:23
5	100170841	−0.61	1e−04	5e−03	10 x 10	chromosome 17 open reading frame 96 [Source:HGNC Symb
6	55258	−0.56	4e−04	5e−03	11 x 9	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
7	64132	−0.55	6e−04	5e−03	10 x 9	xylosyltransferase II [Source:HGNC Symbol;Acc:15517]
8	23338	−0.54	7e−04	5e−03	10 x 12	jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
9	2026	−0.53	8e−04	5e−03	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
10	64847	−0.53	9e−04	6e−03	10 x 9	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
11	56996	−0.51	1e−03	6e−03	10 x 11	solute carrier family 12, member 9 [Source:HGNC Symbol;Ac
12	6722	−0.51	1e−03	1e−02	9 x 12	serum response factor (c−fos serum response element−bindi
13	11000	−0.5	2e−03	2e−02	9 x 11	solute carrier family 27 (fatty acid transporter), member 3 [So
14	84939	−0.47	3e−03	2e−02	10 x 11	melanoma associated antigen (mutated) 1 [Source:HGNC Sy
15	5871	−0.46	4e−03	2e−02	10 x 10	mitogen−activated protein kinase kinase kinase kinase 2 [Sou
16	10898	−0.45	5e−03	2e−02	10 x 12	cleavage and polyadenylation specific factor 4, 30kDa [Sourc
17	114049	−0.44	5e−03	2e−02	11 x 10	Williams Beuren syndrome chromosome region 22 [Source:H
18	2648	−0.43	7e−03	2e−02	11 x 11	K(lysine) acetyltransferase 2A [Source:HGNC Symbol;Acc:42
19	10985	−0.42	8e−03	2e−02	9 x 11	GCN1 general control of amino−acid synthesis 1−like 1 (yeas
20	57176	−0.42	8e−03	2e−02	9 x 11	Valine−−tRNA ligase, mitochondrial [Source:UniProtKB/TrEM



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.57	NULL	1 / 4	miRNA target	hsa−miR−122
2	−9.98	NULL	2 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
3	−8.78	NULL	1 / 10	GSEA C2	KIM_WT1_TARGETS_8HR_DN
4	−8.33	NULL	1 / 11	BP	neuronal stem cell maintenance
5	−8.24	NULL	1 / 15	GSEA C2	KEGG_INOSITOL_PHOSPHATE_METABOLISM
6	−7.95	NULL	1 / 12	BP	response to arsenic−containing substance
7	−7.95	NULL	1 / 12	MMML CGS	MACIEJ_MMML 24
8	−7.95	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
9	−7.61	NULL	1 / 13	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_UP
10	−7.61	NULL	1 / 13	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_DN
11	−7.61	NULL	1 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
12	−7.61	NULL	1 / 13	GSEA C2	WALLACE_JAK2_TARGETS_UP
13	−7.36	NULL	3 / 41	miRNA target−starBase	hsa−miR−532−3p
14	−7.36	NULL	2 / 15	MF	acetylglucosaminyltransferase activity
15	−7.29	NULL	2 / 16	GSEA C2	COLLIS_PRKDC_SUBSTRATES
16	−7.25	NULL	1 / 8	GSEA C2	YEMELYANOV_GR_TARGETS_DN
17	−7.18	NULL	2 / 12	BP	long term synaptic depression
18	−7.04	NULL	1 / 15	GSEA C2	DIRMEIER_LMP1_RESPONSE_LATE_UP
19	−6.9	NULL	2 / 22	MF	N−acetyltransferase activity
20	−6.79	NULL	1 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POC
21	−6.79	NULL	1 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POC
22	−6.66	NULL	2 / 42	BP	inositol phosphate metabolic process
23	−6.56	NULL	1 / 8	GSEA C2	BIOCARTA_STRESS_PATHWAY
24	−6.41	NULL	1 / 10	BP	eyelid development in camera−type eye
25	−6.41	NULL	1 / 10	BP	megakaryocyte development
26	−6.41	NULL	1 / 10	MF	RNA polymerase II transcription factor binding transcription factor a
27	−6.41	NULL	1 / 10	BP	stress fiber assembly
28	−6.41	NULL	1 / 10	GSEA C2	MARTIN_INTERACT_WITH_HDAC
29	−6.25	NULL	1 / 12	BP	heparan sulfate proteoglycan biosynthetic process
30	−6.2	NULL	2 / 30	miRNA target−starBase	hsa−miR−1237
31	−6.11	NULL	3 / 40	BP	histone H3 acetylation
32	−5.98	NULL	3 / 55	miRNA 3UTR	CTGG−296
33	−5.8	NULL	1 / 12	BP	mRNA transcription from RNA polymerase II promoter
34	−5.8	NULL	1 / 12	BP	platelet formation
35	−5.8	NULL	1 / 12	miRNA target−starBase	hsa−miR−1249
36	−5.77	NULL	1 / 13	GSEA C2	REACTOME_GLYCOLYSIS
37	−5.72	NULL	1 / 29	BP	phospholipid biosynthetic process
38	−5.7	NULL	2 / 18	miRNA target−starBase	hsa−miR−564
39	−5.55	NULL	1 / 13	BP	cell migration involved in sprouting angiogenesis
40	−5.55	NULL	1 / 13	BP	positive regulation of smooth muscle contraction

GW_307

Local Summary

%DE = 0.73

metagenes = 28

genes = 361

genes in genesets = 359

genes with fdr < 0.1 = 160 (12 + / 148 −)

genes with fdr < 0.05 = 146 (11 + / 135 −)

genes with fdr < 0.01 = 77 (7 + / 70 −)

<r> metagenes = 0.89

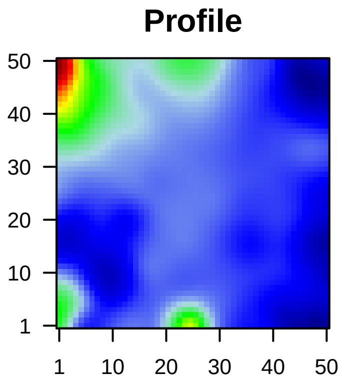
<r> genes = 0.24

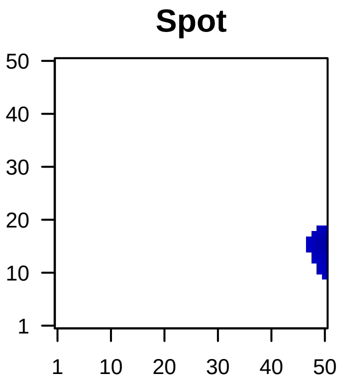
<FC> = −0.26

<shrinkage−t> = −9.15

<p−value> = 0.01

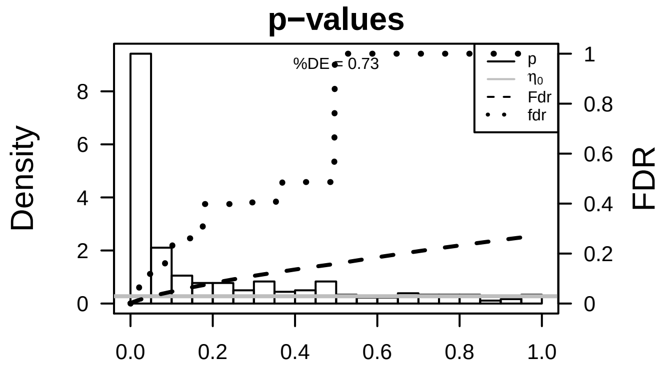
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	728715	1.13	1e−12	2e−09	50 x 18	
2	51316	−1.06	3e−11	4e−09	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
3	29116	−1.04	7e−11	1e−07	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
4	113246	−0.97	1e−09	1e−07	49 x 16	chromosome 12 open reading frame 57 [Source:HGNC Symb
5	2762	−0.94	4e−09	1e−07	50 x 12	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc
6	5382	−0.94	4e−09	2e−07	48 x 15	postmeiotic segregation increased 2 pseudogene 4 [Source:H
7	9071	−0.93	6e−09	1e−06	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
8	498	−0.81	3e−08	1e−06	48 x 15	ATP synthase, H+ transporting, mitochondrial F1 complex, al
9	92747	−0.89	3e−08	1e−06	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
10	79191	0.88	4e−08	1e−06	50 x 15	iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
11	10551	−0.87	5e−08	1e−06	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
12	26018	−0.86	7e−08	1e−06	50 x 16	leucine−rich repeats and immunoglobulin−like domains 1 [So
13	155066	−0.85	8e−08	3e−06	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
14	2205	0.84	1e−07	3e−06	50 x 13	Fc fragment of IgE, high affinity I, receptor for; alpha polypept
15	25840	−0.84	2e−07	3e−06	50 x 11	methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
16	55930	−0.83	2e−07	5e−06	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
17	54102	−0.81	3e−07	5e−06	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
18	9603	−0.81	4e−07	5e−06	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
19	79762	−0.81	4e−07	5e−06	50 x 15	chromosome 1 open reading frame 115 [Source:HGNC Symb
20	79085	−0.81	4e−07	5e−05	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.83	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−10.94	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−7.7	NULL	3 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_UP
4	−7.55	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
5	−7.54	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
6	−7.39	NULL	4 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
7	−7.23	NULL	3 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
8	−7.16	NULL	2 / 9	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
9	−7.04	NULL	1 / 3	miRNA 3UTR	ACGC−210
10	−6.97	NULL	3 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
11	−6.93	NULL	3 / 15	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
12	−6.81	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	−6.81	NULL	4 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
14	−6.71	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
15	−6.33	NULL	2 / 16	GSEA C2	KORKOLA_TERATOMA_UP
16	−5.75	NULL	2 / 12	BP	negative regulation of axon extension
17	−5.57	NULL	1 / 3	miRNA target	miR−148a
18	−5.54	NULL	2 / 12	CC	apical junction complex
19	−5.54	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
20	−5.49	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
21	−5.48	NULL	4 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
22	−5.43	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
23	−5.42	NULL	2 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
24	−5.35	NULL	2 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
25	−5.32	NULL	1 / 10	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_DN
26	−5.32	NULL	3 / 4	miRNA target	miR−204
27	−5.28	NULL	2 / 12	BP	neuron fate specification
28	−5.19	NULL	1 / 7	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_UP
29	−5.18	NULL	1 / 4	GSEA C2	IGARASHI_ATF4_TARGETS_UP
30	−5.17	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
31	−5.15	NULL	1 / 11	BP	negative regulation of multicellular organism growth
32	−5.13	NULL	3 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
33	−5.07	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
34	−4.99	NULL	2 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
35	−4.99	NULL	2 / 10	BP	regulation of dendrite development
36	−4.98	NULL	2 / 14	Cancer	LIU_LIVER_CANCER
37	−4.94	NULL	2 / 29	BP	ATP hydrolysis coupled proton transport
38	−4.78	NULL	2 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
39	−4.76	NULL	2 / 15	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP
40	−4.73	NULL	2 / 11	MF	enhancer sequence−specific DNA binding

GW_307

Local Summary

%DE = 0.72

metagenes = 68

genes = 769

genes in genesets = 763

genes with fdr < 0.1 = 325 (30 + / 295 −)

genes with fdr < 0.05 = 235 (20 + / 215 −)

genes with fdr < 0.01 = 148 (14 + / 134 −)

<r> metagenes = 0.86

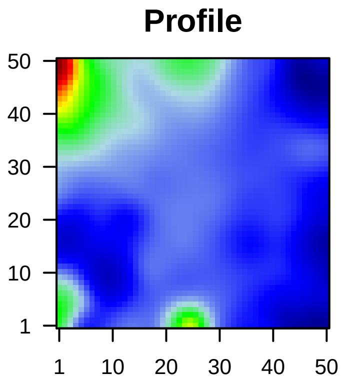
<r> genes = 0.23

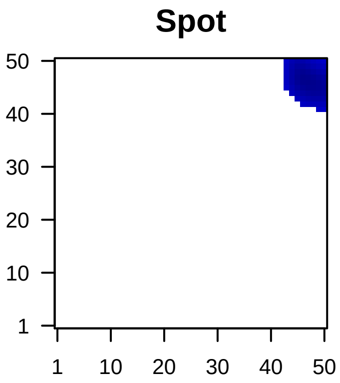
<FC> = −0.25

<shrinkage−t> = −8.89

<p−value> = 0.02

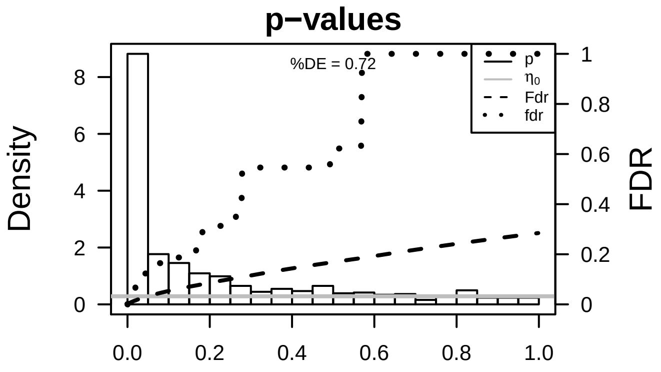
<fdr> = 0.67





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4072	−1.91	2e−16	5e−14	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
2	10643	−1.26	3e−15	5e−11	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:H
3	26227	−1.17	3e−13	1e−10	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
4	2956	−1.14	8e−13	8e−10	47 x 48	mutS homolog 6 [Source:HGNC Symbol;Acc:7329]
5	116832	−1.1	5e−12	3e−07	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
6	26047	−0.95	3e−09	3e−07	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
7	291	−0.95	3e−09	1e−06	50 x 46	solute carrier family 25 (mitochondrial carrier; adenine nucleo
8	2222	−0.92	8e−09	1e−06	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
9	1786	−0.89	3e−08	1e−06	45 x 47	DNA (cytosine−5−)−methyltransferase 1 [Source:HGNC Sym
10	9918	−0.88	3e−08	1e−06	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
11	9076	0.88	3e−08	1e−06	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
12	4172	−0.87	5e−08	1e−06	46 x 47	minichromosome maintenance complex component 3 [Source
13	4922	−0.87	5e−08	1e−06	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
14	51804	−0.87	5e−08	1e−06	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
15	142	−0.87	5e−08	1e−06	47 x 46	poly (ADP−ribose) polymerase 1 [Source:HGNC Symbol;Acc
16	2091	−0.87	5e−08	4e−06	47 x 45	fibrillarin [Source:HGNC Symbol;Acc:3599]
17	26024	−0.85	1e−07	4e−06	49 x 48	pentatricopeptide repeat domain 1 [Source:HGNC Symbol;A
18	899	−0.85	1e−07	4e−06	45 x 46	cyclin F [Source:HGNC Symbol;Acc:1591]
19	7298	−0.84	1e−07	4e−06	46 x 48	thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
20	84171	−0.84	1e−07	4e−06	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.6	NULL	94 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−36.6	NULL	94 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−21.37	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	−19.57	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
5	−19.14	NULL	103 / 370	BP	mitotic cell cycle
6	−18.95	NULL	52 / 149	BP	DNA replication
7	−18.57	NULL	27 / 57	Glio	developing astrocytes
8	−18.3	NULL	115 / 530	Cancer	Lembcke_Normal vs Adenoma
9	−18.16	NULL	19 / 30	BP	DNA strand elongation involved in DNA replication
10	−17.34	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
11	−16.76	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
12	−16.19	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
13	−16.14	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
14	−15.93	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
15	−15.92	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
16	−15.65	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
17	−15.17	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	−15.12	NULL	13 / 22	BP	DNA replication initiation
19	−15.09	NULL	8 / 16	GSEA C2	LY_AGING_PREMATURE_DN
20	−14.9	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
21	−14.49	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
22	−14.3	NULL	62 / 232	BP	mitosis
23	−14.25	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
24	−14.21	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
25	−14.21	NULL	9 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
26	−13.86	NULL	11 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
27	−13.73	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
28	−13.72	NULL	6 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
29	−13.54	NULL	7 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
30	−13.45	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
31	−13.17	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
32	−12.84	NULL	8 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
33	−12.83	NULL	10 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
34	−12.67	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
35	−12.49	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
36	−12.44	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
37	−12.19	NULL	6 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
38	−12.09	NULL	8 / 12	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
39	−12.08	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
40	−12.06	NULL	7 / 15	GSEA C2	LY_AGING_OLD_DN