GW_217

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1722 (1014 + / 708 −)

genes with fdr < 0.1 = 1410 (871 + / 539 −)

genes with fdr < 0.05 = 1172 (746 + / 426 −)

genes with fdr < 0.01 = 801 (542 + / 259 −)

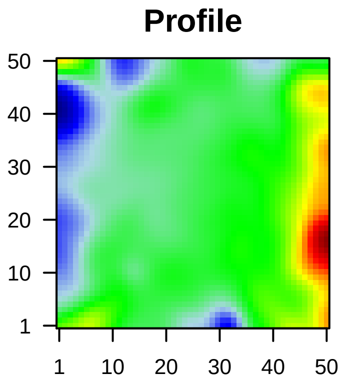
genes in genesets = 16332

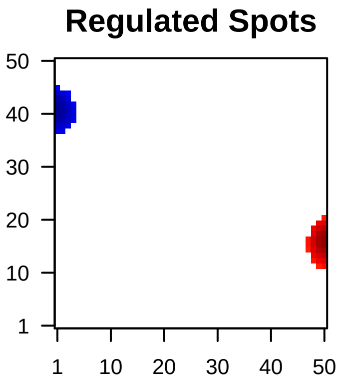
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

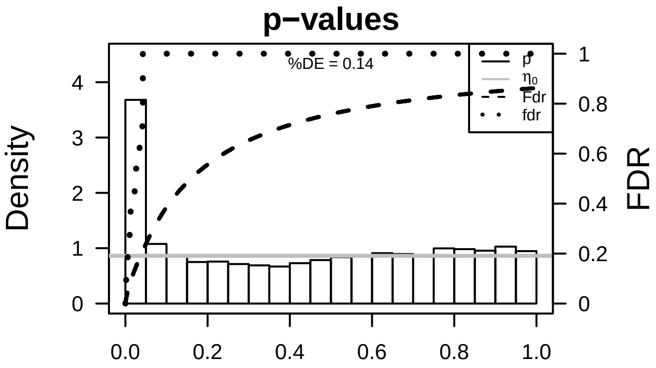
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84532	1.36	2e−16	3e−14	50 x 17	acyl−CoA synthetase short−chain family member 1 [Source:H
2	131	1.76	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	−1.79	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	−1.61	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	216	1.32	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	163782	1.63	2e−16	3e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
7	9915	1.38	2e−16	3e−14	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
8	445	−1.48	2e−16	3e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
9	22809	1.98	2e−16	3e−14	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
10	60370	−1.33	2e−16	3e−14	1 x 39	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
11	684	−1.58	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	25758	1.61	2e−16	3e−14	9 x 3	KIAA1549−like [Source:HGNC Symbol;Acc:24836]
13	64207	−1.54	2e−16	3e−14	50 x 40	interferon regulatory factor 2 binding protein−like [Source:HG
14	343990	1.48	2e−16	3e−14	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
15	260436	2.64	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
16	394263	1.64	2e−16	3e−14	3 x 50	
17	23705	2.01	2e−16	3e−14	50 x 7	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
18	6363	2.34	2e−16	3e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
19	6366	1.92	2e−16	3e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
20	1000	1.87	2e−16	3e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.5	NULL	232	Chr	Chr 18
2	7.88	NULL	280	Chr	Chr 13
3	7.79	NULL	135	H.Tiss	WIRTH_Mucosa
4	6.96	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
5	6.87	NULL	81	BP	viral transcription
6	6.86	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
7	6.85	NULL	1135	Chr	Chr 19
8	6.64	NULL	87	BP	translational termination
9	6.51	NULL	92	BP	translational elongation
10	6.38	NULL	171	miRNA target miRBase	hsa−miR−369−3p
11	6.35	NULL	1749	MF	DNA binding
12	6.19	NULL	128	BP	translational initiation
13	6.11	NULL	1581	BP	regulation of transcription, DNA−dependent
14	6.06	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
15	6.05	NULL	92	BP	viral life cycle
16	5.87	NULL	19	BP	peptide cross−linking
17	5.82	NULL	13	BP	negative regulation of ossification
18	5.76	NULL	375	Disease	GUDJ_psoriasis down
19	5.74	NULL	16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
20	5.71	NULL	15	BP	digestive tract morphogenesis
Underexpressed					
1	−12.98	NULL	717	Chr	Chr 16
2	−12.05	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
3	−11.98	NULL	519	Chr	Chr 14
4	−10.53	NULL	51	BP	type I interferon signaling pathway
5	−10.33	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	−10.31	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	−9.61	NULL	572	Disease	GUDJ_psoriasis up
8	−9.34	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	−9.34	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
10	−8.88	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
11	−8.62	NULL	4	MMML CGS	MACIEJ_MMML 47
12	−8.53	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	−8.51	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
14	−8.32	NULL	31	BP	negative regulation of viral genome replication
15	−8.23	NULL	504	Chr	Chr 15
16	−8.08	NULL	123	BP	defense response to virus
17	−7.54	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
18	−7.19	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
19	−6.3	NULL	109	BP	response to virus
20	−6.17	NULL	127	H.Tiss	WIRTH_Muscle

GW_217

Local Summary

%DE = 0.69

metagenes = 29

genes = 333

genes in genesets = 330

genes with fdr < 0.1 = 196 (193 + / 3 −)

genes with fdr < 0.05 = 159 (156 + / 3 −)

genes with fdr < 0.01 = 128 (127 + / 1 −)

<r> metagenes = 0.91

<r> genes = 0.28

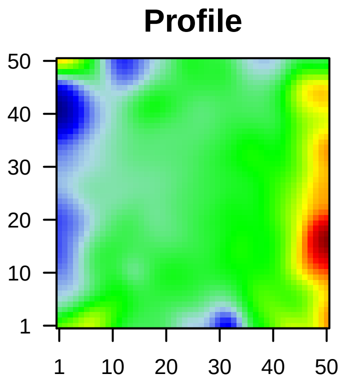
<FC> = 0.47

<shrinkage−t> = 16.57

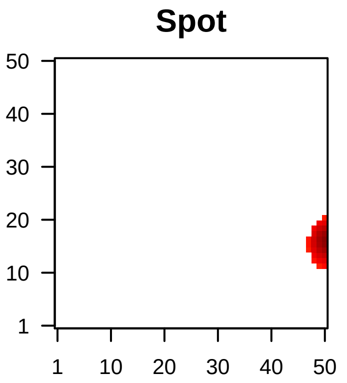
<p−value> = 0

<fdr> = 0.49

Profile



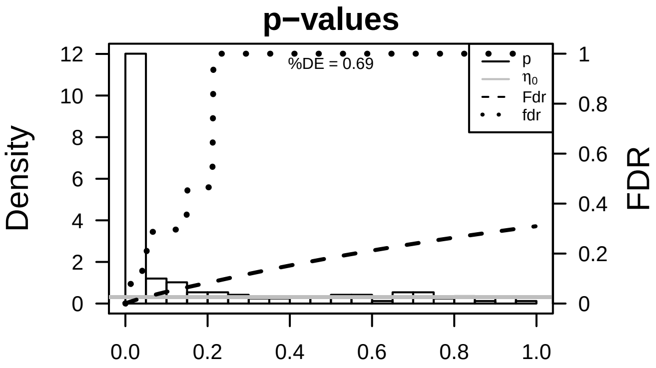
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84532	1.36	2e−16	1e−15	50 x 17	acyl−CoA synthetase short−chain family member 1 [Source:H
2	9915	1.38	2e−16	1e−15	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
3	343990	1.48	2e−16	1e−15	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
4	9071	2.08	2e−16	1e−15	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
5	1298	2.35	2e−16	1e−15	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
6	285016	1.43	2e−16	1e−15	50 x 17	family with sequence similarity 150, member B [Source:HGN
7	8857	1.89	2e−16	1e−15	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
8	2248	1.55	2e−16	1e−15	50 x 19	fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
9	2568	1.55	2e−16	1e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
10	3670	1.67	2e−16	1e−15	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
11	8543	1.5	2e−16	1e−15	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
12	728715	1.62	2e−16	1e−15	50 x 18	
13	440482	1.38	2e−16	1e−15	48 x 13	ankyrin repeat domain 20 family, member A8, pseudogene [S
14	4602	2.28	2e−16	1e−15	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
15	83988	1.46	2e−16	1e−15	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
16	9603	1.9	2e−16	1e−15	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
17	54959	1.46	2e−16	1e−15	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
18	494470	1.79	2e−16	1e−15	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
19	6228	1.76	2e−16	1e−15	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
20	57556	1.41	2e−16	1e−15	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	16.65	NULL	6 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.24	NULL	2 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
3	11.53	NULL	5 / 34	BP	thymus development
4	10.6	NULL	2 / 11	MF	enhancer sequence−specific DNA binding
5	10.49	NULL	3 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
6	10.35	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
7	10.27	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
8	10.09	NULL	4 / 14	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
9	9.77	NULL	1 / 2	miRNA target	miR−153
10	9.35	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
11	9.14	NULL	2 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
12	9.04	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
13	8.81	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
14	8.62	NULL	2 / 15	BP	embryonic digestive tract development
15	8.45	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
16	8.45	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
17	8.42	NULL	2 / 15	GSEA C2	KYNG_DNA_DAMAGE_DN
18	8.01	NULL	1 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
19	7.97	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
20	7.91	NULL	2 / 4	miRNA target	miR−204
21	7.73	NULL	2 / 19	BP	spinal cord motor neuron differentiation
22	7.67	NULL	2 / 16	GSEA C2	WU_HBX_TARGETS_3_UP
23	7.6	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
24	7.58	NULL	4 / 42	BP	B cell differentiation
25	7.51	NULL	1 / 11	BP	homeostasis of number of cells
26	7.51	NULL	1 / 11	Pathw Act	BENTINK_e2f3.2
27	7.51	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
28	7.51	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
29	7.49	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
30	7.14	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
31	7.11	NULL	2 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
32	7.11	NULL	3 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
33	7.07	NULL	4 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
34	7.04	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
35	6.89	NULL	2 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
36	6.83	NULL	2 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
37	6.81	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
38	6.81	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
39	6.76	NULL	3 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
40	6.74	NULL	2 / 16	GSEA C2	NAKAYAMA_FRA2_TARGETS

GW_217

Local Summary

%DE = 0.81

metagenes = 28

genes = 317

genes in genesets = 312

genes with fdr < 0.1 = 210 (7 + / 203 −)

genes with fdr < 0.05 = 176 (5 + / 171 −)

genes with fdr < 0.01 = 136 (5 + / 131 −)

<r> metagenes = 0.96

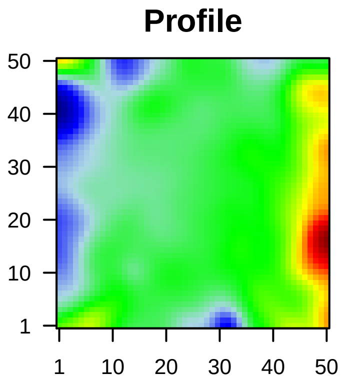
<r> genes = 0.31

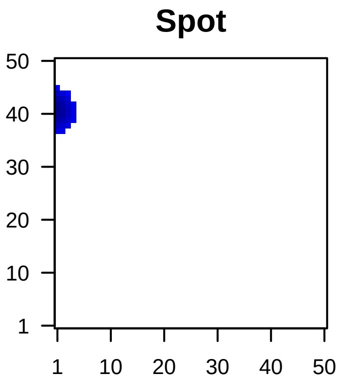
<FC> = −0.4

<shrinkage−t> = −13.98

<p−value> = 0

<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	60370	−1.33	2e−16	3e−15	1 x 39	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
2	3429	−1.79	2e−16	3e−15	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
3	4233	−1.35	2e−16	3e−15	1 x 41	met proto−oncogene [Source:HGNC Symbol;Acc:7029]
4	780854	−1.34	2e−16	3e−15	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
5	780851	−1.27	4e−15	3e−13	2 x 39	small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
6	2167	−1.25	8e−15	7e−12	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
7	50805	1.19	1e−13	2e−11	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
8	8942	−1.17	4e−13	5e−11	1 x 40	kynureninase [Source:HGNC Symbol;Acc:6469]
9	2760	−1.14	1e−12	2e−10	1 x 40	GM2 ganglioside activator [Source:HGNC Symbol;Acc:4367]
10	6513	−1.12	4e−12	2e−10	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
11	760	−1.11	6e−12	2e−09	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	133	−0.98	4e−11	2e−09	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
13	6665	−1.05	7e−11	1e−08	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Symb
14	723790	−1.02	3e−10	1e−08	2 x 38	histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
15	1001	−1	5e−10	1e−08	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
16	51200	−1	6e−10	8e−08	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
17	10397	−0.89	2e−09	8e−08	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
18	7039	0.94	5e−09	8e−08	1 x 44	transforming growth factor, alpha [Source:HGNC Symbol;Acc
19	83882	−0.94	5e−09	8e−08	1 x 43	tetraspanin 10 [Source:HGNC Symbol;Acc:29942]
20	116211	−0.94	6e−09	8e−08	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.64	NULL	2 / 2	miRNA target	miR−199a*
2	−14.63	NULL	1 / 4	MMML CGS	MACIEJ_MMML 47
3	−12.75	NULL	2 / 8	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_UP
4	−11.52	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
5	−11.11	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
6	−10.58	NULL	53 / 572	Disease	GUDJ_psoriasis up
7	−10.25	NULL	3 / 7	MMML CGS	MACIEJ_MMML 9
8	−10.03	NULL	1 / 4	miRNA target	miR−206
9	−9.9	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
10	−8.82	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
11	−8.48	NULL	5 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
12	−8.24	NULL	5 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	−7.93	NULL	1 / 6	GSEA C2	TAKAYAMA_BOUND_BY_AR
14	−7.88	NULL	2 / 12	BP	androgen metabolic process
15	−7.73	NULL	2 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN
16	−7.54	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
17	−7.45	NULL	1 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
18	−7.29	NULL	2 / 8	GSEA C2	WILLIAMS_ESR2_TARGETS_DN
19	−7.27	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
20	−7.27	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
21	−7.25	NULL	1 / 7	GSEA C2	TAKADA_GASTRIC_CANCER_COPY_NUMBER_UP
22	−7.2	NULL	2 / 8	GSEA C2	REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR
23	−7.16	NULL	2 / 11	GSEA C2	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
24	−7.14	NULL	1 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
25	−7.03	NULL	2 / 11	GSEA C2	LEI_MYB_TARGETS
26	−7	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
27	−6.92	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
28	−6.85	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
29	−6.83	NULL	9 / 119	Lymphoma	ROSOLOWSKI_green total
30	−6.82	NULL	5 / 32	CC	cell−cell adherens junction
31	−6.7	NULL	7 / 85	Glio	laffaire_hypermeth_LGG_vs_control
32	−6.52	NULL	4 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
33	−6.32	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
34	−6.26	NULL	5 / 12	BP	hemidesmosome assembly
35	−6.25	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
36	−6.14	NULL	2 / 16	GSEA C2	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN
37	−6.11	NULL	2 / 16	GSEA C2	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
38	−6.07	NULL	3 / 15	GSEA C2	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B
39	−6.06	NULL	2 / 13	GSEA C2	REACTOME_PACKAGING_OF_TELOMERE_ENDS
40	−6.02	NULL	2 / 10	BP	skeletal muscle tissue regeneration