GW_280

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1386 (908 + / 478 −)

genes with fdr < 0.1 = 1141 (775 + / 366 −)

genes with fdr < 0.05 = 858 (618 + / 240 −)

genes with fdr < 0.01 = 625 (474 + / 151 −)

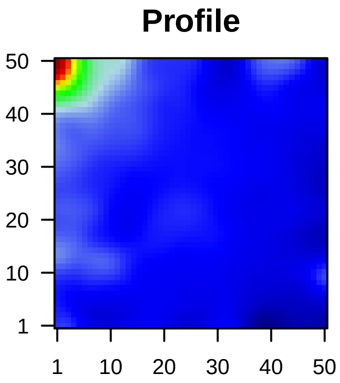
genes in genesets = 16332

<FC> = 0

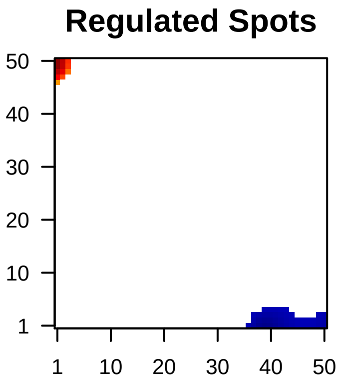
<shrinkage−t> = 0

<p−value> = 0.13

<fdr> = 0.88



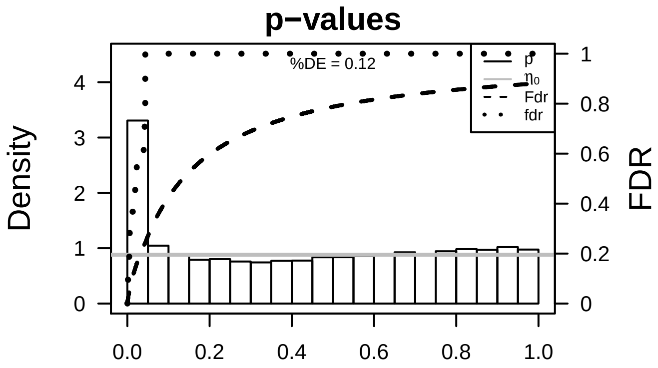
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.27	2e−16	3e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	79852	1.99	2e−16	3e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	84448	1.13	2e−16	3e−14	25 x 1	actin binding LIM protein family, member 2 [Source:HGNC Sy
4	222	1.74	2e−16	3e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	242	1.39	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	55107	2.15	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
7	147495	1.16	2e−16	3e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
8	387695	1.66	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
9	79703	1.13	2e−16	3e−14	1 x 23	chromosome 11 open reading frame 80 [Source:HGNC Sym
10	260436	1.29	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	29113	1.16	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
12	79783	1.17	2e−16	3e−14	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Sym
13	375791	1.13	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
14	51806	1.91	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
15	131076	−1.53	2e−16	3e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
16	79080	1.1	2e−16	3e−14	1 x 14	coiled−coil domain containing 86 [Source:HGNC Symbol;Acc
17	6352	1.33	2e−16	3e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
18	1001	1.29	2e−16	3e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
19	629	1.33	2e−16	3e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
20	1117	1.15	2e−16	3e−14	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	30.91	NULL	135	H.Tiss	WIRTH_Mucosa
2	26.18	NULL	572	Disease	GUDJ_psoriasis up
3	19.11	NULL	21	CC	cornified envelope
4	18	NULL	42	BP	keratinization
5	15.09	NULL	76	BP	epidermis development
6	14.07	NULL	53	BP	keratinocyte differentiation
7	9.35	NULL	19	BP	peptide cross−linking
8	8.76	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	8.74	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
10	8.17	NULL	10	MF	RAGE receptor binding
11	7.85	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
12	7.34	NULL	21	CC	desmosome
13	7.06	NULL	717	Chr	Chr 16
14	7.01	NULL	1182	CC	extracellular region
15	6.92	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
16	6.81	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	6.8	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	6.59	NULL	1146	TF	HEBENSTREIT_low expression TF
19	6.58	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
20	6.43	NULL	14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
Underexpressed					
1	−6.73	NULL	633	Chr	Chr 9
2	−6.5	NULL	504	Chr	Chr 15
3	−6.21	NULL	714	Chr	Chr 6
4	−5.49	NULL	866	Chr	Chr 12
5	−5.35	NULL	15	CC	MHC class II protein complex
6	−4.82	NULL	1749	MF	DNA binding
7	−4.73	NULL	630	Chr	Chr X
8	−4.56	NULL	162	CC	external side of plasma membrane
9	−4.53	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
10	−4.42	NULL	1574	BP	transcription, DNA−templated
11	−4.23	NULL	14	BP	cyclooxygenase pathway
12	−4.15	NULL	10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
13	−4.08	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
14	−3.94	NULL	15	GSEA C2	LE_SKI_TARGETS_UP
15	−3.93	NULL	47	BP	antigen processing and presentation
16	−3.89	NULL	11	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
17	−3.83	NULL	417	H.Tiss	WIRTH_Immune system
18	−3.8	NULL	1581	BP	regulation of transcription, DNA−dependent
19	−3.76	NULL	16	GSEA C2	LIN_APC_TARGETS
20	−3.73	NULL	84	BP	T cell receptor signaling pathway

GW_280

Local Summary

%DE = 0.99

metagenes = 12

genes = 187

genes in genesets = 182

genes with fdr < 0.1 = 182 (171 + / 11 −)

genes with fdr < 0.05 = 171 (162 + / 9 −)

genes with fdr < 0.01 = 163 (155 + / 8 −)

<r> metagenes = 0.97

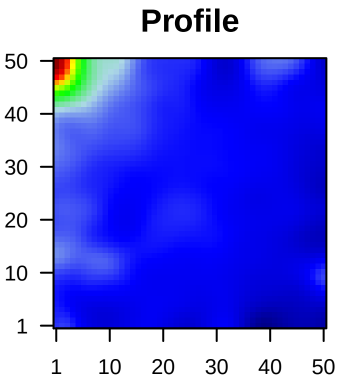
<r> genes = 0.47

<FC> = 0.86

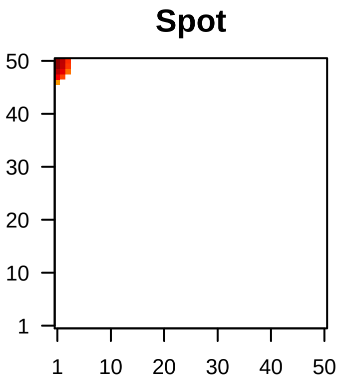
<shrinkage−t> = 30.36

<p−value> = 0

<fdr> = 0.16



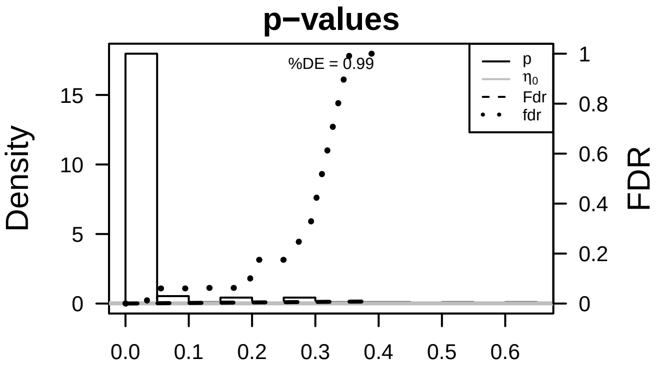
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.27	2e−16	1e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	79852	1.99	2e−16	1e−17	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	222	1.74	2e−16	1e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	242	1.39	2e−16	1e−17	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
5	387695	1.66	2e−16	1e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	29113	1.16	2e−16	1e−17	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
7	375791	1.13	2e−16	1e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
8	84518	1.57	2e−16	1e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
9	49860	1.15	2e−16	1e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1672	1.34	2e−16	1e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	1673	1.82	2e−16	1e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	93099	1.41	2e−16	1e−17	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
13	1828	1.11	2e−16	1e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	10804	2.01	2e−16	1e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	26525	1.78	2e−16	1e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
16	56300	1.75	2e−16	1e−17	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
17	43849	1.37	2e−16	1e−17	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
18	26085	1.31	2e−16	1e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
19	5653	1.18	2e−16	1e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
20	5650	1.64	2e−16	1e−17	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	55.47	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
2	43.04	NULL	18 / 21	CC	cornified envelope
3	37.5	NULL	19 / 42	BP	keratinization
4	32.16	NULL	85 / 572	Disease	GUDJ_psoriasis up
5	28.95	NULL	23 / 53	BP	keratinocyte differentiation
6	28.13	NULL	22 / 76	BP	epidermis development
7	21.45	NULL	5 / 10	MF	RAGE receptor binding
8	18.49	NULL	10 / 19	BP	peptide cross−linking
9	16.96	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	16.96	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
11	15.82	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	15.35	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	14.65	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	14.44	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	13.04	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
16	11.92	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	11.83	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
18	11.4	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
19	11.24	NULL	8 / 21	CC	desmosome
20	10.62	NULL	50 / 1182	CC	extracellular region
21	10.55	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
22	10.52	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
23	10.49	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
24	10.47	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
25	10.31	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
26	10.17	NULL	12 / 79	MF	serine−type endopeptidase inhibitor activity
27	10.16	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
28	9.9	NULL	10 / 52	BP	negative regulation of endopeptidase activity
29	9.84	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
30	9.77	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
31	9.68	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
32	9.58	NULL	2 / 17	Disease	BCHETNIA_EBM up
33	9.55	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
34	9.01	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
35	8.85	NULL	12 / 122	MF	serine−type endopeptidase activity
36	8.85	NULL	3 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
37	8.63	NULL	4 / 23	MF	peptidase inhibitor activity
38	8.45	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
39	8.44	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
40	8.42	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN

GW_280

Local Summary

%DE = 0.56

metagenes = 44

genes = 645

genes in genesets = 614

genes with fdr < 0.1 = 110 (20 + / 90 −)

genes with fdr < 0.05 = 99 (19 + / 80 −)

genes with fdr < 0.01 = 53 (15 + / 38 −)

<r> metagenes = 0.84

<r> genes = 0.37

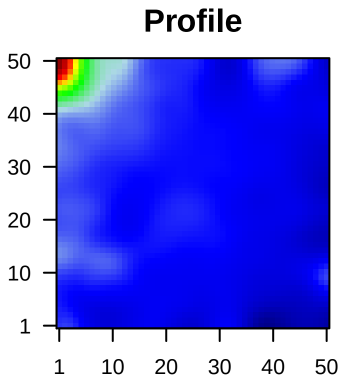
<FC> = −0.13

<shrinkage−t> = −4.68

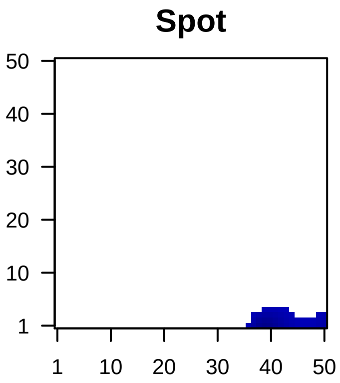
<p−value> = 0.06

<fdr> = 0.79

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	1.29	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	6352	1.33	2e−16	2e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
3	3127	−1.2	2e−16	2e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
4	25849	−1.32	2e−16	2e−14	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
5	3123	1	1e−13	5e−10	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
6	3543	0.87	2e−12	8e−08	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
7	341	0.85	3e−10	4e−07	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
8	3120	−0.81	2e−09	2e−06	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
9	3119	−0.76	1e−08	2e−06	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
10	3113	−0.76	2e−08	3e−05	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
11	9208	−0.71	1e−07	3e−05	37 x 2	leucine rich repeat (in FLII) interacting protein 1 [Source:HGN
12	91368	−0.64	2e−07	2e−04	39 x 1	CDKN2A interacting protein N−terminal like [Source:HGNC S
13	57172	0.64	2e−06	2e−04	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
14	8405	0.64	2e−06	2e−04	41 x 1	speckle−type POZ protein [Source:HGNC Symbol;Acc:11254
15	23324	0.63	3e−06	4e−04	42 x 4	mannosidase, alpha, class 2B, member 2 [Source:HGNC Syr
16	54855	0.62	4e−06	4e−04	49 x 1	family with sequence similarity 46, member C [Source:HGNC
17	399900	−0.56	7e−06	4e−04	39 x 1	
18	618	−0.6	8e−06	4e−04	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
19	5552	−0.6	8e−06	4e−04	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
20	64773	−0.59	1e−05	4e−04	41 x 3	PC−esterase domain containing 1A [Source:HGNC Symbol;A

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.26	NULL	14 / 15	CC	MHC class II protein complex
2	−14.77	NULL	16 / 47	BP	antigen processing and presentation
3	−13.86	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
4	−13.21	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
5	−12.4	NULL	10 / 28	CC	transport vesicle membrane
6	−11.04	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
7	−10.95	NULL	3 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
8	−10.52	NULL	103 / 417	H.Tiss	WIRTH_Immune system
9	−10.51	NULL	9 / 35	CC	trans−Golgi network membrane
10	−10.45	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
11	−9.79	NULL	21 / 60	BP	T cell costimulation
12	−9.1	NULL	16 / 87	BP	antigen processing and presentation of exogenous peptide antigen
13	−9.01	NULL	9 / 46	CC	endocytic vesicle membrane
14	−8.97	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
15	−8.8	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
16	−7.94	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
17	−7.85	NULL	63 / 312	BP	immune response
18	−7.75	NULL	17 / 84	BP	T cell receptor signaling pathway
19	−7.5	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
20	−7.17	NULL	4 / 10	BP	negative thymic T cell selection
21	−7.12	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
22	−6.9	NULL	5 / 12	BP	immunoglobulin mediated immune response
23	−6.73	NULL	12 / 153	CC	endosome membrane
24	−6.53	NULL	19 / 74	BP	regulation of immune response
25	−6.41	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
26	−6.24	NULL	41 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
27	−6.24	NULL	41 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
28	−6.24	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
29	−6.24	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
30	−6.12	NULL	2 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
31	−6.08	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
32	−6.07	NULL	2 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
33	−6.02	NULL	4 / 14	BP	ruffle organization
34	−5.73	NULL	2 / 7	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN
35	−5.68	NULL	1 / 6	GSEA C2	BEIER_GLIOMA_STEM_CELL_DN
36	−5.66	NULL	4 / 17	BP	RNA catabolic process
37	−5.61	NULL	20 / 215	CC	lysosomal membrane
38	−5.61	NULL	2 / 14	GSEA C2	GOLUB_ALL_VS_AML_DN
39	−5.53	NULL	3 / 13	GSEA C2	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
40	−5.51	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN

p−values