GW_191

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1853 (1053 + / 800 −)

genes with fdr < 0.1 = 1512 (883 + / 629 −)

genes with fdr < 0.05 = 1200 (720 + / 480 −)

genes with fdr < 0.01 = 788 (501 + / 287 −)

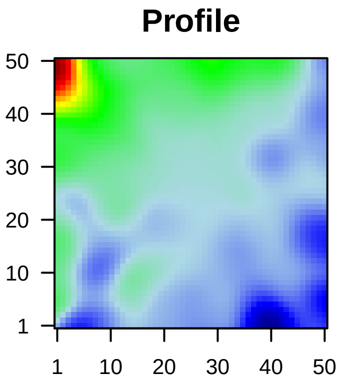
genes in genesets = 16332

<FC> = 0

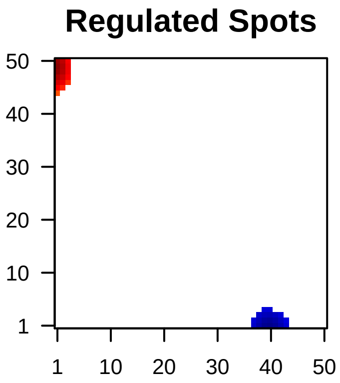
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.85



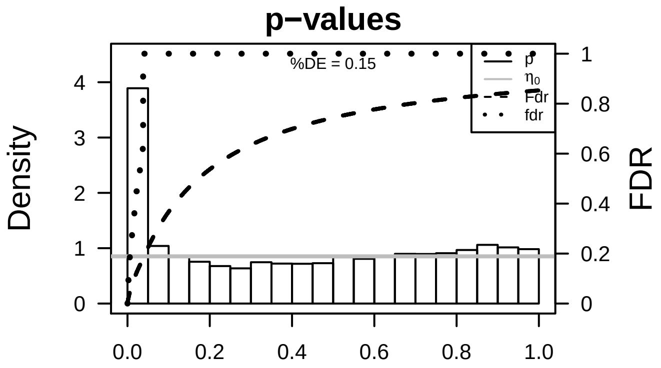
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	−1.39	2e−16	4e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	242	1.71	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
3	164284	1.7	2e−16	4e−14	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:
4	151516	1.89	2e−16	4e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
5	445	1.64	2e−16	4e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
6	10974	1.75	2e−16	4e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
7	387695	1.84	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
8	29113	1.88	2e−16	4e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
9	760	2.17	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
10	84290	1.4	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
11	148170	1.46	2e−16	4e−14	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HG
12	1041	2.57	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
13	84518	1.92	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	441520	1.42	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
15	126410	2.53	2e−16	4e−14	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
16	414325	1.44	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	1673	1.52	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
18	93099	1.94	2e−16	4e−14	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
19	1809	−1.55	2e−16	4e−14	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
20	1823	2.52	2e−16	4e−14	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]



p−values

Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	19.43	NULL	135	H.Tiss	WIRTH_Mucosa
2	18.3	NULL	572	Disease	GUDJ_psoriasis up
3	17.47	NULL	42	BP	keratinization
4	15.82	NULL	21	CC	cornified envelope
5	12.11	NULL	53	BP	keratinocyte differentiation
6	11.06	NULL	76	BP	epidermis development
7	8.33	NULL	82	CC	intermediate filament
8	8.3	NULL	19	BP	peptide cross−linking
9	8.01	NULL	21	CC	desmosome
10	7.6	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
11	7.12	NULL	44	CC	keratin filament
12	6.95	NULL	186	MF	structural molecule activity
13	6.65	NULL	10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
14	6.62	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
15	6.54	NULL	10	MF	RAGE receptor binding
16	6.48	NULL	13	BP	negative regulation of peptidase activity
17	6.11	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
18	6.06	NULL	52	BP	negative regulation of endopeptidase activity
19	5.94	NULL	21	CC	gap junction
20	5.92	NULL	79	MF	serine−type endopeptidase inhibitor activity

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−7.52	NULL	11	MF	platelet−derived growth factor binding
2	−6.3	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−6.06	NULL	12	miRNA target	miR−29c
4	−5.75	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
5	−5.73	NULL	1749	MF	DNA binding
6	−5.63	NULL	12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
7	−5.52	NULL	7	MMML CGS	MACIEJ_MMML 5
8	−5.49	NULL	250	Lymphoma	LENZ_Stromal signature 1
9	−5.41	NULL	16	MMML CGS	MACIEJ_MMML 1
10	−5.28	NULL	190	CC	extracellular matrix
11	−5.27	NULL	69	BP	extracellular matrix disassembly
12	−5.21	NULL	914	Chr	Chr 3
13	−5.08	NULL	10	BP	negative regulation of cell−substrate adhesion
14	−5.07	NULL	68	CC	collagen
15	−5.01	NULL	37	BP	collagen fibril organization
16	−4.95	NULL	743	Chr	Chr 7
17	−4.77	NULL	13	GSEA C2	HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENES
18	−4.77	NULL	274	Lymphoma	SPANG_IL21 DN
19	−4.57	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	−4.57	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up

GW_191

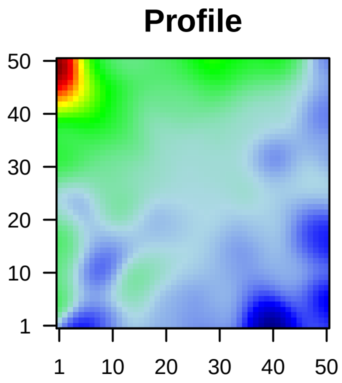
Local Summary

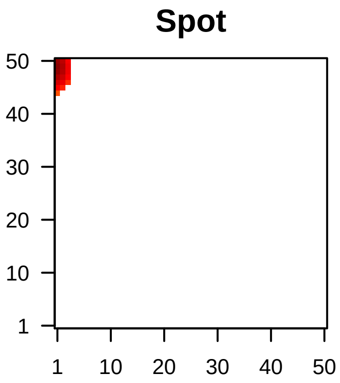
%DE = 0.85
metagenes = 18
genes = 260
genes in genesets = 254

genes with fdr < 0.1 = 199 (189 + / 10 −)
genes with fdr < 0.05 = 187 (179 + / 8 −)
genes with fdr < 0.01 = 172 (168 + / 4 −)

<r> metagenes = 0.93
<r> genes = 0.42

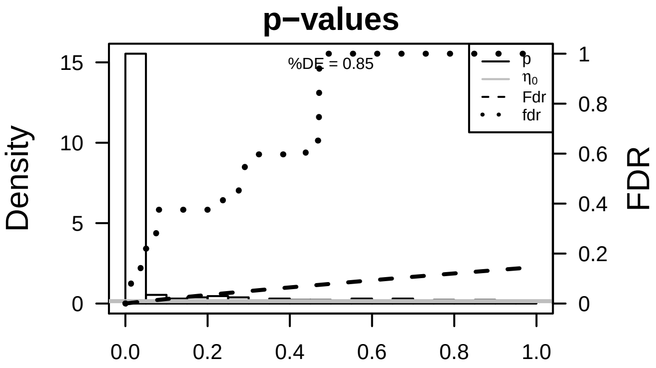
<FC> = 0.82
<shrinkage−t> = 28.87
<p−value> = 0
<fdr> = 0.27


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	242	1.71	2e−16	2e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
2	151516	1.89	2e−16	2e−16	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
3	387695	1.84	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
4	29113	1.88	2e−16	2e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
5	760	2.17	2e−16	2e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
6	84290	1.4	2e−16	2e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	1041	2.57	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
8	84518	1.92	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
9	126410	2.53	2e−16	2e−16	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
10	414325	1.44	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1673	1.52	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	93099	1.94	2e−16	2e−16	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
13	1823	2.52	2e−16	2e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
14	1828	2.62	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	9982	1.36	2e−16	2e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
16	2312	2.11	2e−16	2e−16	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
17	2697	1.85	2e−16	2e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
18	29094	1.93	2e−16	2e−16	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
19	3489	2.29	2e−16	2e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
20	26525	2.06	2e−16	2e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	37.96	NULL	18 / 21	CC	cornified envelope
2	37.77	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
3	30.98	NULL	24 / 53	BP	keratinocyte differentiation
4	28.18	NULL	19 / 42	BP	keratinization
5	25.33	NULL	102 / 572	Disease	GUDJ_psoriasis up
6	19.65	NULL	24 / 76	BP	epidermis development
7	18.61	NULL	12 / 21	CC	desmosome
8	17.68	NULL	10 / 19	BP	peptide cross−linking
9	16.5	NULL	5 / 10	MF	RAGE receptor binding
10	14.73	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	14.26	NULL	19 / 82	CC	intermediate filament
12	13.79	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
13	13.6	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
14	12.94	NULL	26 / 186	MF	structural molecule activity
15	12.75	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	12.63	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
17	12.2	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	12.2	NULL	12 / 44	CC	keratin filament
19	12.02	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
20	11.99	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
21	11.84	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
22	11.76	NULL	10 / 52	BP	negative regulation of endopeptidase activity
23	11.63	NULL	7 / 29	BP	regulation of proteolysis
24	11.56	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
25	10.9	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
26	10.55	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
27	10.42	NULL	4 / 21	CC	gap junction
28	9.73	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
29	9.61	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
30	9.33	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
31	9.31	NULL	6 / 13	BP	negative regulation of peptidase activity
32	9.25	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
33	9.16	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
34	8.8	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
35	8.74	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
36	8.56	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
37	8.43	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
38	8.3	NULL	61 / 1182	CC	extracellular region
39	8.23	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
40	8.17	NULL	3 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING

GW_191

Local Summary

%DE = 0.92

metagenes = 21

genes = 304

genes in genesets = 277

genes with fdr < 0.1 = 254 (5 + / 249 −)

genes with fdr < 0.05 = 230 (4 + / 226 −)

genes with fdr < 0.01 = 177 (3 + / 174 −)

<r> metagenes = 0.96

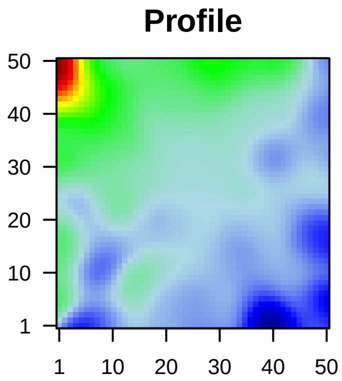
<r> genes = 0.44

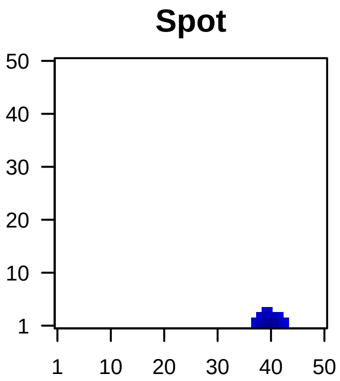
<FC> = −0.44

<shrinkage−t> = −15.4

<p−value> = 0

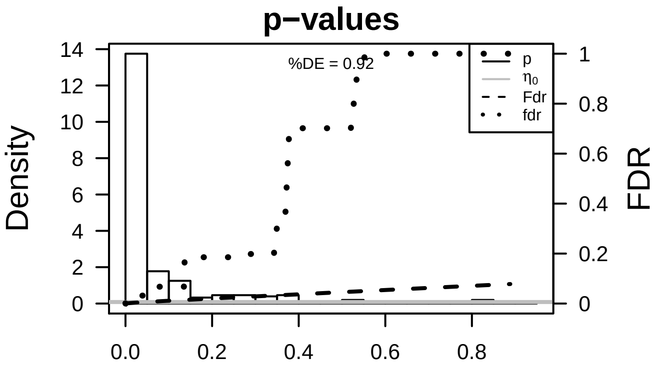
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	641737	−1.12	7e−13	9e−09	40 x 1	
2	126205	−1.05	4e−10	9e−09	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
3	3586	−0.95	1e−09	9e−09	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
4	81033	−0.93	1e−09	9e−09	39 x 1	potassium voltage−gated channel, subfamily H (eag−related),
5	4851	−1.01	2e−09	9e−09	42 x 1	notch 1 [Source:HGNC Symbol;Acc:7881]
6	250	−1.01	2e−09	3e−08	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
7	55719	−0.99	4e−09	3e−08	42 x 1	family with sequence similarity 178, member A [Source:HGN
8	90586	−0.98	5e−09	3e−08	39 x 1	amine oxidase, copper containing 4, pseudogene [Source:HG
9	440353	−0.98	6e−09	1e−07	40 x 1	
10	91368	−0.88	1e−08	1e−07	39 x 1	CDKN2A interacting protein N−terminal like [Source:HGNC S
11	400818	−0.95	2e−08	2e−07	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
12	25862	−0.93	3e−08	2e−07	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
13	79716	−0.93	3e−08	4e−07	41 x 2	aminopeptidase−like 1 [Source:HGNC Symbol;Acc:16244]
14	5143	−0.84	5e−08	4e−07	39 x 1	phosphodiesterase 4C, cAMP−specific [Source:HGNC Symb
15	374882	−0.9	7e−08	4e−07	42 x 1	transmembrane protein 205 [Source:HGNC Symbol;Acc:296
16	255031	−0.9	8e−08	4e−07	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
17	399900	−0.82	9e−08	4e−07	39 x 1	
18	10180	−0.89	1e−07	9e−07	43 x 1	RNA binding motif protein 6 [Source:HGNC Symbol;Acc:990
19	57835	−0.88	1e−07	2e−06	40 x 1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7
20	51326	−0.87	2e−07	2e−06	42 x 1	ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.65	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−9.62	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−7.35	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
4	−7.17	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
5	−6.6	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
6	−6.6	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
7	−6.55	NULL	3 / 19	BP	sprouting angiogenesis
8	−5.94	NULL	1 / 7	GSEA C2	BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
9	−5.86	NULL	2 / 13	BP	positive regulation of JAK−STAT cascade
10	−5.83	NULL	3 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
11	−5.57	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
12	−5.54	NULL	2 / 14	BP	cellular response to estradiol stimulus
13	−5.49	NULL	1 / 8	GSEA C2	KEGG_PRION_DISEASES
14	−5.39	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
15	−5.15	NULL	3 / 24	BP	negative regulation of T cell proliferation
16	−5.11	NULL	1 / 9	GSEA C2	REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES
17	−5.11	NULL	1 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
18	−4.95	NULL	2 / 14	BP	mitochondrion morphogenesis
19	−4.93	NULL	2 / 13	GSEA C2	WU_HBX_TARGETS_1_DN
20	−4.88	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
21	−4.87	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
22	−4.87	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
23	−4.8	NULL	1 / 10	BP	anagen
24	−4.8	NULL	1 / 10	BP	cardiac epithelial to mesenchymal transition
25	−4.8	NULL	1 / 10	BP	inflammatory response to antigenic stimulus
26	−4.8	NULL	1 / 10	BP	negative regulation of cell−substrate adhesion
27	−4.8	NULL	1 / 10	BP	positive regulation of keratinocyte differentiation
28	−4.8	NULL	1 / 10	BP	prostate gland epithelium morphogenesis
29	−4.8	NULL	1 / 10	BP	somatic stem cell division
30	−4.8	NULL	1 / 10	GSEA C2	CAMPS_COLON_CANCER_COPY_NUMBER_UP
31	−4.6	NULL	1 / 11	BP	negative regulation of interleukin−12 production
32	−4.6	NULL	1 / 11	GSEA C2	SU_PANCREAS
33	−4.53	NULL	1 / 11	BP	cardiac muscle tissue morphogenesis
34	−4.53	NULL	1 / 11	BP	negative regulation of myoblast differentiation
35	−4.53	NULL	1 / 11	BP	negative regulation of oligodendrocyte differentiation
36	−4.53	NULL	1 / 11	BP	neuronal stem cell maintenance
37	−4.53	NULL	1 / 11	BP	regulation of epithelial cell proliferation
38	−4.53	NULL	1 / 11	GSEA C2	BIOCARTA_PS1_PATHWAY
39	−4.53	NULL	1 / 11	GSEA C2	REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY
40	−4.52	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS