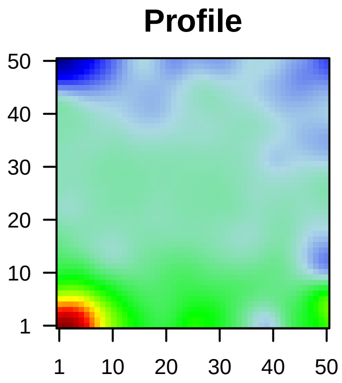
GW_284

Global Summary

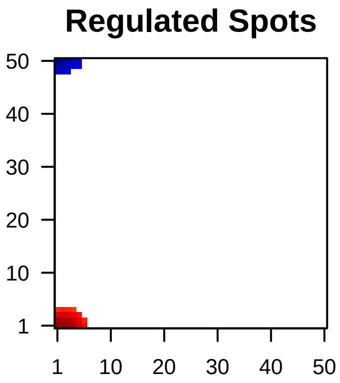
%DE = 0.16
genes with fdr < 0.2 = 1903 (1123 + / 780 −)
genes with fdr < 0.1 = 1611 (999 + / 612 −)
genes with fdr < 0.05 = 1323 (846 + / 477 −)
genes with fdr < 0.01 = 984 (651 + / 333 −)

genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.08
<fdr> = 0.84



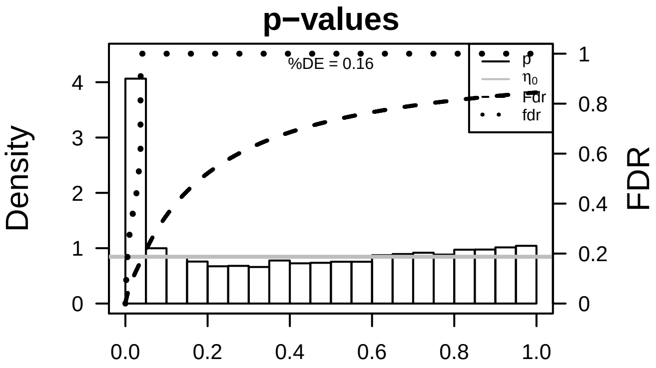
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2	1.42	2e−16	2e−14	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
2	58	2.33	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	59	1.92	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
4	70	2.92	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
5	72	2.2	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
6	131	−2.54	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	165	2.13	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
8	57016	−2.23	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
9	1109	−1.6	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
10	216	−1.37	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
11	220	2.21	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
12	218	−2.91	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
13	23452	1.83	2e−16	2e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
14	118429	1.39	2e−16	2e−14	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
15	366	1.41	2e−16	2e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
16	633	1.83	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
17	387695	−1.64	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
18	114902	1.4	2e−16	2e−14	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
19	84290	−1.81	2e−16	2e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
20	6347	1.88	2e−16	2e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	27.2	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	24.99	NULL	190	CC	extracellular matrix
3	22.26	NULL	242	BP	extracellular matrix organization
4	20.31	NULL	553	Cancer	Lembcke_Colonic Inflammation
5	19.23	NULL	69	BP	extracellular matrix disassembly
6	18.06	NULL	64	BP	collagen catabolic process
7	18.03	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	17.37	NULL	683	CC	extracellular space
9	16.56	NULL	183	CC	proteinaceous extracellular matrix
10	16.36	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	16.36	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	16.36	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	16.36	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	16.36	NULL	16	MMML CGS	MACIEJ_MMML 1
15	16.21	NULL	1182	CC	extracellular region
16	14.52	NULL	57	MF	extracellular matrix structural constituent
17	13.83	NULL	37	BP	collagen fibril organization
18	13.74	NULL	403	BP	cell adhesion
19	13.72	NULL	11	MF	platelet−derived growth factor binding
20	13.09	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
Underexpressed					
1	−25.3	NULL	135	H.Tiss	WIRTH_Mucosa
2	−10.33	NULL	53	BP	keratinocyte differentiation
3	−10.02	NULL	42	BP	keratinization
4	−9.53	NULL	21	CC	cornified envelope
5	−8.5	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
6	−7.98	NULL	4640	CC	nucleus
7	−7.59	NULL	949	CC	nucleoplasm
8	−7.09	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	−7.04	NULL	82	CC	intermediate filament
10	−6.94	NULL	12	BP	cellular aldehyde metabolic process
11	−6.72	NULL	19	BP	peptide cross−linking
12	−6.54	NULL	10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
13	−6.51	NULL	44	CC	keratin filament
14	−6.45	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
15	−6.41	NULL	1720	Chr	Chr 1
16	−6.32	NULL	21	CC	desmosome
17	−6.3	NULL	595	MF	RNA binding
18	−6.13	NULL	10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
19	−6.12	NULL	1318	CC	mitochondrion
20	−6.01	NULL	76	BP	epidermis development

GW_284

Local Summary

%DE = 0.96

metagenes = 21

genes = 314

genes in genesets = 313

genes with fdr < 0.1 = 301 (301 + / 0 −)

genes with fdr < 0.05 = 301 (301 + / 0 −)

genes with fdr < 0.01 = 289 (289 + / 0 −)

<r> metagenes = 0.95

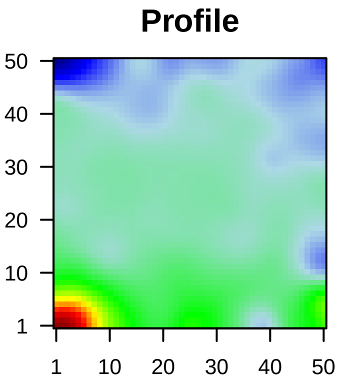
<r> genes = 0.38

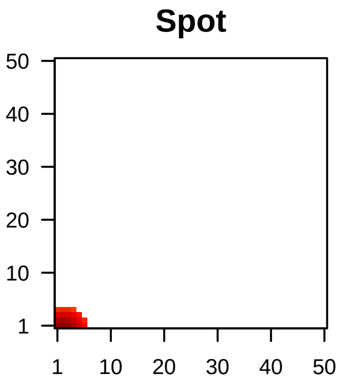
<FC> = 1.13

<shrinkage−t> = 39.58

<p−value> = 0

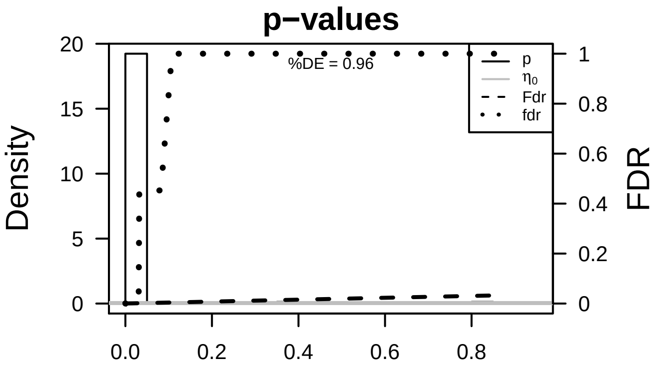
<fdr> = 0.05





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.92	2e−16	3e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	72	2.2	2e−16	3e−17	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
3	165	2.13	2e−16	3e−17	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
4	23452	1.83	2e−16	3e−17	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
5	118429	1.39	2e−16	3e−17	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
6	366	1.41	2e−16	3e−17	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
7	633	1.83	2e−16	3e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
8	114902	1.4	2e−16	3e−17	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
9	1000	1.91	2e−16	3e−17	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
10	1306	1.59	2e−16	3e−17	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
11	1277	2.44	2e−16	3e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	1278	2.14	2e−16	3e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
13	1281	2.17	2e−16	3e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
14	1282	1.49	2e−16	3e−17	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
15	1289	1.9	2e−16	3e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
16	1290	2.06	2e−16	3e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
17	1291	1.97	2e−16	3e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
18	1293	1.83	2e−16	3e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
19	83716	1.86	2e−16	3e−17	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S
20	1437	1.86	2e−16	3e−17	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	41.79	NULL	68 / 190	CC	extracellular matrix
2	38.57	NULL	82 / 250	Lymphoma	LENZ_Stromal signature 1
3	35.72	NULL	33 / 69	BP	extracellular matrix disassembly
4	35.6	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
5	34.39	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	33.87	NULL	68 / 242	BP	extracellular matrix organization
7	33.24	NULL	28 / 64	BP	collagen catabolic process
8	29.27	NULL	8 / 11	MF	platelet−derived growth factor binding
9	26.4	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	25.51	NULL	8 / 12	miRNA target	miR−29c
11	24.12	NULL	91 / 683	CC	extracellular space
12	24.11	NULL	41 / 183	CC	proteinaceous extracellular matrix
13	23.97	NULL	15 / 37	BP	collagen fibril organization
14	23.84	NULL	20 / 57	MF	extracellular matrix structural constituent
15	23.15	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
16	22.44	NULL	117 / 1182	CC	extracellular region
17	21.82	NULL	74 / 553	Cancer	Lembcke_Colonic Inflammation
18	20.16	NULL	11 / 19	MF	extracellular matrix binding
19	19.03	NULL	6 / 12	GSEA C2	LY_AGING_MIDDLE_UP
20	18.83	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
21	18.83	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
22	18.83	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
23	18.83	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
24	18.69	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
25	18.09	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
26	18.06	NULL	12 / 40	BP	cellular response to amino acid stimulus
27	17.75	NULL	12 / 35	Glio	Colman_survival_associated
28	17.68	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
29	17.67	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
30	17.45	NULL	18 / 68	CC	collagen
31	17.39	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
32	17.37	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
33	17.35	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
34	17.25	NULL	23 / 83	CC	basement membrane
35	16.92	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
36	16.61	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
37	16.47	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
38	16.27	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
39	16.14	NULL	24 / 119	Lymphoma	ROSOLOWSKI_green total
40	15.75	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET

GW_284

Local Summary

%DE = 0.96

metagenes = 13

genes = 199

genes in genesets = 195

genes with fdr < 0.1 = 174 (15 + / 159 −)

genes with fdr < 0.05 = 168 (14 + / 154 −)

genes with fdr < 0.01 = 154 (13 + / 141 −)

<r> metagenes = 0.98

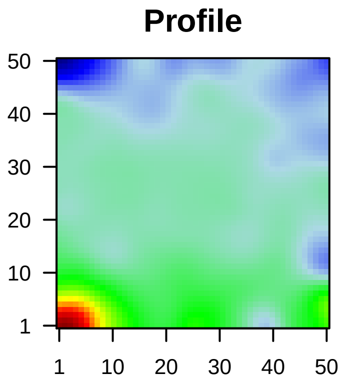
<r> genes = 0.47

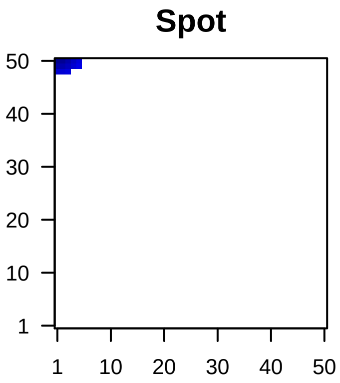
<FC> = −0.75

<shrinkage−t> = −26.31

<p−value> = 0

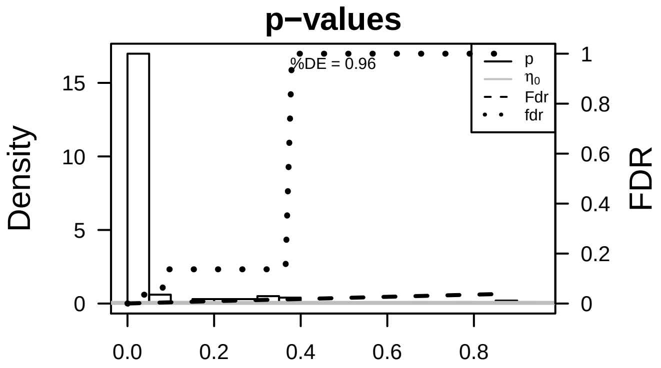
<fdr> = 0.21


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.54	2e−16	5e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.23	2e−16	5e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	218	−2.91	2e−16	5e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	387695	−1.64	2e−16	5e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
5	84290	−1.81	2e−16	5e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	9022	−1.4	2e−16	5e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
7	49860	−2.53	2e−16	5e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
8	1475	−1.75	2e−16	5e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
9	1562	−1.36	2e−16	5e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
10	414325	1.36	2e−16	5e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1673	1.54	2e−16	5e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	1828	−1.5	2e−16	5e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	115572	−1.43	2e−16	5e−17	1 x 48	family with sequence similarity 46, member B [Source:HGNC
14	163351	−1.55	2e−16	5e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
15	2941	−1.36	2e−16	5e−17	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
16	29094	−1.39	2e−16	5e−17	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
17	9314	−1.67	2e−16	5e−17	4 x 50	Kruppel−like factor 4 (gut) [Source:HGNC Symbol;Acc:6348]
18	3860	−3.62	2e−16	5e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
19	192666	−1.96	2e−16	5e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
20	3851	−2.44	2e−16	5e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−56.61	NULL	74 / 135	H.Tiss	WIRTH_Mucosa
2	−27.76	NULL	8 / 19	BP	peptide cross−linking
3	−27.26	NULL	14 / 21	CC	cornified envelope
4	−25.55	NULL	19 / 53	BP	keratinocyte differentiation
5	−25.14	NULL	16 / 42	BP	keratinization
6	−17.78	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
7	−16.2	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
8	−15.78	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
9	−14.2	NULL	3 / 12	BP	cellular aldehyde metabolic process
10	−13.76	NULL	19 / 76	BP	epidermis development
11	−13.69	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
12	−12.95	NULL	13 / 186	MF	structural molecule activity
13	−12.8	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	−12.6	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
15	−12.38	NULL	77 / 572	Disease	GUDJ_psoriasis up
16	−12.26	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
17	−11.99	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
18	−11.49	NULL	5 / 21	CC	desmosome
19	−11.18	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
20	−10.98	NULL	6 / 13	BP	negative regulation of peptidase activity
21	−10.65	NULL	4 / 44	CC	keratin filament
22	−10.33	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
23	−10.26	NULL	6 / 82	CC	intermediate filament
24	−10.1	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
25	−10.09	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
26	−10.02	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
27	−9.83	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
28	−9.47	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
29	−9.17	NULL	4 / 15	MF	retinol dehydrogenase activity
30	−9.08	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
31	−8.81	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
32	−8.8	NULL	2 / 8	TF Tissue	VAQUERIZAS_Tongue
33	−8.68	NULL	4 / 39	BP	retinoid metabolic process
34	−8.66	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
35	−8.39	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
36	−8	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
37	−8	NULL	2 / 13	MF	RNA polymerase II transcription factor binding transcription factor a
38	−7.91	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
39	−7.91	NULL	7 / 38	BP	epithelial cell differentiation
40	−7.67	NULL	5 / 51	MF	protein binding, bridging