GW_039

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1934 (1149 + / 785 −)

genes with fdr < 0.1 = 1662 (1015 + / 647 −)

genes with fdr < 0.05 = 1353 (852 + / 501 −)

genes with fdr < 0.01 = 1001 (653 + / 348 −)

genes in genesets = 16332

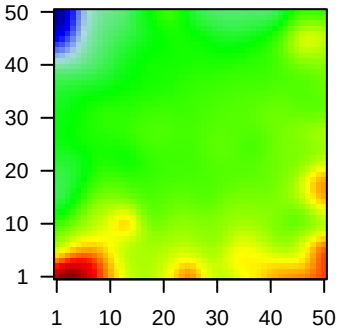
<FC> = 0

<shrinkage−t> = 0

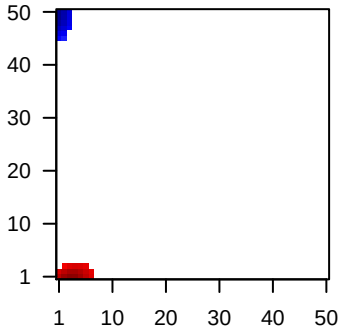
<p−value> = 0.08

<fdr> = 0.85

Profile



Regulated Spots



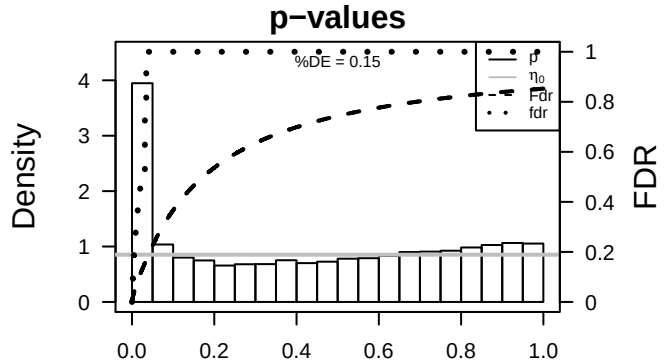
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.45	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	58	2.71	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	59	1.72	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;,
4	70	2.06	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
5	72	1.55	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
6	131	−1.69	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	165	1.96	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
8	57016	−1.66	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
9	441282	−1.47	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
10	8644	−1.41	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syr
11	1109	−1.57	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syr
12	222	−1.39	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
13	23452	1.73	2e−16	2e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
14	347	1.41	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
15	22809	1.54	2e−16	2e−14	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
16	23120	−1.48	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
17	633	1.44	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
18	664	−1.37	2e−16	2e−14	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HG
19	387695	−1.73	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symbo
20	114902	1.59	2e−16	2e−14	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	25.45	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	21.65	NULL	190	CC	extracellular matrix
3	17.11	NULL	242	BP	extracellular matrix organization
4	16.97	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	14.68	NULL	16	MMML C5	GOCIEJ_MMML 1
6	13.96	NULL	57	MF	extracellular matrix structural constituent
7	13.6	NULL	69	BP	extracellular matrix disassembly
8	13.19	NULL	37	BP	collagen fibril organization
9	12.69	NULL	183	CC	proteinaceous extracellular matrix
10	12.27	NULL	64	BP	collagen catabolic process
11	11.43	NULL	36	BP	muscle filament sliding
12	11.16	NULL	11	MF	platelet−derived growth factor binding
13	11.15	NULL	16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
14	11.07	NULL	403	BP	cell adhesion
15	10.5	NULL	553	Cancer	Lembcke_Colonic Inflammation
16	10.25	NULL	85	MF	integrin binding
17	10.07	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
18	10.03	NULL	68	CC	collagen
19	9.99	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
20	9.95	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
Underexpressed					
1	−26.17	NULL	135	H.Tiss	WIRTH_Mucosa
2	−22.26	NULL	572	Disease	GUDJ_psoriasis up
3	−17.93	NULL	21	CC	cornified envelope
4	−15.04	NULL	42	BP	keratinization
5	−13.54	NULL	53	BP	keratinocyte differentiation
6	−10.83	NULL	76	BP	epidermis development
7	−8.81	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
8	−8.46	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−8.36	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	−7.97	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	−7.95	NULL	253	BP	translation
12	−7.43	NULL	153	MF	structural constituent of ribosome
13	−7.34	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
14	−7.14	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
15	−6.84	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	−6.84	NULL	7	MMML C5	GOCIEJ_MMML 5
17	−6.81	NULL	167	CC	ribosome
18	−6.71	NULL	8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
19	−6.63	NULL	14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
20	−6.47	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN

p−values



GW_039

Local Summary

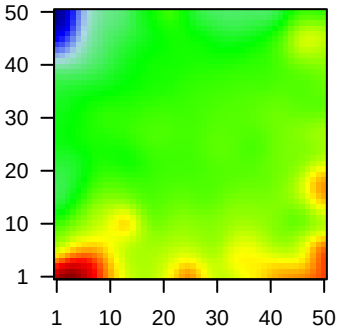
%DE = 0.9
metagenes = 19
genes = 292
genes in genesets = 291

genes with fdr < 0.1 = 259 (240 + / 19 −)
genes with fdr < 0.05 = 241 (227 + / 14 −)
genes with fdr < 0.01 = 218 (209 + / 9 −)

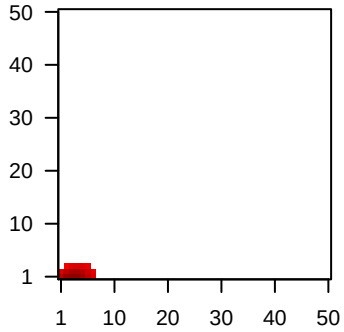
<r> metagenes = 0.96
<r> genes = 0.41

<FC> = 0.79
<shrinkage−t> = 27.5
<p−value> = 0
<fdr> = 0.2

Profile



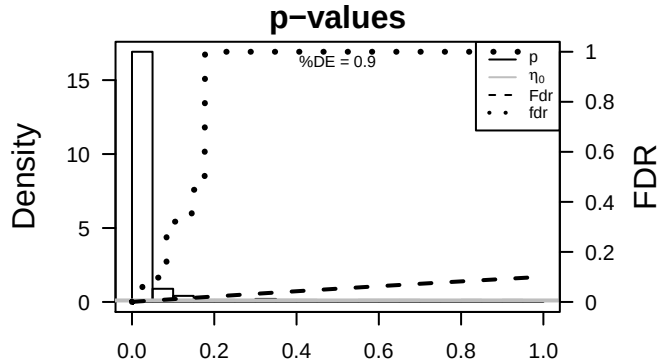
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.72	2e−16	1e−16	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;/
2	72	1.55	2e−16	1e−16	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	165	1.96	2e−16	1e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
4	23452	1.73	2e−16	1e−16	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
5	633	1.44	2e−16	1e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
6	114902	1.59	2e−16	1e−16	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
7	9315	1.43	2e−16	1e−16	3 x 1	neuronal regeneration related protein [Source:HGNC Symbol
8	1009	1.61	2e−16	1e−16	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC
9	1300	1.55	2e−16	1e−16	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
10	1307	1.51	2e−16	1e−16	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
11	1277	2	2e−16	1e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	1278	2	2e−16	1e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
13	1281	1.83	2e−16	1e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
14	1289	2.22	2e−16	1e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
15	1290	1.8	2e−16	1e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
16	1291	1.7	2e−16	1e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
17	1293	1.8	2e−16	1e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
18	81035	1.39	2e−16	1e−16	5 x 1	collectin sub−family member 12 [Source:HGNC Symbol;Acc:1
19	83716	1.74	2e−16	1e−16	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S
20	1490	1.61	2e−16	1e−16	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	42.95	NULL	80 / 250	Lymphoma	LENZ_Stromal signature 1
2	42.28	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	42.12	NULL	66 / 190	CC	extracellular matrix
4	39.71	NULL	14 / 16	MMML C6	CIEJ_MMML 1
5	32.34	NULL	30 / 69	BP	extracellular matrix disassembly
6	31.88	NULL	61 / 242	BP	extracellular matrix organization
7	30.89	NULL	26 / 64	BP	collagen catabolic process
8	30.55	NULL	8 / 11	MF	platelet−derived growth factor binding
9	27.95	NULL	14 / 37	BP	collagen fibril organization
10	27.32	NULL	21 / 57	MF	extracellular matrix structural constituent
11	24.38	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
12	23.76	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
13	23.62	NULL	8 / 12	miRNA target	−29c
14	23.12	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
15	22.56	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
16	21.56	NULL	38 / 183	CC	proteinaceous extracellular matrix
17	20.42	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
18	19.92	NULL	11 / 19	MF	extracellular matrix binding
19	18.95	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
20	18.92	NULL	15 / 68	CC	collagen
21	18.82	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
22	18.53	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
23	18.29	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
24	18.21	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
25	17.89	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
26	17.85	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
27	17.77	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
28	17.55	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
29	17.25	NULL	75 / 683	CC	extracellular space
30	17.17	NULL	10 / 40	BP	cellular response to amino acid stimulus
31	17.03	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
32	16.87	NULL	4 / 10	BP	protein heterotrimerization
33	16.8	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
34	16.02	NULL	23 / 153	CC	endoplasmic reticulum lumen
35	16	NULL	5 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
36	15.81	NULL	103 / 1182	CC	extracellular region
37	15.57	NULL	20 / 83	CC	basement membrane
38	15.3	NULL	4 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
39	15.18	NULL	16 / 85	MF	integrin binding
40	15.15	NULL	68 / 553	Cancer	Lembcke_Colonic Inflammation

GW_039

Local Summary

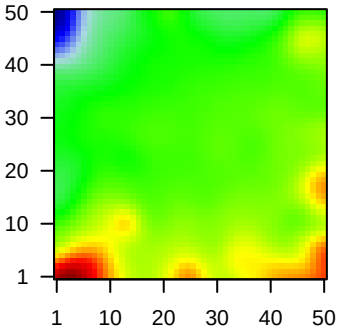
%DE = 0.97
metagenes = 16
genes = 230
genes in genesets = 224

genes with fdr < 0.1 = 207 (4 + / 203 −)
genes with fdr < 0.05 = 207 (4 + / 203 −)
genes with fdr < 0.01 = 204 (4 + / 200 −)

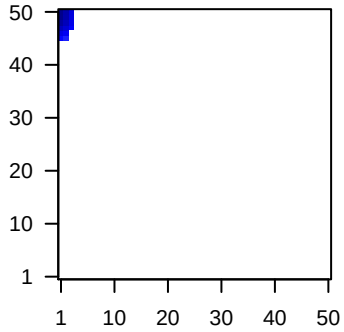
<r> metagenes = 0.94
<r> genes = 0.44

<FC> = −0.98
<shrinkage−t> = −34.37
<p−value> = 0
<fdr> = 0.12

Profile



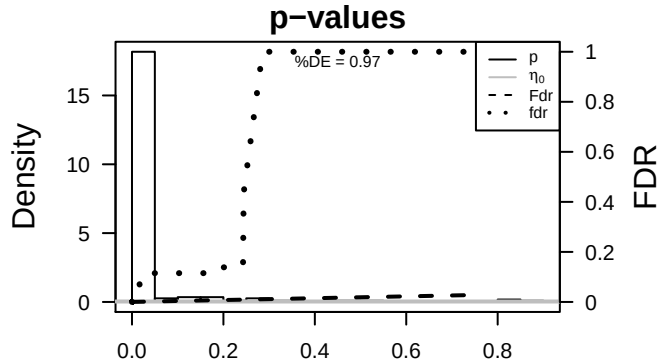
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.69	2e−16	3e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−1.66	2e−16	3e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.47	2e−16	3e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	−1.41	2e−16	3e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syr
5	222	−1.39	2e−16	3e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
6	23120	−1.48	2e−16	3e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
7	387695	−1.73	2e−16	3e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
8	375791	−1.78	2e−16	3e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symt
9	9635	−1.42	2e−16	3e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
10	9022	−1.38	2e−16	3e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
11	84518	−2.02	2e−16	3e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
12	54544	−1.5	2e−16	3e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
13	1672	−1.5	2e−16	3e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
14	55894	−1.62	2e−16	3e−17	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	414325	−2.33	2e−16	3e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1673	−1.44	2e−16	3e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	9982	−1.66	2e−16	3e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Symb
18	10804	−2.04	2e−16	3e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	2877	−1.52	2e−16	3e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
20	26525	−1.78	2e−16	3e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−55.5	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	−47.21	NULL	18 / 21	CC	cornified envelope
3	−35.47	NULL	19 / 42	BP	keratinization
4	−33.27	NULL	24 / 53	BP	keratinocyte differentiation
5	−33.1	NULL	97 / 572	Disease	GUDJ_psoriasis up
6	−24.79	NULL	23 / 76	BP	epidermis development
7	−21.46	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−19.79	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	−19.5	NULL	10 / 19	BP	peptide cross−linking
10	−19.08	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	−19.02	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−15.04	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
13	−14.96	NULL	12 / 21	CC	desmosome
14	−14.47	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
15	−14.46	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
16	−14.35	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
17	−14.27	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
18	−14.03	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
19	−13.74	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
20	−13.44	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
21	−13.41	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	−13.32	NULL	10 / 52	BP	negative regulation of endopeptidase activity
23	−13.32	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
24	−13.2	NULL	5 / 23	MF	peptidase inhibitor activity
25	−13.16	NULL	3 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
26	−12.94	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
27	−12.91	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
28	−12.47	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
29	−12.43	NULL	6 / 13	BP	negative regulation of peptidase activity
30	−11.94	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
31	−11.9	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
32	−11.41	NULL	5 / 10	MF	RAGE receptor binding
33	−11.29	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
34	−11.25	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
35	−10.66	NULL	56 / 1182	CC	extracellular region
36	−10.64	NULL	4 / 27	BP	response to bacterium
37	−10.49	NULL	3 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
38	−10.4	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
39	−10.27	NULL	2 / 11	GSEA C2	LEI_MYB_TARGETS
40	−10.26	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN