GW_057

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1431 (797 + / 634 −)

genes with fdr < 0.1 = 1246 (700 + / 546 −)

genes with fdr < 0.05 = 992 (562 + / 430 −)

genes with fdr < 0.01 = 731 (404 + / 327 −)

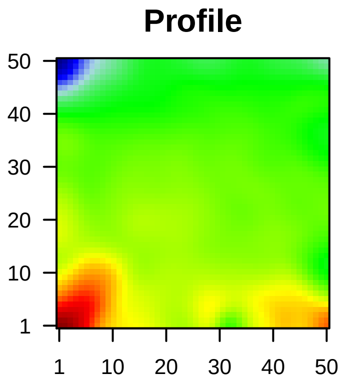
genes in genesets = 16332

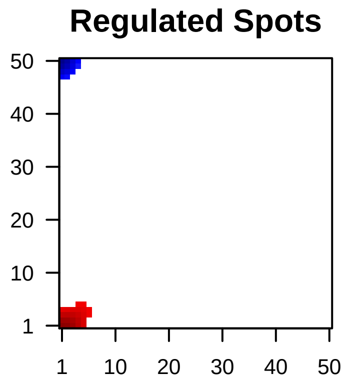
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.12

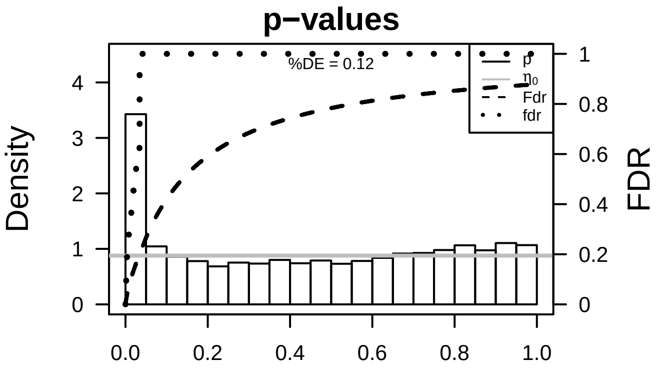
<fdr> = 0.88


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	2.3	2e−16	3e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	70	2.19	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	72	2.81	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
4	131	−3.14	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	57016	−3.72	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	441282	−2.55	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
7	218	−3.43	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
8	366	2.36	2e−16	3e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
9	387695	−2.81	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
10	760	−2.26	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
11	810	−2.89	2e−16	3e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
12	51806	−2.47	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	84290	−2.16	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
14	6364	3.06	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
15	414062	2.85	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
16	4680	−3.19	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
17	22802	−3.05	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	84518	−3.22	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
19	1490	2.22	2e−16	3e−14	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
20	3627	−2.38	2e−16	3e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.45	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	13.44	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
3	13.44	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
4	13.44	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
5	13.44	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
6	10.35	NULL	250	Lymphoma	LENZ_Stromal signature 1
7	9.99	NULL	190	CC	extracellular matrix
8	9.64	NULL	242	BP	extracellular matrix organization
9	9.64	NULL	7	MMML CGS	MACIEJ_MMML 13
10	9.47	NULL	10	BP	cellular response to zinc ion
11	9.3	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
12	9.11	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
13	9.06	NULL	11	Glio	Phillips MES up vs Prolif & PN
14	8.85	NULL	16	MMML CGS	MACIEJ_MMML 1
15	8.28	NULL	269	BP	inflammatory response
16	8	NULL	683	CC	extracellular space
17	7.76	NULL	69	BP	extracellular matrix disassembly
18	7.69	NULL	43	MF	chemokine activity
19	7.62	NULL	15	BP	negative regulation of growth
20	7.57	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
Underexpressed					
1	−32.77	NULL	135	H.Tiss	WIRTH_Mucosa
2	−20.13	NULL	572	Disease	GUDJ_psoriasis up
3	−17.63	NULL	21	CC	cornified envelope
4	−13.83	NULL	53	BP	keratinocyte differentiation
5	−13.43	NULL	42	BP	keratinization
6	−13.12	NULL	76	BP	epidermis development
7	−9.22	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
8	−8.94	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
9	−8.73	NULL	19	BP	peptide cross−linking
10	−7.92	NULL	21	CC	desmosome
11	−7.87	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−7.86	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	−7.68	NULL	12	BP	cellular aldehyde metabolic process
14	−7.61	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
15	−7.59	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
16	−7.34	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
17	−7.12	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	−7.01	NULL	13	H.Tiss	WIRTH_Tonsil
19	−6.85	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
20	−6.79	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E

GW_057

Local Summary

%DE = 0.87

metagenes = 24

genes = 326

genes in genesets = 321

genes with fdr < 0.1 = 255 (241 + / 14 −)

genes with fdr < 0.05 = 242 (230 + / 12 −)

genes with fdr < 0.01 = 213 (203 + / 10 −)

<r> metagenes = 0.96

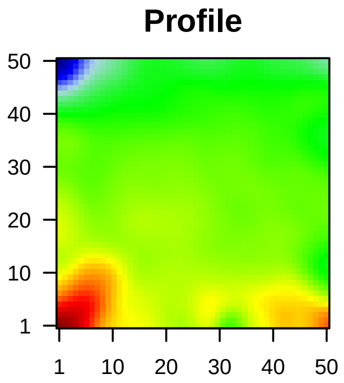
<r> genes = 0.37

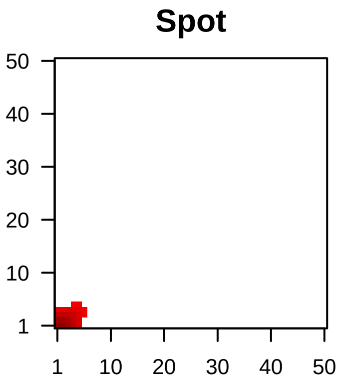
<FC> = 0.97

<shrinkage−t> = 34

<p−value> = 0

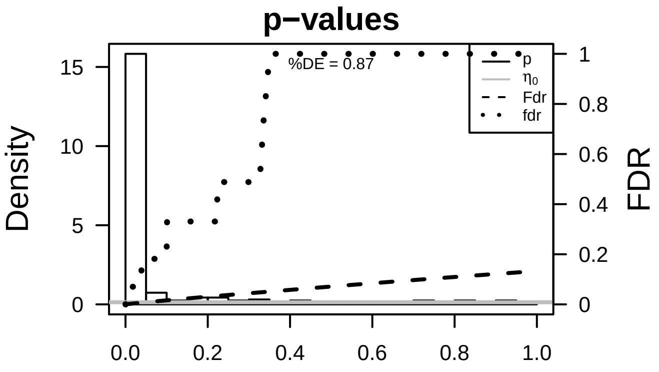
<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	2.3	2e−16	3e−16	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	72	2.81	2e−16	3e−16	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	366	2.36	2e−16	3e−16	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
4	414062	2.85	2e−16	3e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbc
5	1490	2.22	2e−16	3e−16	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
6	2920	2.17	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
7	6374	2.94	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
8	6372	3.07	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
9	3491	2.22	2e−16	3e−16	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
10	3039	2.23	2e−16	3e−16	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
11	3040	2.73	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
12	3043	2.57	2e−16	3e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
13	3553	3.11	2e−16	3e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
14	11009	2.29	2e−16	3e−16	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
15	3569	3.28	2e−16	3e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
16	3576	2.96	2e−16	3e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
17	3678	2.28	2e−16	3e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
18	4312	2.22	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
19	4314	3.31	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
20	4489	1.93	2e−16	3e−16	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.87	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	24.78	NULL	63 / 190	CC	extracellular matrix
3	24.69	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
4	24.08	NULL	68 / 242	BP	extracellular matrix organization
5	23.91	NULL	76 / 250	Lymphoma	LENZ_Stromal signature 1
6	21.79	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
7	20.86	NULL	32 / 69	BP	extracellular matrix disassembly
8	20.76	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
9	20.24	NULL	116 / 1182	CC	extracellular region
10	20.2	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
11	19.62	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
12	19.44	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
13	19.25	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
14	18.98	NULL	9 / 11	MF	platelet−derived growth factor binding
15	18.82	NULL	74 / 553	Cancer	Lembcke_Colonic Inflammation
16	18.55	NULL	88 / 683	CC	extracellular space
17	18.54	NULL	28 / 64	BP	collagen catabolic process
18	18.41	NULL	11 / 19	MF	extracellular matrix binding
19	18.16	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
20	17.3	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
21	17.05	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
22	16.97	NULL	8 / 12	miRNA target	miR−29c
23	16.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
24	16.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
25	16.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
26	16.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
27	16.7	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
28	16.67	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
29	16.62	NULL	8 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
30	16.2	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
31	16.2	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
32	15.81	NULL	8 / 43	MF	chemokine activity
33	15.59	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
34	15.54	NULL	22 / 83	CC	basement membrane
35	15.39	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
36	15.39	NULL	20 / 57	MF	extracellular matrix structural constituent
37	15.31	NULL	6 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
38	15.22	NULL	29 / 269	BP	inflammatory response
39	14.7	NULL	15 / 111	BP	chemotaxis
40	14.68	NULL	4 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN

GW_057

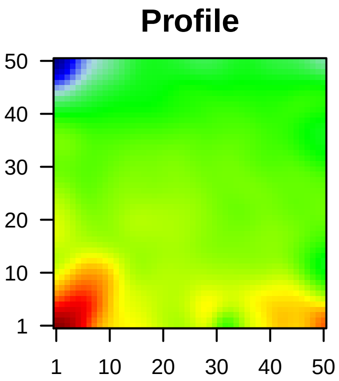
Local Summary

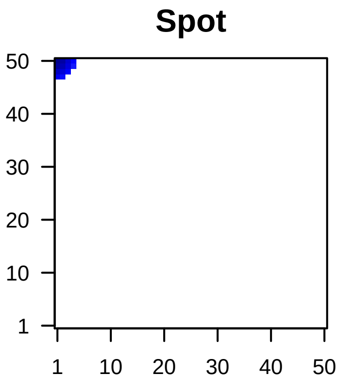
%DE = 0.93
metagenes = 13
genes = 192
genes in genesets = 187

genes with fdr < 0.1 = 170 (2 + / 168 −)
genes with fdr < 0.05 = 164 (2 + / 162 −)
genes with fdr < 0.01 = 156 (2 + / 154 −)

<r> metagenes = 0.98
<r> genes = 0.48

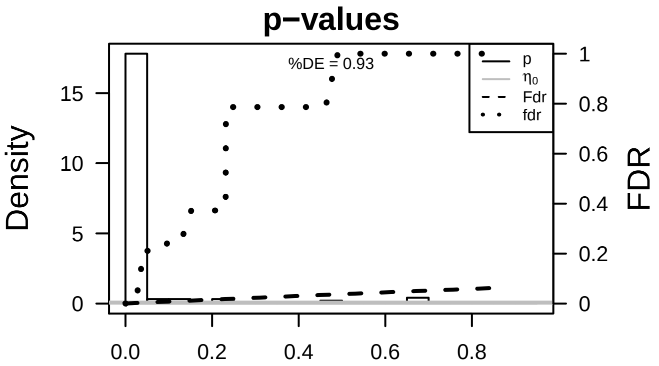
<FC> = −1.45
<shrinkage−t> = −51.2
<p−value> = 0
<fdr> = 0.16


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−3.14	2e−16	6e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−3.72	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−2.55	2e−16	6e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	218	−3.43	2e−16	6e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	387695	−2.81	2e−16	6e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
6	810	−2.89	2e−16	6e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
7	51806	−2.47	2e−16	6e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
8	84290	−2.16	2e−16	6e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	4680	−3.19	2e−16	6e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
10	22802	−3.05	2e−16	6e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	84518	−3.22	2e−16	6e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
12	1673	−2.5	2e−16	6e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1824	−2.34	2e−16	6e−17	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
14	1830	−2.11	2e−16	6e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
15	26298	−2.22	2e−16	6e−17	4 x 50	ets homologous factor [Source:HGNC Symbol;Acc:3246]
16	163351	−2.61	2e−16	6e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
17	2706	−2.23	2e−16	6e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
18	10804	−3.5	2e−16	6e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	2877	−2.42	2e−16	6e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
20	56300	−2.22	2e−16	6e−17	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−63.46	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
2	−41.5	NULL	16 / 21	CC	cornified envelope
3	−32.51	NULL	19 / 42	BP	keratinization
4	−29.31	NULL	21 / 53	BP	keratinocyte differentiation
5	−27.21	NULL	82 / 572	Disease	GUDJ_psoriasis up
6	−24.62	NULL	9 / 19	BP	peptide cross−linking
7	−23.97	NULL	20 / 76	BP	epidermis development
8	−21.08	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	−15.85	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
10	−15.53	NULL	3 / 12	BP	cellular aldehyde metabolic process
11	−14.72	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	−14.6	NULL	6 / 13	BP	negative regulation of peptidase activity
13	−14.3	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
14	−13.48	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
15	−13.26	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
16	−12.67	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
17	−12.38	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
18	−11.81	NULL	5 / 21	CC	desmosome
19	−11.49	NULL	18 / 186	MF	structural molecule activity
20	−11.39	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
21	−11.29	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
22	−10.98	NULL	8 / 44	CC	keratin filament
23	−10.95	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	−10.78	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
25	−10.64	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
26	−10.59	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
27	−10.1	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
28	−10.02	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
29	−9.92	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
30	−9.91	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
31	−9.87	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
32	−9.73	NULL	3 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
33	−9.56	NULL	50 / 1182	CC	extracellular region
34	−9.46	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
35	−9.42	NULL	12 / 122	MF	serine−type endopeptidase activity
36	−9.36	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
37	−8.72	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
38	−8.68	NULL	2 / 15	CC	connexon complex
39	−8.66	NULL	10 / 82	CC	intermediate filament
40	−8.66	NULL	8 / 52	BP	negative regulation of endopeptidase activity