GW_231

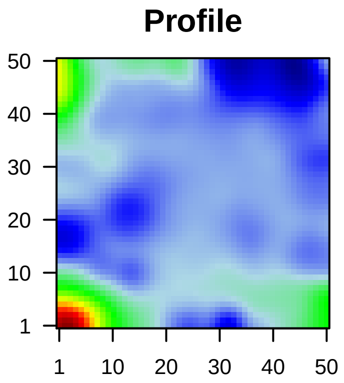
Global Summary

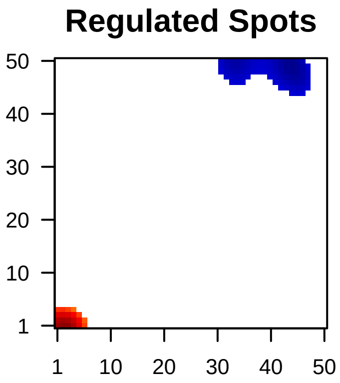
%DE = 0.14

genes with fdr < 0.2 = 1976 (1162 + / 814 −)
genes with fdr < 0.1 = 1437 (915 + / 522 −)
genes with fdr < 0.05 = 1168 (786 + / 382 −)
genes with fdr < 0.01 = 827 (601 + / 226 −)

genes in genesets = 16332

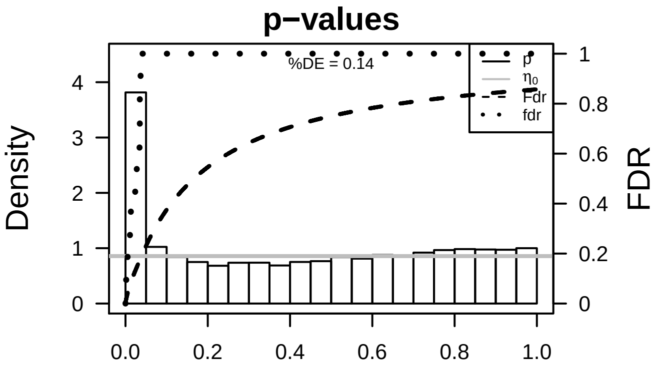
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.1
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.53	2e−16	3e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	131	1.5	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	165	1.94	2e−16	3e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
4	216	1.63	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
5	401138	2.47	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
6	55107	1.72	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
7	200315	1.33	2e−16	3e−14	1 x 40	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
8	60370	1.61	2e−16	3e−14	1 x 39	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
9	9531	1.46	2e−16	3e−14	11 x 50	BCL2−associated athanogene 3 [Source:HGNC Symbol;Acc:
10	25805	1.54	2e−16	3e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
11	633	1.36	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
12	80195	1.27	2e−16	3e−14	7 x 50	transmembrane protein 254 [Source:HGNC Symbol;Acc:258
13	51806	−1.25	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
14	57172	1.36	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
15	6364	1.8	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
16	414062	−1.29	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
17	6355	−1.49	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
18	8900	1.3	2e−16	3e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
19	1000	1.57	2e−16	3e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
20	1300	1.44	2e−16	3e−14	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	24.15	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	21.24	NULL	190	CC	extracellular matrix
3	20.87	NULL	242	BP	extracellular matrix organization
4	15.97	NULL	69	BP	extracellular matrix disassembly
5	15.6	NULL	1182	CC	extracellular region
6	15.55	NULL	183	CC	proteinaceous extracellular matrix
7	15.47	NULL	683	CC	extracellular space
8	15	NULL	64	BP	collagen catabolic process
9	14.44	NULL	403	BP	cell adhesion
10	14.01	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
11	13.77	NULL	135	H.Tiss	WIRTH_Mucosa
12	12.74	NULL	2659	CC	plasma membrane
13	12.74	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	12.52	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
15	12.52	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
16	12.52	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
17	12.52	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
18	12.47	NULL	37	BP	collagen fibril organization
19	11.82	NULL	16	MMML CGS	MACIEJ_MMML 1
20	11.74	NULL	553	Cancer	Lembcke_Colonic Inflammation
Underexpressed					
1	−12.85	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−12.85	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−10.24	NULL	1318	CC	mitochondrion
4	−10.23	NULL	370	BP	mitotic cell cycle
5	−10.15	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	−9.07	NULL	940	MF	nucleic acid binding
7	−8.31	NULL	949	CC	nucleoplasm
8	−7.66	NULL	7	MMML CGS	MACIEJ_MMML 9
9	−7.64	NULL	595	MF	RNA binding
10	−7.37	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
11	−6.91	NULL	83	BP	respiratory electron transport chain
12	−6.61	NULL	304	CC	mitochondrial inner membrane
13	−6.41	NULL	579	CC	nucleolus
14	−6.41	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
15	−6.39	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
16	−6.37	NULL	153	MF	structural constituent of ribosome
17	−6.32	NULL	123	BP	defense response to virus
18	−6.31	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
19	−6.31	NULL	755	Lymphoma	SPANG_BCR UP
20	−6.31	NULL	15	GSEA C2	LY_AGING_MIDDLE_DN

GW_231

Local Summary

%DE = 0.85

metagenes = 21

genes = 314

genes in genesets = 313

genes with fdr < 0.1 = 236 (222 + / 14 −)

genes with fdr < 0.05 = 220 (207 + / 13 −)

genes with fdr < 0.01 = 201 (191 + / 10 −)

<r> metagenes = 0.95

<r> genes = 0.38

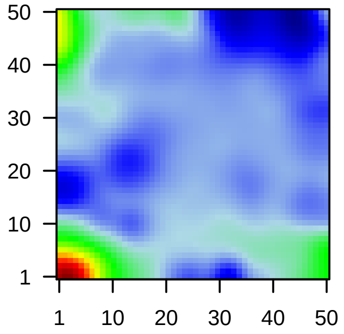
<FC> = 0.6

<shrinkage−t> = 21.19

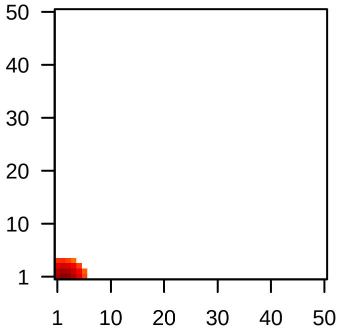
<p−value> = 0

<fdr> = 0.29

Profile

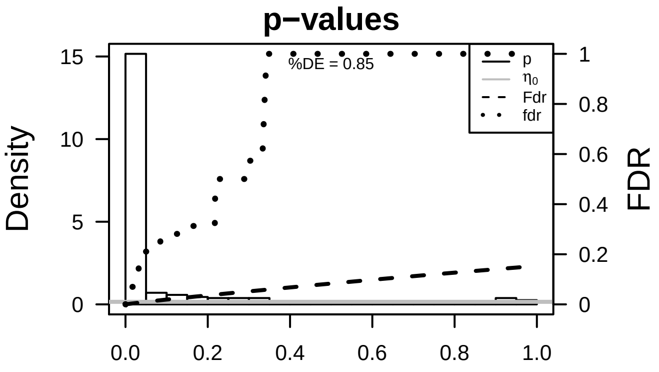


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.53	2e−16	3e−16	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	165	1.94	2e−16	3e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
3	633	1.36	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
4	414062	−1.29	2e−16	3e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
5	1000	1.57	2e−16	3e−16	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
6	1300	1.44	2e−16	3e−16	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
7	1277	1.9	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
8	1278	1.73	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
9	1281	1.39	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
10	1289	1.35	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
11	1290	1.57	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
12	1293	1.52	2e−16	3e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
13	1490	1.46	2e−16	3e−16	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
14	115908	1.45	2e−16	3e−16	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
15	3491	1.51	2e−16	3e−16	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
16	10272	1.26	2e−16	3e−16	1 x 4	follistatin−like 3 (secreted glycoprotein) [Source:HGNC Symb
17	26585	1.41	2e−16	3e−16	2 x 1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbo
18	3678	1.49	2e−16	3e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
19	4319	2.83	2e−16	3e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
20	4320	2.5	2e−16	3e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	40.02	NULL	68 / 190	CC	extracellular matrix
2	37.64	NULL	82 / 250	Lymphoma	LENZ_Stromal signature 1
3	35.62	NULL	68 / 242	BP	extracellular matrix organization
4	34.08	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	33.63	NULL	33 / 69	BP	extracellular matrix disassembly
6	32.71	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
7	32.63	NULL	28 / 64	BP	collagen catabolic process
8	29.77	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
9	28.02	NULL	15 / 37	BP	collagen fibril organization
10	26.23	NULL	11 / 19	MF	extracellular matrix binding
11	25.93	NULL	8 / 11	MF	platelet−derived growth factor binding
12	24.72	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	24.62	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
14	23.14	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
15	22.88	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
16	22.76	NULL	41 / 183	CC	proteinaceous extracellular matrix
17	22.21	NULL	5 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
18	21.61	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
19	21.34	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
20	20.64	NULL	20 / 57	MF	extracellular matrix structural constituent
21	20.46	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
22	20.38	NULL	8 / 12	miRNA target	miR−29c
23	20.37	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
24	19.55	NULL	91 / 683	CC	extracellular space
25	18.99	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
26	18.86	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
27	18.74	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
28	18.59	NULL	18 / 68	CC	collagen
29	17.91	NULL	117 / 1182	CC	extracellular region
30	17.34	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
31	17.33	NULL	4 / 14	GSEA C2	COWLING_MYCN_TARGETS
32	17.32	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
33	17.16	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
34	17.15	NULL	12 / 40	BP	cellular response to amino acid stimulus
35	17.13	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
36	16.79	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
37	16.66	NULL	6 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
38	16.54	NULL	7 / 16	GSEA C2	ZHU_CMV_ALL_DN
39	16.31	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
40	16.31	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up

GW_231

Local Summary

%DE = 0.72

metagenes = 82

genes = 997

genes in genesets = 981

genes with fdr < 0.1 = 415 (22 + / 393 −)

genes with fdr < 0.05 = 342 (20 + / 322 −)

genes with fdr < 0.01 = 167 (9 + / 158 −)

<r> metagenes = 0.73

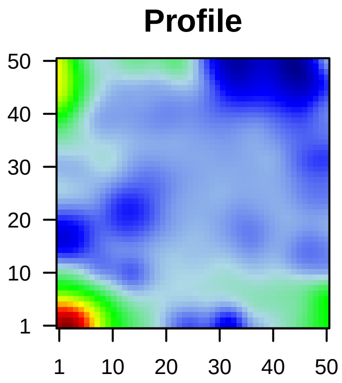
<r> genes = 0.22

<FC> = −0.25

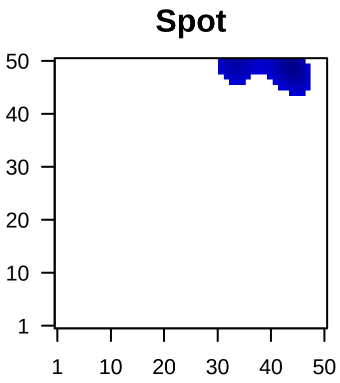
<shrinkage−t> = −8.6

<p−value> = 0.03

<fdr> = 0.66



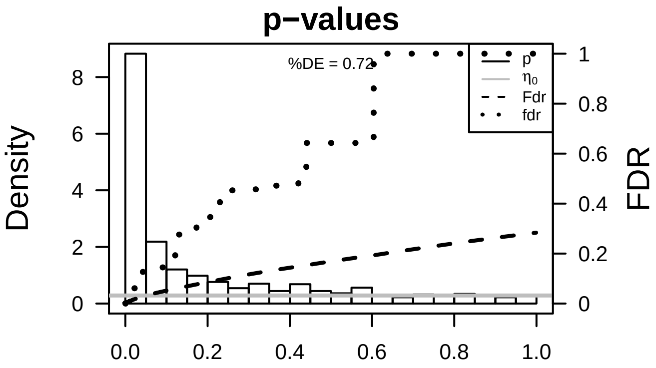
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	899	−0.95	2e−10	2e−07	45 x 46	cyclin F [Source:HGNC Symbol;Acc:1591]
2	100093630	−0.92	1e−09	9e−07	32 x 48	small nucleolar RNA host gene 8 (non−protein coding) [Sourc
3	29088	−0.88	4e−09	1e−06	36 x 50	mitochondrial ribosomal protein L15 [Source:HGNC Symbol;
4	8364	−0.79	1e−08	1e−06	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
5	891	−0.85	1e−08	1e−06	44 x 49	cyclin B1 [Source:HGNC Symbol;Acc:1579]
6	23580	0.84	2e−08	1e−06	47 x 45	CDC42 effector protein (Rho GTPase binding) 4 [Source:HG
7	51053	−0.84	2e−08	8e−06	45 x 49	geminin, DNA replication inhibitor [Source:HGNC Symbol;Ac
8	10799	−0.81	8e−08	8e−06	34 x 50	ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;
9	983	0.8	1e−07	8e−06	44 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:1722]
10	8500	0.79	1e−07	8e−06	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (P
11	1870	−0.79	1e−07	3e−05	46 x 45	E2F transcription factor 2 [Source:HGNC Symbol;Acc:3114]
12	91057	−0.78	2e−07	5e−05	46 x 47	coiled−coil domain containing 34 [Source:HGNC Symbol;Acc
13	890	−0.75	5e−07	5e−05	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]
14	128178	−0.74	7e−07	5e−05	47 x 45	EDAR−associated death domain [Source:HGNC Symbol;Acc
15	79023	−0.74	7e−07	5e−05	42 x 50	nucleoporin 37kDa [Source:HGNC Symbol;Acc:29929]
16	728492	−0.73	1e−06	5e−05	35 x 48	small EDRK−rich factor 1B (centromeric) [Source:HGNC Sym
17	6240	−0.73	1e−06	5e−05	45 x 48	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:104
18	9585	−0.72	1e−06	5e−05	44 x 46	kinesin family member 20B [Source:HGNC Symbol;Acc:7212
19	11198	−0.72	2e−06	5e−05	44 x 46	suppressor of Ty 16 homolog (S. cerevisiae) [Source:HGNC
20	10721	−0.71	2e−06	5e−05	46 x 48	polymerase (DNA directed), theta [Source:HGNC Symbol;Ac



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.21	NULL	102 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−36.21	NULL	102 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−23.48	NULL	136 / 370	BP	mitotic cell cycle
4	−20.28	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	−19.86	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
6	−17.86	NULL	58 / 149	BP	DNA replication
7	−17.34	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
8	−16.74	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
9	−16.62	NULL	176 / 949	CC	nucleoplasm
10	−16.62	NULL	20 / 30	BP	DNA strand elongation involved in DNA replication
11	−16.53	NULL	130 / 530	Cancer	Lembcke_Normal vs Adenoma
12	−15.35	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
13	−14.75	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
14	−14.6	NULL	27 / 56	CC	chromosome, centromeric region
15	−14.28	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
16	−14.13	NULL	11 / 16	Cancer	WOLFER_overlap genes
17	−13.8	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
18	−13.78	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
19	−13.61	NULL	26 / 57	Glio	developing astrocytes
20	−13.51	NULL	15 / 22	BP	DNA replication initiation
21	−13.5	NULL	9 / 11	BP	mitotic metaphase plate congression
22	−13.43	NULL	31 / 66	CC	condensed chromosome kinetochore
23	−13.4	NULL	75 / 232	BP	mitosis
24	−13.15	NULL	14 / 21	BP	telomere maintenance via semi−conservative replication
25	−12.88	NULL	12 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
26	−12.76	NULL	11 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	−12.65	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
28	−12.6	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
29	−12.52	NULL	12 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
30	−12.28	NULL	7 / 10	CC	large ribosomal subunit
31	−12.19	NULL	49 / 153	MF	structural constituent of ribosome
32	−12.18	NULL	14 / 24	BP	telomere maintenance via recombination
33	−12.15	NULL	50 / 148	BP	G1/S transition of mitotic cell cycle
34	−12	NULL	10 / 16	GSEA C2	REACTOME_LAGGING_STRAND_SYNTHESIS
35	−11.84	NULL	11 / 16	GSEA C2	KEGG_MISMATCH_REPAIR
36	−11.71	NULL	13 / 22	BP	CENP−A containing nucleosome assembly at centromere
37	−11.63	NULL	9 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
38	−11.63	NULL	12 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
39	−11.52	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
40	−11.5	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA