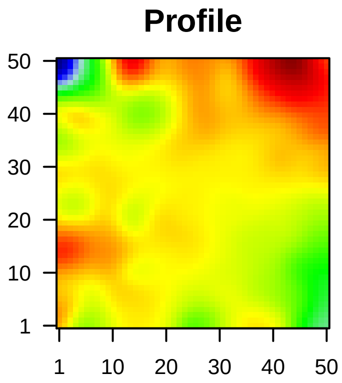
GW_201

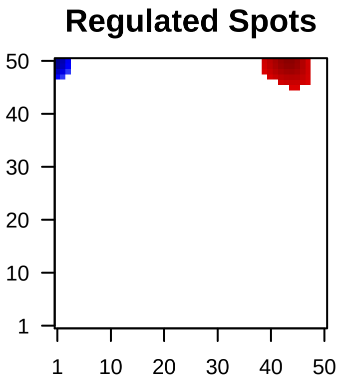
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1718 (873 + / 845 −)
genes with fdr < 0.1 = 1359 (694 + / 665 −)
genes with fdr < 0.05 = 1025 (501 + / 524 −)
genes with fdr < 0.01 = 716 (337 + / 379 −)

genes in genesets = 16332

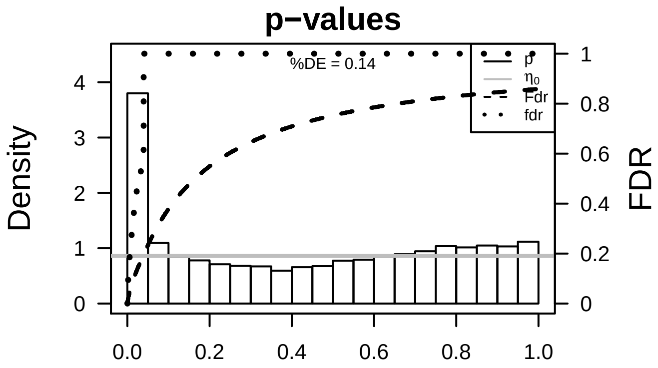
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.12
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	3.01	2e−16	4e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	2.66	2e−16	4e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	57016	1.88	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	8644	3.15	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	2.92	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	501	−1.97	2e−16	4e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
7	387695	−2.13	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
8	339512	1.72	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
9	26256	1.93	2e−16	4e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
10	810	−1.58	2e−16	4e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
11	51806	−1.65	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
12	84290	−1.81	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	1066	2.8	2e−16	4e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
14	22802	−1.76	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	84518	−2.69	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	54544	−1.71	2e−16	4e−14	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	−2.53	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1410	−1.7	2e−16	4e−14	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
19	1475	−1.97	2e−16	4e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
20	1476	−1.65	2e−16	4e−14	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.83	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	12.83	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	10.7	NULL	370	BP	mitotic cell cycle
4	9.48	NULL	1033	Chr	Chr 2
5	8.77	NULL	949	CC	nucleoplasm
6	7.77	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
7	7.57	NULL	530	Cancer	Lembcke_Normal vs Adenoma
8	7.35	NULL	1720	Chr	Chr 1
9	7.23	NULL	1233	TF	KIM_MYC targets
10	7.22	NULL	298	BP	DNA repair
11	7.07	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
12	7.04	NULL	232	BP	mitosis
13	7	NULL	866	Chr	Chr 12
14	6.94	NULL	149	BP	DNA replication
15	6.68	NULL	148	BP	G1/S transition of mitotic cell cycle
16	6.6	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
17	6.58	NULL	15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
18	6.51	NULL	4640	CC	nucleus
19	6.37	NULL	39	BP	retinoid metabolic process
20	5.91	NULL	519	Chr	Chr 14
Underexpressed					
1	−27.2	NULL	135	H.Tiss	WIRTH_Mucosa
2	−22.4	NULL	21	CC	cornified envelope
3	−17.87	NULL	42	BP	keratinization
4	−15.6	NULL	53	BP	keratinocyte differentiation
5	−14.84	NULL	76	BP	epidermis development
6	−12.88	NULL	19	BP	peptide cross−linking
7	−11.04	NULL	699	Chr	Chr 5
8	−10.91	NULL	572	Disease	GUDJ_psoriasis up
9	−10.5	NULL	1135	Chr	Chr 19
10	−8.77	NULL	1182	CC	extracellular region
11	−8.57	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−8.29	NULL	21	CC	desmosome
13	−7.82	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	−7.45	NULL	553	Cancer	Lembcke_Colonic Inflammation
15	−7.43	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
16	−7.3	NULL	14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
17	−7.14	NULL	15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
18	−7.13	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	−6.67	NULL	10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
20	−6.5	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE

GW_201

Local Summary

%DE = 0.64

metagenes = 43

genes = 551

genes in genesets = 547

genes with fdr < 0.1 = 227 (221 + / 6 −)

genes with fdr < 0.05 = 218 (212 + / 6 −)

genes with fdr < 0.01 = 150 (145 + / 5 −)

<r> metagenes = 0.89

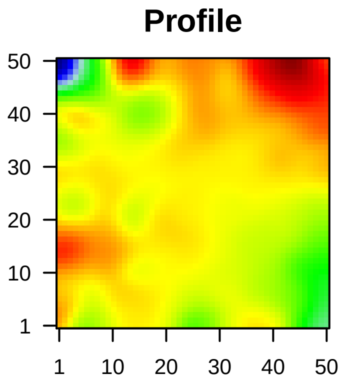
<r> genes = 0.32

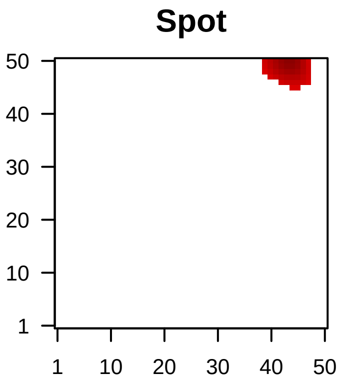
<FC> = 0.38

<shrinkage−t> = 13.21

<p−value> = 0.01

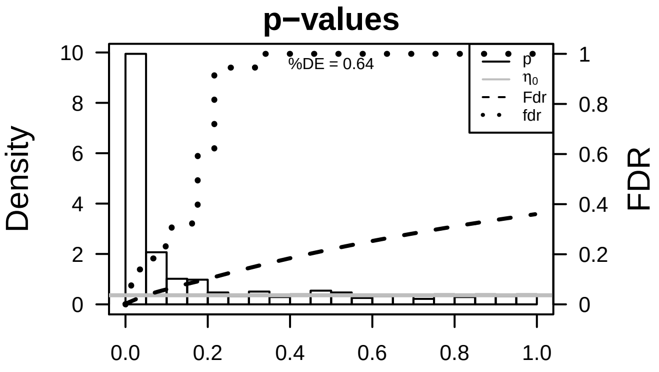
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3992	1.44	3e−13	3e−10	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
2	7153	1.4	2e−12	2e−09	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
3	8500	1.34	1e−11	3e−09	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
4	134147	1.31	3e−11	3e−08	40 x 48	carboxymethylenebutenolidase homolog (Pseudomonas) [So
5	55872	1.26	2e−10	3e−07	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
6	3251	1.17	3e−09	3e−07	42 x 50	hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
7	9918	1.16	4e−09	3e−07	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
8	54517	1.15	5e−09	7e−07	41 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:
9	7272	1.13	9e−09	7e−07	44 x 50	TTK protein kinase [Source:HGNC Symbol;Acc:12401]
10	7804	1.12	1e−08	7e−07	41 x 50	low density lipoprotein receptor−related protein 8, apolipoprot
11	259266	1.12	2e−08	2e−06	45 x 49	asp (abnormal spindle) homolog, microcephaly associated (D
12	9928	1.1	2e−08	2e−06	44 x 50	kinesin family member 14 [Source:HGNC Symbol;Acc:19181]
13	26872	1.09	3e−08	2e−06	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
14	9055	1.08	4e−08	3e−06	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
15	10024	1.06	7e−08	3e−06	45 x 47	trophinin associated protein [Source:HGNC Symbol;Acc:1232
16	81831	1.06	7e−08	3e−06	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym
17	55247	1.06	8e−08	5e−06	43 x 50	nei endonuclease VIII−like 3 (E. coli) [Source:HGNC Symbol;
18	151188	1.05	1e−07	9e−06	43 x 50	ADP−ribosylation−like factor 6 interacting protein 6 [Source:H
19	1163	1.04	2e−07	1e−05	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC S
20	51087	1.02	2e−07	1e−05	47 x 46	Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	42.62	NULL	95 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	42.62	NULL	95 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	26.38	NULL	115 / 370	BP	mitotic cell cycle
4	25.14	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	25.05	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
6	20.92	NULL	24 / 57	Glio	developing astrocytes
7	20.49	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
8	20.27	NULL	9 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
9	19.72	NULL	115 / 530	Cancer	Lembcke_Normal vs Adenoma
10	17.68	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
11	16.94	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
12	16.9	NULL	59 / 232	BP	mitosis
13	16.73	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
14	16.38	NULL	50 / 149	BP	DNA replication
15	16.1	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
16	15.77	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
17	15.66	NULL	13 / 18	BP	spindle organization
18	15.63	NULL	135 / 949	CC	nucleoplasm
19	15.36	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
20	15.18	NULL	41 / 148	BP	G1/S transition of mitotic cell cycle
21	14.7	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
22	14.46	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
23	14.31	NULL	11 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
24	14.16	NULL	11 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
25	13.85	NULL	11 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
26	13.54	NULL	72 / 572	Disease	GUDJ_psoriasis up
27	13.48	NULL	24 / 66	CC	condensed chromosome kinetochore
28	13.48	NULL	11 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
29	13.47	NULL	18 / 30	BP	DNA strand elongation involved in DNA replication
30	13.28	NULL	9 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
31	13.1	NULL	24 / 56	CC	chromosome, centromeric region
32	13.09	NULL	7 / 10	CC	nuclear pore outer ring
33	13.01	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
34	12.99	NULL	15 / 35	BP	mitotic nuclear envelope disassembly
35	12.93	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
36	12.37	NULL	6 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICA
37	12.28	NULL	11 / 15	GSEA C2	CHANG_CYCLING_GENES
38	12.08	NULL	22 / 67	BP	chromosome segregation
39	11.96	NULL	13 / 22	BP	DNA replication initiation
40	11.87	NULL	6 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY

GW_201

Local Summary

%DE = 0.97

metagenes = 11

genes = 165

genes in genesets = 160

genes with fdr < 0.1 = 154 (12 + / 142 −)

genes with fdr < 0.05 = 151 (11 + / 140 −)

genes with fdr < 0.01 = 144 (11 + / 133 −)

<r> metagenes = 0.98

<r> genes = 0.49

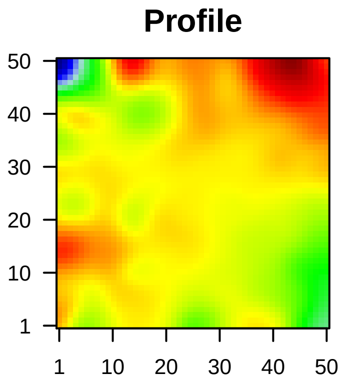
<FC> = −1.15

<shrinkage−t> = −40.82

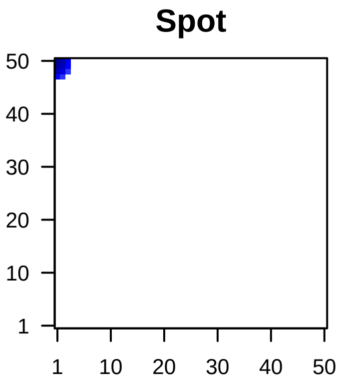
<p−value> = 0

<fdr> = 0.11

Profile



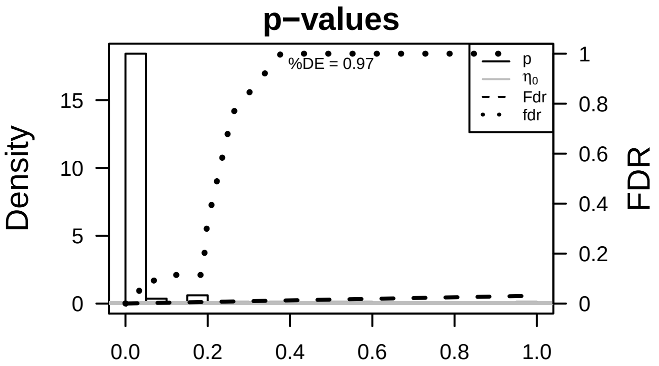
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.88	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	8644	3.15	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	387695	−2.13	2e−16	2e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
4	810	−1.58	2e−16	2e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
5	84290	−1.81	2e−16	2e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	22802	−1.76	2e−16	2e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	−2.69	2e−16	2e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	−1.71	2e−16	2e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	−2.53	2e−16	2e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1475	−1.97	2e−16	2e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	1476	−1.65	2e−16	2e−17	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
12	1672	−1.81	2e−16	2e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	414325	−2.15	2e−16	2e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1673	−3.54	2e−16	2e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
15	1824	−1.83	2e−16	2e−17	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
16	1828	−1.68	2e−16	2e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
17	1830	−1.86	2e−16	2e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
18	2706	−1.94	2e−16	2e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
19	10804	−2.76	2e−16	2e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
20	2877	2.39	2e−16	2e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−52.32	NULL	70 / 135	H.Tiss	WIRTH_Mucosa
2	−52.24	NULL	16 / 21	CC	cornified envelope
3	−41.9	NULL	19 / 42	BP	keratinization
4	−35.49	NULL	21 / 53	BP	keratinocyte differentiation
5	−29.76	NULL	18 / 76	BP	epidermis development
6	−29.33	NULL	9 / 19	BP	peptide cross−linking
7	−25.02	NULL	76 / 572	Disease	GUDJ_psoriasis up
8	−18.29	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−14.94	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	−14.74	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−14.1	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−14.1	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
13	−13.88	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
14	−13.86	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	−13.79	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
16	−13.16	NULL	18 / 186	MF	structural molecule activity
17	−12.78	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
18	−12.54	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
19	−12.19	NULL	5 / 10	MF	RAGE receptor binding
20	−12.17	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
21	−12	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
22	−11.8	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
23	−11.43	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
24	−11.29	NULL	5 / 21	CC	desmosome
25	−10.44	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
26	−10.18	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	−10.09	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
28	−10.01	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
29	−9.77	NULL	6 / 51	MF	protein binding, bridging
30	−9.66	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
31	−9.42	NULL	8 / 44	CC	keratin filament
32	−9.21	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
33	−8.76	NULL	6 / 13	BP	negative regulation of peptidase activity
34	−8.59	NULL	4 / 23	MF	peptidase inhibitor activity
35	−8.49	NULL	3 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
36	−8.46	NULL	2 / 15	CC	connexon complex
37	−8.31	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
38	−8.26	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
39	−8.19	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
40	−8.17	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_