GW_189

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1834 (1013 + / 821 −)

genes with fdr < 0.1 = 1477 (802 + / 675 −)

genes with fdr < 0.05 = 1128 (600 + / 528 −)

genes with fdr < 0.01 = 740 (396 + / 344 −)

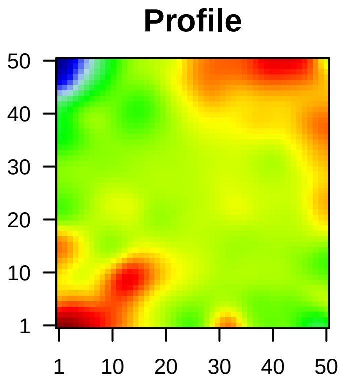
genes in genesets = 16332

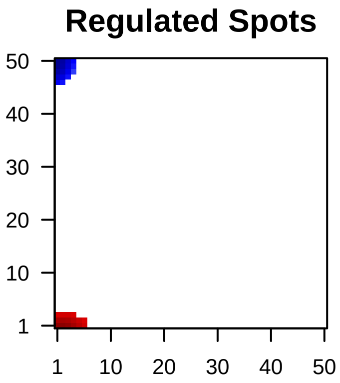
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

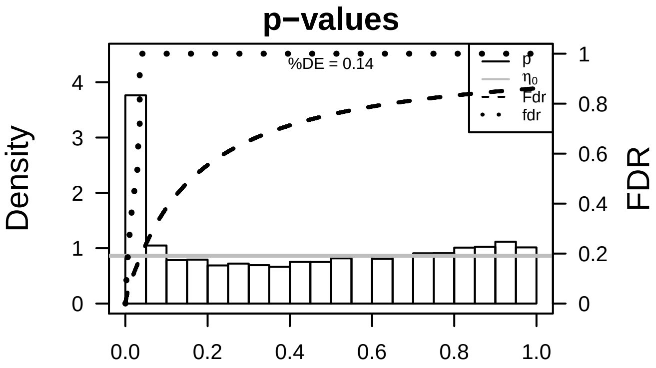
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.56	2e−16	4e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−1.85	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−1.92	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.67	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	220	2.15	2e−16	4e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
6	387695	−2.18	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
7	56892	1.47	2e−16	4e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
8	51806	−1.84	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
9	875	1.65	2e−16	4e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
10	6364	2.55	2e−16	4e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
11	6366	1.39	2e−16	4e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
12	6355	1.67	2e−16	4e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
13	1152	−1.8	2e−16	4e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
14	1308	−1.57	2e−16	4e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
15	1281	1.25	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
16	1363	1.5	2e−16	4e−14	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
17	541466	1.49	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A1 [Source:HGNC S
18	441520	3.05	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
19	441521	1.57	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
20	140690	1.62	2e−16	4e−14	18 x 11	CCCTC−binding factor (zinc finger protein)−like [Source:HGN


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	9.66	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	9.02	NULL	31	BP	negative regulation of viral genome replication
3	8.73	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
4	8.59	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
5	8.31	NULL	534	Chr	Chr 8
6	8.17	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	8.11	NULL	743	Chr	Chr 7
8	7.79	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
9	7.77	NULL	4	MMML CGS	MACIEJ_MMML 47
10	7.75	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	7.4	NULL	51	BP	type I interferon signaling pathway
12	6.94	NULL	123	BP	defense response to virus
13	6.83	NULL	109	BP	response to virus
14	6.71	NULL	253	BP	translation
15	6.68	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
16	6.45	NULL	11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
17	6.34	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
18	6.26	NULL	119	Lymphoma	ROSOLOWSKI_green total
19	6.23	NULL	595	MF	RNA binding
20	6.19	NULL	630	Chr	Chr X
Underexpressed					
1	−23.61	NULL	135	H.Tiss	WIRTH_Mucosa
2	−9.9	NULL	21	CC	cornified envelope
3	−9.71	NULL	42	BP	keratinization
4	−9.51	NULL	76	BP	epidermis development
5	−9.3	NULL	21	CC	desmosome
6	−8.83	NULL	15	CC	MHC class II protein complex
7	−8.11	NULL	82	CC	intermediate filament
8	−7.65	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
9	−7.56	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	−7.46	NULL	53	BP	keratinocyte differentiation
11	−7.36	NULL	633	Chr	Chr 9
12	−6.85	NULL	44	CC	keratin filament
13	−6.79	NULL	13	H.Tiss	WIRTH_Tonsil
14	−6.74	NULL	14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
15	−6.73	NULL	186	MF	structural molecule activity
16	−6.71	NULL	12	BP	hemidesmosome assembly
17	−6.5	NULL	572	Disease	GUDJ_psoriasis up
18	−6.2	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
19	−6.12	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
20	−6	NULL	918	Chr	Chr 17

GW_189

Local Summary

%DE = 0.64

metagenes = 16

genes = 259

genes in genesets = 258

genes with fdr < 0.1 = 127 (119 + / 8 −)

genes with fdr < 0.05 = 121 (115 + / 6 −)

genes with fdr < 0.01 = 88 (84 + / 4 −)

<r> metagenes = 0.96

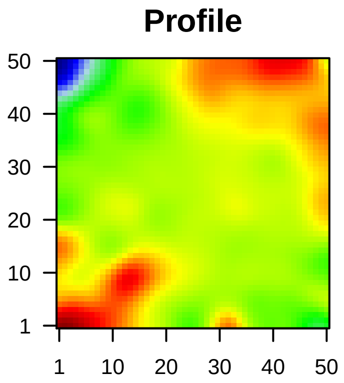
<r> genes = 0.41

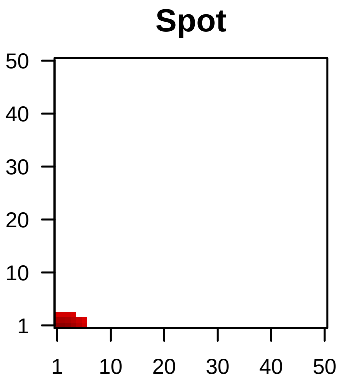
<FC> = 0.41

<shrinkage−t> = 14.26

<p−value> = 0

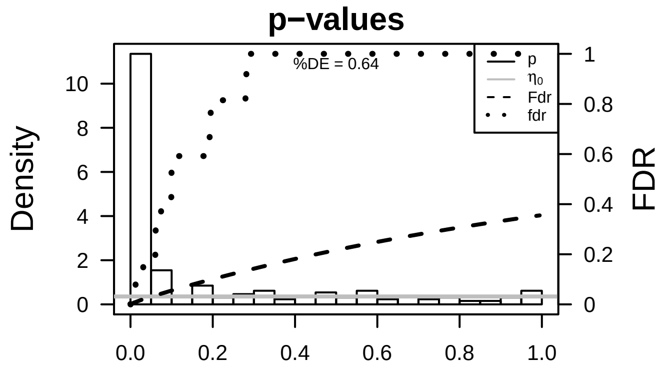
<fdr> = 0.51





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1281	1.25	2e−16	2e−15	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
2	6372	1.41	2e−16	2e−15	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
3	54749	2.16	2e−16	2e−15	5 x 1	ependymin related 1 [Source:HGNC Symbol;Acc:17572]
4	3576	1.75	2e−16	2e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
5	3956	1.44	2e−16	2e−15	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
6	10962	1.61	2e−16	2e−15	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
7	4316	1.47	2e−16	2e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
8	12	3.71	2e−16	2e−15	1 x 1	
9	8910	1.78	2e−16	2e−15	6 x 1	sarcoglycan, epsilon [Source:HGNC Symbol;Acc:10808]
10	8406	2.11	2e−16	2e−15	2 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Syr
11	6781	1.64	2e−16	2e−15	1 x 3	stanniocalcin 1 [Source:HGNC Symbol;Acc:11373]
12	7130	1.42	2e−16	2e−15	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN
13	1462	1.46	2e−16	2e−15	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
14	72	1.32	4e−16	5e−13	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
15	6447	1.26	8e−15	5e−13	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
16	1290	1.25	1e−14	1e−11	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
17	140606	1.2	1e−13	2e−11	5 x 1	Selenoprotein M [Source:UniProtKB/Swiss−Prot;Acc:Q8WW
18	3490	1.18	4e−13	1e−10	3 x 1	insulin−like growth factor binding protein 7 [Source:HGNC Sy
19	221395	1.14	2e−12	2e−10	5 x 1	G protein−coupled receptor 116 [Source:HGNC Symbol;Acc:
20	4314	1.12	4e−12	3e−10	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.33	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	23.83	NULL	8 / 11	MF	platelet−derived growth factor binding
3	22.95	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	22.72	NULL	8 / 12	miRNA target	miR−29c
5	21.33	NULL	67 / 190	CC	extracellular matrix
6	20.99	NULL	76 / 250	Lymphoma	LENZ_Stromal signature 1
7	19.95	NULL	31 / 69	BP	extracellular matrix disassembly
8	18.73	NULL	1 / 2	MMML CGS	MACIEJ_MMML 46
9	17.81	NULL	27 / 64	BP	collagen catabolic process
10	17.41	NULL	61 / 242	BP	extracellular matrix organization
11	17.21	NULL	1 / 2	miRNA target	miR−101b
12	16.49	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
13	15.4	NULL	19 / 57	MF	extracellular matrix structural constituent
14	15.26	NULL	66 / 553	Cancer	Lembcke_Colonic Inflammation
15	14.67	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
16	14.46	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
17	14.39	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	14.39	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	14.39	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	14.39	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	14.39	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
22	14.37	NULL	10 / 40	BP	cellular response to amino acid stimulus
23	14.34	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
24	14.29	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
25	14.04	NULL	78 / 683	CC	extracellular space
26	13.66	NULL	14 / 37	BP	collagen fibril organization
27	13.34	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
28	13.15	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
29	13.15	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
30	12.91	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
31	12.51	NULL	104 / 1182	CC	extracellular region
32	12.13	NULL	6 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
33	11.96	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
34	11.82	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
35	11.64	NULL	3 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
36	11.62	NULL	36 / 183	CC	proteinaceous extracellular matrix
37	11.55	NULL	4 / 14	GSEA C2	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP
38	11.47	NULL	2 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCO
39	11.43	NULL	1 / 6	GSEA C2	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_
40	11.25	NULL	7 / 43	MF	chemokine activity

GW_189

Local Summary

%DE = 0.9

metagenes = 17

genes = 233

genes in genesets = 227

genes with fdr < 0.1 = 183 (9 + / 174 −)

genes with fdr < 0.05 = 175 (9 + / 166 −)

genes with fdr < 0.01 = 151 (5 + / 146 −)

<r> metagenes = 0.96

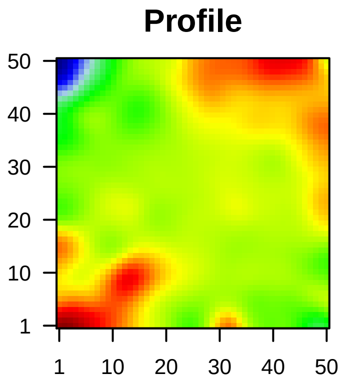
<r> genes = 0.46

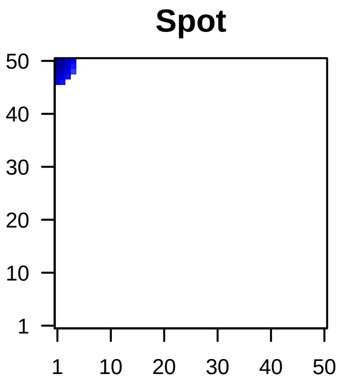
<FC> = −0.65

<shrinkage−t> = −22.78

<p−value> = 0

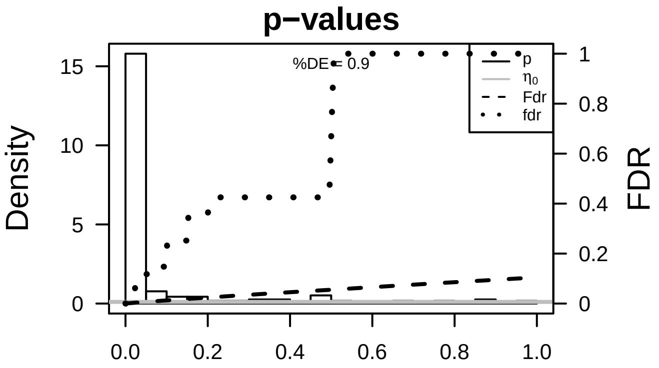
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.56	2e−16	2e−16	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−1.85	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−1.92	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.67	2e−16	2e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	387695	−2.18	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	51806	−1.84	2e−16	2e−16	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
7	9547	−1.95	2e−16	2e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
8	1828	−1.38	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
9	9982	−1.72	2e−16	2e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
10	53833	−1.36	2e−16	2e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
11	3848	−1.73	2e−16	2e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
12	192666	−1.37	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
13	3851	−1.87	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
14	286887	−1.31	2e−16	2e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
15	84648	−1.66	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
16	3963	−1.51	2e−16	2e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
17	653499	−1.41	2e−16	2e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
18	8581	−1.52	2e−16	2e−16	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
19	5493	−1.49	2e−16	2e−16	1 x 50	periplakin [Source:HGNC Symbol;Acc:9273]
20	6337	−1.78	2e−16	2e−16	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−58.46	NULL	88 / 135	H.Tiss	WIRTH_Mucosa
2	−30.67	NULL	19 / 21	CC	cornified envelope
3	−24.74	NULL	19 / 42	BP	keratinization
4	−22.47	NULL	95 / 572	Disease	GUDJ_psoriasis up
5	−21.74	NULL	9 / 21	CC	desmosome
6	−21.44	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
7	−21.37	NULL	24 / 53	BP	keratinocyte differentiation
8	−19.63	NULL	11 / 19	BP	peptide cross−linking
9	−17.44	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
10	−14.5	NULL	24 / 76	BP	epidermis development
11	−14.34	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
12	−13.85	NULL	13 / 82	CC	intermediate filament
13	−13.25	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
14	−12.9	NULL	9 / 44	CC	keratin filament
15	−11.33	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
16	−11.3	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−11.24	NULL	22 / 186	MF	structural molecule activity
18	−10.76	NULL	3 / 12	BP	cellular aldehyde metabolic process
19	−10.52	NULL	4 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
20	−10.5	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
21	−10.42	NULL	4 / 15	MF	retinol dehydrogenase activity
22	−10.34	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
23	−10.14	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
24	−9.9	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
25	−9.5	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
26	−9.06	NULL	2 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
27	−9.01	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
28	−8.99	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
29	−8.92	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
30	−8.77	NULL	4 / 39	BP	retinoid metabolic process
31	−8.7	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
32	−8.7	NULL	2 / 12	MF	retinol binding
33	−8.67	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
34	−8.63	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
35	−8.53	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
36	−8.3	NULL	2 / 13	BP	retinoic acid metabolic process
37	−8.25	NULL	8 / 51	MF	protein binding, bridging
38	−8.21	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
39	−8.1	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
40	−7.84	NULL	8 / 38	BP	epithelial cell differentiation