GW_240

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2147 (1146 + / 1001 −)

genes with fdr < 0.1 = 1593 (884 + / 709 −)

genes with fdr < 0.05 = 1417 (801 + / 616 −)

genes with fdr < 0.01 = 953 (547 + / 406 −)

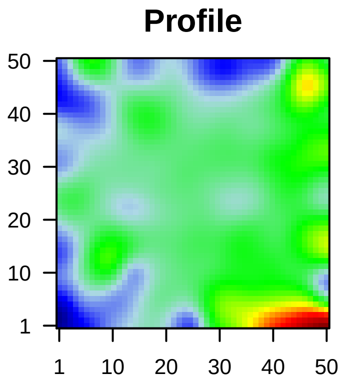
genes in genesets = 16332

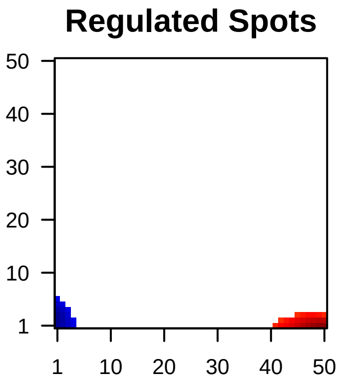
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

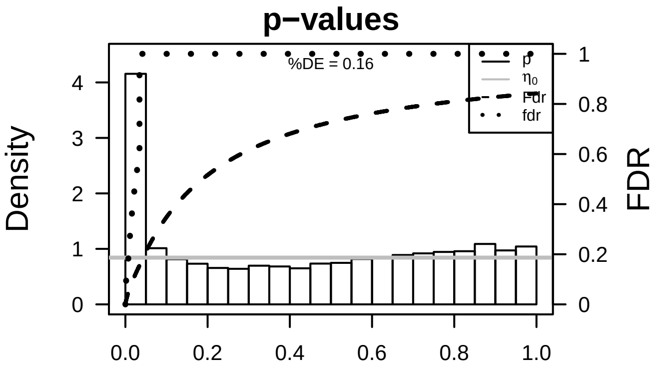
<fdr> = 0.84


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.58	2e−16	3e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	58	−1.44	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	57016	−2.56	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.77	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	1109	−1.61	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
6	218	−2.87	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
7	241	1.36	2e−16	3e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
8	55107	−1.41	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
9	306	−1.43	2e−16	3e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
10	341	2.09	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
11	348	1.82	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
12	121551	−1.56	2e−16	3e−14	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
13	84419	1.62	2e−16	3e−14	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
14	713	1.44	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	59271	1.36	2e−16	3e−14	50 x 48	eva−1 homolog C (C. elegans) [Source:HGNC Symbol;Acc:1
16	260436	4.33	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
17	51806	2.11	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
18	857	−1.4	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
19	6364	2.97	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
20	595	−1.47	2e−16	3e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.29	NULL	15	CC	MHC class II protein complex
2	11.54	NULL	417	H.Tiss	WIRTH_Immune system
3	8.6	NULL	21	CC	clathrin−coated endocytic vesicle membrane
4	8.12	NULL	60	BP	T cell costimulation
5	8.01	NULL	312	BP	immune response
6	7.8	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
7	7.7	NULL	47	BP	antigen processing and presentation
8	7.61	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	6.92	NULL	12	MF	fatty acid binding
10	6.82	NULL	84	BP	T cell receptor signaling pathway
11	6.69	NULL	269	BP	inflammatory response
12	6.42	NULL	13	MMML CGS	MACIEJ_MMML 6
13	6.35	NULL	35	CC	trans−Golgi network membrane
14	6.28	NULL	32	CC	ER to Golgi transport vesicle membrane
15	6.24	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	6.17	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
17	6.04	NULL	14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
18	6.03	NULL	11	BP	positive regulation of bone resorption
19	5.94	NULL	3	MMML CGS	MACIEJ_MMML 7
20	5.94	NULL	60	BP	interferon−gamma−mediated signaling pathway
Underexpressed					
1	−13.72	NULL	957	Chr	Chr 11
2	−8.41	NULL	280	Chr	Chr 13
3	−8.1	NULL	12	BP	hemidesmosome assembly
4	−7.29	NULL	242	BP	extracellular matrix organization
5	−7.19	NULL	190	CC	extracellular matrix
6	−6.66	NULL	9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
7	−6.51	NULL	15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
8	−6.47	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
9	−6.25	NULL	13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
10	−6.14	NULL	15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
11	−6.13	NULL	5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
12	−6.13	NULL	10	BP	cellular response to zinc ion
13	−6.1	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
14	−6.1	NULL	83	CC	basement membrane
15	−6.08	NULL	6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
16	−6.01	NULL	1146	TF	HEBENSTREIT_low expression TF
17	−5.92	NULL	683	CC	extracellular space
18	−5.87	NULL	15	BP	negative regulation of growth
19	−5.79	NULL	14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
20	−5.6	NULL	36	BP	muscle filament sliding

GW_240

Local Summary

%DE = 0.78

metagenes = 25

genes = 373

genes in genesets = 368

genes with fdr < 0.1 = 233 (225 + / 8 −)

genes with fdr < 0.05 = 213 (205 + / 8 −)

genes with fdr < 0.01 = 164 (159 + / 5 −)

<r> metagenes = 0.93

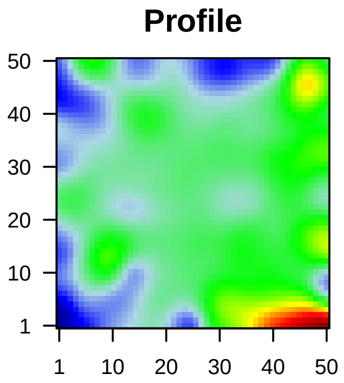
<r> genes = 0.5

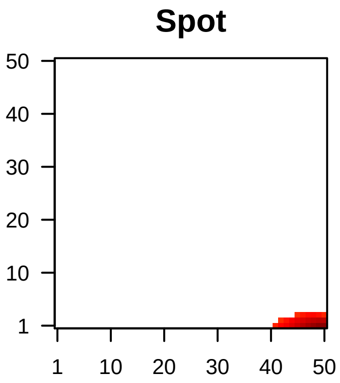
<FC> = 0.49

<shrinkage−t> = 17.12

<p−value> = 0

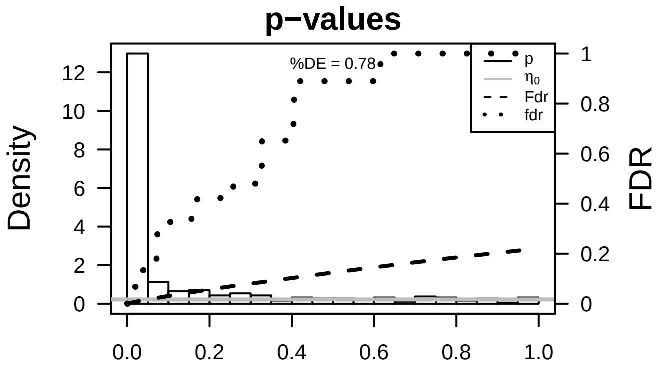
<fdr> = 0.43





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	241	1.36	2e−16	2e−15	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
2	341	2.09	2e−16	2e−15	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
3	348	1.82	2e−16	2e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
4	713	1.44	2e−16	2e−15	50 x 1	complement component 1, q subcomponent, B chain [Source
5	260436	4.33	2e−16	2e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
6	6364	2.97	2e−16	2e−15	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
7	4283	1.61	2e−16	2e−15	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
8	1593	1.45	2e−16	2e−15	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sour
9	3123	2.32	2e−16	2e−15	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
10	3127	3.94	2e−16	2e−15	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
11	3689	1.6	2e−16	2e−15	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
12	4067	1.36	2e−16	2e−15	46 x 2	v−yes−1 Yamaguchi sarcoma viral related oncogene homolog
13	5730	1.34	7e−16	2e−13	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
14	27299	1.3	4e−15	1e−12	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
15	7127	1.26	3e−14	1e−12	43 x 1	tumor necrosis factor, alpha−induced protein 2 [Source:HGN
16	6366	−1.26	3e−14	3e−12	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
17	7351	1.24	8e−14	3e−12	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
18	84868	1.22	2e−13	3e−12	50 x 1	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Ac
19	10537	1.22	2e−13	2e−11	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
20	3108	1.2	4e−13	2e−11	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	39.87	NULL	14 / 15	CC	MHC class II protein complex
2	26.26	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
3	25	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
4	23.94	NULL	105 / 417	H.Tiss	WIRTH_Immune system
5	23.89	NULL	16 / 47	BP	antigen processing and presentation
6	22.46	NULL	9 / 28	CC	transport vesicle membrane
7	20.88	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
8	20.79	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
9	20.28	NULL	20 / 60	BP	T cell costimulation
10	19.88	NULL	9 / 35	CC	trans−Golgi network membrane
11	18.81	NULL	8 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	18.58	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	18.4	NULL	59 / 312	BP	immune response
14	17.72	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
15	17.22	NULL	19 / 84	BP	T cell receptor signaling pathway
16	17.13	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
17	17.09	NULL	9 / 46	CC	endocytic vesicle membrane
18	16.81	NULL	100 / 553	Cancer	Lembcke_Colonic Inflammation
19	16.47	NULL	16 / 87	BP	antigen processing and presentation of exogenous peptide antigen
20	15.99	NULL	9 / 13	Cancer	GENTLES_modul18
21	15.64	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
22	15.15	NULL	42 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
23	15.15	NULL	42 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
24	15.15	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
25	15.15	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
26	14.48	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
27	14.3	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
28	14.07	NULL	7 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
29	13.63	NULL	8 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
30	12.99	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	12.91	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
32	12.59	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
33	12.56	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
34	12.55	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
35	12.42	NULL	5 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
36	12.38	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
37	12.01	NULL	5 / 12	BP	immunoglobulin mediated immune response
38	11.88	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
39	11.76	NULL	4 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
40	11.5	NULL	7 / 77	CC	late endosome membrane

GW_240

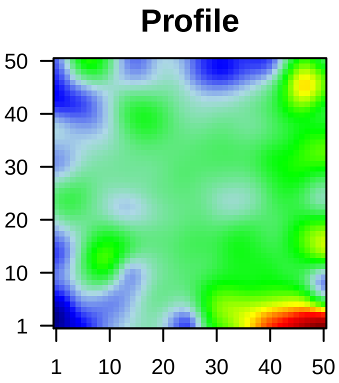
Local Summary

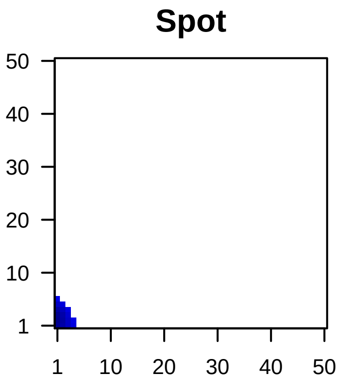
%DE = 0.7
metagenes = 17
genes = 284
genes in genesets = 282

genes with fdr < 0.1 = 158 (23 + / 135 −)
genes with fdr < 0.05 = 145 (21 + / 124 −)
genes with fdr < 0.01 = 98 (13 + / 85 −)

<r> metagenes = 0.95
<r> genes = 0.36

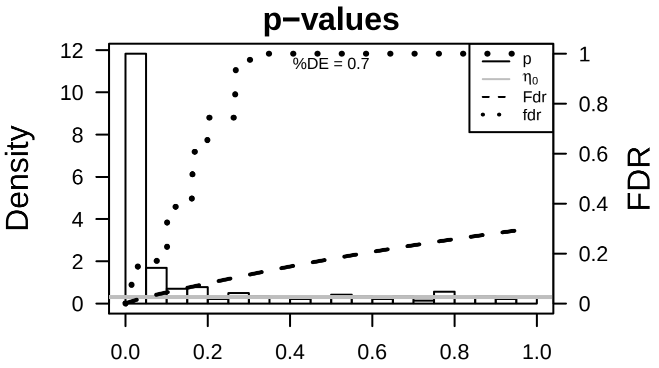
<FC> = −0.34
<shrinkage−t> = −11.91
<p−value> = 0
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	−1.41	2e−16	1e−15	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	857	−1.4	2e−16	1e−15	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
3	595	−1.47	2e−16	1e−15	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
4	2919	1.87	2e−16	1e−15	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
5	27122	−1.96	2e−16	1e−15	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Sy
6	28514	−1.56	2e−16	1e−15	1 x 5	delta−like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
7	4312	−2.41	2e−16	1e−15	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
8	4319	−2.14	2e−16	1e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
9	4314	−2.52	2e−16	1e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
10	4318	2.09	2e−16	1e−15	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
11	4489	−1.41	2e−16	1e−15	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
12	4502	−1.38	2e−16	1e−15	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
13	4628	−1.56	2e−16	1e−15	1 x 5	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
14	12	−1.93	2e−16	1e−15	1 x 1	
15	6696	2.15	2e−16	1e−15	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
16	8406	−1.59	2e−16	1e−15	2 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Sy
17	7045	−1.34	2e−16	1e−15	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
18	3371	−1.9	2e−16	1e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
19	6372	−1.35	4e−16	6e−14	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
20	55959	−1.33	1e−15	1e−13	1 x 3	sulfatase 2 [Source:HGNC Symbol;Acc:20392]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.68	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
2	−19.93	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
3	−18.33	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
4	−17.43	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
5	−16.02	NULL	69 / 242	BP	extracellular matrix organization
6	−15.97	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
7	−15.71	NULL	58 / 190	CC	extracellular matrix
8	−15.31	NULL	13 / 35	Glio	Colman_survival_associated
9	−14.89	NULL	1 / 2	miRNA target	miR−16−1
10	−13.52	NULL	3 / 10	BP	cellular response to zinc ion
11	−13.25	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
12	−12.6	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
13	−12.54	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
14	−12.42	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
15	−12.35	NULL	2 / 12	GSEA C2	WU_HBX_TARGETS_2_DN
16	−12.33	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
17	−12.07	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
18	−12.03	NULL	5 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
19	−12.02	NULL	23 / 83	CC	basement membrane
20	−11.99	NULL	4 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
21	−11.98	NULL	29 / 64	BP	collagen catabolic process
22	−11.97	NULL	3 / 13	GSEA C2	SUZUKI_AMPLIFIED_IN_ORAL_CANCER
23	−11.95	NULL	36 / 183	CC	proteinaceous extracellular matrix
24	−11.89	NULL	2 / 11	GSEA C2	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
25	−11.7	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
26	−11.69	NULL	5 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
27	−11.61	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
28	−11.55	NULL	2 / 4	miRNA target	miR−195
29	−11.47	NULL	6 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
30	−11.38	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
31	−11.33	NULL	32 / 69	BP	extracellular matrix disassembly
32	−11.24	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
33	−11.2	NULL	6 / 51	BP	regulation of cell migration
34	−11.14	NULL	2 / 9	GSEA C2	MARKS_HDAC_TARGETS_DN
35	−10.96	NULL	2 / 16	GSEA C2	REACTOME_BASIGIN_INTERACTIONS
36	−10.88	NULL	7 / 16	MF	fibronectin binding
37	−10.83	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
38	−10.8	NULL	5 / 16	GSEA C2	HENDRICKS_SMARCA4_TARGETS_UP
39	−10.79	NULL	3 / 15	BP	negative regulation of growth
40	−10.76	NULL	4 / 15	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_