GW_165

Global Summary

%DE = 0.11

genes with fdr < 0.2 = 1298 (728 + / 570 −)

genes with fdr < 0.1 = 1131 (642 + / 489 −)

genes with fdr < 0.05 = 895 (527 + / 368 −)

genes with fdr < 0.01 = 626 (395 + / 231 −)

genes in genesets = 16332

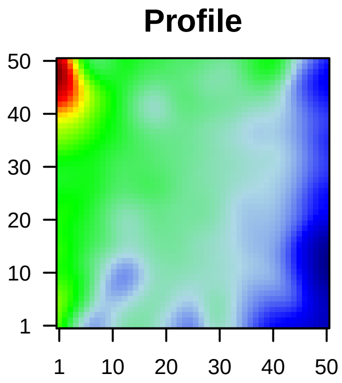
<FC> = 0

<shrinkage−t> = 0

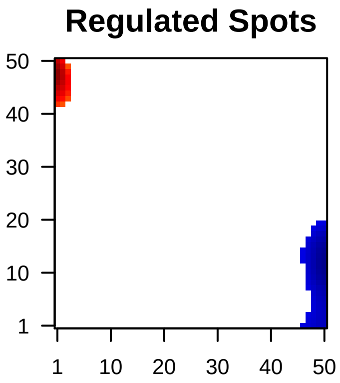
<p−value> = 0.14

<fdr> = 0.89

Profile



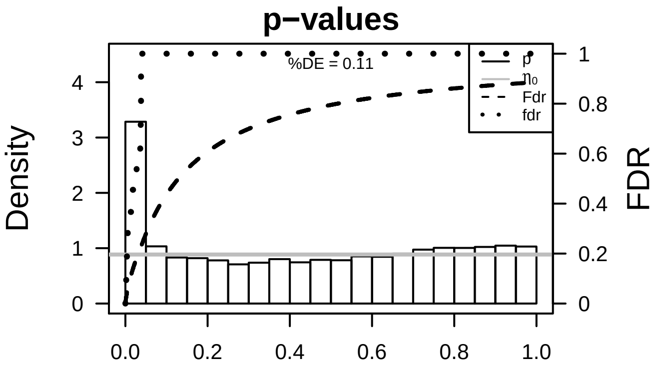
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.82	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	8644	1.96	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	1109	2.04	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	222	1.57	2e−16	4e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	242	2.43	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	387695	1.56	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
7	29113	2.32	2e−16	4e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
8	1041	2.25	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
9	84518	1.65	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
10	54544	1.73	2e−16	4e−14	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
11	49860	−2.03	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
12	92196	−1.56	2e−16	4e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
13	55894	2.13	2e−16	4e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	2.86	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	3	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	1809	−1.58	2e−16	4e−14	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
17	1824	1.6	2e−16	4e−14	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
18	1828	1.97	2e−16	4e−14	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	2064	1.94	2e−16	4e−14	6 x 50	v−erb−b2 avian erythroblastic leukemia viral oncogene homol
20	2167	1.66	2e−16	4e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	25.98	NULL	572	Disease	GUDJ_psoriasis up
2	19.22	NULL	42	BP	keratinization
3	18.88	NULL	21	CC	cornified envelope
4	17.28	NULL	135	H.Tiss	WIRTH_Mucosa
5	13.82	NULL	53	BP	keratinocyte differentiation
6	13.05	NULL	76	BP	epidermis development
7	10.06	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	9.39	NULL	19	BP	peptide cross−linking
9	8.92	NULL	15	MF	interleukin−1 receptor binding
10	8.92	NULL	633	Chr	Chr 9
11	8.61	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
12	8.6	NULL	21	CC	desmosome
13	8.47	NULL	717	Chr	Chr 16
14	8.39	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	8.09	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
16	7.47	NULL	534	Chr	Chr 8
17	7.41	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	6.87	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	6.34	NULL	269	BP	inflammatory response
20	6.21	NULL	15	GSEA C2	BILD_HRAS_ONCOGENIC_SIGNATURE
Underexpressed					
1	−8.6	NULL	375	Disease	GUDJ_psoriasis down
2	−8.3	NULL	15	CC	MHC class II protein complex
3	−7.08	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
4	−6.47	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
5	−6.35	NULL	11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
6	−5.95	NULL	1749	MF	DNA binding
7	−5.68	NULL	918	Chr	Chr 17
8	−5.66	NULL	866	Chr	Chr 12
9	−5.65	NULL	1581	BP	regulation of transcription, DNA−dependent
10	−5.34	NULL	6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
11	−5.27	NULL	81	BP	viral transcription
12	−5.26	NULL	1574	BP	transcription, DNA−templated
13	−5.19	NULL	87	BP	translational termination
14	−5.16	NULL	92	BP	viral life cycle
15	−5.16	NULL	118	Lymphoma	SPANG_LPS 6hrs UP
16	−5.13	NULL	14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
17	−5.12	NULL	28	CC	transport vesicle membrane
18	−5.08	NULL	714	Chr	Chr 6
19	−5.04	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
20	−4.93	NULL	16	GSEA C2	KORKOLA_TERATOMA_UP

GW_165

Local Summary

%DE = 0.84

metagenes = 25

genes = 338

genes in genesets = 331

genes with fdr < 0.1 = 263 (242 + / 21 −)

genes with fdr < 0.05 = 247 (229 + / 18 −)

genes with fdr < 0.01 = 221 (207 + / 14 −)

<r> metagenes = 0.88

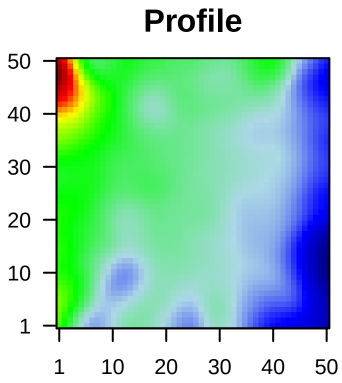
<r> genes = 0.36

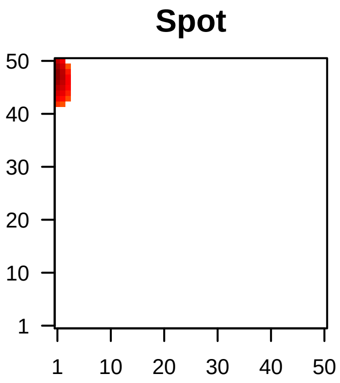
<FC> = 0.8

<shrinkage−t> = 28.25

<p−value> = 0

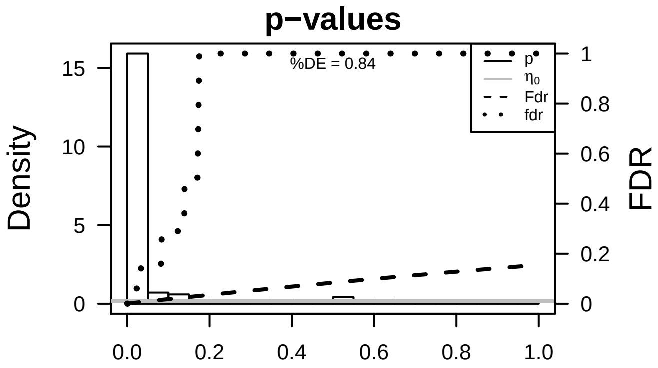
<fdr> = 0.27


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.82	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	8644	1.96	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
3	222	1.57	2e−16	2e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	242	2.43	2e−16	2e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
5	387695	1.56	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	29113	2.32	2e−16	2e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
7	1041	2.25	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
8	84518	1.65	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
9	54544	1.73	2e−16	2e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
10	49860	−2.03	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	55894	2.13	2e−16	2e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	414325	2.86	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	1673	3	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	1824	1.6	2e−16	2e−16	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
15	1828	1.97	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
16	2167	1.66	2e−16	2e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	10804	1.76	2e−16	2e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
18	3489	2.07	2e−16	2e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
19	3552	2.17	2e−16	2e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
20	26525	2.51	2e−16	2e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.71	NULL	18 / 21	CC	cornified envelope
2	33.76	NULL	20 / 42	BP	keratinization
3	32.55	NULL	117 / 572	Disease	GUDJ_psoriasis up
4	31.99	NULL	84 / 135	H.Tiss	WIRTH_Mucosa
5	26.88	NULL	24 / 53	BP	keratinocyte differentiation
6	24.4	NULL	27 / 76	BP	epidermis development
7	17.82	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	16.52	NULL	12 / 21	CC	desmosome
9	16.11	NULL	10 / 19	BP	peptide cross−linking
10	14.29	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	13.12	NULL	5 / 10	MF	RAGE receptor binding
12	13.1	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	12.75	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	12.34	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
15	11.58	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	11.25	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
17	11.2	NULL	3 / 15	MF	interleukin−1 receptor binding
18	11.19	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
19	10.97	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
20	10.59	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
21	10.47	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
22	10.37	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
23	10.13	NULL	10 / 52	BP	negative regulation of endopeptidase activity
24	10.11	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
25	9.81	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
26	9.8	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
27	9.58	NULL	5 / 13	BP	negative regulation of peptidase activity
28	9.5	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
29	9.45	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
30	9.4	NULL	69 / 1182	CC	extracellular region
31	9.31	NULL	5 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
32	9.26	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
33	9.03	NULL	7 / 29	BP	regulation of proteolysis
34	8.92	NULL	2 / 17	Disease	BCHETNIA_EBM up
35	8.76	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
36	8.74	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
37	8.59	NULL	8 / 73	BP	defense response to bacterium
38	8.56	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
39	8.51	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
40	8.34	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN

GW_165

Local Summary

%DE = 0.7

metagenes = 76

genes = 910

genes in genesets = 902

genes with fdr < 0.1 = 419 (13 + / 406 −)

genes with fdr < 0.05 = 347 (11 + / 336 −)

genes with fdr < 0.01 = 217 (5 + / 212 −)

<r> metagenes = 0.76

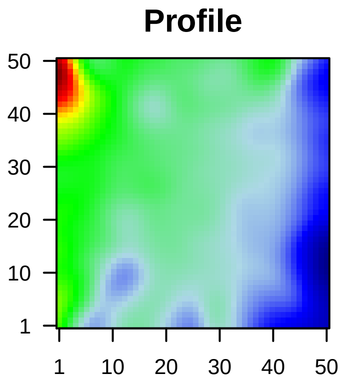
<r> genes = 0.25

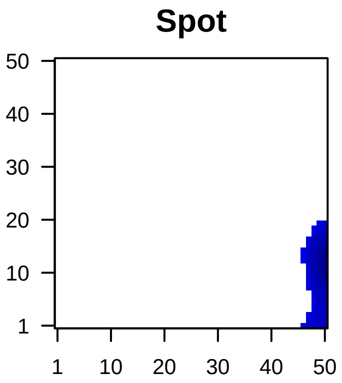
<FC> = −0.38

<shrinkage−t> = −13.27

<p−value> = 0.01

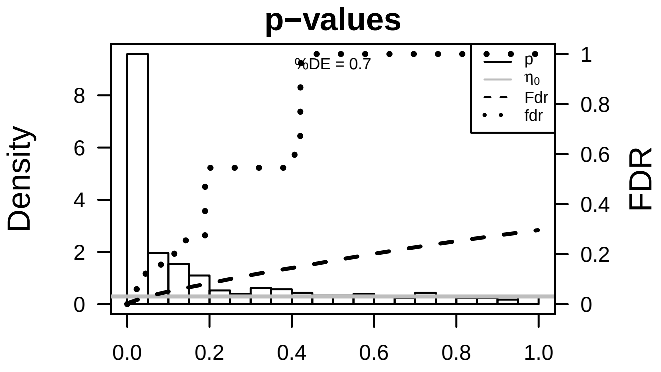
<fdr> = 0.64





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3169	−1.63	2e−16	2e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	93210	1.55	2e−16	2e−14	48 x 13	post−GPI attachment to proteins 3 [Source:HGNC Symbol;Ac
3	10628	−1.85	2e−16	2e−14	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
4	6192	−1.48	5e−15	6e−12	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
5	6364	1.44	3e−14	2e−10	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
6	25849	−1.36	7e−13	2e−10	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
7	494470	−1.33	1e−12	2e−09	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
8	293	−1.28	1e−11	2e−09	50 x 15	solute carrier family 25 (mitochondrial carrier; adenine nucleo
9	348	−1.27	2e−11	2e−09	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	260293	−1.26	2e−11	2e−09	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
11	2878	−1.26	3e−11	6e−09	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
12	341	−1.24	5e−11	7e−09	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
13	25840	−1.23	8e−11	7e−09	50 x 11	methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
14	347	−1.22	1e−10	1e−08	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
15	7033	−1.2	2e−10	1e−08	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
16	894	−1.2	2e−10	2e−08	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
17	84952	−1.19	3e−10	2e−08	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
18	51316	−1.18	4e−10	2e−08	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
19	7018	−1.18	4e−10	2e−08	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
20	1512	−1.17	6e−10	2e−08	47 x 1	cathepsin H [Source:HGNC Symbol;Acc:2535]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.63	NULL	12 / 15	CC	MHC class II protein complex
2	−15.9	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	−12.18	NULL	17 / 47	BP	antigen processing and presentation
4	−10.79	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
5	−10.55	NULL	6 / 16	GSEA C2	KORKOLA_TERATOMA_UP
6	−10.29	NULL	5 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
7	−9.72	NULL	6 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
8	−9.13	NULL	9 / 28	CC	transport vesicle membrane
9	−8.97	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
10	−8.96	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
11	−8.95	NULL	7 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
12	−8.82	NULL	63 / 375	Disease	GUDJ_psoriasis down
13	−8.74	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
14	−8.63	NULL	7 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
15	−8.48	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
16	−8.39	NULL	6 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
17	−8.3	NULL	5 / 14	MF	selenium binding
18	−8.3	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
19	−8.3	NULL	6 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_DN
20	−8.28	NULL	3 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
21	−8.2	NULL	5 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
22	−8.17	NULL	7 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
23	−8.08	NULL	121 / 553	Cancer	Lembcke_Colonic Inflammation
24	−7.72	NULL	6 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
25	−7.63	NULL	15 / 60	BP	T cell costimulation
26	−7.58	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
27	−7.56	NULL	6 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
28	−7.46	NULL	7 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
29	−7.4	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
30	−7.37	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
31	−7.31	NULL	65 / 312	BP	immune response
32	−7.31	NULL	10 / 35	CC	trans−Golgi network membrane
33	−7.07	NULL	4 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
34	−7.03	NULL	4 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
35	−7.02	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
36	−7.02	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
37	−6.88	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
38	−6.85	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
39	−6.73	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
40	−6.61	NULL	5 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP