GW_141

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1504 (714 + / 790 −)

genes with fdr < 0.1 = 1130 (525 + / 605 −)

genes with fdr < 0.05 = 874 (400 + / 474 −)

genes with fdr < 0.01 = 602 (273 + / 329 −)

genes in genesets = 16332

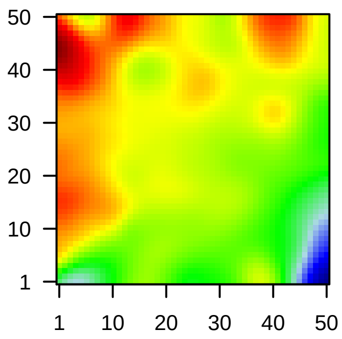
<FC> = 0

<shrinkage−t> = 0

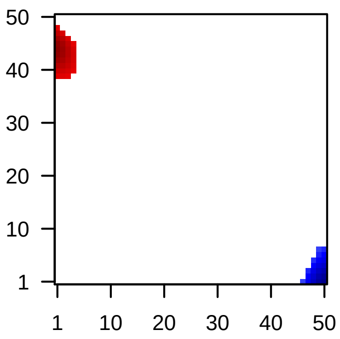
<p−value> = 0.14

<fdr> = 0.88

Profile



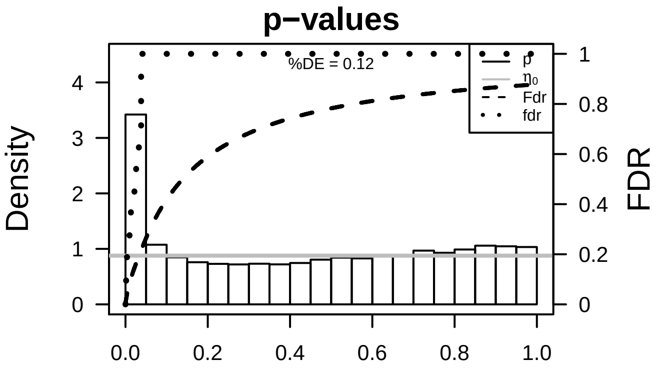
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.7	2e−16	6e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	2.08	2e−16	6e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	2.09	2e−16	6e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	8644	1.64	2e−16	6e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	1.51	2e−16	6e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	445328	1.44	2e−16	6e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
7	84707	−1.71	2e−16	6e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
8	339512	1.93	2e−16	6e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
9	29923	1.53	2e−16	6e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Sy
10	1001	1.44	2e−16	6e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
11	1066	2.55	2e−16	6e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
12	51200	1.6	2e−16	6e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
13	57834	1.69	2e−16	6e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
14	92196	−1.69	2e−16	6e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
15	2167	−1.52	2e−16	6e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	54855	−1.49	2e−16	6e−14	49 x 1	family with sequence similarity 46, member C [Source:HGNC
17	10804	1.65	2e−16	6e−14	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
18	2877	2	2e−16	6e−14	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
19	56169	1.52	2e−16	6e−14	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
20	3040	1.53	2e−16	6e−14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.02	NULL	743	Chr	Chr 7
2	10.76	NULL	21	CC	cornified envelope
3	9.02	NULL	717	Chr	Chr 16
4	8.99	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	8.32	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
6	8.32	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
7	8.27	NULL	135	H.Tiss	WIRTH_Mucosa
8	8.1	NULL	1033	Chr	Chr 2
9	7.92	NULL	76	BP	epidermis development
10	7.89	NULL	53	BP	keratinocyte differentiation
11	7.84	NULL	572	Disease	GUDJ_psoriasis up
12	7.81	NULL	1720	Chr	Chr 1
13	6.81	NULL	42	BP	keratinization
14	6.52	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
15	6.25	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
16	6	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
17	5.71	NULL	4640	CC	nucleus
18	5.69	NULL	370	BP	mitotic cell cycle
19	5.62	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	5.39	NULL	4	MMML CGS	MACIEJ_MMML 23
Underexpressed					
1	−15.32	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−11.94	NULL	914	Chr	Chr 3
3	−11.54	NULL	190	CC	extracellular matrix
4	−11.08	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−10.79	NULL	15	CC	MHC class II protein complex
6	−10.75	NULL	312	BP	immune response
7	−10.71	NULL	630	Chr	Chr X
8	−10.37	NULL	417	H.Tiss	WIRTH_Immune system
9	−10.15	NULL	1182	CC	extracellular region
10	−9.39	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	−9.39	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	−9.39	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	−9.39	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	−9.21	NULL	683	CC	extracellular space
15	−8.96	NULL	866	Chr	Chr 12
16	−8.88	NULL	316	Cancer	SPANG_BCL6−index2
17	−8.53	NULL	47	BP	antigen processing and presentation
18	−8.42	NULL	375	Disease	GUDJ_psoriasis down
19	−8.14	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
20	−8.11	NULL	16	MMML CGS	MACIEJ_MMML 1

GW_141

Local Summary

%DE = 0.68

metagenes = 33

genes = 363

genes in genesets = 356

genes with fdr < 0.1 = 212 (192 + / 20 −)

genes with fdr < 0.05 = 199 (180 + / 19 −)

genes with fdr < 0.01 = 139 (129 + / 10 −)

<r> metagenes = 0.92

<r> genes = 0.34

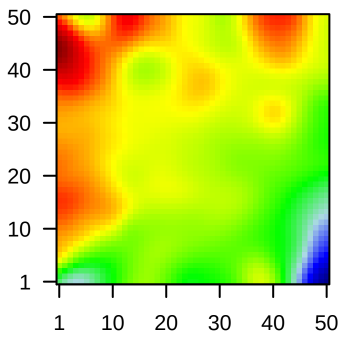
<FC> = 0.4

<shrinkage−t> = 14.23

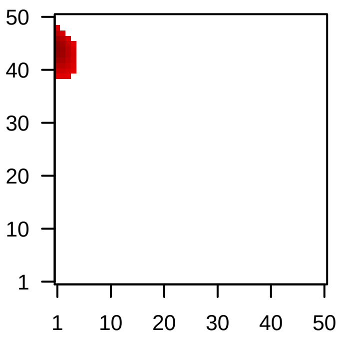
<p−value> = 0

<fdr> = 0.47

Profile

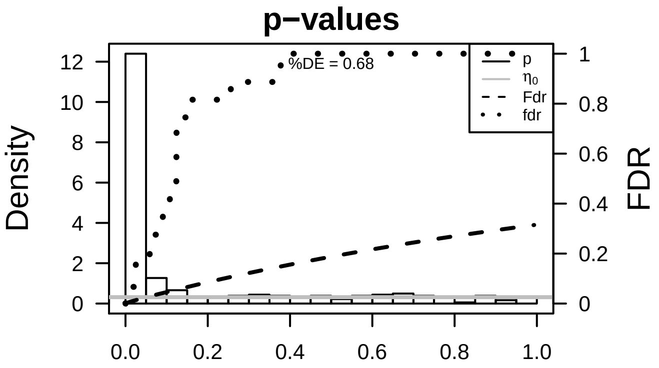


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	29923	1.53	2e−16	2e−15	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Sy
2	1001	1.44	2e−16	2e−15	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
3	51200	1.6	2e−16	2e−15	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
4	2167	−1.52	2e−16	2e−15	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
5	10804	1.65	2e−16	2e−15	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
6	56169	1.52	2e−16	2e−15	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
7	29094	1.71	2e−16	2e−15	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
8	3552	1.59	2e−16	2e−15	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
9	56901	1.76	2e−16	2e−15	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
10	780851	1.96	2e−16	2e−15	2 x 39	small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
11	780853	1.98	2e−16	2e−15	2 x 39	small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc
12	780854	1.95	2e−16	2e−15	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
13	6706	2.33	2e−16	2e−15	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
14	64127	1.44	4e−16	3e−14	1 x 45	nucleotide−binding oligomerization domain containing 2 [Sou
15	414325	1.43	7e−16	3e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	154	1.42	9e−16	2e−12	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:28
17	56300	1.34	3e−14	2e−12	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
18	3861	1.23	3e−14	5e−12	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
19	5803	1.32	8e−14	1e−11	1 x 45	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
20	1828	1.3	2e−13	5e−11	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.15	NULL	91 / 572	Disease	GUDJ_psoriasis up
2	16.48	NULL	39 / 135	H.Tiss	WIRTH_Mucosa
3	15.14	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	14.93	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
5	12.59	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
6	12.49	NULL	18 / 76	BP	epidermis development
7	12.32	NULL	11 / 21	CC	desmosome
8	11.44	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
9	11.33	NULL	5 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
10	10.91	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
11	10.86	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
12	10.76	NULL	5 / 12	BP	hemidesmosome assembly
13	9.99	NULL	5 / 15	CC	connexon complex
14	9.63	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
15	9.31	NULL	19 / 82	CC	intermediate filament
16	9.03	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
17	8.93	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
18	8.85	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
19	8.78	NULL	5 / 21	CC	cornified envelope
20	8.46	NULL	9 / 53	BP	keratinocyte differentiation
21	8	NULL	11 / 82	MF	structural constituent of cytoskeleton
22	7.92	NULL	2 / 15	MF	interleukin−1 receptor binding
23	7.6	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
24	7.42	NULL	4 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
25	7.41	NULL	3 / 25	BP	response to zinc ion
26	7.3	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
27	7.17	NULL	6 / 21	CC	gap junction
28	7.15	NULL	4 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
29	7.12	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
30	7.1	NULL	6 / 42	BP	keratinization
31	7.09	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
32	7.02	NULL	9 / 85	Glio	laffaire_hypermeth_LGG_vs_control
33	6.9	NULL	4 / 10	MF	gap junction channel activity
34	6.82	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
35	6.75	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
36	6.72	NULL	2 / 14	GSEA C2	HOEGERKORP_CD44_TARGETS_DIRECT_UP
37	6.69	NULL	3 / 10	BP	negative regulation of interleukin−2 production
38	6.66	NULL	6 / 32	CC	cell−cell adherens junction
39	6.37	NULL	2 / 21	BP	positive regulation of cytokine production
40	6.33	NULL	7 / 83	Glio	Christensen_hypermethylated_in_secondary_glioblastoma

GW_141

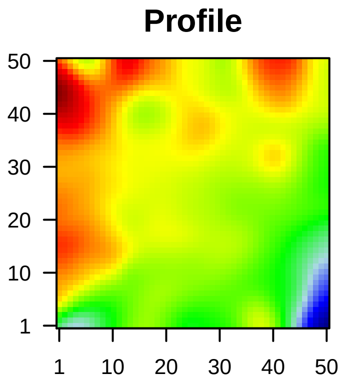
Local Summary

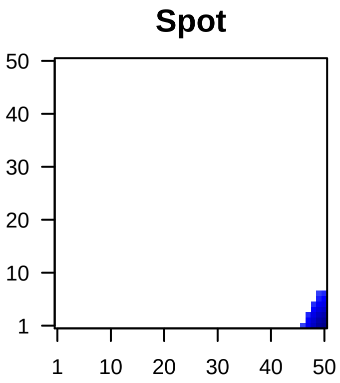
%DE = 0.92
metagenes = 23
genes = 383
genes in genesets = 381

genes with fdr < 0.1 = 339 (0 + / 339 −)
genes with fdr < 0.05 = 298 (0 + / 298 −)
genes with fdr < 0.01 = 227 (0 + / 227 −)

<r> metagenes = 0.94
<r> genes = 0.47

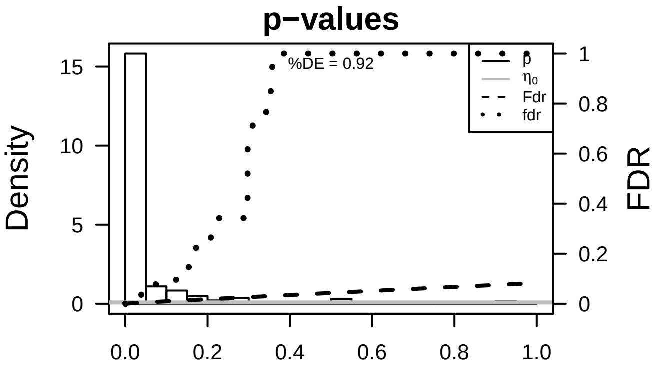
<FC> = −0.58
<shrinkage−t> = −20.29
<p−value> = 0
<fdr> = 0.34


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	54855	−1.49	2e−16	9e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
2	3109	−1.51	2e−16	9e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
3	3122	−1.6	2e−16	9e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
4	3488	−1.54	2e−16	9e−16	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
5	3512	−1.67	2e−16	9e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
6	3543	−2.62	2e−16	9e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
7	23643	−1.45	2e−16	9e−16	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
8	10628	−1.5	2e−16	9e−16	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
9	894	−1.43	9e−16	1e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
10	57172	−1.42	1e−15	7e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
11	5880	−1.39	3e−15	8e−13	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
12	10537	−1.35	3e−14	8e−13	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	3002	−1.33	5e−14	9e−13	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
14	3113	−1.32	1e−13	9e−13	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
15	713	−1.31	1e−13	6e−11	50 x 1	complement component 1, q subcomponent, B chain [Source
16	1363	−1.23	4e−12	6e−11	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
17	348	−1.22	5e−12	6e−11	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
18	260436	−1.22	6e−12	2e−10	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
19	347	−1.2	1e−11	1e−09	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
20	864	−1.15	7e−11	1e−09	46 x 1	runt−related transcription factor 3 [Source:HGNC Symbol;Acc


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.84	NULL	12 / 15	CC	MHC class II protein complex
2	−23.45	NULL	91 / 417	H.Tiss	WIRTH_Immune system
3	−21.8	NULL	109 / 553	Cancer	Lembcke_Colonic Inflammation
4	−20.01	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
5	−19.69	NULL	59 / 312	BP	immune response
6	−16.91	NULL	15 / 47	BP	antigen processing and presentation
7	−15.91	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
8	−15.75	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	−15.75	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	−15.75	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	−15.75	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	−15.19	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
13	−15.04	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
14	−14.75	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
15	−14.25	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	−14.18	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
17	−14.02	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
18	−13.98	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
19	−13.81	NULL	8 / 28	CC	transport vesicle membrane
20	−13.79	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
21	−13.49	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
22	−12.81	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
23	−12.56	NULL	18 / 74	BP	regulation of immune response
24	−12.25	NULL	6 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
25	−12.23	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
26	−12.19	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
27	−12.03	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
28	−11.95	NULL	34 / 316	Cancer	SPANG_BCL6−index2
29	−11.83	NULL	15 / 60	BP	T cell costimulation
30	−11.77	NULL	9 / 35	CC	trans−Golgi network membrane
31	−11.6	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
32	−11.19	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
33	−11.16	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
34	−11.09	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
35	−10.97	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
36	−10.82	NULL	4 / 14	MF	lipid transporter activity
37	−10.74	NULL	4 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
38	−10.72	NULL	16 / 84	BP	T cell receptor signaling pathway
39	−10.67	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
40	−10.64	NULL	4 / 8	Lymphoma	MASCQUE_ABC UP