GW_054

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1789 (938 + / 851 −)

genes with fdr < 0.1 = 1424 (762 + / 662 −)

genes with fdr < 0.05 = 1183 (633 + / 550 −)

genes with fdr < 0.01 = 785 (452 + / 333 −)

genes in genesets = 16332

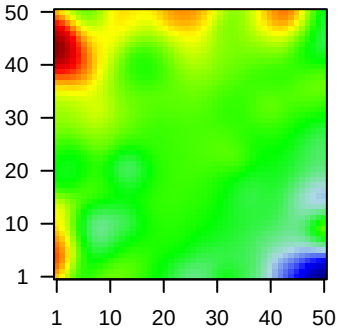
<FC> = 0

<shrinkage−t> = 0

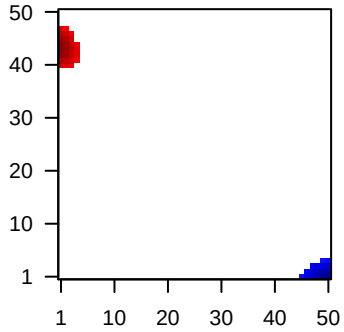
<p−value> = 0.11

<fdr> = 0.86

Profile



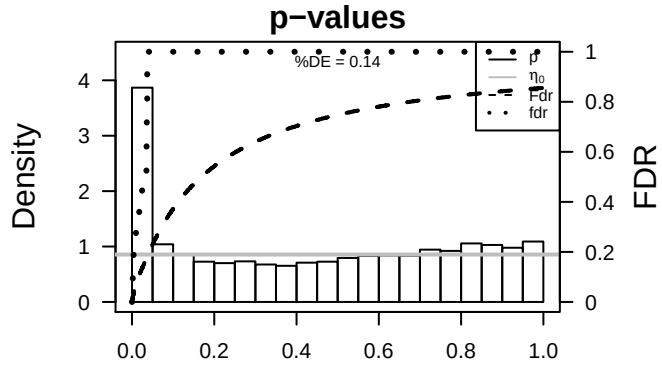
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	1.45	2e−16	5e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	113146	1.64	2e−16	5e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	1.49	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	401138	2.16	2e−16	5e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
5	55107	1.95	2e−16	5e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGI
6	306	1.5	2e−16	5e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
7	348	−1.48	2e−16	5e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
8	80341	1.69	2e−16	5e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
9	92747	1.69	2e−16	5e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
10	29113	2.41	2e−16	5e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
11	760	1.67	2e−16	5e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	51806	2.14	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	55450	1.36	2e−16	5e−14	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
14	6364	−1.46	2e−16	5e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
15	8900	1.69	2e−16	5e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
16	1308	1.83	2e−16	5e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
17	56603	1.51	2e−16	5e−14	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
18	92196	−1.33	2e−16	5e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	55894	1.5	2e−16	5e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	414325	1.88	2e−16	5e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.45	NULL	519	Chr	Chr 14
2	12.01	NULL	633	Chr	Chr 9
3	11.18	NULL	572	Disease	GUDJ_psoriasis up
4	10.36	NULL	135	H.Tiss	WIRTH_Mucosa
5	9.64	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
6	8.63	NULL	12	BP	hemidesmosome assembly
7	8.48	NULL	76	BP	epidermis development
8	7.78	NULL	530	Cancer	Lembcke_Normal vs Adenoma
9	7.6	NULL	21	CC	desmosome
10	7.29	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
11	7.29	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
12	7.1	NULL	370	BP	mitotic cell cycle
13	7	NULL	70	BP	cell junction assembly
14	6.97	NULL	64	BP	collagen catabolic process
15	6.88	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
16	6.82	NULL	242	BP	extracellular matrix organization
17	6.76	NULL	69	BP	extracellular matrix disassembly
18	6.74	NULL	22	MF	cadherin binding
19	6.39	NULL	9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
20	6.25	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
Underexpressed					
1	−13.13	NULL	15	CC	MHC class II protein complex
2	−11.23	NULL	417	H.Tiss	WIRTH_Immune system
3	−9.88	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	−9.44	NULL	312	BP	immune response
5	−8.93	NULL	1135	Chr	Chr 19
6	−8.67	NULL	52	Chr	Chr HSCHR6_MHC_QBL
7	−7.91	NULL	60	BP	T cell costimulation
8	−7.81	NULL	84	BP	T cell receptor signaling pathway
9	−7.38	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	−7.38	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	−7.38	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	−7.38	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	−7.32	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
14	−7.25	NULL	21	CC	clathrin−coated endocytic vesicle membrane
15	−6.9	NULL	47	BP	antigen processing and presentation
16	−6.75	NULL	28	CC	transport vesicle membrane
17	−6.53	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
18	−6.44	NULL	15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	−6.43	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	−6.42	NULL	43	MF	chemokine activity

GW_054

Local Summary

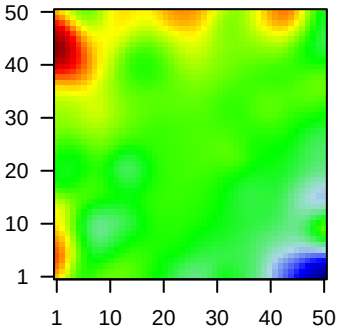
%DE = 0.83
metagenes = 27
genes = 305
genes in genesets = 299

genes with fdr < 0.1 = 215 (205 + / 10 −)
genes with fdr < 0.05 = 213 (203 + / 10 −)
genes with fdr < 0.01 = 178 (170 + / 8 −)

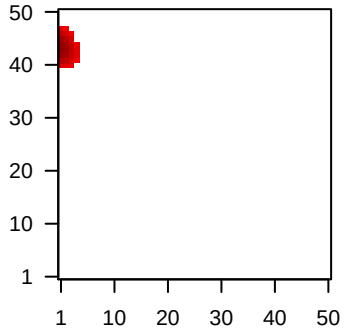
<r> metagenes = 0.94
<r> genes = 0.36

<FC> = 0.53
<shrinkage−t> = 18.68
<p−value> = 0
<fdr> = 0.33

Profile



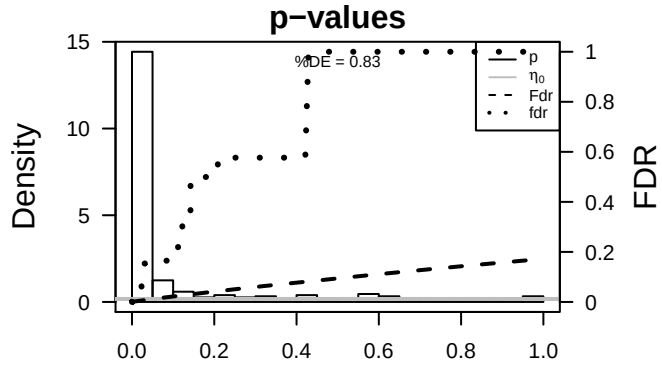
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	113146	1.64	2e−16	8e−16	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	306	1.5	2e−16	8e−16	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
3	29113	2.41	2e−16	8e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbc
4	760	1.67	2e−16	8e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	8900	1.69	2e−16	8e−16	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
6	1308	1.83	2e−16	8e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
7	55894	1.5	2e−16	8e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	2150	1.63	2e−16	8e−16	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGNC
9	3306	2.05	2e−16	8e−16	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
10	3868	1.26	2e−16	8e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
11	387882	1.72	2e−16	8e−16	2 x 41	chromosome 12 open reading frame 75 [Source:HGNC Symt
12	4330	1.37	2e−16	8e−16	1 x 42	meningioma (disrupted in balanced translocation) 1 [Source:H
13	26499	1.36	2e−16	8e−16	1 x 42	pleckstrin 2 [Source:HGNC Symbol;Acc:19238]
14	6339	1.49	2e−16	8e−16	1 x 45	sodium channel, non−voltage−gated 1, delta subunit [Source:
15	116211	1.36	2e−16	8e−16	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/S
16	5268	1.29	1e−15	3e−14	1 x 46	serpin peptidase inhibitor, clade B (ovalbumin), member 5 [Sc
17	1001	1.29	1e−15	5e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
18	8601	1.28	2e−15	6e−14	1 x 44	regulator of G−protein signaling 20 [Source:HGNC Symbol;Ac
19	23002	1.26	4e−15	6e−14	4 x 44	dishevelled associated activator of morphogenesis 1 [Source:
20	653499	1.26	5e−15	6e−14	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.46	NULL	5 / 12	BP	hemidesmosome assembly
2	14.7	NULL	28 / 135	H.Tiss	WIRTH_Mucosa
3	13.94	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
4	13.86	NULL	71 / 572	Disease	GUDJ_psoriasis up
5	13.83	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
6	12.93	NULL	16 / 76	BP	epidermis development
7	12.28	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
8	11.39	NULL	19 / 82	CC	intermediate filament
9	11.26	NULL	8 / 21	CC	desmosome
10	9.89	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
11	9.49	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
12	9.13	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
13	9.08	NULL	2 / 18	BP	male meiosis I
14	9.05	NULL	3 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
15	9.02	NULL	3 / 17	BP	morphogenesis of an epithelium
16	8.44	NULL	3 / 25	BP	response to zinc ion
17	8.4	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
18	8.1	NULL	7 / 48	Glio	Noushmehr_Pron_GCIMP_hypermeth_DN
19	8.01	NULL	9 / 44	CC	keratin filament
20	7.78	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
21	7.73	NULL	2 / 10	BP	positive regulation of Rho protein signal transduction
22	7.64	NULL	11 / 82	MF	structural constituent of cytoskeleton
23	7.59	NULL	6 / 70	BP	cell junction assembly
24	7.51	NULL	3 / 12	BP	keratinocyte proliferation
25	7.44	NULL	3 / 19	MF	laminin binding
26	7.12	NULL	2 / 23	Chr	Chr HSCHR6_MHC_DBB
27	7.01	NULL	4 / 22	MF	cadherin binding
28	6.98	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
29	6.98	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
30	6.95	NULL	19 / 186	MF	structural molecule activity
31	6.94	NULL	3 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
32	6.94	NULL	2 / 16	GSEA C2	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
33	6.88	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
34	6.84	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
35	6.83	NULL	2 / 2	miRNA target	hsa−199a*
36	6.82	NULL	1 / 10	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_5_DN
37	6.78	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
38	6.71	NULL	5 / 32	CC	cell−cell adherens junction
39	6.65	NULL	11 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
40	6.65	NULL	3 / 10	BP	negative regulation of interleukin−2 production

GW_054

Local Summary

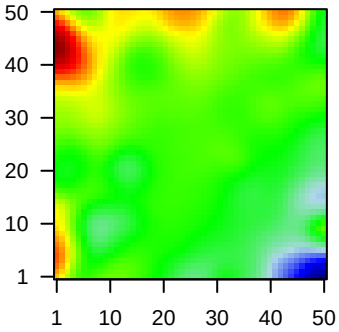
%DE = 0.95
metagenes = 17
genes = 281
genes in genesets = 278

genes with fdr < 0.1 = 254 (4 + / 250 −)
genes with fdr < 0.05 = 247 (3 + / 244 −)
genes with fdr < 0.01 = 221 (1 + / 220 −)

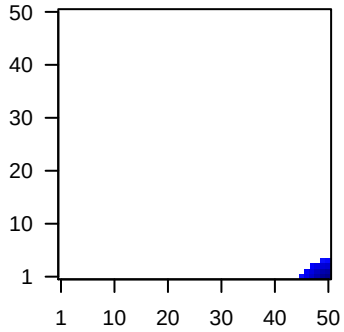
<r> metagenes = 0.99
<r> genes = 0.58

<FC> = −0.6
<shrinkage−t> = −21.1
<p−value> = 0
<fdr> = 0.21

Profile



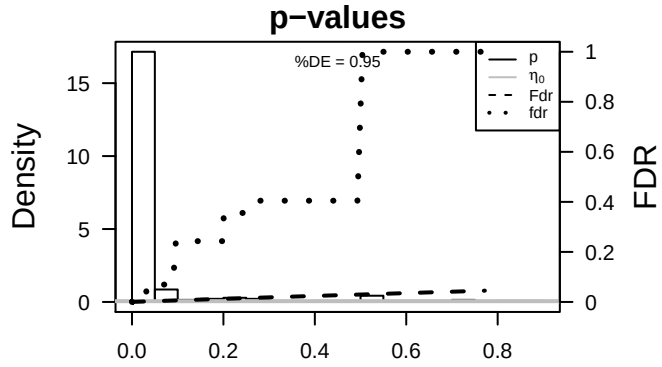
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	−1.48	2e−16	4e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	6364	−1.46	2e−16	4e−16	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
3	3109	−1.64	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
4	3113	−1.39	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
5	3120	−1.37	2e−16	4e−16	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
6	3122	−1.7	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
7	3123	−1.35	2e−16	4e−16	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
8	3936	−1.56	2e−16	4e−16	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
9	9806	−1.33	2e−16	4e−16	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
10	3689	−1.3	7e−16	6e−15	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
11	713	−1.29	1e−15	3e−13	50 x 1	complement component 1, q subcomponent, B chain [Source
12	341	−1.22	4e−14	3e−13	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
13	169044	1.21	7e−14	3e−13	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
14	241	−1.2	8e−14	3e−13	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
15	3108	−1.2	1e−13	3e−13	50 x 1	major histocompatibility complex, class II, DM alpha [Source:H
16	4050	−1.2	1e−13	3e−13	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
17	8635	−1.19	1e−13	9e−13	46 x 1	ribonuclease T2 [Source:HGNC Symbol;Acc:21686]
18	7351	−1.19	2e−13	3e−12	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
19	919	−1.17	4e−13	3e−12	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
20	6363	−1.16	6e−13	7e−12	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−42.49	NULL	13 / 15	CC	MHC class II protein complex
2	−28.93	NULL	92 / 417	H.Tiss	WIRTH_Immune system
3	−25.76	NULL	16 / 47	BP	antigen processing and presentation
4	−23.69	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
5	−23.57	NULL	95 / 553	Cancer	Lembcke_Colonic Inflammation
6	−23.36	NULL	54 / 312	BP	immune response
7	−22.78	NULL	3 / 3	MMML C6	GAJEJ_MMML 7
8	−22.53	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
9	−22.24	NULL	17 / 60	BP	T cell costimulation
10	−20.2	NULL	8 / 28	CC	transport vesicle membrane
11	−20.07	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
12	−20.07	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
13	−20.07	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
14	−20.07	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
15	−19.95	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	−19.35	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	−19.23	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
18	−19.05	NULL	9 / 35	CC	trans−Golgi network membrane
19	−18.75	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
20	−18.68	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
21	−18.17	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
22	−17.9	NULL	17 / 84	BP	T cell receptor signaling pathway
23	−17.08	NULL	12 / 60	BP	interferon−gamma−mediated signaling pathway
24	−16.99	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
25	−16.93	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
26	−16.57	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
27	−16.46	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
28	−16.21	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
29	−16.12	NULL	18 / 74	BP	regulation of immune response
30	−16	NULL	9 / 46	CC	endocytic vesicle membrane
31	−15.7	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
32	−15.32	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
33	−14.95	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
34	−14.55	NULL	7 / 13	Cancer	GENTLES_modul18
35	−14.27	NULL	5 / 12	BP	immunoglobulin mediated immune response
36	−14.15	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
37	−13.97	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
38	−13.83	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
39	−13.7	NULL	25 / 162	CC	external side of plasma membrane
40	−13.43	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS