GW_206

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2132 (1198 + / 934 −)

genes with fdr < 0.1 = 1805 (1047 + / 758 −)

genes with fdr < 0.05 = 1519 (917 + / 602 −)

genes with fdr < 0.01 = 1176 (721 + / 455 −)

genes in genesets = 16332

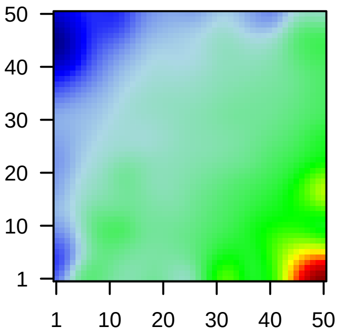
<FC> = 0

<shrinkage−t> = 0

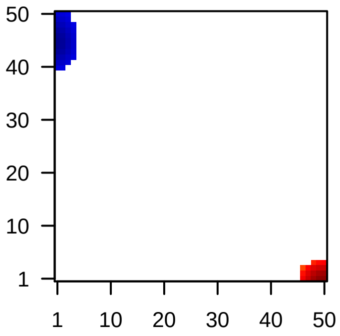
<p−value> = 0.07

<fdr> = 0.84

Profile



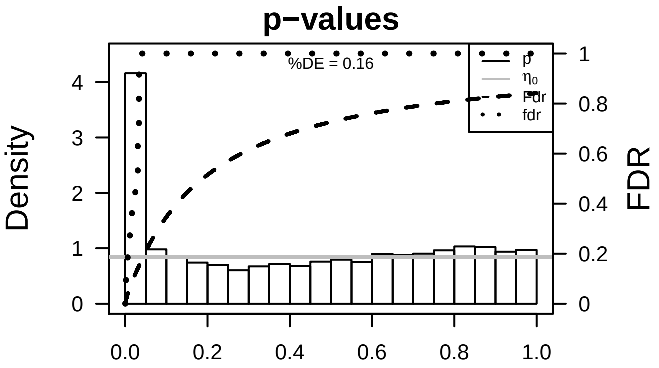
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.63	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	133	−1.73	2e−16	2e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
3	113146	−1.54	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	8644	−1.84	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	−1.95	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	115701	2.19	2e−16	2e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
7	147463	1.9	2e−16	2e−14	25 x 50	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
8	341	1.6	2e−16	2e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
9	348	1.65	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	55843	1.49	2e−16	2e−14	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
11	445328	−1.5	2e−16	2e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
12	92591	1.87	2e−16	2e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
13	22809	1.95	2e−16	2e−14	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
14	713	1.84	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	714	1.63	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
16	260436	2.08	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
17	771	−1.5	2e−16	2e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
18	760	−1.93	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
19	57172	3.1	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
20	6363	2.78	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	23.23	NULL	417	H.Tiss	WIRTH_Immune system
2	16.67	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	16.21	NULL	312	BP	immune response
4	14.63	NULL	15	CC	MHC class II protein complex
5	12.56	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	12.5	NULL	47	BP	antigen processing and presentation
7	11.57	NULL	74	BP	regulation of immune response
8	10.92	NULL	316	Cancer	SPANG_BCL6−index2
9	10.37	NULL	60	BP	interferon−gamma−mediated signaling pathway
10	10.25	NULL	51	BP	type I interferon signaling pathway
11	10.12	NULL	162	CC	external side of plasma membrane
12	9.96	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
13	9.94	NULL	60	BP	T cell costimulation
14	9.88	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
15	9.5	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
16	9.22	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
17	9.16	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
18	8.94	NULL	16	GSEA C2	SU_THYMUS
19	8.88	NULL	84	BP	T cell receptor signaling pathway
20	8.56	NULL	8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
Underexpressed					
1	−18.91	NULL	135	H.Tiss	WIRTH_Mucosa
2	−12.34	NULL	572	Disease	GUDJ_psoriasis up
3	−9.82	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−8.7	NULL	76	BP	epidermis development
5	−8.36	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
6	−8.33	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
7	−8.13	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
8	−7.36	NULL	530	Cancer	Lembcke_Normal vs Adenoma
9	−6.43	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
10	−6.36	NULL	21	CC	cornified envelope
11	−6.34	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
12	−6.34	NULL	53	BP	keratinocyte differentiation
13	−6.2	NULL	13	H.Tiss	WIRTH_Tonsil
14	−6.16	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
15	−5.85	NULL	296	MF	oxidoreductase activity
16	−5.83	NULL	8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
17	−5.75	NULL	21	CC	desmosome
18	−5.72	NULL	12	BP	hemidesmosome assembly
19	−5.64	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
20	−5.49	NULL	1253	BP	small molecule metabolic process

GW_206

Local Summary

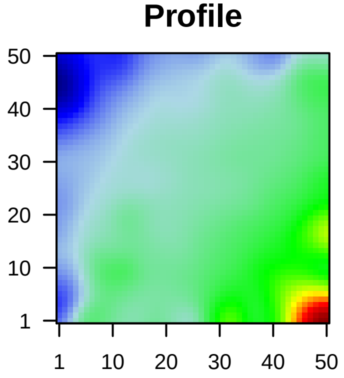
%DE = 0.99
metagenes = 18
genes = 283
genes in genesets = 281

genes with fdr < 0.1 = 278 (278 + / 0 −)
genes with fdr < 0.05 = 278 (278 + / 0 −)
genes with fdr < 0.01 = 277 (277 + / 0 −)

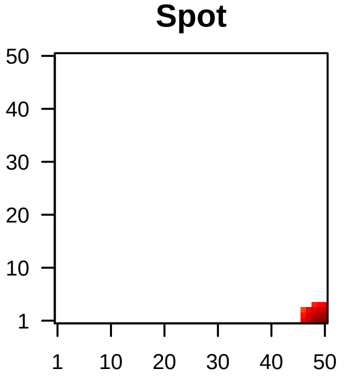
<r> metagenes = 0.99
<r> genes = 0.59

<FC> = 1.32
<shrinkage−t> = 46.35
<p−value> = 0
<fdr> = 0.02

Profile



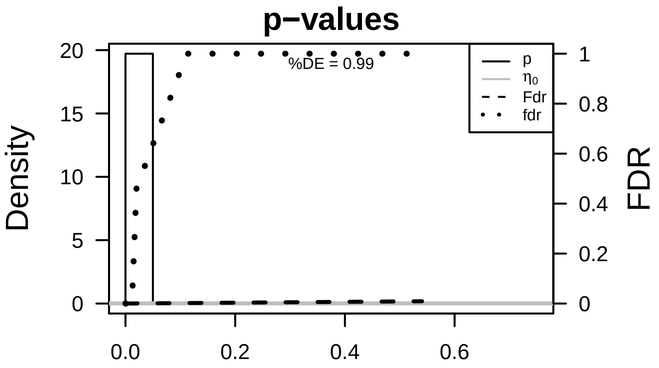
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	115701	2.19	2e−16	9e−18	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
2	341	1.6	2e−16	9e−18	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
3	348	1.65	2e−16	9e−18	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
4	55843	1.49	2e−16	9e−18	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
5	92591	1.87	2e−16	9e−18	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
6	713	1.84	2e−16	9e−18	50 x 1	complement component 1, q subcomponent, B chain [Source
7	714	1.63	2e−16	9e−18	50 x 1	complement component 1, q subcomponent, C chain [Source
8	260436	2.08	2e−16	9e−18	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
9	57172	3.1	2e−16	9e−18	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
10	6363	2.78	2e−16	9e−18	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
11	6364	1.8	2e−16	9e−18	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
12	6366	1.88	2e−16	9e−18	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
13	6352	1.63	2e−16	9e−18	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
14	1236	1.74	2e−16	9e−18	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
15	930	2.11	2e−16	9e−18	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
16	914	1.78	2e−16	9e−18	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
17	919	1.59	2e−16	9e−18	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
18	939	2.11	2e−16	9e−18	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
19	915	1.76	2e−16	9e−18	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
20	962	2.01	2e−16	9e−18	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	34.61	NULL	12 / 15	CC	MHC class II protein complex
2	31.62	NULL	96 / 417	H.Tiss	WIRTH_Immune system
3	27.25	NULL	98 / 553	Cancer	Lembcke_Colonic Inflammation
4	23.52	NULL	54 / 312	BP	immune response
5	21.59	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
6	21.58	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
7	21.28	NULL	15 / 47	BP	antigen processing and presentation
8	18.55	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
9	18.54	NULL	18 / 60	BP	T cell costimulation
10	18.26	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
11	17.47	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
12	17.02	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	17.02	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	17.02	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	17.02	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	16.31	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
17	16.19	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
18	15.99	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
19	15.85	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	15.41	NULL	8 / 13	Cancer	GENTLES_modul18
21	15.4	NULL	18 / 74	BP	regulation of immune response
22	15.37	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
23	14.96	NULL	5 / 12	BP	dendritic cell chemotaxis
24	14.94	NULL	8 / 16	GSEA C2	SU_THYMUS
25	14.81	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
26	14.78	NULL	27 / 162	CC	external side of plasma membrane
27	14.75	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
28	14.32	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
29	14.21	NULL	18 / 84	BP	T cell receptor signaling pathway
30	13.72	NULL	7 / 28	CC	transport vesicle membrane
31	13.6	NULL	5 / 12	BP	immunoglobulin mediated immune response
32	13.47	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
33	13.39	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
34	13.29	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
35	13.17	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
36	13.11	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
37	13.11	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
38	12.99	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
39	12.71	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
40	12.7	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane

GW_206

Local Summary

%DE = 0.97

metagenes = 39

genes = 469

genes in genesets = 458

genes with fdr < 0.1 = 426 (19 + / 407 −)

genes with fdr < 0.05 = 409 (14 + / 395 −)

genes with fdr < 0.01 = 373 (12 + / 361 −)

<r> metagenes = 0.85

<r> genes = 0.33

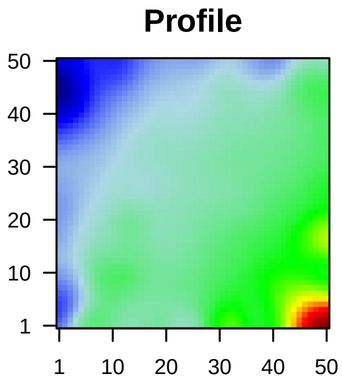
<FC> = −0.72

<shrinkage−t> = −25.28

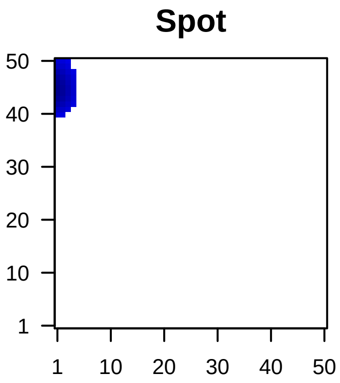
<p−value> = 0

<fdr> = 0.24

Profile



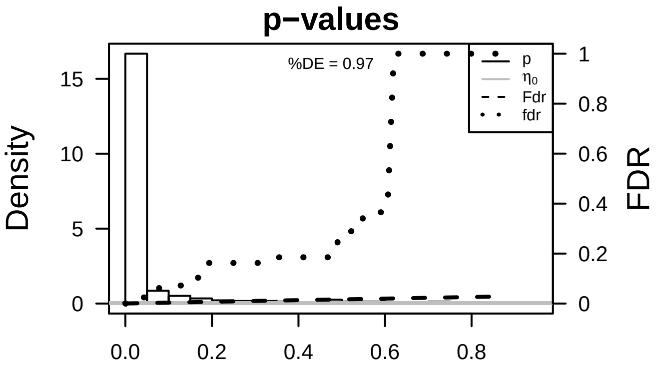
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	133	−1.73	2e−16	9e−17	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
2	113146	−1.54	2e−16	9e−17	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	8644	−1.84	2e−16	9e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	445328	−1.5	2e−16	9e−17	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
5	771	−1.5	2e−16	9e−17	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
6	760	−1.93	2e−16	9e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
7	1001	−1.55	2e−16	9e−17	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
8	9635	−2.02	2e−16	9e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
9	9982	−1.7	2e−16	9e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
10	2706	−1.5	2e−16	9e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
11	10804	−2.21	2e−16	9e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
12	56169	−1.7	2e−16	9e−17	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
13	1839	−1.68	2e−16	9e−17	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Sym
14	3552	−2.18	2e−16	9e−17	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
15	56300	−2.69	2e−16	9e−17	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
16	3613	−1.67	2e−16	9e−17	1 x 46	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC Sy
17	3860	1.38	2e−16	9e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
18	55214	−1.65	2e−16	9e−17	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
19	8581	−1.55	2e−16	9e−17	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
20	27076	−1.53	2e−16	9e−17	1 x 50	LY6/PLAUR domain containing 3 [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.32	NULL	98 / 135	H.Tiss	WIRTH_Mucosa
2	−27.23	NULL	143 / 572	Disease	GUDJ_psoriasis up
3	−18.93	NULL	11 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−17.36	NULL	34 / 76	BP	epidermis development
5	−15.74	NULL	19 / 21	CC	cornified envelope
6	−15.19	NULL	9 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
7	−14.85	NULL	13 / 21	CC	desmosome
8	−14.51	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−14.08	NULL	28 / 53	BP	keratinocyte differentiation
10	−13.82	NULL	7 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
11	−12.94	NULL	6 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
12	−12.48	NULL	6 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
13	−12.45	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
14	−11.32	NULL	7 / 29	BP	regulation of proteolysis
15	−10.98	NULL	7 / 16	GSEA C2	JAEGER_METASTASIS_DN
16	−10.85	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
17	−10.66	NULL	4 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
18	−10.47	NULL	10 / 52	BP	negative regulation of endopeptidase activity
19	−10.46	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
20	−10.29	NULL	7 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
21	−9.93	NULL	3 / 15	MF	interleukin−1 receptor binding
22	−9.85	NULL	25 / 82	CC	intermediate filament
23	−9.51	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
24	−9.39	NULL	20 / 42	BP	keratinization
25	−9.36	NULL	6 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
26	−9.19	NULL	4 / 15	CC	connexon complex
27	−9.13	NULL	9 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
28	−9.12	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
29	−9.02	NULL	2 / 2	miRNA target	miR−199a*
30	−8.46	NULL	15 / 79	MF	serine−type endopeptidase inhibitor activity
31	−8.41	NULL	3 / 16	GSEA C2	SCHAVOLT_TARGETS_OF_TP53_AND_TP63
32	−8.4	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
33	−8.37	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
34	−8.29	NULL	5 / 21	CC	gap junction
35	−8.27	NULL	5 / 12	BP	hemidesmosome assembly
36	−8.24	NULL	6 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
37	−8.1	NULL	3 / 17	BP	morphogenesis of an epithelium
38	−8.04	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
39	−7.99	NULL	3 / 11	GSEA C2	LEI_MYB_TARGETS
40	−7.93	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN