GW_186

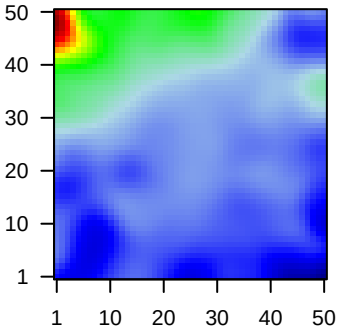
Global Summary

%DE = 0.13
genes with fdr < 0.2 = 1773 (988 + / 785 −)
genes with fdr < 0.1 = 1309 (751 + / 558 −)
genes with fdr < 0.05 = 1040 (617 + / 423 −)
genes with fdr < 0.01 = 701 (434 + / 267 −)

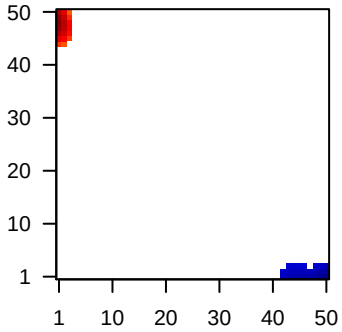
genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.12
<fdr> = 0.87

Profile



Regulated Spots



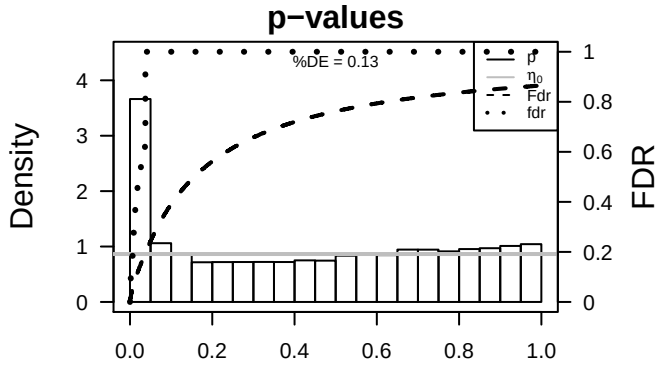
Global Genelist

Rank	ID	log(FC)	fdr p−value		Metagene	Description
1	57016	1.21	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	383	1.2	2e−16	4e−14	7 x 45	arginase 1 [Source:HGNC Symbol;Acc:663]
3	151516	2.61	2e−16	4e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
4	483	1.21	2e−16	4e−14	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
5	25805	−1.46	2e−16	4e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC S
6	684	−1.41	2e−16	4e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
7	387695	1.75	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
8	260436	−1.22	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
9	760	1.91	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
10	57172	1.3	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
11	875	−1.25	2e−16	4e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
12	1041	2.61	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
13	84518	1.36	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	1475	1.31	2e−16	4e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
15	9547	1.31	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;A
16	27065	1.39	2e−16	4e−14	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1)
17	92196	1.21	2e−16	4e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
18	1828	1.34	2e−16	4e−14	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	54855	1.2	2e−16	4e−14	49 x 1	family with sequence similarity 46, member C [Source:HGNC
20	9982	1.2	2e−16	4e−14	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Symb

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	21.43	NULL	21	CC	cornified envelope
2	19.94	NULL	42	BP	keratinization
3	19.47	NULL	135	H.Tiss	WIRTH_Mucosa
4	17.21	NULL	572	Disease	GUDJ_psoriasis up
5	17.16	NULL	53	BP	keratinocyte differentiation
6	15.41	NULL	76	BP	epidermis development
7	8.97	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
8	8.8	NULL	504	Chr	Chr 15
9	8.64	NULL	4	MMML C6	GRACIEJ_MMML 23
10	8.6	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	8.59	NULL	717	Chr	Chr 16
12	7.77	NULL	19	BP	peptide cross−linking
13	7.28	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	7.12	NULL	10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
15	6.98	NULL	186	MF	structural molecule activity
16	6.88	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
17	6.78	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
18	6.55	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
19	6.43	NULL	714	Chr	Chr 6
20	6.33	NULL	488	miRNA target	hsa−miR−15b
Underexpressed					
1	−17.68	NULL	1135	Chr	Chr 19
2	−8.27	NULL	417	H.Tiss	WIRTH_Immune system
3	−6.92	NULL	187	Chr	Chr 21
4	−6.67	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
5	−6.67	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
6	−6.44	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−6.44	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−6.44	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−6.44	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−6.38	NULL	15	CC	MHC class II protein complex
11	−6.02	NULL	11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
12	−5.97	NULL	36	BP	muscle filament sliding
13	−5.71	NULL	16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
14	−5.69	NULL	1095	TF	HEBENSTREIT_high expression TF
15	−5.63	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	−5.56	NULL	44	MF	structural constituent of muscle
17	−5.48	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
18	−5.4	NULL	10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
19	−4.96	NULL	60	BP	T cell costimulation
20	−4.76	NULL	127	H.Tiss	WIRTH_Muscle

p−values



GW_186

Local Summary

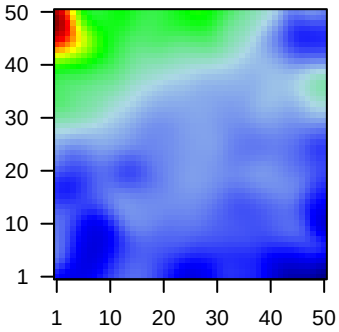
%DE = 0.86
metagenes = 20
genes = 271
genes in genesets = 264

genes with fdr < 0.1 = 217 (204 + / 13 −)
genes with fdr < 0.05 = 212 (199 + / 13 −)
genes with fdr < 0.01 = 175 (163 + / 12 −)

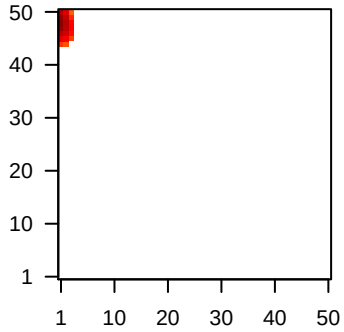
<r> metagenes = 0.92
<r> genes = 0.41

<FC> = 0.66
<shrinkage−t> = 23.37
<p−value> = 0
<fdr> = 0.26

Profile



Spot



Local Genelist

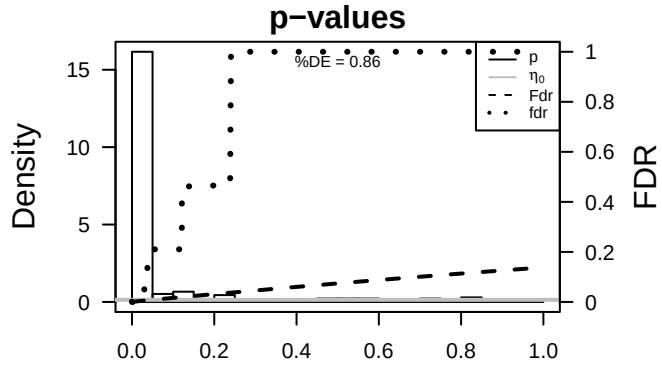
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.21	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	151516	2.61	2e−16	2e−16	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
3	387695	1.75	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
4	760	1.91	2e−16	2e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	1041	2.61	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	84518	1.36	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	1475	1.31	2e−16	2e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
8	9547	1.31	2e−16	2e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;A
9	27065	1.39	2e−16	2e−16	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1)
10	92196	1.21	2e−16	2e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
11	1828	1.34	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
12	9982	1.2	2e−16	2e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Symb
13	2312	1.86	2e−16	2e−16	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
14	10804	1.46	2e−16	2e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	26525	1.36	2e−16	2e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
16	56300	1.27	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
17	5653	1.46	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
18	5650	1.2	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
19	3848	2.69	2e−16	2e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
20	3858	1.75	2e−16	2e−16	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	50.27	NULL	18 / 21	CC	cornified envelope
2	37.87	NULL	87 / 135	H.Tiss	WIRTH_Mucosa
3	37.36	NULL	24 / 53	BP	keratinocyte differentiation
4	31.98	NULL	19 / 42	BP	keratinization
5	28.39	NULL	24 / 76	BP	epidermis development
6	26.89	NULL	104 / 572	Disease	GUDJ_psoriasis up
7	20.13	NULL	5 / 10	MF	RAGE receptor binding
8	18.52	NULL	10 / 19	BP	peptide cross−linking
9	16.39	NULL	12 / 21	CC	desmosome
10	16.32	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
11	15.93	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	15.63	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	15.24	NULL	27 / 186	MF	structural molecule activity
14	15.17	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	14.55	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	14.04	NULL	19 / 82	CC	intermediate filament
17	12.24	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	12.16	NULL	12 / 44	CC	keratin filament
19	11.71	NULL	10 / 52	BP	negative regulation of endopeptidase activity
20	11.66	NULL	7 / 29	BP	regulation of proteolysis
21	11.02	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
22	11	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
23	10.88	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
24	10.78	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
25	10.66	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
26	10.58	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
27	10.42	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
28	10.03	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
29	10.03	NULL	6 / 13	BP	negative regulation of peptidase activity
30	9.98	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
31	9.8	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
32	9.47	NULL	7 / 51	MF	protein binding, bridging
33	9.31	NULL	5 / 25	BP	response to zinc ion
34	9.09	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
35	9.06	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
36	9.04	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
37	8.94	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
38	8.89	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
39	8.88	NULL	62 / 1182	CC	extracellular region
40	8.79	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE

p−values



GW_186

Local Summary

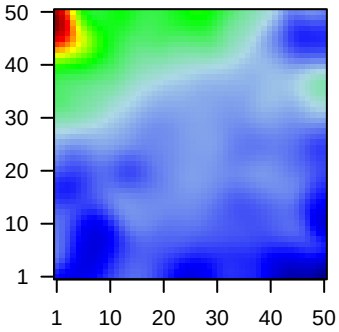
%DE = 0.79
metagenes = 25
genes = 363
genes in genesets = 360

genes with fdr < 0.1 = 240 (26 + / 214 −)
genes with fdr < 0.05 = 177 (23 + / 154 −)
genes with fdr < 0.01 = 125 (18 + / 107 −)

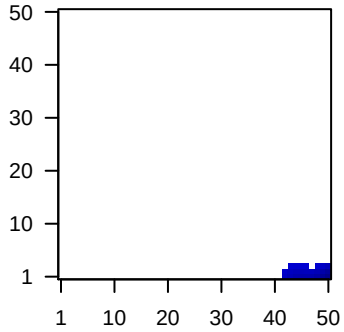
<r> metagenes = 0.94
<r> genes = 0.51

<FC> = −0.27
<shrinkage−t> = −9.33
<p−value> = 0
<fdr> = 0.53

Profile



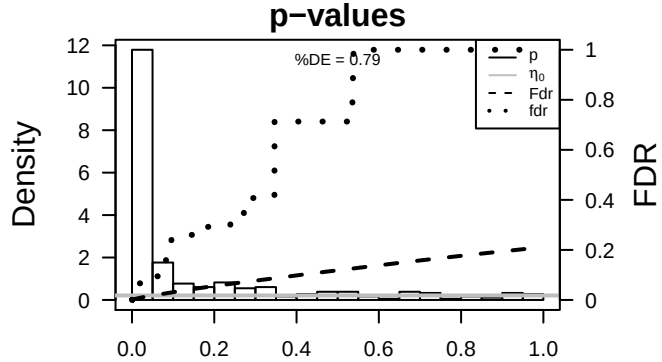
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.22	2e−16	3e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
2	57172	1.3	2e−16	3e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
3	54855	1.2	2e−16	3e−15	49 x 1	family with sequence similarity 46, member C [Source:HGNC
4	3123	−1.51	2e−16	3e−15	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
5	3543	1.13	2e−16	3e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
6	51755	1.04	8e−13	3e−11	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
7	348	−1.04	8e−13	5e−10	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
8	4050	−1	7e−12	8e−09	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
9	3127	−0.94	1e−10	2e−08	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
10	4851	−0.9	5e−10	2e−08	42 x 1	notch 1 [Source:HGNC Symbol;Acc:7881]
11	4069	−0.89	8e−10	2e−08	50 x 2	lysozyme [Source:HGNC Symbol;Acc:6740]
12	341	−0.89	1e−09	2e−08	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
13	9806	−0.88	1e−09	2e−08	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
14	241	−0.88	2e−09	2e−08	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
15	6364	−0.88	2e−09	2e−08	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
16	924	−0.88	2e−09	3e−07	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
17	713	−0.85	6e−09	1e−06	50 x 1	complement component 1, q subcomponent, B chain [Source
18	5880	−0.8	4e−08	1e−06	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small (
19	962	−0.78	7e−08	1e−06	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
20	915	−0.78	8e−08	1e−06	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.5	NULL	14 / 15	CC	MHC class II protein complex
2	−25.11	NULL	106 / 417	H.Tiss	WIRTH_Immune system
3	−20.68	NULL	3 / 3	MMML C6	SOCIEJ_MMML 7
4	−18.75	NULL	8 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
5	−18.1	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
6	−17.78	NULL	9 / 13	Cancer	GENTLES_modul18
7	−16.97	NULL	59 / 312	BP	immune response
8	−16.6	NULL	20 / 60	BP	T cell costimulation
9	−16.14	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
10	−15.72	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
11	−15.49	NULL	16 / 47	BP	antigen processing and presentation
12	−14.95	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
13	−14.86	NULL	7 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
14	−14.48	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
15	−14.42	NULL	5 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
16	−13.95	NULL	7 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
17	−13.9	NULL	5 / 13	MMML C6	SOCIEJ_MMML 6
18	−13.53	NULL	5 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
19	−13.53	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
20	−13.5	NULL	96 / 553	Cancer	Lembcke_Colonic Inflammation
21	−13.42	NULL	9 / 28	CC	transport vesicle membrane
22	−12.87	NULL	19 / 84	BP	T cell receptor signaling pathway
23	−12.72	NULL	5 / 12	GSEA C2	BIOCARTA_CTLA4_PATHWAY
24	−12.7	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
25	−12.64	NULL	6 / 12	CC	T cell receptor complex
26	−12.46	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
27	−12.36	NULL	12 / 45	BP	T cell activation
28	−12.05	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
29	−12.02	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
30	−11.96	NULL	4 / 13	BP	lymph node development
31	−11.85	NULL	9 / 35	CC	trans−Golgi network membrane
32	−11.44	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
33	−11.31	NULL	18 / 74	BP	regulation of immune response
34	−11.24	NULL	5 / 16	GSEA C2	MOREIRA_RESPONSE_TO_TSA_DN
35	−11.15	NULL	40 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
36	−11.15	NULL	40 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
37	−11.15	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
38	−11.15	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
39	−11.09	NULL	5 / 14	GSEA C2	BIOCARTA_STATHMIN_PATHWAY
40	−10.62	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN