GW_155

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1447 (764 + / 683 −)

genes with fdr < 0.1 = 1030 (574 + / 456 −)

genes with fdr < 0.05 = 916 (513 + / 403 −)

genes with fdr < 0.01 = 512 (290 + / 222 −)

genes in genesets = 16332

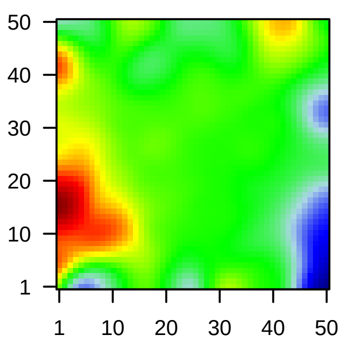
<FC> = 0

<shrinkage−t> = 0

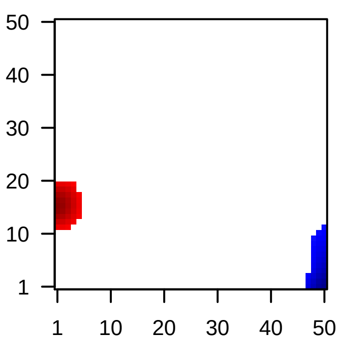
<p−value> = 0.15

<fdr> = 0.87

Profile



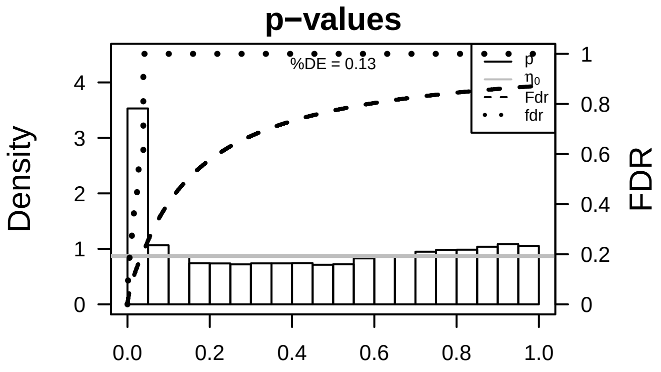
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	220	1.97	2e−16	8e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
2	55107	3.05	2e−16	8e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
3	664	−1.61	2e−16	8e−14	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HG
4	64073	2.04	2e−16	8e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
5	339512	2.22	2e−16	8e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
6	760	2.29	2e−16	8e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
7	595	1.75	2e−16	8e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
8	9547	−1.76	2e−16	8e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
9	1672	−1.93	2e−16	8e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
10	55894	−1.61	2e−16	8e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	−2.15	2e−16	8e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	−2.37	2e−16	8e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1717	2.48	2e−16	8e−14	13 x 50	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
14	2167	3.45	2e−16	8e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
15	8772	1.7	2e−16	8e−14	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
16	10468	1.93	2e−16	8e−14	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
17	3043	−1.76	2e−16	8e−14	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
18	3552	1.69	2e−16	8e−14	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
19	3553	2.08	2e−16	8e−14	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
20	56300	1.74	2e−16	8e−14	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.18	NULL	530	Cancer	Lembcke_Normal vs Adenoma
2	8.55	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	8.55	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	8.36	NULL	504	Chr	Chr 15
5	8	NULL	1720	Chr	Chr 1
6	7.42	NULL	957	Chr	Chr 11
7	7.18	NULL	42	BP	keratinization
8	7	NULL	1135	Chr	Chr 19
9	6.35	NULL	15	GSEA C2	LY_AGING_MIDDLE_DN
10	6.12	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
11	6.11	NULL	572	Disease	GUDJ_psoriasis up
12	5.81	NULL	6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
13	5.73	NULL	13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
14	5.72	NULL	232	Chr	Chr 18
15	5.7	NULL	12	BP	hemidesmosome assembly
16	5.66	NULL	15	MF	interleukin−1 receptor binding
17	5.63	NULL	16	GSEA C2	NOJIMA_SFRP2_TARGETS_DN
18	5.3	NULL	13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
19	5.25	NULL	14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
20	5.23	NULL	51	BP	type I interferon signaling pathway
Underexpressed					
1	−10.58	NULL	1033	Chr	Chr 2
2	−10.34	NULL	633	Chr	Chr 9
3	−9.22	NULL	15	CC	MHC class II protein complex
4	−8.69	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−8.21	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
6	−8.11	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	−8.04	NULL	417	H.Tiss	WIRTH_Immune system
8	−6.61	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	−6.35	NULL	16	MMML CGS	MACIEJ_MMML 1
10	−6.33	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
11	−6.08	NULL	190	CC	extracellular matrix
12	−5.91	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
13	−5.86	NULL	127	H.Tiss	WIRTH_Muscle
14	−5.83	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
15	−5.77	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	−5.72	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
17	−5.62	NULL	36	BP	muscle filament sliding
18	−5.56	NULL	92	BP	translational elongation
19	−5.45	NULL	7	MMML CGS	MACIEJ_MMML 5
20	−5.39	NULL	43	TF Tissue	VAQUERIZAS_Uterus

GW_155

Local Summary

%DE = 0.71

metagenes = 40

genes = 386

genes in genesets = 384

genes with fdr < 0.1 = 166 (165 + / 1 −)

genes with fdr < 0.05 = 127 (126 + / 1 −)

genes with fdr < 0.01 = 67 (67 + / 0 −)

<r> metagenes = 0.93

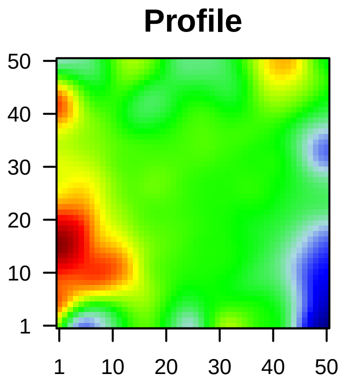
<r> genes = 0.27

<FC> = 0.38

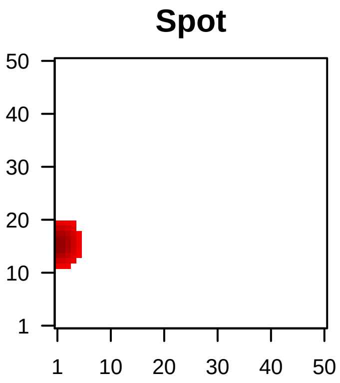
<shrinkage−t> = 13.33

<p−value> = 0.01

<fdr> = 0.66



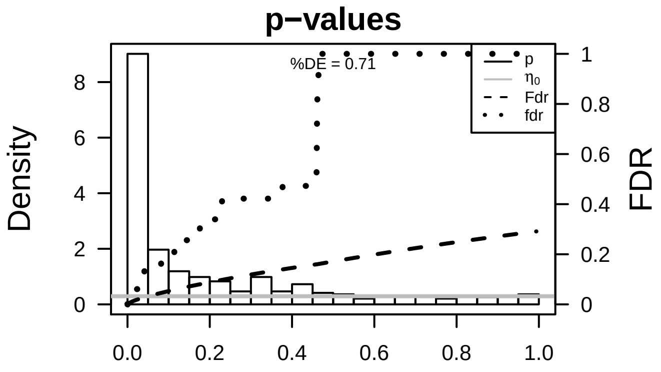
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8772	1.7	2e−16	5e−15	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
2	219927	1.81	2e−16	5e−15	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
3	283869	2.01	2e−16	5e−15	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
4	220064	1.88	2e−16	5e−15	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
5	219931	2.01	2e−16	5e−15	1 x 14	two pore segment channel 2 [Source:HGNC Symbol;Acc:208
6	131076	1.52	3e−15	8e−13	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
7	991	1.49	1e−14	2e−09	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
8	2017	1.29	2e−11	2e−08	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]
9	2932	1.22	2e−10	7e−07	1 x 17	glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc
10	2194	1.12	7e−09	1e−06	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
11	10969	1.06	3e−08	1e−06	1 x 14	EBNA1 binding protein 2 [Source:HGNC Symbol;Acc:15531]
12	3237	1.06	3e−08	3e−06	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
13	3508	1.04	6e−08	7e−06	1 x 14	immunoglobulin mu binding protein 2 [Source:HGNC Symbol;
14	230	1.02	1e−07	2e−05	2 x 17	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A
15	51373	0.97	4e−07	2e−05	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
16	142678	0.95	8e−07	2e−05	1 x 17	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symb
17	51400	0.95	8e−07	2e−05	1 x 18	protein phosphatase methylesterase 1 [Source:HGNC Symbo
18	1374	0.94	1e−06	2e−05	1 x 13	carnitine palmitoyltransferase 1A (liver) [Source:HGNC Symb
19	3326	0.92	1e−06	2e−05	1 x 14	heat shock protein 90kDa alpha (cytosolic), class B member
20	3217	0.93	1e−06	2e−05	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	10.08	NULL	22 / 153	MF	structural constituent of ribosome
2	9.57	NULL	6 / 19	CC	mitochondrial small ribosomal subunit
3	9.56	NULL	26 / 253	BP	translation
4	9.32	NULL	1 / 6	GSEA C2	GALI_TP53_TARGETS_APOPTOTIC_DN
5	8.97	NULL	20 / 167	CC	ribosome
6	8.88	NULL	2 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
7	8.65	NULL	5 / 15	Cancer	GENTLES_modul1
8	8.64	NULL	16 / 96	BP	rRNA processing
9	8.62	NULL	2 / 18	BP	smooth muscle contraction
10	8.15	NULL	1 / 6	GSEA C2	WAESCH_ANAPHASE_PROMOTING_COMPLEX
11	7.95	NULL	2 / 7	GSEA C2	REACTOME_SIGNALING_BY_WNT
12	7.89	NULL	2 / 21	BP	feeding behavior
13	7.87	NULL	85 / 1318	CC	mitochondrion
14	7.72	NULL	3 / 15	GSEA C2	LY_AGING_MIDDLE_DN
15	7.45	NULL	4 / 14	GSEA C2	STEIN_ESRRA_TARGETS_UP
16	7.39	NULL	2 / 10	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_3_DN
17	7.39	NULL	1 / 9	GSEA C2	BIOCARTA_RELA_PATHWAY
18	7.39	NULL	1 / 9	GSEA C2	BIOCARTA_NFKB_PATHWAY
19	7.39	NULL	1 / 9	GSEA C2	BIOCARTA_SODD_PATHWAY
20	7.39	NULL	1 / 9	GSEA C2	REACTOME_DEATH_RECEPTOR_SIGNALLING
21	7.3	NULL	2 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
22	7.14	NULL	2 / 4	TF	MYC_Cell growth and proliferation UP
23	7.13	NULL	4 / 13	GSEA C2	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
24	7.12	NULL	1 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP
25	7.1	NULL	4 / 14	GSEA C2	NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
26	7.03	NULL	4 / 13	GSEA C2	REACTOME_GLYCOLYSIS
27	6.96	NULL	40 / 957	Chr	Chr 11
28	6.96	NULL	2 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
29	6.95	NULL	1 / 10	MF	death receptor binding
30	6.95	NULL	1 / 10	BP	positive regulation of macrophage differentiation
31	6.88	NULL	3 / 14	Pathw Act	BENTINK_myc.1
32	6.77	NULL	40 / 579	CC	nucleolus
33	6.68	NULL	3 / 15	CC	mitochondrial large ribosomal subunit
34	6.66	NULL	2 / 15	GSEA C2	WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE
35	6.65	NULL	3 / 23	BP	positive regulation of proteolysis
36	6.58	NULL	1 / 11	BP	regulation of extrinsic apoptotic signaling pathway in absence of lig
37	6.58	NULL	1 / 11	GSEA C2	HOFMANN_CELL_LYMPHOMA_DN
38	6.58	NULL	1 / 11	GSEA C2	ST_TUMOR_NECROSIS_FACTOR_PATHWAY
39	6.51	NULL	3 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
40	6.48	NULL	2 / 30	BP	extrinsic apoptotic signaling pathway in absence of ligand

GW_155

Local Summary

%DE = 0.77

metagenes = 36

genes = 530

genes in genesets = 527

genes with fdr < 0.1 = 289 (16 + / 273 −)

genes with fdr < 0.05 = 244 (13 + / 231 −)

genes with fdr < 0.01 = 159 (9 + / 150 −)

<r> metagenes = 0.83

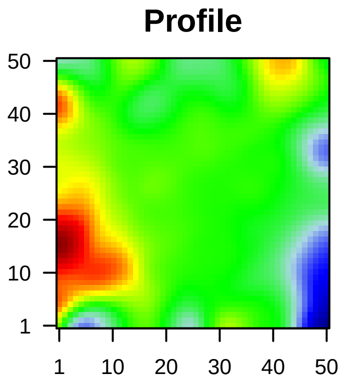
<r> genes = 0.33

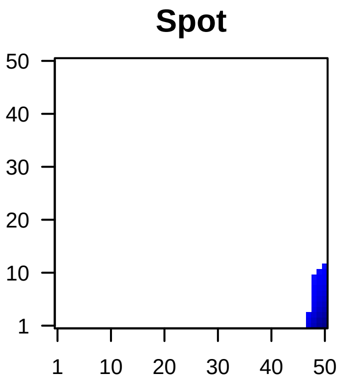
<FC> = −0.38

<shrinkage−t> = −13.31

<p−value> = 0.01

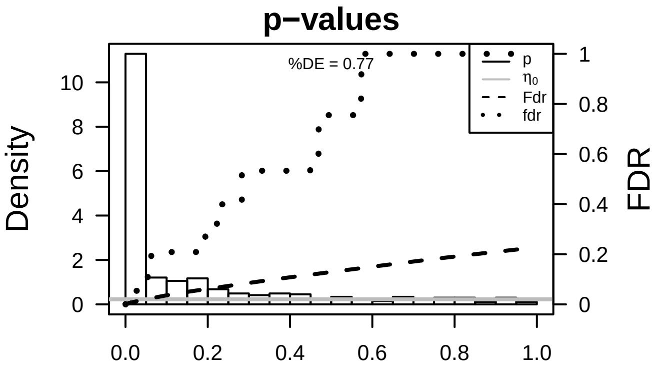
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6192	−1.62	2e−16	3e−14	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
2	79901	−1.43	1e−13	8e−12	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
3	713	−1.42	2e−13	8e−12	50 x 1	complement component 1, q subcomponent, B chain [Source
4	4283	−1.41	3e−13	8e−12	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
5	347733	−1.41	3e−13	4e−11	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
6	1266	−1.38	6e−13	6e−10	50 x 6	calponin 3, acidic [Source:HGNC Symbol;Acc:2157]
7	84952	−1.33	6e−12	4e−09	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
8	10628	−1.24	5e−11	4e−09	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
9	894	−1.26	7e−11	5e−08	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
10	10550	−1.2	5e−10	5e−08	50 x 3	ADP−ribosylation−like factor 6 interacting protein 5 [Source:H
11	3109	−1.18	8e−10	5e−08	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
12	23048	−1.16	2e−09	5e−08	49 x 1	formin binding protein 1 [Source:HGNC Symbol;Acc:17069]
13	10537	−1.16	2e−09	8e−07	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
14	4256	−1.11	8e−09	3e−06	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
15	30061	−1.05	5e−08	3e−06	50 x 5	solute carrier family 40 (iron−regulated transporter), member
16	9806	−1.03	8e−08	3e−06	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
17	81704	−1.02	1e−07	3e−06	50 x 1	dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:19191]
18	3113	−1.02	1e−07	6e−06	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
19	1436	−0.98	3e−07	6e−06	50 x 1	colony stimulating factor 1 receptor [Source:HGNC Symbol;A
20	255231	−0.98	3e−07	6e−06	49 x 1	mucolipin 2 [Source:HGNC Symbol;Acc:13357]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−25.52	NULL	12 / 15	CC	MHC class II protein complex
2	−17.37	NULL	16 / 47	BP	antigen processing and presentation
3	−15.73	NULL	112 / 553	Cancer	Lembcke_Colonic Inflammation
4	−15.62	NULL	90 / 417	H.Tiss	WIRTH_Immune system
5	−15.6	NULL	59 / 312	BP	immune response
6	−15.4	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
7	−14.43	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	−14.12	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	−13.66	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
10	−13.43	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
11	−13.06	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
12	−12.77	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
13	−12.47	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
14	−12.4	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
15	−12.3	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
16	−12.18	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
17	−11.78	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
18	−11.7	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
19	−11.55	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	−11.54	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
21	−11.54	NULL	6 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
22	−11.1	NULL	53 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
23	−11.1	NULL	53 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
24	−11.1	NULL	53 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
25	−11.1	NULL	53 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
26	−11.02	NULL	9 / 28	CC	transport vesicle membrane
27	−10.74	NULL	9 / 35	CC	trans−Golgi network membrane
28	−10.59	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
29	−10.54	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
30	−10.46	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
31	−10.27	NULL	14 / 60	BP	T cell costimulation
32	−10.1	NULL	8 / 16	GSEA C2	SU_THYMUS
33	−10.05	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
34	−9.99	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
35	−9.99	NULL	4 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
36	−9.93	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
37	−9.79	NULL	10 / 46	CC	endocytic vesicle membrane
38	−9.73	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
39	−9.73	NULL	6 / 13	Cancer	GENTLES_modul18
40	−9.56	NULL	3 / 13	GSEA C2	KANG_IMMORTALIZED_BY_TERT_UP