GW_093

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1626 (875 + / 751 −)

genes with fdr < 0.1 = 1255 (681 + / 574 −)

genes with fdr < 0.05 = 1050 (572 + / 478 −)

genes with fdr < 0.01 = 708 (409 + / 299 −)

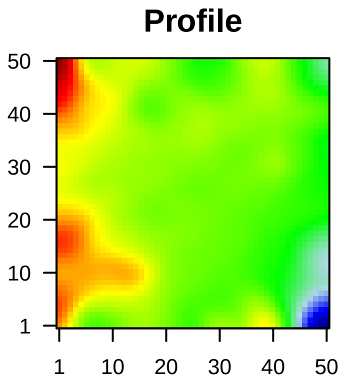
genes in genesets = 16332

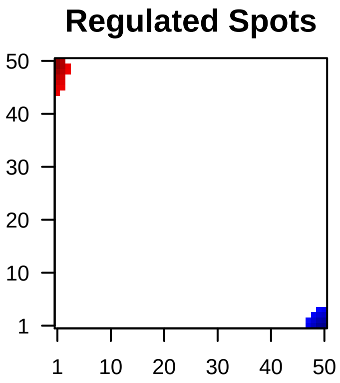
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.87



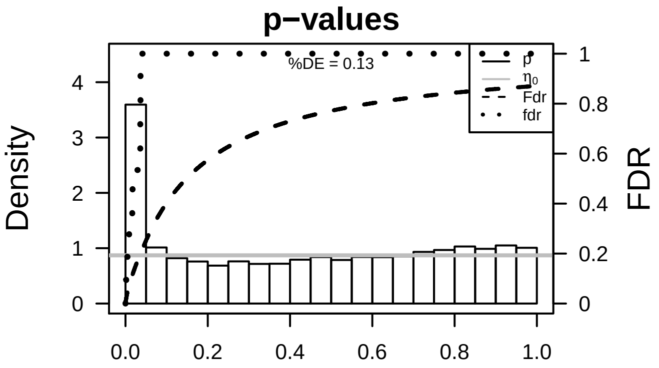


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.94	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	216	−1.54	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	222	1.29	2e−16	4e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	242	1.76	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
5	144193	1.36	2e−16	4e−14	15 x 50	amidohydrolase domain containing 1 [Source:HGNC Symbol;
6	164284	1.34	2e−16	4e−14	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:
7	55971	1.43	2e−16	4e−14	13 x 50	BAI1−associated protein 2−like 1 [Source:HGNC Symbol;Acc
8	387695	1.58	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	260436	−1.32	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
10	51806	−1.6	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
11	57172	−1.47	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	857	1.48	2e−16	4e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
13	972	−1.29	2e−16	4e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
14	4680	1.39	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
15	84518	1.64	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	26047	−1.35	2e−16	4e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
17	49860	1.73	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	126410	1.86	2e−16	4e−14	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
19	92196	−1.62	2e−16	4e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
20	414325	1.41	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	14.2	NULL	572	Disease	GUDJ_psoriasis up
2	13.96	NULL	21	CC	cornified envelope
3	13.94	NULL	135	H.Tiss	WIRTH_Mucosa
4	11.79	NULL	42	BP	keratinization
5	11.29	NULL	743	Chr	Chr 7
6	9.55	NULL	53	BP	keratinocyte differentiation
7	9.21	NULL	1135	Chr	Chr 19
8	8.76	NULL	76	BP	epidermis development
9	8.18	NULL	19	BP	peptide cross−linking
10	7.29	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	7.02	NULL	918	Chr	Chr 17
12	6.57	NULL	699	Chr	Chr 5
13	6.56	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	6.33	NULL	13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
15	6.2	NULL	15	GSEA C2	HOOI_ST7_TARGETS_UP
16	6.19	NULL	11	GSEA C2	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
17	5.8	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	5.77	NULL	14	GSEA C2	PROVENZANI_METASTASIS_DN
19	5.63	NULL	7	MMML CGS	MACIEJ_MMML 9
20	5.41	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
Underexpressed					
1	−12.46	NULL	602	Chr	Chr 10
2	−11.9	NULL	417	H.Tiss	WIRTH_Immune system
3	−9.27	NULL	866	Chr	Chr 12
4	−8.36	NULL	15	CC	MHC class II protein complex
5	−7.33	NULL	312	BP	immune response
6	−6.74	NULL	553	Cancer	Lembcke_Colonic Inflammation
7	−6.62	NULL	47	BP	antigen processing and presentation
8	−6.13	NULL	162	CC	external side of plasma membrane
9	−5.96	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
10	−5.93	NULL	7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
11	−5.87	NULL	280	Chr	Chr 13
12	−5.83	NULL	74	BP	regulation of immune response
13	−5.8	NULL	16	GSEA C2	KORKOLA_TERATOMA_UP
14	−5.47	NULL	8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
15	−5.45	NULL	717	Chr	Chr 16
16	−5.4	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
17	−5.33	NULL	187	Chr	Chr 21
18	−5.32	NULL	84	BP	T cell receptor signaling pathway
19	−5.29	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
20	−5.28	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY



GW_093

Local Summary

%DE = 0.83

metagenes = 15

genes = 234

genes in genesets = 229

genes with fdr < 0.1 = 162 (132 + / 30 −)

genes with fdr < 0.05 = 162 (132 + / 30 −)

genes with fdr < 0.01 = 141 (119 + / 22 −)

<r> metagenes = 0.93

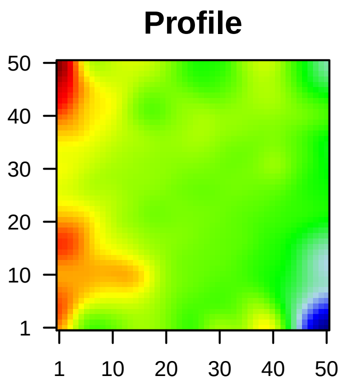
<r> genes = 0.42

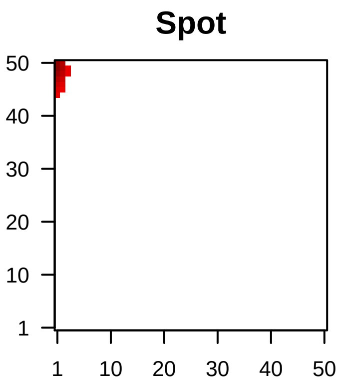
<FC> = 0.5

<shrinkage−t> = 17.74

<p−value> = 0

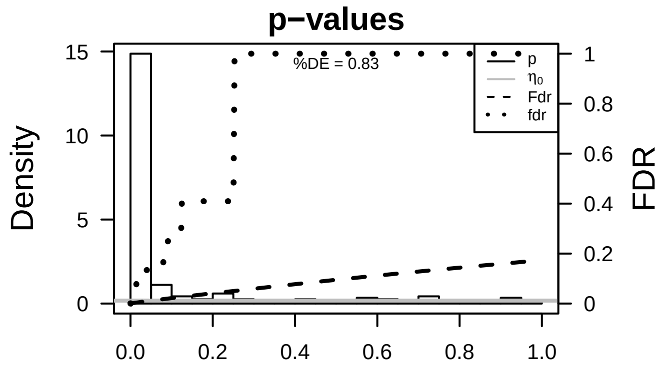
<fdr> = 0.32





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.94	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	222	1.29	2e−16	2e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	242	1.76	2e−16	2e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
4	387695	1.58	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
5	4680	1.39	2e−16	2e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	84518	1.64	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	49860	1.73	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
8	126410	1.86	2e−16	2e−16	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
9	414325	1.41	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	1673	2.59	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	2167	1.5	2e−16	2e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
12	9982	1.22	2e−16	2e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
13	56300	1.38	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
14	43849	1.42	2e−16	2e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
15	26085	1.46	2e−16	2e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
16	5650	1.48	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
17	3848	−1.35	2e−16	2e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
18	192666	1.87	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
19	3851	−2.08	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
20	388533	2.28	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGN



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.86	NULL	18 / 21	CC	cornified envelope
2	34.73	NULL	78 / 135	H.Tiss	WIRTH_Mucosa
3	31.69	NULL	19 / 42	BP	keratinization
4	26.05	NULL	24 / 53	BP	keratinocyte differentiation
5	24.61	NULL	95 / 572	Disease	GUDJ_psoriasis up
6	21.25	NULL	23 / 76	BP	epidermis development
7	20.94	NULL	10 / 19	BP	peptide cross−linking
8	17.19	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	16.28	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	16.06	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	13.75	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	12.12	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	11.76	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
14	10.72	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	10.68	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
16	10.05	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
17	9.92	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
18	9.77	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
19	9.71	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
20	9.63	NULL	12 / 21	CC	desmosome
21	9.54	NULL	3 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
22	9.43	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
23	8.89	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
24	8.66	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
25	8.55	NULL	2 / 10	BP	lipoxygenase pathway
26	8.54	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
27	8.5	NULL	57 / 1182	CC	extracellular region
28	8.35	NULL	5 / 23	MF	peptidase inhibitor activity
29	8.01	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
30	7.98	NULL	26 / 186	MF	structural molecule activity
31	7.77	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
32	7.69	NULL	2 / 12	BP	linoleic acid metabolic process
33	7.44	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
34	7.4	NULL	3 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
35	7.26	NULL	5 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
36	7.24	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
37	7.21	NULL	8 / 73	BP	defense response to bacterium
38	7.2	NULL	2 / 17	Disease	BCHETNIA_EBM up
39	7.11	NULL	13 / 122	MF	serine−type endopeptidase activity
40	7.08	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP

GW_093

Local Summary

%DE = 0.98

metagenes = 13

genes = 245

genes in genesets = 243

genes with fdr < 0.1 = 230 (4 + / 226 −)

genes with fdr < 0.05 = 222 (4 + / 218 −)

genes with fdr < 0.01 = 212 (1 + / 211 −)

<r> metagenes = 0.99

<r> genes = 0.6

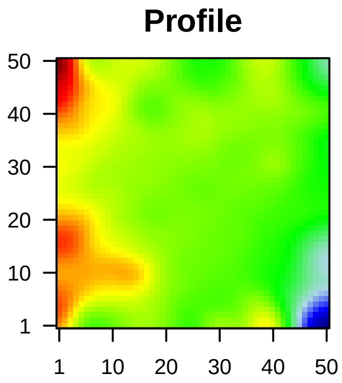
<FC> = −0.59

<shrinkage−t> = −20.55

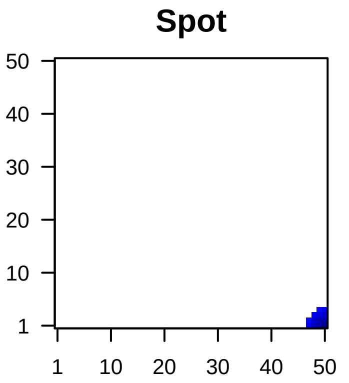
<p−value> = 0

<fdr> = 0.25

Profile



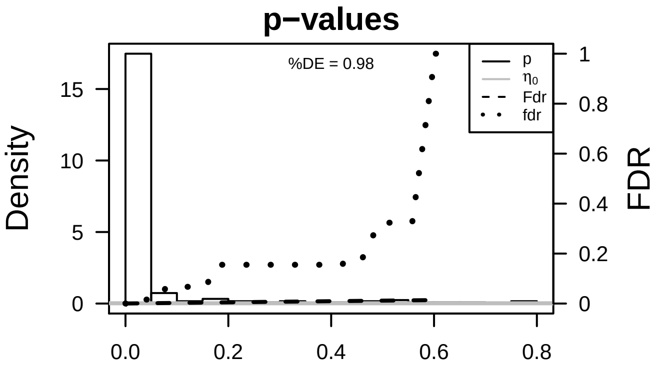
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.32	2e−16	1e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
2	57172	−1.47	2e−16	1e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
3	972	−1.29	2e−16	1e−16	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
4	3113	−1.62	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Sourc
5	3122	−1.26	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
6	3512	−1.61	2e−16	1e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
7	3543	−2.1	2e−16	1e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
8	3936	−1.34	2e−16	1e−16	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
9	6578	−1.28	2e−16	1e−16	50 x 4	solute carrier organic anion transporter family, member 2A1 [
10	3109	−1.23	2e−15	2e−14	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
11	3108	−1.21	7e−15	1e−13	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
12	713	−1.18	3e−14	9e−13	50 x 1	complement component 1, q subcomponent, B chain [Source
13	7351	−1.14	3e−13	9e−13	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
14	241	−1.12	5e−13	9e−13	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
15	51755	−1.12	6e−13	7e−12	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
16	3059	−1.08	4e−12	7e−12	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
17	7305	−1.08	4e−12	1e−11	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
18	83641	−1.06	1e−11	1e−11	50 x 1	family with sequence similarity 107, member B [Source:HGN
19	1436	−1.06	1e−11	1e−11	50 x 1	colony stimulating factor 1 receptor [Source:HGNC Symbol;A
20	714	−1.05	1e−11	2e−11	50 x 1	complement component 1, q subcomponent, C chain [Source

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−38.5	NULL	12 / 15	CC	MHC class II protein complex
2	−27.56	NULL	86 / 417	H.Tiss	WIRTH_Immune system
3	−23.99	NULL	15 / 47	BP	antigen processing and presentation
4	−23.21	NULL	86 / 553	Cancer	Lembcke_Colonic Inflammation
5	−22.65	NULL	47 / 312	BP	immune response
6	−21.39	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
7	−19.71	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
8	−19.16	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
9	−19.15	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
10	−18.96	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
11	−18.21	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
12	−17.51	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	−17.51	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	−17.51	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	−17.51	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	−17	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
17	−16.49	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−16.31	NULL	7 / 28	CC	transport vesicle membrane
19	−16.01	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
20	−15.95	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
21	−15.88	NULL	5 / 12	BP	immunoglobulin mediated immune response
22	−15.62	NULL	13 / 60	BP	T cell costimulation
23	−15.55	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
24	−15.13	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
25	−15.01	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
26	−14.58	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
27	−14.55	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
28	−14.54	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
29	−14.54	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
30	−14.25	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
31	−14.08	NULL	17 / 74	BP	regulation of immune response
32	−13.83	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
33	−13.77	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
34	−13.77	NULL	8 / 35	CC	trans−Golgi network membrane
35	−13.6	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
36	−13.21	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
37	−13.19	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
38	−13.17	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
39	−13.08	NULL	5 / 12	BP	dendritic cell chemotaxis
40	−13.07	NULL	13 / 84	BP	T cell receptor signaling pathway