GW_275

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2062 (1089 + / 973 −)

genes with fdr < 0.1 = 1805 (948 + / 857 −)

genes with fdr < 0.05 = 1558 (809 + / 749 −)

genes with fdr < 0.01 = 1181 (602 + / 579 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.06

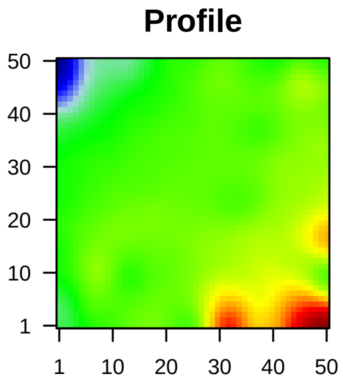
<fdr> = 0.85

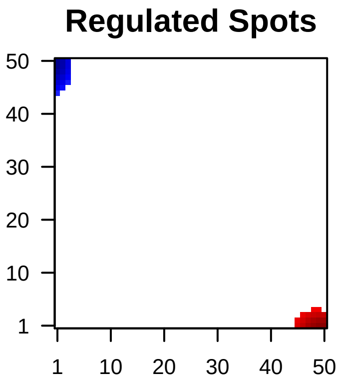
Global Genelist

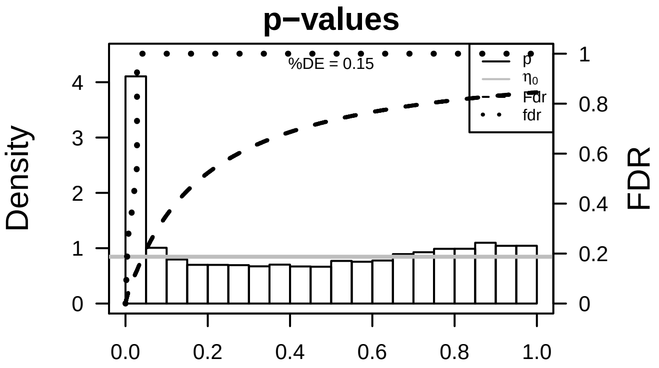
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.68	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	21	2.13	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
3	27299	2.02	2e−16	2e−14	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
4	131	−2.04	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	113146	−2.2	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
6	57016	−2.68	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
7	441282	−2.03	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
8	8644	−2.55	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
9	1109	−1.64	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
10	220	−2.03	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
11	222	−1.85	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
12	55107	−1.87	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
13	301	−1.93	2e−16	2e−14	4 x 48	annexin A1 [Source:HGNC Symbol;Acc:533]
14	348	1.69	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
15	80117	1.61	2e−16	2e−14	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:
16	92591	1.89	2e−16	2e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
17	664	−1.64	2e−16	2e−14	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H
18	121551	−1.76	2e−16	2e−14	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
19	10974	−2.15	2e−16	2e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
20	387695	−2.22	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	19.86	NULL	417	H.Tiss	WIRTH_Immune system
2	16.24	NULL	312	BP	immune response
3	13.79	NULL	51	BP	type I interferon signaling pathway
4	12.51	NULL	316	Cancer	SPANG_BCL6−index2
5	12.45	NULL	204	BP	cytokine−mediated signaling pathway
6	11.81	NULL	553	Cancer	Lembcke_Colonic Inflammation
7	11.77	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	11.73	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	11.6	NULL	274	Lymphoma	SPANG_IL21 DN
10	11.16	NULL	74	BP	regulation of immune response
11	11.02	NULL	60	BP	interferon−gamma−mediated signaling pathway
12	10.96	NULL	123	BP	defense response to virus
13	10.88	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
14	10.57	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
15	9.84	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
16	9.73	NULL	47	BP	antigen processing and presentation
17	9.41	NULL	15	CC	MHC class II protein complex
18	9.41	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
19	9.13	NULL	14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
20	9.12	NULL	109	BP	response to virus
Underexpressed					
1	−36.81	NULL	135	H.Tiss	WIRTH_Mucosa
2	−20.52	NULL	21	CC	cornified envelope
3	−19.63	NULL	76	BP	epidermis development
4	−18.35	NULL	53	BP	keratinocyte differentiation
5	−17.37	NULL	42	BP	keratinization
6	−14.5	NULL	572	Disease	GUDJ_psoriasis up
7	−13.13	NULL	19	BP	peptide cross−linking
8	−12.7	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	−10.49	NULL	186	MF	structural molecule activity
10	−10.22	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
11	−9.92	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
12	−9.8	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	−9.17	NULL	38	BP	epithelial cell differentiation
14	−8.48	NULL	10	MF	RAGE receptor binding
15	−8.43	NULL	1146	TF	HEBENSTREIT_low expression TF
16	−8.38	NULL	82	CC	intermediate filament
17	−8.38	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
18	−8.17	NULL	8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
19	−8.14	NULL	44	CC	keratin filament
20	−8.13	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE







GW_275

Local Summary

%DE = 0.99

metagenes = 19

genes = 288

genes in genesets = 285

genes with fdr < 0.1 = 282 (277 + / 5 −)

genes with fdr < 0.05 = 276 (272 + / 4 −)

genes with fdr < 0.01 = 274 (270 + / 4 −)

<r> metagenes = 0.99

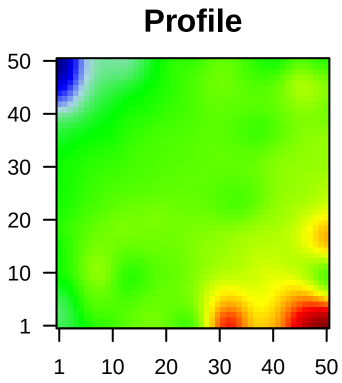
<r> genes = 0.59

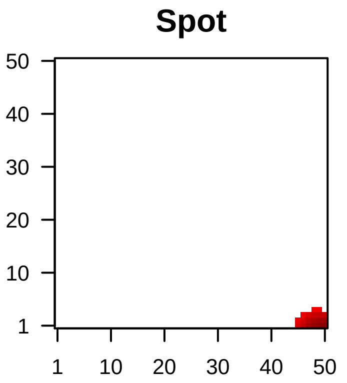
<FC> = 1.12

<shrinkage−t> = 39.19

<p−value> = 0

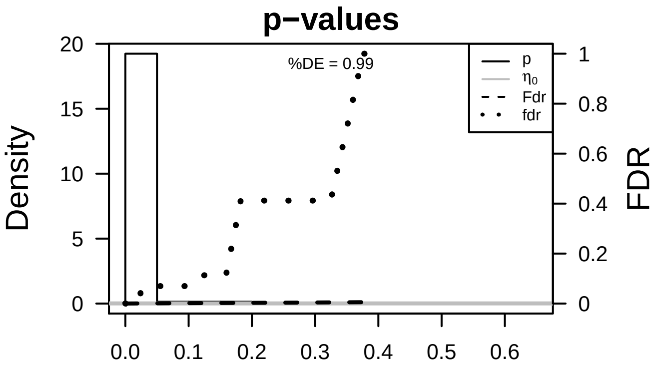
<fdr> = 0.08





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27299	2.02	2e−16	1e−17	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
2	348	1.69	2e−16	1e−17	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	92591	1.89	2e−16	1e−17	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
4	713	2.72	2e−16	1e−17	50 x 1	complement component 1, q subcomponent, B chain [Source
5	714	2.26	2e−16	1e−17	50 x 1	complement component 1, q subcomponent, C chain [Source
6	57172	2.57	2e−16	1e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
7	6363	2.79	2e−16	1e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
8	6364	2.48	2e−16	1e−17	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
9	6352	2.29	2e−16	1e−17	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
10	929	1.61	2e−16	1e−17	50 x 3	CD14 molecule [Source:HGNC Symbol;Acc:1628]
11	962	1.61	2e−16	1e−17	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
12	924	1.73	2e−16	1e−17	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
13	972	1.93	2e−16	1e−17	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
14	925	1.67	2e−16	1e−17	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
15	51755	2.3	2e−16	1e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
16	1436	1.84	2e−16	1e−17	50 x 1	colony stimulating factor 1 receptor [Source:HGNC Symbol;A
17	4283	2.78	2e−16	1e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
18	441168	1.72	2e−16	1e−17	46 x 1	family with sequence similarity 26, member F [Source:HGNC
19	2207	1.85	2e−16	1e−17	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
20	10875	1.85	2e−16	1e−17	50 x 1	fibrinogen−like 2 [Source:HGNC Symbol;Acc:3696]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.5	NULL	101 / 417	H.Tiss	WIRTH_Immune system
2	27.49	NULL	13 / 15	CC	MHC class II protein complex
3	22.95	NULL	56 / 312	BP	immune response
4	22.75	NULL	98 / 553	Cancer	Lembcke_Colonic Inflammation
5	20.22	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
6	19.26	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
7	18.42	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
8	18.19	NULL	41 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	18.19	NULL	41 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	18.19	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	18.19	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	17.89	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
13	17.39	NULL	15 / 47	BP	antigen processing and presentation
14	17.06	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
15	17.05	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
16	16.04	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
17	15.22	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
18	15.1	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
19	14.81	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
20	14.73	NULL	19 / 60	BP	T cell costimulation
21	14.63	NULL	17 / 74	BP	regulation of immune response
22	14.46	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
23	14.31	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
24	14.21	NULL	28 / 162	CC	external side of plasma membrane
25	14.14	NULL	8 / 13	Cancer	GENTLES_modul18
26	14.02	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
27	13.62	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
28	13.5	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
29	13.46	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
30	13.4	NULL	5 / 12	BP	immunoglobulin mediated immune response
31	13.05	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
32	12.48	NULL	9 / 43	BP	positive regulation of T cell proliferation
33	12.28	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
34	12.22	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
35	12.06	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
36	12.04	NULL	4 / 16	BP	cytolysis
37	12.03	NULL	8 / 16	GSEA C2	SU_THYMUS
38	12	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
39	11.83	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
40	11.82	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE

GW_275

Local Summary

%DE = 0.99

metagenes = 18

genes = 260

genes in genesets = 254

genes with fdr < 0.1 = 253 (2 + / 251 −)

genes with fdr < 0.05 = 251 (2 + / 249 −)

genes with fdr < 0.01 = 244 (1 + / 243 −)

<r> metagenes = 0.93

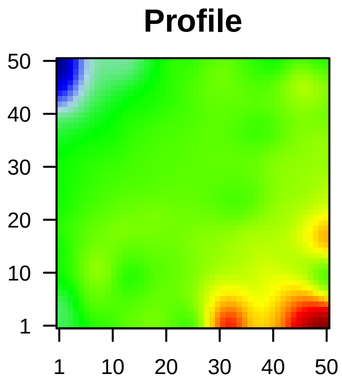
<r> genes = 0.42

<FC> = −1.52

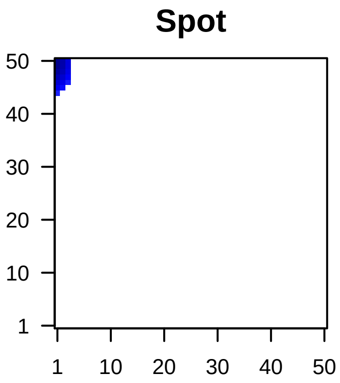
<shrinkage−t> = −53.87

<p−value> = 0

<fdr> = 0.08



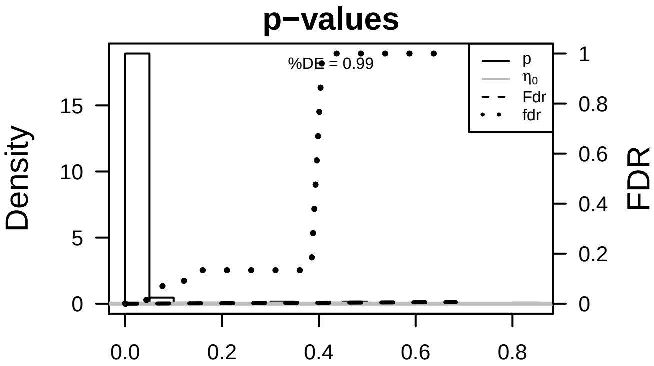
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.68	2e−16	4e−18	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−2.04	2e−16	4e−18	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	113146	−2.2	2e−16	4e−18	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	57016	−2.68	2e−16	4e−18	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	−2.03	2e−16	4e−18	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	8644	−2.55	2e−16	4e−18	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	222	−1.85	2e−16	4e−18	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
8	121551	−1.76	2e−16	4e−18	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Ac
9	387695	−2.22	2e−16	4e−18	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
10	64073	−2.27	2e−16	4e−18	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
11	375791	−2.24	2e−16	4e−18	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
12	771	−2.11	2e−16	4e−18	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
13	760	−2.01	2e−16	4e−18	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
14	810	−2.58	2e−16	4e−18	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
15	4680	−2.52	2e−16	4e−18	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
16	9635	−3.3	2e−16	4e−18	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
17	22802	−2.13	2e−16	4e−18	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	84518	−3.44	2e−16	4e−18	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
19	1382	−1.88	2e−16	4e−18	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
20	49860	−2.7	2e−16	4e−18	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−62.14	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
2	−40.5	NULL	18 / 21	CC	cornified envelope
3	−33.1	NULL	19 / 42	BP	keratinization
4	−32.95	NULL	24 / 53	BP	keratinocyte differentiation
5	−32.4	NULL	102 / 572	Disease	GUDJ_psoriasis up
6	−30.73	NULL	24 / 76	BP	epidermis development
7	−22.37	NULL	10 / 19	BP	peptide cross−linking
8	−21.35	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−20.83	NULL	5 / 10	MF	RAGE receptor binding
10	−19.69	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	−18.82	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−17.16	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	−15.47	NULL	12 / 21	CC	desmosome
14	−15.01	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	−14.57	NULL	12 / 44	CC	keratin filament
16	−14.55	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	−14.19	NULL	26 / 186	MF	structural molecule activity
18	−14.14	NULL	19 / 82	CC	intermediate filament
19	−13.95	NULL	5 / 25	BP	response to zinc ion
20	−13.77	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
21	−13.55	NULL	10 / 52	BP	negative regulation of endopeptidase activity
22	−13.42	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
23	−13.36	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
24	−13.23	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
25	−13.06	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
26	−12.96	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
27	−11.99	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
28	−11.88	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
29	−11.85	NULL	7 / 29	BP	regulation of proteolysis
30	−11.49	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
31	−11.3	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
32	−11.12	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
33	−11.1	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
34	−10.87	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
35	−10.76	NULL	6 / 13	BP	negative regulation of peptidase activity
36	−10.71	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
37	−10.7	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
38	−10.59	NULL	61 / 1182	CC	extracellular region
39	−10.54	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
40	−10.38	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN