GW_301

Global Summary

%DE = 0.17

genes with fdr < 0.2 = 2288 (1251 + / 1037 −)

genes with fdr < 0.1 = 1844 (1018 + / 826 −)

genes with fdr < 0.05 = 1563 (876 + / 687 −)

genes with fdr < 0.01 = 1263 (732 + / 531 −)

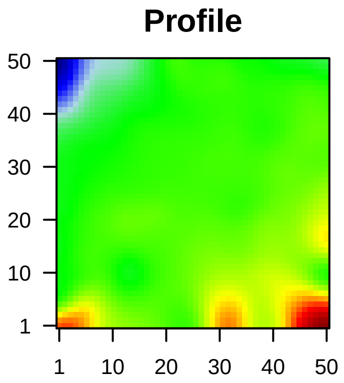
genes in genesets = 16332

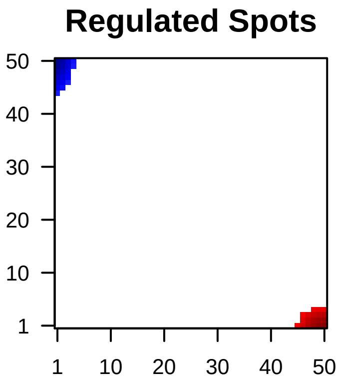
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.06

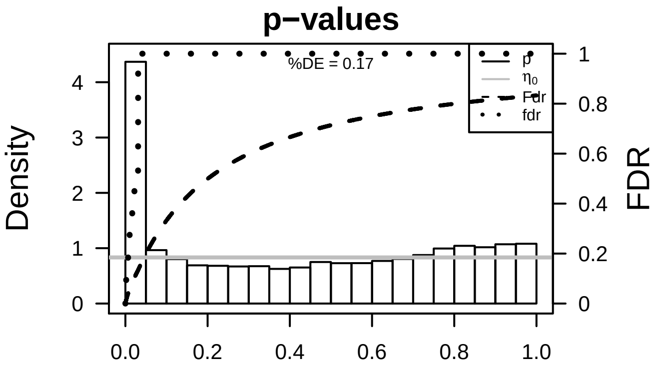
<fdr> = 0.83





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.78	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	72	2.12	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	27299	1.56	2e−16	2e−14	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
4	131	−2.16	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	113146	−1.63	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
6	57016	−2.44	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
7	441282	−1.64	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
8	8644	−2.7	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
9	1109	−2.14	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
10	220	−1.94	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
11	218	−2.65	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
12	222	−1.6	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
13	241	1.42	2e−16	2e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
14	55107	−1.98	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
15	366	2.06	2e−16	2e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
16	9915	1.56	2e−16	2e−14	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
17	92591	1.9	2e−16	2e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
18	330	1.7	2e−16	2e−14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
19	655	−1.47	2e−16	2e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
20	10974	−1.89	2e−16	2e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	25.01	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	18.75	NULL	312	BP	immune response
3	16.59	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	16.59	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	16.59	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	16.59	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	16.49	NULL	417	H.Tiss	WIRTH_Immune system
8	12.83	NULL	43	MF	chemokine activity
9	12.1	NULL	269	BP	inflammatory response
10	11.76	NULL	316	Cancer	SPANG_BCL6−index2
11	11.36	NULL	274	Lymphoma	SPANG_IL21 DN
12	11.05	NULL	51	BP	type I interferon signaling pathway
13	11.05	NULL	60	BP	interferon−gamma−mediated signaling pathway
14	10.95	NULL	111	BP	chemotaxis
15	10.84	NULL	204	BP	cytokine−mediated signaling pathway
16	10.69	NULL	15	CC	MHC class II protein complex
17	10.59	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
18	10.35	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
19	10.31	NULL	22	Lymphoma	DAVE_NFkB BL DN
20	10.08	NULL	47	BP	antigen processing and presentation

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−33.35	NULL	135	H.Tiss	WIRTH_Mucosa
2	−16.95	NULL	21	CC	cornified envelope
3	−15.34	NULL	42	BP	keratinization
4	−14.96	NULL	76	BP	epidermis development
5	−14.32	NULL	53	BP	keratinocyte differentiation
6	−11.25	NULL	572	Disease	GUDJ_psoriasis up
7	−9.24	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
8	−8.54	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	−8.49	NULL	519	Chr	Chr 14
10	−8.16	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−8.05	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−7.81	NULL	19	BP	peptide cross−linking
13	−7.77	NULL	602	Chr	Chr 10
14	−7.56	NULL	186	MF	structural molecule activity
15	−6.93	NULL	14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
16	−6.92	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	−6.88	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
18	−6.44	NULL	21	CC	desmosome
19	−6.43	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
20	−6.42	NULL	12	BP	cellular aldehyde metabolic process

GW_301

Local Summary

%DE = 0.95

metagenes = 19

genes = 296

genes in genesets = 293

genes with fdr < 0.1 = 265 (261 + / 4 −)

genes with fdr < 0.05 = 259 (255 + / 4 −)

genes with fdr < 0.01 = 236 (232 + / 4 −)

<r> metagenes = 0.99

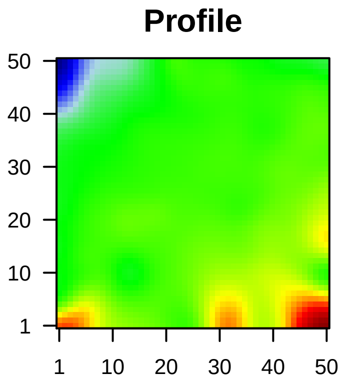
<r> genes = 0.57

<FC> = 0.89

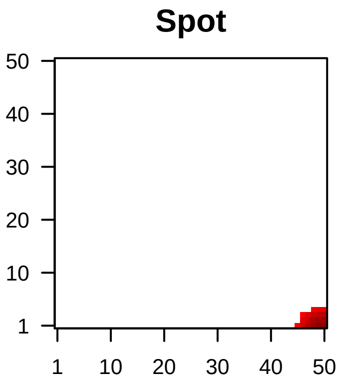
<shrinkage−t> = 31.03

<p−value> = 0

<fdr> = 0.17



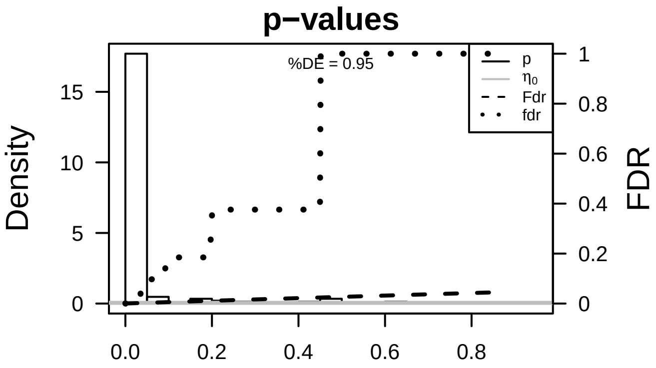
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27299	1.56	2e−16	7e−17	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
2	241	1.42	2e−16	7e−17	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
3	92591	1.9	2e−16	7e−17	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
4	330	1.7	2e−16	7e−17	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
5	57172	2.71	2e−16	7e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
6	6363	1.57	2e−16	7e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	6347	1.48	2e−16	7e−17	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
8	6364	2.7	2e−16	7e−17	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
9	1116	1.72	2e−16	7e−17	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
10	51755	2.48	2e−16	7e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	10563	1.88	2e−16	7e−17	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
12	4283	1.51	2e−16	7e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
13	1593	1.74	2e−16	7e−17	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sour
14	5168	1.66	2e−16	7e−17	50 x 2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
15	54855	2.24	2e−16	7e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
16	2207	1.69	2e−16	7e−17	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
17	80307	1.45	2e−16	7e−17	45 x 1	
18	51303	1.89	2e−16	7e−17	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
19	2745	1.58	2e−16	7e−17	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
20	3002	1.44	2e−16	7e−17	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	31.24	NULL	13 / 15	CC	MHC class II protein complex
2	27.27	NULL	97 / 417	H.Tiss	WIRTH_Immune system
3	23.57	NULL	99 / 553	Cancer	Lembcke_Colonic Inflammation
4	21.82	NULL	56 / 312	BP	immune response
5	21.33	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
6	19.8	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	19.8	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	19.8	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	19.8	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	18.98	NULL	16 / 47	BP	antigen processing and presentation
11	18.76	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
12	17.43	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
13	16.06	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
14	15.82	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
15	14.69	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	14.58	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
17	14.35	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP
18	13.85	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
19	13.72	NULL	19 / 60	BP	T cell costimulation
20	13.31	NULL	27 / 162	CC	external side of plasma membrane
21	12.77	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
22	12.69	NULL	8 / 16	GSEA C2	SU_THYMUS
23	12.45	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
24	12.4	NULL	9 / 35	CC	trans−Golgi network membrane
25	12.37	NULL	8 / 28	CC	transport vesicle membrane
26	12.06	NULL	18 / 74	BP	regulation of immune response
27	11.78	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
28	11.6	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
29	11.47	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
30	11.45	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
31	11.44	NULL	19 / 84	BP	T cell receptor signaling pathway
32	11.4	NULL	32 / 316	Cancer	SPANG_BCL6−index2
33	11.35	NULL	12 / 60	BP	interferon−gamma−mediated signaling pathway
34	11.07	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
35	11.03	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
36	10.92	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
37	10.83	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
38	10.79	NULL	5 / 12	BP	immunoglobulin mediated immune response
39	10.63	NULL	9 / 46	CC	endocytic vesicle membrane
40	10.53	NULL	8 / 43	MF	chemokine activity

GW_301

Local Summary

%DE = 0.95

metagenes = 20

genes = 287

genes in genesets = 281

genes with fdr < 0.1 = 265 (7 + / 258 −)

genes with fdr < 0.05 = 255 (5 + / 250 −)

genes with fdr < 0.01 = 250 (5 + / 245 −)

<r> metagenes = 0.93

<r> genes = 0.41

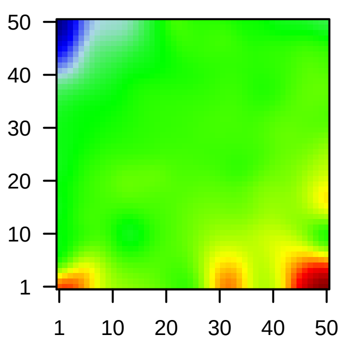
<FC> = −1.07

<shrinkage−t> = −37.66

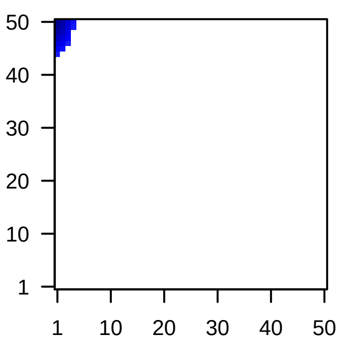
<p−value> = 0

<fdr> = 0.12

Profile



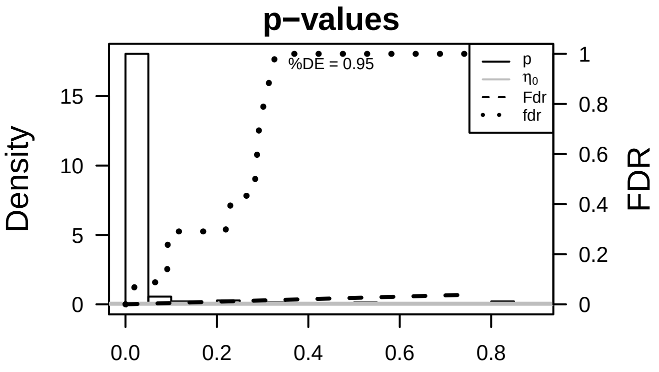
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.16	2e−16	4e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	113146	−1.63	2e−16	4e−17	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	−2.44	2e−16	4e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
4	441282	−1.64	2e−16	4e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	−2.7	2e−16	4e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	−2.65	2e−16	4e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	222	−1.6	2e−16	4e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
8	387695	−1.64	2e−16	4e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
9	64073	−2.13	2e−16	4e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
10	375791	−2.02	2e−16	4e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
11	810	−2.15	2e−16	4e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
12	1048	−1.44	2e−16	4e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	4680	−2.39	2e−16	4e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	9635	−2.03	2e−16	4e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	22802	−1.44	2e−16	4e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	84518	−2.68	2e−16	4e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	49860	−2.14	2e−16	4e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1515	−1.75	2e−16	4e−17	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
19	9547	−1.75	2e−16	4e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
20	1672	−1.95	2e−16	4e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−64.9	NULL	92 / 135	H.Tiss	WIRTH_Mucosa
2	−38.21	NULL	18 / 21	CC	cornified envelope
3	−32.43	NULL	19 / 42	BP	keratinization
4	−31.87	NULL	24 / 53	BP	keratinocyte differentiation
5	−29.9	NULL	108 / 572	Disease	GUDJ_psoriasis up
6	−27.71	NULL	26 / 76	BP	epidermis development
7	−21.17	NULL	10 / 19	BP	peptide cross−linking
8	−17.42	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−17.1	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	−17.01	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	−15.67	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	−15.2	NULL	12 / 21	CC	desmosome
13	−14.22	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	−13.72	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−13.02	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
16	−12.63	NULL	26 / 186	MF	structural molecule activity
17	−12.09	NULL	3 / 12	BP	cellular aldehyde metabolic process
18	−11.99	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
19	−11.99	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	−11.95	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
21	−11.94	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
22	−11.68	NULL	12 / 44	CC	keratin filament
23	−11.46	NULL	19 / 82	CC	intermediate filament
24	−11.34	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
25	−11	NULL	7 / 29	BP	regulation of proteolysis
26	−10.63	NULL	10 / 52	BP	negative regulation of endopeptidase activity
27	−10.51	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
28	−10.5	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
29	−10.5	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
30	−10.48	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
31	−10.04	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
32	−9.93	NULL	65 / 1182	CC	extracellular region
33	−9.8	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
34	−9.7	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
35	−9.67	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
36	−9.58	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
37	−9.58	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
38	−9.54	NULL	5 / 10	MF	RAGE receptor binding
39	−9.25	NULL	4 / 15	MF	retinol dehydrogenase activity
40	−8.79	NULL	5 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP