GW_152

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2145 (1167 + / 978 −)

genes with fdr < 0.1 = 1732 (963 + / 769 −)

genes with fdr < 0.05 = 1330 (735 + / 595 −)

genes with fdr < 0.01 = 987 (531 + / 456 −)

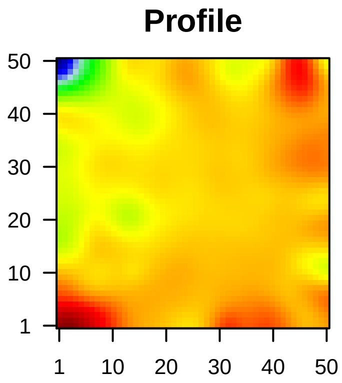
genes in genesets = 16332

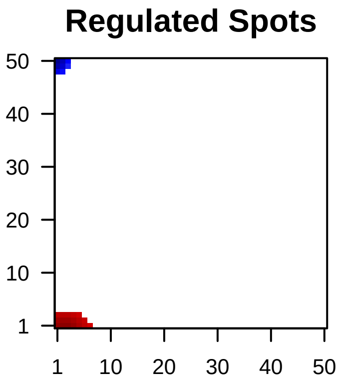
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

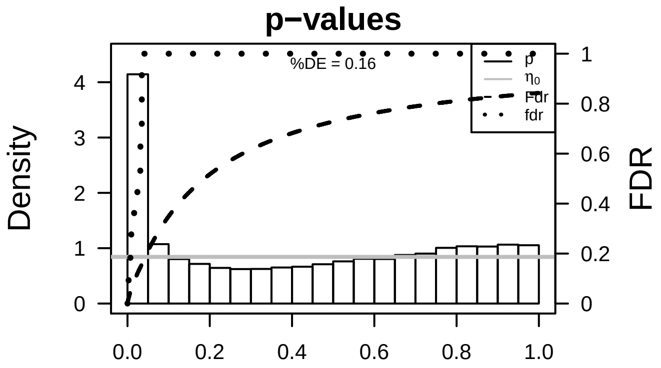
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.95	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−2.81	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−2.11	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.6	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	1646	−1.84	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
6	8644	−1.43	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	−2.18	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	216	−1.39	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
9	220	−1.84	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
10	218	−2.05	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	222	−2.77	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
12	242	−1.54	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
13	118932	−1.38	2e−16	2e−14	4 x 50	ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:28321]
14	9823	1.52	2e−16	2e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
15	633	1.28	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
16	387695	−2.81	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
17	343990	1.61	2e−16	2e−14	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
18	375791	−2.5	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
19	760	1.96	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
20	51806	1.5	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	13.85	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	13.69	NULL	190	CC	extracellular matrix
3	13.13	NULL	242	BP	extracellular matrix organization
4	12.58	NULL	69	BP	extracellular matrix disassembly
5	12.02	NULL	16	MMML CGS	MACIEJ_MMML 1
6	11.78	NULL	11	MF	platelet−derived growth factor binding
7	11.3	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	11.11	NULL	64	BP	collagen catabolic process
9	9.7	NULL	83	CC	basement membrane
10	9.35	NULL	8023	MF	protein binding
11	9.19	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
12	9.19	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
13	9.08	NULL	57	MF	extracellular matrix structural constituent
14	8.71	NULL	119	Lymphoma	ROSOLOWSKI_green total
15	8.67	NULL	4640	CC	nucleus
16	8.45	NULL	370	BP	mitotic cell cycle
17	8.39	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
18	8.26	NULL	16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
19	8.24	NULL	68	CC	collagen
20	7.87	NULL	37	BP	collagen fibril organization
Underexpressed					
1	−34.78	NULL	135	H.Tiss	WIRTH_Mucosa
2	−25.28	NULL	21	CC	cornified envelope
3	−23.26	NULL	42	BP	keratinization
4	−20.1	NULL	53	BP	keratinocyte differentiation
5	−18.19	NULL	572	Disease	GUDJ_psoriasis up
6	−15.22	NULL	19	BP	peptide cross−linking
7	−14.73	NULL	76	BP	epidermis development
8	−13.42	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−10.45	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	−10.13	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−9.44	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
12	−9.4	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
13	−8.98	NULL	186	MF	structural molecule activity
14	−8.92	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
15	−8.69	NULL	52	BP	negative regulation of endopeptidase activity
16	−8.66	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
17	−8.46	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
18	−8.25	NULL	10	MF	RAGE receptor binding
19	−8.16	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
20	−8.15	NULL	10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP

GW_152

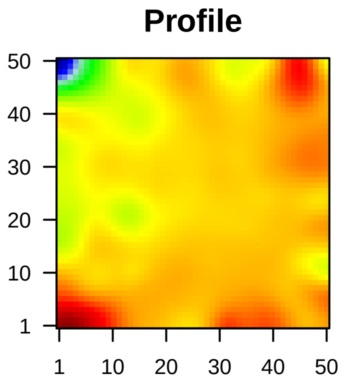
Local Summary

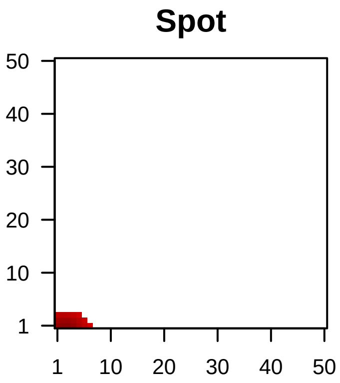
%DE = 0.87
metagenes = 18
genes = 300
genes in genesets = 299

genes with fdr < 0.1 = 204 (194 + / 10 −)
genes with fdr < 0.05 = 201 (191 + / 10 −)
genes with fdr < 0.01 = 177 (169 + / 8 −)

<r> metagenes = 0.96
<r> genes = 0.4

<FC> = 0.58
<shrinkage−t> = 20.21
<p−value> = 0
<fdr> = 0.36





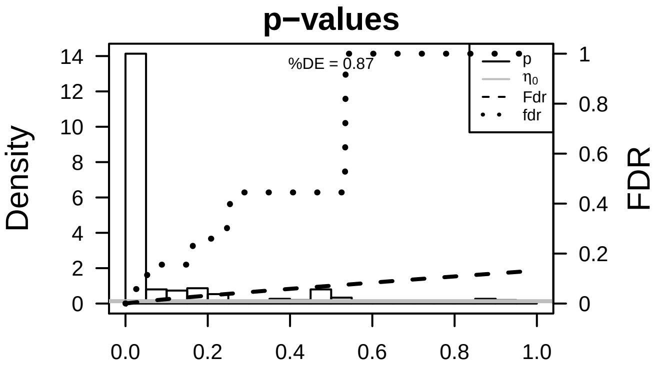
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9823	1.52	2e−16	4e−16	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
2	633	1.28	2e−16	4e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	57124	1.52	2e−16	4e−16	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
4	1277	1.72	2e−16	4e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	1.93	2e−16	4e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1281	1.81	2e−16	4e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
7	1289	1.97	2e−16	4e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	1.74	2e−16	4e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1291	2.05	2e−16	4e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
10	1293	1.81	2e−16	4e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	84624	1.51	2e−16	4e−16	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
12	2619	1.98	2e−16	4e−16	2 x 1	growth arrest−specific 1 [Source:HGNC Symbol;Acc:4165]
13	3569	1.76	2e−16	4e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
14	4060	1.53	2e−16	4e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
15	4312	1.51	2e−16	4e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
16	4314	1.4	2e−16	4e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
17	4318	1.61	2e−16	4e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
18	25878	1.58	2e−16	4e−16	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
19	5156	1.67	2e−16	4e−16	5 x 1	platelet−derived growth factor receptor, alpha polypeptide [So
20	5159	1.52	2e−16	4e−16	3 x 1	platelet−derived growth factor receptor, beta polypeptide [Sou

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	41.63	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
2	41.41	NULL	8 / 11	MF	platelet−derived growth factor binding
3	41.22	NULL	69 / 190	CC	extracellular matrix
4	39.19	NULL	82 / 250	Lymphoma	LENZ_Stromal signature 1
5	36.76	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	33.89	NULL	31 / 69	BP	extracellular matrix disassembly
7	33.16	NULL	64 / 242	BP	extracellular matrix organization
8	32.5	NULL	27 / 64	BP	collagen catabolic process
9	28.61	NULL	8 / 12	miRNA target	miR−29c
10	28.09	NULL	21 / 57	MF	extracellular matrix structural constituent
11	25.4	NULL	11 / 19	MF	extracellular matrix binding
12	23.91	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
13	23.41	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
14	23.15	NULL	14 / 37	BP	collagen fibril organization
15	22.71	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
16	22.36	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
17	22.24	NULL	10 / 40	BP	cellular response to amino acid stimulus
18	21.04	NULL	4 / 10	BP	protein heterotrimerization
19	20.71	NULL	39 / 183	CC	proteinaceous extracellular matrix
20	20.25	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
21	20.21	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
22	20.2	NULL	16 / 68	CC	collagen
23	19.37	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
24	18.71	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
25	18.61	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
26	18.34	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
27	17.92	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
28	17.69	NULL	83 / 683	CC	extracellular space
29	17.69	NULL	113 / 1182	CC	extracellular region
30	17.68	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
31	17.49	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
32	17.42	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
33	17.38	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
34	17.36	NULL	23 / 153	CC	endoplasmic reticulum lumen
35	17.33	NULL	21 / 83	CC	basement membrane
36	17.19	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
37	16.81	NULL	4 / 16	GSEA C2	REACTOME_AXON_GUIDANCE
38	16.81	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
39	16.73	NULL	8 / 28	BP	odontogenesis
40	16.46	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST



GW_152

Local Summary

%DE = 0.99

metagenes = 8

genes = 137

genes in genesets = 134

genes with fdr < 0.1 = 135 (1 + / 134 −)

genes with fdr < 0.05 = 135 (1 + / 134 −)

genes with fdr < 0.01 = 134 (1 + / 133 −)

<r> metagenes = 0.99

<r> genes = 0.52

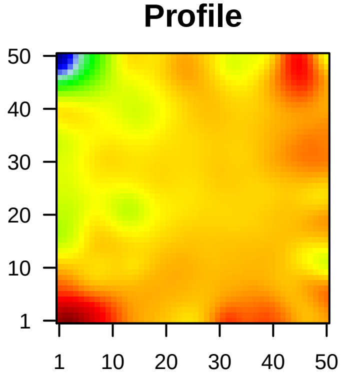
<FC> = −1.73

<shrinkage−t> = −61.32

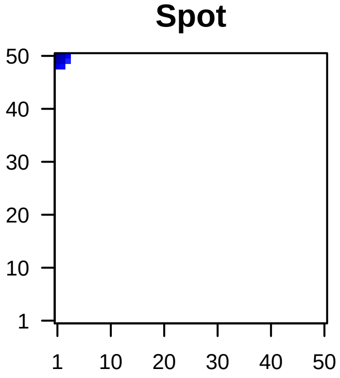
<p−value> = 0

<fdr> = 0.02

Profile

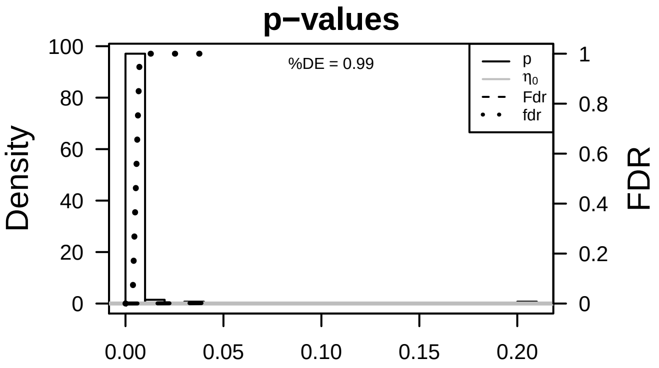


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.95	2e−16	3e−18	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−2.81	2e−16	3e−18	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−2.11	2e−16	3e−18	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.6	2e−16	3e−18	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	−1.43	2e−16	3e−18	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	−2.05	2e−16	3e−18	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	222	−2.77	2e−16	3e−18	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
8	242	−1.54	2e−16	3e−18	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
9	387695	−2.81	2e−16	3e−18	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
10	375791	−2.5	2e−16	3e−18	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
11	84290	−1.99	2e−16	3e−18	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
12	1048	−1.54	2e−16	3e−18	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	4680	−2.7	2e−16	3e−18	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	22802	−2.29	2e−16	3e−18	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	9022	−1.58	2e−16	3e−18	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
16	84518	−3.78	2e−16	3e−18	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	54544	−1.87	2e−16	3e−18	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
18	49860	−2.81	2e−16	3e−18	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
19	1475	−1.81	2e−16	3e−18	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
20	1476	−1.3	2e−16	3e−18	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−57.04	NULL	63 / 135	H.Tiss	WIRTH_Mucosa
2	−51.07	NULL	14 / 21	CC	cornified envelope
3	−42.64	NULL	16 / 42	BP	keratinization
4	−40.15	NULL	19 / 53	BP	keratinocyte differentiation
5	−33.65	NULL	8 / 19	BP	peptide cross−linking
6	−28.03	NULL	16 / 76	BP	epidermis development
7	−27.77	NULL	65 / 572	Disease	GUDJ_psoriasis up
8	−25.13	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−21.41	NULL	4 / 10	MF	RAGE receptor binding
10	−21.26	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	−18.09	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
12	−17.89	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	−17.59	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
14	−17.19	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
15	−16.22	NULL	6 / 13	BP	negative regulation of peptidase activity
16	−15.99	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
17	−15.63	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
18	−15.61	NULL	8 / 52	BP	negative regulation of endopeptidase activity
19	−15.56	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
20	−15.54	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
21	−15.09	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
22	−14.99	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
23	−14.79	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
24	−14.67	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
25	−14.45	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
26	−14.15	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
27	−14.08	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
28	−13.68	NULL	4 / 23	MF	peptidase inhibitor activity
29	−13.05	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
30	−12.98	NULL	13 / 186	MF	structural molecule activity
31	−12.8	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
32	−12.4	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
33	−12.23	NULL	3 / 12	BP	cellular aldehyde metabolic process
34	−11.78	NULL	5 / 29	BP	regulation of proteolysis
35	−11.75	NULL	2 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
36	−11.75	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
37	−11.65	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
38	−11.29	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
39	−11.18	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
40	−11.12	NULL	41 / 1182	CC	extracellular region