GW_199

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1339 (747 + / 592 −)

genes with fdr < 0.1 = 1122 (639 + / 483 −)

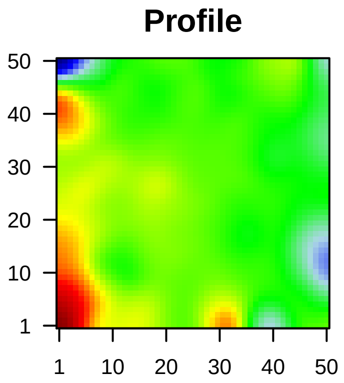
genes with fdr < 0.05 = 899 (513 + / 386 −)

genes with fdr < 0.01 = 540 (313 + / 227 −)

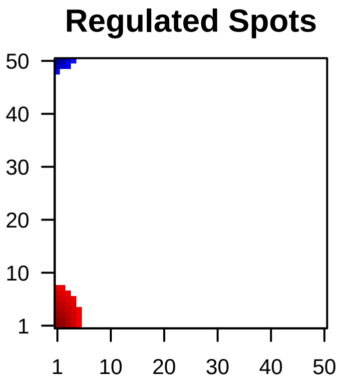
genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.14
<fdr> = 0.88

Profile



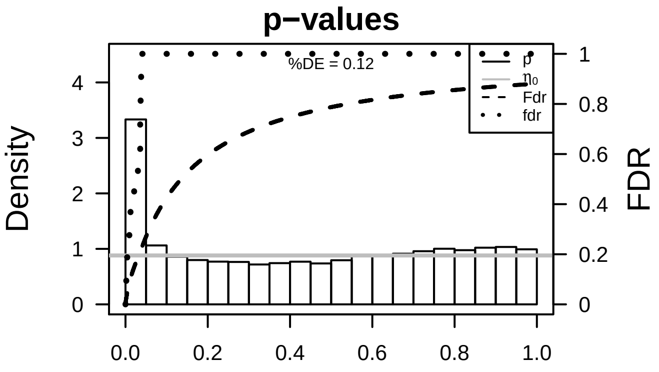
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.5	2e−16	6e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.33	2e−16	6e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	329	1.87	2e−16	6e−14	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
4	330	2.32	2e−16	6e−14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
5	140851	1.75	2e−16	6e−14	1 x 5	
6	768	1.82	2e−16	6e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
7	22802	−1.77	2e−16	6e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	84518	−2.24	2e−16	6e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
9	49860	−2.14	2e−16	6e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1469	1.78	2e−16	6e−14	9 x 6	cystatin SN [Source:HGNC Symbol;Acc:2473]
11	3627	2.77	2e−16	6e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
12	6373	2.3	2e−16	6e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
13	4283	1.86	2e−16	6e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
14	84259	1.84	2e−16	6e−14	5 x 42	DCN1, defective in cullin neddylation 1, domain containing 5 [
15	1672	−1.74	2e−16	6e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
16	1673	−1.91	2e−16	6e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1917	1.89	2e−16	6e−14	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
18	8857	−2.31	2e−16	6e−14	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;A
19	115362	1.85	2e−16	6e−14	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
20	2731	2.65	2e−16	6e−14	1 x 38	glycine dehydrogenase (decarboxylating) [Source:HGNC Syn

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.88	NULL	7	MMML CGS	MACIEJ_MMML 13
2	11.41	NULL	10	BP	cellular response to zinc ion
3	10.36	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	10.21	NULL	242	BP	extracellular matrix organization
5	10.11	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	10.11	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	10.11	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	10.11	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	9.89	NULL	8023	MF	protein binding
10	9.22	NULL	15	BP	negative regulation of growth
11	9.13	NULL	190	CC	extracellular matrix
12	8.55	NULL	69	BP	extracellular matrix disassembly
13	7.95	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	7.74	NULL	8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
15	7.67	NULL	11	Glio	Phillips MES up vs Prolif & PN
16	7.34	NULL	13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
17	7.34	NULL	7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
18	7.33	NULL	12	BP	positive regulation of leukocyte chemotaxis
19	7.31	NULL	608	BP	apoptotic process
20	7.26	NULL	64	BP	collagen catabolic process
Underexpressed					
1	−17.14	NULL	135	H.Tiss	WIRTH_Mucosa
2	−13.21	NULL	21	CC	cornified envelope
3	−11.62	NULL	42	BP	keratinization
4	−10.95	NULL	53	BP	keratinocyte differentiation
5	−9.97	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
6	−8.11	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
7	−7.73	NULL	10	MF	RAGE receptor binding
8	−6.89	NULL	76	BP	epidermis development
9	−6.85	NULL	12	BP	cellular aldehyde metabolic process
10	−6.8	NULL	19	BP	peptide cross−linking
11	−6.6	NULL	618	Chr	Chr 4
12	−6.56	NULL	119	BP	xenobiotic metabolic process
13	−6.48	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
14	−6.42	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	−6.15	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
16	−5.97	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	−5.86	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
18	−5.58	NULL	10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
19	−5.5	NULL	940	MF	nucleic acid binding
20	−5.47	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN

GW_199

Local Summary

%DE = 0.73

metagenes = 33

genes = 486

genes in genesets = 482

genes with fdr < 0.1 = 287 (280 + / 7 −)

genes with fdr < 0.05 = 243 (238 + / 5 −)

genes with fdr < 0.01 = 192 (187 + / 5 −)

<r> metagenes = 0.91

<r> genes = 0.3

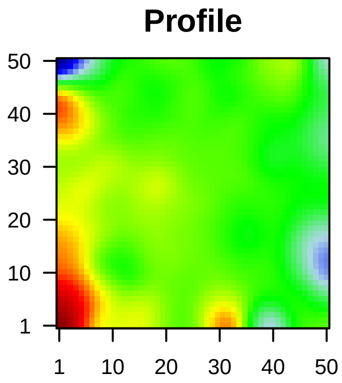
<FC> = 0.54

<shrinkage−t> = 19.09

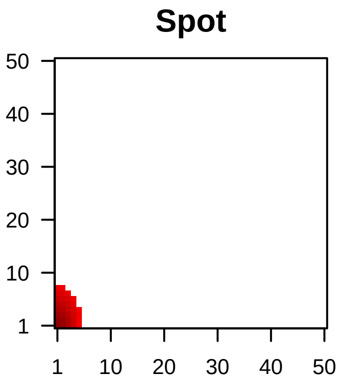
<p−value> = 0

<fdr> = 0.49

Profile



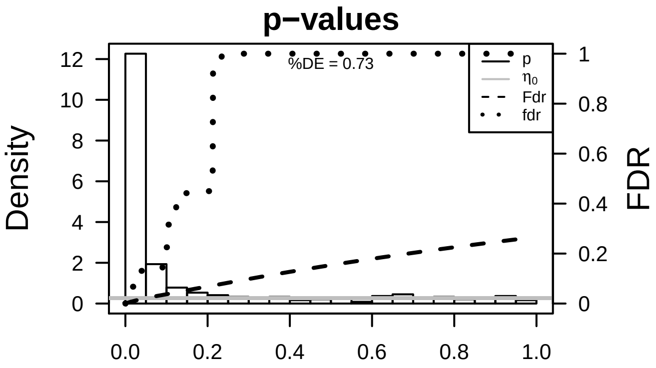
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	140851	1.75	2e−16	2e−15	1 x 5	
2	768	1.82	2e−16	2e−15	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	3039	1.7	2e−16	2e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3040	1.89	2e−16	2e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3553	1.76	2e−16	2e−15	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
6	3678	1.85	2e−16	2e−15	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
7	4320	1.95	2e−16	2e−15	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
8	4489	1.74	2e−16	2e−15	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
9	4502	2.29	2e−16	2e−15	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
10	644314	1.96	2e−16	2e−15	1 x 5	
11	10631	1.71	2e−16	2e−15	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
12	6515	1.73	2e−16	2e−15	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
13	8406	1.78	2e−16	2e−15	2 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Syr
14	25907	1.61	9e−15	1e−12	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HGN
15	55450	1.59	2e−14	1e−12	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
16	414062	1.58	3e−14	1e−12	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
17	857	1.57	4e−14	4e−11	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
18	3491	1.51	4e−13	7e−11	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
19	1397	1.47	2e−12	7e−11	4 x 3	cysteine−rich protein 2 [Source:HGNC Symbol;Acc:2361]
20	60675	1.46	2e−12	7e−11	1 x 1	prokineticin 2 [Source:HGNC Symbol;Acc:18455]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.87	NULL	85 / 250	Lymphoma	LENZ_Stromal signature 1
2	24.38	NULL	67 / 190	CC	extracellular matrix
3	23.82	NULL	84 / 242	BP	extracellular matrix organization
4	23.14	NULL	10 / 11	Glio	Phillips MES up vs Prolif & PN
5	21.04	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
6	20.29	NULL	34 / 69	BP	extracellular matrix disassembly
7	19.55	NULL	5 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
8	18.95	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
9	18.88	NULL	7 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
10	18.56	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
11	18.55	NULL	30 / 64	BP	collagen catabolic process
12	18.15	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
13	16.91	NULL	53 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	16.91	NULL	53 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	16.91	NULL	53 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	16.91	NULL	53 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	16.39	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
18	16.25	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
19	16.04	NULL	16 / 37	BP	collagen fibril organization
20	15.77	NULL	5 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
21	15.55	NULL	6 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
22	15.48	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
23	15.47	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
24	15.29	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
25	15.19	NULL	147 / 1182	CC	extracellular region
26	14.99	NULL	13 / 35	Glio	Colman_survival_associated
27	14.86	NULL	5 / 11	GSEA C2	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP
28	14.81	NULL	3 / 10	BP	cellular response to zinc ion
29	14.32	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
30	14.05	NULL	82 / 553	Cancer	Lembcke_Colonic Inflammation
31	13.83	NULL	22 / 85	MF	integrin binding
32	13.76	NULL	98 / 683	CC	extracellular space
33	13.72	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
34	13.5	NULL	9 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
35	13.46	NULL	71 / 403	BP	cell adhesion
36	13.38	NULL	9 / 16	MF	fibronectin binding
37	13.23	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
38	13.1	NULL	5 / 14	GSEA C2	HALMOS_CEBPA_TARGETS_DN
39	13.05	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
40	12.8	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST

GW_199

Local Summary

%DE = 0.94

metagenes = 8

genes = 154

genes in genesets = 151

genes with fdr < 0.1 = 140 (3 + / 137 −)

genes with fdr < 0.05 = 139 (3 + / 136 −)

genes with fdr < 0.01 = 126 (2 + / 124 −)

<r> metagenes = 0.99

<r> genes = 0.5

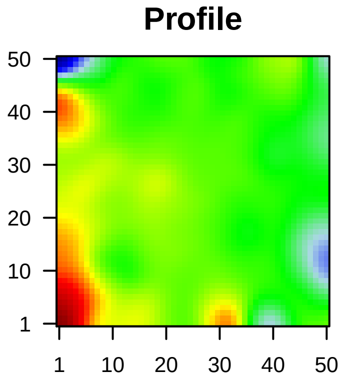
<FC> = −1.06

<shrinkage−t> = −37.41

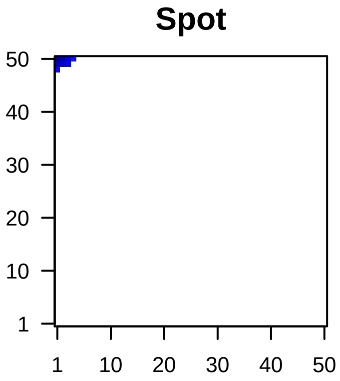
<p−value> = 0

<fdr> = 0.15

Profile

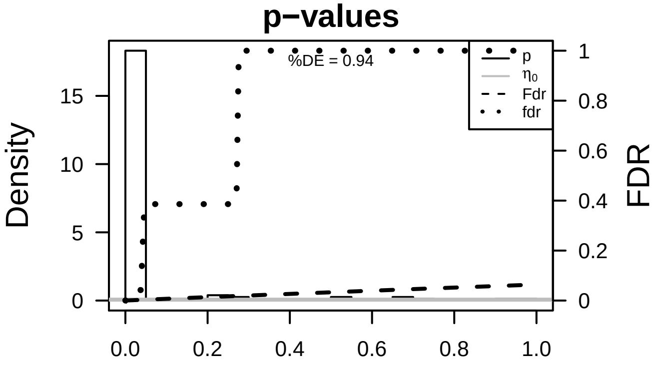


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.5	2e−16	8e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.33	2e−16	8e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	22802	−1.77	2e−16	8e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
4	84518	−2.24	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
5	49860	−2.14	2e−16	8e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	1672	−1.74	2e−16	8e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
7	1673	−1.91	2e−16	8e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	2877	−2.16	2e−16	8e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
9	2941	−1.74	2e−16	8e−17	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
10	5653	−1.78	2e−16	8e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
11	3860	−1.94	2e−16	8e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
12	192666	−1.75	2e−16	8e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
13	3851	−2.81	2e−16	8e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
14	3934	−2.2	2e−16	8e−17	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
15	4118	−2.3	2e−16	8e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
16	342897	−1.89	2e−16	8e−17	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebraf
17	5266	−1.62	2e−16	8e−17	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
18	6278	−3.54	2e−16	8e−17	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
19	338324	−2.44	2e−16	8e−17	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
20	6286	−1.8	2e−16	8e−17	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−50.38	NULL	66 / 135	H.Tiss	WIRTH_Mucosa
2	−35.69	NULL	13 / 21	CC	cornified envelope
3	−32.08	NULL	17 / 53	BP	keratinocyte differentiation
4	−30.45	NULL	15 / 42	BP	keratinization
5	−25.44	NULL	69 / 572	Disease	GUDJ_psoriasis up
6	−24.92	NULL	18 / 76	BP	epidermis development
7	−24.22	NULL	4 / 10	MF	RAGE receptor binding
8	−23.41	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−20.91	NULL	7 / 19	BP	peptide cross−linking
10	−15.14	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	−15.02	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
12	−14.61	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
13	−14.48	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
14	−13.21	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
15	−12.76	NULL	4 / 15	MF	retinol dehydrogenase activity
16	−12.63	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
17	−12.29	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
18	−12.05	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
19	−11.81	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	−11.24	NULL	4 / 27	BP	response to bacterium
21	−11.19	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
22	−11.13	NULL	3 / 12	BP	cellular aldehyde metabolic process
23	−11.04	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
24	−10.64	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
25	−10.57	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
26	−10.56	NULL	4 / 23	MF	peptidase inhibitor activity
27	−10.54	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
28	−10.35	NULL	44 / 1182	CC	extracellular region
29	−10.05	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
30	−10.03	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
31	−10.02	NULL	12 / 186	MF	structural molecule activity
32	−9.85	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
33	−9.8	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
34	−9.79	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
35	−9.67	NULL	6 / 38	BP	epithelial cell differentiation
36	−9.53	NULL	2 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
37	−9.38	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
38	−9.38	NULL	6 / 13	BP	negative regulation of peptidase activity
39	−9.36	NULL	4 / 39	BP	retinoid metabolic process
40	−9.25	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN