GW_202

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1709 (953 + / 756 −)

genes with fdr < 0.1 = 1353 (788 + / 565 −)

genes with fdr < 0.05 = 1240 (723 + / 517 −)

genes with fdr < 0.01 = 859 (521 + / 338 −)

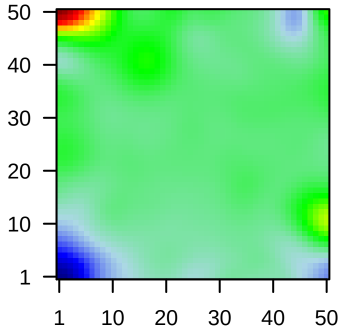
genes in genesets = 16332

<FC> = 0

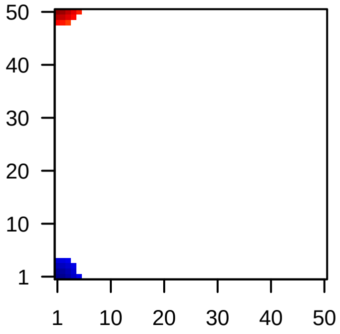
<shrinkage−t> = 0

<p−value> = 0.09

<fdr> = 0.87



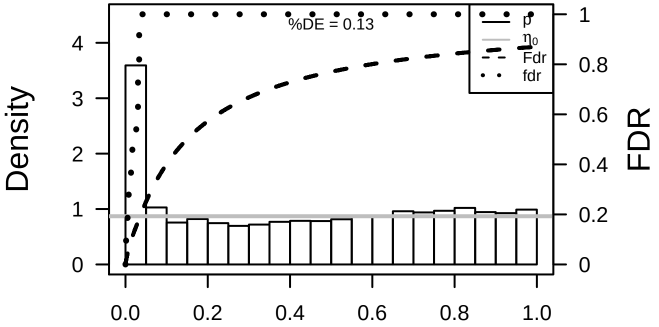
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.65	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	59	−1.27	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	131	1.9	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	10551	1.4	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	57016	1.58	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	1109	2.02	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	218	1.51	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
8	55107	−1.71	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
9	151516	2.04	2e−16	2e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
10	23120	1.38	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
11	344905	2.07	2e−16	2e−14	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
12	8424	1.3	2e−16	2e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
13	205428	1.24	2e−16	2e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
14	394263	1.77	2e−16	2e−14	3 x 50	
15	352999	2.52	2e−16	2e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
16	375791	2.06	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
17	760	1.9	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	51806	2.17	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
19	6364	−1.95	2e−16	2e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
20	1009	−1.24	2e−16	2e−14	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	29.32	NULL	135	H.Tiss	WIRTH_Mucosa
2	18.66	NULL	21	CC	cornified envelope
3	14.41	NULL	53	BP	keratinocyte differentiation
4	12.65	NULL	42	BP	keratinization
5	10.58	NULL	76	BP	epidermis development
6	9.7	NULL	572	Disease	GUDJ_psoriasis up
7	9.68	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	8.82	NULL	19	BP	peptide cross−linking
9	8.65	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
10	8.32	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	7.52	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	7.42	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
13	7.27	NULL	119	BP	xenobiotic metabolic process
14	7.01	NULL	1720	Chr	Chr 1
15	6.9	NULL	618	Chr	Chr 4
16	6.49	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
17	6.48	NULL	13	BP	cellular response to cadmium ion
18	6.47	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
19	6.29	NULL	17	Disease	BCHETNIA_EBM up
20	6.2	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
Underexpressed					
1	−16.36	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	−15.38	NULL	242	BP	extracellular matrix organization
3	−14.92	NULL	190	CC	extracellular matrix
4	−14.48	NULL	69	BP	extracellular matrix disassembly
5	−14	NULL	11	MF	platelet−derived growth factor binding
6	−13.68	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	−12.99	NULL	64	BP	collagen catabolic process
8	−12.53	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	−12.53	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	−12.53	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	−12.53	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	−12.09	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
13	−12.01	NULL	553	Cancer	Lembcke_Colonic Inflammation
14	−11.97	NULL	12	miRNA target	miR−29c
15	−11.62	NULL	16	MMML CGS	MACIEJ_MMML 1
16	−10.55	NULL	68	CC	collagen
17	−10.2	NULL	37	BP	collagen fibril organization
18	−10.01	NULL	403	BP	cell adhesion
19	−9.83	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
20	−9.56	NULL	57	MF	extracellular matrix structural constituent

GW_202

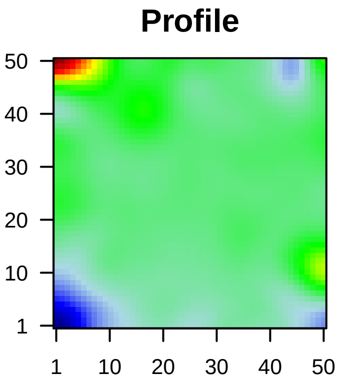
Local Summary

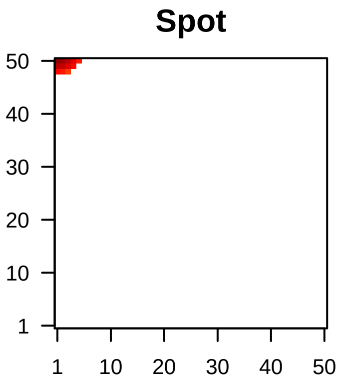
%DE = 0.97
metagenes = 12
genes = 196
genes in genesets = 192

genes with fdr < 0.1 = 189 (185 + / 4 −)
genes with fdr < 0.05 = 189 (185 + / 4 −)
genes with fdr < 0.01 = 181 (177 + / 4 −)

<r> metagenes = 0.98
<r> genes = 0.47

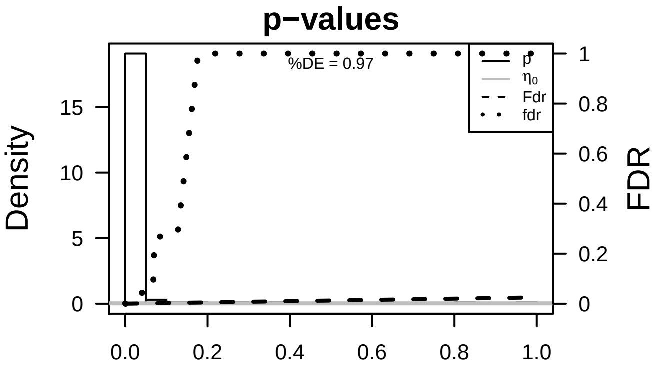
<FC> = 1.08
<shrinkage−t> = 38.12
<p−value> = 0
<fdr> = 0.08





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.65	2e−16	1e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	1.9	2e−16	1e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.58	2e−16	1e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	218	1.51	2e−16	1e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	23120	1.38	2e−16	1e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
6	8424	1.3	2e−16	1e−17	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamm
7	394263	1.77	2e−16	1e−17	3 x 50	
8	375791	2.06	2e−16	1e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
9	51806	2.17	2e−16	1e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
10	1048	1.69	2e−16	1e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
11	4680	1.74	2e−16	1e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
12	1087	1.24	2e−16	1e−17	4 x 50	carcinoembryonic antigen−related cell adhesion molecule 7 [
13	22802	2.06	2e−16	1e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	9022	1.6	2e−16	1e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
15	84518	1.92	2e−16	1e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	54544	1.66	2e−16	1e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	3.33	2e−16	1e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	1.39	2e−16	1e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1577	1.31	2e−16	1e−17	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
20	414325	−1.35	2e−16	1e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	53.77	NULL	72 / 135	H.Tiss	WIRTH_Mucosa
2	39.07	NULL	14 / 21	CC	cornified envelope
3	30.45	NULL	19 / 53	BP	keratinocyte differentiation
4	29.31	NULL	16 / 42	BP	keratinization
5	24.38	NULL	19 / 76	BP	epidermis development
6	22.95	NULL	8 / 19	BP	peptide cross−linking
7	20.74	NULL	76 / 572	Disease	GUDJ_psoriasis up
8	19.16	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	16.19	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	14.05	NULL	5 / 10	MF	RAGE receptor binding
11	12.93	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	12.92	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	12.79	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	12.68	NULL	6 / 13	BP	negative regulation of peptidase activity
15	12.66	NULL	7 / 38	BP	epithelial cell differentiation
16	11.64	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
17	11.25	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
18	11.23	NULL	13 / 186	MF	structural molecule activity
19	11.06	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
20	9.67	NULL	4 / 44	CC	keratin filament
21	9.66	NULL	12 / 122	MF	serine−type endopeptidase activity
22	9.18	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
23	8.93	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
24	8.92	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
25	8.91	NULL	6 / 82	CC	intermediate filament
26	8.83	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
27	8.76	NULL	2 / 17	Disease	BCHETNIA_EBM up
28	8.56	NULL	3 / 12	BP	cellular aldehyde metabolic process
29	8.41	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
30	8.27	NULL	4 / 27	BP	response to bacterium
31	8.13	NULL	49 / 1182	CC	extracellular region
32	8.02	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
33	8	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
34	7.99	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
35	7.74	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
36	7.58	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
37	7.57	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
38	7.46	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
39	7.39	NULL	4 / 15	MF	retinol dehydrogenase activity
40	7.33	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP

GW_202

Local Summary

%DE = 0.96

metagenes = 16

genes = 259

genes in genesets = 258

genes with fdr < 0.1 = 228 (8 + / 220 −)

genes with fdr < 0.05 = 228 (8 + / 220 −)

genes with fdr < 0.01 = 209 (7 + / 202 −)

<r> metagenes = 0.96

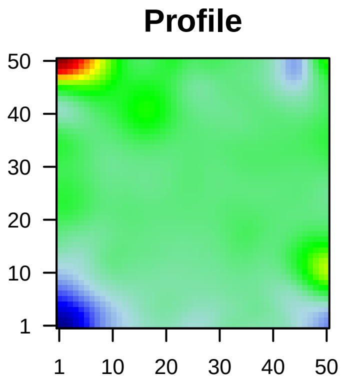
<r> genes = 0.4

<FC> = −0.67

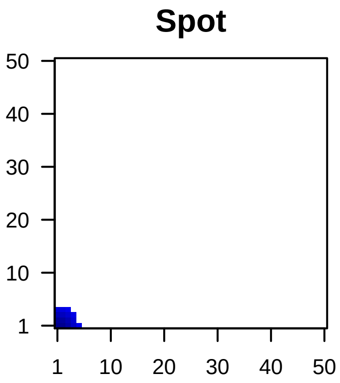
<shrinkage−t> = −23.56

<p−value> = 0

<fdr> = 0.2



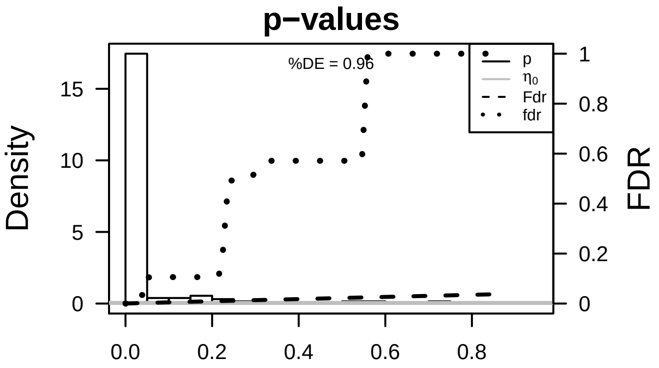
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	−1.27	2e−16	8e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	1009	−1.24	2e−16	8e−17	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC
3	1307	−1.39	2e−16	8e−17	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
4	1277	−2.39	2e−16	8e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	−2.11	2e−16	8e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1281	−2.05	2e−16	8e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
7	1282	−1.77	2e−16	8e−17	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
8	1289	−1.91	2e−16	8e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
9	1290	−1.96	2e−16	8e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
10	1291	−1.73	2e−16	8e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
11	1293	−1.82	2e−16	8e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	83716	−1.44	2e−16	8e−17	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S
13	1687	−1.24	2e−16	8e−17	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
14	3576	−1.26	2e−16	8e−17	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
15	3956	−1.96	2e−16	8e−17	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
16	4312	−1.82	2e−16	8e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
17	4320	−1.32	2e−16	8e−17	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
18	4318	−1.65	2e−16	8e−17	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
19	5159	−1.31	2e−16	8e−17	3 x 1	platelet−derived growth factor receptor, beta polypeptide [Sou
20	5328	−1.6	2e−16	8e−17	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−42.97	NULL	8 / 11	MF	platelet−derived growth factor binding
2	−40.38	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−39.81	NULL	62 / 190	CC	extracellular matrix
4	−39.5	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
5	−39.27	NULL	31 / 69	BP	extracellular matrix disassembly
6	−38.28	NULL	28 / 64	BP	collagen catabolic process
7	−37.64	NULL	8 / 12	miRNA target	miR−29c
8	−36.18	NULL	71 / 250	Lymphoma	LENZ_Stromal signature 1
9	−34.95	NULL	67 / 242	BP	extracellular matrix organization
10	−31.66	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	−26.18	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
12	−25.52	NULL	15 / 37	BP	collagen fibril organization
13	−24.97	NULL	20 / 57	MF	extracellular matrix structural constituent
14	−24.42	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
15	−24.24	NULL	12 / 40	BP	cellular response to amino acid stimulus
16	−23.27	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
17	−23.1	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	−23.1	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	−23.1	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	−23.1	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	−22.97	NULL	18 / 68	CC	collagen
22	−22.53	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
23	−22.31	NULL	4 / 10	BP	protein heterotrimerization
24	−21.66	NULL	12 / 35	Glio	Colman_survival_associated
25	−21.03	NULL	75 / 683	CC	extracellular space
26	−20.79	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
27	−20.75	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
28	−20.14	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
29	−20.11	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
30	−19.67	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
31	−19.33	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
32	−19.18	NULL	101 / 1182	CC	extracellular region
33	−19.11	NULL	25 / 153	CC	endoplasmic reticulum lumen
34	−19.06	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
35	−19.05	NULL	14 / 68	Glio	cultured astroglia vs. in vivo astrocytes
36	−19.04	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
37	−19.03	NULL	22 / 83	CC	basement membrane
38	−18.84	NULL	11 / 19	MF	extracellular matrix binding
39	−18.74	NULL	37 / 183	CC	proteinaceous extracellular matrix
40	−18.74	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF