GW_129

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1720 (991 + / 729 −)

genes with fdr < 0.1 = 1443 (858 + / 585 −)

genes with fdr < 0.05 = 1099 (662 + / 437 −)

genes with fdr < 0.01 = 830 (508 + / 322 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

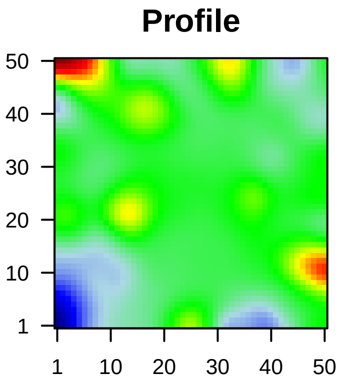
<fdr> = 0.86

Global Genelist

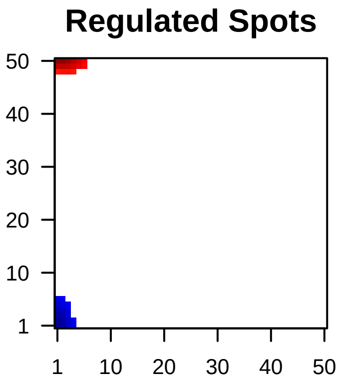
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.82	2e−16	4e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.02	2e−16	4e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	1.99	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	216	2.06	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
5	374569	1.96	2e−16	4e−14	4 x 50	asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
6	64073	1.73	2e−16	4e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
7	92747	3.22	2e−16	4e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
8	394263	1.99	2e−16	4e−14	3 x 50	
9	375791	2.21	2e−16	4e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
10	1158	2.82	2e−16	4e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
11	22802	2.5	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	9022	1.83	2e−16	4e−14	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
13	84518	1.94	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	1277	−2.53	2e−16	4e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	1278	−2.03	2e−16	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
16	1281	−1.9	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
17	1282	−1.71	2e−16	4e−14	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
18	1289	−1.71	2e−16	4e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
19	1293	−2.17	2e−16	4e−14	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
20	54544	1.97	2e−16	4e−14	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987

Global Geneset Analysis

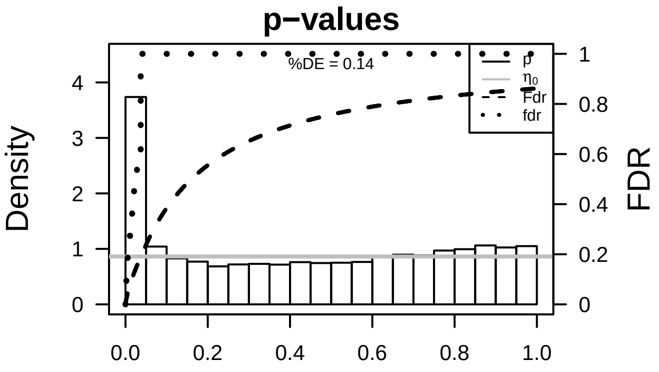
Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	22.82	NULL	135	H.Tiss	WIRTH_Mucosa
2	11.18	NULL	83	BP	respiratory electron transport chain
3	10.78	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	10.39	NULL	152	BP	cellular metabolic process
5	10.32	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
6	10.23	NULL	304	CC	mitochondrial inner membrane
7	10.01	NULL	153	MF	structural constituent of ribosome
8	9.97	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
9	9.91	NULL	1318	CC	mitochondrion
10	9.29	NULL	16	H.Tiss	WIRTH_Hippocampus
11	8.76	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
12	8.67	NULL	81	BP	viral transcription
13	8.56	NULL	87	BP	translational termination
14	8.37	NULL	92	BP	translational elongation
15	8.2	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	8.06	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
17	8.02	NULL	167	CC	ribosome
18	7.96	NULL	127	H.Tiss	WIRTH_Muscle
19	7.92	NULL	119	BP	xenobiotic metabolic process
20	7.84	NULL	36	CC	mitochondrial respiratory chain complex I
Underexpressed					
1	−15.69	NULL	242	BP	extracellular matrix organization
2	−14.24	NULL	69	BP	extracellular matrix disassembly
3	−14.03	NULL	64	BP	collagen catabolic process
4	−12.97	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
5	−12.47	NULL	8023	MF	protein binding
6	−11.62	NULL	250	Lymphoma	LENZ_Stromal signature 1
7	−11.43	NULL	190	CC	extracellular matrix
8	−10.5	NULL	403	BP	cell adhesion
9	−10.33	NULL	11	MF	platelet−derived growth factor binding
10	−10.22	NULL	553	Cancer	Lembcke_Colonic Inflammation
11	−10.03	NULL	83	CC	basement membrane
12	−9.41	NULL	4640	CC	nucleus
13	−9.16	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	−9.14	NULL	16	MMML CGS	MACIEJ_MMML 1
15	−9.1	NULL	12	miRNA target	miR−29c
16	−9.06	NULL	153	CC	endoplasmic reticulum lumen
17	−8.94	NULL	37	BP	collagen fibril organization
18	−8.9	NULL	51	BP	type I interferon signaling pathway
19	−8.89	NULL	57	MF	extracellular matrix structural constituent
20	−8.74	NULL	274	Lymphoma	SPANG_IL21 DN



Profile



Regulated Spots



p−values

GW_129

Local Summary

%DE = 0.97

metagenes = 16

genes = 243

genes in genesets = 239

genes with fdr < 0.1 = 230 (219 + / 11 −)

genes with fdr < 0.05 = 218 (209 + / 9 −)

genes with fdr < 0.01 = 202 (196 + / 6 −)

<r> metagenes = 0.98

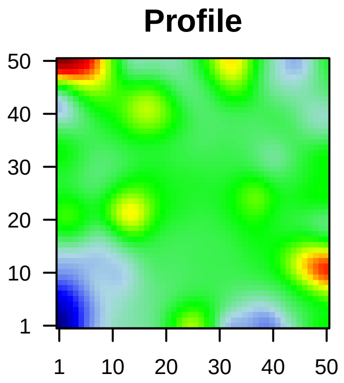
<r> genes = 0.45

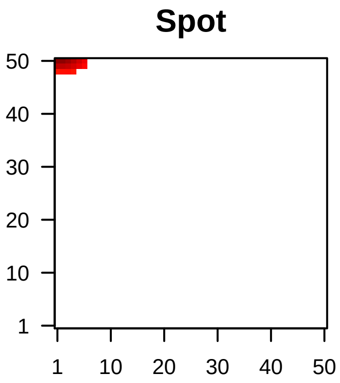
<FC> = 1.03

<shrinkage−t> = 36.04

<p−value> = 0

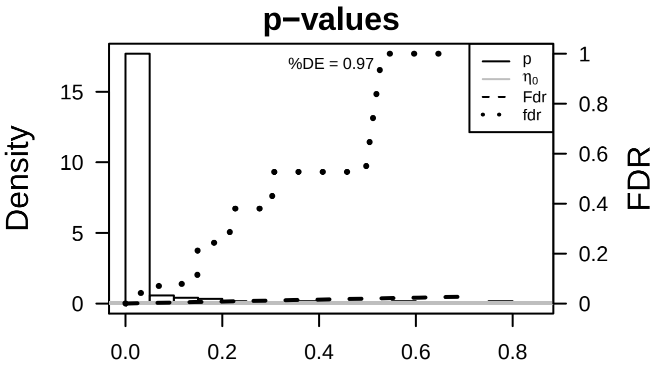
<fdr> = 0.17





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.99	2e−16	4e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	374569	1.96	2e−16	4e−17	4 x 50	asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
3	394263	1.99	2e−16	4e−17	3 x 50	
4	375791	2.21	2e−16	4e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
5	22802	2.5	2e−16	4e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
6	9022	1.83	2e−16	4e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
7	84518	1.94	2e−16	4e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	1.97	2e−16	4e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	2.9	2e−16	4e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1475	2	2e−16	4e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	1571	1.79	2e−16	4e−17	5 x 50	cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
12	1577	2.29	2e−16	4e−17	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
13	92196	1.9	2e−16	4e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
14	131177	2.54	2e−16	4e−17	3 x 50	family with sequence similarity 3, member D [Source:HGNC
15	163351	2.01	2e−16	4e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
16	9245	2.17	2e−16	4e−17	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
17	79153	1.67	2e−16	4e−17	3 x 50	glycerophosphodiester phosphodiesterase domain containing
18	192666	2.58	2e−16	4e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
19	3851	3.57	2e−16	4e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
20	196374	2.47	2e−16	4e−17	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	53.92	NULL	78 / 135	H.Tiss	WIRTH_Mucosa
2	18.85	NULL	81 / 572	Disease	GUDJ_psoriasis up
3	16.48	NULL	9 / 19	BP	peptide cross−linking
4	15.27	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
5	14.69	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
6	13.23	NULL	7 / 38	BP	epithelial cell differentiation
7	12.99	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
8	12.82	NULL	15 / 21	CC	cornified envelope
9	12.72	NULL	20 / 53	BP	keratinocyte differentiation
10	12.52	NULL	5 / 10	MF	RAGE receptor binding
11	12.43	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
12	12.07	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
13	11.97	NULL	5 / 13	H.Tiss	WIRTH_Tonsil
14	11.95	NULL	6 / 13	BP	negative regulation of peptidase activity
15	11.29	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
16	11.03	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
17	10.9	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	10.22	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
19	10.09	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
20	10	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
21	9.61	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
22	9.55	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
23	9.55	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
24	9.51	NULL	3 / 13	BP	retinoic acid metabolic process
25	9.5	NULL	16 / 42	BP	keratinization
26	9.44	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	9.36	NULL	57 / 1182	CC	extracellular region
28	9.22	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
29	9.16	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
30	9.04	NULL	10 / 52	BP	negative regulation of endopeptidase activity
31	9.02	NULL	4 / 15	MF	retinol dehydrogenase activity
32	8.9	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
33	8.59	NULL	16 / 186	MF	structural molecule activity
34	8.53	NULL	4 / 23	MF	peptidase inhibitor activity
35	8.47	NULL	2 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
36	8.18	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
37	8.09	NULL	4 / 44	CC	keratin filament
38	7.97	NULL	19 / 76	BP	epidermis development
39	7.92	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
40	7.87	NULL	6 / 82	CC	intermediate filament

GW_129

Local Summary

%DE = 0.9

metagenes = 19

genes = 295

genes in genesets = 293

genes with fdr < 0.1 = 239 (5 + / 234 −)

genes with fdr < 0.05 = 239 (5 + / 234 −)

genes with fdr < 0.01 = 194 (3 + / 191 −)

<r> metagenes = 0.94

<r> genes = 0.36

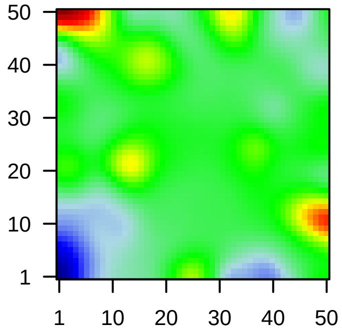
<FC> = −0.77

<shrinkage−t> = −27.18

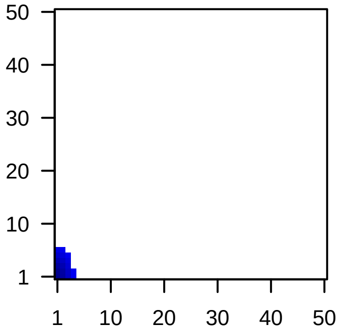
<p−value> = 0

<fdr> = 0.29

Profile



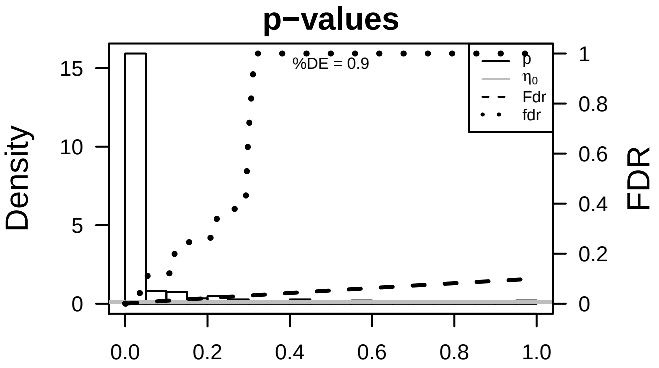
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1277	−2.53	2e−16	5e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	1278	−2.03	2e−16	5e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	−1.9	2e−16	5e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	1282	−1.71	2e−16	5e−16	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
5	1289	−1.71	2e−16	5e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1293	−2.17	2e−16	5e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
7	115908	−1.85	2e−16	5e−16	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
8	6624	−1.55	2e−16	5e−16	1 x 6	fascin homolog 1, actin−bundling protein (Strongylocentrotus
9	3576	−2.83	2e−16	5e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
10	4312	−2.45	2e−16	5e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
11	4319	−2.27	2e−16	5e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
12	4314	−2.2	2e−16	5e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
13	4318	−1.69	2e−16	5e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
14	5054	−1.79	2e−16	5e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
15	1051	−1.51	7e−16	5e−15	1 x 4	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGN
16	1290	−1.64	9e−16	7e−15	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
17	4060	−1.65	9e−16	7e−15	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
18	4316	−1.64	9e−16	7e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
19	3490	−1.64	1e−15	7e−15	3 x 1	insulin−like growth factor binding protein 7 [Source:HGNC Sy
20	7045	−1.5	1e−15	3e−14	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.4	NULL	29 / 64	BP	collagen catabolic process
2	−37.27	NULL	32 / 69	BP	extracellular matrix disassembly
3	−36.5	NULL	69 / 242	BP	extracellular matrix organization
4	−36.49	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
5	−35.58	NULL	58 / 190	CC	extracellular matrix
6	−32.17	NULL	7 / 11	MF	platelet−derived growth factor binding
7	−31.59	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
8	−29.55	NULL	68 / 250	Lymphoma	LENZ_Stromal signature 1
9	−28.86	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
10	−28.43	NULL	8 / 12	miRNA target	miR−29c
11	−23.96	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
12	−23.61	NULL	15 / 37	BP	collagen fibril organization
13	−22.64	NULL	21 / 57	MF	extracellular matrix structural constituent
14	−22.16	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
15	−21.88	NULL	11 / 40	BP	cellular response to amino acid stimulus
16	−21.05	NULL	76 / 683	CC	extracellular space
17	−20.83	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
18	−20.82	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
19	−20.79	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
20	−20.42	NULL	106 / 1182	CC	extracellular region
21	−19.51	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
22	−19.46	NULL	56 / 403	BP	cell adhesion
23	−19.3	NULL	42 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
24	−19.3	NULL	42 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
25	−19.3	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
26	−19.3	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
27	−19.22	NULL	37 / 183	CC	proteinaceous extracellular matrix
28	−19.02	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
29	−18.69	NULL	63 / 553	Cancer	Lembcke_Colonic Inflammation
30	−18.67	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
31	−18.4	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
32	−18.33	NULL	23 / 83	CC	basement membrane
33	−18.24	NULL	13 / 35	Glio	Colman_survival_associated
34	−17.83	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
35	−17.67	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
36	−17.66	NULL	4 / 10	BP	protein heterotrimerization
37	−17.2	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
38	−17.06	NULL	12 / 19	MF	extracellular matrix binding
39	−17.03	NULL	16 / 68	CC	collagen
40	−16.78	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY