GW_159

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1724 (951 + / 773 −)

genes with fdr < 0.1 = 1398 (780 + / 618 −)

genes with fdr < 0.05 = 1243 (690 + / 553 −)

genes with fdr < 0.01 = 772 (451 + / 321 −)

genes in genesets = 16332

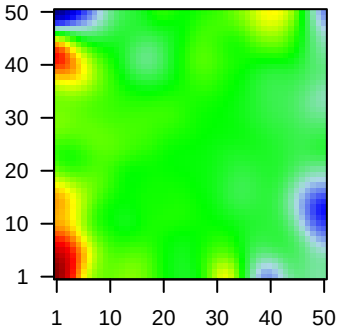
<FC> = 0

<shrinkage−t> = 0

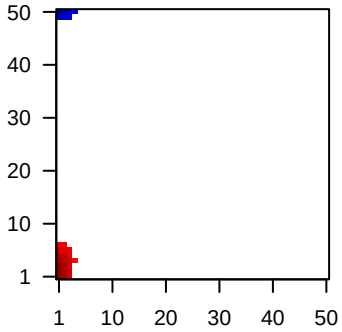
<p−value> = 0.11

<fdr> = 0.85

Profile



Regulated Spots



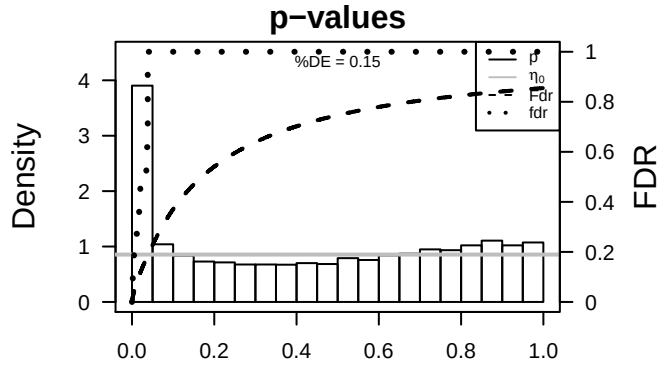
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.93	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.97	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.55	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	218	−2.7	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	55107	1.61	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGI
6	306	1.73	2e−16	4e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
7	80115	1.75	2e−16	4e−14	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
8	387695	−1.61	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
9	793	1.57	2e−16	4e−14	39 x 50	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
10	55450	1.7	2e−16	4e−14	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
11	84290	−1.75	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
12	414062	1.58	2e−16	4e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbc
13	1000	1.61	2e−16	4e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
14	1048	−1.57	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
15	22802	−2.33	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	49860	−2.57	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
17	441520	1.82	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
18	1515	1.79	2e−16	4e−14	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
19	6373	1.6	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;A
20	6374	2.22	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.4	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	11	NULL	242	BP	extracellular matrix organization
3	8.96	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	8.7	NULL	190	CC	extracellular matrix
5	8.52	NULL	69	BP	extracellular matrix disassembly
6	8.52	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
7	8.14	NULL	1720	Chr	Chr 1
8	7.99	NULL	64	BP	collagen catabolic process
9	7.8	NULL	51	BP	type I interferon signaling pathway
10	7.76	NULL	35	Glio	Colman_survival_associated
11	7.57	NULL	6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
12	7.42	NULL	15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
13	7.29	NULL	117	Glio	GIEZELT_GBM_WT_up_VS_mut
14	7.04	NULL	16	GSEA C2	LU_TUMOR_VASCULATURE_UP
15	7.04	NULL	16	GSEA C2	TIAN_TNF_SIGNALING_VIA_NFKB
16	6.95	NULL	957	Chr	Chr 11
17	6.89	NULL	13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
18	6.87	NULL	6	Glio	Martinez_Glio_hypometh
19	6.69	NULL	16	BP	decidualization
20	6.66	NULL	530	Cancer	Lembcke_Normal vs Adenoma
Underexpressed					
1	−18.75	NULL	135	H.Tiss	WIRTH_Mucosa
2	−8.12	NULL	232	Chr	Chr 18
3	−7.93	NULL	630	Chr	Chr X
4	−7.68	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
5	−7.53	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
6	−6.95	NULL	1033	Chr	Chr 2
7	−6.88	NULL	119	BP	xenobiotic metabolic process
8	−6.77	NULL	10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
9	−6.73	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
10	−6.63	NULL	12	BP	cellular aldehyde metabolic process
11	−6.57	NULL	42	BP	keratinization
12	−6.15	NULL	53	BP	keratinocyte differentiation
13	−6.15	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
14	−5.91	NULL	21	CC	cornified envelope
15	−5.88	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
16	−5.72	NULL	19	BP	peptide cross−linking
17	−5.69	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
18	−5.56	NULL	296	MF	oxidoreductase activity
19	−5.46	NULL	6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
20	−5.45	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E

p−values



GW_159

Local Summary

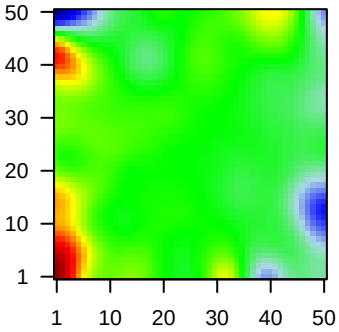
%DE = 0.81
metagenes = 21
genes = 315
genes in genesets = 312

genes with fdr < 0.1 = 213 (210 + / 3 −)
genes with fdr < 0.05 = 195 (193 + / 2 −)
genes with fdr < 0.01 = 167 (167 + / 0 −)

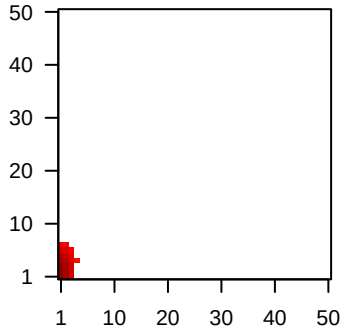
<r> metagenes = 0.94
<r> genes = 0.34

<FC> = 0.67
<shrinkage−t> = 23.68
<p−value> = 0
<fdr> = 0.36

Profile



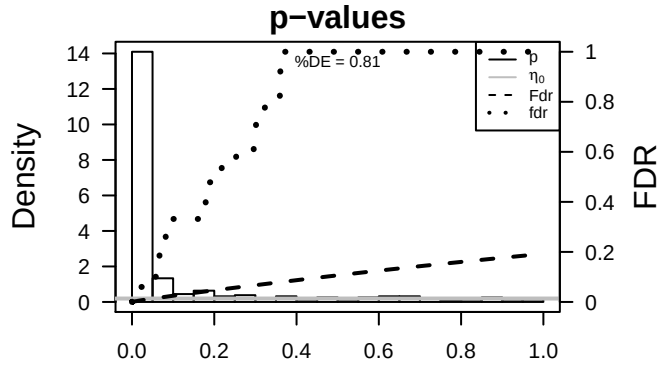
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	1.61	2e−16	6e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	55450	1.7	2e−16	6e−16	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
3	414062	1.58	2e−16	6e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
4	6374	2.22	2e−16	6e−16	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
5	1687	1.57	2e−16	6e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
6	3678	1.71	2e−16	6e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
7	3918	1.62	2e−16	6e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
8	4312	1.56	2e−16	6e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
9	4319	2.08	2e−16	6e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
10	4320	1.71	2e−16	6e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
11	4318	2.12	2e−16	6e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
12	10630	1.6	2e−16	6e−16	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
13	5210	1.74	2e−16	6e−16	1 x 5	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 4 [S
14	5270	1.6	2e−16	6e−16	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
15	871	1.56	2e−16	6e−16	1 x 1	serpin peptidase inhibitor, clade H (heat shock protein 47), m
16	284111	1.62	2e−16	6e−16	1 x 7	solute carrier family 13 (sodium−dependent citrate transporte
17	8877	1.6	2e−16	6e−16	3 x 5	sphingosine kinase 1 [Source:HGNC Symbol;Acc:11240]
18	6696	2.47	2e−16	6e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
19	8406	2.17	2e−16	6e−16	2 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Syr
20	7045	1.74	2e−16	6e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	31.65	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	24.91	NULL	62 / 242	BP	extracellular matrix organization
3	22.05	NULL	3 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
4	20.82	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
5	20.18	NULL	47 / 190	CC	extracellular matrix
6	20.01	NULL	61 / 250	Lymphoma	ENZ_Stromal signature 1
7	19.92	NULL	24 / 64	BP	collagen catabolic process
8	19.49	NULL	8 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
9	19.09	NULL	26 / 69	BP	extracellular matrix disassembly
10	18.41	NULL	12 / 35	Glio	Colman_survival_associated
11	17.49	NULL	76 / 683	CC	extracellular space
12	17.26	NULL	3 / 6	Glio	Martinez_Glio_hypometh
13	16.77	NULL	14 / 37	BP	collagen fibril organization
14	16.68	NULL	107 / 1182	CC	extracellular region
15	16.42	NULL	14 / 68	Glio	cultured astroglia vs. in vivo astrocytes
16	15.47	NULL	8 / 19	MF	extracellular matrix binding
17	15.09	NULL	9 / 16	MF	fibronectin binding
18	14.95	NULL	32 / 183	CC	proteinaceous extracellular matrix
19	14.65	NULL	58 / 553	Cancer	Lembcke_Colonic Inflammation
20	14.64	NULL	6 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
21	14.3	NULL	5 / 13	BP	response to vitamin D
22	14.28	NULL	56 / 403	BP	cell adhesion
23	14.26	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
24	14.14	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
25	14	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
26	13.93	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
27	13.93	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
28	13.93	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
29	13.93	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
30	13.68	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
31	13.38	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
32	13.35	NULL	3 / 10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
33	13.27	NULL	14 / 16	MMML C6	GRACIEJ_MMML 1
34	12.96	NULL	4 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
35	12.71	NULL	5 / 16	BP	decidualization
36	12.69	NULL	7 / 49	Glio	Christensen_hypomethylated_in_primary_glioblastoma
37	12.42	NULL	6 / 12	BP	hemidesmosome assembly
38	12.27	NULL	4 / 16	GSEA C2	KEGG_BLADDER_CANCER
39	12.27	NULL	6 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
40	12.19	NULL	4 / 16	GSEA C2	LU_TUMOR_ANGIOGENESIS_UP

GW_159

Local Summary

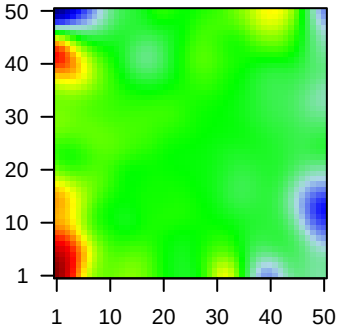
%DE = 0.94
metagenes = 7
genes = 135
genes in genesets = 132

genes with fdr < 0.1 = 116 (6 + / 110 −)
genes with fdr < 0.05 = 109 (3 + / 106 −)
genes with fdr < 0.01 = 101 (3 + / 98 −)

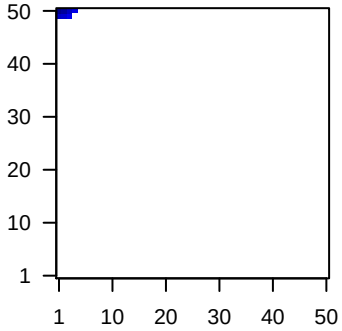
<r> metagenes = 0.99
<r> genes = 0.51

<FC> = −1.01
<shrinkage−t> = −35.81
<p−value> = 0
<fdr> = 0.24

Profile



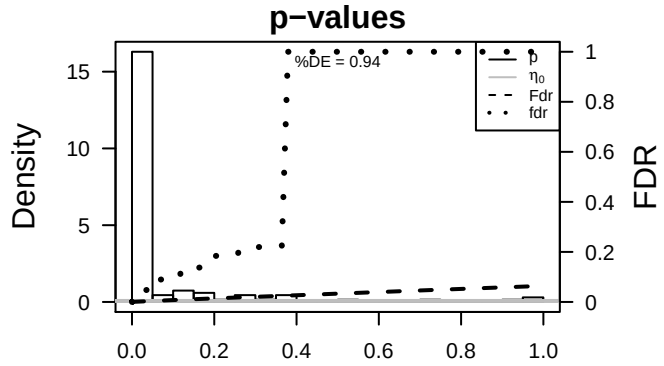
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.93	2e−16	6e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.97	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.55	2e−16	6e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	218	−2.7	2e−16	6e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	387695	−1.61	2e−16	6e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
6	84290	−1.75	2e−16	6e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	1048	−1.57	2e−16	6e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
8	22802	−2.33	2e−16	6e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	49860	−2.57	2e−16	6e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1562	−1.61	2e−16	6e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
11	92196	−1.54	2e−16	6e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
12	1673	−1.78	2e−16	6e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	3860	−3.89	2e−16	6e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
14	192666	−1.96	2e−16	6e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
15	3851	−2.96	2e−16	6e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
16	196374	−1.61	2e−16	6e−17	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
17	4118	−2.96	2e−16	6e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
18	5307	−1.65	2e−16	6e−17	3 x 50	paired−like homeodomain 1 [Source:HGNC Symbol;Acc:900
19	5493	−1.6	2e−16	6e−17	1 x 50	periplakin [Source:HGNC Symbol;Acc:9273]
20	6337	−2.41	2e−16	6e−17	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−53.51	NULL	57 / 135	H.Tiss	WIRTH_Mucosa
2	−21.2	NULL	16 / 53	BP	keratinocyte differentiation
3	−19.91	NULL	7 / 19	BP	peptide cross−linking
4	−18.94	NULL	13 / 42	BP	keratinization
5	−17.49	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
6	−17.49	NULL	55 / 572	Disease	GUDJ_psoriasis up
7	−17.29	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
8	−16.14	NULL	12 / 21	CC	cornified envelope
9	−15.99	NULL	3 / 12	BP	cellular aldehyde metabolic process
10	−13.24	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−13.02	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
12	−12.84	NULL	16 / 76	BP	epidermis development
13	−12.82	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
14	−12.69	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
15	−12.64	NULL	4 / 15	MF	retinol dehydrogenase activity
16	−12.6	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
17	−12.54	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
18	−12.51	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	−11.9	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
20	−11.88	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
21	−11.87	NULL	5 / 13	BP	negative regulation of peptidase activity
22	−11.74	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
23	−11.48	NULL	4 / 44	CC	keratin filament
24	−11.1	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
25	−10.96	NULL	4 / 39	BP	retinoid metabolic process
26	−10.51	NULL	12 / 186	MF	structural molecule activity
27	−10.46	NULL	6 / 82	CC	intermediate filament
28	−10.46	NULL	6 / 38	BP	epithelial cell differentiation
29	−10.27	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
30	−9.84	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
31	−9.34	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
32	−9.21	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
33	−9.16	NULL	9 / 79	MF	serine−type endopeptidase inhibitor activity
34	−9.09	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
35	−8.79	NULL	3 / 27	BP	response to bacterium
36	−8.74	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
37	−8.74	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
38	−8.69	NULL	41 / 1182	CC	extracellular region
39	−8.47	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
40	−8.45	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN