GW_183

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1719 (950 + / 769 −)

genes with fdr < 0.1 = 1315 (744 + / 571 −)

genes with fdr < 0.05 = 997 (585 + / 412 −)

genes with fdr < 0.01 = 635 (382 + / 253 −)

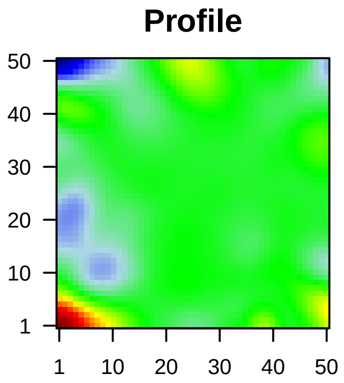
genes in genesets = 16332

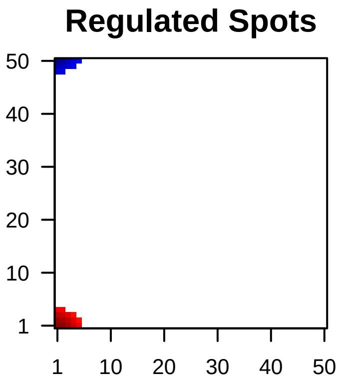
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

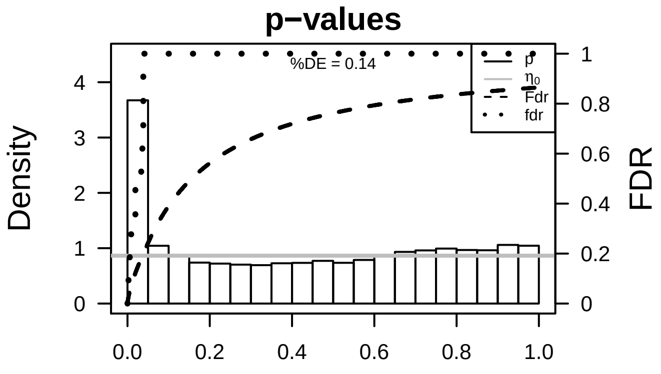
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−2.51	2e−16	6e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	222	−1.63	2e−16	6e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	401138	3.45	2e−16	6e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
4	260436	1.7	2e−16	6e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
5	810	−2.35	2e−16	6e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
6	22802	−1.65	2e−16	6e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	9076	−2.01	2e−16	6e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
8	1300	1.64	2e−16	6e−14	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
9	1281	1.74	2e−16	6e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
10	1290	1.84	2e−16	6e−14	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
11	51200	1.95	2e−16	6e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
12	49860	−2.39	2e−16	6e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
13	1513	1.8	2e−16	6e−14	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
14	9547	1.65	2e−16	6e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
15	2167	−1.63	2e−16	6e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	10468	2.03	2e−16	6e−14	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
17	10804	−2.12	2e−16	6e−14	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
18	3006	1.63	2e−16	6e−14	5 x 20	histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
19	3123	1.89	2e−16	6e−14	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
20	3127	2.39	2e−16	6e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	19.2	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	15.41	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	15.13	NULL	190	CC	extracellular matrix
4	14.34	NULL	242	BP	extracellular matrix organization
5	12.82	NULL	69	BP	extracellular matrix disassembly
6	12.72	NULL	64	BP	collagen catabolic process
7	12.15	NULL	16	MMML CGS	MACIEJ_MMML 1
8	11.5	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	11.5	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	11.5	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	11.5	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	11.47	NULL	183	CC	proteinaceous extracellular matrix
13	11.03	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	10.27	NULL	683	CC	extracellular space
15	9.98	NULL	83	CC	basement membrane
16	9.34	NULL	1182	CC	extracellular region
17	9.22	NULL	403	BP	cell adhesion
18	9.01	NULL	119	Lymphoma	ROSOLOWSKI_green total
19	8.98	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
20	8.76	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
Underexpressed					
1	−18.85	NULL	135	H.Tiss	WIRTH_Mucosa
2	−12.7	NULL	1135	Chr	Chr 19
3	−10.22	NULL	42	BP	keratinization
4	−9.46	NULL	21	CC	cornified envelope
5	−8.44	NULL	918	Chr	Chr 17
6	−7.81	NULL	717	Chr	Chr 16
7	−7.81	NULL	45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
8	−7.58	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
9	−7.5	NULL	1318	CC	mitochondrion
10	−6.76	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−6.54	NULL	304	CC	mitochondrial inner membrane
12	−6.5	NULL	53	BP	keratinocyte differentiation
13	−6.26	NULL	572	Disease	GUDJ_psoriasis up
14	−6.22	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
15	−5.81	NULL	220	CC	mitochondrial matrix
16	−5.77	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
17	−5.69	NULL	14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
18	−5.64	NULL	19	BP	peptide cross−linking
19	−5.47	NULL	152	BP	cellular metabolic process
20	−4.98	NULL	38	BP	epithelial cell differentiation

GW_183

Local Summary

%DE = 0.85

metagenes = 16

genes = 258

genes in genesets = 257

genes with fdr < 0.1 = 193 (188 + / 5 −)

genes with fdr < 0.05 = 185 (181 + / 4 −)

genes with fdr < 0.01 = 153 (153 + / 0 −)

<r> metagenes = 0.96

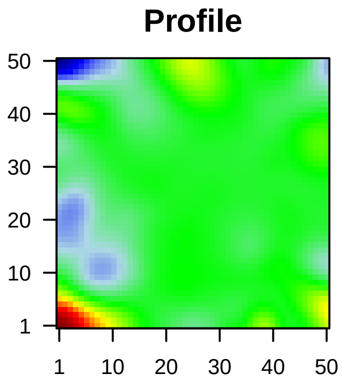
<r> genes = 0.4

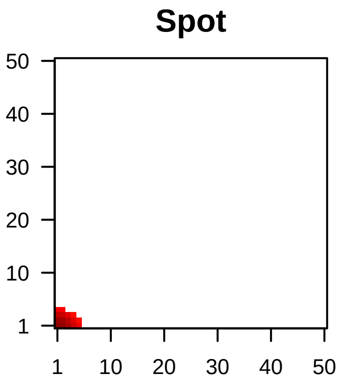
<FC> = 0.78

<shrinkage−t> = 27.26

<p−value> = 0

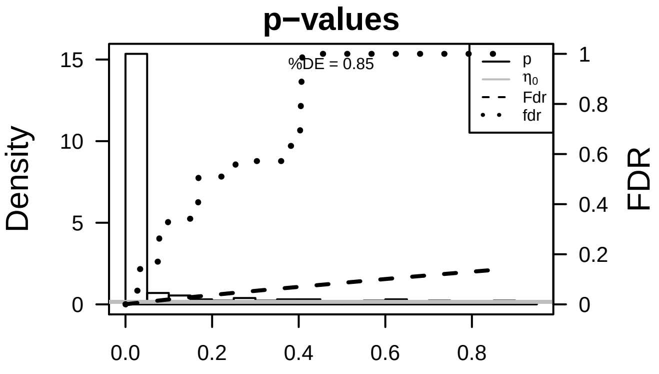
<fdr> = 0.3


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1300	1.64	2e−16	5e−16	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
2	1281	1.74	2e−16	5e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
3	1290	1.84	2e−16	5e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
4	1513	1.8	2e−16	5e−16	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
5	11009	2.03	2e−16	5e−16	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
6	3918	1.64	2e−16	5e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
7	4060	1.81	2e−16	5e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
8	4312	1.82	2e−16	5e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
9	4319	2.04	2e−16	5e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
10	4322	3.32	2e−16	5e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
11	4314	2	2e−16	5e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
12	4318	1.94	2e−16	5e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
13	4907	1.62	2e−16	5e−16	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
14	10631	2.35	2e−16	5e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;A
15	6447	1.97	2e−16	5e−16	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
16	6678	1.85	2e−16	5e−16	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
17	6696	2.26	2e−16	5e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
18	3371	1.66	2e−16	5e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
19	1464	1.55	3e−15	5e−14	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
20	1278	1.55	3e−15	5e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	36.18	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	36.1	NULL	30 / 69	BP	extracellular matrix disassembly
3	35.42	NULL	27 / 64	BP	collagen catabolic process
4	35.14	NULL	62 / 190	CC	extracellular matrix
5	33.09	NULL	65 / 242	BP	extracellular matrix organization
6	31.64	NULL	71 / 250	Lymphoma	LENZ_Stromal signature 1
7	31.16	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	29.92	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
9	25.2	NULL	8 / 12	miRNA target	miR−29c
10	24.97	NULL	8 / 11	MF	platelet−derived growth factor binding
11	22.98	NULL	35 / 183	CC	proteinaceous extracellular matrix
12	22.79	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
13	22.35	NULL	76 / 683	CC	extracellular space
14	21.91	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
15	21.74	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
16	21.72	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
17	20.81	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
18	20.3	NULL	102 / 1182	CC	extracellular region
19	18.89	NULL	11 / 19	MF	extracellular matrix binding
20	18.78	NULL	5 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
21	18.74	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
22	18.72	NULL	19 / 57	MF	extracellular matrix structural constituent
23	18.72	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
24	18.32	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
25	18.3	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
26	17.89	NULL	12 / 40	BP	cellular response to amino acid stimulus
27	17.34	NULL	14 / 37	BP	collagen fibril organization
28	17.13	NULL	5 / 16	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_UP
29	17.08	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
30	16.49	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
31	16.16	NULL	21 / 83	CC	basement membrane
32	15.8	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
33	15.76	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
34	15.73	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
35	15.4	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
36	14.89	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
37	14.77	NULL	10 / 73	MF	metallopeptidase activity
38	14.77	NULL	10 / 81	MF	metalloendopeptidase activity
39	14.74	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
40	14.64	NULL	14 / 68	Glio	cultured astroglia vs. in vivo astrocytes

GW_183

Local Summary

%DE = 0.87

metagenes = 11

genes = 192

genes in genesets = 188

genes with fdr < 0.1 = 150 (7 + / 143 −)

genes with fdr < 0.05 = 141 (7 + / 134 −)

genes with fdr < 0.01 = 126 (5 + / 121 −)

<r> metagenes = 0.98

<r> genes = 0.48

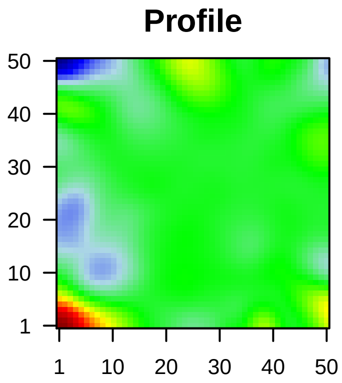
<FC> = −0.77

<shrinkage−t> = −27.32

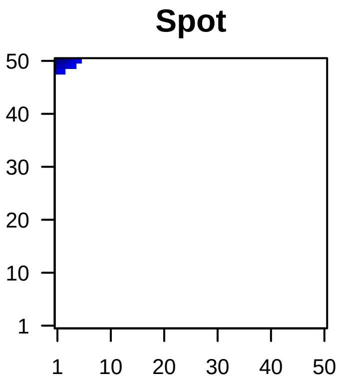
<p−value> = 0

<fdr> = 0.27

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−2.51	2e−16	3e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	222	−1.63	2e−16	3e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	810	−2.35	2e−16	3e−16	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
4	22802	−1.65	2e−16	3e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	49860	−2.39	2e−16	3e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	3860	−3.19	2e−16	3e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
7	192666	−1.72	2e−16	3e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
8	3851	−2.42	2e−16	3e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
9	4118	−2.26	2e−16	3e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
10	342897	−1.64	2e−16	3e−16	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebra
11	5307	−2.28	2e−16	3e−16	3 x 50	paired−like homeodomain 1 [Source:HGNC Symbol;Acc:900
12	51458	−1.62	2e−16	3e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
13	6700	−2.21	2e−16	3e−16	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
14	6702	−1.64	2e−16	3e−16	1 x 50	
15	6705	−1.91	2e−16	3e−16	1 x 50	small proline−rich protein 2F [Source:HGNC Symbol;Acc:112
16	6707	−3.38	2e−16	3e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
17	7053	−2.18	2e−16	3e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
18	1992	−1.58	1e−15	5e−13	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [S
19	9368	−1.5	3e−14	5e−13	5 x 50	solute carrier family 9, subfamily A (NHE3, cation proton anti
20	6701	−1.49	4e−14	5e−13	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−53.41	NULL	71 / 135	H.Tiss	WIRTH_Mucosa
2	−29.38	NULL	14 / 21	CC	cornified envelope
3	−28.08	NULL	16 / 42	BP	keratinization
4	−25.72	NULL	19 / 53	BP	keratinocyte differentiation
5	−24.4	NULL	8 / 19	BP	peptide cross−linking
6	−22.02	NULL	75 / 572	Disease	GUDJ_psoriasis up
7	−20.88	NULL	19 / 76	BP	epidermis development
8	−16.4	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	−14.57	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
10	−13.01	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	−11.92	NULL	6 / 13	BP	negative regulation of peptidase activity
12	−11.66	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
13	−11.36	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	−11.31	NULL	13 / 186	MF	structural molecule activity
15	−11	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	−10.83	NULL	2 / 8	TF Tissue	VAQUERIZAS_Tongue
17	−10.58	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
18	−10.57	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
19	−10.55	NULL	7 / 38	BP	epithelial cell differentiation
20	−10.18	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
21	−10	NULL	3 / 12	BP	cellular aldehyde metabolic process
22	−9.97	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
23	−9.96	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
24	−9.95	NULL	4 / 44	CC	keratin filament
25	−9.78	NULL	6 / 29	BP	regulation of proteolysis
26	−9.72	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
27	−9.4	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
28	−9.37	NULL	9 / 52	BP	negative regulation of endopeptidase activity
29	−9.15	NULL	6 / 82	CC	intermediate filament
30	−9.12	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
31	−9.09	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
32	−9.01	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
33	−8.93	NULL	2 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
34	−8.63	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
35	−8.26	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
36	−8.19	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
37	−8.18	NULL	12 / 122	MF	serine−type endopeptidase activity
38	−8.17	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
39	−8.01	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
40	−8	NULL	3 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP

p−values