GW_255

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1826 (1064 + / 762 −)

genes with fdr < 0.1 = 1461 (879 + / 582 −)

genes with fdr < 0.05 = 1098 (678 + / 420 −)

genes with fdr < 0.01 = 784 (518 + / 266 −)

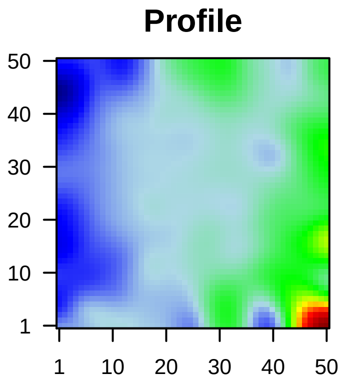
genes in genesets = 16332

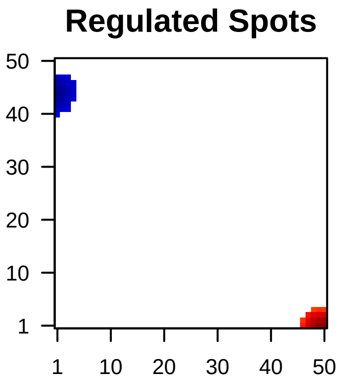
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

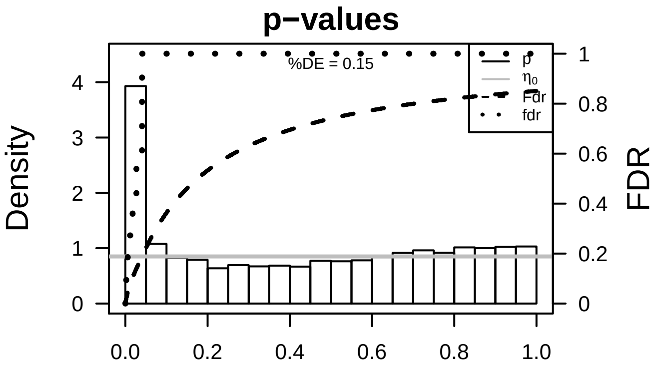
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.58	2e−16	3e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	124	1.83	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	1.58	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
4	8644	−1.71	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	55107	−1.65	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
6	341	1.66	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
7	366	1.57	2e−16	3e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
8	445328	−1.84	2e−16	3e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
9	80117	1.84	2e−16	3e−14	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:
10	92591	1.65	2e−16	3e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
11	57172	3.02	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	6347	2.71	2e−16	3e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
13	6364	2.51	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
14	414062	1.75	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
15	9560	2.04	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
16	6355	1.59	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
17	909	1.47	2e−16	3e−14	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
18	10428	−1.48	2e−16	3e−14	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
19	9076	1.63	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
20	54102	1.47	2e−16	3e−14	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.92	NULL	417	H.Tiss	WIRTH_Immune system
2	17.31	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	14.73	NULL	312	BP	immune response
4	13.01	NULL	316	Cancer	SPANG_BCL6−index2
5	11.87	NULL	15	CC	MHC class II protein complex
6	10.88	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	10.88	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	10.88	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	10.88	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	10.55	NULL	47	BP	antigen processing and presentation
11	10.42	NULL	269	BP	inflammatory response
12	9.89	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
13	9.45	NULL	60	BP	interferon−gamma−mediated signaling pathway
14	9.31	NULL	36	BP	neutrophil chemotaxis
15	8.83	NULL	43	MF	chemokine activity
16	8.73	NULL	49	Glio	Donson−innate immunity−associated with LTS in HGA
17	8.66	NULL	10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
18	8.32	NULL	530	BP	innate immune response
19	8.26	NULL	111	BP	chemotaxis
20	8.22	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
Underexpressed					
1	−11.38	NULL	135	H.Tiss	WIRTH_Mucosa
2	−9.46	NULL	519	Chr	Chr 14
3	−8.29	NULL	717	Chr	Chr 16
4	−8.29	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	−6.89	NULL	449	Chr	Chr 20
6	−6.15	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
7	−6.15	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
8	−5.74	NULL	957	Chr	Chr 11
9	−5.6	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
10	−5.51	NULL	84	BP	muscle contraction
11	−4.75	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
12	−4.68	NULL	13	GSEA C2	NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON
13	−4.64	NULL	15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
14	−4.57	NULL	16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
15	−4.46	NULL	602	Chr	Chr 10
16	−4.42	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
17	−4.4	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
18	−4.37	NULL	15	BP	negative regulation of growth
19	−4.28	NULL	16	GSEA C2	GRATIAS_RETINOBLASTOMA_16Q24
20	−4.27	NULL	45	CC	stress fiber

GW_255

Local Summary

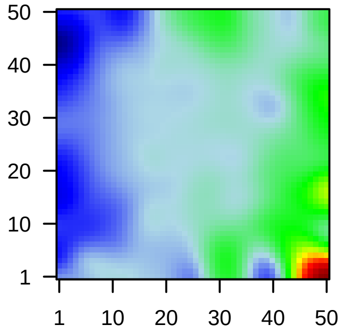
%DE = 0.99
metagenes = 17
genes = 276
genes in genesets = 274

genes with fdr < 0.1 = 268 (264 + / 4 −)
genes with fdr < 0.05 = 259 (257 + / 2 −)
genes with fdr < 0.01 = 247 (245 + / 2 −)

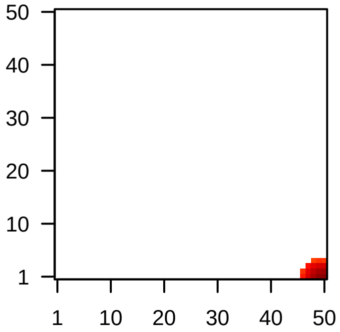
<r> metagenes = 0.99
<r> genes = 0.59

<FC> = 0.88
<shrinkage−t> = 30.77
<p−value> = 0
<fdr> = 0.18

Profile



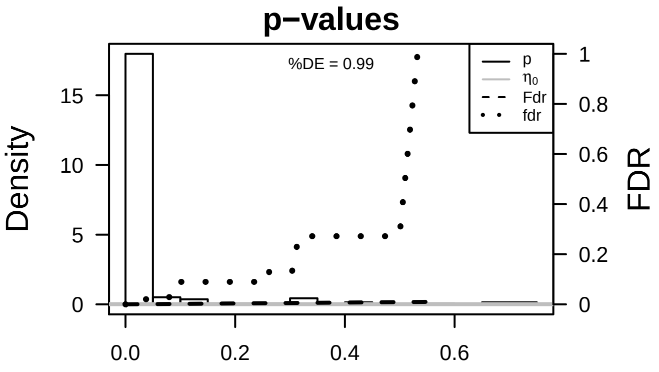
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	1.66	2e−16	3e−17	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	92591	1.65	2e−16	3e−17	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
3	57172	3.02	2e−16	3e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
4	6347	2.71	2e−16	3e−17	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
5	6364	2.51	2e−16	3e−17	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
6	51755	2.64	2e−16	3e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
7	4283	1.76	2e−16	3e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
8	1545	1.88	2e−16	3e−17	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
9	1593	1.81	2e−16	3e−17	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sou
10	55619	1.82	2e−16	3e−17	50 x 1	dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:2347
11	54855	1.88	2e−16	3e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
12	3113	1.58	2e−16	3e−17	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
13	3119	1.52	2e−16	3e−17	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
14	3120	2.19	2e−16	3e−17	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
15	3122	1.48	2e−16	3e−17	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
16	3128	2.1	2e−16	3e−17	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
17	3512	2.33	2e−16	3e−17	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
18	3543	1.5	2e−16	3e−17	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
19	91353	1.85	2e−16	3e−17	48 x 1	
20	3936	1.63	2e−16	3e−17	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	35.09	NULL	12 / 15	CC	MHC class II protein complex
2	25.75	NULL	92 / 417	H.Tiss	WIRTH_Immune system
3	23	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
4	22.43	NULL	96 / 553	Cancer	Lembcke_Colonic Inflammation
5	21.95	NULL	52 / 312	BP	immune response
6	20.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	20.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	20.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	20.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	20.57	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
11	20.15	NULL	15 / 47	BP	antigen processing and presentation
12	17.62	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
13	16.74	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
14	15.74	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
15	15.48	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
16	15.35	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
17	15.03	NULL	17 / 60	BP	T cell costimulation
18	14.97	NULL	7 / 28	CC	transport vesicle membrane
19	14.96	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	14.74	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
21	14.33	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
22	14.27	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
23	14.23	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
24	13.87	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
25	13.68	NULL	8 / 35	CC	trans−Golgi network membrane
26	13.59	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
27	13.5	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
28	13.41	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
29	13.26	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
30	13.24	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
31	13.09	NULL	8 / 16	GSEA C2	SU_THYMUS
32	12.97	NULL	17 / 84	BP	T cell receptor signaling pathway
33	12.69	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
34	12.59	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
35	12.45	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
36	12.45	NULL	18 / 74	BP	regulation of immune response
37	12.42	NULL	5 / 12	BP	immunoglobulin mediated immune response
38	12.25	NULL	8 / 46	CC	endocytic vesicle membrane
39	11.98	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
40	11.73	NULL	25 / 162	CC	external side of plasma membrane

GW_255

Local Summary

%DE = 0.81

metagenes = 26

genes = 305

genes in genesets = 299

genes with fdr < 0.1 = 209 (12 + / 197 −)

genes with fdr < 0.05 = 176 (10 + / 166 −)

genes with fdr < 0.01 = 148 (7 + / 141 −)

<r> metagenes = 0.93

<r> genes = 0.36

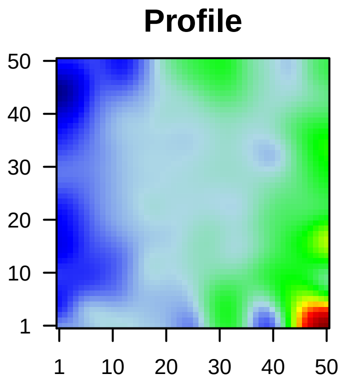
<FC> = −0.46

<shrinkage−t> = −16.22

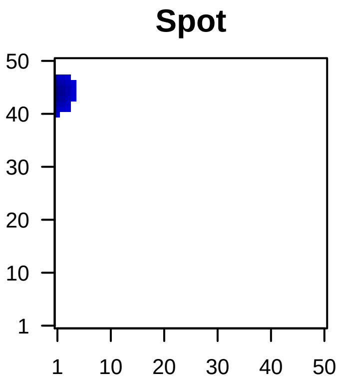
<p−value> = 0

<fdr> = 0.43

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	445328	−1.84	2e−16	1e−15	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
2	1515	−1.52	2e−16	1e−15	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
3	3858	1.6	2e−16	1e−15	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]
4	3861	−1.65	2e−16	1e−15	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
5	3868	−1.39	2e−16	1e−15	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
6	3872	−1.37	2e−16	1e−15	1 x 43	keratin 17 [Source:HGNC Symbol;Acc:6427]
7	5744	−1.62	2e−16	1e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
8	29984	−1.59	2e−16	1e−15	1 x 45	ras homolog family member D [Source:HGNC Symbol;Acc:67
9	6273	−1.47	2e−16	1e−15	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
10	8710	1.54	2e−16	1e−15	1 x 46	serpin peptidase inhibitor, clade B (ovalbumin), member 7 [Sc
11	8140	−1.47	2e−16	1e−15	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
12	23682	−1.45	4e−16	1e−14	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
13	771	−1.44	7e−16	4e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
14	9635	−1.42	1e−15	4e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	5836	−1.41	2e−15	3e−12	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:97
16	3963	−1.34	6e−14	2e−11	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
17	2810	−1.18	5e−13	2e−11	1 x 45	stratifin [Source:HGNC Symbol;Acc:10773]
18	51200	−1.27	9e−13	2e−11	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
19	84985	−1.26	2e−12	2e−11	1 x 44	family with sequence similarity 83, member A [Source:HGNC
20	113146	−1.26	2e−12	2e−11	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.59	NULL	30 / 135	H.Tiss	WIRTH_Mucosa
2	−16.95	NULL	73 / 572	Disease	GUDJ_psoriasis up
3	−12.54	NULL	15 / 76	BP	epidermis development
4	−12.27	NULL	11 / 82	MF	structural constituent of cytoskeleton
5	−12.03	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
6	−12.02	NULL	4 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
7	−11.84	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
8	−11.65	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
9	−10.92	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
10	−9.94	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
11	−9.39	NULL	18 / 82	CC	intermediate filament
12	−9.27	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
13	−8.82	NULL	3 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
14	−8.78	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
15	−8.64	NULL	3 / 35	CC	cell periphery
16	−8.48	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
17	−8.39	NULL	3 / 25	BP	response to zinc ion
18	−8.24	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
19	−7.95	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
20	−7.8	NULL	2 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
21	−7.68	NULL	2 / 10	MF	neutral amino acid transmembrane transporter activity
22	−7.57	NULL	8 / 21	CC	desmosome
23	−7.39	NULL	2 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
24	−7.16	NULL	3 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
25	−7.16	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA
26	−7.11	NULL	2 / 11	BP	positive regulation of positive chemotaxis
27	−7.11	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
28	−7.05	NULL	1 / 6	Glio	Martinez_Glio_hypometh
29	−7.03	NULL	1 / 6	miRNA target−starBase	hsa−miR−126
30	−6.96	NULL	3 / 15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
31	−6.96	NULL	2 / 15	Pathw Act	GUSTAFSON_PI3K_DN
32	−6.9	NULL	2 / 12	BP	neutral amino acid transport
33	−6.88	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
34	−6.84	NULL	2 / 12	MF	fatty acid binding
35	−6.69	NULL	2 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
36	−6.51	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
37	−6.47	NULL	2 / 10	BP	positive regulation of Rho protein signal transduction
38	−6.43	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
39	−6.39	NULL	3 / 17	BP	morphogenesis of an epithelium
40	−6.39	NULL	8 / 44	BP	skin development

p−values