GW_020

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1892 (1037 + / 855 −)

genes with fdr < 0.1 = 1497 (820 + / 677 −)

genes with fdr < 0.05 = 1271 (689 + / 582 −)

genes with fdr < 0.01 = 926 (483 + / 443 −)

genes in genesets = 16332

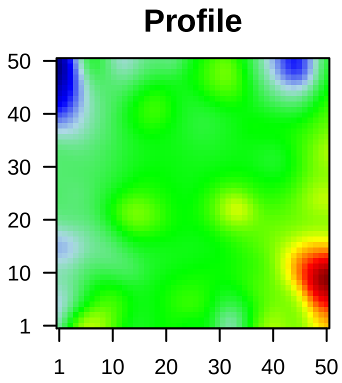
<FC> = 0

<shrinkage−t> = −0.01

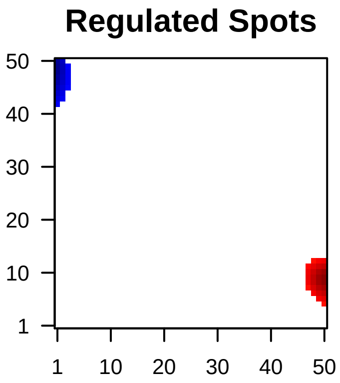
<p−value> = 0.09

<fdr> = 0.85

Profile



Regulated Spots



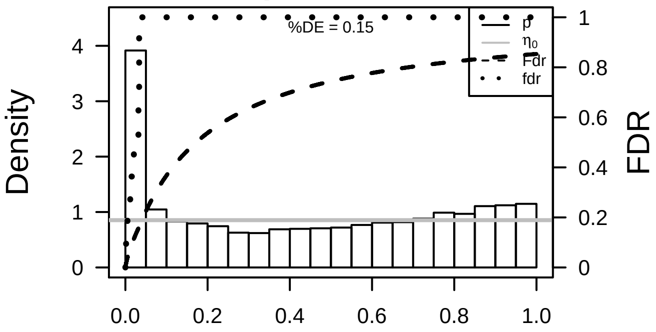
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	2.01	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Symb
2	133	−1.89	2e−16	3e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
3	10551	2.52	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	222	−1.98	2e−16	3e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	347	2.84	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
6	80341	2.64	2e−16	3e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
7	387695	−2.06	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
8	260436	3.71	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
9	352999	2.48	2e−16	3e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symb
10	375791	−2.7	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
11	57172	2.1	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	1001	−2.03	2e−16	3e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
13	4680	2.23	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	9635	−2.77	2e−16	3e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	9071	2.07	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
16	84518	−3.04	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	1308	−1.99	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	10321	2.2	2e−16	3e−14	50 x 10	cysteine−rich secretory protein 3 [Source:HGNC Symbol;Acc
19	49860	−2.98	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
20	1475	−2.11	2e−16	3e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.51	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	10.98	NULL	375	Disease	GUDJ_psoriasis down
3	8.65	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
4	8.36	NULL	3274	CC	integral to membrane
5	7.63	NULL	482	BP	cellular protein metabolic process
6	7.3	NULL	87	BP	translational termination
7	7.25	NULL	81	BP	viral transcription
8	7.08	NULL	92	BP	translational elongation
9	6.99	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
10	6.6	NULL	128	BP	translational initiation
11	6.52	NULL	14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
12	6.38	NULL	16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
13	6.23	NULL	92	BP	viral life cycle
14	5.88	NULL	14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
15	5.88	NULL	170	BP	post−translational protein modification
16	5.82	NULL	13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
17	5.79	NULL	10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP
18	5.78	NULL	253	BP	translation
19	5.63	NULL	10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
20	5.58	NULL	15	GSEA C2	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
Underexpressed					
1	−30.88	NULL	572	Disease	GUDJ_psoriasis up
2	−30.11	NULL	135	H.Tiss	WIRTH_Mucosa
3	−19.03	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	−19.03	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	−17.12	NULL	21	CC	cornified envelope
6	−17	NULL	76	BP	epidermis development
7	−15.45	NULL	53	BP	keratinocyte differentiation
8	−14.91	NULL	42	BP	keratinization
9	−13.84	NULL	530	Cancer	Lembcke_Normal vs Adenoma
10	−12.76	NULL	370	BP	mitotic cell cycle
11	−11.03	NULL	82	CC	intermediate filament
12	−10.66	NULL	19	BP	peptide cross−linking
13	−10.63	NULL	57	Glio	developing astrocytes
14	−9.96	NULL	949	CC	nucleoplasm
15	−9.29	NULL	44	CC	keratin filament
16	−9.11	NULL	186	MF	structural molecule activity
17	−8.77	NULL	4310	CC	cytoplasm
18	−8.76	NULL	10	MF	RAGE receptor binding
19	−8.4	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
20	−8.02	NULL	15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN

p−values



GW_020

Local Summary

%DE = 0.92

metagenes = 29

genes = 317

genes in genesets = 314

genes with fdr < 0.1 = 274 (266 + / 8 −)

genes with fdr < 0.05 = 247 (244 + / 3 −)

genes with fdr < 0.01 = 233 (231 + / 2 −)

<r> metagenes = 0.89

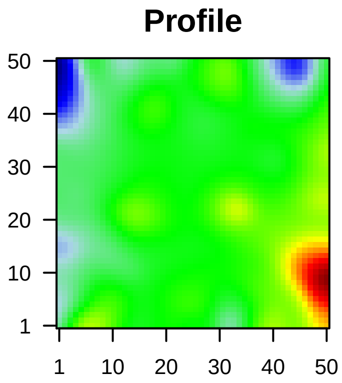
<r> genes = 0.26

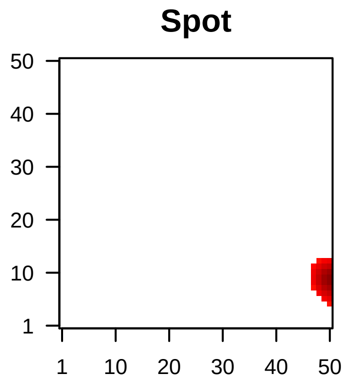
<FC> = 1.02

<shrinkage−t> = 35.51

<p−value> = 0

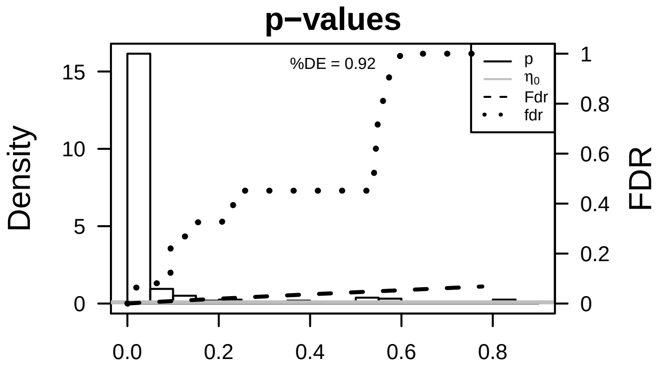
<fdr> = 0.24





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	2.52	2e−16	2e−16	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	347	2.84	2e−16	2e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
3	80341	2.64	2e−16	2e−16	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
4	352999	2.48	2e−16	2e−16	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
5	9071	2.07	2e−16	2e−16	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
6	10321	2.2	2e−16	2e−16	50 x 10	cysteine−rich secretory protein 3 [Source:HGNC Symbol;Acc
7	1805	2.02	2e−16	2e−16	50 x 5	dermatopontin [Source:HGNC Symbol;Acc:3011]
8	8857	2.25	2e−16	2e−16	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
9	57535	2.37	2e−16	2e−16	50 x 10	KIAA1324 [Source:HGNC Symbol;Acc:29618]
10	124220	3.02	2e−16	2e−16	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
11	389816	2.7	2e−16	2e−16	50 x 10	leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
12	4057	2.01	2e−16	2e−16	50 x 10	lactotransferrin [Source:HGNC Symbol;Acc:6720]
13	4256	2.31	2e−16	2e−16	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
14	79083	2.11	2e−16	2e−16	50 x 10	melanophilin [Source:HGNC Symbol;Acc:29643]
15	4589	2.29	2e−16	2e−16	50 x 10	mucin 7, secreted [Source:HGNC Symbol;Acc:7518]
16	4824	2.23	2e−16	2e−16	50 x 10	NK3 homeobox 1 [Source:HGNC Symbol;Acc:7838]
17	5284	2.9	2e−16	2e−16	50 x 10	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	5304	3.04	2e−16	2e−16	50 x 10	prolactin−induced protein [Source:HGNC Symbol;Acc:8993]
19	8842	2.97	2e−16	2e−16	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
20	11272	2.45	2e−16	2e−16	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.37	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	14.22	NULL	4 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
3	14.1	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
4	13.88	NULL	6 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
5	13.73	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
6	13.57	NULL	44 / 375	Disease	GUDJ_psoriasis down
7	12.16	NULL	65 / 1182	CC	extracellular region
8	12.07	NULL	7 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
9	11.95	NULL	4 / 13	Cancer	GENTLES_modul17
10	11.87	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
11	11.07	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
12	10.93	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
13	10.78	NULL	4 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
14	10.36	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
15	9.79	NULL	5 / 20	BP	complement activation
16	9.37	NULL	2 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
17	9.31	NULL	47 / 683	CC	extracellular space
18	9.03	NULL	4 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN
19	8.98	NULL	3 / 14	BP	negative regulation of epithelial to mesenchymal transition
20	8.85	NULL	2 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
21	8.84	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
22	8.79	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
23	8.78	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
24	8.75	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
25	8.51	NULL	3 / 17	BP	iron ion transport
26	8.24	NULL	3 / 13	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
27	8.16	NULL	3 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
28	8.12	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
29	8.06	NULL	4 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
30	8.02	NULL	4 / 17	MF	metallocarboxypeptidase activity
31	8.02	NULL	3 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
32	8.01	NULL	3 / 7	TF Tissue	VAQUERIZAS_Appendix
33	7.91	NULL	3 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
34	7.81	NULL	4 / 15	GSEA C2	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
35	7.75	NULL	2 / 15	GSEA C2	ABE_INNER_EAR
36	7.64	NULL	3 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
37	7.6	NULL	7 / 61	CC	secretory granule
38	7.48	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
39	7.46	NULL	3 / 14	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
40	7.42	NULL	4 / 15	Cancer	GENTLES_modul13

GW_020

Local Summary

%DE = 0.94

metagenes = 22

genes = 316

genes in genesets = 309

genes with fdr < 0.1 = 272 (12 + / 260 −)

genes with fdr < 0.05 = 268 (12 + / 256 −)

genes with fdr < 0.01 = 254 (12 + / 242 −)

<r> metagenes = 0.89

<r> genes = 0.37

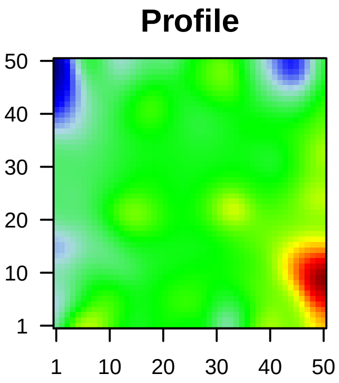
<FC> = −1.16

<shrinkage−t> = −41.1

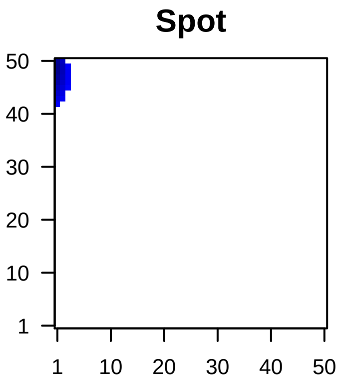
<p−value> = 0

<fdr> = 0.19

Profile



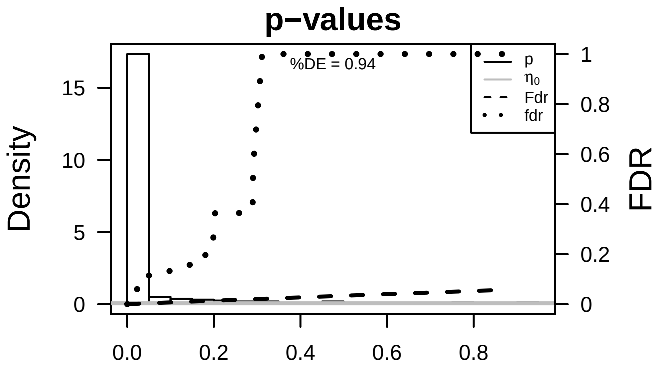
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	133	−1.89	2e−16	7e−17	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
2	222	−1.98	2e−16	7e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	387695	−2.06	2e−16	7e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
4	375791	−2.7	2e−16	7e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
5	1001	−2.03	2e−16	7e−17	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
6	4680	2.23	2e−16	7e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
7	9635	−2.77	2e−16	7e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
8	84518	−3.04	2e−16	7e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
9	1308	−1.99	2e−16	7e−17	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
10	49860	−2.98	2e−16	7e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	1475	−2.11	2e−16	7e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
12	1672	3	2e−16	7e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	1673	−2.53	2e−16	7e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	1830	−2.29	2e−16	7e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
15	2171	−2.12	2e−16	7e−17	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
16	9982	−2.9	2e−16	7e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
17	2706	−2.43	2e−16	7e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
18	10804	−2.76	2e−16	7e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	3429	−2.18	2e−16	7e−17	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
20	3552	−2.12	2e−16	7e−17	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−57.41	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	−38.26	NULL	18 / 21	CC	cornified envelope
3	−31.48	NULL	113 / 572	Disease	GUDJ_psoriasis up
4	−31.46	NULL	20 / 42	BP	keratinization
5	−31.02	NULL	24 / 53	BP	keratinocyte differentiation
6	−29.7	NULL	27 / 76	BP	epidermis development
7	−24.24	NULL	10 / 19	BP	peptide cross−linking
8	−20.74	NULL	21 / 82	CC	intermediate filament
9	−20.71	NULL	13 / 44	CC	keratin filament
10	−19.93	NULL	5 / 10	MF	RAGE receptor binding
11	−18.97	NULL	30 / 186	MF	structural molecule activity
12	−16.78	NULL	12 / 21	CC	desmosome
13	−15.53	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	−14.4	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
15	−14.09	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	−14.07	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
17	−13.15	NULL	2 / 5	miRNA target	miR−196a
18	−12.5	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
19	−12.18	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	−11.6	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
21	−11.44	NULL	7 / 29	BP	regulation of proteolysis
22	−10.98	NULL	4 / 12	BP	hemidesmosome assembly
23	−10.95	NULL	5 / 13	BP	negative regulation of peptidase activity
24	−10.93	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
25	−10.85	NULL	3 / 10	BP	chronic inflammatory response
26	−10.56	NULL	2 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
27	−10.31	NULL	7 / 38	BP	epithelial cell differentiation
28	−10.2	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
29	−9.95	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
30	−9.82	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
31	−9.76	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
32	−9.75	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
33	−9.38	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
34	−9.36	NULL	3 / 14	BP	defense response to fungus
35	−9.12	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
36	−8.91	NULL	11 / 82	MF	structural constituent of cytoskeleton
37	−8.81	NULL	5 / 25	BP	response to zinc ion
38	−8.62	NULL	3 / 15	CC	connexon complex
39	−8.45	NULL	4 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
40	−8.45	NULL	4 / 13	H.Tiss	WIRTH_Tonsil