GW_143

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1298 (737 + / 561 −)

genes with fdr < 0.1 = 995 (570 + / 425 −)

genes with fdr < 0.05 = 741 (439 + / 302 −)

genes with fdr < 0.01 = 452 (291 + / 161 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.16

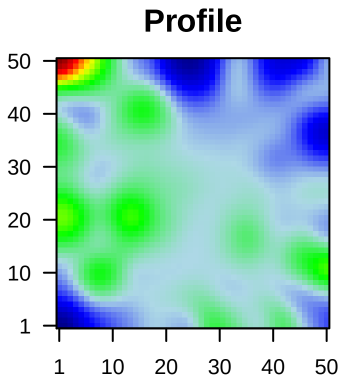
<fdr> = 0.88

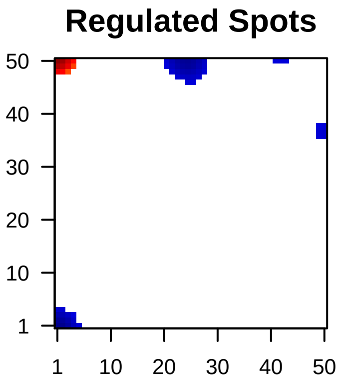
Global Genelist

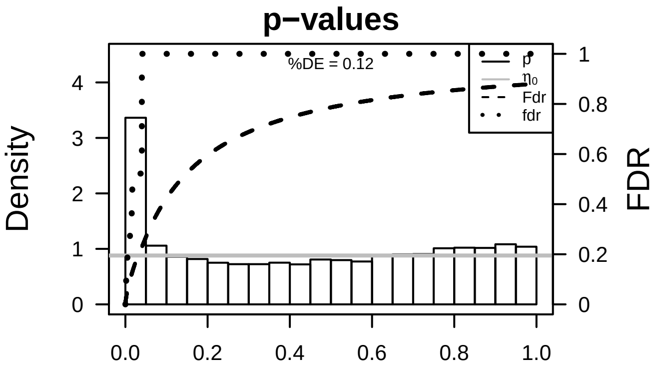
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.8	2e−16	9e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	387695	2.09	2e−16	9e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	64073	1.79	2e−16	9e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
4	375791	2.21	2e−16	9e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
5	4680	1.81	2e−16	9e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	84518	1.92	2e−16	9e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	1278	−1.81	2e−16	9e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
8	49860	3.28	2e−16	9e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	1562	1.82	2e−16	9e−14	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
10	1577	1.84	2e−16	9e−14	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
11	1673	2.72	2e−16	9e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	131177	2.02	2e−16	9e−14	3 x 50	family with sequence similarity 3, member D [Source:HGNC
13	2312	2.16	2e−16	9e−14	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
14	3127	1.79	2e−16	9e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
15	3576	−1.99	2e−16	9e−14	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
16	43849	2.1	2e−16	9e−14	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
17	5653	1.8	2e−16	9e−14	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
18	5650	2.26	2e−16	9e−14	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
19	448834	1.76	2e−16	9e−14	1 x 48	keratinocyte proline−rich protein [Source:HGNC Symbol;Acc:
20	3851	2.97	2e−16	9e−14	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	28.54	NULL	135	H.Tiss	WIRTH_Mucosa
2	12.75	NULL	42	BP	keratinization
3	11.6	NULL	21	CC	cornified envelope
4	9.98	NULL	76	BP	epidermis development
5	9.74	NULL	1135	Chr	Chr 19
6	9.25	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	8.65	NULL	572	Disease	GUDJ_psoriasis up
8	8.44	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	8.28	NULL	53	BP	keratinocyte differentiation
10	7.67	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	7.42	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	6.9	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
13	6.75	NULL	14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
14	6.45	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	6.34	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
16	6.27	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
17	6.13	NULL	122	MF	serine−type endopeptidase activity
18	5.86	NULL	19	BP	peptide cross−linking
19	5.75	NULL	38	BP	epithelial cell differentiation
20	5.69	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
Underexpressed					
1	−12.17	NULL	436	miRNA target starBase	hsa−miR−548n
2	−11.9	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−11.28	NULL	315	miRNA target starBase	hsa−miR−30e
4	−10.53	NULL	262	miRNA target starBase	hsa−miR−548l
5	−10.27	NULL	278	miRNA target starBase	hsa−miR−30c
6	−10.24	NULL	336	miRNA target starBase	hsa−miR−548d−5p
7	−10.13	NULL	8023	MF	protein binding
8	−10.05	NULL	268	miRNA target starBase	hsa−miR−30b
9	−10.03	NULL	307	miRNA target starBase	hsa−miR−548c−5p
10	−9.97	NULL	336	miRNA target starBase	hsa−miR−548b−5p
11	−9.73	NULL	852	Lymphoma	SPANG_BCR DN
12	−9.66	NULL	302	miRNA target starBase	hsa−miR−548i
13	−9.48	NULL	313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
14	−9.48	NULL	313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
15	−9.48	NULL	313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up
16	−9.47	NULL	264	miRNA target starBase	hsa−miR−30a
17	−9.43	NULL	268	miRNA target starBase	hsa−miR−30d
18	−9.43	NULL	242	BP	extracellular matrix organization
19	−9.3	NULL	300	miRNA target starBase	hsa−miR−548c−3p
20	−9.22	NULL	321	miRNA target starBase	hsa−miR−548a−5p







GW_143

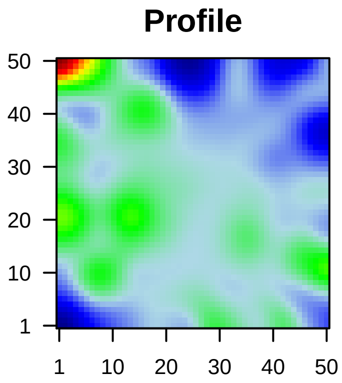
Local Summary

%DE = 0.89
metagenes = 11
genes = 168
genes in genesets = 165

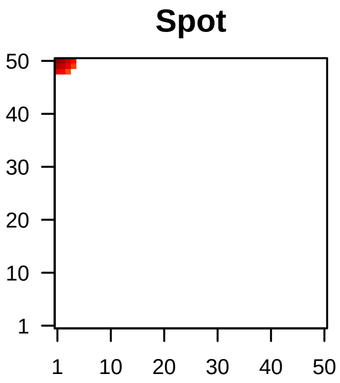
genes with fdr < 0.1 = 145 (142 + / 3 −)
genes with fdr < 0.05 = 145 (142 + / 3 −)
genes with fdr < 0.01 = 131 (130 + / 1 −)

<r> metagenes = 0.99
<r> genes = 0.49

<FC> = 1.16
<shrinkage−t> = 40.87
<p−value> = 0
<fdr> = 0.17



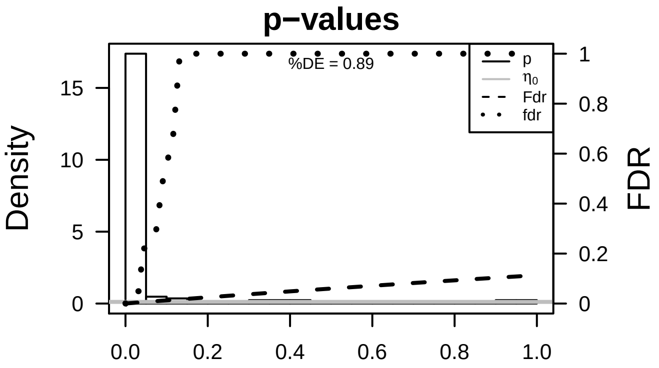
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.8	2e−16	1e−16	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	387695	2.09	2e−16	1e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	375791	2.21	2e−16	1e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	4680	1.81	2e−16	1e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
5	84518	1.92	2e−16	1e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
6	49860	3.28	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
7	1562	1.82	2e−16	1e−16	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
8	1577	1.84	2e−16	1e−16	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
9	1673	2.72	2e−16	1e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	131177	2.02	2e−16	1e−16	3 x 50	family with sequence similarity 3, member D [Source:HGNC
11	2312	2.16	2e−16	1e−16	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
12	43849	2.1	2e−16	1e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
13	5653	1.8	2e−16	1e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
14	5650	2.26	2e−16	1e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
15	448834	1.76	2e−16	1e−16	1 x 48	keratinocyte proline−rich protein [Source:HGNC Symbol;Acc:
16	3851	2.97	2e−16	1e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
17	137797	2.37	2e−16	1e−16	1 x 50	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
18	4118	2.51	2e−16	1e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
19	342897	2.07	2e−16	1e−16	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebraf
20	51458	1.87	2e−16	1e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	57.55	NULL	71 / 135	H.Tiss	WIRTH_Mucosa
2	25.67	NULL	14 / 21	CC	cornified envelope
3	23.75	NULL	72 / 572	Disease	GUDJ_psoriasis up
4	23.31	NULL	16 / 42	BP	keratinization
5	23.1	NULL	19 / 53	BP	keratinocyte differentiation
6	19.28	NULL	8 / 19	BP	peptide cross−linking
7	18.61	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	18.27	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	17.47	NULL	18 / 76	BP	epidermis development
10	16.15	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	14.95	NULL	6 / 13	BP	negative regulation of peptidase activity
12	13.44	NULL	5 / 10	MF	RAGE receptor binding
13	12.67	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	11.78	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
15	11.68	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
16	10.95	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
17	10.74	NULL	46 / 1182	CC	extracellular region
18	10.69	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
19	10.47	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
20	10.18	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
21	10.07	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
22	9.87	NULL	6 / 38	BP	epithelial cell differentiation
23	9.8	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
24	9.79	NULL	10 / 122	MF	serine−type endopeptidase activity
25	9.63	NULL	3 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
26	9.17	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
27	8.86	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
28	8.79	NULL	2 / 11	GSEA C2	REACTOME_XENOBIOTICS
29	8.76	NULL	3 / 12	BP	cellular aldehyde metabolic process
30	8.55	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
31	8.43	NULL	2 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
32	8.24	NULL	13 / 186	MF	structural molecule activity
33	8.06	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
34	7.91	NULL	4 / 44	CC	keratin filament
35	7.73	NULL	3 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
36	7.66	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
37	7.35	NULL	6 / 82	CC	intermediate filament
38	7.29	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
39	7.08	NULL	4 / 23	MF	peptidase inhibitor activity
40	7.06	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP

GW_143

Local Summary

%DE = 0.76

metagenes = 15

genes = 254

genes in genesets = 253

genes with fdr < 0.1 = 147 (5 + / 142 −)

genes with fdr < 0.05 = 139 (5 + / 134 −)

genes with fdr < 0.01 = 99 (4 + / 95 −)

<r> metagenes = 0.96

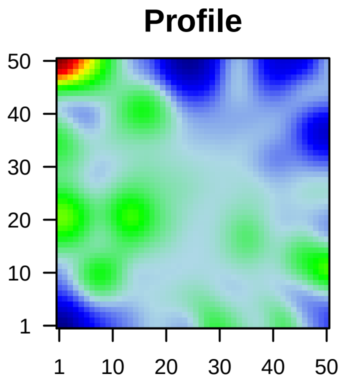
<r> genes = 0.4

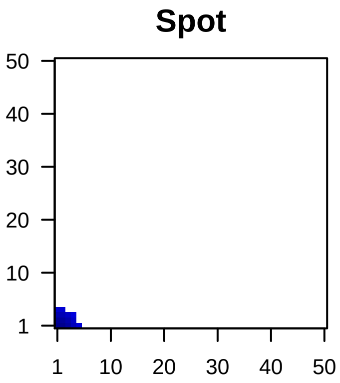
<FC> = −0.52

<shrinkage−t> = −18.23

<p−value> = 0

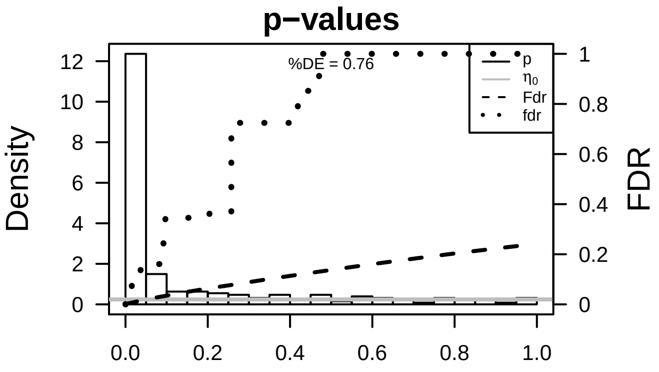
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1278	−1.81	2e−16	3e−15	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
2	3576	−1.99	2e−16	3e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
3	4060	−1.97	2e−16	3e−15	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
4	7057	−1.86	2e−16	3e−15	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
5	5743	−1.71	1e−15	5e−12	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
6	1293	−1.59	1e−13	5e−12	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
7	7431	−1.57	2e−13	5e−12	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
8	3490	−1.56	2e−13	8e−10	3 x 1	insulin−like growth factor binding protein 7 [Source:HGNC Sy
9	3553	−1.44	1e−11	5e−09	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
10	1281	−1.27	9e−11	3e−08	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
11	3491	−1.3	1e−09	3e−08	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
12	3685	−1.3	1e−09	7e−08	1 x 4	integrin, alpha V [Source:HGNC Symbol;Acc:6150]
13	1009	−1.27	2e−09	6e−07	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN
14	1277	−1.22	1e−08	2e−06	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	6591	−1.16	5e−08	2e−06	1 x 4	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
16	414062	−1.15	8e−08	2e−06	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
17	1291	−1.14	9e−08	2e−06	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
18	7130	−1.13	1e−07	2e−06	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN
19	7128	−1.12	2e−07	2e−06	1 x 1	tumor necrosis factor, alpha−induced protein 3 [Source:HGN
20	5066	−1.11	2e−07	2e−06	2 x 3	peptidylglycine alpha−amidating monooxygenase [Source:HG



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.2	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	−33.35	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−31.24	NULL	61 / 190	CC	extracellular matrix
4	−30.62	NULL	8 / 11	MF	platelet−derived growth factor binding
5	−29.85	NULL	65 / 242	BP	extracellular matrix organization
6	−29.19	NULL	70 / 250	Lymphoma	LENZ_Stromal signature 1
7	−28.14	NULL	30 / 69	BP	extracellular matrix disassembly
8	−27.76	NULL	8 / 12	miRNA target	miR−29c
9	−26.99	NULL	27 / 64	BP	collagen catabolic process
10	−26.1	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	−25.63	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
12	−25.5	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
13	−25.15	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
14	−24.12	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
15	−23.62	NULL	11 / 19	MF	extracellular matrix binding
16	−23.55	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
17	−23.25	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
18	−22.04	NULL	14 / 37	BP	collagen fibril organization
19	−21.89	NULL	19 / 57	MF	extracellular matrix structural constituent
20	−21.66	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
21	−21.22	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
22	−21.21	NULL	75 / 683	CC	extracellular space
23	−21.2	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
24	−20.9	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
25	−20.77	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
26	−20.74	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
27	−20.35	NULL	6 / 16	GSEA C2	ZHU_CMV_24_HR_DN
28	−20.35	NULL	6 / 16	GSEA C2	ZHU_CMV_ALL_DN
29	−19.96	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
30	−19.38	NULL	100 / 1182	CC	extracellular region
31	−18.89	NULL	6 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
32	−18.77	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
33	−18.73	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
34	−18.58	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
35	−18.22	NULL	4 / 10	BP	protein heterotrimerization
36	−18.04	NULL	12 / 40	BP	cellular response to amino acid stimulus
37	−17.82	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
38	−17.73	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
39	−17.47	NULL	4 / 13	GSEA C2	REACTOME_FORMATION_OF_PLATELET_PLUG
40	−17.47	NULL	4 / 13	GSEA C2	REACTOME_PLATELET_ACTIVATION

GW_143

Local Summary

%DE = 0.89

metagenes = 6

genes = 122

genes in genesets = 122

genes with fdr < 0.1 = 101 (0 + / 101 −)

genes with fdr < 0.05 = 87 (0 + / 87 −)

genes with fdr < 0.01 = 40 (0 + / 40 −)

<r> metagenes = 0.99

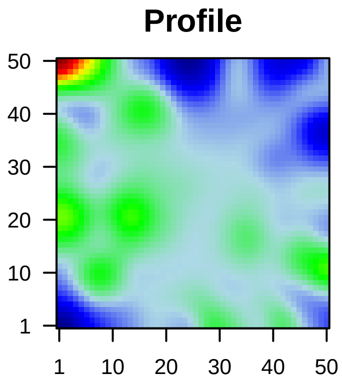
<r> genes = 0.32

<FC> = −0.46

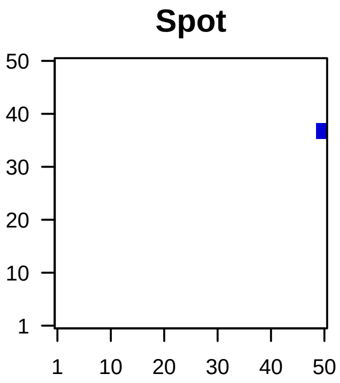
<shrinkage−t> = −16.08

<p−value> = 0.02

<fdr> = 0.59



Profile



Spot

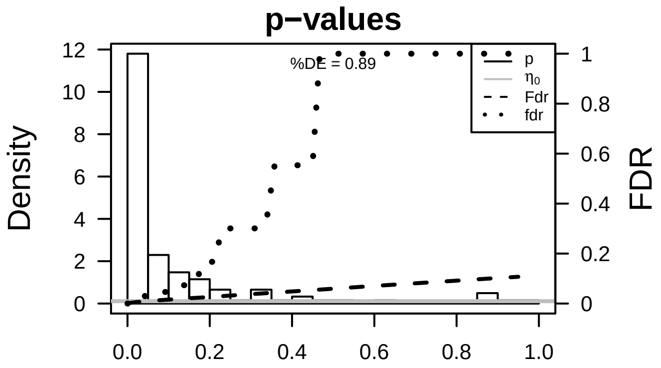
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23215	−1.02	2e−06	7e−05	50 x 37	proline−rich coiled−coil 2C [Source:HGNC Symbol;Acc:2490
2	27075	−0.96	7e−06	5e−04	50 x 38	tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
3	7764	−0.87	5e−05	5e−04	50 x 37	zinc finger protein 217 [Source:HGNC Symbol;Acc:13009]
4	84928	−0.83	1e−04	5e−04	50 x 37	transmembrane protein 209 [Source:HGNC Symbol;Acc:218
5	171586	−0.82	1e−04	5e−04	50 x 37	abhydrolase domain containing 3 [Source:HGNC Symbol;Acc
6	5431	−0.79	2e−04	5e−04	50 x 37	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [
7	64393	−0.78	2e−04	5e−04	50 x 37	zinc finger, matrin−type 3 [Source:HGNC Symbol;Acc:29983]
8	23505	−0.77	3e−04	5e−04	50 x 37	transmembrane protein 131 [Source:HGNC Symbol;Acc:303
9	60481	−0.77	3e−04	5e−04	50 x 37	ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213
10	4254	−0.76	4e−04	5e−04	50 x 36	KIT ligand [Source:HGNC Symbol;Acc:6343]
11	1655	−0.69	4e−04	5e−04	50 x 36	DEAD (Asp−Glu−Ala−Asp) box helicase 5 [Source:HGNC Sy
12	23049	−0.75	4e−04	5e−04	49 x 37	SMG1 phosphatidylinositol 3−kinase−related kinase [Source:
13	7844	−0.75	4e−04	1e−03	50 x 37	RNF103−CHMP3 readthrough [Source:HGNC Symbol;Acc:3
14	64083	−0.74	5e−04	2e−03	50 x 37	golgi phosphoprotein 3 (coat−protein) [Source:HGNC Symbol
15	10257	−0.73	6e−04	2e−03	50 x 36	ATP−binding cassette, sub−family C (CFTR/MRP), member 4
16	55251	−0.71	8e−04	2e−03	50 x 37	protein−L−isoaspartate (D−aspartate) O−methyltransferase d
17	10672	−0.71	9e−04	2e−03	49 x 36	guanine nucleotide binding protein (G protein), alpha 13 [Sou
18	23318	−0.7	1e−03	2e−03	50 x 37	zinc finger, CCHC domain containing 11 [Source:HGNC Sym
19	6634	−0.69	1e−03	2e−03	50 x 38	small nuclear ribonucleoprotein D3 polypeptide 18kDa [Sourc
20	84343	−0.68	1e−03	2e−03	49 x 38	Hermansky−Pudlak syndrome 3 [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.15	NULL	2 / 10	GSEA C2	CROONQUIST_STROMAL_STIMULATION_DN
2	−12.07	NULL	1 / 2	MMML CGS	MACIEJ_MMML 38
3	−11.18	NULL	2 / 11	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
4	−10.7	NULL	3 / 11	MF	AU−rich element binding
5	−10.26	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
6	−9.42	NULL	1 / 4	GSEA C2	LUCAS_HNF4A_TARGETS_DN
7	−8.87	NULL	10 / 189	miRNA target starBase	hsa−miR−1283
8	−8.75	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_3
9	−8.62	NULL	6 / 51	miRNA target starBase	hsa−miR−556−3p
10	−8.32	NULL	2 / 11	GSEA C2	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEM
11	−7.78	NULL	2 / 14	GSEA C2	AIYAR_COBRA1_TARGETS_DN
12	−7.73	NULL	8 / 163	BP	mRNA splicing, via spliceosome
13	−7.68	NULL	13 / 271	miRNA target starBase	hsa−miR−101
14	−7.57	NULL	2 / 26	miRNA target starBase	hsa−miR−337−5p
15	−7.34	NULL	4 / 41	BP	mRNA 3'−end processing
16	−7.27	NULL	2 / 30	miRNA target starBase	hsa−miR−486−5p
17	−7.25	NULL	1 / 3	miRNA target	miR−197
18	−7.23	NULL	6 / 95	miRNA target starBase	hsa−miR−1259
19	−7.21	NULL	6 / 157	miRNA target starBase	hsa−miR−548o
20	−7.04	NULL	4 / 44	BP	termination of RNA polymerase II transcription
21	−7.02	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
22	−7.01	NULL	1 / 6	GSEA C2	CLAUS_PGR_POSITIVE_MENINGIOMA_UP
23	−6.95	NULL	3 / 52	miRNA target starBase	hsa−miR−191
24	−6.79	NULL	7 / 130	miRNA target starBase	hsa−miR−194
25	−6.67	NULL	18 / 595	MF	RNA binding
26	−6.63	NULL	9 / 155	miRNA target starBase	hsa−miR−298
27	−6.53	NULL	6 / 58	miRNA target starBase	hsa−miR−455−5p
28	−6.47	NULL	1 / 8	GSEA C2	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN
29	−6.4	NULL	1 / 7	MMML CGS	MACIEJ_MMML 48
30	−6.37	NULL	1 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_DN
31	−6.37	NULL	2 / 20	BP	protein secretion
32	−6.27	NULL	15 / 412	miRNA target starBase	hsa−miR−372
33	−6.23	NULL	7 / 186	miRNA target starBase	hsa−miR−382
34	−6.23	NULL	7 / 121	miRNA target starBase	hsa−miR−543
35	−6.2	NULL	2 / 16	GSEA C2	CROMER_METASTASIS_UP
36	−6.19	NULL	8 / 159	miRNA target starBase	hsa−miR−512−3p
37	−6.12	NULL	1 / 15	MMML CGS	MACIEJ_MMML 16
38	−6.12	NULL	1 / 15	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D9
39	−5.94	NULL	11 / 215	miRNA target starBase	hsa−miR−203
40	−5.91	NULL	5 / 81	miRNA target starBase	hsa−miR−188−5p



p−values

GW_143

Local Summary

%DE = 0.87

metagenes = 30

genes = 368

genes in genesets = 363

genes with fdr < 0.1 = 289 (0 + / 289 −)

genes with fdr < 0.05 = 223 (0 + / 223 −)

genes with fdr < 0.01 = 118 (0 + / 118 −)

<r> metagenes = 0.94

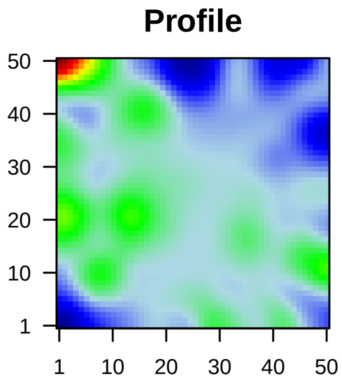
<r> genes = 0.26

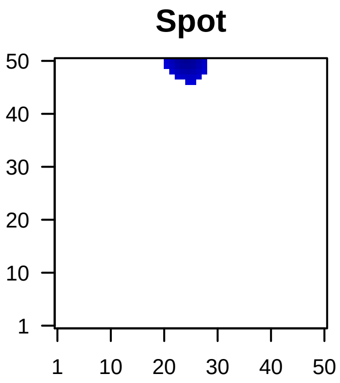
<FC> = −0.48

<shrinkage−t> = −16.66

<p−value> = 0.01

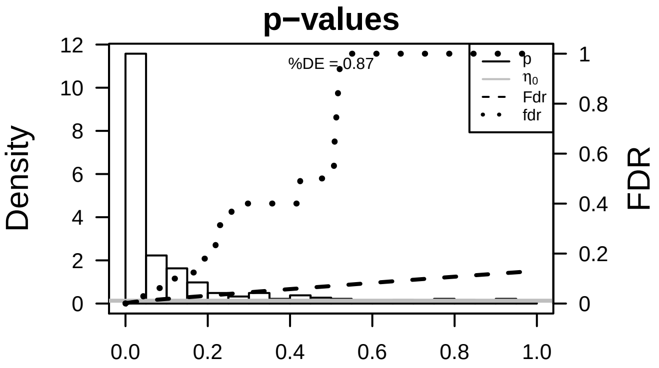
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2353	−1.37	2e−12	3e−09	22 x 50	FBJ murine osteosarcoma viral oncogene homolog [Source:H
2	1843	−1.27	7e−11	1e−07	22 x 50	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30
3	23645	−1.28	2e−09	1e−07	22 x 50	protein phosphatase 1, regulatory subunit 15A [Source:HGNC
4	25800	−1.25	4e−09	1e−07	25 x 50	solute carrier family 39 (zinc transporter), member 6 [Source:
5	10972	−1.23	7e−09	1e−06	25 x 50	transmembrane emp24−like trafficking protein 10 (yeast) [Sou
6	114908	−1.18	3e−08	1e−06	26 x 50	transmembrane protein 123 [Source:HGNC Symbol;Acc:3013
7	4609	−1.16	5e−08	1e−06	22 x 50	v−myc avian myelocytomatosis viral oncogene homolog [Sou
8	1958	−1.15	7e−08	3e−06	22 x 50	early growth response 1 [Source:HGNC Symbol;Acc:3238]
9	678	−1.12	1e−07	3e−06	23 x 50	ZFP36 ring finger protein−like 2 [Source:HGNC Symbol;Acc:1
10	10787	−1.1	3e−07	3e−06	25 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]
11	57132	−1.1	3e−07	5e−05	22 x 50	charged multivesicular body protein 1B [Source:HGNC Symb
12	6386	−1.01	2e−06	5e−05	25 x 50	syndecan binding protein (syntenin) [Source:HGNC Symbol;A
13	51014	−0.99	4e−06	5e−05	26 x 50	transmembrane emp24 protein transport domain containing 7
14	7538	−0.96	5e−06	5e−05	22 x 50	ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
15	9188	−0.97	6e−06	5e−05	26 x 50	DEAD (Asp−Glu−Ala−Asp) box helicase 21 [Source:HGNC S
16	51030	−0.96	6e−06	5e−05	26 x 50	trans−golgi network vesicle protein 23 homolog B (S. cerevisi
17	9643	−0.96	6e−06	7e−05	26 x 50	mortality factor 4 like 2 [Source:HGNC Symbol;Acc:16849]
18	26092	−0.95	8e−06	7e−05	25 x 49	torsin A interacting protein 1 [Source:HGNC Symbol;Acc:294
19	81533	−0.95	9e−06	9e−05	26 x 50	integrin alpha FG−GAP repeat containing 1 [Source:HGNC S
20	55854	−0.93	1e−05	9e−05	28 x 50	zinc finger CCCH−type containing 15 [Source:HGNC Symbol



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.6	NULL	6 / 10	GSEA C2	CHASSOT_SKIN_WOUND
2	−20.43	NULL	8 / 16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
3	−19.16	NULL	6 / 15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
4	−16.41	NULL	7 / 16	GSEA C2	AMIT_DELAYED_EARLY_GENES
5	−16.18	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_40_MCF10A
6	−15.64	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
7	−14.12	NULL	5 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
8	−13.81	NULL	4 / 8	MMML CGS	MACIEJ_MMML 50
9	−13.77	NULL	4 / 14	BP	response to light stimulus
10	−13.63	NULL	3 / 11	GSEA C2	AMIT_EGF_RESPONSE_20_HELA
11	−13.11	NULL	2 / 7	GSEA C2	TURJANSKI_MAPK7_TARGETS
12	−12.95	NULL	6 / 16	TF Tissue	VAQUERIZAS_Pancreas
13	−12.89	NULL	54 / 436	miRNA target−starBase	hsa−miR−548n
14	−12.71	NULL	4 / 14	GSEA C2	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
15	−12.42	NULL	4 / 14	GSEA C2	BIOCARTA_IL2_PATHWAY
16	−12.18	NULL	4 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
17	−11.51	NULL	2 / 5	miRNA target	miR−101
18	−11.48	NULL	1 / 2	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
19	−11.47	NULL	3 / 10	GSEA C2	BIOCARTA_CDMAC_PATHWAY
20	−11.4	NULL	5 / 24	TF Tissue	VAQUERIZAS_Trachea
21	−11.03	NULL	4 / 16	GSEA C2	JI_RESPONSE_TO_FSH_DN
22	−10.83	NULL	4 / 15	GSEA C2	DIRMEIER_LMP1_RESPONSE_EARLY
23	−10.81	NULL	22 / 151	miRNA target−starBase	hsa−miR−429
24	−10.65	NULL	23 / 150	miRNA target−starBase	hsa−miR−200c
25	−10.49	NULL	3 / 12	GSEA C2	BIOCARTA_DREAM_PATHWAY
26	−10.44	NULL	3 / 10	GSEA C2	REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSC
27	−10.43	NULL	4 / 16	GSEA C2	BIOCARTA_ETS_PATHWAY
28	−10.38	NULL	38 / 310	miRNA target−starBase	hsa−miR−340
29	−10.37	NULL	38 / 269	miRNA target−starBase	hsa−miR−1244
30	−10.27	NULL	33 / 318	miRNA target−starBase	hsa−miR−590−3p
31	−10.2	NULL	3 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
32	−10.17	NULL	22 / 155	miRNA target−starBase	hsa−miR−200b
33	−10.16	NULL	2 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
34	−10.13	NULL	37 / 336	miRNA target−starBase	hsa−miR−548d−5p
35	−10.12	NULL	26 / 167	miRNA target−starBase	hsa−miR−548g
36	−10.06	NULL	35 / 307	miRNA target−starBase	hsa−miR−548c−5p
37	−10.05	NULL	4 / 13	BP	COPI coating of Golgi vesicle
38	−9.95	NULL	14 / 61	miRNA target−starBase	hsa−miR−1278
39	−9.92	NULL	26 / 232	miRNA 3UTR	UCTT−142−5P
40	−9.83	NULL	28 / 281	miRNA target−starBase	hsa−miR−570

GW_143

Local Summary

%DE = 0.66

metagenes = 3

genes = 81

genes in genesets = 81

genes with fdr < 0.1 = 41 (0 + / 41 −)

genes with fdr < 0.05 = 25 (0 + / 25 −)

genes with fdr < 0.01 = 5 (0 + / 5 −)

<r> metagenes = 0.99

<r> genes = 0.4

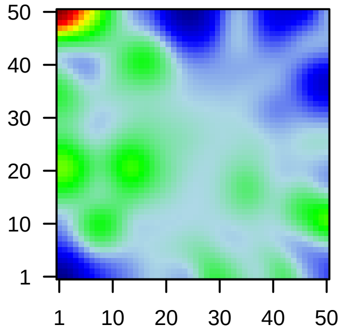
<FC> = −0.38

<shrinkage−t> = −13.41

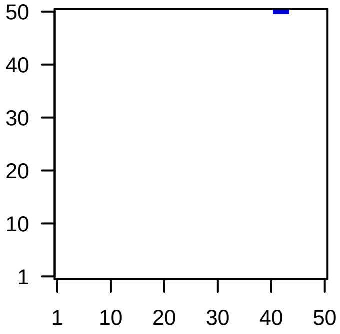
<p−value> = 0.04

<fdr> = 0.67

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	151188	−0.97	5e−06	7e−05	43 x 50	ADP−ribosylation−like factor 6 interacting protein 6 [Source:H
2	3251	−0.97	5e−06	4e−04	42 x 50	hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
3	6873	−0.91	2e−05	5e−04	41 x 50	TAF2 RNA polymerase II, TATA box binding protein (TBP)−as
4	23279	−0.88	4e−05	9e−04	42 x 50	nucleoporin 160kDa [Source:HGNC Symbol;Acc:18017]
5	6611	−0.85	7e−05	5e−03	42 x 50	spermine synthase [Source:HGNC Symbol;Acc:11123]
6	3161	−0.78	3e−04	1e−02	43 x 50	hyaluronan−mediated motility receptor (RHAMM) [Source:HG
7	6241	−0.69	1e−03	1e−02	43 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:104
8	51001	−0.68	1e−03	1e−02	41 x 50	MTERF domain containing 1 [Source:HGNC Symbol;Acc:242
9	3376	−0.67	2e−03	1e−02	41 x 50	isoleucyl−tRNA synthetase [Source:HGNC Symbol;Acc:5330
10	440145	−0.65	2e−03	1e−02	41 x 50	mitotic spindle organizing protein 1 [Source:HGNC Symbol;A
11	54443	−0.63	3e−03	1e−02	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
12	51068	−0.63	3e−03	1e−02	41 x 50	NMD3 ribosome export adaptor [Source:HGNC Symbol;Acc:
13	26774	−0.62	3e−03	1e−02	41 x 50	growth arrest−specific 5 (non−protein coding) [Source:HGNC
14	8520	−0.62	3e−03	1e−02	42 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:4821]
15	51319	−0.61	4e−03	1e−02	43 x 50	arginine/serine−rich coiled−coil 1 [Source:HGNC Symbol;Acc
16	7027	−0.6	5e−03	1e−02	43 x 50	transcription factor Dp−1 [Source:HGNC Symbol;Acc:11749]
17	10606	−0.6	5e−03	2e−02	43 x 50	phosphoribosylaminoimidazole carboxylase, phosphoribosyla
18	10576	−0.59	6e−03	2e−02	41 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
19	10797	−0.58	7e−03	2e−02	43 x 50	methylenetetrahydrofolate dehydrogenase (NADP+ depender
20	7443	−0.57	7e−03	2e−02	43 x 50	vaccinia related kinase 1 [Source:HGNC Symbol;Acc:12718]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.12	NULL	0 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	−17.44	NULL	3 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
3	−16.74	NULL	3 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−16.14	NULL	3 / 15	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
5	−16.12	NULL	3 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
6	−16	NULL	4 / 16	GSEA C2	BIDUS_METASTASIS_UP
7	−15.71	NULL	3 / 16	GSEA C2	REACTOME_REV_MEDIATED_NUCLEAR_EXPORT_OF_HIV1_
8	−15.23	NULL	3 / 10	CC	nuclear pore outer ring
9	−15.05	NULL	2 / 6	GSEA C2	LOPEZ_MBD_TARGETS
10	−14.96	NULL	3 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
11	−14.63	NULL	2 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
12	−14.14	NULL	3 / 16	GSEA C2	REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MA
13	−13.85	NULL	2 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
14	−13.71	NULL	3 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
15	−13.33	NULL	2 / 13	GSEA C2	WELCSH_BRCA1_TARGETS_1_UP
16	−12.37	NULL	2 / 14	GSEA C2	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN
17	−12.37	NULL	2 / 14	GSEA C2	REACTOME_GLUCOSE_TRANSPORT
18	−12.31	NULL	2 / 15	GSEA C2	GAL_LEUKEMIC_STEM_CELL_DN
19	−12.31	NULL	2 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
20	−12.02	NULL	1 / 5	Glio	Phillips Prolif up vs PN & MES
21	−11.97	NULL	3 / 18	BP	spindle organization
22	−11.9	NULL	2 / 15	GSEA C2	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_
23	−11.9	NULL	2 / 15	GSEA C2	REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_E
24	−11.88	NULL	2 / 16	GSEA C2	WILCOX_PRESPONSE_TO_ROGESTERONE_UP
25	−11.88	NULL	2 / 16	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
26	−11.88	NULL	2 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
27	−11.88	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
28	−11.79	NULL	3 / 16	GSEA C2	FUJII_YBX1_TARGETS_DN
29	−11.58	NULL	2 / 10	GSEA C2	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
30	−11.48	NULL	2 / 16	GSEA C2	REACTOME_VPR_MEDIATED_NUCLEAR_IMPORT_OF_PICS
31	−11.48	NULL	2 / 16	GSEA C2	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKI
32	−11.2	NULL	5 / 35	BP	mitotic nuclear envelope disassembly
33	−11.13	NULL	2 / 10	CC	microtubule plus−end
34	−10.73	NULL	2 / 12	GSEA C2	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN
35	−10.73	NULL	2 / 12	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_DN
36	−10.68	NULL	2 / 11	GSEA C2	NUYTTEN_EZH2_TARGETS_DN
37	−10.52	NULL	2 / 13	GSEA C2	ALONSO_METASTASIS_UP
38	−10.52	NULL	1 / 4	MMML CGS	MACIEJ_MMML 41
39	−10.4	NULL	2 / 16	Cancer	WOLFER_overlap genes
40	−10.31	NULL	2 / 10	Cancer	GENTLES_modul3

p−values