GW_085

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1664 (1006 + / 658 −)

genes with fdr < 0.1 = 1302 (820 + / 482 −)

genes with fdr < 0.05 = 1097 (716 + / 381 −)

genes with fdr < 0.01 = 778 (541 + / 237 −)

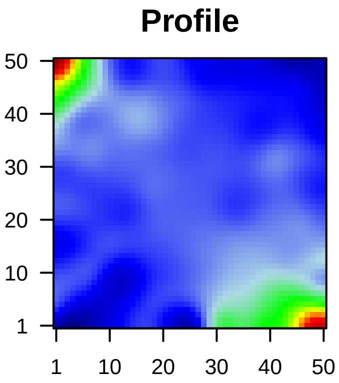
genes in genesets = 16332

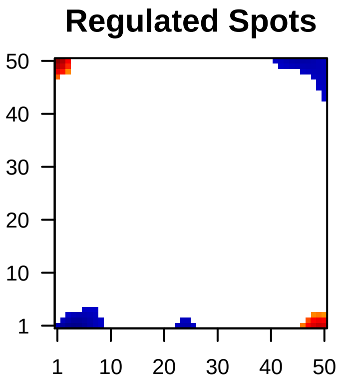
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

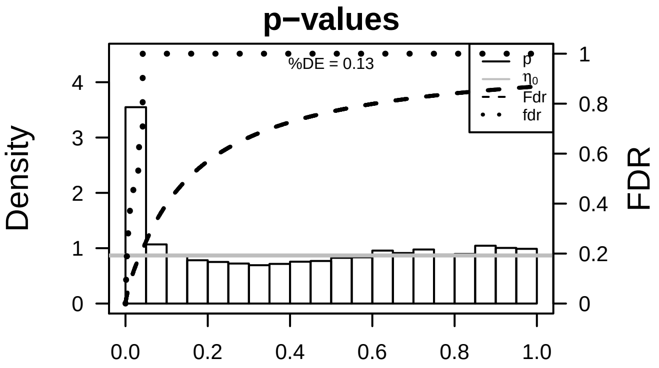
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	−1.44	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	401138	2.58	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
3	55107	1.48	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
4	23120	1.09	2e−16	3e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
5	387695	1.17	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	375791	1.25	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
7	760	1.36	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	57172	1.42	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
9	84290	1.15	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	6363	2.47	2e−16	3e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
11	8900	1.58	2e−16	3e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
12	1236	1.19	2e−16	3e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
13	930	1.44	2e−16	3e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
14	919	1.09	2e−16	3e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
15	915	1.3	2e−16	3e−14	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
16	1048	1.47	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
17	1117	1.39	2e−16	3e−14	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]
18	22802	1.64	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
19	9071	1.76	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
20	84518	1.58	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	23.34	NULL	135	H.Tiss	WIRTH_Mucosa
2	19.74	NULL	572	Disease	GUDJ_psoriasis up
3	15.85	NULL	417	H.Tiss	WIRTH_Immune system
4	14.93	NULL	42	BP	keratinization
5	14.17	NULL	21	CC	cornified envelope
6	13.01	NULL	76	BP	epidermis development
7	12.1	NULL	553	Cancer	Lembcke_Colonic Inflammation
8	11.97	NULL	312	BP	immune response
9	10.9	NULL	53	BP	keratinocyte differentiation
10	9.3	NULL	74	BP	regulation of immune response
11	8.66	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
12	8.37	NULL	2659	CC	plasma membrane
13	7.9	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
14	7.74	NULL	162	CC	external side of plasma membrane
15	7.69	NULL	15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
16	7.67	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
17	7.58	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
18	7.38	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	7.36	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	7.36	NULL	316	Cancer	SPANG_BCL6−index2
Underexpressed					
1	−8.48	NULL	127	H.Tiss	WIRTH_Muscle
2	−8.19	NULL	36	BP	muscle filament sliding
3	−8.18	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	−8	NULL	1033	Chr	Chr 2
5	−7.69	NULL	449	Chr	Chr 20
6	−6.53	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	−6.45	NULL	44	MF	structural constituent of muscle
8	−6.18	NULL	743	Chr	Chr 7
9	−5.95	NULL	16	H.Tiss	WIRTH_Hippocampus
10	−5.85	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
11	−5.85	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
12	−5.4	NULL	16	MMML CGS	MACIEJ_MMML 1
13	−5.34	NULL	37	BP	collagen fibril organization
14	−5.27	NULL	375	Disease	GUDJ_psoriasis down
15	−4.79	NULL	12	CC	myosin filament
16	−4.69	NULL	11	MMML CGS	MACIEJ_MMML 31
17	−4.49	NULL	7	MMML CGS	MACIEJ_MMML 13
18	−4.44	NULL	37	CC	sarcomere
19	−4.4	NULL	84	BP	muscle contraction
20	−4.24	NULL	914	Chr	Chr 3

GW_085

Local Summary

%DE = 0.87

metagenes = 12

genes = 236

genes in genesets = 234

genes with fdr < 0.1 = 181 (180 + / 1 −)

genes with fdr < 0.05 = 181 (180 + / 1 −)

genes with fdr < 0.01 = 166 (165 + / 1 −)

<r> metagenes = 0.99

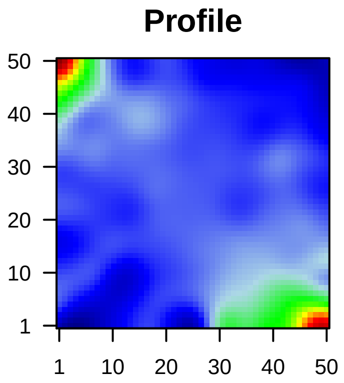
<r> genes = 0.62

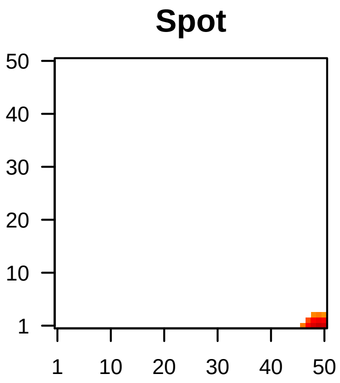
<FC> = 0.57

<shrinkage−t> = 19.98

<p−value> = 0

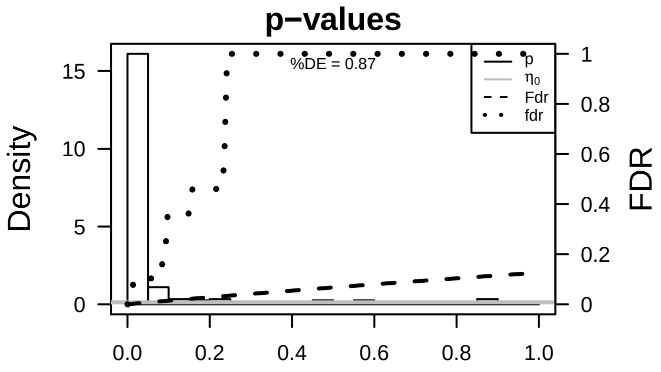
<fdr> = 0.26





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	1.42	2e−16	3e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	6363	2.47	2e−16	3e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	1236	1.19	2e−16	3e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
4	930	1.44	2e−16	3e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
5	919	1.09	2e−16	3e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
6	915	1.3	2e−16	3e−16	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
7	51755	1.12	2e−16	3e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:2422
8	4283	1.99	2e−16	3e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
9	54855	1.38	2e−16	3e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
10	115361	1.19	2e−16	3e−16	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
11	3512	1.27	2e−16	3e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	3543	1.24	2e−16	3e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
13	91353	1.58	2e−16	3e−16	48 x 1	
14	126306	1.32	2e−16	3e−16	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
15	4050	1.5	2e−16	3e−16	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
16	11040	1.56	2e−16	3e−16	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
17	5730	1.64	2e−16	3e−16	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
18	5790	1.15	2e−16	3e−16	49 x 1	protein tyrosine phosphatase, receptor type, C−associated pr
19	9806	1.17	2e−16	3e−16	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
20	10537	2.23	2e−16	3e−16	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	31.45	NULL	86 / 417	H.Tiss	WIRTH_Immune system
2	28.79	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	25.29	NULL	85 / 553	Cancer	Lembcke_Colonic Inflammation
4	23.89	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	22.17	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
6	20.56	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
7	20.31	NULL	5 / 12	BP	dendritic cell chemotaxis
8	20.11	NULL	49 / 312	BP	immune response
9	19.73	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
10	19.66	NULL	12 / 15	CC	MHC class II protein complex
11	19.08	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
12	19.02	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	18.88	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
14	18.29	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
15	16.81	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
16	16.37	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
17	16.07	NULL	5 / 13	Cancer	GENTLES_modul18
18	15.86	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
19	15.06	NULL	14 / 60	BP	T cell costimulation
20	14.45	NULL	2 / 10	BP	positive regulation of chemotaxis
21	14.38	NULL	25 / 162	CC	external side of plasma membrane
22	14.22	NULL	16 / 74	BP	regulation of immune response
23	14.15	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
24	14.08	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
25	13.93	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
26	13.8	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
27	13.4	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
28	13.27	NULL	3 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
29	13.19	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
30	13.13	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	13.02	NULL	4 / 22	BP	positive regulation of interleukin−12 production
32	13	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
33	12.94	NULL	5 / 11	BP	positive regulation of B cell differentiation
34	12.94	NULL	7 / 43	MF	chemokine activity
35	12.64	NULL	4 / 27	BP	release of sequestered calcium ion into cytosol
36	12.4	NULL	3 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
37	12.34	NULL	3 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
38	12.32	NULL	8 / 16	GSEA C2	SU_THYMUS
39	12.12	NULL	9 / 43	BP	positive regulation of T cell proliferation
40	11.93	NULL	4 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN

GW_085

Local Summary

%DE = 0.83

metagenes = 10

genes = 162

genes in genesets = 157

genes with fdr < 0.1 = 124 (118 + / 6 −)

genes with fdr < 0.05 = 124 (118 + / 6 −)

genes with fdr < 0.01 = 120 (114 + / 6 −)

<r> metagenes = 0.98

<r> genes = 0.49

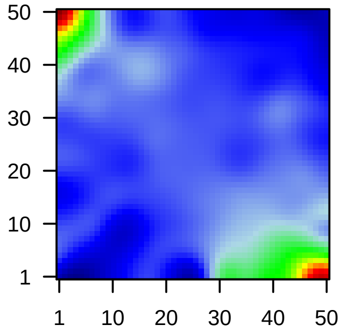
<FC> = 0.7

<shrinkage−t> = 24.66

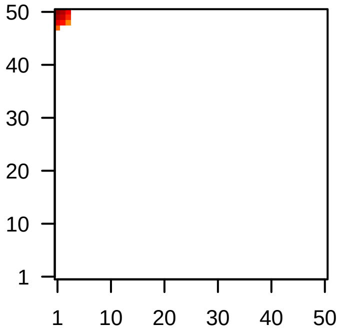
<p−value> = 0

<fdr> = 0.22

Profile



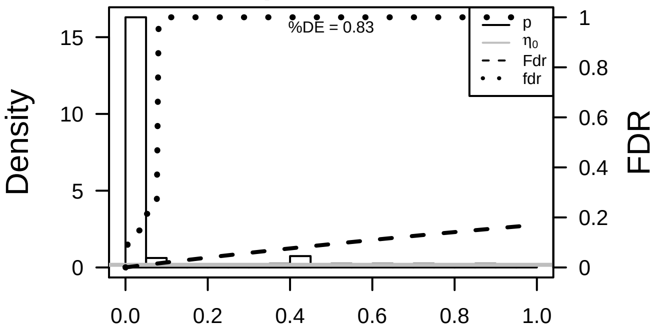
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23120	1.09	2e−16	2e−16	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
2	387695	1.17	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	375791	1.25	2e−16	2e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	84290	1.15	2e−16	2e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
5	1048	1.47	2e−16	2e−16	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
6	22802	1.64	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	1.58	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	49860	1.47	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	1673	1.15	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	131177	1.45	2e−16	2e−16	3 x 50	family with sequence similarity 3, member D [Source:HGNC
11	163351	1.31	2e−16	2e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
12	2941	1.72	2e−16	2e−16	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
13	26085	1.47	2e−16	2e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
14	5653	1.52	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
15	3860	1.65	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	2.72	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
17	3851	2.87	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
18	196374	1.12	2e−16	2e−16	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
19	388533	1.62	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
20	84648	1.49	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	51.68	NULL	68 / 135	H.Tiss	WIRTH_Mucosa
2	38	NULL	15 / 21	CC	cornified envelope
3	33.98	NULL	18 / 42	BP	keratinization
4	26.85	NULL	20 / 53	BP	keratinocyte differentiation
5	21.76	NULL	18 / 76	BP	epidermis development
6	21.63	NULL	74 / 572	Disease	GUDJ_psoriasis up
7	19.45	NULL	8 / 19	BP	peptide cross−linking
8	18.15	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	18.07	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	17.05	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	11.35	NULL	5 / 10	MF	RAGE receptor binding
12	11.28	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
13	11.21	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	10.95	NULL	11 / 122	MF	serine−type endopeptidase activity
15	10.85	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
16	10.78	NULL	17 / 186	MF	structural molecule activity
17	10.72	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	10.14	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
19	9.79	NULL	10 / 82	CC	intermediate filament
20	9.7	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
21	9.44	NULL	8 / 44	CC	keratin filament
22	9.21	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
23	9.19	NULL	2 / 17	Disease	BCHETNIA_EBM up
24	9.17	NULL	1 / 11	Glio	VERHAAK_Brain
25	8.94	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
26	8.74	NULL	6 / 13	BP	negative regulation of peptidase activity
27	8.7	NULL	1 / 12	MF	channel activity
28	8.36	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
29	8.3	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
30	8.26	NULL	45 / 1182	CC	extracellular region
31	7.98	NULL	5 / 38	BP	epithelial cell differentiation
32	7.96	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
33	7.81	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
34	7.61	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
35	7.61	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
36	7.33	NULL	1 / 16	Cancer	GENTLES_modul11
37	7.32	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
38	7.27	NULL	5 / 21	CC	desmosome
39	7.16	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
40	7.12	NULL	2 / 38	BP	myelination

GW_085

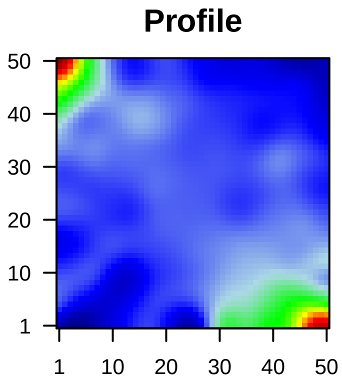
Local Summary

%DE = 0.56
metagenes = 26
genes = 382
genes in genesets = 377

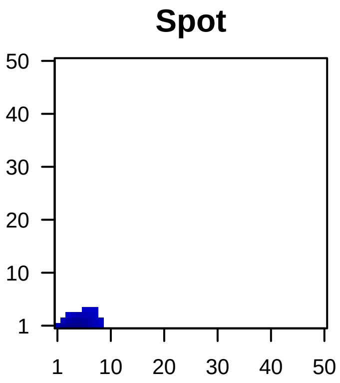
genes with fdr < 0.1 = 136 (11 + / 125 −)
genes with fdr < 0.05 = 95 (6 + / 89 −)
genes with fdr < 0.01 = 79 (6 + / 73 −)

<r> metagenes = 0.96
<r> genes = 0.38

<FC> = −0.2
<shrinkage−t> = −7.17
<p−value> = 0.01
<fdr> = 0.66



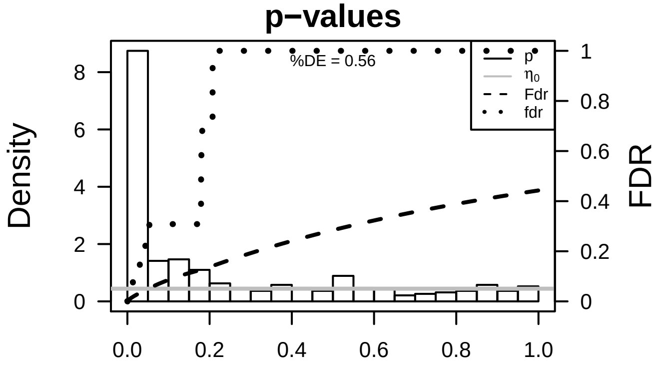
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10962	−1.3	2e−16	8e−15	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
2	4316	−1.32	2e−16	8e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
3	4318	1.73	2e−16	8e−15	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
4	12	−1.21	2e−16	8e−15	1 x 1	
5	9697	1.11	2e−16	8e−15	8 x 1	translocation associated membrane protein 2 [Source:HGNC
6	1290	−1.02	1e−14	1e−11	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	3576	−0.99	9e−14	1e−11	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
8	1281	−0.9	1e−13	6e−10	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
9	25805	−0.92	3e−12	1e−09	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
10	55714	0.9	9e−12	3e−09	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
11	7058	−0.88	3e−11	1e−08	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
12	8076	−0.86	9e−11	1e−08	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
13	1278	−0.85	2e−10	1e−08	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
14	6678	−0.84	2e−10	1e−08	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
15	4320	−0.83	3e−10	3e−08	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
16	118429	0.82	5e−10	3e−07	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
17	8463	−0.78	4e−09	3e−07	8 x 3	TEA domain family member 2 [Source:HGNC Symbol;Acc:11
18	7169	−0.77	5e−09	3e−07	3 x 1	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
19	7130	−0.77	6e−09	3e−07	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN
20	84624	−0.76	8e−09	3e−06	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.98	NULL	14 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−26.13	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
3	−21.06	NULL	94 / 250	Lymphoma	LENZ_Stromal signature 1
4	−20.89	NULL	15 / 37	BP	collagen fibril organization
5	−20.79	NULL	71 / 190	CC	extracellular matrix
6	−19.24	NULL	8 / 11	MF	platelet−derived growth factor binding
7	−17.75	NULL	24 / 57	MF	extracellular matrix structural constituent
8	−17.72	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
9	−17.51	NULL	8 / 12	miRNA target	miR−29c
10	−16.11	NULL	62 / 242	BP	extracellular matrix organization
11	−14.53	NULL	27 / 69	BP	extracellular matrix disassembly
12	−14.12	NULL	23 / 64	BP	collagen catabolic process
13	−13.38	NULL	74 / 553	Cancer	Lembcke_Colonic Inflammation
14	−13.29	NULL	45 / 183	CC	proteinaceous extracellular matrix
15	−13.29	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
16	−12.94	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
17	−12.71	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
18	−12.4	NULL	5 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
19	−12.31	NULL	82 / 683	CC	extracellular space
20	−12.23	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
21	−12.07	NULL	9 / 40	BP	cellular response to amino acid stimulus
22	−12.03	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
23	−12.03	NULL	2 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
24	−12	NULL	7 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
25	−11.92	NULL	110 / 1182	CC	extracellular region
26	−11.87	NULL	41 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
27	−11.87	NULL	41 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
28	−11.87	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
29	−11.87	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
30	−11.72	NULL	6 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
31	−11.61	NULL	24 / 153	CC	endoplasmic reticulum lumen
32	−11.06	NULL	10 / 19	MF	extracellular matrix binding
33	−11	NULL	1 / 5	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
34	−10.85	NULL	8 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_N
35	−10.84	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
36	−10.82	NULL	12 / 68	Glio	cultured astroglia vs. in vivo astrocytes
37	−10.73	NULL	6 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
38	−10.47	NULL	5 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
39	−10.22	NULL	4 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
40	−10	NULL	4 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP

GW_085

Local Summary

%DE = 0.81

metagenes = 6

genes = 99

genes in genesets = 99

genes with fdr < 0.1 = 64 (3 + / 61 −)

genes with fdr < 0.05 = 49 (1 + / 48 −)

genes with fdr < 0.01 = 35 (1 + / 34 −)

<r> metagenes = 1

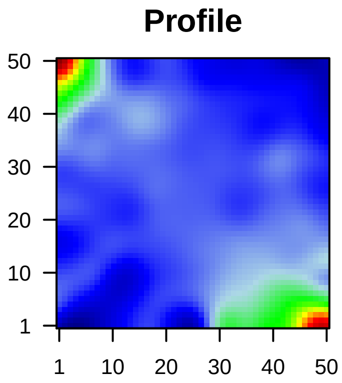
<r> genes = 0.66

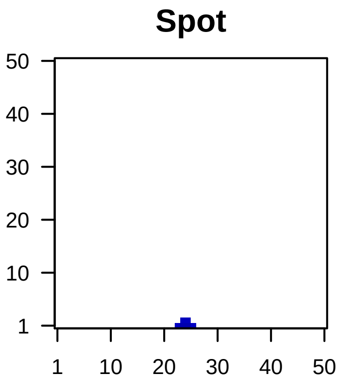
<FC> = −0.33

<shrinkage−t> = −11.68

<p−value> = 0

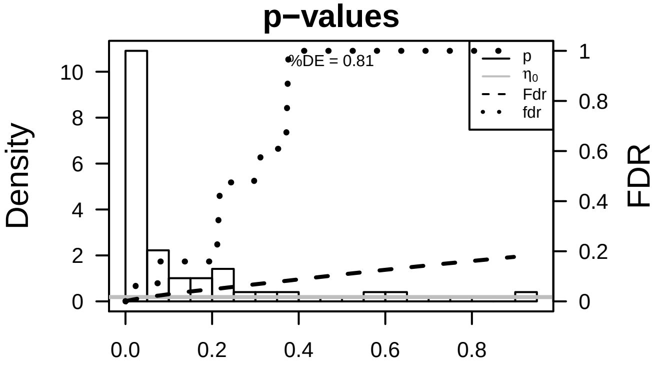
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	−1.44	2e−16	2e−15	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	6588	−1.24	2e−16	2e−15	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
3	70	−0.99	8e−14	8e−11	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	4703	−0.92	4e−12	1e−10	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
5	1917	−0.9	1e−11	3e−09	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
6	1158	−0.85	2e−10	5e−08	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
7	4151	−0.78	3e−09	1e−07	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
8	7060	−0.75	1e−08	1e−07	25 x 1	thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
9	1410	−0.75	2e−08	2e−06	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
10	4608	−0.7	1e−07	9e−06	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
11	10324	−0.66	6e−07	9e−06	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
12	4633	−0.65	1e−06	2e−05	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
13	7134	−0.62	3e−06	2e−05	25 x 1	troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
14	4620	−0.61	4e−06	2e−04	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
15	9499	−0.58	1e−05	2e−04	25 x 1	myotilin [Source:HGNC Symbol;Acc:12399]
16	7140	−0.56	2e−05	2e−04	25 x 1	troponin T type 3 (skeletal, fast) [Source:HGNC Symbol;Acc:1
17	4625	−0.55	3e−05	2e−04	25 x 1	myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC S
18	8557	−0.54	4e−05	4e−04	25 x 1	titin−cap [Source:HGNC Symbol;Acc:11610]
19	29895	−0.52	8e−05	4e−04	25 x 1	myosin light chain, phosphorylatable, fast skeletal muscle [So
20	4606	−0.51	1e−04	4e−04	25 x 1	myosin binding protein C, fast type [Source:HGNC Symbol;Ac



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−58.63	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
2	−54.38	NULL	23 / 36	BP	muscle filament sliding
3	−50.82	NULL	55 / 127	H.Tiss	WIRTH_Muscle
4	−50	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	−40.39	NULL	21 / 44	MF	structural constituent of muscle
6	−37.81	NULL	10 / 12	CC	myosin filament
7	−34.26	NULL	8 / 14	CC	contractile fiber
8	−28.79	NULL	23 / 84	BP	muscle contraction
9	−28.7	NULL	12 / 37	CC	sarcomere
10	−26.28	NULL	8 / 13	CC	muscle myosin complex
11	−23.95	NULL	9 / 20	CC	I band
12	−23.14	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
13	−22.93	NULL	20 / 88	CC	Z disc
14	−22.67	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
15	−22.5	NULL	14 / 34	CC	myofibril
16	−20.84	NULL	9 / 37	BP	cardiac muscle contraction
17	−20.79	NULL	3 / 15	Cancer	BEN−PORATH_UP
18	−19.41	NULL	6 / 12	MF	titin binding
19	−18.2	NULL	6 / 12	BP	skeletal muscle contraction
20	−17.05	NULL	2 / 20	MF	myosin binding
21	−16.97	NULL	6 / 18	BP	regulation of muscle contraction
22	−16.88	NULL	2 / 10	BP	heart contraction
23	−16.36	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
24	−16.31	NULL	7 / 15	BP	striated muscle contraction
25	−15.86	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
26	−15.86	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
27	−15.34	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
28	−14.94	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
29	−14.94	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
30	−14.91	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
31	−14.68	NULL	8 / 16	CC	M band
32	−14.51	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
33	−13.95	NULL	2 / 15	GSEA C2	BIOCARTA_INTEGRIN_PATHWAY
34	−13.9	NULL	2 / 15	BP	skeletal muscle fiber development
35	−13.42	NULL	1 / 12	GSEA C2	BIOCARTA_NO1_PATHWAY
36	−13.42	NULL	1 / 12	GSEA C2	BIOCARTA_RAB_PATHWAY
37	−13.4	NULL	3 / 37	CC	actin filament
38	−13.35	NULL	8 / 42	CC	myosin complex
39	−13.12	NULL	3 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
40	−13.04	NULL	25 / 297	MF	actin binding

GW_085

Local Summary

%DE = 0.64

metagenes = 33

genes = 478

genes in genesets = 475

genes with fdr < 0.1 = 162 (30 + / 132 −)

genes with fdr < 0.05 = 131 (25 + / 106 −)

genes with fdr < 0.01 = 82 (15 + / 67 −)

<r> metagenes = 0.84

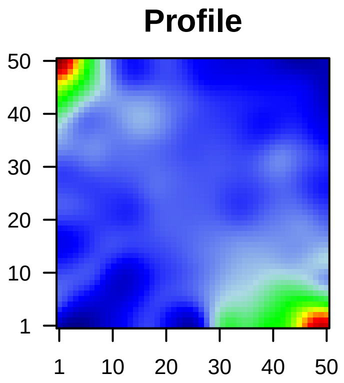
<r> genes = 0.24

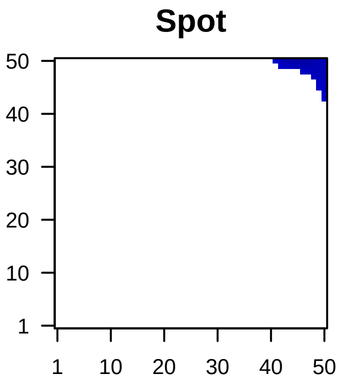
<FC> = −0.16

<shrinkage−t> = −5.77

<p−value> = 0.01

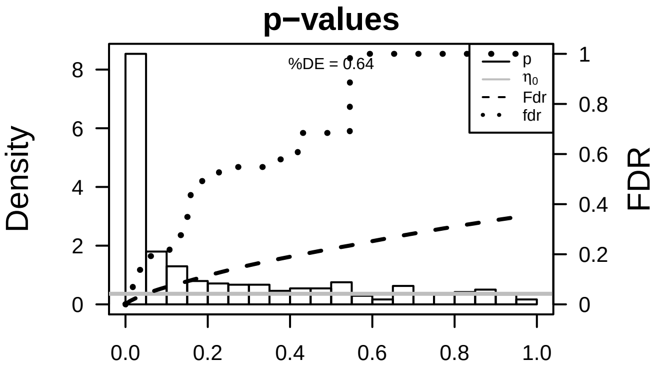
<fdr> = 0.67





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	26047	1.33	2e−16	1e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
2	3856	−1.35	2e−16	1e−14	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
3	4953	1.11	2e−16	1e−14	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
4	7419	1.03	2e−15	5e−12	50 x 47	voltage−dependent anion channel 3 [Source:HGNC Symbol;
5	5625	1	3e−14	2e−11	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ac
6	200810	−0.98	1e−13	2e−11	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
7	4072	−0.97	2e−13	4e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
8	655	−0.86	7e−11	4e−09	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
9	3880	−0.86	7e−11	4e−09	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
10	3790	−0.86	7e−11	2e−08	50 x 50	potassium voltage−gated channel, delayed−rectifier, subfamil
11	57549	−0.84	2e−10	3e−08	49 x 47	immunoglobulin superfamily, member 9 [Source:HGNC Symb
12	3149	0.83	4e−10	2e−07	47 x 50	high mobility group box 3 [Source:HGNC Symbol;Acc:5004]
13	1164	−0.79	2e−09	2e−07	44 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
14	1163	−0.78	4e−09	2e−07	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
15	875	−0.78	4e−09	9e−07	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
16	10857	−0.76	9e−09	7e−06	47 x 50	progesterone receptor membrane component 1 [Source:HGN
17	6659	−0.71	7e−08	7e−06	50 x 45	SRY (sex determining region Y)−box 4 [Source:HGNC Symb
18	3202	−0.7	1e−07	7e−06	49 x 47	homeobox A5 [Source:HGNC Symbol;Acc:5106]
19	55190	−0.7	1e−07	1e−05	47 x 50	nudix (nucleoside diphosphate linked moiety X)−type motif 11
20	256764	−0.68	2e−07	1e−05	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.75	NULL	64 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−19.75	NULL	64 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−13.05	NULL	90 / 914	Chr	Chr 3
4	−12.69	NULL	9 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
5	−11.87	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
6	−11.63	NULL	11 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	−11.36	NULL	8 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
8	−11.05	NULL	10 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
9	−11.03	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
10	−10.85	NULL	4 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
11	−10.64	NULL	8 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
12	−10.56	NULL	20 / 57	Glio	developing astrocytes
13	−10.52	NULL	8 / 16	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
14	−10.06	NULL	8 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
15	−10.05	NULL	7 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
16	−9.84	NULL	7 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
17	−9.8	NULL	10 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
18	−9.8	NULL	7 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
19	−9.63	NULL	9 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
20	−9.44	NULL	6 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
21	−9.29	NULL	1 / 2	miRNA target	miR−129
22	−9.02	NULL	6 / 14	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
23	−8.97	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
24	−8.93	NULL	12 / 68	Cancer	SHAUGHNESSY_MM high risk
25	−8.93	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
26	−8.85	NULL	7 / 15	GSEA C2	LY_AGING_OLD_DN
27	−8.84	NULL	7 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
28	−8.8	NULL	8 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
29	−8.46	NULL	9 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
30	−8.15	NULL	6 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
31	−8.08	NULL	6 / 15	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
32	−8.08	NULL	11 / 18	BP	spindle organization
33	−7.86	NULL	68 / 530	Cancer	Lembcke_Normal vs Adenoma
34	−7.71	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
35	−7.68	NULL	6 / 15	GSEA C2	CHANG_CYCLING_GENES
36	−7.45	NULL	3 / 19	BP	maternal process involved in female pregnancy
37	−7.23	NULL	4 / 15	Cancer	RHODES_CANCER_META_SIGNATURE
38	−7.15	NULL	4 / 37	CC	lateral plasma membrane
39	−7.11	NULL	6 / 15	GSEA C2	KAUFFMANN_MELANOMA_RELAPSE_UP
40	−7.05	NULL	4 / 12	GSEA C2	SHEPARD_BMYB_TARGETS