GW_124

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1396 (821 + / 575 −)

genes with fdr < 0.1 = 1039 (647 + / 392 −)

genes with fdr < 0.05 = 804 (524 + / 280 −)

genes with fdr < 0.01 = 452 (328 + / 124 −)

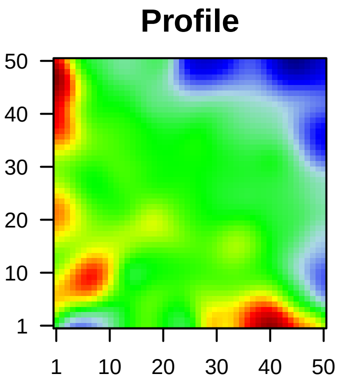
genes in genesets = 16332

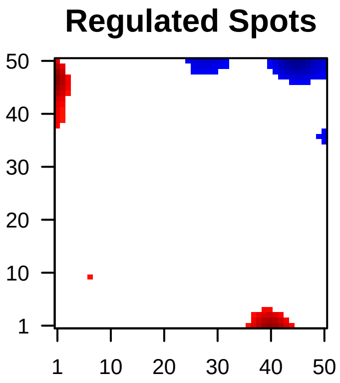
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.16

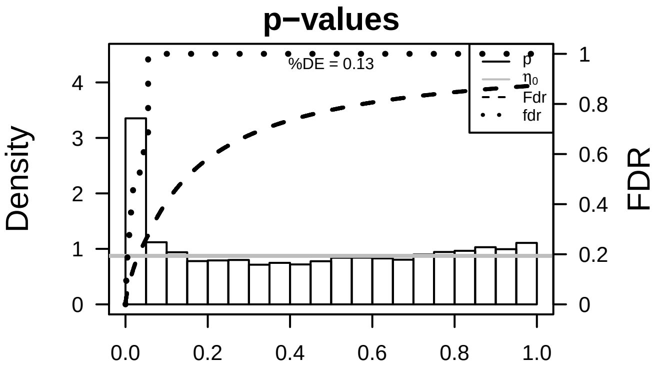
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	2.14	2e−16	1e−13	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	1281	−1.74	2e−16	1e−13	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
3	51755	1.89	2e−16	1e−13	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
4	55894	2.31	2e−16	1e−13	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
5	414325	2.2	2e−16	1e−13	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
6	1673	2.78	2e−16	1e−13	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
7	1839	1.81	2e−16	1e−13	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Sym
8	3552	2.14	2e−16	1e−13	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
9	56300	2.13	2e−16	1e−13	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
10	126306	1.95	2e−16	1e−13	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC S
11	3880	−3.09	2e−16	1e−13	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
12	84648	1.99	2e−16	1e−13	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
13	3963	1.85	2e−16	1e−13	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
14	8581	1.94	2e−16	1e−13	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
15	4312	1.87	2e−16	1e−13	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
16	4319	2.99	2e−16	1e−13	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC S
17	4314	1.98	2e−16	1e−13	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
18	4316	2.09	2e−16	1e−13	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
19	283869	2.03	2e−16	1e−13	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
20	5217	−1.81	2e−16	1e−13	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.29	NULL	1135	Chr	Chr 19
2	14.31	NULL	135	H.Tiss	WIRTH_Mucosa
3	10.64	NULL	76	BP	epidermis development
4	10.1	NULL	21	CC	cornified envelope
5	8.9	NULL	42	BP	keratinization
6	8.62	NULL	572	Disease	GUDJ_psoriasis up
7	7.54	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
8	7.15	NULL	717	Chr	Chr 16
9	6.96	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
10	6.78	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
11	6.78	NULL	14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
12	6.73	NULL	53	BP	keratinocyte differentiation
13	6.72	NULL	957	Chr	Chr 11
14	6.47	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	6.42	NULL	918	Chr	Chr 17
16	6.13	NULL	17	BP	negative regulation of interleukin−6 production
17	5.8	NULL	12	GSEA C2	SHI_SPARC_TARGETS_UP
18	5.7	NULL	15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
19	5.68	NULL	10	BP	cellular response to zinc ion
20	5.55	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
Underexpressed					
1	−11.83	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−11.83	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−9.2	NULL	914	Chr	Chr 3
4	−8.88	NULL	370	BP	mitotic cell cycle
5	−8.42	NULL	16	MMML CGS	MACIEJ_MMML 1
6	−8.3	NULL	618	Chr	Chr 4
7	−8.16	NULL	280	Chr	Chr 13
8	−7.63	NULL	12	miRNA target	miR−29c
9	−7.29	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
10	−7.07	NULL	11	MF	platelet−derived growth factor binding
11	−7.04	NULL	232	BP	mitosis
12	−6.88	NULL	436	miRNA target starBase	hsa−miR−548n
13	−6.53	NULL	2378	CC	cytosol
14	−6.48	NULL	1233	TF	KIM_MYC targets
15	−6.36	NULL	318	miRNA target starBase	hsa−miR−590−3p
16	−6.35	NULL	300	miRNA target starBase	hsa−miR−561
17	−6.22	NULL	264	miRNA target starBase	hsa−miR−449a
18	−6.12	NULL	169	miRNA target starBase	hsa−miR−183
19	−6.11	NULL	336	miRNA target starBase	hsa−miR−548b−5p
20	−6.06	NULL	293	miRNA target starBase	hsa−miR−186

GW_124

Local Summary

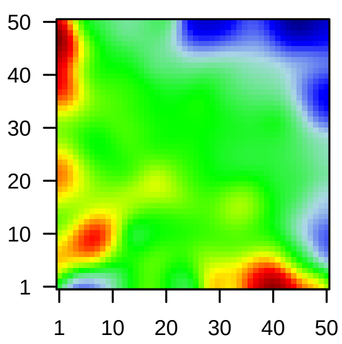
%DE = 0.73
metagenes = 24
genes = 343
genes in genesets = 315

genes with fdr < 0.1 = 174 (173 + / 1 −)
genes with fdr < 0.05 = 137 (137 + / 0 −)
genes with fdr < 0.01 = 88 (88 + / 0 −)

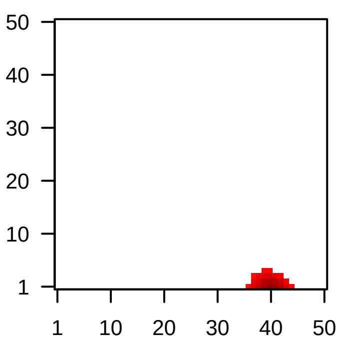
<r> metagenes = 0.95
<r> genes = 0.42

<FC> = 0.46
<shrinkage−t> = 16.05
<p−value> = 0.01
<fdr> = 0.59

Profile



Spot



Local Genelist

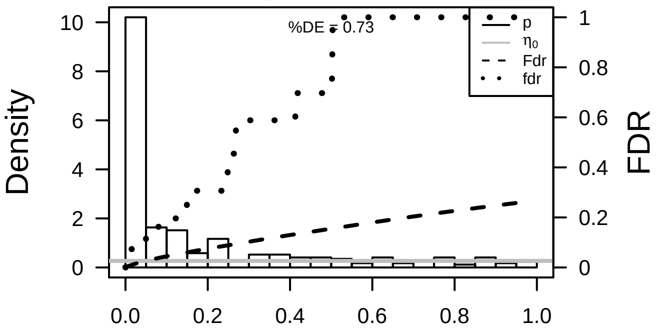
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	400818	1.62	2e−13	1e−08	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
2	84446	1.4	2e−10	5e−06	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
3	22809	1.18	8e−08	5e−06	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
4	100132406	1.15	2e−07	5e−06	39 x 1	neuroblastoma breakpoint family, member 10 [Source:HGNC
5	8837	1.15	2e−07	5e−06	44 x 1	CASP8 and FADD−like apoptosis regulator [Source:HGNC S
6	28996	1.13	3e−07	5e−06	40 x 1	homeodomain interacting protein kinase 2 [Source:HGNC Sy
7	55142	1.12	3e−07	5e−06	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symbo
8	57835	1.11	4e−07	5e−06	40 x 1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7
9	440275	1.11	5e−07	5e−06	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
10	348094	1.1	5e−07	5e−06	43 x 1	ankyrin repeat and death domain containing 1A [Source:HGN
11	25862	1.1	5e−07	5e−06	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
12	26279	1.1	6e−07	5e−06	40 x 1	phospholipase A2, group IID [Source:HGNC Symbol;Acc:903
13	202134	1.09	6e−07	5e−06	40 x 1	family with sequence similarity 153, member B [Source:HGN
14	57464	1.09	7e−07	2e−05	40 x 1	striatin interacting protein 2 [Source:HGNC Symbol;Acc:2220
15	401494	1.07	1e−06	2e−05	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [Sou
16	29797	1.07	1e−06	2e−05	40 x 1	
17	6376	1.06	2e−06	2e−05	44 x 1	chemokine (C−X3−C motif) ligand 1 [Source:HGNC Symbol;
18	125050	1.05	2e−06	2e−05	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
19	113277	1.05	2e−06	4e−05	40 x 1	transmembrane protein 106A [Source:HGNC Symbol;Acc:28
20	79792	1.03	3e−06	4e−05	44 x 1	gasdermin D [Source:HGNC Symbol;Acc:25697]

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	11.85	NULL	1 / 2	miRNA target	miR−193a
2	8.87	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
3	7.46	NULL	3 / 16	BP	negative regulation of neurogenesis
4	7.09	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
5	6.79	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
6	6.53	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
7	6.22	NULL	1 / 6	GSEA C2	SA_FAS_SIGNALING
8	6.13	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
9	6	NULL	2 / 14	BP	cellular response to estradiol stimulus
10	5.63	NULL	2 / 15	GSEA C2	FIRESTEIN_PROLIFERATION
11	5.54	NULL	49 / 1135	Chr	Chr 19
12	5.5	NULL	2 / 12	BP	macrophage chemotaxis
13	5.39	NULL	1 / 11	MF	tau−protein kinase activity
14	5.37	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
15	5.3	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
16	5.27	NULL	2 / 11	GSEA C2	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
17	5.22	NULL	3 / 24	BP	negative regulation of T cell proliferation
18	5.21	NULL	2 / 19	BP	establishment of cell polarity
19	5.05	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
20	5.05	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
21	5.04	NULL	2 / 14	GSEA C2	MITSIADES_RESPONSE_TO_APLIDIN_DN
22	4.89	NULL	1 / 9	GSEA C2	REACTOME_DEATH_RECEPTOR_SIGNALLING
23	4.82	NULL	1 / 9	GSEA C2	BROWNE_HCMV_INFECTION_1HR_DN
24	4.81	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
25	4.81	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
26	4.81	NULL	1 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
27	4.7	NULL	2 / 19	CC	histone methyltransferase complex
28	4.7	NULL	2 / 19	BP	negative regulation of extrinsic apoptotic signaling pathway via dea
29	4.65	NULL	1 / 14	BP	centrosome duplication
30	4.61	NULL	3 / 23	BP	G2 DNA damage checkpoint
31	4.59	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
32	4.59	NULL	1 / 10	BP	skeletal muscle tissue regeneration
33	4.49	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
34	4.47	NULL	1 / 11	GSEA C2	TRACEY_RESISTANCE_TO_IFNA2_DN
35	4.45	NULL	1 / 6	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_UP
36	4.45	NULL	1 / 6	GSEA C2	ST_INTERLEUKIN_13_PATHWAY
37	4.45	NULL	1 / 6	GSEA C2	ST_IL_13_PATHWAY
38	4.42	NULL	1 / 7	GSEA C2	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_UP
39	4.36	NULL	3 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
40	4.35	NULL	3 / 48	MF	cysteine−type endopeptidase activity

p−values



GW_124

Local Summary

%DE = 0.83

metagenes = 1

genes = 15

genes in genesets = 15

genes with fdr < 0.1 = 9 (9 + / 0 −)

genes with fdr < 0.05 = 8 (8 + / 0 −)

genes with fdr < 0.01 = 5 (5 + / 0 −)

<r> metagenes = NA

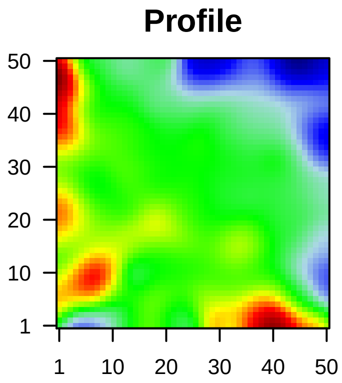
<r> genes = 0.48

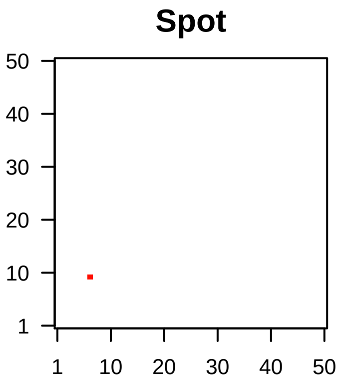
<FC> = 0.5

<shrinkage−t> = 17.55

<p−value> = 0.01

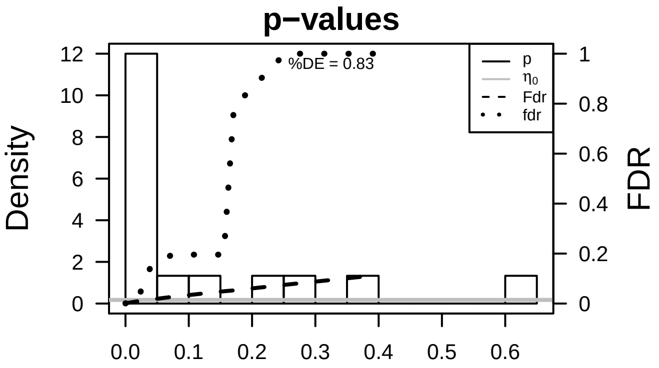
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55661	1.02	3e−06	4e−04	7 x 10	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
2	6195	0.83	2e−04	5e−04	7 x 10	ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:H
3	126208	0.78	4e−04	4e−03	7 x 10	zinc finger protein 787 [Source:HGNC Symbol;Acc:26998]
4	22870	0.68	2e−03	4e−03	7 x 10	protein phosphatase 6, regulatory subunit 1 [Source:HGNC S
5	7782	0.64	4e−03	7e−03	7 x 10	solute carrier family 30 (zinc transporter), member 4 [Source:
6	10078	0.6	6e−03	3e−02	7 x 10	tumor suppressing subtransferable candidate 4 [Source:HGN
7	83985	0.48	3e−02	3e−02	7 x 10	spinster homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:
8	11140	0.43	3e−02	3e−02	7 x 10	cell division cycle 37 [Source:HGNC Symbol;Acc:1735]
9	4287	0.46	4e−02	5e−02	7 x 10	
10	26229	0.41	6e−02	1e−01	7 x 10	beta−1,3−glucuronyltransferase 3 (glucuronosyltransferase I)
11	55559	0.35	1e−01	2e−01	7 x 10	HAUS augmin−like complex, subunit 7 [Source:HGNC Symbo
12	10025	0.26	2e−01	2e−01	7 x 10	mediator complex subunit 16 [Source:HGNC Symbol;Acc:175
13	10844	0.25	3e−01	8e−01	7 x 10	tubulin, gamma complex associated protein 2 [Source:HGNC
14	9277	0.19	4e−01	1e+00	7 x 10	WD repeat domain 46 [Source:HGNC Symbol;Acc:13923]
15	54971	0.11	6e−01	1e+00	7 x 10	BTG3 associated nuclear protein [Source:HGNC Symbol;Acc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.42	NULL	2 / 16	GSEA C2	SCHEIDEREIT_IKK_INTERACTING_PROTEINS
2	21.12	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
3	17.93	NULL	1 / 13	GSEA C2	LAMB_CCND1_TARGETS
4	17.93	NULL	1 / 13	GSEA C2	REACTOME_CREB_PHOPHORYLATION_THROUGH_THE_ACT
5	17.03	NULL	1 / 14	GSEA C2	BIOCARTA_ERK5_PATHWAY
6	16.24	NULL	1 / 15	GSEA C2	FIRESTEIN_CTNNB1_PATHWAY
7	16.24	NULL	1 / 15	GSEA C2	BIOCARTA_G2_PATHWAY
8	16.24	NULL	1 / 15	GSEA C2	BIOCARTA_GH_PATHWAY
9	16.24	NULL	1 / 15	GSEA C2	BIOCARTA_IGF1R_PATHWAY
10	16.24	NULL	1 / 15	GSEA C2	BIOCARTA_BAD_PATHWAY
11	16.24	NULL	1 / 15	GSEA C2	BIOCARTA_CREB_PATHWAY
12	16.24	NULL	1 / 15	GSEA C2	REACTOME_ERK_MAPK_TARGETS
13	16.24	NULL	1 / 15	GSEA C2	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPT
14	16.24	NULL	1 / 15	GSEA C2	SA_B_CELL_RECEPTOR_COMPLEXES
15	15.55	NULL	1 / 16	GSEA C2	BIOCARTA_ERK_PATHWAY
16	15.55	NULL	1 / 16	GSEA C2	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED
17	15.55	NULL	1 / 16	GSEA C2	ST_ERK1_ERK2_MAPK_PATHWAY
18	14.67	NULL	1 / 12	BP	zinc ion transmembrane transport
19	14.67	NULL	1 / 12	MF	zinc ion transmembrane transporter activity
20	13.88	NULL	1 / 19	MF	cysteine−type endopeptidase inhibitor activity involved in apoptotic
21	13.37	NULL	2 / 34	miRNA target starBase	hsa−miR−1226
22	12.21	NULL	1 / 10	MF	protein kinase B binding
23	11.11	NULL	1 / 18	MF	cation transmembrane transporter activity
24	10.67	NULL	1 / 12	miRNA target starBase	hsa−miR−1249
25	10.06	NULL	1 / 11	GSEA C2	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
26	9.99	NULL	1 / 32	Glio	Donson−Misc immune function−associated with LTS in HGA
27	9.8	NULL	1 / 33	BP	positive regulation of cell differentiation
28	9.57	NULL	1 / 14	MF	Hsp90 protein binding
29	9.44	NULL	1 / 12	BP	heparan sulfate proteoglycan biosynthetic process
30	9.35	NULL	2 / 62	miRNA target starBase	hsa−miR−637
31	9.12	NULL	1 / 15	GSEA C2	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN
32	8.73	NULL	1 / 16	BP	regulation of interferon−gamma−mediated signaling pathway
33	8.73	NULL	1 / 16	BP	regulation of type I interferon−mediated signaling pathway
34	8.73	NULL	1 / 16	GSEA C2	DORSAM_HOXA9_TARGETS_DN
35	8.73	NULL	1 / 16	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_UP
36	8.46	NULL	1 / 14	GSEA C2	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
37	8.46	NULL	1 / 14	GSEA C2	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_S
38	8.07	NULL	1 / 15	MF	glucuronosyltransferase activity
39	8.07	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_4HR_DN
40	8.07	NULL	1 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP

GW_124

Local Summary

%DE = 0.73

metagenes = 28

genes = 405

genes in genesets = 396

genes with fdr < 0.1 = 245 (223 + / 22 −)

genes with fdr < 0.05 = 218 (200 + / 18 −)

genes with fdr < 0.01 = 184 (173 + / 11 −)

<r> metagenes = 0.86

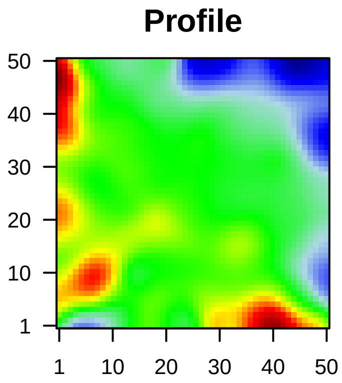
<r> genes = 0.32

<FC> = 0.54

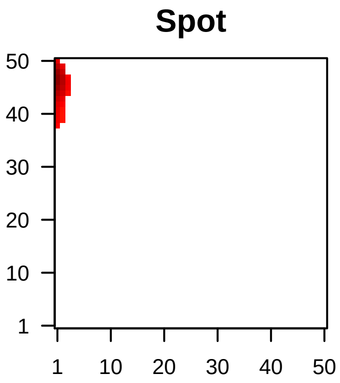
<shrinkage−t> = 18.95

<p−value> = 0

<fdr> = 0.43



Profile



Spot

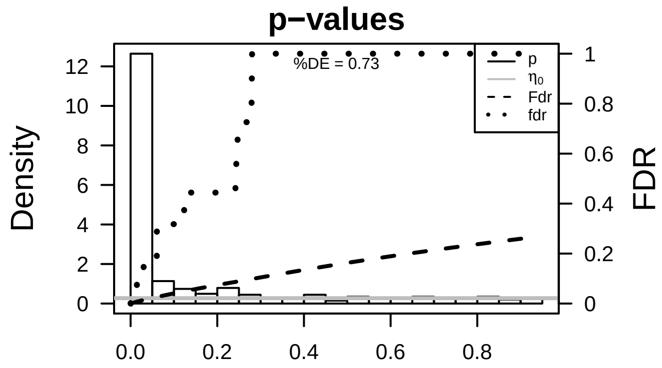
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55894	2.31	2e−16	2e−15	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
2	414325	2.2	2e−16	2e−15	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
3	1673	2.78	2e−16	2e−15	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
4	1839	1.81	2e−16	2e−15	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Symb
5	3552	2.14	2e−16	2e−15	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
6	56300	2.13	2e−16	2e−15	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
7	84648	1.99	2e−16	2e−15	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
8	3963	1.85	2e−16	2e−15	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
9	8581	1.94	2e−16	2e−15	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
10	6274	1.8	2e−16	2e−15	1 x 43	S100 calcium binding protein A3 [Source:HGNC Symbol;Acc:
11	6278	1.76	2e−16	2e−15	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
12	338324	2.84	2e−16	2e−15	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
13	374897	1.91	2e−16	2e−15	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
14	6701	2.75	2e−16	2e−15	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
15	6702	1.85	2e−16	2e−15	1 x 50	
16	6706	2.59	2e−16	2e−15	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
17	5650	1.76	9e−16	3e−13	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
18	348938	1.73	4e−15	1e−12	1 x 46	NIPA−like domain containing 4 [Source:HGNC Symbol;Acc:2
19	64073	1.69	1e−14	2e−12	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
20	388533	1.67	3e−14	3e−11	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.49	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	27.04	NULL	18 / 21	CC	cornified envelope
3	26.18	NULL	125 / 572	Disease	GUDJ_psoriasis up
4	23.41	NULL	28 / 76	BP	epidermis development
5	22.93	NULL	20 / 42	BP	keratinization
6	15.85	NULL	25 / 53	BP	keratinocyte differentiation
7	14.95	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
8	13.03	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	12.73	NULL	5 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
10	12.32	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
11	11.3	NULL	3 / 15	MF	interleukin−1 receptor binding
12	11.09	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	10.5	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
14	10.28	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
15	9.29	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
16	9.22	NULL	10 / 19	BP	peptide cross−linking
17	9.12	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
18	9.06	NULL	8 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	8.9	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
20	8.9	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
21	8.74	NULL	4 / 10	MF	RAGE receptor binding
22	8.65	NULL	12 / 21	CC	desmosome
23	8.24	NULL	6 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
24	8.02	NULL	7 / 73	BP	defense response to bacterium
25	7.94	NULL	6 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
26	7.91	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
27	7.79	NULL	2 / 17	Disease	BCHETNIA_EBM up
28	7.47	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
29	7.39	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
30	7.24	NULL	2 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
31	7.11	NULL	22 / 82	CC	intermediate filament
32	7.01	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
33	6.92	NULL	7 / 32	CC	cell−cell adherens junction
34	6.9	NULL	4 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
35	6.85	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
36	6.65	NULL	3 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
37	6.63	NULL	3 / 12	GSEA C2	SESTO_RESPONSE_TO_UV_C3
38	6.56	NULL	1 / 5	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
39	6.52	NULL	5 / 25	BP	brown fat cell differentiation
40	6.39	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE



p−values

GW_124

Local Summary

%DE = 0.77

metagenes = 4

genes = 109

genes in genesets = 109

genes with fdr < 0.1 = 75 (0 + / 75 −)

genes with fdr < 0.05 = 37 (0 + / 37 −)

genes with fdr < 0.01 = 18 (0 + / 18 −)

<r> metagenes = 0.99

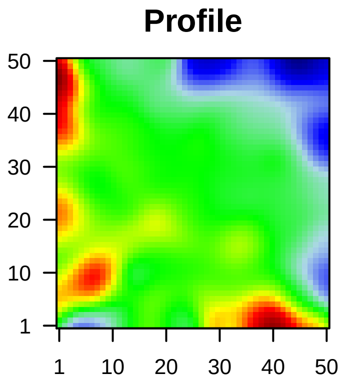
<r> genes = 0.34

<FC> = −0.41

<shrinkage−t> = −14.25

<p−value> = 0.04

<fdr> = 0.68



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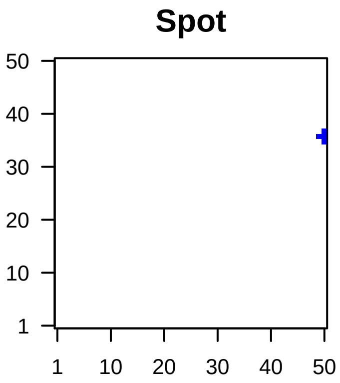
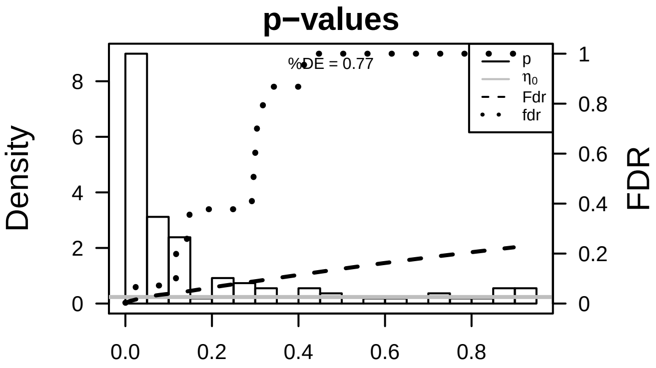


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	60481	−1.17	1e−07	0.003	50 x 37	ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213
2	4942	−0.81	2e−04	0.003	50 x 35	ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
3	25972	−0.77	4e−04	0.003	50 x 37	unc−50 homolog (C. elegans) [Source:HGNC Symbol;Acc:16
4	57092	−0.77	5e−04	0.003	50 x 35	PEST proteolytic signal containing nuclear protein [Source:H
5	80209	−0.76	6e−04	0.003	50 x 36	proline and serine rich 1 [Source:HGNC Symbol;Acc:20291]
6	23505	−0.75	6e−04	0.005	50 x 37	transmembrane protein 131 [Source:HGNC Symbol;Acc:303
7	5431	−0.7	1e−03	0.005	50 x 37	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [
8	22889	−0.7	1e−03	0.005	50 x 37	KIAA0907 [Source:HGNC Symbol;Acc:29145]
9	5934	−0.69	2e−03	0.005	50 x 36	retinoblastoma−like 2 (p130) [Source:HGNC Symbol;Acc:989
10	7764	−0.69	2e−03	0.005	50 x 37	zinc finger protein 217 [Source:HGNC Symbol;Acc:13009]
11	10257	−0.69	2e−03	0.005	50 x 36	ATP−binding cassette, sub−family C (CFTR/MRP), member 4
12	4254	−0.69	2e−03	0.005	50 x 36	KIT ligand [Source:HGNC Symbol;Acc:6343]
13	7342	−0.68	2e−03	0.005	50 x 35	upstream binding protein 1 (LBP−1a) [Source:HGNC Symbol
14	7520	−0.68	2e−03	0.005	50 x 35	X−ray repair complementing defective repair in Chinese ham
15	80208	−0.67	2e−03	0.005	50 x 35	spastic paraplegia 11 (autosomal recessive) [Source:HGNC
16	9802	−0.61	2e−03	0.009	50 x 35	DAZ associated protein 2 [Source:HGNC Symbol;Acc:2684]
17	6599	−0.65	3e−03	0.009	50 x 36	SWI/SNF related, matrix associated, actin dependent regulat
18	11064	−0.65	3e−03	0.009	50 x 35	centriolin [Source:HGNC Symbol;Acc:1858]
19	10099	−0.64	4e−03	0.011	50 x 37	tetraspanin 3 [Source:HGNC Symbol;Acc:17752]
20	57088	−0.63	4e−03	0.017	50 x 36	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.93	NULL	1 / 2	miRNA target	miR−98
2	−11.9	NULL	1 / 4	miRNA target	let−7c
3	−11.9	NULL	1 / 4	miRNA target	let−7g
4	−11.1	NULL	1 / 3	miRNA target	miR−197
5	−10.14	NULL	6 / 51	miRNA target−starBase	hsa−miR−556−3p
6	−10.12	NULL	1 / 4	GSEA C2	LUCAS_HNF4A_TARGETS_DN
7	−9.72	NULL	1 / 11	BP	alpha−linolenic acid metabolic process
8	−9.72	NULL	1 / 11	BP	unsaturated fatty acid metabolic process
9	−9.72	NULL	4 / 47	miRNA target−starBase	hsa−miR−302b*
10	−9.49	NULL	14 / 271	miRNA target−starBase	hsa−miR−101
11	−9.43	NULL	1 / 6	miRNA target	let−7b
12	−9.43	NULL	1 / 6	miRNA target	let−7d
13	−9.43	NULL	1 / 6	miRNA target	miR−26a
14	−9.25	NULL	1 / 12	BP	linoleic acid metabolic process
15	−8.88	NULL	3 / 32	miRNA target−starBase	hsa−miR−589
16	−8.77	NULL	2 / 10	GSEA C2	CROONQUIST_STROMAL_STIMULATION_DN
17	−8.67	NULL	2 / 11	miRNA target−starBase	hsa−miR−487b
18	−8.43	NULL	4 / 38	miRNA target−starBase	hsa−miR−770−5p
19	−8.28	NULL	3 / 29	TF Tissue	VAQUERIZAS_Lymph node
20	−8.18	NULL	5 / 69	miRNA target−starBase	hsa−miR−299−5p
21	−8.14	NULL	6 / 100	miRNA target−starBase	hsa−miR−544
22	−8.1	NULL	2 / 16	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_DN
23	−7.99	NULL	5 / 103	miRNA target−starBase	hsa−miR−1284
24	−7.97	NULL	13 / 433	miRNA target−starBase	hsa−miR−19b
25	−7.87	NULL	1 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
26	−7.85	NULL	10 / 177	miRNA target−starBase	hsa−miR−300
27	−7.74	NULL	10 / 181	miRNA target−starBase	hsa−miR−381
28	−7.61	NULL	1 / 5	miRNA target−starBase	hsa−miR−585
29	−7.6	NULL	2 / 38	miRNA target−starBase	hsa−miR−1308
30	−7.6	NULL	1 / 17	BP	long−chain fatty−acyl−CoA biosynthetic process
31	−7.54	NULL	4 / 39	miRNA target−starBase	hsa−miR−502−3p
32	−7.53	NULL	3 / 52	miRNA target−starBase	hsa−miR−191
33	−7.48	NULL	1 / 9	miRNA target	miR−125b
34	−7.45	NULL	9 / 172	miRNA target−starBase	hsa−miR−607
35	−7.32	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
36	−7.3	NULL	11 / 281	miRNA target−starBase	hsa−miR−570
37	−7.23	NULL	4 / 38	miRNA target−starBase	hsa−miR−1277
38	−7.18	NULL	2 / 15	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D6
39	−7.18	NULL	6 / 58	miRNA target−starBase	hsa−miR−455−5p
40	−7.17	NULL	5 / 86	miRNA target−starBase	hsa−miR−595

GW_124

Local Summary

%DE = 0.74

metagenes = 45

genes = 608

genes in genesets = 603

genes with fdr < 0.1 = 301 (12 + / 289 −)

genes with fdr < 0.05 = 239 (10 + / 229 −)

genes with fdr < 0.01 = 108 (4 + / 104 −)

<r> metagenes = 0.84

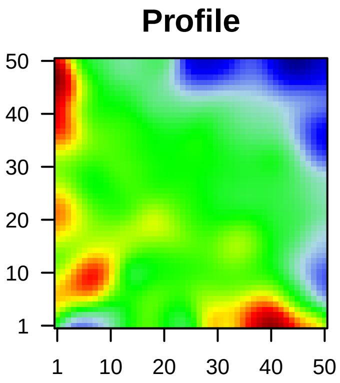
<r> genes = 0.26

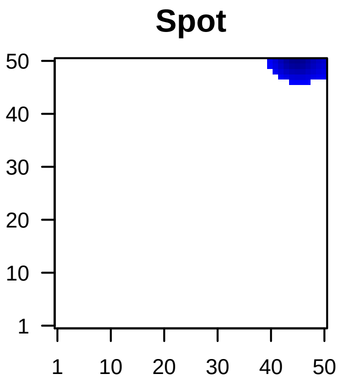
<FC> = −0.38

<shrinkage−t> = −13.41

<p−value> = 0.02

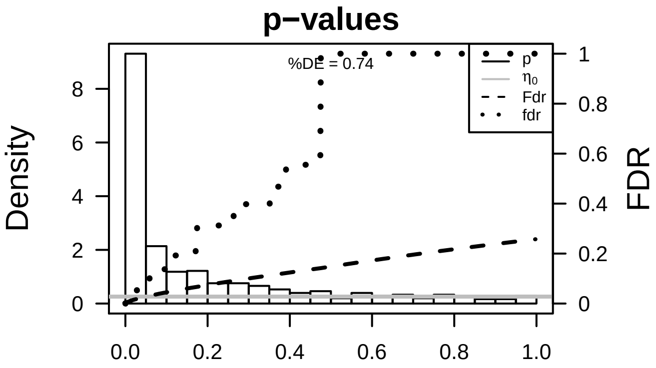
<fdr> = 0.65


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3880	−3.09	2e−16	3e−14	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
2	216	−1.78	7e−16	1e−11	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	4072	−1.65	6e−14	1e−08	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
4	4922	−1.43	8e−11	5e−07	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
5	79844	1.28	6e−09	5e−07	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
6	84171	1.27	7e−09	1e−06	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
7	28978	−1.25	1e−08	4e−06	49 x 50	transmembrane protein 14A [Source:HGNC Symbol;Acc:210
8	7153	−1.19	7e−08	4e−06	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
9	2956	−1.18	7e−08	2e−05	47 x 48	mutS homolog 6 [Source:HGNC Symbol;Acc:7329]
10	81831	−1.15	2e−07	2e−05	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym
11	928	−1.13	3e−07	1e−04	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
12	7419	−1.02	2e−06	1e−04	50 x 47	voltage−dependent anion channel 3 [Source:HGNC Symbol;
13	3428	−1.04	2e−06	2e−04	45 x 50	interferon, gamma−inducible protein 16 [Source:HGNC Symb
14	5984	−1.01	4e−06	2e−04	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn
15	3945	−1	5e−06	2e−04	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
16	79866	−0.99	7e−06	2e−04	43 x 50	bora, aurora kinase A activator [Source:HGNC Symbol;Acc:2
17	3856	−0.99	7e−06	2e−04	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
18	25975	−0.99	7e−06	4e−04	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
19	86	−0.96	1e−05	4e−04	46 x 50	actin−like 6A [Source:HGNC Symbol;Acc:24124]
20	255758	−0.96	1e−05	4e−04	50 x 50	Tctex1 domain containing 2 [Source:HGNC Symbol;Acc:284


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−35.54	NULL	91 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−35.54	NULL	91 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−22.83	NULL	109 / 370	BP	mitotic cell cycle
4	−21.25	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	−19.62	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
6	−19.18	NULL	24 / 57	Glio	developing astrocytes
7	−18.21	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
8	−17.94	NULL	8 / 11	GSEA C2	KALMA_E2F1_TARGETS
9	−17.54	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
10	−16.73	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
11	−16.08	NULL	11 / 16	Cancer	WOLFER_overlap genes
12	−15.85	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
13	−15.82	NULL	17 / 30	BP	DNA strand elongation involved in DNA replication
14	−15.74	NULL	9 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
15	−14.71	NULL	43 / 149	BP	DNA replication
16	−14.24	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	−14.21	NULL	108 / 530	Cancer	Lembcke_Normal vs Adenoma
18	−14.18	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
19	−14.03	NULL	12 / 18	BP	spindle organization
20	−13.88	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
21	−13.81	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
22	−13.43	NULL	10 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
23	−13.39	NULL	54 / 232	BP	mitosis
24	−13.33	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
25	−13.31	NULL	11 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
26	−13.29	NULL	10 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	−13.11	NULL	11 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
28	−13.09	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
29	−13.01	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
30	−12.87	NULL	24 / 66	CC	condensed chromosome kinetochore
31	−12.8	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
32	−12.65	NULL	39 / 148	BP	G1/S transition of mitotic cell cycle
33	−12.62	NULL	70 / 572	Disease	GUDJ_psoriasis up
34	−12.52	NULL	7 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
35	−12.44	NULL	10 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
36	−12.42	NULL	18 / 61	CC	kinetochore
37	−12.35	NULL	20 / 56	CC	chromosome, centromeric region
38	−12.18	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
39	−11.96	NULL	120 / 949	CC	nucleoplasm
40	−11.57	NULL	8 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK

GW_124

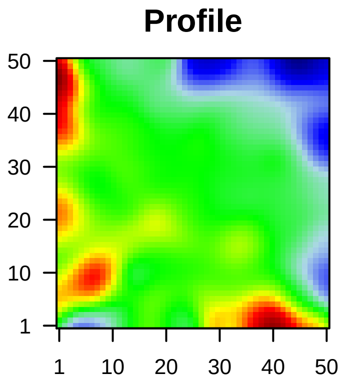
Local Summary

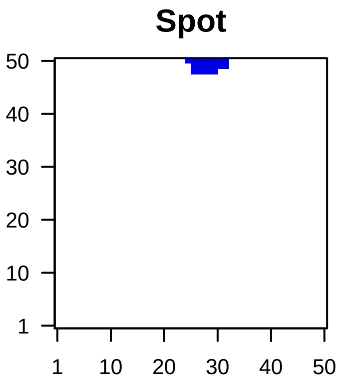
%DE = 0.8
metagenes = 20
genes = 336
genes in genesets = 331

genes with fdr < 0.1 = 181 (1 + / 180 −)
genes with fdr < 0.05 = 165 (1 + / 164 −)
genes with fdr < 0.01 = 50 (0 + / 50 −)

<r> metagenes = 0.92
<r> genes = 0.3

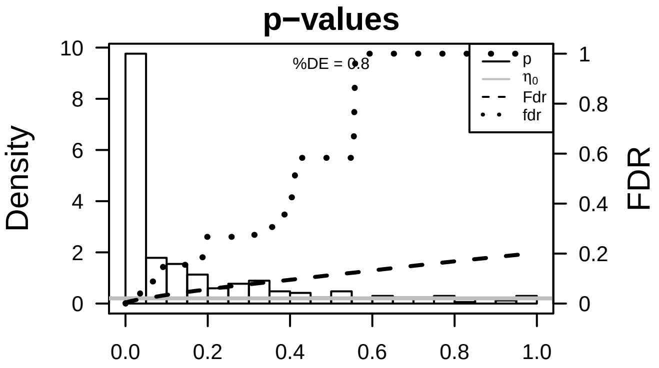
<FC> = −0.4
<shrinkage−t> = −13.93
<p−value> = 0.04
<fdr> = 0.66





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	509	−1.14	2e−07	2e−04	31 x 50	ATP synthase, H+ transporting, mitochondrial F1 complex, ga
2	9643	−1	5e−06	2e−04	26 x 50	mortality factor 4 like 2 [Source:HGNC Symbol;Acc:16849]
3	10935	−0.99	6e−06	2e−04	29 x 50	peroxiredoxin 3 [Source:HGNC Symbol;Acc:9354]
4	10787	−0.96	1e−05	2e−04	25 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]
5	3839	−0.94	2e−05	2e−04	26 x 50	karyopherin alpha 3 (importin alpha 4) [Source:HGNC Symbo
6	10972	−0.94	2e−05	2e−04	25 x 50	transmembrane emp24−like trafficking protein 10 (yeast) [Sou
7	55848	−0.94	2e−05	2e−03	31 x 50	plasminogen receptor, C−terminal lysine transmembrane prot
8	25831	−0.88	6e−05	2e−03	25 x 50	HECT domain containing E3 ubiquitin protein ligase 1 [Source
9	9188	−0.85	1e−04	2e−03	26 x 50	DEAD (Asp−Glu−Ala−Asp) box helicase 21 [Source:HGNC S
10	11260	−0.84	1e−04	2e−03	25 x 50	exportin, tRNA [Source:HGNC Symbol;Acc:12826]
11	6386	−0.84	1e−04	2e−03	25 x 50	syndecan binding protein (syntenin) [Source:HGNC Symbol;
12	3799	−0.83	2e−04	2e−03	25 x 50	kinesin family member 5B [Source:HGNC Symbol;Acc:6324]
13	54918	−0.81	2e−04	2e−03	25 x 50	CKLF−like MARVEL transmembrane domain containing 6 [So
14	130814	−0.8	3e−04	2e−03	27 x 48	PQ loop repeat containing 3 [Source:HGNC Symbol;Acc:285
15	8803	−0.8	3e−04	2e−03	27 x 50	succinate−CoA ligase, ADP−forming, beta subunit [Source:H
16	29079	−0.79	3e−04	2e−03	27 x 48	mediator complex subunit 4 [Source:HGNC Symbol;Acc:179
17	51019	−0.79	3e−04	2e−03	31 x 49	coiled−coil domain containing 53 [Source:HGNC Symbol;Acc
18	515	−0.78	4e−04	2e−03	30 x 50	ATP synthase, H+ transporting, mitochondrial Fo complex, su
19	10175	−0.78	4e−04	4e−03	28 x 50	cornichon family AMPA receptor auxiliary protein 1 [Source:H
20	9375	−0.77	4e−04	5e−03	27 x 48	transmembrane 9 superfamily member 2 [Source:HGNC Sym



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.16	NULL	2 / 4	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN
2	−10.73	NULL	5 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
3	−10.29	NULL	5 / 14	BP	mitochondrial ATP synthesis coupled proton transport
4	−10.13	NULL	4 / 8	MMML CGS	MACIEJ_MMML 50
5	−9.9	NULL	5 / 15	BP	ATP synthesis coupled proton transport
6	−9.29	NULL	5 / 24	CC	endoplasmic reticulum−Golgi intermediate compartment membran
7	−9.29	NULL	4 / 11	MMML CGS	MACIEJ_MMML 49
8	−8.89	NULL	3 / 14	GSEA C2	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN
9	−8.85	NULL	6 / 62	Glio	Stuehler_Proteins_up_in_STS
10	−8.65	NULL	5 / 19	CC	mitochondrial proton−transporting ATP synthase complex
11	−8.25	NULL	10 / 83	BP	respiratory electron transport chain
12	−8.19	NULL	4 / 25	miRNA target−starBase	hsa−miR−1273
13	−7.97	NULL	14 / 152	BP	cellular metabolic process
14	−7.65	NULL	2 / 12	BP	oxidative phosphorylation
15	−7.64	NULL	3 / 16	GSEA C2	REACTOME_CITRIC_ACID_CYCLE
16	−7.48	NULL	4 / 15	BP	COPII vesicle coating
17	−7.42	NULL	2 / 10	BP	maternal placenta development
18	−7.03	NULL	16 / 169	Glio	willscher_GBM_proteomics_wtOnly_Differencelist_
19	−7.01	NULL	17 / 184	miRNA target−starBase	hsa−miR−586
20	−6.9	NULL	9 / 86	Lymphoma	ROSOLOWSKI_red total
21	−6.63	NULL	9 / 70	Glio	willscher_GBM_proteomics_wtOnly_SpotJ
22	−6.52	NULL	14 / 146	miRNA target−starBase	hsa−miR−494
23	−6.41	NULL	3 / 12	GSEA C2	DAZARD_RESPONSE_TO_UV_SCC_UP
24	−6.41	NULL	2 / 5	MMML CGS	MACIEJ_MMML 28
25	−6.35	NULL	26 / 269	miRNA target−starBase	hsa−miR−1244
26	−6.31	NULL	3 / 13	GSEA C2	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
27	−6.26	NULL	3 / 10	BP	ubiquitin−dependent protein catabolic process via the multivesicula
28	−6.24	NULL	21 / 318	miRNA target−starBase	hsa−miR−590−3p
29	−6.21	NULL	9 / 99	miRNA target−starBase	hsa−miR−653
30	−6.18	NULL	2 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
31	−6.14	NULL	2 / 13	BP	COPI coating of Golgi vesicle
32	−6.1	NULL	2 / 13	BP	viral entry into host cell
33	−5.97	NULL	7 / 67	miRNA target−starBase	hsa−miR−1246
34	−5.88	NULL	11 / 210	miRNA target−starBase	hsa−miR−29b
35	−5.85	NULL	18 / 290	BP	intracellular protein transport
36	−5.82	NULL	6 / 49	BP	ER to Golgi vesicle−mediated transport
37	−5.79	NULL	10 / 170	miRNA target−starBase	hsa−miR−29a
38	−5.74	NULL	3 / 14	CC	eukaryotic 43S preinitiation complex
39	−5.67	NULL	2 / 10	CC	oligosaccharyltransferase complex
40	−5.65	NULL	16 / 198	BP	vesicle−mediated transport