GW_130

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1959 (1082 + / 877 −)

genes with fdr < 0.1 = 1563 (866 + / 697 −)

genes with fdr < 0.05 = 1329 (748 + / 581 −)

genes with fdr < 0.01 = 967 (551 + / 416 −)

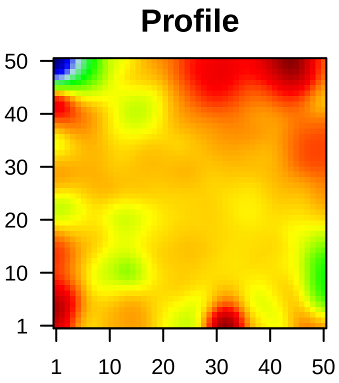
genes in genesets = 16332

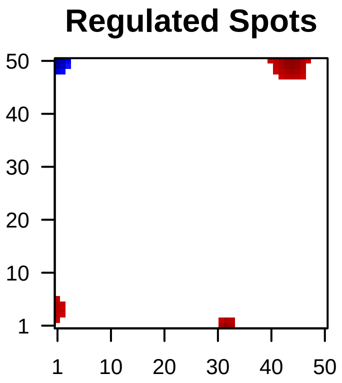
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

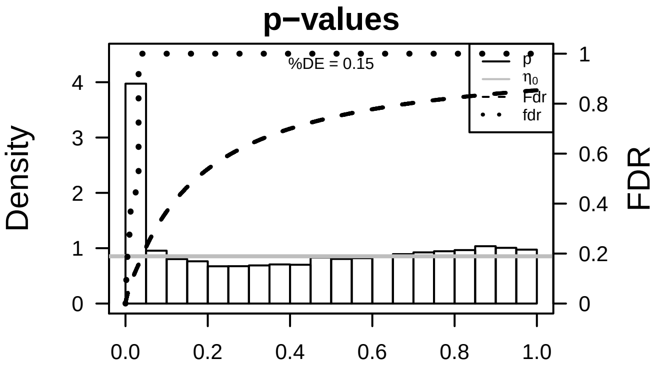
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	1.3	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	57016	−2.01	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.52	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	220	−1.66	2e−16	3e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
5	222	−1.46	2e−16	3e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
6	10409	−1.25	2e−16	3e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
7	387695	−1.59	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
8	84830	1.19	2e−16	3e−14	15 x 1	androgen−dependent TFPI−regulating protein [Source:HGNC
9	79783	1.42	2e−16	3e−14	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Sym
10	768	1.42	2e−16	3e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
11	57172	−1.19	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	857	1.43	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
13	131076	1.18	2e−16	3e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
14	100133941	−1.49	2e−16	3e−14	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
15	972	1.15	2e−16	3e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
16	22802	−1.59	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	9076	1.71	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
18	84518	−1.43	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
19	1308	1.41	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
20	1288	1.31	2e−16	3e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	14.59	NULL	15	CC	MHC class II protein complex
2	13.04	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
3	12.36	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	12.36	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	12.1	NULL	47	BP	antigen processing and presentation
6	11.38	NULL	60	BP	interferon−gamma−mediated signaling pathway
7	11.01	NULL	32	CC	ER to Golgi transport vesicle membrane
8	10.66	NULL	633	Chr	Chr 9
9	10.16	NULL	3	MMML CGS	MACIEJ_MMML 7
10	9.57	NULL	204	BP	cytokine−mediated signaling pathway
11	9.41	NULL	51	BP	type I interferon signaling pathway
12	9.02	NULL	21	CC	clathrin−coated endocytic vesicle membrane
13	8.5	NULL	370	BP	mitotic cell cycle
14	8.23	NULL	6	Lymphoma	DAVE_MHCCII BL DN
15	8.18	NULL	12	BP	hemidesmosome assembly
16	7.93	NULL	534	Chr	Chr 8
17	7.86	NULL	28	CC	transport vesicle membrane
18	7.84	NULL	123	BP	defense response to virus
19	7.8	NULL	16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
20	7.5	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
Underexpressed					
1	−19.4	NULL	135	H.Tiss	WIRTH_Mucosa
2	−16.4	NULL	21	CC	cornified envelope
3	−14.42	NULL	42	BP	keratinization
4	−13.87	NULL	504	Chr	Chr 15
5	−11.38	NULL	53	BP	keratinocyte differentiation
6	−8.62	NULL	76	BP	epidermis development
7	−7.8	NULL	10	MF	RAGE receptor binding
8	−7.06	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
9	−6.9	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
10	−6.69	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
11	−6.48	NULL	19	BP	peptide cross−linking
12	−6.12	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	−6.08	NULL	15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
14	−6.05	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−5.62	NULL	21	CC	desmosome
16	−5.58	NULL	12	BP	cellular aldehyde metabolic process
17	−5.57	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	−5.5	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
19	−5.46	NULL	10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
20	−5.41	NULL	1720	Chr	Chr 1

GW_130

Local Summary

%DE = 0.82

metagenes = 6

genes = 114

genes in genesets = 112

genes with fdr < 0.1 = 83 (83 + / 0 −)

genes with fdr < 0.05 = 75 (75 + / 0 −)

genes with fdr < 0.01 = 69 (69 + / 0 −)

<r> metagenes = 1

<r> genes = 0.47

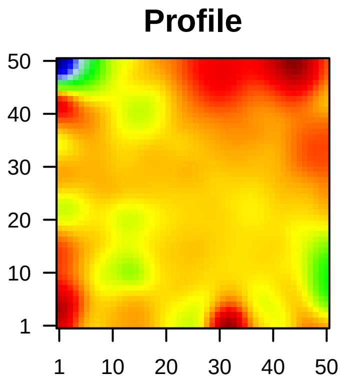
<FC> = 0.55

<shrinkage−t> = 19.5

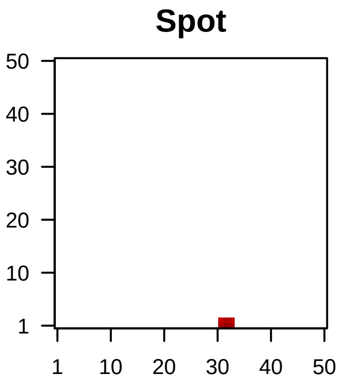
<p−value> = 0

<fdr> = 0.33

Profile



Spot



Local Genelist

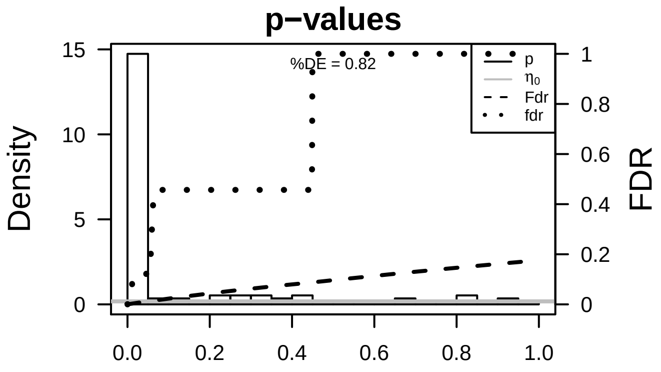
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3627	1.5	2e−16	6e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
2	6373	1.77	2e−16	6e−16	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;A
3	94240	1.18	2e−16	6e−16	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
4	10866	1.28	2e−16	6e−16	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
5	3106	1.27	2e−16	6e−16	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
6	3135	1.98	2e−16	6e−16	32 x 1	major histocompatibility complex, class I, G [Source:HGNC Sy
7	3136	1.63	2e−16	6e−16	32 x 1	
8	7453	1.26	2e−16	6e−16	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
9	3134	1.1	2e−15	3e−14	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
10	10581	1.01	2e−15	3e−14	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC S
11	629	1.09	4e−15	4e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
12	8519	1.08	6e−15	7e−13	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
13	3458	1.05	4e−14	1e−12	32 x 1	interferon, gamma [Source:HGNC Symbol;Acc:5438]
14	5698	1.03	1e−13	1e−12	32 x 1	proteasome (prosome, macropain) subunit, beta type, 9 [Sour
15	10346	1.03	2e−13	8e−12	32 x 1	tripartite motif containing 22 [Source:HGNC Symbol;Acc:163
16	6890	1	8e−13	8e−12	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
17	55601	0.99	1e−12	8e−12	32 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 60 [Source:HGN
18	23780	0.99	1e−12	2e−11	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
19	10964	0.98	2e−12	7e−11	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
20	2633	0.96	6e−12	2e−10	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	49.64	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
2	45.75	NULL	29 / 51	BP	type I interferon signaling pathway
3	43.25	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
4	39.96	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	38.37	NULL	7 / 10	CC	MHC class I protein complex
6	37.11	NULL	1 / 2	miRNA target	miR−152
7	35.94	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	34.95	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	33.89	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	33.68	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
11	33.14	NULL	31 / 123	BP	defense response to virus
12	31.68	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
13	31.01	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
14	30.59	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	30.37	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
16	29.65	NULL	7 / 18	MF	peptide antigen binding
17	29.52	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
18	27.6	NULL	13 / 31	BP	negative regulation of viral genome replication
19	27.41	NULL	27 / 109	BP	response to virus
20	27.29	NULL	1 / 3	miRNA target	miR−148a
21	26.72	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
22	26.01	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
23	25.94	NULL	34 / 204	BP	cytokine−mediated signaling pathway
24	25.45	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
25	25.3	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
26	23.61	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
27	23.3	NULL	3 / 5	GSEA C2	BROWNE_INTERFERON_RESPONSIVE_GENES
28	22.2	NULL	9 / 47	BP	antigen processing and presentation
29	21.84	NULL	28 / 312	BP	immune response
30	20.98	NULL	2 / 10	BP	positive regulation of cAMP−mediated signaling
31	20.63	NULL	5 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
32	20.48	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
33	20.4	NULL	12 / 70	BP	antigen processing and presentation of exogenous peptide antigen
34	19.93	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
35	19.78	NULL	12 / 74	BP	antigen processing and presentation of exogenous peptide antigen
36	19.5	NULL	46 / 572	Disease	GUDJ_psoriasis up
37	19.11	NULL	5 / 18	BP	response to interferon−gamma
38	18.91	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
39	18.84	NULL	2 / 12	BP	positive regulation of leukocyte chemotaxis
40	18.84	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA

p−values



GW_130

Local Summary

%DE = 0.79

metagenes = 8

genes = 143

genes in genesets = 141

genes with fdr < 0.1 = 88 (65 + / 23 −)

genes with fdr < 0.05 = 73 (53 + / 20 −)

genes with fdr < 0.01 = 67 (50 + / 17 −)

<r> metagenes = 0.98

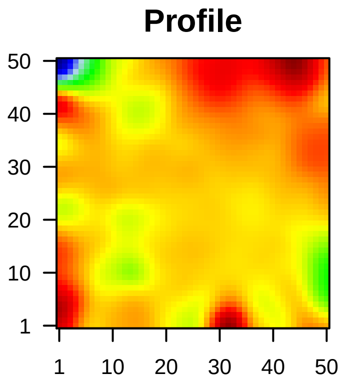
<r> genes = 0.38

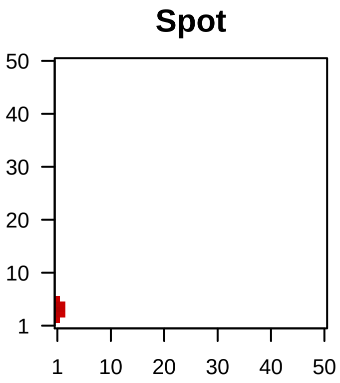
<FC> = 0.27

<shrinkage−t> = 9.5

<p−value> = 0

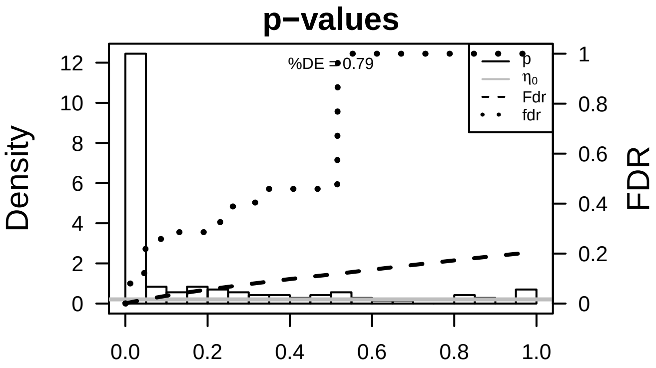
<fdr> = 0.46





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10409	−1.25	2e−16	5e−16	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
2	79783	1.42	2e−16	5e−16	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
3	768	1.42	2e−16	5e−16	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
4	857	1.43	2e−16	5e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
5	1687	1.17	2e−16	5e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
6	2201	1.61	2e−16	5e−16	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
7	10468	1.54	2e−16	5e−16	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
8	3918	1.44	2e−16	5e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
9	4322	2.25	2e−16	5e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
10	4907	1.21	2e−16	5e−16	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
11	169611	1.48	2e−16	5e−16	1 x 5	olfactomedin−like 2A [Source:HGNC Symbol;Acc:27270]
12	5328	1.29	2e−16	5e−16	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
13	7045	−1.21	2e−16	5e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
14	3371	1.17	2e−16	5e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
15	10644	1.11	1e−15	1e−13	1 x 6	insulin−like growth factor 2 mRNA binding protein 2 [Source:
16	8727	1.09	6e−15	2e−13	1 x 5	catenin (cadherin−associated protein), alpha−like 1 [Source:
17	4489	0.98	1e−14	3e−12	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
18	3909	1.03	1e−13	3e−12	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
19	4502	1.02	2e−13	3e−11	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
20	3486	−0.99	1e−12	5e−11	1 x 6	insulin−like growth factor binding protein 3 [Source:HGNC Sy



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.24	NULL	3 / 10	BP	cellular response to zinc ion
2	17.01	NULL	3 / 12	BP	hemidesmosome assembly
3	15.13	NULL	1 / 8	miRNA target	miR−9
4	14.41	NULL	3 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC
5	13.68	NULL	3 / 15	BP	negative regulation of growth
6	13.65	NULL	2 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
7	13.4	NULL	2 / 7	MMML CGS	MACIEJ_MMML 13
8	13.26	NULL	2 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
9	12.65	NULL	3 / 12	MF	activin binding
10	11.65	NULL	3 / 15	BP	negative regulation of anoikis
11	11.42	NULL	1 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
12	11.38	NULL	2 / 13	BP	hematopoietic progenitor cell differentiation
13	10.76	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
14	10.64	NULL	2 / 15	GSEA C2	MUELLER_METHYLATED_IN_GLIOBLASTOMA
15	10.53	NULL	1 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
16	10.23	NULL	1 / 2	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
17	10.15	NULL	1 / 16	GSEA C2	MURATA_VIRULENCE_OF_H_PILORI
18	9.98	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
19	9.98	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
20	9.6	NULL	2 / 13	BP	cellular response to cadmium ion
21	9.58	NULL	2 / 16	BP	negative regulation of peptidyl−serine phosphorylation
22	9.4	NULL	3 / 16	CC	microvillus membrane
23	9.34	NULL	1 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
24	9.22	NULL	24 / 242	BP	extracellular matrix organization
25	9.21	NULL	3 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
26	9.08	NULL	2 / 10	BP	positive regulation of peptidase activity
27	9.06	NULL	2 / 15	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP
28	8.52	NULL	1 / 12	GSEA C2	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_DN
29	8.38	NULL	1 / 10	CC	acrosomal membrane
30	8.38	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
31	8.38	NULL	1 / 10	GSEA C2	REACTOME_METABOLISM_OF_NITRIC_OXIDE
32	8.15	NULL	1 / 12	MF	heparan sulfate proteoglycan binding
33	8.08	NULL	4 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
34	8.04	NULL	1 / 5	miRNA target	miR−126
35	7.95	NULL	2 / 32	BP	positive regulation of intrinsic apoptotic signaling pathway
36	7.94	NULL	2 / 13	Cancer	GENTLES_modul16
37	7.93	NULL	1 / 11	GSEA C2	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
38	7.93	NULL	1 / 11	GSEA C2	TRACEY_RESISTANCE_TO_IFNA2_DN
39	7.93	NULL	1 / 11	GSEA C2	REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_
40	7.91	NULL	9 / 151	BP	response to hypoxia

GW_130

Local Summary

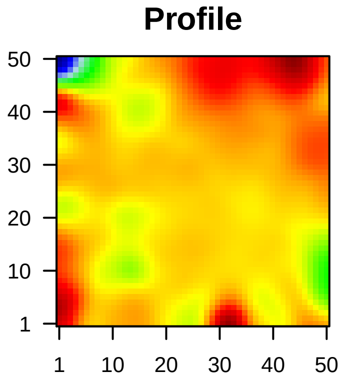
%DE = 0.52
metagenes = 25
genes = 374
genes in genesets = 371

genes with fdr < 0.1 = 143 (138 + / 5 −)
genes with fdr < 0.05 = 102 (98 + / 4 −)
genes with fdr < 0.01 = 66 (63 + / 3 −)

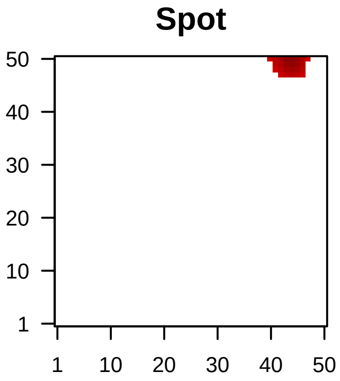
<r> metagenes = 0.94
<r> genes = 0.37

<FC> = 0.24
<shrinkage−t> = 8.47
<p−value> = 0.01
<fdr> = 0.65

Profile



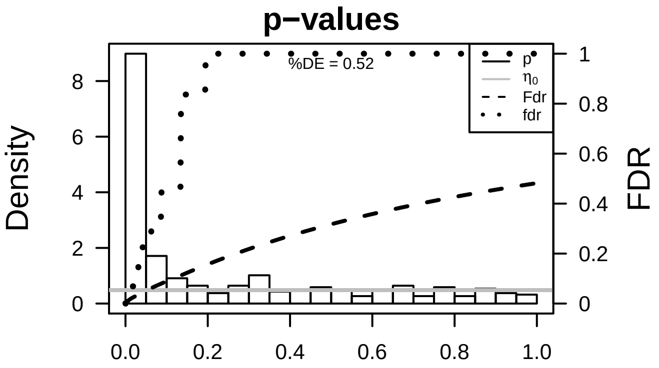
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	891	1.11	2e−15	1e−10	44 x 49	cyclin B1 [Source:HGNC Symbol;Acc:1579]
2	55872	1	7e−13	8e−10	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
3	116832	0.96	5e−12	7e−09	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:17094
4	1164	0.9	8e−11	7e−09	44 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
5	51659	0.9	8e−11	6e−08	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
6	26255	0.87	4e−10	3e−07	44 x 48	pituitary tumor−transforming 3, pseudogene [Source:HGNC
7	10732	0.82	4e−09	3e−07	40 x 50	transcription factor−like 5 (basic helix−loop−helix) [Source:HG
8	137392	0.81	5e−09	3e−07	40 x 50	family with sequence similarity 92, member A1 [Source:HGN
9	54443	0.81	6e−09	5e−07	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
10	9787	0.8	9e−09	5e−07	43 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
11	10112	0.79	1e−08	5e−07	44 x 49	kinesin family member 20A [Source:HGNC Symbol;Acc:9787
12	8833	0.79	1e−08	5e−07	45 x 50	guanine monphosphate synthase [Source:HGNC Symbol;Acc
13	387103	0.78	2e−08	2e−06	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
14	7298	0.77	3e−08	3e−06	46 x 48	thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
15	7083	0.76	5e−08	3e−06	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
16	7991	−0.76	5e−08	1e−05	46 x 50	tumor suppressor candidate 3 [Source:HGNC Symbol;Acc:30
17	64151	0.74	1e−07	2e−05	44 x 48	non−SMC condensin I complex, subunit G [Source:HGNC Sy
18	4291	0.72	2e−07	2e−05	46 x 50	myeloid leukemia factor 1 [Source:HGNC Symbol;Acc:7125]
19	26872	0.71	3e−07	3e−05	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
20	890	0.69	6e−07	3e−05	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	52.01	NULL	87 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	52.01	NULL	87 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	30.91	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	29.2	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
5	25.23	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
6	25.12	NULL	5 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
7	24.57	NULL	95 / 370	BP	mitotic cell cycle
8	24.57	NULL	23 / 57	Glio	developing astrocytes
9	23.69	NULL	12 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
10	23.6	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	23.12	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
12	22.72	NULL	12 / 18	BP	spindle organization
13	21.7	NULL	8 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
14	21.02	NULL	87 / 530	Cancer	Lembcke_Normal vs Adenoma
15	20.15	NULL	8 / 15	GSEA C2	LY_AGING_MIDDLE_DN
16	19.77	NULL	8 / 11	BP	mitotic metaphase plate congression
17	19.34	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
18	18.74	NULL	8 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
19	18.62	NULL	7 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
20	18.52	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
21	18.11	NULL	66 / 572	Disease	GUDJ_psoriasis up
22	17.92	NULL	47 / 232	BP	mitosis
23	16.69	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
24	16.39	NULL	20 / 56	CC	chromosome, centromeric region
25	16.07	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
26	15.15	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
27	14.1	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
28	14.05	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
29	13.96	NULL	6 / 13	GSEA C2	REN_BOUND_BY_E2F
30	13.87	NULL	3 / 6	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_DN
31	13.76	NULL	4 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
32	13.76	NULL	9 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
33	13.38	NULL	17 / 67	BP	chromosome segregation
34	13.35	NULL	6 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
35	13.34	NULL	8 / 15	GSEA C2	CHANG_CYCLING_GENES
36	13.21	NULL	36 / 149	BP	DNA replication
37	13.14	NULL	5 / 15	GSEA C2	REACTOME_CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2
38	13.04	NULL	5 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
39	12.86	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
40	12.85	NULL	10 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN

GW_130

Local Summary

%DE = 0.89

metagenes = 8

genes = 137

genes in genesets = 134

genes with fdr < 0.1 = 115 (4 + / 111 −)

genes with fdr < 0.05 = 115 (4 + / 111 −)

genes with fdr < 0.01 = 109 (4 + / 105 −)

<r> metagenes = 0.99

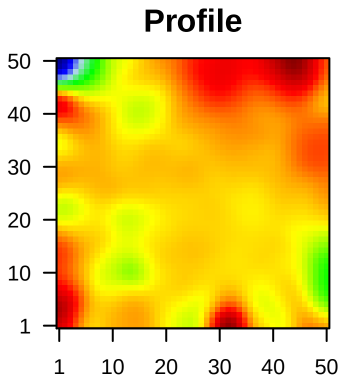
<r> genes = 0.52

<FC> = −0.86

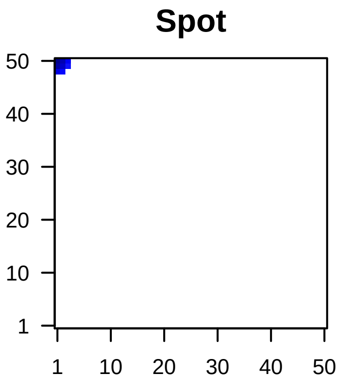
<shrinkage−t> = −30.52

<p−value> = 0

<fdr> = 0.16



Profile



Spot

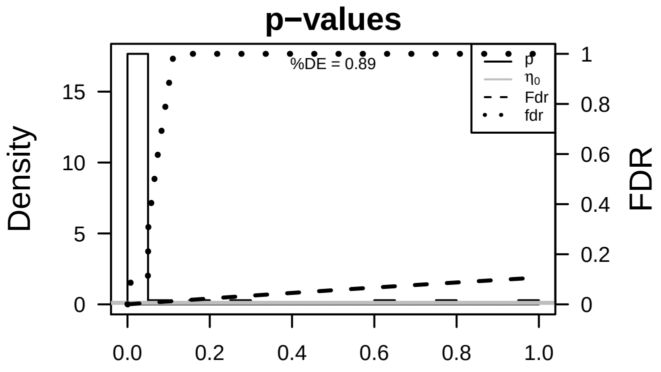
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−2.01	2e−16	8e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	−1.52	2e−16	8e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	222	−1.46	2e−16	8e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	387695	−1.59	2e−16	8e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
5	100133941	−1.49	2e−16	8e−17	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
6	22802	−1.59	2e−16	8e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	−1.43	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	−1.33	2e−16	8e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	−1.63	2e−16	8e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	92196	−1.19	2e−16	8e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
11	414325	−1.71	2e−16	8e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	−2.54	2e−16	8e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1824	−1.14	2e−16	8e−17	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
14	1828	−1.4	2e−16	8e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	3851	−2.15	2e−16	8e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
16	84648	−1.81	2e−16	8e−17	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
17	4118	−1.28	2e−16	8e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
18	5266	−1.05	2e−16	8e−17	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
19	51458	−1.38	2e−16	8e−17	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
20	84659	−1.41	2e−16	8e−17	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−50.31	NULL	63 / 135	H.Tiss	WIRTH_Mucosa
2	−45.7	NULL	14 / 21	CC	cornified envelope
3	−38.67	NULL	16 / 42	BP	keratinization
4	−35.05	NULL	19 / 53	BP	keratinocyte differentiation
5	−27.53	NULL	65 / 572	Disease	GUDJ_psoriasis up
6	−26.88	NULL	16 / 76	BP	epidermis development
7	−19.95	NULL	4 / 10	MF	RAGE receptor binding
8	−19.9	NULL	8 / 19	BP	peptide cross−linking
9	−17.8	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	−16.4	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	−16.14	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−14.85	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
13	−14.44	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
14	−13.97	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−13.69	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	−13.2	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
17	−11.93	NULL	3 / 12	BP	cellular aldehyde metabolic process
18	−11.39	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
19	−11.22	NULL	6 / 13	BP	negative regulation of peptidase activity
20	−10.85	NULL	5 / 21	CC	desmosome
21	−10.78	NULL	6 / 73	BP	defense response to bacterium
22	−10.73	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
23	−10.43	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
24	−10.14	NULL	41 / 1182	CC	extracellular region
25	−9.9	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
26	−9.89	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
27	−9.51	NULL	2 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
28	−8.9	NULL	4 / 38	BP	epithelial cell differentiation
29	−8.88	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
30	−8.74	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
31	−8.67	NULL	1 / 5	miRNA target	miR−196a
32	−8.54	NULL	2 / 14	BP	defense response to fungus
33	−8.52	NULL	4 / 23	MF	peptidase inhibitor activity
34	−8.02	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
35	−7.76	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
36	−7.69	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
37	−7.53	NULL	1 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
38	−7.49	NULL	1 / 15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
39	−7.42	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
40	−7.33	NULL	8 / 52	BP	negative regulation of endopeptidase activity



p−values