GW_025

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1759 (1036 + / 723 −)

genes with fdr < 0.1 = 1272 (799 + / 473 −)

genes with fdr < 0.05 = 969 (640 + / 329 −)

genes with fdr < 0.01 = 681 (481 + / 200 −)

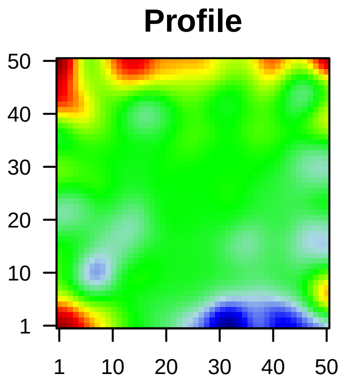
genes in genesets = 16332

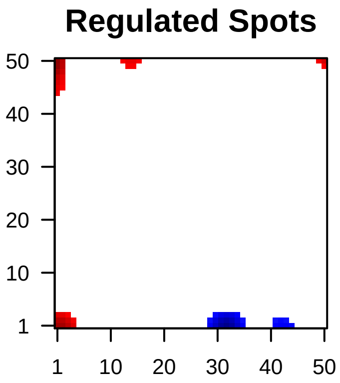
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

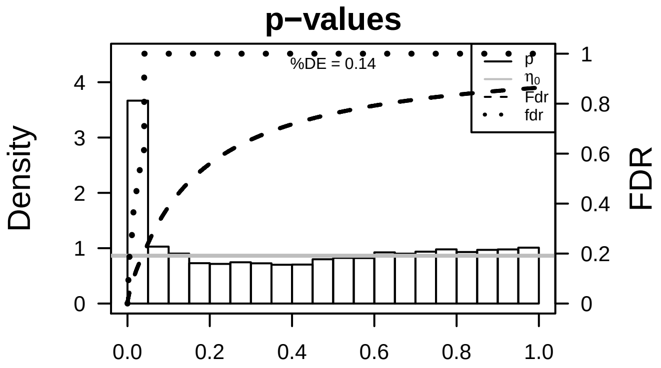
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	24	1.67	2e−16	4e−14	16 x 50	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
2	131	1.78	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.94	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.82	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	1.64	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
6	1109	1.52	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
7	216	1.95	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
8	218	1.92	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
9	655	1.71	2e−16	4e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
10	387695	1.24	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
11	339512	1.39	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
12	92747	1.26	2e−16	4e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
13	56892	1.3	2e−16	4e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
14	51806	−1.48	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
15	57172	1.32	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
16	9073	1.65	2e−16	4e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
17	49860	1.76	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1469	1.31	2e−16	4e−14	9 x 6	cystatin SN [Source:HGNC Symbol;Acc:2473]
19	2919	1.45	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
20	6372	1.51	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.11	NULL	135	H.Tiss	WIRTH_Mucosa
2	12.09	NULL	21	CC	cornified envelope
3	11.88	NULL	53	BP	keratinocyte differentiation
4	11.67	NULL	42	BP	keratinization
5	11.52	NULL	1182	CC	extracellular region
6	11.52	NULL	76	BP	epidermis development
7	10.48	NULL	190	CC	extracellular matrix
8	10.43	NULL	534	Chr	Chr 8
9	9.87	NULL	683	CC	extracellular space
10	9.81	NULL	13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
11	9.81	NULL	242	BP	extracellular matrix organization
12	9.24	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
13	9.14	NULL	519	Chr	Chr 14
14	9.14	NULL	19	BP	peptide cross−linking
15	8.84	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
16	8.34	NULL	64	BP	collagen catabolic process
17	8.3	NULL	250	Lymphoma	LENZ_Stromal signature 1
18	8.02	NULL	186	MF	structural molecule activity
19	7.97	NULL	183	CC	proteinaceous extracellular matrix
20	7.82	NULL	22	MF	insulin−like growth factor binding
Underexpressed					
1	−12.03	NULL	51	BP	type I interferon signaling pathway
2	−11.28	NULL	633	Chr	Chr 9
3	−11.12	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	−10.91	NULL	1135	Chr	Chr 19
5	−10.54	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	−10	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
7	−9.77	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
8	−9.65	NULL	123	BP	defense response to virus
9	−8.97	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	−8.77	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
11	−8.76	NULL	417	H.Tiss	WIRTH_Immune system
12	−8.32	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
13	−8.23	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
14	−8.17	NULL	31	BP	negative regulation of viral genome replication
15	−8.08	NULL	204	BP	cytokine−mediated signaling pathway
16	−7.4	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	−7.34	NULL	60	BP	interferon−gamma−mediated signaling pathway
18	−7.08	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
19	−6.86	NULL	14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
20	−6.83	NULL	4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP

GW_025

Local Summary

%DE = 0.79

metagenes = 11

genes = 174

genes in genesets = 174

genes with fdr < 0.1 = 95 (89 + / 6 −)

genes with fdr < 0.05 = 89 (84 + / 5 −)

genes with fdr < 0.01 = 64 (61 + / 3 −)

<r> metagenes = 0.98

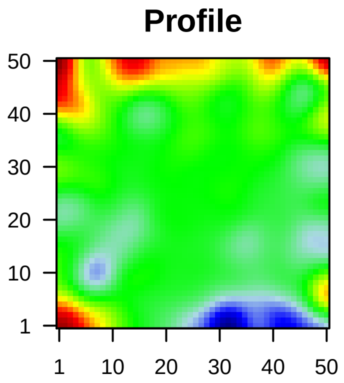
<r> genes = 0.45

<FC> = 0.41

<shrinkage−t> = 14.27

<p−value> = 0

<fdr> = 0.49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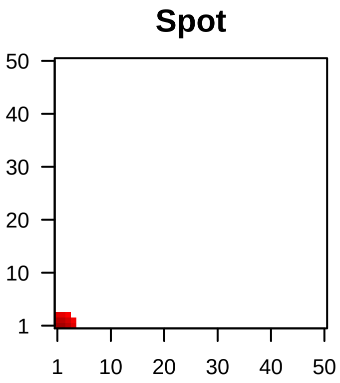
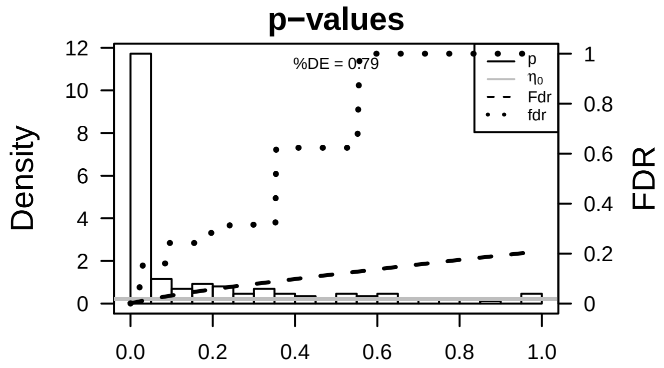

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2919	1.45	2e−16	9e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
2	6372	1.51	2e−16	9e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
3	11009	1.26	2e−16	9e−16	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
4	4312	1.97	2e−16	9e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
5	4319	1.44	2e−16	9e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
6	4314	2.55	2e−16	9e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
7	4316	1.44	2e−16	9e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
8	5054	1.73	2e−16	9e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
9	7057	1.23	2e−16	9e−16	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
10	3569	1.18	1e−15	2e−14	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
11	1306	1.17	2e−15	2e−13	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
12	3371	1.13	1e−14	2e−13	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
13	3576	1.13	1e−14	7e−13	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
14	6423	1.11	4e−14	7e−13	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
15	51050	1.1	7e−14	7e−13	1 x 2	peptidase inhibitor 15 [Source:HGNC Symbol;Acc:8946]
16	3491	1.1	7e−14	7e−13	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
17	6374	1.09	1e−13	7e−13	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
18	26585	1.09	1e−13	2e−12	2 x 1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbo
19	1009	1.08	2e−13	2e−10	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC
20	5270	0.99	1e−11	2e−10	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.46	NULL	55 / 190	CC	extracellular matrix
2	31.01	NULL	30 / 69	BP	extracellular matrix disassembly
3	30.53	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	30.34	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
5	29.82	NULL	27 / 64	BP	collagen catabolic process
6	28.15	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
7	26.28	NULL	6 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
8	26.24	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
9	25.78	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
10	25.28	NULL	54 / 242	BP	extracellular matrix organization
11	25	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
12	24.63	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
13	24.6	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
14	23.17	NULL	8 / 12	miRNA target	miR−29c
15	22.94	NULL	63 / 683	CC	extracellular space
16	22.59	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
17	21.57	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
18	21.32	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
19	20.49	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
20	20.46	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
21	19.78	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
22	19.75	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
23	19.56	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
24	19.51	NULL	12 / 35	Glio	Colman_survival_associated
25	19.39	NULL	58 / 250	Lymphoma	LENZ_Stromal signature 1
26	19.32	NULL	30 / 183	CC	proteinaceous extracellular matrix
27	19.28	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
28	18.86	NULL	3 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
29	18.56	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
30	18.32	NULL	13 / 37	BP	collagen fibril organization
31	18.27	NULL	82 / 1182	CC	extracellular region
32	18.16	NULL	2 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
33	17.77	NULL	6 / 16	GSEA C2	ZHU_CMV_24_HR_DN
34	17.77	NULL	6 / 16	GSEA C2	ZHU_CMV_ALL_DN
35	17.64	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
36	17.34	NULL	3 / 13	GSEA C2	REACTOME_FORMATION_OF_PLATELET_PLUG
37	17.34	NULL	3 / 13	GSEA C2	REACTOME_PLATELET_ACTIVATION
38	17.27	NULL	3 / 14	GSEA C2	KOYAMA_SEMA3B_TARGETS_UP
39	16.85	NULL	7 / 11	MF	platelet−derived growth factor binding
40	16.43	NULL	52 / 553	Cancer	Lembcke_Colonic Inflammation

GW_025

Local Summary

%DE = 0.69

metagenes = 13

genes = 229

genes in genesets = 224

genes with fdr < 0.1 = 118 (103 + / 15 −)

genes with fdr < 0.05 = 102 (91 + / 11 −)

genes with fdr < 0.01 = 90 (82 + / 8 −)

<r> metagenes = 0.93

<r> genes = 0.42

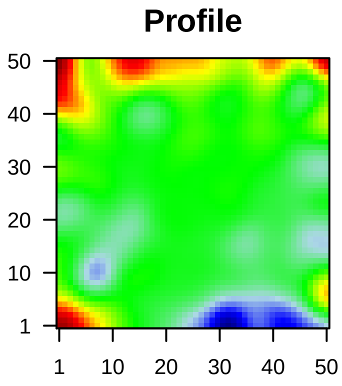
<FC> = 0.4

<shrinkage−t> = 14.04

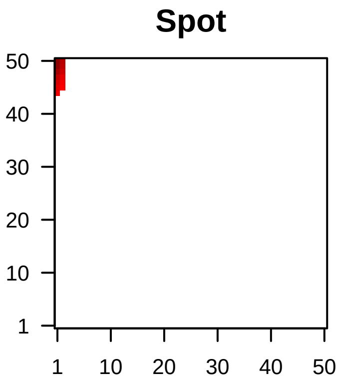
<p−value> = 0

<fdr> = 0.5

Profile



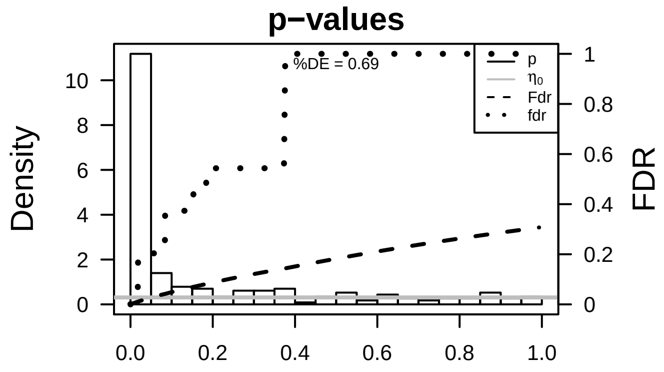
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.78	2e−16	7e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.94	2e−16	7e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	1.82	2e−16	7e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	1.64	2e−16	7e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	218	1.92	2e−16	7e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	387695	1.24	2e−16	7e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
7	49860	1.76	2e−16	7e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
8	2877	2.51	2e−16	7e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
9	3489	1.49	2e−16	7e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
10	3868	1.34	2e−16	7e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
11	9119	1.6	2e−16	7e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
12	388533	1.46	2e−16	7e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
13	4014	2.34	2e−16	7e−16	2 x 48	loricrin [Source:HGNC Symbol;Acc:6663]
14	4753	1.98	2e−16	7e−16	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
15	338324	1.78	2e−16	7e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
16	143686	1.64	2e−16	7e−16	1 x 44	sestrin 3 [Source:HGNC Symbol;Acc:23060]
17	84651	1.21	2e−16	7e−16	1 x 50	serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
18	6699	1.26	2e−16	7e−16	1 x 50	small proline−rich protein 1B [Source:HGNC Symbol;Acc:112
19	6700	1.47	2e−16	7e−16	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
20	6702	1.6	2e−16	7e−16	1 x 50	

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.96	NULL	18 / 21	CC	cornified envelope
2	35.1	NULL	24 / 53	BP	keratinocyte differentiation
3	34.68	NULL	19 / 42	BP	keratinization
4	32.63	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
5	23.79	NULL	23 / 76	BP	epidermis development
6	23.11	NULL	10 / 19	BP	peptide cross−linking
7	18.12	NULL	26 / 186	MF	structural molecule activity
8	17.91	NULL	12 / 44	CC	keratin filament
9	17.37	NULL	93 / 572	Disease	GUDJ_psoriasis up
10	16.33	NULL	19 / 82	CC	intermediate filament
11	15.69	NULL	3 / 12	BP	cellular aldehyde metabolic process
12	13.09	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	10.99	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
14	10.54	NULL	12 / 21	CC	desmosome
15	10.37	NULL	3 / 15	MF	retinol dehydrogenase activity
16	10.31	NULL	2 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
17	10.22	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
18	10.21	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
19	9.78	NULL	4 / 39	BP	retinoid metabolic process
20	9.49	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
21	9.27	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
22	9.27	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
23	8.84	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
24	8.59	NULL	1 / 13	BP	temperature homeostasis
25	8.52	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
26	8.48	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
27	8.41	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
28	8.39	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
29	8.28	NULL	3 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
30	8.23	NULL	1 / 14	MF	glutathione peroxidase activity
31	8.19	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
32	8.05	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
33	7.89	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
34	7.85	NULL	9 / 82	MF	structural constituent of cytoskeleton
35	7.85	NULL	1 / 10	GSEA C2	KIM_MYCL1_AMPLIFICATION_TARGETS_UP
36	7.83	NULL	4 / 25	BP	response to zinc ion
37	7.8	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
38	7.76	NULL	2 / 12	GSEA C2	ODONNELL_METASTASIS_DN
39	7.75	NULL	7 / 51	MF	protein binding, bridging
40	7.7	NULL	1 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM

GW_025

Local Summary

%DE = 0.74

metagenes = 6

genes = 111

genes in genesets = 110

genes with fdr < 0.1 = 67 (61 + / 6 −)

genes with fdr < 0.05 = 51 (47 + / 4 −)

genes with fdr < 0.01 = 38 (35 + / 3 −)

<r> metagenes = 0.99

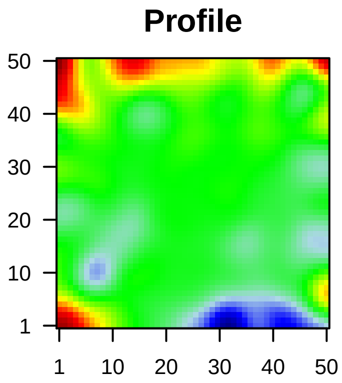
<r> genes = 0.26

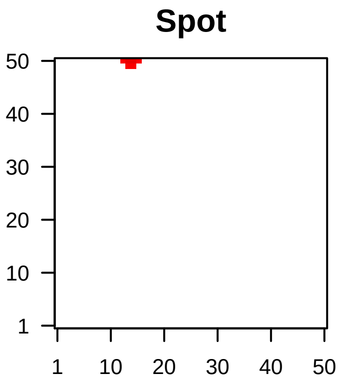
<FC> = 0.35

<shrinkage−t> = 12.16

<p−value> = 0

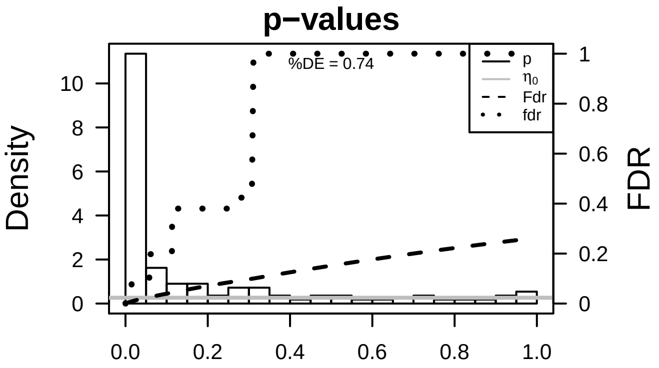
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	24	1.67	2e−16	1e−15	16 x 50	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
2	1109	1.52	2e−16	1e−15	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
3	1956	1.37	2e−16	1e−15	15 x 50	epidermal growth factor receptor [Source:HGNC Symbol;Acc:
4	4741	1.35	2e−16	1e−15	15 x 50	neurofilament, medium polypeptide [Source:HGNC Symbol;A
5	5217	1.44	2e−16	1e−15	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]
6	7102	1.43	2e−16	1e−15	15 x 50	tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
7	100288413	1.1	7e−14	1e−12	14 x 50	endogenous retrovirus group MER34, member 1 [Source:HG
8	145407	1.09	9e−14	1e−12	16 x 50	chromosome 14 open reading frame 37 [Source:HGNC Sym
9	65997	1.09	1e−13	7e−11	15 x 50	RAS−like, family 11, member B [Source:HGNC Symbol;Acc:2
10	7062	1.03	2e−12	4e−09	13 x 50	trichohyalin [Source:HGNC Symbol;Acc:11791]
11	483	0.94	2e−10	3e−08	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
12	4055	0.9	1e−09	1e−07	14 x 50	lymphotoxin beta receptor (TNFR superfamily, member 3) [Sc
13	1646	0.86	5e−09	3e−07	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
14	5909	−0.83	2e−08	7e−07	14 x 50	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
15	10457	0.81	4e−08	7e−07	13 x 50	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
16	23428	0.79	6e−08	1e−05	14 x 50	solute carrier family 7 (amino acid transporter light chain, L sy
17	1066	0.73	6e−07	2e−05	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
18	2736	0.71	1e−06	2e−05	14 x 50	GLI family zinc finger 2 [Source:HGNC Symbol;Acc:4318]
19	57834	0.7	2e−06	4e−05	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
20	8626	0.68	4e−06	2e−04	13 x 50	tumor protein p63 [Source:HGNC Symbol;Acc:15979]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.93	NULL	1 / 4	miRNA target	miR−128b
2	18.93	NULL	1 / 4	miRNA target	miR−7
3	16.42	NULL	1 / 5	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
4	16.42	NULL	1 / 5	GSEA C2	DING_LUNG_CANCER_MUTATED_RECURRENTLY
5	13.9	NULL	3 / 39	BP	retinoid metabolic process
6	13.34	NULL	1 / 7	GSEA C2	RUGO_STRESS_RESPONSE_SUBSET_F
7	13.34	NULL	1 / 7	GSEA C2	KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION
8	12.46	NULL	1 / 11	CC	photoreceptor disc membrane
9	12.31	NULL	1 / 8	GSEA C2	TCGA_GLIOBLASTOMA_MUTATED
10	11.28	NULL	1 / 10	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESISTANCE
11	11.16	NULL	2 / 14	BP	bile acid and bile salt transport
12	10.83	NULL	1 / 14	MF	phospholipid−translocating ATPase activity
13	10.78	NULL	1 / 10	BP	ovulation cycle
14	10.78	NULL	1 / 10	GSEA C2	HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2
15	10.78	NULL	1 / 10	GSEA C2	BIOCARTA_EGFR_SMRTE_PATHWAY
16	10.77	NULL	1 / 12	BP	androgen metabolic process
17	10.63	NULL	3 / 63	BP	phototransduction, visible light
18	10.61	NULL	3 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
19	10.51	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
20	10.43	NULL	2 / 16	GSEA C2	REACTOME_BASIGIN_INTERACTIONS
21	10.19	NULL	1 / 11	BP	positive regulation of catenin import into nucleus
22	10.19	NULL	1 / 11	BP	response to lipid
23	10.19	NULL	1 / 11	GSEA C2	REACTOME_GAB1_SIGNALOSOME
24	10.02	NULL	1 / 16	GSEA C2	ASTIER_INTEGRIN_SIGNALING
25	10.02	NULL	3 / 35	BP	hair follicle development
26	9.68	NULL	1 / 12	BP	positive regulation of synaptic transmission, glutamatergic
27	9.68	NULL	1 / 12	BP	regulation of peptidyl−tyrosine phosphorylation
28	9.24	NULL	1 / 13	GSEA C2	SUZUKI_AMPLIFIED_IN_ORAL_CANCER
29	9.24	NULL	1 / 13	GSEA C2	HASINA_NOL7_TARGETS_DN
30	9.24	NULL	1 / 13	GSEA C2	BIOCARTA_CBL_PATHWAY
31	9.24	NULL	1 / 13	GSEA C2	REACTOME_GRB2_EVENTS_IN_EGFR_SIGNALING
32	9.23	NULL	2 / 16	GSEA C2	KEGG_DORSO_VENTRAL_AXIS_FORMATION
33	9.16	NULL	5 / 32	MF	ATPase activity, coupled to transmembrane movement of substanc
34	9.15	NULL	1 / 13	BP	intermediate filament cytoskeleton organization
35	8.95	NULL	2 / 16	GSEA C2	BIOCARTA_TFF_PATHWAY
36	8.9	NULL	1 / 15	Cancer	GENTLES_modul13
37	8.9	NULL	1 / 15	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP
38	8.9	NULL	1 / 15	GSEA C2	VALK_AML_CLUSTER_4
39	8.85	NULL	1 / 14	BP	cellular response to epidermal growth factor stimulus
40	8.85	NULL	1 / 14	BP	cellular response to estradiol stimulus

GW_025

Local Summary

%DE = 0.59
metagenes = 3
genes = 106
genes in genesets = 105

genes with fdr < 0.1 = 54 (49 + / 5 −)
genes with fdr < 0.05 = 48 (44 + / 4 −)
genes with fdr < 0.01 = 40 (38 + / 2 −)

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<r> genes = 0.33

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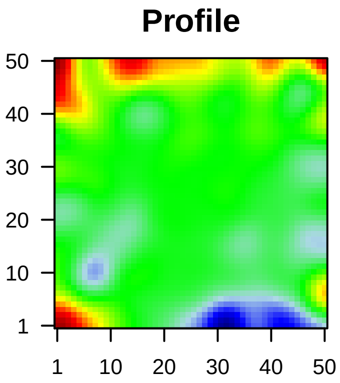
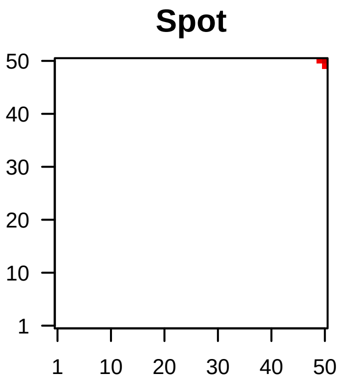
<shrinkage−t> = 15.45
<p−value> = 0
<fdr> = 0.48

Profile



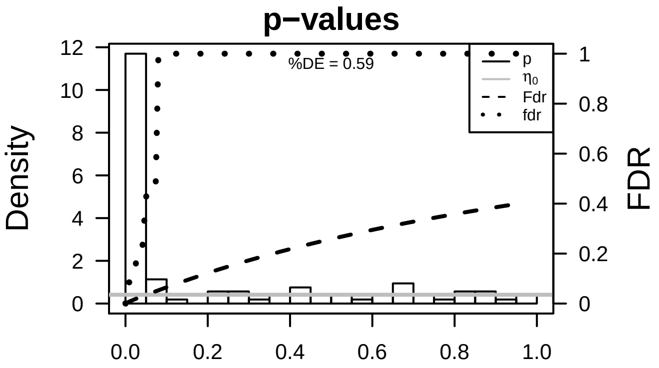
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.95	2e−16	9e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	655	1.71	2e−16	9e−16	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
3	339512	1.39	2e−16	9e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	1780	1.28	2e−16	9e−16	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
5	4072	1.44	2e−16	9e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
6	4915	1.22	2e−16	9e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
7	4922	3.91	2e−16	9e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
8	54575	1.63	2e−16	9e−16	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A10 [Sour
9	54578	1.3	2e−16	9e−16	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
10	256764	1.87	2e−16	9e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
11	79844	1.46	2e−16	9e−16	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
12	2730	1.15	4e−15	7e−14	50 x 50	glutamate−cysteine ligase, modifier subunit [Source:HGNC S
13	928	1.15	4e−15	7e−14	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
14	57110	1.15	5e−15	3e−13	50 x 50	HRAS−like suppressor [Source:HGNC Symbol;Acc:14922]
15	3866	1.12	2e−14	3e−13	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
16	4953	1.12	2e−14	8e−11	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
17	26256	1.03	2e−12	8e−10	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
18	2719	0.98	2e−11	2e−09	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
19	214	0.96	7e−11	2e−09	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
20	1592	0.95	9e−11	9e−08	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sour

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.03	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	25.92	NULL	3 / 13	BP	regulation of blood vessel size
3	21.86	NULL	1 / 11	Glio	neurons_glio
4	18.22	NULL	1 / 15	MF	neuropeptide hormone activity
5	16.48	NULL	3 / 15	BP	lipid glycosylation
6	15.76	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
7	15.76	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
8	15.51	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	15.03	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
10	14.28	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
11	13.56	NULL	2 / 15	MF	glucuronosyltransferase activity
12	13.37	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
13	12.77	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
14	12.22	NULL	2 / 12	BP	cellular aldehyde metabolic process
15	12.22	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
16	12.22	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
17	11.47	NULL	1 / 8	GSEA C2	MCCABE_HOXC6_TARGETS_UP
18	11.46	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
19	11.46	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
20	10.35	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
21	10.26	NULL	1 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
22	10.25	NULL	1 / 41	CC	transport vesicle
23	10	NULL	1 / 10	BP	branching involved in salivary gland morphogenesis
24	10	NULL	1 / 10	BP	mesonephros development
25	9.82	NULL	3 / 37	MF	transferase activity, transferring hexosyl groups
26	9.62	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
27	9.39	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
28	9.36	NULL	1 / 14	MF	Ras GTPase activator activity
29	9.36	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
30	9.36	NULL	1 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
31	9.29	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
32	9.23	NULL	1 / 6	GSEA C2	KORKOLA_CHORIOCARCINOMA_UP
33	8.98	NULL	1 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
34	8.97	NULL	2 / 14	CC	membrane−bounded vesicle
35	8.95	NULL	1 / 12	BP	positive regulation of peptidyl−threonine phosphorylation
36	8.95	NULL	1 / 12	Lymphoma	DAVE_BL UP
37	8.61	NULL	2 / 19	BP	anatomical structure formation involved in morphogenesis
38	8.59	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
39	8.58	NULL	1 / 5	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_DN
40	8.53	NULL	1 / 13	BP	response to vitamin D

GW_025

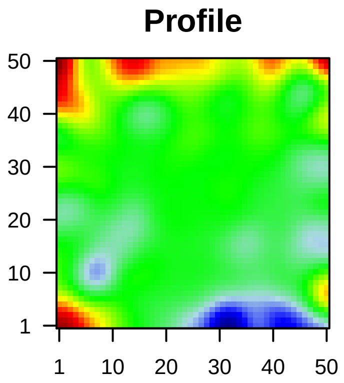
Local Summary

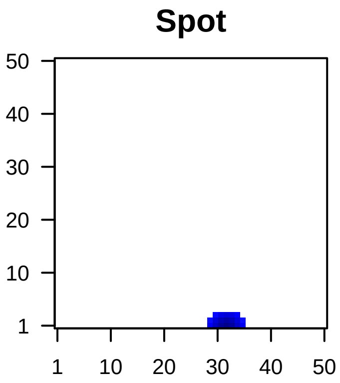
%DE = 0.85
metagenes = 19
genes = 181
genes in genesets = 178

genes with fdr < 0.1 = 127 (4 + / 123 −)
genes with fdr < 0.05 = 121 (4 + / 117 −)
genes with fdr < 0.01 = 98 (4 + / 94 −)

<r> metagenes = 0.94
<r> genes = 0.35

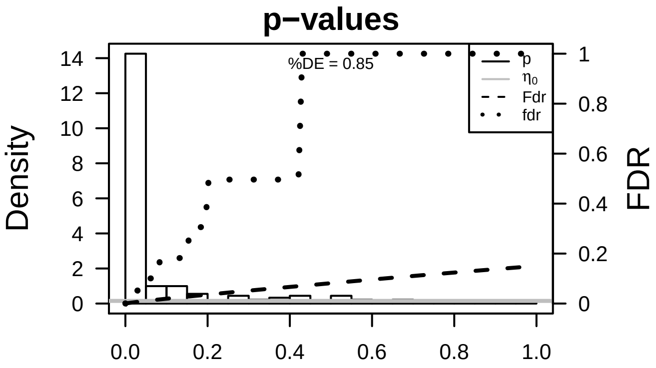
<FC> = −0.44
<shrinkage−t> = −15.39
<p−value> = 0
<fdr> = 0.38





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1591	1.39	2e−16	1e−15	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
2	10561	−1.24	2e−16	1e−15	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
3	10964	−1.68	2e−16	1e−15	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
4	9636	−1.6	2e−16	1e−15	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
5	4599	−1.16	2e−16	1e−15	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
6	2537	−1.17	1e−15	4e−12	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
7	51191	−1.08	2e−13	2e−11	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
8	3430	−1.04	1e−12	2e−11	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
9	6890	−1.04	1e−12	5e−11	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
10	684	−1.01	5e−12	5e−11	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
11	3665	−1.01	5e−12	8e−11	32 x 1	interferon regulatory factor 7 [Source:HGNC Symbol;Acc:612
12	3627	−1	8e−12	1e−10	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
13	94240	−0.99	1e−11	1e−10	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
14	85441	−0.99	2e−11	2e−10	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
15	6772	−0.98	3e−11	2e−10	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
16	64761	−0.97	4e−11	2e−10	32 x 1	poly (ADP−ribose) polymerase family, member 12 [Source:H
17	55008	−0.97	5e−11	2e−10	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
18	219285	−0.97	5e−11	4e−09	32 x 1	sterile alpha motif domain containing 9−like [Source:HGNC S
19	54739	−0.93	2e−10	5e−09	32 x 1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
20	51296	−0.92	4e−10	7e−09	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−49.78	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
2	−49.14	NULL	29 / 51	BP	type I interferon signaling pathway
3	−47.97	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	−45.72	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	−44.89	NULL	12 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
6	−43.51	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
7	−40.57	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	−39.22	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
9	−36.03	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	−35.37	NULL	33 / 123	BP	defense response to virus
11	−35.03	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
12	−34.69	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	−33.85	NULL	16 / 31	BP	negative regulation of viral genome replication
14	−33.31	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
15	−31.71	NULL	27 / 109	BP	response to virus
16	−28.64	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
17	−28.22	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
18	−27.51	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
19	−26.54	NULL	34 / 204	BP	cytokine−mediated signaling pathway
20	−25.64	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
21	−25.57	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
22	−24.5	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
23	−24.45	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
24	−24.38	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
25	−24.36	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
26	−22.49	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
27	−22.46	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
28	−22.11	NULL	5 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
29	−21.6	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
30	−21.57	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
31	−20.16	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
32	−19.78	NULL	51 / 572	Disease	GUDJ_psoriasis up
33	−19.47	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	−19.47	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	−19.47	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
36	−19.25	NULL	6 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
37	−19.06	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
38	−18.6	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
39	−18.49	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
40	−16.6	NULL	8 / 18	MF	peptide antigen binding

GW_025

Local Summary

%DE = 0.69

metagenes = 7

genes = 95

genes in genesets = 93

genes with fdr < 0.1 = 50 (2 + / 48 −)

genes with fdr < 0.05 = 49 (2 + / 47 −)

genes with fdr < 0.01 = 39 (1 + / 38 −)

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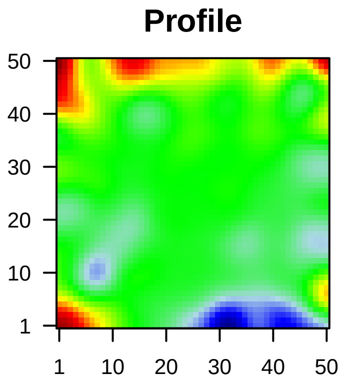
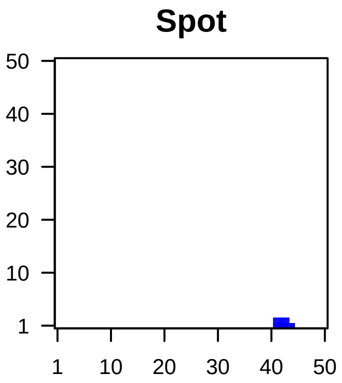
<p−value> = 0.01

<fdr> = 0.5


Profile


Spot

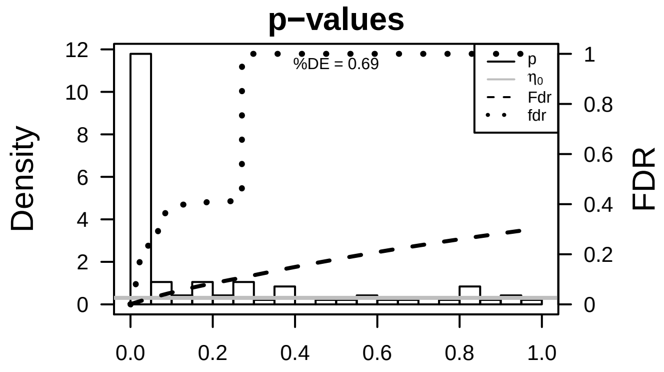
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	−0.94	2e−10	3e−07	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	401261	−0.84	1e−08	2e−06	41 x 1	
3	10908	−0.79	9e−08	4e−06	42 x 1	patatin−like phospholipase domain containing 6 [Source:HGN
4	348094	−0.76	2e−07	3e−05	43 x 1	ankyrin repeat and death domain containing 1A [Source:HGN
5	10347	−0.71	1e−06	4e−05	42 x 2	ATP−binding cassette, sub−family A (ABC1), member 7 [Sour
6	80233	−0.69	3e−06	9e−05	41 x 1	chromosome 17 open reading frame 70 [Source:HGNC Symb
7	4851	−0.65	9e−06	9e−05	42 x 1	notch 1 [Source:HGNC Symbol;Acc:7881]
8	51281	−0.65	9e−06	1e−04	42 x 1	ankyrin repeat and MYND domain containing 1 [Source:HGN
9	148867	−0.63	2e−05	1e−04	42 x 2	
10	79058	−0.63	2e−05	1e−04	41 x 1	alveolar soft part sarcoma chromosome region, candidate 1 [
11	7297	−0.62	2e−05	1e−04	44 x 1	tyrosine kinase 2 [Source:HGNC Symbol;Acc:12440]
12	30827	−0.62	2e−05	1e−03	43 x 1	CXXC finger protein 1 [Source:HGNC Symbol;Acc:24343]
13	11322	−0.57	1e−04	1e−03	44 x 1	transmembrane channel−like 6 [Source:HGNC Symbol;Acc:1
14	23466	0.55	2e−04	1e−03	41 x 1	chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
15	286257	−0.55	2e−04	1e−03	42 x 2	chromosome 9 open reading frame 142 [Source:HGNC Symb
16	375775	−0.54	2e−04	1e−03	41 x 1	patatin−like phospholipase domain containing 7 [Source:HGN
17	8175	−0.54	2e−04	1e−03	42 x 1	splicing factor 3a, subunit 2, 66kDa [Source:HGNC Symbol;A
18	808	−0.54	3e−04	1e−03	42 x 2	calmodulin 3 (phosphorylase kinase, delta) [Source:HGNC Sy
19	8837	−0.53	3e−04	1e−03	44 x 1	CASP8 and FADD−like apoptosis regulator [Source:HGNC Sy
20	22809	−0.53	3e−04	1e−03	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.13	NULL	1 / 2	miRNA target	miR−193a
2	−14.73	NULL	3 / 16	BP	negative regulation of neurogenesis
3	−12.86	NULL	2 / 10	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
4	−12.27	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
5	−11.35	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
6	−11.35	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
7	−9.93	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
8	−9.49	NULL	1 / 6	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_UP
9	−9.49	NULL	1 / 6	GSEA C2	ST_INTERLEUKIN_13_PATHWAY
10	−9.49	NULL	1 / 6	GSEA C2	ST_IL_13_PATHWAY
11	−9.45	NULL	2 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
12	−9.06	NULL	1 / 7	GSEA C2	BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
13	−8.94	NULL	2 / 16	GSEA C2	KEGG_DORSO_VENTRAL_AXIS_FORMATION
14	−8.91	NULL	2 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
15	−8.47	NULL	1 / 15	CC	MHC class II protein complex
16	−8.44	NULL	1 / 11	GSEA C2	NAKAJIMA_EOSINOPHIL
17	−8.38	NULL	1 / 8	GSEA C2	KEGG_PRION_DISEASES
18	−8.12	NULL	1 / 6	GSEA C2	SA_FAS_SIGNALING
19	−8.11	NULL	2 / 19	BP	negative regulation of extrinsic apoptotic signaling pathway via dea
20	−8.02	NULL	1 / 12	MF	lysophospholipase activity
21	−8.02	NULL	1 / 8	GSEA C2	ST_TYPE_I_INTERFERON_PATHWAY
22	−7.82	NULL	1 / 9	GSEA C2	REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES
23	−7.82	NULL	1 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
24	−7.64	NULL	2 / 15	GSEA C2	REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_O
25	−7.58	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
26	−7.36	NULL	1 / 10	BP	anagen
27	−7.36	NULL	1 / 10	BP	cardiac epithelial to mesenchymal transition
28	−7.36	NULL	1 / 10	BP	inflammatory response to antigenic stimulus
29	−7.36	NULL	1 / 10	BP	negative regulation of cell−substrate adhesion
30	−7.36	NULL	1 / 10	BP	positive regulation of keratinocyte differentiation
31	−7.36	NULL	1 / 10	BP	prostate gland epithelium morphogenesis
32	−7.36	NULL	1 / 10	BP	somatic stem cell division
33	−7.36	NULL	1 / 10	GSEA C2	CAMPS_COLON_CANCER_COPY_NUMBER_UP
34	−6.99	NULL	1 / 21	CC	clathrin−coated endocytic vesicle membrane
35	−6.96	NULL	1 / 11	BP	cardiac muscle tissue morphogenesis
36	−6.96	NULL	1 / 11	BP	negative regulation of myoblast differentiation
37	−6.96	NULL	1 / 11	BP	negative regulation of oligodendrocyte differentiation
38	−6.96	NULL	1 / 11	BP	neuronal stem cell maintenance
39	−6.96	NULL	1 / 11	BP	regulation of epithelial cell proliferation
40	−6.96	NULL	1 / 11	GSEA C2	BIOCARTA_PS1_PATHWAY


p−values