GW_219

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1776 (1022 + / 754 −)

genes with fdr < 0.1 = 1497 (899 + / 598 −)

genes with fdr < 0.05 = 1262 (794 + / 468 −)

genes with fdr < 0.01 = 853 (586 + / 267 −)

genes in genesets = 16332

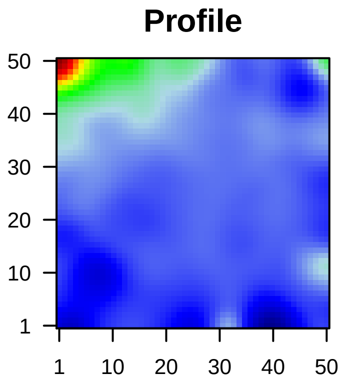
<FC> = 0

<shrinkage−t> = 0

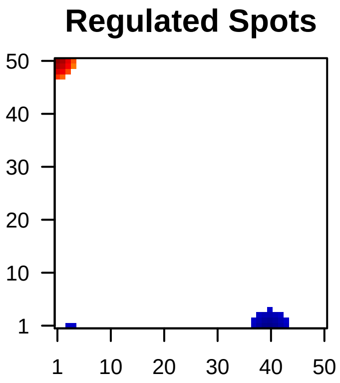
<p−value> = 0.09

<fdr> = 0.85

Profile



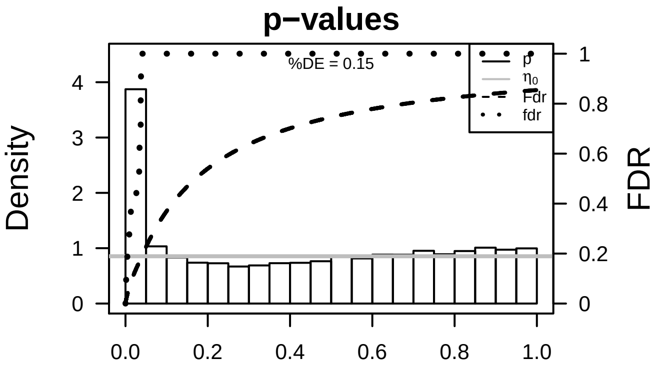
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.15	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	8745	1.36	2e−16	2e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	131	2.41	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.77	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.67	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	1646	1.6	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
7	8644	2.73	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
8	1109	2.99	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
9	218	2.1	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	401138	2.23	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
11	8416	1.19	2e−16	2e−14	5 x 50	annexin A9 [Source:HGNC Symbol;Acc:547]
12	23120	1.16	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
13	329	1.29	2e−16	2e−14	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
14	387695	1.58	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
15	339512	1.32	2e−16	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
16	92747	1.23	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
17	391267	1.21	2e−16	2e−14	50 x 13	ankyrin repeat domain 20 family, member A11, pseudogene [
18	260436	−1.43	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
19	29113	1.67	2e−16	2e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
20	394263	1.67	2e−16	2e−14	3 x 50	

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	32.02	NULL	135	H.Tiss	WIRTH_Mucosa
2	20.8	NULL	572	Disease	GUDJ_psoriasis up
3	17.19	NULL	21	CC	cornified envelope
4	16.56	NULL	53	BP	keratinocyte differentiation
5	14.23	NULL	42	BP	keratinization
6	13.03	NULL	76	BP	epidermis development
7	10.68	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
8	9.59	NULL	38	BP	epithelial cell differentiation
9	9.3	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
10	9.04	NULL	34	BP	glutathione metabolic process
11	8.71	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
12	8.41	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	8.24	NULL	19	BP	peptide cross−linking
14	8.22	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
15	8.15	NULL	119	BP	xenobiotic metabolic process
16	7.94	NULL	15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
17	7.71	NULL	21	CC	desmosome
18	7.48	NULL	16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
19	7.38	NULL	186	MF	structural molecule activity
20	7.37	NULL	51	BP	type I interferon signaling pathway
Underexpressed					
1	−6.87	NULL	127	H.Tiss	WIRTH_Muscle
2	−6.32	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−5.79	NULL	36	BP	muscle filament sliding
4	−5.5	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
5	−4.93	NULL	68	CC	collagen
6	−4.92	NULL	4	MMML CGS	MACIEJ_MMML 23
7	−4.89	NULL	940	MF	nucleic acid binding
8	−4.89	NULL	57	MF	extracellular matrix structural constituent
9	−4.81	NULL	12	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
10	−4.71	NULL	19	MF	L−ascorbic acid binding
11	−4.67	NULL	918	Chr	Chr 17
12	−4.64	NULL	250	Lymphoma	LENZ_Stromal signature 1
13	−4.55	NULL	16	H.Tiss	WIRTH_Hippocampus
14	−4.5	NULL	11	MF	platelet−derived growth factor binding
15	−4.48	NULL	44	MF	structural constituent of muscle
16	−4.33	NULL	10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
17	−4.31	NULL	11	MF	oxygen transporter activity
18	−4.31	NULL	37	BP	collagen fibril organization
19	−4.31	NULL	29	MF	oxidoreductase activity, acting on paired donors, with incorporation
20	−4.29	NULL	149	BP	DNA replication

GW_219

Local Summary

%DE = 0.95

metagenes = 13

genes = 192

genes in genesets = 187

genes with fdr < 0.1 = 175 (169 + / 6 −)

genes with fdr < 0.05 = 174 (168 + / 6 −)

genes with fdr < 0.01 = 160 (157 + / 3 −)

<r> metagenes = 0.98

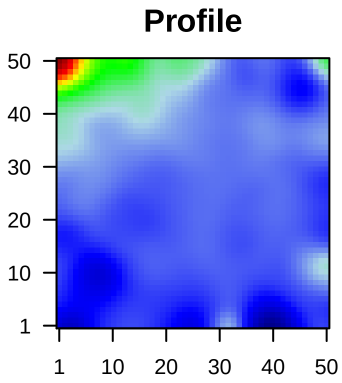
<r> genes = 0.48

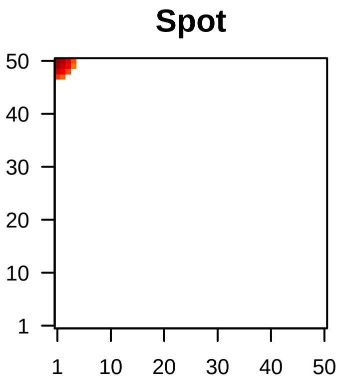
<FC> = 0.98

<shrinkage−t> = 34.49

<p−value> = 0

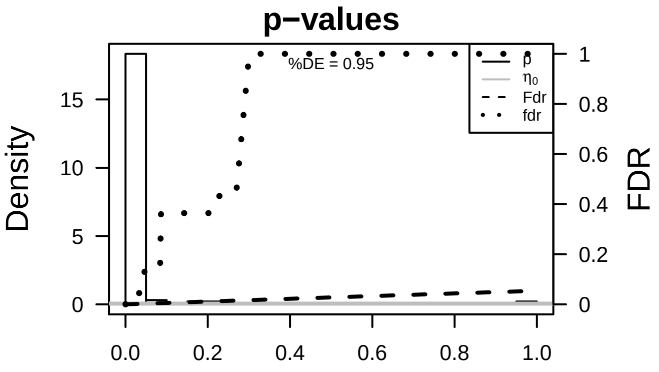
<fdr> = 0.13





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.15	2e−16	3e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	2.41	2e−16	3e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.77	2e−16	3e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.67	2e−16	3e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	2.73	2e−16	3e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	2.1	2e−16	3e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	23120	1.16	2e−16	3e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
8	387695	1.58	2e−16	3e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	29113	1.67	2e−16	3e−17	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
10	394263	1.67	2e−16	3e−17	3 x 50	
11	375791	1.45	2e−16	3e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
12	84290	1.22	2e−16	3e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	1048	1.4	2e−16	3e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
14	22802	1.76	2e−16	3e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	84518	1.73	2e−16	3e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	54544	1.38	2e−16	3e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	2.82	2e−16	3e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	92196	1.31	2e−16	3e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	414325	1.24	2e−16	3e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1830	1.15	2e−16	3e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	56.74	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
2	36.01	NULL	16 / 21	CC	cornified envelope
3	31.83	NULL	19 / 42	BP	keratinization
4	29.39	NULL	21 / 53	BP	keratinocyte differentiation
5	23.4	NULL	82 / 572	Disease	GUDJ_psoriasis up
6	20.98	NULL	20 / 76	BP	epidermis development
7	18.85	NULL	9 / 19	BP	peptide cross−linking
8	17.48	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	16.45	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	14.05	NULL	4 / 15	MF	retinol dehydrogenase activity
11	13.26	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	13.15	NULL	7 / 38	BP	epithelial cell differentiation
13	12.57	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
14	12.14	NULL	3 / 12	BP	cellular aldehyde metabolic process
15	11.42	NULL	8 / 44	CC	keratin filament
16	10.86	NULL	18 / 186	MF	structural molecule activity
17	10.64	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	10.58	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
19	10.46	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
20	10.17	NULL	10 / 82	CC	intermediate filament
21	10.15	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
22	9.93	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
23	9.48	NULL	5 / 10	MF	RAGE receptor binding
24	9.42	NULL	4 / 39	BP	retinoid metabolic process
25	9.25	NULL	6 / 13	BP	negative regulation of peptidase activity
26	9.23	NULL	5 / 21	CC	desmosome
27	9.08	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
28	8.81	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
29	8.41	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
30	8.37	NULL	2 / 12	MF	retinol binding
31	8.36	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
32	8.29	NULL	4 / 23	MF	peptidase inhibitor activity
33	8.18	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
34	8.08	NULL	3 / 19	MF	laminin binding
35	8	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
36	7.98	NULL	2 / 13	BP	retinoic acid metabolic process
37	7.68	NULL	50 / 1182	CC	extracellular region
38	7.65	NULL	4 / 27	BP	response to bacterium
39	7.55	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
40	7.43	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL

GW_219

Local Summary

%DE = 0.91

metagenes = 2

genes = 65

genes in genesets = 65

genes with fdr < 0.1 = 48 (1 + / 47 −)

genes with fdr < 0.05 = 44 (1 + / 43 −)

genes with fdr < 0.01 = 36 (0 + / 36 −)

<r> metagenes = 1

<r> genes = 0.58

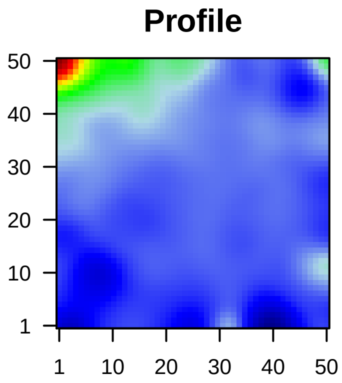
<FC> = −0.4

<shrinkage−t> = −14.13

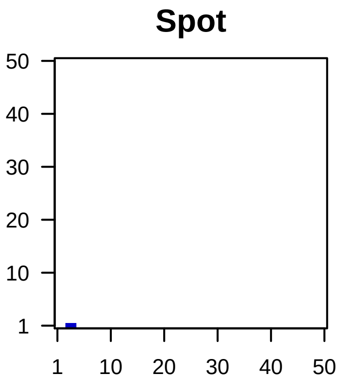
<p−value> = 0

<fdr> = 0.4

Profile



Spot



Local Genelist

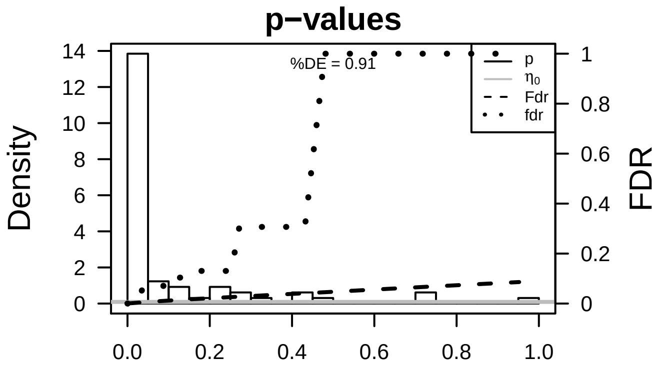
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3040	−1.3	2e−16	1e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	1462	−1.09	8e−15	1e−12	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
3	4320	−1.03	3e−13	1e−12	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
4	59	−1.02	4e−13	2e−10	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
5	7070	−0.93	3e−11	9e−09	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801
6	7169	−0.85	2e−09	2e−08	3 x 1	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
7	3671	−0.82	4e−09	1e−07	4 x 1	immunoglobulin superfamily containing leucine−rich repeat [S
8	633	−0.73	2e−08	3e−07	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
9	8076	−0.76	7e−08	5e−07	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
10	1490	−0.72	2e−07	5e−07	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
11	7043	−0.72	2e−07	8e−06	4 x 1	transforming growth factor, beta 3 [Source:HGNC Symbol;Ac
12	6678	−0.66	2e−06	8e−06	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
13	165	−0.66	3e−06	4e−05	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
14	493869	−0.62	9e−06	1e−04	3 x 1	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;A
15	10979	−0.56	6e−05	1e−04	4 x 1	fermitin family member 2 [Source:HGNC Symbol;Acc:15767]
16	115908	−0.56	7e−05	1e−04	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
17	5159	−0.56	7e−05	5e−04	3 x 1	platelet−derived growth factor receptor, beta polypeptide [Sou
18	72	−0.53	2e−04	5e−04	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
19	7076	−0.51	3e−04	5e−04	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
20	114902	−0.49	5e−04	5e−04	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.19	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
2	−25.66	NULL	4 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
3	−25.3	NULL	7 / 19	MF	extracellular matrix binding
4	−25.26	NULL	1 / 2	miRNA target	miR−18
5	−25.09	NULL	28 / 250	Lymphoma	LENZ_Stromal signature 1
6	−24.27	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
7	−23.97	NULL	22 / 190	CC	extracellular matrix
8	−23.62	NULL	1 / 4	MMML CGS	MACIEJ_MMML 23
9	−22.8	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
10	−21.74	NULL	3 / 11	BP	dermatan sulfate biosynthetic process
11	−21.51	NULL	3 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
12	−20.3	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
13	−19.91	NULL	3 / 15	Cancer	LIU_PROSTATE_CANCER_DN
14	−18.96	NULL	2 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
15	−18.86	NULL	3 / 14	BP	chondroitin sulfate catabolic process
16	−18.41	NULL	2 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
17	−17.95	NULL	3 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
18	−17.02	NULL	2 / 14	CC	endocytic vesicle lumen
19	−16.96	NULL	19 / 242	BP	extracellular matrix organization
20	−16.36	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
21	−16.36	NULL	1 / 7	GSEA C2	SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_
22	−16.33	NULL	4 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
23	−15.53	NULL	2 / 14	GSEA C2	DANG_REGULATED_BY_MYC_DN
24	−15.5	NULL	3 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
25	−15.38	NULL	2 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
26	−15.33	NULL	3 / 20	BP	positive regulation of collagen biosynthetic process
27	−15.21	NULL	12 / 183	CC	proteinaceous extracellular matrix
28	−15.06	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
29	−14.92	NULL	3 / 21	MF	glycosaminoglycan binding
30	−14.21	NULL	3 / 13	GSEA C2	ZIRN_TRETINOIN_RESPONSE_UP
31	−14.05	NULL	2 / 8	GSEA C2	ZHAN_MULTIPLE_MYELOMA_SPIKED
32	−13.81	NULL	2 / 15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
33	−13.69	NULL	2 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
34	−13.62	NULL	3 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
35	−13.5	NULL	3 / 25	BP	chondroitin sulfate biosynthetic process
36	−13.14	NULL	1 / 10	CC	hemoglobin complex
37	−12.97	NULL	3 / 16	GSEA C2	NEWMAN_ERCC6_TARGETS_DN
38	−12.96	NULL	2 / 14	GSEA C2	MAINA_VHL_TARGETS_DN
39	−12.72	NULL	1 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
40	−12.62	NULL	2 / 10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP

p−values



GW_219

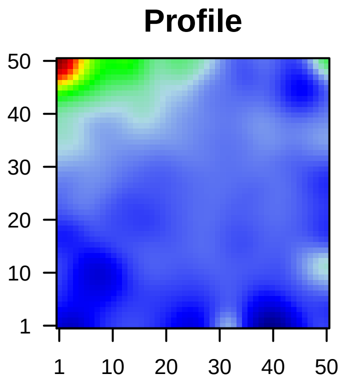
Local Summary

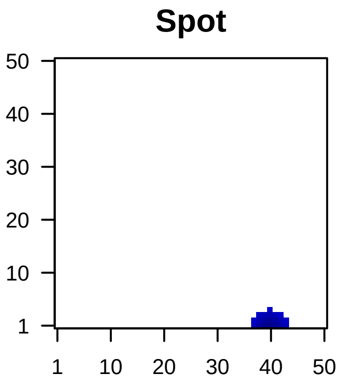
%DE = 0.88
metagenes = 20
genes = 300
genes in genesets = 273

genes with fdr < 0.1 = 202 (8 + / 194 −)
genes with fdr < 0.05 = 177 (7 + / 170 −)
genes with fdr < 0.01 = 124 (5 + / 119 −)

<r> metagenes = 0.96
<r> genes = 0.44

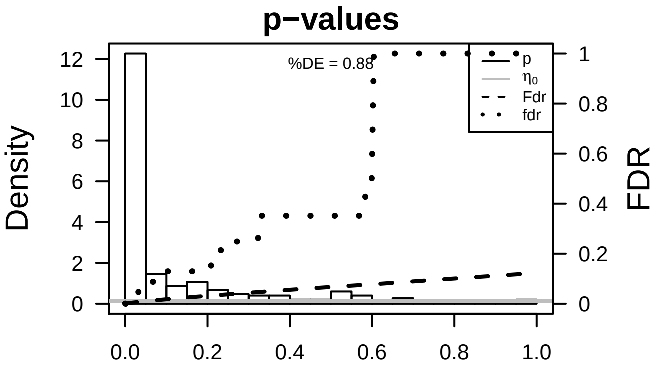
<FC> = −0.33
<shrinkage−t> = −11.69
<p−value> = 0
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	618	−1.06	5e−14	3e−11	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
2	641737	−0.93	1e−12	1e−09	40 x 1	
3	9747	−0.85	3e−11	1e−09	39 x 1	family with sequence similarity 115, member A [Source:HGN
4	55142	−0.92	6e−11	8e−09	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symbo
5	400818	−0.87	5e−10	8e−09	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
6	3586	−0.8	8e−10	8e−09	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
7	401494	−0.86	8e−10	8e−09	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [Sou
8	57464	−0.85	1e−09	8e−09	40 x 1	striatin interacting protein 2 [Source:HGNC Symbol;Acc:2220
9	440275	−0.85	1e−09	3e−08	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
10	255031	−0.84	2e−09	5e−08	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
11	250	−0.82	5e−09	5e−08	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
12	90586	−0.81	7e−09	5e−08	39 x 1	amine oxidase, copper containing 4, pseudogene [Source:HG
13	5143	−0.74	7e−09	5e−08	39 x 1	phosphodiesterase 4C, cAMP−specific [Source:HGNC Symb
14	7813	−0.81	8e−09	5e−08	40 x 1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:3
15	126205	−0.81	9e−09	2e−07	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
16	729603	−0.73	1e−08	7e−07	40 x 1	
17	136051	−0.78	3e−08	1e−06	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
18	26580	−0.75	1e−07	1e−06	43 x 1	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
19	140771	−0.74	1e−07	3e−06	40 x 1	Smith−Magenis syndrome chromosome region, candidate 5 (
20	441087	−0.73	2e−07	4e−06	39 x 1	



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.1	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−13.73	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−10.16	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	−7.65	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
5	−7.17	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
6	−7.11	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
7	−7.11	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
8	−7.03	NULL	2 / 14	BP	cellular response to estradiol stimulus
9	−6.89	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
10	−6.89	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	−6.23	NULL	2 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_DN
12	−6.19	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
13	−5.87	NULL	3 / 24	BP	negative regulation of T cell proliferation
14	−5.84	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
15	−5.47	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
16	−5.43	NULL	2 / 14	BP	mitochondrion morphogenesis
17	−5.36	NULL	2 / 15	GSEA C2	REACTOME_DARPP32_EVENTS
18	−5.26	NULL	4 / 100	Lymphoma	ROSOLOWSKI_blue total
19	−5.12	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
20	−5.12	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
21	−5.07	NULL	2 / 15	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_DN
22	−5	NULL	2 / 16	GSEA C2	YANAGIHARA_ESX1_TARGETS
23	−4.84	NULL	1 / 11	BP	negative regulation of interleukin−12 production
24	−4.84	NULL	1 / 11	GSEA C2	SU_PANCREAS
25	−4.79	NULL	1 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
26	−4.59	NULL	1 / 12	BP	negative regulation of growth of symbiont in host
27	−4.59	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS
28	−4.51	NULL	1 / 4	GSEA C2	KORKOLA_CHORIOCARCINOMA
29	−4.49	NULL	3 / 15	GSEA C2	WANG_CLIM2_TARGETS_UP
30	−4.48	NULL	3 / 38	MF	methylated histone residue binding
31	−4.47	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
32	−4.37	NULL	1 / 13	BP	negative regulation of B cell proliferation
33	−4.37	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
34	−4.37	NULL	1 / 13	GSEA C2	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
35	−4.37	NULL	1 / 13	GSEA C2	BIOCARTA_DC_PATHWAY
36	−4.3	NULL	1 / 12	BP	cAMP catabolic process
37	−4.3	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
38	−4.3	NULL	1 / 12	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_DN
39	−4.29	NULL	2 / 14	GSEA C2	VALK_AML_CLUSTER_5
40	−4.23	NULL	2 / 25	CC	primary cilium