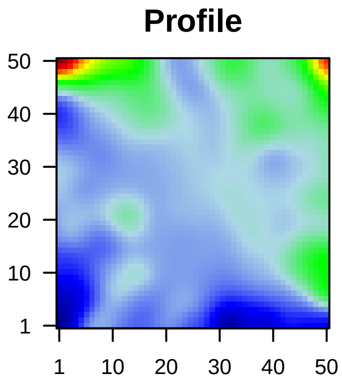
GW_188

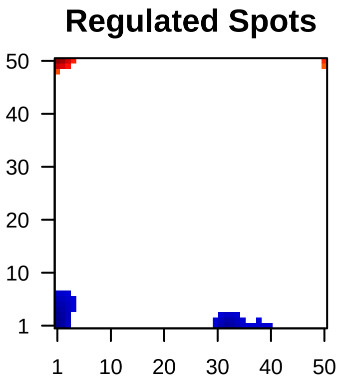
Global Summary

%DE = 0.13
genes with fdr < 0.2 = 1550 (910 + / 640 −)
genes with fdr < 0.1 = 1261 (761 + / 500 −)
genes with fdr < 0.05 = 984 (606 + / 378 −)
genes with fdr < 0.01 = 724 (469 + / 255 −)

genes in genesets = 16332

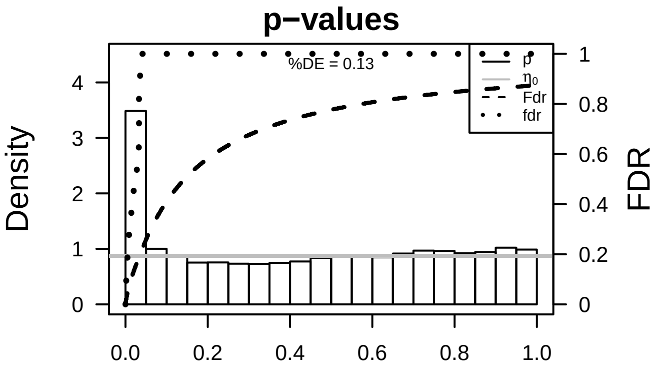
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10057	1.24	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
2	79852	1.39	2e−16	3e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	8745	1.56	2e−16	3e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
4	124	1.36	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
5	57016	1.47	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	1646	1.46	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
7	8644	2.62	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
8	1109	2.61	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
9	216	1.61	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
10	218	2.68	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	347	1.65	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
12	9823	1.36	2e−16	3e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
13	84707	1.76	2e−16	3e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
14	56271	1.54	2e−16	3e−14	50 x 12	brain expressed, X−linked 4 [Source:HGNC Symbol;Acc:254
15	655	1.44	2e−16	3e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
16	64207	1.24	2e−16	3e−14	50 x 40	interferon regulatory factor 2 binding protein−like [Source:HG
17	260436	−1.13	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
18	375791	1.43	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
19	6364	−1.18	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
20	414062	−1.4	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb


p−values

Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	21.04	NULL	135	H.Tiss	WIRTH_Mucosa
2	10.85	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
3	8.94	NULL	12	BP	cellular aldehyde metabolic process
4	8.8	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
5	8.59	NULL	914	Chr	Chr 3
6	8.46	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
7	8.4	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
8	7.91	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
9	7.32	NULL	20	MF	glutathione transferase activity
10	7.16	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	7.13	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
12	7.11	NULL	434	BP	oxidation−reduction process
13	7.09	NULL	34	Chr	Chr Y
14	7.04	NULL	34	BP	glutathione metabolic process
15	6.8	NULL	296	MF	oxidoreductase activity
16	6.62	NULL	918	Chr	Chr 17
17	6.61	NULL	53	BP	keratinocyte differentiation
18	6.59	NULL	38	BP	epithelial cell differentiation
19	6.52	NULL	18	MF	acyl−CoA dehydrogenase activity
20	6.48	NULL	25	BP	glutathione derivative biosynthetic process

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−10.56	NULL	51	BP	type I interferon signaling pathway
2	−9.35	NULL	312	BP	immune response
3	−9.35	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	−9.3	NULL	717	Chr	Chr 16
5	−9.29	NULL	123	BP	defense response to virus
6	−8.81	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	−8.4	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
8	−8.36	NULL	204	BP	cytokine−mediated signaling pathway
9	−7.97	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	−7.86	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	−7.69	NULL	1720	Chr	Chr 1
12	−7.31	NULL	60	BP	interferon−gamma−mediated signaling pathway
13	−7.14	NULL	119	Lymphoma	ROSOLOWSKI_green total
14	−7.12	NULL	553	Cancer	Lembcke_Colonic Inflammation
15	−7.07	NULL	4	MMML CGS	MACIEJ_MMML 47
16	−7.06	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
17	−7.05	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
18	−7.02	NULL	31	BP	negative regulation of viral genome replication
19	−6.93	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	−6.93	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up

GW_188

Local Summary

%DE = 0.91

metagenes = 8

genes = 154

genes in genesets = 151

genes with fdr < 0.1 = 131 (122 + / 9 −)

genes with fdr < 0.05 = 117 (111 + / 6 −)

genes with fdr < 0.01 = 117 (111 + / 6 −)

<r> metagenes = 0.99

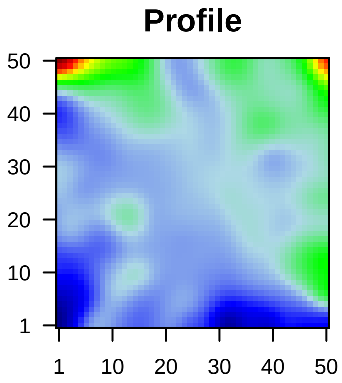
<r> genes = 0.5

<FC> = 0.75

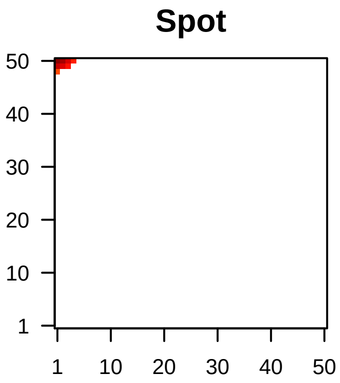
<shrinkage−t> = 26.62

<p−value> = 0

<fdr> = 0.23



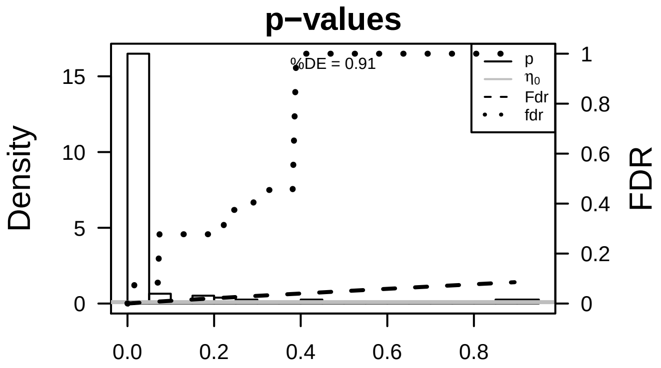
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.39	2e−16	8e−17	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	57016	1.47	2e−16	8e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	8644	2.62	2e−16	8e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	218	2.68	2e−16	8e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	375791	1.43	2e−16	8e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
6	4680	1.73	2e−16	8e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
7	1087	1.22	2e−16	8e−17	4 x 50	carcinoembryonic antigen−related cell adhesion molecule 7 [
8	22802	2.03	2e−16	8e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	84518	1.3	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
10	49860	2.57	2e−16	8e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	1475	1.33	2e−16	8e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
12	92196	2.38	2e−16	8e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
13	2877	2.11	2e−16	8e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
14	26085	1.53	2e−16	8e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
15	5653	1.58	2e−16	8e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
16	5650	1.3	2e−16	8e−17	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
17	3860	1.47	2e−16	8e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
18	192666	1.48	2e−16	8e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
19	3851	2.25	2e−16	8e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
20	388533	1.24	2e−16	8e−17	1 x 49	keratinocyte differentiation−associated protein [Source:HGN



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	51.18	NULL	66 / 135	H.Tiss	WIRTH_Mucosa
2	20.9	NULL	69 / 572	Disease	GUDJ_psoriasis up
3	20.83	NULL	17 / 53	BP	keratinocyte differentiation
4	19.5	NULL	13 / 21	CC	cornified envelope
5	19.49	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
6	19.34	NULL	7 / 19	BP	peptide cross−linking
7	18.28	NULL	4 / 10	MF	RAGE receptor binding
8	18.27	NULL	6 / 13	BP	negative regulation of peptidase activity
9	18.02	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
10	16.08	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	15.62	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
12	15.57	NULL	15 / 42	BP	keratinization
13	14.37	NULL	3 / 12	BP	cellular aldehyde metabolic process
14	13.54	NULL	4 / 15	MF	retinol dehydrogenase activity
15	12.47	NULL	18 / 76	BP	epidermis development
16	11.29	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
17	11.21	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
18	10.97	NULL	10 / 122	MF	serine−type endopeptidase activity
19	10.66	NULL	6 / 38	BP	epithelial cell differentiation
20	10.36	NULL	8 / 52	BP	negative regulation of endopeptidase activity
21	10.27	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
22	10.21	NULL	5 / 29	BP	regulation of proteolysis
23	10.12	NULL	5 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
24	9.94	NULL	44 / 1182	CC	extracellular region
25	9.88	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
26	9.85	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
27	9.84	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
28	9.59	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
29	9.46	NULL	1 / 11	Glio	VERHAAK_Brain
30	9.42	NULL	1 / 10	BP	positive regulation of endothelial cell apoptotic process
31	9.42	NULL	1 / 10	BP	retinal metabolic process
32	9.28	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
33	9.03	NULL	4 / 39	BP	retinoid metabolic process
34	8.97	NULL	1 / 12	MF	channel activity
35	8.89	NULL	1 / 11	BP	prostaglandin metabolic process
36	8.86	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
37	8.75	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
38	8.7	NULL	12 / 186	MF	structural molecule activity
39	8.64	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
40	8.55	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES

GW_188

Local Summary

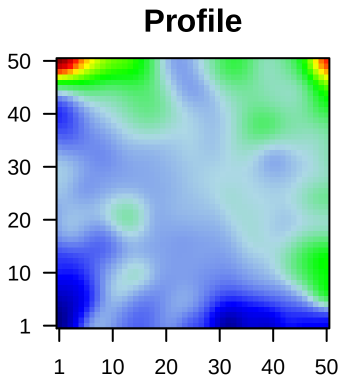
%DE = 0.95
metagenes = 2
genes = 94
genes in genesets = 93

genes with fdr < 0.1 = 81 (80 + / 1 −)
genes with fdr < 0.05 = 75 (74 + / 1 −)
genes with fdr < 0.01 = 64 (63 + / 1 −)

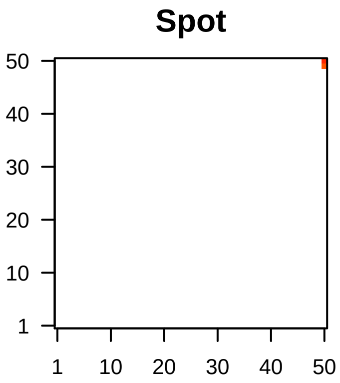
<r> metagenes = 1
<r> genes = 0.34

<FC> = 0.69
<shrinkage−t> = 24
<p−value> = 0
<fdr> = 0.27

Profile



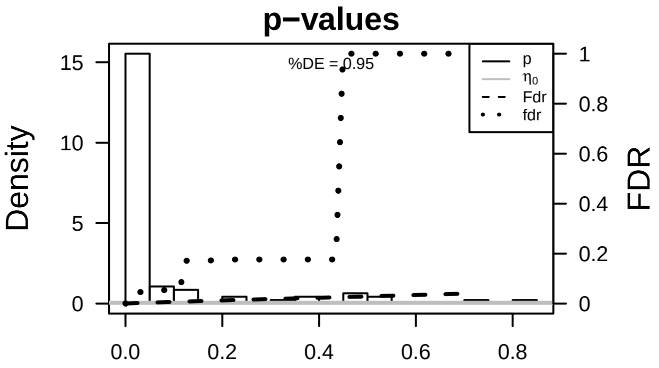
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10057	1.24	2e−16	6e−17	50 x 50	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
2	8745	1.56	2e−16	6e−17	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	216	1.61	2e−16	6e−17	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	655	1.44	2e−16	6e−17	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
5	1056	1.26	2e−16	6e−17	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	4072	1.27	2e−16	6e−17	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
7	2947	1.29	2e−16	6e−17	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symb
8	3866	2.33	2e−16	6e−17	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
9	3880	1.65	2e−16	6e−17	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
10	4915	1.65	2e−16	6e−17	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
11	4922	3.38	2e−16	6e−17	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
12	4953	1.23	2e−16	6e−17	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
13	55244	1.16	2e−16	6e−17	50 x 50	solute carrier family 47 (multidrug and toxin extrusion), memb
14	83959	1.47	2e−16	6e−17	50 x 50	solute carrier family 4, sodium borate transporter, member 11
15	6657	1.43	2e−16	6e−17	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
16	89894	1.41	2e−16	6e−17	50 x 50	transmembrane protein 116 [Source:HGNC Symbol;Acc:250
17	2946	1.13	4e−16	6e−14	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
18	54578	1.06	2e−14	6e−14	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
19	224	1.05	3e−14	6e−14	50 x 50	aldehyde dehydrogenase 3 family, member A2 [Source:HGN
20	205428	1.05	4e−14	6e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	35.12	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	33.98	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	19.44	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
4	19.05	NULL	3 / 13	BP	regulation of blood vessel size
5	17.92	NULL	1 / 11	Glio	neurons_glio
6	15.51	NULL	3 / 11	MF	glutathione binding
7	15.51	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
8	14.86	NULL	1 / 15	MF	neuropeptide hormone activity
9	14.5	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
10	13.34	NULL	2 / 12	BP	cellular aldehyde metabolic process
11	13.22	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
12	12.94	NULL	6 / 25	BP	glutathione derivative biosynthetic process
13	12.91	NULL	8 / 34	BP	glutathione metabolic process
14	12.9	NULL	5 / 20	MF	glutathione transferase activity
15	12.55	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
16	12.46	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
17	12.46	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
18	11.87	NULL	2 / 14	CC	membrane−bounded vesicle
19	11.25	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
20	11.13	NULL	2 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
21	11.03	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
22	10.94	NULL	2 / 19	BP	anatomical structure formation involved in morphogenesis
23	10.44	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
24	10.32	NULL	2 / 16	GSEA C2	GOUYER_TATI_TARGETS_DN
25	10.16	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
26	10.02	NULL	2 / 22	BP	eye development
27	10.01	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
28	9.98	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
29	9.98	NULL	1 / 7	miRNA target	miR−145
30	9.92	NULL	11 / 119	BP	xenobiotic metabolic process
31	9.77	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
32	9.56	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
33	9.56	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
34	9.35	NULL	2 / 21	BP	feeding behavior
35	9.2	NULL	1 / 8	GSEA C2	MCCABE_HOXC6_TARGETS_UP
36	9.2	NULL	1 / 10	BP	regulation of dendrite development
37	9.2	NULL	1 / 10	BP	regulation of MAPK cascade
38	9.15	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
39	9.15	NULL	1 / 8	miRNA 3UTR	CTGCA−450
40	9.01	NULL	2 / 20	BP	long−term memory

GW_188

Local Summary

%DE = 0.72

metagenes = 24

genes = 345

genes in genesets = 342

genes with fdr < 0.1 = 185 (18 + / 167 −)

genes with fdr < 0.05 = 164 (14 + / 150 −)

genes with fdr < 0.01 = 116 (7 + / 109 −)

<r> metagenes = 0.94

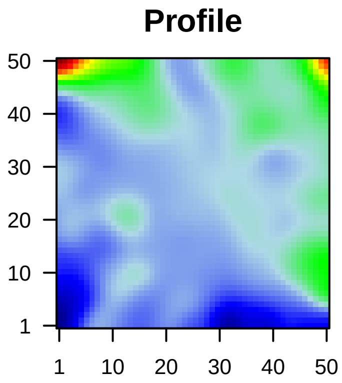
<r> genes = 0.33

<FC> = −0.3

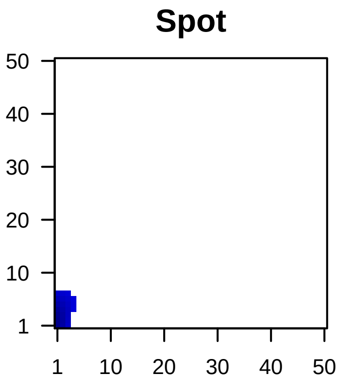
<shrinkage−t> = −10.38

<p−value> = 0

<fdr> = 0.53



Profile



Spot

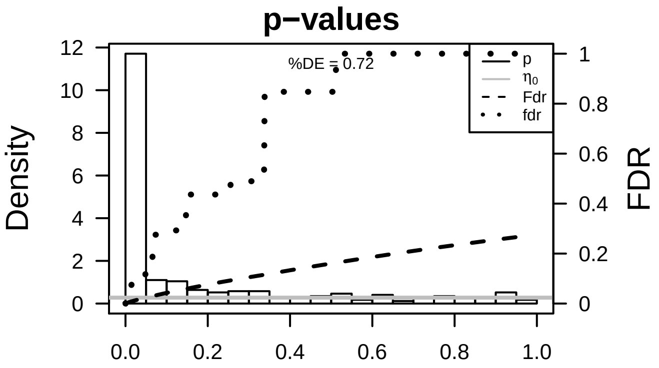
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	414062	−1.4	2e−16	2e−15	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
2	3918	−1.43	2e−16	2e−15	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
3	4316	−1.16	2e−16	2e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
4	4318	−1.19	2e−16	2e−15	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
5	4502	−1.36	2e−16	2e−15	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
6	5054	−1.25	2e−16	2e−15	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
7	6515	−1.38	2e−16	2e−15	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
8	7078	−1.24	2e−16	2e−15	2 x 1	TIMP metallopeptidase inhibitor 3 [Source:HGNC Symbol;Ac
9	3371	1.27	2e−16	2e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
10	6696	−1.12	7e−16	4e−13	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
11	4907	−1.08	5e−15	1e−12	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
12	3491	−1.05	3e−14	3e−11	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
13	25907	1.05	3e−14	3e−11	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HG
14	51330	−1.01	3e−13	5e−10	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
15	55107	−0.95	6e−12	5e−10	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
16	164284	−0.94	1e−11	6e−10	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:
17	4489	−0.86	2e−11	6e−10	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
18	91663	−0.92	3e−11	6e−10	2 x 1	myeloid−associated differentiation marker [Source:HGNC Sy
19	79783	−0.92	3e−11	7e−09	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
20	768	−0.89	1e−10	7e−09	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.57	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	−21.91	NULL	7 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
3	−21.84	NULL	4 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
4	−19.18	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
5	−18.71	NULL	4 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
6	−18.63	NULL	3 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
7	−18.52	NULL	62 / 242	BP	extracellular matrix organization
8	−17.04	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
9	−17.02	NULL	8 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
10	−16.59	NULL	63 / 250	Lymphoma	LENZ_Stromal signature 1
11	−16.51	NULL	6 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
12	−16.31	NULL	5 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
13	−15.73	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
14	−15.62	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
15	−15.41	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
16	−15.3	NULL	3 / 6	Glio	Martinez_Glio_hypometh
17	−15.24	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
18	−14.74	NULL	3 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
19	−14.57	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
20	−14.41	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
21	−14.41	NULL	8 / 19	MF	extracellular matrix binding
22	−14.36	NULL	4 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
23	−14.23	NULL	6 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
24	−13.93	NULL	6 / 12	BP	hemidesmosome assembly
25	−13.39	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
26	−13.37	NULL	5 / 14	GSEA C2	HALMOS_CEBPA_TARGETS_DN
27	−13.06	NULL	3 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
28	−12.99	NULL	4 / 11	GSEA C2	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP
29	−12.99	NULL	48 / 190	CC	extracellular matrix
30	−12.85	NULL	26 / 69	BP	extracellular matrix disassembly
31	−12.67	NULL	4 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_32HR_DN
32	−12.67	NULL	4 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_48HR_DN
33	−12.58	NULL	24 / 64	BP	collagen catabolic process
34	−12.25	NULL	5 / 16	GSEA C2	GU_PDEF_TARGETS_UP
35	−12.22	NULL	9 / 16	MF	fibronectin binding
36	−12.07	NULL	4 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
37	−11.99	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
38	−11.95	NULL	4 / 16	GSEA C2	LEONARD_HYPOXIA
39	−11.88	NULL	5 / 16	GSEA C2	KIM_WT1_TARGETS_UP
40	−11.81	NULL	14 / 68	Glio	cultured astroglia vs. in vivo astrocytes



p−values

GW_188

Local Summary

%DE = 0.8

metagenes = 22

genes = 332

genes in genesets = 307

genes with fdr < 0.1 = 205 (7 + / 198 −)

genes with fdr < 0.05 = 152 (5 + / 147 −)

genes with fdr < 0.01 = 102 (2 + / 100 −)

<r> metagenes = 0.79

<r> genes = 0.28

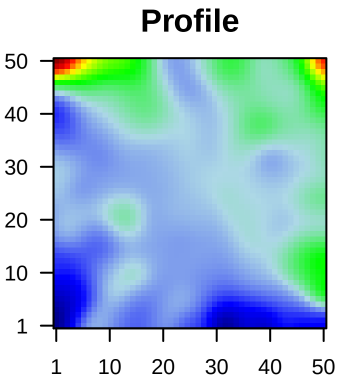
<FC> = −0.33

<shrinkage−t> = −11.58

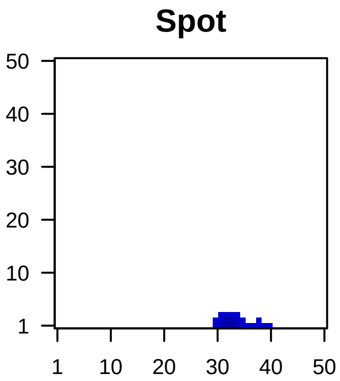
<p−value> = 0

<fdr> = 0.56

Profile



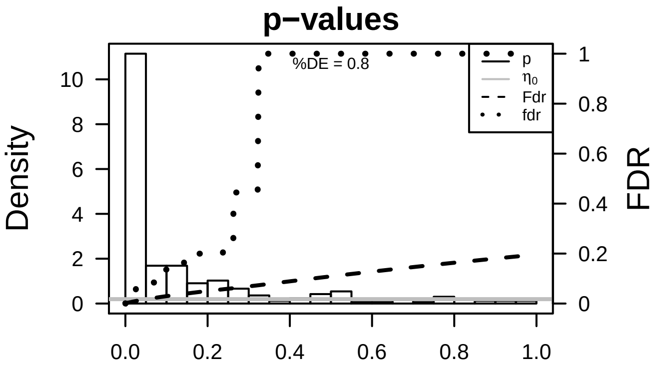
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3627	−1.4	2e−16	5e−15	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
2	10561	−1.26	2e−16	5e−15	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
3	9636	−1.44	2e−16	5e−15	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
4	684	−1.13	4e−16	6e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
5	2537	−1.11	1e−15	2e−13	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
6	94240	−1.08	5e−15	4e−12	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
7	4321	−1.04	7e−14	4e−11	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
8	4061	−1	6e−13	2e−10	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
9	10964	−0.95	7e−12	2e−10	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
10	84061	−0.95	9e−12	2e−10	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
11	3136	−0.95	9e−12	6e−09	32 x 1	
12	3134	−0.89	1e−10	7e−09	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
13	9560	−0.88	2e−10	6e−08	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
14	51191	−0.84	1e−09	6e−08	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
15	4600	−0.83	2e−09	1e−07	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
16	55601	−0.81	5e−09	1e−07	32 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 60 [Source:HGN
17	2633	−0.8	6e−09	2e−07	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN
18	3106	−0.72	1e−08	2e−07	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
19	91543	−0.78	2e−08	2e−07	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:I
20	51296	−0.78	2e−08	2e−06	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−42.53	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	−41.75	NULL	13 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	−38.39	NULL	29 / 51	BP	type I interferon signaling pathway
4	−30.98	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
5	−30.5	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	−29.91	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
7	−28.83	NULL	35 / 123	BP	defense response to virus
8	−28.72	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
9	−28.46	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
10	−26.66	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
11	−26	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−25.5	NULL	28 / 109	BP	response to virus
13	−25.09	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	−25.08	NULL	15 / 31	BP	negative regulation of viral genome replication
15	−23.91	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
16	−23.18	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
17	−23.13	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
18	−22.54	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
19	−22.22	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
20	−21.5	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
21	−21.2	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
22	−21.09	NULL	34 / 204	BP	cytokine−mediated signaling pathway
23	−20.78	NULL	7 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
24	−20.72	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
25	−20.56	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
26	−20.36	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
27	−19.73	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
28	−19.31	NULL	7 / 10	CC	MHC class I protein complex
29	−18.12	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
30	−17.98	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
31	−17.98	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
32	−17.9	NULL	8 / 18	MF	peptide antigen binding
33	−17.89	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
34	−17.69	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
35	−17.52	NULL	49 / 572	Disease	GUDJ_psoriasis up
36	−17.31	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
37	−17.23	NULL	34 / 274	Lymphoma	SPANG_IL21 DN
38	−17.13	NULL	5 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
39	−15.92	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
40	−13.98	NULL	3 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY