GW_005

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1801 (959 + / 842 −)

genes with fdr < 0.1 = 1612 (858 + / 754 −)

genes with fdr < 0.05 = 1281 (676 + / 605 −)

genes with fdr < 0.01 = 937 (505 + / 432 −)

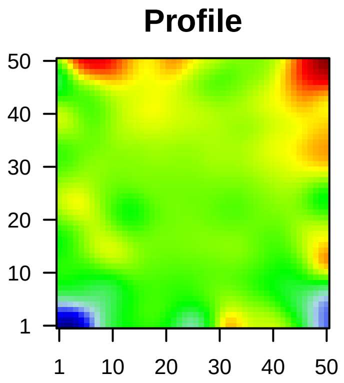
genes in genesets = 16332

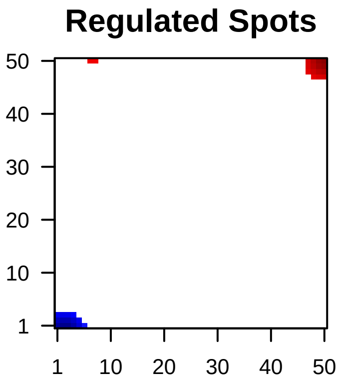
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

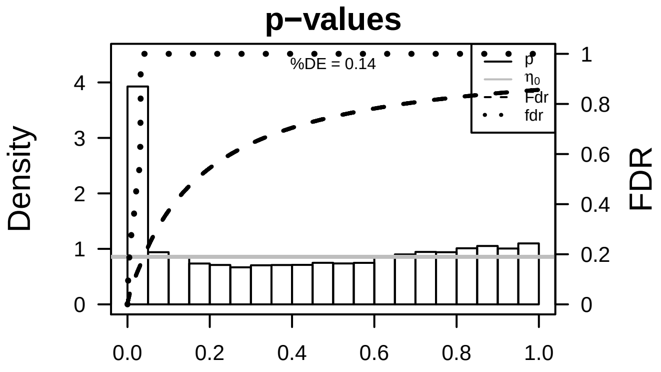
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.47	2e−16	3e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	8745	1.74	2e−16	3e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	124	1.74	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
4	126	1.49	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
5	165	−1.59	2e−16	3e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
6	216	1.51	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
7	501	−1.88	2e−16	3e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
8	154796	1.42	2e−16	3e−14	50 x 12	angiomotin [Source:HGNC Symbol;Acc:17810]
9	23780	1.53	2e−16	3e−14	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
10	23120	1.49	2e−16	3e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
11	633	−2.28	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
12	64073	−2	2e−16	3e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
13	339512	2.28	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
14	56892	1.42	2e−16	3e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
15	57172	−1.68	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
16	6364	1.84	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
17	595	−2.14	2e−16	3e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
18	1048	1.62	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
19	1056	2.31	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
20	1951	1.4	2e−16	3e−14	9 x 13	cadherin, EGF LAG seven−pass G−type receptor 3 [Source:H



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.6	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	9.49	NULL	572	Disease	GUDJ_psoriasis up
3	8.93	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
4	8.44	NULL	274	Lymphoma	SPANG_IL21 DN
5	8.35	NULL	630	Chr	Chr X
6	7.24	NULL	123	BP	defense response to virus
7	6.92	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
8	6.92	NULL	31	BP	negative regulation of viral genome replication
9	6.62	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
10	6.36	NULL	914	Chr	Chr 3
11	6.11	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	6.06	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
13	5.97	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
14	5.97	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
15	5.59	NULL	24	TF Tissue	VAQUERIZAS_Trachea
16	5.54	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
17	5.34	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
18	5.33	NULL	10	GSEA C2	DAUER_STAT3_TARGETS_DN
19	5.3	NULL	135	H.Tiss	WIRTH_Mucosa
20	5.28	NULL	633	Chr	Chr 9
Underexpressed					
1	−17.87	NULL	190	CC	extracellular matrix
2	−15.35	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−13.58	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
4	−13.34	NULL	11	MF	platelet−derived growth factor binding
5	−12.38	NULL	16	MMML CGS	MACIEJ_MMML 1
6	−11.71	NULL	242	BP	extracellular matrix organization
7	−11.71	NULL	64	BP	collagen catabolic process
8	−11.55	NULL	69	BP	extracellular matrix disassembly
9	−11.1	NULL	57	MF	extracellular matrix structural constituent
10	−10.81	NULL	12	miRNA target	miR−29c
11	−10	NULL	957	Chr	Chr 11
12	−9.55	NULL	183	CC	proteinaceous extracellular matrix
13	−9.37	NULL	553	Cancer	Lembcke_Colonic Inflammation
14	−9.19	NULL	37	BP	collagen fibril organization
15	−8.72	NULL	1182	CC	extracellular region
16	−8.38	NULL	683	CC	extracellular space
17	−8.2	NULL	19	MF	extracellular matrix binding
18	−7.95	NULL	8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
19	−7.9	NULL	40	BP	cellular response to amino acid stimulus
20	−7.86	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP

GW_005

Local Summary

%DE = 0.73

metagenes = 15

genes = 207

genes in genesets = 205

genes with fdr < 0.1 = 133 (119 + / 14 −)

genes with fdr < 0.05 = 115 (104 + / 11 −)

genes with fdr < 0.01 = 91 (85 + / 6 −)

<r> metagenes = 0.96

<r> genes = 0.28

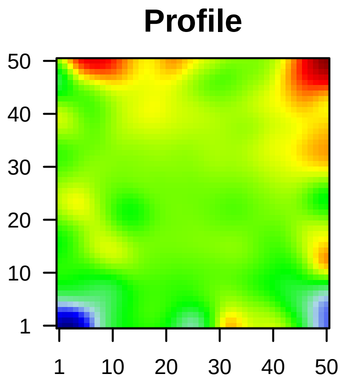
<FC> = 0.45

<shrinkage−t> = 15.65

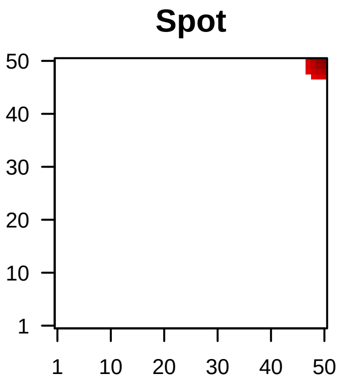
<p−value> = 0

<fdr> = 0.43

Profile



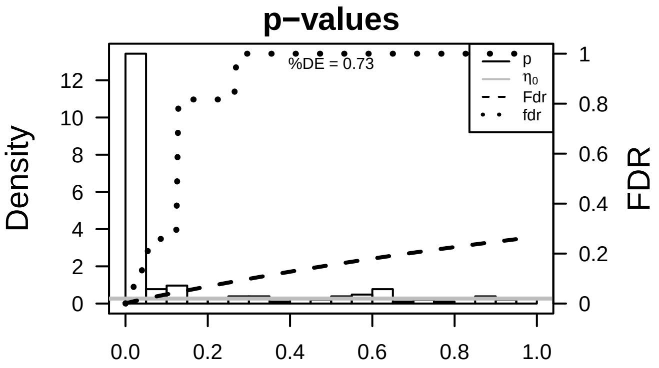
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	1.74	2e−16	1e−15	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	216	1.51	2e−16	1e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	339512	2.28	2e−16	1e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	1056	2.31	2e−16	1e−15	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
5	9076	1.54	2e−16	1e−15	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
6	3866	2.31	2e−16	1e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
7	3880	1.64	2e−16	1e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
8	3856	1.95	2e−16	1e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
9	4922	1.99	2e−16	1e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	59342	1.38	2e−16	1e−15	50 x 47	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
11	6657	1.35	4e−16	2e−14	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
12	445	1.34	9e−16	2e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
13	7037	1.22	1e−15	2e−14	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
14	139728	1.33	2e−15	5e−11	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
15	154664	1.19	1e−12	5e−11	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
16	2946	−1.17	2e−12	5e−11	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
17	10057	1.17	2e−12	7e−11	50 x 50	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
18	255758	1.15	4e−12	7e−11	50 x 50	Tctex1 domain containing 2 [Source:HGNC Symbol;Acc:284
19	2944	−1.15	5e−12	2e−10	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
20	3304	1.04	9e−12	4e−10	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.99	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	17.6	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	17.55	NULL	3 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
4	16.94	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
5	16.27	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
6	15.71	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
7	15.16	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
8	13.31	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
9	12.37	NULL	4 / 13	BP	regulation of blood vessel size
10	11.53	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
11	11.2	NULL	1 / 8	GSEA C2	KEGG_GLYCEROLIPID_METABOLISM
12	10.99	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
13	10.23	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
14	10.17	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
15	9.91	NULL	1 / 2	miRNA target	miR−127
16	9.31	NULL	1 / 11	GSEA C2	BROWNE_HCMV_INFECTION_10HR_UP
17	9.17	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
18	8.97	NULL	2 / 6	GSEA C2	YAGUE_PRETUMOR_DRUG_RESISTANCE_UP
19	8.86	NULL	2 / 8	GSEA C2	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
20	8.7	NULL	2 / 16	GSEA C2	KEGG_STEROID_BIOSYNTHESIS
21	8.61	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
22	8.61	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
23	8.52	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
24	8.46	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
25	8.46	NULL	1 / 13	MF	triglyceride lipase activity
26	8.42	NULL	1 / 5	miRNA target	miR−320
27	8.29	NULL	4 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
28	8.1	NULL	1 / 14	GSEA C2	WATANABE_COLON_CANCER_MSI_VS_MSS_DN
29	7.99	NULL	1 / 11	Glio	neurons_glio
30	7.88	NULL	3 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
31	7.85	NULL	1 / 4	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_DN
32	7.79	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
33	7.74	NULL	2 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
34	7.63	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
35	7.63	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
36	7.55	NULL	2 / 12	BP	cellular aldehyde metabolic process
37	7.5	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
38	7.41	NULL	2 / 16	GSEA C2	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
39	7.33	NULL	2 / 13	GSEA C2	LENAOUR_DENDRITIC_CELL_MATURATION_UP
40	7.23	NULL	53 / 914	Chr	Chr 3

GW_005

Local Summary

%DE = 0.87

metagenes = 2

genes = 59

genes in genesets = 59

genes with fdr < 0.1 = 44 (40 + / 4 −)

genes with fdr < 0.05 = 30 (29 + / 1 −)

genes with fdr < 0.01 = 24 (24 + / 0 −)

<r> metagenes = 1

<r> genes = 0.36

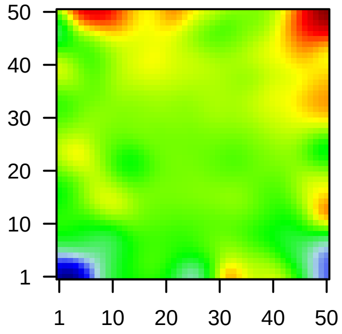
<FC> = 0.39

<shrinkage−t> = 13.83

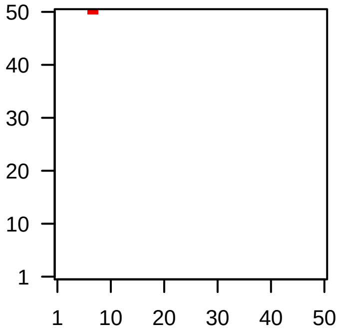
<p−value> = 0

<fdr> = 0.52

Profile



Spot



Local Genelist

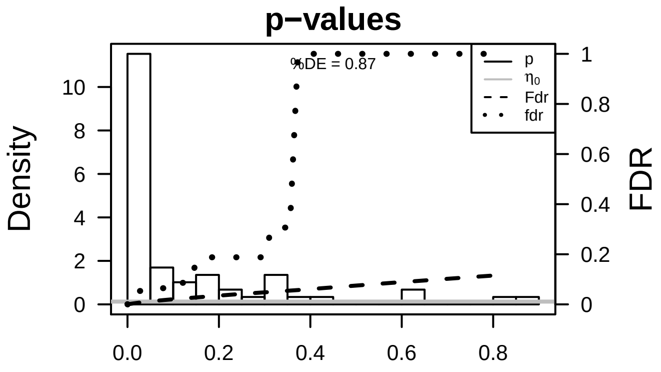
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4128	1.8	2e−16	2e−15	7 x 50	monoamine oxidase A [Source:HGNC Symbol;Acc:6833]
2	157506	1.33	2e−15	2e−08	8 x 50	retinol dehydrogenase 10 (all−trans) [Source:HGNC Symbol;
3	7105	0.99	3e−09	3e−07	7 x 50	tetraspanin 6 [Source:HGNC Symbol;Acc:11858]
4	57530	0.92	4e−08	1e−06	7 x 50	cingulin [Source:HGNC Symbol;Acc:17429]
5	9524	0.87	2e−07	2e−06	7 x 50	trans−2,3−enoyl−CoA reductase [Source:HGNC Symbol;Acc:
6	79956	0.84	4e−07	5e−06	7 x 50	endoplasmic reticulum metallopeptidase 1 [Source:HGNC Sy
7	8000	0.8	2e−06	5e−06	7 x 50	prostate stem cell antigen [Source:HGNC Symbol;Acc:9500]
8	4070	0.73	2e−06	5e−06	7 x 50	tumor−associated calcium signal transducer 2 [Source:HGNC
9	55552	0.78	3e−06	5e−06	8 x 50	zinc finger protein 823 [Source:HGNC Symbol;Acc:30936]
10	201501	0.77	4e−06	5e−06	7 x 50	zinc finger and BTB domain containing 7C [Source:HGNC Sy
11	200942	0.76	5e−06	5e−06	7 x 50	kelch domain containing 8B [Source:HGNC Symbol;Acc:2855
12	3157	0.76	5e−06	5e−06	7 x 50	3−hydroxy−3−methylglutaryl−CoA synthase 1 (soluble) [Sour
13	11261	0.76	5e−06	1e−05	7 x 50	calcineurin−like EF−hand protein 1 [Source:HGNC Symbol;A
14	54677	0.75	7e−06	6e−05	8 x 50	carnitine O−octanoyltransferase [Source:HGNC Symbol;Acc:
15	9957	0.72	2e−05	2e−04	7 x 50	heparan sulfate (glucosamine) 3−O−sulfotransferase 1 [Sour
16	50506	0.69	4e−05	6e−04	8 x 50	dual oxidase 2 [Source:HGNC Symbol;Acc:13273]
17	58489	0.62	2e−04	6e−04	7 x 50	abhydrolase domain containing 17C [Source:HGNC Symbol;
18	121273	0.61	2e−04	6e−04	8 x 50	chromosome 12 open reading frame 54 [Source:HGNC Symb
19	55030	0.61	3e−04	6e−04	8 x 50	F−box protein 34 [Source:HGNC Symbol;Acc:20201]
20	55602	0.6	3e−04	9e−04	7 x 50	CDKN2A interacting protein [Source:HGNC Symbol;Acc:2432

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.5	NULL	1 / 2	Cancer	GENTLES_modul8
2	22.11	NULL	1 / 8	GSEA C2	SCHURINGA_STAT5A_TARGETS_UP
3	19.29	NULL	1 / 10	GSEA C2	REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELE
4	18.21	NULL	1 / 11	BP	neurotransmitter biosynthetic process
5	17.29	NULL	1 / 12	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION
6	15.78	NULL	1 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
7	14.2	NULL	1 / 10	BP	embryonic camera−type eye development
8	14.2	NULL	1 / 10	BP	retinal metabolic process
9	13.62	NULL	2 / 13	GSEA C2	SABATES_COLORECTAL_ADENOMA_SIZE_DN
10	13.4	NULL	1 / 11	BP	ear development
11	13.4	NULL	1 / 11	BP	embryonic viscerocranium morphogenesis
12	12.59	NULL	1 / 5	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_DN
13	11.65	NULL	1 / 6	Glio	Martinez_Glio_hypometh
14	11.6	NULL	1 / 14	BP	neural crest cell development
15	11.27	NULL	1 / 25	BP	behavior
16	11.14	NULL	1 / 15	MF	retinol dehydrogenase activity
17	11.14	NULL	1 / 15	GSEA C2	BEIER_GLIOMA_STEM_CELL_UP
18	10.53	NULL	1 / 7	GSEA C2	DE_YY1_TARGETS_UP
19	10.44	NULL	2 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
20	10.35	NULL	1 / 17	miRNA 3UTR	AGTC−151
21	10.01	NULL	1 / 18	BP	retinol metabolic process
22	9.67	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
23	9.14	NULL	1 / 21	BP	embryonic organ development
24	8.86	NULL	2 / 16	miRNA target−starBase	hsa−miR−1298
25	8.71	NULL	1 / 12	CC	apical junction complex
26	8.67	NULL	1 / 23	BP	gonad development
27	8.55	NULL	2 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
28	8.54	NULL	2 / 15	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
29	8.41	NULL	3 / 82	miRNA target−starBase	hsa−miR−567
30	8.38	NULL	1 / 42	BP	neurotransmitter secretion
31	8.06	NULL	1 / 10	GSEA C2	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS
32	7.94	NULL	1 / 11	BP	regulation of epithelial cell proliferation
33	7.62	NULL	1 / 15	GSEA C2	OZEN_MIR125B1_TARGETS
34	7.6	NULL	1 / 11	BP	positive regulation of protein targeting to membrane
35	7.58	NULL	1 / 29	BP	embryonic forelimb morphogenesis
36	7.54	NULL	1 / 12	GSEA C2	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
37	7.48	NULL	1 / 11	BP	fatty acid beta−oxidation using acyl−CoA oxidase
38	7.44	NULL	2 / 66	MF	flavin adenine dinucleotide binding
39	7.32	NULL	2 / 14	GSEA C2	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
40	7.25	NULL	1 / 10	BP	hormone biosynthetic process

p−values



GW_005

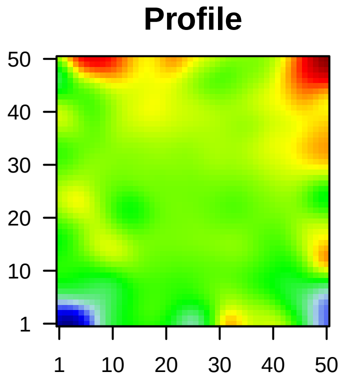
Local Summary

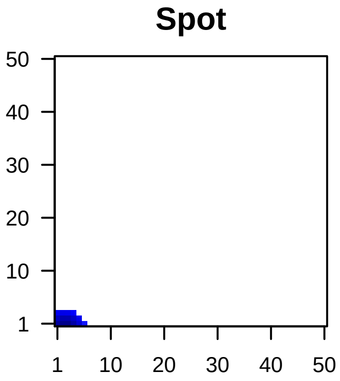
%DE = 0.86
metagenes = 15
genes = 254
genes in genesets = 253

genes with fdr < 0.1 = 208 (13 + / 195 −)
genes with fdr < 0.05 = 205 (13 + / 192 −)
genes with fdr < 0.01 = 166 (9 + / 157 −)

<r> metagenes = 0.97
<r> genes = 0.42

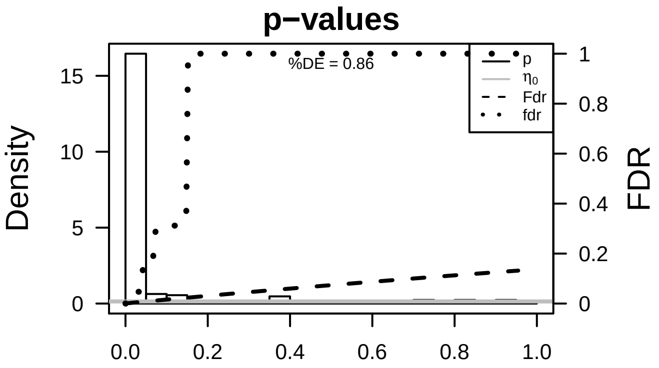
<FC> = −0.63
<shrinkage−t> = −22.22
<p−value> = 0
<fdr> = 0.26


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	165	−1.59	2e−16	3e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
2	633	−2.28	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	1277	−2.44	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	−2.29	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	−2.64	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1289	−1.6	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1290	−1.75	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	1291	−1.7	2e−16	3e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
9	1293	−2.16	2e−16	3e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	1397	−1.44	2e−16	3e−16	4 x 3	cysteine−rich protein 2 [Source:HGNC Symbol;Acc:2361]
11	1513	−1.57	2e−16	3e−16	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
12	2199	−1.6	2e−16	3e−16	4 x 1	fibulin 2 [Source:HGNC Symbol;Acc:3601]
13	11167	−1.59	2e−16	3e−16	3 x 1	follistatin−like 1 [Source:HGNC Symbol;Acc:3972]
14	3040	−1.5	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
15	3043	−1.54	2e−16	3e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
16	3956	−1.59	2e−16	3e−16	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
17	4312	−1.8	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
18	4316	−1.42	2e−16	3e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
19	4692	−1.39	2e−16	3e−16	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
20	10631	−1.64	2e−16	3e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−43.41	NULL	67 / 190	CC	extracellular matrix
2	−42.82	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−42.12	NULL	8 / 11	MF	platelet−derived growth factor binding
4	−41.34	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
5	−38.37	NULL	76 / 250	Lymphoma	LENZ_Stromal signature 1
6	−37.58	NULL	31 / 69	BP	extracellular matrix disassembly
7	−36.18	NULL	27 / 64	BP	collagen catabolic process
8	−33.76	NULL	8 / 12	miRNA target	miR−29c
9	−33.51	NULL	61 / 242	BP	extracellular matrix organization
10	−29.22	NULL	19 / 57	MF	extracellular matrix structural constituent
11	−27.64	NULL	14 / 37	BP	collagen fibril organization
12	−24.84	NULL	11 / 19	MF	extracellular matrix binding
13	−23.56	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
14	−23.52	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
15	−22.84	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
16	−22.81	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
17	−22.16	NULL	4 / 10	BP	protein heterotrimerization
18	−22.05	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
19	−21.91	NULL	10 / 40	BP	cellular response to amino acid stimulus
20	−21.43	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
21	−21.27	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
22	−21.04	NULL	36 / 183	CC	proteinaceous extracellular matrix
23	−20.52	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
24	−20.25	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
25	−20.13	NULL	16 / 68	CC	collagen
26	−18.57	NULL	6 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
27	−18.09	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
28	−18.06	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
29	−17.9	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
30	−17.79	NULL	102 / 1182	CC	extracellular region
31	−17.78	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
32	−17.54	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
33	−17.46	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
34	−16.95	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
35	−16.78	NULL	77 / 683	CC	extracellular space
36	−16.64	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
37	−16.61	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
38	−16.56	NULL	12 / 35	Glio	Colman_survival_associated
39	−16.35	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
40	−16.24	NULL	7 / 16	GSEA C2	ZHU_CMV_ALL_DN