GW_142

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1343 (694 + / 649 −)

genes with fdr < 0.1 = 967 (495 + / 472 −)

genes with fdr < 0.05 = 809 (418 + / 391 −)

genes with fdr < 0.01 = 528 (261 + / 267 −)

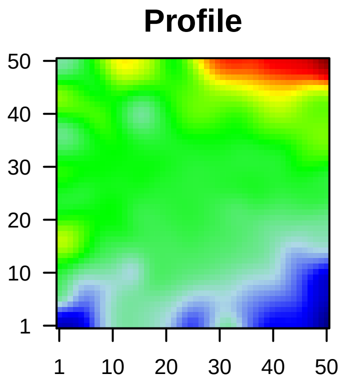
genes in genesets = 16332

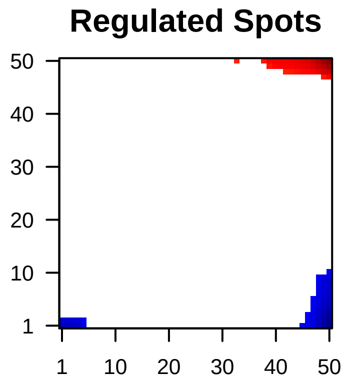
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.15

<fdr> = 0.88


Profile

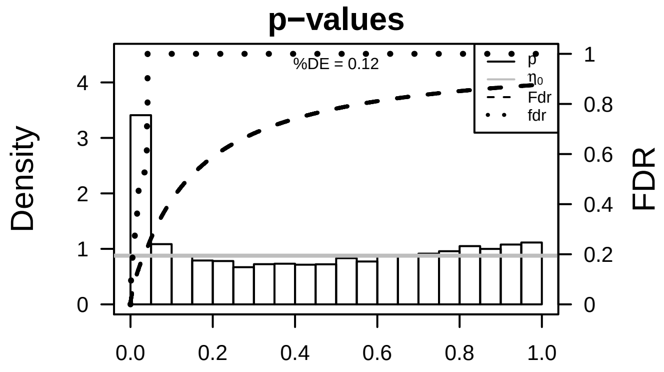

Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	1.8	2e−16	8e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	218	1.92	2e−16	8e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	501	−1.56	2e−16	8e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
4	445	1.73	2e−16	8e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
5	655	1.64	2e−16	8e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
6	10974	−1.76	2e−16	8e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
7	339512	1.45	2e−16	8e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
8	51806	−1.54	2e−16	8e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
9	875	1.47	2e−16	8e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
10	1673	−1.74	2e−16	8e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	115572	−1.48	2e−16	8e−14	1 x 48	family with sequence similarity 46, member B [Source:HGNC
12	2353	−1.56	2e−16	8e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog [Source:
13	10457	1.71	2e−16	8e−14	13 x 50	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
14	2938	1.51	2e−16	8e−14	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
15	2944	1.92	2e−16	8e−14	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
16	283120	−1.94	2e−16	8e−14	25 x 1	H19, imprinted maternally expressed transcript (non−protein
17	3040	−2	2e−16	8e−14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
18	3043	−2.09	2e−16	8e−14	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
19	3123	1.79	2e−16	8e−14	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
20	8988	1.77	2e−16	8e−14	1 x 4	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:524

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.31	NULL	534	Chr	Chr 8
2	9.78	NULL	1318	CC	mitochondrion
3	9.69	NULL	699	Chr	Chr 5
4	9.41	NULL	1233	TF	KIM_MYC targets
5	9.3	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
6	9.3	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
7	7.72	NULL	83	BP	respiratory electron transport chain
8	7.59	NULL	370	BP	mitotic cell cycle
9	7.14	NULL	304	CC	mitochondrial inner membrane
10	7.12	NULL	152	BP	cellular metabolic process
11	7.04	NULL	530	Cancer	Lembcke_Normal vs Adenoma
12	6.22	NULL	1253	BP	small molecule metabolic process
13	6.1	NULL	649	BP	gene expression
14	6.05	NULL	253	BP	translation
15	5.98	NULL	25	BP	glutathione derivative biosynthetic process
16	5.97	NULL	44	BP	tRNA aminoacylation for protein translation
17	5.94	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
18	5.85	NULL	298	BP	DNA repair
19	5.84	NULL	579	CC	nucleolus
20	5.81	NULL	595	MF	RNA binding
Underexpressed					
1	−16.79	NULL	633	Chr	Chr 9
2	−13.25	NULL	519	Chr	Chr 14
3	−10.34	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	−10	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	−10	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	−10	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	−10	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	−9.33	NULL	280	Chr	Chr 13
9	−8.76	NULL	312	BP	immune response
10	−8.71	NULL	1135	Chr	Chr 19
11	−7.91	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
12	−7.76	NULL	269	BP	inflammatory response
13	−7.74	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
14	−7.51	NULL	683	CC	extracellular space
15	−7.48	NULL	1182	CC	extracellular region
16	−7.4	NULL	250	Lymphoma	LENZ_Stromal signature 1
17	−7.27	NULL	190	CC	extracellular matrix
18	−6.92	NULL	2659	CC	plasma membrane
19	−6.79	NULL	4	MMML CGS	MACIEJ_MMML 23
20	−6.68	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D


p−values

GW_142

Local Summary

%DE = 0.68

metagenes = 36

genes = 572

genes in genesets = 566

genes with fdr < 0.1 = 255 (245 + / 10 −)

genes with fdr < 0.05 = 203 (195 + / 8 −)

genes with fdr < 0.01 = 126 (119 + / 7 −)

<r> metagenes = 0.81

<r> genes = 0.25

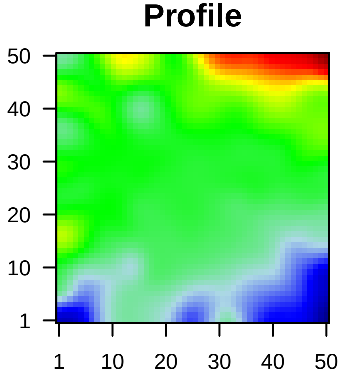
<FC> = 0.32

<shrinkage−t> = 11.29

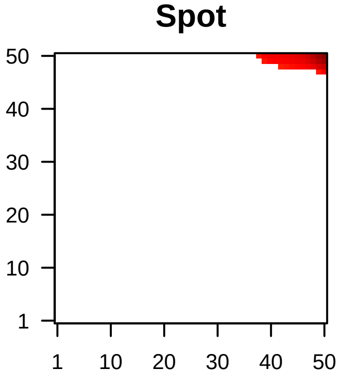
<p−value> = 0.01

<fdr> = 0.63

Profile



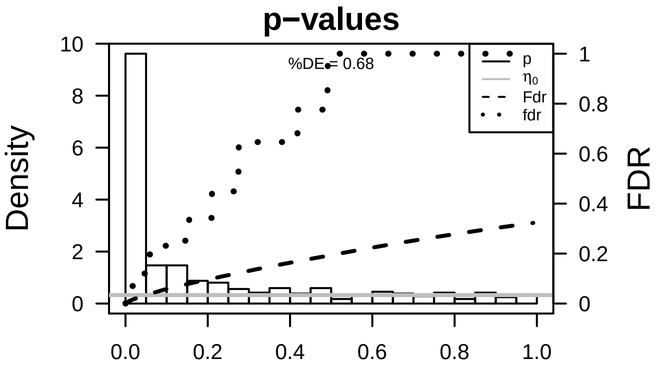
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	445	1.73	2e−16	5e−15	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:758
2	655	1.64	2e−16	5e−15	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
3	339512	1.45	2e−16	5e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	875	1.47	2e−16	5e−15	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
5	2938	1.51	2e−16	5e−15	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
6	2944	1.92	2e−16	5e−15	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
7	3866	2.16	2e−16	5e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
8	4922	1.68	2e−16	5e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
9	216	1.42	1e−15	3e−12	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
10	94234	1.36	2e−14	2e−11	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
11	2946	1.31	1e−13	1e−10	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
12	2719	1.27	1e−12	1e−10	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
13	80896	1.25	2e−12	3e−09	50 x 50	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
14	3856	1.19	2e−11	5e−09	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
15	1780	1.15	8e−11	5e−09	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
16	59271	1.15	8e−11	5e−09	50 x 48	eva−1 homolog C (C. elegans) [Source:HGNC Symbol;Acc:1
17	4780	1.15	1e−10	8e−09	50 x 50	nuclear factor, erythroid 2−like 2 [Source:HGNC Symbol;Acc:
18	55244	1.13	2e−10	8e−09	50 x 50	solute carrier family 47 (multidrug and toxin extrusion), memb
19	79190	1.13	2e−10	8e−09	50 x 47	iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
20	29785	1.13	2e−10	3e−08	50 x 50	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.24	NULL	75 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	19.24	NULL	75 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	16.57	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
4	14.04	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
5	13.51	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
6	13.02	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
7	12.79	NULL	5 / 20	MF	glutathione transferase activity
8	12.2	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
9	12.05	NULL	9 / 34	BP	glutathione metabolic process
10	11.83	NULL	7 / 25	BP	glutathione derivative biosynthetic process
11	11.49	NULL	3 / 11	MF	glutathione binding
12	11.49	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	11.3	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	10.84	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
15	10.6	NULL	10 / 16	Cancer	WOLFER_overlap genes
16	10.33	NULL	4 / 13	BP	regulation of blood vessel size
17	10.01	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
18	10.01	NULL	5 / 15	Cancer	BEN−PORATH_UP
19	9.96	NULL	22 / 57	Glio	developing astrocytes
20	9.95	NULL	78 / 370	BP	mitotic cell cycle
21	9.91	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
22	9.84	NULL	80 / 530	Cancer	Lembcke_Normal vs Adenoma
23	9.64	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
24	9.57	NULL	11 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
25	9.57	NULL	10 / 30	BP	DNA strand elongation involved in DNA replication
26	9.42	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
27	9.4	NULL	8 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
28	9.13	NULL	6 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
29	9.05	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
30	8.82	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
31	8.46	NULL	13 / 119	BP	xenobiotic metabolic process
32	8.41	NULL	18 / 66	CC	condensed chromosome kinetochore
33	8.35	NULL	13 / 35	BP	mitotic nuclear envelope disassembly
34	8.27	NULL	43 / 232	BP	mitosis
35	8.23	NULL	7 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
36	8.02	NULL	2 / 14	CC	membrane−bounded vesicle
37	7.89	NULL	7 / 15	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
38	7.82	NULL	3 / 6	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_DN
39	7.81	NULL	7 / 11	BP	mitotic metaphase plate congression
40	7.68	NULL	16 / 100	Lymphoma	ROSOLOWSKI_blue total

GW_142

Local Summary

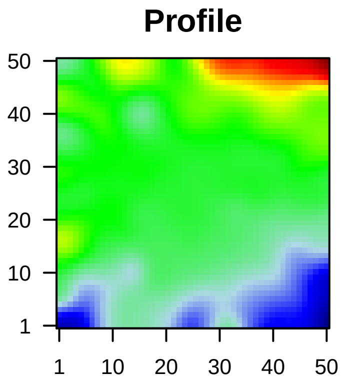
%DE = 0.65
metagenes = 1
genes = 16
genes in genesets = 15

genes with fdr < 0.1 = 5 (5 + / 0 −)
genes with fdr < 0.05 = 3 (3 + / 0 −)
genes with fdr < 0.01 = 2 (2 + / 0 −)

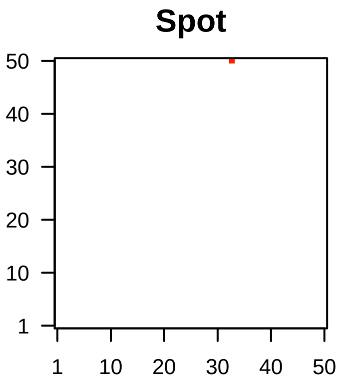
<r> metagenes = NA
<r> genes = 0.39

<FC> = 0.26
<shrinkage−t> = 9.27
<p−value> = 0.04
<fdr> = 0.7

Profile



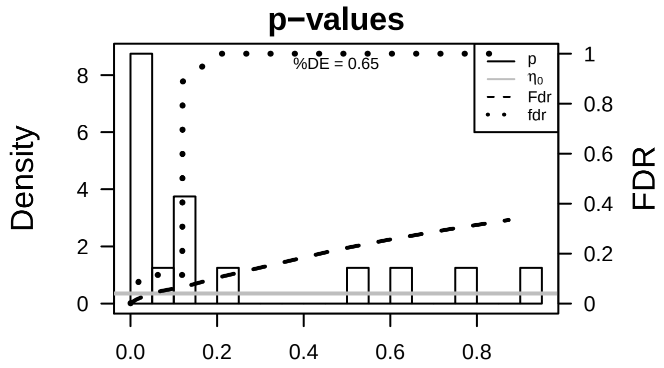
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4724	0.67	2e−04	8e−04	33 x 50	NADH dehydrogenase (ubiquinone) Fe−S protein 4, 18kDa (N
2	7388	0.64	3e−04	1e−02	33 x 50	ubiquinol−cytochrome c reductase hinge protein [Source:HGN
3	10987	0.55	2e−03	1e−02	33 x 50	COP9 signalosome subunit 5 [Source:HGNC Symbol;Acc:224
4	1349	0.5	5e−03	5e−02	33 x 50	cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;Ac
5	63933	0.43	1e−02	6e−02	33 x 50	mitochondrial calcium uniporter regulator 1 [Source:HGNC Sy
6	64801	0.4	3e−02	1e−01	33 x 50	ARV1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:29
7	29093	0.35	5e−02	1e−01	33 x 50	mitochondrial ribosomal protein L22 [Source:HGNC Symbol;A
8	27089	0.29	7e−02	1e−01	33 x 50	ubiquinol−cytochrome c reductase, complex III subunit VII, 9.5
9	84833	−0.28	1e−01	1e−01	33 x 50	up−regulated during skeletal muscle growth 5 homolog (mous
10	4709	0.27	1e−01	1e−01	33 x 50	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12
11	401505	0.27	1e−01	9e−01	33 x 50	translocase of outer mitochondrial membrane 5 homolog (yea
12	4729	0.22	2e−01	1e+00	33 x 50	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa [So
13	27109	−0.12	5e−01	1e+00	33 x 50	ATP synthase, H+ transporting, mitochondrial Fo complex, su
14	9978	0.09	6e−01	1e+00	33 x 50	ring−box 1, E3 ubiquitin protein ligase [Source:HGNC Symbo
15	10597	−0.05	8e−01	1e+00	33 x 50	
16	285381	−0.02	9e−01	1e+00	33 x 50	diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:2771

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	30.05	NULL	2 / 13	CC	mitochondrial respiratory chain
2	25.49	NULL	6 / 83	BP	respiratory electron transport chain
3	22.6	NULL	1 / 10	MF	oxidoreductase activity, acting on NAD(P)H
4	19.05	NULL	3 / 34	MF	NADH dehydrogenase (ubiquinone) activity
5	18.74	NULL	3 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
6	18.45	NULL	3 / 36	CC	mitochondrial respiratory chain complex I
7	18.42	NULL	6 / 152	BP	cellular metabolic process
8	16.92	NULL	1 / 16	BP	cellular respiration
9	16.92	NULL	1 / 16	BP	mitochondrial respiratory chain complex I assembly
10	16.34	NULL	1 / 12	BP	oxidative phosphorylation
11	16.32	NULL	1 / 17	BP	cAMP−mediated signaling
12	15.69	NULL	1 / 13	BP	regulation of JNK cascade
13	14.67	NULL	1 / 10	CC	integral to mitochondrial inner membrane
14	14.39	NULL	1 / 15	CC	eukaryotic translation initiation factor 3 complex
15	14.39	NULL	1 / 15	GSEA C2	BIOCARTA_HIF_PATHWAY
16	12.69	NULL	1 / 16	Cancer	GENTLES_modul10
17	12.69	NULL	1 / 16	GSEA C2	BARIS_THYROID_CANCER_UP
18	12.45	NULL	1 / 13	BP	calcium ion import
19	12.19	NULL	1 / 28	BP	regulation of protein phosphorylation
20	12.01	NULL	1 / 20	BP	aerobic respiration
21	11.93	NULL	1 / 10	CC	large ribosomal subunit
22	11.72	NULL	1 / 30	BP	reactive oxygen species metabolic process
23	10.64	NULL	1 / 12	GSEA C2	SHEPARD_CRUSH_AND_BURN_MUTANT_UP
24	10.6	NULL	8 / 304	CC	mitochondrial inner membrane
25	10.51	NULL	1 / 22	miRNA target starBase	hsa−miR−1250
26	10.24	NULL	1 / 38	BP	positive regulation of fibroblast proliferation
27	10.24	NULL	1 / 23	miRNA target starBase	hsa−miR−1225−5p
28	10.09	NULL	1 / 39	BP	response to cAMP
29	10.06	NULL	1 / 11	BP	cerebellar Purkinje cell layer development
30	9.53	NULL	1 / 26	MF	cytochrome−c oxidase activity
31	9.32	NULL	1 / 18	BP	cholesterol transport
32	9.22	NULL	1 / 32	CC	COP9 signalosome
33	8.4	NULL	1 / 54	Glio	willscher_GBM_proteomics_wtOnly_SpotG
34	8.29	NULL	1 / 38	miRNA target starBase	hsa−miR−1224−5p
35	6.85	NULL	1 / 54	MF	translation initiation factor activity
36	6.77	NULL	1 / 31	BP	bile acid metabolic process
37	6.65	NULL	1 / 56	BP	protein heterooligomerization
38	6.42	NULL	1 / 23	BP	midbrain development
39	5.96	NULL	1 / 59	miRNA target starBase	hsa−miR−556−5p
40	5.81	NULL	1 / 71	miRNA target starBase	hsa−miR−1254

GW_142

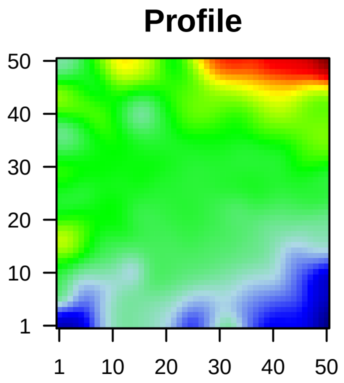
Local Summary

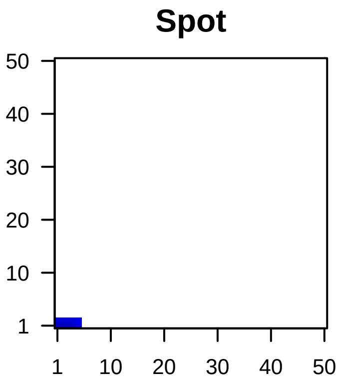
%DE = 0.72
metagenes = 10
genes = 186
genes in genesets = 185

genes with fdr < 0.1 = 101 (7 + / 94 −)
genes with fdr < 0.05 = 70 (5 + / 65 −)
genes with fdr < 0.01 = 47 (3 + / 44 −)

<r> metagenes = 0.98
<r> genes = 0.45

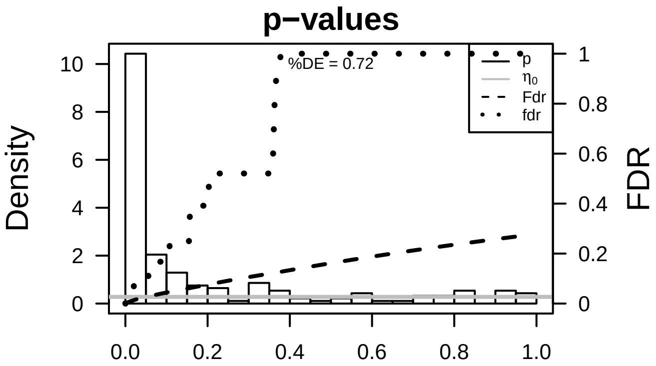
<FC> = −0.37
<shrinkage−t> = −12.94
<p−value> = 0
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3040	−2	2e−16	4e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	3043	−2.09	2e−16	4e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
3	4314	−1.48	2e−16	4e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
4	12	−1.41	2e−15	5e−14	1 x 1	
5	3956	−1.41	2e−15	5e−14	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
6	4318	−1.4	3e−15	7e−13	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
7	2919	−1.36	2e−14	9e−13	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
8	3039	−1.35	3e−14	7e−10	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	4060	1.2	1e−11	8e−09	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
10	4320	1.13	2e−10	7e−08	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
11	91663	−1.07	1e−09	2e−07	2 x 1	myeloid−associated differentiation marker [Source:HGNC Sy
12	6696	−1.02	8e−09	2e−07	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
13	5054	−1.02	1e−08	8e−07	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
14	3553	−0.99	3e−08	2e−06	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
15	6515	−0.96	6e−08	3e−06	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
16	7431	−0.94	1e−07	3e−05	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
17	25878	−0.85	2e−06	3e−05	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
18	7076	−0.84	2e−06	3e−05	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
19	4692	−0.84	2e−06	3e−05	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
20	2014	−0.84	2e−06	7e−05	1 x 1	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:33



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.73	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
2	−29.6	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
3	−23.56	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
4	−23.27	NULL	3 / 11	MF	oxygen transporter activity
5	−22.29	NULL	2 / 10	CC	hemoglobin complex
6	−21.61	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
7	−21.54	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
8	−21.13	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
9	−20.64	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
10	−20.07	NULL	5 / 19	MF	peroxidase activity
11	−20.03	NULL	57 / 190	CC	extracellular matrix
12	−19.34	NULL	3 / 14	CC	endocytic vesicle lumen
13	−18.14	NULL	60 / 250	Lymphoma	LENZ_Stromal signature 1
14	−17.95	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
15	−17.77	NULL	3 / 19	BP	hydrogen peroxide catabolic process
16	−17.34	NULL	55 / 242	BP	extracellular matrix organization
17	−16.67	NULL	29 / 69	BP	extracellular matrix disassembly
18	−16.43	NULL	5 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
19	−15.76	NULL	3 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CA
20	−15.74	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
21	−15.74	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN
22	−15.73	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
23	−15.33	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
24	−15.16	NULL	4 / 29	BP	positive regulation of cell death
25	−15.05	NULL	4 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
26	−14.84	NULL	26 / 64	BP	collagen catabolic process
27	−14.75	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
28	−14.75	NULL	10 / 35	Glio	Colman_survival_associated
29	−14.74	NULL	3 / 15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
30	−14.66	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
31	−14.49	NULL	4 / 26	MF	oxygen binding
32	−14.41	NULL	5 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
33	−14.37	NULL	2 / 22	BP	bicarbonate transport
34	−14.22	NULL	2 / 6	Glio	Martinez_Glio_hypometh
35	−14.19	NULL	83 / 1182	CC	extracellular region
36	−14.08	NULL	4 / 26	BP	positive regulation of nitric oxide biosynthetic process
37	−13.97	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
38	−13.94	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
39	−13.68	NULL	4 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
40	−13.63	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP

GW_142

Local Summary

%DE = 0.78

metagenes = 41

genes = 572

genes in genesets = 568

genes with fdr < 0.1 = 288 (30 + / 258 −)

genes with fdr < 0.05 = 225 (29 + / 196 −)

genes with fdr < 0.01 = 135 (21 + / 114 −)

<r> metagenes = 0.85

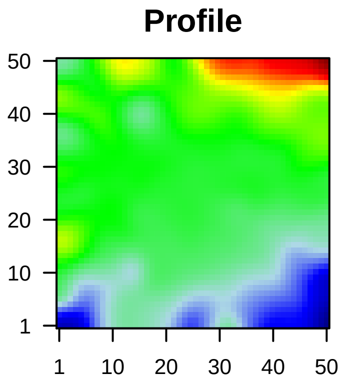
<r> genes = 0.35

<FC> = −0.28

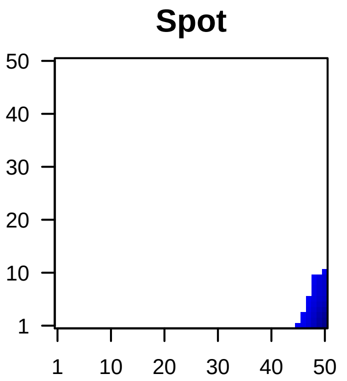
<shrinkage−t> = −9.81

<p−value> = 0.01

<fdr> = 0.63



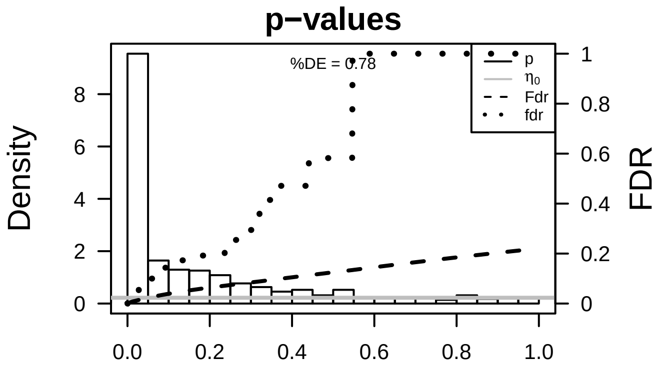
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3123	1.79	2e−16	1e−14	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
2	5920	1.61	2e−16	1e−14	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
3	6192	−1.44	4e−16	1e−12	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
4	3543	1.26	9e−15	4e−12	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
5	3512	1.34	4e−14	5e−12	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
6	10628	−1.3	8e−14	1e−10	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
7	2878	−1.26	1e−12	2e−08	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
8	10232	−1.13	2e−10	2e−08	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
9	1675	−1.12	3e−10	1e−07	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
10	3120	−1.07	1e−09	3e−07	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
11	92304	−1.04	4e−09	3e−07	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
12	6422	−1.04	5e−09	4e−07	50 x 8	secreted frizzled−related protein 1 [Source:HGNC Symbol;Ac
13	6363	−1.02	9e−09	4e−07	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
14	1512	1	2e−08	4e−07	47 x 1	cathepsin H [Source:HGNC Symbol;Acc:2535]
15	23048	−1	2e−08	4e−07	49 x 1	formin binding protein 1 [Source:HGNC Symbol;Acc:17069]
16	84952	−0.99	2e−08	4e−07	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
17	2934	−0.99	2e−08	4e−07	50 x 9	gelsolin [Source:HGNC Symbol;Acc:4620]
18	260436	−0.99	3e−08	2e−06	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
19	2532	−0.97	4e−08	2e−06	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
20	25891	0.97	5e−08	2e−06	50 x 8	peptidase domain containing associated with muscle regener



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.72	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−16.23	NULL	130 / 553	Cancer	Lembcke_Colonic Inflammation
3	−15.09	NULL	59 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	−15.09	NULL	59 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	−15.09	NULL	59 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	−15.09	NULL	59 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	−14.71	NULL	103 / 417	H.Tiss	WIRTH_Immune system
8	−13.6	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
9	−12.21	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
10	−11.57	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
11	−11.47	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
12	−11.34	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
13	−11.02	NULL	12 / 43	MF	chemokine activity
14	−10.55	NULL	7 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
15	−10.35	NULL	5 / 14	BP	ruffle organization
16	−10.32	NULL	68 / 312	BP	immune response
17	−10.27	NULL	4 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
18	−10.15	NULL	73 / 683	CC	extracellular space
19	−9.94	NULL	3 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
20	−9.92	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
21	−9.91	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
22	−9.87	NULL	6 / 20	BP	actin filament polymerization
23	−9.85	NULL	4 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
24	−9.76	NULL	5 / 12	BP	dendritic cell chemotaxis
25	−9.6	NULL	4 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
26	−9.43	NULL	4 / 10	BP	actin polymerization or depolymerization
27	−9.38	NULL	4 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
28	−9.16	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
29	−9.09	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
30	−8.93	NULL	15 / 76	BP	defense response
31	−8.7	NULL	4 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
32	−8.7	NULL	4 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
33	−8.29	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
34	−8.04	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
35	−7.97	NULL	2 / 7	GSEA C2	LEE_NAIVE_T_LYMPHOCYTE
36	−7.96	NULL	4 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
37	−7.9	NULL	3 / 14	GSEA C2	GOLUB_ALL_VS_AML_DN
38	−7.87	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
39	−7.85	NULL	4 / 16	GSEA C2	BROWNE_HCMV_INFECTION_2HR_UP
40	−7.84	NULL	106 / 1182	CC	extracellular region