GW_091

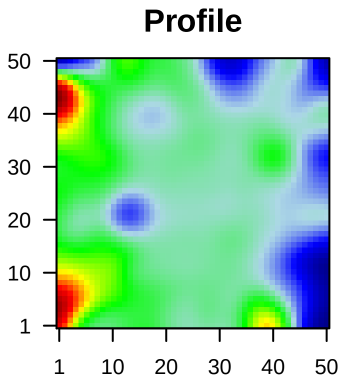
Global Summary

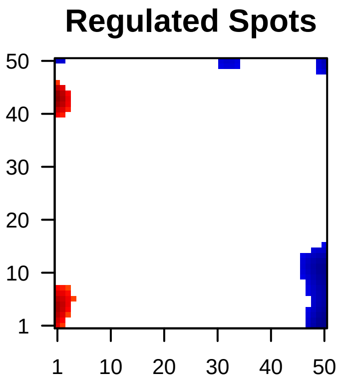
%DE = 0.14

genes with fdr < 0.2 = 1828 (1030 + / 798 −)
genes with fdr < 0.1 = 1473 (844 + / 629 −)
genes with fdr < 0.05 = 1160 (669 + / 491 −)
genes with fdr < 0.01 = 801 (476 + / 325 −)

genes in genesets = 16332

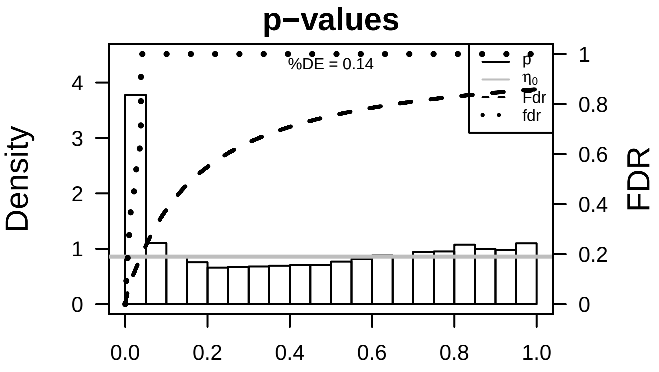
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.29	2e−16	4e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	−1.82	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	−1.5	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	−1.78	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	216	−1.58	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	218	−2.7	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	23120	−1.28	2e−16	4e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
8	633	1.22	2e−16	4e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
9	260436	−1.31	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
10	760	1.36	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
11	768	1.49	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
12	1001	1.42	2e−16	4e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
13	1048	−1.6	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
14	4680	−1.75	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
15	22802	−1.85	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	1258	1.48	2e−16	4e−14	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symb
17	1308	1.45	2e−16	4e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	1277	1.37	2e−16	4e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
19	1289	1.33	2e−16	4e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
20	51200	1.56	2e−16	4e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.96	NULL	918	Chr	Chr 17
2	10.66	NULL	717	Chr	Chr 16
3	9.17	NULL	866	Chr	Chr 12
4	8.7	NULL	12	BP	hemidesmosome assembly
5	8.19	NULL	242	BP	extracellular matrix organization
6	7.38	NULL	117	Glio	GIEZELT_GBM_WT_up_VS_mut
7	7.28	NULL	534	Chr	Chr 8
8	6.98	NULL	403	BP	cell adhesion
9	6.86	NULL	69	BP	extracellular matrix disassembly
10	6.58	NULL	16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
11	6.46	NULL	76	BP	epidermis development
12	6.34	NULL	2659	CC	plasma membrane
13	6.27	NULL	70	BP	cell junction assembly
14	6.22	NULL	633	Chr	Chr 9
15	6.16	NULL	64	BP	collagen catabolic process
16	6.04	NULL	21	CC	desmosome
17	6.02	NULL	250	Lymphoma	LENZ_Stromal signature 1
18	6.02	NULL	16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
19	5.95	NULL	16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
20	5.93	NULL	16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
Underexpressed					
1	−12.59	NULL	699	Chr	Chr 5
2	−8.01	NULL	83	BP	respiratory electron transport chain
3	−7.47	NULL	15	CC	MHC class II protein complex
4	−7.17	NULL	52	Chr	Chr HSCHR6_MHC_QBL
5	−7.13	NULL	13	BP	negative regulation of peptidase activity
6	−7.12	NULL	152	BP	cellular metabolic process
7	−6.73	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
8	−6.65	NULL	119	BP	xenobiotic metabolic process
9	−6.5	NULL	153	MF	structural constituent of ribosome
10	−6.48	NULL	167	CC	ribosome
11	−6.4	NULL	1318	CC	mitochondrion
12	−6.36	NULL	47	BP	antigen processing and presentation
13	−6.29	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
14	−6.28	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−6.22	NULL	12	BP	cellular aldehyde metabolic process
16	−6.21	NULL	304	CC	mitochondrial inner membrane
17	−6.1	NULL	253	BP	translation
18	−5.93	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
19	−5.77	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
20	−5.59	NULL	34	MF	NADH dehydrogenase (ubiquinone) activity

GW_091

Local Summary

%DE = 0.68

metagenes = 23

genes = 344

genes in genesets = 341

genes with fdr < 0.1 = 207 (193 + / 14 −)

genes with fdr < 0.05 = 180 (171 + / 9 −)

genes with fdr < 0.01 = 152 (146 + / 6 −)

<r> metagenes = 0.94

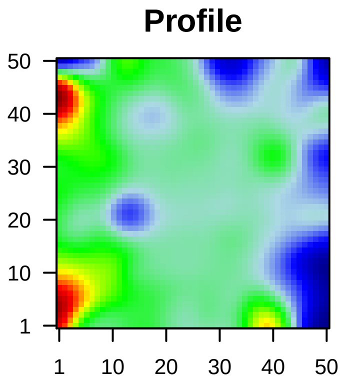
<r> genes = 0.32

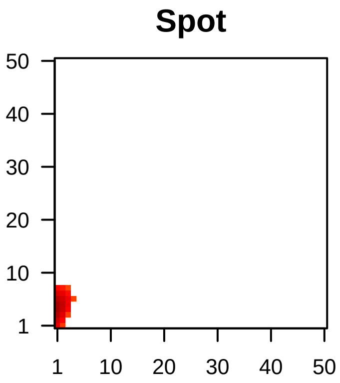
<FC> = 0.38

<shrinkage−t> = 13.29

<p−value> = 0

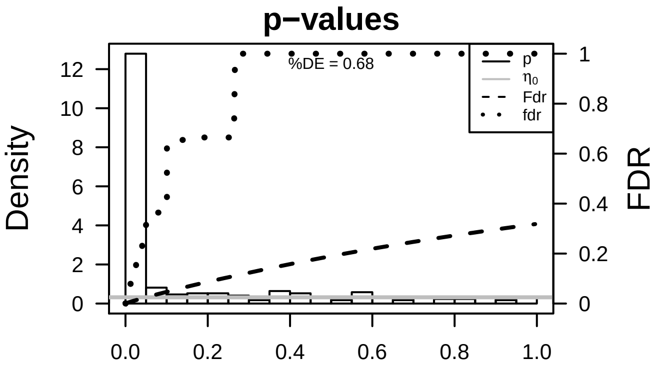
<fdr> = 0.43





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	768	1.49	2e−16	2e−15	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
2	1258	1.48	2e−16	2e−15	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
3	1277	1.37	2e−16	2e−15	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1289	1.33	2e−16	2e−15	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	285761	1.57	2e−16	2e−15	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
6	2195	1.28	2e−16	2e−15	1 x 5	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
7	3678	1.38	2e−16	2e−15	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
8	4311	1.57	2e−16	2e−15	2 x 1	membrane metallo−endopeptidase [Source:HGNC Symbol;A
9	169611	1.25	2e−16	2e−15	1 x 5	olfactomedin−like 2A [Source:HGNC Symbol;Acc:27270]
10	8877	1.26	2e−16	2e−15	3 x 5	sphingosine kinase 1 [Source:HGNC Symbol;Acc:11240]
11	7078	1.27	2e−16	2e−15	2 x 1	TIMP metallopeptidase inhibitor 3 [Source:HGNC Symbol;Ac
12	3371	1.95	2e−16	2e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
13	90226	1.23	2e−16	2e−15	1 x 5	urocortin 2 [Source:HGNC Symbol;Acc:18414]
14	56603	1.19	7e−16	7e−14	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
15	60675	1.19	7e−16	7e−14	1 x 1	prokineticin 2 [Source:HGNC Symbol;Acc:18455]
16	1294	1.18	1e−15	7e−13	1 x 5	collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
17	401138	1.15	8e−15	2e−12	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
18	3918	1.12	4e−14	2e−12	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
19	4316	−1.11	5e−14	2e−12	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
20	8632	1.11	6e−14	2e−11	1 x 8	dynein, axonemal, heavy chain 17 [Source:HGNC Symbol;Ac



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.5	NULL	59 / 242	BP	extracellular matrix organization
2	20.35	NULL	6 / 11	MF	platelet−derived growth factor binding
3	19.89	NULL	8 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
4	18.79	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
5	18.45	NULL	5 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
6	17.59	NULL	21 / 64	BP	collagen catabolic process
7	17.24	NULL	22 / 69	BP	extracellular matrix disassembly
8	16.79	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
9	15.27	NULL	5 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
10	15.18	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	15.18	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	15.18	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	15.18	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	14.96	NULL	44 / 250	Lymphoma	LENZ_Stromal signature 1
15	14.69	NULL	37 / 190	CC	extracellular matrix
16	14.44	NULL	55 / 403	BP	cell adhesion
17	14.43	NULL	11 / 35	Glio	Colman_survival_associated
18	13.93	NULL	12 / 37	BP	collagen fibril organization
19	13.88	NULL	10 / 16	MMML CGS	MACIEJ_MMML 1
20	13.71	NULL	3 / 10	BP	protein heterotrimerization
21	13.58	NULL	11 / 40	BP	cellular response to amino acid stimulus
22	13.15	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
23	12.88	NULL	3 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
24	12.81	NULL	3 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
25	12.78	NULL	4 / 13	GSEA C2	HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENES
26	12.7	NULL	6 / 12	miRNA target	miR−29c
27	12.47	NULL	20 / 153	CC	endoplasmic reticulum lumen
28	12.34	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
29	12.28	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
30	11.9	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
31	11.86	NULL	8 / 27	CC	integrin complex
32	11.73	NULL	3 / 8	GSEA C2	HUANG_DASATINIB_RESISTANCE_UP
33	11.65	NULL	17 / 83	CC	basement membrane
34	11.61	NULL	6 / 12	BP	hemidesmosome assembly
35	11.5	NULL	4 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
36	11.24	NULL	6 / 19	MF	L−ascorbic acid binding
37	11.08	NULL	100 / 1182	CC	extracellular region
38	10.89	NULL	15 / 106	BP	leukocyte migration
39	10.83	NULL	5 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
40	10.74	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY

GW_091

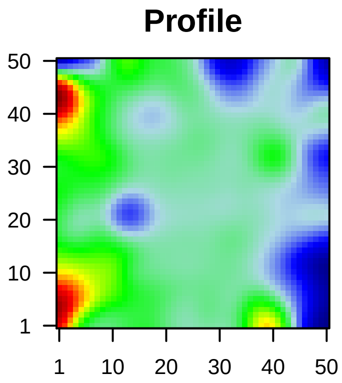
Local Summary

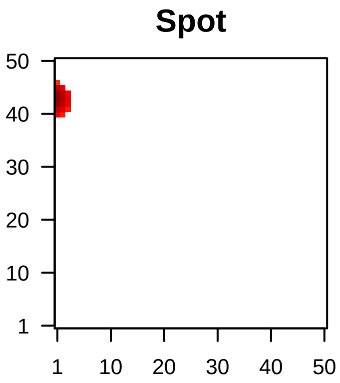
%DE = 0.78
metagenes = 17
genes = 229
genes in genesets = 226

genes with fdr < 0.1 = 144 (135 + / 9 −)
genes with fdr < 0.05 = 134 (126 + / 8 −)
genes with fdr < 0.01 = 116 (108 + / 8 −)

<r> metagenes = 0.96
<r> genes = 0.36

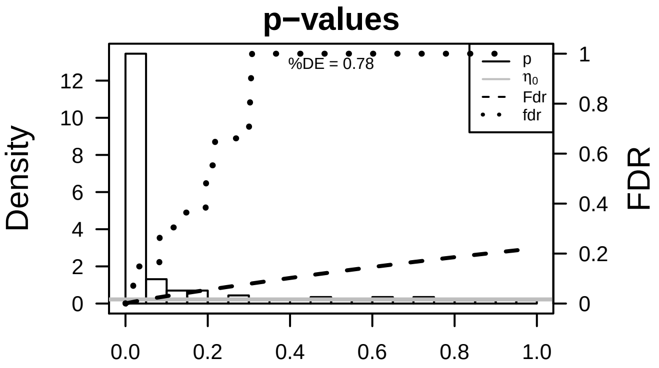
<FC> = 0.47
<shrinkage−t> = 16.65
<p−value> = 0
<fdr> = 0.39





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	760	1.36	2e−16	7e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	1001	1.42	2e−16	7e−16	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
3	1308	1.45	2e−16	7e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
4	51200	1.56	2e−16	7e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
5	2167	1.59	2e−16	7e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
6	126917	1.6	2e−16	7e−16	1 x 45	intermediate filament family orphan 2 [Source:HGNC Symbol
7	3489	2.17	2e−16	7e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
8	53833	1.32	2e−16	7e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
9	3861	1.33	2e−16	7e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
10	3868	1.38	2e−16	7e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
11	9119	2.07	2e−16	7e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
12	10397	1.21	2e−16	7e−16	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
13	56901	1.58	2e−16	7e−16	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
14	5738	1.21	2e−16	7e−16	1 x 41	prostaglandin F2 receptor inhibitor [Source:HGNC Symbol;Ac
15	5744	1.81	2e−16	7e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
16	404203	1.71	2e−16	7e−16	1 x 43	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
17	5317	1.19	9e−16	2e−14	1 x 46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
18	84985	1.18	2e−15	2e−14	1 x 44	family with sequence similarity 83, member A [Source:HGNC
19	8601	1.18	2e−15	2e−14	1 x 44	regulator of G−protein signaling 20 [Source:HGNC Symbol;A
20	113146	1.18	2e−15	1e−13	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.17	NULL	5 / 12	BP	hemidesmosome assembly
2	17.62	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	16.27	NULL	14 / 82	CC	intermediate filament
4	14.63	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
5	14.45	NULL	12 / 76	BP	epidermis development
6	14.08	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
7	13.53	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
8	12.57	NULL	19 / 135	H.Tiss	WIRTH_Mucosa
9	12.08	NULL	2 / 2	miRNA target	miR−199a*
10	11.41	NULL	5 / 44	CC	keratin filament
11	11.34	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
12	11.33	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
13	11.28	NULL	6 / 21	CC	desmosome
14	11.11	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
15	10.68	NULL	3 / 25	BP	response to zinc ion
16	10.07	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
17	9.49	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
18	9.32	NULL	3 / 38	BP	epithelial cell differentiation
19	9.28	NULL	3 / 10	BP	negative regulation of interleukin−2 production
20	9.27	NULL	10 / 82	MF	structural constituent of cytoskeleton
21	9.24	NULL	3 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
22	9.2	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
23	9.13	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
24	8.95	NULL	2 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
25	8.95	NULL	2 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
26	8.94	NULL	3 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
27	8.93	NULL	6 / 70	BP	cell junction assembly
28	8.92	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
29	8.78	NULL	12 / 186	MF	structural molecule activity
30	8.77	NULL	54 / 572	Disease	GUDJ_psoriasis up
31	8.71	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
32	8.68	NULL	5 / 32	CC	cell−cell adherens junction
33	8.62	NULL	4 / 20	MF	scaffold protein binding
34	8.44	NULL	3 / 12	CC	fascia adherens
35	8.42	NULL	2 / 10	GSEA C2	RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
36	8.42	NULL	2 / 10	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
37	8.4	NULL	2 / 12	MF	fatty acid binding
38	8.36	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
39	8.28	NULL	2 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
40	8.23	NULL	2 / 10	BP	skeletal muscle tissue regeneration

GW_091

Local Summary

%DE = 0.65

metagenes = 63

genes = 771

genes in genesets = 762

genes with fdr < 0.1 = 269 (29 + / 240 −)

genes with fdr < 0.05 = 236 (26 + / 210 −)

genes with fdr < 0.01 = 150 (13 + / 137 −)

<r> metagenes = 0.79

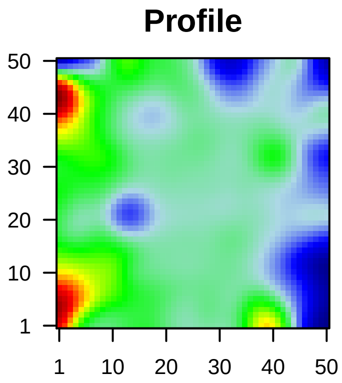
<r> genes = 0.27

<FC> = −0.24

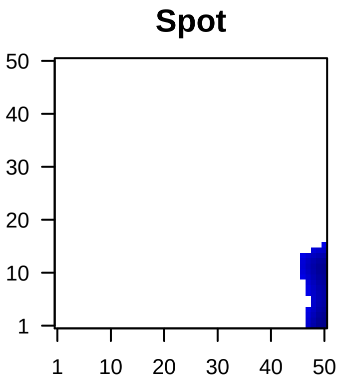
<shrinkage−t> = −8.31

<p−value> = 0.01

<fdr> = 0.65



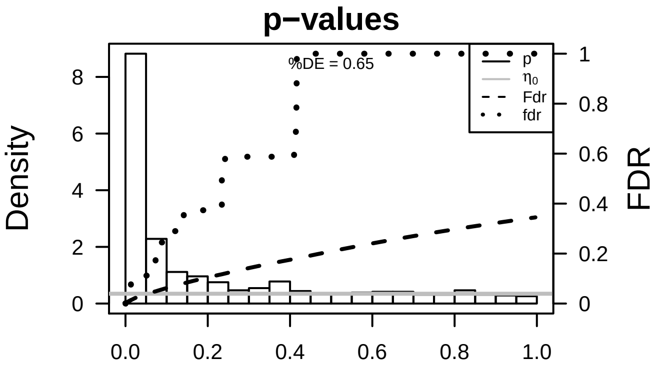
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.31	2e−16	1e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
2	3169	−1.32	2e−16	1e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
3	3512	−1.5	2e−16	1e−14	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
4	6192	−1.27	2e−16	1e−14	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
5	10537	−1.38	2e−16	1e−14	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
6	894	−1.19	9e−16	4e−13	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
7	3122	−1.09	2e−15	1e−12	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
8	5996	−1.15	7e−15	4e−12	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
9	2568	−1.13	3e−14	4e−12	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
10	83699	−1.12	4e−14	3e−11	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
11	51316	−1.08	2e−13	3e−11	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
12	7033	−1.07	4e−13	3e−11	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
13	1396	1.07	4e−13	5e−10	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
14	3128	−1.04	2e−12	1e−09	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
15	2745	−1.01	8e−12	2e−09	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
16	399959	−1	1e−11	2e−09	50 x 6	
17	26002	−0.99	2e−11	2e−08	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
18	57559	−0.94	2e−10	2e−08	48 x 2	STAM binding protein−like 1 [Source:HGNC Symbol;Acc:241
19	54855	−0.94	2e−10	2e−08	49 x 1	family with sequence similarity 46, member C [Source:HGNC
20	10551	−0.94	2e−10	2e−08	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.07	NULL	12 / 15	CC	MHC class II protein complex
2	−16.3	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	−15.57	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
4	−12.43	NULL	17 / 47	BP	antigen processing and presentation
5	−10.98	NULL	4 / 7	MMML CGS	MACIEJ_MMML 5
6	−10.69	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
7	−10.64	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
8	−10.2	NULL	4 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
9	−10.14	NULL	4 / 10	BP	epoxygenase P450 pathway
10	−9.91	NULL	7 / 15	GSEA C2	NAKAJIMA_MAST_CELL
11	−9.65	NULL	5 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
12	−9.43	NULL	4 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
13	−9.38	NULL	4 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
14	−9.35	NULL	6 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
15	−9.32	NULL	9 / 16	GSEA C2	SU_THYMUS
16	−9.3	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	−8.99	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
18	−8.94	NULL	9 / 28	CC	transport vesicle membrane
19	−8.77	NULL	123 / 553	Cancer	Lembcke_Colonic Inflammation
20	−8.75	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
21	−8.7	NULL	62 / 312	BP	immune response
22	−8.36	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
23	−8.3	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
24	−8.29	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
25	−8.22	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
26	−8.2	NULL	3 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
27	−7.94	NULL	4 / 18	MF	aromatase activity
28	−7.92	NULL	10 / 35	CC	trans−Golgi network membrane
29	−7.8	NULL	2 / 11	GSEA C2	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
30	−7.79	NULL	5 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
31	−7.71	NULL	5 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
32	−7.71	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
33	−7.64	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
34	−7.48	NULL	4 / 15	GSEA C2	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
35	−7.48	NULL	7 / 35	MF	monooxygenase activity
36	−7.37	NULL	2 / 5	Lymphoma	WRIGHT_custom ABC−DLBCL UP
37	−7.33	NULL	4 / 26	Disease	BCHETNIA_EBM−DM up
38	−7.22	NULL	14 / 60	BP	T cell costimulation
39	−7.18	NULL	3 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
40	−7.11	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP

GW_091

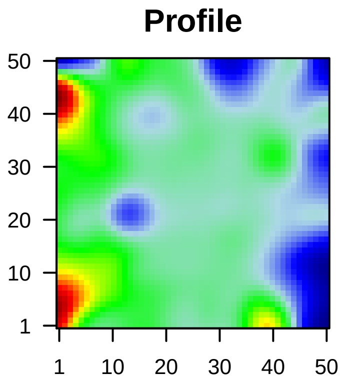
Local Summary

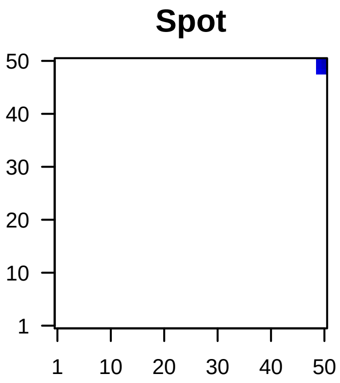
%DE = 0.57
metagenes = 6
genes = 120
genes in genesets = 119

genes with fdr < 0.1 = 51 (5 + / 46 −)
genes with fdr < 0.05 = 40 (3 + / 37 −)
genes with fdr < 0.01 = 31 (2 + / 29 −)

<r> metagenes = 0.99
<r> genes = 0.31

<FC> = −0.28
<shrinkage−t> = −9.9
<p−value> = 0
<fdr> = 0.59


Profile


Spot

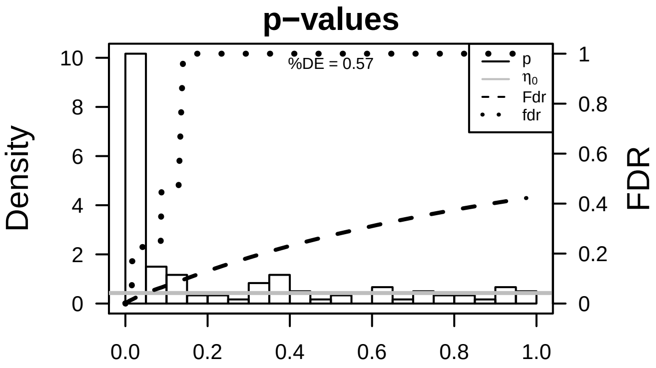
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.58	2e−16	4e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	3866	−1.27	2e−16	4e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
3	4922	−1.6	2e−16	4e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
4	339512	−1.2	4e−16	7e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
5	6657	−1.18	2e−15	1e−13	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
6	154664	−1.16	4e−15	1e−12	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
7	11166	−1.13	3e−14	2e−09	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
8	8745	−0.97	5e−11	1e−08	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
9	4915	−0.94	2e−10	2e−06	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
10	5635	0.81	5e−08	2e−05	50 x 50	phosphoribosyl pyrophosphate synthetase−associated protei
11	79679	−0.75	3e−07	2e−05	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:
12	8544	−0.72	1e−06	2e−05	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
13	4953	−0.71	2e−06	2e−05	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
14	1528	−0.7	2e−06	2e−05	50 x 50	cytochrome b5 type A (microsomal) [Source:HGNC Symbol;
15	83959	−0.7	2e−06	2e−05	50 x 50	solute carrier family 4, sodium borate transporter, member 11
16	2938	−0.7	2e−06	8e−05	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
17	256764	−0.68	4e−06	2e−04	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
18	5625	−0.66	9e−06	6e−04	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
19	57291	−0.63	2e−05	6e−04	50 x 50	differentiation antagonizing non−protein coding RNA [Source:
20	120	−0.61	3e−05	9e−04	50 x 50	adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.94	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	−28.49	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	−17.98	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
4	−17.98	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
5	−16.42	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
6	−16	NULL	3 / 13	BP	regulation of blood vessel size
7	−14.21	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
8	−14.19	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
9	−14.19	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
10	−14.07	NULL	2 / 12	BP	cellular aldehyde metabolic process
11	−13.36	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
12	−13.36	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
13	−12.81	NULL	1 / 11	Glio	neurons_glio
14	−12.79	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
15	−12.38	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
16	−12.21	NULL	2 / 23	BP	stem cell differentiation
17	−12.16	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
18	−12.16	NULL	1 / 7	miRNA target	miR−145
19	−12.03	NULL	1 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
20	−11.91	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
21	−11.25	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
22	−11.25	NULL	1 / 8	miRNA 3UTR	CTGCA−450
23	−11.19	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
24	−11.17	NULL	8 / 34	BP	glutathione metabolic process
25	−11.02	NULL	1 / 14	MF	Ras GTPase activator activity
26	−11.02	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
27	−11.02	NULL	1 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
28	−10.74	NULL	1 / 15	MF	neuropeptide hormone activity
29	−10.66	NULL	11 / 119	BP	xenobiotic metabolic process
30	−10.6	NULL	1 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
31	−10.44	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
32	−10.25	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
33	−9.88	NULL	1 / 10	MF	miRNA binding
34	−9.73	NULL	6 / 25	BP	glutathione derivative biosynthetic process
35	−9.6	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
36	−9.56	NULL	1 / 18	BP	positive regulation of Ras GTPase activity
37	−9.56	NULL	1 / 18	BP	retinol metabolic process
38	−9.47	NULL	1 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
39	−9.44	NULL	2 / 19	BP	anatomical structure formation involved in morphogenesis
40	−9.35	NULL	1 / 11	BP	neuronal stem cell maintenance


p−values

GW_091

Local Summary

%DE = 0.65

metagenes = 8

genes = 135

genes in genesets = 132

genes with fdr < 0.1 = 67 (0 + / 67 −)

genes with fdr < 0.05 = 35 (0 + / 35 −)

genes with fdr < 0.01 = 15 (0 + / 15 −)

<r> metagenes = 0.98

<r> genes = 0.31

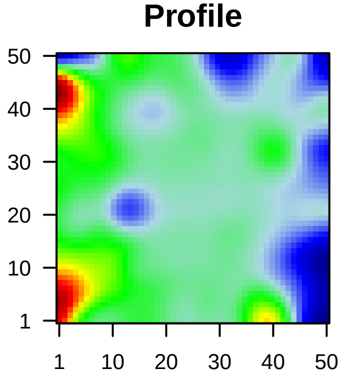
<FC> = −0.26

<shrinkage−t> = −9.28

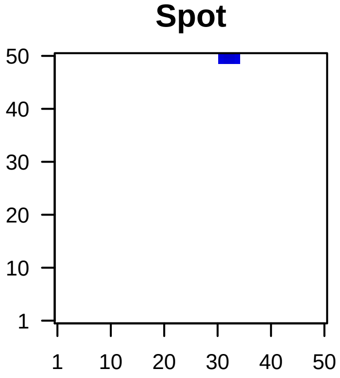
<p−value> = 0.04

<fdr> = 0.69

Profile



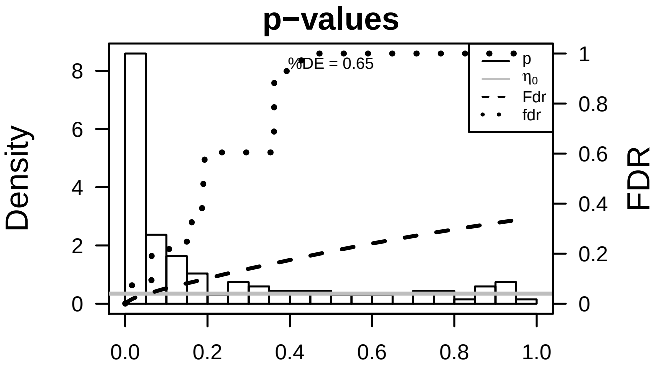
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4724	−0.63	2e−05	2e−04	33 x 50	NADH dehydrogenase (ubiquinone) Fe−S protein 4, 18kDa (
2	7388	−0.63	2e−05	2e−04	33 x 50	ubiquinol−cytochrome c reductase hinge protein [Source:HG
3	1349	−0.63	2e−05	2e−04	33 x 50	cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;Ac
4	64801	−0.63	2e−05	2e−04	33 x 50	ARV1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:2
5	5423	−0.63	2e−05	1e−03	34 x 50	polymerase (DNA directed), beta [Source:HGNC Symbol;Acc
6	1340	−0.6	4e−05	1e−03	34 x 50	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
7	3094	−0.54	8e−05	2e−03	32 x 50	histidine triad nucleotide binding protein 1 [Source:HGNC Sy
8	27089	−0.52	1e−04	2e−03	33 x 50	ubiquinol−cytochrome c reductase, complex III subunit VII, 9.
9	51074	−0.56	2e−04	2e−03	31 x 49	APAF1 interacting protein [Source:HGNC Symbol;Acc:17581]
10	29093	−0.54	3e−04	2e−03	33 x 50	mitochondrial ribosomal protein L22 [Source:HGNC Symbol;
11	7386	−0.53	3e−04	2e−03	34 x 50	ubiquinol−cytochrome c reductase, Rieske iron−sulfur polype
12	653147	−0.53	3e−04	2e−03	34 x 50	
13	10632	−0.53	4e−04	2e−03	32 x 49	ATP synthase, H+ transporting, mitochondrial Fo complex, su
14	10412	−0.52	4e−04	5e−03	31 x 49	NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:
15	10190	−0.51	5e−04	9e−03	31 x 50	thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:
16	57002	−0.5	7e−04	1e−02	34 x 50	Yae1 domain containing 1 [Source:HGNC Symbol;Acc:24857
17	539	−0.49	1e−03	1e−02	32 x 50	ATP synthase, H+ transporting, mitochondrial F1 complex, O
18	54534	−0.48	1e−03	1e−02	31 x 50	mitochondrial ribosomal protein L50 [Source:HGNC Symbol;
19	23421	−0.46	2e−03	1e−02	32 x 50	integrin beta 3 binding protein (beta3−endonexin) [Source:H
20	139886	−0.45	2e−03	1e−02	31 x 50	spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−33.43	NULL	24 / 83	BP	respiratory electron transport chain
2	−24.25	NULL	24 / 152	BP	cellular metabolic process
3	−20.39	NULL	31 / 304	CC	mitochondrial inner membrane
4	−17.13	NULL	5 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
5	−16.49	NULL	9 / 34	MF	NADH dehydrogenase (ubiquinone) activity
6	−16.47	NULL	5 / 14	BP	mitochondrial ATP synthesis coupled proton transport
7	−15.99	NULL	9 / 36	CC	mitochondrial respiratory chain complex I
8	−15.88	NULL	5 / 15	BP	ATP synthesis coupled proton transport
9	−15.43	NULL	4 / 10	CC	large ribosomal subunit
10	−15.42	NULL	8 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
11	−15.33	NULL	3 / 13	CC	mitochondrial respiratory chain
12	−13.37	NULL	6 / 19	CC	mitochondrial proton−transporting ATP synthase complex
13	−13.36	NULL	4 / 16	Cancer	GENTLES_modul10
14	−13.12	NULL	4 / 12	BP	oxidative phosphorylation
15	−12.29	NULL	5 / 26	MF	cytochrome−c oxidase activity
16	−12.2	NULL	3 / 11	GSEA C2	BIOCARTA_ETC_PATHWAY
17	−11.68	NULL	48 / 1318	CC	mitochondrion
18	−9.9	NULL	3 / 20	BP	aerobic respiration
19	−9.89	NULL	3 / 18	MF	2 iron, 2 sulfur cluster binding
20	−9.79	NULL	3 / 16	GSEA C2	BARIS_THYROID_CANCER_UP
21	−9.27	NULL	2 / 15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
22	−9.13	NULL	3 / 16	BP	mitochondrial respiratory chain complex I assembly
23	−8.63	NULL	3 / 19	BP	ATP biosynthetic process
24	−8.54	NULL	2 / 11	GSEA C2	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE
25	−8.36	NULL	3 / 11	Cancer	GENTLES_modul5
26	−8.22	NULL	5 / 50	MF	transmembrane transporter activity
27	−8.21	NULL	4 / 25	MF	hydrogen ion transmembrane transporter activity
28	−8.15	NULL	29 / 1253	BP	small molecule metabolic process
29	−8.06	NULL	15 / 153	MF	structural constituent of ribosome
30	−7.83	NULL	2 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
31	−7.63	NULL	2 / 15	GSEA C2	MOOTHA_TCA
32	−7.57	NULL	14 / 167	CC	ribosome
33	−7.49	NULL	1 / 2	miRNA target	miR−375
34	−7.34	NULL	2 / 9	GSEA C2	KEGG_RIBOSOME
35	−7.34	NULL	2 / 9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
36	−7.34	NULL	2 / 9	GSEA C2	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_
37	−7.34	NULL	2 / 9	GSEA C2	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_
38	−7.34	NULL	2 / 9	GSEA C2	REACTOME_PEPTIDE_CHAIN_ELONGATION
39	−7.34	NULL	2 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
40	−7.34	NULL	2 / 9	GSEA C2	REACTOME_VIRAL_MRNA_TRANSLATION

GW_091

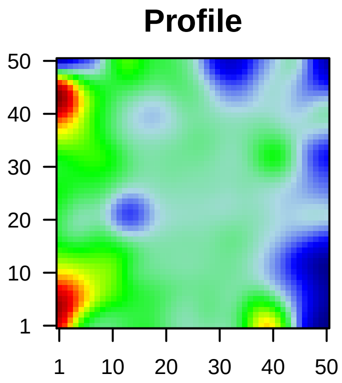
Local Summary

%DE = 0.9
metagenes = 2
genes = 71
genes in genesets = 70

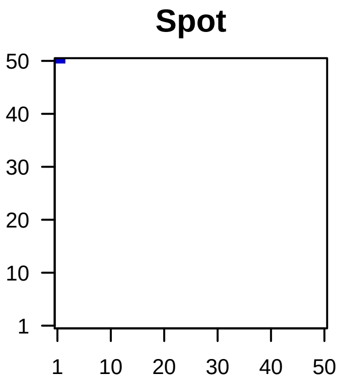
genes with fdr < 0.1 = 58 (14 + / 44 −)
genes with fdr < 0.05 = 54 (12 + / 42 −)
genes with fdr < 0.01 = 51 (11 + / 40 −)

<r> metagenes = 1
<r> genes = 0.58

<FC> = −0.71
<shrinkage−t> = −25.06
<p−value> = 0
<fdr> = 0.25



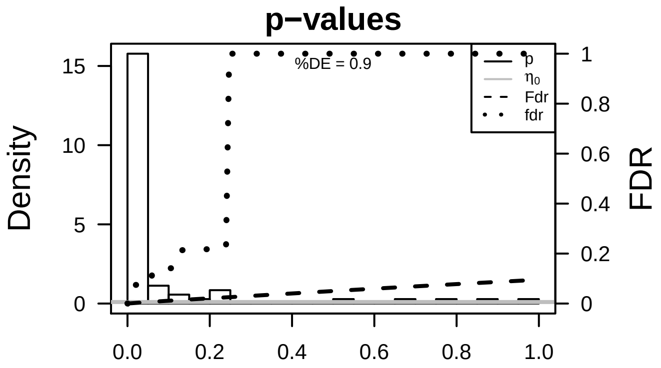
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.82	2e−16	7e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	−1.5	2e−16	7e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	218	−2.7	2e−16	7e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	23120	−1.28	2e−16	7e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
5	1048	−1.6	2e−16	7e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
6	4680	−1.75	2e−16	7e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
7	22802	−1.85	2e−16	7e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	49860	−3.23	2e−16	7e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	1475	−1.66	2e−16	7e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
10	1562	−1.5	2e−16	7e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sour
11	3860	−3.09	2e−16	7e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
12	192666	−2.1	2e−16	7e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
13	3851	−2.33	2e−16	7e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
14	196374	−1.25	2e−16	7e−17	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
15	4118	−2.22	2e−16	7e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
16	5275	−1.23	2e−16	7e−17	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 13 [S
17	11005	−1.68	2e−16	7e−17	1 x 50	serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
18	6707	−3.07	2e−16	7e−17	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
19	6947	−1.84	2e−16	7e−17	2 x 50	transcobalamin I (vitamin B12 binding protein, R binder family
20	7053	−2.25	2e−16	7e−17	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−30.41	NULL	39 / 135	H.Tiss	WIRTH_Mucosa
2	−22.49	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
3	−18.93	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	−18.29	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
5	−17.8	NULL	3 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
6	−17.62	NULL	7 / 19	BP	peptide cross−linking
7	−15.88	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
8	−15.19	NULL	3 / 13	BP	negative regulation of peptidase activity
9	−14.93	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
10	−13.62	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
11	−13.61	NULL	3 / 44	CC	keratin filament
12	−12.54	NULL	4 / 82	CC	intermediate filament
13	−12.15	NULL	2 / 15	MF	retinol dehydrogenase activity
14	−12.14	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
15	−10.95	NULL	10 / 186	MF	structural molecule activity
16	−10.74	NULL	1 / 13	MF	oxidoreductase activity, acting on the aldehyde or oxo group of don
17	−10.26	NULL	1 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
18	−10.17	NULL	2 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
19	−10.14	NULL	12 / 53	BP	keratinocyte differentiation
20	−9.95	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
21	−9.83	NULL	1 / 11	Glio	VERHAAK_Brain
22	−9.75	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
23	−9.75	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
24	−9.63	NULL	3 / 38	BP	epithelial cell differentiation
25	−9.41	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
26	−9.41	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
27	−9.29	NULL	1 / 12	MF	channel activity
28	−9.16	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
29	−9.02	NULL	1 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
30	−8.9	NULL	2 / 12	BP	cellular aldehyde metabolic process
31	−8.83	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
32	−8.78	NULL	1 / 18	MF	acyl−CoA dehydrogenase activity
33	−8.61	NULL	1 / 27	BP	response to radiation
34	−8.16	NULL	2 / 13	H.Tiss	WIRTH_Tonsil
35	−8.07	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
36	−8.07	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
37	−8.07	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
38	−7.86	NULL	1 / 10	BP	anagen
39	−7.76	NULL	1 / 10	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
40	−7.75	NULL	1 / 16	Cancer	GENTLES_modul11