GW_012

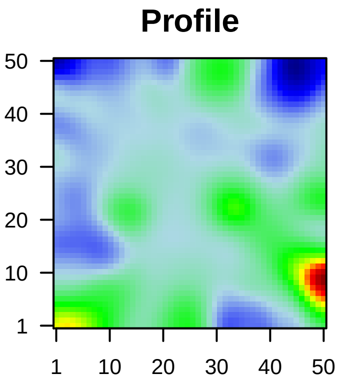
Global Summary

%DE = 0.15

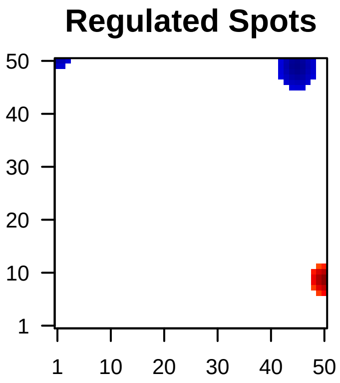
genes with fdr < 0.2 = 1874 (1100 + / 774 −)
genes with fdr < 0.1 = 1492 (906 + / 586 −)
genes with fdr < 0.05 = 1288 (793 + / 495 −)
genes with fdr < 0.01 = 887 (578 + / 309 −)

genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.09
<fdr> = 0.85



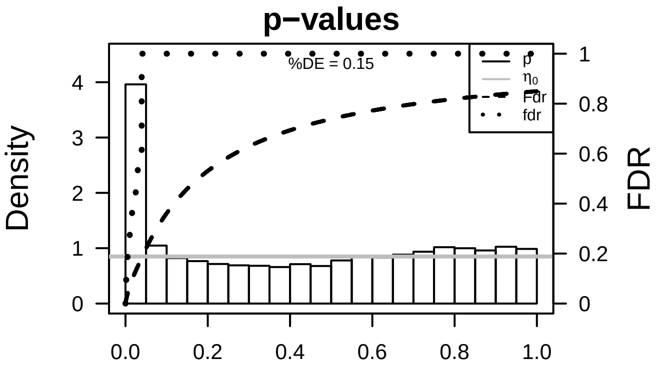
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.34	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:1
2	72	2.27	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
3	131	−2.18	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	10551	3.21	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	155465	1.64	2e−16	3e−14	50 x 10	anterior gradient 3 [Source:HGNC Symbol;Acc:24167]
6	57016	−1.87	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
7	216	1.58	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	218	−1.99	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
9	347	2.82	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
10	80117	1.51	2e−16	3e−14	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:
11	525	1.85	2e−16	3e−14	12 x 8	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1
12	563	2.09	2e−16	3e−14	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
13	80341	3.11	2e−16	3e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
14	387695	−1.69	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
15	149563	1.63	2e−16	3e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symb
16	92747	5.31	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
17	375791	−1.75	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
18	810	−1.52	2e−16	3e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
19	57172	1.7	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
20	84290	−1.6	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	20.5	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	13.36	NULL	190	CC	extracellular matrix
3	12.52	NULL	1182	CC	extracellular region
4	12.42	NULL	375	Disease	GUDJ_psoriasis down
5	12.14	NULL	250	Lymphoma	LENZ_Stromal signature 1
6	12.12	NULL	683	CC	extracellular space
7	10.18	NULL	183	CC	proteinaceous extracellular matrix
8	9.6	NULL	957	Chr	Chr 11
9	9.55	NULL	3274	CC	integral to membrane
10	9.41	NULL	482	BP	cellular protein metabolic process
11	8.64	NULL	14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
12	8.21	NULL	242	BP	extracellular matrix organization
13	8.01	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
14	7.75	NULL	69	BP	extracellular matrix disassembly
15	7.58	NULL	16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
16	7.46	NULL	13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
17	7.4	NULL	15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_IN
18	7.4	NULL	10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
19	7.32	NULL	59	Lymphoma	LENZ_Stromal signature 2
20	7.15	NULL	64	BP	collagen catabolic process
Underexpressed					
1	−19.2	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−19.2	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−18.73	NULL	572	Disease	GUDJ_psoriasis up
4	−18.29	NULL	135	H.Tiss	WIRTH_Mucosa
5	−14.06	NULL	370	BP	mitotic cell cycle
6	−13.06	NULL	949	CC	nucleoplasm
7	−12.71	NULL	4640	CC	nucleus
8	−11.56	NULL	530	Cancer	Lembcke_Normal vs Adenoma
9	−9.62	NULL	149	BP	DNA replication
10	−9.49	NULL	232	BP	mitosis
11	−8.97	NULL	57	Glio	developing astrocytes
12	−8.59	NULL	1749	MF	DNA binding
13	−8.57	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
14	−8.3	NULL	4310	CC	cytoplasm
15	−8.22	NULL	298	BP	DNA repair
16	−8.22	NULL	274	Lymphoma	SPANG_IL21 DN
17	−8.1	NULL	1344	MF	ATP binding
18	−8.02	NULL	8023	MF	protein binding
19	−7.84	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
20	−7.74	NULL	417	H.Tiss	WIRTH_Immune system

GW_012

Local Summary

%DE = 0.87

metagenes = 16

genes = 202

genes in genesets = 201

genes with fdr < 0.1 = 168 (165 + / 3 −)

genes with fdr < 0.05 = 157 (157 + / 0 −)

genes with fdr < 0.01 = 153 (153 + / 0 −)

<r> metagenes = 0.93

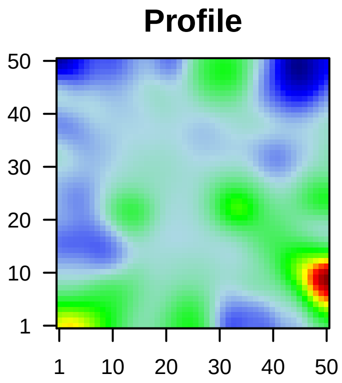
<r> genes = 0.29

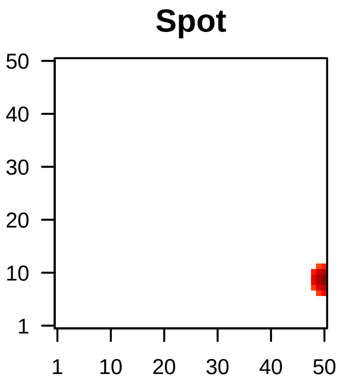
<FC> = 1.08

<shrinkage−t> = 37.82

<p−value> = 0

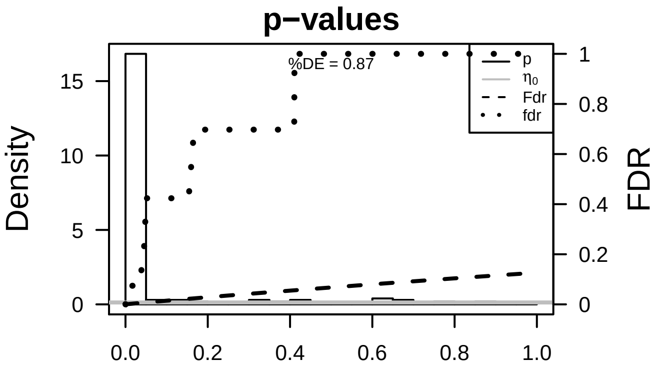
<fdr> = 0.21





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	3.21	2e−16	1e−16	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	155465	1.64	2e−16	1e−16	50 x 10	anterior gradient 3 [Source:HGNC Symbol;Acc:24167]
3	347	2.82	2e−16	1e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
4	563	2.09	2e−16	1e−16	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
5	80341	3.11	2e−16	1e−16	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
6	92747	5.31	2e−16	1e−16	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
7	6358	1.69	2e−16	1e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
8	148170	1.55	2e−16	1e−16	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HG
9	1675	1.76	2e−16	1e−16	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
10	84952	2.33	2e−16	1e−16	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
11	9071	2.53	2e−16	1e−16	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
12	1363	1.75	2e−16	1e−16	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
13	10321	2.38	2e−16	1e−16	50 x 10	cysteine−rich secretory protein 3 [Source:HGNC Symbol;Acc
14	1511	1.76	2e−16	1e−16	50 x 7	cathepsin G [Source:HGNC Symbol;Acc:2532]
15	1755	2.04	2e−16	1e−16	50 x 10	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
16	283229	1.67	2e−16	1e−16	50 x 10	EF−hand calcium binding domain 4A [Source:HGNC Symbol;
17	219970	1.51	2e−16	1e−16	50 x 10	glycine−N−acyltransferase−like 2 [Source:HGNC Symbol;Acc
18	3158	1.87	2e−16	1e−16	50 x 10	3−hydroxy−3−methylglutaryl−CoA synthase 2 (mitochondrial)
19	57535	2.34	2e−16	1e−16	50 x 10	KIAA1324 [Source:HGNC Symbol;Acc:29618]
20	124220	3.02	2e−16	1e−16	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	44.76	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	16.52	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	15.14	NULL	3 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
4	15.1	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
5	12.32	NULL	4 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
6	12.32	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
7	12.03	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
8	11.69	NULL	33 / 375	Disease	GUDJ_psoriasis down
9	11.58	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
10	11.32	NULL	2 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
11	11.15	NULL	48 / 1182	CC	extracellular region
12	11.03	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
13	10.84	NULL	38 / 683	CC	extracellular space
14	10.74	NULL	2 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
15	10.03	NULL	3 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
16	9.32	NULL	1 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
17	8.98	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
18	8.66	NULL	7 / 61	CC	secretory granule
19	8.47	NULL	3 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
20	8.42	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
21	8.26	NULL	2 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
22	8.12	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
23	7.9	NULL	4 / 17	MF	metallocarboxypeptidase activity
24	7.88	NULL	2 / 13	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
25	7.74	NULL	5 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
26	7.46	NULL	3 / 37	BP	digestion
27	7.44	NULL	3 / 14	BP	negative regulation of epithelial to mesenchymal transition
28	7.44	NULL	5 / 115	MF	lipid binding
29	7.33	NULL	4 / 15	GSEA C2	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
30	7.29	NULL	2 / 12	BP	urogenital system development
31	7.25	NULL	1 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
32	7.09	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
33	7.07	NULL	2 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
34	7.06	NULL	3 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
35	7	NULL	2 / 10	BP	angiotensin maturation
36	6.97	NULL	2 / 14	GSEA C2	PENG_RAPAMYCIN_RESPONSE_UP
37	6.97	NULL	3 / 15	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
38	6.9	NULL	2 / 16	GSEA C2	AIYAR_COBRA1_TARGETS_UP
39	6.9	NULL	2 / 7	TF Tissue	VAQUERIZAS_Appendix
40	6.79	NULL	3 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN

GW_012

Local Summary

%DE = 0.82

metagenes = 36

genes = 405

genes in genesets = 403

genes with fdr < 0.1 = 268 (2 + / 266 −)

genes with fdr < 0.05 = 247 (1 + / 246 −)

genes with fdr < 0.01 = 176 (0 + / 176 −)

<r> metagenes = 0.91

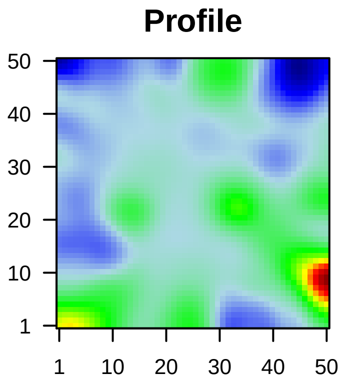
<r> genes = 0.36

<FC> = −0.49

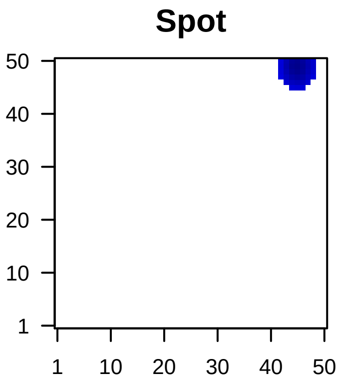
<shrinkage−t> = −17.23

<p−value> = 0

<fdr> = 0.45



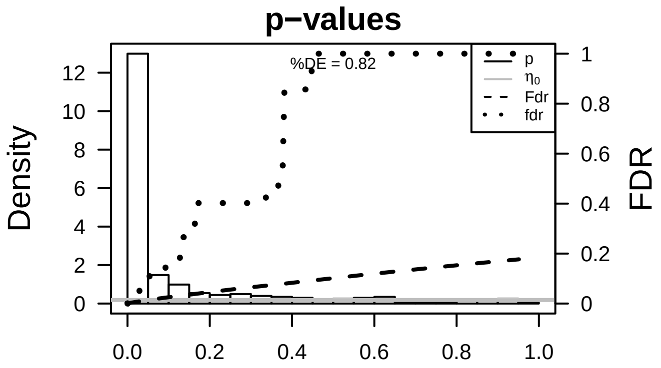
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51659	−1.64	2e−16	2e−14	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
2	55165	−1.35	2e−13	2e−11	44 x 50	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
3	10643	−1.34	4e−13	2e−11	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
4	8318	−1.32	7e−13	2e−10	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
5	259266	−1.29	3e−12	3e−10	45 x 49	asp (abnormal spindle) homolog, microcephaly associated (D
6	113130	−1.26	8e−12	3e−10	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
7	84823	−1.25	1e−11	3e−10	44 x 49	lamin B2 [Source:HGNC Symbol;Acc:6638]
8	4173	−1.24	1e−11	3e−10	44 x 50	minichromosome maintenance complex component 4 [Source
9	7153	−1.24	2e−11	3e−10	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
10	1870	−1.23	2e−11	9e−09	46 x 45	E2F transcription factor 2 [Source:HGNC Symbol;Acc:3114]
11	81620	−1.18	1e−10	1e−08	45 x 47	chromatin licensing and DNA replication factor 1 [Source:HG
12	116028	−1.16	3e−10	1e−08	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
13	10635	−1.15	4e−10	1e−08	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
14	9212	−1.14	5e−10	5e−08	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
15	7546	−1.11	2e−09	5e−08	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
16	1164	−1.1	2e−09	5e−08	44 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
17	9787	−1.1	3e−09	2e−07	43 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
18	84223	−1.08	5e−09	3e−07	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
19	3833	−1.05	1e−08	3e−07	45 x 48	kinesin family member C1 [Source:HGNC Symbol;Acc:6389]
20	26255	−1.04	2e−08	3e−07	44 x 48	pituitary tumor−transforming 3, pseudogene [Source:HGNC



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−67.34	NULL	95 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−67.34	NULL	95 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−35.78	NULL	105 / 370	BP	mitotic cell cycle
4	−35.55	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	−31.23	NULL	25 / 57	Glio	developing astrocytes
6	−30.06	NULL	108 / 530	Cancer	Lembcke_Normal vs Adenoma
7	−29.83	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
8	−29.63	NULL	50 / 149	BP	DNA replication
9	−28.56	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
10	−28.55	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
11	−28.21	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
12	−27.79	NULL	19 / 30	BP	DNA strand elongation involved in DNA replication
13	−27.17	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
14	−26.47	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
15	−25.26	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
16	−24.29	NULL	57 / 232	BP	mitosis
17	−23.9	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
18	−23.79	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
19	−23.42	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
20	−23.39	NULL	13 / 22	BP	DNA replication initiation
21	−23.24	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
22	−22.95	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
23	−22.84	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
24	−22.61	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
25	−22.13	NULL	11 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
26	−21.98	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
27	−21.71	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
28	−21.65	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
29	−21.29	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
30	−20.45	NULL	23 / 56	CC	chromosome, centromeric region
31	−20.31	NULL	13 / 18	BP	spindle organization
32	−20.25	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
33	−19.98	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
34	−19.87	NULL	10 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
35	−19.68	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
36	−19.5	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
37	−19.42	NULL	61 / 572	Disease	GUDJ_psoriasis up
38	−19.36	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
39	−19.08	NULL	34 / 148	BP	G1/S transition of mitotic cell cycle
40	−18.96	NULL	8 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN

GW_012

Local Summary

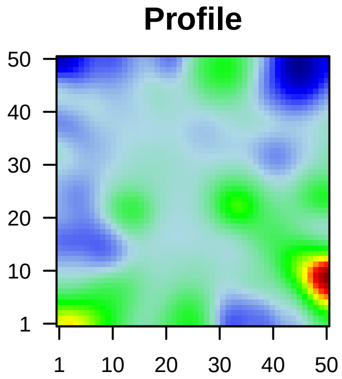
%DE = 0.92
metagenes = 5
genes = 112
genes in genesets = 109

genes with fdr < 0.1 = 96 (17 + / 79 −)
genes with fdr < 0.05 = 95 (17 + / 78 −)
genes with fdr < 0.01 = 84 (15 + / 69 −)

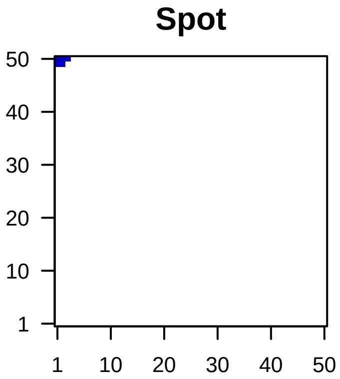
<r> metagenes = 1
<r> genes = 0.54

<FC> = −0.66
<shrinkage−t> = −23.35
<p−value> = 0
<fdr> = 0.18

Profile



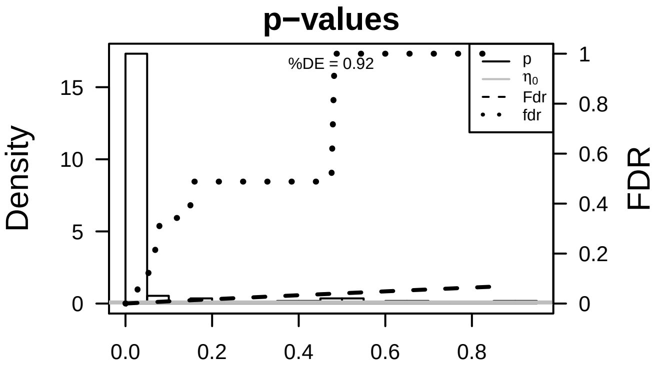
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.18	2e−16	7e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−1.87	2e−16	7e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	218	−1.99	2e−16	7e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	387695	−1.69	2e−16	7e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
5	375791	−1.75	2e−16	7e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
6	810	−1.52	2e−16	7e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
7	84290	−1.6	2e−16	7e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
8	4680	1.55	2e−16	7e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
9	49860	−2.45	2e−16	7e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	92196	−1.55	2e−16	7e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
11	1672	2.18	2e−16	7e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
12	1673	−2.23	2e−16	7e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	131177	2.5	2e−16	7e−17	3 x 50	family with sequence similarity 3, member D [Source:HGNC
14	163351	−1.79	2e−16	7e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
15	3860	−3.14	2e−16	7e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	−1.62	2e−16	7e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
17	3851	−1.92	2e−16	7e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
18	4118	−2.13	2e−16	7e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
19	7851	−1.7	2e−16	7e−17	1 x 50	mal, T−cell differentiation protein−like [Source:HGNC Symbol
20	51458	−1.61	2e−16	7e−17	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−46.69	NULL	53 / 135	H.Tiss	WIRTH_Mucosa
2	−27.29	NULL	7 / 19	BP	peptide cross−linking
3	−25.36	NULL	13 / 42	BP	keratinization
4	−23.92	NULL	12 / 21	CC	cornified envelope
5	−18.98	NULL	16 / 53	BP	keratinocyte differentiation
6	−16.42	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
7	−16.36	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
8	−12.97	NULL	5 / 13	BP	negative regulation of peptidase activity
9	−12.59	NULL	49 / 572	Disease	GUDJ_psoriasis up
10	−11.97	NULL	12 / 186	MF	structural molecule activity
11	−11.95	NULL	14 / 76	BP	epidermis development
12	−11.93	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
13	−11.26	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
14	−11.24	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−10.99	NULL	4 / 44	CC	keratin filament
16	−10.86	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	−10.47	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
18	−10.43	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
19	−9.7	NULL	3 / 12	BP	cellular aldehyde metabolic process
20	−9.64	NULL	6 / 82	CC	intermediate filament
21	−9.42	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
22	−8.56	NULL	4 / 38	BP	epithelial cell differentiation
23	−8.43	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
24	−8.06	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
25	−7.77	NULL	2 / 15	GSEA C2	LI_AMPLIFIED_IN_LUNG_CANCER
26	−7.53	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
27	−7.34	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
28	−7.33	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
29	−6.95	NULL	1 / 11	Glio	VERHAAK_Brain
30	−6.88	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
31	−6.83	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
32	−6.83	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
33	−6.75	NULL	1 / 12	MF	retinol binding
34	−6.71	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
35	−6.62	NULL	1 / 27	BP	response to radiation
36	−6.59	NULL	1 / 12	MF	channel activity
37	−6.52	NULL	4 / 29	BP	regulation of proteolysis
38	−6.44	NULL	1 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
39	−6.43	NULL	1 / 13	BP	retinoic acid metabolic process
40	−6.3	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP