GW_177

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2029 (1165 + / 864 −)

genes with fdr < 0.1 = 1617 (970 + / 647 −)

genes with fdr < 0.05 = 1393 (856 + / 537 −)

genes with fdr < 0.01 = 1016 (644 + / 372 −)

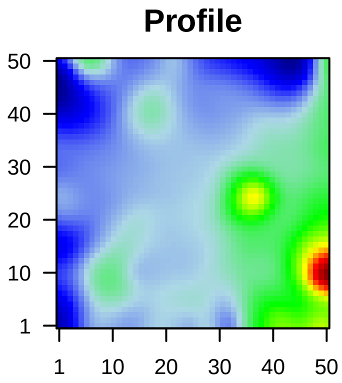
genes in genesets = 16332

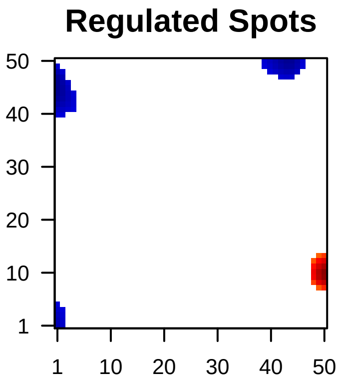
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

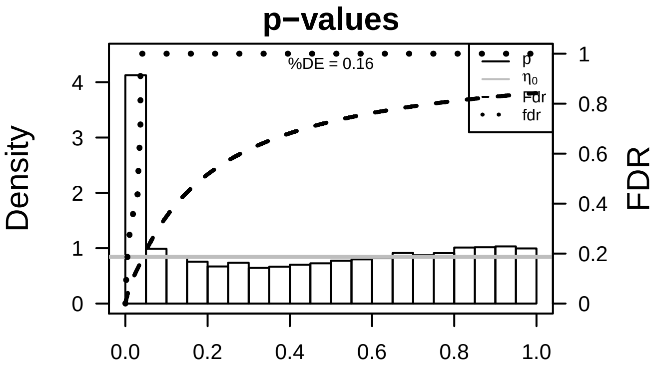
<fdr> = 0.84


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.25	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	72	1.56	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	124	2.39	2e−16	2e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
4	126	2.17	2e−16	2e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
5	131	1.76	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
6	10551	2.63	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
7	214	1.75	2e−16	2e−14	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
8	216	2.32	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	10840	1.64	2e−16	2e−14	50 x 12	aldehyde dehydrogenase 1 family, member L1 [Source:HGNC
10	218	1.64	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
11	347	2.24	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
12	479	1.78	2e−16	2e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
13	563	1.91	2e−16	2e−14	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
14	80341	2.83	2e−16	2e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
15	79949	1.73	2e−16	2e−14	50 x 10	pleckstrin homology domain containing, family S member 1 [S
16	144809	1.53	2e−16	2e−14	45 x 8	family with sequence similarity 216, member B [Source:HGNC
17	339512	2.66	2e−16	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
18	92747	4.37	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
19	343990	1.56	2e−16	2e−14	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
20	352999	3.14	2e−16	2e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	22.18	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	10.71	NULL	51	Glio	willscher_GBM_Verhaak−PNmut_expression_G_down
3	9.74	NULL	24	TF Tissue	VAQUERIZAS_Trachea
4	8.86	NULL	375	Disease	GUDJ_psoriasis down
5	8.17	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
6	8.06	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
7	7.97	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
8	6.62	NULL	15	CC	MHC class II protein complex
9	6.42	NULL	13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
10	6.4	NULL	16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_N
11	6.32	NULL	7	GSEA C2	NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
12	6.24	NULL	7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	6.09	NULL	7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
14	6.03	NULL	10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP
15	5.96	NULL	85	Glio	GIEZELT_GBM_STS_down_VS_LTS
16	5.75	NULL	16	TF Tissue	VAQUERIZAS_Salivary gland
17	5.7	NULL	14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
18	5.64	NULL	15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
19	5.6	NULL	19	BP	calcium−independent cell−cell adhesion
20	5.56	NULL	76	Glio	GIEZELT_GBM_STSwt_up_VS_LTSwt
Underexpressed					
1	−21.21	NULL	572	Disease	GUDJ_psoriasis up
2	−17.07	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	−17.07	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	−12.65	NULL	21	CC	cornified envelope
5	−11.62	NULL	370	BP	mitotic cell cycle
6	−11.18	NULL	42	BP	keratinization
7	−10.56	NULL	53	BP	keratinocyte differentiation
8	−10.5	NULL	76	BP	epidermis development
9	−9.69	NULL	64	BP	collagen catabolic process
10	−9.48	NULL	530	Cancer	Lembcke_Normal vs Adenoma
11	−9.22	NULL	69	BP	extracellular matrix disassembly
12	−9.05	NULL	242	BP	extracellular matrix organization
13	−8.63	NULL	11	MF	platelet−derived growth factor binding
14	−8.36	NULL	16	MMML CGS	MACIEJ_MMML 1
15	−8.28	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
16	−7.85	NULL	16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
17	−7.8	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
18	−7.8	NULL	949	CC	nucleoplasm
19	−7.51	NULL	190	CC	extracellular matrix
20	−7.45	NULL	135	H.Tiss	WIRTH_Mucosa

GW_177

Local Summary

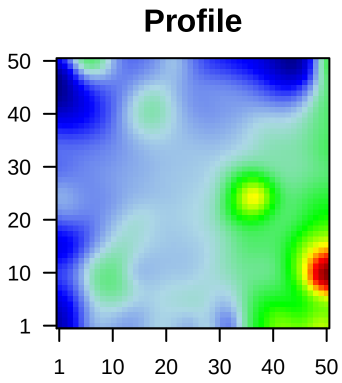
%DE = 0.92
metagenes = 19
genes = 210
genes in genesets = 207

genes with fdr < 0.1 = 184 (180 + / 4 −)
genes with fdr < 0.05 = 180 (178 + / 2 −)
genes with fdr < 0.01 = 162 (160 + / 2 −)

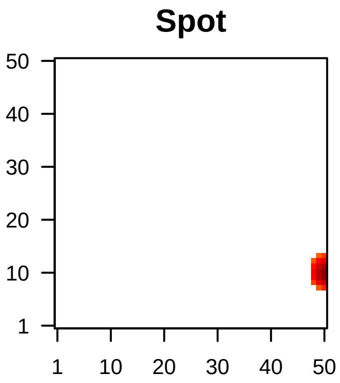
<r> metagenes = 0.93
<r> genes = 0.27

<FC> = 1.18
<shrinkage−t> = 41.3
<p−value> = 0
<fdr> = 0.16

Profile

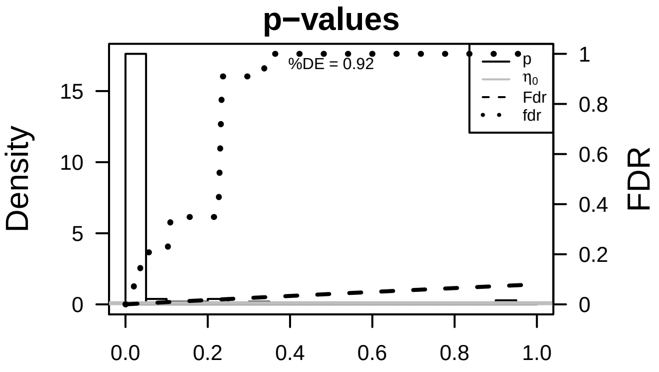


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.39	2e−16	7e−17	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	2.17	2e−16	7e−17	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	10551	2.63	2e−16	7e−17	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	10840	1.64	2e−16	7e−17	50 x 12	aldehyde dehydrogenase 1 family, member L1 [Source:HGNC
5	563	1.91	2e−16	7e−17	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
6	80341	2.83	2e−16	7e−17	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
7	79949	1.73	2e−16	7e−17	50 x 10	pleckstrin homology domain containing, family S member 1 [S
8	92747	4.37	2e−16	7e−17	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
9	343990	1.56	2e−16	7e−17	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
10	352999	3.14	2e−16	7e−17	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
11	401546	1.73	2e−16	7e−17	50 x 11	chromosome 9 open reading frame 152 [Source:HGNC Symb
12	92291	1.65	2e−16	7e−17	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
13	148170	1.67	2e−16	7e−17	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HGN
14	83539	1.69	2e−16	7e−17	50 x 11	carbohydrate (N−acetylgalactosamine 4−0) sulfotransferase
15	9071	1.86	2e−16	7e−17	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
16	54102	2.32	2e−16	7e−17	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
17	1755	2.08	2e−16	7e−17	50 x 10	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
18	283229	1.95	2e−16	7e−17	50 x 10	EF−hand calcium binding domain 4A [Source:HGNC Symbol;
19	8857	2.4	2e−16	7e−17	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
20	2327	1.86	2e−16	7e−17	50 x 11	flavin containing monooxygenase 2 (non−functional) [Source:



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	44.69	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	16.35	NULL	3 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
3	14.72	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
4	14.7	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
5	13.17	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
6	12.33	NULL	5 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
7	12.18	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
8	11.78	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
9	11.36	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
10	11.21	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
11	11.02	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
12	10.4	NULL	3 / 7	TF Tissue	VAQUERIZAS_Appendix
13	9.88	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
14	9.77	NULL	2 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
15	9.52	NULL	2 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
16	9.28	NULL	2 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
17	9.1	NULL	3 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
18	8.92	NULL	2 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
19	8.69	NULL	2 / 7	GSEA C2	NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
20	8.4	NULL	29 / 375	Disease	GUDJ_psoriasis down
21	8.37	NULL	3 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
22	8.02	NULL	1 / 15	Cancer	LIU_PROSTATE_CANCER_DN
23	8.01	NULL	2 / 8	GSEA C2	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
24	8	NULL	36 / 1182	CC	extracellular region
25	7.99	NULL	2 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
26	7.93	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
27	7.88	NULL	4 / 21	BP	drug metabolic process
28	7.86	NULL	4 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
29	7.78	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
30	7.77	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
31	7.76	NULL	2 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
32	7.62	NULL	2 / 13	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
33	7.62	NULL	2 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
34	7.57	NULL	2 / 11	CC	photoreceptor outer segment membrane
35	7.56	NULL	2 / 17	BP	iron ion transport
36	7.51	NULL	3 / 16	GSEA C2	AIYAR_COBRA1_TARGETS_UP
37	7.4	NULL	2 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
38	7.27	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
39	7.23	NULL	5 / 61	CC	secretory granule
40	7.19	NULL	2 / 10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP

GW_177

Local Summary

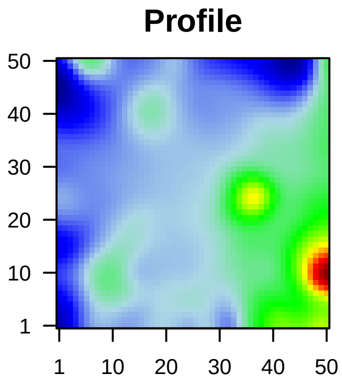
%DE = 0.89
metagenes = 9
genes = 171
genes in genesets = 169

genes with fdr < 0.1 = 134 (8 + / 126 −)
genes with fdr < 0.05 = 134 (8 + / 126 −)
genes with fdr < 0.01 = 99 (6 + / 93 −)

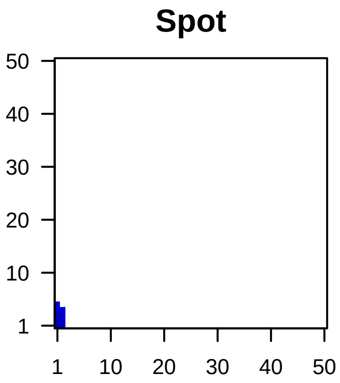
<r> metagenes = 0.98
<r> genes = 0.38

<FC> = −0.58
<shrinkage−t> = −20.47
<p−value> = 0
<fdr> = 0.34

Profile



Spot



Local Genelist

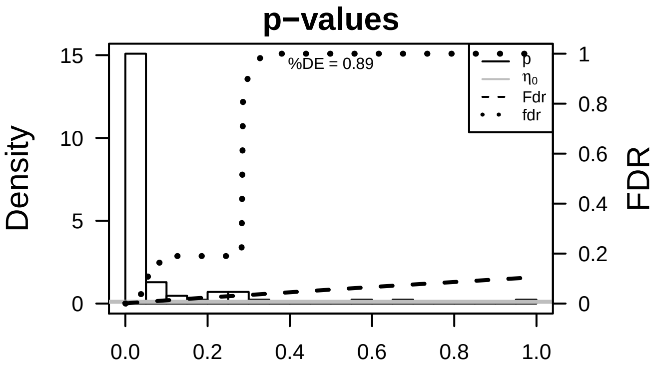
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1277	−2.25	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	1281	−1.81	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
3	1282	−1.85	2e−16	3e−16	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
4	1290	−1.69	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
5	1293	−1.64	2e−16	3e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
6	3553	−1.71	2e−16	3e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
7	3576	−1.68	2e−16	3e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
8	4060	−1.73	2e−16	3e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
9	4312	−2.61	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
10	4314	−2.54	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
11	5328	−1.83	2e−16	3e−16	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
12	12	3.12	2e−16	3e−16	1 x 1	
13	5054	−1.55	2e−16	3e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
14	1278	−1.5	1e−15	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
15	7045	−1.35	4e−15	4e−14	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
16	4502	−1.47	5e−15	8e−13	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
17	857	−1.41	5e−14	9e−12	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
18	7058	−1.35	6e−13	2e−11	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
19	11098	1.32	2e−12	3e−11	1 x 1	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
20	10631	−1.3	3e−12	6e−11	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.12	NULL	6 / 11	MF	platelet−derived growth factor binding
2	−34.46	NULL	10 / 16	MMML CGS	MACIEJ_MMML 1
3	−31.6	NULL	6 / 12	miRNA target	miR−29c
4	−30.8	NULL	19 / 64	BP	collagen catabolic process
5	−30.16	NULL	20 / 69	BP	extracellular matrix disassembly
6	−27.27	NULL	45 / 242	BP	extracellular matrix organization
7	−26.55	NULL	33 / 190	CC	extracellular matrix
8	−25.98	NULL	7 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	−25.83	NULL	10 / 40	BP	cellular response to amino acid stimulus
10	−25.24	NULL	10 / 37	BP	collagen fibril organization
11	−24.53	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
12	−22.8	NULL	4 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
13	−22.02	NULL	12 / 57	MF	extracellular matrix structural constituent
14	−21.49	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
15	−19.1	NULL	3 / 10	BP	protein heterotrimerization
16	−18.63	NULL	29 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
17	−18.63	NULL	29 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
18	−18.63	NULL	29 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
19	−18.63	NULL	29 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
20	−18.55	NULL	4 / 11	Glio	Phillips MES up vs Prolif & PN
21	−18.13	NULL	35 / 250	Lymphoma	LENZ_Stromal signature 1
22	−17.79	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
23	−17.09	NULL	9 / 35	Glio	Colman_survival_associated
24	−16.93	NULL	53 / 683	CC	extracellular space
25	−16.91	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
26	−16.62	NULL	4 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
27	−16.44	NULL	9 / 68	CC	collagen
28	−16.2	NULL	3 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
29	−16.2	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
30	−16.14	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
31	−15.85	NULL	3 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
32	−15.85	NULL	72 / 1182	CC	extracellular region
33	−15.79	NULL	16 / 153	CC	endoplasmic reticulum lumen
34	−15.71	NULL	2 / 7	Glio	KIM_epithelial−mesenchymal−transition related genes_decreased
35	−15.62	NULL	2 / 12	GSEA C2	GEISS_RESPONSE_TO_DSRNA_DN
36	−15.51	NULL	6 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
37	−15.23	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
38	−15.09	NULL	5 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
39	−14.92	NULL	4 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
40	−14.72	NULL	3 / 11	GSEA C2	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGE

p−values



GW_177

Local Summary

%DE = 0.87

metagenes = 29

genes = 344

genes in genesets = 336

genes with fdr < 0.1 = 250 (16 + / 234 −)

genes with fdr < 0.05 = 249 (16 + / 233 −)

genes with fdr < 0.01 = 190 (7 + / 183 −)

<r> metagenes = 0.9

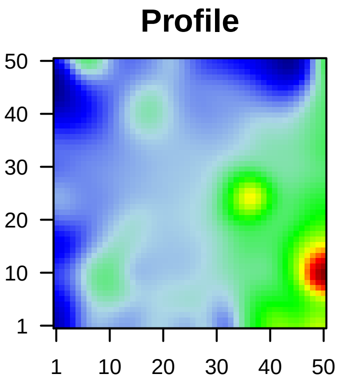
<r> genes = 0.36

<FC> = −0.61

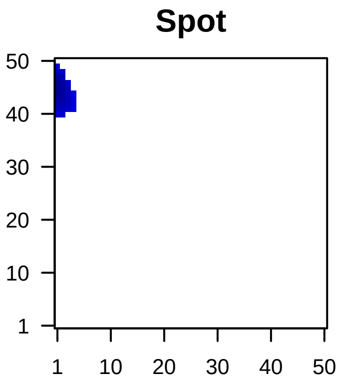
<shrinkage−t> = −21.62

<p−value> = 0

<fdr> = 0.36



Profile



Spot

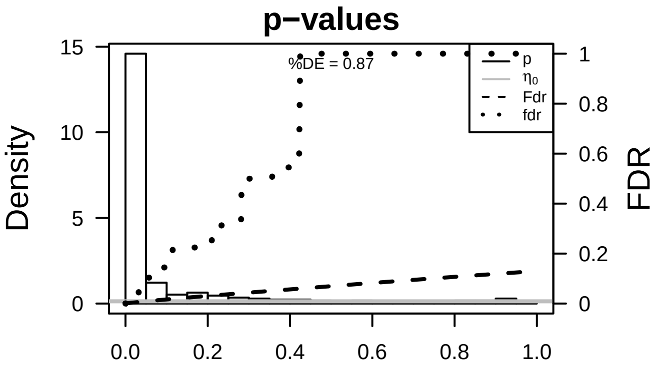
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	414325	−2.37	2e−16	4e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
2	1673	−2.42	2e−16	4e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
3	1828	−1.68	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
4	2697	−1.96	2e−16	4e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
5	10804	−1.82	2e−16	4e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
6	3552	−2.5	2e−16	4e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
7	56300	−2.19	2e−16	4e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
8	5650	−1.6	2e−16	4e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
9	3861	−1.74	2e−16	4e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
10	3868	−2.28	2e−16	4e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
11	286887	−3.34	2e−16	4e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
12	388533	−3.31	2e−16	4e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
13	84648	−2.25	2e−16	4e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
14	55214	−1.67	2e−16	4e−16	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
15	3963	−1.99	2e−16	4e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
16	653499	−2.02	2e−16	4e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
17	5266	−1.65	2e−16	4e−16	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
18	5744	−1.73	2e−16	4e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
19	84659	−1.54	2e−16	4e−16	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
20	6283	−1.68	2e−16	4e−16	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−23.24	NULL	22 / 76	BP	epidermis development
2	−23.21	NULL	98 / 572	Disease	GUDJ_psoriasis up
3	−19.77	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
4	−18.02	NULL	44 / 135	H.Tiss	WIRTH_Mucosa
5	−16.84	NULL	21 / 82	CC	intermediate filament
6	−16.63	NULL	14 / 53	BP	keratinocyte differentiation
7	−15.4	NULL	10 / 44	CC	keratin filament
8	−15.34	NULL	8 / 21	CC	cornified envelope
9	−15.28	NULL	3 / 10	MF	RAGE receptor binding
10	−14.93	NULL	11 / 21	CC	desmosome
11	−13.98	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
12	−13.35	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
13	−13.3	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
14	−12.89	NULL	9 / 42	BP	keratinization
15	−12.7	NULL	3 / 15	MF	interleukin−1 receptor binding
16	−12.63	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
17	−12.58	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	−11.73	NULL	4 / 15	CC	connexon complex
19	−11.1	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
20	−11.01	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
21	−10.97	NULL	5 / 21	CC	gap junction
22	−10.82	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
23	−10.01	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
24	−9.94	NULL	3 / 10	MF	gap junction channel activity
25	−9.92	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
26	−9.42	NULL	22 / 186	MF	structural molecule activity
27	−9.32	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
28	−9.24	NULL	5 / 12	BP	hemidesmosome assembly
29	−9.05	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	−8.92	NULL	4 / 25	BP	response to zinc ion
31	−8.52	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
32	−8.41	NULL	12 / 82	MF	structural constituent of cytoskeleton
33	−8.3	NULL	4 / 38	BP	epithelial cell differentiation
34	−8.2	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
35	−8.2	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
36	−8.15	NULL	3 / 11	GSEA C2	LEI_MYB_TARGETS
37	−7.87	NULL	2 / 16	BP	response to reactive oxygen species
38	−7.83	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
39	−7.54	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
40	−7.5	NULL	2 / 2	miRNA target	miR−199a*



p−values

GW_177

Local Summary

%DE = 0.93

metagenes = 25

genes = 370

genes in genesets = 367

genes with fdr < 0.1 = 328 (3 + / 325 −)

genes with fdr < 0.05 = 286 (0 + / 286 −)

genes with fdr < 0.01 = 219 (0 + / 219 −)

<r> metagenes = 0.94

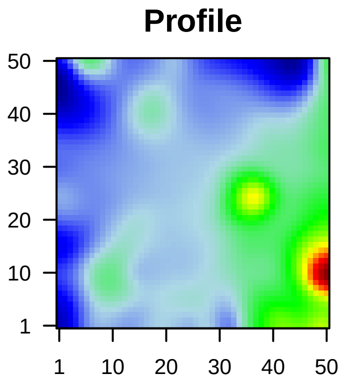
<r> genes = 0.36

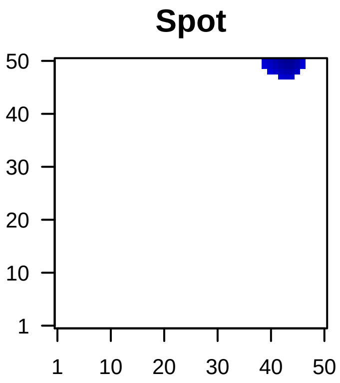
<FC> = −0.52

<shrinkage−t> = −18.2

<p−value> = 0

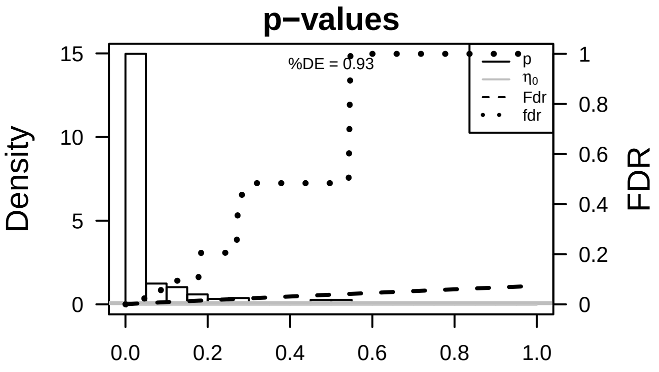
<fdr> = 0.4





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55165	−1.33	1e−12	2e−11	44 x 50	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
2	7083	−1.32	2e−12	2e−10	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
3	51659	−1.28	8e−12	1e−09	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
4	1164	−1.23	6e−11	1e−08	44 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
5	9055	−1.15	8e−10	1e−08	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
6	8318	−1.15	8e−10	2e−07	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
7	1033	−1.06	1e−08	2e−07	43 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	8836	−1.05	2e−08	2e−07	40 x 50	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
9	29089	−1.04	3e−08	2e−07	45 x 49	ubiquitin−conjugating enzyme E2T (putative) [Source:HGNC
10	3992	−1.04	3e−08	2e−07	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
11	6790	−1.04	3e−08	2e−07	44 x 50	aurora kinase A [Source:HGNC Symbol;Acc:11393]
12	55839	−1.03	4e−08	2e−07	44 x 50	centromere protein N [Source:HGNC Symbol;Acc:30873]
13	64151	−1.02	5e−08	3e−07	44 x 48	non−SMC condensin I complex, subunit G [Source:HGNC Sy
14	51203	−1.01	7e−08	3e−07	45 x 48	nucleolar and spindle associated protein 1 [Source:HGNC Sy
15	54443	−1.01	8e−08	3e−07	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
16	9833	−1	9e−08	3e−07	44 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
17	9212	−1	1e−07	3e−07	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
18	1163	−1	1e−07	3e−07	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
19	113130	−0.99	1e−07	3e−07	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
20	22974	−0.99	1e−07	3e−07	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−54.36	NULL	75 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−54.36	NULL	75 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−32.38	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
4	−27.51	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
5	−27.43	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
6	−26.96	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	−26.88	NULL	80 / 370	BP	mitotic cell cycle
8	−25.56	NULL	10 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
9	−25.35	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
10	−25.34	NULL	20 / 57	Glio	developing astrocytes
11	−24.68	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
12	−24.19	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	−22.62	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
14	−22.5	NULL	67 / 572	Disease	GUDJ_psoriasis up
15	−22.35	NULL	12 / 18	BP	spindle organization
16	−22.18	NULL	76 / 530	Cancer	Lembcke_Normal vs Adenoma
17	−21.19	NULL	10 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
18	−20.91	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
19	−20.04	NULL	9 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	−19.75	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
21	−19.33	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
22	−19.3	NULL	9 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
23	−19.1	NULL	43 / 232	BP	mitosis
24	−18.53	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
25	−18.16	NULL	8 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
26	−17.9	NULL	8 / 11	BP	mitotic metaphase plate congression
27	−17.33	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
28	−17.04	NULL	7 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
29	−16.93	NULL	18 / 56	CC	chromosome, centromeric region
30	−16.72	NULL	7 / 15	GSEA C2	CHANG_CYCLING_GENES
31	−16.63	NULL	4 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
32	−16.62	NULL	9 / 16	Cancer	WOLFER_overlap genes
33	−16.14	NULL	7 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
34	−16.04	NULL	7 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
35	−16.03	NULL	6 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
36	−15.92	NULL	6 / 13	GSEA C2	REN_BOUND_BY_E2F
37	−15.83	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
38	−15.72	NULL	7 / 15	GSEA C2	LY_AGING_MIDDLE_DN
39	−14.92	NULL	86 / 949	CC	nucleoplasm
40	−14.91	NULL	6 / 15	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP