GW_294

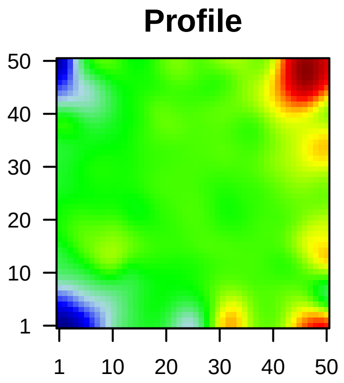
Global Summary

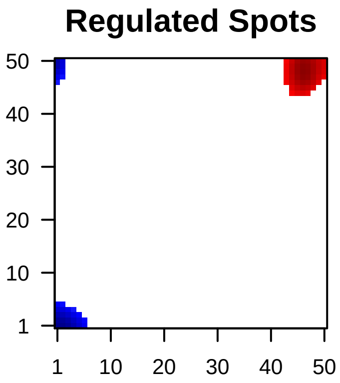
%DE = 0.15

genes with fdr < 0.2 = 1970 (1078 + / 892 −)
genes with fdr < 0.1 = 1563 (843 + / 720 −)
genes with fdr < 0.05 = 1287 (688 + / 599 −)
genes with fdr < 0.01 = 998 (527 + / 471 −)

genes in genesets = 16332

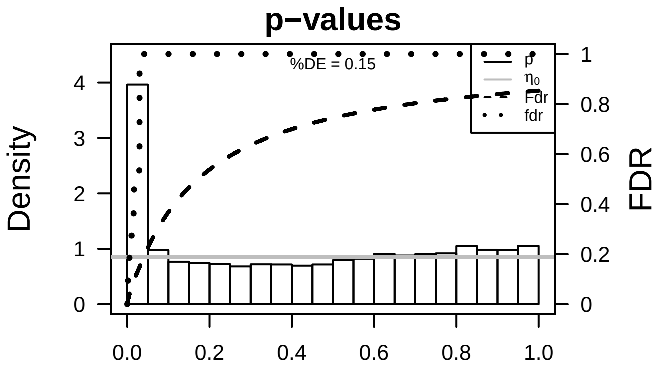
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.09
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.28	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	154664	1.9	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
3	131	1.86	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	8644	−1.68	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	−1.55	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	216	1.75	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
7	501	−1.31	2e−16	2e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
8	341	1.3	2e−16	2e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
9	25805	−1.37	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
10	64207	−2.13	2e−16	2e−14	50 x 40	interferon regulatory factor 2 binding protein−like [Source:HG
11	254528	1.31	2e−16	2e−14	12 x 14	meiosis specific with OB domains [Source:HGNC Symbol;Ac
12	116028	1.43	2e−16	2e−14	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
13	339512	2.51	2e−16	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
14	713	1.34	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	387103	1.83	2e−16	2e−14	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
16	810	−1.21	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
17	57172	1.31	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
18	595	−1.99	2e−16	2e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
19	100133941	−1.39	2e−16	2e−14	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
20	1029	1.33	2e−16	2e−14	45 x 45	cyclin−dependent kinase inhibitor 2A [Source:HGNC Symbol;



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.37	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	11.37	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	9.66	NULL	370	BP	mitotic cell cycle
4	9.66	NULL	13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
5	9.51	NULL	914	Chr	Chr 3
6	8.39	NULL	949	CC	nucleoplasm
7	7.67	NULL	15	CC	MHC class II protein complex
8	7.64	NULL	149	BP	DNA replication
9	7.23	NULL	4640	CC	nucleus
10	7.23	NULL	417	H.Tiss	WIRTH_Immune system
11	7.12	NULL	30	BP	DNA strand elongation involved in DNA replication
12	7.04	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	6.97	NULL	1720	Chr	Chr 1
14	6.78	NULL	11	GSEA C2	KALMA_E2F1_TARGETS
15	6.69	NULL	47	BP	antigen processing and presentation
16	6.52	NULL	298	BP	DNA repair
17	6.44	NULL	1318	CC	mitochondrion
18	6.42	NULL	22	BP	CENP−A containing nucleosome assembly at centromere
19	6.37	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
20	6.26	NULL	1749	MF	DNA binding
Underexpressed					
1	−17.46	NULL	21	CC	cornified envelope
2	−16.02	NULL	42	BP	keratinization
3	−12.88	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	−12.68	NULL	53	BP	keratinocyte differentiation
5	−12.5	NULL	190	CC	extracellular matrix
6	−12.27	NULL	76	BP	epidermis development
7	−11.27	NULL	242	BP	extracellular matrix organization
8	−10.72	NULL	135	H.Tiss	WIRTH_Mucosa
9	−10.56	NULL	19	BP	peptide cross−linking
10	−10.26	NULL	1182	CC	extracellular region
11	−9.26	NULL	183	CC	proteinaceous extracellular matrix
12	−8.54	NULL	683	CC	extracellular space
13	−7.95	NULL	16	MMML CGS	MACIEJ_MMML 1
14	−7.86	NULL	69	BP	extracellular matrix disassembly
15	−7.81	NULL	13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
16	−7.71	NULL	375	Disease	GUDJ_psoriasis down
17	−7.7	NULL	83	CC	basement membrane
18	−7.7	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	−7.47	NULL	186	MF	structural molecule activity
20	−7.45	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5

GW_294

Local Summary

%DE = 0.72

metagenes = 48

genes = 564

genes in genesets = 560

genes with fdr < 0.1 = 340 (313 + / 27 −)

genes with fdr < 0.05 = 288 (266 + / 22 −)

genes with fdr < 0.01 = 220 (207 + / 13 −)

<r> metagenes = 0.88

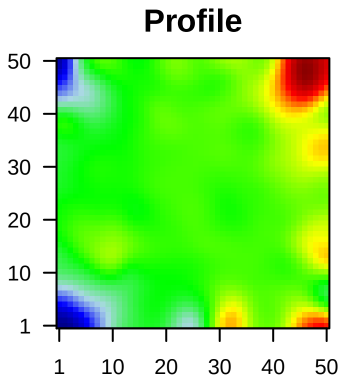
<r> genes = 0.26

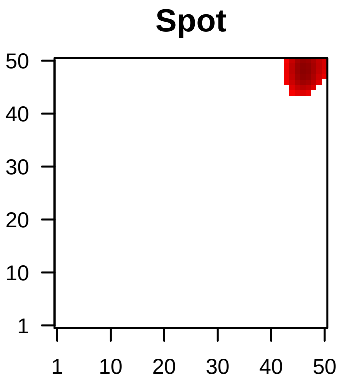
<FC> = 0.38

<shrinkage−t> = 13.5

<p−value> = 0

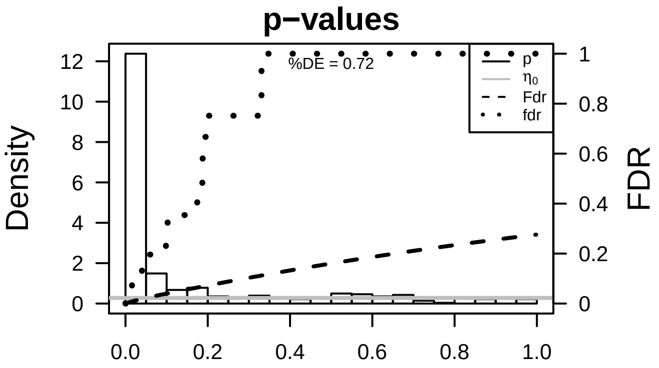
<fdr> = 0.48





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.9	2e−16	2e−15	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	216	1.75	2e−16	2e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
3	116028	1.43	2e−16	2e−15	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
4	339512	2.51	2e−16	2e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
5	387103	1.83	2e−16	2e−15	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
6	1029	1.33	2e−16	2e−15	45 x 45	cyclin−dependent kinase inhibitor 2A [Source:HGNC Symbol;
7	1056	1.73	2e−16	2e−15	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
8	3787	1.43	2e−16	2e−15	46 x 45	potassium voltage−gated channel, delayed−rectifier, subfamil
9	283212	1.53	2e−16	2e−15	46 x 44	kelch−like family member 35 [Source:HGNC Symbol;Acc:265
10	3880	2.17	2e−16	2e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
11	4171	1.39	2e−16	2e−15	46 x 48	minichromosome maintenance complex component 2 [Source
12	4744	1.5	2e−16	2e−15	45 x 44	neurofilament, heavy polypeptide [Source:HGNC Symbol;Acc
13	349565	1.29	2e−16	2e−15	50 x 50	nicotinamide nucleotide adenylyltransferase 3 [Source:HGNC
14	4922	3.69	2e−16	2e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
15	10388	1.61	2e−16	2e−15	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
16	11073	1.4	2e−16	2e−15	47 x 48	topoisomerase (DNA) II binding protein 1 [Source:HGNC Sym
17	84215	1.29	2e−16	2e−15	46 x 45	zinc finger protein 541 [Source:HGNC Symbol;Acc:25294]
18	200810	1.27	4e−16	2e−12	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransferas
19	6596	1.2	2e−14	2e−12	46 x 50	helicase−like transcription factor [Source:HGNC Symbol;Acc:
20	79844	1.19	3e−14	3e−12	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	30.8	NULL	94 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	30.8	NULL	94 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	23.15	NULL	6 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
4	20.64	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	20.15	NULL	101 / 370	BP	mitotic cell cycle
6	18.08	NULL	49 / 149	BP	DNA replication
7	17.69	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
8	16.78	NULL	19 / 30	BP	DNA strand elongation involved in DNA replication
9	15.18	NULL	109 / 530	Cancer	Lembcke_Normal vs Adenoma
10	14.93	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
11	14.77	NULL	10 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
12	14.18	NULL	26 / 57	Glio	developing astrocytes
13	14.1	NULL	9 / 16	Cancer	WOLFER_overlap genes
14	13.95	NULL	13 / 22	BP	DNA replication initiation
15	13.79	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
16	13.49	NULL	11 / 22	BP	CENP−A containing nucleosome assembly at centromere
17	13.46	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
18	13.22	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
19	13.16	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
20	13.15	NULL	14 / 24	BP	telomere maintenance via recombination
21	13.07	NULL	13 / 21	BP	telomere maintenance via semi−conservative replication
22	12.89	NULL	9 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
23	12.76	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
24	12.73	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
25	12.5	NULL	8 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
26	12.46	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
27	12.34	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
28	12.23	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
29	12.17	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
30	12.03	NULL	32 / 148	BP	G1/S transition of mitotic cell cycle
31	12.02	NULL	7 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
32	11.98	NULL	6 / 13	GSEA C2	VECCHI_GASTRIC_CANCER_EARLY_UP
33	11.97	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
34	11.91	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
35	11.76	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
36	11.63	NULL	9 / 18	BP	nucleotide−excision repair, DNA gap filling
37	11.61	NULL	24 / 56	CC	chromosome, centromeric region
38	11.44	NULL	6 / 9	GSEA C2	REACTOME_MITOTIC_M_M_G1_PHASES
39	11.43	NULL	9 / 16	GSEA C2	KEGG_MISMATCH_REPAIR
40	11.38	NULL	6 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP

GW_294

Local Summary

%DE = 0.83

metagenes = 23

genes = 354

genes in genesets = 351

genes with fdr < 0.1 = 250 (11 + / 239 −)

genes with fdr < 0.05 = 226 (9 + / 217 −)

genes with fdr < 0.01 = 186 (8 + / 178 −)

<r> metagenes = 0.94

<r> genes = 0.35

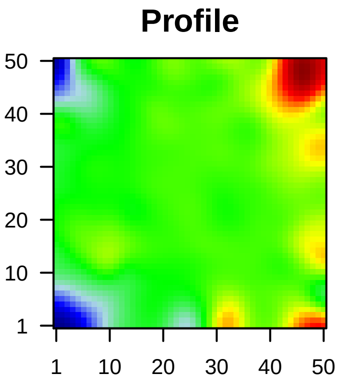
<FC> = −0.47

<shrinkage−t> = −16.28

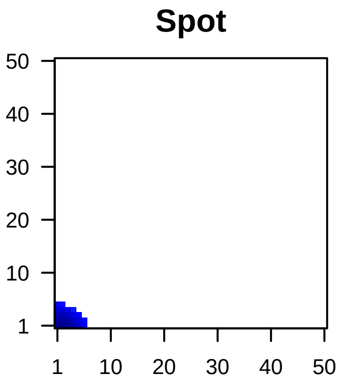
<p−value> = 0

<fdr> = 0.4

Profile



Spot



Local Genelist

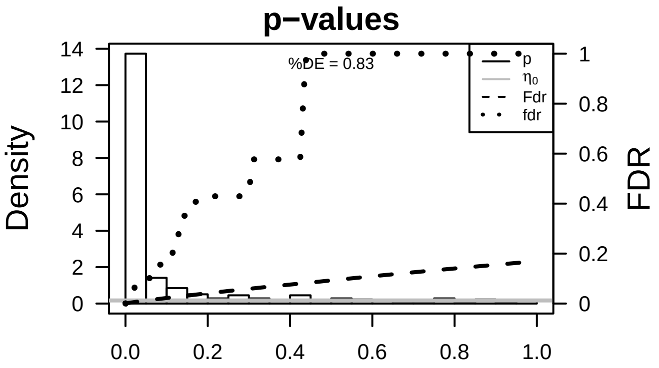
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	28514	−1.36	2e−16	1e−15	1 x 5	delta−like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
2	1948	−1.38	2e−16	1e−15	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]
3	10468	−1.41	2e−16	1e−15	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
4	3039	−1.34	2e−16	1e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3040	−1.99	2e−16	1e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
6	3043	−2.04	2e−16	1e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
7	5654	−1.4	2e−16	1e−15	2 x 1	HtrA serine peptidase 1 [Source:HGNC Symbol;Acc:9476]
8	4319	−1.45	2e−16	1e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
9	10630	−1.47	2e−16	1e−15	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
10	5270	−1.29	2e−16	1e−15	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
11	3371	−1.75	2e−16	1e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
12	55714	−1.24	2e−15	8e−14	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
13	4316	−1.24	3e−15	3e−13	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
14	7058	−1.22	7e−15	4e−13	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
15	857	−1.2	2e−14	4e−13	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
16	25878	−1.2	2e−14	4e−13	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
17	55450	−1.19	3e−14	3e−12	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
18	26064	−1.16	1e−13	3e−12	4 x 1	retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
19	4628	−1.16	1e−13	3e−12	1 x 5	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol;
20	10409	−1.16	2e−13	5e−12	1 x 2	brain abundant, membrane attached signal protein 1 [Source:

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−30.8	NULL	87 / 250	Lymphoma	LENZ_Stromal signature 1
2	−30.58	NULL	70 / 190	CC	extracellular matrix
3	−27.3	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
4	−25.66	NULL	75 / 242	BP	extracellular matrix organization
5	−23.81	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	−22.55	NULL	34 / 69	BP	extracellular matrix disassembly
7	−22.3	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
8	−20.05	NULL	29 / 64	BP	collagen catabolic process
9	−19.55	NULL	43 / 183	CC	proteinaceous extracellular matrix
10	−18.73	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
11	−18.4	NULL	127 / 1182	CC	extracellular region
12	−17.46	NULL	26 / 83	CC	basement membrane
13	−17.15	NULL	12 / 35	Glio	Colman_survival_associated
14	−16.94	NULL	7 / 11	MMML CGS	MACIEJ_MMML 31
15	−16.73	NULL	21 / 57	MF	extracellular matrix structural constituent
16	−16.35	NULL	8 / 11	MF	platelet−derived growth factor binding
17	−16.33	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
18	−15.96	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
19	−15.37	NULL	7 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
20	−15.26	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
21	−15.25	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
22	−15.15	NULL	94 / 683	CC	extracellular space
23	−15.01	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
24	−14.86	NULL	47 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
25	−14.86	NULL	47 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
26	−14.86	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
27	−14.86	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
28	−14.72	NULL	8 / 11	Glio	Phillips MES up vs Prolif & PN
29	−14.7	NULL	58 / 403	BP	cell adhesion
30	−14.67	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
31	−14.58	NULL	5 / 19	MF	peroxidase activity
32	−14.12	NULL	3 / 11	MF	oxygen transporter activity
33	−14.1	NULL	21 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
34	−13.9	NULL	24 / 119	Lymphoma	ROSOLOWSKI_green total
35	−13.86	NULL	76 / 553	Cancer	Lembcke_Colonic Inflammation
36	−13.78	NULL	6 / 12	GSEA C2	LY_AGING_MIDDLE_UP
37	−13.4	NULL	3 / 14	CC	endocytic vesicle lumen
38	−13.28	NULL	2 / 10	CC	hemoglobin complex
39	−12.83	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
40	−12.8	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET

p−values



GW_294

Local Summary

%DE = 0.92

metagenes = 9

genes = 165

genes in genesets = 161

genes with fdr < 0.1 = 136 (27 + / 109 −)

genes with fdr < 0.05 = 127 (22 + / 105 −)

genes with fdr < 0.01 = 118 (18 + / 100 −)

<r> metagenes = 0.97

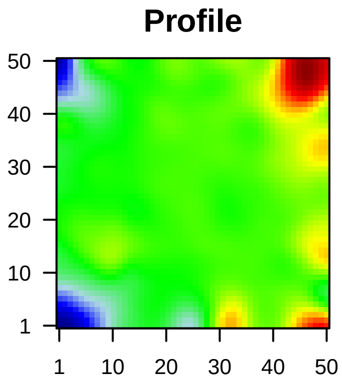
<r> genes = 0.49

<FC> = −0.59

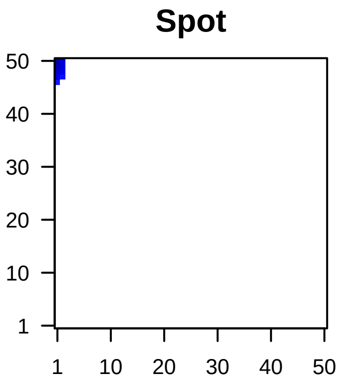
<shrinkage−t> = −20.9

<p−value> = 0

<fdr> = 0.25



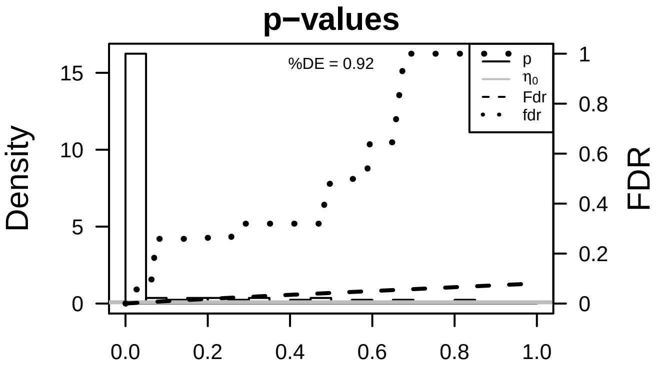
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.28	2e−16	7e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	1.86	2e−16	7e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	−1.68	2e−16	7e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	810	−1.21	2e−16	7e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
5	4680	−1.34	2e−16	7e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	22802	1.61	2e−16	7e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	−3.19	2e−16	7e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	−1.7	2e−16	7e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	−2.08	2e−16	7e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	9547	−2.19	2e−16	7e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
11	414325	−1.63	2e−16	7e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1828	−1.7	2e−16	7e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	128876	1.57	2e−16	7e−17	1 x 48	family with sequence similarity 83, member C [Source:HGNC
14	10804	−1.81	2e−16	7e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	26525	−1.5	2e−16	7e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
16	53833	1.51	2e−16	7e−17	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
17	5653	−1.53	2e−16	7e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
18	5650	−1.51	2e−16	7e−17	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
19	3854	−1.59	2e−16	7e−17	1 x 47	keratin 6B [Source:HGNC Symbol;Acc:6444]
20	388533	−3.36	2e−16	7e−17	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−52.01	NULL	18 / 21	CC	cornified envelope
2	−43.88	NULL	19 / 42	BP	keratinization
3	−35.68	NULL	23 / 53	BP	keratinocyte differentiation
4	−27.84	NULL	70 / 135	H.Tiss	WIRTH_Mucosa
5	−27.65	NULL	10 / 19	BP	peptide cross−linking
6	−25.23	NULL	21 / 76	BP	epidermis development
7	−17.22	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
8	−16.79	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
9	−16.69	NULL	78 / 572	Disease	GUDJ_psoriasis up
10	−14.85	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−12.33	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
12	−11.85	NULL	4 / 23	MF	peptidase inhibitor activity
13	−11.5	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
14	−11.47	NULL	20 / 186	MF	structural molecule activity
15	−11.27	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	−11.14	NULL	3 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
17	−11.08	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
18	−10.92	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
19	−10.8	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
20	−10.69	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
21	−10.48	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
22	−10.32	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
23	−10.21	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
24	−10.16	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
25	−9.26	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
26	−9.15	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
27	−9.1	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
28	−8.94	NULL	9 / 44	CC	keratin filament
29	−8.84	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
30	−8.72	NULL	8 / 21	CC	desmosome
31	−8.71	NULL	4 / 34	MF	endopeptidase inhibitor activity
32	−8.51	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
33	−8.5	NULL	7 / 51	MF	protein binding, bridging
34	−8.29	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
35	−8.27	NULL	3 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
36	−8.18	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
37	−8.02	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
38	−7.94	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
39	−7.84	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
40	−7.74	NULL	2 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC