GW_166

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2152 (1128 + / 1024 −)

genes with fdr < 0.1 = 1894 (1004 + / 890 −)

genes with fdr < 0.05 = 1583 (853 + / 730 −)

genes with fdr < 0.01 = 1179 (640 + / 539 −)

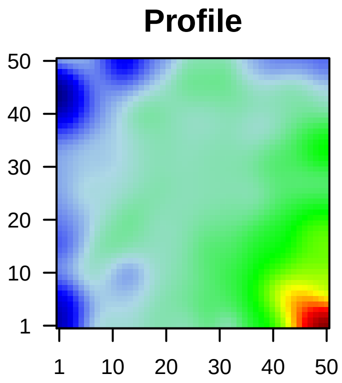
genes in genesets = 16332

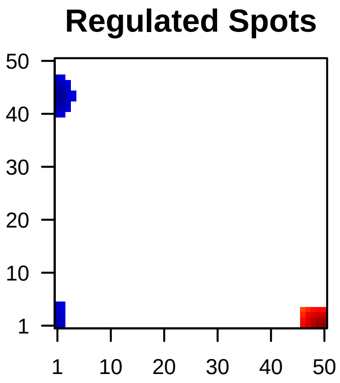
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.06

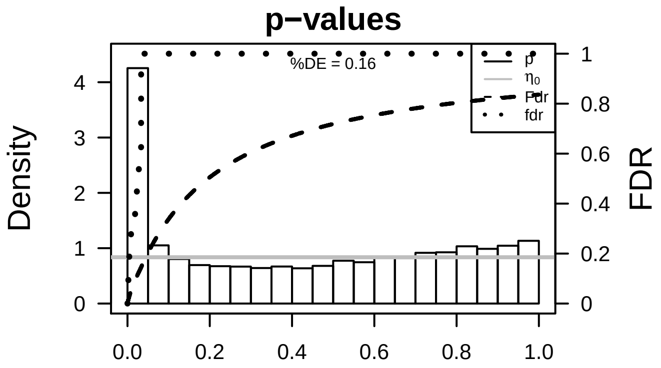
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9744	1.85	2e−16	1e−14	49 x 1	ArfGAP with coiled−coil, ankyrin repeat and PH domains 1 [S
2	8728	1.79	2e−16	1e−14	50 x 3	ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
3	27299	1.63	2e−16	1e−14	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
4	133	−2.18	2e−16	1e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
5	10551	1.54	2e−16	1e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
6	113146	−1.93	2e−16	1e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
7	80709	1.58	2e−16	1e−14	49 x 1	AT−hook transcription factor [Source:HGNC Symbol;Acc:241
8	57016	−1.86	2e−16	1e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
9	441282	−1.85	2e−16	1e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
10	8644	−1.78	2e−16	1e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
11	1109	−1.75	2e−16	1e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
12	115701	2.03	2e−16	1e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
13	55107	−1.89	2e−16	1e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
14	54518	1.92	2e−16	1e−14	50 x 1	amyloid beta (A4) precursor protein−binding, family B, membe
15	55843	1.94	2e−16	1e−14	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
16	393	1.61	2e−16	1e−14	49 x 1	Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
17	64333	1.87	2e−16	1e−14	50 x 1	Rho GTPase activating protein 9 [Source:HGNC Symbol;Acc:
18	397	1.59	2e−16	1e−14	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Sy
19	9459	1.95	2e−16	1e−14	50 x 1	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
20	640	1.55	2e−16	1e−14	46 x 4	B lymphoid tyrosine kinase [Source:HGNC Symbol;Acc:1057]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	29.66	NULL	417	H.Tiss	WIRTH_Immune system
2	14.89	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	13.99	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	13.15	NULL	15	CC	MHC class II protein complex
5	11.66	NULL	60	BP	T cell costimulation
6	10.97	NULL	84	BP	T cell receptor signaling pathway
7	10.73	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
8	10.63	NULL	28	BP	B cell receptor signaling pathway
9	10.39	NULL	312	BP	immune response
10	10.08	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
11	9.81	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	9.8	NULL	16	GSEA C2	SU_THYMUS
13	9.29	NULL	13	Cancer	GENTLES_modul18
14	9.28	NULL	162	CC	external side of plasma membrane
15	9.19	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
16	9.15	NULL	74	BP	regulation of immune response
17	8.7	NULL	14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
18	8.61	NULL	10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
19	8.58	NULL	28	BP	B cell activation
20	8.48	NULL	8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
Underexpressed					
1	−13.88	NULL	242	BP	extracellular matrix organization
2	−11.89	NULL	572	Disease	GUDJ_psoriasis up
3	−11.54	NULL	64	BP	collagen catabolic process
4	−11.5	NULL	69	BP	extracellular matrix disassembly
5	−10.91	NULL	190	CC	extracellular matrix
6	−10.43	NULL	76	BP	epidermis development
7	−10.23	NULL	83	CC	basement membrane
8	−9.39	NULL	12	BP	hemidesmosome assembly
9	−8.92	NULL	530	Cancer	Lembcke_Normal vs Adenoma
10	−8.35	NULL	11	MF	platelet−derived growth factor binding
11	−8.28	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	−8.25	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
13	−8.2	NULL	16	MMML CGS	MACIEJ_MMML 1
14	−8.09	NULL	12	miRNA target	miR−29c
15	−7.65	NULL	57	MF	extracellular matrix structural constituent
16	−7.58	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
17	−7.48	NULL	117	Glio	GIEZELT_GBM_WT_up_VS_mut
18	−7.46	NULL	37	BP	collagen fibril organization
19	−7.33	NULL	135	H.Tiss	WIRTH_Mucosa
20	−7.32	NULL	250	Lymphoma	LENZ_Stromal signature 1

GW_166

Local Summary

%DE = 0.97

metagenes = 20

genes = 314

genes in genesets = 312

genes with fdr < 0.1 = 294 (293 + / 1 −)

genes with fdr < 0.05 = 294 (293 + / 1 −)

genes with fdr < 0.01 = 287 (286 + / 1 −)

<r> metagenes = 0.99

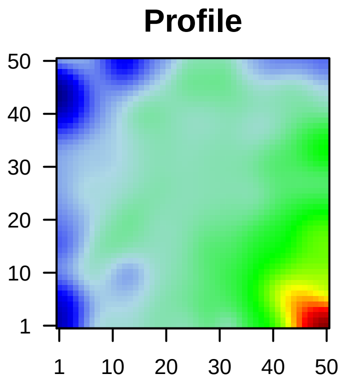
<r> genes = 0.59

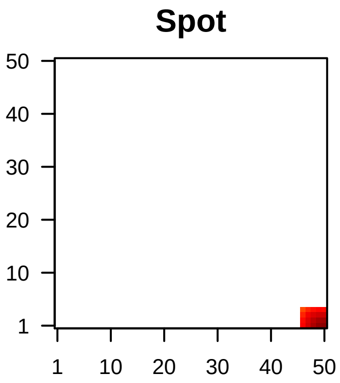
<FC> = 1.3

<shrinkage−t> = 45.47

<p−value> = 0

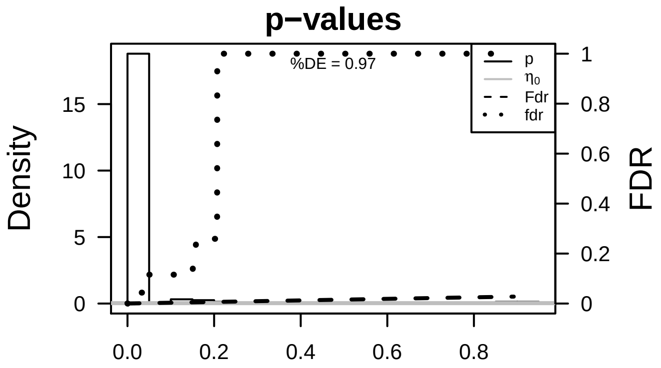
<fdr> = 0.09





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9744	1.85	2e−16	2e−17	49 x 1	ArfGAP with coiled−coil, ankyrin repeat and PH domains 1 [S
2	8728	1.79	2e−16	2e−17	50 x 3	ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
3	27299	1.63	2e−16	2e−17	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
4	80709	1.58	2e−16	2e−17	49 x 1	AT−hook transcription factor [Source:HGNC Symbol;Acc:241
5	115701	2.03	2e−16	2e−17	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
6	54518	1.92	2e−16	2e−17	50 x 1	amyloid beta (A4) precursor protein−binding, family B, membe
7	55843	1.94	2e−16	2e−17	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
8	393	1.61	2e−16	2e−17	49 x 1	Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
9	64333	1.87	2e−16	2e−17	50 x 1	Rho GTPase activating protein 9 [Source:HGNC Symbol;Acc:
10	397	1.59	2e−16	2e−17	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Sy
11	9459	1.95	2e−16	2e−17	50 x 1	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
12	640	1.55	2e−16	2e−17	46 x 4	B lymphoid tyrosine kinase [Source:HGNC Symbol;Acc:1057]
13	695	1.64	2e−16	2e−17	49 x 1	Bruton agammaglobulinemia tyrosine kinase [Source:HGNC
14	260436	2.89	2e−16	2e−17	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
15	6363	3.83	2e−16	2e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
16	6366	3.12	2e−16	2e−17	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
17	1236	2.61	2e−16	2e−17	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
18	930	3.28	2e−16	2e−17	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
19	914	1.96	2e−16	2e−17	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
20	919	2.12	2e−16	2e−17	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.36	NULL	103 / 417	H.Tiss	WIRTH_Immune system
2	31.79	NULL	113 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.76	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
4	22.56	NULL	12 / 15	CC	MHC class II protein complex
5	20.06	NULL	60 / 312	BP	immune response
6	19.11	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
7	18.79	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
8	18.74	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	18.52	NULL	12 / 28	BP	B cell receptor signaling pathway
10	18.18	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
11	17.25	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
12	16.89	NULL	8 / 16	GSEA C2	SU_THYMUS
13	16.8	NULL	8 / 13	Cancer	GENTLES_modul18
14	16.7	NULL	19 / 60	BP	T cell costimulation
15	16.42	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
16	15.95	NULL	5 / 12	BP	dendritic cell chemotaxis
17	15.8	NULL	51 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	15.8	NULL	51 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	15.8	NULL	51 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	15.8	NULL	51 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	15.3	NULL	18 / 74	BP	regulation of immune response
22	15.09	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
23	15.01	NULL	28 / 162	CC	external side of plasma membrane
24	14.86	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
25	14.29	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
26	14.22	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
27	13.51	NULL	15 / 47	BP	antigen processing and presentation
28	13.18	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
29	12.97	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
30	12.9	NULL	6 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
31	12.86	NULL	5 / 11	BP	positive regulation of B cell differentiation
32	12.6	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
33	12.49	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
34	12.45	NULL	19 / 84	BP	T cell receptor signaling pathway
35	11.97	NULL	4 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
36	11.96	NULL	6 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
37	11.83	NULL	10 / 45	BP	T cell activation
38	11.68	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
39	11.65	NULL	2 / 10	BP	positive regulation of chemotaxis
40	11.64	NULL	4 / 14	BP	ruffle organization

GW_166

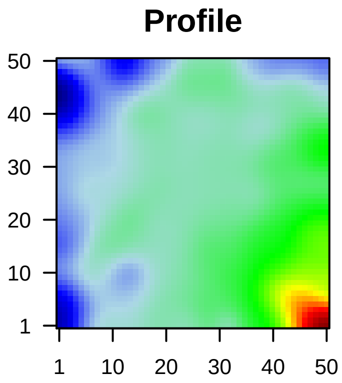
Local Summary

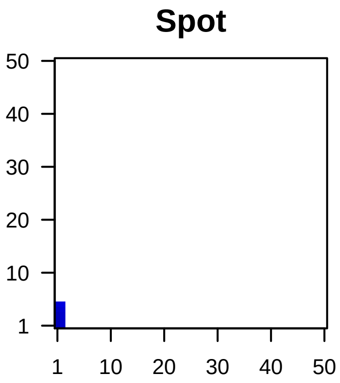
%DE = 0.94
metagenes = 10
genes = 177
genes in genesets = 175

genes with fdr < 0.1 = 163 (7 + / 156 −)
genes with fdr < 0.05 = 160 (7 + / 153 −)
genes with fdr < 0.01 = 143 (6 + / 137 −)

<r> metagenes = 0.97
<r> genes = 0.38

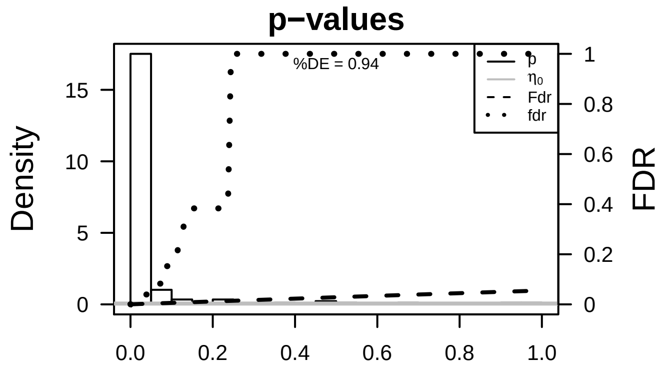
<FC> = −0.87
<shrinkage−t> = −30.64
<p−value> = 0
<fdr> = 0.18





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	−1.89	2e−16	8e−17	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	857	−1.53	2e−16	8e−17	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
3	1277	−2.5	2e−16	8e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	−1.67	2e−16	8e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	−1.75	2e−16	8e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1282	−1.78	2e−16	8e−17	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
7	1289	−1.97	2e−16	8e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	−1.79	2e−16	8e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1293	−1.73	2e−16	8e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	1294	−2.07	2e−16	8e−17	1 x 5	collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
11	2919	−1.63	2e−16	8e−17	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
12	285761	−1.65	2e−16	8e−17	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
13	2195	−2.1	2e−16	8e−17	1 x 5	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
14	8870	−1.56	2e−16	8e−17	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:539
15	3576	−2.52	2e−16	8e−17	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
16	3918	−1.66	2e−16	8e−17	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
17	4312	−2.48	2e−16	8e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
18	4319	−2.11	2e−16	8e−17	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
19	4314	−2.25	2e−16	8e−17	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
20	4502	−1.73	2e−16	8e−17	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.51	NULL	6 / 11	MF	platelet−derived growth factor binding
2	−31.23	NULL	46 / 242	BP	extracellular matrix organization
3	−30.32	NULL	19 / 64	BP	collagen catabolic process
4	−30.28	NULL	20 / 69	BP	extracellular matrix disassembly
5	−29.73	NULL	10 / 16	MMML CGS	MACIEJ_MMML 1
6	−27.85	NULL	6 / 12	miRNA target	miR−29c
7	−27.58	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
8	−27.18	NULL	7 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	−26.74	NULL	33 / 190	CC	extracellular matrix
10	−25.86	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	−22.66	NULL	10 / 40	BP	cellular response to amino acid stimulus
12	−21.02	NULL	12 / 57	MF	extracellular matrix structural constituent
13	−21	NULL	10 / 37	BP	collagen fibril organization
14	−20.8	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP
15	−20.16	NULL	35 / 250	Lymphoma	LENZ_Stromal signature 1
16	−20.06	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
17	−19.33	NULL	4 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
18	−19.25	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
19	−18.7	NULL	30 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	−18.7	NULL	30 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
21	−18.7	NULL	30 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
22	−18.7	NULL	30 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
23	−17.79	NULL	14 / 83	CC	basement membrane
24	−17.74	NULL	73 / 1182	CC	extracellular region
25	−17.42	NULL	5 / 11	Glio	Phillips MES up vs Prolif & PN
26	−17.39	NULL	53 / 683	CC	extracellular space
27	−17.28	NULL	4 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
28	−16.93	NULL	5 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
29	−16.75	NULL	38 / 403	BP	cell adhesion
30	−16.71	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
31	−16.32	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
32	−16.16	NULL	4 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
33	−16.12	NULL	4 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
34	−15.8	NULL	41 / 553	Cancer	Lembcke_Colonic Inflammation
35	−15.77	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
36	−15.52	NULL	16 / 153	CC	endoplasmic reticulum lumen
37	−15.49	NULL	9 / 68	CC	collagen
38	−15.47	NULL	5 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
39	−15.21	NULL	3 / 10	BP	protein heterotrimerization
40	−14.53	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL

GW_166

Local Summary

%DE = 0.97

metagenes = 24

genes = 286

genes in genesets = 280

genes with fdr < 0.1 = 269 (2 + / 267 −)

genes with fdr < 0.05 = 259 (2 + / 257 −)

genes with fdr < 0.01 = 237 (0 + / 237 −)

<r> metagenes = 0.93

<r> genes = 0.36

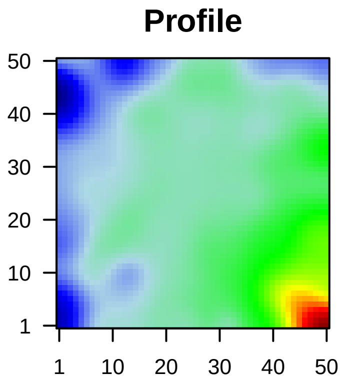
<FC> = −0.85

<shrinkage−t> = −29.92

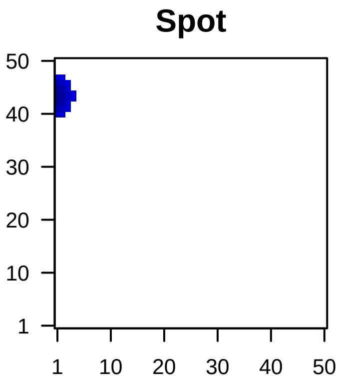
<p−value> = 0

<fdr> = 0.19

Profile



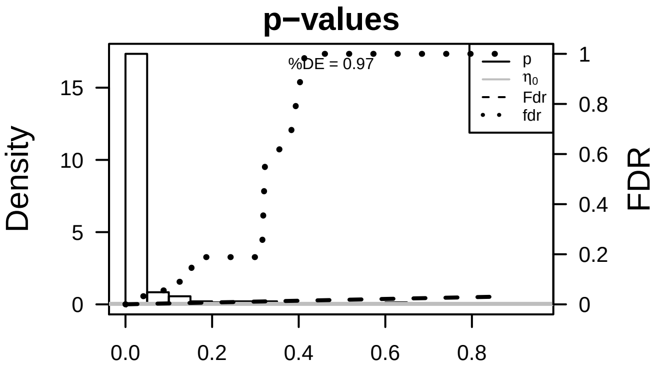
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	133	−2.18	2e−16	8e−17	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
2	113146	−1.93	2e−16	8e−17	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	760	−1.81	2e−16	8e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
4	1001	−1.96	2e−16	8e−17	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
5	1308	−1.85	2e−16	8e−17	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
6	51200	−1.83	2e−16	8e−17	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
7	1515	−1.77	2e−16	8e−17	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
8	2150	−1.55	2e−16	8e−17	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGNC
9	2171	−2	2e−16	8e−17	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
10	2697	−2.05	2e−16	8e−17	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
11	10804	−1.81	2e−16	8e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
12	3429	−1.41	2e−16	8e−17	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
13	50805	−1.81	2e−16	8e−17	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
14	3848	−1.75	2e−16	8e−17	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
15	3861	−1.63	2e−16	8e−17	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
16	3868	−3.04	2e−16	8e−17	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
17	3872	−2.93	2e−16	8e−17	1 x 43	keratin 17 [Source:HGNC Symbol;Acc:6427]
18	3852	−1.52	2e−16	8e−17	1 x 44	keratin 5 [Source:HGNC Symbol;Acc:6442]
19	286887	−2.27	2e−16	8e−17	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
20	55214	−1.86	2e−16	8e−17	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.79	NULL	18 / 82	CC	intermediate filament
2	−20.35	NULL	28 / 135	H.Tiss	WIRTH_Mucosa
3	−19.92	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−18.4	NULL	15 / 76	BP	epidermis development
5	−16.56	NULL	5 / 12	BP	hemidesmosome assembly
6	−16.43	NULL	68 / 572	Disease	GUDJ_psoriasis up
7	−16.2	NULL	9 / 44	CC	keratin filament
8	−15.25	NULL	2 / 2	miRNA target	miR−199a*
9	−14.82	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
10	−12.84	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
11	−12.17	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−12.13	NULL	11 / 82	MF	structural constituent of cytoskeleton
13	−11.86	NULL	8 / 21	CC	desmosome
14	−11.54	NULL	3 / 17	BP	morphogenesis of an epithelium
15	−11.48	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
16	−11.44	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
17	−11.42	NULL	18 / 186	MF	structural molecule activity
18	−11.3	NULL	4 / 15	CC	connexon complex
19	−11.04	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
20	−10.89	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
21	−10.87	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
22	−10.42	NULL	3 / 12	GSEA C2	MIZUKAMI_HYPOXIA_UP
23	−10.39	NULL	3 / 25	BP	response to zinc ion
24	−10.39	NULL	3 / 35	CC	cell periphery
25	−10.32	NULL	5 / 21	CC	gap junction
26	−10.32	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
27	−9.67	NULL	4 / 38	BP	epithelial cell differentiation
28	−9.58	NULL	3 / 10	MF	gap junction channel activity
29	−9.49	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
30	−9.48	NULL	4 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
31	−9.4	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
32	−9.13	NULL	4 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
33	−9.08	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
34	−9.06	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
35	−9.03	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
36	−9.03	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
37	−8.84	NULL	3 / 26	BP	positive regulation of vasodilation
38	−8.81	NULL	8 / 85	Glio	laffaire_hypermeth_LGG_vs_control
39	−8.8	NULL	4 / 20	MF	scaffold protein binding
40	−8.8	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN