GW_081

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2019 (1092 + / 927 −)

genes with fdr < 0.1 = 1593 (880 + / 713 −)

genes with fdr < 0.05 = 1346 (758 + / 588 −)

genes with fdr < 0.01 = 1021 (577 + / 444 −)

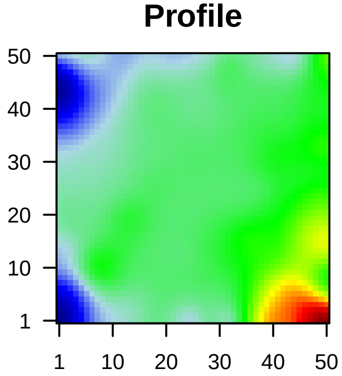
genes in genesets = 16332

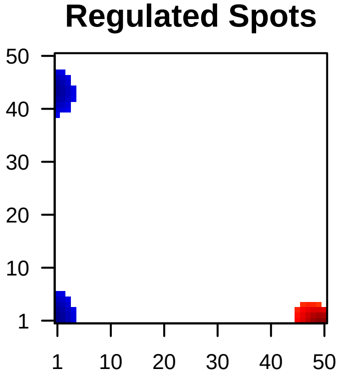
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

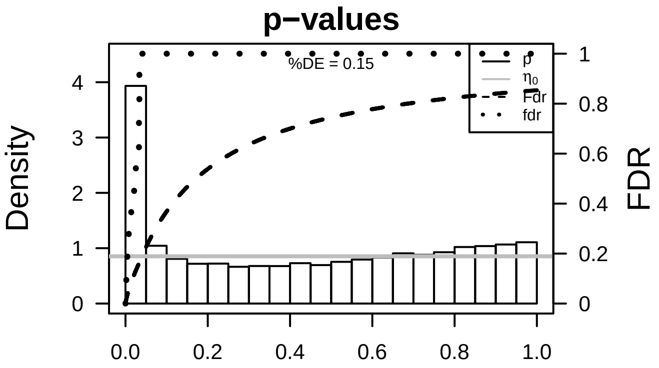
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	2.52	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	2.92	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	1109	2.32	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	216	2.1	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
5	218	1.72	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	393	1.76	2e−16	2e−14	49 x 1	Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
7	695	1.59	2e−16	2e−14	49 x 1	Bruton agammaglobulinemia tyrosine kinase [Source:HGNC
8	387695	−1.74	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
9	399948	1.63	2e−16	2e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
10	260436	2.19	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	760	−2.01	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	57172	1.7	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
13	857	−1.8	2e−16	2e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
14	6363	2.53	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
15	6366	2.26	2e−16	2e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
16	1236	2.2	2e−16	2e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
17	930	2.96	2e−16	2e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
18	919	1.65	2e−16	2e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
19	939	1.81	2e−16	2e−14	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
20	915	1.61	2e−16	2e−14	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	23.02	NULL	417	H.Tiss	WIRTH_Immune system
2	11.1	NULL	15	CC	MHC class II protein complex
3	10.69	NULL	28	BP	B cell receptor signaling pathway
4	9.67	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
5	8.63	NULL	16	GSEA C2	SU_THYMUS
6	8.38	NULL	28	BP	B cell activation
7	7.93	NULL	940	MF	nucleic acid binding
8	7.8	NULL	10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
9	7.78	NULL	60	BP	T cell costimulation
10	7.48	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
11	7.45	NULL	15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	7.41	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	7.38	NULL	84	BP	T cell receptor signaling pathway
14	7.15	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
15	7.1	NULL	74	BP	regulation of immune response
16	6.9	NULL	81	BP	viral transcription
17	6.76	NULL	14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
18	6.71	NULL	87	BP	translational termination
19	6.65	NULL	8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
20	6.64	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
Underexpressed					
1	−17.89	NULL	572	Disease	GUDJ_psoriasis up
2	−14.72	NULL	242	BP	extracellular matrix organization
3	−13.73	NULL	190	CC	extracellular matrix
4	−13.66	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−13.61	NULL	1182	CC	extracellular region
6	−12.47	NULL	69	BP	extracellular matrix disassembly
7	−11.95	NULL	64	BP	collagen catabolic process
8	−11.9	NULL	76	BP	epidermis development
9	−11.51	NULL	683	CC	extracellular space
10	−10.38	NULL	16	MMML CGS	MACIEJ_MMML 1
11	−9.72	NULL	11	MF	platelet−derived growth factor binding
12	−9.12	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
13	−9.07	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	−8.78	NULL	183	CC	proteinaceous extracellular matrix
15	−8.61	NULL	83	CC	basement membrane
16	−8.49	NULL	57	MF	extracellular matrix structural constituent
17	−8.45	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
18	−8.45	NULL	37	BP	collagen fibril organization
19	−8.42	NULL	12	miRNA target	miR−29c
20	−8.4	NULL	135	H.Tiss	WIRTH_Mucosa

GW_081

Local Summary

%DE = 0.88

metagenes = 22

genes = 328

genes in genesets = 325

genes with fdr < 0.1 = 272 (269 + / 3 −)

genes with fdr < 0.05 = 265 (262 + / 3 −)

genes with fdr < 0.01 = 240 (238 + / 2 −)

<r> metagenes = 0.99

<r> genes = 0.59

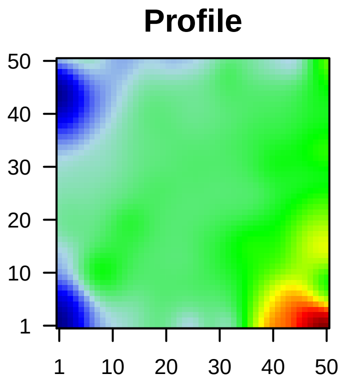
<FC> = 0.96

<shrinkage−t> = 33.67

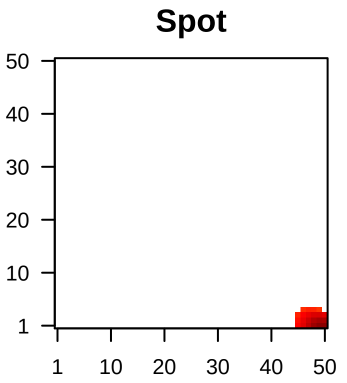
<p−value> = 0

<fdr> = 0.19

Profile



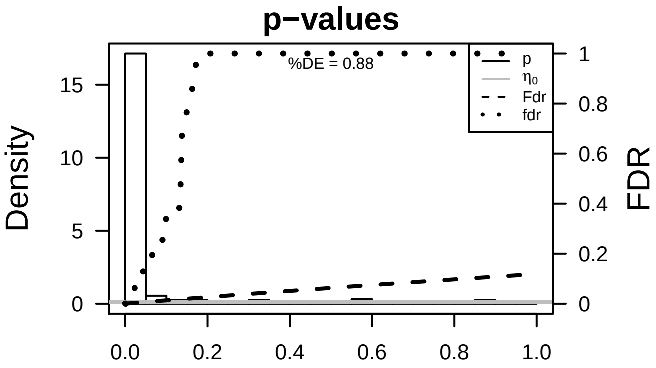
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	393	1.76	2e−16	1e−16	49 x 1	Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
2	695	1.59	2e−16	1e−16	49 x 1	Bruton agammaglobulinemia tyrosine kinase [Source:HGNC
3	260436	2.19	2e−16	1e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
4	57172	1.7	2e−16	1e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
5	6363	2.53	2e−16	1e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
6	6366	2.26	2e−16	1e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
7	1236	2.2	2e−16	1e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
8	930	2.96	2e−16	1e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
9	919	1.65	2e−16	1e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
10	939	1.81	2e−16	1e−16	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
11	915	1.61	2e−16	1e−16	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
12	962	2.23	2e−16	1e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
13	1043	2.25	2e−16	1e−16	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
14	963	1.56	2e−16	1e−16	50 x 1	CD53 molecule [Source:HGNC Symbol;Acc:1686]
15	974	1.7	2e−16	1e−16	48 x 1	CD79b molecule, immunoglobulin−associated beta [Source:H
16	11151	1.66	2e−16	1e−16	50 x 1	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
17	51755	1.68	2e−16	1e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
18	10563	1.66	2e−16	1e−16	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
19	26999	1.73	2e−16	1e−16	49 x 1	cytoplasmic FMR1 interacting protein 2 [Source:HGNC Symb
20	1794	1.64	2e−16	1e−16	50 x 1	dedicator of cytokinesis 2 [Source:HGNC Symbol;Acc:2988]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	35.25	NULL	110 / 417	H.Tiss	WIRTH_Immune system
2	31.54	NULL	114 / 553	Cancer	Lembcke_Colonic Inflammation
3	28.42	NULL	13 / 15	CC	MHC class II protein complex
4	20.7	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	19.51	NULL	12 / 28	BP	B cell receptor signaling pathway
6	19.04	NULL	62 / 312	BP	immune response
7	18.49	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
8	18.21	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
9	17.85	NULL	8 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
10	16.46	NULL	21 / 60	BP	T cell costimulation
11	16.11	NULL	15 / 47	BP	antigen processing and presentation
12	15.13	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
13	15.12	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
14	15	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
15	14.89	NULL	5 / 12	BP	dendritic cell chemotaxis
16	14.71	NULL	8 / 16	GSEA C2	SU_THYMUS
17	14.67	NULL	9 / 13	Cancer	GENTLES_modul18
18	14.46	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
19	14.31	NULL	47 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	14.31	NULL	47 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
21	14.31	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
22	14.31	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
23	14.24	NULL	5 / 11	BP	positive regulation of B cell differentiation
24	14.04	NULL	7 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
25	13.78	NULL	30 / 162	CC	external side of plasma membrane
26	13.74	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
27	13.19	NULL	20 / 84	BP	T cell receptor signaling pathway
28	13.1	NULL	18 / 74	BP	regulation of immune response
29	13.09	NULL	6 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
30	13.08	NULL	5 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
31	12.72	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
32	11.97	NULL	5 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
33	11.81	NULL	4 / 13	BP	lymph node development
34	11.67	NULL	5 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
35	11.53	NULL	7 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
36	11.52	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
37	11.47	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
38	11.45	NULL	7 / 15	GSEA C2	BIOCARTA_TCR_PATHWAY
39	11.41	NULL	4 / 10	BP	negative thymic T cell selection
40	11.36	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP

GW_081

Local Summary

%DE = 0.9

metagenes = 20

genes = 301

genes in genesets = 299

genes with fdr < 0.1 = 263 (3 + / 260 −)

genes with fdr < 0.05 = 248 (3 + / 245 −)

genes with fdr < 0.01 = 207 (1 + / 206 −)

<r> metagenes = 0.94

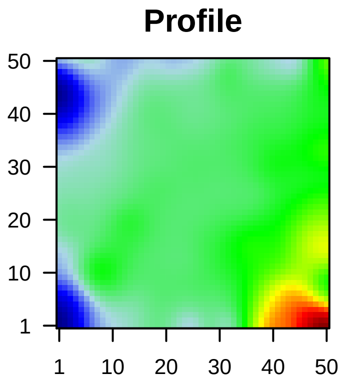
<r> genes = 0.36

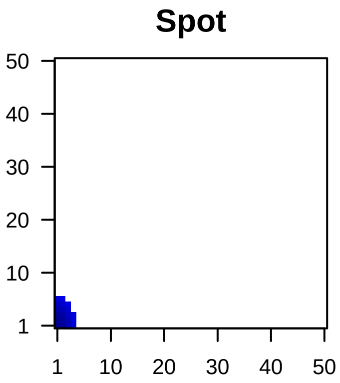
<FC> = −0.72

<shrinkage−t> = −25.12

<p−value> = 0

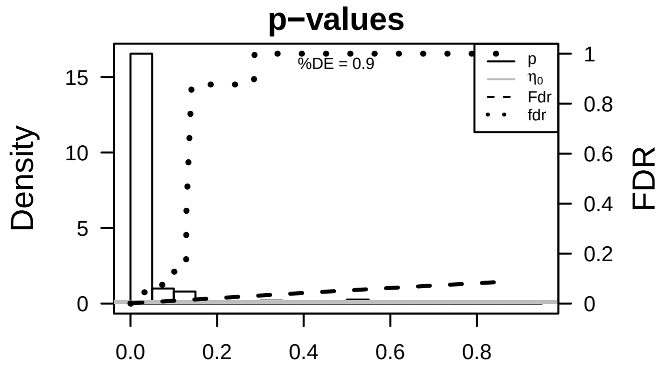
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	857	−1.8	2e−16	3e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
2	1277	−2.2	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	−1.9	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	−1.65	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1289	−1.82	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1290	−1.54	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1291	−1.54	2e−16	3e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
8	2919	−1.57	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
9	2195	−1.86	2e−16	3e−16	1 x 5	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
10	3040	−1.96	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
11	3576	−2.43	2e−16	3e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
12	4312	−2.09	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
13	4314	−1.95	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
14	4489	−1.57	2e−16	3e−16	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
15	4502	−1.68	2e−16	3e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
16	4430	−1.53	2e−16	3e−16	1 x 5	myosin IB [Source:HGNC Symbol;Acc:7596]
17	5328	−2	2e−16	3e−16	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
18	5743	−1.58	2e−16	3e−16	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
19	51330	−1.73	2e−16	3e−16	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
20	1948	−1.5	4e−16	6e−15	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.67	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	−33.04	NULL	70 / 242	BP	extracellular matrix organization
3	−32.71	NULL	59 / 190	CC	extracellular matrix
4	−31.53	NULL	29 / 64	BP	collagen catabolic process
5	−31.21	NULL	32 / 69	BP	extracellular matrix disassembly
6	−31.02	NULL	7 / 11	MF	platelet−derived growth factor binding
7	−30.61	NULL	69 / 250	Lymphoma	LENZ_Stromal signature 1
8	−30.37	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	−28.31	NULL	8 / 12	miRNA target	miR−29c
10	−23.45	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
11	−23.44	NULL	16 / 37	BP	collagen fibril organization
12	−22.78	NULL	21 / 57	MF	extracellular matrix structural constituent
13	−22.5	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	−22.33	NULL	11 / 40	BP	cellular response to amino acid stimulus
15	−21.52	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
16	−21.52	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
17	−21.52	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
18	−21.52	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
19	−20.97	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
20	−19.84	NULL	76 / 683	CC	extracellular space
21	−19.84	NULL	106 / 1182	CC	extracellular region
22	−19.21	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
23	−18.8	NULL	65 / 553	Cancer	Lembcke_Colonic Inflammation
24	−18.73	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
25	−18.31	NULL	4 / 10	BP	protein heterotrimerization
26	−18.27	NULL	12 / 19	MF	extracellular matrix binding
27	−18.17	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
28	−18.11	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
29	−17.78	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
30	−17.77	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
31	−17.63	NULL	16 / 68	CC	collagen
32	−17.51	NULL	56 / 403	BP	cell adhesion
33	−17.32	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
34	−17.29	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
35	−17.26	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
36	−17.26	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
37	−16.91	NULL	27 / 153	CC	endoplasmic reticulum lumen
38	−16.84	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
39	−16.83	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
40	−16.82	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR

GW_081

Local Summary

%DE = 0.93

metagenes = 27

genes = 316

genes in genesets = 310

genes with fdr < 0.1 = 279 (3 + / 276 −)

genes with fdr < 0.05 = 266 (3 + / 263 −)

genes with fdr < 0.01 = 223 (1 + / 222 −)

<r> metagenes = 0.93

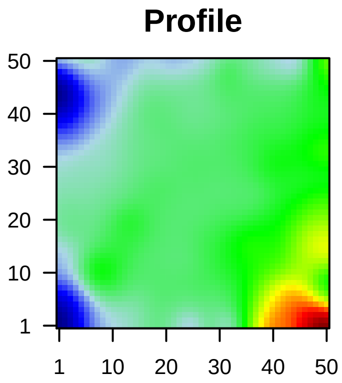
<r> genes = 0.35

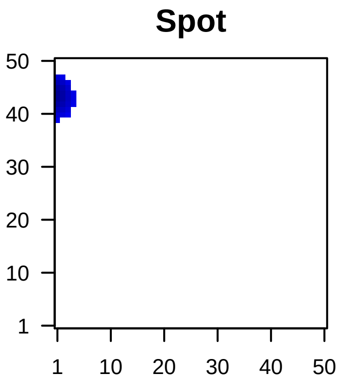
<FC> = −0.69

<shrinkage−t> = −24.25

<p−value> = 0

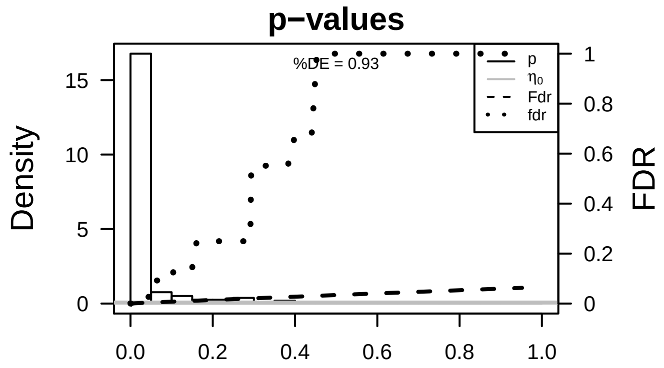
<fdr> = 0.29





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	760	−2.01	2e−16	3e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	1001	−1.54	2e−16	3e−16	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
3	1308	−1.95	2e−16	3e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
4	51200	−1.52	2e−16	3e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
5	2697	−1.98	2e−16	3e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
6	2706	−1.82	2e−16	3e−16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
7	10804	−1.86	2e−16	3e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
8	3306	−1.52	2e−16	3e−16	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
9	3489	−2.19	2e−16	3e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
10	56300	−1.68	2e−16	3e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
11	3868	−2.45	2e−16	3e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
12	5836	−1.51	2e−16	3e−16	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:97
13	5947	−1.8	2e−16	3e−16	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
14	2810	−1.41	2e−16	3e−16	1 x 45	stratifin [Source:HGNC Symbol;Acc:10773]
15	7280	−1.7	2e−16	3e−16	1 x 45	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
16	3854	−1.51	4e−16	9e−15	1 x 47	keratin 6B [Source:HGNC Symbol;Acc:6444]
17	3848	−1.49	9e−16	1e−14	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
18	3861	−1.36	2e−15	1e−13	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
19	9982	−1.35	1e−14	1e−13	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
20	6713	−1.43	1e−14	3e−13	2 x 43	squalene epoxidase [Source:HGNC Symbol;Acc:11279]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.47	NULL	71 / 572	Disease	GUDJ_psoriasis up
2	−18.2	NULL	5 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
3	−17.73	NULL	29 / 135	H.Tiss	WIRTH_Mucosa
4	−17.55	NULL	19 / 82	CC	intermediate filament
5	−16.17	NULL	16 / 76	BP	epidermis development
6	−16.06	NULL	5 / 15	CC	connexon complex
7	−14.93	NULL	4 / 10	MF	gap junction channel activity
8	−14.78	NULL	6 / 21	CC	gap junction
9	−14.56	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
10	−14.51	NULL	9 / 44	CC	keratin filament
11	−14.33	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
12	−14.16	NULL	5 / 12	BP	hemidesmosome assembly
13	−13.51	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
14	−13.11	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
15	−12.06	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
16	−11.75	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
17	−11.73	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
18	−11.63	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
19	−11.58	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
20	−11.33	NULL	11 / 82	MF	structural constituent of cytoskeleton
21	−11.27	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
22	−11.19	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
23	−11.14	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
24	−10.72	NULL	3 / 25	BP	response to zinc ion
25	−9.74	NULL	19 / 186	MF	structural molecule activity
26	−9.59	NULL	8 / 21	CC	desmosome
27	−9.54	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
28	−9.47	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
29	−9.32	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
30	−8.99	NULL	2 / 2	miRNA target	miR−199a*
31	−8.92	NULL	3 / 17	BP	morphogenesis of an epithelium
32	−8.72	NULL	3 / 12	CC	fascia adherens
33	−8.71	NULL	8 / 85	Glio	laffaire_hypermeth_LGG_vs_control
34	−8.7	NULL	4 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
35	−8.66	NULL	9 / 44	BP	skin development
36	−8.39	NULL	3 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
37	−8.38	NULL	4 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
38	−8.37	NULL	4 / 38	BP	epithelial cell differentiation
39	−8.19	NULL	2 / 12	GSEA C2	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
40	−8.18	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN