GW_095

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1864 (969 + / 895 −)

genes with fdr < 0.1 = 1592 (829 + / 763 −)

genes with fdr < 0.05 = 1381 (712 + / 669 −)

genes with fdr < 0.01 = 1025 (524 + / 501 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

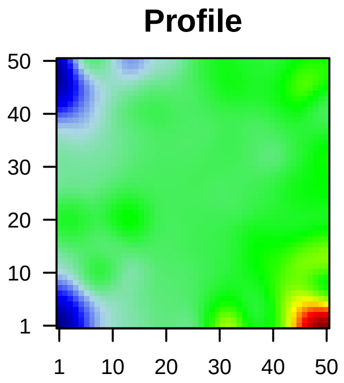
<fdr> = 0.85

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.65	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	133	−1.37	2e−16	2e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
3	113146	−1.96	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	501	−1.61	2e−16	2e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
5	242	−1.58	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sy
6	55107	−1.87	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
7	341	2.42	2e−16	2e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
8	348	1.71	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
9	445328	−1.87	2e−16	2e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
10	445	2.04	2e−16	2e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
11	25805	−1.66	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
12	10974	1.65	2e−16	2e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
13	113802	1.43	2e−16	2e−14	46 x 46	HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:H
14	713	1.88	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	771	−1.41	2e−16	2e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
16	51806	1.58	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
17	57172	1.5	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
18	6363	2.09	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
19	6364	−2.38	2e−16	2e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
20	6352	1.66	2e−16	2e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	21.99	NULL	417	H.Tiss	WIRTH_Immune system
2	13.72	NULL	15	CC	MHC class II protein complex
3	11.68	NULL	47	BP	antigen processing and presentation
4	11.2	NULL	74	BP	regulation of immune response
5	10.32	NULL	312	BP	immune response
6	9.5	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
7	9.39	NULL	60	BP	interferon−gamma−mediated signaling pathway
8	9.17	NULL	1135	Chr	Chr 19
9	9.12	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	8.72	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	8.69	NULL	84	BP	T cell receptor signaling pathway
12	8.66	NULL	32	CC	ER to Golgi transport vesicle membrane
13	8.6	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
14	8.35	NULL	60	BP	T cell costimulation
15	8.26	NULL	14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
16	8.1	NULL	13	Cancer	GENTLES_modul18
17	8.04	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
18	7.74	NULL	15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
19	7.72	NULL	10	BP	positive regulation of cAMP−mediated signaling
20	7.68	NULL	162	CC	external side of plasma membrane
Underexpressed					
1	−18.17	NULL	21	CC	cornified envelope
2	−16.31	NULL	42	BP	keratinization
3	−15.39	NULL	242	BP	extracellular matrix organization
4	−14.94	NULL	53	BP	keratinocyte differentiation
5	−14.47	NULL	190	CC	extracellular matrix
6	−14.3	NULL	76	BP	epidermis development
7	−13.44	NULL	69	BP	extracellular matrix disassembly
8	−13.24	NULL	64	BP	collagen catabolic process
9	−12.18	NULL	250	Lymphoma	LENZ_Stromal signature 1
10	−11.86	NULL	11	MF	platelet−derived growth factor binding
11	−11.67	NULL	135	H.Tiss	WIRTH_Mucosa
12	−11.3	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	−11.04	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
14	−10.79	NULL	1182	CC	extracellular region
15	−10.29	NULL	16	MMML CGS	MACIEJ_MMML 1
16	−9.95	NULL	572	Disease	GUDJ_psoriasis up
17	−9.68	NULL	183	CC	proteinaceous extracellular matrix
18	−9.29	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
19	−9.16	NULL	683	CC	extracellular space
20	−9.12	NULL	12	miRNA target	miR−29c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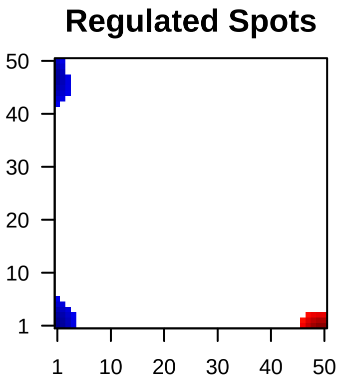
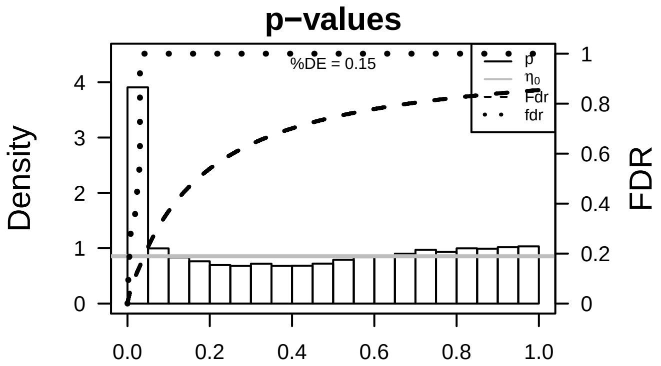

Regulated Spots


p−values

GW_095

Local Summary

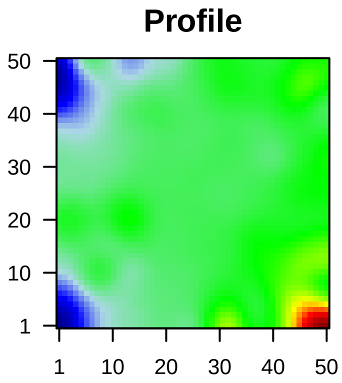
%DE = 0.98
metagenes = 14
genes = 247
genes in genesets = 245

genes with fdr < 0.1 = 233 (230 + / 3 −)
genes with fdr < 0.05 = 233 (230 + / 3 −)
genes with fdr < 0.01 = 230 (227 + / 3 −)

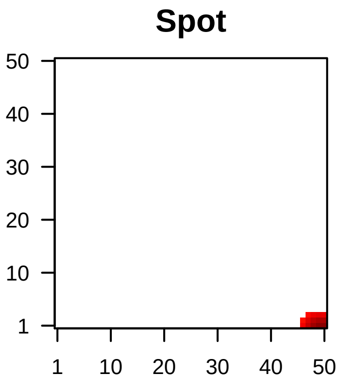
<r> metagenes = 0.99
<r> genes = 0.62

<FC> = 1
<shrinkage−t> = 34.95
<p−value> = 0
<fdr> = 0.07

Profile



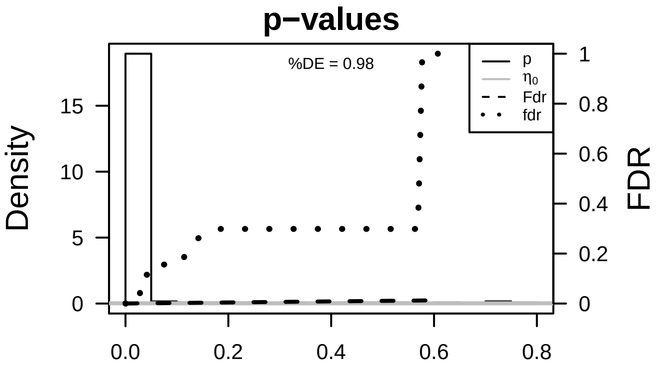
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	2.42	2e−16	2e−17	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	348	1.71	2e−16	2e−17	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	713	1.88	2e−16	2e−17	50 x 1	complement component 1, q subcomponent, B chain [Source
4	57172	1.5	2e−16	2e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
5	6363	2.09	2e−16	2e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
6	6364	−2.38	2e−16	2e−17	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
7	6352	1.66	2e−16	2e−17	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
8	930	1.48	2e−16	2e−17	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
9	914	1.54	2e−16	2e−17	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
10	919	1.43	2e−16	2e−17	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
11	939	1.47	2e−16	2e−17	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
12	915	1.87	2e−16	2e−17	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
13	962	1.78	2e−16	2e−17	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
14	1043	1.71	2e−16	2e−17	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
15	924	1.38	2e−16	2e−17	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
16	925	1.65	2e−16	2e−17	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
17	51755	1.45	2e−16	2e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
18	4283	2.98	2e−16	2e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
19	8320	1.57	2e−16	2e−17	48 x 1	eomesodermin [Source:HGNC Symbol;Acc:3372]
20	54855	1.56	2e−16	2e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.39	NULL	12 / 15	CC	MHC class II protein complex
2	32.22	NULL	89 / 417	H.Tiss	WIRTH_Immune system
3	24.55	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
4	23.99	NULL	89 / 553	Cancer	Lembcke_Colonic Inflammation
5	23.39	NULL	14 / 47	BP	antigen processing and presentation
6	23.03	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
7	22.88	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	22.71	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
9	22.42	NULL	50 / 312	BP	immune response
10	19.56	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
11	19.19	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	18.95	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	18.91	NULL	16 / 60	BP	T cell costimulation
14	18.69	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
15	18.58	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
16	18.45	NULL	7 / 13	Cancer	GENTLES_modul18
17	17.29	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
18	16.78	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
19	16.7	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
20	16.63	NULL	7 / 28	CC	transport vesicle membrane
21	16.61	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
22	15.92	NULL	15 / 84	BP	T cell receptor signaling pathway
23	15.83	NULL	17 / 74	BP	regulation of immune response
24	15.75	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
25	15.53	NULL	8 / 16	GSEA C2	SU_THYMUS
26	15.47	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
27	15.42	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
28	15.37	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
29	15.37	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
30	15.37	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
31	15.37	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
32	14.82	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
33	14.65	NULL	7 / 35	CC	trans−Golgi network membrane
34	14.6	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
35	14.59	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
36	14.38	NULL	4 / 16	BP	cytolysis
37	14.34	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
38	14.17	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
39	14.12	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
40	14.01	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_

GW_095

Local Summary

%DE = 0.91

metagenes = 18

genes = 290

genes in genesets = 288

genes with fdr < 0.1 = 260 (7 + / 253 −)

genes with fdr < 0.05 = 231 (3 + / 228 −)

genes with fdr < 0.01 = 204 (0 + / 204 −)

<r> metagenes = 0.95

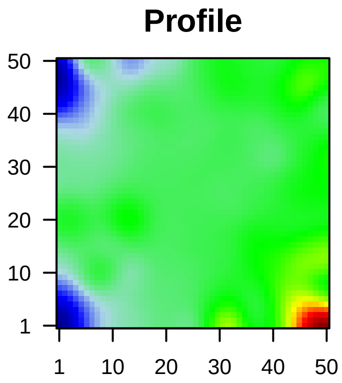
<r> genes = 0.36

<FC> = −0.73

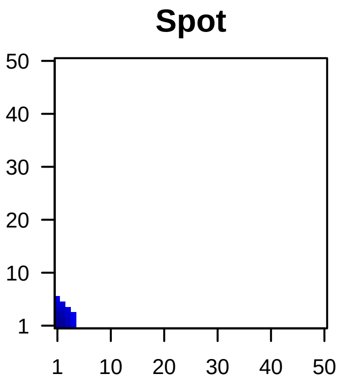
<shrinkage−t> = −25.46

<p−value> = 0

<fdr> = 0.24



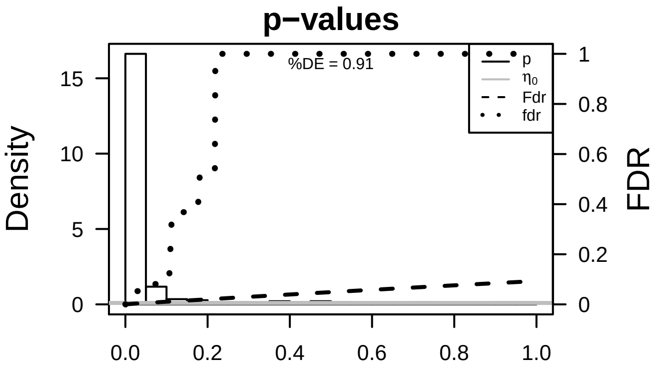
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	−1.87	2e−16	2e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	595	−1.32	2e−16	2e−16	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
3	1277	−2.28	2e−16	2e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	−1.61	2e−16	2e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	−1.77	2e−16	2e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1282	−1.86	2e−16	2e−16	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
7	1289	−2.32	2e−16	2e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	−1.53	2e−16	2e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1291	−1.92	2e−16	2e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
10	2919	−1.86	2e−16	2e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
11	1687	−1.38	2e−16	2e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
12	1948	−1.6	2e−16	2e−16	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]
13	8870	−1.86	2e−16	2e−16	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:539
14	3553	−2.25	2e−16	2e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
15	3576	−2.55	2e−16	2e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
16	3693	−1.39	2e−16	2e−16	1 x 5	integrin, beta 5 [Source:HGNC Symbol;Acc:6160]
17	4312	−1.81	2e−16	2e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
18	4319	−1.62	2e−16	2e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
19	4314	−2.75	2e−16	2e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
20	4316	−1.89	2e−16	2e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−35.83	NULL	7 / 11	MF	platelet−derived growth factor binding
2	−34.79	NULL	59 / 190	CC	extracellular matrix
3	−33.1	NULL	70 / 242	BP	extracellular matrix organization
4	−32.88	NULL	32 / 69	BP	extracellular matrix disassembly
5	−32.88	NULL	29 / 64	BP	collagen catabolic process
6	−32.04	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
7	−29.39	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	−29.07	NULL	8 / 12	miRNA target	miR−29c
9	−28.09	NULL	69 / 250	Lymphoma	LENZ_Stromal signature 1
10	−24.09	NULL	20 / 57	MF	extracellular matrix structural constituent
11	−23.02	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
12	−22.21	NULL	15 / 37	BP	collagen fibril organization
13	−22.05	NULL	11 / 40	BP	cellular response to amino acid stimulus
14	−21.78	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
15	−20.91	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
16	−20.64	NULL	76 / 683	CC	extracellular space
17	−20.36	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
18	−20.17	NULL	37 / 183	CC	proteinaceous extracellular matrix
19	−19.8	NULL	42 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	−19.8	NULL	42 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
21	−19.8	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
22	−19.8	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
23	−19.49	NULL	104 / 1182	CC	extracellular region
24	−19.28	NULL	63 / 553	Cancer	Lembcke_Colonic Inflammation
25	−19.11	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
26	−18.81	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
27	−18.52	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
28	−18.43	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
29	−18.32	NULL	4 / 10	BP	protein heterotrimerization
30	−18.03	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN
31	−17.87	NULL	13 / 35	Glio	Colman_survival_associated
32	−17.65	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
33	−17.64	NULL	56 / 403	BP	cell adhesion
34	−17.46	NULL	23 / 83	CC	basement membrane
35	−17.16	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
36	−16.85	NULL	16 / 68	CC	collagen
37	−16.26	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
38	−16.2	NULL	16 / 68	Glio	cultured astroglia vs. in vivo astrocytes
39	−15.8	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
40	−15.75	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN

GW_095

Local Summary

%DE = 0.91

metagenes = 21

genes = 319

genes in genesets = 312

genes with fdr < 0.1 = 266 (21 + / 245 −)

genes with fdr < 0.05 = 266 (21 + / 245 −)

genes with fdr < 0.01 = 229 (13 + / 216 −)

<r> metagenes = 0.9

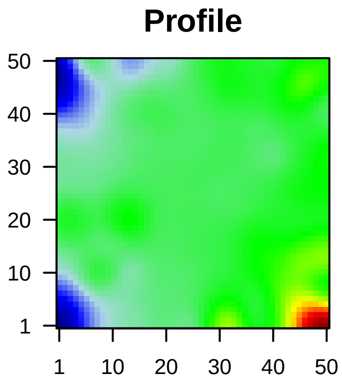
<r> genes = 0.37

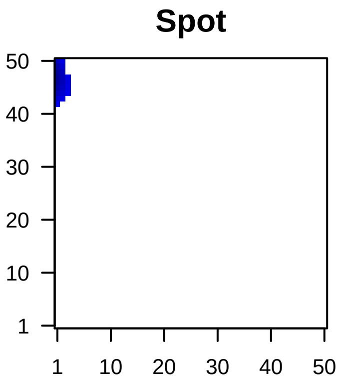
<FC> = −0.79

<shrinkage−t> = −27.78

<p−value> = 0

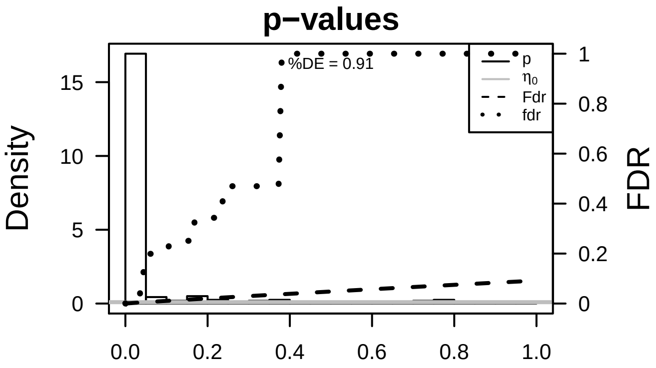
<fdr> = 0.23





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.65	2e−16	1e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	133	−1.37	2e−16	1e−16	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
3	113146	−1.96	2e−16	1e−16	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	242	−1.58	2e−16	1e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
5	771	−1.41	2e−16	1e−16	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
6	22802	1.38	2e−16	1e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	−1.57	2e−16	1e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	1308	−1.93	2e−16	1e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
9	54544	−1.42	2e−16	1e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
10	1515	−1.73	2e−16	1e−16	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
11	9547	−1.43	2e−16	1e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
12	1672	−1.71	2e−16	1e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	55894	−1.72	2e−16	1e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	−2.52	2e−16	1e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	−3.32	2e−16	1e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	2167	−2.06	2e−16	1e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	163351	1.53	2e−16	1e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
18	2706	−2.76	2e−16	1e−16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
19	10804	−2.39	2e−16	1e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
20	1839	−1.86	2e−16	1e−16	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Sym



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−43.27	NULL	18 / 21	CC	cornified envelope
2	−35.67	NULL	20 / 42	BP	keratinization
3	−32.59	NULL	24 / 53	BP	keratinocyte differentiation
4	−30.82	NULL	27 / 76	BP	epidermis development
5	−27.79	NULL	112 / 572	Disease	GUDJ_psoriasis up
6	−26.39	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
7	−24.32	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−20.21	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
9	−15.34	NULL	10 / 19	BP	peptide cross−linking
10	−14.52	NULL	4 / 10	MF	RAGE receptor binding
11	−13.36	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−13.26	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	−13.22	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
14	−13.21	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
15	−12.18	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
16	−11.77	NULL	3 / 15	MF	interleukin−1 receptor binding
17	−11.69	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
18	−10.95	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
19	−10.93	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	−10.86	NULL	30 / 186	MF	structural molecule activity
21	−10.72	NULL	3 / 15	CC	connexon complex
22	−10.58	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
23	−10.47	NULL	21 / 82	CC	intermediate filament
24	−10.47	NULL	12 / 21	CC	desmosome
25	−10.24	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
26	−10.05	NULL	66 / 1182	CC	extracellular region
27	−9.58	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
28	−9.51	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
29	−9.43	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
30	−9.39	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
31	−9.21	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
32	−9.19	NULL	5 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
33	−9.17	NULL	4 / 21	CC	gap junction
34	−9.12	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
35	−9.07	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
36	−8.85	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
37	−8.78	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
38	−8.78	NULL	2 / 11	GSEA C2	LEI_MYB_TARGETS
39	−8.7	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
40	−8.7	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL