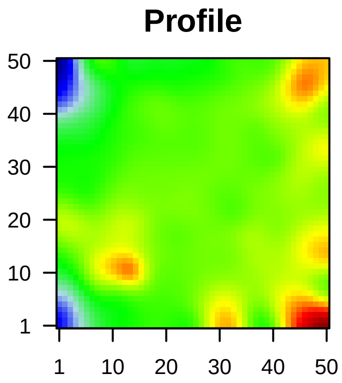
GW_224

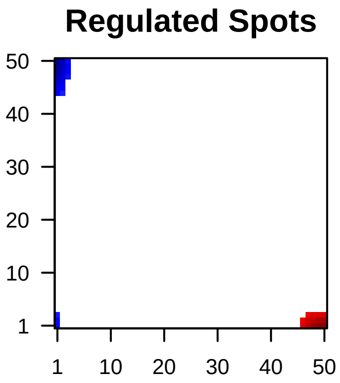
Global Summary

%DE = 0.15
genes with fdr < 0.2 = 1958 (992 + / 966 −)
genes with fdr < 0.1 = 1553 (769 + / 784 −)
genes with fdr < 0.05 = 1296 (633 + / 663 −)
genes with fdr < 0.01 = 975 (474 + / 501 −)

genes in genesets = 16332

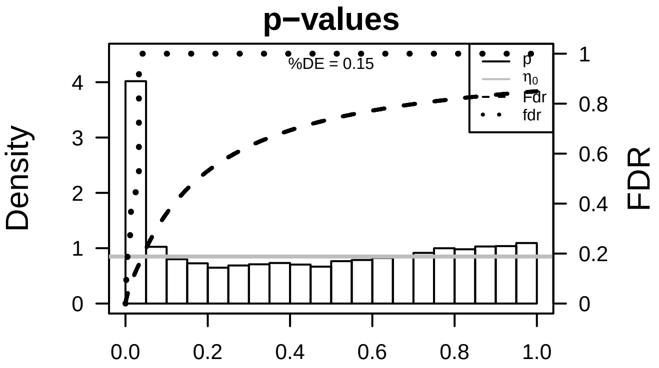
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.08
<fdr> = 0.85


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.11	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	27299	1.94	2e−16	2e−14	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
3	216	2.55	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
4	218	−3.05	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	65124	−2.16	2e−16	2e−14	1 x 45	sosondowah ankyrin repeat domain family member C [Source
6	341	2.58	2e−16	2e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
7	348	2.11	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
8	664	−1.82	2e−16	2e−14	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HG
9	339512	2.65	2e−16	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
10	713	2.04	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
11	260436	3.87	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
12	375791	−2.11	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
13	92291	2.25	2e−16	2e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
14	875	1.89	2e−16	2e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
15	6363	1.67	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
16	595	−2.01	2e−16	2e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
17	962	1.59	2e−16	2e−14	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
18	1048	−1.59	2e−16	2e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
19	4680	−2.84	2e−16	2e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
20	56994	1.58	2e−16	2e−14	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.15	NULL	417	H.Tiss	WIRTH_Immune system
2	9.21	NULL	914	Chr	Chr 3
3	6.48	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
4	6.11	NULL	13	MMML CGS	MACIEJ_MMML 6
5	6.08	NULL	11	GSEA C2	APPEL_IMATINIB_RESPONSE
6	5.91	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
7	5.79	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
8	5.66	NULL	74	BP	regulation of immune response
9	5.39	NULL	7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
10	5.38	NULL	49	Glio	Donson−innate immunity−associated with LTS in HGA
11	5.32	NULL	14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
12	5.11	NULL	7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	5.08	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
14	5.08	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
15	5.05	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
16	5	NULL	15	CC	high−density lipoprotein particle
17	4.95	NULL	32	Glio	Donson−Misc immune function−associated with LTS in HGA
18	4.9	NULL	16	BP	cytolysis
19	4.87	NULL	13	Cancer	GENTLES_modul18
20	4.79	NULL	553	Cancer	Lembcke_Colonic Inflammation
Underexpressed					
1	−20.19	NULL	135	H.Tiss	WIRTH_Mucosa
2	−19.27	NULL	42	BP	keratinization
3	−19.09	NULL	21	CC	cornified envelope
4	−16.59	NULL	76	BP	epidermis development
5	−15.2	NULL	53	BP	keratinocyte differentiation
6	−12.52	NULL	19	BP	peptide cross−linking
7	−12.43	NULL	242	BP	extracellular matrix organization
8	−10.84	NULL	190	CC	extracellular matrix
9	−10.54	NULL	186	MF	structural molecule activity
10	−9.67	NULL	572	Disease	GUDJ_psoriasis up
11	−9.41	NULL	64	BP	collagen catabolic process
12	−9.32	NULL	69	BP	extracellular matrix disassembly
13	−8.71	NULL	12	BP	hemidesmosome assembly
14	−8.5	NULL	1182	CC	extracellular region
15	−8.4	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
16	−8.33	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−8.33	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	−8.31	NULL	250	Lymphoma	LENZ_Stromal signature 1
19	−8.17	NULL	44	CC	keratin filament
20	−8.07	NULL	15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH

GW_224

Local Summary

%DE = 0.89

metagenes = 14

genes = 247

genes in genesets = 245

genes with fdr < 0.1 = 188 (181 + / 7 −)

genes with fdr < 0.05 = 179 (173 + / 6 −)

genes with fdr < 0.01 = 156 (152 + / 4 −)

<r> metagenes = 0.99

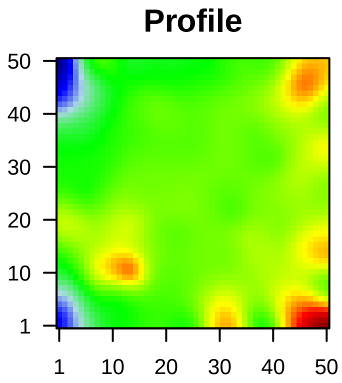
<r> genes = 0.62

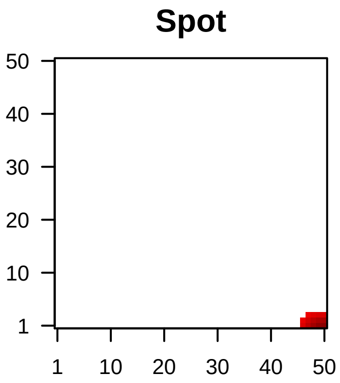
<FC> = 0.73

<shrinkage−t> = 25.52

<p−value> = 0

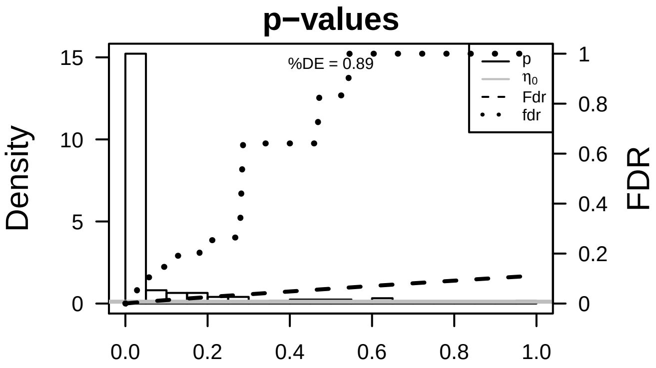
<fdr> = 0.31





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27299	1.94	2e−16	4e−16	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
2	341	2.58	2e−16	4e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
3	348	2.11	2e−16	4e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
4	713	2.04	2e−16	4e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
5	260436	3.87	2e−16	4e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
6	6363	1.67	2e−16	4e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	962	1.59	2e−16	4e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
8	4283	2.06	2e−16	4e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
9	3002	1.61	2e−16	4e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
10	3109	1.64	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
11	3620	1.75	2e−16	4e−16	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
12	3512	1.89	2e−16	4e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
13	3820	1.59	2e−16	4e−16	50 x 1	killer cell lectin−like receptor subfamily B, member 1 [Source:
14	7305	1.76	2e−16	4e−16	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
15	10537	2.39	2e−16	4e−16	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	5730	1.53	2e−15	4e−14	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
17	1593	1.52	4e−15	4e−14	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sour
18	2517	1.52	4e−15	1e−13	48 x 3	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:4
19	3689	1.5	8e−15	1e−12	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
20	84868	1.44	1e−13	1e−12	50 x 1	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;A



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.88	NULL	89 / 417	H.Tiss	WIRTH_Immune system
2	21.14	NULL	89 / 553	Cancer	Lembcke_Colonic Inflammation
3	20.78	NULL	12 / 15	CC	MHC class II protein complex
4	20.32	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
5	20.16	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
6	19.71	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
7	19.62	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
8	17.9	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
9	17.43	NULL	3 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
10	17.41	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
11	17.08	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	16.99	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
13	16.95	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
14	16.85	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
15	16.81	NULL	50 / 312	BP	immune response
16	16.34	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
17	16.34	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
18	16.34	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
19	16.34	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
20	15.82	NULL	7 / 13	Cancer	GENTLES_modul18
21	14.98	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
22	14.8	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
23	14.43	NULL	17 / 74	BP	regulation of immune response
24	14.35	NULL	4 / 13	MMML CGS	MACIEJ_MMML 6
25	14.26	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
26	14.19	NULL	8 / 16	GSEA C2	SU_THYMUS
27	13.72	NULL	14 / 47	BP	antigen processing and presentation
28	13.41	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
29	13.09	NULL	2 / 11	BP	high−density lipoprotein particle remodeling
30	13.02	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
31	12.98	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
32	12.46	NULL	16 / 60	BP	T cell costimulation
33	12.42	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
34	12.4	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
35	12.34	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
36	12.34	NULL	3 / 11	GSEA C2	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
37	12.18	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
38	11.83	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
39	11.64	NULL	5 / 11	BP	positive regulation of B cell differentiation
40	11.42	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG

GW_224

Local Summary

%DE = 0.91

metagenes = 3

genes = 66

genes in genesets = 66

genes with fdr < 0.1 = 54 (4 + / 50 −)

genes with fdr < 0.05 = 51 (3 + / 48 −)

genes with fdr < 0.01 = 46 (2 + / 44 −)

<r> metagenes = 0.99

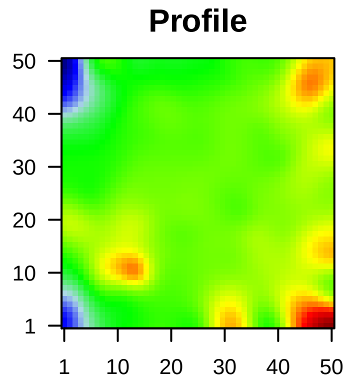
<r> genes = 0.43

<FC> = −0.87

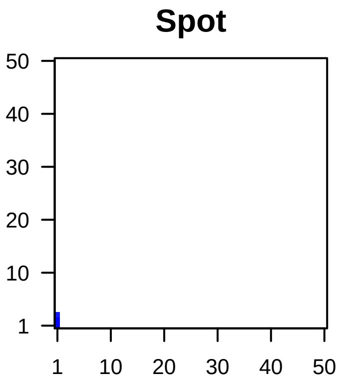
<shrinkage−t> = −30.69

<p−value> = 0

<fdr> = 0.23



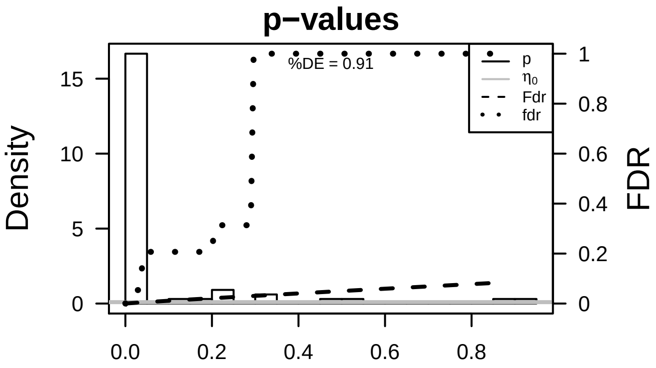
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27122	−1.95	2e−16	1e−16	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Sy
2	3553	−2.25	2e−16	1e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
3	3576	−2.63	2e−16	1e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
4	4312	−2.31	2e−16	1e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
5	4319	−2.26	2e−16	1e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
6	4314	−3.02	2e−16	1e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
7	55714	−1.8	2e−16	1e−16	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
8	7045	−1.83	2e−16	1e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
9	7057	−1.68	2e−16	1e−16	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
10	25907	−1.56	7e−16	3e−14	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HGN
11	5270	−1.51	5e−15	7e−13	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
12	3371	−1.44	1e−13	1e−12	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
13	10630	−1.41	3e−13	2e−12	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
14	1307	−1.39	6e−13	3e−11	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
15	56937	−1.32	1e−11	3e−11	1 x 1	prostate transmembrane protein, androgen induced 1 [Source
16	11098	−1.32	1e−11	5e−11	1 x 1	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
17	3569	−1.29	3e−11	5e−11	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
18	5054	−1.28	4e−11	5e−11	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
19	4973	1.28	4e−11	5e−11	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
20	4907	−1.27	5e−11	4e−10	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:802



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−35.37	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
2	−35.23	NULL	4 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
3	−32.98	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
4	−28.29	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
5	−26.08	NULL	5 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
6	−25.68	NULL	8 / 35	Glio	Colman_survival_associated
7	−25.61	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
8	−23.48	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
9	−22.45	NULL	2 / 12	GSEA C2	LY_AGING_MIDDLE_UP
10	−22.02	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
11	−21.67	NULL	1 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCO
12	−21.2	NULL	3 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
13	−21.12	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
14	−20.31	NULL	7 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
15	−19.36	NULL	4 / 37	Glio	Christensen_hypomethylated_in_ependymoma
16	−19.33	NULL	2 / 11	GSEA C2	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
17	−19.3	NULL	1 / 2	miRNA target	miR−101b
18	−19	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
19	−18.99	NULL	1 / 6	GSEA C2	MIZUKAMI_HYPOXIA_DN
20	−18.99	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
21	−18.97	NULL	2 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
22	−18.85	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
23	−18.79	NULL	2 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
24	−18.6	NULL	3 / 15	BP	positive regulation vascular endothelial growth factor production
25	−17.88	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
26	−17.57	NULL	2 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
27	−17.56	NULL	2 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
28	−17.08	NULL	2 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
29	−17.06	NULL	1 / 7	GSEA C2	BIOCARTA_FREE_PATHWAY
30	−16.81	NULL	17 / 242	BP	extracellular matrix organization
31	−16.74	NULL	12 / 190	CC	extracellular matrix
32	−16.7	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
33	−16.65	NULL	8 / 64	BP	collagen catabolic process
34	−16.46	NULL	2 / 12	GSEA C2	WU_HBX_TARGETS_2_DN
35	−16.14	NULL	29 / 683	CC	extracellular space
36	−15.96	NULL	8 / 69	BP	extracellular matrix disassembly
37	−15.58	NULL	1 / 8	GSEA C2	OSAWA_TNF_TARGETS
38	−15.25	NULL	2 / 13	BP	positive regulation of vascular endothelial growth factor receptor sig
39	−14.91	NULL	3 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
40	−14.66	NULL	2 / 10	BP	negative regulation of fibroblast growth factor receptor signaling pa

GW_224

Local Summary

%DE = 0.91

metagenes = 18

genes = 260

genes in genesets = 254

genes with fdr < 0.1 = 223 (25 + / 198 −)

genes with fdr < 0.05 = 222 (25 + / 197 −)

genes with fdr < 0.01 = 209 (22 + / 187 −)

<r> metagenes = 0.92

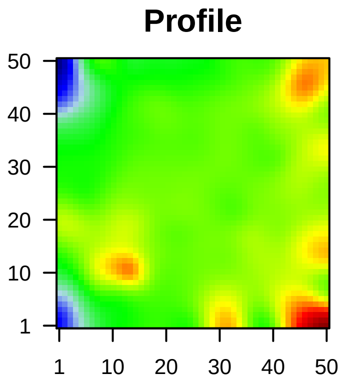
<r> genes = 0.41

<FC> = −0.97

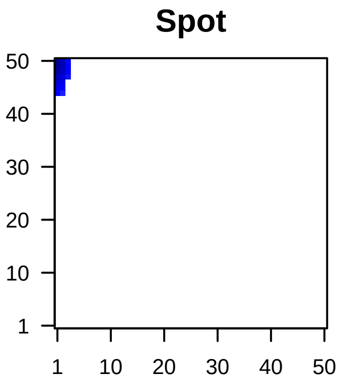
<shrinkage−t> = −34.43

<p−value> = 0

<fdr> = 0.16



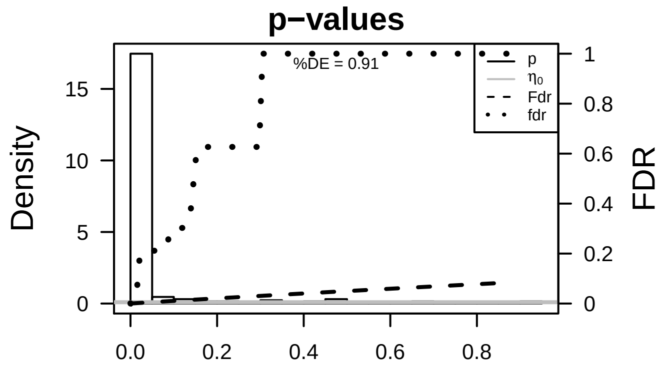
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−3.05	2e−16	8e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
2	65124	−2.16	2e−16	8e−17	1 x 45	sosondowah ankyrin repeat domain family member C [Source
3	375791	−2.11	2e−16	8e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	1048	−1.59	2e−16	8e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
5	4680	−2.84	2e−16	8e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (r
6	9022	−1.8	2e−16	8e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:20
7	84518	−3.35	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	1382	−1.69	2e−16	8e−17	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
9	54544	−1.76	2e−16	8e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
10	49860	−3.17	2e−16	8e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	9547	−1.91	2e−16	8e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
12	414325	−2.58	2e−16	8e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	93099	−2.25	2e−16	8e−17	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
14	1828	−1.8	2e−16	8e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	2167	−1.6	2e−16	8e−17	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	9982	−1.92	2e−16	8e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
17	2697	−2.37	2e−16	8e−17	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
18	2706	−2.68	2e−16	8e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
19	10804	−2.49	2e−16	8e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
20	3489	−2.18	2e−16	8e−17	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−43.31	NULL	18 / 21	CC	cornified envelope
2	−41.05	NULL	86 / 135	H.Tiss	WIRTH_Mucosa
3	−37.23	NULL	19 / 42	BP	keratinization
4	−30.68	NULL	24 / 53	BP	keratinocyte differentiation
5	−28.08	NULL	24 / 76	BP	epidermis development
6	−24.3	NULL	10 / 19	BP	peptide cross−linking
7	−20.83	NULL	102 / 572	Disease	GUDJ_psoriasis up
8	−18.28	NULL	12 / 44	CC	keratin filament
9	−17	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	−16.5	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	−16.41	NULL	19 / 82	CC	intermediate filament
12	−16.22	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	−15.66	NULL	26 / 186	MF	structural molecule activity
14	−15.55	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	−15.07	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
16	−14.46	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
17	−13.3	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	−13.26	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
19	−13.21	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
20	−13.07	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
21	−12.94	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
22	−12.58	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
23	−12.56	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
24	−12.38	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
25	−12.38	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
26	−12.36	NULL	3 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
27	−12.13	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
28	−11.49	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
29	−11.46	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
30	−11.39	NULL	3 / 15	CC	connexon complex
31	−11.05	NULL	12 / 21	CC	desmosome
32	−11.03	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
33	−11.02	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
34	−10.66	NULL	5 / 23	MF	peptidase inhibitor activity
35	−10.61	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
36	−10.6	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
37	−10.47	NULL	7 / 38	BP	epithelial cell differentiation
38	−10.25	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
39	−10.23	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
40	−10.15	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP