GW_071

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2111 (1122 + / 989 −)

genes with fdr < 0.1 = 1793 (957 + / 836 −)

genes with fdr < 0.05 = 1422 (766 + / 656 −)

genes with fdr < 0.01 = 1098 (587 + / 511 −)

genes in genesets = 16332

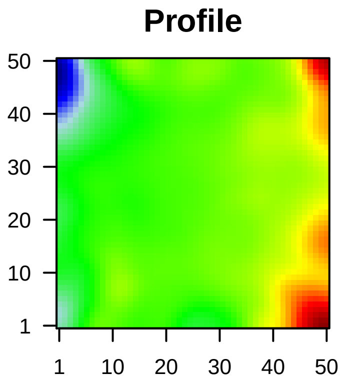
<FC> = 0

<shrinkage−t> = 0

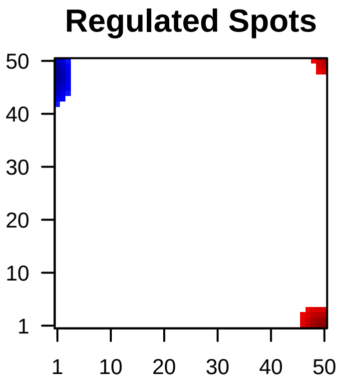
<p−value> = 0.07

<fdr> = 0.84

Profile



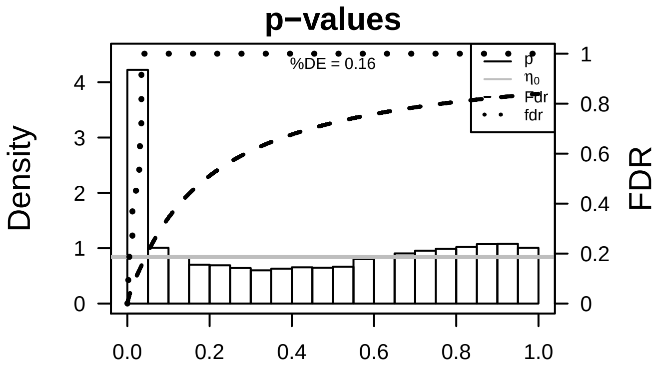
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.29	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [So
2	86	1.75	2e−16	2e−14	46 x 50	actin−like 6A [Source:HGNC Symbol;Acc:24124]
3	8745	2.17	2e−16	2e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
4	131	2.62	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	8644	2.16	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	1.76	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	216	2.31	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	218	1.89	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
9	9823	1.77	2e−16	2e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
10	387695	−2	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
11	64073	−1.98	2e−16	2e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
12	375791	−2.4	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
13	760	−2.21	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
14	57172	2.41	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
15	84290	−1.51	2e−16	2e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	6363	2.78	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
17	6347	1.71	2e−16	2e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
18	6364	1.63	2e−16	2e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
19	1236	1.72	2e−16	2e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
20	930	2.34	2e−16	2e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.02	NULL	417	H.Tiss	WIRTH_Immune system
2	8.75	NULL	162	CC	external side of plasma membrane
3	8.7	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	8.53	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
5	7.8	NULL	914	Chr	Chr 3
6	7.07	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
7	6.88	NULL	28	BP	B cell receptor signaling pathway
8	6.73	NULL	866	Chr	Chr 12
9	6.7	NULL	20	MF	glutathione transferase activity
10	6.53	NULL	630	Chr	Chr X
11	6.28	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
12	6.18	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
13	5.96	NULL	119	BP	xenobiotic metabolic process
14	5.79	NULL	3274	CC	integral to membrane
15	5.74	NULL	25	BP	glutathione derivative biosynthetic process
16	5.71	NULL	34	BP	glutathione metabolic process
17	5.68	NULL	15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
18	5.65	NULL	16	GSEA C2	SU_THYMUS
19	5.64	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
20	5.59	NULL	15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
Underexpressed					
1	−27.88	NULL	135	H.Tiss	WIRTH_Mucosa
2	−21.78	NULL	21	CC	cornified envelope
3	−17.57	NULL	76	BP	epidermis development
4	−17.04	NULL	572	Disease	GUDJ_psoriasis up
5	−16.77	NULL	42	BP	keratinization
6	−15.61	NULL	53	BP	keratinocyte differentiation
7	−11.72	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	−9.93	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
9	−9.91	NULL	19	BP	peptide cross−linking
10	−9.14	NULL	186	MF	structural molecule activity
11	−9.08	NULL	1720	Chr	Chr 1
12	−8.94	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
13	−8.93	NULL	82	CC	intermediate filament
14	−8.66	NULL	12	BP	hemidesmosome assembly
15	−8.51	NULL	44	CC	keratin filament
16	−8.25	NULL	21	CC	desmosome
17	−8.22	NULL	633	Chr	Chr 9
18	−7.85	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	−7.83	NULL	13	BP	negative regulation of peptidase activity
20	−7.55	NULL	957	Chr	Chr 11

GW_071

Local Summary

%DE = 0.93

metagenes = 19

genes = 295

genes in genesets = 293

genes with fdr < 0.1 = 249 (244 + / 5 −)

genes with fdr < 0.05 = 237 (232 + / 5 −)

genes with fdr < 0.01 = 219 (216 + / 3 −)

<r> metagenes = 0.99

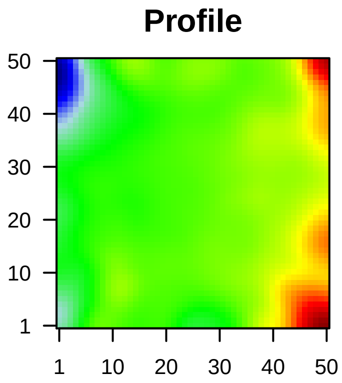
<r> genes = 0.59

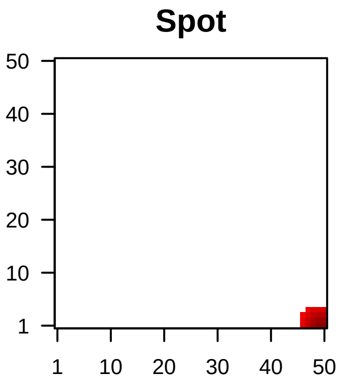
<FC> = 0.77

<shrinkage−t> = 27.04

<p−value> = 0

<fdr> = 0.24





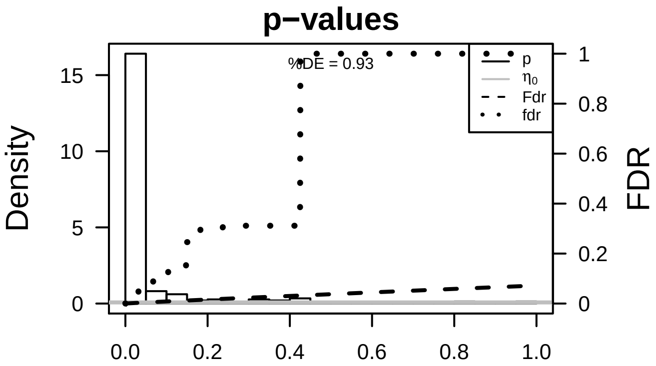
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	2.41	2e−16	2e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	6363	2.78	2e−16	2e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	6347	1.71	2e−16	2e−16	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
4	6364	1.63	2e−16	2e−16	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
5	1236	1.72	2e−16	2e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
6	930	2.34	2e−16	2e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
7	939	1.5	2e−16	2e−16	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
8	962	1.54	2e−16	2e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
9	1116	1.69	2e−16	2e−16	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
10	51755	1.97	2e−16	2e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	10563	1.73	2e−16	2e−16	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
12	54855	2.27	2e−16	2e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
13	3059	1.97	2e−16	2e−16	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
14	3512	3.09	2e−16	2e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
15	3543	1.42	2e−16	2e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC S
16	3394	1.61	2e−16	2e−16	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
17	11040	1.87	2e−16	2e−16	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
18	5450	1.65	2e−16	2e−16	48 x 1	POU class 2 associating factor 1 [Source:HGNC Symbol;Acc:
19	5730	1.99	2e−16	2e−16	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
20	9806	1.49	2e−16	2e−16	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	30.11	NULL	99 / 417	H.Tiss	WIRTH_Immune system
2	28.5	NULL	105 / 553	Cancer	Lembcke_Colonic Inflammation
3	23.58	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
4	21.54	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	18.38	NULL	55 / 312	BP	immune response
6	17.86	NULL	12 / 15	CC	MHC class II protein complex
7	16.21	NULL	49 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
8	16.21	NULL	49 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
9	16.21	NULL	49 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
10	16.21	NULL	49 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
11	16.21	NULL	11 / 28	BP	B cell receptor signaling pathway
12	15.66	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
13	15.32	NULL	8 / 16	GSEA C2	SU_THYMUS
14	15.26	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	15.04	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
16	14.45	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
17	14.4	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
18	14.27	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
19	14.08	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
20	13.98	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
21	13.83	NULL	6 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
22	13.8	NULL	27 / 162	CC	external side of plasma membrane
23	13.76	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
24	13.75	NULL	5 / 12	BP	dendritic cell chemotaxis
25	13.24	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP
26	13	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
27	12.76	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
28	12.65	NULL	18 / 74	BP	regulation of immune response
29	12.27	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
30	12.22	NULL	15 / 47	BP	antigen processing and presentation
31	11.9	NULL	8 / 43	MF	chemokine activity
32	11.84	NULL	6 / 27	MF	antigen binding
33	11.76	NULL	18 / 60	BP	T cell costimulation
34	11.68	NULL	8 / 13	Cancer	GENTLES_modul18
35	11.62	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
36	11.31	NULL	33 / 316	Cancer	SPANG_BCL6−index2
37	11.18	NULL	4 / 22	BP	positive regulation of interleukin−12 production
38	10.99	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
39	10.71	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
40	10.64	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY



GW_071

Local Summary

%DE = 0.77

metagenes = 7

genes = 141

genes in genesets = 140

genes with fdr < 0.1 = 103 (99 + / 4 −)

genes with fdr < 0.05 = 103 (99 + / 4 −)

genes with fdr < 0.01 = 85 (83 + / 2 −)

<r> metagenes = 0.99

<r> genes = 0.31

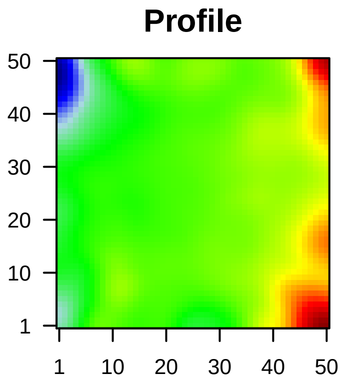
<FC> = 0.87

<shrinkage−t> = 30.58

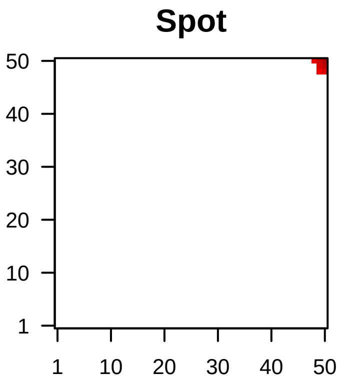
<p−value> = 0

<fdr> = 0.28

Profile



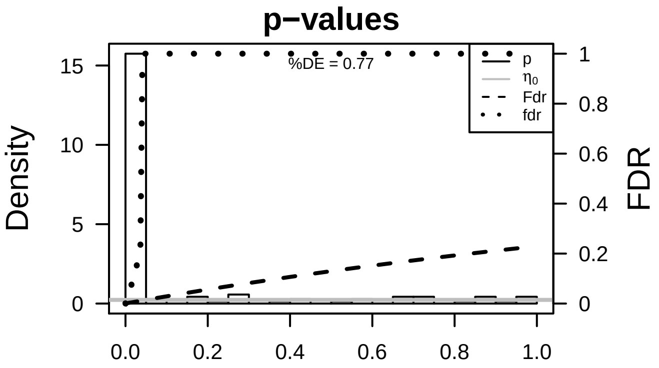
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.29	2e−16	3e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	2.17	2e−16	3e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	216	2.31	2e−16	3e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	928	1.52	2e−16	3e−16	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
5	1056	2.17	2e−16	3e−16	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	56548	1.86	2e−16	3e−16	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7
7	4072	2.13	2e−16	3e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
8	2719	2.58	2e−16	3e−16	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
9	2938	3.6	2e−16	3e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
10	2939	1.66	2e−16	3e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
11	2944	2.37	2e−16	3e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
12	2946	1.51	2e−16	3e−16	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
13	3880	2.33	2e−16	3e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
14	3856	1.88	2e−16	3e−16	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
15	56922	1.85	2e−16	3e−16	50 x 50	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
16	4915	1.66	2e−16	3e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
17	4922	4.88	2e−16	3e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
18	57526	1.49	2e−16	3e−16	50 x 50	protocadherin 19 [Source:HGNC Symbol;Acc:14270]
19	139728	2.14	2e−16	3e−16	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
20	9182	1.75	2e−16	3e−16	50 x 50	Ras association (RalGDS/AF−6) domain family (N−terminal)

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.59	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	21.89	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	19.43	NULL	5 / 20	MF	glutathione transferase activity
4	18.72	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
5	17.67	NULL	3 / 13	BP	regulation of blood vessel size
6	17.18	NULL	8 / 34	BP	glutathione metabolic process
7	16.87	NULL	6 / 25	BP	glutathione derivative biosynthetic process
8	16.24	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
9	15.32	NULL	1 / 11	Glio	neurons_glio
10	15	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
11	14.49	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
12	14.41	NULL	3 / 11	MF	glutathione binding
13	14.41	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
14	14.3	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
15	12.77	NULL	1 / 15	MF	neuropeptide hormone activity
16	12.61	NULL	11 / 119	BP	xenobiotic metabolic process
17	12.6	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
18	11.82	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
19	11.16	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
20	10.72	NULL	3 / 15	BP	lipid glycosylation
21	10.33	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
22	10.33	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
23	10.09	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
24	10.09	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
25	9.99	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
26	9.38	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
27	9.31	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
28	9.31	NULL	1 / 7	miRNA target	miR−145
29	9.16	NULL	2 / 23	BP	stem cell differentiation
30	9.11	NULL	4 / 32	BP	glycosaminoglycan biosynthetic process
31	8.9	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
32	8.62	NULL	1 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
33	8.6	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
34	8.57	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
35	8.57	NULL	1 / 8	miRNA 3UTR	CTGCA−450
36	8.5	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
37	8.45	NULL	2 / 10	BP	biotin metabolic process
38	8.25	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
39	8.11	NULL	1 / 8	GSEA C2	KEGG_GLYCEROLIPID_METABOLISM
40	8.03	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN

GW_071

Local Summary

%DE = 0.92

metagenes = 24

genes = 341

genes in genesets = 333

genes with fdr < 0.1 = 307 (17 + / 290 −)

genes with fdr < 0.05 = 302 (14 + / 288 −)

genes with fdr < 0.01 = 287 (11 + / 276 −)

<r> metagenes = 0.89

<r> genes = 0.36

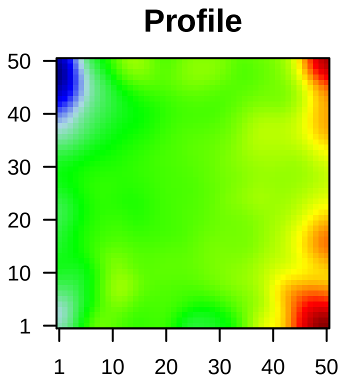
<FC> = −1.06

<shrinkage−t> = −37.28

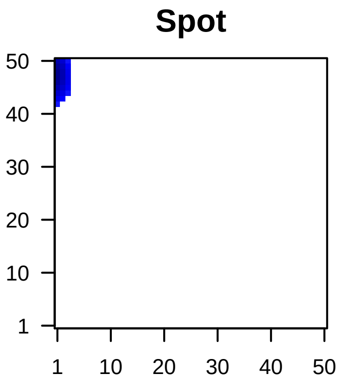
<p−value> = 0

<fdr> = 0.12

Profile



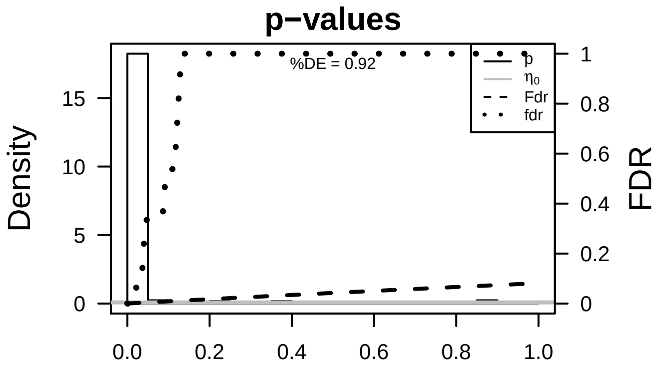
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	2.62	2e−16	7e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	2.16	2e−16	7e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	218	1.89	2e−16	7e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	387695	−2	2e−16	7e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
5	64073	−1.98	2e−16	7e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
6	375791	−2.4	2e−16	7e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
7	760	−2.21	2e−16	7e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	84290	−1.51	2e−16	7e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	1001	−1.77	2e−16	7e−17	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
10	9635	−2.55	2e−16	7e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
11	9022	−1.81	2e−16	7e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
12	84518	−3.13	2e−16	7e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
13	1308	−2.1	2e−16	7e−17	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
14	51200	−1.85	2e−16	7e−17	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
15	1382	−1.77	2e−16	7e−17	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
16	54544	−1.73	2e−16	7e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	−2.4	2e−16	7e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	−2.65	2e−16	7e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1515	−1.91	2e−16	7e−17	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
20	92196	2.24	2e−16	7e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−47.5	NULL	89 / 135	H.Tiss	WIRTH_Mucosa
2	−43.28	NULL	18 / 21	CC	cornified envelope
3	−31.04	NULL	28 / 76	BP	epidermis development
4	−30.69	NULL	20 / 42	BP	keratinization
5	−29.28	NULL	119 / 572	Disease	GUDJ_psoriasis up
6	−28.84	NULL	24 / 53	BP	keratinocyte differentiation
7	−18.3	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	−18.06	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
9	−17.98	NULL	10 / 19	BP	peptide cross−linking
10	−16.34	NULL	12 / 21	CC	desmosome
11	−15.59	NULL	5 / 10	MF	RAGE receptor binding
12	−15.55	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
13	−15.49	NULL	13 / 44	CC	keratin filament
14	−15.36	NULL	21 / 82	CC	intermediate filament
15	−14.99	NULL	30 / 186	MF	structural molecule activity
16	−13.91	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
17	−13.79	NULL	5 / 25	BP	response to zinc ion
18	−13.22	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
19	−13.07	NULL	4 / 12	BP	hemidesmosome assembly
20	−13	NULL	6 / 13	BP	negative regulation of peptidase activity
21	−12.68	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
22	−12.64	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
23	−12.57	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
24	−11.85	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
25	−11.67	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
26	−11.52	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	−11.03	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
28	−10.9	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
29	−10.69	NULL	8 / 38	BP	epithelial cell differentiation
30	−10.66	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
31	−10.2	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
32	−10.2	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
33	−9.99	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
34	−9.84	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
35	−9.6	NULL	10 / 52	BP	negative regulation of endopeptidase activity
36	−9.6	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
37	−9.51	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
38	−9.51	NULL	4 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
39	−9.36	NULL	3 / 15	CC	connexon complex
40	−9.17	NULL	71 / 1182	CC	extracellular region