GW_179

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1723 (919 + / 804 −)

genes with fdr < 0.1 = 1275 (702 + / 573 −)

genes with fdr < 0.05 = 1109 (621 + / 488 −)

genes with fdr < 0.01 = 818 (482 + / 336 −)

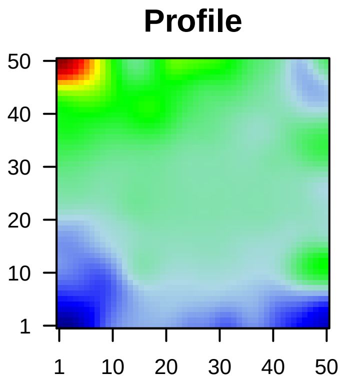
genes in genesets = 16332

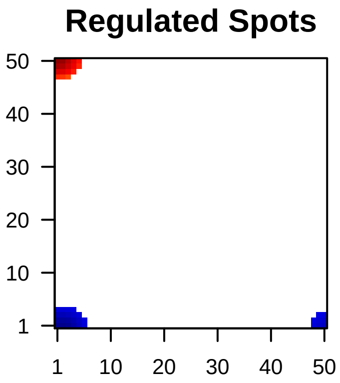
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

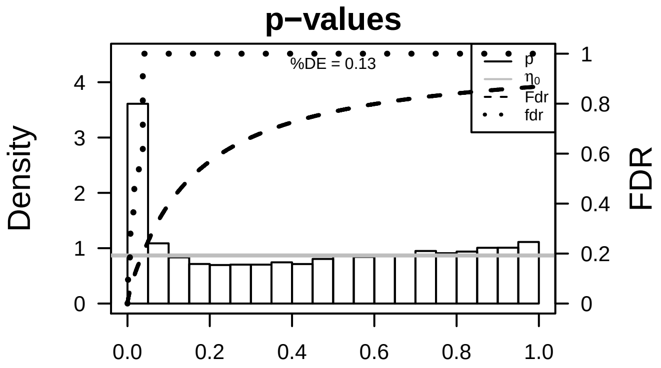
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.68	2e−16	3e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	55	1.39	2e−16	3e−14	4 x 50	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	218	1.35	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	239	1.4	2e−16	3e−14	5 x 49	arachidonate 12−lipoxygenase [Source:HGNC Symbol;Acc:4
5	353322	1.52	2e−16	3e−14	6 x 48	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:29593]
6	360	1.41	2e−16	3e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	633	−1.5	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
8	387695	1.48	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	399948	1.4	2e−16	3e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
10	148304	1.43	2e−16	3e−14	1 x 41	chromosome 1 open reading frame 74 [Source:HGNC Symb
11	394263	1.85	2e−16	3e−14	3 x 50	
12	375791	1.83	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
13	57172	−1.58	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
14	1048	1.37	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
15	4680	1.48	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
16	1056	3.22	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
17	22802	1.5	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	9071	1.54	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
19	9022	1.57	2e−16	3e−14	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
20	84518	1.62	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	35.36	NULL	135	H.Tiss	WIRTH_Mucosa
2	16.17	NULL	572	Disease	GUDJ_psoriasis up
3	12.24	NULL	21	CC	cornified envelope
4	11	NULL	53	BP	keratinocyte differentiation
5	10.72	NULL	76	BP	epidermis development
6	10.11	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
7	9.48	NULL	42	BP	keratinization
8	9.38	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	8.85	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	8.41	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
11	8.4	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
12	8.31	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
13	7.79	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
14	7.75	NULL	16	GSEA C2	AMIT_DELAYED_EARLY_GENES
15	7.64	NULL	24	TF Tissue	VAQUERIZAS_Trachea
16	7.63	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
17	7.58	NULL	19	BP	peptide cross−linking
18	7.01	NULL	13	BP	negative regulation of peptidase activity
19	6.77	NULL	82	CC	intermediate filament
20	6.76	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
Underexpressed					
1	−15.89	NULL	190	CC	extracellular matrix
2	−15.38	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	−14.2	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	−13.38	NULL	242	BP	extracellular matrix organization
5	−13.26	NULL	69	BP	extracellular matrix disassembly
6	−12.2	NULL	64	BP	collagen catabolic process
7	−10.82	NULL	183	CC	proteinaceous extracellular matrix
8	−10.41	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	−10.1	NULL	11	MF	platelet−derived growth factor binding
10	−9.93	NULL	57	MF	extracellular matrix structural constituent
11	−9.73	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
12	−9.73	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
13	−9.73	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
14	−9.73	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
15	−9.46	NULL	16	MMML CGS	MACIEJ_MMML 1
16	−9.42	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
17	−9.06	NULL	403	BP	cell adhesion
18	−8.83	NULL	683	CC	extracellular space
19	−8.78	NULL	153	CC	endoplasmic reticulum lumen
20	−8.07	NULL	312	BP	immune response

GW_179

Local Summary

%DE = 0.98

metagenes = 17

genes = 235

genes in genesets = 229

genes with fdr < 0.1 = 223 (221 + / 2 −)

genes with fdr < 0.05 = 223 (221 + / 2 −)

genes with fdr < 0.01 = 217 (215 + / 2 −)

<r> metagenes = 0.97

<r> genes = 0.46

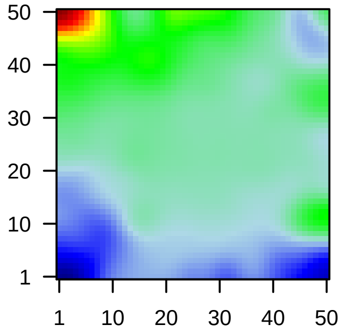
<FC> = 1.03

<shrinkage−t> = 36.1

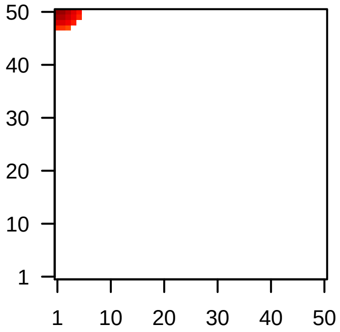
<p−value> = 0

<fdr> = 0.09

Profile

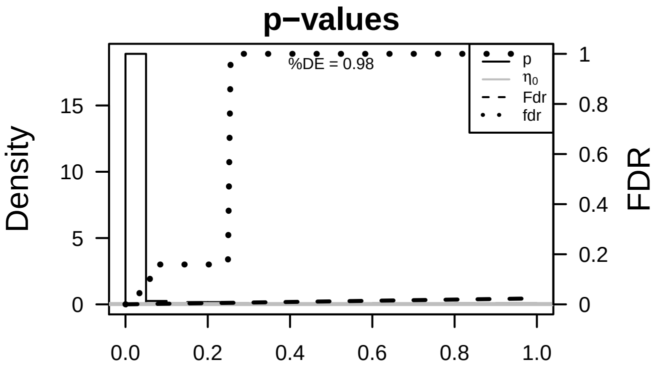


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.68	2e−16	2e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	55	1.39	2e−16	2e−17	4 x 50	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	218	1.35	2e−16	2e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	239	1.4	2e−16	2e−17	5 x 49	arachidonate 12−lipoxygenase [Source:HGNC Symbol;Acc:4
5	360	1.41	2e−16	2e−17	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	387695	1.48	2e−16	2e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
7	394263	1.85	2e−16	2e−17	3 x 50	
8	375791	1.83	2e−16	2e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
9	1048	1.37	2e−16	2e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
10	4680	1.48	2e−16	2e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
11	22802	1.5	2e−16	2e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	9022	1.57	2e−16	2e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
13	84518	1.62	2e−16	2e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	54544	1.8	2e−16	2e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
15	49860	3.11	2e−16	2e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
16	1475	1.86	2e−16	2e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
17	1562	1.72	2e−16	2e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
18	1577	1.53	2e−16	2e−17	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
19	414325	1.4	2e−16	2e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	2.27	2e−16	2e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	65.55	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	28.5	NULL	17 / 21	CC	cornified envelope
3	26.27	NULL	91 / 572	Disease	GUDJ_psoriasis up
4	22.44	NULL	19 / 42	BP	keratinization
5	21.58	NULL	22 / 53	BP	keratinocyte differentiation
6	20.44	NULL	21 / 76	BP	epidermis development
7	20.3	NULL	10 / 19	BP	peptide cross−linking
8	18.86	NULL	9 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
9	17.74	NULL	6 / 13	BP	negative regulation of peptidase activity
10	17.26	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	16.92	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
12	14.5	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	13.87	NULL	8 / 38	BP	epithelial cell differentiation
14	12.53	NULL	6 / 29	BP	regulation of proteolysis
15	12.27	NULL	15 / 122	MF	serine−type endopeptidase activity
16	12.17	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
17	11.91	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
18	11.13	NULL	56 / 1182	CC	extracellular region
19	10.9	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	10.84	NULL	8 / 44	CC	keratin filament
21	10.78	NULL	9 / 52	BP	negative regulation of endopeptidase activity
22	10.71	NULL	5 / 10	MF	RAGE receptor binding
23	10.48	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
24	10.44	NULL	20 / 186	MF	structural molecule activity
25	10.35	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
26	9.51	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	9.03	NULL	10 / 82	CC	intermediate filament
28	8.99	NULL	5 / 21	CC	desmosome
29	8.92	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
30	8.5	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
31	8.35	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
32	8.11	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
33	8.04	NULL	8 / 53	MF	serine−type peptidase activity
34	7.9	NULL	3 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
35	7.67	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
36	7.55	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
37	7.55	NULL	4 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
38	7.45	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
39	7.44	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
40	7.4	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP

GW_179

Local Summary

%DE = 0.93

metagenes = 21

genes = 314

genes in genesets = 313

genes with fdr < 0.1 = 282 (10 + / 272 −)

genes with fdr < 0.05 = 261 (9 + / 252 −)

genes with fdr < 0.01 = 202 (7 + / 195 −)

<r> metagenes = 0.95

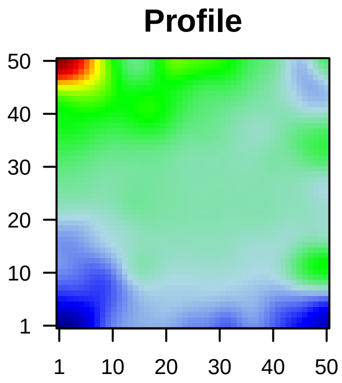
<r> genes = 0.38

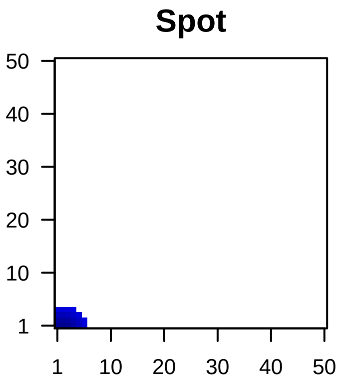
<FC> = −0.59

<shrinkage−t> = −20.52

<p−value> = 0

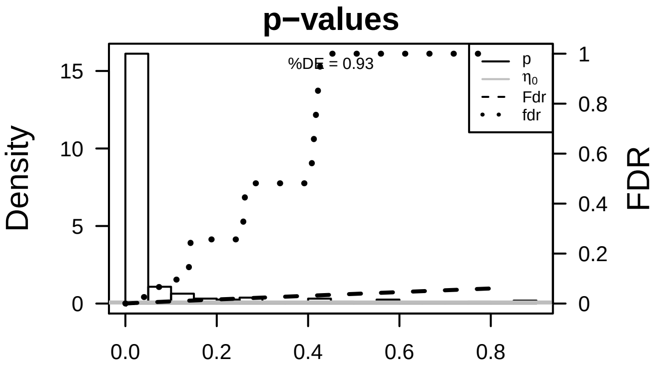
<fdr> = 0.31





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	633	−1.5	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
2	1278	−1.48	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	−1.26	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	1289	−1.4	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	1291	−1.37	2e−16	3e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
6	3040	−1.79	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
7	3043	−2.28	2e−16	3e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
8	5654	−1.41	2e−16	3e−16	2 x 1	HtrA serine peptidase 1 [Source:HGNC Symbol;Acc:9476]
9	3956	−1.86	2e−16	3e−16	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
10	4312	−2.05	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
11	4319	−1.49	2e−16	3e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
12	4314	−1.9	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
13	4318	−1.88	2e−16	3e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
14	12	−1.83	2e−16	3e−16	1 x 1	
15	7045	−1.31	2e−16	3e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
16	1293	−1.31	1e−15	3e−14	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
17	1277	−1.3	3e−15	7e−13	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
18	115908	−1.25	3e−14	1e−12	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
19	1462	−1.22	1e−13	1e−12	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
20	7431	−1.22	1e−13	8e−12	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.95	NULL	68 / 190	CC	extracellular matrix
2	−37.94	NULL	33 / 69	BP	extracellular matrix disassembly
3	−37.33	NULL	82 / 250	Lymphoma	LENZ_Stromal signature 1
4	−35.08	NULL	28 / 64	BP	collagen catabolic process
5	−34.6	NULL	68 / 242	BP	extracellular matrix organization
6	−34.04	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
7	−31.1	NULL	8 / 11	MF	platelet−derived growth factor binding
8	−30.69	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	−28.1	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	−25.17	NULL	41 / 183	CC	proteinaceous extracellular matrix
11	−25.07	NULL	8 / 12	miRNA target	miR−29c
12	−24.17	NULL	20 / 57	MF	extracellular matrix structural constituent
13	−22.7	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
14	−22.24	NULL	15 / 37	BP	collagen fibril organization
15	−21.25	NULL	91 / 683	CC	extracellular space
16	−21.11	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
17	−20.46	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
18	−20.41	NULL	11 / 19	MF	extracellular matrix binding
19	−20.29	NULL	117 / 1182	CC	extracellular region
20	−19.83	NULL	12 / 35	Glio	Colman_survival_associated
21	−19.39	NULL	12 / 40	BP	cellular response to amino acid stimulus
22	−18.6	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
23	−17.94	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
24	−17.94	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
25	−17.94	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
26	−17.94	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
27	−17.75	NULL	74 / 553	Cancer	Lembcke_Colonic Inflammation
28	−17.63	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
29	−17.39	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
30	−17.2	NULL	18 / 68	CC	collagen
31	−16.78	NULL	23 / 83	CC	basement membrane
32	−16.57	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
33	−16.47	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
34	−16.31	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
35	−15.93	NULL	7 / 11	MMML CGS	MACIEJ_MMML 31
36	−15.91	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
37	−15.78	NULL	24 / 119	Lymphoma	ROSOLOWSKI_green total
38	−15.64	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
39	−15.56	NULL	4 / 10	BP	protein heterotrimerization
40	−15.53	NULL	5 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP

GW_179

Local Summary

%DE = 0.88

metagenes = 8

genes = 197

genes in genesets = 195

genes with fdr < 0.1 = 166 (7 + / 159 −)

genes with fdr < 0.05 = 140 (4 + / 136 −)

genes with fdr < 0.01 = 107 (1 + / 106 −)

<r> metagenes = 1

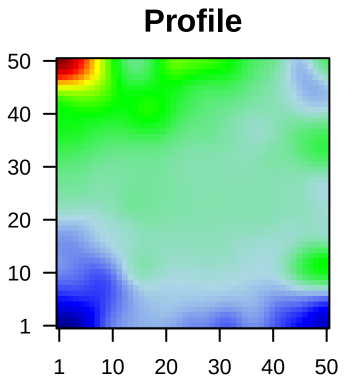
<r> genes = 0.64

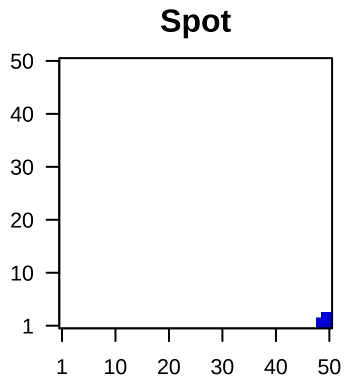
<FC> = −0.47

<shrinkage−t> = −16.51

<p−value> = 0

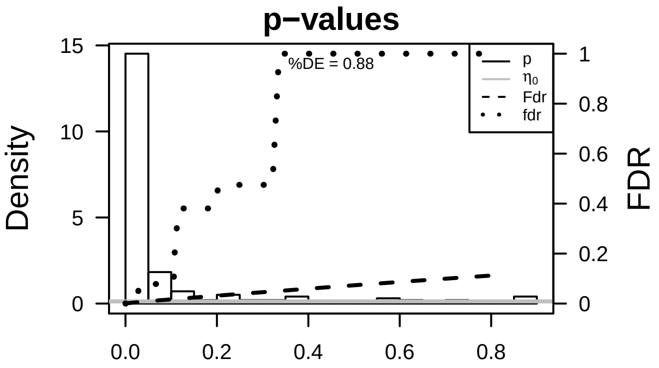
<fdr> = 0.38





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	−1.58	2e−16	2e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	3512	−1.43	2e−16	2e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	3543	−1.58	2e−16	2e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
4	54855	−1.26	2e−14	3e−11	49 x 1	family with sequence similarity 46, member C [Source:HGNC
5	11040	−1.17	1e−12	7e−11	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
6	51755	−1.14	5e−12	7e−11	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
7	5880	−1.13	7e−12	1e−10	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
8	3575	−1.12	1e−11	1e−10	50 x 2	interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
9	126306	−1.11	2e−11	5e−09	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
10	348	−1.04	2e−10	1e−08	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
11	23231	−1.02	7e−10	3e−07	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
12	4050	−0.93	1e−08	4e−07	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
13	55303	−0.89	6e−08	4e−07	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
14	260436	−0.89	6e−08	4e−07	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
15	3669	−0.88	9e−08	4e−07	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
16	3001	0.88	1e−07	4e−07	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
17	7351	−0.88	1e−07	2e−06	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
18	3936	−0.86	2e−07	3e−06	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
19	3689	−0.84	3e−07	3e−06	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
20	3109	−0.83	4e−07	3e−06	50 x 1	major histocompatibility complex, class II, DM beta [Source:H



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.38	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
2	−24.14	NULL	73 / 417	H.Tiss	WIRTH_Immune system
3	−21.19	NULL	11 / 15	CC	MHC class II protein complex
4	−20.52	NULL	72 / 553	Cancer	Lembcke_Colonic Inflammation
5	−19.19	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−18.4	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
7	−17.39	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
8	−16.73	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
9	−16.03	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
10	−15.44	NULL	4 / 13	BP	lymph node development
11	−15.43	NULL	32 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
12	−15.43	NULL	32 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
13	−15.43	NULL	32 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
14	−15.43	NULL	32 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
15	−14.23	NULL	5 / 12	BP	immunoglobulin mediated immune response
16	−14.13	NULL	41 / 312	BP	immune response
17	−14.06	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
18	−12.54	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
19	−12.39	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
20	−12.13	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
21	−12.02	NULL	4 / 14	BP	ruffle organization
22	−12	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
23	−11.83	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
24	−11.65	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
25	−11.42	NULL	4 / 27	MF	antigen binding
26	−11.4	NULL	2 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
27	−11.33	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
28	−11.32	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
29	−11.22	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
30	−11.15	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
31	−10.93	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
32	−10.89	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
33	−10.8	NULL	3 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
34	−10.77	NULL	14 / 74	BP	regulation of immune response
35	−10.62	NULL	2 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
36	−10.52	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
37	−10.24	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
38	−10.18	NULL	4 / 12	BP	dendritic cell chemotaxis
39	−10.14	NULL	6 / 28	Lymphoma	DAVE_Immune response 1
40	−10.12	NULL	12 / 47	BP	antigen processing and presentation