GW_174

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1591 (937 + / 654 −)

genes with fdr < 0.1 = 1161 (705 + / 456 −)

genes with fdr < 0.05 = 955 (599 + / 356 −)

genes with fdr < 0.01 = 671 (442 + / 229 −)

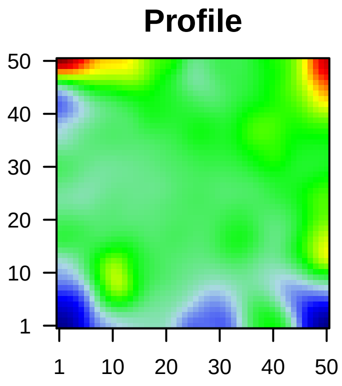
genes in genesets = 16332

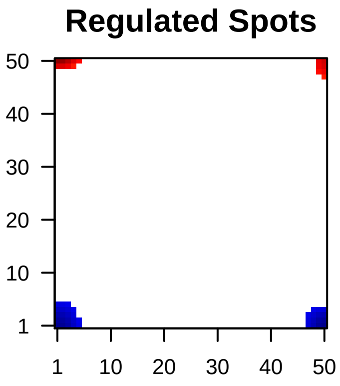
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.13

<fdr> = 0.87


Profile

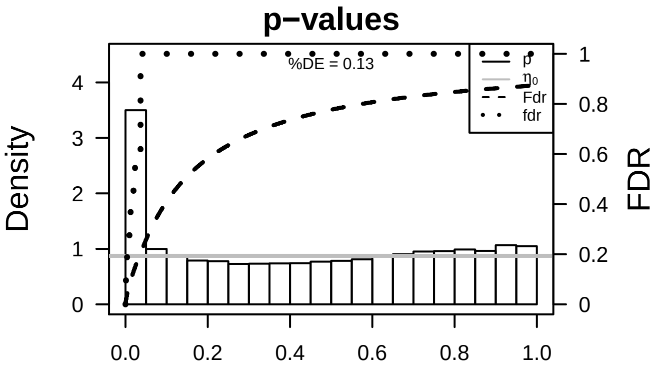

Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	1.32	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	218	1.71	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	375791	1.6	2e−16	5e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	760	−1.3	2e−16	5e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	857	−1.29	2e−16	5e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
6	1050	1.39	2e−16	5e−14	6 x 50	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HG
7	22802	2.11	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	169044	1.38	2e−16	5e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
9	1298	1.39	2e−16	5e−14	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
10	49860	3.28	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	441520	1.37	2e−16	5e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
12	57834	2.38	2e−16	5e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
13	414325	−1.34	2e−16	5e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	146754	1.37	2e−16	5e−14	13 x 10	dynein, axonemal, heavy chain 2 [Source:HGNC Symbol;Acc
15	1999	1.28	2e−16	5e−14	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
16	2012	1.19	2e−16	5e−14	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
17	4072	1.6	2e−16	5e−14	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
18	2167	−1.28	2e−16	5e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
19	401237	1.39	2e−16	5e−14	6 x 1	cancer susceptibility candidate 15 (non−protein coding) [Sour
20	2354	1.29	2e−16	5e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.52	NULL	135	H.Tiss	WIRTH_Mucosa
2	8.96	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
3	8.75	NULL	1749	MF	DNA binding
4	8.43	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
5	8.42	NULL	16	TF Tissue	VAQUERIZAS_Pancreas
6	8.18	NULL	4640	CC	nucleus
7	7.4	NULL	1581	BP	regulation of transcription, DNA−dependent
8	6.94	NULL	1574	BP	transcription, DNA−templated
9	6.69	NULL	12	BP	cellular aldehyde metabolic process
10	6.65	NULL	918	Chr	Chr 17
11	6.61	NULL	940	MF	nucleic acid binding
12	6.6	NULL	823	MF	sequence−specific DNA binding transcription factor activity
13	6.36	NULL	24	TF Tissue	VAQUERIZAS_Trachea
14	6.22	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
15	6.22	NULL	23	BP	hair follicle morphogenesis
16	6.03	NULL	500	MF	sequence−specific DNA binding
17	5.93	NULL	318	MF	chromatin binding
18	5.91	NULL	119	BP	xenobiotic metabolic process
19	5.45	NULL	99	MF	double−stranded DNA binding
20	5.39	NULL	18	MF	acyl−CoA dehydrogenase activity
Underexpressed					
1	−14.46	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−11.33	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
3	−11.33	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
4	−11.33	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
5	−11.33	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
6	−10.72	NULL	386	Chr	Chr 22
7	−10.43	NULL	250	Lymphoma	LENZ_Stromal signature 1
8	−10.09	NULL	1182	CC	extracellular region
9	−10.03	NULL	683	CC	extracellular space
10	−9.78	NULL	190	CC	extracellular matrix
11	−9.36	NULL	417	H.Tiss	WIRTH_Immune system
12	−9.31	NULL	312	BP	immune response
13	−9.29	NULL	242	BP	extracellular matrix organization
14	−8.59	NULL	69	BP	extracellular matrix disassembly
15	−8.13	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
16	−7.66	NULL	185	Cancer	SPANG_LPS−index2
17	−7.32	NULL	2659	CC	plasma membrane
18	−7.27	NULL	316	Cancer	SPANG_BCL6−index2
19	−7.22	NULL	64	BP	collagen catabolic process
20	−6.75	NULL	16	MMML CGS	MACIEJ_MMML 1


p−values

GW_174

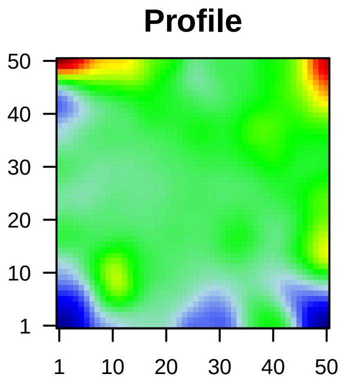
Local Summary

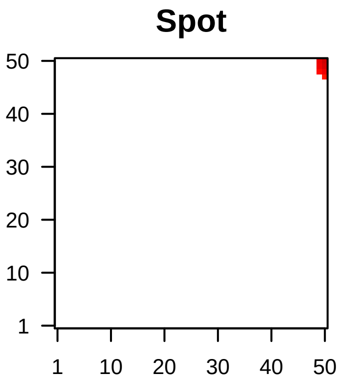
%DE = 0.73
metagenes = 7
genes = 134
genes in genesets = 133

genes with fdr < 0.1 = 74 (70 + / 4 −)
genes with fdr < 0.05 = 73 (69 + / 4 −)
genes with fdr < 0.01 = 62 (60 + / 2 −)

<r> metagenes = 0.99
<r> genes = 0.3

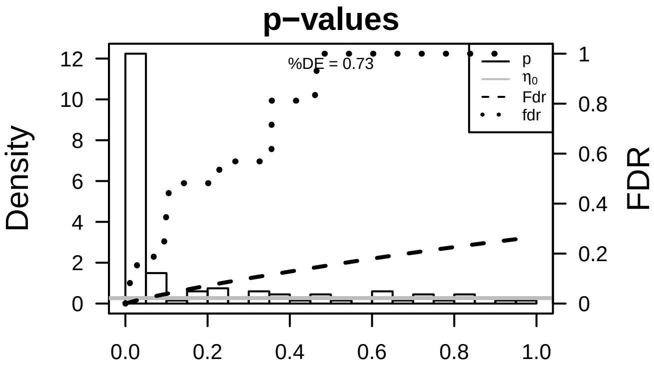
<FC> = 0.44
<shrinkage−t> = 15.46
<p−value> = 0
<fdr> = 0.46





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4072	1.6	2e−16	1e−15	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
2	2719	1.9	2e−16	1e−15	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
3	2938	2.05	2e−16	1e−15	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
4	3866	1.38	2e−16	1e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
5	4922	2.24	2e−16	1e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
6	23321	1.34	2e−16	1e−15	50 x 50	tripartite motif containing 2 [Source:HGNC Symbol;Acc:1597
7	216	1.26	9e−16	1e−12	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	94234	1.27	9e−16	1e−12	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
9	6657	1.19	4e−14	2e−12	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
10	2304	1.16	1e−13	2e−12	50 x 50	forkhead box E1 (thyroid transcription factor 2) [Source:HGN
11	139728	1.16	2e−13	2e−12	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
12	214	1.15	2e−13	2e−11	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC S
13	56977	1.13	8e−13	3e−11	50 x 49	storkhead box 2 [Source:HGNC Symbol;Acc:25450]
14	9182	1.11	2e−12	3e−11	50 x 50	Ras association (RalGDS/AF−6) domain family (N−terminal)
15	5013	1.1	3e−12	2e−10	50 x 50	orthodenticle homeobox 1 [Source:HGNC Symbol;Acc:8521]
16	1056	1.07	9e−12	2e−10	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
17	120	1.06	1e−11	2e−10	50 x 50	adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]
18	11166	1.05	2e−11	1e−08	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
19	79190	0.99	3e−10	1e−08	50 x 47	iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
20	56963	0.97	6e−10	4e−08	50 x 50	repulsive guidance molecule family member a [Source:HGNC



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.21	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	23.65	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	19.71	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
4	13.72	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
5	13.06	NULL	3 / 13	BP	regulation of blood vessel size
6	12.54	NULL	1 / 11	Glio	neurons_glio
7	12.44	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
8	11.37	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
9	10.6	NULL	2 / 12	BP	cellular aldehyde metabolic process
10	10.46	NULL	1 / 15	MF	neuropeptide hormone activity
11	10.1	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
12	10.1	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
13	10.09	NULL	1 / 12	MF	heparan sulfate proteoglycan binding
14	10.05	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
15	9.63	NULL	1 / 13	BP	positive regulation of endocytosis
16	9.61	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
17	9.19	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
18	9.17	NULL	3 / 32	BP	glycosaminoglycan biosynthetic process
19	9.02	NULL	3 / 33	BP	regulation of sequence−specific DNA binding transcription factor ac
20	8.91	NULL	2 / 23	BP	hair follicle morphogenesis
21	8.85	NULL	1 / 15	BP	anterior/posterior axis specification
22	8.85	NULL	1 / 15	BP	negative regulation of growth
23	8.85	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
24	8.65	NULL	3 / 15	BP	lipid glycosylation
25	8.63	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
26	8.63	NULL	1 / 7	miRNA target	miR−145
27	8.45	NULL	5 / 20	MF	glutathione transferase activity
28	8.37	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
29	8.36	NULL	2 / 15	MF	glucuronosyltransferase activity
30	8.25	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
31	8.2	NULL	1 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
32	8.19	NULL	2 / 23	BP	stem cell differentiation
33	8.17	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
34	8.13	NULL	2 / 10	BP	biotin metabolic process
35	8.03	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
36	7.96	NULL	1 / 18	CC	anchored to plasma membrane
37	7.96	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
38	7.96	NULL	1 / 8	miRNA 3UTR	CTGCA−450
39	7.89	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
40	7.89	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION

GW_174

Local Summary

%DE = 0.88

metagenes = 9

genes = 168

genes in genesets = 164

genes with fdr < 0.1 = 125 (111 + / 14 −)

genes with fdr < 0.05 = 125 (111 + / 14 −)

genes with fdr < 0.01 = 99 (88 + / 11 −)

<r> metagenes = 0.99

<r> genes = 0.49

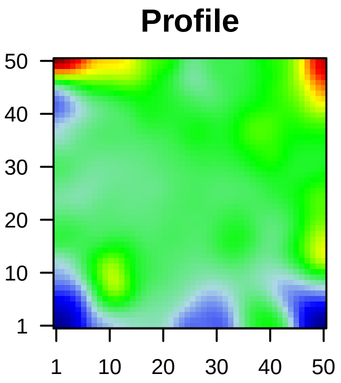
<FC> = 0.56

<shrinkage−t> = 19.89

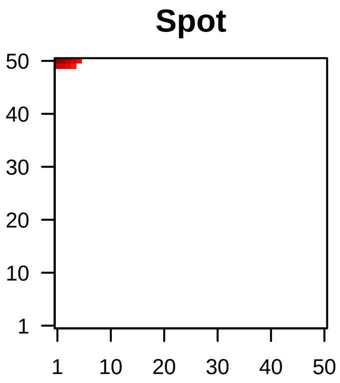
<p−value> = 0

<fdr> = 0.32

Profile



Spot



Local Genelist

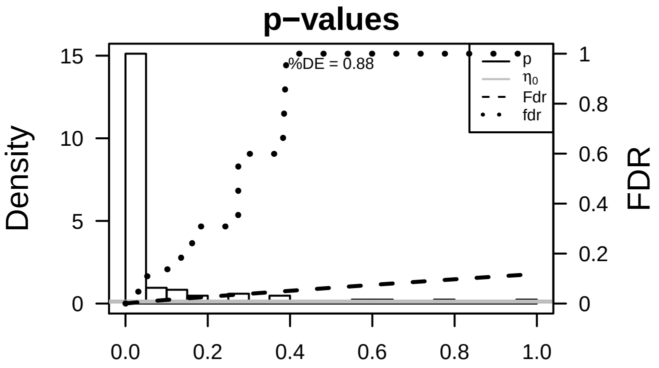
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	1.32	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	218	1.71	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	375791	1.6	2e−16	2e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
4	22802	2.11	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	49860	3.28	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	1999	1.28	2e−16	2e−16	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
7	2012	1.19	2e−16	2e−16	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
8	163351	1.31	2e−16	2e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
9	2877	1.64	2e−16	2e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
10	3860	1.6	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
11	192666	1.3	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
12	3851	2.76	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
13	196374	1.94	2e−16	2e−16	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
14	4118	2.84	2e−16	2e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
15	83886	1.31	2e−16	2e−16	1 x 50	protease, serine 27 [Source:HGNC Symbol;Acc:15475]
16	51458	1.63	2e−16	2e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
17	11005	1.35	2e−16	2e−16	1 x 50	serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
18	84651	1.83	2e−16	2e−16	1 x 50	serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
19	6707	1.82	2e−16	2e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
20	7053	1.89	2e−16	2e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	44.23	NULL	61 / 135	H.Tiss	WIRTH_Mucosa
2	21.24	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
3	16.73	NULL	7 / 38	BP	epithelial cell differentiation
4	14.37	NULL	7 / 19	BP	peptide cross−linking
5	13.77	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
6	13.01	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
7	12.51	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
8	11.34	NULL	3 / 12	BP	cellular aldehyde metabolic process
9	11.03	NULL	60 / 572	Disease	GUDJ_psoriasis up
10	10.84	NULL	4 / 44	CC	keratin filament
11	10.2	NULL	1 / 11	Glio	VERHAAK_Brain
12	10.04	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	10	NULL	6 / 82	CC	intermediate filament
14	10	NULL	5 / 13	BP	negative regulation of peptidase activity
15	9.99	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
16	9.69	NULL	1 / 12	MF	channel activity
17	9.25	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
18	9.09	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
19	8.98	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
20	8.95	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
21	8.79	NULL	4 / 15	MF	retinol dehydrogenase activity
22	8.62	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
23	8.58	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
24	8.5	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
25	8.5	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
26	8.38	NULL	16 / 53	BP	keratinocyte differentiation
27	8.26	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
28	8.19	NULL	1 / 16	Cancer	GENTLES_modul11
29	7.8	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
30	7.79	NULL	10 / 201	CC	apical plasma membrane
31	7.66	NULL	1 / 10	MF	monosaccharide binding
32	7.54	NULL	4 / 10	MF	RAGE receptor binding
33	7.42	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
34	7.29	NULL	12 / 186	MF	structural molecule activity
35	7.26	NULL	13 / 42	BP	keratinization
36	7.21	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
37	7.21	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUN
38	7.19	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
39	6.92	NULL	3 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
40	6.87	NULL	3 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP

p−values



GW_174

Local Summary

%DE = 0.82

metagenes = 21

genes = 318

genes in genesets = 315

genes with fdr < 0.1 = 199 (28 + / 171 −)

genes with fdr < 0.05 = 196 (28 + / 168 −)

genes with fdr < 0.01 = 141 (20 + / 121 −)

<r> metagenes = 0.95

<r> genes = 0.36

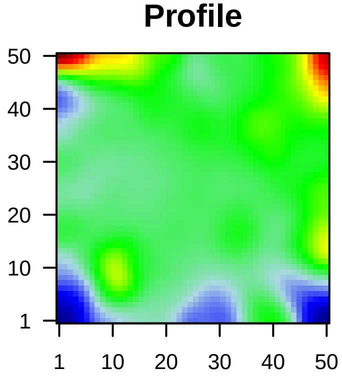
<FC> = −0.29

<shrinkage−t> = −10.31

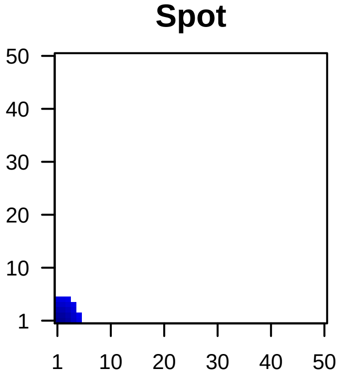
<p−value> = 0

<fdr> = 0.46

Profile



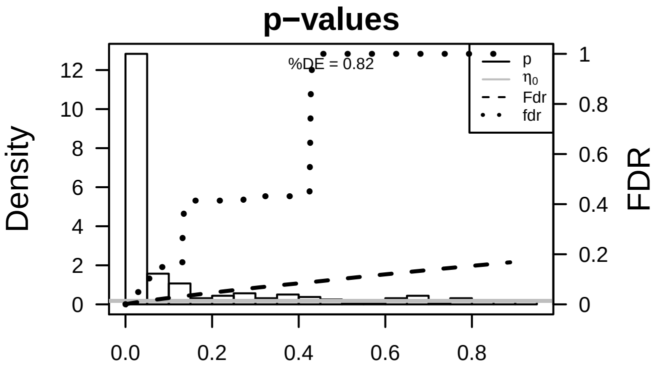
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	857	−1.29	2e−16	2e−15	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
2	26508	1.57	2e−16	2e−15	3 x 1	hes−related family bHLH transcription factor with YRPW motif
3	10962	2.05	2e−16	2e−15	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
4	4319	−1.38	2e−16	2e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
5	10630	2.13	2e−16	2e−15	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
6	6447	1.75	2e−16	2e−15	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
7	3371	1.62	2e−16	2e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
8	4314	−1.27	7e−16	7e−13	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
9	55714	−1.21	1e−14	3e−11	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
10	2619	−1.13	5e−13	1e−10	2 x 1	growth arrest−specific 1 [Source:HGNC Symbol;Acc:4165]
11	3553	−1.1	2e−12	2e−10	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
12	118429	−1.08	8e−12	2e−10	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
13	1291	−1.08	8e−12	7e−10	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
14	7431	−1.05	2e−11	7e−10	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
15	5997	−1.04	3e−11	2e−09	5 x 1	regulator of G−protein signaling 2, 24kDa [Source:HGNC Syn
16	29940	−1.03	6e−11	8e−09	1 x 4	dermatan sulfate epimerase [Source:HGNC Symbol;Acc:211
17	4502	−1	2e−10	2e−08	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
18	5351	0.96	9e−10	2e−08	1 x 3	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 1 [Source
19	112464	−0.96	1e−09	2e−08	1 x 1	protein kinase C, delta binding protein [Source:HGNC Symbo
20	7058	−0.95	2e−09	2e−08	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−29.5	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	−26.58	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−23.91	NULL	33 / 69	BP	extracellular matrix disassembly
4	−23.35	NULL	77 / 250	Lymphoma	LENZ_Stromal signature 1
5	−23.15	NULL	65 / 190	CC	extracellular matrix
6	−22.44	NULL	29 / 64	BP	collagen catabolic process
7	−20.52	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
8	−20.21	NULL	8 / 12	miRNA target	miR−29c
9	−19.57	NULL	8 / 11	MF	platelet−derived growth factor binding
10	−18.97	NULL	74 / 242	BP	extracellular matrix organization
11	−16.3	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
12	−16.17	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
13	−14.68	NULL	82 / 683	CC	extracellular space
14	−14.67	NULL	12 / 40	BP	cellular response to amino acid stimulus
15	−14.48	NULL	22 / 57	MF	extracellular matrix structural constituent
16	−13.52	NULL	117 / 1182	CC	extracellular region
17	−13.23	NULL	6 / 15	GSEA C2	GILDEA_METASTASIS
18	−13.05	NULL	4 / 10	BP	protein heterotrimerization
19	−12.62	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
20	−12.25	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
21	−11.76	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
22	−11.44	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
23	−11.43	NULL	40 / 183	CC	proteinaceous extracellular matrix
24	−11.34	NULL	6 / 16	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_UP
25	−11.32	NULL	3 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
26	−11.27	NULL	67 / 553	Cancer	Lembcke_Colonic Inflammation
27	−11.08	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
28	−11.08	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
29	−11.08	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
30	−11.08	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
31	−11	NULL	27 / 153	CC	endoplasmic reticulum lumen
32	−10.96	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
33	−10.95	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
34	−10.89	NULL	16 / 37	BP	collagen fibril organization
35	−10.76	NULL	5 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
36	−10.45	NULL	7 / 28	BP	odontogenesis
37	−10.24	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
38	−10.17	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
39	−9.99	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
40	−9.77	NULL	25 / 83	CC	basement membrane

GW_174

Local Summary

%DE = 0.92

metagenes = 15

genes = 260

genes in genesets = 258

genes with fdr < 0.1 = 204 (14 + / 190 −)

genes with fdr < 0.05 = 178 (12 + / 166 −)

genes with fdr < 0.01 = 114 (7 + / 107 −)

<r> metagenes = 0.99

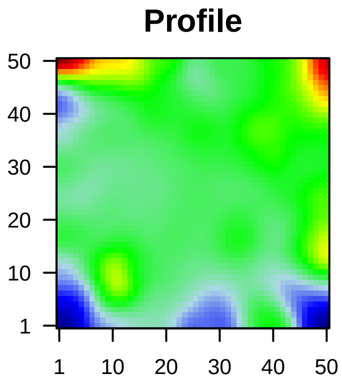
<r> genes = 0.59

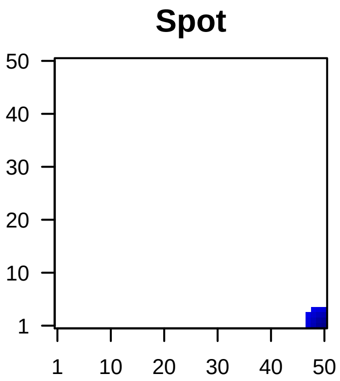
<FC> = −0.32

<shrinkage−t> = −11.02

<p−value> = 0.01

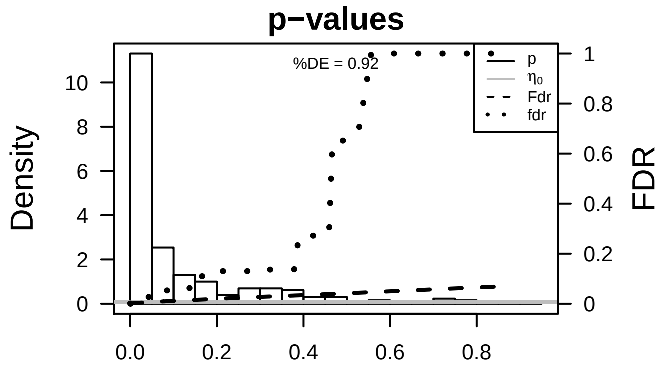
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.08	6e−12	1e−10	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	4283	−1.07	1e−11	3e−10	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
3	23180	−1.05	2e−11	2e−08	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
4	4069	−0.96	1e−09	3e−07	50 x 2	lysozyme [Source:HGNC Symbol;Acc:6740]
5	7305	−0.89	1e−08	5e−07	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
6	3620	−0.86	5e−08	5e−07	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
7	10563	−0.85	6e−08	3e−06	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
8	3109	−0.8	4e−07	3e−06	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
9	6347	−0.8	4e−07	3e−06	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
10	1545	−0.79	5e−07	7e−06	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
11	152007	−0.75	2e−06	7e−06	50 x 3	GLI pathogenesis−related 2 [Source:HGNC Symbol;Acc:180
12	5552	−0.75	2e−06	7e−06	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
13	23643	−0.75	2e−06	7e−06	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
14	115701	−0.75	2e−06	7e−06	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
15	91523	−0.74	2e−06	9e−06	48 x 1	PC−esterase domain containing 1B [Source:HGNC Symbol;
16	894	0.73	3e−06	9e−06	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
17	1116	−0.73	3e−06	1e−05	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
18	3059	−0.73	4e−06	1e−05	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
19	3113	−0.72	4e−06	2e−05	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
20	2207	−0.71	6e−06	2e−05	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.71	NULL	89 / 417	H.Tiss	WIRTH_Immune system
2	−25.3	NULL	92 / 553	Cancer	Lembcke_Colonic Inflammation
3	−23.89	NULL	12 / 15	CC	MHC class II protein complex
4	−19.75	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	−19.75	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	−19.75	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	−19.75	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	−15.6	NULL	48 / 312	BP	immune response
9	−15.17	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
10	−14.83	NULL	15 / 47	BP	antigen processing and presentation
11	−14.66	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
12	−14.54	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
13	−13.71	NULL	5 / 12	BP	immunoglobulin mediated immune response
14	−13.27	NULL	17 / 74	BP	regulation of immune response
15	−12.82	NULL	8 / 16	GSEA C2	SU_THYMUS
16	−12.19	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
17	−12.11	NULL	7 / 45	BP	cellular defense response
18	−12.11	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	−11.72	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
20	−11.67	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEME
21	−11.34	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
22	−10.75	NULL	3 / 13	GSEA C2	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN
23	−10.58	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
24	−10.53	NULL	23 / 162	CC	external side of plasma membrane
25	−10.39	NULL	5 / 11	BP	positive regulation of B cell differentiation
26	−10.2	NULL	4 / 14	BP	ruffle organization
27	−10.01	NULL	7 / 43	MF	chemokine activity
28	−9.81	NULL	3 / 16	GSEA C2	KAAB_FAILED_HEART_VENTRICLE_DN
29	−9.76	NULL	4 / 13	BP	lymph node development
30	−9.76	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
31	−9.67	NULL	23 / 269	BP	inflammatory response
32	−9.66	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
33	−9.64	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
34	−9.55	NULL	2 / 14	GSEA C2	CHEOK_RESPONSE_TO_HD_MTX_UP
35	−9.54	NULL	1 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
36	−9.27	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
37	−9.17	NULL	3 / 10	BP	negative thymic T cell selection
38	−8.88	NULL	4 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
39	−8.84	NULL	3 / 14	Lymphoma	WRIGHT_GCB UP
40	−8.82	NULL	3 / 13	GSEA C2	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION