GW_128

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1973 (1083 + / 890 −)

genes with fdr < 0.1 = 1493 (873 + / 620 −)

genes with fdr < 0.05 = 1249 (761 + / 488 −)

genes with fdr < 0.01 = 923 (590 + / 333 −)

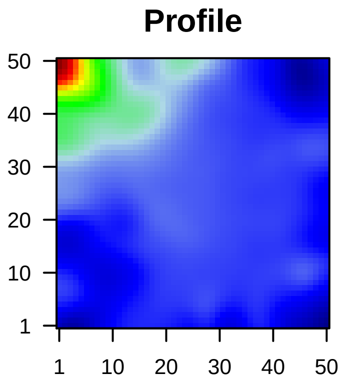
genes in genesets = 16332

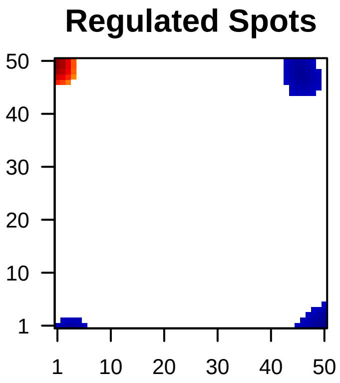
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.49	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	59	−1.41	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	441282	1.45	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	222	1.6	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	242	2.19	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	360	1.44	2e−16	2e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	383	1.4	2e−16	2e−14	7 x 45	arginase 1 [Source:HGNC Symbol;Acc:663]
8	151516	2.64	2e−16	2e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
9	387695	1.71	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
10	29113	2.68	2e−16	2e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
11	375791	2.05	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
12	760	2.13	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	51806	2.29	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
14	595	−1.35	2e−16	2e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
15	948	1.73	2e−16	2e−14	6 x 44	CD36 molecule (thrombospondin receptor) [Source:HGNC S
16	1041	3.12	2e−16	2e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
17	1048	2	2e−16	2e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
18	4680	1.73	2e−16	2e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
19	629	−1.76	2e−16	2e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
20	10370	1.36	2e−16	2e−14	46 x 9	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo

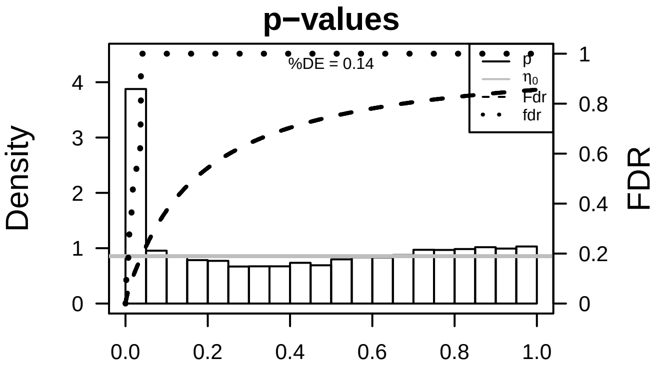
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	36.35	NULL	135	H.Tiss	WIRTH_Mucosa
2	23.33	NULL	42	BP	keratinization
3	20.6	NULL	572	Disease	GUDJ_psoriasis up
4	20.19	NULL	21	CC	cornified envelope
5	18.4	NULL	53	BP	keratinocyte differentiation
6	16.82	NULL	76	BP	epidermis development
7	12.21	NULL	19	BP	peptide cross−linking
8	11.31	NULL	21	CC	desmosome
9	10.78	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
10	9.73	NULL	82	CC	intermediate filament
11	9.52	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	9.4	NULL	186	MF	structural molecule activity
13	9.05	NULL	44	CC	keratin filament
14	8.16	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	7.9	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	7.38	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
17	7.25	NULL	10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
18	7.22	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	7.14	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	7.07	NULL	16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−12.97	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−12.97	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−9.89	NULL	190	CC	extracellular matrix
4	−8.89	NULL	149	BP	DNA replication
5	−8.79	NULL	370	BP	mitotic cell cycle
6	−8.32	NULL	949	CC	nucleoplasm
7	−7.43	NULL	30	BP	DNA strand elongation involved in DNA replication
8	−7.38	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
9	−7.21	NULL	57	Glio	developing astrocytes
10	−7.19	NULL	11	MF	platelet−derived growth factor binding
11	−7.02	NULL	553	Cancer	Lembcke_Colonic Inflammation
12	−7.01	NULL	51	BP	type I interferon signaling pathway
13	−6.98	NULL	242	BP	extracellular matrix organization
14	−6.97	NULL	250	Lymphoma	LENZ_Stromal signature 1
15	−6.9	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
16	−6.81	NULL	153	CC	endoplasmic reticulum lumen
17	−6.7	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
18	−6.66	NULL	69	BP	extracellular matrix disassembly
19	−6.61	NULL	417	H.Tiss	WIRTH_Immune system
20	−6.49	NULL	11	GSEA C2	KALMA_E2F1_TARGETS



GW_128

Local Summary

%DE = 0.99

metagenes = 19

genes = 245

genes in genesets = 238

genes with fdr < 0.1 = 242 (242 + / 0 −)

genes with fdr < 0.05 = 242 (242 + / 0 −)

genes with fdr < 0.01 = 229 (229 + / 0 −)

<r> metagenes = 0.96

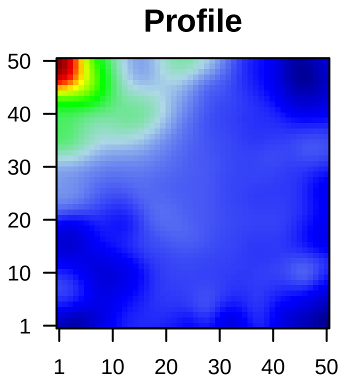
<r> genes = 0.45

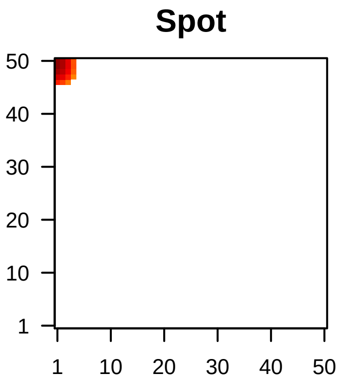
<FC> = 1.35

<shrinkage−t> = 47.43

<p−value> = 0

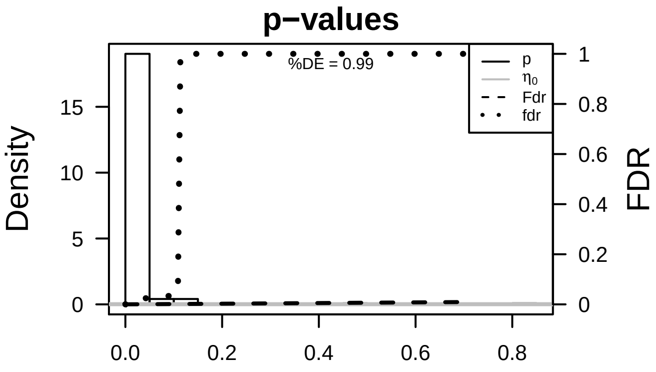
<fdr> = 0.06





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.49	2e−16	6e−18	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	441282	1.45	2e−16	6e−18	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	222	1.6	2e−16	6e−18	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
4	242	2.19	2e−16	6e−18	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
5	360	1.44	2e−16	6e−18	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	151516	2.64	2e−16	6e−18	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
7	387695	1.71	2e−16	6e−18	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
8	29113	2.68	2e−16	6e−18	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
9	375791	2.05	2e−16	6e−18	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
10	51806	2.29	2e−16	6e−18	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
11	1041	3.12	2e−16	6e−18	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
12	1048	2	2e−16	6e−18	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	4680	1.73	2e−16	6e−18	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	22802	1.8	2e−16	6e−18	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	26285	1.46	2e−16	6e−18	4 x 48	claudin 17 [Source:HGNC Symbol;Acc:2038]
16	9022	1.88	2e−16	6e−18	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
17	84518	1.92	2e−16	6e−18	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
18	54544	2.25	2e−16	6e−18	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
19	49860	2.94	2e−16	6e−18	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
20	126410	2.3	2e−16	6e−18	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	57.85	NULL	90 / 135	H.Tiss	WIRTH_Mucosa
2	38.98	NULL	19 / 21	CC	cornified envelope
3	31.99	NULL	25 / 53	BP	keratinocyte differentiation
4	30.42	NULL	19 / 42	BP	keratinization
5	28.01	NULL	96 / 572	Disease	GUDJ_psoriasis up
6	25.16	NULL	26 / 76	BP	epidermis development
7	24.94	NULL	12 / 19	BP	peptide cross−linking
8	18.03	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	17.87	NULL	9 / 21	CC	desmosome
10	17.84	NULL	7 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	14.91	NULL	22 / 186	MF	structural molecule activity
12	14.51	NULL	13 / 82	CC	intermediate filament
13	14.06	NULL	9 / 44	CC	keratin filament
14	13.55	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
15	12.85	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
16	12.45	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
17	12.25	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
18	12.05	NULL	5 / 10	MF	RAGE receptor binding
19	11.87	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
20	11.21	NULL	6 / 13	BP	negative regulation of peptidase activity
21	10.93	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
22	10.89	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
23	10.75	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
24	10.52	NULL	58 / 1182	CC	extracellular region
25	10.34	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
26	10.15	NULL	13 / 122	MF	serine−type endopeptidase activity
27	10.06	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
28	9.81	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
29	9.74	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	9.52	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
31	9.51	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
32	9.46	NULL	8 / 38	BP	epithelial cell differentiation
33	8.76	NULL	8 / 51	MF	protein binding, bridging
34	8.6	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
35	8.2	NULL	5 / 23	MF	peptidase inhibitor activity
36	8.15	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
37	8.11	NULL	4 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
38	8.07	NULL	10 / 52	BP	negative regulation of endopeptidase activity
39	7.94	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
40	7.93	NULL	5 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN

GW_128

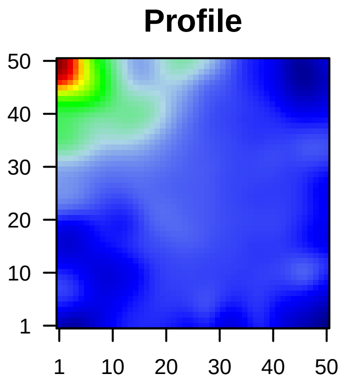
Local Summary

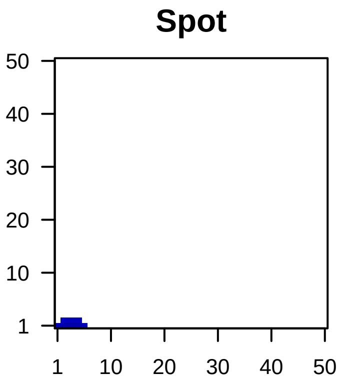
%DE = 0.77
metagenes = 10
genes = 205
genes in genesets = 204

genes with fdr < 0.1 = 118 (10 + / 108 −)
genes with fdr < 0.05 = 115 (9 + / 106 −)
genes with fdr < 0.01 = 86 (5 + / 81 −)

<r> metagenes = 0.98
<r> genes = 0.45

<FC> = −0.44
<shrinkage−t> = −15.36
<p−value> = 0
<fdr> = 0.46


Profile


Spot

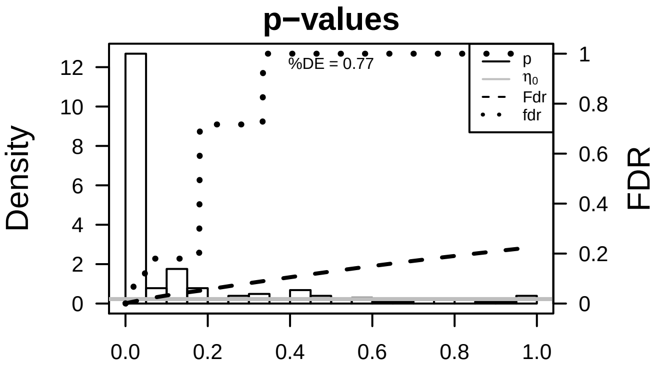
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	−1.41	2e−16	1e−15	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	1278	−1.4	2e−16	1e−15	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1289	−1.36	2e−16	1e−15	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
4	3043	−1.54	2e−16	1e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
5	4320	−1.42	2e−16	1e−15	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
6	4316	−1.7	2e−16	1e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
7	12	−1.43	2e−16	1e−15	1 x 1	
8	6678	−1.45	2e−16	1e−15	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
9	1462	−1.4	2e−16	1e−15	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
10	633	−1.23	1e−15	2e−13	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
11	3956	−1.3	7e−15	2e−13	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
12	3040	−1.29	9e−15	2e−13	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
13	1277	−1.29	1e−14	4e−12	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
14	6696	−1.24	9e−14	8e−11	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
15	1513	−1.18	2e−12	3e−09	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
16	165	−1.07	1e−10	3e−09	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
17	23213	−1.07	1e−10	5e−09	2 x 1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]
18	7070	−1.05	3e−10	5e−09	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801
19	84624	−1.05	3e−10	1e−08	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
20	6515	−1.03	6e−10	1e−08	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.76	NULL	8 / 11	MF	platelet−derived growth factor binding
2	−34.77	NULL	58 / 190	CC	extracellular matrix
3	−32.67	NULL	8 / 12	miRNA target	miR−29c
4	−31.93	NULL	66 / 250	Lymphoma	LENZ_Stromal signature 1
5	−31.8	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
6	−30.97	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	−29.17	NULL	26 / 69	BP	extracellular matrix disassembly
8	−27.92	NULL	49 / 242	BP	extracellular matrix organization
9	−27.87	NULL	22 / 64	BP	collagen catabolic process
10	−26.17	NULL	19 / 57	MF	extracellular matrix structural constituent
11	−23.79	NULL	10 / 19	MF	extracellular matrix binding
12	−23.21	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	−22.94	NULL	11 / 37	BP	collagen fibril organization
14	−21.99	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
15	−21.88	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
16	−21.76	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
17	−21.17	NULL	9 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
18	−20.01	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
19	−19.85	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
20	−19.72	NULL	4 / 10	BP	protein heterotrimerization
21	−19.37	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
22	−19.21	NULL	29 / 183	CC	proteinaceous extracellular matrix
23	−19.07	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
24	−18.99	NULL	15 / 68	CC	collagen
25	−18.85	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
26	−18.83	NULL	5 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE
27	−17.65	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
28	−16.63	NULL	3 / 14	CC	endocytic vesicle lumen
29	−16.52	NULL	4 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
30	−16.47	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
31	−16.16	NULL	6 / 16	GSEA C2	GU_PDEF_TARGETS_UP
32	−16.12	NULL	61 / 683	CC	extracellular space
33	−16.03	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
34	−16.03	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
35	−16.02	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
36	−15.96	NULL	9 / 40	BP	cellular response to amino acid stimulus
37	−15.59	NULL	4 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
38	−15.47	NULL	4 / 16	GSEA C2	REACTOME_AXON_GUIDANCE
39	−15.47	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
40	−15.38	NULL	83 / 1182	CC	extracellular region


p−values

GW_128

Local Summary

%DE = 0.83

metagenes = 19

genes = 308

genes in genesets = 305

genes with fdr < 0.1 = 229 (18 + / 211 −)

genes with fdr < 0.05 = 162 (14 + / 148 −)

genes with fdr < 0.01 = 126 (14 + / 112 −)

<r> metagenes = 0.98

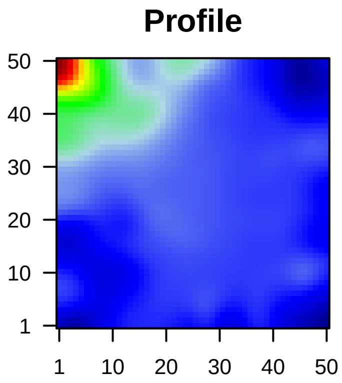
<r> genes = 0.55

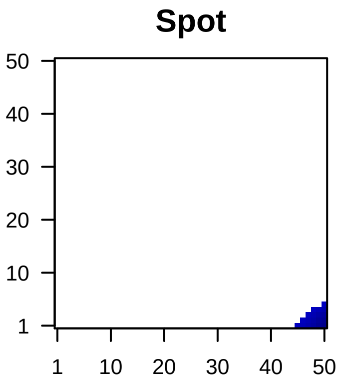
<FC> = −0.36

<shrinkage−t> = −12.49

<p−value> = 0

<fdr> = 0.49


Profile


Spot

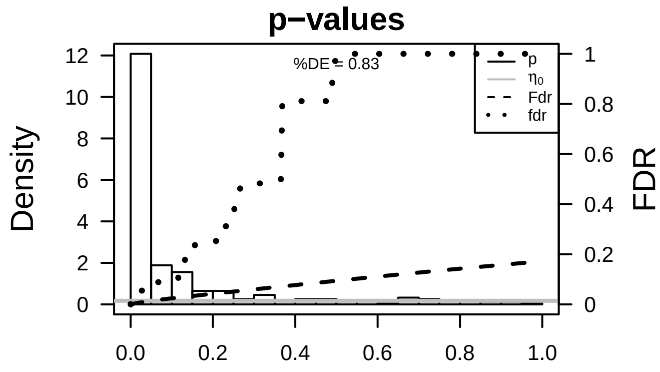
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1545	2.62	2e−16	6e−15	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
2	2745	1.4	2e−16	6e−15	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
3	5996	−1.36	4e−16	3e−13	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
4	3620	1.3	7e−15	1e−09	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
5	341	−1.12	2e−11	2e−09	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
6	348	−1.1	5e−11	3e−09	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	7351	−1.08	1e−10	6e−09	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
8	260436	−1.05	4e−10	6e−09	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
9	713	−1.05	4e−10	6e−09	50 x 1	complement component 1, q subcomponent, B chain [Source
10	64759	−1.04	4e−10	2e−08	50 x 4	tensin 3 [Source:HGNC Symbol;Acc:21616]
11	9806	−1.03	8e−10	2e−08	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
12	10563	−1.02	1e−09	2e−08	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
13	25849	−1.01	2e−09	2e−08	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
14	6363	−1.01	2e−09	1e−07	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
15	10537	−0.98	4e−09	1e−07	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	9308	−0.97	6e−09	1e−07	50 x 3	CD83 molecule [Source:HGNC Symbol;Acc:1703]
17	347733	−0.97	7e−09	2e−07	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
18	6364	−0.95	1e−08	4e−07	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
19	5920	−0.94	2e−08	7e−07	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
20	4283	0.92	3e−08	1e−06	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.94	NULL	13 / 15	CC	MHC class II protein complex
2	−18.89	NULL	93 / 417	H.Tiss	WIRTH_Immune system
3	−17.82	NULL	97 / 553	Cancer	Lembcke_Colonic Inflammation
4	−17.43	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
5	−16.17	NULL	55 / 312	BP	immune response
6	−15.75	NULL	5 / 13	MMML CGS	MACIEJ_MMML 6
7	−14.91	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
8	−14.85	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	−14.85	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	−14.85	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	−14.85	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	−14.79	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
13	−14.68	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
14	−14.02	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
15	−13.68	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	−13.65	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
17	−13.42	NULL	16 / 47	BP	antigen processing and presentation
18	−13.4	NULL	5 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
19	−12.97	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
20	−12.91	NULL	5 / 12	BP	immunoglobulin mediated immune response
21	−12.89	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	−12.87	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
23	−12.8	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
24	−12.7	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
25	−12.55	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
26	−12.28	NULL	18 / 60	BP	T cell costimulation
27	−12.15	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
28	−12	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
29	−11.6	NULL	18 / 74	BP	regulation of immune response
30	−11.52	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
31	−11.51	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
32	−11.22	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
33	−11.11	NULL	5 / 12	BP	dendritic cell chemotaxis
34	−10.92	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
35	−10.82	NULL	25 / 162	CC	external side of plasma membrane
36	−10.41	NULL	26 / 204	BP	cell surface receptor signaling pathway
37	−10.01	NULL	4 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
38	−10	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
39	−9.94	NULL	15 / 87	BP	antigen processing and presentation of exogenous peptide antigen
40	−9.92	NULL	4 / 13	BP	lymph node development


p−values

GW_128

Local Summary

%DE = 0.8

metagenes = 44

genes = 438

genes in genesets = 435

genes with fdr < 0.1 = 250 (5 + / 245 −)

genes with fdr < 0.05 = 196 (3 + / 193 −)

genes with fdr < 0.01 = 132 (1 + / 131 −)

<r> metagenes = 0.9

<r> genes = 0.33

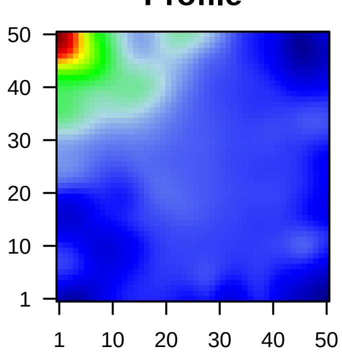
<FC> = −0.37

<shrinkage−t> = −12.95

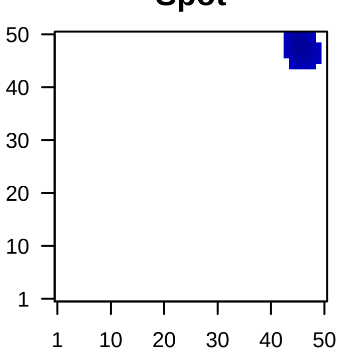
<p−value> = 0.01

<fdr> = 0.58

Profile



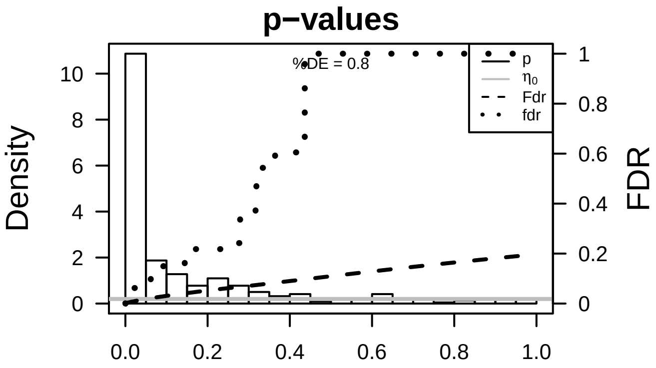
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	7037	−1.54	2e−16	2e−14	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
2	4171	−1.12	2e−11	2e−08	46 x 48	minichromosome maintenance complex component 2 [Source
3	4175	−1.05	3e−10	3e−08	46 x 47	minichromosome maintenance complex component 6 [Source
4	7083	−1.03	7e−10	3e−08	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
5	5984	−1.02	9e−10	4e−08	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sym
6	8318	−1	2e−09	4e−08	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
7	7153	−1	2e−09	5e−08	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
8	4172	−1	2e−09	3e−07	46 x 47	minichromosome maintenance complex component 3 [Source
9	51659	−0.97	6e−09	3e−07	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
10	11065	−0.96	1e−08	3e−07	44 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
11	1163	−0.95	1e−08	3e−07	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
12	9918	−0.95	1e−08	2e−06	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
13	1019	−0.91	5e−08	2e−06	46 x 47	cyclin−dependent kinase 4 [Source:HGNC Symbol;Acc:1773]
14	10024	−0.9	7e−08	2e−06	45 x 47	trophinin associated protein [Source:HGNC Symbol;Acc:1232
15	113130	−0.9	7e−08	2e−06	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
16	57570	−0.89	9e−08	3e−06	46 x 45	tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141
17	142	−0.88	1e−07	3e−06	47 x 46	poly (ADP−ribose) polymerase 1 [Source:HGNC Symbol;Acc
18	1063	−0.88	2e−07	3e−06	46 x 48	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac
19	4174	−0.87	2e−07	1e−05	46 x 46	minichromosome maintenance complex component 5 [Source
20	1786	−0.84	5e−07	1e−05	45 x 47	DNA (cytosine−5−)−methyltransferase 1 [Source:HGNC Sym

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−50.52	NULL	94 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−50.52	NULL	94 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−31.43	NULL	19 / 30	BP	DNA strand elongation involved in DNA replication
4	−29.82	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
5	−29.34	NULL	101 / 370	BP	mitotic cell cycle
6	−29.03	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
7	−28.94	NULL	49 / 149	BP	DNA replication
8	−28.34	NULL	26 / 57	Glio	developing astrocytes
9	−28.18	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
10	−25.9	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
11	−25.78	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
12	−24.41	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
13	−23.12	NULL	13 / 22	BP	DNA replication initiation
14	−22.67	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−22.59	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	−22.33	NULL	103 / 530	Cancer	Lembcke_Normal vs Adenoma
17	−22.19	NULL	11 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
18	−21.96	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
19	−20.9	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
20	−20.79	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
21	−20.5	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
22	−20.24	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
23	−20.21	NULL	8 / 16	GSEA C2	LY_AGING_PREMATURE_DN
24	−19.71	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
25	−19.59	NULL	13 / 21	BP	telomere maintenance via semi−conservative replication
26	−19.58	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
27	−19.41	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
28	−19.34	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
29	−19.16	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
30	−19.13	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
31	−19.11	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
32	−18.81	NULL	54 / 232	BP	mitosis
33	−18.65	NULL	10 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
34	−18.5	NULL	10 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
35	−18.33	NULL	9 / 15	GSEA C2	KEGG_DNA_REPLICATION
36	−18.32	NULL	7 / 15	GSEA C2	LY_AGING_OLD_DN
37	−18.23	NULL	14 / 24	BP	telomere maintenance via recombination
38	−18.14	NULL	6 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
39	−18.01	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
40	−17.91	NULL	109 / 949	CC	nucleoplasm