GW_266

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1756 (939 + / 817 −)

genes with fdr < 0.1 = 1375 (755 + / 620 −)

genes with fdr < 0.05 = 1062 (591 + / 471 −)

genes with fdr < 0.01 = 717 (436 + / 281 −)

genes in genesets = 16332

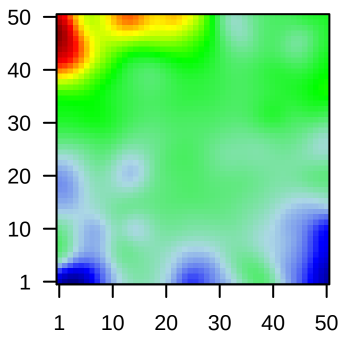
<FC> = 0

<shrinkage−t> = 0

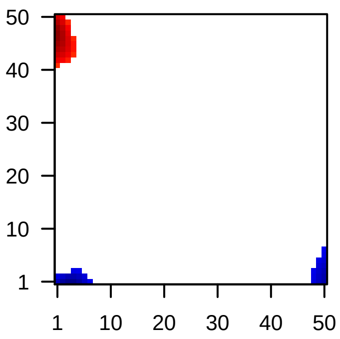
<p−value> = 0.11

<fdr> = 0.86

Profile



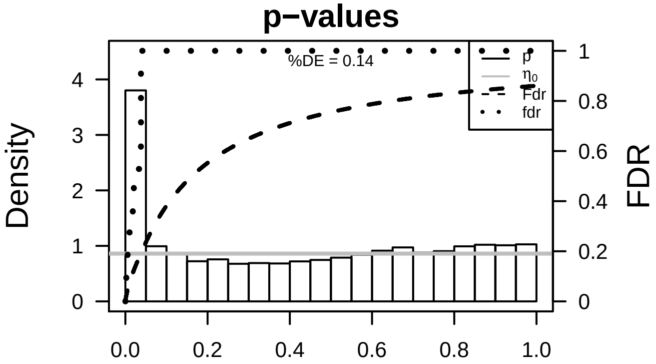
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.77	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	154	1.53	2e−16	4e−14	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286
3	84632	1.36	2e−16	4e−14	1 x 41	actin filament associated protein 1−like 2 [Source:HGNC Sym
4	57016	2.02	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.89	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
6	8644	1.88	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	1.77	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	216	−1.33	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
9	55107	1.36	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
10	91947	1.32	2e−16	4e−14	4 x 43	arrestin domain containing 4 [Source:HGNC Symbol;Acc:280
11	387695	2.07	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
12	760	1.52	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	84290	1.46	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
14	1066	1.64	2e−16	4e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
15	9073	1.96	2e−16	4e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
16	1281	−1.19	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
17	1282	−1.49	2e−16	4e−14	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
18	1591	2.03	2e−16	4e−14	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
19	57834	1.3	2e−16	4e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sou
20	92196	1.73	2e−16	4e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2

p−values



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	14.18	NULL	135	H.Tiss	WIRTH_Mucosa
2	13.68	NULL	572	Disease	GUDJ_psoriasis up
3	10.32	NULL	76	BP	epidermis development
4	9.54	NULL	1033	Chr	Chr 2
5	9.52	NULL	53	BP	keratinocyte differentiation
6	9.16	NULL	21	CC	cornified envelope
7	9.01	NULL	602	Chr	Chr 10
8	7.81	NULL	42	BP	keratinization
9	7.53	NULL	717	Chr	Chr 16
10	7.27	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
11	7.14	NULL	25	BP	glutathione derivative biosynthetic process
12	6.87	NULL	504	Chr	Chr 15
13	6.7	NULL	20	MF	glutathione transferase activity
14	6.67	NULL	534	Chr	Chr 8
15	6.31	NULL	16	GSEA C2	AMIT_DELAYED_EARLY_GENES
16	6.06	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
17	5.89	NULL	10	BP	white fat cell differentiation
18	5.85	NULL	16	TF Tissue	VAQUERIZAS_Pancreas
19	5.82	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
20	5.65	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−14.81	NULL	633	Chr	Chr 9
2	−8.97	NULL	11	MF	platelet−derived growth factor binding
3	−8.96	NULL	190	CC	extracellular matrix
4	−8.82	NULL	553	Cancer	Lembcke_Colonic Inflammation
5	−8.32	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	−7.74	NULL	714	Chr	Chr 6
7	−7.51	NULL	15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
8	−7.33	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
9	−7.19	NULL	1135	Chr	Chr 19
10	−7.11	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
11	−6.97	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
12	−6.82	NULL	7	MMML CGS	MACIEJ_MMML 5
13	−6.6	NULL	57	MF	extracellular matrix structural constituent
14	−6.48	NULL	250	Lymphoma	LENZ_Stromal signature 1
15	−6.44	NULL	12	miRNA target	miR−29c
16	−6.39	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
17	−6.07	NULL	36	BP	muscle filament sliding
18	−6.06	NULL	44	MF	structural constituent of muscle
19	−5.92	NULL	253	BP	translation
20	−5.86	NULL	683	CC	extracellular space

GW_266

Local Summary

%DE = 0.8

metagenes = 31

genes = 390

genes in genesets = 383

genes with fdr < 0.1 = 247 (216 + / 31 −)

genes with fdr < 0.05 = 220 (195 + / 25 −)

genes with fdr < 0.01 = 194 (173 + / 21 −)

<r> metagenes = 0.88

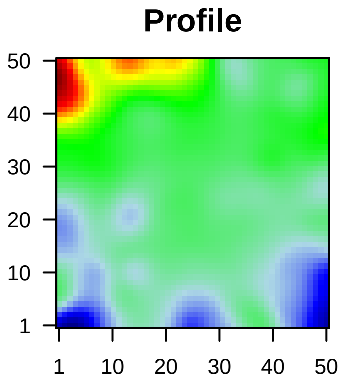
<r> genes = 0.35

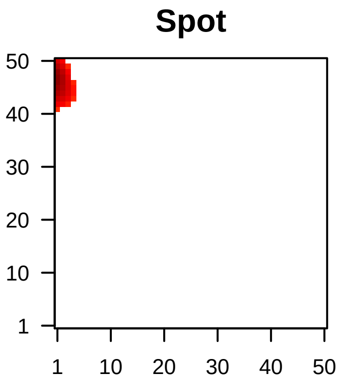
<FC> = 0.46

<shrinkage−t> = 16.18

<p−value> = 0

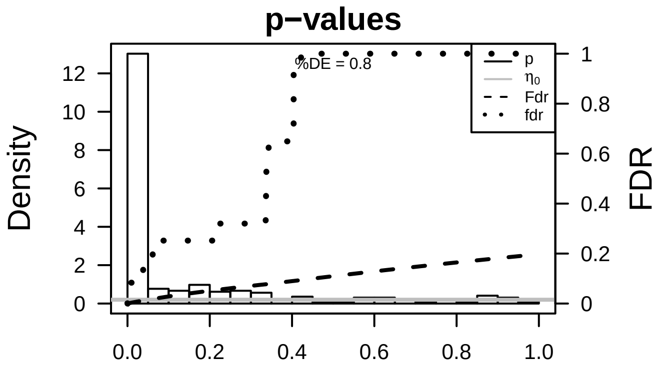
<fdr> = 0.41


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.77	2e−16	4e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	84632	1.36	2e−16	4e−16	1 x 41	actin filament associated protein 1−like 2 [Source:HGNC Sym
3	57016	2.02	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.89	2e−16	4e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	1.88	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	91947	1.32	2e−16	4e−16	4 x 43	arrestin domain containing 4 [Source:HGNC Symbol;Acc:280
7	387695	2.07	2e−16	4e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
8	760	1.52	2e−16	4e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	84290	1.46	2e−16	4e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	1672	1.49	2e−16	4e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	55894	1.88	2e−16	4e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	414325	2.19	2e−16	4e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	1673	2.42	2e−16	4e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	1828	1.33	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	2167	3.6	2e−16	4e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	10804	1.54	2e−16	4e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
17	56169	1.4	2e−16	4e−16	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
18	3306	1.8	2e−16	4e−16	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
19	29094	1.62	2e−16	4e−16	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
20	3848	2.06	2e−16	4e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	27.5	NULL	87 / 135	H.Tiss	WIRTH_Mucosa
2	23.2	NULL	18 / 21	CC	cornified envelope
3	22.09	NULL	29 / 76	BP	epidermis development
4	21.93	NULL	127 / 572	Disease	GUDJ_psoriasis up
5	20.86	NULL	26 / 53	BP	keratinocyte differentiation
6	16.03	NULL	20 / 42	BP	keratinization
7	13	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
8	12.32	NULL	13 / 21	CC	desmosome
9	11.95	NULL	4 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
10	11.23	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	11.09	NULL	2 / 12	MF	fatty acid binding
12	10.97	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
13	10.96	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
14	10.42	NULL	23 / 82	CC	intermediate filament
15	10.26	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	9.74	NULL	5 / 10	MF	RAGE receptor binding
17	9.61	NULL	1 / 10	BP	white fat cell differentiation
18	9.45	NULL	3 / 15	MF	retinol dehydrogenase activity
19	9.1	NULL	1 / 11	GSEA C2	REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_
20	9.02	NULL	13 / 44	CC	keratin filament
21	8.95	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
22	8.93	NULL	4 / 13	BP	retinoic acid metabolic process
23	8.83	NULL	3 / 12	BP	cellular aldehyde metabolic process
24	8.78	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
25	8.5	NULL	6 / 16	GSEA C2	JAEGER_METASTASIS_DN
26	8.47	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
27	8.44	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
28	8.39	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
29	8.36	NULL	3 / 14	GSEA C2	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
30	8.27	NULL	1 / 13	BP	cellular response to lithium ion
31	8.26	NULL	8 / 73	BP	defense response to bacterium
32	8.22	NULL	4 / 25	BP	brown fat cell differentiation
33	8.11	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
34	8.09	NULL	5 / 25	BP	response to zinc ion
35	8.03	NULL	2 / 10	BP	retinal metabolic process
36	8.01	NULL	32 / 186	MF	structural molecule activity
37	7.9	NULL	5 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
38	7.88	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
39	7.86	NULL	4 / 12	BP	hemidesmosome assembly
40	7.78	NULL	6 / 39	BP	retinoid metabolic process

GW_266

Local Summary

%DE = 0.82

metagenes = 15

genes = 272

genes in genesets = 271

genes with fdr < 0.1 = 212 (19 + / 193 −)

genes with fdr < 0.05 = 176 (17 + / 159 −)

genes with fdr < 0.01 = 146 (13 + / 133 −)

<r> metagenes = 0.97

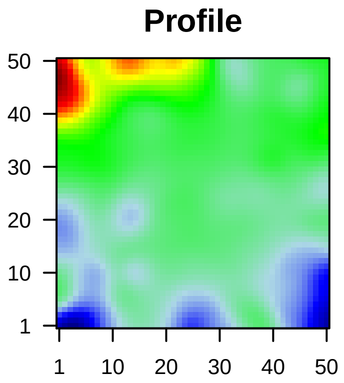
<r> genes = 0.42

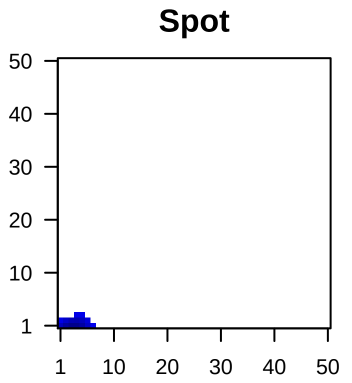
<FC> = −0.42

<shrinkage−t> = −14.7

<p−value> = 0

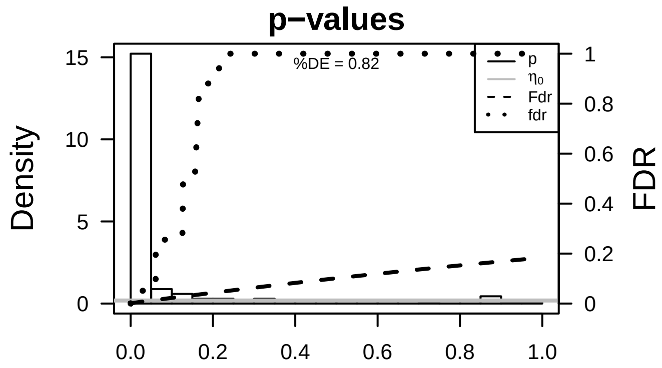
<fdr> = 0.36





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1281	−1.19	2e−16	2e−15	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
2	1282	−1.49	2e−16	2e−15	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
3	3043	−1.45	2e−16	2e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
4	3956	−1.33	2e−16	2e−15	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
5	4316	1.75	2e−16	2e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
6	55714	−1.47	2e−16	2e−15	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
7	12	1.72	2e−16	2e−15	1 x 1	
8	3040	−1.29	4e−16	1e−14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	1462	−1.28	7e−16	1e−12	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
10	7070	−1.2	4e−14	1e−12	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801
11	633	−1.1	6e−14	1e−12	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
12	5159	−1.19	7e−14	4e−12	3 x 1	platelet−derived growth factor receptor, beta polypeptide [Sou
13	6696	−1.17	2e−13	5e−12	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
14	118429	−1.16	3e−13	5e−12	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
15	7431	−1.15	4e−13	5e−12	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
16	7837	−1.15	5e−13	7e−11	2 x 1	peroxidasin homolog (Drosophila) [Source:HGNC Symbol;Ac
17	1289	−1.12	2e−12	1e−10	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
18	10631	−1.1	4e−12	1e−10	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
19	3039	−1.09	7e−12	6e−10	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
20	1293	−1.06	3e−11	6e−10	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−33.94	NULL	8 / 11	MF	platelet−derived growth factor binding
2	−30.12	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−28.33	NULL	76 / 250	Lymphoma	LENZ_Stromal signature 1
4	−28.29	NULL	65 / 190	CC	extracellular matrix
5	−25.54	NULL	8 / 12	miRNA target	miR−29c
6	−23.23	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
7	−22.21	NULL	60 / 242	BP	extracellular matrix organization
8	−21.6	NULL	30 / 69	BP	extracellular matrix disassembly
9	−20.72	NULL	21 / 57	MF	extracellular matrix structural constituent
10	−20.36	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
11	−20.2	NULL	26 / 64	BP	collagen catabolic process
12	−19.43	NULL	11 / 19	MF	extracellular matrix binding
13	−18.94	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
14	−18.52	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
15	−18.11	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
16	−17.43	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
17	−17.2	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
18	−17	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
19	−16.76	NULL	15 / 68	CC	collagen
20	−16.71	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
21	−16.03	NULL	14 / 37	BP	collagen fibril organization
22	−15.77	NULL	68 / 553	Cancer	Lembcke_Colonic Inflammation
23	−15.43	NULL	10 / 40	BP	cellular response to amino acid stimulus
24	−14.92	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
25	−14.73	NULL	5 / 15	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
26	−14.63	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
27	−14.23	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
28	−14.18	NULL	5 / 19	MF	peroxidase activity
29	−14.03	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
30	−13.9	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
31	−13.75	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
32	−13.56	NULL	4 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
33	−13.39	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
34	−13.03	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
35	−12.98	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
36	−12.8	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
37	−12.76	NULL	3 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
38	−12.72	NULL	4 / 10	BP	negative regulation of cell−substrate adhesion
39	−12.6	NULL	3 / 14	CC	endocytic vesicle lumen
40	−12.54	NULL	36 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up

GW_266

Local Summary

%DE = 0.75

metagenes = 15

genes = 315

genes in genesets = 313

genes with fdr < 0.1 = 177 (13 + / 164 −)

genes with fdr < 0.05 = 143 (12 + / 131 −)

genes with fdr < 0.01 = 87 (9 + / 78 −)

<r> metagenes = 0.95

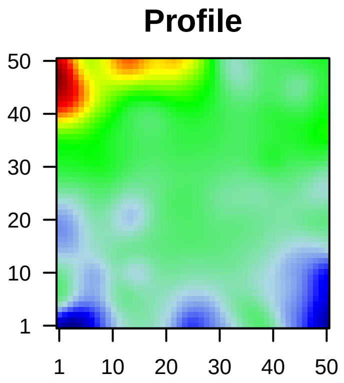
<r> genes = 0.48

<FC> = −0.29

<shrinkage−t> = −10.11

<p−value> = 0.01

<fdr> = 0.58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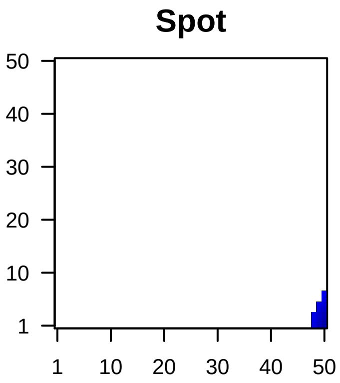
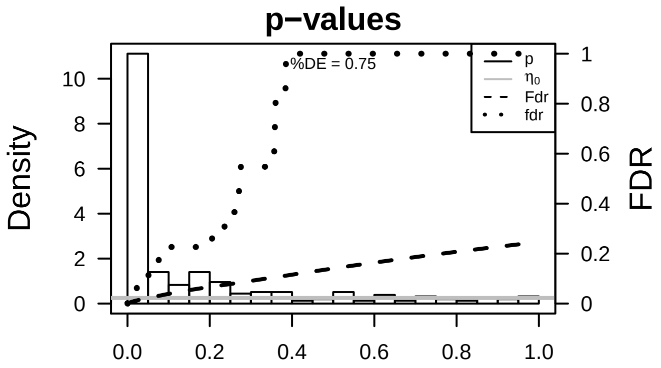

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.23	9e−15	2e−11	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
2	347733	−1.17	2e−13	3e−09	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
3	10537	−1.03	8e−11	3e−09	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
4	3488	−1.03	9e−11	3e−09	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
5	3543	0.94	1e−10	2e−08	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
6	6363	−1	4e−10	3e−08	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	6347	−0.98	7e−10	2e−07	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
8	347	−0.93	5e−09	2e−07	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
9	152007	−0.93	5e−09	3e−07	50 x 3	GLI pathogenesis−related 2 [Source:HGNC Symbol;Acc:180
10	3669	−0.91	1e−08	3e−07	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
11	6578	−0.9	2e−08	3e−07	50 x 4	solute carrier organic anion transporter family, member 2A1 [
12	338773	−0.89	2e−08	9e−06	50 x 5	transmembrane protein 119 [Source:HGNC Symbol;Acc:278
13	8404	−0.82	2e−07	9e−06	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
14	5341	−0.82	3e−07	1e−05	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
15	5920	0.79	7e−07	1e−05	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
16	51176	−0.78	8e−07	1e−05	50 x 5	lymphoid enhancer−binding factor 1 [Source:HGNC Symbol;
17	399959	−0.78	8e−07	1e−05	50 x 6	
18	115701	−0.78	1e−06	1e−05	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
19	55303	−0.77	1e−06	2e−05	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
20	3398	0.77	1e−06	1e−04	49 x 5	inhibitor of DNA binding 2, dominant negative helix−loop−hel


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.62	NULL	11 / 15	CC	MHC class II protein complex
2	−18.1	NULL	91 / 553	Cancer	Lembcke_Colonic Inflammation
3	−14.63	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	−14.63	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	−14.63	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	−14.63	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	−14.57	NULL	76 / 417	H.Tiss	WIRTH_Immune system
8	−14.11	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
9	−13.95	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
10	−13.72	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
11	−13.09	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
12	−12.98	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
13	−12.68	NULL	5 / 12	BP	dendritic cell chemotaxis
14	−12.05	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
15	−12.01	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	−11.7	NULL	4 / 14	BP	ruffle organization
17	−11.45	NULL	9 / 43	MF	chemokine activity
18	−10.86	NULL	4 / 13	BP	positive regulation of endocytosis
19	−10.74	NULL	4 / 14	Lymphoma	WRIGHT_GCB UP
20	−10.71	NULL	16 / 74	BP	regulation of immune response
21	−10.69	NULL	48 / 312	BP	immune response
22	−10.13	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
23	−9.91	NULL	4 / 22	BP	positive regulation of interleukin−12 production
24	−9.84	NULL	4 / 10	GSEA C2	FERRANDO_LYL1_NEIGHBORS
25	−9.62	NULL	27 / 162	CC	external side of plasma membrane
26	−9.57	NULL	4 / 13	BP	lymph node development
27	−9.29	NULL	5 / 12	BP	immunoglobulin mediated immune response
28	−9.23	NULL	12 / 60	BP	T cell costimulation
29	−9.13	NULL	2 / 10	BP	positive regulation of chemotaxis
30	−9.1	NULL	13 / 47	BP	antigen processing and presentation
31	−9.04	NULL	2 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
32	−9	NULL	3 / 14	MF	lipid transporter activity
33	−8.99	NULL	4 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
34	−8.81	NULL	4 / 14	BP	positive regulation of interleukin−10 production
35	−8.54	NULL	8 / 35	CC	trans−Golgi network membrane
36	−8.48	NULL	2 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
37	−8.43	NULL	9 / 43	BP	positive regulation of T cell proliferation
38	−8.42	NULL	3 / 7	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN
39	−8.33	NULL	3 / 7	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
40	−8.3	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane