GW_209

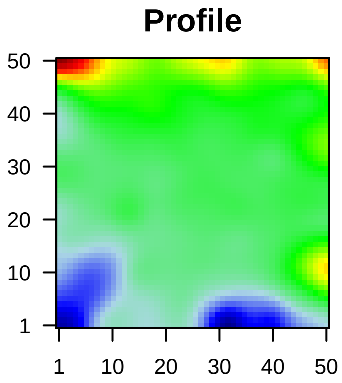
Global Summary

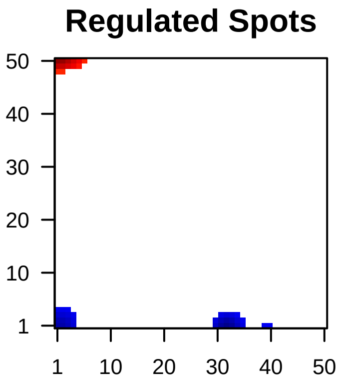
%DE = 0.14

genes with fdr < 0.2 = 1798 (1019 + / 779 −)
genes with fdr < 0.1 = 1461 (831 + / 630 −)
genes with fdr < 0.05 = 1254 (720 + / 534 −)
genes with fdr < 0.01 = 891 (530 + / 361 −)

genes in genesets = 16332

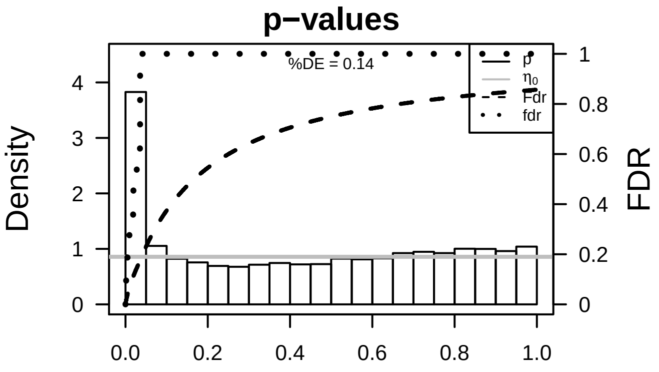
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.09
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	2.57	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	165	−1.27	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
3	57016	2.07	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.9	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	1.48	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	1.84	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	216	2.1	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	218	2.22	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
9	25805	1.59	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
10	633	−1.75	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
11	684	−2.26	2e−16	2e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	399948	1.33	2e−16	2e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
13	92747	2.03	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
14	375791	1.29	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
15	6347	1.5	2e−16	2e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
16	414062	−1.54	2e−16	2e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
17	969	1.26	2e−16	2e−14	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
18	22802	1.67	2e−16	2e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
19	9071	2.06	2e−16	2e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
20	7122	1.76	2e−16	2e−14	50 x 6	claudin 5 [Source:HGNC Symbol;Acc:2047]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.8	NULL	135	H.Tiss	WIRTH_Mucosa
2	8.94	NULL	21	CC	cornified envelope
3	8.72	NULL	12	BP	cellular aldehyde metabolic process
4	8.16	NULL	53	BP	keratinocyte differentiation
5	7.8	NULL	1318	CC	mitochondrion
6	7.74	NULL	1253	BP	small molecule metabolic process
7	7.58	NULL	434	BP	oxidation−reduction process
8	7.56	NULL	10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
9	7.45	NULL	119	BP	xenobiotic metabolic process
10	7.26	NULL	42	BP	keratinization
11	6.94	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
12	6.86	NULL	19	BP	peptide cross−linking
13	6.85	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
14	6.83	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
15	6.74	NULL	633	Chr	Chr 9
16	6.72	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
17	6.71	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
18	6.69	NULL	296	MF	oxidoreductase activity
19	6.67	NULL	1033	Chr	Chr 2
20	6.3	NULL	304	CC	mitochondrial inner membrane
Underexpressed					
1	−18.06	NULL	51	BP	type I interferon signaling pathway
2	−15.38	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	−14.78	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	−14.25	NULL	190	CC	extracellular matrix
5	−14.18	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	−14.08	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
7	−13.91	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	−13.68	NULL	69	BP	extracellular matrix disassembly
9	−12.84	NULL	64	BP	collagen catabolic process
10	−12.79	NULL	123	BP	defense response to virus
11	−12.62	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	−12.55	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
13	−12.48	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	−12.46	NULL	31	BP	negative regulation of viral genome replication
15	−11.82	NULL	242	BP	extracellular matrix organization
16	−11.05	NULL	11	MF	platelet−derived growth factor binding
17	−10.99	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
18	−10.47	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
19	−10.05	NULL	10	GSEA C2	DAUER_STAT3_TARGETS_DN
20	−9.87	NULL	250	Lymphoma	LENZ_Stromal signature 1

GW_209

Local Summary

%DE = 0.89

metagenes = 13

genes = 230

genes in genesets = 226

genes with fdr < 0.1 = 183 (175 + / 8 −)

genes with fdr < 0.05 = 174 (168 + / 6 −)

genes with fdr < 0.01 = 165 (160 + / 5 −)

<r> metagenes = 0.98

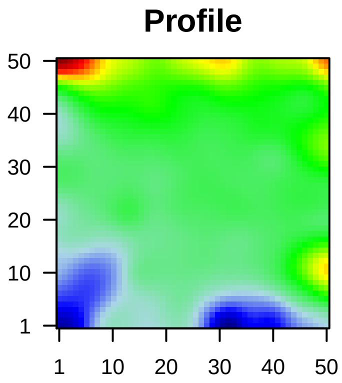
<r> genes = 0.45

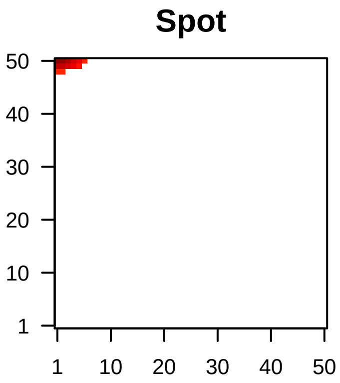
<FC> = 0.69

<shrinkage−t> = 24.39

<p−value> = 0

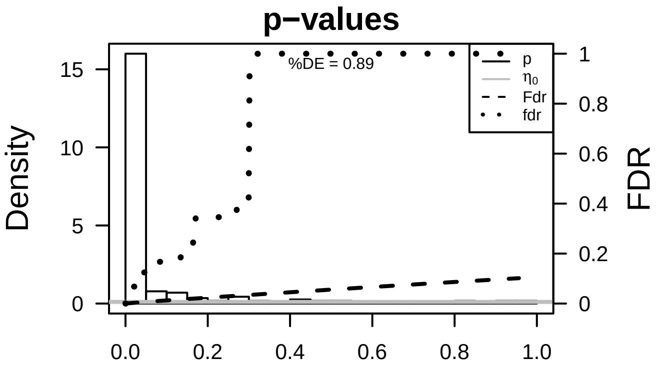
<fdr> = 0.25





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	2.57	2e−16	1e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	2.07	2e−16	1e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	1.9	2e−16	1e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	1.48	2e−16	1e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
5	218	2.22	2e−16	1e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	375791	1.29	2e−16	1e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
7	22802	1.67	2e−16	1e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	9022	1.2	2e−16	1e−16	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
9	49860	2.1	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1562	1.21	2e−16	1e−16	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
11	1571	1.42	2e−16	1e−16	5 x 50	cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
12	1577	1.25	2e−16	1e−16	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
13	1672	1.21	2e−16	1e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
14	131177	1.38	2e−16	1e−16	3 x 50	family with sequence similarity 3, member D [Source:HGNC
15	163351	1.72	2e−16	1e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC Sy
16	9245	1.28	2e−16	1e−16	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
17	2877	1.78	2e−16	1e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syı
18	29094	1.53	2e−16	1e−16	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
19	3860	1.57	2e−16	1e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
20	192666	2.53	2e−16	1e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	50.54	NULL	75 / 135	H.Tiss	WIRTH_Mucosa
2	26.54	NULL	14 / 21	CC	cornified envelope
3	23.49	NULL	19 / 53	BP	keratinocyte differentiation
4	22.87	NULL	8 / 19	BP	peptide cross−linking
5	22.72	NULL	16 / 42	BP	keratinization
6	18.94	NULL	78 / 572	Disease	GUDJ_psoriasis up
7	17.93	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
8	14.92	NULL	19 / 76	BP	epidermis development
9	14.5	NULL	3 / 12	BP	cellular aldehyde metabolic process
10	14.03	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
11	13.15	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
12	11.91	NULL	4 / 15	MF	retinol dehydrogenase activity
13	11.84	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
14	11.44	NULL	3 / 13	BP	retinoic acid metabolic process
15	11.14	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	11.12	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
17	11.01	NULL	7 / 38	BP	epithelial cell differentiation
18	10.41	NULL	14 / 186	MF	structural molecule activity
19	10.29	NULL	4 / 10	MF	RAGE receptor binding
20	10.17	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
21	10.09	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	9.9	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
23	9.74	NULL	4 / 39	BP	retinoid metabolic process
24	9.39	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
25	9.35	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
26	9.22	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
27	9.06	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
28	9.06	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
29	8.97	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
30	8.76	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
31	8.73	NULL	2 / 14	BP	cyclooxygenase pathway
32	8.72	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
33	8.63	NULL	4 / 44	BP	steroid metabolic process
34	8.42	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
35	8.38	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
36	8.16	NULL	6 / 82	CC	intermediate filament
37	8.1	NULL	5 / 21	CC	desmosome
38	8.04	NULL	2 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
39	7.95	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
40	7.77	NULL	5 / 13	H.Tiss	WIRTH_Tonsil

GW_209

Local Summary

%DE = 0.87

metagenes = 15

genes = 223

genes in genesets = 223

genes with fdr < 0.1 = 169 (12 + / 157 −)

genes with fdr < 0.05 = 166 (11 + / 155 −)

genes with fdr < 0.01 = 147 (11 + / 136 −)

<r> metagenes = 0.97

<r> genes = 0.41

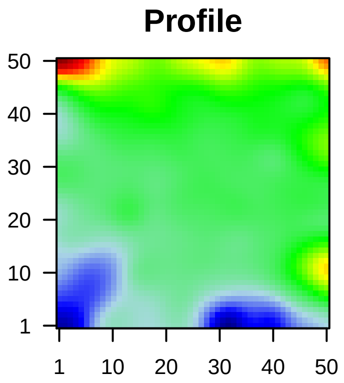
<FC> = −0.49

<shrinkage−t> = −17.26

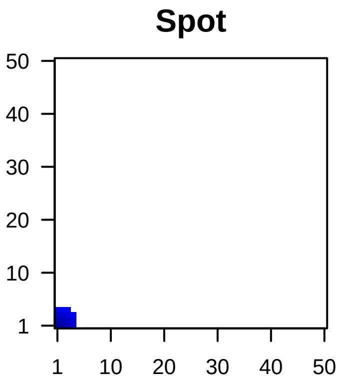
<p−value> = 0

<fdr> = 0.29

Profile



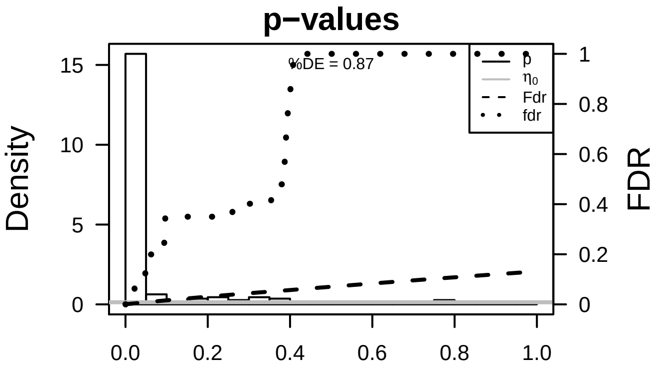
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	165	−1.27	2e−16	3e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
2	633	−1.75	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	414062	−1.54	2e−16	3e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbc
4	1277	−1.98	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	−1.63	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1281	−1.5	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
7	1289	−1.81	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	−1.41	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1291	−1.31	2e−16	3e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
10	1293	−1.47	2e−16	3e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	115908	−1.2	2e−16	3e−16	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
12	3040	−1.73	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
13	4312	−1.63	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
14	4314	−1.78	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
15	4318	−1.41	2e−16	3e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
16	25878	−1.47	2e−16	3e−16	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
17	10631	−1.38	2e−16	3e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
18	5743	1.28	2e−16	3e−16	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
19	7045	−1.12	2e−16	3e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
20	7058	−1.25	2e−16	3e−16	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−44.48	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−42.84	NULL	31 / 69	BP	extracellular matrix disassembly
3	−41.87	NULL	28 / 64	BP	collagen catabolic process
4	−41.04	NULL	57 / 190	CC	extracellular matrix
5	−40.26	NULL	7 / 11	MF	platelet−derived growth factor binding
6	−39.15	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
7	−33.62	NULL	62 / 242	BP	extracellular matrix organization
8	−30.27	NULL	64 / 250	Lymphoma	LENZ_Stromal signature 1
9	−29.87	NULL	8 / 12	miRNA target	miR−29c
10	−27.61	NULL	15 / 37	BP	collagen fibril organization
11	−27.6	NULL	19 / 57	MF	extracellular matrix structural constituent
12	−27.41	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
13	−24.69	NULL	11 / 40	BP	cellular response to amino acid stimulus
14	−23.79	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
15	−23.34	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
16	−23.07	NULL	4 / 10	BP	protein heterotrimerization
17	−22.81	NULL	11 / 19	MF	extracellular matrix binding
18	−22.56	NULL	16 / 68	CC	collagen
19	−22.19	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
20	−20.95	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
21	−20.86	NULL	35 / 183	CC	proteinaceous extracellular matrix
22	−20.83	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
23	−20.75	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
24	−19.89	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
25	−19.22	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
26	−19.18	NULL	25 / 153	CC	endoplasmic reticulum lumen
27	−18.47	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
28	−18.32	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
29	−18.32	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
30	−18.32	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
31	−18.32	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
32	−18.27	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
33	−18.19	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
34	−17.99	NULL	5 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
35	−17.78	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
36	−17.7	NULL	90 / 1182	CC	extracellular region
37	−17.34	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
38	−17.15	NULL	4 / 16	GSEA C2	REACTOME_AXON_GUIDANCE
39	−17.15	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
40	−17.05	NULL	20 / 83	CC	basement membrane

GW_209

Local Summary

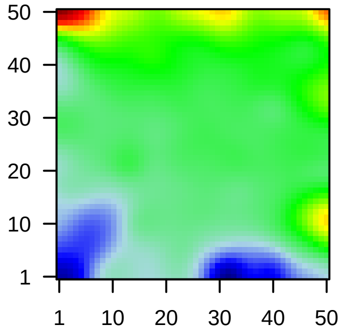
%DE = 0.91
metagenes = 16
genes = 163
genes in genesets = 160

genes with fdr < 0.1 = 127 (1 + / 126 −)
genes with fdr < 0.05 = 123 (1 + / 122 −)
genes with fdr < 0.01 = 113 (0 + / 113 −)

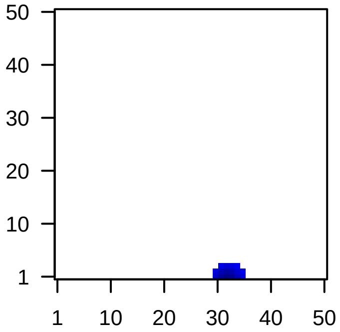
<r> metagenes = 0.96
<r> genes = 0.38

<FC> = −0.69
<shrinkage−t> = −24.22
<p−value> = 0
<fdr> = 0.26

Profile



Spot



Local Genelist

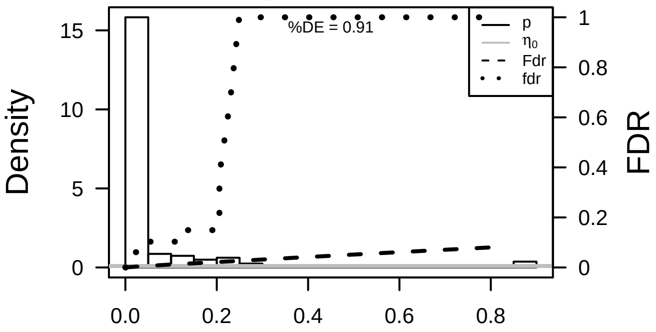
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−2.26	2e−16	1e−16	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	3627	−1.78	2e−16	1e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
3	94240	−2.07	2e−16	1e−16	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
4	51191	−1.93	2e−16	1e−16	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
5	3106	−1.55	2e−16	1e−16	32 x 1	major histocompatibility complex, class I, B [Source:HGNC S
6	3430	−1.3	2e−16	1e−16	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
7	10561	−1.89	2e−16	1e−16	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
8	10964	−1.94	2e−16	1e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
9	2537	−2.48	2e−16	1e−16	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
10	3433	−1.63	2e−16	1e−16	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
11	8519	−1.33	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
12	10410	−1.16	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
13	9636	−2.69	2e−16	1e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
14	4061	−1.24	2e−16	1e−16	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
15	4321	−1.26	2e−16	1e−16	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
16	4599	−1.52	2e−16	1e−16	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
17	4600	−1.31	2e−16	1e−16	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
18	85441	−1.38	2e−16	1e−16	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
19	51296	−1.32	2e−16	1e−16	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [
20	6772	−1.31	2e−16	1e−16	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−55.14	NULL	29 / 51	BP	type I interferon signaling pathway
2	−53.81	NULL	12 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	−48.77	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	−48.68	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	−45.03	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	−45	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
7	−43.86	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
8	−41.14	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
9	−40.52	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	−38.74	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
11	−38.07	NULL	15 / 31	BP	negative regulation of viral genome replication
12	−37.48	NULL	33 / 123	BP	defense response to virus
13	−36.17	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
14	−35.22	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
15	−33.39	NULL	27 / 109	BP	response to virus
16	−32.39	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
17	−30.51	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
18	−30.2	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
19	−29.95	NULL	34 / 204	BP	cytokine−mediated signaling pathway
20	−29.12	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
21	−28.73	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	−28.5	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
23	−26.77	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
24	−26.65	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
25	−26.49	NULL	7 / 10	CC	MHC class I protein complex
26	−26.16	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
27	−25.93	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
28	−24.4	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
29	−24.38	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
30	−24.3	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
31	−24.03	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
32	−23.38	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
33	−23.27	NULL	49 / 572	Disease	GUDJ_psoriasis up
34	−21.62	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
35	−21.37	NULL	3 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
36	−21.3	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
37	−21.3	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
38	−21.22	NULL	6 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
39	−21.14	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
40	−20.46	NULL	8 / 18	MF	peptide antigen binding

p−values



GW_209

Local Summary

%DE = 0.97

metagenes = 2

genes = 106

genes in genesets = 86

genes with fdr < 0.1 = 101 (0 + / 101 −)

genes with fdr < 0.05 = 99 (0 + / 99 −)

genes with fdr < 0.01 = 83 (0 + / 83 −)

<r> metagenes = 1

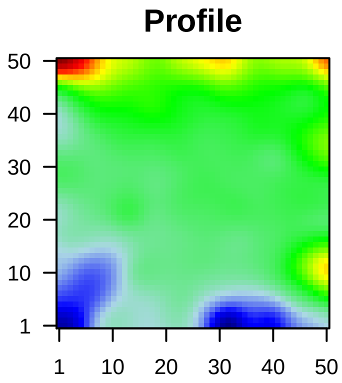
<r> genes = 0.66

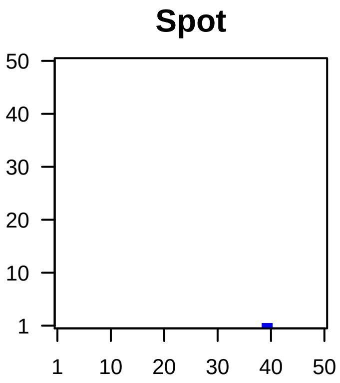
<FC> = −0.46

<shrinkage−t> = −16.16

<p−value> = 0

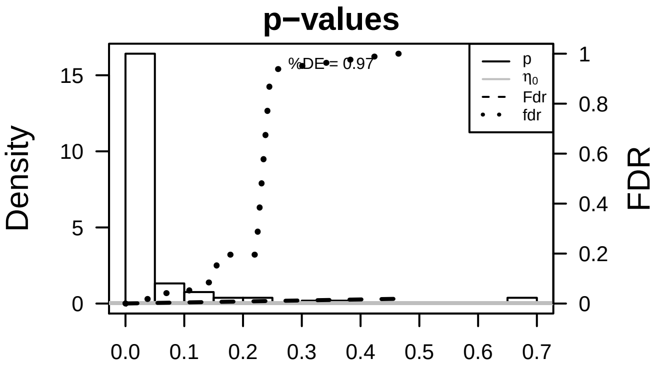
<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84061	−1.06	4e−13	1e−12	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
2	400818	−1.04	7e−13	3e−09	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
3	641737	−0.82	1e−09	3e−09	40 x 1	
4	100132406	−0.87	2e−09	3e−08	39 x 1	neuroblastoma breakpoint family, member 10 [Source:HGNC
5	136051	−0.83	1e−08	4e−07	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
6	25862	−0.77	1e−07	6e−07	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
7	319085	−0.73	4e−07	6e−07	39 x 1	ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
8	399900	−0.67	6e−07	6e−07	39 x 1	
9	7813	−0.72	8e−07	1e−06	40 x 1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:3
10	400866	−0.71	1e−06	1e−06	39 x 1	long intergenic non−protein coding RNA 114 [Source:HGNC
11	23162	−0.7	1e−06	1e−06	39 x 1	mitogen−activated protein kinase 8 interacting protein 3 [Sou
12	91368	−0.64	2e−06	5e−06	39 x 1	CDKN2A interacting protein N−terminal like [Source:HGNC S
13	100128274	−0.67	5e−06	5e−06	39 x 1	
14	3586	−0.61	6e−06	5e−06	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
15	90586	−0.64	1e−05	5e−06	39 x 1	amine oxidase, copper containing 4, pseudogene [Source:HG
16	85452	−0.64	1e−05	5e−06	39 x 1	chromosome 1 open reading frame 222 [Source:HGNC Sym
17	8548	−0.63	1e−05	5e−06	39 x 1	basic leucine zipper nuclear factor 1 [Source:HGNC Symbol;
18	1762	−0.63	1e−05	5e−06	40 x 1	dystrophia myotonica, WD repeat containing [Source:HGNC
19	440275	−0.63	1e−05	5e−06	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
20	9747	−0.58	1e−05	2e−05	39 x 1	family with sequence similarity 115, member A [Source:HGN



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−21.04	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−14.25	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−13.05	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	−10.3	NULL	1 / 10	CC	oligosaccharyltransferase complex
5	−9.71	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
6	−9.66	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
7	−9.45	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
8	−8.82	NULL	1 / 13	MF	magnesium ion transmembrane transporter activity
9	−8.66	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
10	−8.66	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	−8.44	NULL	1 / 14	BP	magnesium ion transport
12	−8.42	NULL	2 / 14	BP	cellular response to estradiol stimulus
13	−7.8	NULL	1 / 16	BP	cognition
14	−7.39	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
15	−7.25	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
16	−6.87	NULL	2 / 24	BP	negative regulation of T cell proliferation
17	−6.75	NULL	1 / 10	BP	lung morphogenesis
18	−6.37	NULL	1 / 11	CC	axolemma
19	−6.32	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
20	−6.32	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
21	−6.28	NULL	1 / 23	BP	protein N−linked glycosylation
22	−6.21	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
23	−6.21	NULL	1 / 12	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_DN
24	−5.97	NULL	1 / 11	BP	negative regulation of interleukin−12 production
25	−5.97	NULL	1 / 11	GSEA C2	SU_PANCREAS
26	−5.93	NULL	1 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
27	−5.92	NULL	1 / 13	GSEA C2	WANG_RESPONSE_TO_ANDROGEN_UP
28	−5.82	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
29	−5.76	NULL	1 / 13	BP	regulation of JNK cascade
30	−5.76	NULL	1 / 13	CC	smooth endoplasmic reticulum
31	−5.7	NULL	1 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
32	−5.66	NULL	1 / 12	BP	negative regulation of growth of symbiont in host
33	−5.66	NULL	1 / 14	GSEA C2	WANG_RESPONSE_TO_FORSKOLIN_UP
34	−5.5	NULL	1 / 14	MF	mitogen−activated protein kinase kinase binding
35	−5.5	NULL	1 / 14	GSEA C2	ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS
36	−5.43	NULL	1 / 10	BP	cellular response to peptide hormone stimulus
37	−5.43	NULL	1 / 10	BP	T−helper 1 type immune response
38	−5.39	NULL	1 / 13	BP	negative regulation of B cell proliferation
39	−5.39	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
40	−5.39	NULL	1 / 13	GSEA C2	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP