GW_192

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1739 (994 + / 745 −)

genes with fdr < 0.1 = 1396 (819 + / 577 −)

genes with fdr < 0.05 = 1085 (663 + / 422 −)

genes with fdr < 0.01 = 768 (508 + / 260 −)

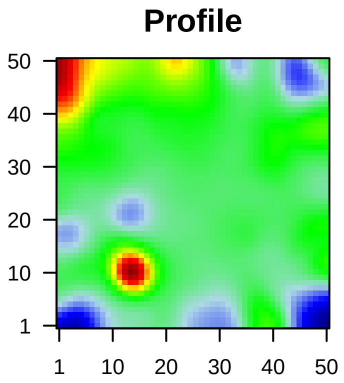
genes in genesets = 16332

<FC> = 0

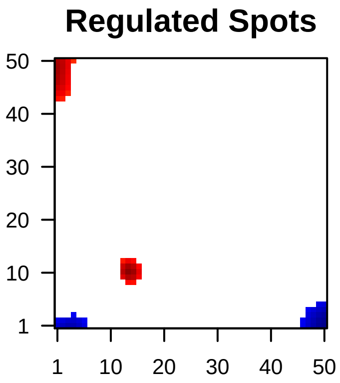
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



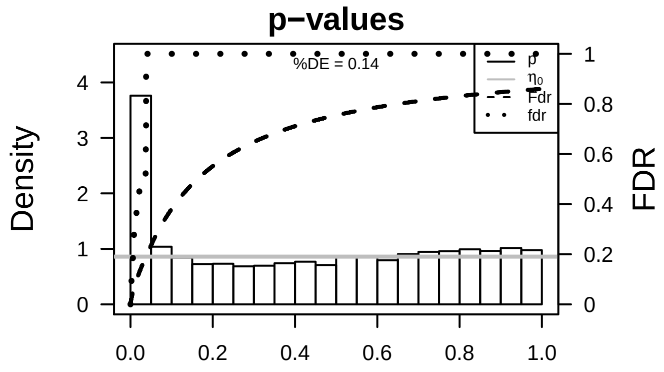
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	−1.3	2e−16	4e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	222	2.38	2e−16	4e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	131076	−1.39	2e−16	4e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
4	6347	−1.32	2e−16	4e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
5	948	2.31	2e−16	4e−14	6 x 44	CD36 molecule (thrombospondin receptor) [Source:HGNC S
6	22802	2.07	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	169044	1.62	2e−16	4e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
8	49860	1.73	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	2919	1.37	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimul
10	1577	1.74	2e−16	4e−14	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
11	1672	1.72	2e−16	4e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
12	2167	2.26	2e−16	4e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
13	2354	1.73	2e−16	4e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
14	729428	3.02	2e−16	4e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
15	729422	3.19	2e−16	4e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
16	100008586	2.49	2e−16	4e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
17	645073	3.01	2e−16	4e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	729442	3.19	2e−16	4e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	26748	2.77	2e−16	4e−14	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
20	729396	2.13	2e−16	4e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.97	NULL	135	H.Tiss	WIRTH_Mucosa
2	12.43	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
3	11.65	NULL	957	Chr	Chr 11
4	11.02	NULL	280	Chr	Chr 13
5	10.48	NULL	76	BP	epidermis development
6	8.32	NULL	618	Chr	Chr 4
7	7.99	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
8	7.93	NULL	714	Chr	Chr 6
9	7.85	NULL	10	GSEA C2	BIOCARTA_PPARA_PATHWAY
10	7.71	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
11	7.06	NULL	53	BP	keratinocyte differentiation
12	6.65	NULL	24	TF Tissue	VAQUERIZAS_Trachea
13	6.59	NULL	82	CC	intermediate filament
14	6.32	NULL	44	CC	keratin filament
15	6.29	NULL	4640	CC	nucleus
16	6.26	NULL	10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
17	6.11	NULL	16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
18	6.06	NULL	823	MF	sequence−specific DNA binding transcription factor activity
19	5.93	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
20	5.87	NULL	1749	MF	DNA binding
Underexpressed					
1	−10.65	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−10.65	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−9.66	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	−8.37	NULL	190	CC	extracellular matrix
5	−8.29	NULL	449	Chr	Chr 20
6	−7.86	NULL	699	Chr	Chr 5
7	−7.44	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	−7.06	NULL	386	Chr	Chr 22
9	−7.01	NULL	232	Chr	Chr 18
10	−6.83	NULL	683	CC	extracellular space
11	−6.62	NULL	417	H.Tiss	WIRTH_Immune system
12	−6.57	NULL	152	BP	cellular metabolic process
13	−6.52	NULL	530	Cancer	Lembcke_Normal vs Adenoma
14	−6.44	NULL	183	CC	proteinaceous extracellular matrix
15	−6.21	NULL	83	BP	respiratory electron transport chain
16	−6.21	NULL	153	MF	structural constituent of ribosome
17	−5.99	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	−5.99	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	−5.99	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	−5.99	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down

GW_192

Local Summary

%DE = 0.72

metagenes = 17

genes = 82

genes in genesets = 58

genes with fdr < 0.1 = 50 (49 + / 1 −)

genes with fdr < 0.05 = 49 (49 + / 0 −)

genes with fdr < 0.01 = 44 (44 + / 0 −)

<r> metagenes = 0.98

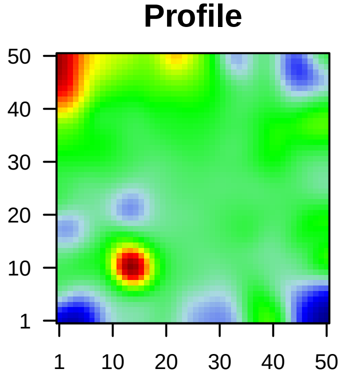
<r> genes = 0.33

<FC> = 0.85

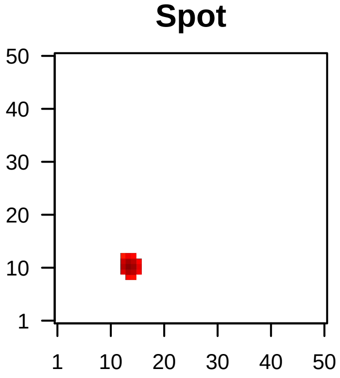
<shrinkage−t> = 29.85

<p−value> = 0

<fdr> = 0.36



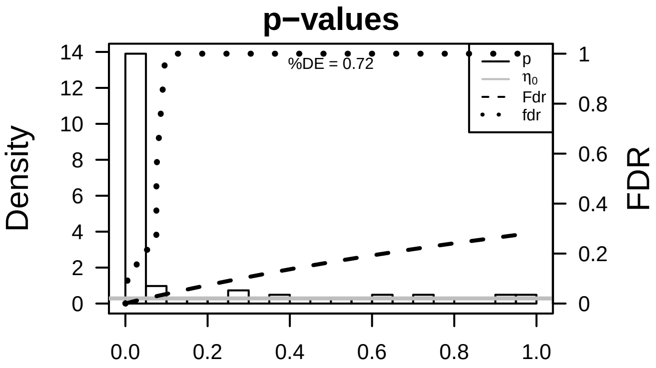
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	3.02	2e−16	3e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	3.19	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100008586	2.49	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	645073	3.01	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	729442	3.19	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	26748	2.77	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
7	729396	2.13	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
8	729447	2.14	2e−16	3e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
9	645037	3.43	2e−16	3e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
10	26749	2.28	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
11	2576	3.06	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
12	2577	2.94	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2578	1.6	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2579	1.87	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
15	100101629	1.66	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
16	4100	1.76	2e−16	3e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
17	55655	1.63	2e−16	3e−16	15 x 11	NLR family, pyrin domain containing 2 [Source:HGNC Symbo
18	5746	1.34	2e−16	3e−16	14 x 10	parathyroid hormone 2 receptor [Source:HGNC Symbol;Acc:
19	441520	1.14	6e−13	5e−12	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
20	51481	1.14	6e−13	5e−12	13 x 11	variable charge, X−linked 3A [Source:HGNC Symbol;Acc:181



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.38	NULL	1 / 2	miRNA target	miR−107
2	17.19	NULL	30 / 630	Chr	Chr X
3	14.2	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
4	13.92	NULL	3 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
5	8.38	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
6	7.97	NULL	1 / 17	BP	positive regulation of interleukin−1 beta secretion
7	7.91	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
8	7.56	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
9	7.33	NULL	1 / 5	miRNA target	miR−181a
10	6.63	NULL	1 / 7	GSEA C2	REACTOME_AMINE_LIGAND_BINDING_RECEPTORS
11	6.36	NULL	1 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16
12	6.36	NULL	1 / 6	miRNA target	miR−181b
13	6.3	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
14	5.91	NULL	1 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
15	5.73	NULL	1 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_DN
16	5.67	NULL	1 / 7	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9
17	5.03	NULL	2 / 23	BP	calcium−dependent cell−cell adhesion
18	4.94	NULL	1 / 37	BP	positive regulation of cysteine−type endopeptidase activity involved
19	4.78	NULL	1 / 21	BP	chromatin organization
20	4.76	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
21	4.51	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
22	4.41	NULL	1 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_DN
23	4.41	NULL	1 / 10	miRNA target	hsa−miR−933
24	4.33	NULL	1 / 13	BP	positive regulation of smooth muscle contraction
25	4.23	NULL	1 / 13	CC	mitochondrial respiratory chain
26	4.02	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
27	4.01	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
28	3.94	NULL	1 / 15	GSEA C2	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_ACE
29	3.89	NULL	1 / 12	BP	organ growth
30	3.77	NULL	1 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
31	3.73	NULL	2 / 37	BP	synapse assembly
32	3.69	NULL	9 / 549	MF	molecular_function
33	3.69	NULL	2 / 48	Cancer	KUIPER_MM poor survival
34	3.68	NULL	1 / 68	MF	histone deacetylase binding
35	3.64	NULL	1 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
36	3.64	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
37	3.63	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
38	3.63	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
39	3.49	NULL	1 / 18	BP	smooth muscle contraction
40	3.48	NULL	1 / 16	GSEA C2	JAEGER_METASTASIS_UP

GW_192

Local Summary

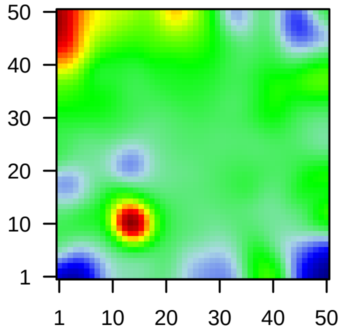
%DE = 0.73
metagenes = 24
genes = 334
genes in genesets = 326

genes with fdr < 0.1 = 196 (160 + / 36 −)
genes with fdr < 0.05 = 162 (135 + / 27 −)
genes with fdr < 0.01 = 150 (129 + / 21 −)

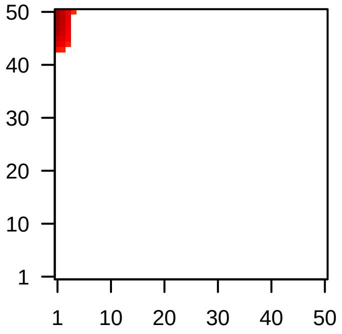
<r> metagenes = 0.89
<r> genes = 0.37

<FC> = 0.36
<shrinkage−t> = 12.67
<p−value> = 0
<fdr> = 0.46

Profile

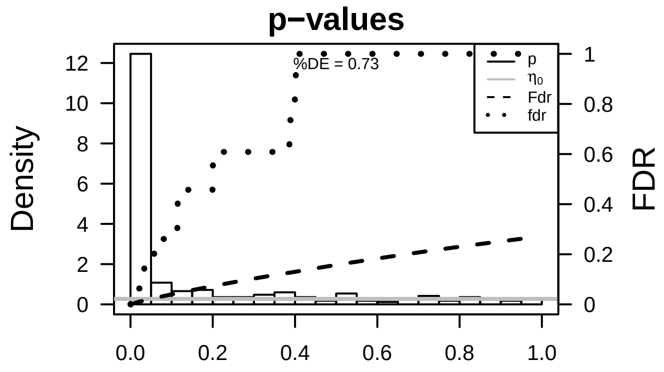


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	222	2.38	2e−16	7e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
2	22802	2.07	2e−16	7e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
3	49860	1.73	2e−16	7e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
4	1577	1.74	2e−16	7e−16	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
5	1672	1.72	2e−16	7e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
6	2167	2.26	2e−16	7e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
7	2697	1.64	2e−16	7e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
8	2706	1.25	2e−16	7e−16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
9	10804	1.77	2e−16	7e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
10	2941	1.38	2e−16	7e−16	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
11	1839	1.56	2e−16	7e−16	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Sym
12	53833	1.63	2e−16	7e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
13	3848	3.24	2e−16	7e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
14	3858	1.76	2e−16	7e−16	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]
15	3860	1.47	2e−16	7e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	2.05	2e−16	7e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
17	3851	2.44	2e−16	7e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
18	3934	1.63	2e−16	7e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
19	8581	1.52	2e−16	7e−16	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
20	118430	1.74	2e−16	7e−16	2 x 44	mucin−like 1 [Source:HGNC Symbol;Acc:30588]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.36	NULL	92 / 135	H.Tiss	WIRTH_Mucosa
2	21.38	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	18.8	NULL	21 / 82	CC	intermediate filament
4	18.64	NULL	29 / 76	BP	epidermis development
5	16.9	NULL	13 / 44	CC	keratin filament
6	15.95	NULL	24 / 53	BP	keratinocyte differentiation
7	15.78	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
8	15.39	NULL	5 / 10	MF	RAGE receptor binding
9	14.48	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
10	14.47	NULL	4 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
11	14.46	NULL	118 / 572	Disease	GUDJ_psoriasis up
12	13.78	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
13	13.25	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	12.46	NULL	2 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
15	12.43	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	12.28	NULL	18 / 21	CC	cornified envelope
17	12.17	NULL	3 / 15	CC	connexon complex
18	12	NULL	6 / 16	GSEA C2	JAEGER_METASTASIS_DN
19	11.96	NULL	3 / 15	GSEA C2	STOSSI_RESPONSE_TO_ESTRADIOL
20	11.95	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
21	11.92	NULL	10 / 19	BP	peptide cross−linking
22	11.78	NULL	30 / 186	MF	structural molecule activity
23	11.34	NULL	2 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
24	10.89	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
25	10.7	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
26	10.65	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
27	10.62	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
28	10.49	NULL	4 / 21	CC	gap junction
29	10.45	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	10.03	NULL	10 / 38	BP	epithelial cell differentiation
31	9.9	NULL	3 / 12	BP	cellular aldehyde metabolic process
32	9.51	NULL	2 / 10	MF	gap junction channel activity
33	9.44	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
34	9.16	NULL	12 / 21	CC	desmosome
35	8.96	NULL	3 / 10	BP	chronic inflammatory response
36	8.86	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
37	8.86	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
38	8.77	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
39	8.73	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
40	8.59	NULL	2 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP

GW_192

Local Summary

%DE = 0.81

metagenes = 13

genes = 231

genes in genesets = 230

genes with fdr < 0.1 = 138 (16 + / 122 −)

genes with fdr < 0.05 = 121 (15 + / 106 −)

genes with fdr < 0.01 = 96 (12 + / 84 −)

<r> metagenes = 0.97

<r> genes = 0.43

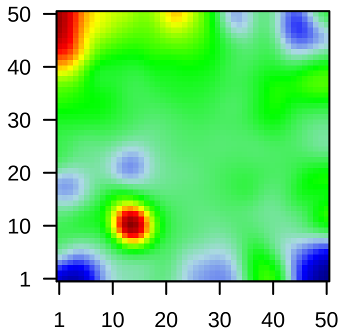
<FC> = −0.32

<shrinkage−t> = −11.32

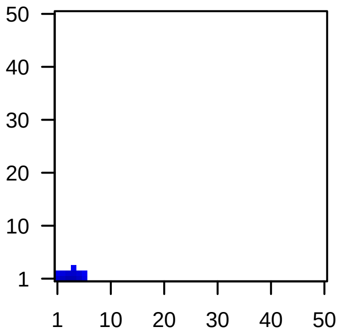
<p−value> = 0

<fdr> = 0.46

Profile



Spot



Local Genelist

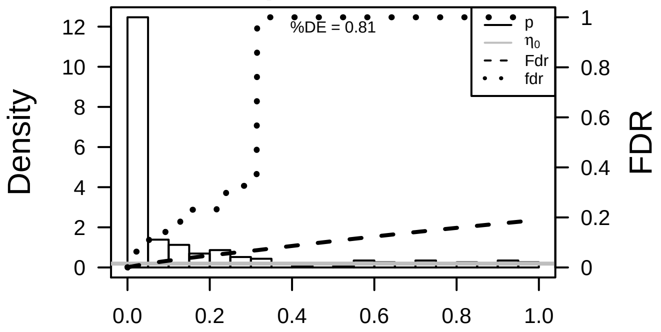
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	−1.3	2e−16	1e−15	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	2919	1.37	2e−16	1e−15	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
3	4311	1.3	2e−16	1e−15	2 x 1	membrane metallo−endopeptidase [Source:HGNC Symbol;A
4	4312	−1.67	2e−16	1e−15	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
5	4314	−1.76	2e−16	1e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
6	4692	1.57	2e−16	1e−15	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
7	144165	1.46	2e−16	1e−15	5 x 1	prickle homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:1
8	25907	−1.18	9e−14	2e−12	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HGN
9	6372	−1.18	1e−13	3e−11	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
10	3553	−1.13	8e−13	8e−11	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
11	84624	−1.11	3e−12	8e−10	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
12	7058	−1.05	3e−11	8e−10	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
13	1307	1.04	4e−11	8e−10	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
14	7045	−0.95	6e−11	2e−09	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
15	23213	−1.02	1e−10	5e−09	2 x 1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]
16	1513	−0.98	6e−10	5e−09	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
17	10962	−0.98	6e−10	5e−09	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
18	1462	−0.98	6e−10	5e−09	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
19	4322	0.98	6e−10	5e−09	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
20	7070	−0.97	7e−10	4e−08	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−29.46	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−27.19	NULL	63 / 190	CC	extracellular matrix
3	−24.95	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	−24.54	NULL	70 / 250	Lymphoma	LENZ_Stromal signature 1
5	−18.95	NULL	10 / 35	Glio	Colman_survival_associated
6	−17.91	NULL	57 / 242	BP	extracellular matrix organization
7	−16.92	NULL	30 / 69	BP	extracellular matrix disassembly
8	−16.88	NULL	5 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
9	−16.08	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	−15.97	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
11	−15.95	NULL	5 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
12	−15.45	NULL	4 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
13	−15.42	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	−15.26	NULL	8 / 12	miRNA target	miR−29c
15	−15.05	NULL	26 / 64	BP	collagen catabolic process
16	−14.83	NULL	8 / 11	MF	platelet−derived growth factor binding
17	−14.15	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
18	−14.11	NULL	33 / 183	CC	proteinaceous extracellular matrix
19	−13.48	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
20	−13.45	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
21	−13.37	NULL	11 / 19	MF	extracellular matrix binding
22	−13.24	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
23	−12.99	NULL	3 / 14	GSEA C2	OZANNE_AP1_TARGETS_UP
24	−12.97	NULL	92 / 1182	CC	extracellular region
25	−12.7	NULL	67 / 683	CC	extracellular space
26	−12.25	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
27	−11.97	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
28	−11.81	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
29	−11.78	NULL	3 / 15	Cancer	LIU_PROSTATE_CANCER_DN
30	−11.75	NULL	4 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
31	−11.68	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
32	−11.61	NULL	19 / 57	MF	extracellular matrix structural constituent
33	−11.6	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
34	−11.53	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
35	−11.3	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
36	−11.26	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
37	−11.1	NULL	3 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
38	−11.04	NULL	4 / 16	GSEA C2	HENDRICKS_SMARCA4_TARGETS_UP
39	−11	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
40	−10.75	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN

p−values



GW_192

Local Summary

%DE = 0.81

metagenes = 20

genes = 311

genes in genesets = 309

genes with fdr < 0.1 = 175 (13 + / 162 −)

genes with fdr < 0.05 = 166 (13 + / 153 −)

genes with fdr < 0.01 = 80 (10 + / 70 −)

<r> metagenes = 0.98

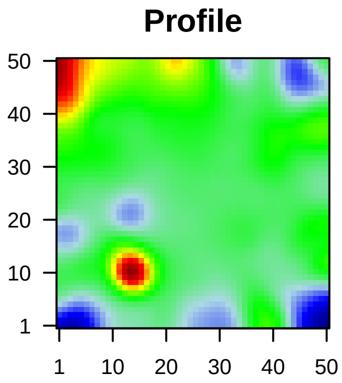
<r> genes = 0.56

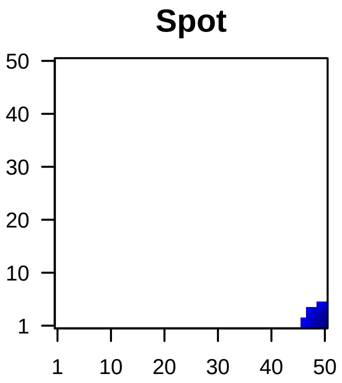
<FC> = −0.28

<shrinkage−t> = −9.78

<p−value> = 0.01

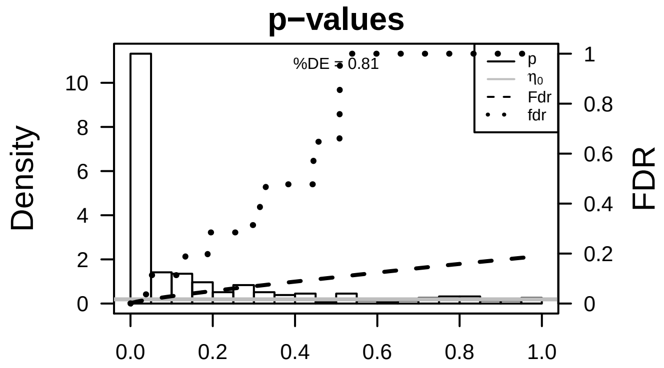
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6347	−1.32	2e−16	4e−15	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
2	3512	1.61	2e−16	4e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	10365	1.31	2e−16	4e−15	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
4	894	1.2	3e−14	9e−12	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
5	1545	1.16	2e−13	4e−10	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
6	23231	1.09	7e−12	3e−07	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
7	10563	−0.92	7e−09	3e−07	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
8	347733	−0.9	1e−08	3e−07	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
9	10791	−0.89	2e−08	3e−07	50 x 4	vesicle−associated membrane protein 5 [Source:HGNC Sym
10	5341	−0.89	2e−08	2e−06	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
11	260436	−0.86	5e−08	5e−06	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
12	10537	−0.84	1e−07	7e−06	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	2219	−0.82	2e−07	1e−05	50 x 5	ficolin (collagen/fibrinogen domain containing) 1 [Source:HG
14	55303	−0.79	6e−07	1e−05	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
15	2	−0.79	6e−07	3e−05	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
16	7412	−0.77	1e−06	4e−05	50 x 1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
17	3620	−0.76	2e−06	5e−05	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
18	3398	−0.74	3e−06	1e−04	49 x 5	inhibitor of DNA binding 2, dominant negative helix−loop−heli
19	2113	−0.72	6e−06	1e−04	50 x 3	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
20	2634	0.71	7e−06	1e−04	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HG



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.88	NULL	95 / 417	H.Tiss	WIRTH_Immune system
2	−20.56	NULL	103 / 553	Cancer	Lembcke_Colonic Inflammation
3	−19.35	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
4	−19.15	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
5	−17.54	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−15.47	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
7	−15.18	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
8	−15.18	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
9	−15.18	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
10	−15.18	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
11	−14.44	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
12	−13.41	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
13	−13.19	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
14	−12.74	NULL	5 / 12	BP	dendritic cell chemotaxis
15	−12.6	NULL	8 / 43	MF	chemokine activity
16	−12.31	NULL	18 / 74	BP	regulation of immune response
17	−12.24	NULL	5 / 15	GSEA C2	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
18	−12.1	NULL	2 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
19	−11.39	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	−11.23	NULL	8 / 16	GSEA C2	SU_THYMUS
21	−10.64	NULL	4 / 21	BP	cellular response to interferon−gamma
22	−10.57	NULL	4 / 14	BP	ruffle organization
23	−10.41	NULL	5 / 27	BP	lipopolysaccharide−mediated signaling pathway
24	−10.14	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
25	−10.03	NULL	25 / 162	CC	external side of plasma membrane
26	−10.02	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
27	−10.01	NULL	2 / 12	BP	macrophage chemotaxis
28	−10.01	NULL	2 / 12	GSEA C2	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
29	−9.84	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
30	−9.69	NULL	27 / 269	BP	inflammatory response
31	−9.66	NULL	3 / 21	BP	chemokine−mediated signaling pathway
32	−9.66	NULL	9 / 43	BP	positive regulation of T cell proliferation
33	−9.64	NULL	3 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN
34	−9.61	NULL	1 / 6	GSEA C2	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP
35	−9.55	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
36	−9.42	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
37	−9.37	NULL	55 / 312	BP	immune response
38	−9.28	NULL	2 / 10	BP	chronic inflammatory response
39	−9.25	NULL	3 / 13	GSEA C2	ZIRN_TRETINOIN_RESPONSE_UP
40	−9.25	NULL	3 / 7	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN