

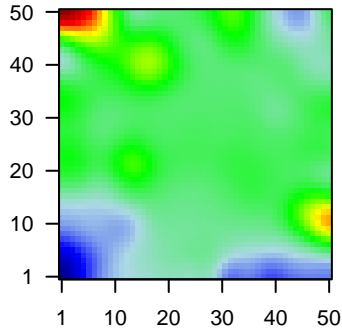
GW_237

Global Summary

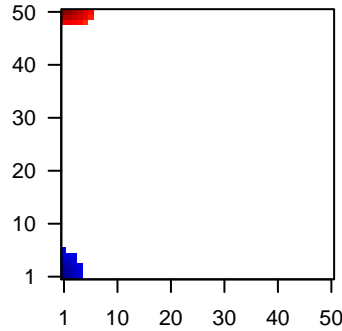
%DE = 0.14
 # genes with fdr < 0.2 = 1874 (985 + / 889 -)
 # genes with fdr < 0.1 = 1514 (819 + / 695 -)
 # genes with fdr < 0.05 = 1359 (737 + / 622 -)
 # genes with fdr < 0.01 = 888 (500 + / 388 -)
 # genes in genesets = 16332

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

Profile



Regulated Spots



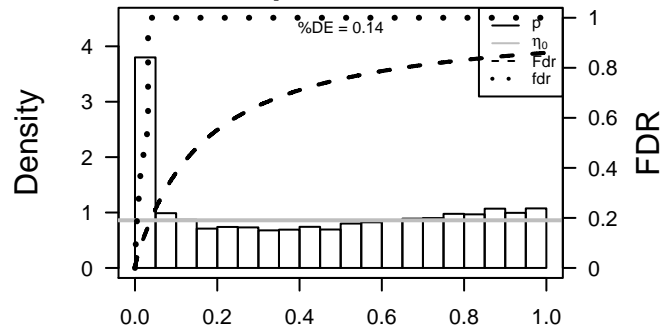
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.01	2e-16	3e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.59	2e-16	3e-14	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.6	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	216	2.09	2e-16	3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	374569	1.77	2e-16	3e-14	4 x 50 asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
6	684	-1.55	2e-16	3e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
7	387695	1.8	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
8	64073	1.65	2e-16	3e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Symt
9	92747	2.87	2e-16	3e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbo
10	391267	1.57	2e-16	3e-14	50 x 13 ankyrin repeat domain 20 family, member A11, pseudogene [
11	29113	3.07	2e-16	3e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
12	394263	2.15	2e-16	3e-14	3 x 50
13	375791	2.55	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
14	84290	1.56	2e-16	3e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
15	414062	-1.59	2e-16	3e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
16	634	1.64	2e-16	3e-14	50 x 12 carcinoembryonic antigen-related cell adhesion molecule 1 (l
17	1048	2.29	2e-16	3e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 (l
18	4680	2.28	2e-16	3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (l
19	1087	1.91	2e-16	3e-14	4 x 50 carcinoembryonic antigen-related cell adhesion molecule 7 (l
20	84952	1.6	2e-16	3e-14	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	30.87	NULL	135	H.Tiss WIRTH_Mucosa
2	11.99	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
3	11.93	NULL	21	CC cornified envelope
4	9.24	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
5	8.53	NULL	53	BP keratinocyte differentiation
6	8.34	NULL	16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
7	7.96	NULL	15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
8	7.76	NULL	15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
9	7.76	NULL	81	BP viral transcription
10	7.76	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
11	7.57	NULL	153	MF structural constituent of ribosome
12	7.56	NULL	87	BP translational termination
13	7.53	NULL	92	BP translational elongation
14	7.39	NULL	42	BP keratinization
15	7.33	NULL	83	BP respiratory electron transport chain
16	7.26	NULL	16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
17	7.25	NULL	119	BP xenobiotic metabolic process
18	7.25	NULL	152	BP cellular metabolic process
19	7.22	NULL	128	BP translational initiation
20	6.94	NULL	16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
<i>Underexpressed</i>				
1	-16.11	NULL	553	Cancer Lembecke_Colonc Inflammation
2	-14.9	NULL	242	BP extracellular matrix organization
3	-13.98	NULL	64	BP collagen catabolic process
4	-13.9	NULL	69	BP extracellular matrix disassembly
5	-13.55	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
6	-12.96	NULL	250	LymphomaLENZ_Stromal signature 1
7	-12.19	NULL	190	CC extracellular matrix
8	-11.78	NULL	11	MF platelet-derived growth factor binding
9	-11.27	NULL	403	BP cell adhesion
10	-10.47	NULL	83	CC basement membrane
11	-10.37	NULL	12	miRNA target-29c
12	-10.08	NULL	153	CC endoplasmic reticulum lumen
13	-9.98	NULL	51	BP type I interferon signaling pathway
14	-9.94	NULL	8023	MF protein binding
15	-9.8	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
16	-9.76	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
17	-9.76	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
18	-9.76	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
19	-9.76	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
20	-9.73	NULL	16	MMML C2SCIEJ_MMML 1

p-values



GW_237

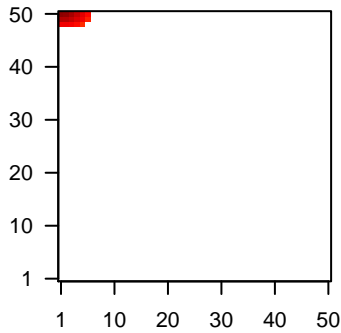
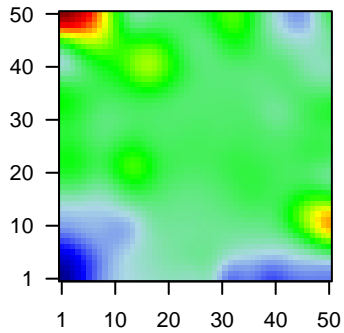
Local Summary

%DE = 0.95
 # metagenes = 17
 # genes = 259
 # genes in genesets = 254
 # genes with $fdr < 0.1$ = 237 (233 + / 4 -)
 # genes with $fdr < 0.05$ = 236 (232 + / 4 -)
 # genes with $fdr < 0.01$ = 235 (232 + / 3 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.44
 $\langle FC \rangle = 1.19$
 $\langle \text{shrinkage-t} \rangle = 41.69$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.09$

Profile

Spot



Local Genelist

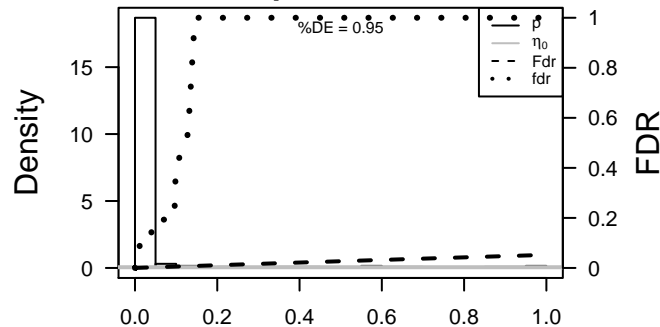
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.01	2e-16	5e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.59	2e-16	5e-17	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.6	2e-16	5e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	374569	1.77	2e-16	5e-17	4 x 50 asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
5	387695	1.8	2e-16	5e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
6	394263	2.15	2e-16	5e-17	3 x 50
7	375791	2.55	2e-16	5e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
8	84290	1.56	2e-16	5e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	1048	2.29	2e-16	5e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
10	4680	2.28	2e-16	5e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
11	1087	1.91	2e-16	5e-17	4 x 50 carcinoembryonic antigen-related cell adhesion molecule 7 [
12	22802	2.64	2e-16	5e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	9022	2.13	2e-16	5e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
14	84518	2.08	2e-16	5e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	54544	1.99	2e-16	5e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
16	49860	3.23	2e-16	5e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1562	1.77	2e-16	5e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
18	1577	2.03	2e-16	5e-17	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
19	92196	1.96	2e-16	5e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
20	1672	1.9	2e-16	5e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	59.87	NULL	80 / 135	H.Tiss WIRTH_Mucosa
2	25.89	NULL	15 / 21	CC cornified envelope
3	22.18	NULL	85 / 572	Disease GUDJ_pсориазис up
4	20.32	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
5	19.48	NULL	20 / 53	BP keratinocyte differentiation
6	19.41	NULL	16 / 42	BP keratinization
7	16.11	NULL	9 / 19	BP peptide cross-linking
8	15.48	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	14.53	NULL	19 / 76	BP epidermis development
10	14.37	NULL	9 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
11	13.88	NULL	6 / 13	BP negative regulation of peptidase activity
12	13.05	NULL	7 / 38	BP epithelial cell differentiation
13	11.62	NULL	6 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
14	11.48	NULL	5 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
15	10.92	NULL	5 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
16	10.88	NULL	6 / 13	H.Tiss WIRTH_Tonsil
17	10.48	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
18	10.15	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
19	10.06	NULL	3 / 11	GSEA C2REACTOME_XENOBIOTICS
20	9.64	NULL	57 / 1182	CC extracellular region
21	9.46	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
22	9.19	NULL	11 / 79	MF serine-type endopeptidase inhibitor activity
23	9.13	NULL	5 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
24	9.04	NULL	7 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
25	8.99	NULL	8 / 83	CC anchored to membrane
26	8.95	NULL	13 / 122	MF serine-type endopeptidase activity
27	8.47	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
28	8.38	NULL	3 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
29	8.3	NULL	10 / 52	BP negative regulation of endopeptidase activity
30	8.3	NULL	6 / 29	BP regulation of proteolysis
31	8.29	NULL	3 / 16	GSEA C2CHECK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_
32	8.27	NULL	17 / 186	MF structural molecule activity
33	8.23	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
34	8.17	NULL	5 / 10	MF RAGE receptor binding
35	8.15	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
36	7.86	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
37	7.84	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
38	7.68	NULL	4 / 27	BP response to bacterium
39	7.66	NULL	3 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
40	7.65	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP

p-values



GW_237

Local Summary

%DE = 0.93
 # metagenes = 19
 # genes = 300
 # genes in genesets = 298

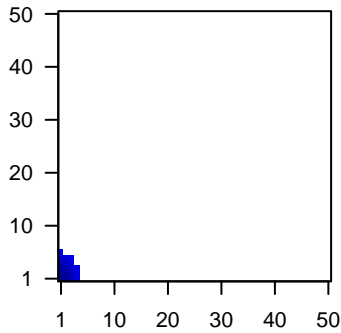
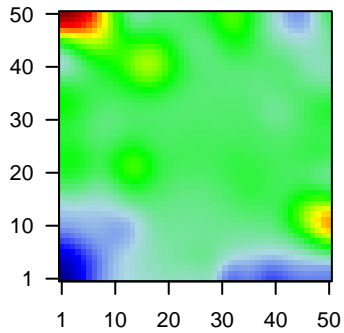
genes with $fdr < 0.1 = 263$ (4 + / 259 -)
 # genes with $fdr < 0.05 = 253$ (4 + / 249 -)
 # genes with $fdr < 0.01 = 225$ (3 + / 222 -)

<r> metagenes = 0.95
 <r> genes = 0.36

<FC> = -0.81
 <shrinkage-t> = -28.51
 <p-value> = 0
 <fdr> = 0.21

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	414062	-1.59	2e-16	2e-16	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:2197]
2	1277	-2.68	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	-2.26	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	-1.99	2e-16	2e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1282	-1.84	2e-16	2e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
6	1289	-1.95	2e-16	2e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1290	-1.62	2e-16	2e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	1291	-1.63	2e-16	2e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
9	1293	-2.07	2e-16	2e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	1294	-1.68	2e-16	2e-16	1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
11	2919	-1.55	2e-16	2e-16	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula
12	3491	-1.74	2e-16	2e-16	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
13	10468	-1.55	2e-16	2e-16	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
14	3553	-1.95	2e-16	2e-16	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
15	3576	-2.32	2e-16	2e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
16	3678	-1.67	2e-16	2e-16	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
17	4312	-2.45	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi
18	4320	-1.94	2e-16	2e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
19	4314	-2.43	2e-16	2e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
20	4318	-2.21	2e-16	2e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9;

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-36.92	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
2	-36.78	NULL	32 / 69	BP extracellular matrix disassembly
3	-36.35	NULL	70 / 242	BP extracellular matrix organization
4	-36.24	NULL	29 / 64	BP collagen catabolic process
5	-35.32	NULL	59 / 190	CC extracellular matrix
6	-34.17	NULL	7 / 11	MF platelet-derived growth factor binding
7	-33.04	NULL	15 / 16	MMML C2SCIEJ_MMML 1
8	-30.51	NULL	8 / 12	miRNA target-29c
9	-29.9	NULL	69 / 250	Lymphocyte-stromal signature 1
10	-28.1	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
11	-25.66	NULL	16 / 37	BP collagen fibril organization
12	-23.96	NULL	21 / 57	MF extracellular matrix structural constituent
13	-21.98	NULL	12 / 19	MF extracellular matrix binding
14	-21.97	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
15	-21.9	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
16	-21.2	NULL	11 / 40	BP cellular response to amino acid stimulus
17	-21.19	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
18	-20.99	NULL	44 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
19	-20.99	NULL	44 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
20	-20.99	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
21	-20.99	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
22	-20.9	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
23	-20.85	NULL	76 / 683	CC extracellular space
24	-20.74	NULL	106 / 1182	CC extracellular region
25	-20.7	NULL	13 / 35	Glio Colman_survival_associated
26	-20.56	NULL	38 / 183	CC proteinaceous extracellular matrix
27	-20.13	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
28	-20.06	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
29	-19.98	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
30	-19.5	NULL	23 / 83	CC basement membrane
31	-19.03	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
32	-18.85	NULL	56 / 403	BP cell adhesion
33	-18.66	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
34	-18.61	NULL	65 / 553	Cancer Lembcke_Colonc Inflammation
35	-18.49	NULL	4 / 10	BP protein heterotrimerization
36	-18.15	NULL	6 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
37	-17.97	NULL	5 / 11	GSEA C2BIOCARTA_PLATELETAPP_PATHWAY
38	-17.81	NULL	27 / 153	CC endoplasmic reticulum lumen
39	-17.55	NULL	16 / 68	Glio cultured astroglia vs. in vivo astrocytes
40	-17.47	NULL	16 / 68	CC collagen

p-values

