

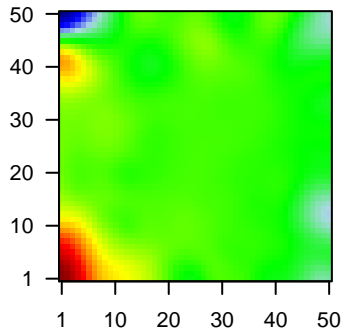
GW_220

Global Summary

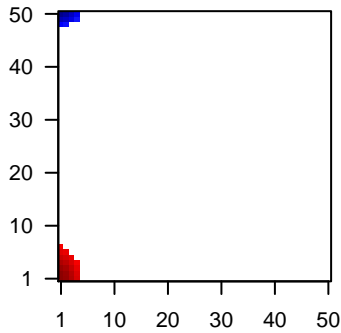
%DE = 0.16
 # genes with $fdr < 0.2$ = 2223 (1174 + / 1049 -)
 # genes with $fdr < 0.1$ = 1801 (971 + / 830 -)
 # genes with $fdr < 0.05$ = 1452 (799 + / 653 -)
 # genes with $fdr < 0.01$ = 1063 (594 + / 469 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.07
 <fdr> = 0.84

Profile



Regulated Spots



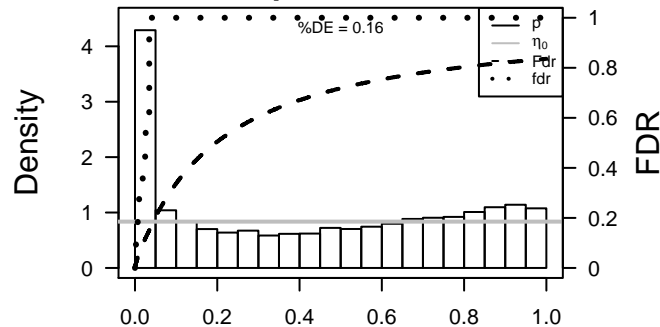
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-2.01	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	87	1.97	2e-16	2e-14	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
3	8728	1.7	2e-16	2e-14	50 x 3 ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
4	131	-2.77	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	113146	1.68	2e-16	2e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
6	57016	-2.98	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
7	441282	-1.9	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
8	216	-1.86	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	220	1.7	2e-16	2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
10	218	-3.24	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
11	222	-1.94	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
12	401138	2.21	2e-16	2e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
13	163782	1.68	2e-16	2e-14	1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
14	118429	1.74	2e-16	2e-14	2 x 1 anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
15	164284	2.35	2e-16	2e-14	1 x 3 adenomatosis polyposis coli down-regulated 1-like [Source:t
16	10409	2.14	2e-16	2e-14	1 x 2 brain abundant, membrane attached signal protein 1 [Source:
17	387695	-2.28	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
18	375791	-2.61	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
19	810	-1.5	2e-16	2e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
20	55450	1.8	2e-16	2e-14	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	19.87	NULL	250	LymphomaTENZ_Stromal signature 1
2	18.23	NULL	242	BP extracellular matrix organization
3	16.67	NULL	190	CC extracellular matrix
4	13.06	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
5	12.55	NULL	69	BP extracellular matrix disassembly
6	12.44	NULL	16	MMML C6SCIEJ_MMML 1
7	12.34	NULL	403	BP cell adhesion
8	12.22	NULL	386	Chr Chr 22
9	12.12	NULL	83	CC basement membrane
10	11.45	NULL	64	BP collagen catabolic process
11	11.2	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
12	10.96	NULL	183	CC proteinaceous extracellular matrix
13	10.58	NULL	57	MF extracellular matrix structural constituent
14	10.38	NULL	11	MF platelet-derived growth factor binding
15	9.89	NULL	153	CC endoplasmic reticulum lumen
16	9.7	NULL	299	BP axon guidance
17	9.5	NULL	37	BP collagen fibril organization
18	8.83	NULL	85	MF integrin binding
19	8.8	NULL	15	GSEA C2ONDER_CDH1_TARGETS_2_UP
20	8.66	NULL	10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
<i>Underexpressed</i>				
1	-28.21	NULL	135	H.Tiss WIRTH_Mucosa
2	-15.59	NULL	572	Disease GUDJ_psooriasis up
3	-14.25	NULL	21	CC cornified envelope
4	-13.11	NULL	42	BP keratinization
5	-11.45	NULL	8	GSEA C2LIU_CD_X2_TARGETS_DN
6	-10.25	NULL	53	BP keratinocyte differentiation
7	-10.01	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
8	-9.63	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	-9.13	NULL	1135	Chr Chr 19
10	-7.99	NULL	12	BP cellular aldehyde metabolic process
11	-7.83	NULL	19	BP peptide cross-linking
12	-7.41	NULL	13	H.Tiss WIRTH_Tonsil
13	-7.32	NULL	16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	-7.29	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
15	-7.28	NULL	232	Chr Chr 18
16	-7.03	NULL	14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
17	-7.01	NULL	304	CC mitochondrial inner membrane
18	-6.91	NULL	6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
19	-6.67	NULL	83	BP respiratory electron transport chain
20	-6.6	NULL	417	H.Tiss WIRTH_Immune system

p-values



GW_220

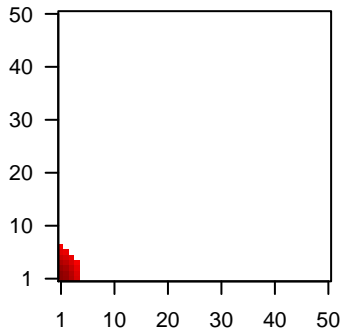
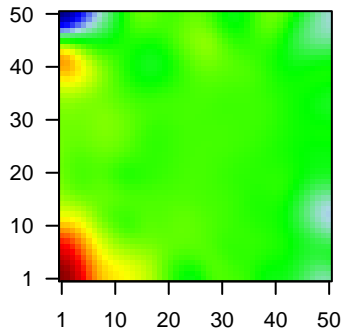
Local Summary

%DE = 0.91
 # metagenes = 22
 # genes = 343
 # genes in genesets = 341
 # genes with $fdr < 0.1$ = 298 (291 + / 7 -)
 # genes with $fdr < 0.05$ = 286 (280 + / 6 -)
 # genes with $fdr < 0.01$ = 273 (270 + / 3 -)

<r> metagenes = 0.94
 <r> genes = 0.34
 <FC> = 0.97
 <shrinkage-t> = 34.19
 <p-value> = 0
 <fdr> = 0.18

Profile

Spot



Local Genelist

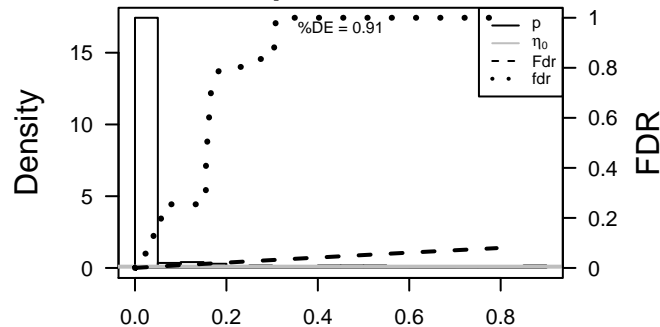
Rank	ID	log(FC)	fdr	p-value	Description
1	87	1.97	2e-16	1e-16	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	401138	2.21	2e-16	1e-16	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
3	163782	1.68	2e-16	1e-16	1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
4	118429	1.74	2e-16	1e-16	2 x 1 anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
5	164284	2.35	2e-16	1e-16	1 x 3 adenomatosis polyposis coli down-regulated 1-like [Source:t
6	10409	2.14	2e-16	1e-16	1 x 2 brain abundant, membrane attached signal protein 1 [Source:
7	55450	1.8	2e-16	1e-16	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [S
8	114335	1.75	2e-16	1e-16	1 x 7 chorionic gonadotropin, beta polypeptide [Source:HGNC Syrr
9	1277	1.9	2e-16	1e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
10	1278	1.91	2e-16	1e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
11	1281	1.83	2e-16	1e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
12	1289	2.06	2e-16	1e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
13	1290	2.25	2e-16	1e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
14	1291	2.06	2e-16	1e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
15	1293	1.86	2e-16	1e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
16	1464	1.83	2e-16	1e-16	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
17	115908	1.97	2e-16	1e-16	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
18	131566	1.92	2e-16	1e-16	1 x 4 discoidin, CUB and LCCL domain containing 2 [Source:HGNC
19	22943	1.82	2e-16	1e-16	1 x 7 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
20	27122	2.1	2e-16	1e-16	1 x 3 dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	34.45	NULL	15 / 16	MMML C63CIEJ_MMML 1
2	34.14	NULL	70 / 250	Lymphoma ENZ_Stromal signature 1
3	33.3	NULL	60 / 190	CC extracellular matrix
4	32.87	NULL	73 / 242	BP extracellular matrix organization
5	31.52	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	26.33	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
7	26.28	NULL	33 / 69	BP extracellular matrix disassembly
8	25.36	NULL	29 / 64	BP collagen catabolic process
9	24.58	NULL	7 / 11	MF platelet-derived growth factor binding
10	22.69	NULL	6 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
11	21.76	NULL	12 / 19	MF extracellular matrix binding
12	21.62	NULL	21 / 57	MF extracellular matrix structural constituent
13	21.58	NULL	60 / 403	BP cell adhesion
14	21.47	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
15	20.95	NULL	16 / 37	BP collagen fibril organization
16	20.6	NULL	8 / 12	miRNA target-29c
17	20.32	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
18	19.51	NULL	25 / 83	CC basement membrane
19	19.5	NULL	38 / 183	CC proteinaceous extracellular matrix
20	19.2	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
21	18.96	NULL	7 / 11	Glio Phillips MES up vs Prolif & PN
22	18.92	NULL	82 / 683	CC extracellular space
23	18.91	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
24	18.42	NULL	116 / 1182	CC extracellular region
25	18.25	NULL	24 / 119	Lymphoma OSOLOWSKI_green total
26	18.01	NULL	45 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
27	18.01	NULL	45 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
28	18.01	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
29	18.01	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
30	17.95	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
31	17.46	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
32	17.46	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
33	17.33	NULL	6 / 11	MMML C63CIEJ_MMML 31
34	17.3	NULL	13 / 35	Glio Colman_survival_associated
35	16.66	NULL	5 / 11	GSEA C2BIOCARTA_PLATELETAPP_PATHWAY
36	16.65	NULL	3 / 5	GSEA C2DASU_IL6_SIGNALING_UP
37	16.27	NULL	6 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
38	16.14	NULL	5 / 16	GSEA C2JRS_ADIPOCYTE_DIFFERENTIATION_DN
39	16.07	NULL	16 / 68	CC collagen
40	15.68	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP

p-values



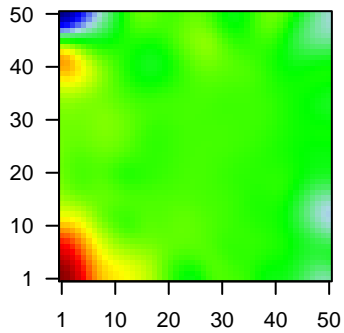
GW_220

Local Summary

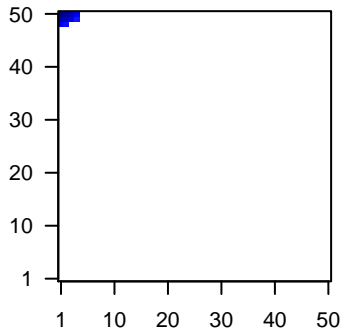
%DE = 0.99
 # metagenes = 10
 # genes = 164
 # genes in genesets = 161
 # genes with $fdr < 0.1$ = 161 (2 + / 159 -)
 # genes with $fdr < 0.05$ = 154 (1 + / 153 -)
 # genes with $fdr < 0.01$ = 151 (0 + / 151 -)

<r> metagenes = 0.99
 <r> genes = 0.5
 <FC> = -1.47
 <shrinkage-t> = -52.04
 <p-value> = 0
 <fdr> = 0.09

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-2.01	2e-16	7e-18	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	-2.77	2e-16	7e-18	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-2.98	2e-16	7e-18	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	-1.9	2e-16	7e-18	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	218	-3.24	2e-16	7e-18	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	222	-1.94	2e-16	7e-18	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
7	387695	-2.28	2e-16	7e-18	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
8	375791	-2.61	2e-16	7e-18	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
9	810	-1.5	2e-16	7e-18	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
10	1048	-1.76	2e-16	7e-18	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
11	4680	-3.7	2e-16	7e-18	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
12	548596	-2.26	2e-16	7e-18	4 x 50 creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc
13	22802	-2	2e-16	7e-18	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	84518	-2.82	2e-16	7e-18	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	49860	-3.23	2e-16	7e-18	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
16	1475	-1.65	2e-16	7e-18	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
17	1476	-1.87	2e-16	7e-18	1 x 50 cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
18	92196	-1.66	2e-16	7e-18	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
19	1672	-2.69	2e-16	7e-18	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
20	414325	-1.82	2e-16	7e-18	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-62.91	NULL	70 / 135	H.Tiss WIRTH_Mucosa
2	-35.35	NULL	14 / 21	CC cornified envelope
3	-32.66	NULL	16 / 42	BP keratinization
4	-27.17	NULL	19 / 53	BP keratinocyte differentiation
5	-25.83	NULL	8 / 19	BP peptide cross-linking
6	-24.83	NULL	71 / 572	Disease GUDJ_psooriasis up
7	-20.61	NULL	18 / 76	BP epidermis development
8	-19.69	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	-16.95	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
10	-16.53	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
11	-16.38	NULL	6 / 13	BP negative regulation of peptidase activity
12	-15.51	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
13	-15.18	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
14	-15.05	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
15	-14.85	NULL	3 / 12	BP cellular aldehyde metabolic process
16	-13.52	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
17	-13.2	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
18	-13.07	NULL	2 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
19	-12.83	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
20	-12.77	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
21	-12.53	NULL	5 / 16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
22	-12.47	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
23	-12.13	NULL	8 / 52	BP negative regulation of endopeptidase activity
24	-11.59	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
25	-11.35	NULL	6 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
26	-11.08	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
27	-10.72	NULL	13 / 186	MF structural molecule activity
28	-10.67	NULL	4 / 13	H.Tiss WIRTH_Tonsil
29	-10.33	NULL	3 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
30	-10.26	NULL	5 / 29	BP regulation of proteolysis
31	-10.1	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HP31_DN
32	-10.01	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
33	-10.01	NULL	4 / 16	GSEA C2JAEGER_METASTASIS_DN
34	-9.97	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_U
35	-9.88	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
36	-9.85	NULL	4 / 44	CC keratin filament
37	-9.31	NULL	6 / 38	BP epithelial cell differentiation
38	-9.31	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
39	-9.23	NULL	4 / 23	MF peptidase inhibitor activity
40	-9.03	NULL	45 / 1182	CC extracellular region

p-values

