

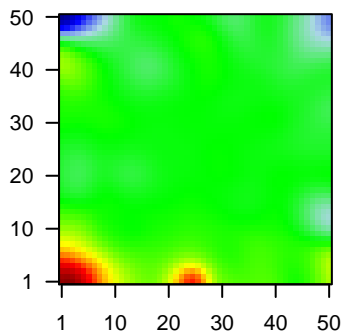
GW_011

Global Summary

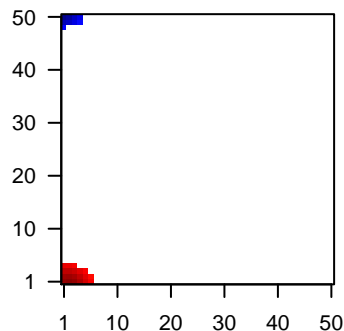
%DE = 0.16
 # genes with fdr < 0.2 = 2093 (1157 + / 936 -)
 # genes with fdr < 0.1 = 1819 (1023 + / 796 -)
 # genes with fdr < 0.05 = 1608 (913 + / 695 -)
 # genes with fdr < 0.01 = 1186 (690 + / 496 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.06
 <fdr> = 0.84

Profile



Regulated Spots



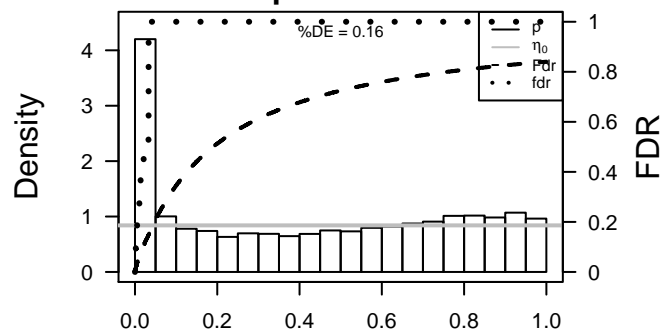
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-1.68	2e-16	1e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	154664	-1.37	2e-16	1e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [So
3	58	3.41	2e-16	1e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
4	59	1.55	2e-16	1e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
5	70	3.87	2e-16	1e-14	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
6	72	1.49	2e-16	1e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
7	131	-3.05	2e-16	1e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
8	165	1.97	2e-16	1e-14	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
9	113146	1.38	2e-16	1e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
10	57016	-1.65	2e-16	1e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
11	8644	-1.37	2e-16	1e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
12	1109	-1.5	2e-16	1e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
13	216	-1.89	2e-16	1e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
14	220	-1.58	2e-16	1e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
15	218	-3.44	2e-16	1e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
16	115701	1.83	2e-16	1e-14	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
17	23452	1.76	2e-16	1e-14	3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490]
18	27063	1.54	2e-16	1e-14	25 x 1 ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Syr
19	163782	1.82	2e-16	1e-14	1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
20	306	-1.36	2e-16	1e-14	4 x 42 annexin A3 [Source:HGNC Symbol;Acc:541]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	25.84	NULL	250	LymphomaTENZ_Stromal signature 1
2	23.46	NULL	190	CC extracellular matrix
3	20.92	NULL	242	BP extracellular matrix organization
4	19.73	NULL	36	BP muscle filament sliding
5	19.26	NULL	127	H.Tiss WIRTH_Muscle
6	17.85	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
7	17.45	NULL	69	BP extracellular matrix disassembly
8	16.79	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
9	16.15	NULL	16	MMML C6ACIEJ_MMML 1
10	15.97	NULL	64	BP collagen catabolic process
11	14.99	NULL	183	CC proteinaceous extracellular matrix
12	14.67	NULL	57	MF extracellular matrix structural constituent
13	14.08	NULL	403	BP cell adhesion
14	13.61	NULL	37	BP collagen fibril organization
15	13.59	NULL	83	CC basement membrane
16	12.99	NULL	44	MF structural constituent of muscle
17	12.87	NULL	84	BP muscle contraction
18	12.68	NULL	11	MF platelet-derived growth factor binding
19	12.55	NULL	16	H.Tiss WIRTH_Hippocampus
20	12.29	NULL	68	CC collagen
<i>Underexpressed</i>				
1	-25.02	NULL	135	H.Tiss WIRTH_Mucosa
2	-17.82	NULL	21	CC cornified envelope
3	-17.8	NULL	572	Disease GUDJ_pсориаз up
4	-15.19	NULL	42	BP keratinization
5	-13.08	NULL	53	BP keratinocyte differentiation
6	-9.67	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
7	-8.85	NULL	16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
8	-8.76	NULL	232	Chr Chr 18
9	-8.47	NULL	16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
10	-8.27	NULL	19	BP peptide cross-linking
11	-8.24	NULL	16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
12	-7.9	NULL	76	BP epidermis development
13	-7.59	NULL	1318	CC mitochondrion
14	-7.45	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
15	-7.1	NULL	1253	BP small molecule metabolic process
16	-6.67	NULL	18	BP retinol metabolic process
17	-6.63	NULL	15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
18	-6.63	NULL	296	MF oxidoreductase activity
19	-6.59	NULL	504	Chr Chr 15
20	-6.59	NULL	304	CC mitochondrial inner membrane

p-values



GW_011

Local Summary

%DE = 0.92
 # metagenes = 20
 # genes = 309
 # genes in genesets = 308

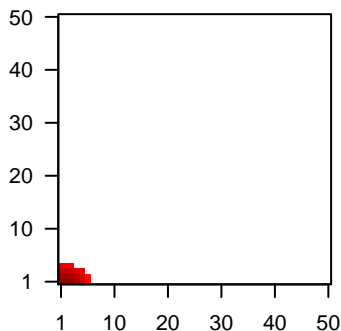
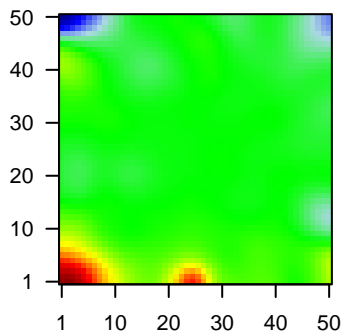
genes with $fdr < 0.1 = 274$ (265 + / 9 -)
 # genes with $fdr < 0.05 = 268$ (260 + / 8 -)
 # genes with $fdr < 0.01 = 255$ (249 + / 6 -)

<r> metagenes = 0.95
 <r> genes = 0.38

<FC> = 0.97
 <shrinkage-t> = 34.12
 <p-value> = 0
 <fdr> = 0.14

Profile

Spot



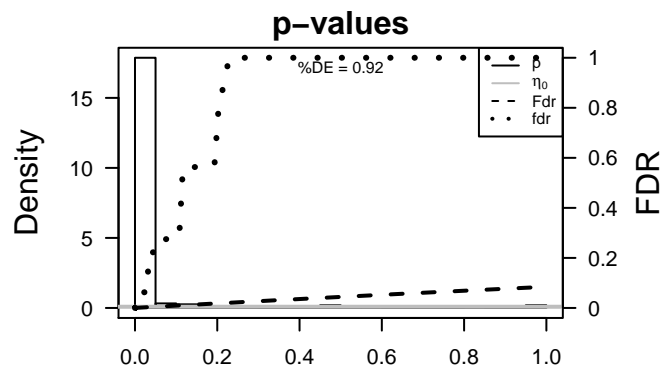
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	1.55	2e-16	6e-17	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	72	1.49	2e-16	6e-17	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	165	1.97	2e-16	6e-17	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
4	23452	1.76	2e-16	6e-17	3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490]
5	163782	1.82	2e-16	6e-17	1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
6	10409	1.65	2e-16	6e-17	1 x 2 brain abundant, membrane attached signal protein 1 [Source:
7	633	1.41	2e-16	6e-17	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
8	114902	1.33	2e-16	6e-17	4 x 1 C1q and tumor necrosis factor related protein 5 [Source:HGN
9	51313	1.31	2e-16	6e-17	4 x 1 family with sequence similarity 198, member B [Source:HGN
10	9315	1.31	2e-16	6e-17	3 x 1 neuronal regeneration related protein [Source:HGNC Symbol
11	800	1.39	2e-16	6e-17	2 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:1441]
12	55450	1.34	2e-16	6e-17	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
13	857	1.5	2e-16	6e-17	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;#
14	1009	1.43	2e-16	6e-17	3 x 1 cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC
15	1000	1.95	2e-16	6e-17	4 x 1 cadherin 2, type 1, N-cadherin (neuronal) [Source:HGNC Sy
16	1300	1.78	2e-16	6e-17	3 x 1 collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
17	1301	1.46	2e-16	6e-17	4 x 1 collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:2186]
18	1307	1.62	2e-16	6e-17	1 x 2 collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
19	1277	2.53	2e-16	6e-17	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
20	1278	2.45	2e-16	6e-17	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	41.78	NULL	68 / 190	CC extracellular matrix
2	41.22	NULL	82 / 250	Lymphocyte_ENZ_Stromal signature 1
3	40.13	NULL	15 / 16	MMML C27C1EJ_MMML 1
4	38.91	NULL	12 / 16	GSEA C27FARMER_BREAST_CANCER_CLUSTER_5
5	35.59	NULL	68 / 242	BP extracellular matrix organization
6	34.15	NULL	32 / 69	BP extracellular matrix disassembly
7	33.19	NULL	28 / 64	BP collagen catabolic process
8	30.06	NULL	8 / 11	MF platelet-derived growth factor binding
9	28.6	NULL	15 / 37	BP collagen fibril organization
10	24.86	NULL	20 / 57	MF extracellular matrix structural constituent
11	23.92	NULL	8 / 12	miRNA target-29c
12	23.8	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
13	23.27	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
14	22.9	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
15	22.3	NULL	41 / 183	CC proteinaceous extracellular matrix
16	22.25	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_T
17	21.7	NULL	11 / 19	MF extracellular matrix binding
18	20.07	NULL	18 / 68	CC collagen
19	19.81	NULL	12 / 40	BP cellular response to amino acid stimulus
20	19.67	NULL	88 / 683	CC extracellular space
21	19.59	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
22	19.58	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
23	19.32	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
24	18.93	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
25	18.76	NULL	24 / 119	Lymphocyte_SOLOWSKI_green total
26	18.52	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
27	18.46	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
28	18.11	NULL	8 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
29	17.82	NULL	7 / 16	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC
30	17.61	NULL	5 / 15	GSEA C2CHANG_POU5F1_TARGETS_UP
31	17.56	NULL	43 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
32	17.56	NULL	43 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
33	17.56	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
34	17.56	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
35	17.53	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
36	17.34	NULL	12 / 35	Glio Colman_survival_associated
37	17.31	NULL	5 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
38	17.28	NULL	23 / 83	CC basement membrane
39	16.92	NULL	48 / 403	BP cell adhesion
40	16.85	NULL	26 / 153	CC endoplasmic reticulum lumen



GW_011

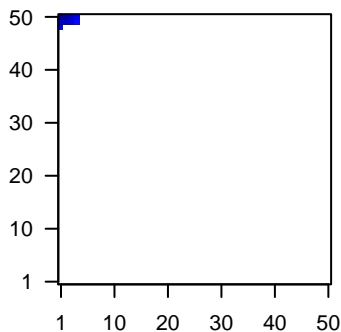
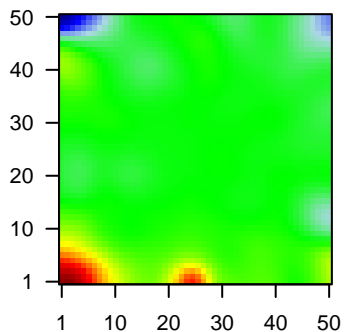
Local Summary

%DE = 0.97
 # metagenes = 9
 # genes = 159
 # genes in genesets = 156
 # genes with $fdr < 0.1$ = 153 (6 + / 147 -)
 # genes with $fdr < 0.05$ = 153 (6 + / 147 -)
 # genes with $fdr < 0.01$ = 143 (5 + / 138 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.5
 $\langle FC \rangle = -1.28$
 $\langle \text{shrinkage-t} \rangle = -45.36$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.08$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-1.68	2e-16	1e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	-3.05	2e-16	1e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-1.65	2e-16	1e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	8644	-1.37	2e-16	1e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym
5	218	-3.44	2e-16	1e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	375791	-2.1	2e-16	1e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
7	810	-1.42	2e-16	1e-17	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
8	51806	-2.57	2e-16	1e-17	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
9	1048	-1.52	2e-16	1e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
10	4680	-2.66	2e-16	1e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (f
11	548596	-1.47	2e-16	1e-17	4 x 50 creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc
12	22802	-2.31	2e-16	1e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	9022	-1.46	2e-16	1e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
14	84518	-2.8	2e-16	1e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	49860	-2.39	2e-16	1e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
16	1475	-2.39	2e-16	1e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
17	1476	-1.67	2e-16	1e-17	1 x 50 cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
18	92196	-2.12	2e-16	1e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
19	1672	-1.63	2e-16	1e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
20	1673	-1.85	2e-16	1e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-57.28	NULL	69 / 135	H.Tiss WIRTH_Mucosa
2	-42.87	NULL	13 / 21	CC cornified envelope
3	-35.15	NULL	15 / 42	BP keratinization
4	-31.69	NULL	17 / 53	BP keratinocyte differentiation
5	-27.56	NULL	7 / 19	BP peptide cross-linking
6	-25.6	NULL	70 / 572	Disease GUDJ_psooriasis up
7	-25.38	NULL	18 / 76	BP epidermis development
8	-18.64	NULL	6 / 13	BP negative regulation of peptidase activity
9	-18.39	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
10	-17.55	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	-15.93	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	-15.16	NULL	8 / 52	BP negative regulation of endopeptidase activity
13	-14.91	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
14	-14.85	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
15	-14.83	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
16	-14.6	NULL	4 / 10	MF RAGE receptor binding
17	-14.17	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
18	-14.12	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
19	-13.88	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
20	-13.21	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
21	-12.98	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
22	-12.97	NULL	3 / 12	BP cellular aldehyde metabolic process
23	-12.82	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_DN
24	-12.66	NULL	2 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
25	-12.47	NULL	12 / 186	MF structural molecule activity
26	-12.32	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
27	-12.3	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
28	-12.17	NULL	5 / 29	BP regulation of proteolysis
29	-12.17	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
30	-11.98	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
31	-11.83	NULL	4 / 23	MF peptidase inhibitor activity
32	-11.67	NULL	5 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
33	-11.54	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
34	-11.44	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
35	-11.36	NULL	4 / 16	GSEA C2JAEGER_METASTASIS_DN
36	-11.27	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
37	-11.27	NULL	4 / 27	BP response to bacterium
38	-10.96	NULL	3 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
39	-10.95	NULL	4 / 13	H.Tiss WIRTH_Tonsil
40	-10.9	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN

p-values

