

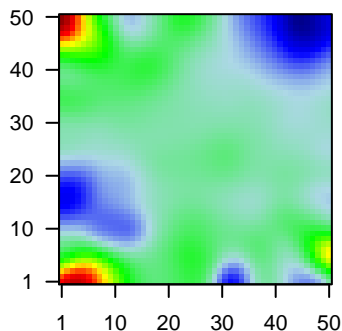
GW_242

Global Summary

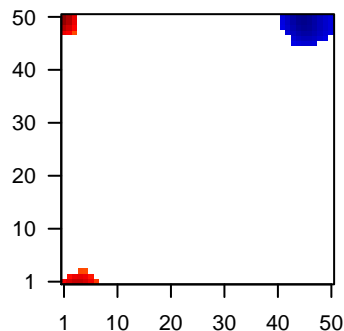
%DE = 0.15
 # genes with $fdr < 0.2$ = 2044 (1186 + / 858 -)
 # genes with $fdr < 0.1$ = 1566 (963 + / 603 -)
 # genes with $fdr < 0.05$ = 1403 (881 + / 522 -)
 # genes with $fdr < 0.01$ = 1018 (680 + / 338 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.08
 <fdr> = 0.85

Profile



Regulated Spots



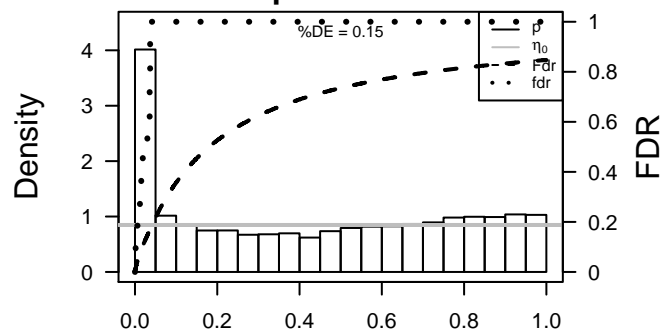
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.87	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	59	1.53	2e-16	2e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	72	1.77	2e-16	2e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
4	57016	1.54	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
5	441282	1.44	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
6	23452	1.79	2e-16	2e-14	3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490]
7	684	-1.79	2e-16	2e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
8	387695	1.73	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
9	260436	-1.51	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
10	375791	2.03	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
11	978	1.91	2e-16	2e-14	1 x 46 cytidine deaminase [Source:HGNC Symbol;Acc:1712]
12	9022	1.86	2e-16	2e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
13	84518	1.88	2e-16	2e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
14	26047	1.81	2e-16	2e-14	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
15	1277	2.14	2e-16	2e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
16	1278	2.03	2e-16	2e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
17	1281	2.03	2e-16	2e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
18	1289	2.06	2e-16	2e-14	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
19	1290	1.8	2e-16	2e-14	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
20	1291	1.92	2e-16	2e-14	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.22	NULL	135	H.Tiss WIRTH_Mucosa
2	25.22	NULL	250	LymphoENZ_Stromal signature 1
3	22.58	NULL	190	CC extracellular matrix
4	16.61	NULL	1182	CC extracellular region
5	16.11	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	15.84	NULL	683	CC extracellular space
7	15.4	NULL	242	BP extracellular matrix organization
8	15.09	NULL	16	MMML C6SCIEJ_MMML_1
9	14.6	NULL	21	CC cornified envelope
10	12.63	NULL	183	CC proteinaceous extracellular matrix
11	12.43	NULL	57	MF extracellular matrix structural constituent
12	12.25	NULL	42	BP keratinization
13	12.23	NULL	11	MF platelet-derived growth factor binding
14	12.18	NULL	53	BP keratinocyte differentiation
15	12.12	NULL	1146	TF HEBENSTREIT_low expression TF
16	11.55	NULL	69	BP extracellular matrix disassembly
17	11.41	NULL	76	BP epidermis development
18	11.34	NULL	37	BP collagen fibril organization
19	11.13	NULL	19	BP peptide cross-linking
20	10.92	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
<i>Underexpressed</i>				
1	-19.63	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-19.63	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-14.57	NULL	370	BP mitotic cell cycle
4	-12.53	NULL	949	CC nucleoplasm
5	-12.21	NULL	530	Cancer Lembecke_Normal vs Adenoma
6	-10.06	NULL	1233	TF KIM_MYC targets
7	-9.95	NULL	298	BP DNA repair
8	-9.92	NULL	51	BP type I interferon signaling pathway
9	-9.83	NULL	4640	CC nucleus
10	-9.66	NULL	149	BP DNA replication
11	-9.5	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
12	-9.24	NULL	417	H.Tiss WIRTH_Immune system
13	-9.22	NULL	232	BP mitosis
14	-8.98	NULL	148	BP G1/S transition of mitotic cell cycle
15	-8.97	NULL	595	MF RNA binding
16	-8.86	NULL	30	BP DNA strand elongation involved in DNA replication
17	-8.69	NULL	16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
18	-8.49	NULL	123	BP defense response to virus
19	-8.42	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
20	-8.34	NULL	1318	CC mitochondrion

p-values



GW_242

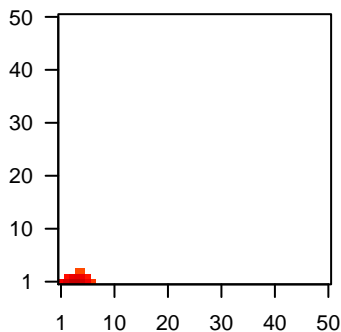
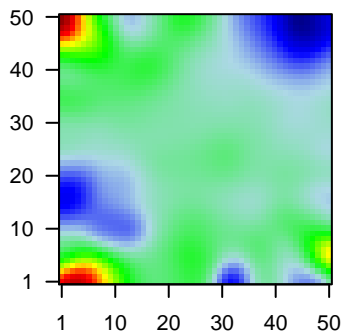
Local Summary

%DE = 0.97
 # metagenes = 14
 # genes = 257
 # genes in genesets = 256
 # genes with $fdr < 0.1$ = 239 (235 + / 4 -)
 # genes with $fdr < 0.05$ = 236 (234 + / 2 -)
 # genes with $fdr < 0.01$ = 228 (227 + / 1 -)

<r> metagenes = 0.97
 <r> genes = 0.43
 <FC> = 0.94
 <shrinkage-t> = 32.77
 <p-value> = 0
 <fdr> = 0.1

Profile

Spot



Local Genelist

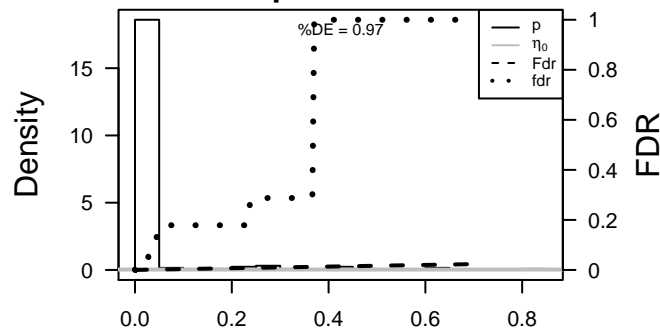
Rank	ID	log(FC)	fdr	p-value	Description
1	59	1.53	2e-16	4e-17	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	72	1.77	2e-16	4e-17	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Symb]
3	23452	1.79	2e-16	4e-17	3 x 1 angiopoietin-like 2 [Source:HGNC Symbol;Acc:490]
4	1277	2.14	2e-16	4e-17	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	2.03	2e-16	4e-17	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1281	2.03	2e-16	4e-17	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
7	1289	2.06	2e-16	4e-17	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	1.8	2e-16	4e-17	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1291	1.92	2e-16	4e-17	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
10	1293	1.56	2e-16	4e-17	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	83716	1.69	2e-16	4e-17	2 x 1 cysteine-rich secretory protein LCCL domain containing 2 [S]
12	1490	1.5	2e-16	4e-17	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2
13	115908	1.62	2e-16	4e-17	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
14	1513	1.71	2e-16	4e-17	4 x 1 cathepsin K [Source:HGNC Symbol;Acc:2536]
15	6374	2.47	2e-16	4e-17	1 x 1 chemokine (C-X-C motif) ligand 5 [Source:HGNC Symbol;Ac
16	6372	2.09	2e-16	4e-17	1 x 1 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Ac
17	1809	1.49	2e-16	4e-17	6 x 1 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:3015]
18	84624	1.9	2e-16	4e-17	3 x 1 fibronectin type III domain containing 1 [Source:HGNC Symb]
19	11167	1.63	2e-16	4e-17	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
20	5654	1.45	2e-16	4e-17	2 x 1 HtrA serine peptidase 1 [Source:HGNC Symbol;Acc:9476]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	40.41	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
2	40.01	NULL	73 / 250	Lymphoma_TENZ_Stromal signature 1
3	40	NULL	14 / 16	MMML C6SCIEJ_MMML 1
4	38.16	NULL	61 / 190	CC extracellular matrix
5	33.56	NULL	8 / 11	MF platelet-derived growth factor binding
6	29.62	NULL	8 / 12	miRNA target-29c
7	27.95	NULL	21 / 57	MF extracellular matrix structural constituent
8	27.61	NULL	53 / 242	BP extracellular matrix organization
9	26.24	NULL	26 / 69	BP extracellular matrix disassembly
10	24.25	NULL	22 / 64	BP collagen catabolic process
11	23.97	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
12	22.55	NULL	12 / 37	BP collagen fibril organization
13	20.95	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
14	20.91	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
15	20.88	NULL	10 / 19	MF extracellular matrix binding
16	20.08	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
17	19.18	NULL	64 / 553	Cancer Lembecke_Colonc Inflammation
18	19.14	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
19	18.8	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
20	18.71	NULL	15 / 68	CC collagen
21	18.32	NULL	67 / 683	CC extracellular space
22	18.24	NULL	94 / 1182	CC extracellular region
23	18.13	NULL	4 / 10	BP protein heterotrimerization
24	18.06	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
25	17.83	NULL	21 / 119	Lymphoma_SOLOWSKI_green total
26	17.73	NULL	8 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
27	17.45	NULL	7 / 16	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC
28	17.26	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
29	17.05	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
30	17.04	NULL	19 / 83	CC basement membrane
31	16.6	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
32	16.26	NULL	6 / 11	MMML C6SCIEJ_MMML 31
33	16.22	NULL	33 / 183	CC proteinaceous extracellular matrix
34	15.93	NULL	9 / 40	BP cellular response to amino acid stimulus
35	15.84	NULL	6 / 16	GSEA C2GU_PDEF_TARGETS_UP
36	15.42	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
37	15.36	NULL	6 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
38	15.36	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
39	15.26	NULL	5 / 16	GSEA C2JRS_ADIPOCYTE_DIFFERENTIATION_DN
40	15.25	NULL	6 / 12	GSEA C2Y_AGING_MIDDLE_UP

p-values



GW_242

Local Summary

%DE = 0.92
 # metagenes = 12
 # genes = 171
 # genes in genesets = 166

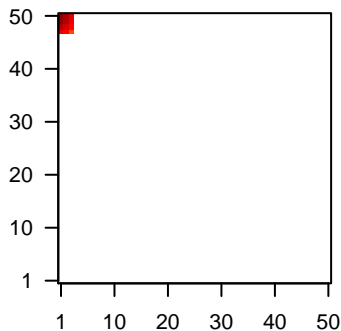
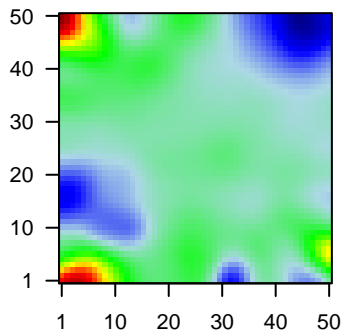
genes with $fdr < 0.1 = 152$ (147 + / 5 -)
 # genes with $fdr < 0.05 = 147$ (143 + / 4 -)
 # genes with $fdr < 0.01 = 140$ (136 + / 4 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.49

$\langle FC \rangle = 1.1$
 $\langle \text{shrinkage-t} \rangle = 38.8$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.14$

Profile

Spot



Local Genelist

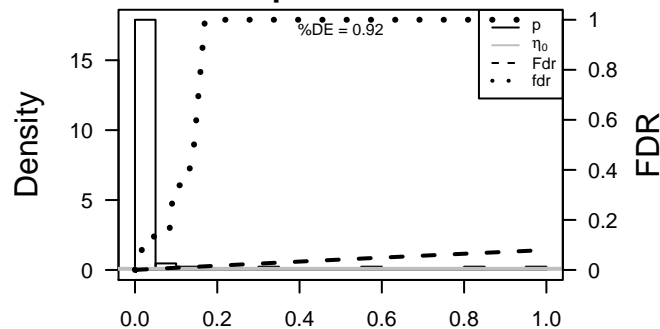
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.87	2e-16	5e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	57016	1.54	2e-16	5e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.44	2e-16	5e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	387695	1.73	2e-16	5e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
5	375791	2.03	2e-16	5e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
6	9022	1.86	2e-16	5e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
7	84518	1.88	2e-16	5e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	1382	1.51	2e-16	5e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
9	54544	2.33	2e-16	5e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
10	49860	3.17	2e-16	5e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
11	126410	1.44	2e-16	5e-17	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
12	1672	1.71	2e-16	5e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	55894	1.79	2e-16	5e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	2.39	2e-16	5e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	2.25	2e-16	5e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	93099	1.69	2e-16	5e-17	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
17	1828	2.56	2e-16	5e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	115572	1.55	2e-16	5e-17	1 x 48 family with sequence similarity 46, member B [Source:HGNC
19	2312	1.8	2e-16	5e-17	1 x 49 filaggrin [Source:HGNC Symbol;Acc:3748]
20	80157	1.75	2e-16	5e-17	1 x 48 cell wall biogenesis 43 C-terminal homolog (S. cerevisiae) [S

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	56.92	NULL	71 / 135	H.Tiss WIRTH_Mucosa
2	39.39	NULL	16 / 21	CC cornified envelope
3	34.75	NULL	19 / 42	BP keratinization
4	27.67	NULL	21 / 53	BP keratinocyte differentiation
5	24.52	NULL	78 / 572	Disease GUDJ_psooriasis up
6	23.61	NULL	18 / 76	BP epidermis development
7	21.49	NULL	9 / 19	BP peptide cross-linking
8	16.49	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	16.32	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	15.11	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
11	15	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	12.99	NULL	5 / 21	CC desmosome
13	12.38	NULL	6 / 13	BP negative regulation of peptidase activity
14	12.05	NULL	8 / 44	CC keratin filament
15	10.87	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
16	10.83	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
17	10.78	NULL	12 / 122	MF serine-type endopeptidase activity
18	10.41	NULL	18 / 186	MF structural molecule activity
19	9.83	NULL	46 / 1182	CC extracellular region
20	9.82	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
21	9.81	NULL	7 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
22	8.95	NULL	2 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
23	8.85	NULL	6 / 53	MF serine-type peptidase activity
24	8.77	NULL	3 / 16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
25	8.65	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
26	8.58	NULL	10 / 82	CC intermediate filament
27	8.53	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
28	8.29	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
29	8.23	NULL	3 / 15	GSEA C2AIGNER_ZEB1_TARGETS
30	8.19	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
31	7.96	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
32	7.9	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
33	7.83	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
34	7.41	NULL	5 / 38	BP epithelial cell differentiation
35	7.32	NULL	7 / 73	BP defense response to bacterium
36	7.24	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
37	7.15	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
38	7.1	NULL	4 / 27	BP response to bacterium
39	7.1	NULL	2 / 17	Disease BCHETNIA_EBM up
40	7.09	NULL	3 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN

p-values



GW_242

Local Summary

%DE = 0.88
 # metagenes = 51
 # genes = 631
 # genes in genesets = 627

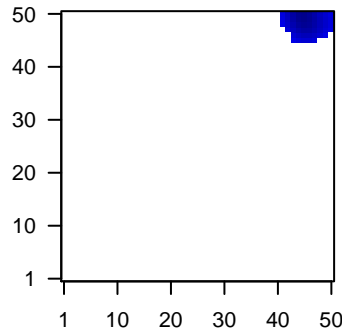
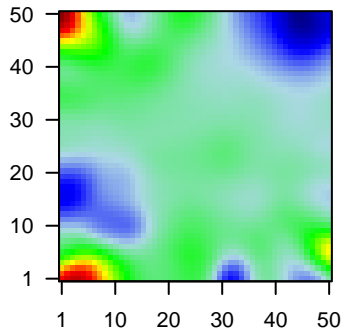
genes with $fdr < 0.1 = 476$ (7 + / 469 -)
 # genes with $fdr < 0.05 = 457$ (7 + / 450 -)
 # genes with $fdr < 0.01 = 326$ (5 + / 321 -)

$\langle r \rangle$ metagenes = 0.85
 $\langle r \rangle$ genes = 0.26

$\langle FC \rangle = -0.48$
 $\langle \text{shrinkage-t} \rangle = -16.83$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.42$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	26047	1.81	2e-16	4e-15	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Acc:26047]
2	4072	-1.56	2e-16	4e-15	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:4072]
3	4171	-1.4	2e-16	4e-15	46 x 48 minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:4171]
4	256764	-1.99	2e-16	4e-15	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
5	3856	-1.38	4e-16	2e-13	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
6	4922	-1.33	6e-15	2e-13	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
7	94234	-1.32	8e-15	2e-13	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
8	7153	-1.32	9e-15	2e-12	45 x 49 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbol;Acc:7153]
9	8318	-1.28	5e-14	2e-12	45 x 49 cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
10	25975	1.28	7e-14	2e-12	48 x 50 EGF-like-domain, multiple 6 [Source:HGNC Symbol;Acc:32222]
11	55165	-1.27	7e-14	6e-12	44 x 50 centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161]
12	3880	-1.26	1e-13	2e-11	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
13	7083	-1.23	6e-13	2e-11	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183]
14	339512	-1.22	1e-12	2e-11	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt:339512]
15	84707	-1.21	1e-12	2e-11	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
16	259266	-1.21	1e-12	2e-11	45 x 49 asp (abnormal spindle) homolog, microcephaly associated (D) [Source:HGNC Symbol;Acc:259266]
17	113130	-1.2	2e-12	9e-11	44 x 49 cell division cycle associated 5 [Source:HGNC Symbol;Acc:113130]
18	200634	-1.19	3e-12	8e-10	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc:200634]
19	5984	-1.14	2e-11	8e-10	46 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Symbol;Acc:5984]
20	3202	-1.14	2e-11	2e-09	49 x 47 homeobox A5 [Source:HGNC Symbol;Acc:5106]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-51.85	NULL	96 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-51.85	NULL	96 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-28.73	NULL	112 / 370	BP mitotic cell cycle
4	-27.05	NULL	16 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
5	-25.68	NULL	26 / 57	Glio developing astrocytes
6	-25.38	NULL	119 / 530	Cancer Lembecke_Normal vs Adenoma
7	-23.62	NULL	53 / 149	BP DNA replication
8	-23.57	NULL	13 / 14	MMML C6SCIEJ_MMML_4
9	-23.28	NULL	12 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
10	-23.15	NULL	19 / 30	BP DNA strand elongation involved in DNA replication
11	-22.67	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
12	-22.33	NULL	14 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
13	-21.75	NULL	9 / 11	GSEA C2KALMA_E2F1_TARGETS
14	-21.12	NULL	13 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
15	-20.99	NULL	8 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
16	-20.98	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
17	-20.29	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	-20.28	NULL	12 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
19	-20.26	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
20	-19.95	NULL	11 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTANT_DN
21	-19.68	NULL	12 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
22	-19.56	NULL	12 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
23	-19.41	NULL	58 / 232	BP mitosis
24	-19.36	NULL	12 / 15	GSEA C2CHANG_CYCLING_GENES
25	-19.17	NULL	10 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
26	-18.93	NULL	10 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
27	-18.64	NULL	12 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
28	-18.46	NULL	11 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
29	-18.2	NULL	13 / 18	BP spindle organization
30	-18.09	NULL	11 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
31	-17.77	NULL	13 / 22	BP DNA replication initiation
32	-17.57	NULL	10 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
33	-17.37	NULL	8 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
34	-17.35	NULL	9 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
35	-17.05	NULL	23 / 56	CC chromosome, centromeric region
36	-16.7	NULL	11 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
37	-16.43	NULL	127 / 949	CC nucleoplasm
38	-16.31	NULL	9 / 15	GSEA C2Y_AGING_MIDDLE_DN
39	-16.29	NULL	11 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
40	-16.07	NULL	8 / 16	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP

