

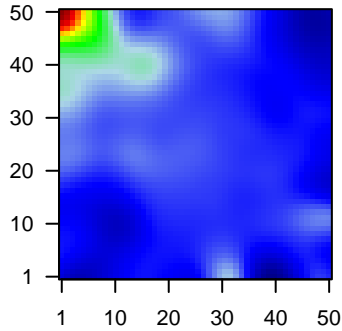
GW_288

Global Summary

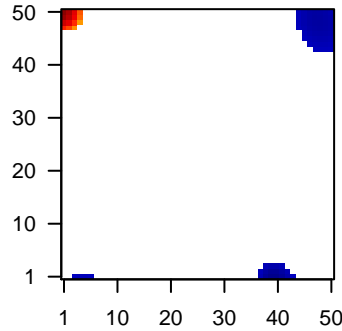
%DE = 0.13
 # genes with fdr < 0.2 = 1738 (1006 + / 732 -)
 # genes with fdr < 0.1 = 1341 (828 + / 513 -)
 # genes with fdr < 0.05 = 1156 (738 + / 418 -)
 # genes with fdr < 0.01 = 783 (567 + / 216 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.87

Profile



Regulated Spots



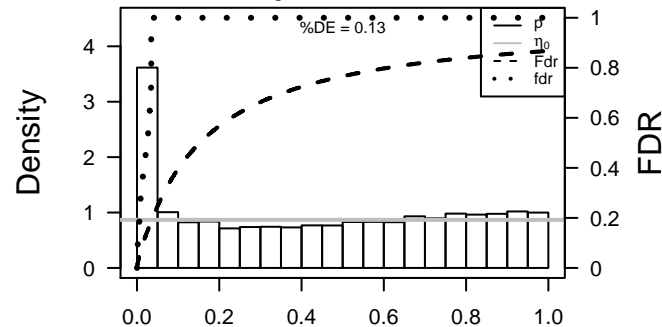
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.19	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	57016	1.64	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.54	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	222	1.68	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
5	8416	1.36	2e-16	2e-14	5 x 50 annexin A9 [Source:HGNC Symbol;Acc:547]
6	360	1.64	2e-16	2e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	50617	1.32	2e-16	2e-14	5 x 50 ATPase, H+ transporting, lysosomal V0 subunit a4 [Source:H
8	387695	2.21	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
9	84419	1.5	2e-16	2e-14	5 x 50 chromosome 15 open reading frame 48 [Source:HGNC Synt
10	64073	1.33	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt
11	260436	1.71	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
12	394263	1.76	2e-16	2e-14	3 x 50
13	375791	2.76	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
14	760	1.32	2e-16	2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	55450	1.39	2e-16	2e-14	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
16	6352	1.73	2e-16	2e-14	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
17	50489	1.33	2e-16	2e-14	5 x 48 CD207 molecule, langerin [Source:HGNC Symbol;Acc:17935
18	978	2.1	2e-16	2e-14	1 x 46 cytidine deaminase [Source:HGNC Symbol;Acc:1712]
19	22802	2.02	2e-16	2e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
20	9071	2.09	2e-16	2e-14	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	38.73	NULL	135	H.Tiss WIRTH_Mucosa
2	32.17	NULL	572	Disease GUDJ_psooriasis up
3	21.41	NULL	21	CC cornified envelope
4	19.07	NULL	42	BP keratinization
5	17.15	NULL	53	BP keratinocyte differentiation
6	16.39	NULL	76	BP epidermis development
7	11.55	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
8	10.49	NULL	19	BP peptide cross-linking
9	10.33	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
10	10.32	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	9.89	NULL	16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
12	9.87	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
13	9.36	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
14	9.33	NULL	16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
15	9.17	NULL	14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
16	8.98	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	8.91	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	8.82	NULL	31	BP negative regulation of viral genome replication
19	8.71	NULL	186	MF structural molecule activity
20	8.63	NULL	16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
<i>Underexpressed</i>				
1	-8.55	NULL	1749	MF DNA binding
2	-7.55	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
3	-7.49	NULL	4640	CC nucleus
4	-7.25	NULL	7	MMML C6ACIEJ_MMML 5
5	-7.09	NULL	949	CC nucleoplasm
6	-6.81	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
7	-6.8	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
8	-6.73	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
9	-6.73	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
10	-6.65	NULL	823	MF sequence-specific DNA binding transcription factor activity
11	-6.61	NULL	1574	BP transcription, DNA-templated
12	-6.31	NULL	1581	BP regulation of transcription, DNA-dependent
13	-6.31	NULL	370	BP mitotic cell cycle
14	-6.14	NULL	250	LymphocyteENZ_Stromal signature 1
15	-6.11	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
16	-5.99	NULL	149	BP DNA replication
17	-5.94	NULL	743	BP Chr 7
18	-5.89	NULL	16	MMML C6ACIEJ_MMML 1
19	-5.76	NULL	36	BP muscle filament sliding
20	-5.75	NULL	16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN

p-values



GW_288

Local Summary

%DE = 0.98
 # metagenes = 15
 # genes = 204
 # genes in genesets = 199

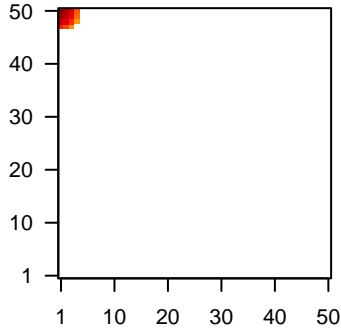
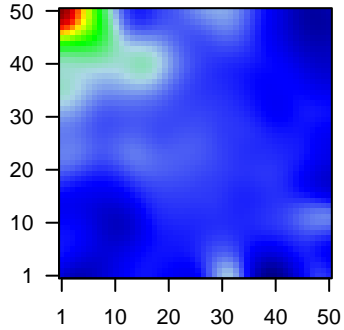
 # genes with $fdr < 0.1$ = 197 (196 + / 1 -)
 # genes with $fdr < 0.05$ = 194 (194 + / 0 -)
 # genes with $fdr < 0.01$ = 191 (191 + / 0 -)

<r> metagenes = 0.98
 <r> genes = 0.48

 <FC> = 1.49
 <shrinkage-t> = 52.47
 <p-value> = 0
 <fdr> = 0.05

Profile

Spot



Local Genelist

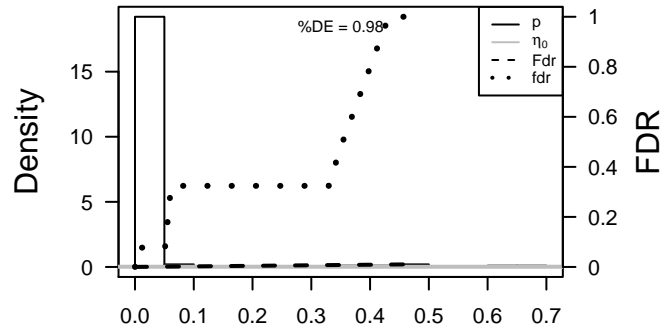
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.19	2e-16	6e-18	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	57016	1.64	2e-16	6e-18	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.54	2e-16	6e-18	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	222	1.68	2e-16	6e-18	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
5	360	1.64	2e-16	6e-18	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	387695	2.21	2e-16	6e-18	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	394263	1.76	2e-16	6e-18	3 x 50
8	375791	2.76	2e-16	6e-18	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
9	22802	2.02	2e-16	6e-18	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	26285	1.32	2e-16	6e-18	4 x 48 claudin 17 [Source:HGNC Symbol;Acc:2038]
11	9022	2.38	2e-16	6e-18	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
12	84518	2.34	2e-16	6e-18	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
13	54544	3.09	2e-16	6e-18	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:29871
14	49860	3.23	2e-16	6e-18	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	1474	1.7	2e-16	6e-18	1 x 47 cystatin E/M [Source:HGNC Symbol;Acc:2478]
16	1562	1.71	2e-16	6e-18	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
17	126410	1.58	2e-16	6e-18	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
18	1672	1.41	2e-16	6e-18	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
19	55894	3.01	2e-16	6e-18	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	414325	3.53	2e-16	6e-18	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	58.7	NULL	80 / 135	H.Tiss WIRTH_Mucosa
2	38.26	NULL	17 / 21	CC cornified envelope
3	31.95	NULL	19 / 42	BP keratinization
4	29.2	NULL	86 / 572	Disease GUDJ_psooriasis up
5	27.74	NULL	22 / 53	BP keratinocyte differentiation
6	22.24	NULL	20 / 76	BP epidermis development
7	19.73	NULL	10 / 19	BP peptide cross-linking
8	19.3	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	15.34	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	14.87	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
11	14.83	NULL	7 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
12	14.52	NULL	8 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	12.75	NULL	5 / 10	MF RAGE receptor binding
14	12.65	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	12.46	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
16	12.22	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
17	11.88	NULL	13 / 122	MF serine-type endopeptidase activity
18	11.64	NULL	52 / 1182	CC extracellular region
19	11.62	NULL	20 / 186	MF structural molecule activity
20	11.23	NULL	4 / 15	GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
21	10.48	NULL	4 / 16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
22	10.47	NULL	10 / 82	CC intermediate filament
23	10.24	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
24	10.12	NULL	8 / 44	CC keratin filament
25	9.99	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
26	9.94	NULL	6 / 13	BP negative regulation of peptidase activity
27	9.79	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
28	9.54	NULL	4 / 23	MF peptidase inhibitor activity
29	9.48	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
30	9.42	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
31	9.23	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
32	9.2	NULL	4 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
33	9.14	NULL	8 / 73	BP defense response to bacterium
34	9.06	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
35	8.97	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
36	8.93	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
37	8.82	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
38	8.81	NULL	4 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
39	8.72	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
40	8.71	NULL	5 / 21	CC desmosome

p-values



GW_288

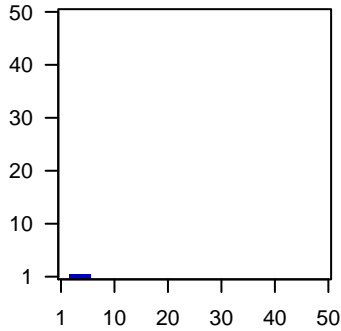
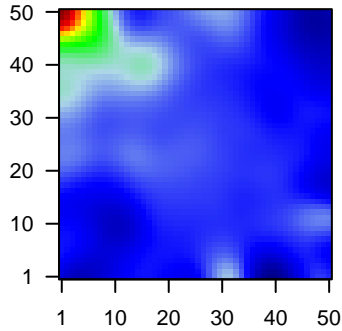
Local Summary

%DE = 0.79
 # metagenes = 4
 # genes = 135
 # genes in genesets = 134
 # genes with $fdr < 0.1 = 75$ (0 + / 75 -)
 # genes with $fdr < 0.05 = 70$ (0 + / 70 -)
 # genes with $fdr < 0.01 = 52$ (0 + / 52 -)

<r> metagenes = 0.99
 <r> genes = 0.49
 <FC> = -0.36
 <shrinkage-t> = -12.74
 <p-value> = 0.01
 <fdr> = 0.52

Profile

Spot



Local Genelist

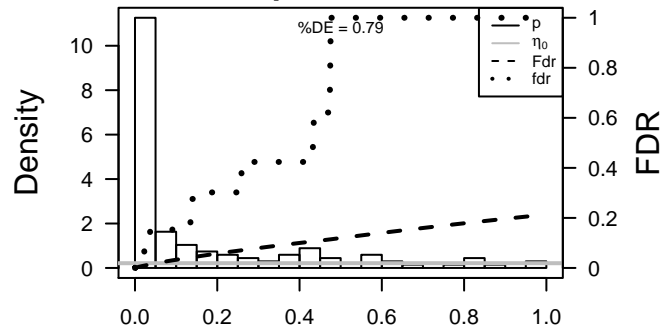
Rank	ID	log(FC)	fdr	p-value	Description
1	6423	-1.08	1e-11	1e-09	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:10444]
2	59	-1.05	5e-11	7e-09	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Acc:10444]
3	633	-0.93	3e-10	2e-07	3 x 1 biglycan [Source:HGNC Symbol;Acc:10444]
4	1306	-0.92	8e-09	5e-07	4 x 1 collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
5	54749	-0.89	3e-08	7e-06	5 x 1 ependymin related 1 [Source:HGNC Symbol;Acc:17572]
6	6678	-0.82	3e-07	8e-06	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:2536]
7	1513	-0.8	6e-07	8e-06	4 x 1 cathepsin K [Source:HGNC Symbol;Acc:2536]
8	1462	-0.78	1e-06	8e-06	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
9	1490	-0.78	1e-06	5e-05	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2464]
10	187	-0.75	3e-06	9e-05	5 x 1 apelin receptor [Source:HGNC Symbol;Acc:339]
11	165	-0.71	8e-06	9e-05	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
12	1634	-0.71	9e-06	2e-04	4 x 1 decorin [Source:HGNC Symbol;Acc:2705]
13	11167	-0.68	2e-05	2e-04	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
14	6876	-0.67	3e-05	2e-04	3 x 1 transgelin [Source:HGNC Symbol;Acc:11553]
15	3487	-0.67	3e-05	2e-04	5 x 1 insulin-like growth factor binding protein 4 [Source:HGNC Symbol;Acc:3601]
16	2199	-0.66	3e-05	4e-04	4 x 1 fibulin 2 [Source:HGNC Symbol;Acc:3601]
17	26064	-0.65	5e-05	4e-04	4 x 1 retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
18	5118	-0.64	7e-05	4e-04	4 x 1 procollagen C-endopeptidase enhancer [Source:HGNC Symbol;Acc:15855]
19	22918	-0.63	7e-05	4e-04	4 x 1 CD93 molecule [Source:HGNC Symbol;Acc:15855]
20	2882	-0.63	9e-05	4e-04	6 x 1 glutathione peroxidase 7 [Source:HGNC Symbol;Acc:4559]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-27.2	NULL	44 / 250	Lymphoma_TENZ_Stromal signature 1
2	-24.98	NULL	7 / 19	MF extracellular matrix binding
3	-22.89	NULL	3 / 5	GSEA C2COLLER_MYC_TARGETS_DN
4	-22.39	NULL	32 / 190	CC extracellular matrix
5	-21.48	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	-19.86	NULL	3 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
7	-19.37	NULL	3 / 11	BP dermatan sulfate biosynthetic process
8	-19.24	NULL	4 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
9	-19.2	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
10	-18.32	NULL	4 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_CARCINOMA
11	-16.97	NULL	3 / 14	BP chondroitin sulfate catabolic process
12	-16.68	NULL	5 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
13	-16	NULL	5 / 16	MMML C6SCIEJ_MMML 1
14	-15.99	NULL	5 / 25	BP chondroitin sulfate biosynthetic process
15	-15.94	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_CARCINOMA
16	-15.85	NULL	1 / 2	miRNA target-18
17	-15.15	NULL	2 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
18	-15.02	NULL	3 / 15	Cancer LIU_PROSTATE_CANCER_DN
19	-13.85	NULL	4 / 21	MF glycosaminoglycan binding
20	-13.23	NULL	2 / 8	GSEA C2ZHAN_MULTIPLE_MYELOMA_SPIKED
21	-13.22	NULL	4 / 11	MMML C6SCIEJ_MMML 31
22	-13.15	NULL	25 / 242	BP extracellular matrix organization
23	-13.08	NULL	3 / 15	GSEA C2EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
24	-12.92	NULL	1 / 5	GSEA C2OHM_EMBRYONIC_CARCINOMA_UP
25	-12.89	NULL	3 / 10	GSEA C2MAINA_VHL_TARGETS_UP
26	-12.84	NULL	4 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS
27	-12.83	NULL	2 / 12	miRNA target-29c
28	-12.49	NULL	2 / 7	GSEA C2TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_DN
29	-12.4	NULL	17 / 183	CC proteinaceous extracellular matrix
30	-12.35	NULL	8 / 57	MF extracellular matrix structural constituent
31	-12.17	NULL	3 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_CARCINOMA
32	-12.04	NULL	3 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
33	-11.68	NULL	2 / 16	MF fibronectin binding
34	-11.56	NULL	5 / 45	BP chondroitin sulfate metabolic process
35	-11.37	NULL	4 / 15	GSEA C2SENESE_HDAC2_TARGETS_DN
36	-11.16	NULL	4 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
37	-10.77	NULL	2 / 14	GSEA C2MAINA_VHL_TARGETS_DN
38	-10.7	NULL	3 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
39	-10.69	NULL	3 / 13	GSEA C2WART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
40	-10.56	NULL	31 / 683	CC extracellular space

p-values



GW_288

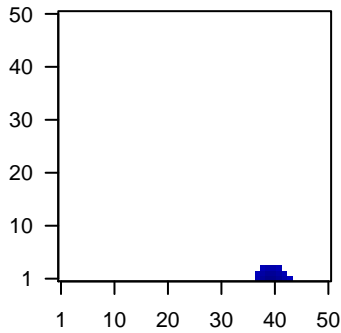
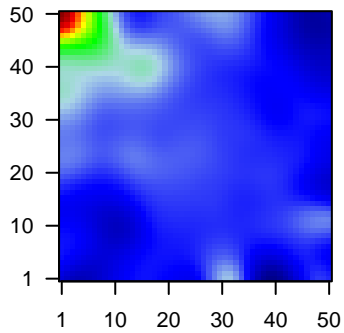
Local Summary

%DE = 0.85
 # metagenes = 17
 # genes = 281
 # genes in genesets = 255
 # genes with $fdr < 0.1$ = 213 (1 + / 212 -)
 # genes with $fdr < 0.05$ = 163 (1 + / 162 -)
 # genes with $fdr < 0.01$ = 120 (1 + / 119 -)

<r> metagenes = 0.97
 <r> genes = 0.46
 <FC> = -0.4
 <shrinkage-t> = -14.27
 <p-value> = 0
 <fdr> = 0.5

Profile

Spot



Local Genelist

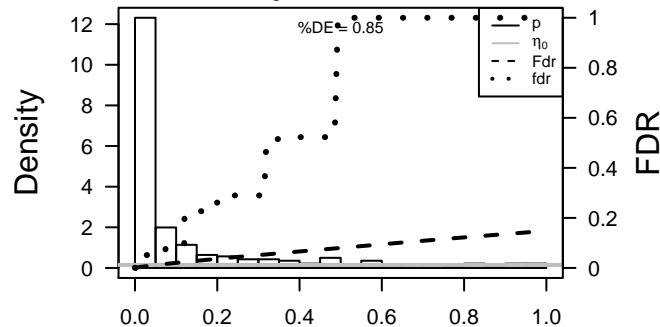
Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	399900	-1.16	2e-15	6e-11	39 x 1
2	91368	-1.04	1e-12	3e-10	39 x 1
3	84061	-1.09	7e-12	3e-10	39 x 1
4	23466	-1.08	1e-11	2e-08	41 x 1
5	250	-0.97	1e-09	2e-08	40 x 1
6	387700	-0.89	1e-09	2e-08	40 x 1
7	90586	-0.97	1e-09	4e-08	39 x 1
8	9747	-0.87	3e-09	4e-08	39 x 1
9	440353	-0.94	4e-09	4e-08	40 x 1
10	440157	-0.94	4e-09	9e-08	39 x 1
11	400866	-0.92	9e-09	9e-08	39 x 1
12	3127	-0.91	1e-08	9e-08	43 x 1
13	5143	-0.84	1e-08	9e-08	39 x 1
14	641737	-0.85	1e-08	3e-07	40 x 1
15	84278	-0.89	3e-08	3e-07	39 x 1
16	100132247	-0.88	4e-08	3e-07	39 x 3
17	729603	-0.81	4e-08	6e-07	40 x 1
18	100190938	-0.8	5e-08	1e-06	39 x 1
19	642947	-0.78	1e-07	1e-06	39 x 1
20	81033	-0.78	1e-07	1e-06	39 x 1

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-12.62	NULL	3 / 14	MMML C69CIEJ_MMML 8
2	-12.2	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
3	-7.78	NULL	2 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
4	-7.41	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
5	-6.93	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
6	-6.79	NULL	2 / 14	BP cellular response to estradiol stimulus
7	-6.37	NULL	3 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
8	-6.24	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
9	-6.24	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
10	-6.09	NULL	1 / 10	CC oligosaccharyltransferase complex
11	-5.99	NULL	2 / 16	BP cognition
12	-5.73	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
13	-5.6	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
14	-5.57	NULL	2 / 15	GSEA C2REACTOME_DARPP32_EVENTS
15	-5.46	NULL	2 / 10	MF endodeoxyribonuclease activity
16	-5.36	NULL	2 / 19	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
17	-5.27	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
18	-5.21	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
19	-5.09	NULL	1 / 11	GSEA C2KEGG_FOLATE_BIOSYNTHESIS
20	-5.07	NULL	2 / 23	BP protein N-linked glycosylation
21	-5.06	NULL	2 / 15	BP female gamete generation
22	-4.99	NULL	1 / 14	BP magnesium ion transport
23	-4.89	NULL	3 / 24	BP negative regulation of T cell proliferation
24	-4.88	NULL	2 / 12	GSEA C2BARRIER_COLON_CANCER_RECURRENCE_DN
25	-4.79	NULL	3 / 19	BP sprouting angiogenesis
26	-4.62	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process
27	-4.62	NULL	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
28	-4.53	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOLESTEROL
29	-4.49	NULL	1 / 12	BP cAMP catabolic process
30	-4.46	NULL	4 / 69	miRNA target-miR-396
31	-4.38	NULL	1 / 14	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_UP
32	-4.37	NULL	2 / 14	BP mitochondrion morphogenesis
33	-4.36	NULL	2 / 13	GSEA C2REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
34	-4.36	NULL	1 / 11	BP negative regulation of interleukin-12 production
35	-4.36	NULL	1 / 11	GSEA C2SU_PANCREAS
36	-4.28	NULL	1 / 10	BP negative regulation of cell-matrix adhesion
37	-4.26	NULL	1 / 14	Cancer LIU_COMMON_CANCER_GENES
38	-4.25	NULL	4 / 100	Lymphoma ROSOLOWSKI_blue total
39	-4.14	NULL	2 / 15	GSEA C2REACTOME_LYSOSOME_VESICLE_BIOGENESIS
40	-4.13	NULL	1 / 12	BP negative regulation of growth of symbiont in host

p-values



GW_288

Local Summary

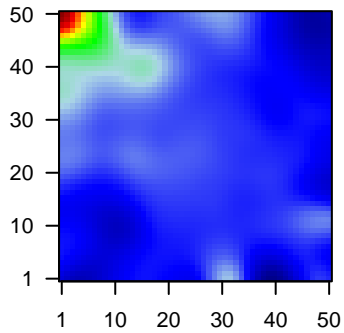
%DE = 0.8
 # metagenes = 49
 # genes = 567
 # genes in genesets = 562

genes with $fdr < 0.1 = 298$ (9 + / 289 -)
 # genes with $fdr < 0.05 = 222$ (7 + / 215 -)
 # genes with $fdr < 0.01 = 118$ (5 + / 113 -)

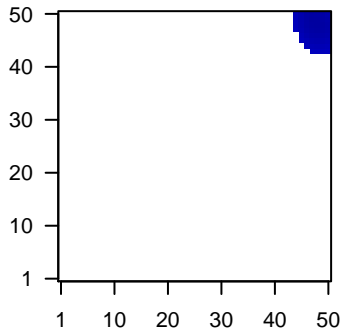
$\langle r \rangle$ metagenes = 0.88
 $\langle r \rangle$ genes = 0.24

$\langle FC \rangle = -0.3$
 $\langle \text{shrinkage-t} \rangle = -10.51$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.66$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4072	-1.34	2e-16	8e-15	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:...
2	4922	-1.48	2e-16	8e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
3	256764	-1.31	2e-16	8e-15	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
4	7037	-1.14	6e-15	4e-12	47 x 50 transferrin receptor [Source:HGNC Symbol;Acc:11763]
5	875	-1.21	4e-14	3e-11	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:151...
6	3856	-1.16	3e-13	1e-07	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
7	10655	-0.97	1e-09	1e-07	50 x 50 doublesex and mab-3 related transcription factor 2 [Source:H...
8	3202	-0.95	2e-09	2e-07	49 x 47 homeobox A5 [Source:HGNC Symbol;Acc:5106]
9	1974	-0.86	5e-09	2e-07	49 x 47 eukaryotic translation initiation factor 4A2 [Source:HGNC Syn...
10	4953	-0.93	6e-09	3e-07	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	55689	-0.92	9e-09	4e-07	46 x 50 YEATS domain containing 2 [Source:HGNC Symbol;Acc:2541...
12	139728	-0.91	1e-08	2e-06	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l...
13	54800	-0.89	3e-08	4e-06	50 x 48 kelch-like family member 24 [Source:HGNC Symbol;Acc:259...
14	2938	-0.85	1e-07	4e-06	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Ac...
15	7546	-0.84	1e-07	4e-06	48 x 50 Zic family member 2 [Source:HGNC Symbol;Acc:12873]
16	5984	-0.84	2e-07	4e-06	46 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn...
17	154664	-0.84	2e-07	4e-06	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [So...
18	339512	-0.83	2e-07	1e-05	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt...
19	6596	-0.82	3e-07	2e-05	46 x 50 helicase-like transcription factor [Source:HGNC Symbol;Acc:...
20	1780	-0.8	5e-07	3e-05	50 x 50 dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S...

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-23.72	NULL	76 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-23.72	NULL	76 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-15.68	NULL	14 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
4	-15.08	NULL	25 / 57	Glio developing astrocytes
5	-14.5	NULL	16 / 30	BP DNA strand elongation involved in DNA replication
6	-14.19	NULL	10 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
7	-13.89	NULL	3 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
8	-13.78	NULL	80 / 370	BP mitotic cell cycle
9	-13.35	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
10	-13.18	NULL	40 / 149	BP DNA replication
11	-12.91	NULL	9 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
12	-12.86	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	-12.67	NULL	8 / 11	GSEA C2KALMA_E2F1_TARGETS
14	-12.34	NULL	9 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
15	-12.13	NULL	10 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
16	-11.9	NULL	7 / 16	GSEA C2Y_AGING_PREMATURE_DN
17	-11.49	NULL	9 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
18	-11.45	NULL	6 / 11	GSEA C2ODONNELL_TFRC_TARGETS_DN
19	-11.35	NULL	8 / 15	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G23_UP
20	-11.22	NULL	87 / 530	Cancer Lembecke_Normal vs Adenoma
21	-11.1	NULL	6 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
22	-11.07	NULL	4 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
23	-11.01	NULL	9 / 15	GSEA C2ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
24	-10.89	NULL	10 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
25	-10.83	NULL	4 / 13	BP regulation of blood vessel size
26	-10.77	NULL	85 / 914	Chr Chr 3
27	-10.73	NULL	7 / 16	Cancer WOLFER_overlap genes
28	-10.66	NULL	7 / 15	GSEA C2Y_AGING_OLD_DN
29	-10.6	NULL	3 / 9	GSEA C2BROWNE_HCMV_INFECTION_8HR_UP
30	-10.58	NULL	9 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
31	-10.58	NULL	10 / 16	GSEA C2SCIEN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
32	-10.42	NULL	6 / 9	GSEA C2REACTOME_CELL_CYCLE_CHECKPOINTS
33	-10.38	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
34	-10.37	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
35	-10.36	NULL	6 / 14	GSEA C2ANTVEER_BREAST_CANCER_METASTASIS_DN
36	-10.19	NULL	3 / 11	GSEA C2DANG_MYC_TARGETS_UP
37	-10.09	NULL	18 / 66	CC condensed chromosome kinetochore
38	-10.09	NULL	7 / 15	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
39	-9.99	NULL	9 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
40	-9.99	NULL	11 / 22	BP DNA replication initiation

p-values

