

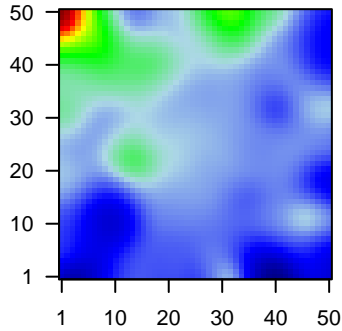
GW_256

Global Summary

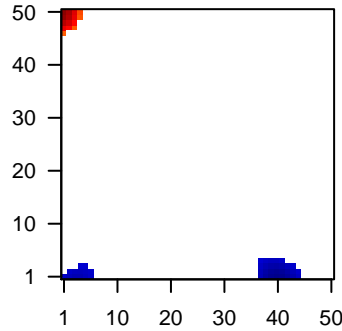
%DE = 0.13
 # genes with fdr < 0.2 = 1456 (757 + / 699 -)
 # genes with fdr < 0.1 = 1062 (587 + / 475 -)
 # genes with fdr < 0.05 = 823 (477 + / 346 -)
 # genes with fdr < 0.01 = 561 (364 + / 197 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.14
 <fdr> = 0.87

Profile



Regulated Spots



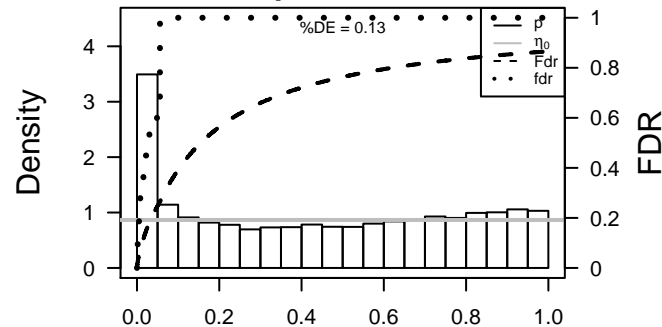
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	144568	1.71	2e-16 4e-14 1 x 50	alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	59	-1.71	2e-16 4e-14 3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	8424	1.95	2e-16 4e-14 3 x 48	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
4	387695	1.96	2e-16 4e-14 1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
5	64207	-1.98	2e-16 4e-14 50 x 40	interferon regulatory factor 2 binding protein-like [Source:HG
6	375791	2.21	2e-16 4e-14 1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symt
7	22802	2.27	2e-16 4e-14 1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	9022	1.84	2e-16 4e-14 1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
9	84518	2.05	2e-16 4e-14 1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
10	54544	2.31	2e-16 4e-14 1 x 50	cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
11	49860	4.24	2e-16 4e-14 1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
12	1475	2.04	2e-16 4e-14 1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
13	1562	1.7	2e-16 4e-14 1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
14	1571	1.65	2e-16 4e-14 5 x 50	cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
15	126410	2.05	2e-16 4e-14 1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
16	92196	1.97	2e-16 4e-14 3 x 50	death associated protein-like 1 [Source:HGNC Symbol;Acc:2
17	1672	2.06	2e-16 4e-14 1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	55894	1.85	2e-16 4e-14 1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	414325	1.98	2e-16 4e-14 1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	1.92	2e-16 4e-14 1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	32.3	NULL	135	H.Tiss WIRTH_Mucosa
2	25.08	NULL	572	Disease GUDJ_psooriasis up
3	16.49	NULL	21	CC cornified envelope
4	13.9	NULL	42	BP keratinization
5	13.62	NULL	53	BP keratinocyte differentiation
6	11.19	NULL	76	BP epidermis development
7	9.8	NULL	153	MF structural constituent of ribosome
8	9.8	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	9.46	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	8.84	NULL	13	BP negative regulation of peptidase activity
11	8.78	NULL	19	BP peptide cross-linking
12	8.71	NULL	253	BP translation
13	8.45	NULL	1318	CC mitochondrion
14	8.22	NULL	44	CC keratin filament
15	8.11	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
16	8.09	NULL	167	CC ribosome
17	7.49	NULL	81	BP viral transcription
18	7.47	NULL	87	BP translational termination
19	7.19	NULL	92	BP translational elongation
20	7.16	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
<i>Underexpressed</i>				
1	-10.92	NULL	250	LymphomaL1ENZ_Stromal signature 1
2	-9.96	NULL	190	CC extracellular matrix
3	-9.25	NULL	8023	MF protein binding
4	-8.73	NULL	823	MF sequence-specific DNA binding transcription factor activity
5	-8.56	NULL	1749	MF DNA binding
6	-8.21	NULL	242	BP extracellular matrix organization
7	-8.04	NULL	1581	BP regulation of transcription, DNA-dependent
8	-7.64	NULL	1574	BP transcription, DNA-templated
9	-7.53	NULL	553	Cancer Lembecke_Colonc Inflammation
10	-7.47	NULL	11	MF platelet-derived growth factor binding
11	-7.37	NULL	16	MMML C6SCIEJ_MMML 1
12	-7.27	NULL	403	BP cell adhesion
13	-7.07	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
14	-7.04	NULL	676	BP positive regulation of transcription from RNA polymerase II promot
15	-7	NULL	4640	CC nucleus
16	-6.93	NULL	504	BP positive regulation of transcription, DNA-dependent
17	-6.78	NULL	386	Chr Chr 22
18	-6.73	NULL	57	MF extracellular matrix structural constituent
19	-6.67	NULL	85	MF integrin binding
20	-6.6	NULL	183	CC proteinaceous extracellular matrix

p-values



GW_256

Local Summary

%DE = 0.98
 # metagenes = 15
 # genes = 220
 # genes in genesets = 215

genes with $fdr < 0.1$ = 212 (211 + / 1 -)
 # genes with $fdr < 0.05$ = 205 (205 + / 0 -)
 # genes with $fdr < 0.01$ = 195 (195 + / 0 -)

<r> metagenes = 0.97
 <r> genes = 0.46

<FC> = 1.34
 <shrinkage-t> = 47.04
 <p-value> = 0
 <fdr> = 0.1

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.71	2e-16	1e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	8424	1.95	2e-16	1e-17	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxxygenase (gamma
3	387695	1.96	2e-16	1e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
4	375791	2.21	2e-16	1e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
5	22802	2.27	2e-16	1e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
6	9022	1.84	2e-16	1e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
7	84518	2.05	2e-16	1e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	2.31	2e-16	1e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987:
9	49860	4.24	2e-16	1e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
10	1475	2.04	2e-16	1e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	1562	1.7	2e-16	1e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
12	126410	2.05	2e-16	1e-17	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
13	92196	1.97	2e-16	1e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
14	1672	2.06	2e-16	1e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
15	55894	1.85	2e-16	1e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	414325	1.98	2e-16	1e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	1673	1.92	2e-16	1e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
18	1828	2.88	2e-16	1e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	131177	1.68	2e-16	1e-17	3 x 50 family with sequence similarity 3, member D [Source:HGNC
20	2312	2.4	2e-16	1e-17	1 x 49 filaggrin [Source:HGNC Symbol;Acc:3748]

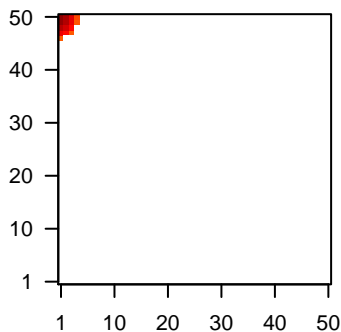
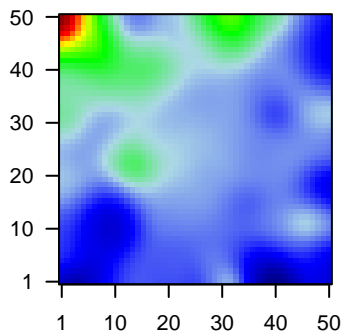
Local Geneset Analysis

Overexpression

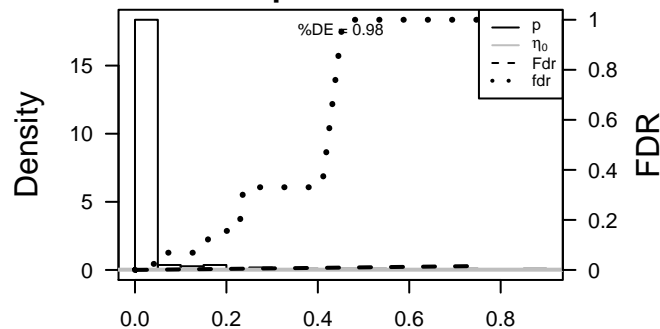
Rank	GSZ	p-value	#in/all	Geneset
1	57.65	NULL	85 / 135	H.Tiss WIRTH_Mucosa
2	34.38	NULL	18 / 21	CC cornified envelope
3	28.3	NULL	93 / 572	Disease GUDJ_pсориазис up
4	27.96	NULL	19 / 42	BP keratinization
5	26.57	NULL	23 / 53	BP keratinocyte differentiation
6	21.54	NULL	24 / 76	BP epidermis development
7	21.04	NULL	10 / 19	BP peptide cross-linking
8	19.9	NULL	6 / 13	BP negative regulation of peptidase activity
9	17.99	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
10	15.18	NULL	7 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
11	13.92	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	13.55	NULL	12 / 79	MF serine-type endopeptidase inhibitor activity
13	13.43	NULL	5 / 10	MF RAGE receptor binding
14	13.4	NULL	8 / 38	BP epithelial cell differentiation
15	13.28	NULL	9 / 44	CC keratin filament
16	12.29	NULL	7 / 29	BP regulation of proteolysis
17	12.21	NULL	54 / 1182	CC extracellular region
18	12.12	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
19	12	NULL	20 / 186	MF structural molecule activity
20	11.8	NULL	10 / 52	BP negative regulation of endopeptidase activity
21	11.52	NULL	13 / 82	CC intermediate filament
22	11.24	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
23	10.97	NULL	12 / 122	MF serine-type endopeptidase activity
24	10.93	NULL	7 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
25	10.4	NULL	6 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
26	10.39	NULL	8 / 21	CC desmosome
27	9.74	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
28	9.58	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
29	9.52	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	9.02	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
31	8.99	NULL	5 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
32	8.9	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
33	8.88	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
34	8.83	NULL	4 / 23	MF peptidase inhibitor activity
35	8.6	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
36	8.26	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
37	8.23	NULL	5 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
38	8.13	NULL	4 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPVP31_DN
39	7.88	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
40	7.76	NULL	6 / 53	MF serine-type peptidase activity

Profile

Spot



p-values



GW_256

Local Summary

%DE = 0.86
 # metagenes = 13
 # genes = 223
 # genes in genesets = 222

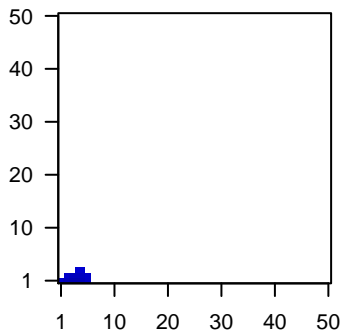
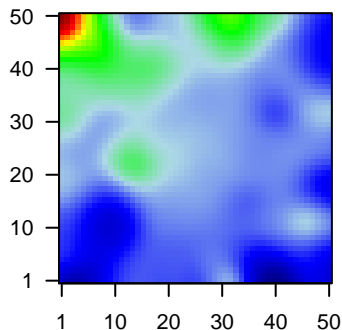
genes with $fdr < 0.1$ = 165 (9 + / 156 -)
 # genes with $fdr < 0.05$ = 133 (7 + / 126 -)
 # genes with $fdr < 0.01$ = 105 (3 + / 102 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.44

$\langle FC \rangle = -0.48$
 $\langle \text{shrinkage-t} \rangle = -16.83$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.47$

Profile

Spot



Local Genelist

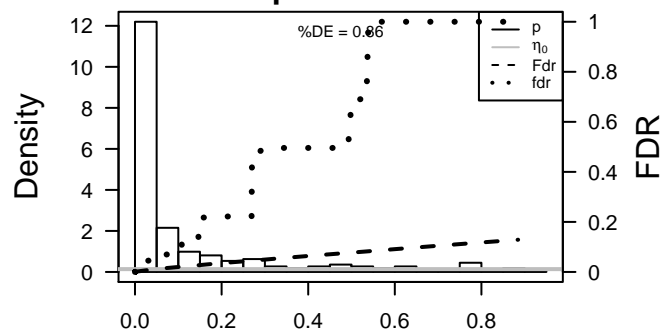
Rank	ID	log(FC)	fdr	p-value	Description
1	59	-1.71	2e-16	7e-15	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Acc:1044]
2	3040	1.61	2e-15	5e-13	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
3	1809	-1.54	2e-14	2e-12	6 x 1 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:3015]
4	7431	-1.5	1e-13	2e-12	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]
5	633	-1.37	2e-13	5e-12	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
6	6423	-1.46	4e-13	5e-12	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:12692]
7	3039	1.45	5e-13	2e-10	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	3043	1.39	5e-12	2e-10	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
9	1278	-1.36	1e-11	7e-10	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
10	1293	-1.33	4e-11	9e-10	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	1277	-1.3	1e-10	9e-10	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	1281	-1.19	1e-10	9e-10	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
13	1289	-1.29	1e-10	7e-09	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
14	3490	-1.26	3e-10	6e-08	3 x 1 insulin-like growth factor binding protein 7 [Source:HGNC Symbol;Acc:1044]
15	1291	-1.2	2e-09	2e-07	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
16	1009	-1.14	1e-08	2e-07	3 x 1 cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC Symbol;Acc:1044]
17	5159	-1.13	2e-08	2e-07	3 x 1 platelet-derived growth factor receptor, beta polypeptide [Source:HGNC Symbol;Acc:1044]
18	7070	-1.11	3e-08	2e-07	4 x 1 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:11801]
19	1462	-1.11	3e-08	1e-06	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
20	7057	-1.07	1e-07	1e-06	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-37.98	NULL	68 / 250	Lymphoma_TENZ_Stromal signature 1
2	-37.64	NULL	14 / 16	MMML_C63CIEJ_MMML 1
3	-35.26	NULL	8 / 11	MF platelet-derived growth factor binding
4	-34.8	NULL	59 / 190	CC extracellular matrix
5	-30.3	NULL	12 / 16	GSEA_C2FARMER_BREAST_CANCER_CLUSTER_5
6	-26.19	NULL	50 / 242	BP extracellular matrix organization
7	-26.08	NULL	8 / 12	miRNA target-29c
8	-26.07	NULL	26 / 69	BP extracellular matrix disassembly
9	-24.19	NULL	5 / 10	GSEA_C2KEGG_ECM_RECEPTOR_INTERACTION
10	-23.57	NULL	10 / 19	MF extracellular matrix binding
11	-23.45	NULL	19 / 57	MF extracellular matrix structural constituent
12	-23.07	NULL	22 / 64	BP collagen catabolic process
13	-22.74	NULL	4 / 5	GSEA_C2COLLER_MYC_TARGETS_DN
14	-22.73	NULL	6 / 13	GSEA_C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
15	-22.54	NULL	7 / 16	GSEA_C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
16	-21.41	NULL	9 / 15	GSEA_C2ONDER_CDH1_TARGETS_2_UP
17	-21.16	NULL	12 / 37	BP collagen fibril organization
18	-20.17	NULL	5 / 13	GSEA_C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
19	-20.15	NULL	5 / 10	GSEA_C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
20	-19.97	NULL	4 / 8	GSEA_C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
21	-19.41	NULL	4 / 10	BP protein heterotrimerization
22	-19.09	NULL	4 / 12	GSEA_C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
23	-18.86	NULL	7 / 15	GSEA_C2DASU_IL6_SIGNALING_SCAR_DN
24	-18.64	NULL	5 / 16	GSEA_C2REACTOME_SIGNALING_BY_PDGF
25	-18.49	NULL	8 / 15	GSEA_C2CROMER_TUMORIGENESIS_UP
26	-18.48	NULL	7 / 16	GSEA_C2ROZANOV_MMP14_TARGETS_SUBSET
27	-18.44	NULL	21 / 119	Lymphoma_SOLOWSKI_green total
28	-18.15	NULL	5 / 13	GSEA_C2TAI_RESPONSE_TO_RADIATION_THERAPY
29	-18.07	NULL	6 / 16	GSEA_C2ZHU_CMV_ALL_DN
30	-17.67	NULL	6 / 16	GSEA_C2CROONQUIST_STROMAL_STIMULATION_UP
31	-17.08	NULL	15 / 68	CC collagen
32	-17.01	NULL	5 / 16	GSEA_C2JRS_ADIPOCYTE_DIFFERENTIATION_DN
33	-16.92	NULL	6 / 11	MMML_C63CIEJ_MMML 31
34	-16.87	NULL	7 / 16	GSEA_C2LIEN_BREAST_CARCINOMA_METAPLASTIC
35	-16.85	NULL	65 / 683	CC extracellular space
36	-16.62	NULL	4 / 10	GSEA_C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
37	-16.38	NULL	14 / 85	MF integrin binding
38	-16.27	NULL	31 / 183	CC proteinaceous extracellular matrix
39	-16.16	NULL	2 / 3	GSEA_C2KONDO_HYPOXIA
40	-16.08	NULL	5 / 16	GSEA_C2ZHU_CMV_24_HR_DN

p-values



GW_256

Local Summary

%DE = 0.86
 # metagenes = 28
 # genes = 379
 # genes in genesets = 351
 # genes with $fdr < 0.1$ = 281 (1 + / 280 -)
 # genes with $fdr < 0.05$ = 225 (1 + / 224 -)
 # genes with $fdr < 0.01$ = 148 (0 + / 148 -)

<r> metagenes = 0.94

<r> genes = 0.41

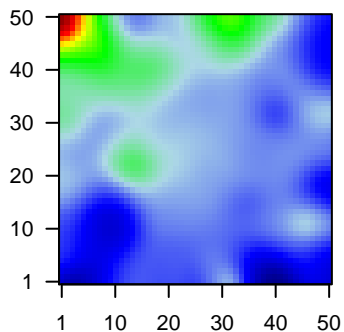
<FC> = -0.48

<shrinkage-t> = -16.79

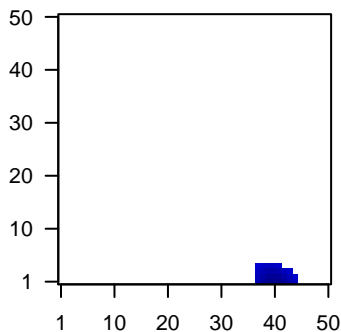
<p-value> = 0.01

<fdr> = 0.52

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	23466	-1.27	3e-10	4e-07	41 x 1 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
2	100132406	-1.14	1e-08	4e-07	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
3	399900	-1.04	2e-08	4e-07	39 x 1
4	440353	-1.13	2e-08	8e-07	40 x 1
5	3127	-1.1	5e-08	8e-07	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:
6	9612	-1.09	5e-08	8e-07	38 x 1 nuclear receptor corepressor 2 [Source:HGNC Symbol;Acc:7
7	641737	-1.01	7e-08	8e-07	40 x 1
8	91368	-0.99	8e-08	1e-06	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC S
9	114785	-1.07	1e-07	1e-06	39 x 1 methyl-CpG binding domain protein 6 [Source:HGNC Symbo
10	9747	-0.97	1e-07	2e-06	39 x 1 family with sequence similarity 115, member A [Source:HGNC
11	25777	-1.04	2e-07	2e-06	42 x 2 Sad1 and UNC84 domain containing 2 [Source:HGNC Symbr
12	442578	-1.04	2e-07	8e-06	39 x 1
13	729603	-0.93	5e-07	8e-06	40 x 1
14	400818	-1.01	6e-07	8e-06	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
15	8216	-0.99	8e-07	8e-06	38 x 3 leucine-zipper-like transcription regulator 1 [Source:HGNC S
16	25862	-0.99	8e-07	1e-05	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2c
17	5660	-0.9	1e-06	2e-05	43 x 1 prosaposin [Source:HGNC Symbol;Acc:9498]
18	4924	-0.89	2e-06	2e-05	42 x 1 nucleobindin 1 [Source:HGNC Symbol;Acc:8043]
19	404093	-0.96	2e-06	4e-05	39 x 1 CUE domain containing 1 [Source:HGNC Symbol;Acc:31350]
20	84061	-0.95	3e-06	5e-05	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.26	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-8.53	NULL	4 / 14	MMML C2BIOCIEJ_MMML_8
3	-7.13	NULL	3 / 13	GSEA C2ST_GAQ_PATHWAY
4	-7.06	NULL	4 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
5	-6.71	NULL	1 / 2	miRNA target-193a
6	-6.17	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
7	-6.07	NULL	2 / 12	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
8	-5.88	NULL	55 / 1135	Chr Chr 19
9	-5.73	NULL	3 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
10	-5.73	NULL	3 / 16	GSEA C2REACTOME_TRKA_SIGNALLING_FROM_THE_PLASMA_MEMB
11	-5.73	NULL	2 / 12	GSEA C2BARRIER_COLON_CANCER_RECURRENCE_DN
12	-5.64	NULL	2 / 10	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
13	-5.64	NULL	2 / 16	GSEA C2PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
14	-5.46	NULL	4 / 29	CC histone deacetylase complex
15	-5.23	NULL	2 / 20	MF ligand-dependent nuclear receptor binding
16	-5.18	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
17	-5.05	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
18	-4.99	NULL	2 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
19	-4.77	NULL	2 / 14	GSEA C2BIOCARTA_IL12_PATHWAY
20	-4.75	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
21	-4.73	NULL	2 / 14	BP cellular response to estradiol stimulus
22	-4.71	NULL	3 / 16	BP negative regulation of neurogenesis
23	-4.7	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
24	-4.7	NULL	2 / 13	GSEA C2ST_GA13_PATHWAY
25	-4.7	NULL	3 / 16	GSEA C2POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP
26	-4.64	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
27	-4.64	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
28	-4.58	NULL	3 / 12	GSEA C2BIOCARTA_HDAC_PATHWAY
29	-4.57	NULL	2 / 14	GSEA C2REACTOME_FURTHER_PLATELET_RELEASE
30	-4.55	NULL	3 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
31	-4.51	NULL	2 / 15	GSEA C2WONG_IFNA2_RESISTANCE_DN
32	-4.47	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
33	-4.47	NULL	1 / 6	GSEA C2TURJANSKI_MAPK8_AND_MAPK9_TARGETS
34	-4.42	NULL	1 / 6	GSEA C2PENG_GlutAMINE_DEPRIVATION_UP
35	-4.42	NULL	1 / 6	GSEA C2ST_INTERLEUKIN_13_PATHWAY
36	-4.42	NULL	1 / 6	GSEA C2ST_IL_13_PATHWAY
37	-4.41	NULL	2 / 16	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G24
38	-4.36	NULL	3 / 13	GSEA C2BIOCARTA_MEF2D_PATHWAY
39	-4.31	NULL	3 / 16	GSEA C2SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
40	-4.31	NULL	2 / 15	GSEA C2FIRESTEIN_PROLIFERATION

p-values

