

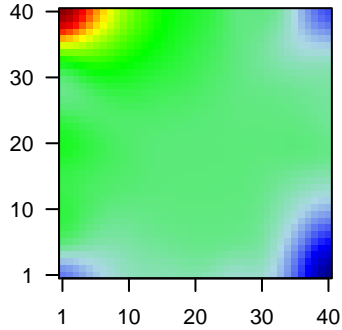
11_nH

Global Summary

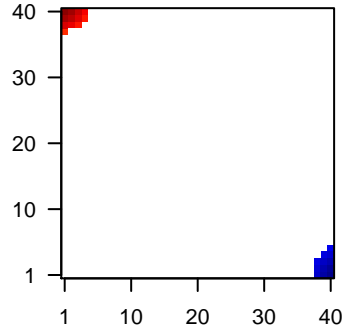
%DE = 0.25
 # genes with fdr < 0.2 = 4595 (2159 + / 2436 -)
 # genes with fdr < 0.1 = 4174 (1962 + / 2212 -)
 # genes with fdr < 0.05 = 3724 (1754 + / 1970 -)
 # genes with fdr < 0.01 = 3229 (1536 + / 1693 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0.01
 <fdr> = 0.75

Profile



Regulated Spots



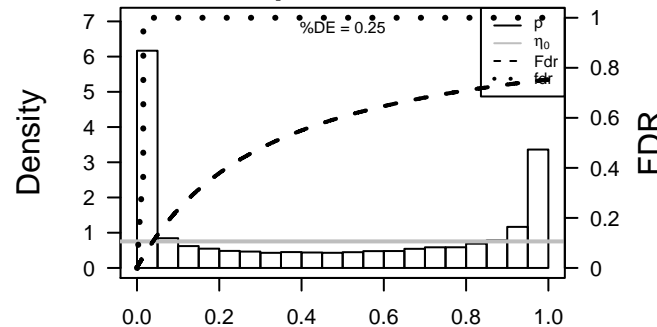
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000000000	0.27	2e-16	3e-15	6 x 38 period circadian clock 3 [Source:HGNC Symbol;Acc:HGNC:8
2	ENSG000000000	0.24	2e-16	3e-15	7 x 37 urotensin 2 [Source:HGNC Symbol;Acc:HGNC:12636]
3	ENSG000000000	-0.26	2e-16	3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
4	ENSG000000001	0.28	2e-16	3e-15	9 x 38 angiotensin-like 7 [Source:HGNC Symbol;Acc:HGNC:24078
5	ENSG000000001	0.28	2e-16	3e-15	7 x 38 mitofusin 2 [Source:HGNC Symbol;Acc:HGNC:16877]
6	ENSG000000000	-0.24	2e-16	3e-15	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Sour
7	ENSG000000001	-0.26	2e-16	3e-15	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;
8	ENSG000000001	0.47	2e-16	3e-15	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [
9	ENSG000000001	-0.28	2e-16	3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;A
10	ENSG000000001	-0.25	2e-16	3e-15	25 x 1 aldo-keto reductase family 7, member A3 (aflatoxin aldehyde
11	ENSG000000001	0.28	2e-16	3e-15	8 x 40 phospholipase A2, group V [Source:HGNC Symbol;Acc:HGNC
12	ENSG000000001	-0.29	2e-16	3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
13	ENSG000000001	0.37	2e-16	3e-15	1 x 33 low density lipoprotein receptor class A domain containing 2 [
14	ENSG000000001	0.31	2e-16	3e-15	1 x 35 heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:H
15	ENSG000000000	-0.29	2e-16	3e-15	40 x 6 lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:673
16	ENSG000000001	-0.23	2e-16	3e-15	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:Hi
17	ENSG000000001	-0.33	2e-16	3e-15	38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:H
18	ENSG000000001	0.54	2e-16	3e-15	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
19	ENSG000000001	-0.68	2e-16	3e-15	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HC
20	ENSG000000001	-0.54	2e-16	3e-15	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]

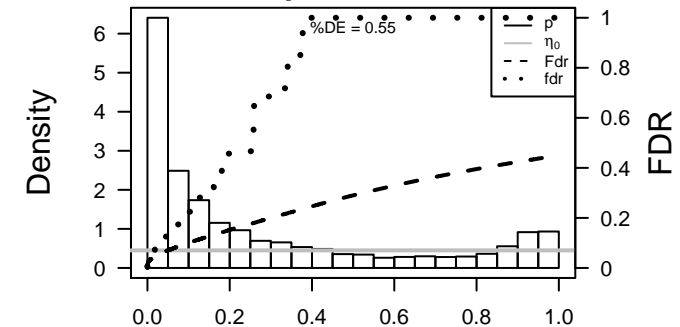
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	32.8	0e+00	132	Colon CaMrisa_CRC-cluster-b
2	28.59	1e-03	16	Cancer LIU_PROSTATE_CANCER_DN
3	23.23	6e-06	22	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
4	21.5	9e-06	478	GSEA C2LIM_MAMMARY_STEM_CELL_UP
5	21.26	9e-06	40	GSEA C2TOMLINS_PROSTATE_CANCER_DN
6	20.67	1e-05	160	GSEA C2BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
7	20.2	1e-05	18	GSEA C2NIELSEN_LEIOMYOSARCOMA_CNN1_UP
8	18.74	2e-05	44	GSEA C2REACTOME_MUSCLE_CONTRACTION
9	18.03	2e-05	40	GSEA C2PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE
10	17.92	2e-05	303	GSEA C2PASINI_SUZ12_TARGETS_DN
11	17.39	2e-05	294	GSEA C2ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODE
12	17.25	2e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
13	17.06	2e-05	105	BP muscle contraction
14	16.45	2e-05	10278	Brain Overlap_fetal_midbrain_ReprPCWk
15	16.43	2e-05	445	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
16	16.4	2e-05	6320	Brain Overlap_fetal_midbrain_HetRpts
17	16.33	2e-05	535	GSEA C2CHICAS_RB1_TARGETS_CONFLUENT
18	16.28	2e-05	10239	Brain Overlap_fetal_midbrain_ReprPC
19	15.39	3e-05	198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
20	14.97	3e-05	399	Disease GUDJ_psooriasis down
<i>Underexpressed</i>				
1	-18.05	2e-05	251	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
2	-17.39	2e-05	608	Disease GUDJ_psooriasis up
3	-17.11	2e-05	429	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
4	-16.44	2e-05	455	GSEA C2ONDER_CDH1_TARGETS_2_DN
5	-14.93	3e-05	126	GSEA C2VECCI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
6	-14.62	3e-05	222	GSEA C2OLDREN_GEFITINIB_RESISTANCE_DN
7	-14.57	3e-05	104	Colon CaMrisa_CRC_TCGA_group.over_A_normal_UP
8	-14.54	3e-05	643	Colon CaMrisa_CRC_TCGA_meth_kmeans_J_CIMP_H_DN
9	-14.5	3e-05	412	GSEA C2LIM_MAMMARY_STEM_CELL_DN
10	-14.47	3e-05	115	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
11	-14.06	4e-05	144	LymphomaWIRTH_lymphoma937_spot G
12	-13.44	4e-05	174	GSEA C2LI_AMPLIFIED_IN_LUNG_CANCER
13	-13.33	4e-05	142	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression
14	-13.11	4e-05	132	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
15	-12.94	5e-05	110	Colon CaMrisa_CRC-cluster-h
16	-12.62	6e-05	220	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
17	-11.86	8e-05	49	Colon CaMrisa_CRC-cluster-f
18	-11.63	9e-05	210	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
19	-11.55	1e-04	109	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
20	-11.51	1e-04	688	Colon CaMrisa_CRC_TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN

p-values



p-values



11_nH

Local Summary

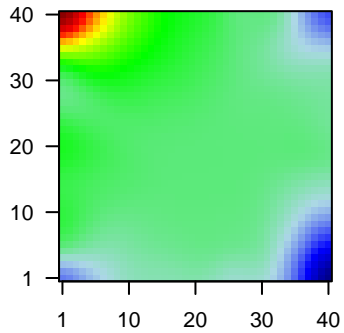
%DE = 1
 # metagenes = 12
 # genes = 256
 # genes in genesets = 254

 # genes with $fdr < 0.1 = 254$ (254 + / 0 -)
 # genes with $fdr < 0.05 = 254$ (254 + / 0 -)
 # genes with $fdr < 0.01 = 254$ (254 + / 0 -)

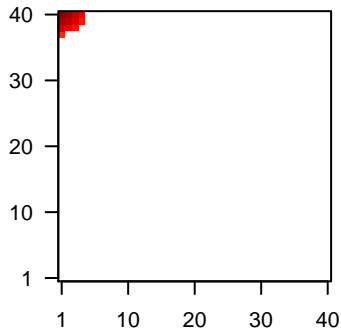
$\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.82

 $\langle FC \rangle = 0.63$
 $\langle t\text{-score} \rangle = 12.73$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0$

Profile



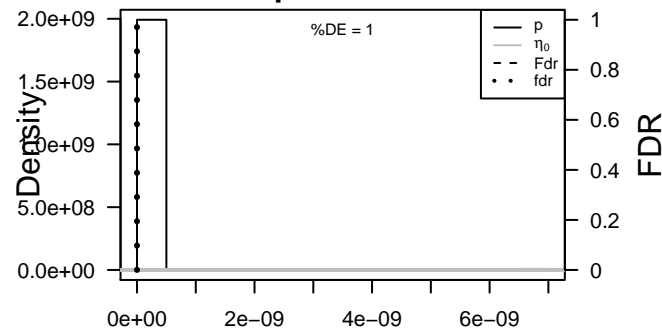
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.47	2e-16	9e-19	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [
2	ENSG0000001	0.54	2e-16	9e-19	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
3	ENSG0000001	0.42	2e-16	9e-19	4 x 40 syndecan 3 [Source:HGNC Symbol;Acc:HGNC:10660]
4	ENSG0000001	0.4	2e-16	9e-19	4 x 40 wntless Wnt ligand secretion mediator [Source:HGNC Symbc
5	ENSG0000001	0.63	2e-16	9e-19	1 x 40 nexilin (F actin binding protein) [Source:HGNC Symbol;Acc:H
6	ENSG0000001	0.32	2e-16	9e-19	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
7	ENSG0000001	0.59	2e-16	9e-19	2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f
8	ENSG0000000	0.48	2e-16	9e-19	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
9	ENSG0000001	0.7	2e-16	9e-19	1 x 40 tetraspanin 2 [Source:HGNC Symbol;Acc:HGNC:20659]
10	ENSG0000001	0.82	2e-16	9e-19	1 x 40 calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
11	ENSG0000001	0.56	2e-16	9e-19	4 x 40 prostaglandin F2 receptor inhibitor [Source:HGNC Symbol;Ac
12	ENSG0000001	0.31	2e-16	9e-19	1 x 38
13	ENSG0000000	0.44	2e-16	9e-19	1 x 39 pleckstrin homology domain containing, family O member 1 [f
14	ENSG0000001	0.47	2e-16	9e-19	1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:
15	ENSG0000000	0.42	2e-16	9e-19	3 x 40 ATPase, Na+/K+ transporting, alpha 2 polypeptide [Source:H
16	ENSG0000001	0.47	2e-16	9e-19	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
17	ENSG0000001	0.55	2e-16	9e-19	2 x 40 discoidin domain receptor tyrosine kinase 2 [Source:HGNC S
18	ENSG0000001	0.79	2e-16	9e-19	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc
19	ENSG0000001	1.07	2e-16	9e-19	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
20	ENSG0000001	0.54	2e-16	9e-19	3 x 40 angiotensin-like 1 [Source:HGNC Symbol;Acc:HGNC:489]

p-values



11_nH

Local Summary

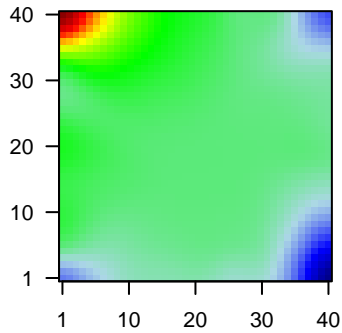
%DE = 1
 # metagenes = 12
 # genes = 250
 # genes in genesets = 247

 # genes with $fdr < 0.1$ = 248 (0 + / 248 -)
 # genes with $fdr < 0.05$ = 248 (0 + / 248 -)
 # genes with $fdr < 0.01$ = 248 (0 + / 248 -)

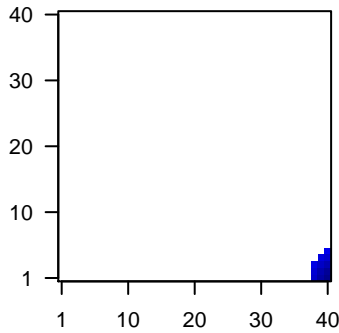
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.66

 $\langle FC \rangle$ = -0.45
 $\langle t\text{-score} \rangle$ = -9.13
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.28	2e-16	9e-19	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:1712]
2	ENSG0000001	-0.29	2e-16	9e-19	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
3	ENSG0000001	-0.33	2e-16	9e-19	38 x 1 fucosidase, alpha-L- 1, tissue [Source:HGNC Symbol;Acc:HGNC:1712]
4	ENSG0000001	-0.68	2e-16	9e-19	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC Symbol;Acc:HGNC:1712]
5	ENSG0000001	-0.33	2e-16	9e-19	39 x 4 ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:1712]
6	ENSG0000001	-0.87	2e-16	9e-19	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
7	ENSG0000001	-0.43	2e-16	9e-19	40 x 1 serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:23201]
8	ENSG0000001	-0.29	2e-16	9e-19	40 x 5 KIAA1522 [Source:HGNC Symbol;Acc:HGNC:29301]
9	ENSG0000001	-0.62	2e-16	9e-19	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:20657]
10	ENSG0000000	-0.52	2e-16	9e-19	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:21297]
11	ENSG0000001	-0.97	2e-16	9e-19	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:21297]
12	ENSG0000002	-0.27	2e-16	9e-19	38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symbol;Acc:HGNC:20657]
13	ENSG0000001	-1.02	2e-16	9e-19	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
14	ENSG0000001	-0.4	2e-16	9e-19	40 x 5 24-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:HGNC:21297]
15	ENSG0000000	-0.59	2e-16	9e-19	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:21297]
16	ENSG0000001	-0.5	2e-16	9e-19	40 x 3 EPS8-like 3 [Source:HGNC Symbol;Acc:HGNC:21297]
17	ENSG0000001	-0.51	2e-16	9e-19	40 x 4 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:21297]
18	ENSG0000001	-0.48	2e-16	9e-19	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:21297]
19	ENSG0000001	-0.48	2e-16	9e-19	38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
20	ENSG0000001	-0.31	2e-16	9e-19	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:21297]

p-values

