

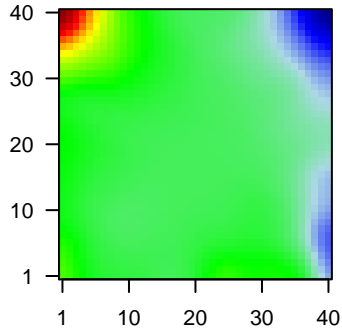
other_normHNPC vs

Global Summary

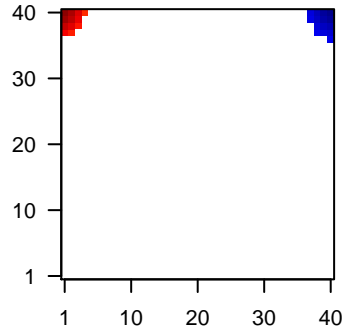
%DE = 0.32
 # genes with fdr < 0.2 = 165 (19 + / 146 -)
 # genes with fdr < 0.1 = 42 (1 + / 41 -)
 # genes with fdr < 0.05 = 7 (0 + / 7 -)
 # genes with fdr < 0.01 = 1 (0 + / 1 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0.27
 <fdr> = 0.68

Profile



Regulated Spots



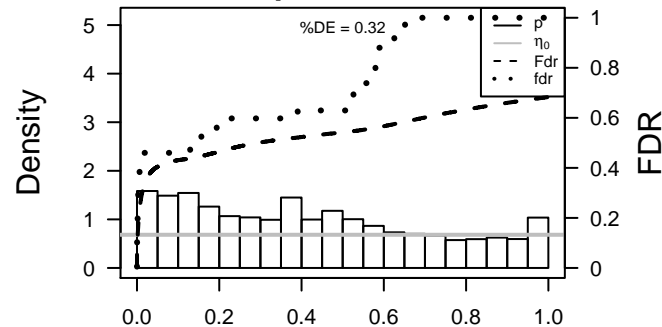
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000001	-0.14	6e-07	0.005	37 x 35 IQ motif containing GTPase activating protein 3 [Source:HGNC
2	ENSG00000001	-0.21	8e-07	0.016	37 x 36 MYC-associated zinc finger protein (purine-binding transcrip
3	ENSG00000001	-0.01	2e-06	0.038	26 x 40 S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
4	ENSG00000001	-0.06	8e-06	0.038	35 x 31 jagged 2 [Source:HGNC Symbol;Acc:HGNC:6189]
5	ENSG00000002	-0.29	1e-05	0.038	35 x 40 translocase of outer mitochondrial membrane 6 homolog (yea
6	ENSG00000001	-0.08	1e-05	0.038	33 x 32 PARP1 binding protein [Source:HGNC Symbol;Acc:HGNC:26
7	ENSG00000000	-0.11	2e-05	0.038	35 x 34 origin recognition complex, subunit 1 [Source:HGNC Symbol;
8	ENSG00000002	-0.18	2e-05	0.077	37 x 38 phosphoglycerate mutase family member 5 [Source:HGNC S
9	ENSG00000000	-0.06	2e-05	0.077	27 x 35 tRNA methyltransferase 6 [Source:HGNC Symbol;Acc:HGNC
10	ENSG00000001	-0.18	4e-05	0.077	38 x 36 5'-nucleotidase domain containing 2 [Source:HGNC Symbol;
11	ENSG00000001	-0.04	4e-05	0.077	31 x 28 Rho GTPase activating protein 11B [Source:HGNC Symbol;A
12	ENSG00000001	-0.04	5e-05	0.077	29 x 28 BRCA1 interacting protein C-terminal helicase 1 [Source:HG
13	ENSG00000000	-0.04	5e-05	0.077	29 x 28 claspin [Source:HGNC Symbol;Acc:HGNC:19715]
14	ENSG00000001	-0.01	6e-05	0.077	25 x 28 ripply transcriptional repressor 3 [Source:HGNC Symbol;Acc:
15	ENSG00000002	-0.01	6e-05	0.077	28 x 23
16	ENSG00000001	-0.06	6e-05	0.085	31 x 31
17	ENSG00000001	0.19	8e-05	0.085	1 x 31 serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigm
18	ENSG00000001	-0.13	8e-05	0.085	36 x 37 angiotensin II receptor-associated protein [Source:HGNC Sy
19	ENSG00000001	-0.25	9e-05	0.085	37 x 38 marker of proliferation Ki-67 [Source:HGNC Symbol;Acc:HGI
20	ENSG00000001	-0.19	9e-05	0.085	40 x 38 hes family bHLH transcription factor 6 [Source:HGNC Symbol

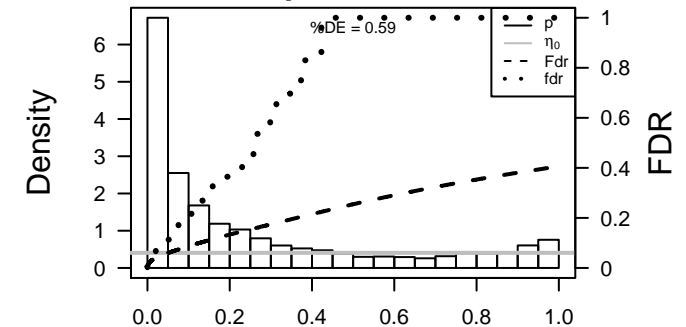
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.86	4e-05	4879	Colon CaQuest1_Colon
2	13.81	4e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
3	13.67	4e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	13.63	4e-05	478	GSEA C2LIM_MAMMARY_STEM_CELL_UP
5	13.49	4e-05	3109	Colon CaQuestP_Colon
6	13.14	4e-05	5039	LymphomaL1OPP_Repressed
7	12.68	6e-05	368	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B
8	12.36	6e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
9	12.17	6e-05	148	Colon CaQuesta_CRC-cluster-a
10	12	6e-05	692	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
11	11.76	7e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
12	11.69	7e-05	3406	Colon CaQuestPC_Colon
13	11.52	8e-05	2947	Colon CaQuestPCWk_Colon
14	11.45	8e-05	132	Colon CaQuesta_CRC-cluster-b
15	11.18	9e-05	336	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_DN
16	11.02	1e-02	16	Cancer LIU_PROSTATE_CANCER_DN
17	10.98	9e-05	418	GSEA C2SWEET_LUNG_CANCER_KRAS_DN
18	10.95	9e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
19	10.72	1e-04	476	Tissue WIRTH_Nervous System
20	10.43	1e-04	844	Colon CaQuestbcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
<i>Underexpressed</i>				
1	-28.14	0e+00	550	Cancer Lembecke_Normal vs Adenoma
2	-26.67	0e+00	807	LymphomaL1opp_June14_MML937_tumors+controls_group.overexpression
3	-26.4	0e+00	811	LymphomaL1WIRTH_lymphoma937_spot D
4	-22.92	0e+00	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
5	-22.59	0e+00	145	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
6	-22.37	0e+00	546	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	-22.15	0e+00	400	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
8	-21.99	0e+00	316	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	-20.77	0e+00	282	GSEA C2MANALO_HYPOXIA_DN
10	-20.52	0e+00	713	Colon CaQuesttrack_CRC_TCGA_group.over_C_normal_DN
11	-20.43	0e+00	830	Colon CaQuesttrack_CRC_TCGA_corr_R_normal_DN
12	-19.68	3e-06	1298	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
13	-18.84	5e-06	668	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
14	-18.61	1e-05	859	GSEA C2LEE_BMP2_TARGETS_DN
15	-18.53	2e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	-18.02	1e-05	1563	GSEA C2PUJANA_BRCA1_PCC_NETWORK
17	-17.76	1e-05	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
18	-17.45	1e-05	446	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
19	-17.37	1e-05	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
20	-17.09	2e-05	8123	Colon CaQuestF_Colon

p-values



p-values



other_normHNPC vs

Local Summary

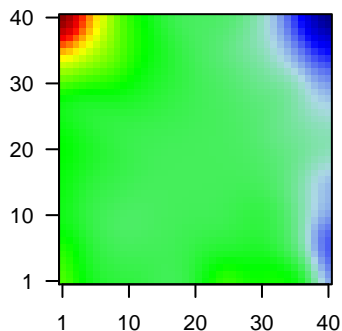
%DE = 0.99
 # metagenes = 12
 # genes = 253
 # genes in genesets = 251

 # genes with $fdr < 0.1$ = 249 (249 + / 0 -)
 # genes with $fdr < 0.05$ = 249 (249 + / 0 -)
 # genes with $fdr < 0.01$ = 233 (233 + / 0 -)

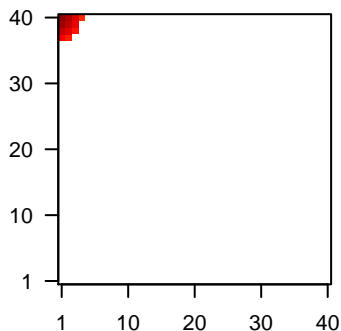
<r> metagenes = 1
 <r> genes = 0.91

<FC> = 0.42
 <t-score> = 2.29
 <p-value> = 0.08
 <fdr> = 0.48

Profile



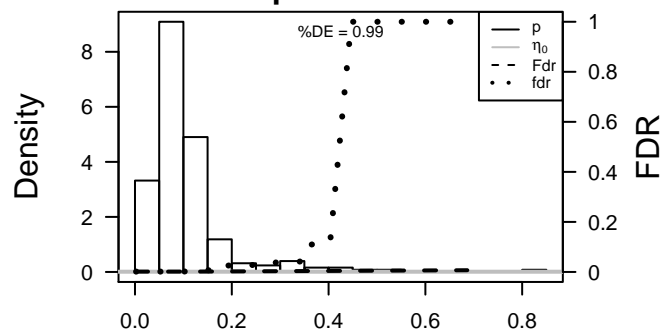
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000000	0.41	0.003	0.001	1 x 37 phosphatidic acid phosphatase type 2A [Source:HGNC Symb
2	ENSG000000	0.64	0.008	0.001	1 x 40 insulin-like growth factor binding protein 7 [Source:HGNC Sy
3	ENSG000000	0.55	0.009	0.001	1 x 39 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HG
4	ENSG000000	0.83	0.011	0.001	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
5	ENSG000000	0.4	0.012	0.001	1 x 37 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:I
6	ENSG000000	0.61	0.014	0.001	1 x 38 chromosome 8 open reading frame 4 [Source:HGNC Symbol
7	ENSG000000	0.63	0.014	0.001	1 x 40 microfibrillar-associated protein 4 [Source:HGNC Symbol;Ac
8	ENSG000000	0.44	0.015	0.001	3 x 40 related RAS viral (r-ras) oncogene homolog [Source:HGNC
9	ENSG000000	0.35	0.020	0.001	1 x 38 alpha-2-macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
10	ENSG000000	0.39	0.021	0.001	2 x 37 fibrinogen-like 2 [Source:HGNC Symbol;Acc:HGNC:3696]
11	ENSG000000	1.38	0.021	0.001	1 x 40 desmin [Source:HGNC Symbol;Acc:HGNC:2770]
12	ENSG000000	0.43	0.022	0.001	3 x 40 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
13	ENSG000000	1.23	0.022	0.001	1 x 40 transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
14	ENSG000000	0.37	0.023	0.001	1 x 37 decorin [Source:HGNC Symbol;Acc:HGNC:2705]
15	ENSG000000	0.38	0.024	0.001	1 x 38 annexin A6 [Source:HGNC Symbol;Acc:HGNC:544]
16	ENSG000000	0.51	0.026	0.001	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
17	ENSG000000	0.68	0.027	0.001	1 x 40 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
18	ENSG000000	0.34	0.028	0.001	3 x 40 necdin, melanoma antigen (MAGE) family member [Source:H
19	ENSG000000	1.36	0.028	0.001	1 x 40 myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:I
20	ENSG000000	0.57	0.029	0.001	2 x 40 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC

p-values



other_normHNPC vs

Local Summary

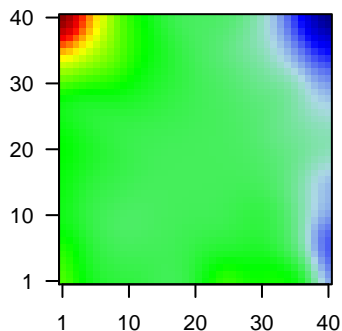
%DE = 0.99
 # metagenes = 15
 # genes = 340
 # genes in genesets = 335

 # genes with $fdr < 0.1$ = 336 (4 + / 332 -)
 # genes with $fdr < 0.05$ = 334 (4 + / 330 -)
 # genes with $fdr < 0.01$ = 318 (2 + / 316 -)

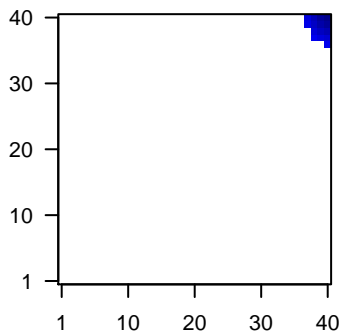
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.86

 $\langle FC \rangle$ = -0.3
 $\langle t\text{-score} \rangle$ = -3.68
 $\langle p\text{-value} \rangle$ = 0.07
 $\langle fdr \rangle$ = 0.49

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.19	9e-05	9e-05	40 x 38 hes family bHLH transcription factor 6 [Source:HGNC Symbol]
2	ENSG0000001	-0.34	1e-04	9e-05	40 x 40 peroxiredoxin 4 [Source:HGNC Symbol;Acc:HGNC:17169]
3	ENSG0000001	-0.35	1e-04	9e-05	40 x 39 Tu translation elongation factor, mitochondrial [Source:HGNC]
4	ENSG0000001	-0.57	1e-04	9e-05	40 x 40 malectin [Source:HGNC Symbol;Acc:HGNC:28973]
5	ENSG0000001	-0.19	2e-04	9e-05	38 x 38 translocase of outer mitochondrial membrane 40 homolog (ye
6	ENSG0000001	-0.18	2e-04	9e-05	38 x 38 transmembrane protein 97 [Source:HGNC Symbol;Acc:HGNC]
7	ENSG0000000	-0.34	2e-04	9e-05	38 x 39 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:H
8	ENSG0000001	-0.29	2e-04	1e-04	40 x 39 prohibitin [Source:HGNC Symbol;Acc:HGNC:8912]
9	ENSG0000001	-0.34	3e-04	1e-04	40 x 40 transmembrane emp24 protein transport domain containing 3
10	ENSG0000001	-0.23	3e-04	1e-04	39 x 38 stomatin (EPB72)-like 2 [Source:HGNC Symbol;Acc:HGNC:1
11	ENSG0000001	-0.28	4e-04	2e-04	39 x 40 serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
12	ENSG0000000	-0.22	5e-04	2e-04	37 x 40 eukaryotic translation initiation factor 3, subunit I [Source:HGI
13	ENSG0000001	-1.5	5e-04	2e-04	40 x 40 lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
14	ENSG0000001	-0.34	5e-04	2e-04	39 x 40 heat shock 10kDa protein 1 [Source:HGNC Symbol;Acc:HGNC]
15	ENSG0000001	-0.23	6e-04	2e-04	38 x 40 solute carrier family 39 (zinc transporter), member 8 [Source:
16	ENSG0000000	-0.23	8e-04	2e-04	40 x 37 cytochrome b561 [Source:HGNC Symbol;Acc:HGNC:2571]
17	ENSG0000001	-0.28	9e-04	2e-04	37 x 40 solute carrier family 35 (adenosine 3'-phospho 5'-phospho
18	ENSG0000001	-0.24	9e-04	2e-04	38 x 40 emopamil binding protein-like [Source:HGNC Symbol;Acc:HGNC]
19	ENSG0000001	-0.2	9e-04	2e-04	38 x 37 proteasome (prosome, macropain) assembly chaperone 1 [S
20	ENSG0000001	-0.39	1e-03	2e-04	40 x 38 ribophorin II [Source:HGNC Symbol;Acc:HGNC:10382]

p-values

