

# other\_normHNPC vs

## Global Summary

%DE = 0.47  
 # genes with fdr < 0.2 = 1571 ( 292 + / 1279 -)  
 # genes with fdr < 0.1 = 891 ( 118 + / 773 -)  
 # genes with fdr < 0.05 = 512 ( 49 + / 463 -)  
 # genes with fdr < 0.01 = 65 ( 3 + / 62 -)  
  
 # genes in genesets = 18990  
  
 <FC> = 0  
 <t-score> = -0.17  
 <p-value> = 0.17  
 <fdr> = 0.53

## Global Genelist

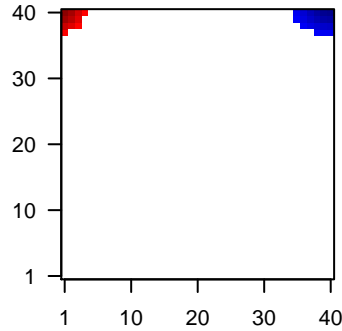
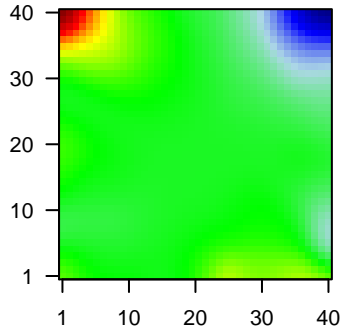
Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	ENSG00000001	-0.25	6e-08	4e-04 36 x 40 dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Acc:HGNC:100001]
2	ENSG00000001	-0.04	8e-08	1e-03 36 x 26 p21 protein (Cdc42/Rac)-activated kinase 6 [Source:HGNC Symbol;Acc:HGNC:100001]
3	ENSG00000000	-0.13	2e-07	1e-03 35 x 36 thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:100001]
4	ENSG00000001	-0.24	3e-07	4e-03 37 x 40 proliferation-associated 2G4, 38kDa [Source:HGNC Symbol;Acc:HGNC:100001]
5	ENSG00000001	-0.17	1e-06	4e-03 37 x 36 pseudouridylyl synthase 1 [Source:HGNC Symbol;Acc:HGNC:100001]
6	ENSG00000001	-0.59	2e-06	4e-03 40 x 40 ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:HGNC:100001]
7	ENSG00000001	-0.23	2e-06	4e-03 39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;Acc:HGNC:100001]
8	ENSG00000001	-0.48	3e-06	4e-03 40 x 40 protein disulfide isomerase family A, member 4 [Source:HGNC Symbol;Acc:HGNC:100001]
9	ENSG00000001	-0.12	3e-06	4e-03 38 x 34 proline/serine-rich coiled-coil 1 [Source:HGNC Symbol;Acc:HGNC:100001]
10	ENSG00000001	-0.1	3e-06	4e-03 31 x 38 GTP binding protein 4 [Source:HGNC Symbol;Acc:HGNC:100001]
11	ENSG00000001	-0.37	3e-06	4e-03 35 x 40 nucleophosmin (nucleolar phosphoprotein B23, numatrin) [Source:HGNC Symbol;Acc:HGNC:100001]
12	ENSG00000001	-0.08	4e-06	4e-03 30 x 36 polymerase (RNA) I polypeptide B, 128kDa [Source:HGNC Symbol;Acc:HGNC:100001]
13	ENSG00000001	-0.08	4e-06	4e-03 34 x 34 GINS complex subunit 1 (Psf1 homolog) [Source:HGNC Symbol;Acc:HGNC:100001]
14	ENSG00000001	-0.22	5e-06	4e-03 36 x 38 protein phosphatase, Mg2+/Mn2+ dependent, 1G [Source:HGNC Symbol;Acc:HGNC:100001]
15	ENSG00000001	-0.05	5e-06	4e-03 38 x 26 X-ray repair complementing defective repair in Chinese hamster cells 1 [Source:HGNC Symbol;Acc:HGNC:100001]
16	ENSG00000001	-0.16	5e-06	4e-03 37 x 36 GrpE-like 1, mitochondrial (E. coli) [Source:HGNC Symbol;Acc:HGNC:100001]
17	ENSG00000001	-0.25	5e-06	4e-03 40 x 38 forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:3818]
18	ENSG00000002	-0.17	6e-06	4e-03 38 x 36
19	ENSG00000000	-0.06	7e-06	4e-03 29 x 35 spindle apparatus coiled-coil protein 1 [Source:HGNC Symbol;Acc:HGNC:100001]
20	ENSG00000001	-0.07	7e-06	4e-03 33 x 33 polo-like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]

## Global Geneset Analysis

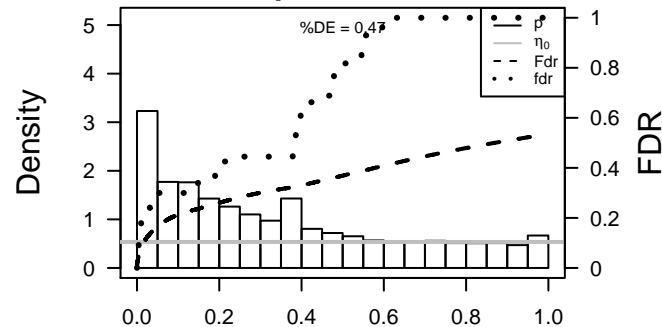
Rank	GSZ	p-value	#all	Geneset
<b>Overexpressed</b>				
1	17.65	1e-05	4879	Colon CaRectal_Colon
2	16.69	2e-05	5039	LymphomaLymphoma_Repressed
3	15.48	2e-05	507	Colon CaRectal_CRC_TCGA_corr_C_normal_UP
4	14.73	3e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
5	14.4	3e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
6	13.92	4e-05	336	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_DN
7	13.44	4e-05	2947	Colon CaRectalPCWk_Colon
8	13.43	4e-05	3109	Colon CaRectal_P_Colon
9	13.11	4e-05	3406	Colon CaRectalPC_Colon
10	13.04	4e-05	436	GSEA C2MID_BREAST_CANCER_NORMAL_LIKE_UP
11	12.44	6e-05	4327	Colon CaRectalWk2_Colon
12	12.34	2e-02	16	Cancer LIU_PROSTATE_CANCER_DN
13	12.31	6e-05	2658	LymphomaLymphoma_Repetitive
14	12.03	6e-05	132	Colon CaRectal_CRC-cluster-b
15	11.83	6e-05	476	Tissue WIRTH_Nervous System
16	11.7	7e-05	2838	LymphomaLymphoma_Poised_promoter
17	11.55	8e-05	1279	Brain Overlap_fetal_midbrain_Enh
18	11.54	8e-05	3507	CC plasma membrane
19	11.45	8e-05	1753	Colon CaRectal_Colon
20	11.05	9e-05	420	GSEA C2SHEN_SMARCA2_TARGETS_UP
<b>Underexpressed</b>				
1	-36.45	0	807	LymphomaLymphoma_June14_MMLL937_tumors+controls_group.overexpression
2	-35.94	0	811	LymphomaWIRTH_lymphoma937_spot D
3	-35	0	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
4	-34.99	0	1298	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	-33.86	0	713	Colon CaRectal_CRC_TCGA_group.over_C_normal_DN
6	-33.7	0	550	Cancer Lembecke_Normal vs Adenoma
7	-30.42	0	546	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	-30.2	0	830	Colon CaRectal_CRC_TCGA_corr_R_normal_DN
9	-29.82	0	859	GSEA C2LEE_BMP2_TARGETS_DN
10	-29.41	0	316	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
11	-29.18	0	1563	GSEA C2PUJANA_BRCA1_PCC_NETWORK
12	-28.96	0	145	Glio WILLSCHER_GBM_Verhaak-CL_up ( C)
13	-28.68	0	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
14	-28.67	0	747	GSEA C2PUJANA_CHEK2_PCC_NETWORK
15	-28.63	0	400	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
16	-28.43	0	282	GSEA C2MANALO_HYPOXIA_DN
17	-27.26	0	327	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
18	-27.03	0	1228	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
19	-26.78	0	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
20	-26.44	0	446	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6

Profile

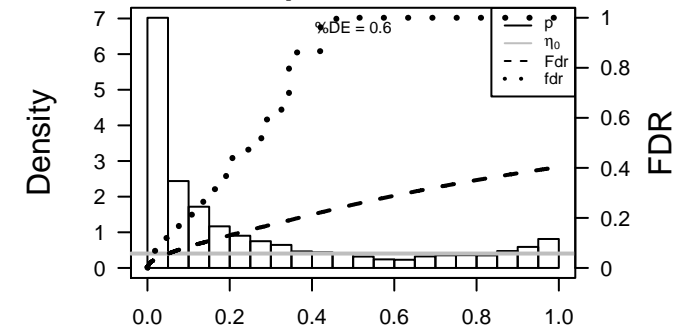
Regulated Spots



p-values



p-values



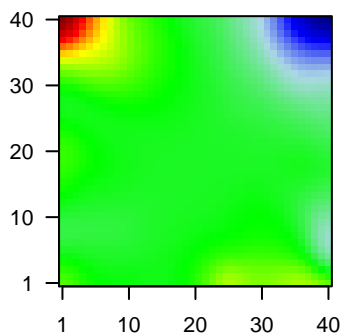
# other\_normHNPC vs

## Local Summary

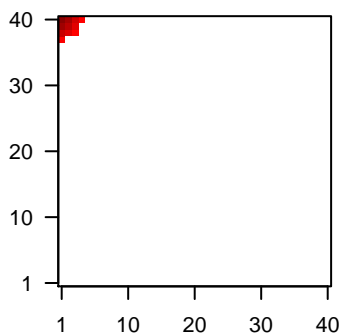
%DE = 0.94  
 # metagenes = 11  
 # genes = 251  
 # genes in genesets = 250  
  
 # genes with  $fdr < 0.1$  = 229 ( 229 + / 0 -)  
 # genes with  $fdr < 0.05$  = 208 ( 208 + / 0 -)  
 # genes with  $fdr < 0.01$  = 0 ( 0 + / 0 -)

<r> metagenes = 1  
 <r> genes = 0.91  
  
 <FC> = 0.37  
 <t-score> = 2.04  
 <p-value> = 0.1  
 <fdr> = 0.34

Profile



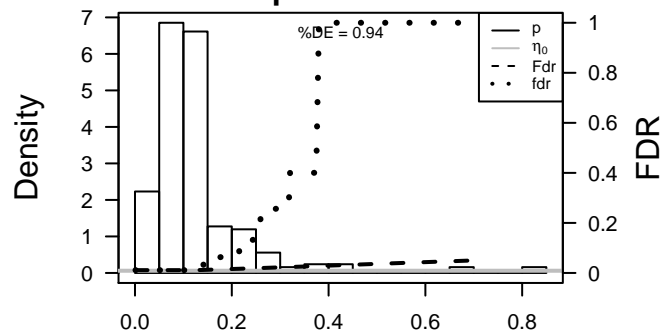
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.4	0.001	0.01	3 x 38 Shwachman-Bodian-Diamond syndrome [Source:HGNC Sym
2	ENSG0000000	0.38	0.003	0.01	1 x 37 phosphatidic acid phosphatase type 2A [Source:HGNC Symb
3	ENSG0000001	0.71	0.015	0.01	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
4	ENSG0000001	0.57	0.018	0.01	1 x 40 microfibrillar-associated protein 4 [Source:HGNC Symbol;Acc
5	ENSG0000001	0.34	0.019	0.01	1 x 38 alpha-2-macroglobulin [Source:HGNC Symbol;Acc:HGNC:7,
6	ENSG0000000	0.43	0.022	0.01	3 x 40 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
7	ENSG0000001	1.31	0.024	0.01	1 x 40 desmin [Source:HGNC Symbol;Acc:HGNC:2770]
8	ENSG0000001	0.44	0.025	0.01	1 x 40 stomatin [Source:HGNC Symbol;Acc:HGNC:3383]
9	ENSG0000001	0.41	0.026	0.01	1 x 38 brain expressed, X-linked 4 [Source:HGNC Symbol;Acc:HGNC
10	ENSG0000001	0.39	0.027	0.01	2 x 39 gelsolin [Source:HGNC Symbol;Acc:HGNC:4620]
11	ENSG0000001	0.32	0.027	0.01	4 x 40 protein kinase (cAMP-dependent, catalytic) inhibitor gamma
12	ENSG0000001	0.34	0.028	0.01	3 x 40 necdin, melanoma antigen (MAGE) family member [Source:H
13	ENSG0000001	0.43	0.028	0.01	1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:
14	ENSG0000001	0.35	0.030	0.01	1 x 38 annexin A6 [Source:HGNC Symbol;Acc:HGNC:544]
15	ENSG0000001	0.4	0.031	0.01	1 x 39 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC
16	ENSG0000000	0.51	0.033	0.01	1 x 40 myosin, light chain 6, alkali, smooth muscle and non-muscle
17	ENSG0000001	0.37	0.036	0.01	3 x 40 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:]
18	ENSG0000001	0.59	0.036	0.01	2 x 40 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
19	ENSG0000001	0.35	0.036	0.01	3 x 40 related RAS viral (r-ras) oncogene homolog [Source:HGNC
20	ENSG0000001	0.37	0.038	0.01	1 x 40 receptor (G protein-coupled) activity modifying protein 1 [Sou

p-values



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## Local Summary

%DE = 1  
 # metagenes = 20  
 # genes = 414  
 # genes in genesets = 408  
  
 # genes with  $fdr < 0.1$  = 411 ( 0 + / 411 -)  
 # genes with  $fdr < 0.05$  = 409 ( 0 + / 409 -)  
 # genes with  $fdr < 0.01$  = 376 ( 0 + / 376 -)

<r> metagenes = 0.99

<r> genes = 0.84

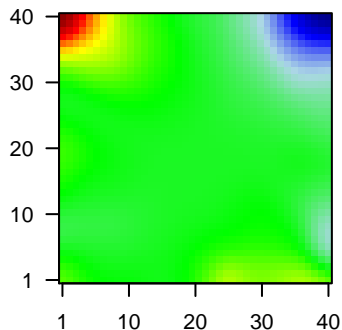
<FC> = -0.3

<t-score> = -5.05

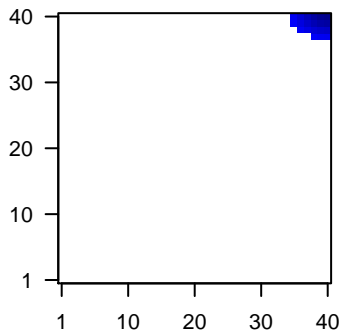
<p-value> = 0

<fdr> = 0.13

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.25	6e-08	4e-07	36 x 40 dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Ac
2	ENSG0000001	-0.24	3e-07	2e-06	37 x 40 proliferation-associated 2G4, 38kDa [Source:HGNC Symbol;
3	ENSG0000001	-0.59	2e-06	2e-06	40 x 40 ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:HGI
4	ENSG0000001	-0.23	2e-06	2e-06	39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;/
5	ENSG0000001	-0.48	3e-06	2e-06	40 x 40 protein disulfide isomerase family A, member 4 [Source:HGNC
6	ENSG0000001	-0.37	3e-06	2e-06	35 x 40 nucleophosmin (nucleolar phosphoprotein B23, numatrin) [Sc
7	ENSG0000001	-0.22	5e-06	2e-06	36 x 38 protein phosphatase, Mg2+/Mn2+ dependent, 1G [Source:HC
8	ENSG0000001	-0.25	5e-06	2e-06	40 x 38 forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:3818]
9	ENSG0000000	-0.45	7e-06	2e-06	38 x 40 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:HGN
10	ENSG0000001	-0.64	7e-06	2e-06	38 x 40 ribosomal protein S2 [Source:HGNC Symbol;Acc:HGNC:104I
11	ENSG0000001	-0.18	8e-06	4e-06	35 x 39 WD repeat domain 77 [Source:HGNC Symbol;Acc:HGNC:29I
12	ENSG0000001	-0.22	1e-05	4e-06	36 x 38 minichromosome maintenance complex component 4 [Source
13	ENSG0000001	-0.23	2e-05	4e-06	38 x 40 Aly/REF export factor [Source:HGNC Symbol;Acc:HGNC:19C
14	ENSG0000000	-0.49	2e-05	4e-06	40 x 40 NME/NM23 nucleoside diphosphate kinase 2 [Source:HGNC
15	ENSG0000001	-0.3	2e-05	4e-06	36 x 40 NOP56 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
16	ENSG0000001	-0.43	2e-05	4e-06	39 x 40 eukaryotic translation initiation factor 5A [Source:HGNC SymI
17	ENSG0000001	-0.22	2e-05	4e-06	35 x 40 chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
18	ENSG0000001	-0.31	3e-05	4e-06	36 x 40 regulator of chromosome condensation 2 [Source:HGNC Syn
19	ENSG0000001	-0.29	3e-05	4e-06	36 x 40 guanine nucleotide binding protein-like 3 (nucleolar) [Source:
20	ENSG0000001	-0.25	3e-05	4e-06	36 x 40 NIN1/RPN12 binding protein 1 homolog [Source:HGNC Synt

p-values

