

## Supplementary figure legends

**Supplementary figure1: Race based expression analysis of hepatocellular carcinoma associated genes.** (A) Screen shot of the left side panel in UALCAN analysis page, which directs to heatmap of top differentially expressed genes. (B) Heatmap showing top 25 over-expressed genes in liver hepatocellular carcinoma [LIHC]. Each row shows expression level of specific gene across tumor (n=371) and normal (n=50) samples. Gene names on heatmap is linked to gene expression analysis page. Boxplots (C-F) depict expression level of GPC3, LCN2, SPP1 and UBE2C in caucasian, african american and asian LIHC patients.

**Supplementary figure2: Cancer stage specific expression analysis of bladder urothelial carcinoma associated genes.** (A) Heatmap showing top 25 over-expressed genes in bladder urothelial carcinoma [BLCA]. Each row shows expression level of specific gene across tumor (n=408) and normal(n=19) samples. Gene names on heatmap is linked to gene expression analysis page. Boxplots (B-D) depict expression level of CST6, CDKN2A and MMP11 in stage1, stage2, stage3 and stage4 BLCA patients.

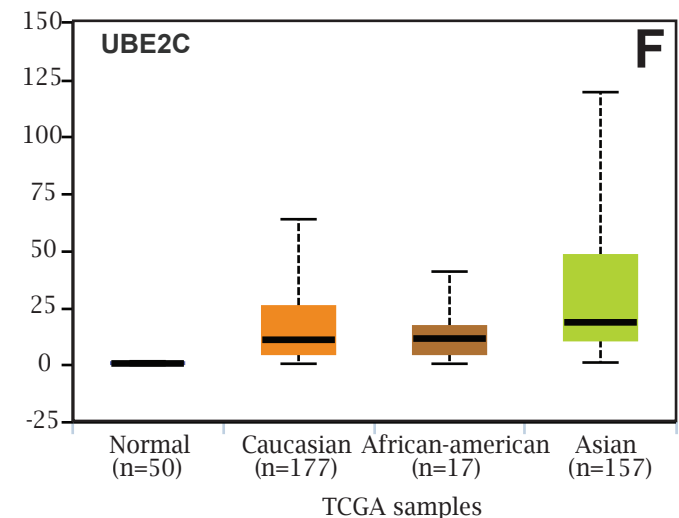
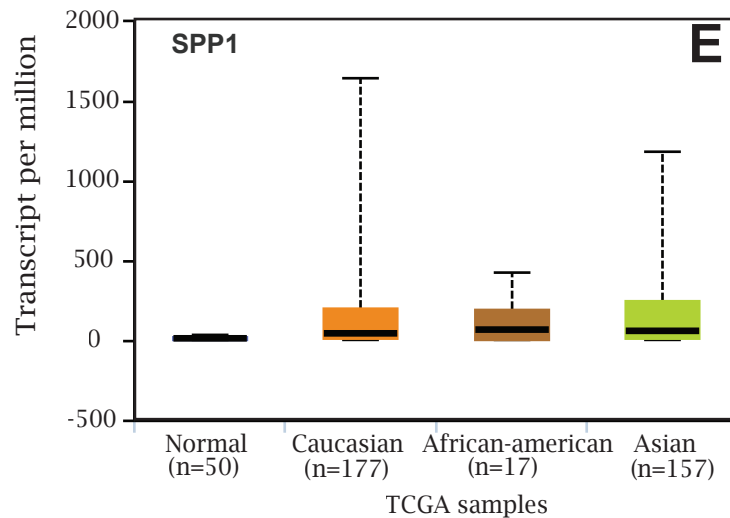
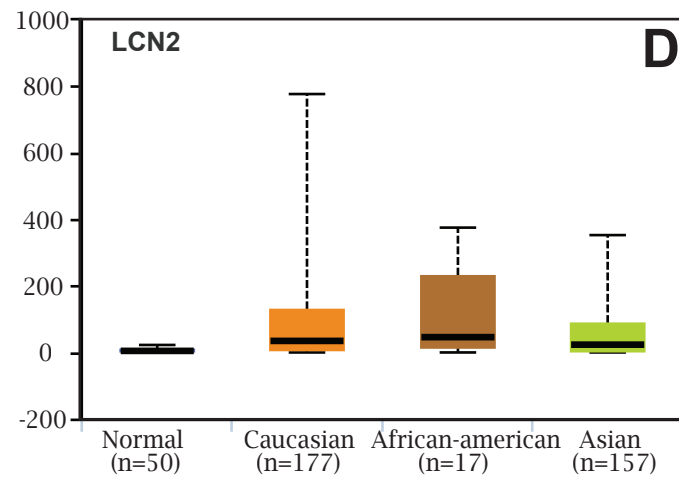
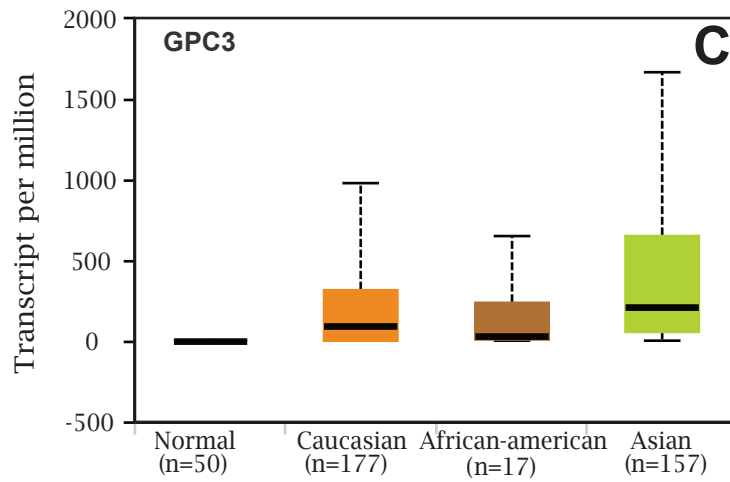
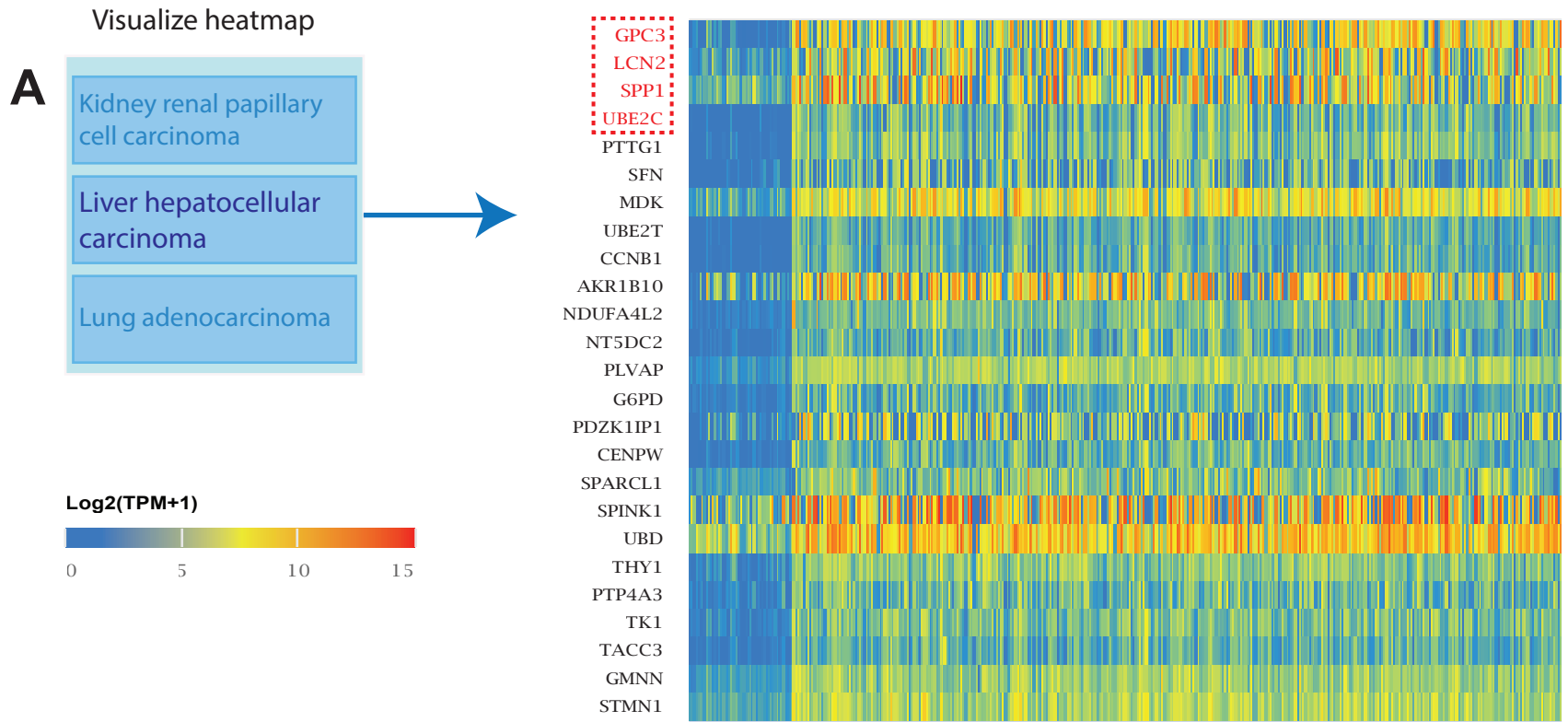
**Supplementary figure3: Pan cancer analysis of P53 signaling pathway genes.** (A) Screen shot of the panel in analysis page that facilitates to scan UALCAN with precompiled gene class. (B) Screen shot of the output page providing bird's eye view on expression and survival profile of each gene across 31 TCGA cancer types. Each button links to gene's expression profile in different cancers. The styles of the button indicate the expression status (Over-/under-regulation or No change) and overall survival impact (significant/not significant) of gene.

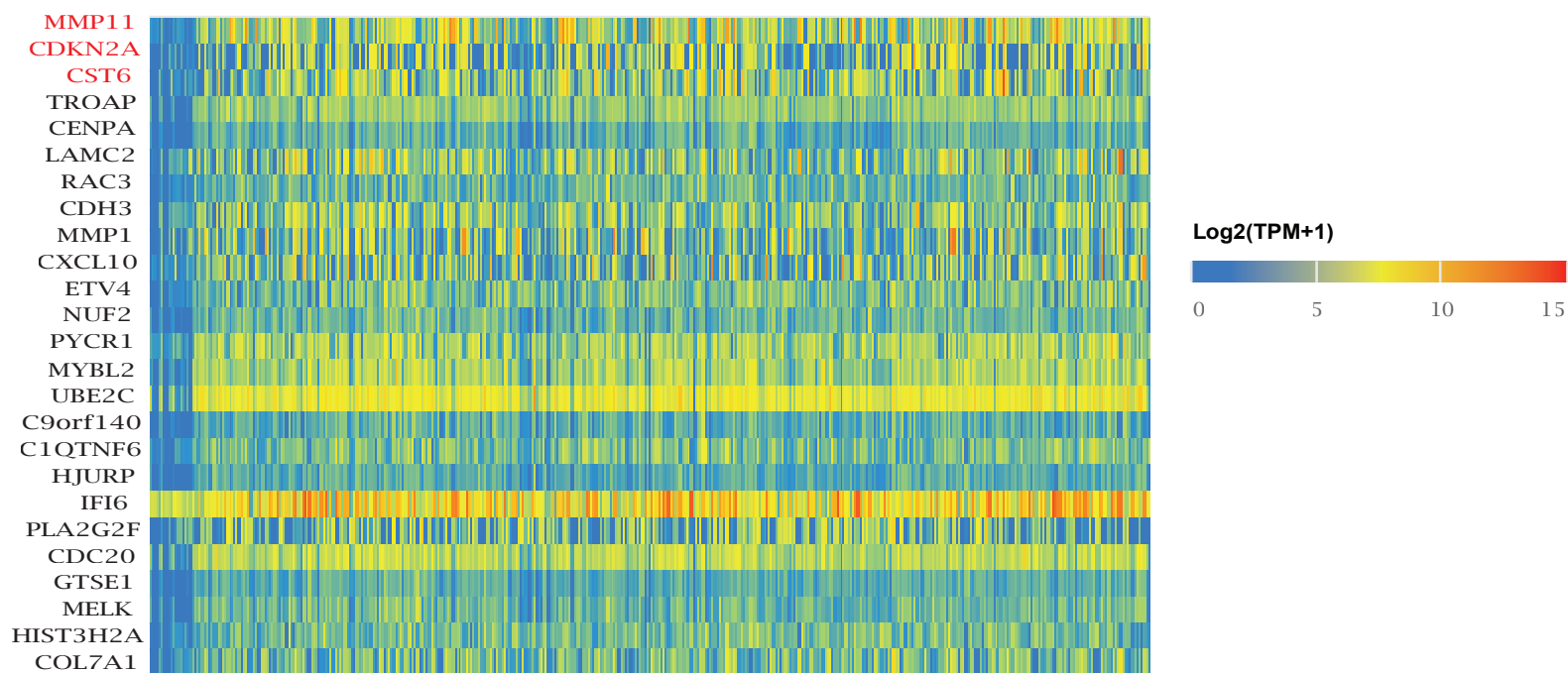
**Supplementary figure4: Assessment of combined impact of CDKN1A expression and patient's race on overall survival of head and neck squamous cell carcinoma [HNSC] patients.** (A) Screen shot of UALCAN output page providing links to survival and gene expression analysis. (B) Kaplan meier plot showing result of multivariate overall survival analysis considering CDKN1A expression and patient's race. (C-D) Kaplan meier plot showing influence of CDKN1A expression level on overall survival of Caucasian and African American patients.

**Supplementary figure5: Breast cancer subtype specific gene expression analysis.** (A) Heatmap showing top 25 over-expressed genes in breast invasive carcinoma [BRCA]. (B-C) Boxplots showing expression profile of BIRC5 and UBE2C in BRCA patients with luminal (n=566), HER2 positive (n=37) and TNBC (n=116) types of breast cancer. (D-E) Boxplots showing BIRC5 and UBE2C expression in TNBC sutypes (samples categorized using TNBCtype tool).

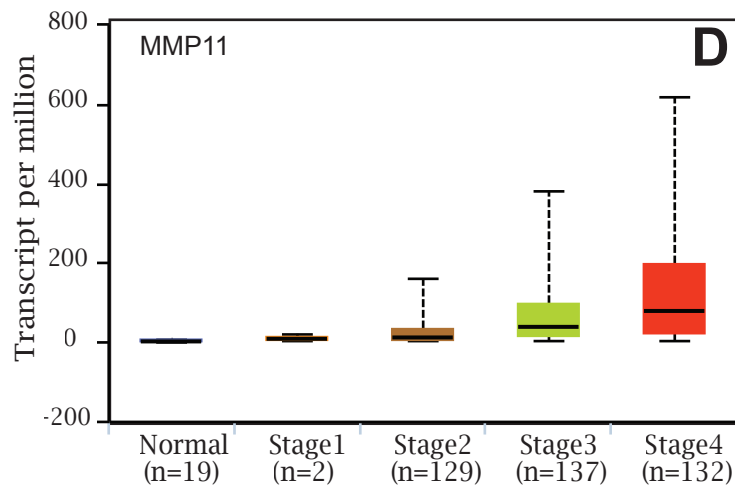
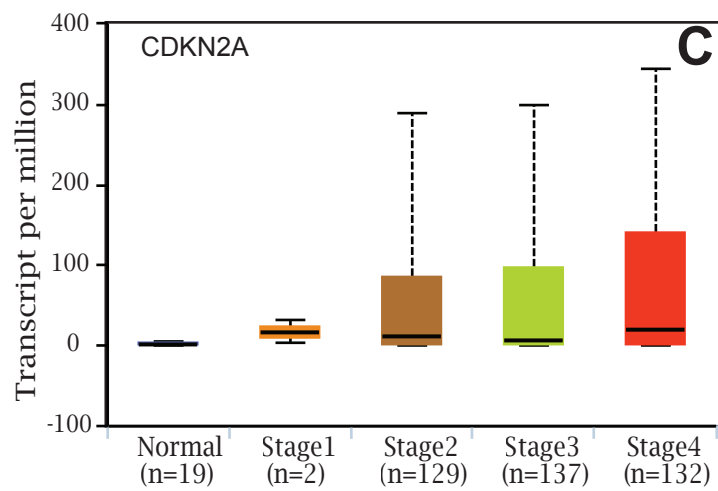
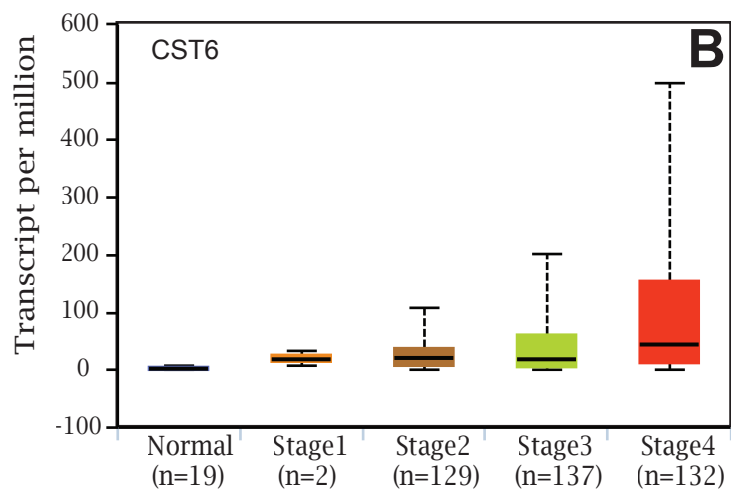
**B**

Top 25 over-expressed genes in Liver hepatocellular carcinoma (LIHC)



**A** Top 25 over-expressed genes in Bladder urothelial carcinoma (BLCA)

Expression profile in bladder urothelial carcinoma based on pathological stages



# Chandrashekar et al., Supplementary Figure 3

**A**

Scan by gene classes

Gene class

**B**

Gene	Links to expression/survival information	External links		
CDK2	<div style="display: flex; justify-content: space-between;"> <span>BLCA</span><span>BRCA</span><span>COAD</span><span>LUAD</span><span>KIRC</span><span>PAAD</span><span>PRAD</span><span>LGG</span> </div> <div style="display: flex; justify-content: space-between;"> <span>LUSC</span><span>HNSC</span><span>KIRP</span><span>ESCA</span><span>OV</span><span>LIHC</span><span>CESC</span><span>READ</span> </div> <div style="display: flex; justify-content: space-between;"> <span>UCEC</span><span>THYM</span><span>THCA</span><span>GBM</span><span>SARC</span><span>PCPG</span><span>ACC</span><span>UVM</span> </div> <div style="display: flex; justify-content: space-between;"> <span>MESO</span><span>UCS</span><span>TGCT</span><span>CHOL</span><span>KICH</span><span>DLBC</span><span>SKCM</span> </div>	<input type="button" value="Genecards"/> <input type="button" value="TargetScan"/> <input type="button" value="PubMed-Cancer"/> <input type="button" value="Human Protein Atlas"/>		
	CDK4		<div style="display: flex; justify-content: space-between;"> <span>BLCA</span><span>BRCA</span><span>COAD</span><span>LUAD</span><span>KIRC</span><span>PAAD</span><span>PRAD</span><span>LGG</span> </div> <div style="display: flex; justify-content: space-between;"> <span>LUSC</span><span>HNSC</span><span>KIRP</span><span>ESCA</span><span>OV</span><span>LIHC</span><span>CESC</span><span>READ</span> </div> <div style="display: flex; justify-content: space-between;"> <span>UCEC</span><span>THYM</span><span>THCA</span><span>GBM</span><span>SARC</span><span>PCPG</span><span>ACC</span><span>UVM</span> </div> <div style="display: flex; justify-content: space-between;"> <span>MESO</span><span>UCS</span><span>TGCT</span><span>CHOL</span><span>KICH</span><span>DLBC</span><span>SKCM</span> </div>	<input type="button" value="Genecards"/> <input type="button" value="TargetScan"/> <input type="button" value="PubMed-Cancer"/> <input type="button" value="Human Protein Atlas"/>

**Cancer** Gene regulation: Over  
Overall survival: Not significant

**Cancer** Gene regulation: Under  
Overall survival: Significant

**Cancer** Gene regulation: Over  
Overall survival: Significant

**Cancer** Gene regulation: No change  
Overall survival: Not significant

**Cancer** Gene regulation: Under  
Overall survival: Not significant

**Cancer** Gene regulation: No change  
Overall survival: Significant

**A**

CDKN1A

GEx Profile

Survival Profile

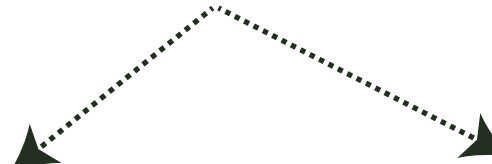
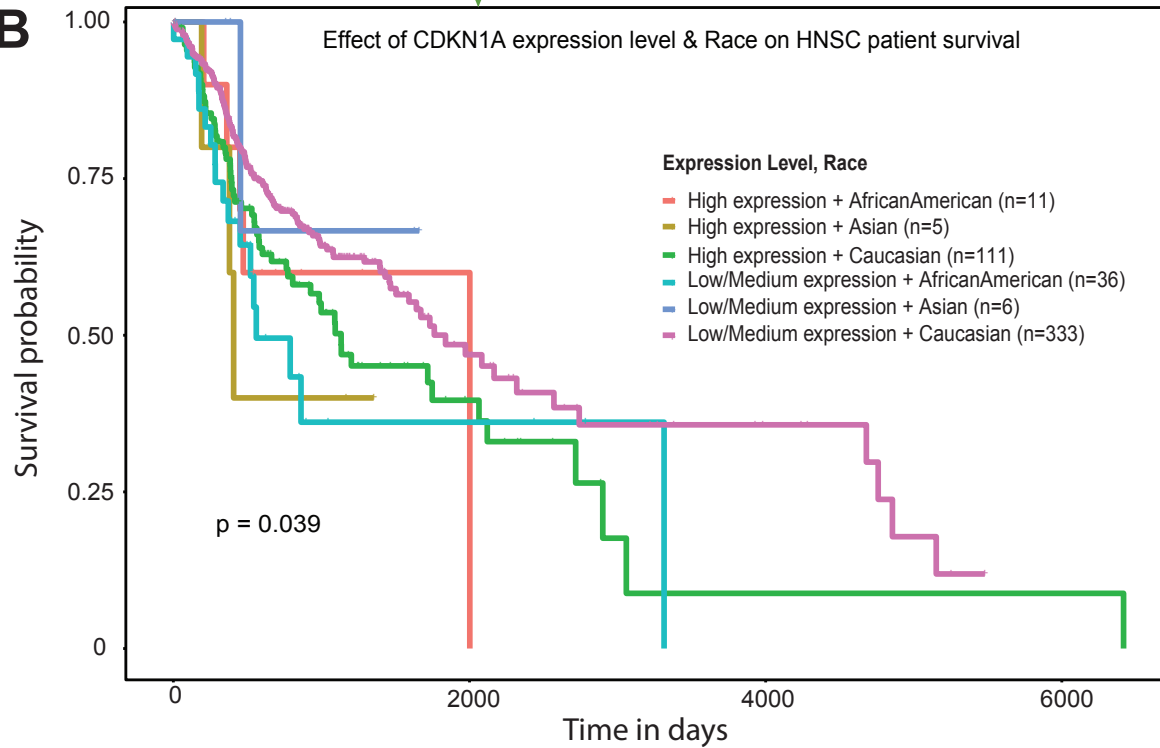
Genecards

TargetScan

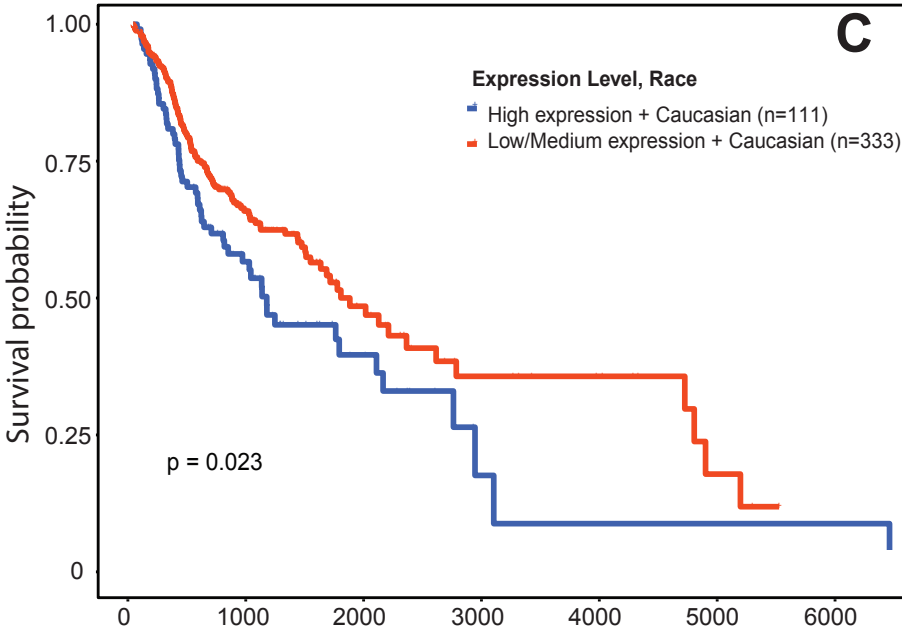
PubMed-Cancer

Human Protein Atlas

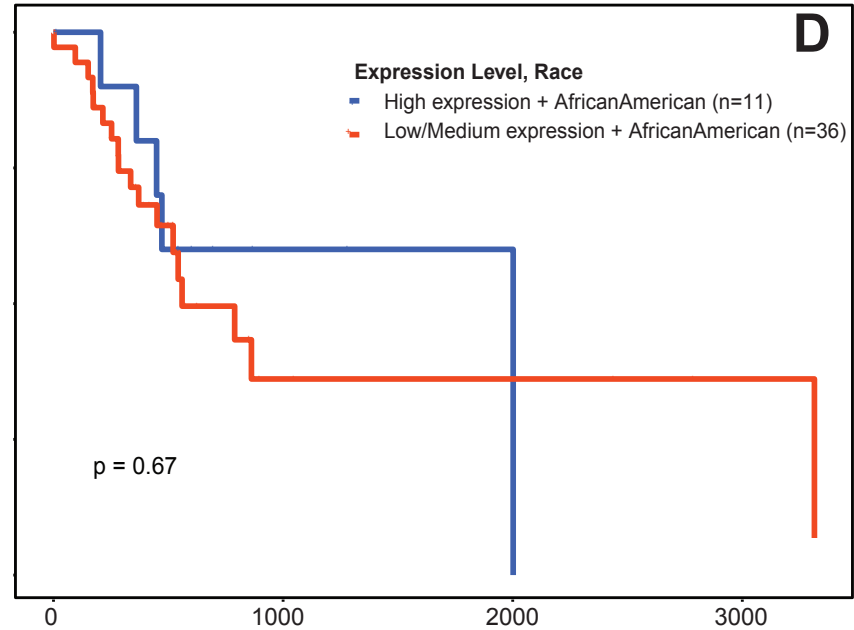
**B**



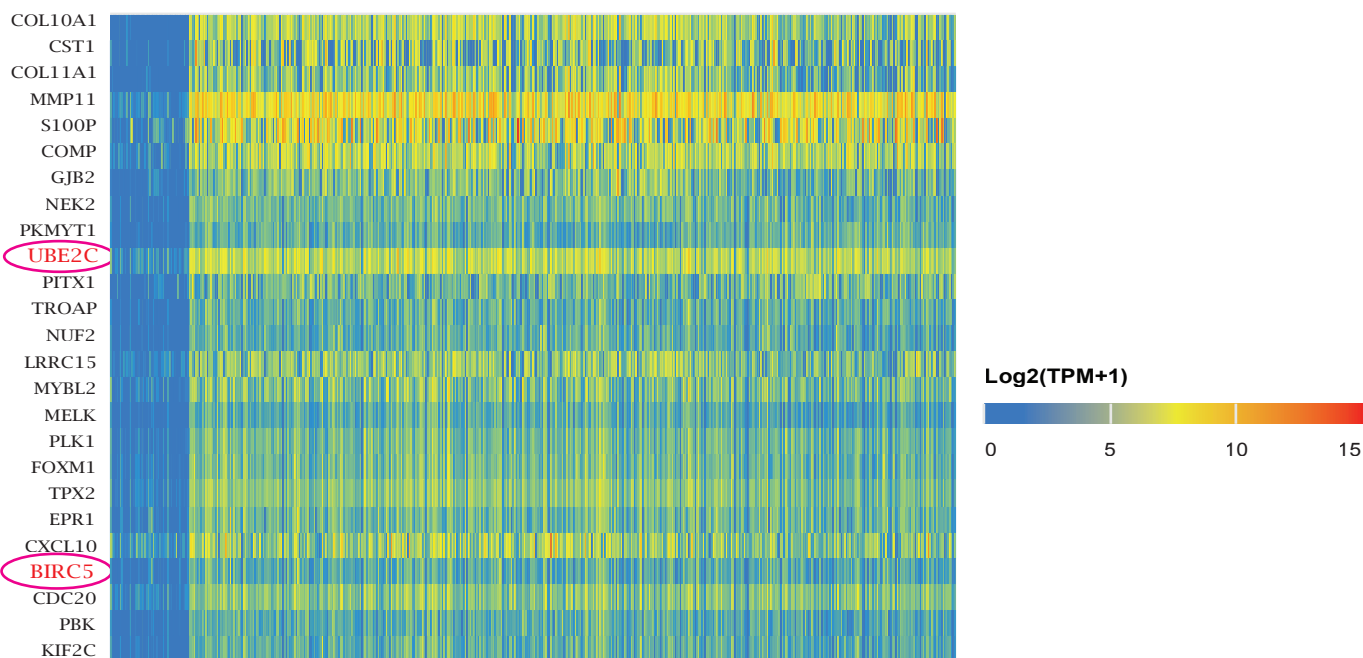
**C**



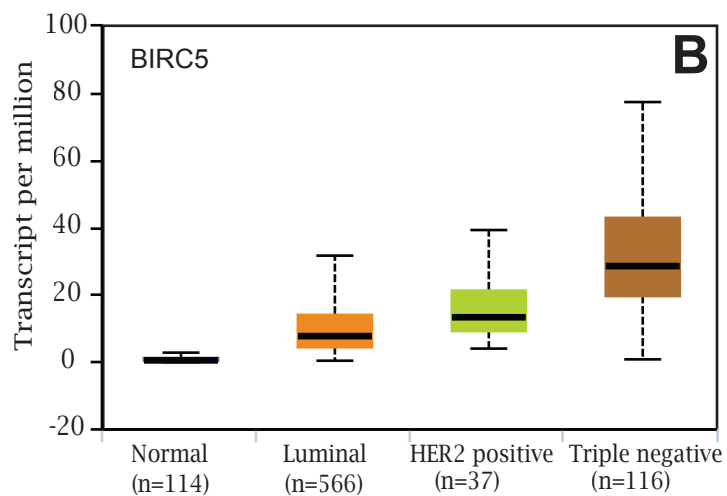
**D**



**A** Top 25 over-expressed genes in Breast invasive carcinoma (BRCA)



Expression profile in BRCA based on subtypes



Expression profile in BRCA based on TNBC subtypes

