**Supplementary figure legends:**

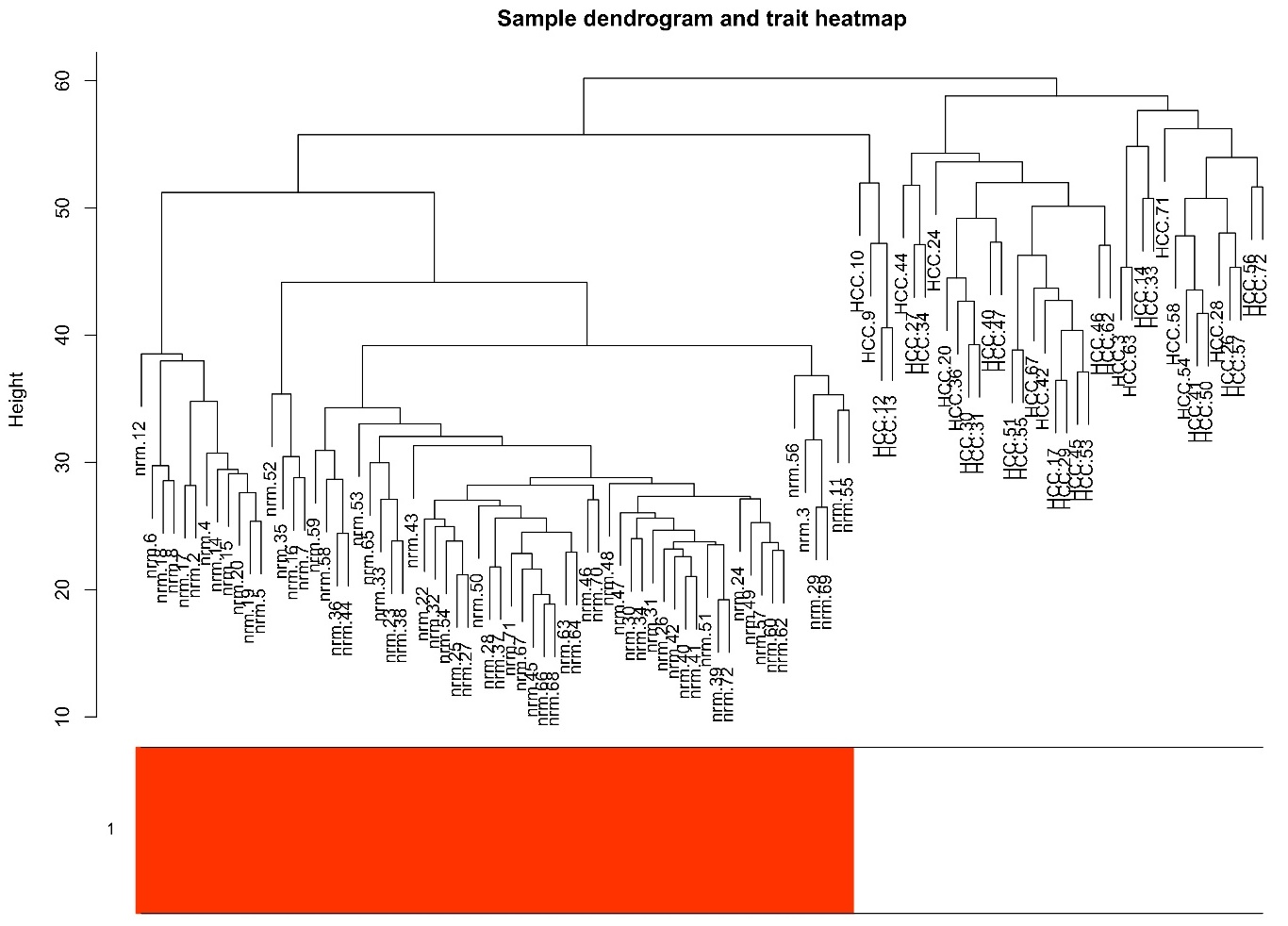
**Figure S1:** Sample clustering to detect outliers: sample dendrogram and trait indicator. The color is proportional to pathological stage (Red=normal samples and white=HCC samples).

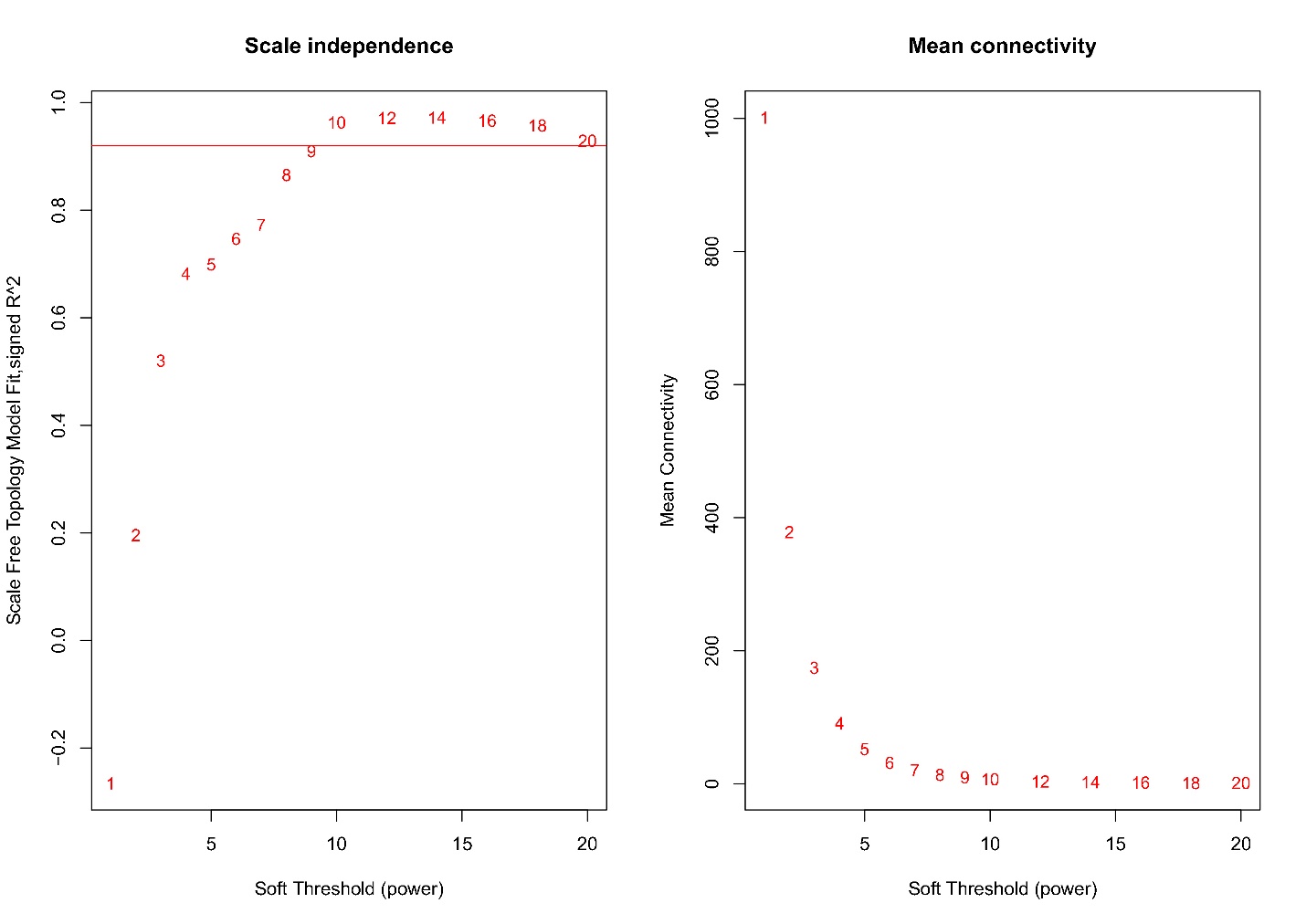
**Figure S2:** Validation of the gene expression levels between HCC and normal tissue samples from GEPIA.

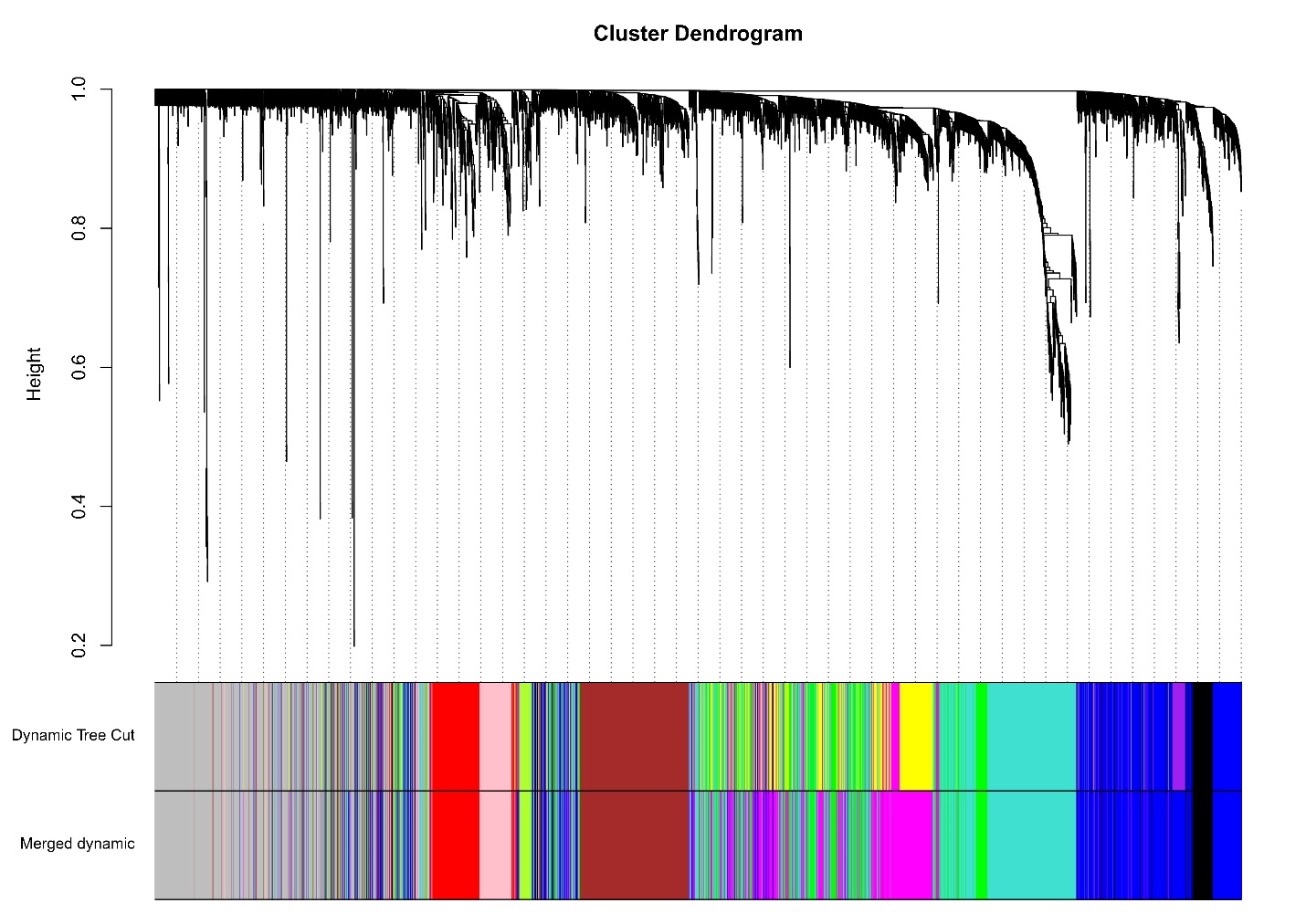
**Figure S3:** Validation of the gene expression levels between HCC sample and normal tissue with immunohistochemistry analysis.

**Figure S4:** Kaplan-Meier survival plots for overall survival in hub genes. Red line represented the samples with gene highly expressed and the blue line was for the samples with gene lowly expressed. The X and Y axes represent survival time (months) and percent of survival, respectively. HR, hazard ratio.

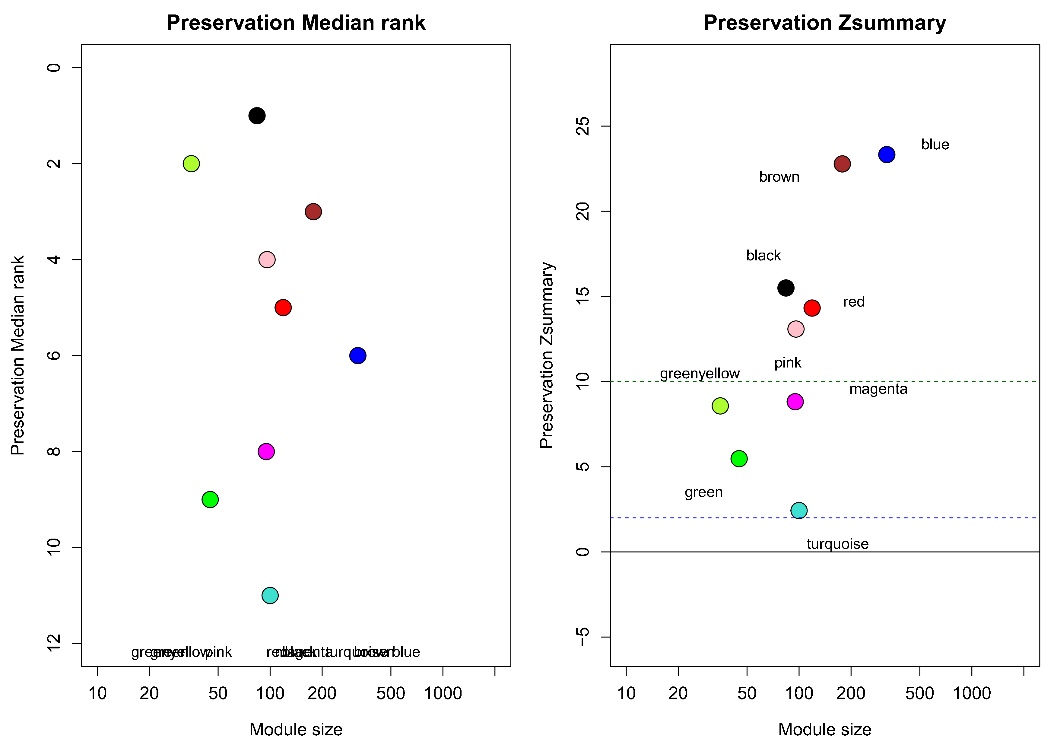
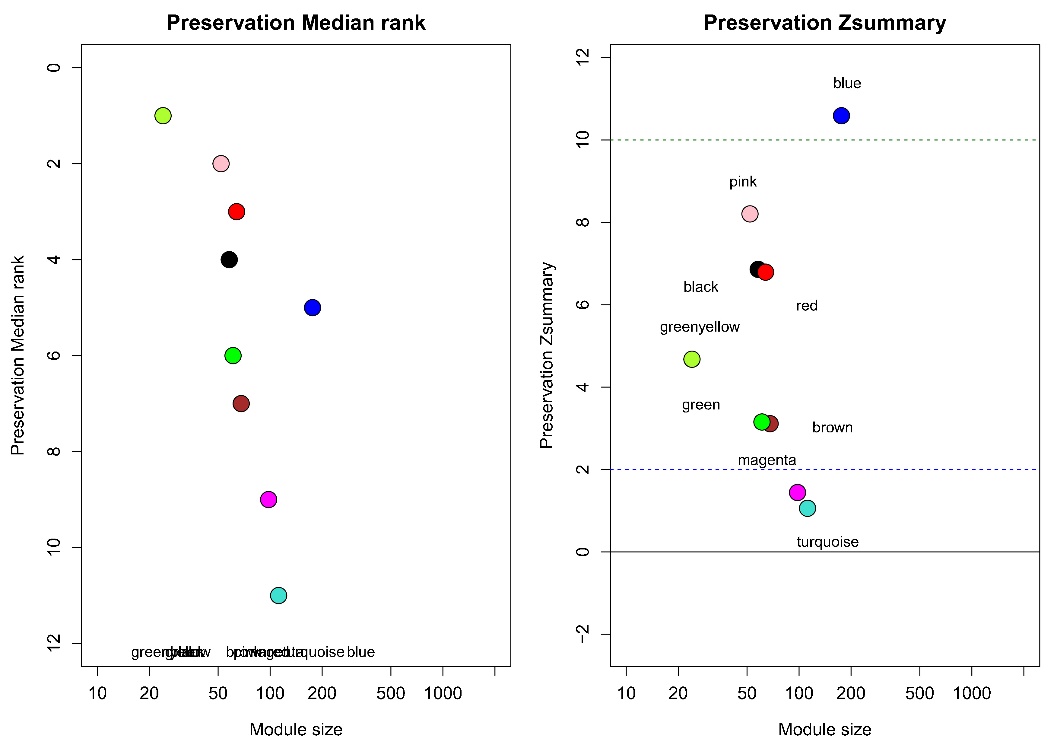
**Figure S1:**

**Figure S2:**



**Figure S3:**

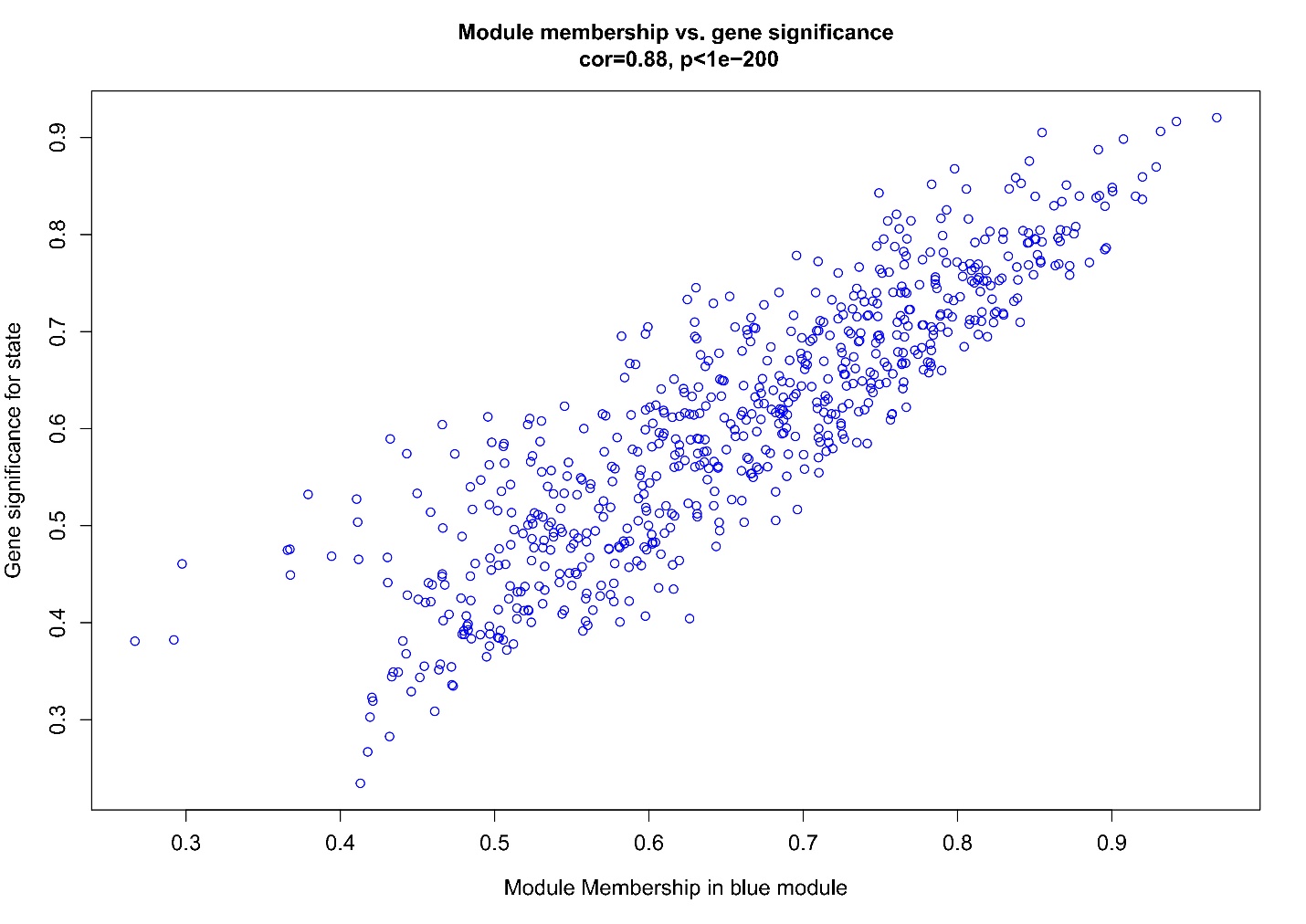
**Figure S4:**



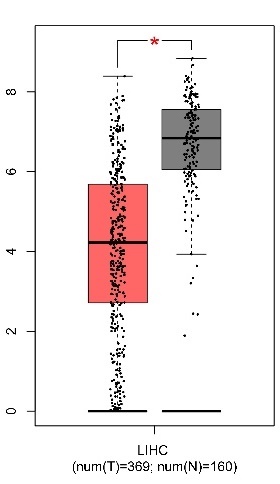
**A**

**B**

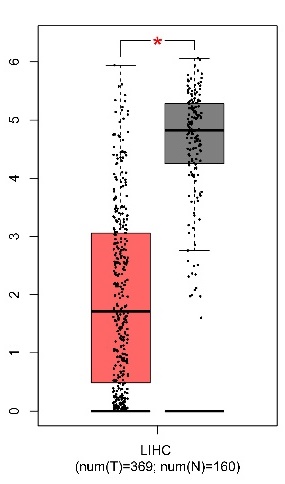
**Figure S5:**



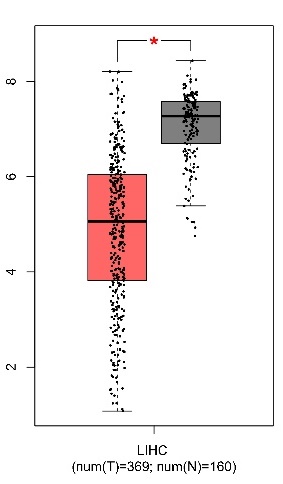
**Figure S6:**



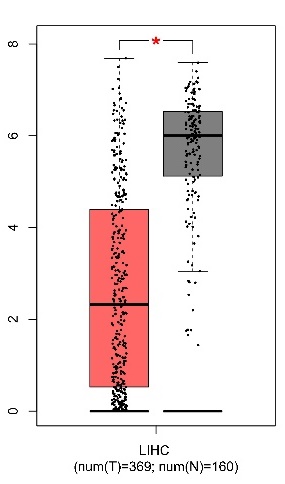
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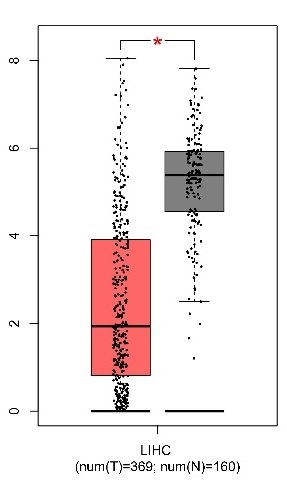
NAT2



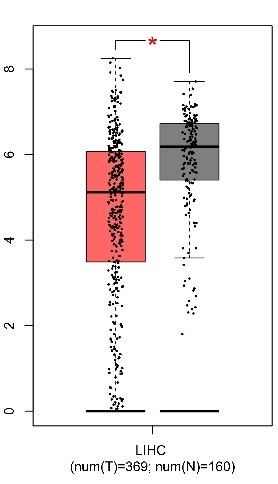
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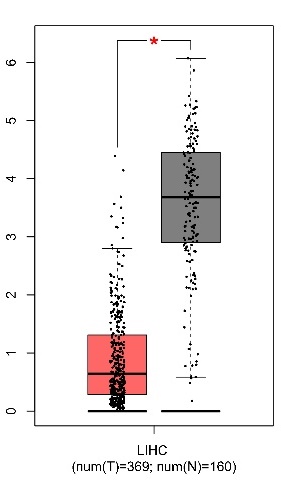
TTC36



IGFALS

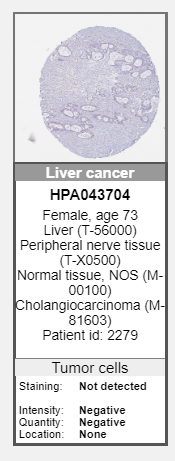
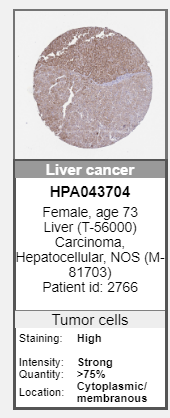


ASPDH

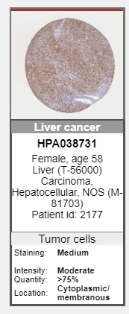
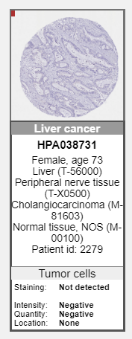


VIPR1

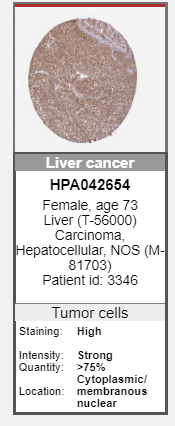
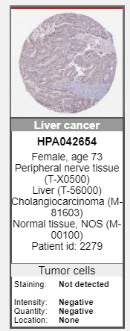
**Figure S7:**



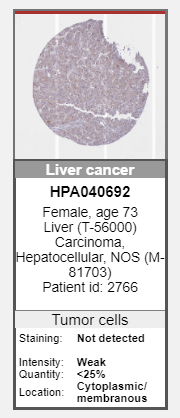
NAT2



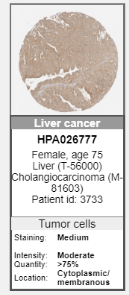
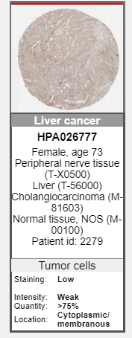
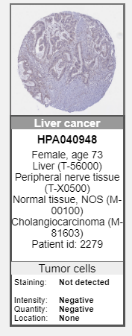
TTC36



ASPDH



IGFALS



VIPR1

**Figure S8:**

