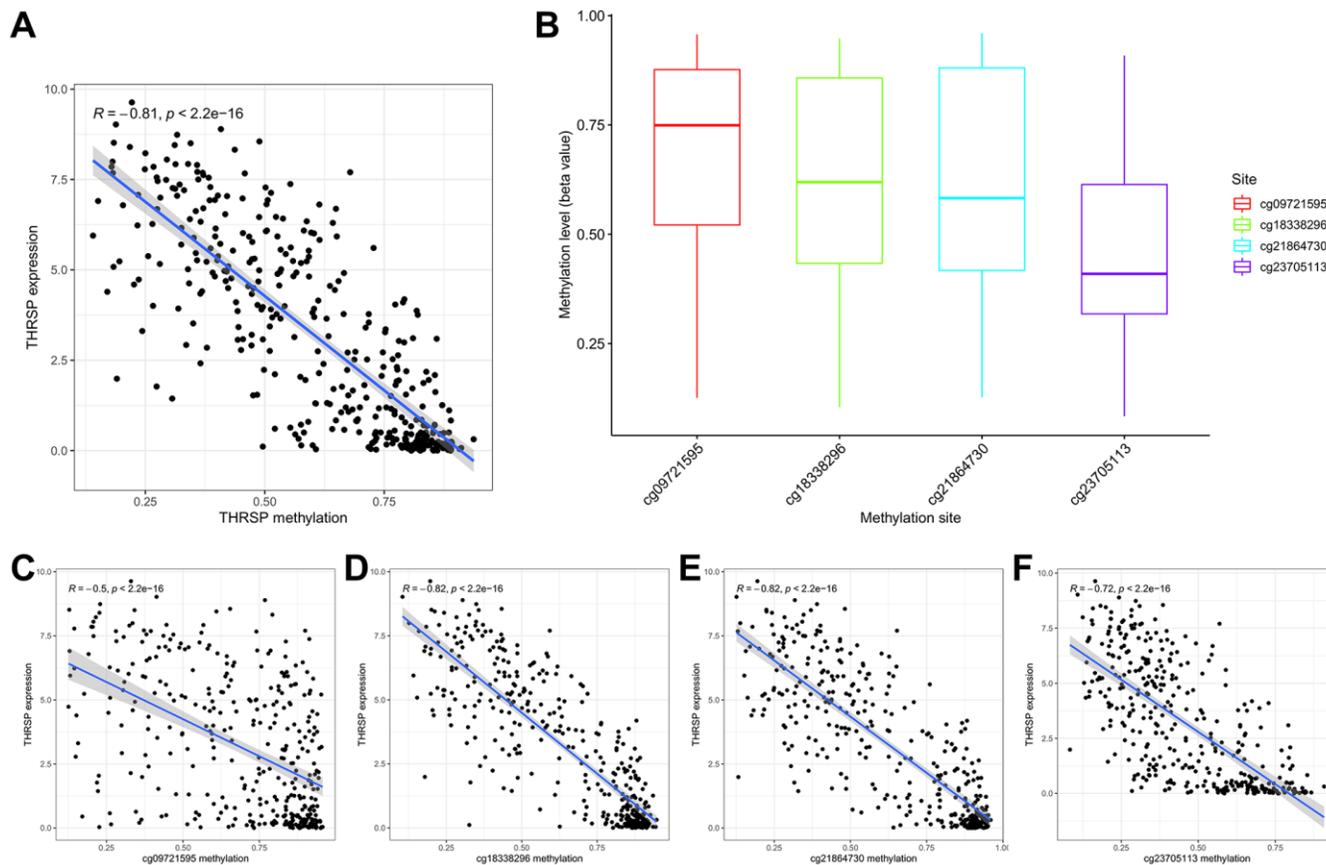
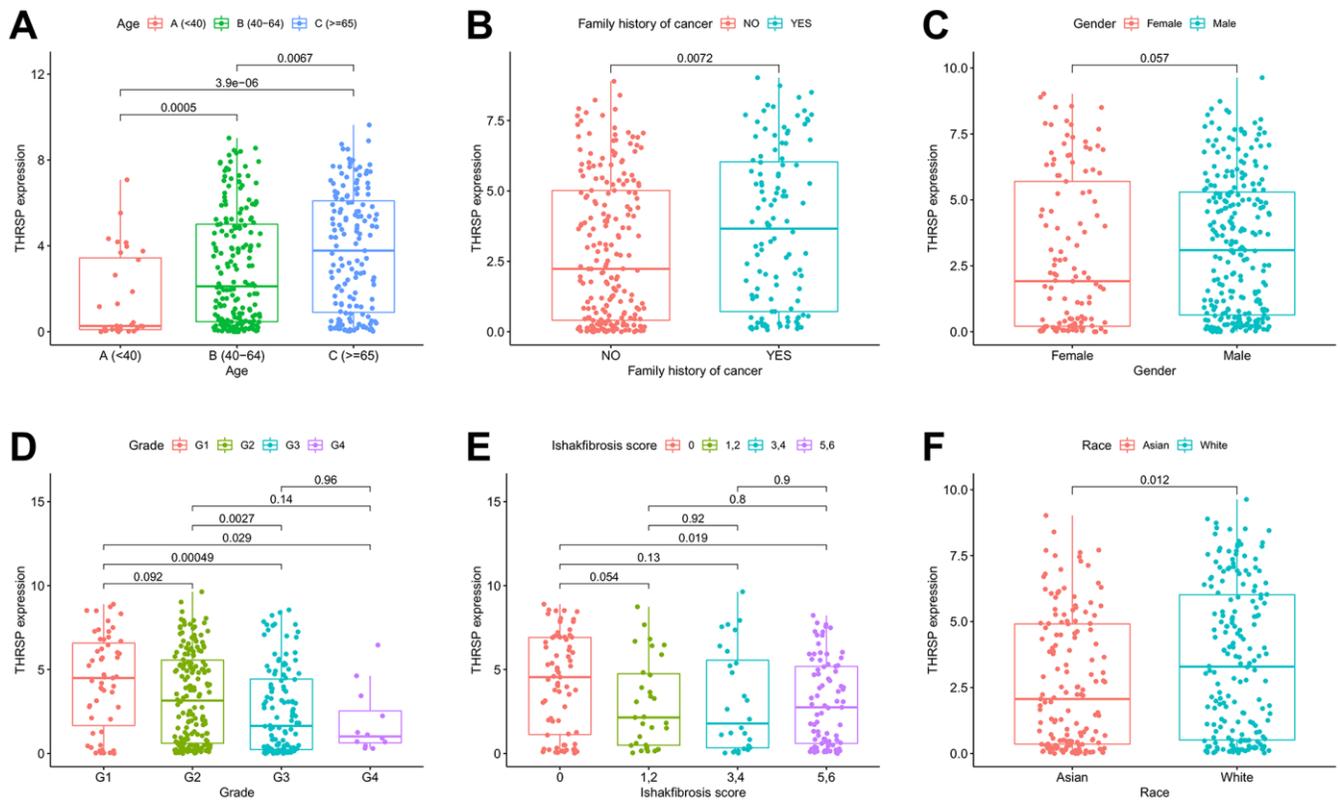


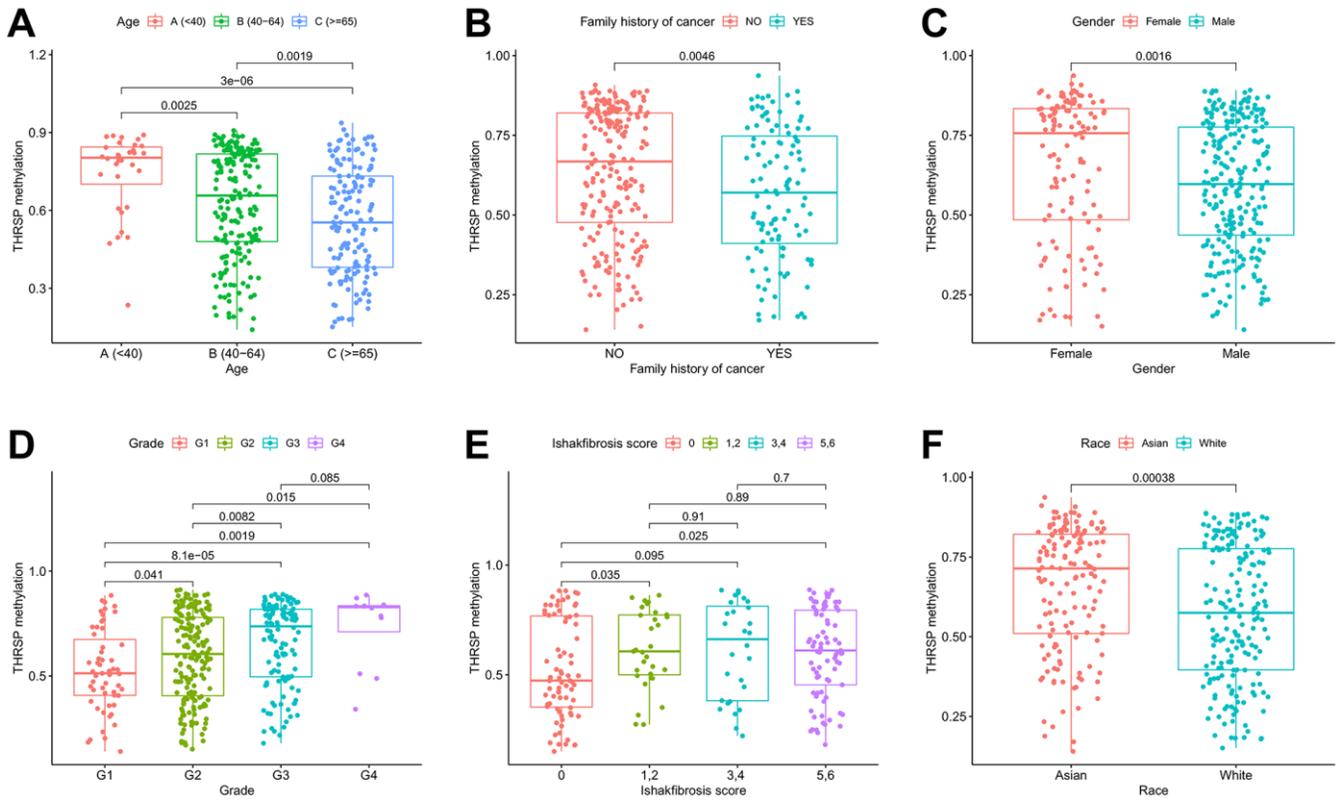
SUPPLEMENTARY FIGURES



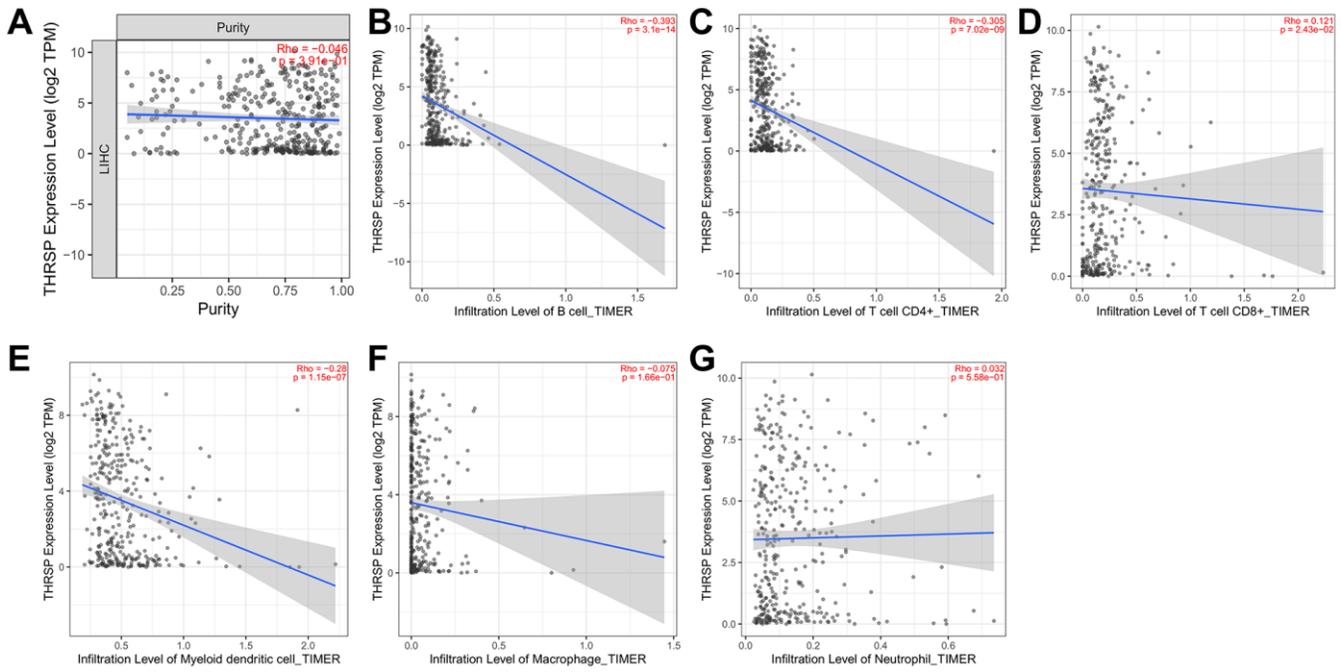
Supplementary Figure 1. Relationship between THRSP mRNA expression and DNA methylation. (A) THRSP expression was negatively correlated with DNA methylation ($R = -0.81, p < 2.2e-16$). (B) The distribution of four THRSP DNA promoter CpG sites. (C–F) THRSP expression was negatively correlated with the methylation levels of the four CpG sites. From the left to right were cg09721595 ($R = -0.5, p < 2.2e-16$), cg18338296 ($R = -0.82, p < 2.2e-16$), cg21864730 ($R = -0.82, p < 2.2e-16$) and cg23705113 ($R = -0.72, p < 2.2e-16$).



Supplementary Figure 2. The correlation between THRSF expression and the clinical features. THRSF mRNA expression was stratified by (A) age, (B) family history of cancer, (C) gender, (D) grade, (E) Ishak fibrosis score, and (F) race.



Supplementary Figure 3. The correlation between THRSF methylation and the clinical features. THRSF methylation was stratified by (A) age, (B) family history of cancer, (C) gender, (D) grade, (E) Ishak fibrosis score, and (F) race.



Supplementary Figure 4. The correlation between THRSP expression and immune infiltration levels in HCC. (A) No association between THRSP expression and tumor purity ($R = -0.046$, $p = 0.391$). **(B–G)** THRSP expression was significantly negatively correlated with infiltrating levels of B cells, CD4+ T cells, and dendritic cells, positively correlated with CD8+ T cells, but not correlated with macrophages or neutrophils.