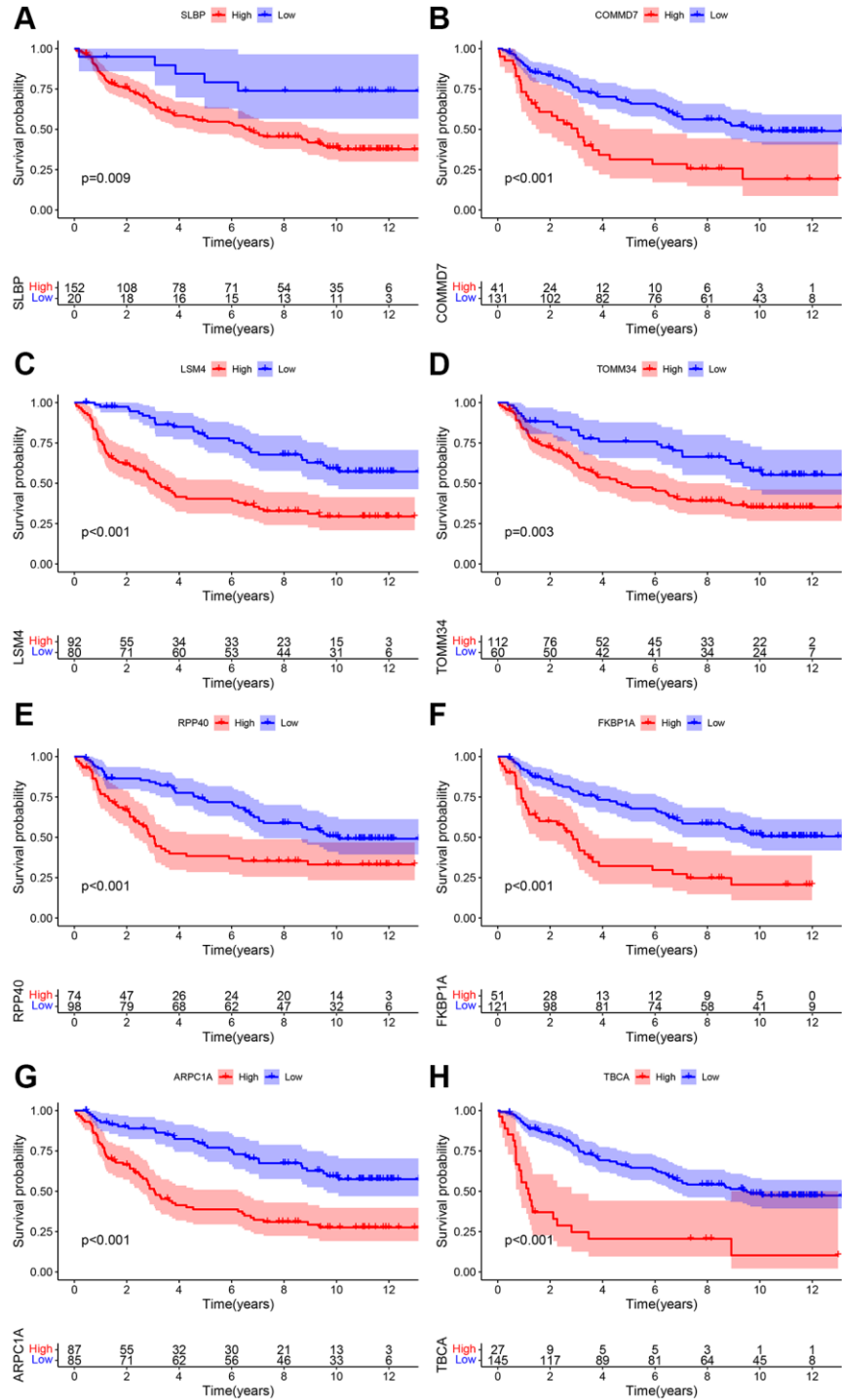
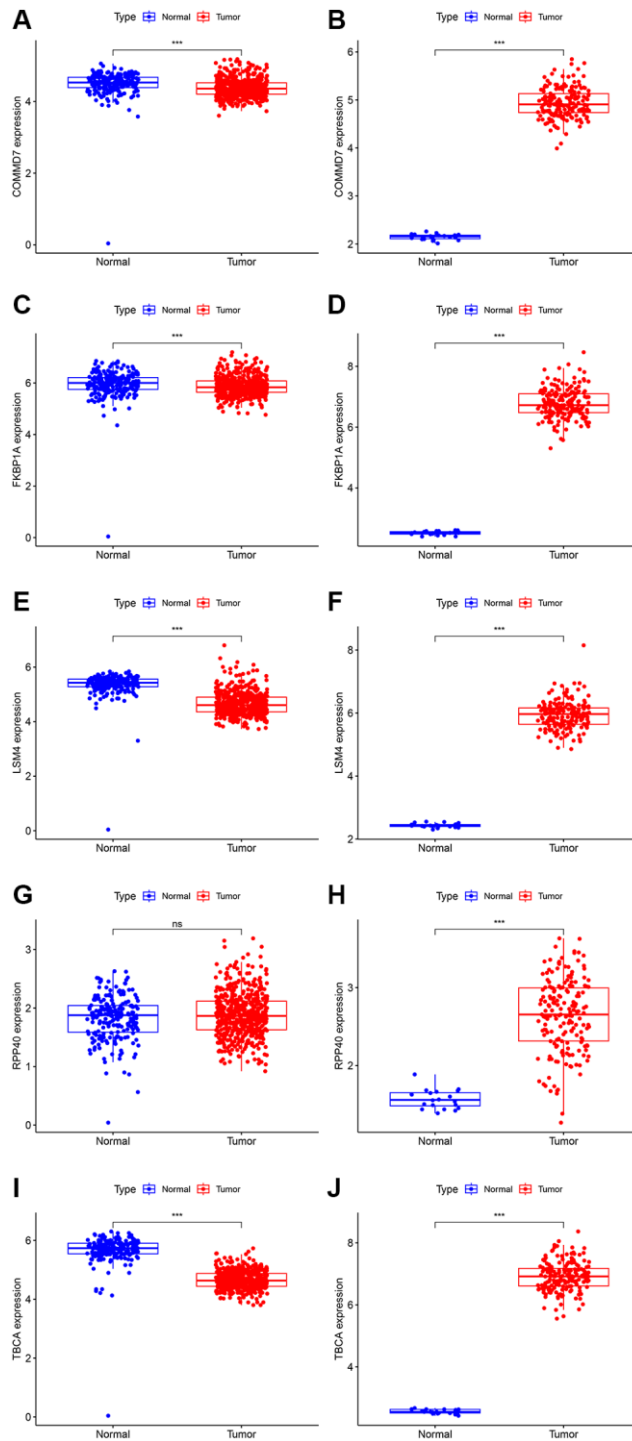


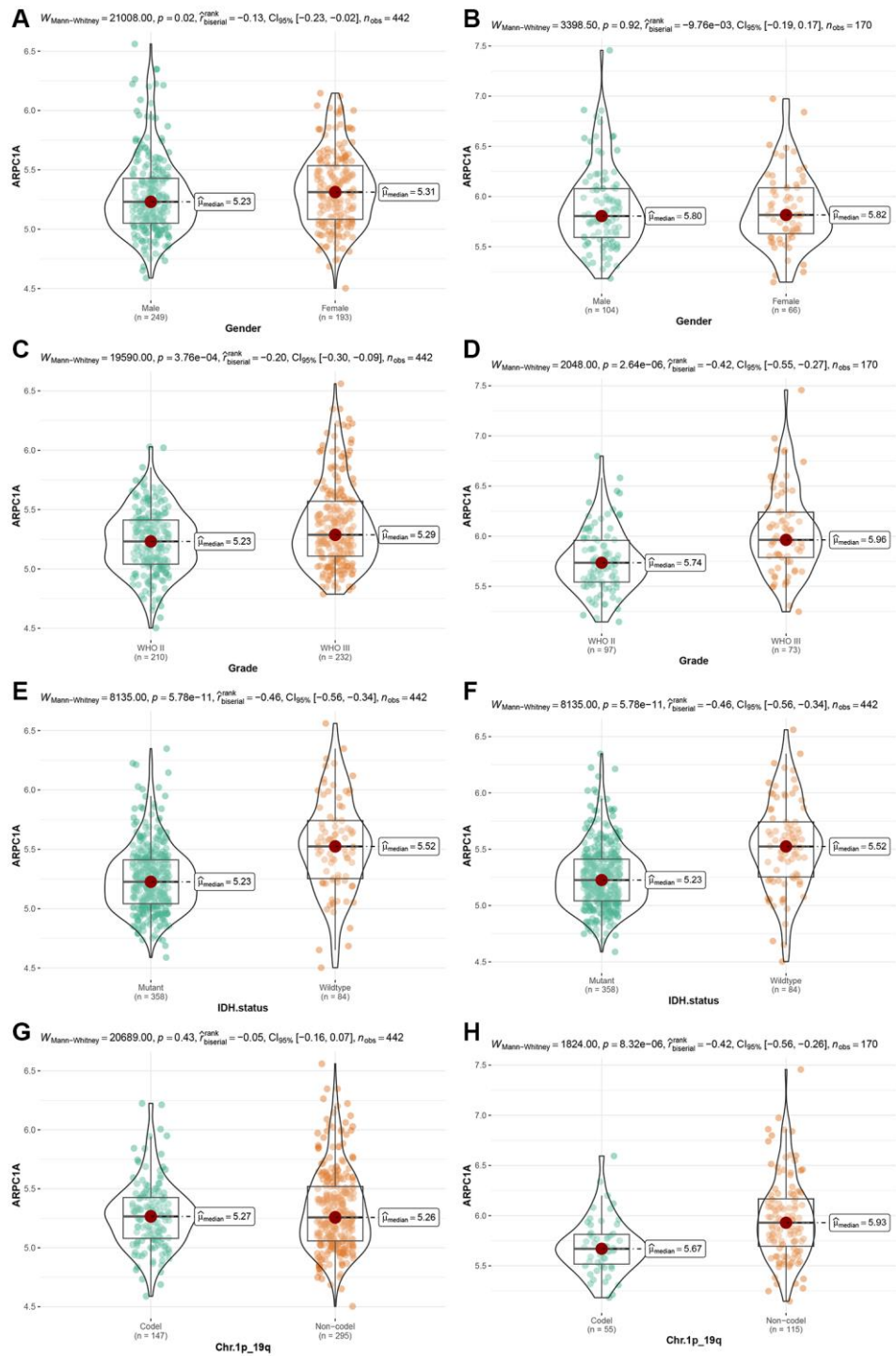
**SUPPLEMENTARY FIGURES**



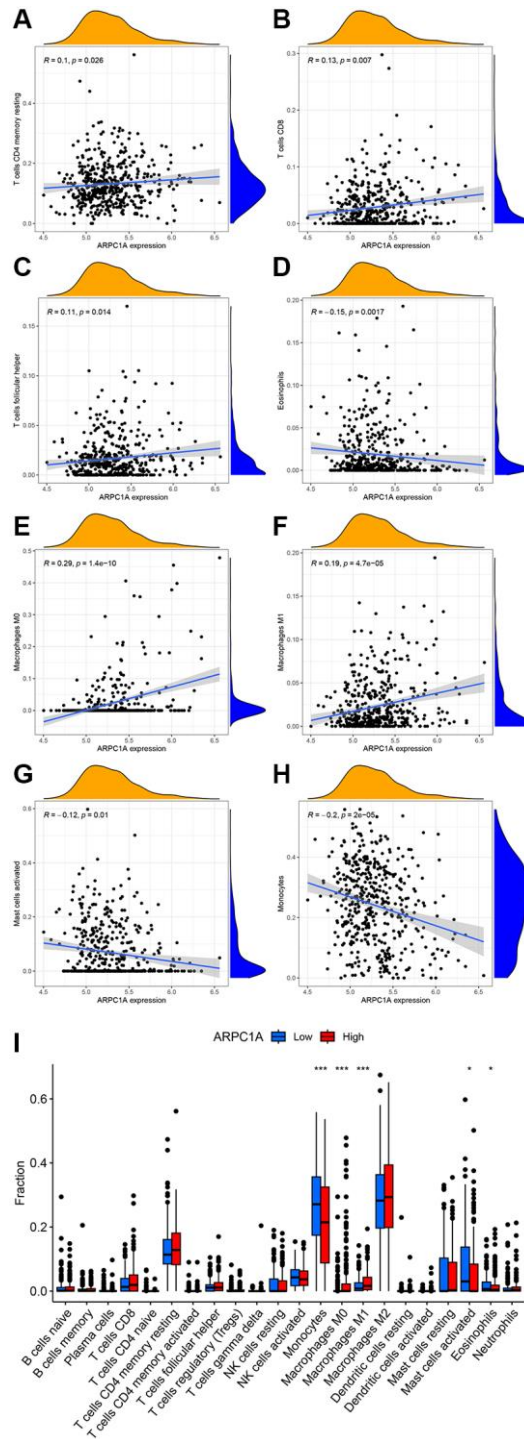
**Supplementary Figure 1.** (A–H) KM survival analysis curves of eight genes: SLBP, COMMD7, LSM4, TOMM34, RPP40, FKBP1A, ARPC1A, and TBCA based on the expression data and prognostic information of the CGGA database.



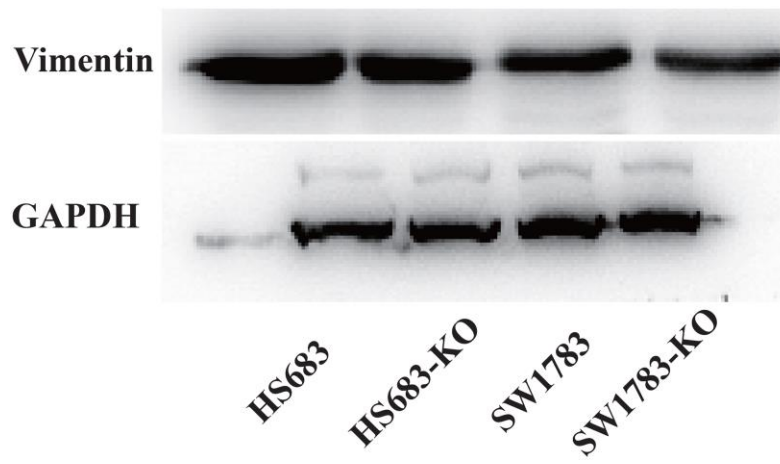
**Supplementary Figure 2.** (A, B) Differential expression of analysis of COMMD7 based on TCGA and CGGA expression. (C, D) Differential expression of analysis of FKBP1A based on TCGA and CGGA expression. (E, F) Differential expression of analysis of LSM4 based on TCGA and CGGA expression. (G, H) Differential expression of analysis of RPP40 based on TCGA and CGGA expression. (I, J) Differential expression of analysis of TBCA based on TCGA and CGGA expression.



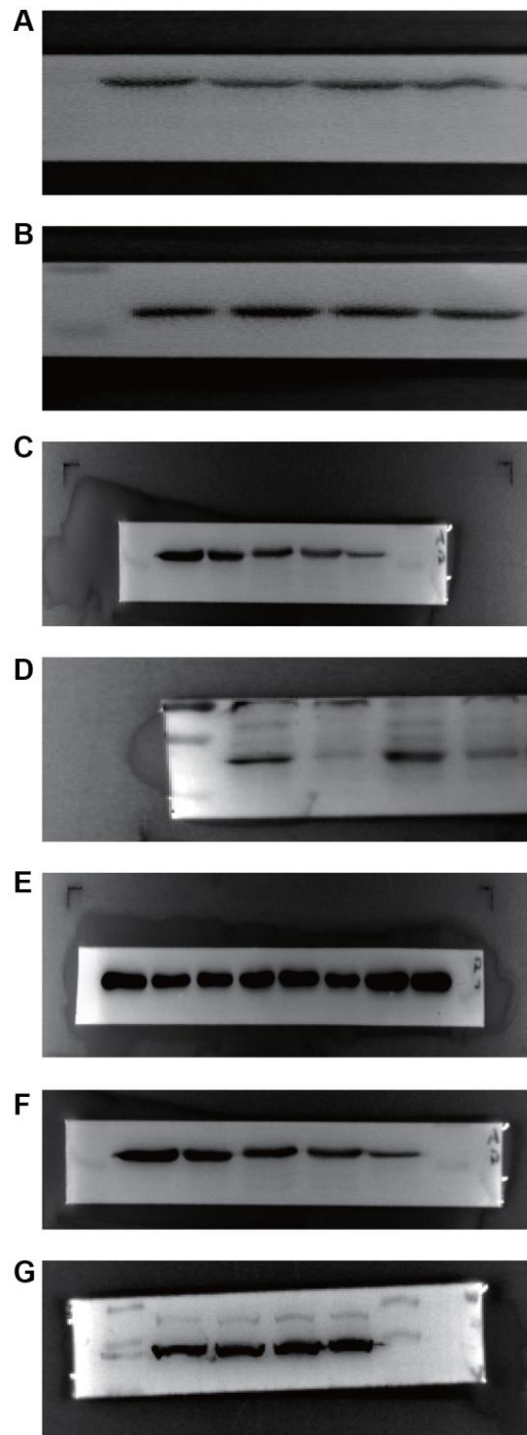
**Supplementary Figure 3. Correlation analysis of ARPC1A expression with clinical risk factors for TCGA and CGGA analysis. (A, B) Gender; (C, D) Grade; (E, F) IDH mutation status; (G, H) 1p19q co-deletion state.**



**Supplementary Figure 4. Immune cell infiltration correlation analysis.** (A) T cells CD8; (B) T cells CD4 memory resting; (C) T cells follicular helper; (D) Monocytes; (E) Macrophages M0; (F) Macrophages M1; (G) Mast cells activated; (H) Eosinophils; (I) Analysis of ARPC1A differential expression and immune cell infiltration.



Supplementary Figure 5. Analysis of vimentin protein in four cell lines.



**Supplementary Figure 6.** (A–G) Summary of protein expression from the WB experiments involved in this study.