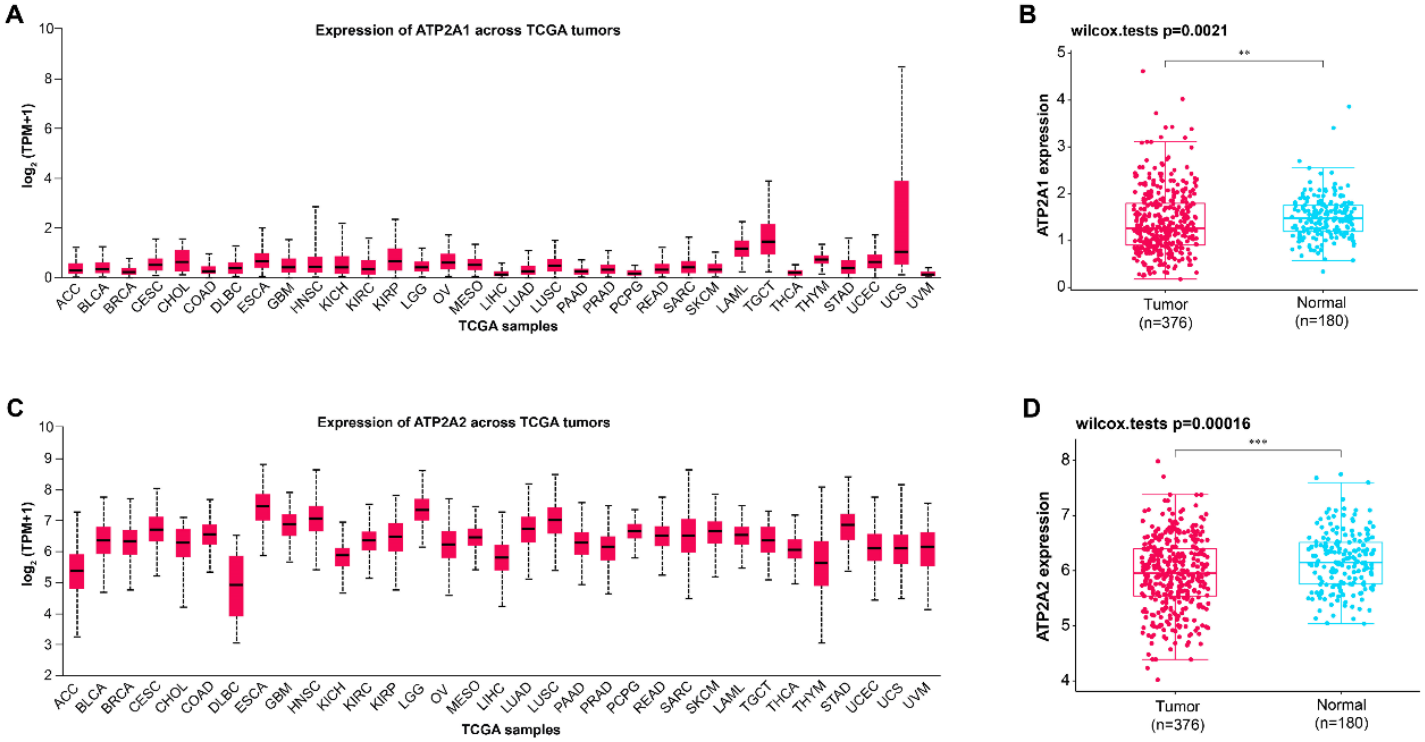
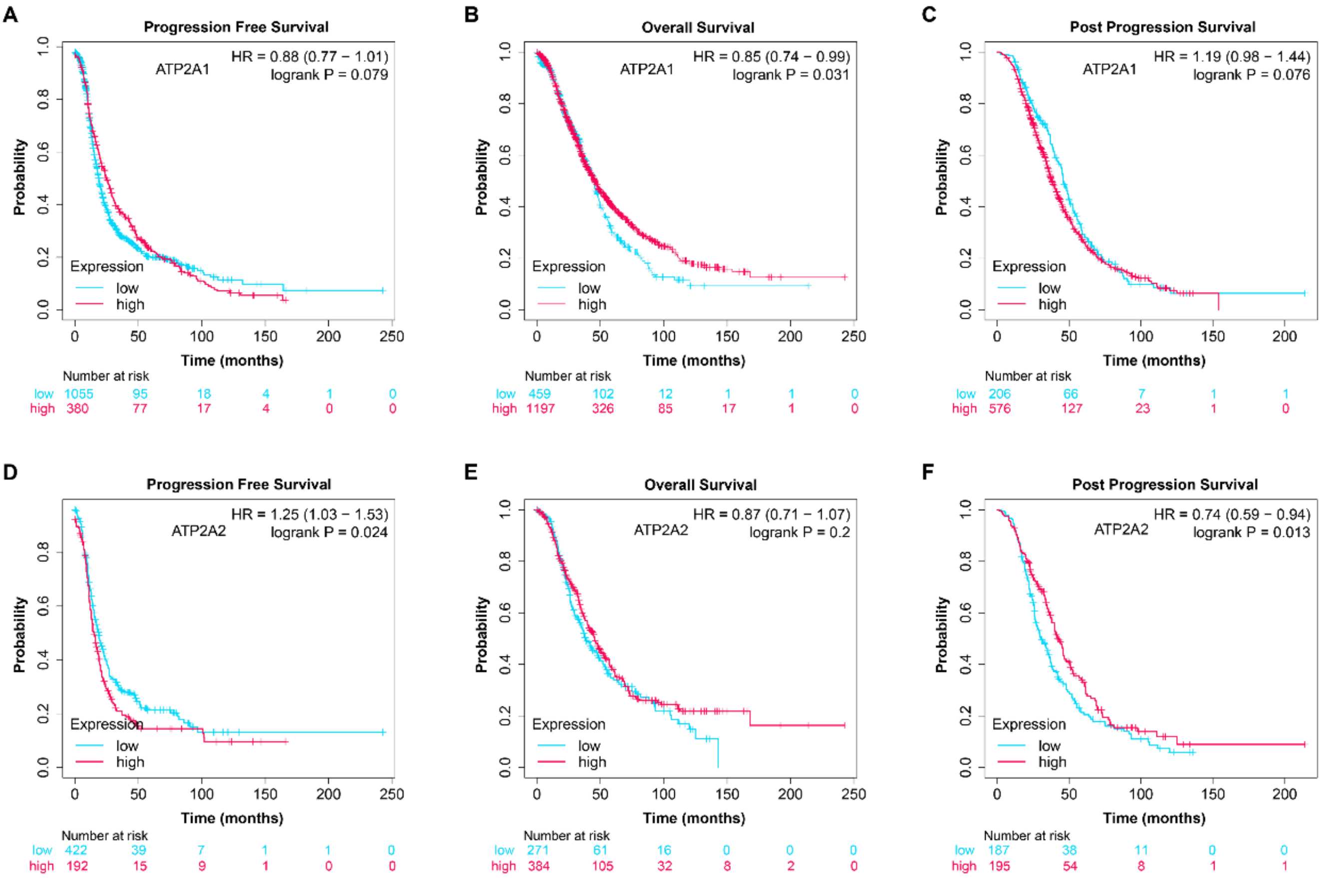
Supplementary Figure S1. Comparative analysis of ATP2A1 and ATP2A2 expression. **A–C** – UALCAN database detected expression of ATP2A1 and ATP2A2 in 33 tumor samples. **B–D** – Wilcoxon detection of expression pattern of ATP2A1 and ATP2A2 between TCGA-OSC samples and GTEx-control samples. ***P* < 0.01, ****P* < 0.001



Supplementary Figure S2. Prognostic impact of ATP2A1 and ATP2A2 expression levels in OV patients. **A–F** – KM survival curve, the effect of differential expression of ATP2A1 and ATP2A2 on the probability of PFS, OS and PPS of patients



Supplementary Figure S3. Immunohistochemical analysis reveals the correlation between ATP2A3 protein expression and OV clinicopathological features. **A** – Comparative analysis of ATP2A3 protein levels between primary OV tumor samples and normal counterparts using the HPA database. **B–E** – Correlation of ATP2A3 protein expression with cancer stage, race, age and tumor grade was measured by the CPTAC database. Z-value is a statistical indicator used to measure the significance of the difference between two different pathological stages (or groups), and *P* values were used to measure statistical significance.