

Fig S1. Using the ONCOMINE databases, a comparative analysis transcription levels of Na+/K+-ATPase genes was performed on cancer tissues and adjacent normal tissue.



Fig S2. Using the GEPIA databases, a comparative analysis transcription levels of Na+/K+-ATPase genes was performed on cancer tissues and adjacent normal tissue.



Fig S3. ATP1A1, ATP1B1 and ATP1B3 expression levels in different cancer types from TCGA data in TIMER. \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.



[Fig S4](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6977647/figure/f2/).ATP1B3expression in HCC **patients with different clinical feature using UALCAN.** The t-test was used to estimate the significance of difference in gene expression levels between groups. \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001.



Fig S5. ATP1B3 co-expressed genes showed the significant correlations with tumor purity and varying degree with immune cells.



Fig S6. the relationship between ATP1B3 and 50 top positive co-expressed genes were confirmed using the CPTAC database.



Fig S7. the relationship between ATP1B3 and 50 top negative co-expressed genes were confirmed using the CPTAC database.



Fig S8. The correlation between ATP1B3 and immune gene were also confirmed using the CPTAC database.