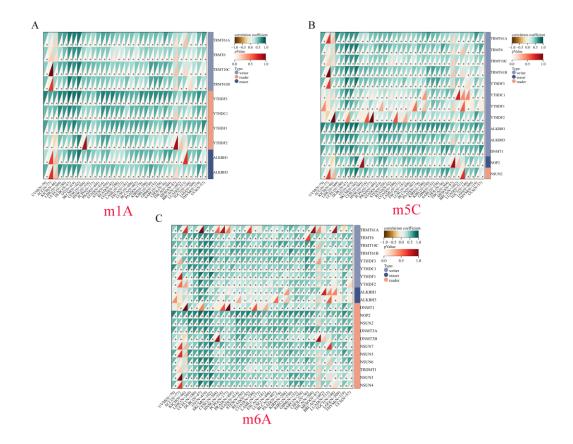
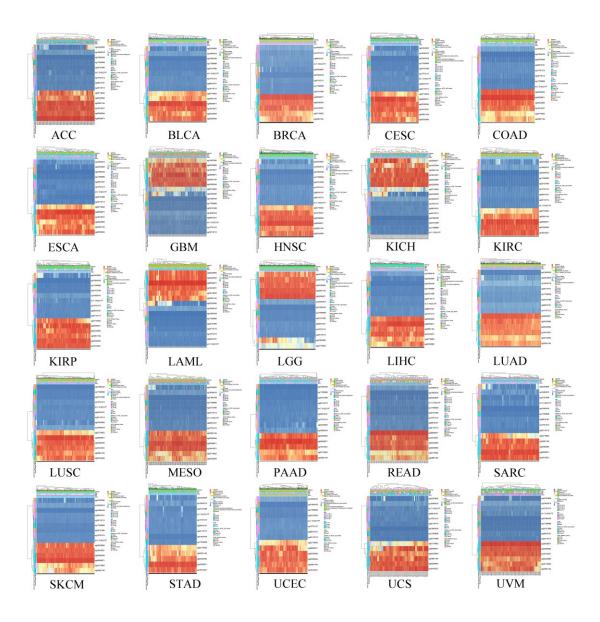


Supplementary file 1: Figure S1. **Mutation analysis of EZH2.** (**A**) the main mutation type of EZH2. (**B**) The primary single nucleotide variation (SNV) class type of EZH2. (**C**) Correlation between EZH2 expression and different mutated types. (**D**) The mutation spectrum of EZH2. (**E**) Association between EZH2 expression and copy number variation (CNV). (**F**) Correlation between EZH2 expression and SNV.

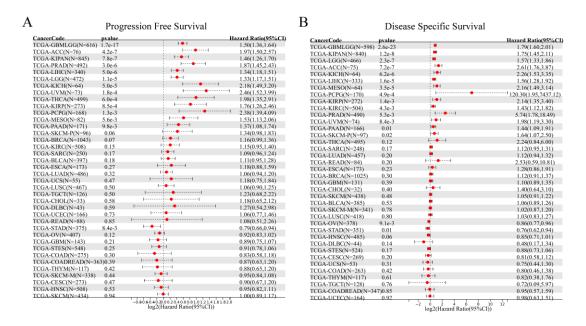


Supplementary file 2: Figure S2. Correlation between EZH2 expression and RNA methylation regulators (i.e., m1A, m5C, m6A). (A) m1A. (B) m5C. (C) m6A.

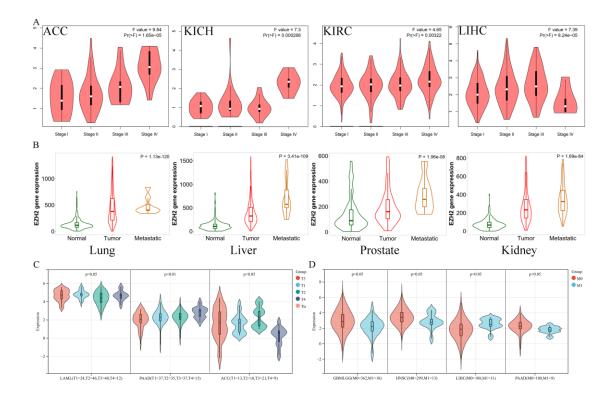


 $\textbf{Supplementary file 3:} \ \textbf{Figure S3.} \ \textbf{Heatmap of DNA methylation level of EZH2 in various cancers.}$

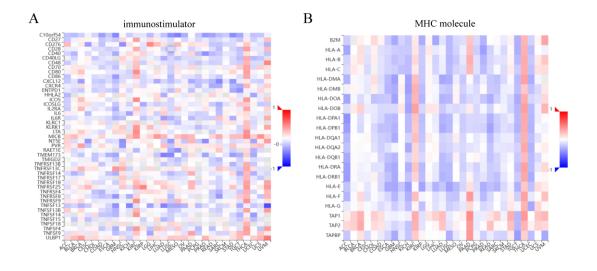
High-expression (red); low-expression (bule).



Supplementary file 4: Figure S4. Correlation between EZH2 expression and survival prognosis of TCGA pan-cancer patients. (A) Progression free survival. (B) Disease specific survival.



Supplementary file 5: Figure S5. **Association analysis of EZH2 expression with clinicopathological features. (A)** The association between EZH2 expression and pathological stages. **(B)** Violin plots showing differential EZH2 expression levels in different metastasis. **(C-D)** Correlation between EZH2 expression and TNM classification (T and M stages).



Supplementary file 6: Table S6. **The correlation between EZH2 expression and several immunotherapy-related molecules.** (A) Immunostimulator. (B) MHC.