

**Figure S1. The unsupervised clustering of DNA methylation regulators and consensus matrix heatmaps.** (A) Cumulative distribution function (CDF) curve. (B) CDF Delta area curve, which indicates the relative change in the area under the CDF curve for each category number  $k$  compared with  $k-1$ . (C) The consensus matrix heatmaps for  $k = 2$ , and  $k = 4-9$ .

Figure S2

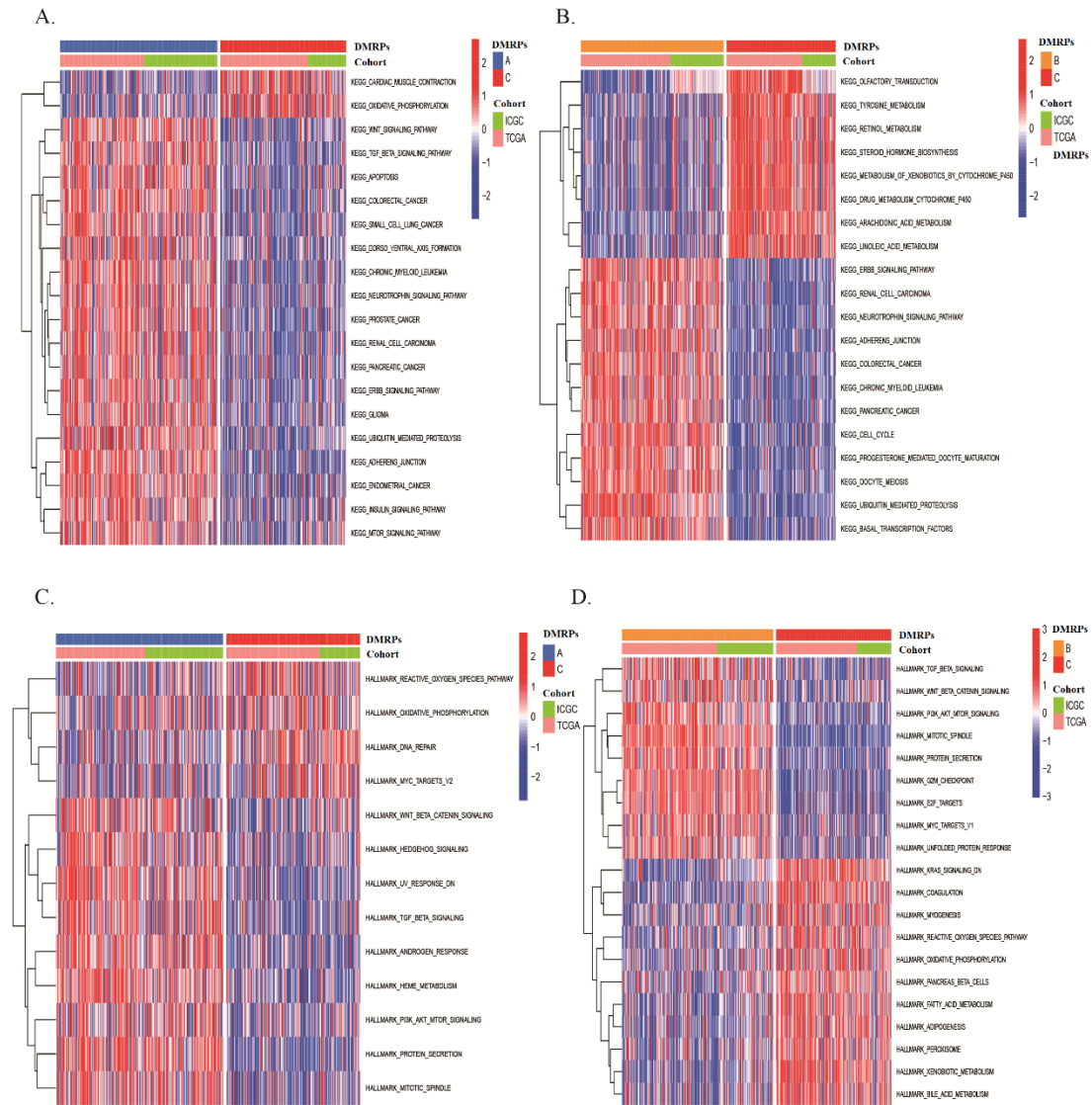
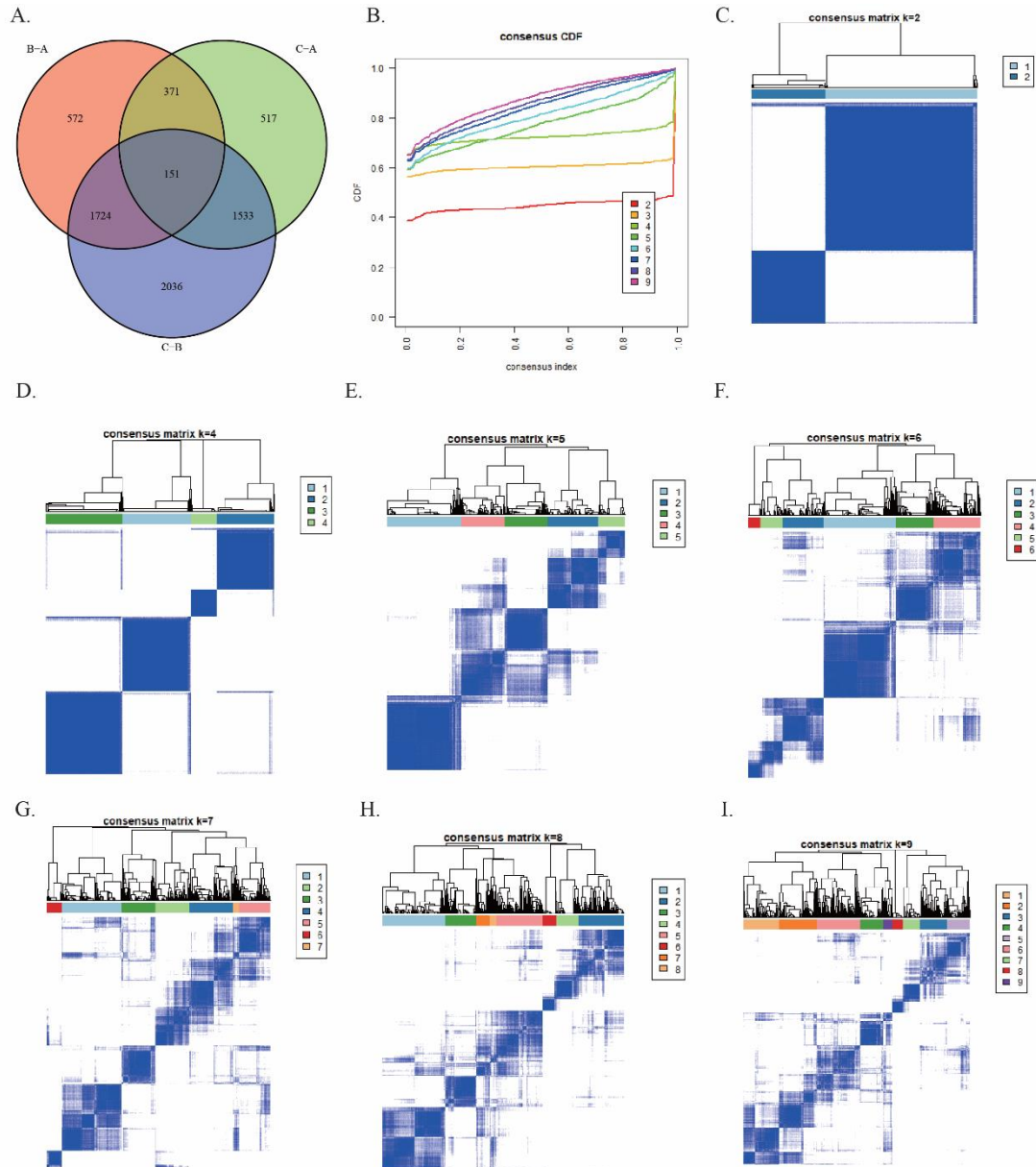
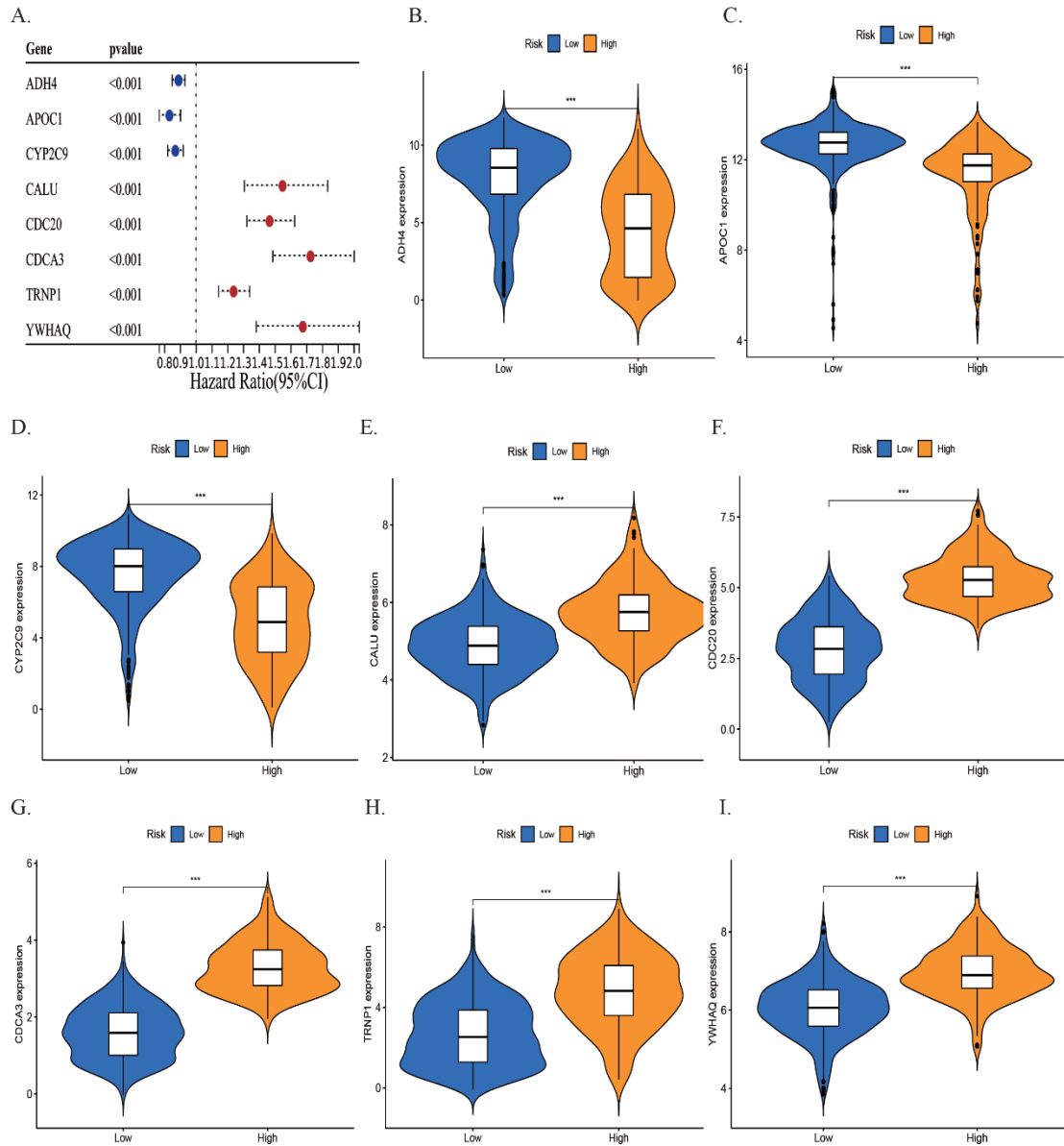


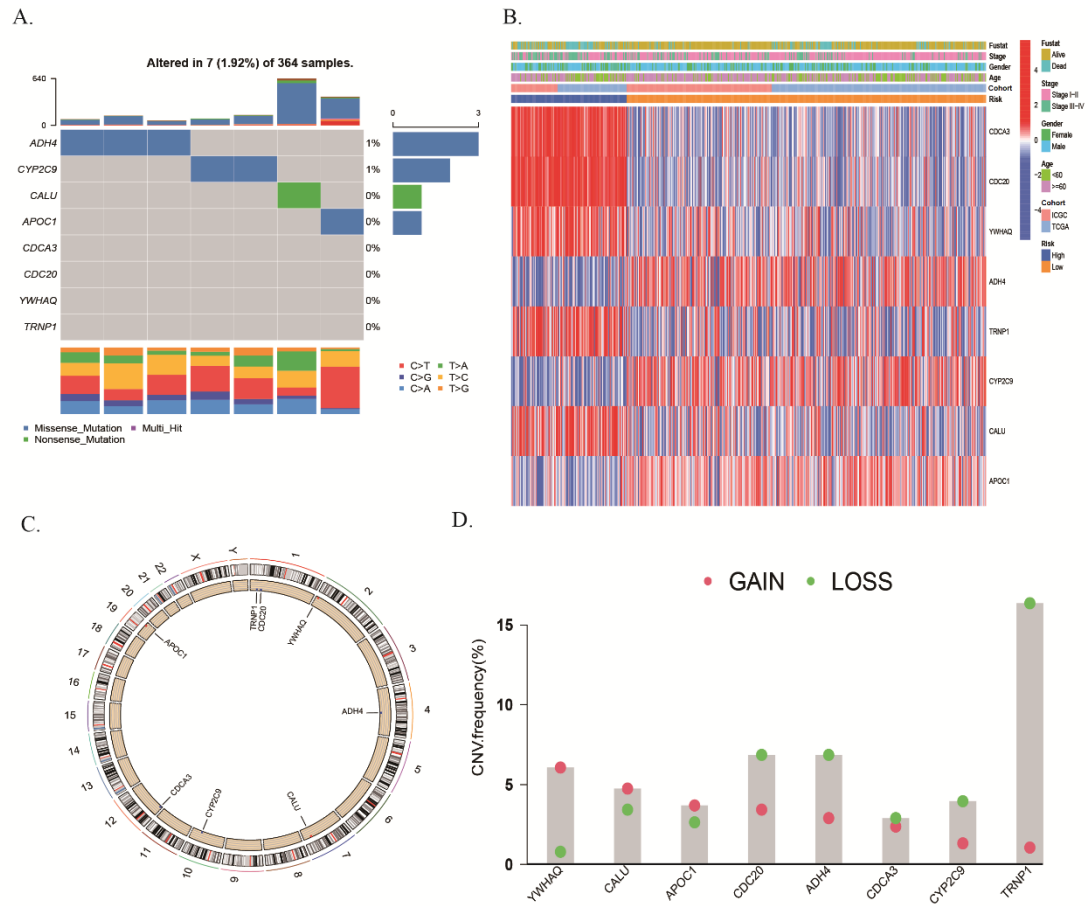
Figure S2. The GSEA analysis of DNA methylator regulators-related patterns between pattern A-C and pattern B-C.



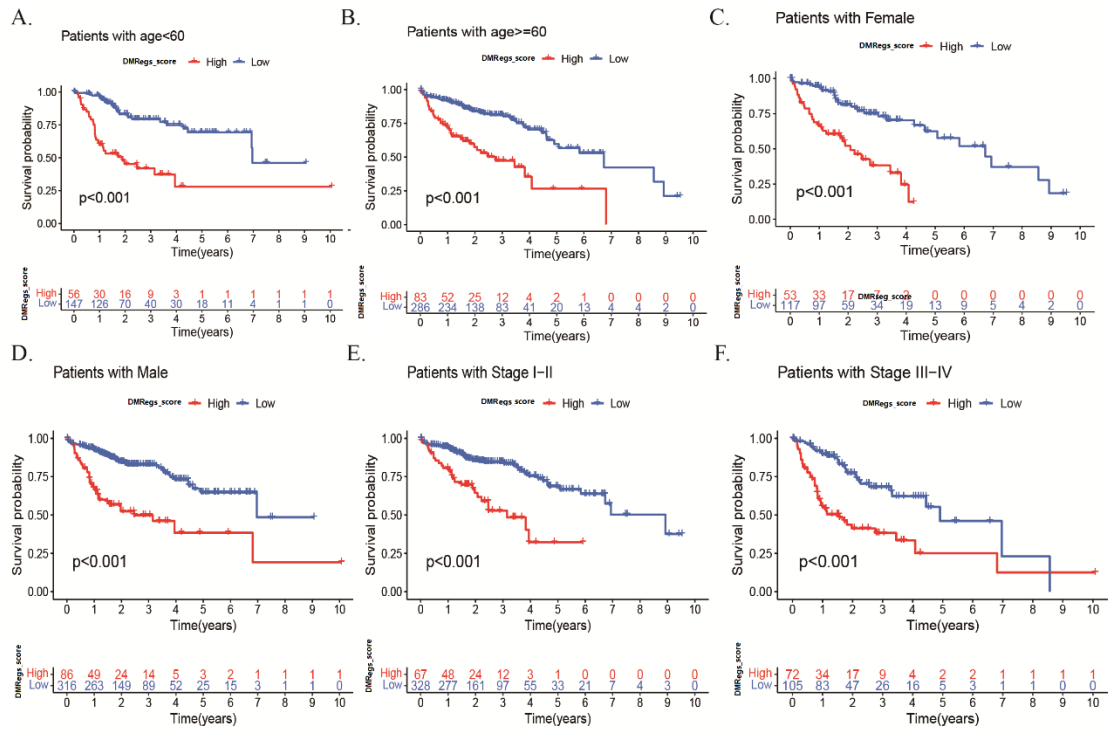
**Figure S3. The unsupervised clustering of DNA methylation regulators-related DEGs and consensus matrix heatmaps.** (A) Venn diagram of DEGs among three DNA methylation regulators-related patterns. (B) CDF Delta area curve. (C) The consensus matrix heatmaps for k = 2, and k= 4-9.



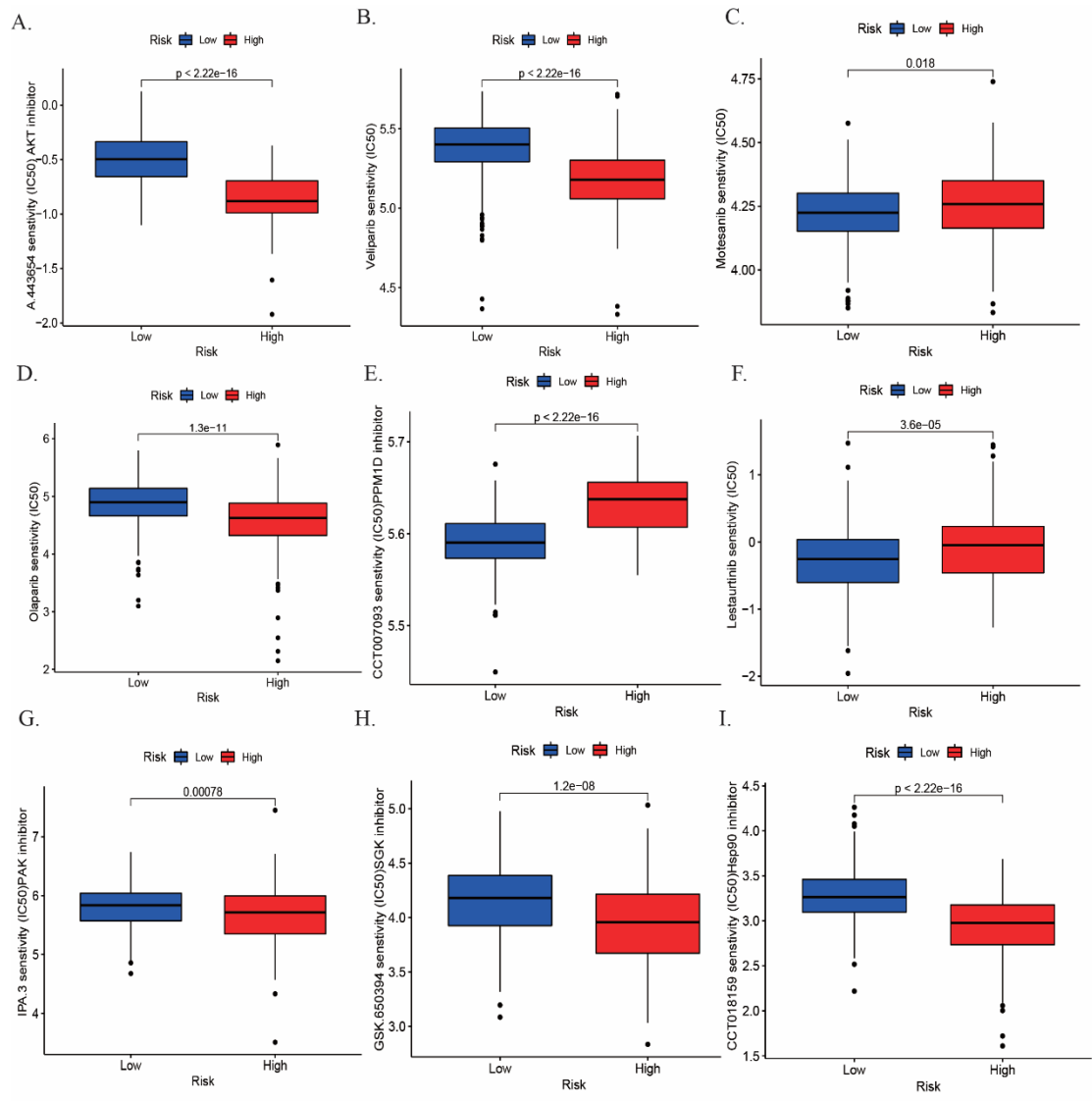
**Figure S4. Characteristics of eight genes in the risk model. (A)** The prognosis of eight genes in HCC patients. **(B-I)** The expression differences of eight genes in two risk groups.



**Figure S5. Landscape of genetic variations and transcriptional expression of eight genes.** (A) The expression level of eight genes between different risk groups with clinical features. (B) 7 of the 364 patients occurred genetic variations of eight genes with 1.92% mutation frequencies. (C) The locations of CNV variations in eight genes on 23 chromosomes. (D) The frequency of CNV gain or loss among eight genes.

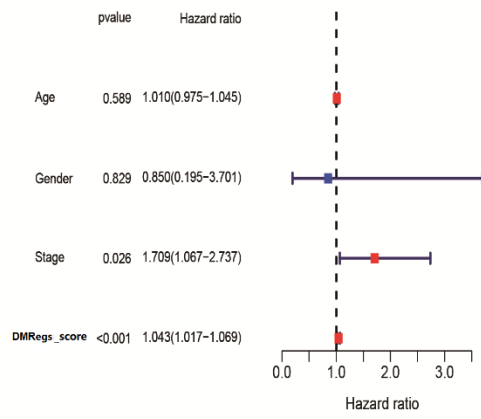


**Figure S6. Stratification analysis of the DMRegs\_ score in HCC. (A-B) Age (age ≤ 60 and age > 60 years old). (C-D) Gender (female and male). (E-F) Tumor stage (I-II or III-IV).**

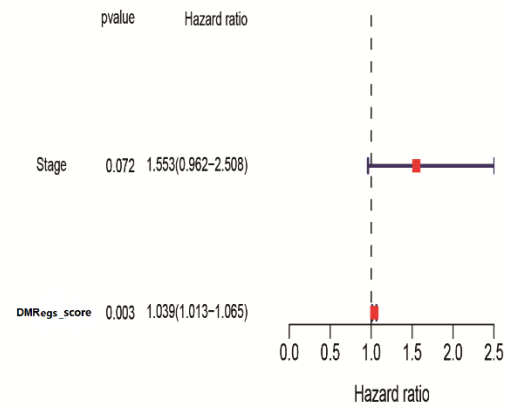


**Figure S7. The relationship between DMRegs\_score and therapeutic sensitivity.**

A.



B.



**Figure S8. The univariate and multivariate cox analysis of DMRegs\_score in validating set.**