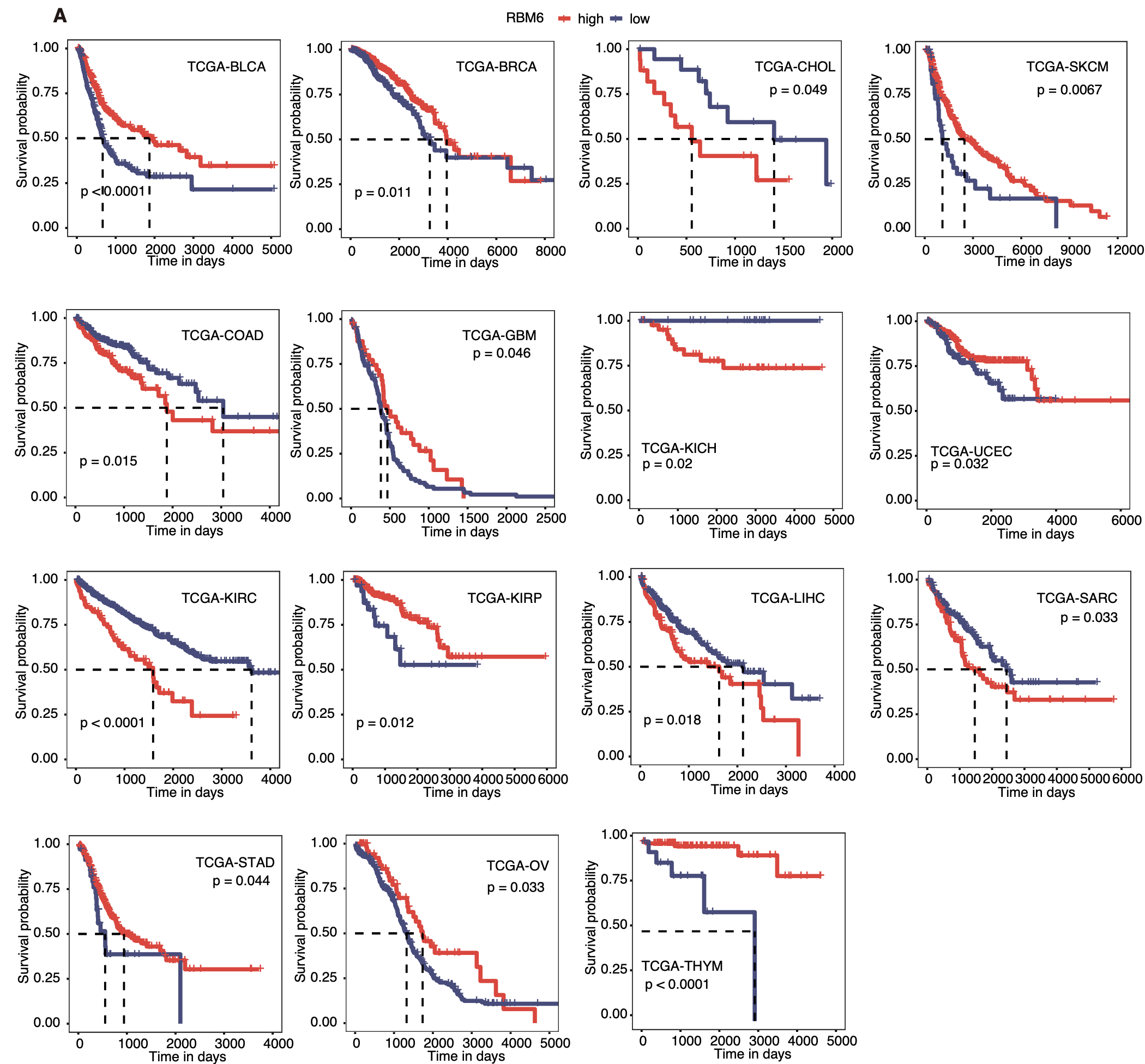
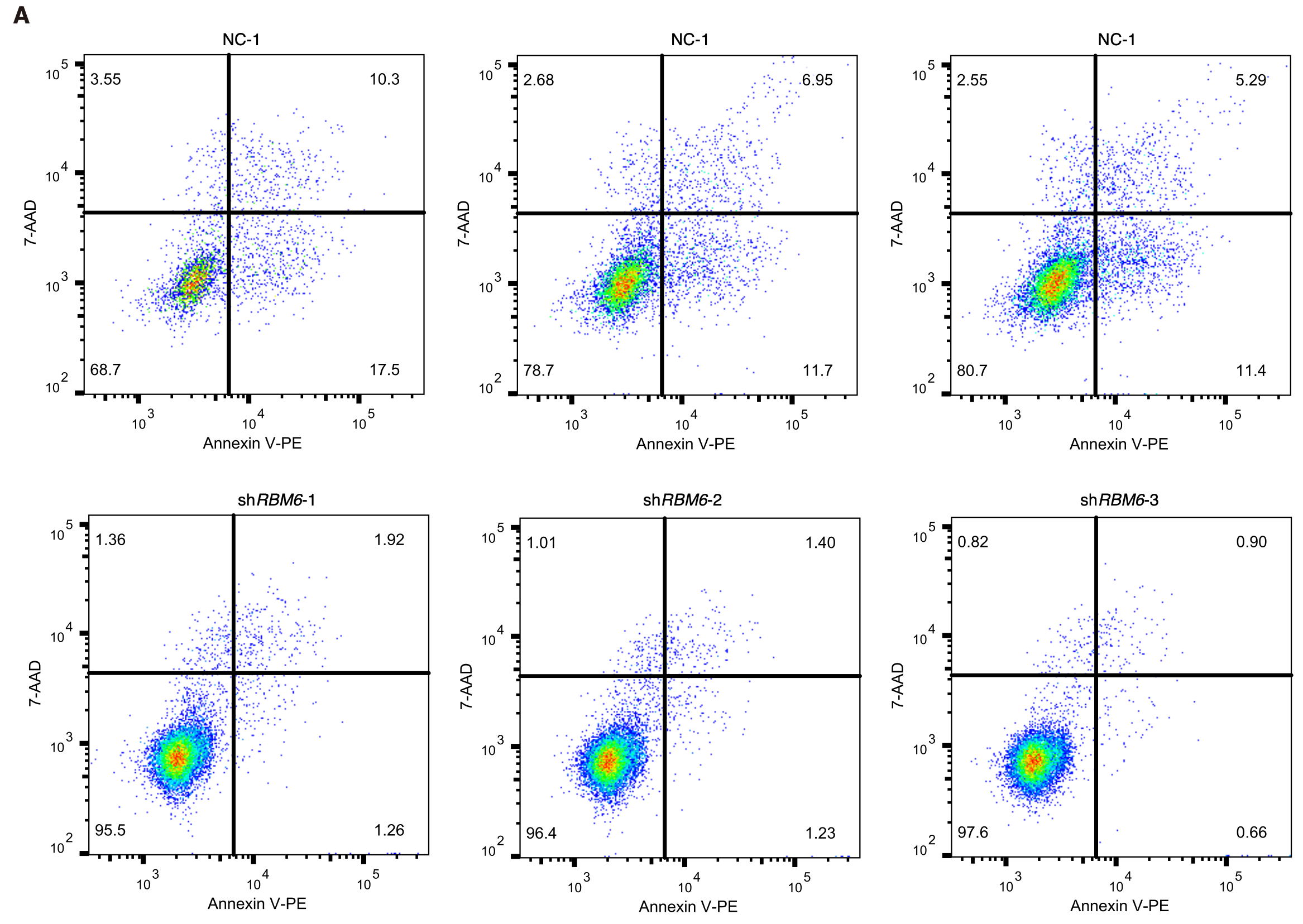
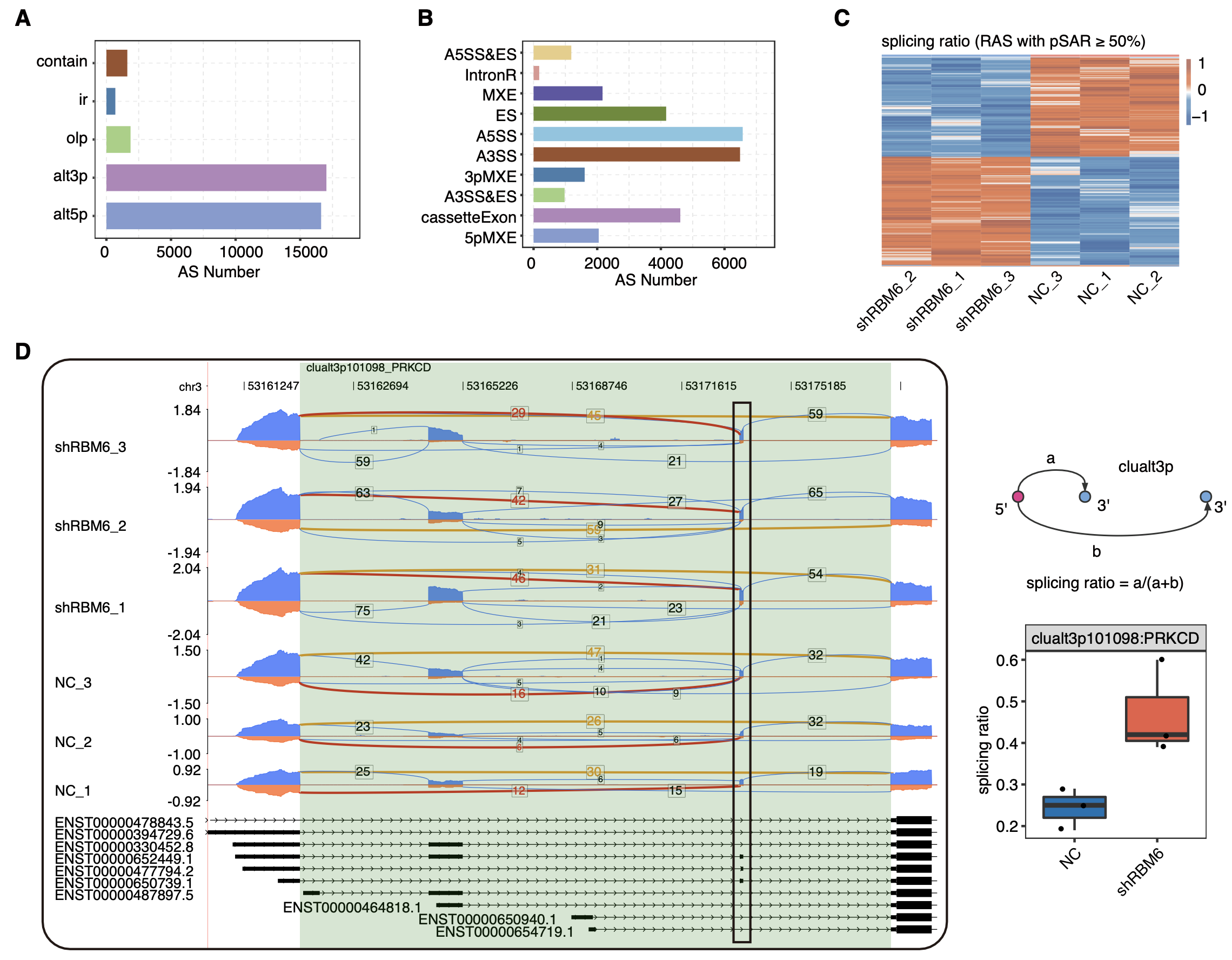
Supplementary Figures



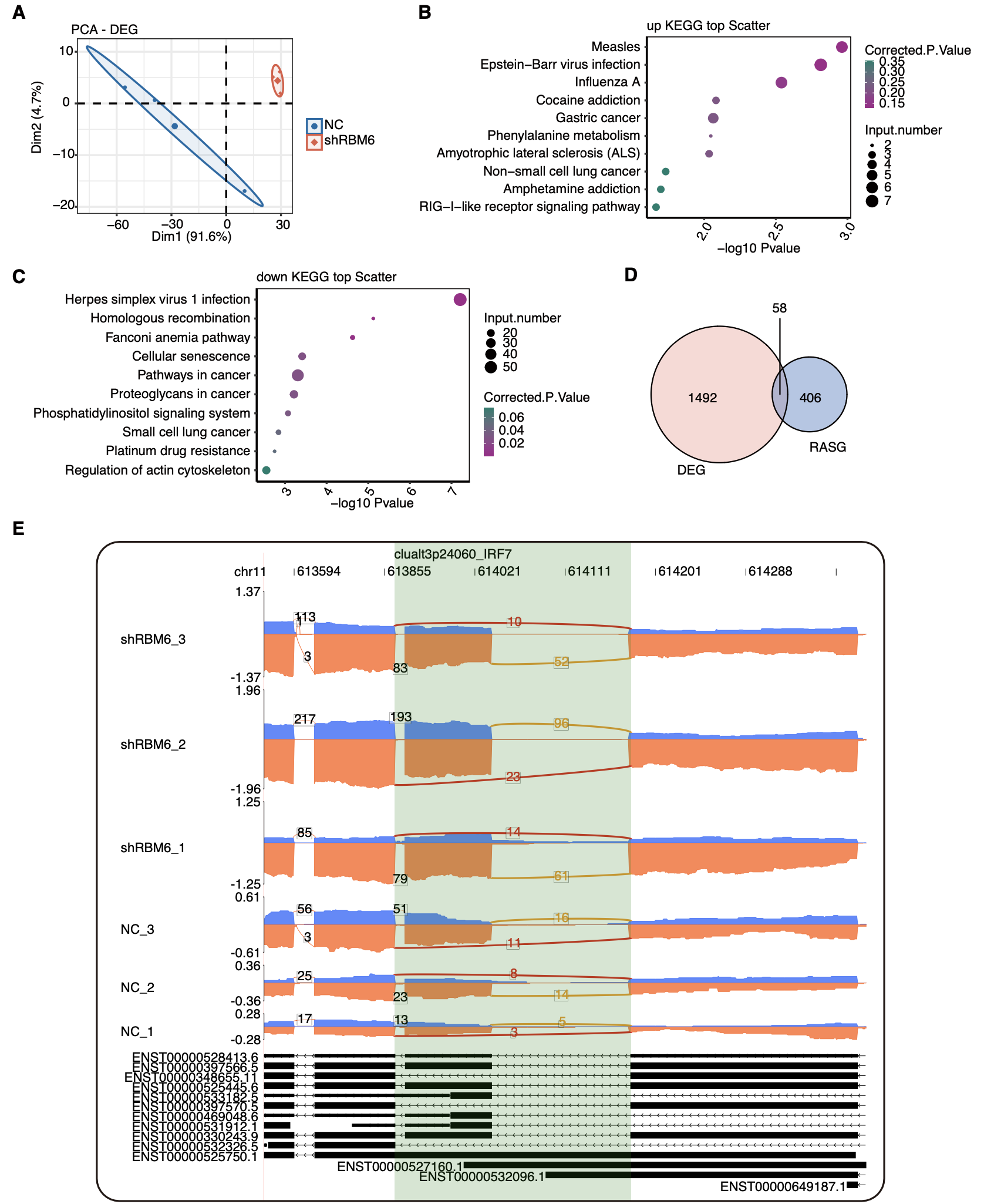
**Supplementary Fig. 1. Pan-cancer analysis shows that high RBM6 expression is associated with a good prognosis in several tumor types.** The survival curve shows the prognosis of RBM6 in the 15 cancer types of TCGA.



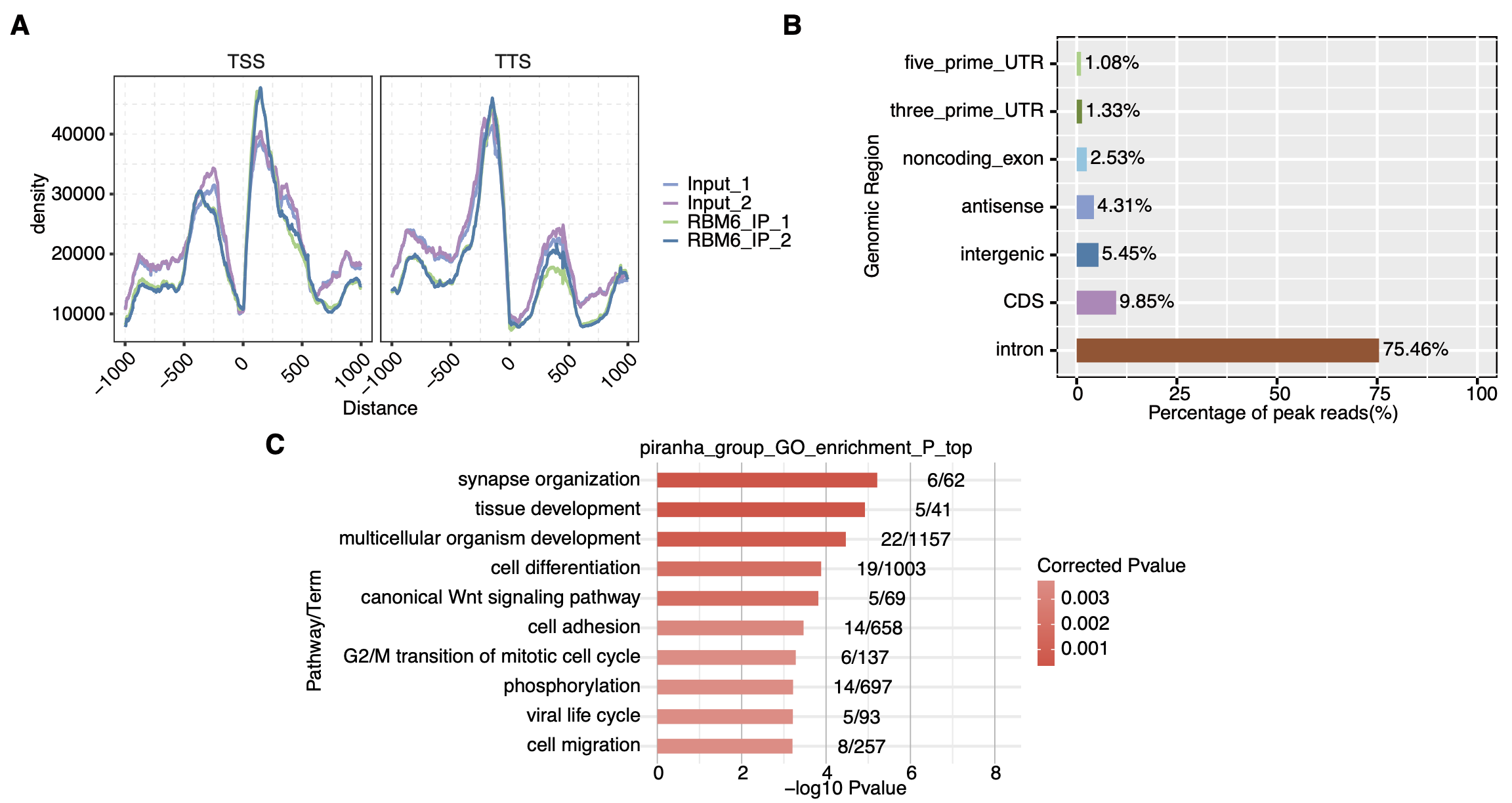
**Supplementary Fig. 2. RBM6 knockdown significantly promotes proliferation and inhibits apoptosis.** Annexin *V*-*PE*/7-AAD staining assay.



**Supplementary Fig. 3. RBM6 regulates the AS of genes associated with DNA damage response- and cell survival-related pathways.** A. The bar plot shows all detected ASEs by SUVA in each group. B. Splice junction constituting ASEs detected by SUVA is annotated to classical ASE types. And the number of each classical ASE type is shown in the bar plot. C. The heatmap shows the splicing ratios of RAS (PSAR ≥ 50%). D. Reads distribution diagram shows clualt3p101098 PRKCD. The boxplot in the right panel shows the splicing ratio of clualt3p101098 PRKCD.



**Supplementary Fig. 4. RBM6 regulates the expression of genes involved in type I interferon signaling pathways, cell cycle, and cellular responses to DNA damage, which may be mediated by TFs with RBM6-RAS.** A. PCA based on DEGs. The ellipse for each group is the confidence ellipse. B. The bar plot shows the top 10 enriched KEGG pathways of the up-regulated genes. C. The bar plot shows the top 10 enriched KEGG pathways of the down-regulated genes. D. Venn diagram shows the overlap of DEGs and RASGs. E. Reads distribution diagram shows clualt3p24060 IRF7.



**Supplementary Fig. 5. RBM6-mRNA interaction map in HeLa cells.** A. Distribution RBM6 binding reads around transcription start/terminate sites (TSS/TTS). B. The bar plot shows the distribution of peak reads across genomic regions. C. The top 10 enriched GO terms of RBM6 peak associated genes.