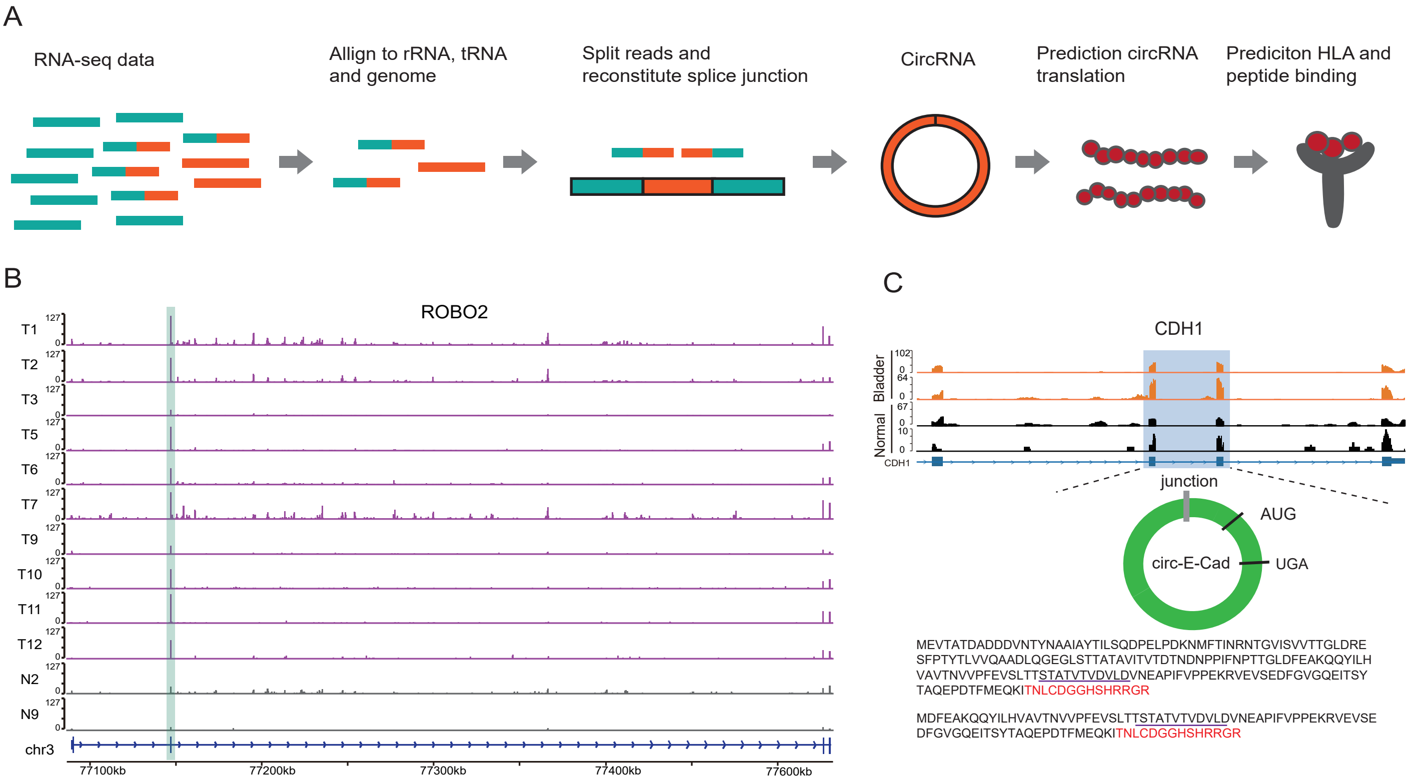
Figure S1



Supplementary Figure 1. The workflow for the identification of neoepitopes using CIRC-neo. **(A)** Flowcharts for the number of circRNA or circRNA-derived neoepitope peptides identified at each stage of the analysis. **(B)** The second exon of ROBO2 forming the circRNA track. Purple represents the GBM samples and gray represents the normal samples. **(C)** The novel proteins and neoepitopes generated from circ-E-Cad. The red letters represent the novel peptide sequences while the purple lines represent HLA class I-binding neoepitopes.