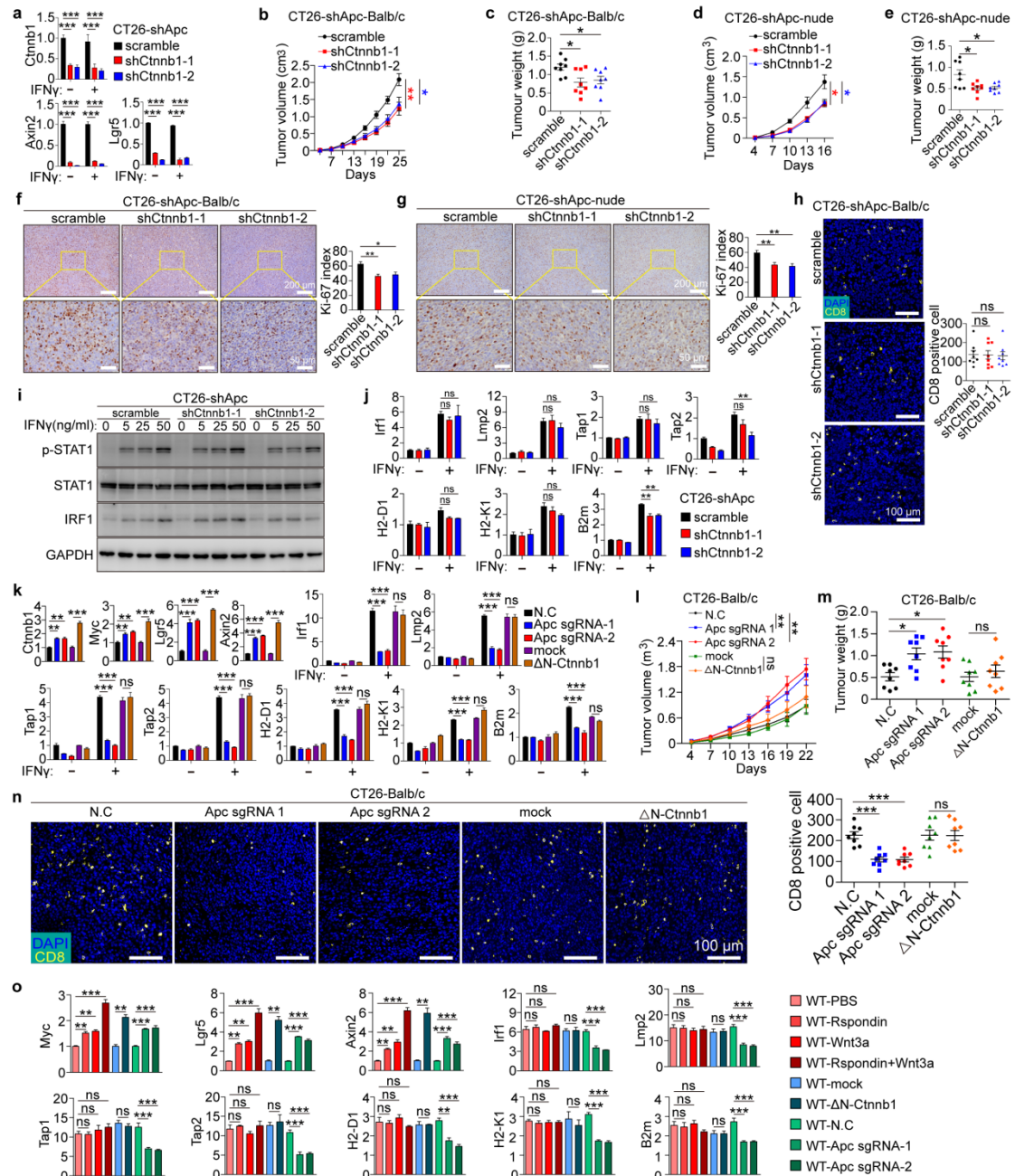




Supplementary information, Fig. S5. Role of β -catenin in APC-loss-induced CRC immune evasion and inactivation of IFN γ -STAT1-IRF1-MHC-I antigen presentation signaling. **a**, Ctnnb1, Axin2 and Lgr5 mRNA expression (qPCR) in indicated cells with 12 h exposure to IFN γ (50 ng ml⁻¹) before collection from three independent experiments. One-way ANOVA. **b-e**, Indicated cells were transplanted subcutaneously into Balb/c or nude mice. Tumor growth was monitored at indicated times. $n = 8$, two-way ANOVA. Tumor weight was measured. $n = 8$, one-way ANOVA. **f, g**, Representative images and quantification of immunohistochemistry staining against Ki-67 in tumor tissues. $n = 8$ for each group, one-way ANOVA. **h**, Frozen sections from indicated tumors were subjected to immunostaining analysis of CD8 (red) along with DAPI for DNA (cyan), and the number of CD8⁺ cells were quantified. $n = 8$. one-way ANOVA. **i**, Cell lysates from gradient concentration IFN γ -stimulated cells were subjected to immunoblot analysis with antibodies to the indicated proteins. Data collected from three independent experiments. **j**, Irf1, Lmp2, Tap1, Tap2, H2-D1, H2K1 and B2m mRNA

expression (qPCR) in indicated cells with 12 h exposure to IFN γ (50 ng ml⁻¹) before collection from three independent experiments. one-way ANOVA. **k**, Apc was knocked out or Δ N-Ctnnb1 was overexpressed in CT26 cells, and Ctnnb1, Myc, Lgr5, Axin2, Irf1, Lmp2, Tap1, Tap2, H2-D1, H2K1 and B2m mRNA expression were determined by qPCR. Data were from three independent experiments. one-way ANOVA. **l**, Indicated CT26 cells were transplanted into Balb/c mice and tumor growth was monitored. Significance for tumor growth kinetics were calculated by two-way ANOVA test. **m**, Scatter plots show tumor weight of indicated cells formed in Balb/c mice. $n = 8$, one-way ANOVA. **n**, Representative immunofluorescence staining of CD8 in tumor tissues and scatter plots show number of CD8⁺ cell in all three groups. $n = 8$, one-way ANOVA. **o**, Myc, Lgr5, and Axin2 were quantified by qPCR in organoids with indicated treatment, and Irf1, Lmp2, Tap1, Tap2, H2-D1, H2K1 and B2m mRNA expression were quantified by qPCR in indicated organoids with 12 h exposure to IFN γ (50 ng ml⁻¹) before collection from three independent experiments. one-way ANOVA.