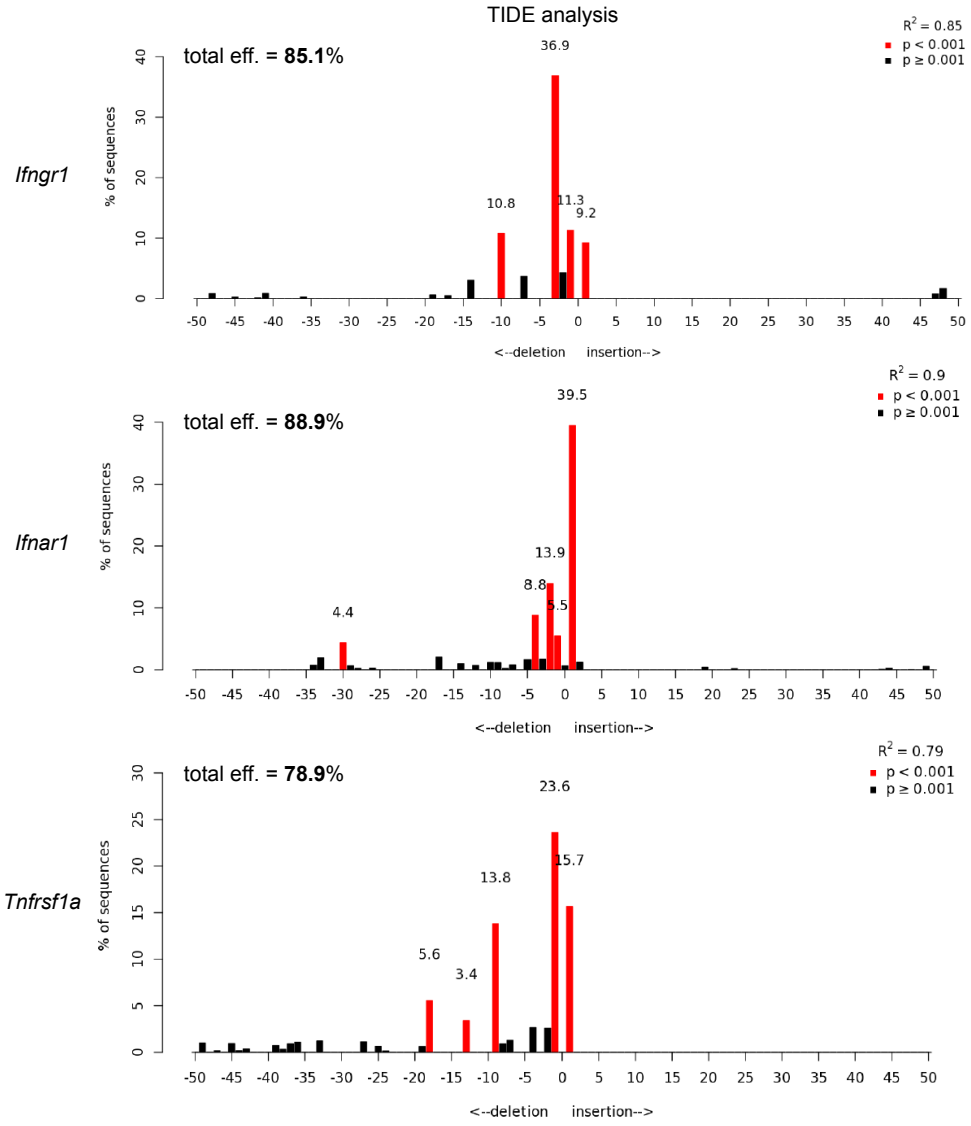
Figure S2

A

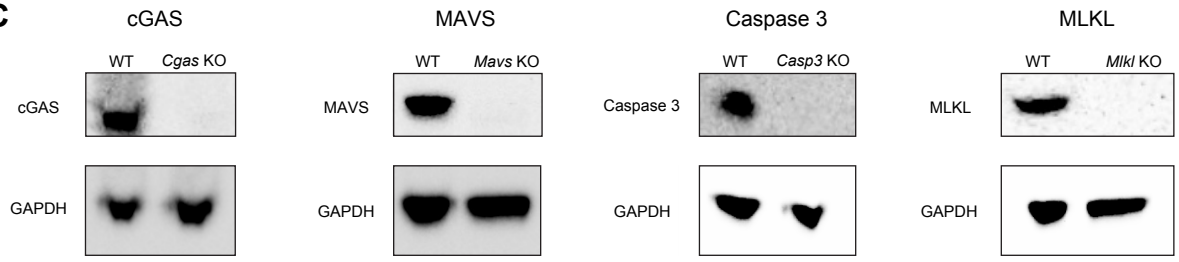


B

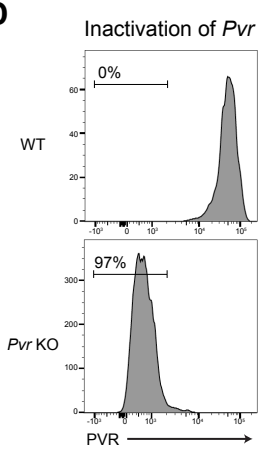
Summary of TIDE analysis

	Control	*Ifngr1*	*Ifnar1*	*Tnfrsf1a*	*Fas*	*Gne*
Editing efficiency	95.2%	85.1%	88.9%	78.9%	95.4%	98.2%

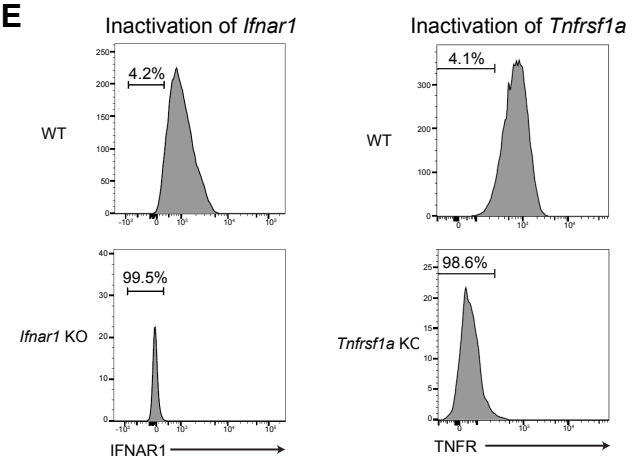
C



D



E



Supplementary Fig. S2. Efficiency of gene editing in tumor cell lines for co-dependency screen.

(**A**) TIDE analysis of *Ifngr1*, *Ifnar1*, and *Tnfrsf1a* gene editing efficiency in *Ifngr1*-KO, *Ifnar1*-KO, and *Tnfrsf1a*-KO B16F10-Cas9 cells, respectively.

(**B**) Summary of editing efficiency by TIDE analysis for genes edited in B16F10-Cas9 cells that were used for co-dependency screens.

(**C**) Western blot analysis of cell lysates from parental B16F10-Cas9 cells (WT) or indicated gene edited B16F10-Cas9 cells. GAPDH is shown as a loading control.

(**D**) Histogram of flow cytometry analysis for PVR expression. Parental B16F10-Cas9 cells (WT) or B16F10-Cas9 *Pvr*-KO cells were analysed.

(**E**) Histogram of flow cytometry analysis for IFNAR1 and TNFR expression. Parental B16F10-Cas9 cells (WT) and B16F10-Cas9 *Ifnar1*-KO cells, or B16F10-Cas9 *Tnfrsf1a*-KO cells were analysed, respectively.