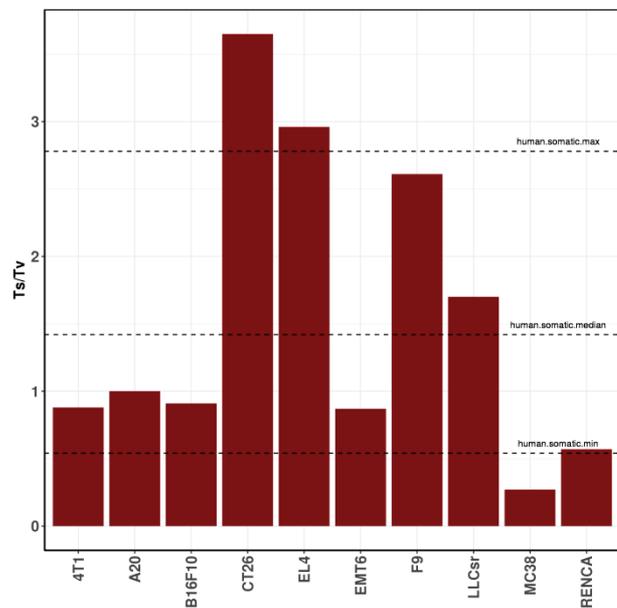


Figure S1. Mutation landscape of syngeneic models and types of somatic variants for each model.

A.



B.

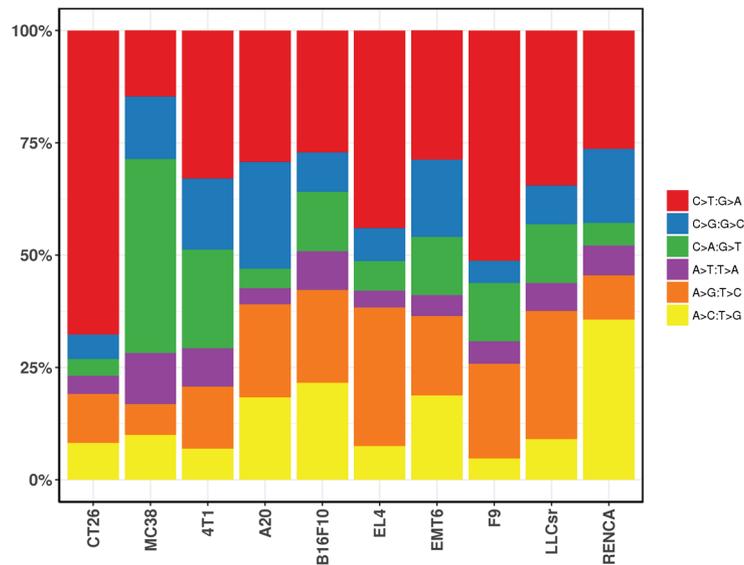


Figure S2. A. Ratio of Ts (Transition) to Tv (Transversion) substitution mutation in each syngeneic model; dashed lines represent maximum, median and minimum of median Ts/Tv from each human tumor types (data from (Alexandrov et al. 2013)) respectively. B. Single nucleotide mutation changes in each syngeneic model.

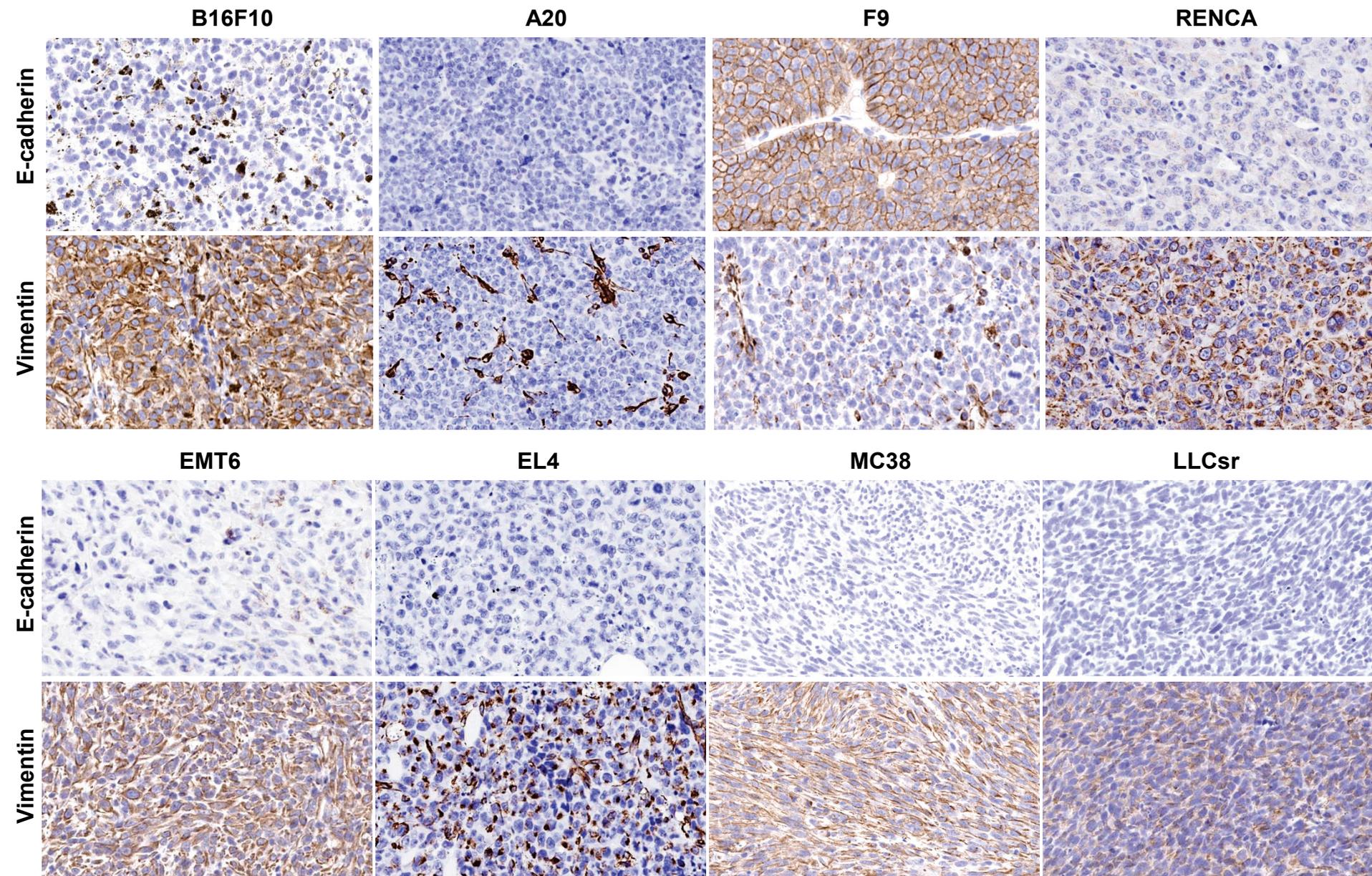


Figure S3. E-cadherin and vimentin stain in syngeneic models.

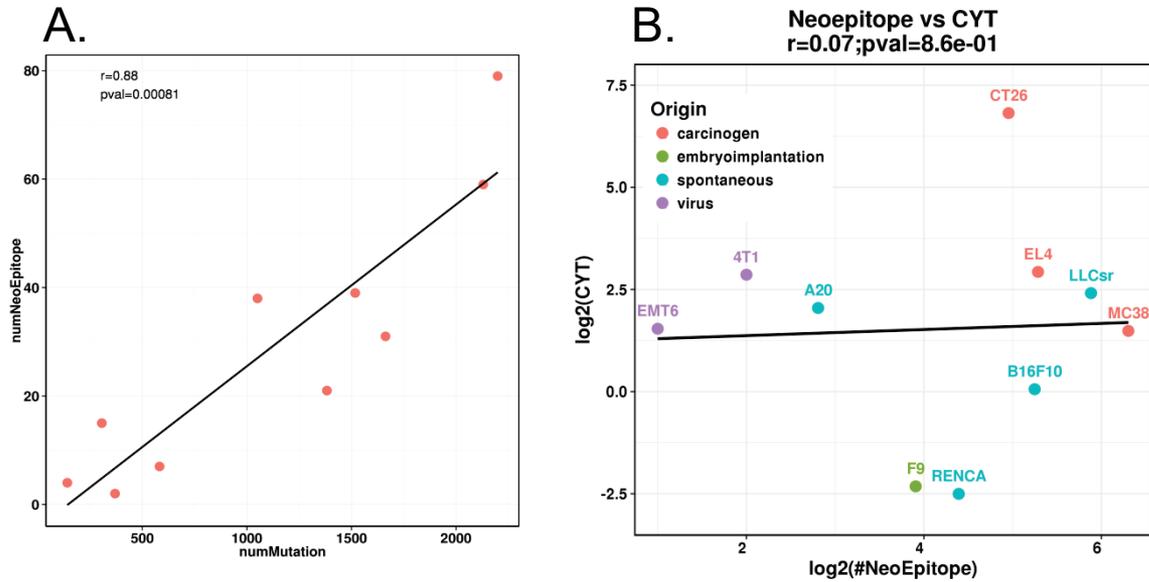


Figure S4. A. Correlation of neoantigen with mutational load in syngeneic models.  
 B. Correlation of neoantigen with cytolytic activity in syngeneic models.  
 The correlation was calculated using spearman method in R.  
 numMutation: number of missense mutation.

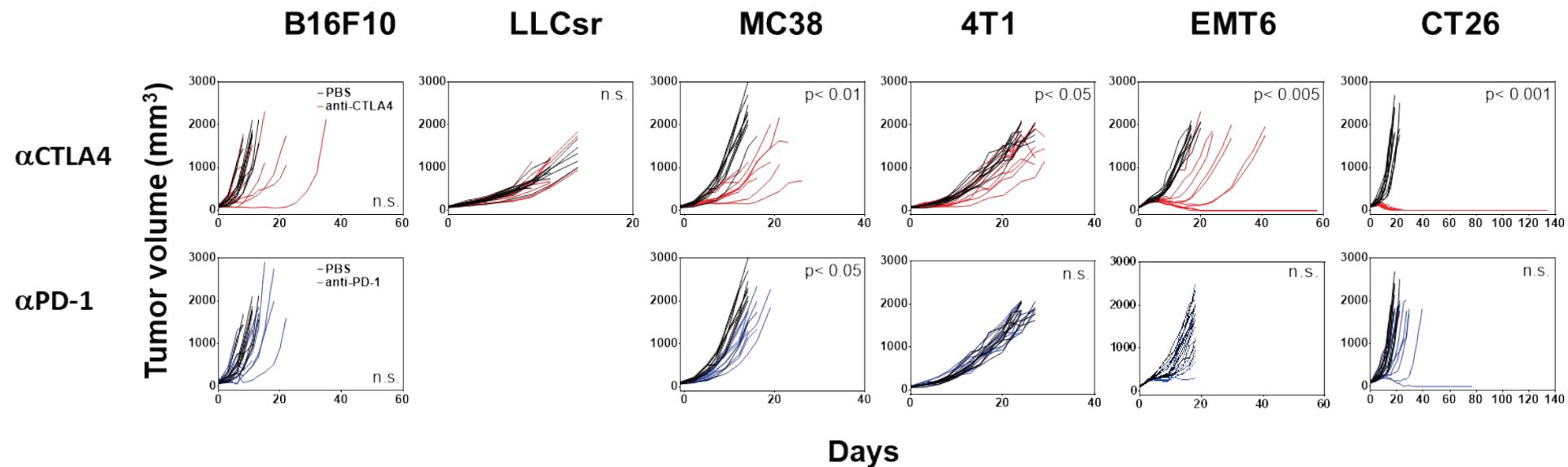
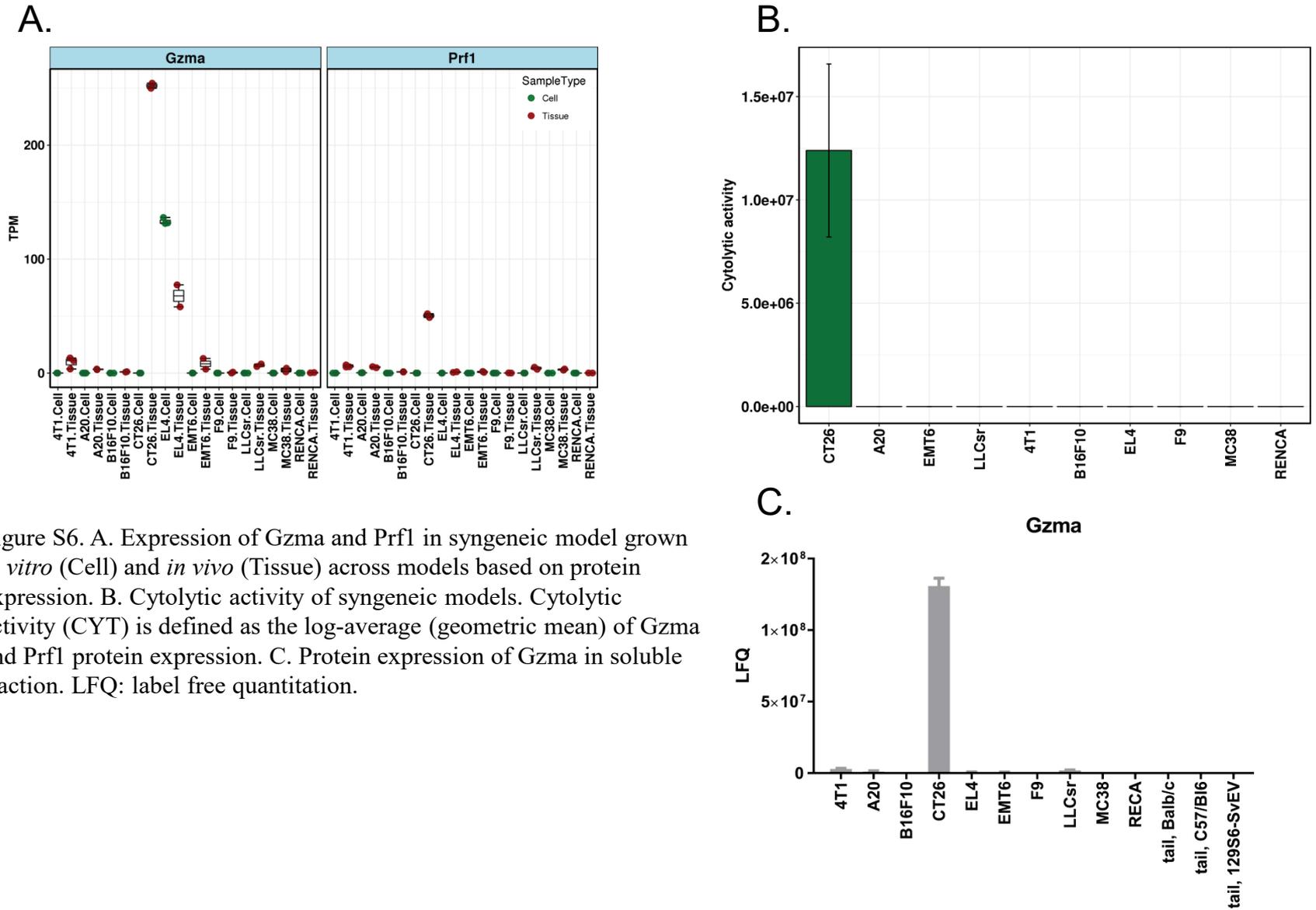
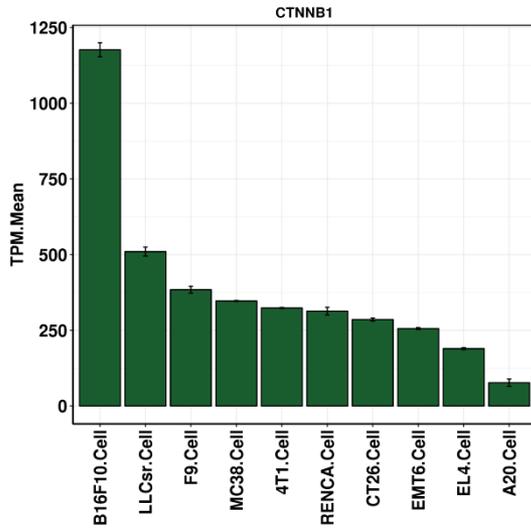


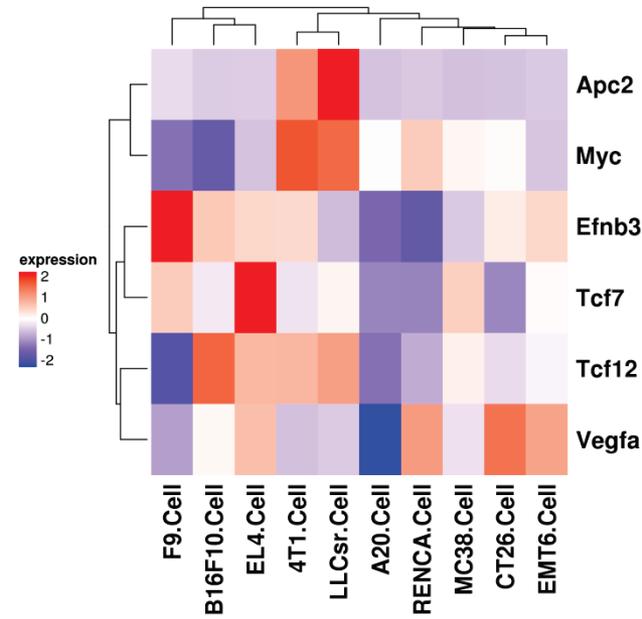
Figure S5. Response of syngeneic tumor models to anti-CTLA4, or anti PD-1. All mice were dosed intravenously. Individual tumor volumes are shown for 10 mice treated with PBS (black) or 10 mg/kg anti-CTLA4 (9H10) (red trace), or 10 mg/kg anti-PD-1 (RMP 1-14) (blue trace). All 10 mice bearing CT26 tumors dosed with anti-CTLA4 had no measurable tumor from study day 25 until measurements ended on study day 238. Comparison of mean tumor volumes was analyzed using log-transformed ANOVA. P-values are shown if there was a statistical difference between vehicle and antibody-treated groups. n.s. not significant.



## $\beta$ -catenin



## $\beta$ -catenin target genes



## Epigenetic modulators

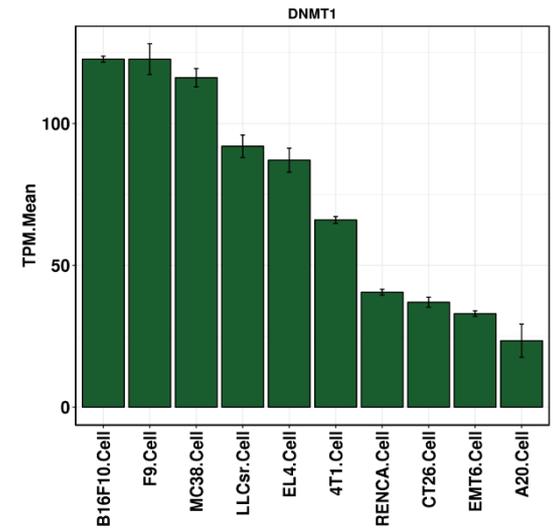
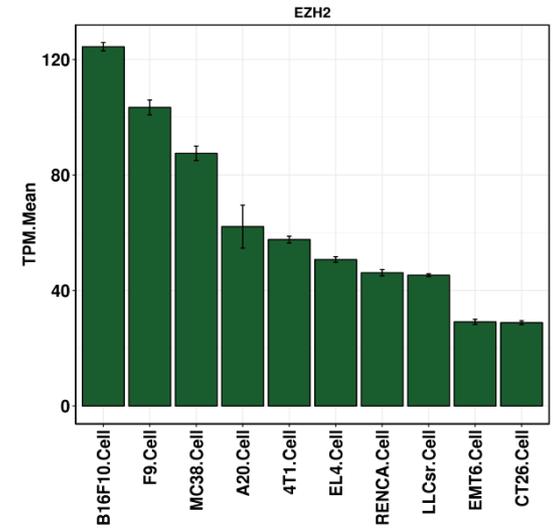


Figure S7. Gene expression of  $\beta$ -catenin,  $\beta$ -catenin target genes (gene list from (Spranger et al. 2015)) and epigenetic modulators (Ezh2, Dnmt1) across syngeneic models.

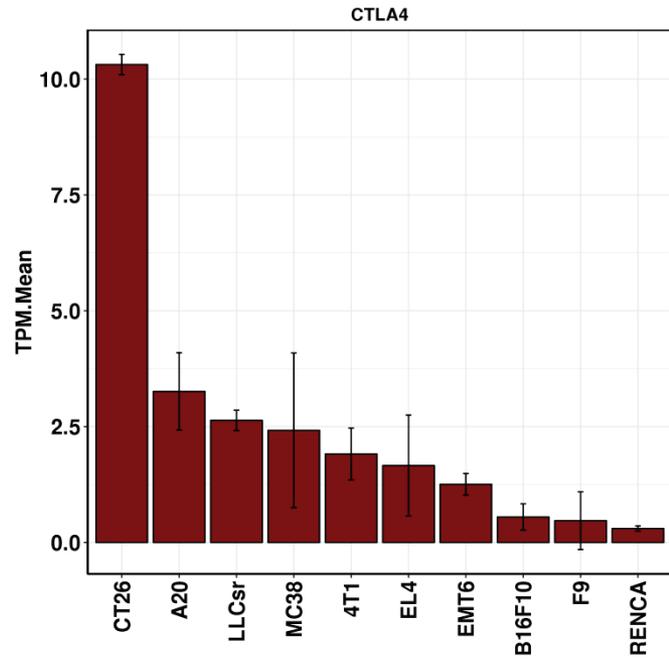


Figure S8. CTLA4 expression in syngeneic *in vivo* tumor samples.