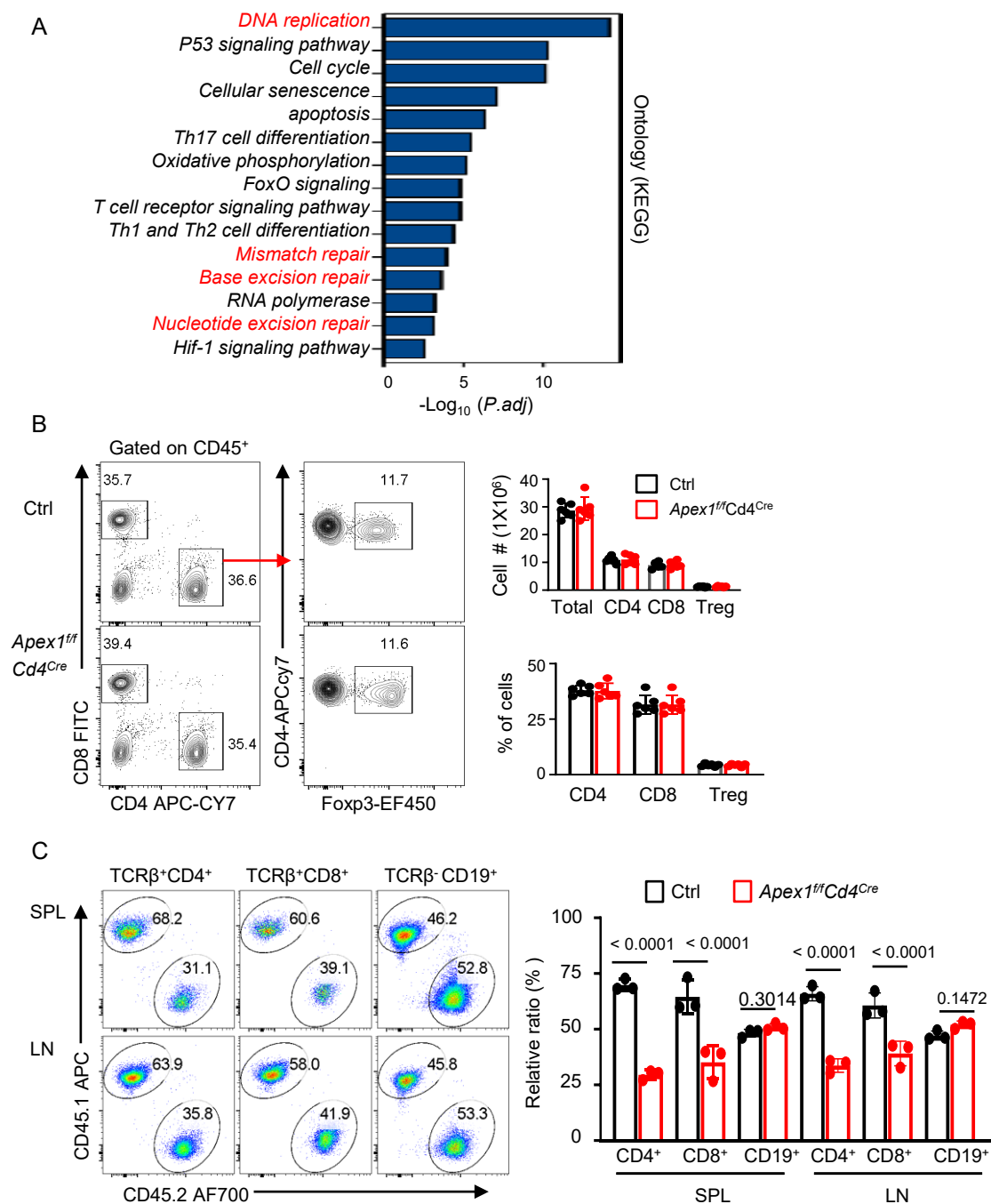
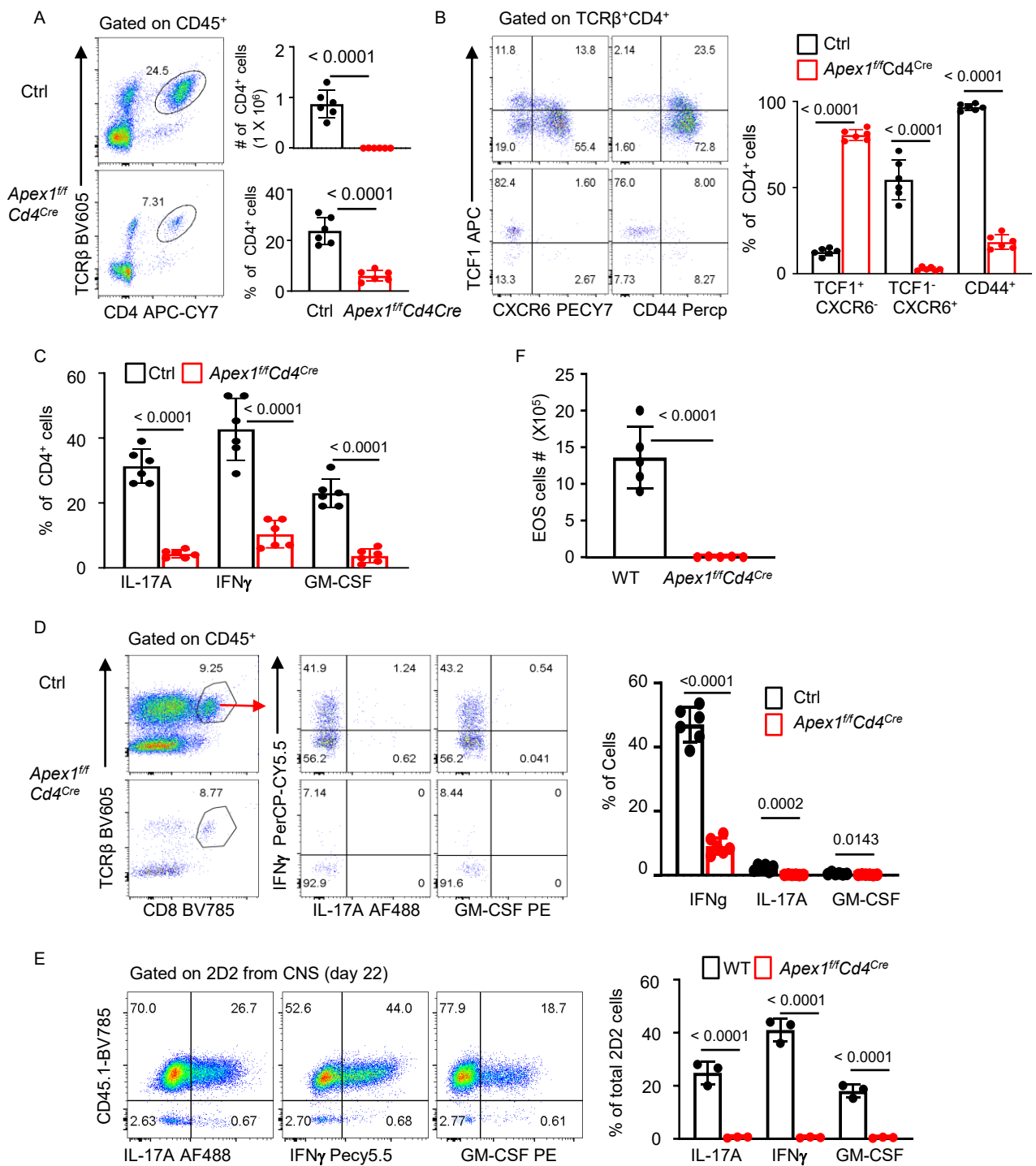




Supplemental Fig 1. See next page for caption.

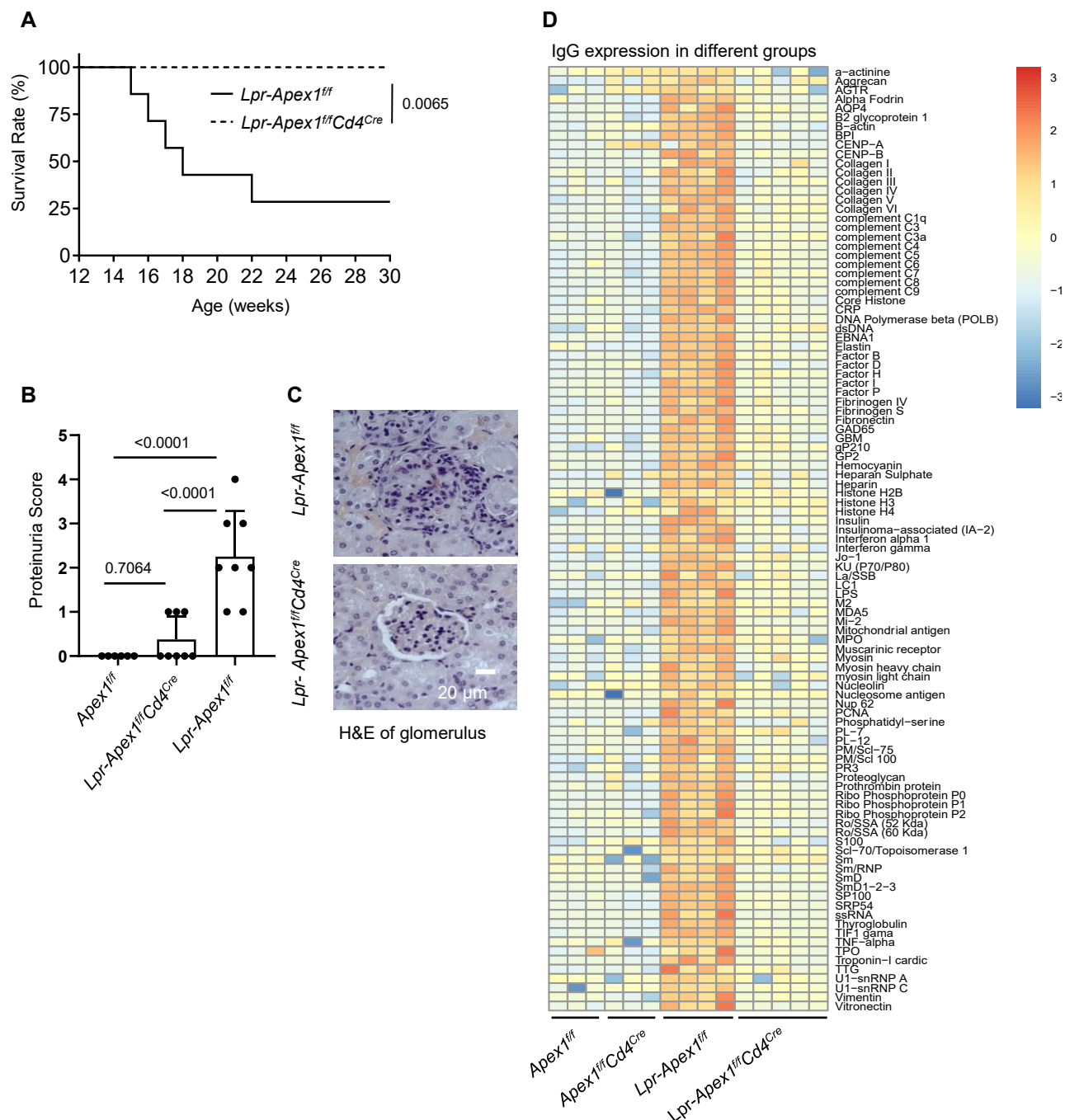
Supplemental Fig 1. Pathway enrichment analysis, conditional *Apex1* deletion, and T cell subsets in WT and *Apex1^{ff}Cd4^{Cre}* mice. (A) Gene Set Enrichment Analysis of RNA-seq dataset showing the highly induced top pathways enriched in 48h-activated WT CD4⁺ T cells versus naive CD4⁺ T cells (n=3 biologically independent replicates). (B) lymph nodes (LN) of *Apex1^{ff}Cd4^{Cre}* and WT control mice were analyzed for the presence of CD4⁺, CD8⁺, and Foxp3⁺ subsets by flow cytometry (left). The percentage and absolute cell number of the indicated subsets were shown in the bar graphs (right) (n=6 mice per group). (C) The lethally irradiated (9 Gy) *Rag1^{-/-}* mice were reconstituted with mixed bone marrow stem cells from WT CD45.1^{+/+} and *Apex1^{ff}Cd4^{Cre}* (CD45.2⁺) mice (1:1 ratio, 10 million each), and T cells in the spleen (SPL) and LN in the chimeric mice were examined 8 weeks later and shown. CD19⁺ B cells were included as an internal control and each group included 3 mice. Data are presented as mean $\pm$ s.d. p values are calculated by a two-tailed unpaired (B) and paired (C) Student's *t*-test.



Supplemental Fig 2. See next page for caption.

Supplemental Fig 2. Critical role of Apex1 in the induction of cytopathic T

effector cells *in vivo*. (A) Flow cytometry plots (left) and bar graphs (right) showing the percentage and absolute cell number of TCR β +CD4+ T cells obtained from CNS of EAE mice as stated in Fig. 2C (n=6 mice per group). (B) Flow cytometry plots (left) and bar graphs (right) showing the effector phenotype of TCR β +CD4+ T cells from the EAE mice in supplemental Fig. 1A (n=6 mice per group). (C) Bar graph showing the relative percentage of cytokine-producing TCR β +CD4+ cells from CNS of EAE mice as stated in Fig. 2C (n=6 mice per group). (D) Flow cytometry plots showing CD8+ T cells from the spinal cords of MOG-immunized control and Apex1f/fCd4Cre mice, the bar graph on the right is the summary of 6 mice in each group. (E) Absolute eosinophil numbers obtained from BAL of OVA-immunized and challenged mice as in Fig. 2G (n=5 mice per group). (F) WT 2D2 (CD45.1+/-) and Apex1f/fCd4Cre 2D2 T cells (CD45.2+) were mixed at a 1:1 ratio (2 million each) and co-transferred into CD45.1+/+ control B6 mice 1 day before EAE induction, and expression of inflammatory cytokines on day 22 by the 2D2 cells from CNS were analyzed and shown (n=3 mice). Data are presented as mean $\pm$ s.d. and the p values are from a two-tailed unpaired Student's t-test (A-F).



Supplemental Figure 3. Conditional deletion of *Apex1* in T cells in MRL^{lpr/lpr} mice prevents lupus development and reduces autoantibody production. **A**, Survival curves of *Lpr*, *Apex1^{fl/fl}* mice (n=7) and *Lpr-Apex1^{fl/fl}Cd4^{Cre}* mice (n=7). **B** and **C**, bar graphs showing proteinuria measurements (**B**) and representative H&E staining of glomeruli (**C**) of 16 weeks old female littermates of *Apex1^{fl/fl}* mice (n=6), *Lpr-Apex1^{fl/fl}Cd4^{Cre}* mice (n=8) and *Lpr-Apex1^{fl/fl}* mice (n=8). Scale bar represents 20μm. **D**, Autoantibodies heatmap of IgG against full array of 124 antigens measured in serum of *Apex1^{fl/fl}* mice (n=3), *Apex1^{fl/fl}Cd4^{Cre}* mice (n=3), *Lpr-Apex1^{fl/fl}* mice (n=4), *Lpr-Apex1^{fl/fl}Cd4^{Cre}* mice (n=5), each column represents individual mice in each group. The p value was calculated by Gehan-Breslow-Wilcoxon test for survival analysis (A) and one-way ANOVA (B). Data are representative of three independent experiments (C).