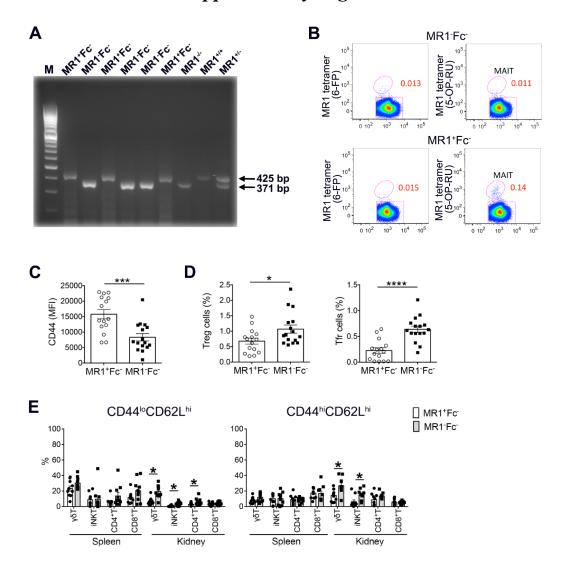


Supplementary Figure 3



Supplementary Figure 3. Genotyping of MR1 knockout and flow cytometric analysis of B and T cell subsets in MR1^{+/+} (MR1⁺Fc⁻) and MR1^{-/-} FcγRIIb^{-/-}Yaa (MR1⁻Fc⁻) mice. (A) PCR Genotyping of MR1^{-/-} FcγRIIb^{-/-} Yaa (MR1⁻Fc⁻) and MR1^{+/+} FcγRIIb^{-/-} Yaa (MR1⁺Fc⁻) mice and MR1^{-/-}, MR1^{+/+} and MR1^{+/-} C57BL/6J mice using DNA isolated from tail biopsies. A representative agarose gel electrophoresis image is shown. M, DNA markers. (B) Representative flow cytometry images of F4/80 CD3⁺γδTCR CD1d/PBS-57 tetramer lymphocytes in the spleen from MR1⁺ and MR1 Fc⁻ mice. (C) Mean fluorescence intensity (MFI) of CD44 on plasma cells. (D) Frequencies of T regulatory cells (Treg) (CD3⁺CD4⁺Foxp3⁺CD25⁺) and T follicular regulatory cells (Tfr) (CD3⁺CD4⁺CD69⁺Foxp3⁺CD25^{lo}CXCR5⁺Bcl6⁺). (E) Frequencies of naïve T cells (CD44^{lo}CD62L^{hi}) and central memory T cells (CD44^{hi}CD62L^{hi}) among γδT cells, iNKT cells, CD4⁺T cells and CD8⁺T cells. Each symbol represents the value of one individual. Values in C-E are shown as the mean ± SEM. *p*-values were determined by two-tailed Mann-Whitney *U*-test (**p* < 0.05).