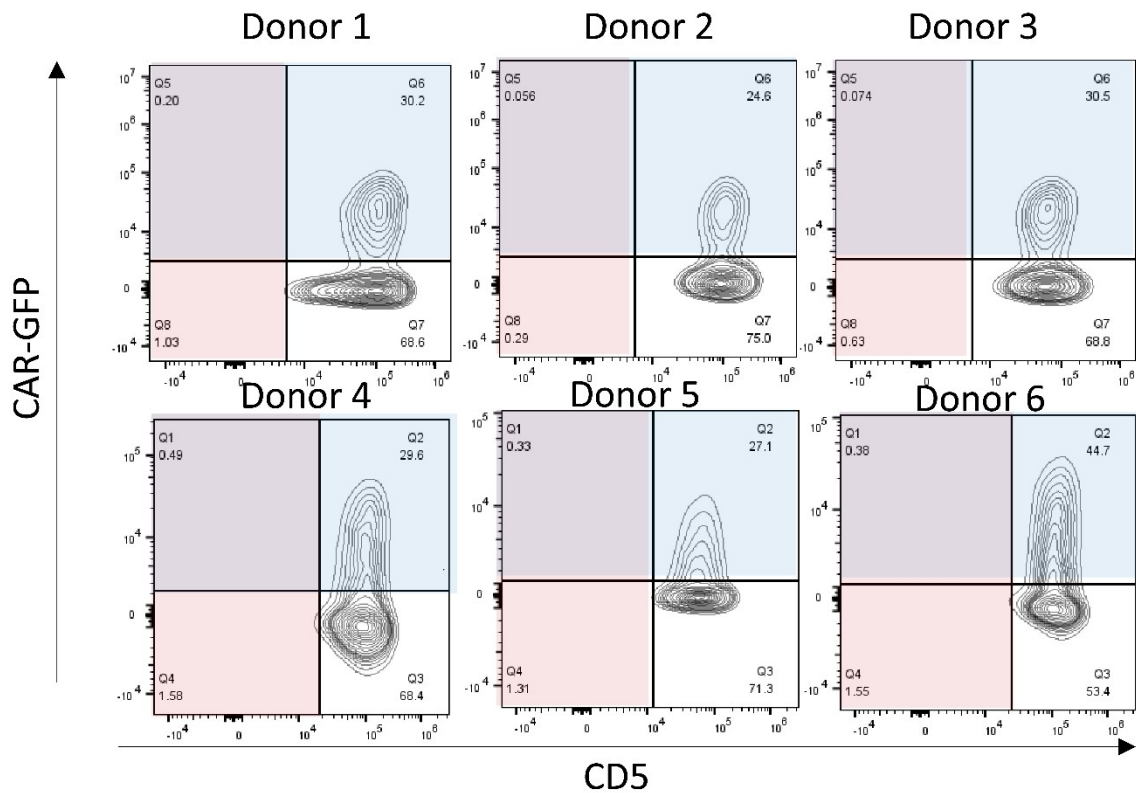
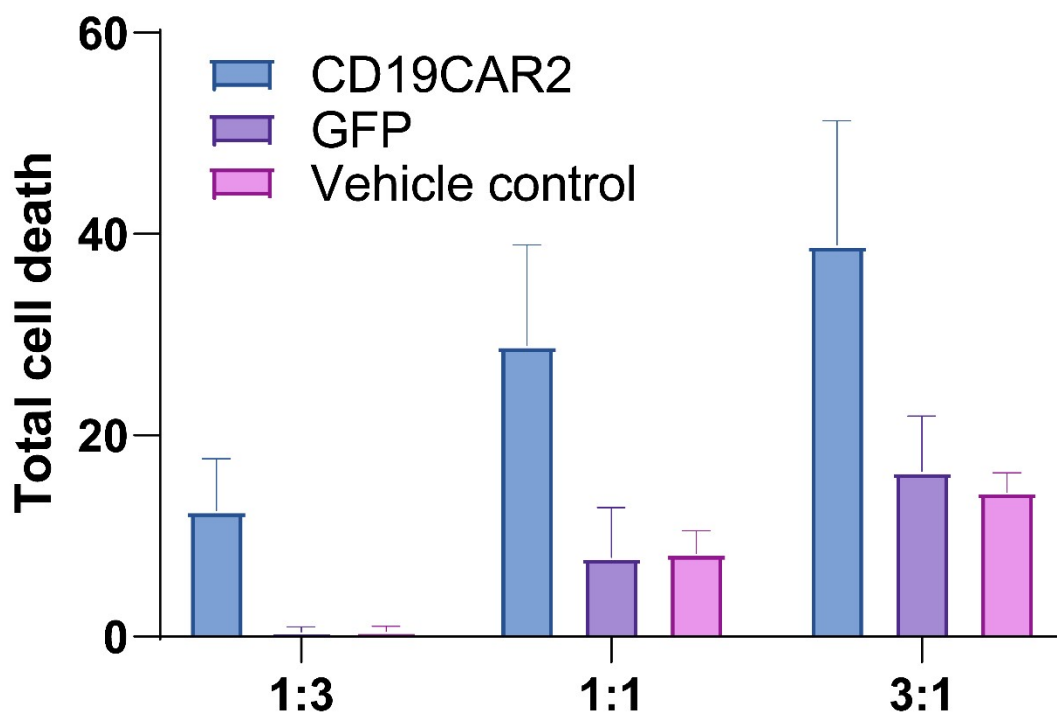


Supplement figure 1: Sanger sequencing confirms CD5 disruption at genetic level. A) chromatogram showing control (top) and VECT-processed (bottom) population. Due to indel formation, CD5 sequence among VECT-processed T cells shows a convoluted pattern. Guide RNA sequence is highlighted in red with blue underline showing the PAM region. Due to the use of primer upstream of PAM, PAM region appears convoluted. B) Indel frequency analysis indicates an estimated editing efficiency of 52.4%.



Supplement figure 2: CD5 expression and transduction efficiency in no device control is used to place gates. Exemplary flow cytometry contour plots from no device groups with CD5 expression on the x-axis and CD19 CAR – GFP expression on the y-axis. CD5 – population is shown in red box. GFP expression level is used to gate CD19 CAR + population, which is shown in blue box.



Supplement figure 3: Cytotoxicity data from No device treatment control showing the percentage cell death resulted from coculturing with T cells in CD19CAR transduced, GFP vector transduced, and polybrene vehicle only groups. The low baseline cell death from GFP vector and vehicle control is used to show CD19CAR-specific cytotoxicity.