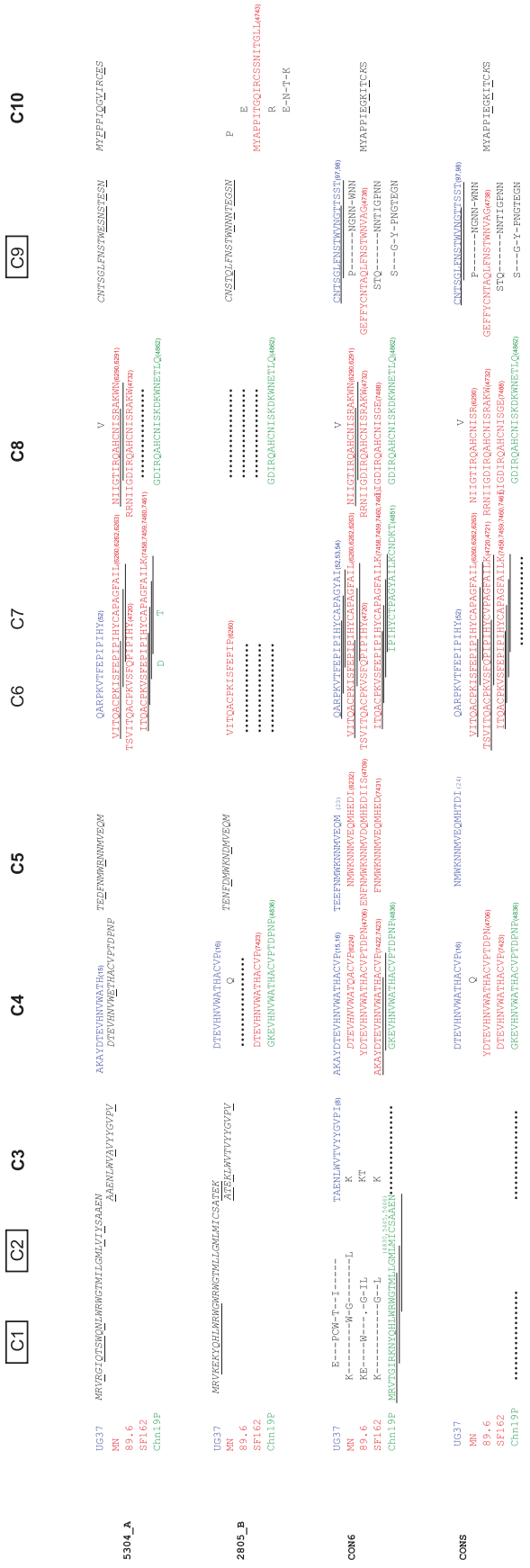


SUPPLEMENTAL FIG. 1. T-cell epitope mapping of CON6, CON-S, and subtype Env immunogens. T-cell responses were determined in BALB/c mice with five overlapping Env peptide sets. The T-cell epitopes were first screened with Env overlapping peptides and then confirmed with individual peptides by performing ELISpot assays. One subtype A (92UG037_A), three subtypes B (MN_B, 89.6_B and SF162P3_B), and one subtype C (Chn19_C) overlapping peptide sets were used for the analysis. Positive subtypes A, B, and C peptide sequences were indicated by red, blue, and green colors, respectively. Peptide sequences that were positive for stimulating the T-cell response are shown, and lines underneath the peptide sequences indicate the overlapping peptides. The mutations that may responsible for not stimulating the T-cell responses are indicated with substituted amino acid(s) at the corresponding position(s). When the similar mutation patterns are shared among different immunogens, only the first is shown for clarity purposes. For the epitopes that are missing in the immunogen, the corresponding epitope sequences from the immunogen are shown in italics, and the mutations that may be potentially responsible for not inducing the T-cell responses are highlighted with underlines. When peptides that have an overlap of fewer than four amino acids, they are considered to contain two independent T-cell epitopes. Epitope B7 is boxed, indicating that the epitope was identified in CD8 T cells and is a MHC I-restricted CTL epitope. Peptide ID numbers corresponding to the NIH AIDS Research and Reference Reagent Program catalog number are indicated at the end of the peptide sequences.



SUPPLEMENTAL FIG. 2. T-cell epitope mapping of CON6 and subtype Env immunogens. T-cell responses were determined in C57BL/6 mice with five overlapping Env peptide sets. The T-cell epitopes were first screened with Env overlapping peptides and then confirmed with individual peptides by performing ELISpot assays. One subtype A (92UG037_A), three subtypes B (MN_B, 89.6_B and SFI62P3_B), and one subtype C (Chn19_C) overlapping peptide sets were used for the analysis. Positive subtype A, B, and C peptide sequences were indicated by red, blue, and green colors, respectively. Peptide sequences that were positive for stimulating the T-cell response are shown, and lines underneath the peptide sequences indicate the overlapping peptides. The mutations that may be responsible for not stimulating the T-cell responses are indicated with substituted amino acid(s) at the corresponding position(s). When the similar mutation patterns are shared among different immunogens, only the first is shown for clarity purposes. For the epitopes that are missing in the immunogen, the corresponding epitope sequences from the immunogen are shown in italics, and the mutations that may be potentially responsible for not inducing the T-cell responses are highlighted with underlines. When peptides that have an overlap of fewer than four amino acids, they are considered to contain two independent T-cell epitopes. Epitopes C1, C2, and C9 are boxed, indicating that the epitopes were identified in CD8 T cells and are MHC I-restricted CTL epitopes. Peptide ID numbers corresponding to the NIH AIDS Research and Reference Reagent Program catalog number are indicated at the end of the peptide sequences.