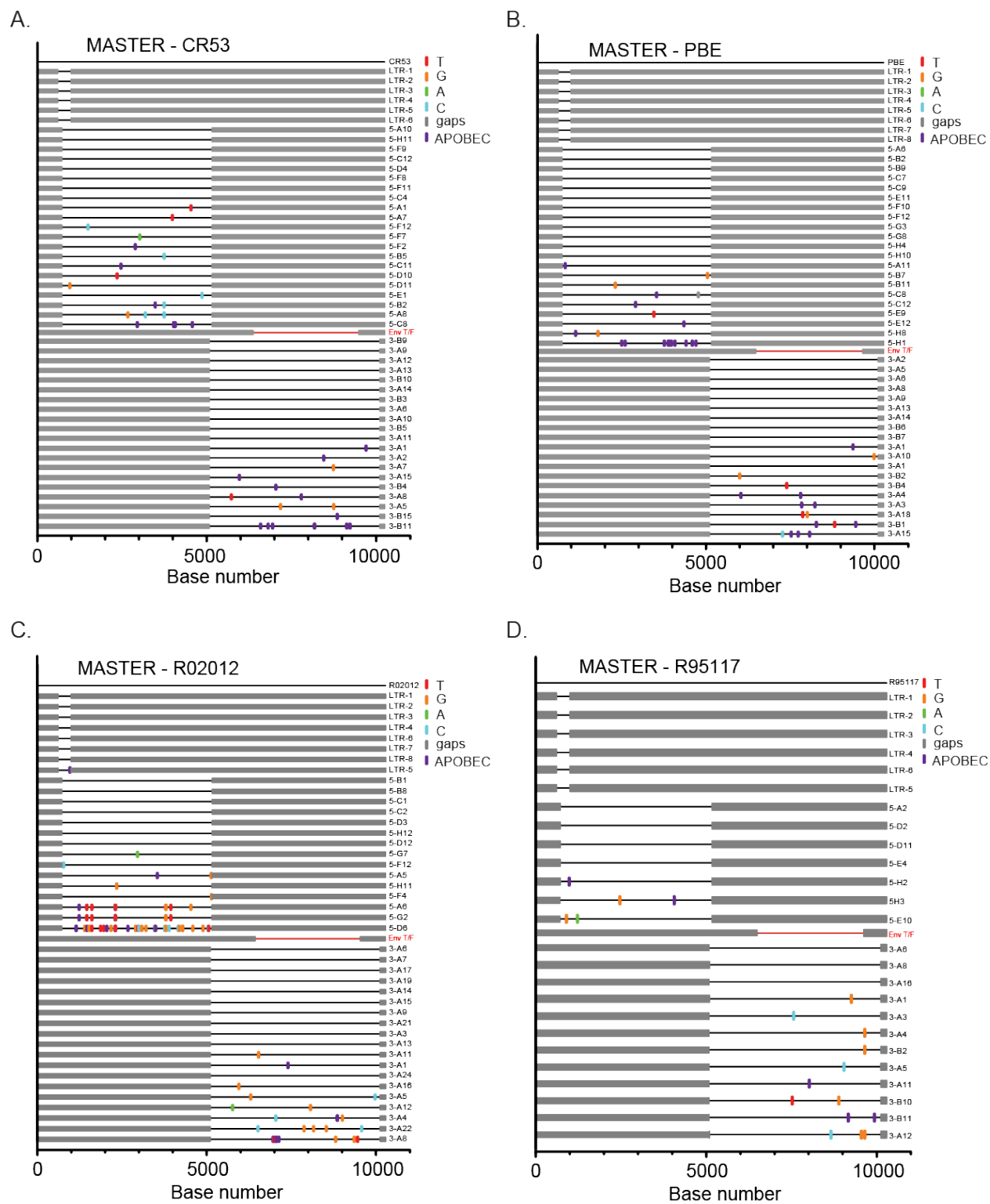
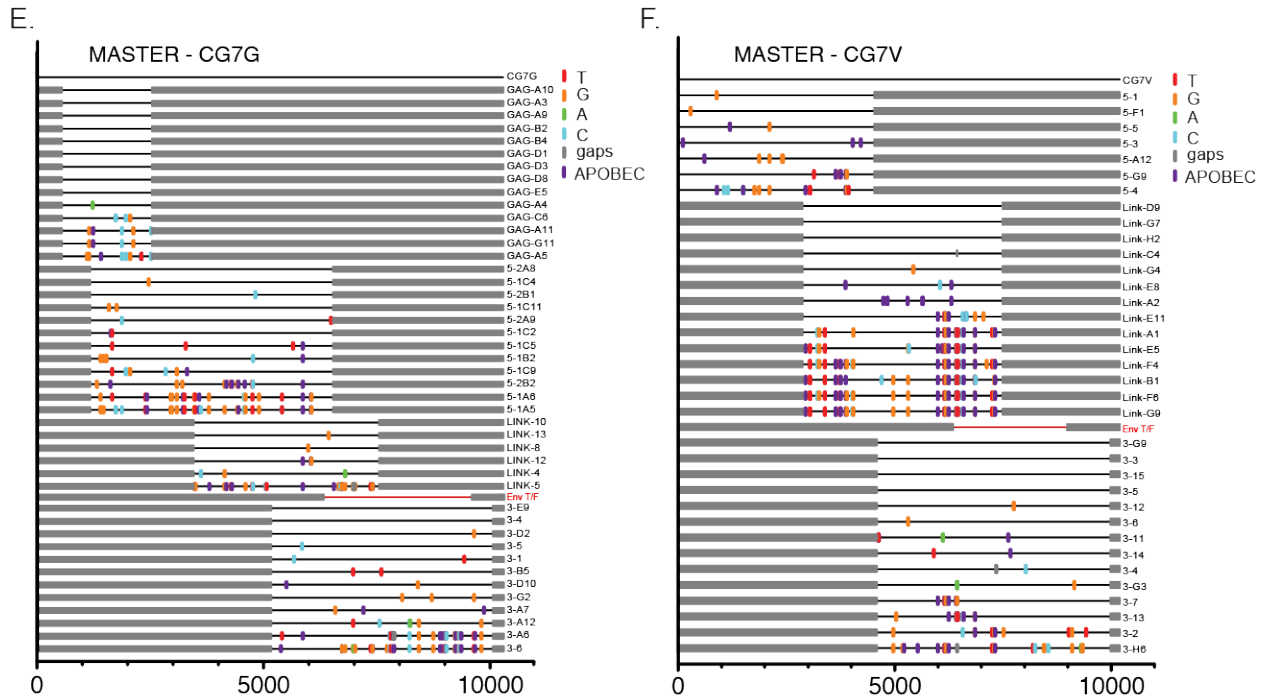


# Supplemental Figures





Supplemental Figure 1. Highlighter alignments of 5' and 3' half genomes from animals CR53 (A) and PBE (B), R02012 (C), R95117 (D), CG7G (E), CG7V (F). Single nucleotide polymorphisms to the consensus sequences are denoted by colored tick marks, gaps are shown in grey, and G-to-A mutations are purple. Overlapping amplicons are shown in black and the previously determined T/F env sequence is shown in red (Env T/F). The full-genome consensus sequence was identified using the overlapping genomes.

