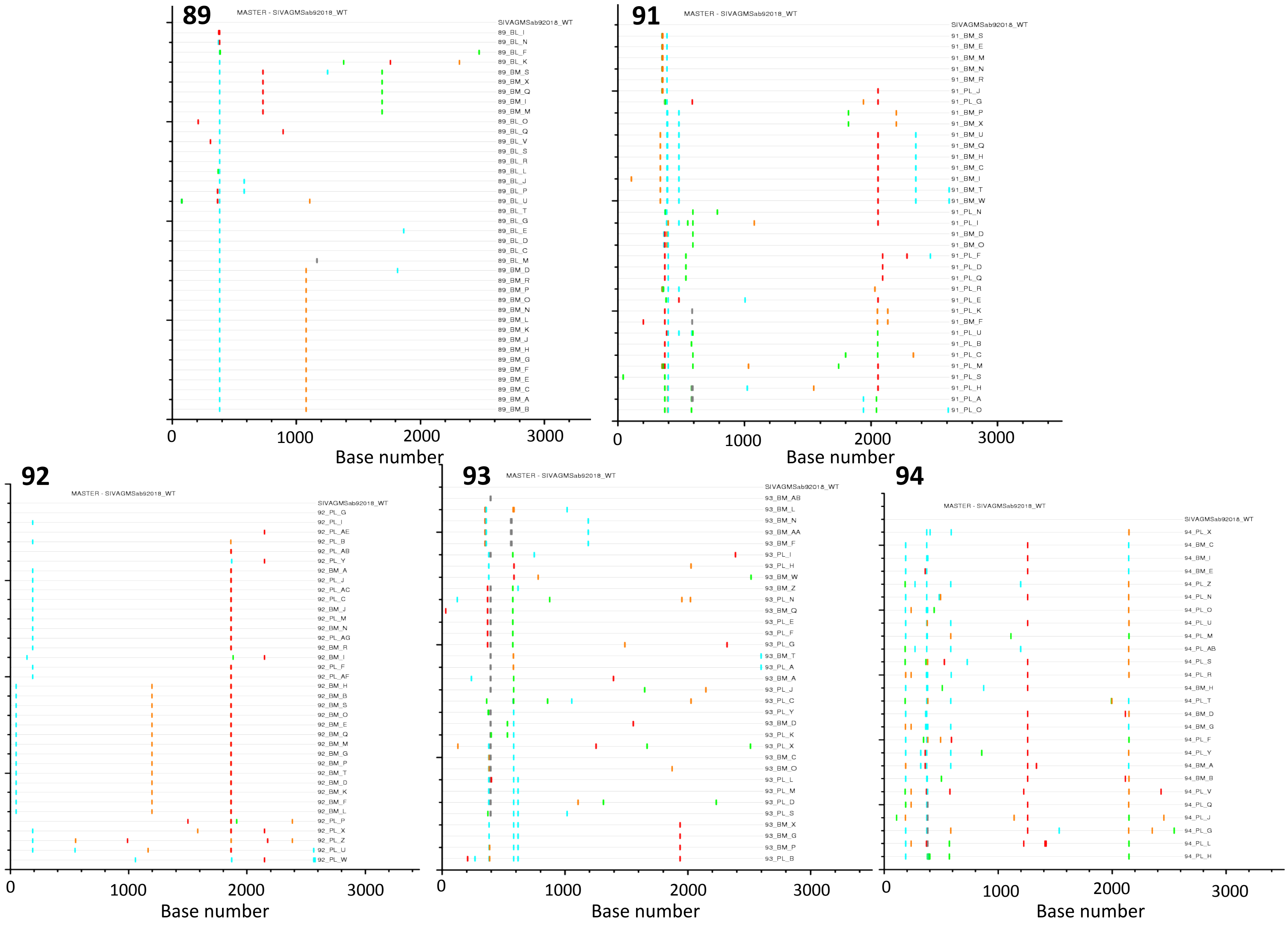

Figure S1. Sequence alignments of plasma and breast milk SIVSab92018ivTF *env* virus variants from five AGMs at five months post-infection. The sequences are aligned against the cloned SIVsab92018ivTF challenge virus. There were no identified mutations in the breast milk virus variants that appeared across all the animals. The colors correspond with the nucleotide mutation (green: A, red: T, orange: C, light blue: G).

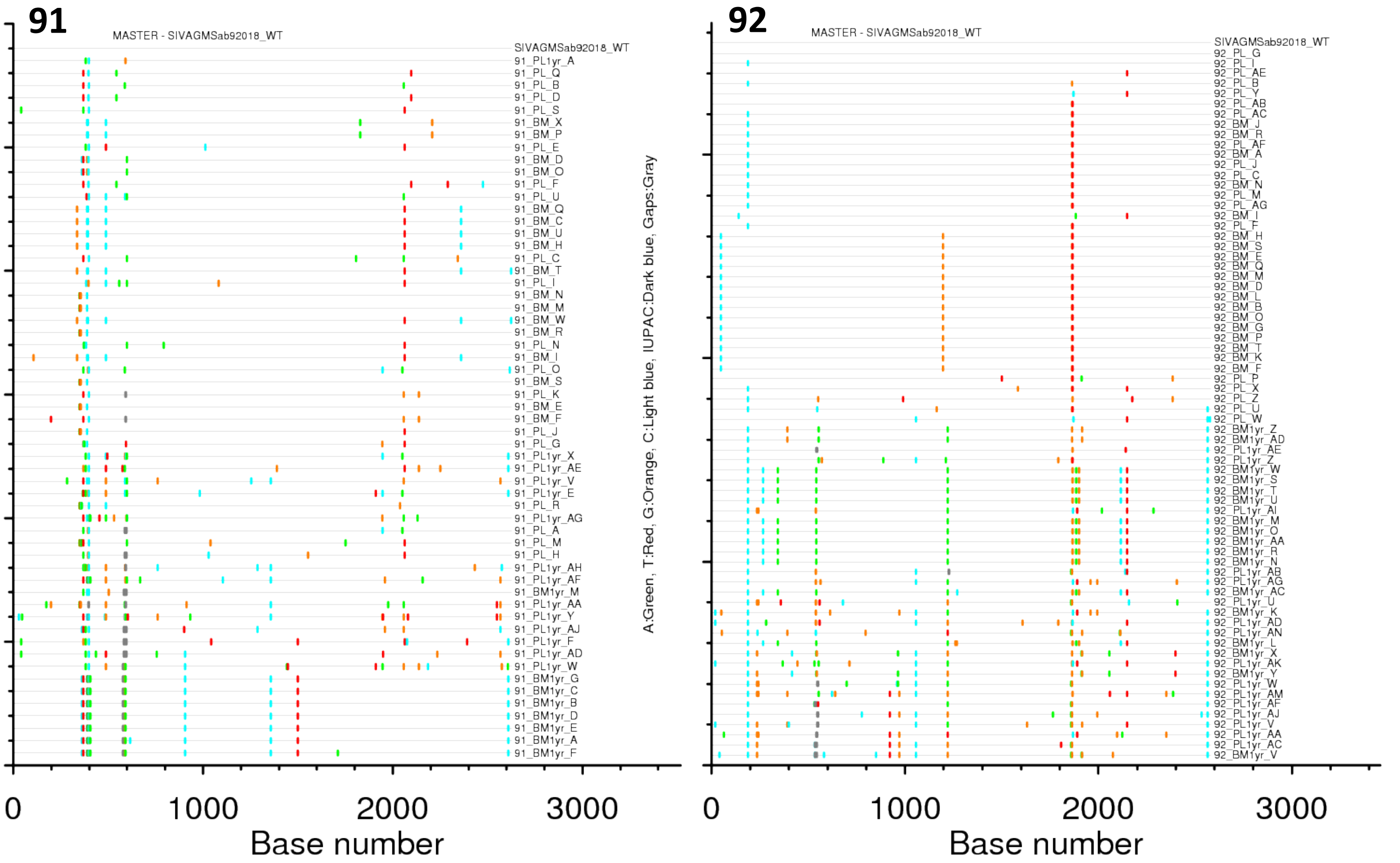

Figure S2. Longitudinal sequence alignments of plasma and breast milk SIVSab92018ivTF *env* variants from two AGMs at five months and one year post-infection. The sequences are aligned against the cloned SIVsab92018ivTF challenge virus. There are no distinct breast milk virus variant mutations that appear across both time points within each animal. The colors correspond with the nucleotide mutation (green: A, red: T, orange: C, light blue: G).

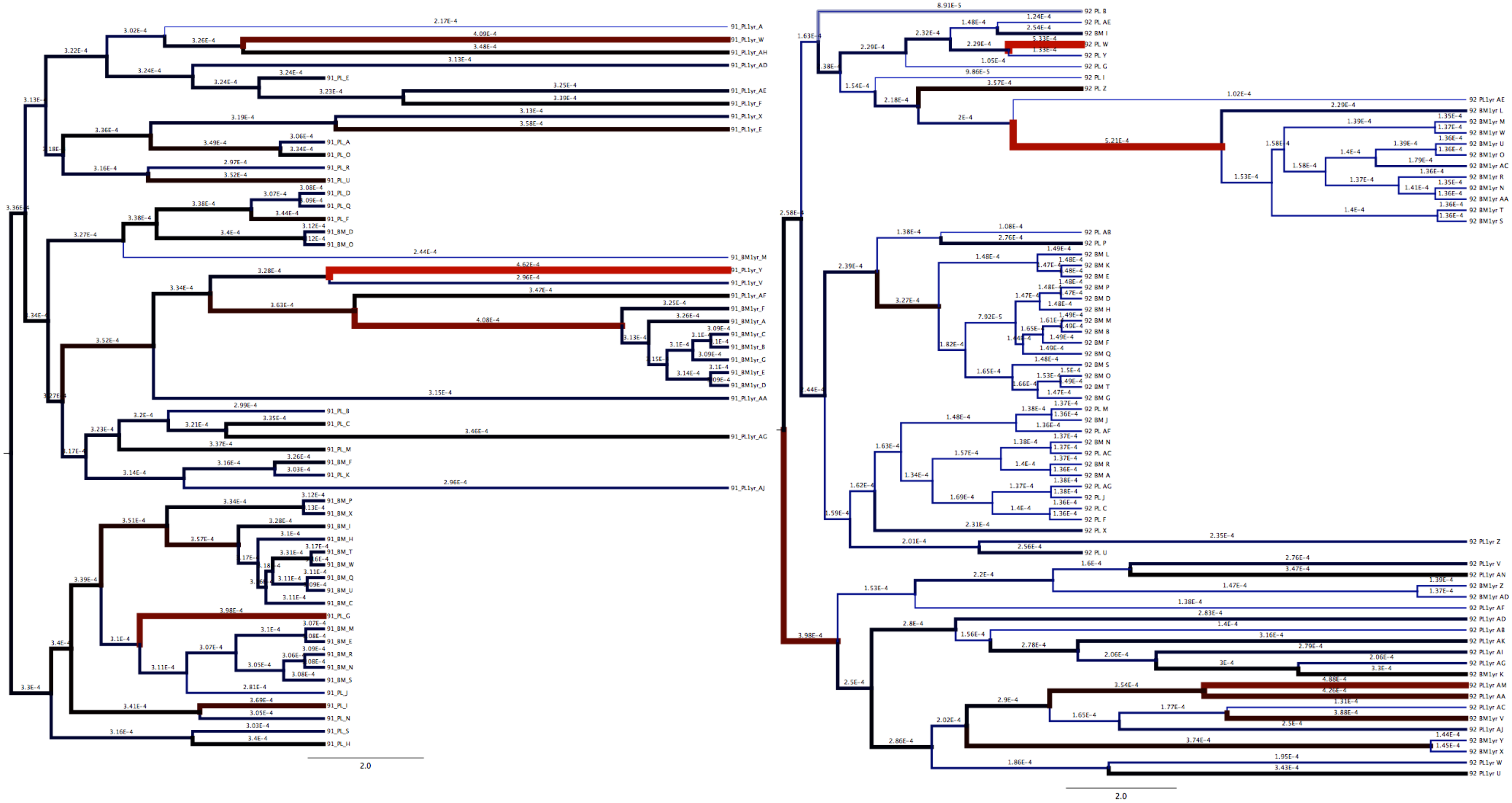

Figure S3. BEAST trees showing substitution rates of plasma and breast milk SIVSab92018ivTF *env* variants from two AGMs at five months and one year post-infection. There is no consistent pattern to indicate a significant difference between the evolutionary rates of plasma (PL) and breast milk (BM) virus lineages. The branch labels show the number of nucleotide substitutions per site per month, and the scale bar represents two months. SIV variants from one year post-infection are labeled accordingly. The branch widths and colors indicate the substitution rate, with larger widths and red branches indicating higher rates.