

Figure S1. Productive infection by two divergent HIV-1 T/F viruses in subject 3156. ML tree and *Highlighter* plot of gp160 *env* sequences demonstrate one or more low-diversity lineages of CRF01_AE sequences (in black), a second highly divergent Subtype B (in magenta), and two recombinant sequences (in orange). The recombinant sequences do not share breakpoints with known circulating recombinant forms (data not shown), thus reinforcing their likely inpatient origin.

Figure S2. Acute-to-acute HIV-1 transmission in VAX003 subjects 3090 and 3184. ML tree and *Highlighter* plot of gp160 *env* sequences from placebo recipient subject 3090 (in blue) and vaccine recipient subject 3184 (in green) reveal near-identity between the T/F virus infecting subject 3184 and one of the multiple T/F lineages infecting subject 3090. Each sequence lineage from subject 3090 is substantially more homogeneous compared with the diversity evident 3184 sequences, consistent with the Fiebig staging of these two subjects (Fiebig II versus VI) and the timing estimate for the most recent common ancestors of the respective T/F sequence lineages (15 days \pm 6 versus 91 days \pm 12; see Table 1)

Figure S3. Acute-to-acute HIV-1 transmission in VAX003 subjects 3017 and 3212. ML tree and *Highlighter* plot of gp160 *env* sequences from placebo recipient subject 3017 (in blue) and vaccine recipient subject 3212 (in green) reveal productive infection with highly similar viruses (the single variant in 3212 and the minor variant in 3017). Possible explanations include acute-to-acute transmission between these two subjects or transmission from a common, unidentified third subject to both subjects 3017 and 3212.

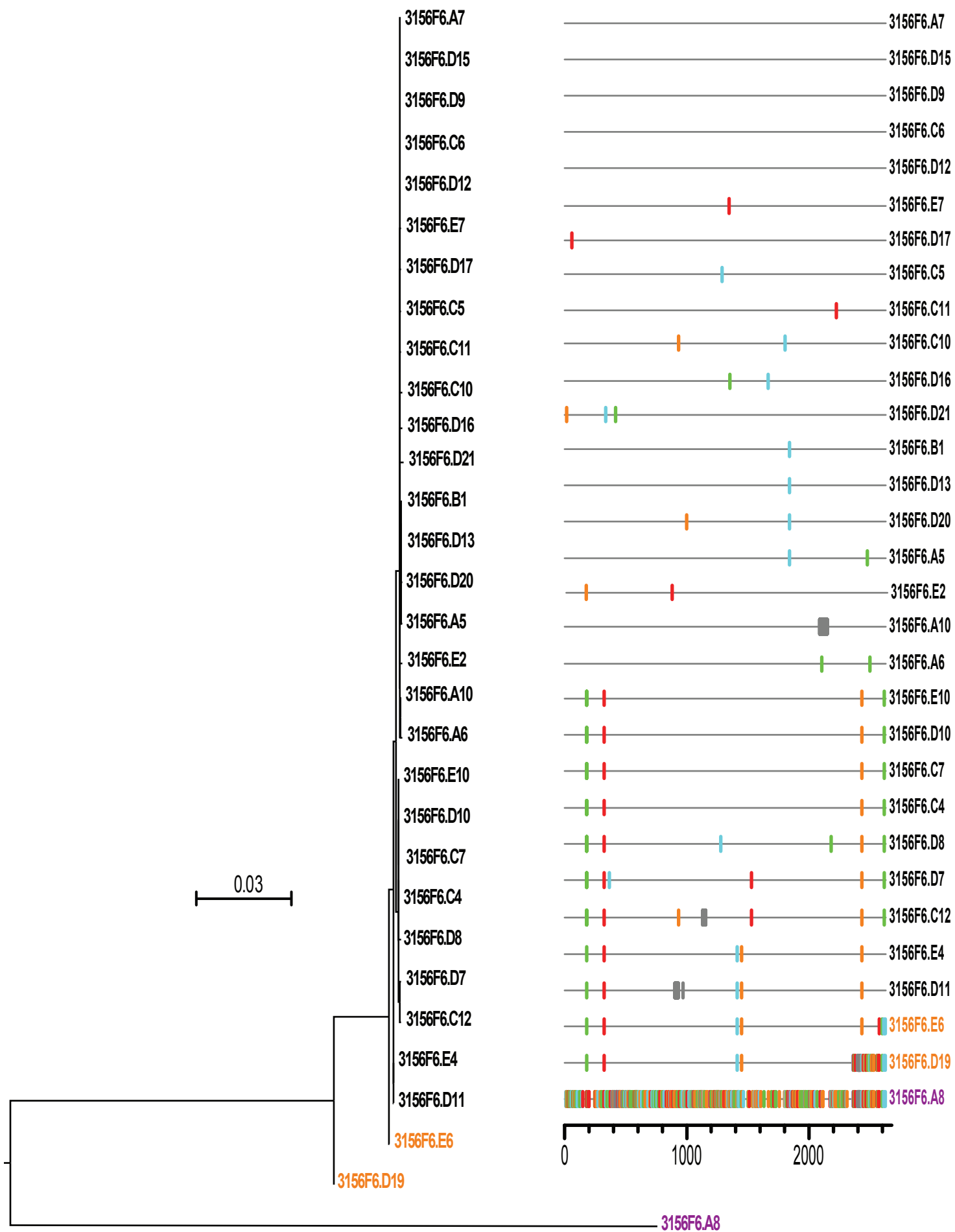


Fig. S1

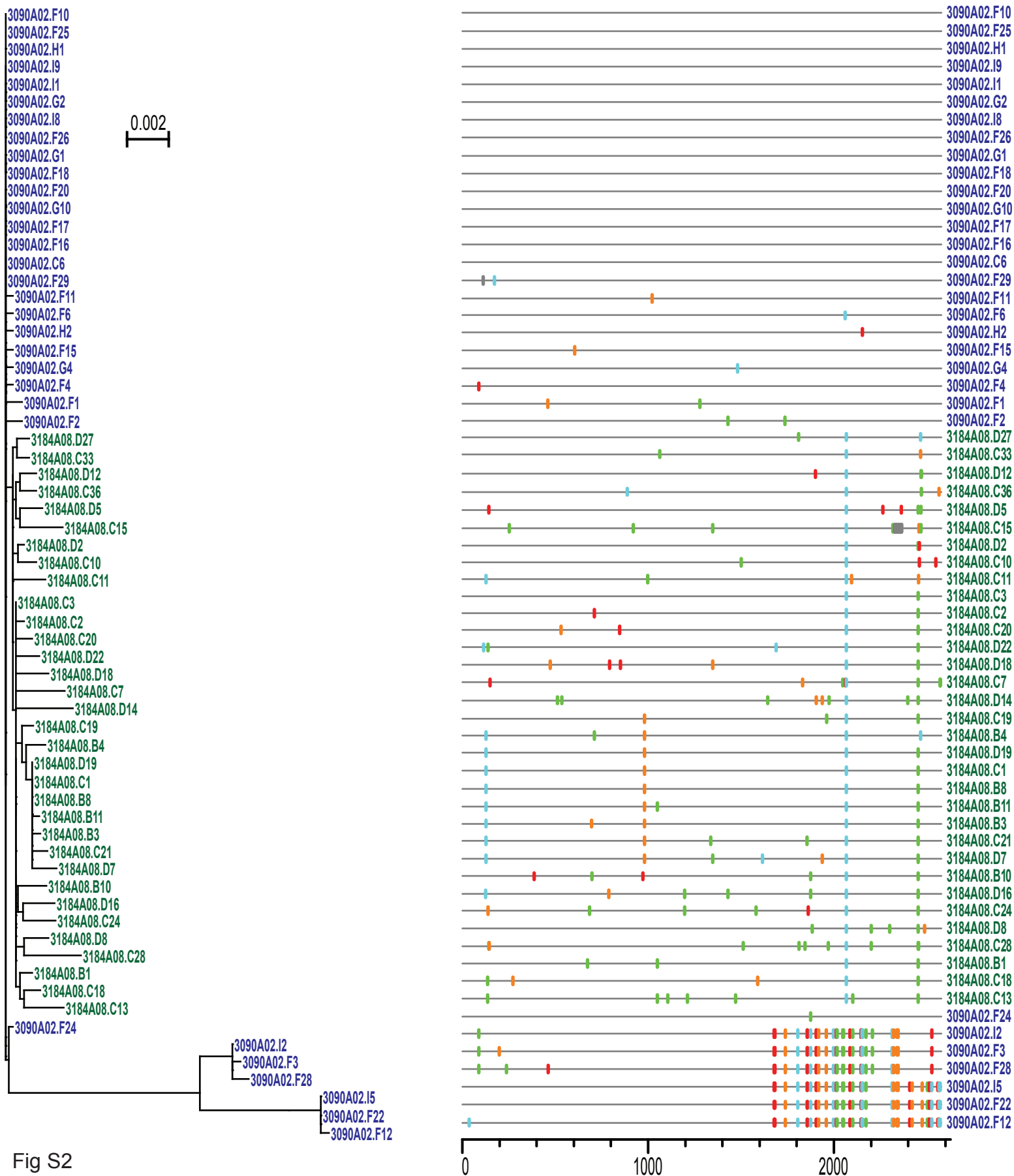


Fig S2

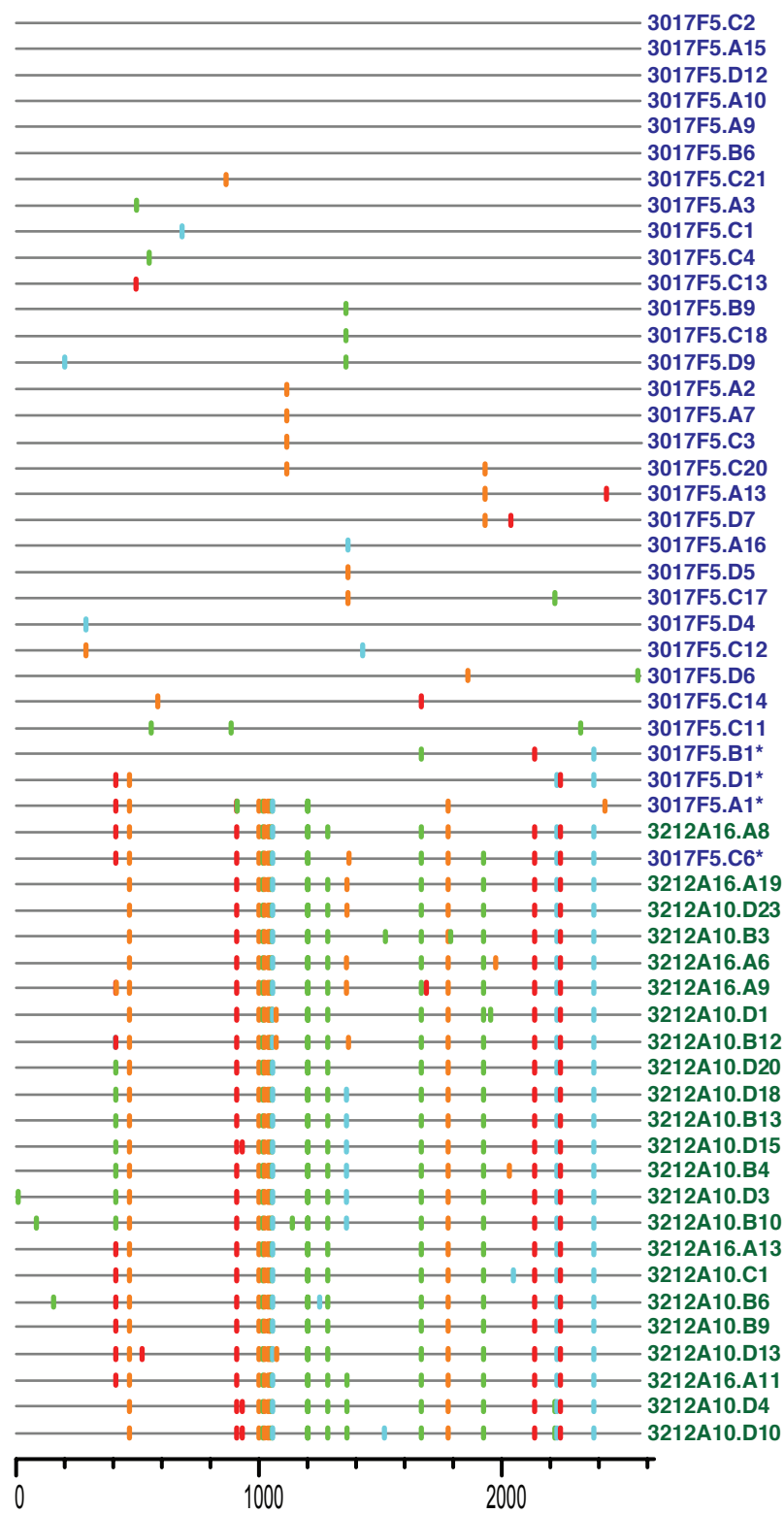
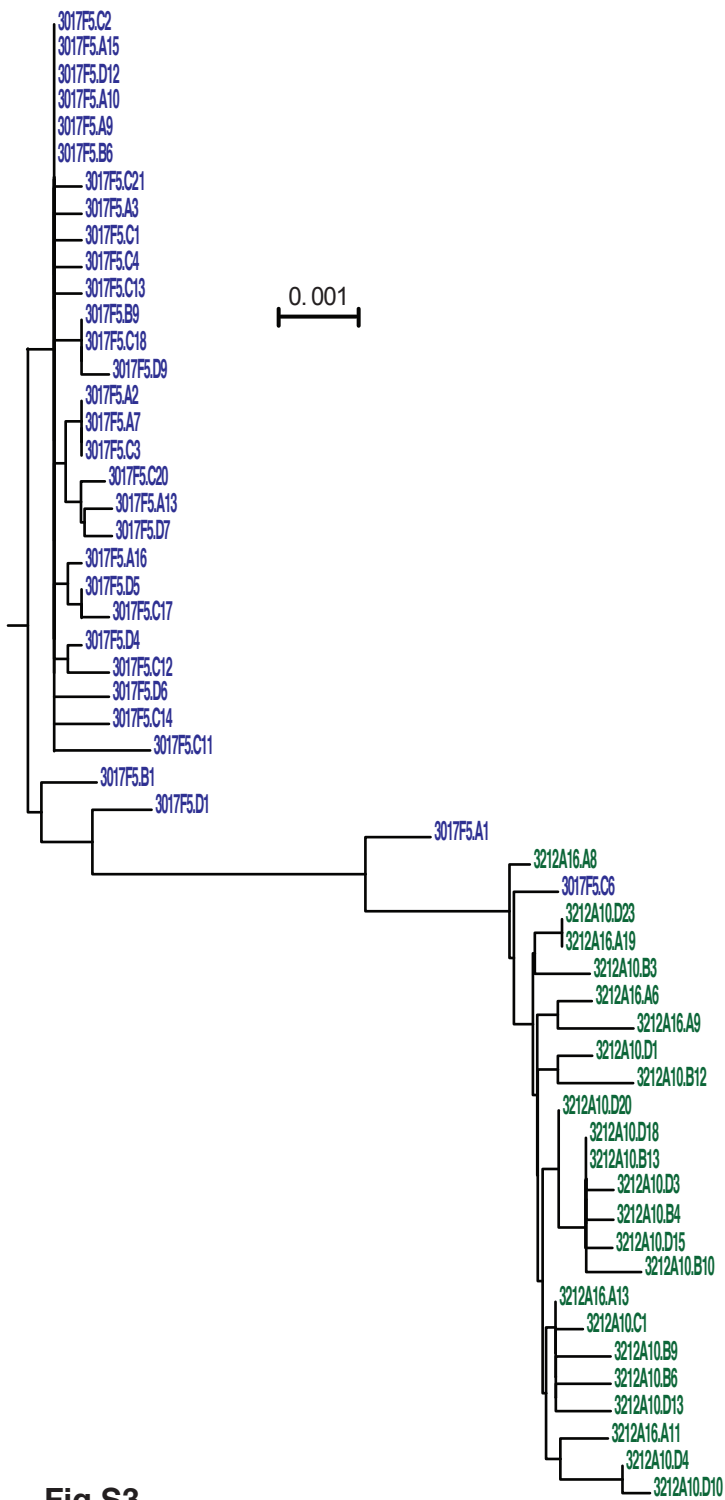


Fig.S3