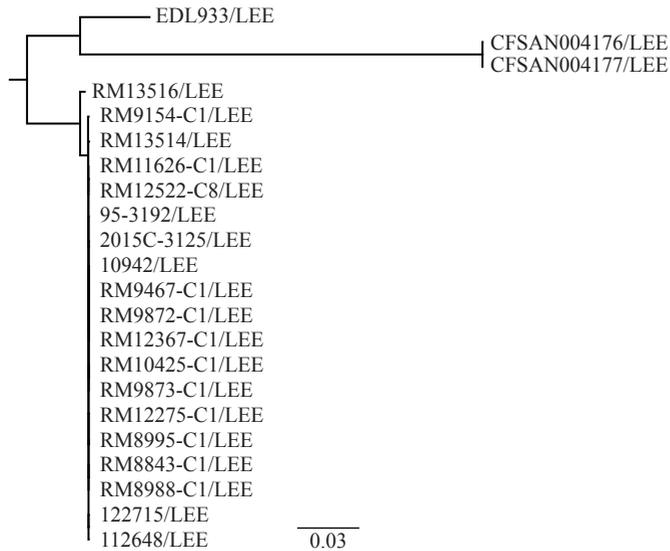
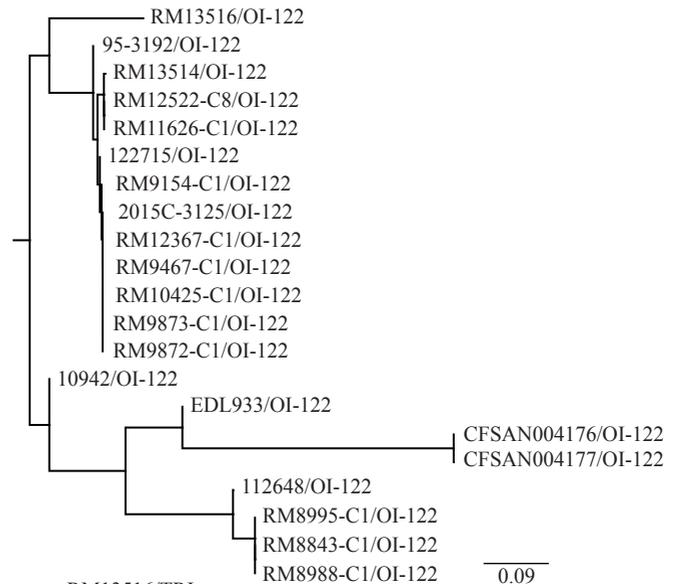


Figure S2. Comparative analyses of PAIs in STEC strains. A: Relatedness of LEE islands; B: Relatedness of the OI-122 islands; C: Relatedness of the OI-57 islands; D: Relatedness of the TRIs. The DNA sequences of 22 LEE islands (A), 21 OI-122 islands (B), 20 OI-57 islands (C), and 24 TRIs (D) were aligned in Geneious Prime®, correspondingly, using Clustal Omega, followed by constructing a consensus tree using Jukes-Cantor Genetic Distance Model and Neighbor-Joining Tree Build Method without an outgroup as detailed in the Materials and Methods section.

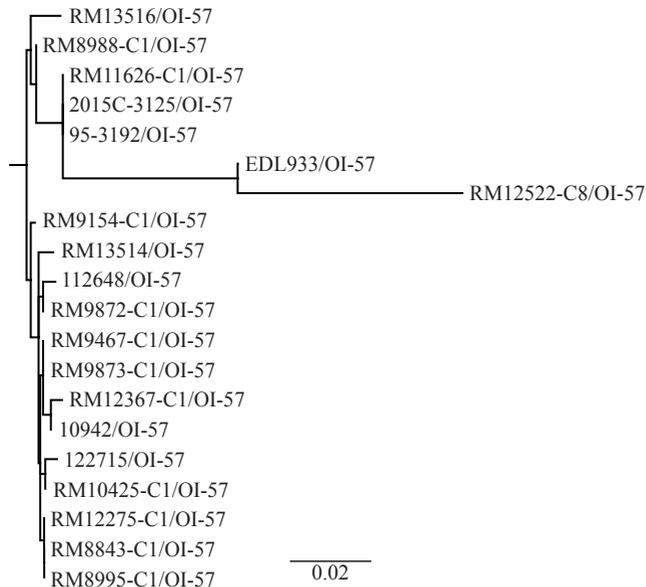
A



B



C



D

