

Fig 1. Identifying amino acid substitutions of *tnaA* protein sequences of 0395, M010, N16961, V52, V51, 2740-80, and S35 strains with SeaView, where red box shows amino acid substitution and its position on the *tnaA* protein sequences within the strains

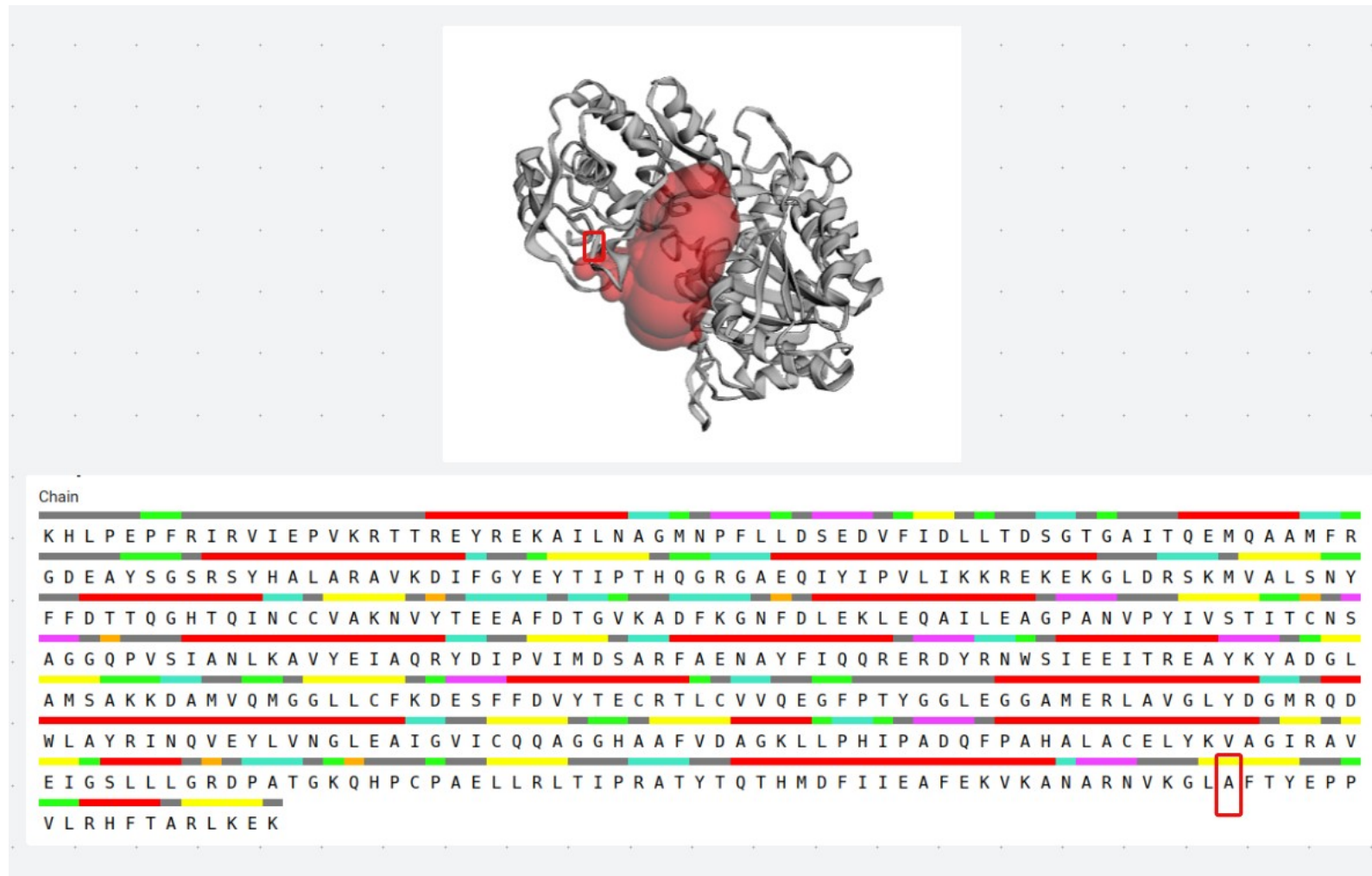


Fig2. Identifying amino acid substitution position of Ala453 in *tnaA* protein sequence by CASTp, where red box represents Ala453 position on the *tna* protein sequence and *tna* protein structure, and red pocket on the protein structure displays the active site of the enzyme.

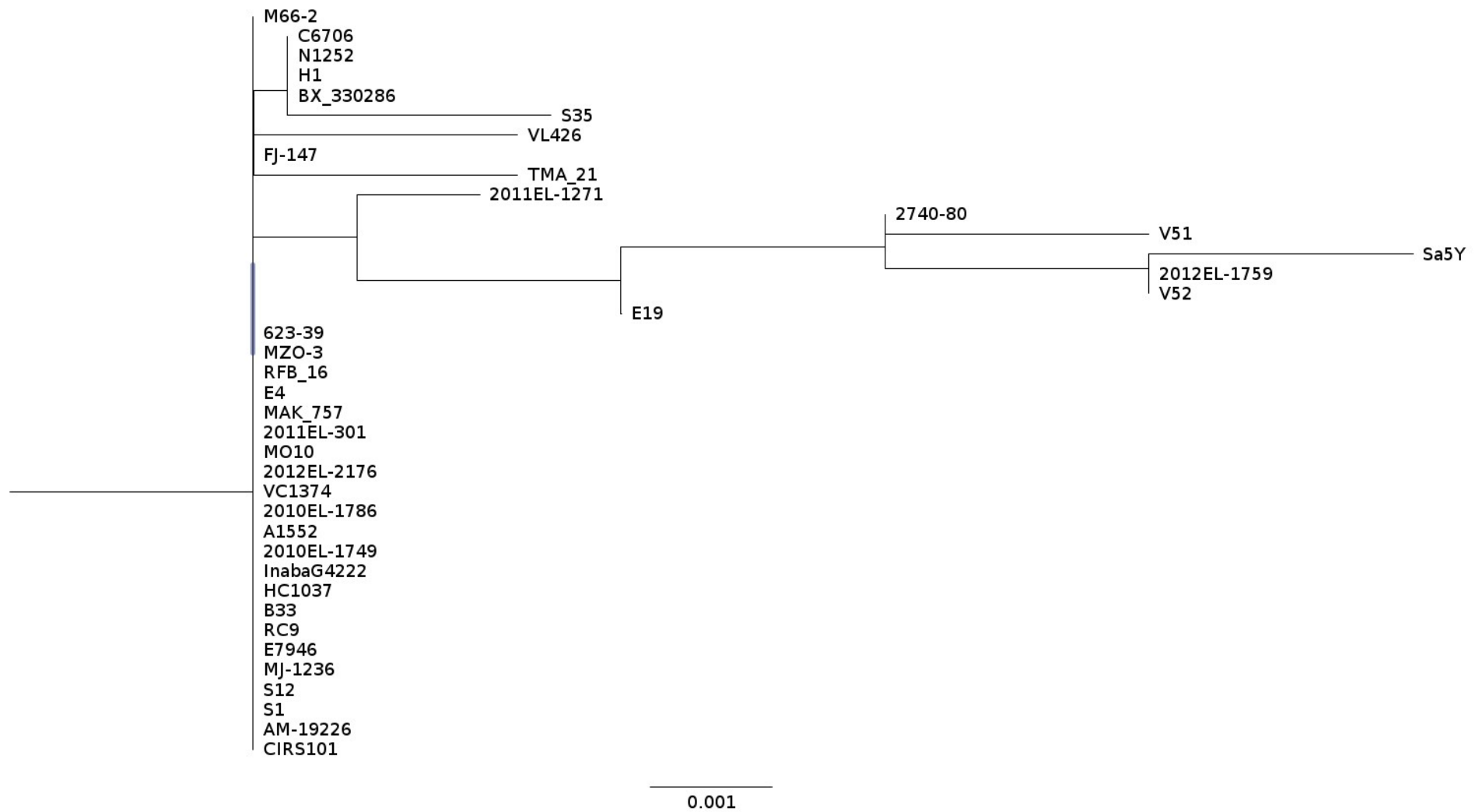


Fig 3. Maximum likelihood phylogenetic tree of *tnaA* protein sequences within *V.cholerae* species.



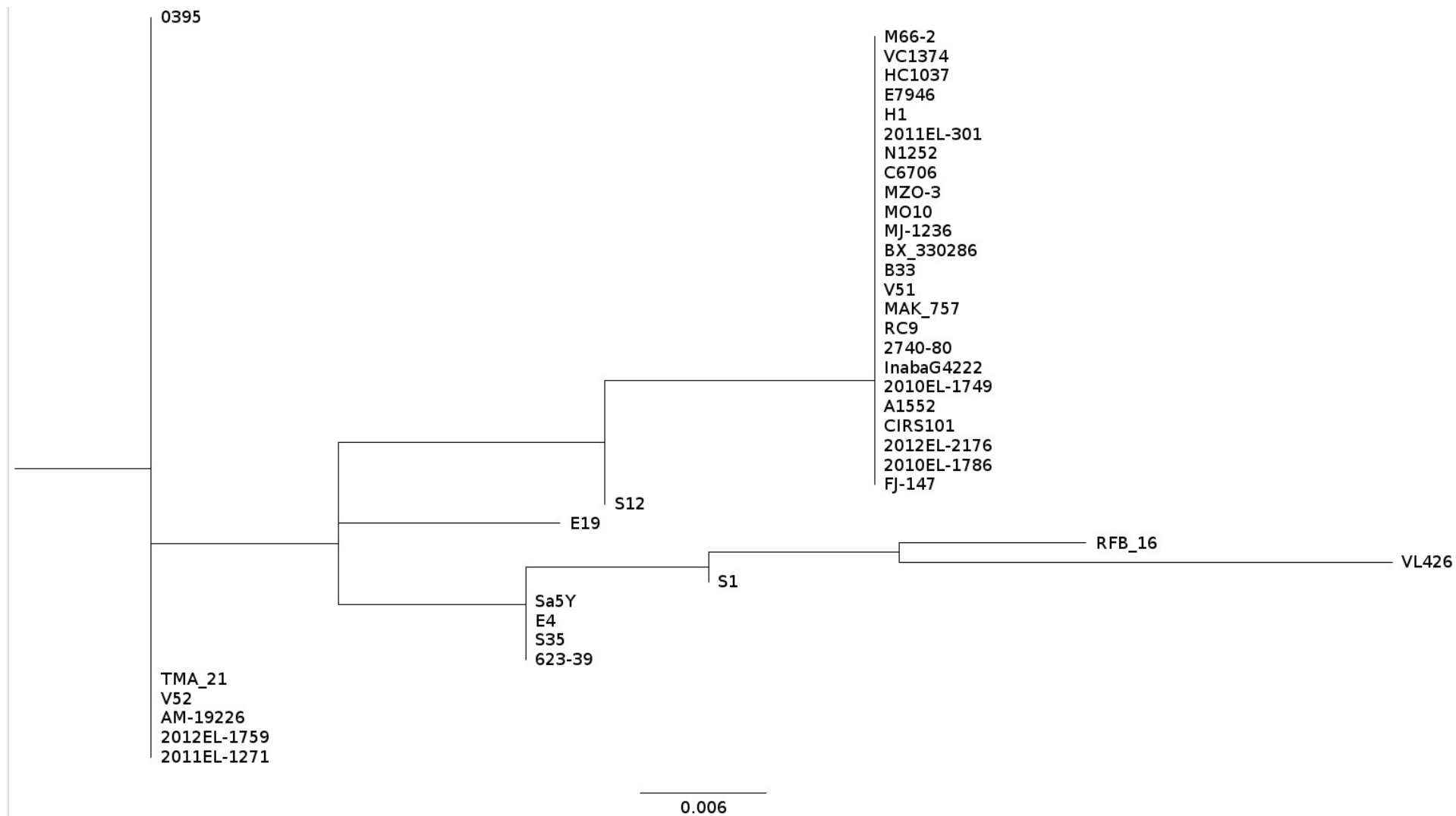


Fig 4. Maximum likelihood phylogenetic tree of *trpR* protein sequences within *V. cholerae* species.

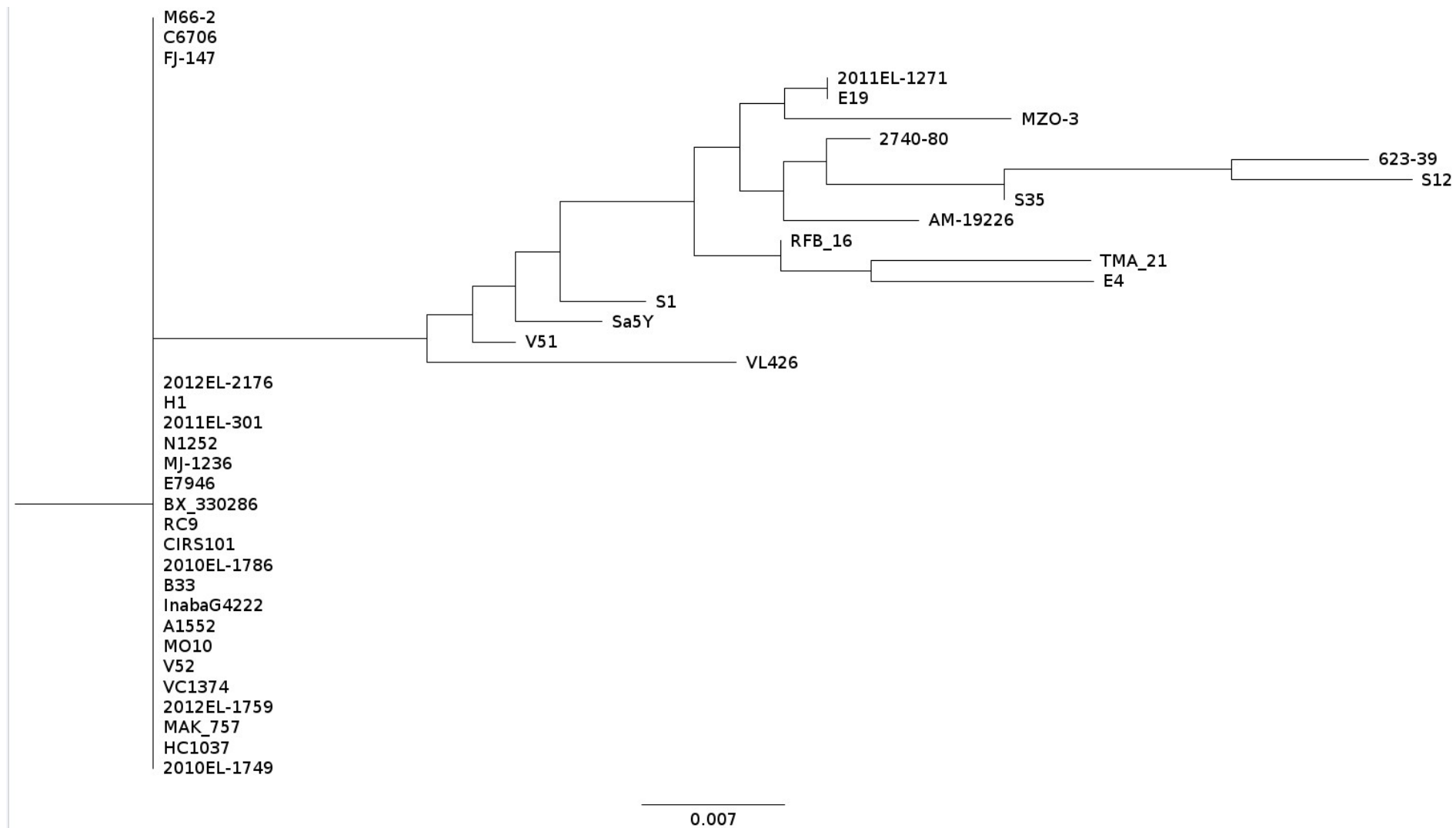


Fig 5. Maximum likelihood phylogenetic tree of *trpC.F* protein sequences within *V.cholerae* species.

