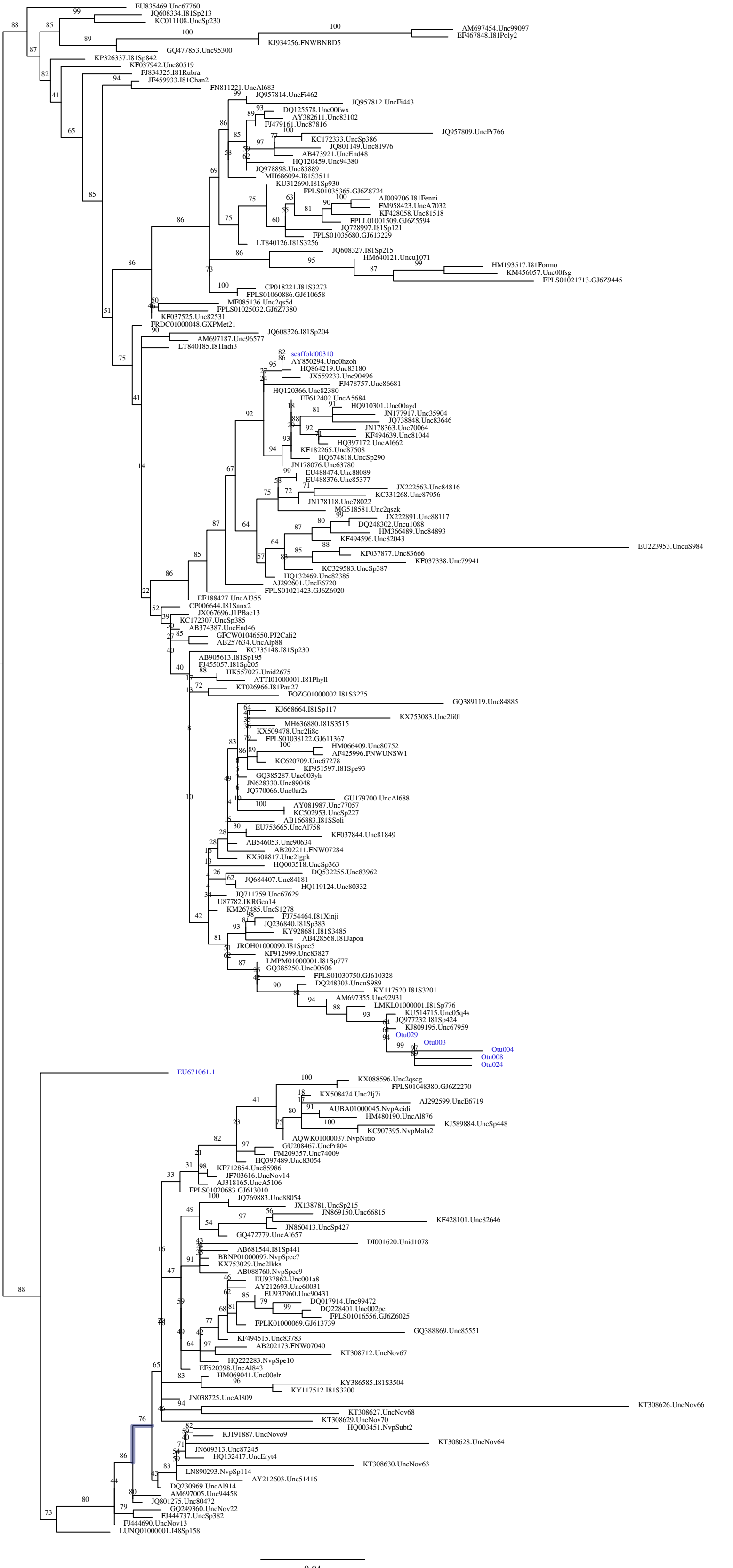


**Supplementary Figure S1A:** a maximum likelihood phylogenetic tree built on alignment columns corresponding to 16S amplicon. All strains associated with *F. radians* are shown in blue.



0.04

**Supplementary Figure S1B:** a maximum likelihood phylogenetic tree built on a complete 16S alignment. All strains associated with *F. radians* are shown in blue.

