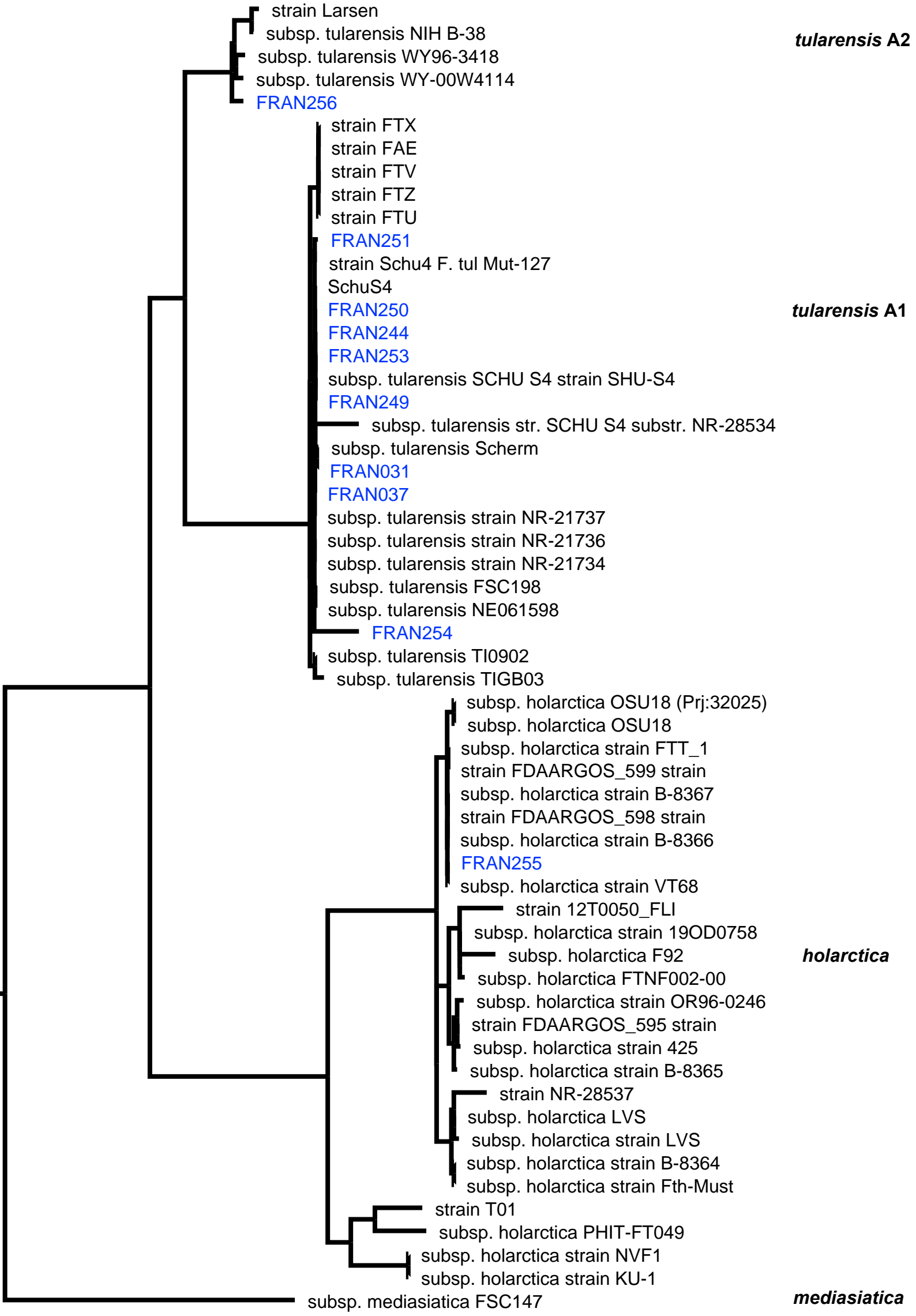


Supplementary Figure 1. Percentage difference between each strain based on average nucleotide identity calculated by mutual BLAST.
 Green indicates a greater distance between strains, red indicates greater similarity.



6.0E-4

Supplementary Figure 2. Phylogeny of *F. tularensis* strains with completed genomes. The tree is comprised of *F. tularensis* subsp. *holarctica*, *tularensis* and *mediasiatica* strains that have complete genomes, including the newly sequenced strains in our panel, indicated in blue. The PATRIC phylogenetic tree service was used to generate a RaxML tree based on 100 conserved genes found within each strain. The genomes fall within three main clades corresponding to *holarctica*, *tularensis* type A2 and *tularensis* type A1. Phylogenetic distance, measured by substitutions/site, is indicated on the x-axis.



Supplementary Figure 3. Colony appearance of *F. tularensis* Schu S4 (left) and FRAN255 (right) after 2 days of growth on Remel chocolate agar plates.