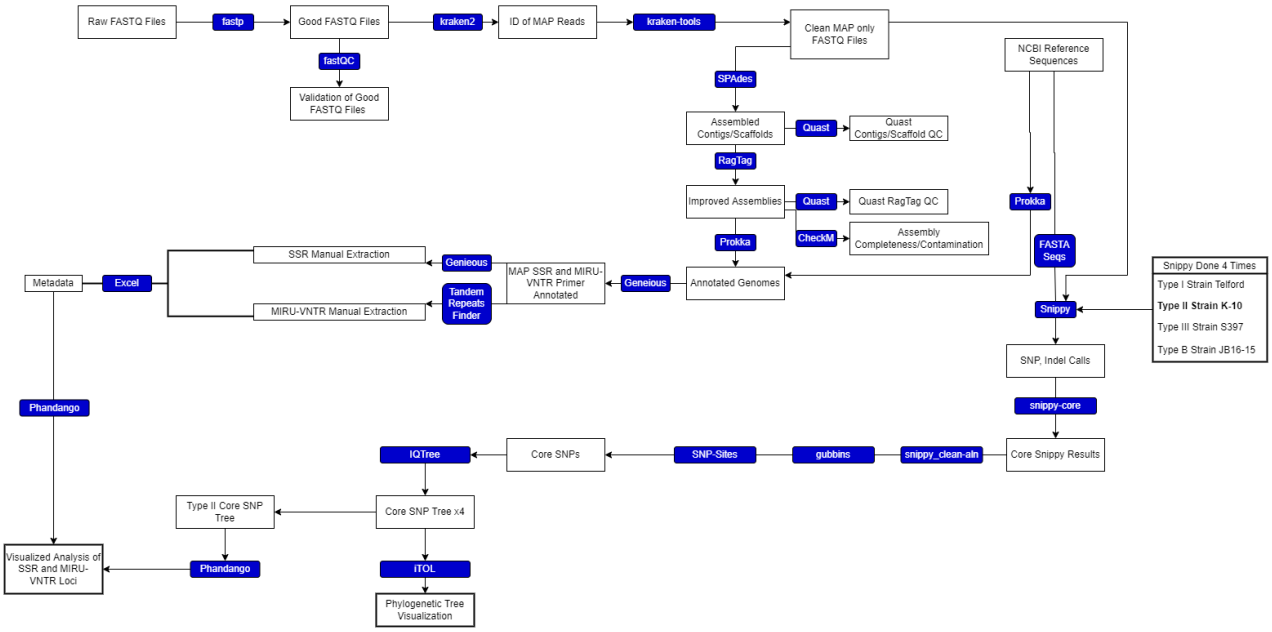
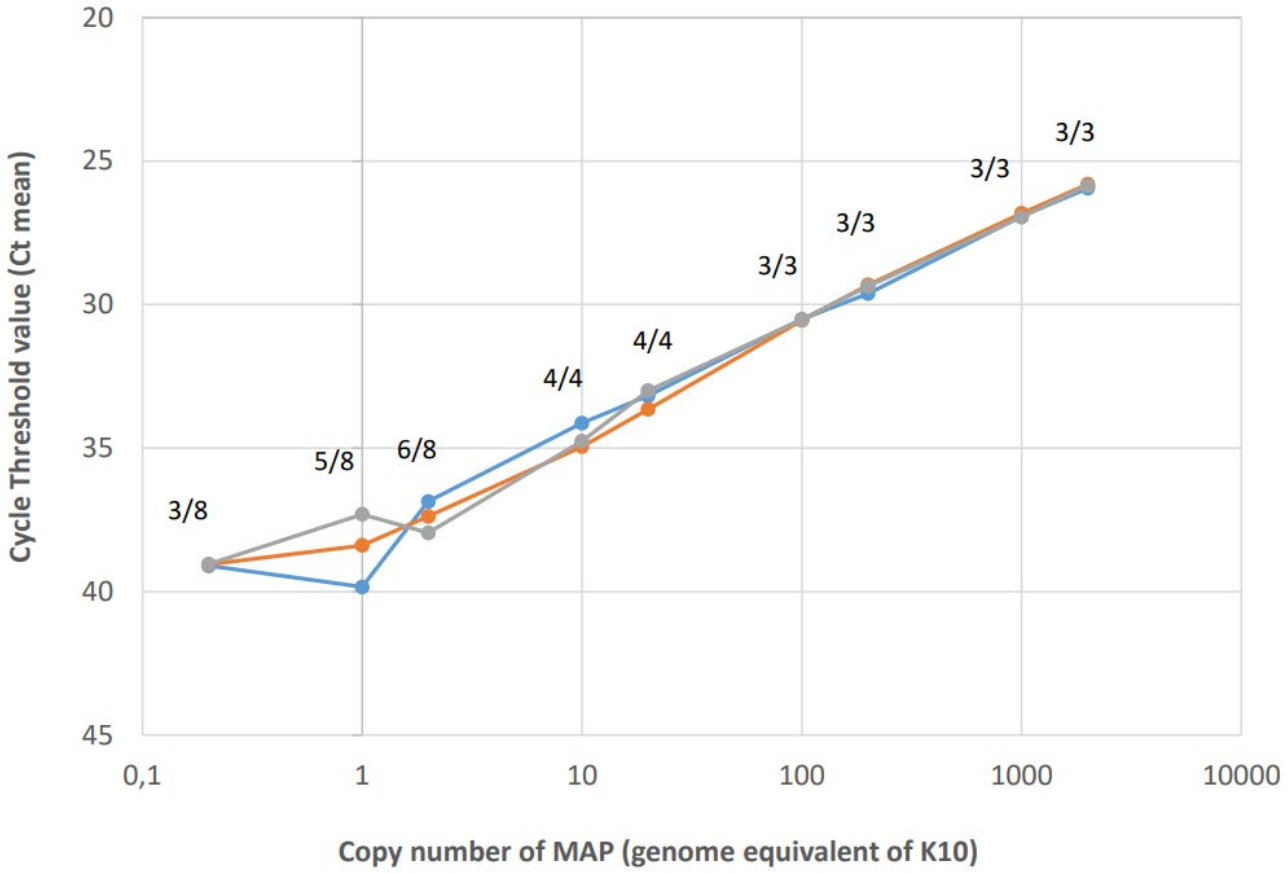
Supplementary Material

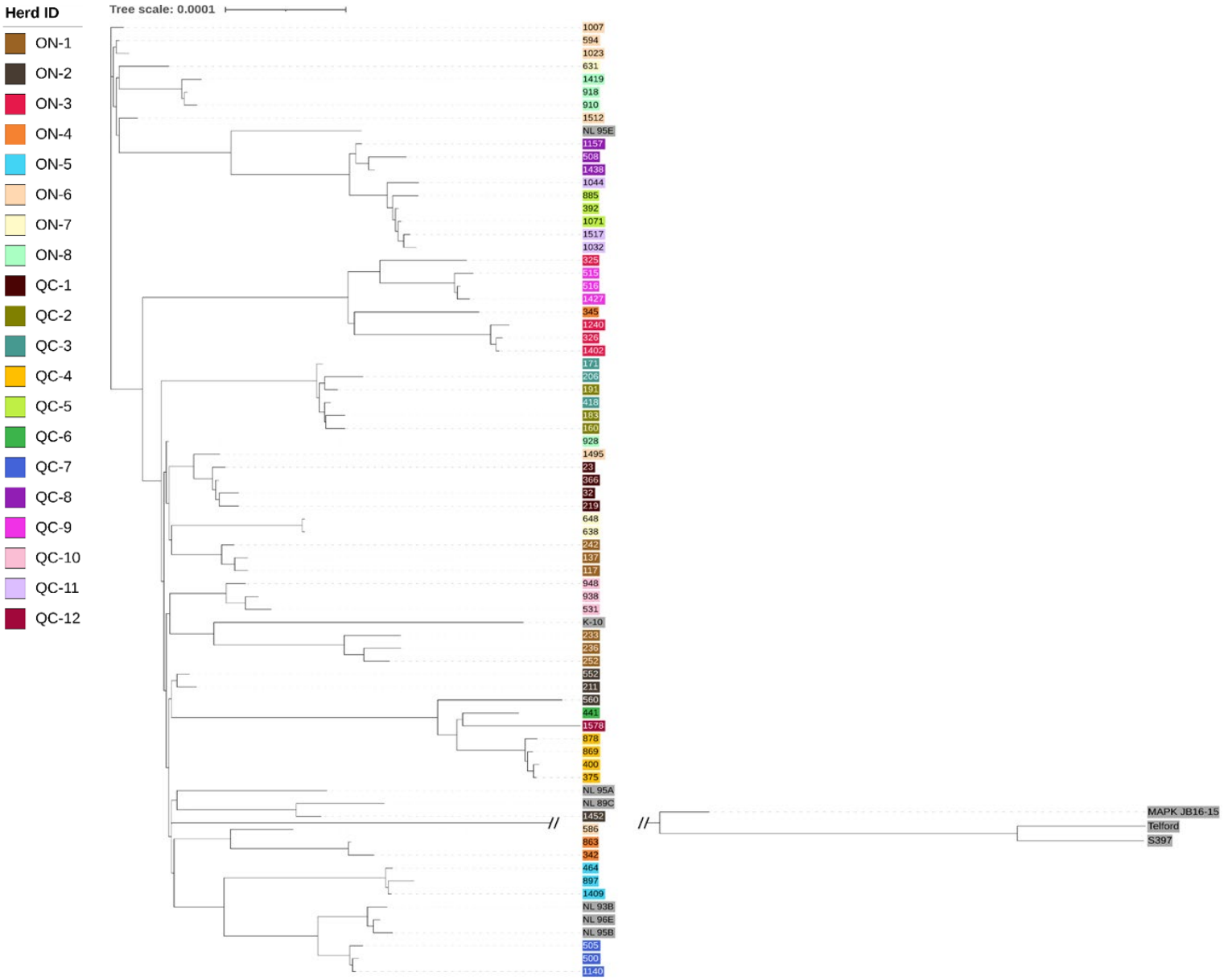


Supplementary Figure S1: Pipeline of bioinformatic tools (blue) and files (white) used to analyze whole genome sequencing data. Exact parameters used for each tool are described in the main manuscript.



Supplementary Figure S2: Detection of K10 strain (ATCC BAA-968D-5) of Mycobacterium avium subsp. paratuberculosis (MAP) by quantitative PCR (qPCR). Serial dilutions of DNA corresponding to known quantities of genome equivalents (Ge) were quantified by qPCR. Three independent serial dilution curves were made. Each dilution point was quantified eight times for the dilutions of 0.2, 1 and 2 Ge, four times for 10 and 20 Ge, and three times for the dilutions of 100, 200, 1000 and 2000 Ge.

A)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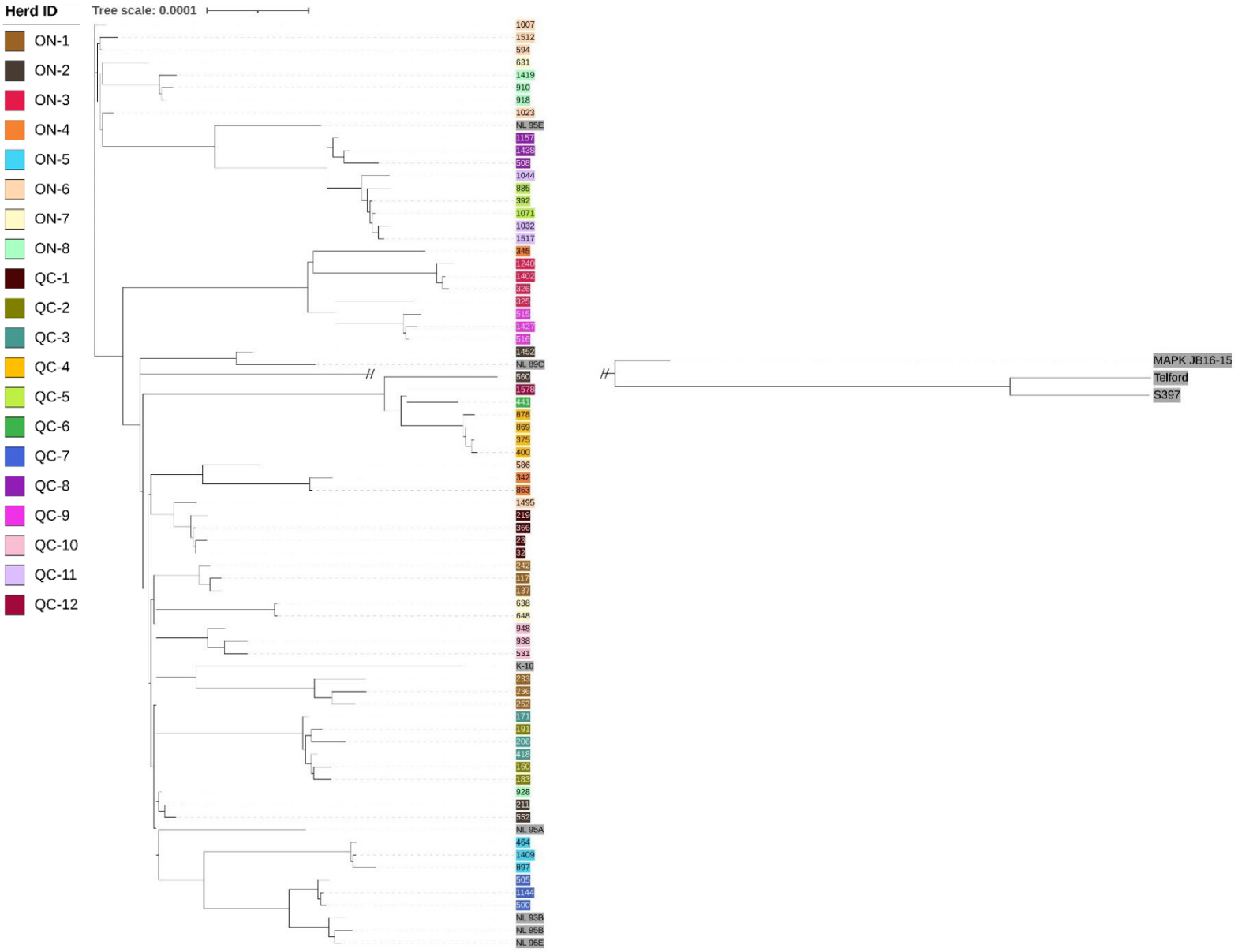
B)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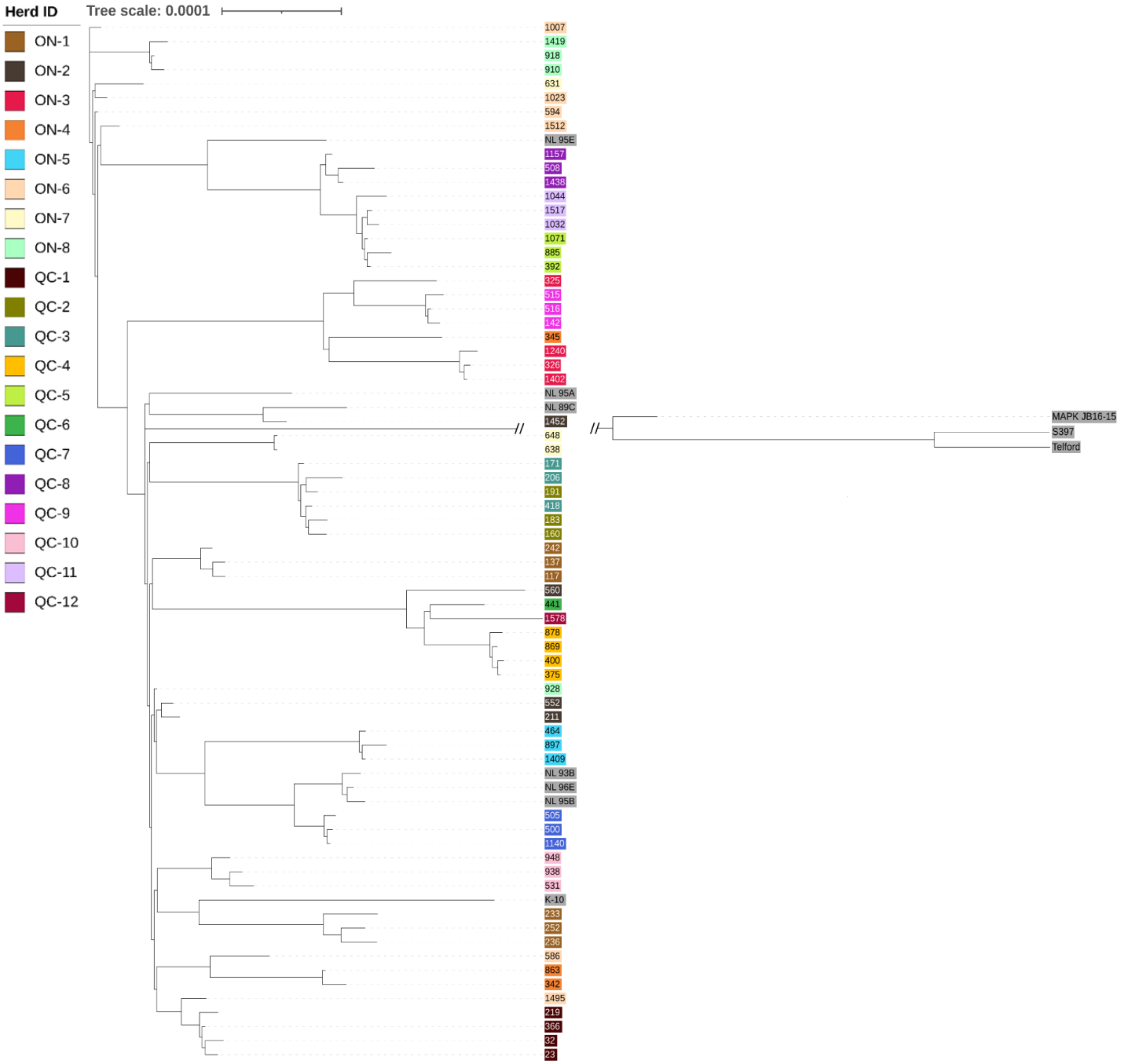
C)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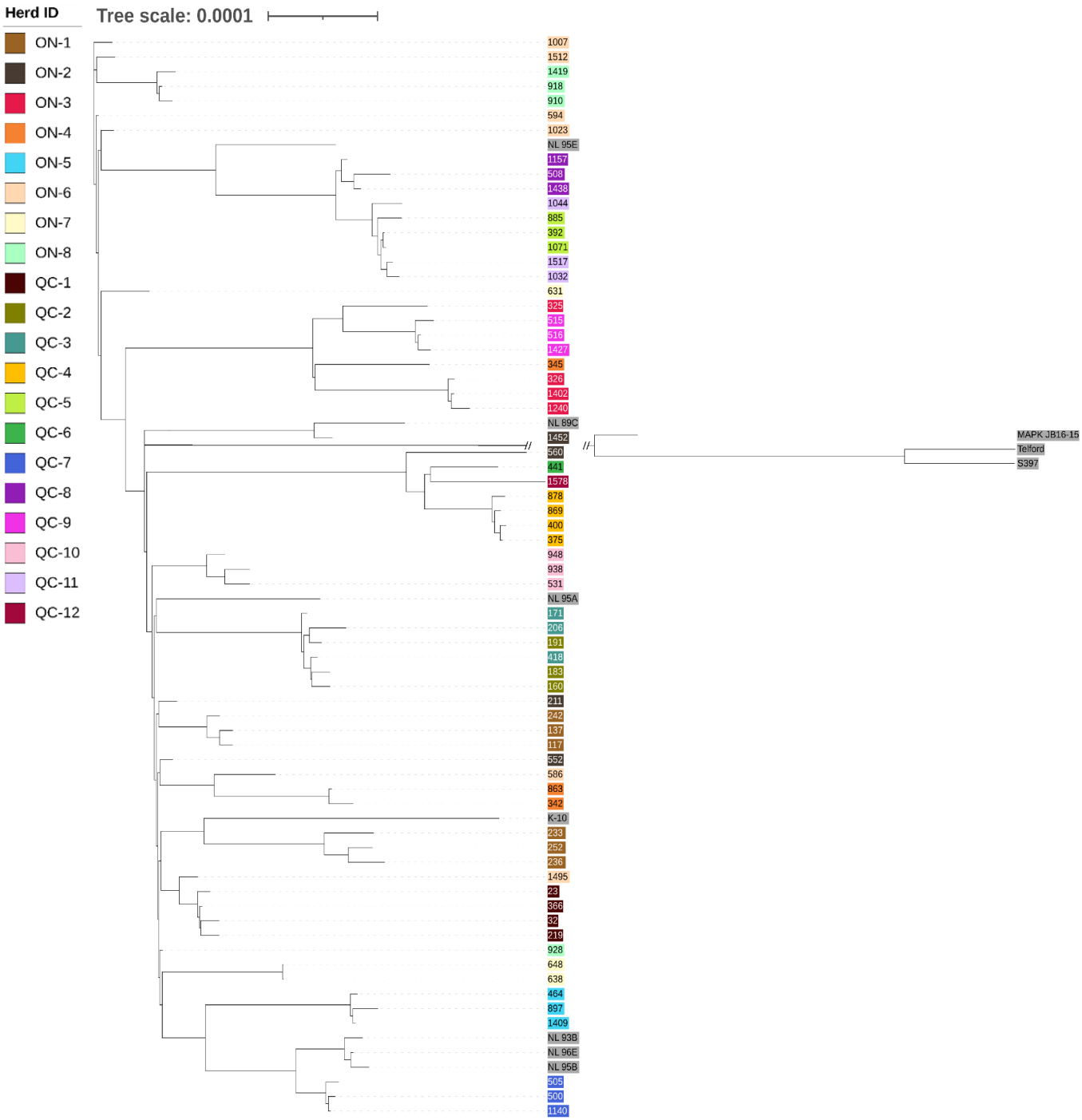
D)



Supplementary Figure S3: Core SNP phylogenies of MAP isolates (n=67) from ON and QC herds along with select reference sequences from NCBI (n=10). Each phylogeny was constructed based on

four separate core SNP analysis, each done using a different reference strain. A) used the type I reference strain Telford (NZ_CP033688.1), B) used the type II reference strain K-10 (NC_002944.2), C) used the type III reference strain S397 (NZ_CP053749.1), and D) used the type B reference strain MAPK_JB16/15 (NZ_CP033911.1). Each of 67 field isolates are colored by herd according to the listed key, while NCBI reference sequences are all colored in grey.