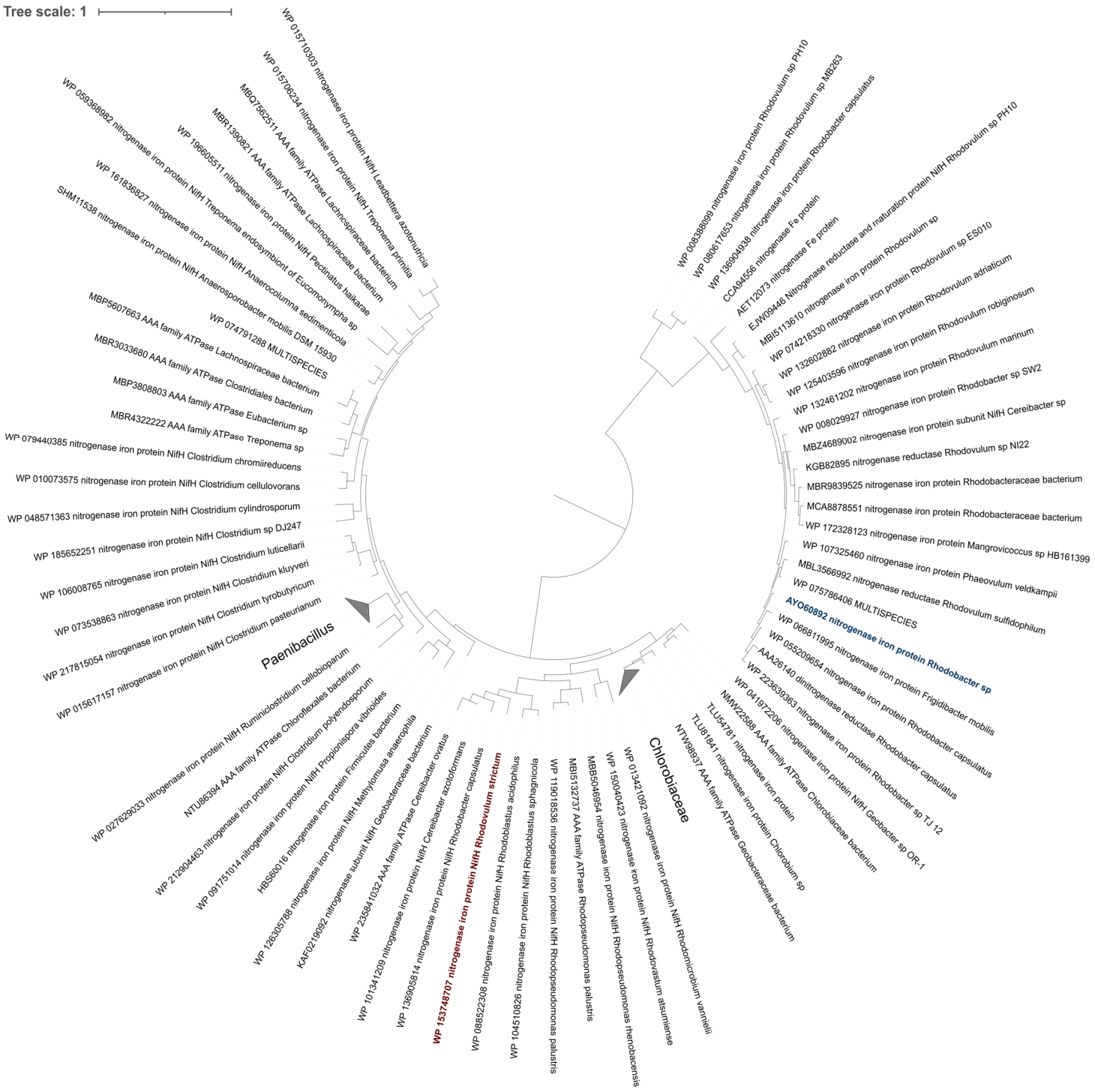

Figure S1. Phylogenetic tree of *nifH* gene across *Bacteria*. The tree includes *nifH* homologues missing in *R. steppense* and *R. tesquicola* (blue) and appearing in the three strains (red). The tree is scaled by evolutionary distance (count of substitutions per site) and rooted at the midpoint.