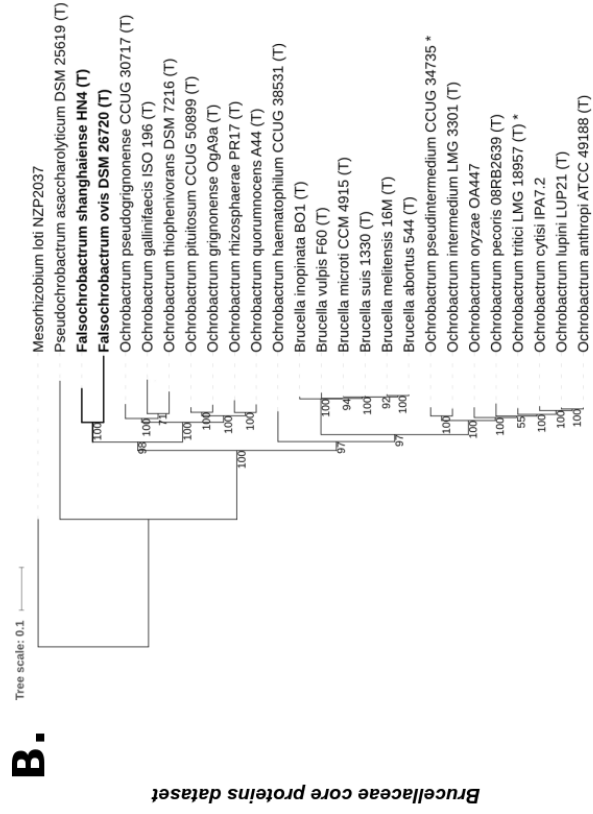
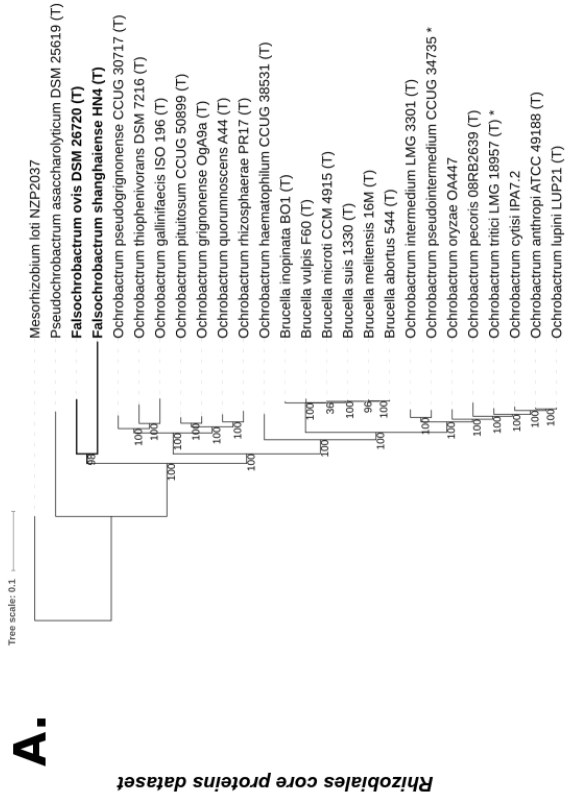
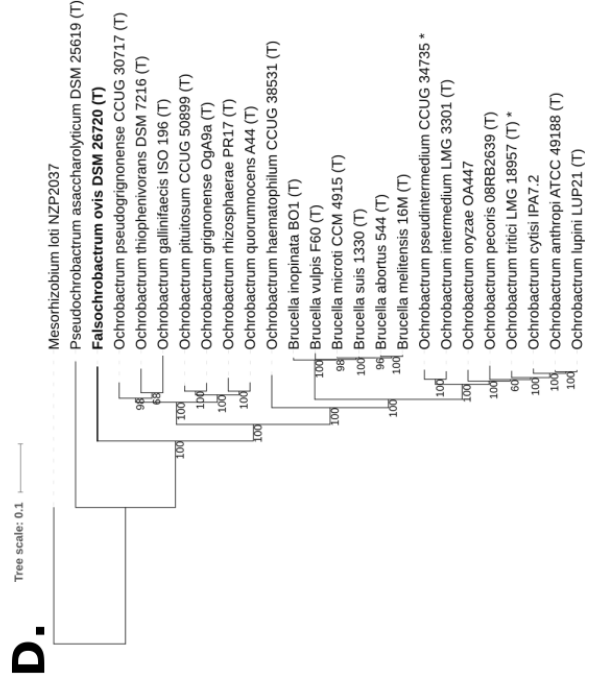
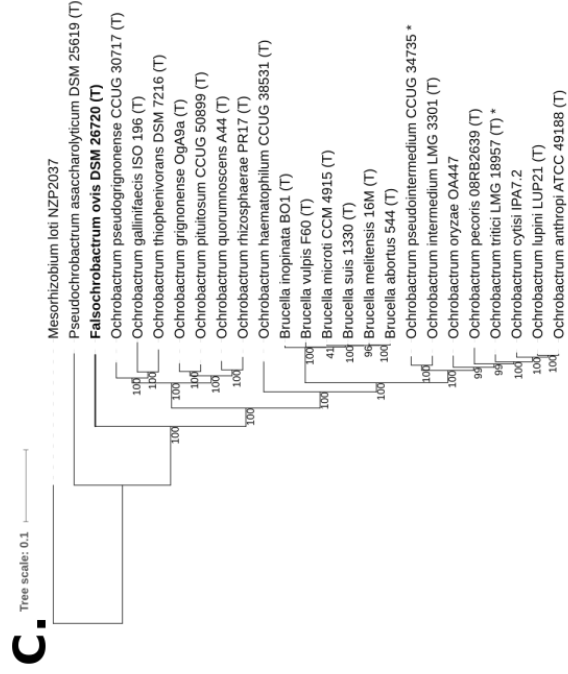


F. ovis & F. shanghaiense



F. ovis alone



F. shanghaiense alone

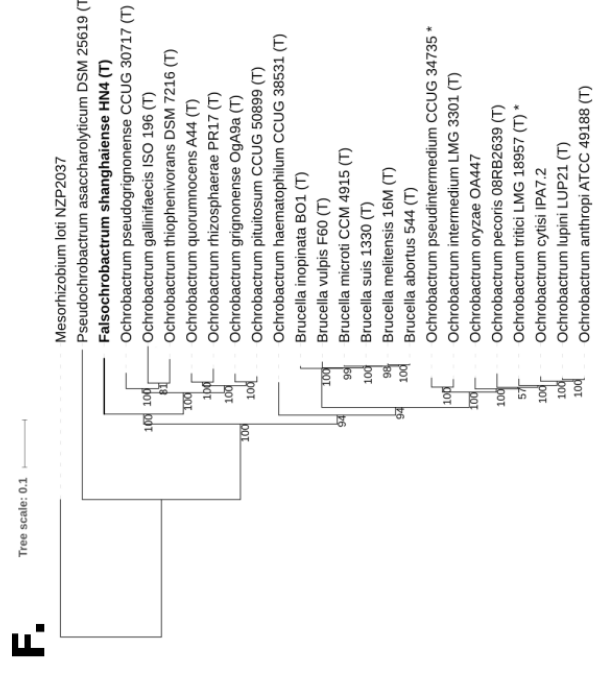
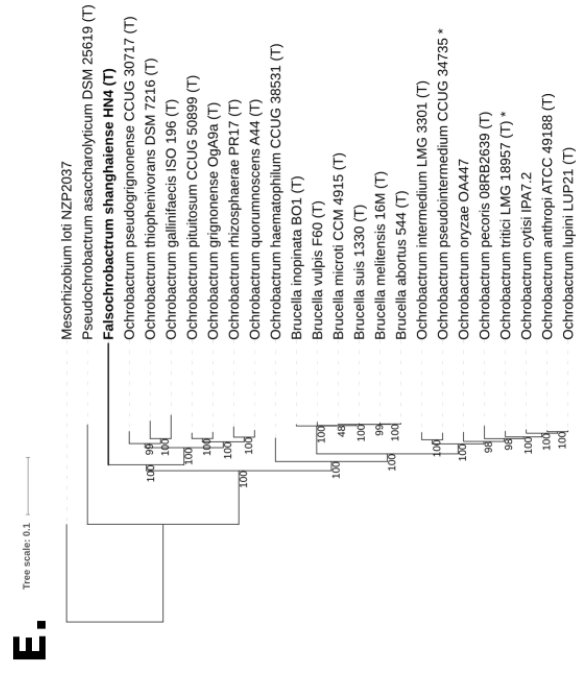


Figure S3. Position of Falsochrobacterium spp. among the family Brucellaceae. Various ML phylogenetic trees were computed using RaxML from the alignment of 145 and 195 core proteins (A,C,E and B,D,F, respectively), on datasets including representative *Brucellaceae* and both *Falsochrobacterium* (A,B), *F. ovis* only (C,D), or *F. shanghaiense* only (E,F). All trees were rooted using the *Mesorhizobium loti* genome. Branching support was estimated using 100 bootstrap replicates.