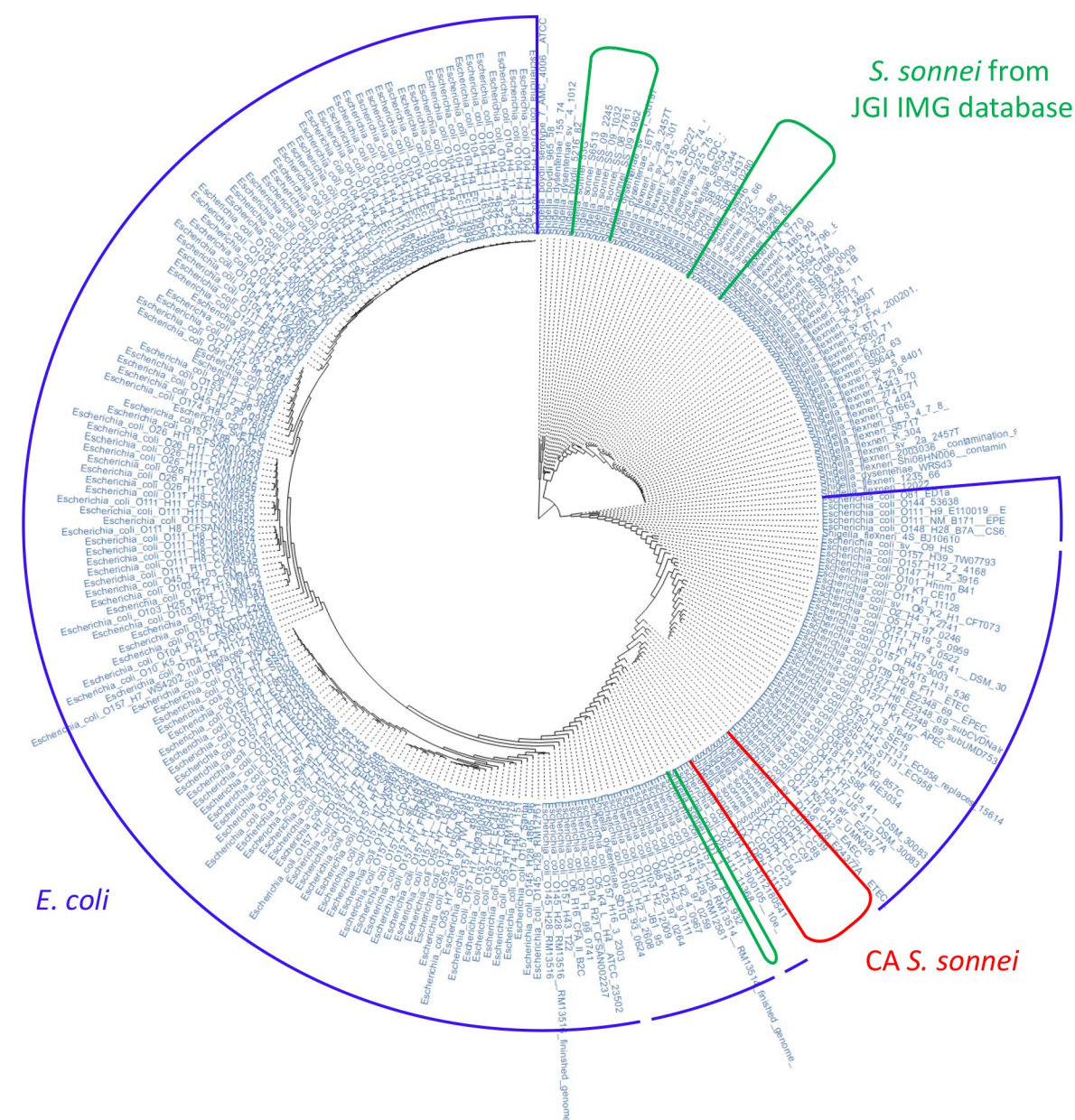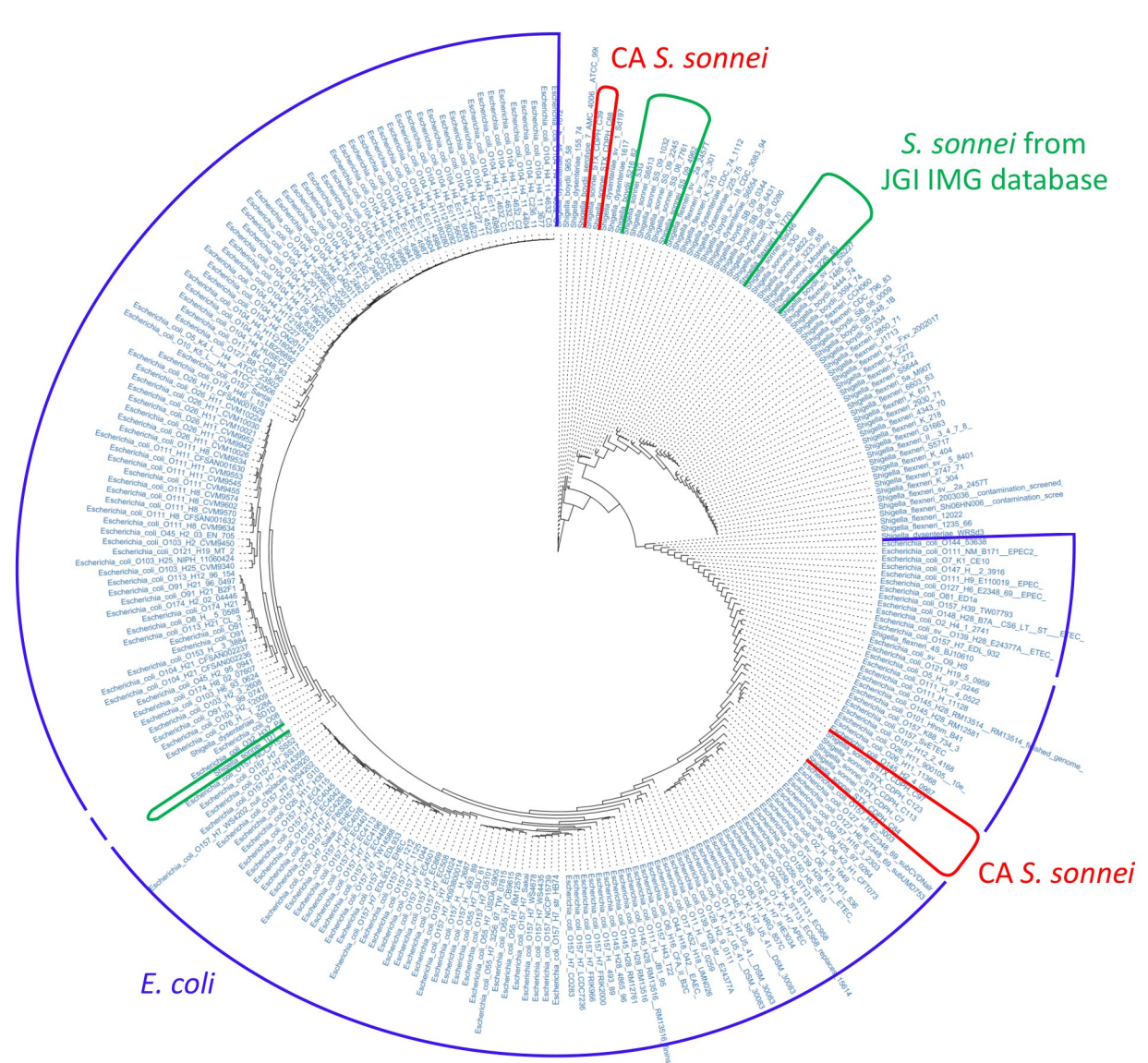# Figure S2. Comparison of CA *S. sonnei* with other *Shigella* and *E. coli* species
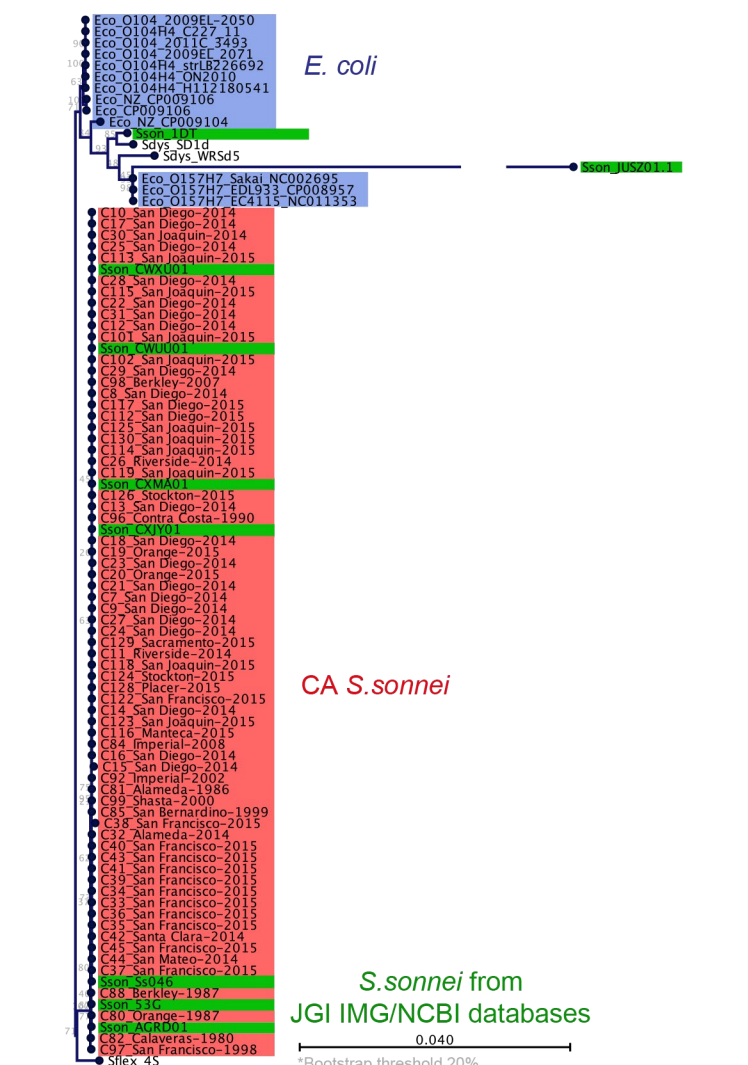
A. Hierarchical Clustering of CA representative *S. sonnei* isolates with other *Shigella* and *E. coli* from JGI IMG database based on COG profiles (abundance). Color of the brackets: Red- representative *S. sonnei* from California; Green- other *S. sonnei* from JGI IMG database; Blue- *E. coli* strains from JGI IMG database.

B. Hierarchical Clustering of CA representative *S. sonnei* isolates with other *Shigella* and *E. coli* from JGI IMG database based on pfam profiles (abundance). Color of the brackets: Red- representative *S. sonnei* from California; Green- other *S. sonnei* from JGI IMG database; Blue- *E. coli* strains from JGI IMG database.

C. Comparison of CA *S. sonnei* with other *Shigella* and *E. coli* publicly-available genomes based on nucleotide sequence. Maximum likelihood clustering from PhyloSift nucleotide-based phylogeny. Background color: Red- *S.sonnei* from California; Green- other *S.sonnei* from JGI IMG and NCBI databases; Blue- *E.coli* strains from JGI IMG database. Bootstrap threshold 20%.

D. Comparison of CA *S. sonnei* with other *Shigella* and *E. coli* publicly-available genomes based on nucleotide sequence. Maximum likelihood phylogeny of CA *S. sonnei*, *E.coli*, and publicly-available *S. sonnei* genomes based on genome-wide hqSNPs. Background color: Red- *S.sonnei* from California; Green- other *S. sonnei* from JGI IMG and NCBI databases; Blue- *E.coli* strains from JGI IMG database. Bootstrap threshold 50%.