

Figure S1. Whole-genome Average Nucleotide Identity (ANI) and sequence type: A) 140 peruvian and global *Salmonella* Typhimurium strains B) 90 peruvian *Salmonella* Typhimurium strains.

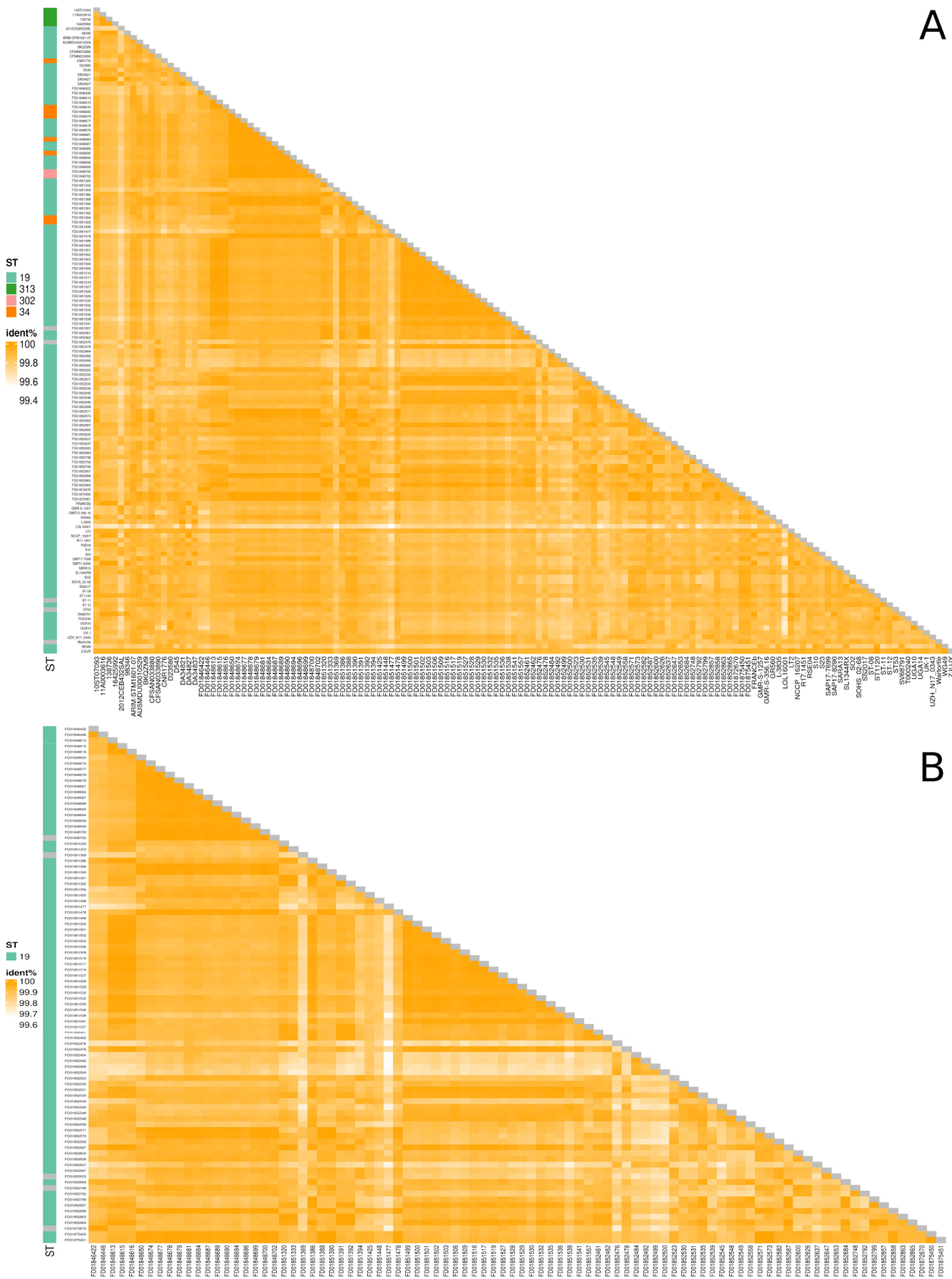


Figure S2. Nucleotide similarity and sequence type: A) 140 peruvian and global *Salmonella* Typhimurium strains B) 90 peruvian *Salmonella* Typhimurium strains.

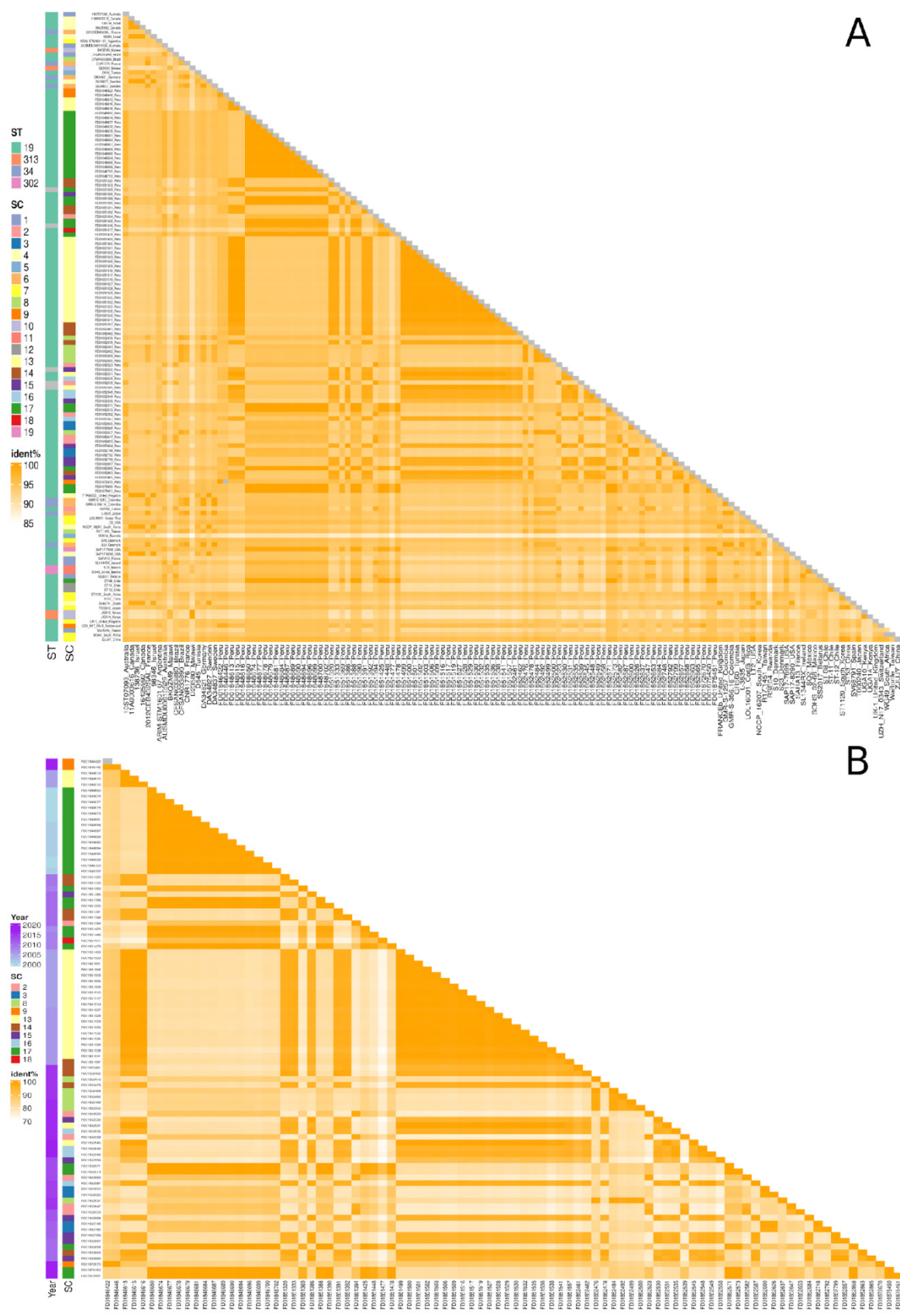


Figure S3. Phylogenetic tree was generated using a maximum likelihood method with 1000 replicates of bootstrap using GTR+GAMMA to estimate evolutionary distance between 140 global isolates. The phylogenetic tree was clustered into at least two large clades and segregated into at least nineteen sub-clades.

