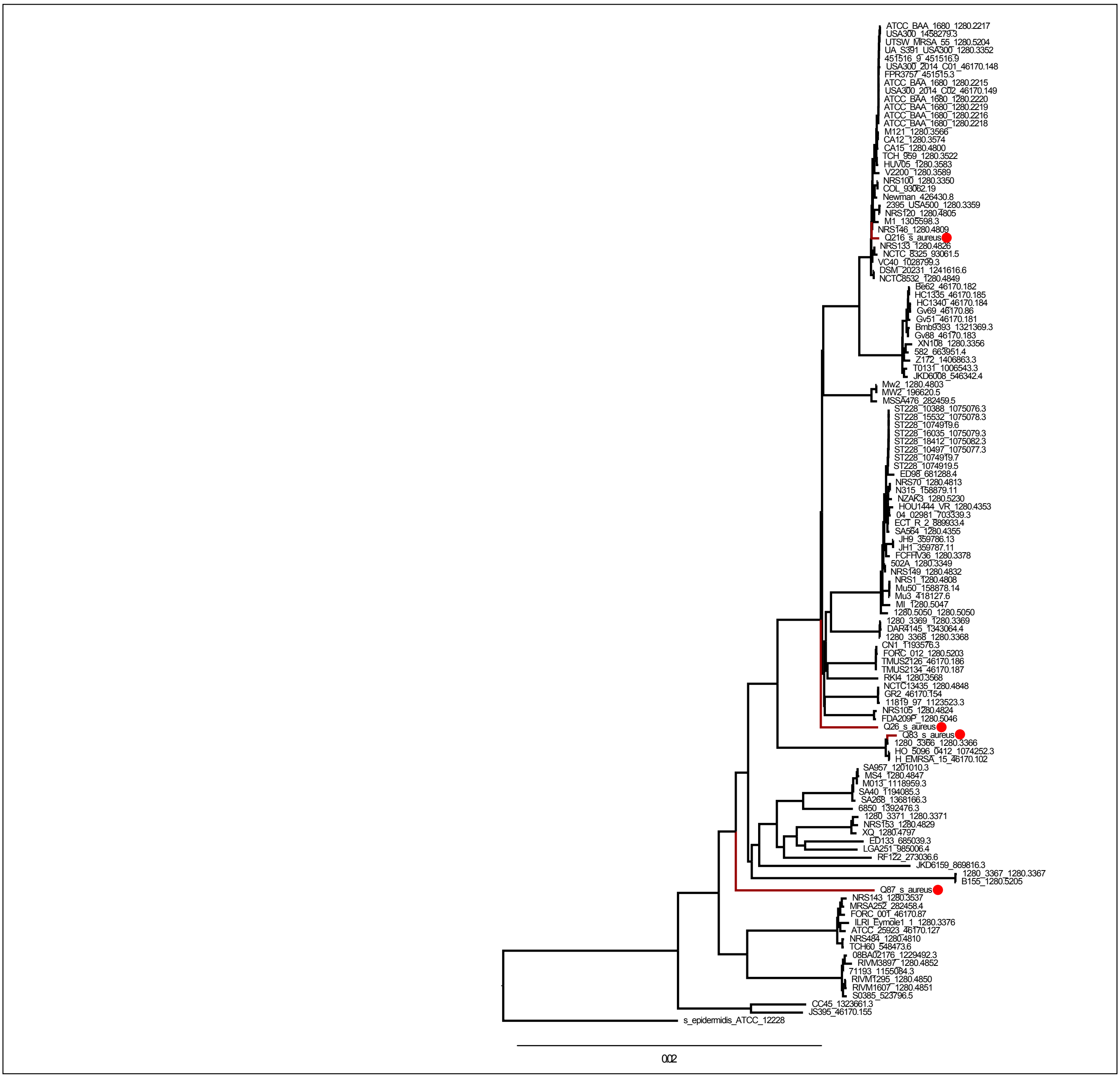

Figure S3. *S. aureus* phylogeny. Neighbor-joining tree built using estimated distances between a collection of 118 complete *S. aureus* genomes, and assembled *S. aureus* genomes from 4 preterm infant metagenomes. Genomes derived from the premature infant samples are highlighted in red. *S. epidermidis* used as the outlier, and this branch has been truncated for presentation purposes. Scale bar shows number of nucleotide substitutions per site.