

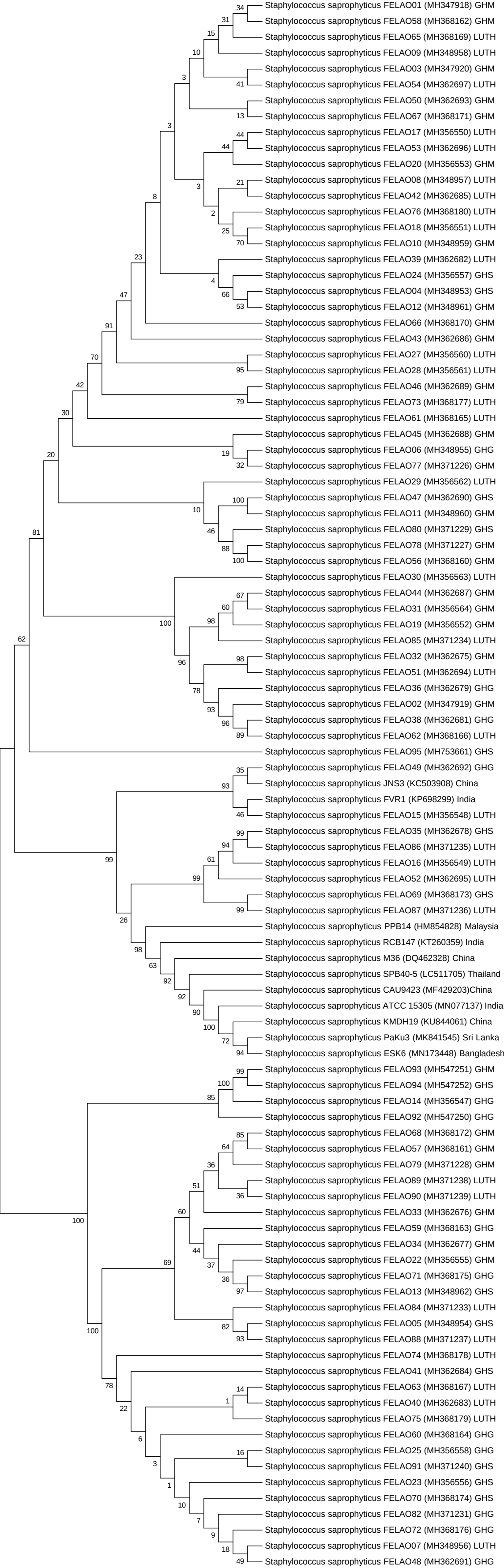


Figure 2: Neighbour-joining tree showing the phylogenetic relationships among *S. saprophyticus* isolates based on a comparison of 1500bp 16SrRNA gene sequences. Bootstrap values based on 1000 replicates are given at the branching points when they are above 50%. NCBI accession numbers are in parentheses followed by sampling site.