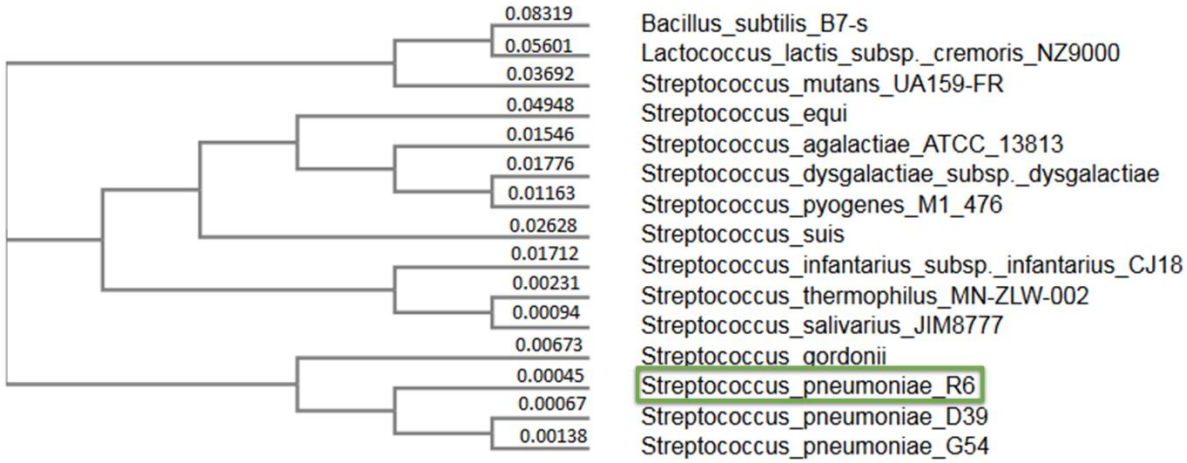
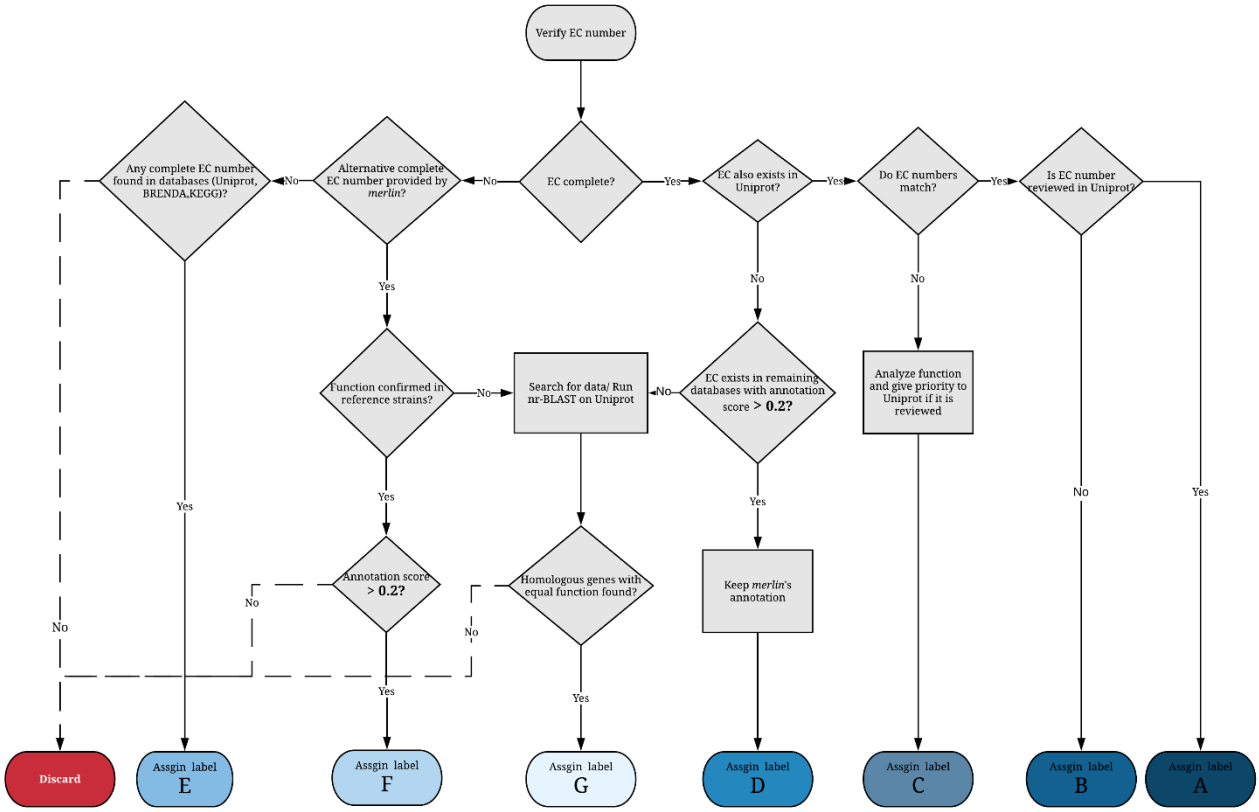
Supplementary Material

1 Supplementary Figures



Supplementary Figure 1. Phylogenetic tree of Streptococcus pneumoniae relative organisms. This tree was built using EMBL-EBI Clustal OMEGA multiple sequence alignment tool (Sievers et al., 2011). Numbers above each line represent the branch lengths to each node generated automatically by the tool using the Neighbor-joining method (Saitou and Nei, 1987).



Supplementary Figure 2. Re-annotation workflow for model iDS372.