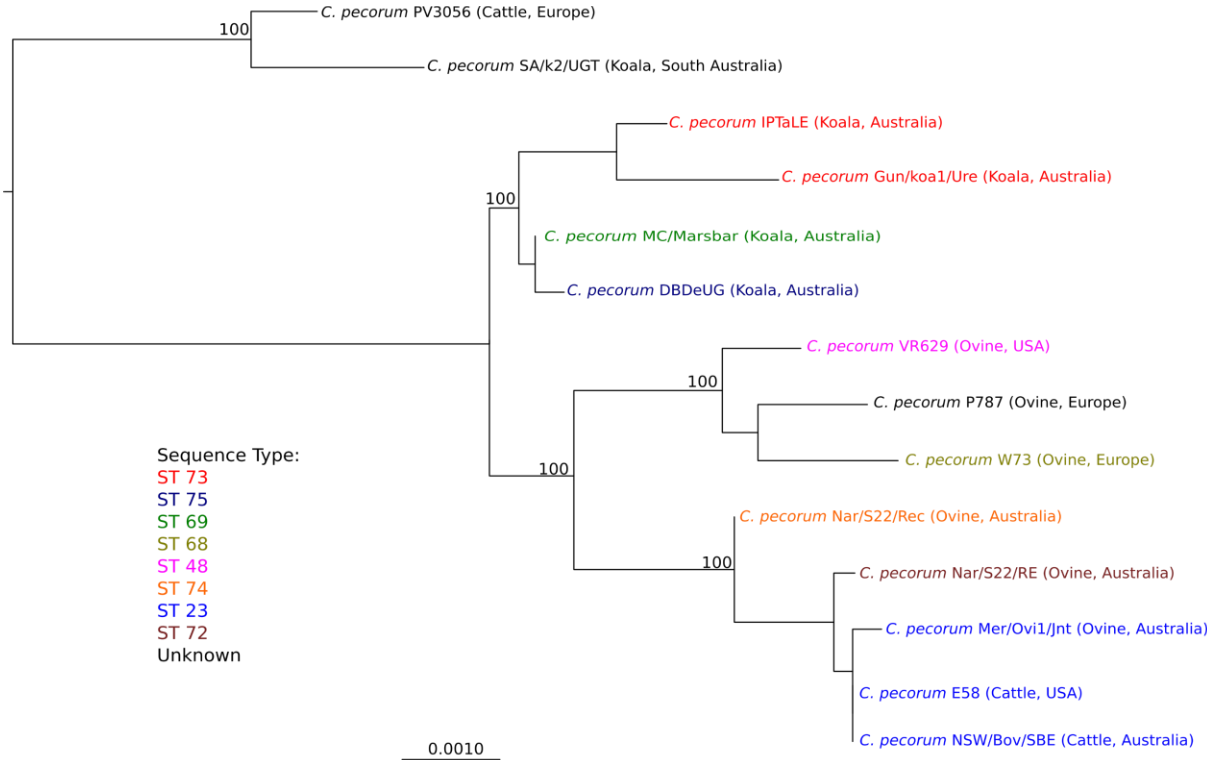

Supplementary Figure 1: Maximum-likelihood tree based on the concatenation of seven housekeeping genes. The seven housekeeping genes used to build the phylogeny includes *oppA*, *hflX*, *hemN*, *gidA*, *gatA*, *fumC* and *enoA*. The phylogenetic tree was constructed using PhyML with the GTR substitution model. Bootstrap values are shown as percentages of 1000 replicates. The scale bar represents the number of substitutions per site. Sequence types are based on MLST typing of seven housekeeping genes.