



Supplemental Figure S6. Maximum likelihood phylogenetic trees of *Pneumocystis* from hares and other mammals based on the dihydropteroate synthase (*dhps*) gene (**A**) and nuclear rRNA operon (**B**). The trees were constructed using nucleotide sequences from each *Pneumocystis* species or strain, with GenBank accession numbers listed in Table S6. The order of species and strains in panel B was rotated, without changing the clustering relationships, to facilitate visual comparison with other trees. Numbers at each node are SH-aLRT support (%)/ultrafast bootstrap support (%). The 2 variants of *P. sp. 'townsendii'* from hares identified in this study are represented by Ph_v1 and Ph_v2.