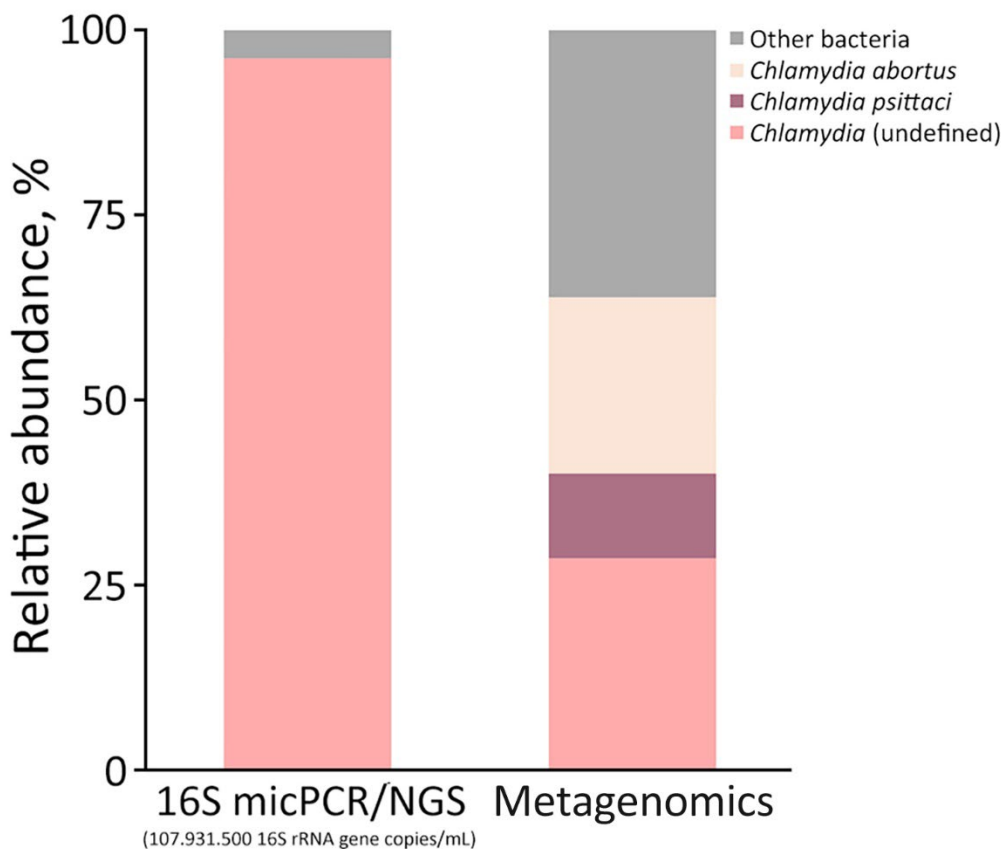
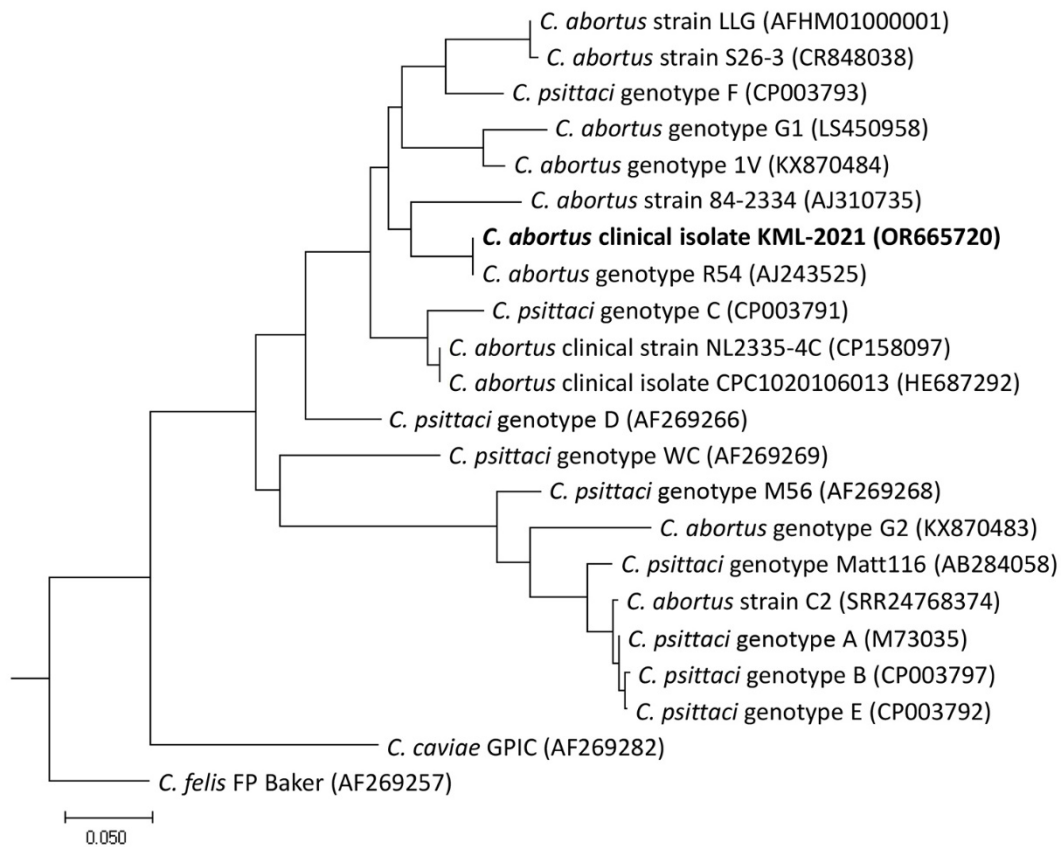


# Community-Acquired Pneumonia Caused by Avian *Chlamydia abortus*, the Netherlands

## Appendix



**Appendix Figure 1.** Bacterial microbiota profiles of the lower respiratory tract in a patient with community-acquired pneumonia caused by avian *Chlamydia abortus*, the Netherlands. A high relative abundance of *Chlamydia* spp. was detected in the lower respiratory tract by using quantitative 16S rRNA gene micelle PCR with next-generation sequencing analysis (micPCR/NGS) and shotgun metagenomics.



**Appendix Figure 2.** Chlamydial genotyping in a patient with community-acquired pneumonia caused by avian *Chlamydia abortus*, the Netherlands. For genotyping, an 850-bp alignment of *ompA* gene sequences from clinical isolate KML-2021 shown in bold (GenBank accession no. OR665720) and reference *Chlamydia* strains (GenBank accessions) was used. The tree was rooted with the *C. felis* (FP Baker) reference strain.