



Figure S1. Core-genome comparison of *C. sedlakii* 3347089 II with all *C. sedlakii* genome assemblies deposited in the NCBI genome database and three assemblies deposited as *Citrobacter* spp. (strains 50677481, RHB21-C05, and RHB21-C01) (accessed on 03/17/2021). The assemblies are presented in a SNVs hierarchical clustering dendrogram tree obtained from the core-genome analysis performed using Parsnp (v1.2) and visualized with iTOL (<https://itol.embl.de/>). The core-genome represents the total coverage (85.3%) among all sequences corresponding to 75'495 SNVs. The Δ SNV values indicate the number of non-identical SNVs between two strains. The grey circles on the branches indicate that the branch is supported by a bootstrap value >89. For each strain, the GenBank accession is reported in brackets.