



Supplementary Figure S1. Whole-genome synteny analysis of predicted genes between Sanger-sequenced *FoI4287* (*FoI 2010*) and PacBio-

sequenced *FoI4287* (*FoI 2020*) assemblies. The grey lines in the background indicate the collinear genes between the two assemblies, while the red lines highlight the collinear genes in the lineage-specific regions.