



Supplementary Figure S1. Whole-genome synteny analysis of predicted genes between Sanger-sequenced Fol4287 (*Fol* 2010) and PacBio-sequenced Fol4287 (*Fol* 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.