



Supplementary Fig. S1 | *tra* genes and adjacent elements detected in 'Ca. Midichloriaceae' genomes. Each column represents genes classified as orthologous by OrthoFinder. Colours distinguish different genomes. The relative order of the *tra* genes and adjacent elements as they appear along the contigs is conserved. Length and average k-mer coverage are reported for all relevant contigs on the right column (N/A: not available). Consensus tree topology derived from phylogenomic analysis is reported on the left. TNP/INT: putative transposase/integrase; SSDB: single-strand DNA binding protein. A single asterisk marks genes annotated by KEGG; two asterisks mark genes annotated by Prokka; three asterisks mark genes annotated by TXSScan

gene detected by annotation softwares and identity corroborated by BLASTp
 gene detected by annotation softwares but identity not corroborated by BLASTp
 open reading frame not recognized by annotation softwares (identified by BLASTp and OrthoFinder)
 contiguous on a contig
 same contig, but separated by other genes / open reading frames (not reported)