APPENDIX S1. Schematic MITObim workflow (Hahn et al., 2013). In the first step, genomic reads of *Crescentia cujete* were mapped on the reference guide plastome of *Tanaecium tetragonolobum*. Contigs were created and used as a new reference in the second step. Baiting was performed with a 31-bp overlap with the reference contigs. Extension of the contigs was done iteratively until a complete genome was achieved.