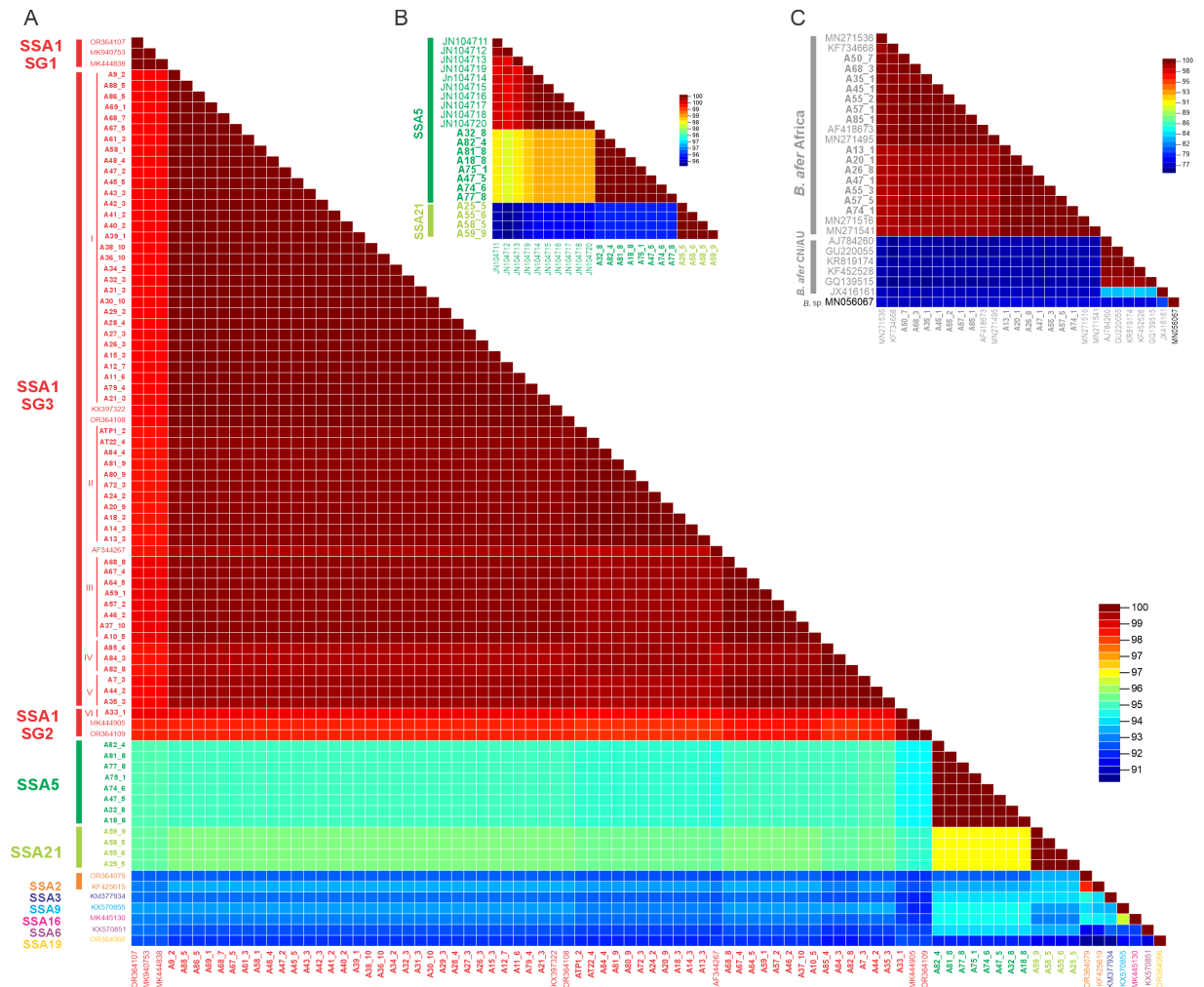
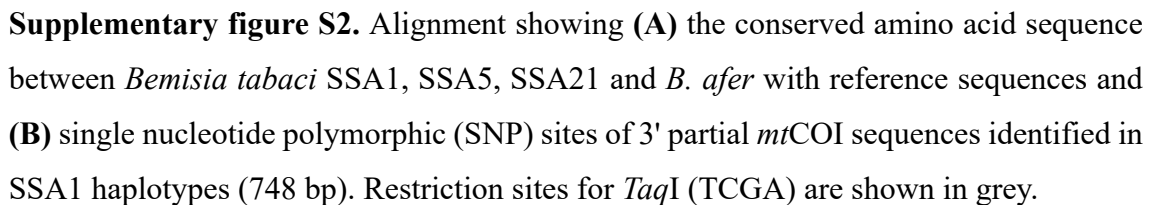




Supplementary figure S1. Nucleotide divergence of whitefly species sequenced from Mozambique. Data sets were comprised of **(A)** 3' *mtCOI* sequence (657 bp) of *B. tabaci* cryptic species within Sub-Saharan Africa clade, **(B)** 3' *mtCOI* sequence (630 bp) of *B. tabaci* SSA5 and SSA21, and **(C)** 3' *mtCOI* sequence (657 bp) of *Bemisia afer*. Each data set was aligned using the MUSCLE algorithm (Edgar, 2004) implemented in MEGA X (Kumar *et al.*, 2018) and analyzed using the SDT v. 1.3 program (Muhire *et al.*, 2014).



Supplementary figure S2. Alignment showing **(A)** the conserved amino acid sequence between *Bemisia tabaci* SSA1, SSA5, SSA21 and *B. afer* with reference sequences and **(B)** single nucleotide polymorphic (SNP) sites of 3' partial *mtCOI* sequences identified in SSA1 haplotypes (748 bp). Restriction sites for *TaqI* (TCGA) are shown in grey.