Figure S1 ITS partition strategy through ASAP algorithm.
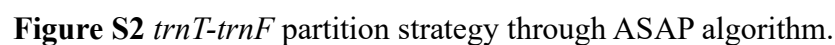
Figure S2 *trnT-trnF* partition strategy through ASAP algorithm.
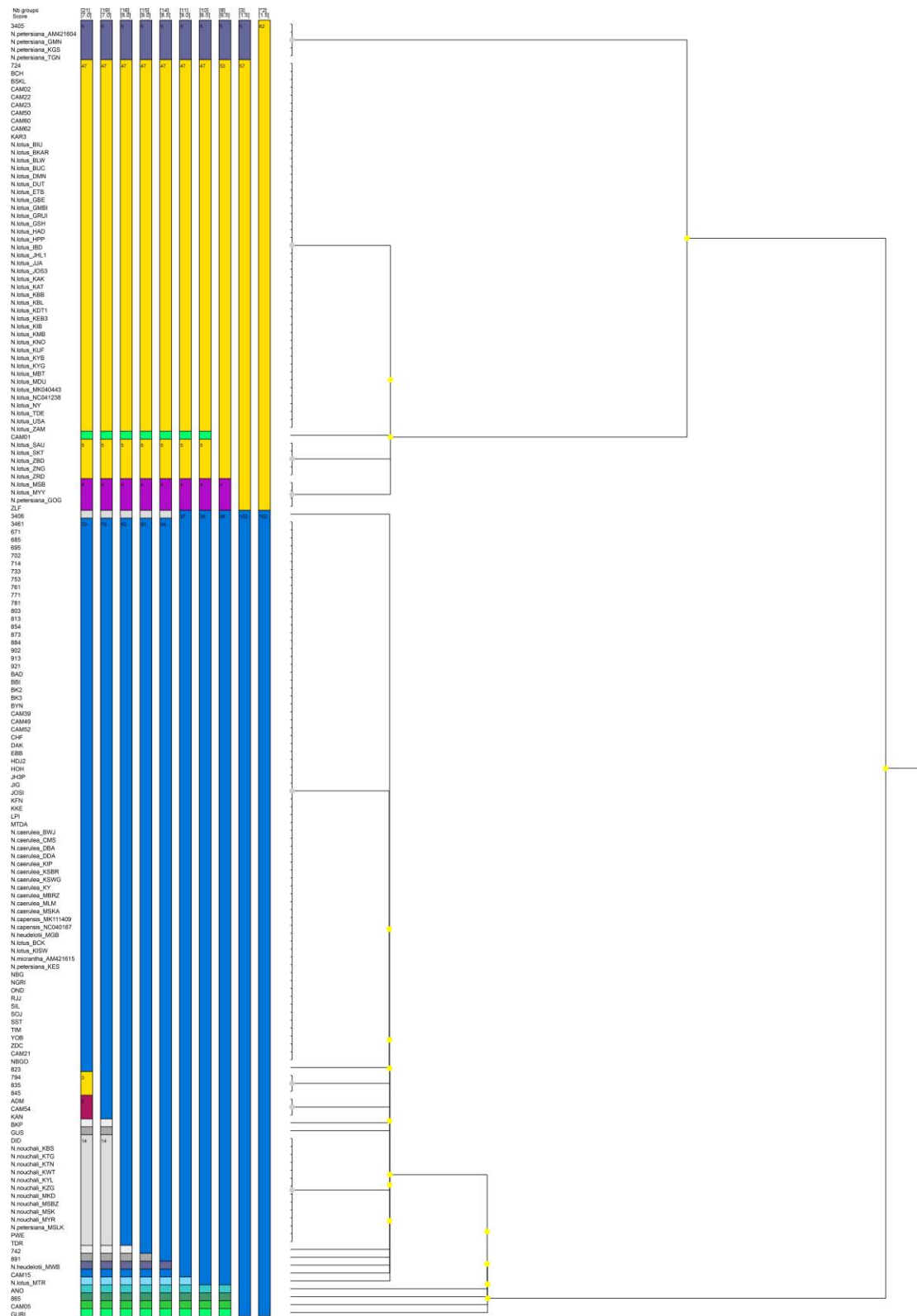
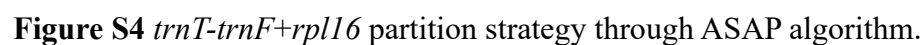**Figure S3** *rpl16* partition strategy through ASAP algorithm.

Figure S4 *trnT-trnF+rpl16* partition strategy through ASAP algorithm.
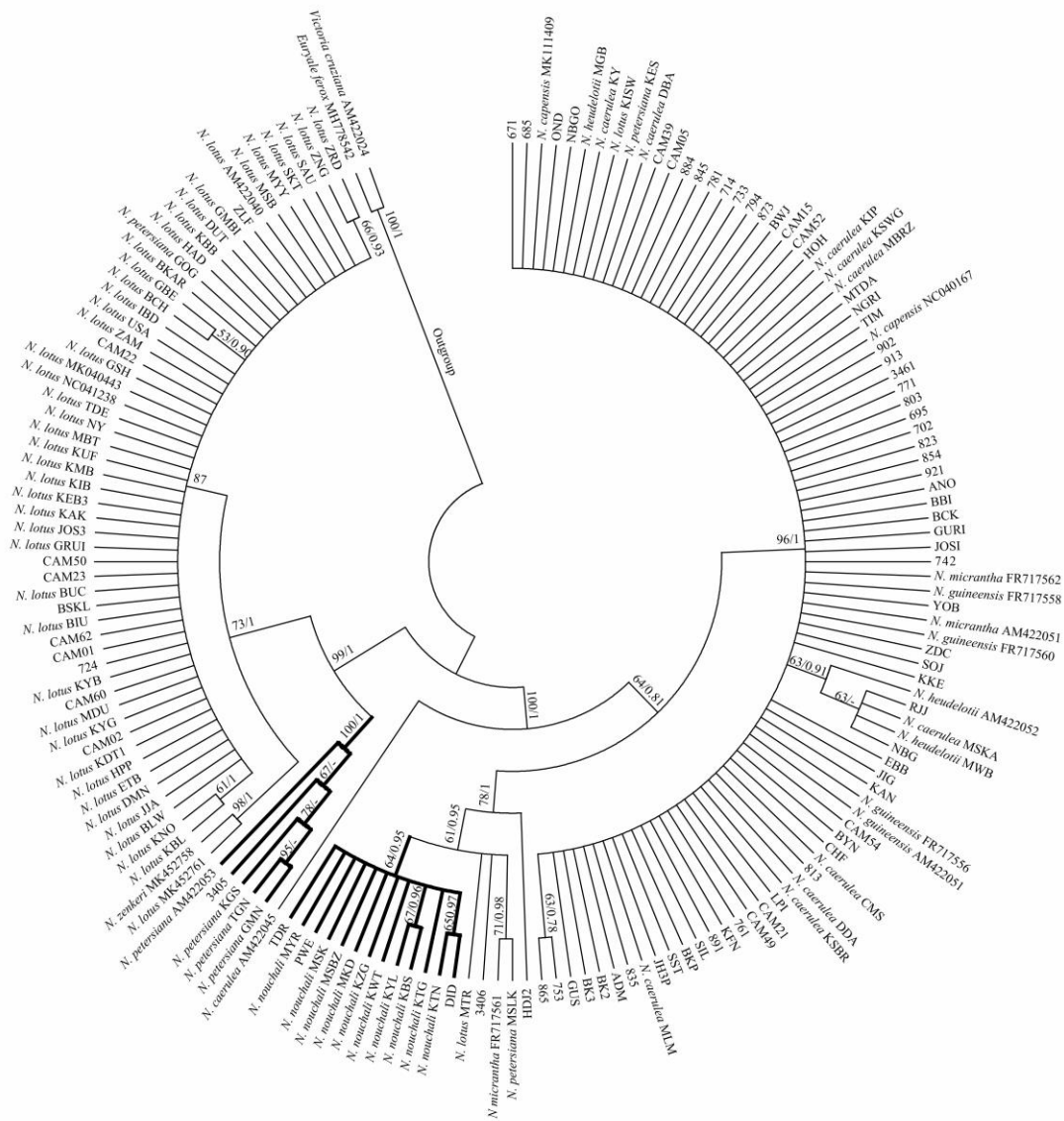
Figure S5 Phylogenetic tree constructed based on 167 *trnT-trnF* sequences of *Nymphaea*. Bootstrap values (> 50) and posterior probabilities (>0.5) based on NJ and BI analysis are shown above the branches. The rough branches mean identified species by *trnT-trnF* tree.
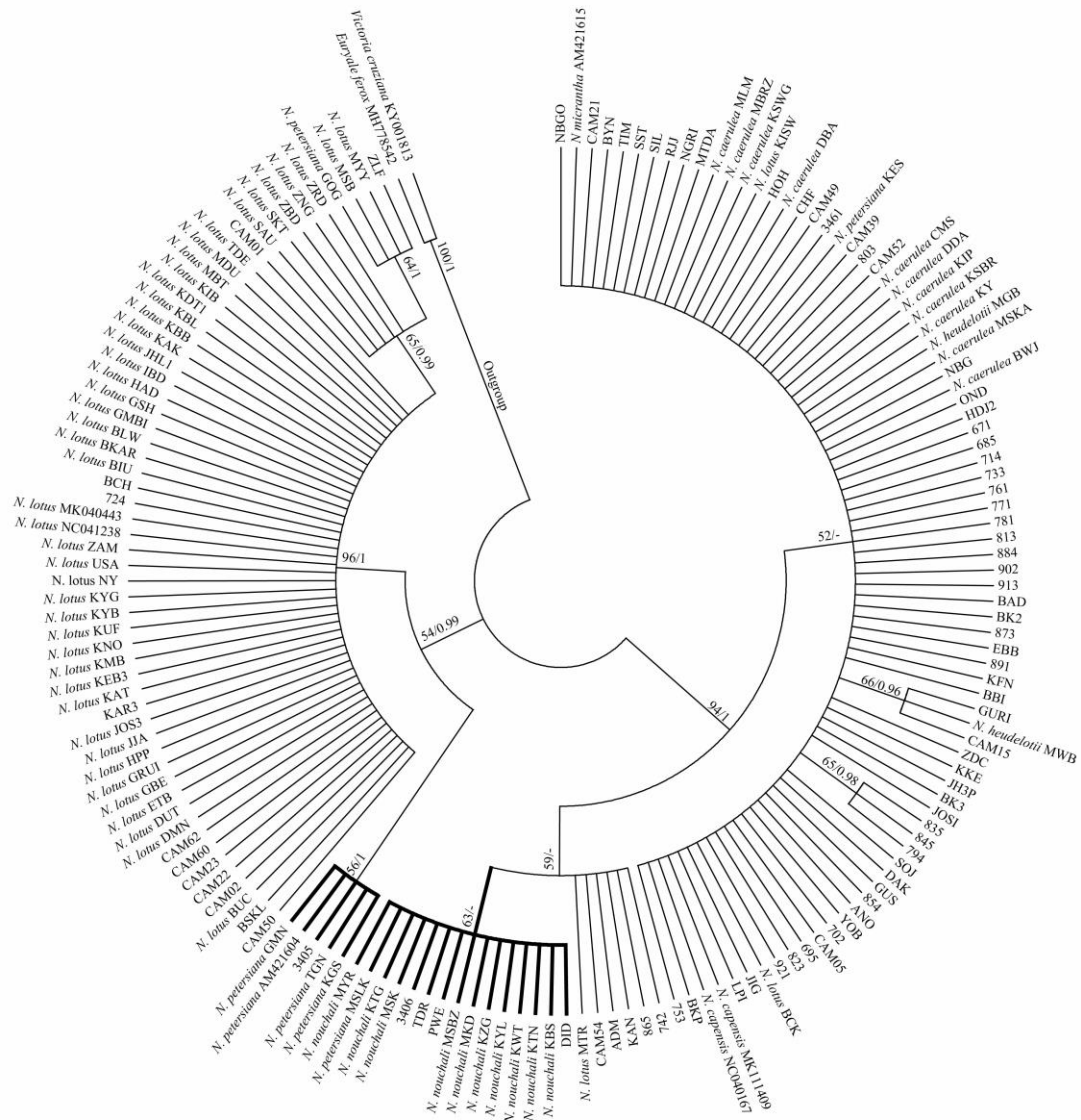
Figure S6 Phylogenetic tree constructed based on 164 *rpl16* sequences of *Nymphaea*. Bootstrap values (> 50) and posterior probabilities (>0.5) based on NJ and BI analysis are shown above the branches. The rough branches mean identified species by *rpl16* tree.
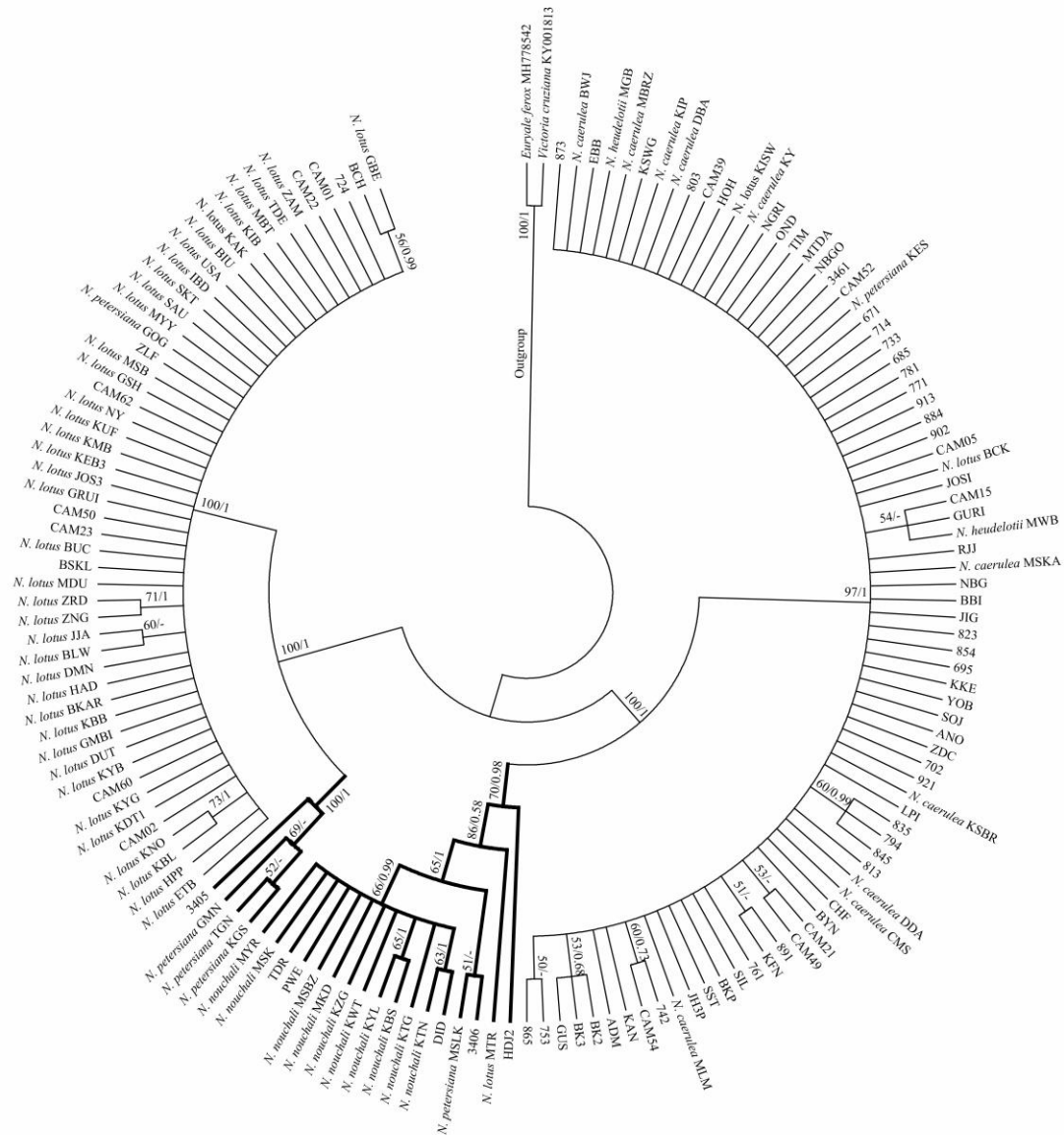
Figure S7 Phylogenetic tree constructed based on 152 *trnT-trnF+rpl16* sequences of *Nymphaea*. Bootstrap values (> 50) and posterior probabilities (>0.5) based on NJ and BI analysis are shown above the branches. The rough branches mean identified species by *trnT-trnF+rpl16* tree.