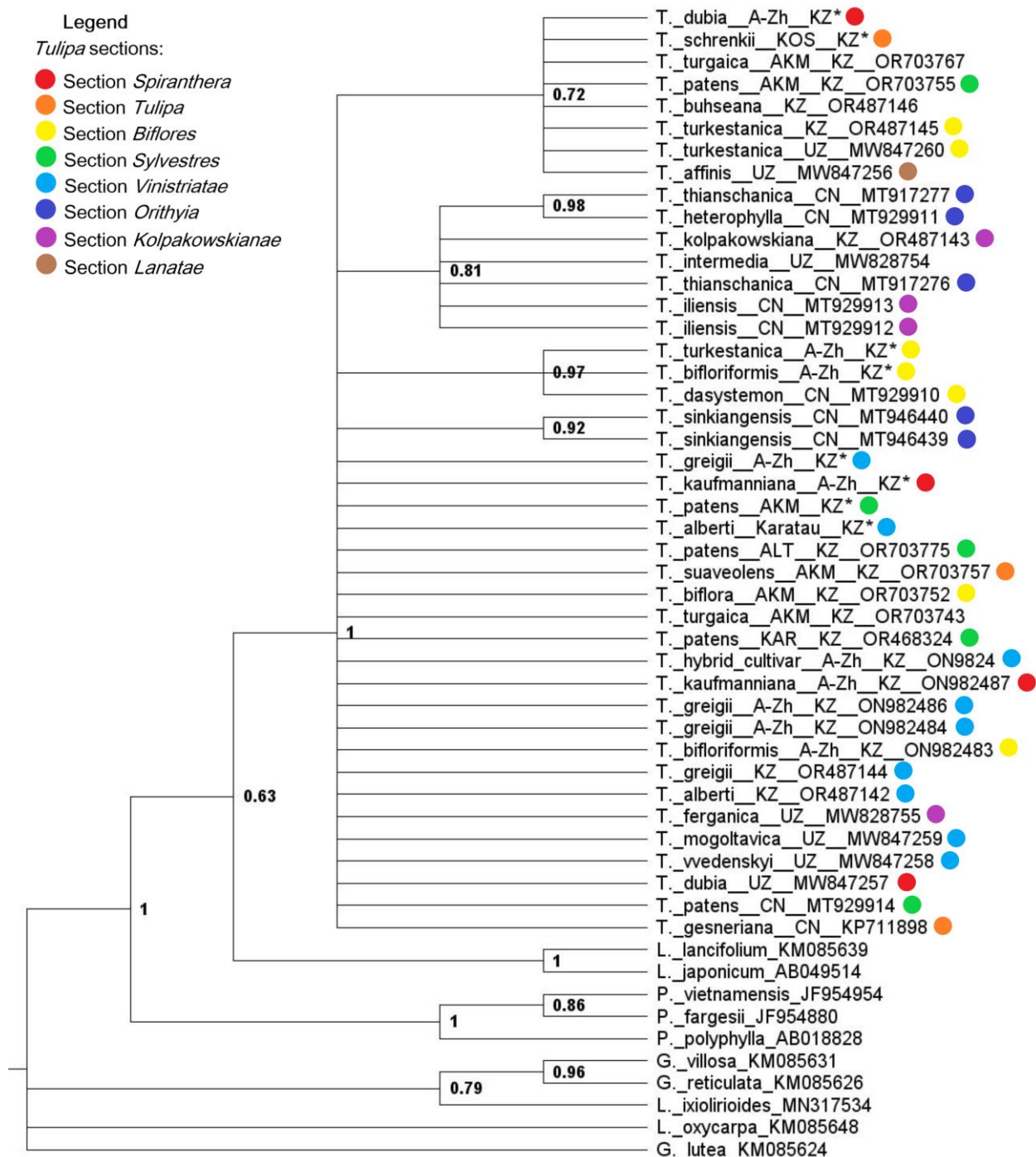
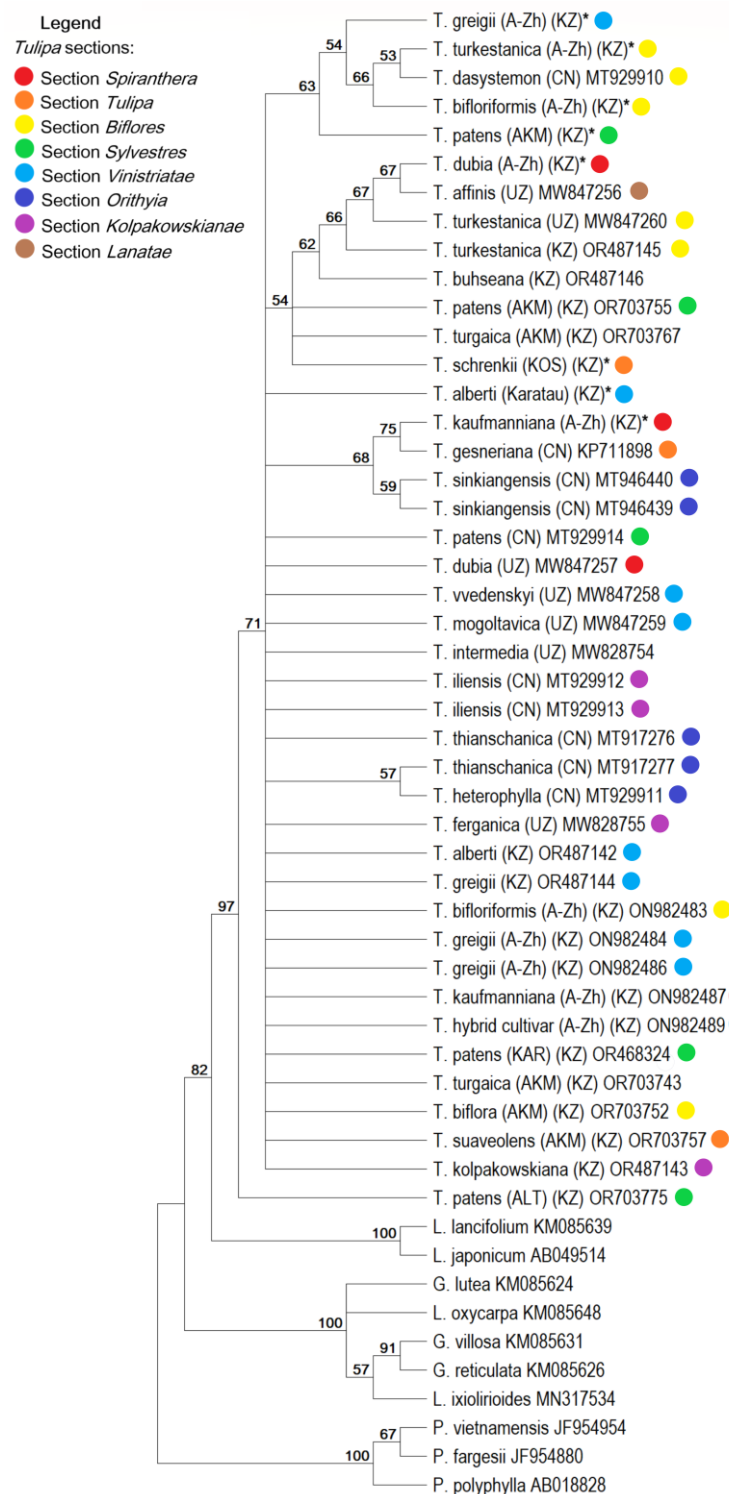


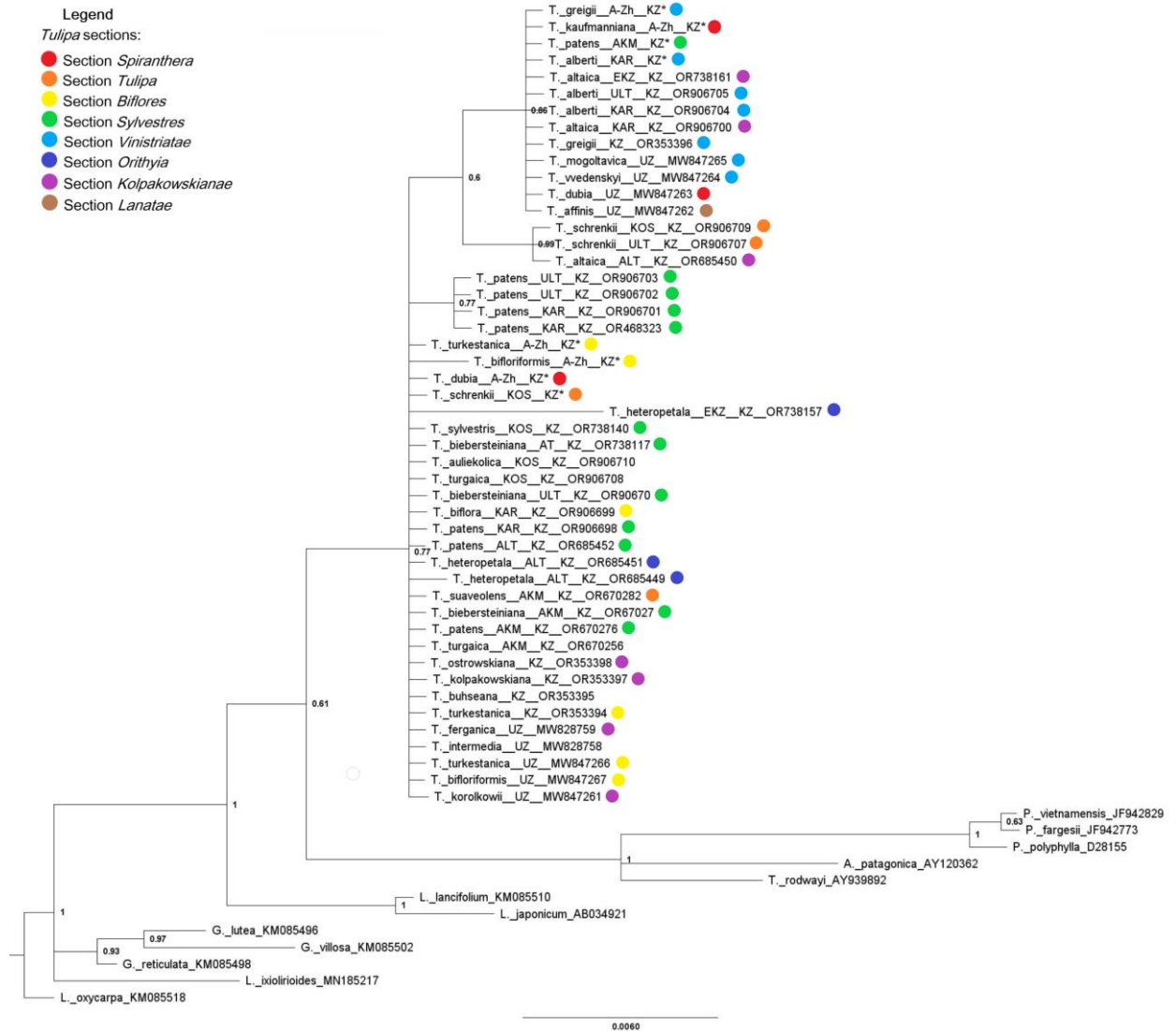
## Supplementary figure legends



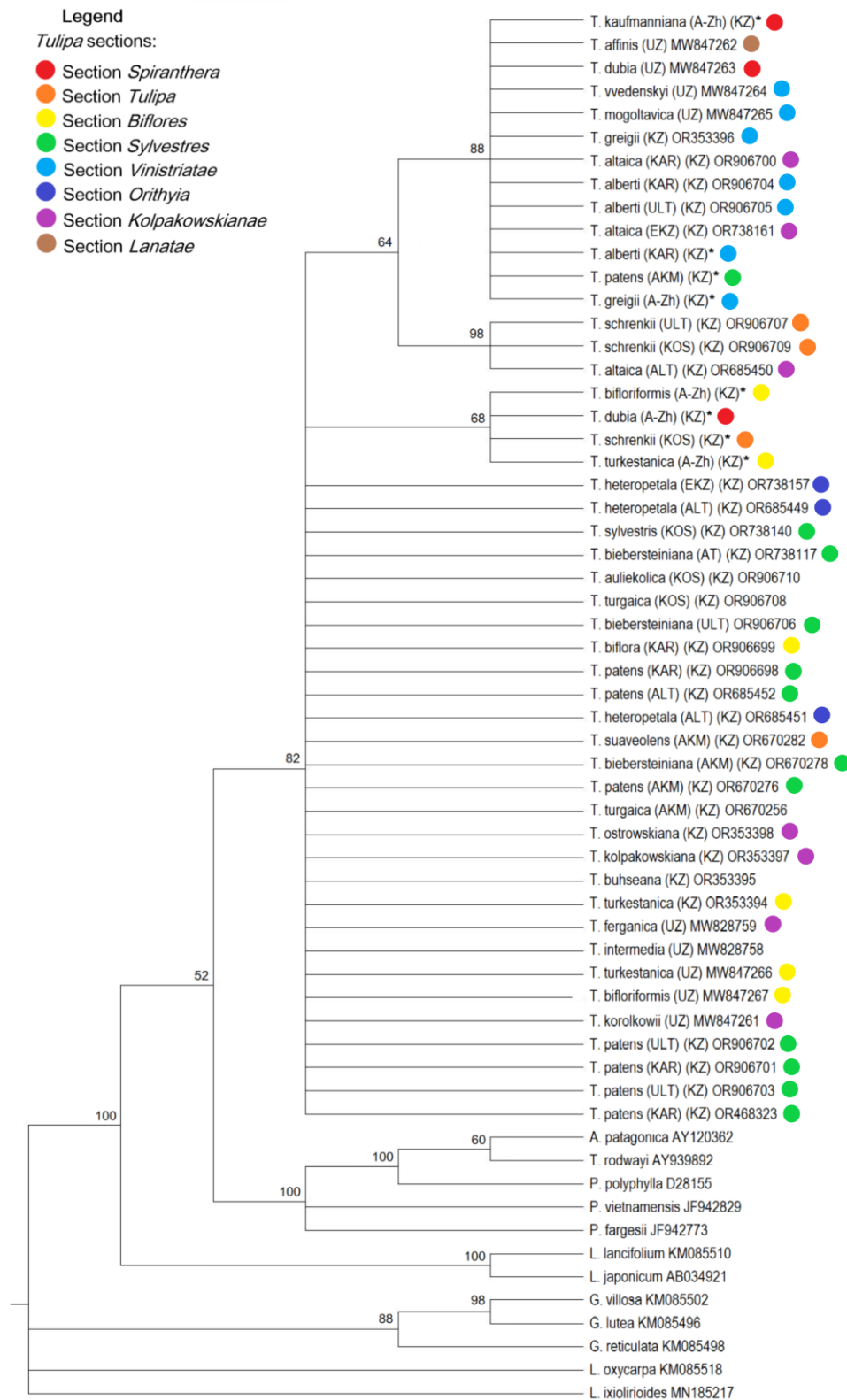
**Figure S1.** Bayesian inference 50% majority rule consensus tree based on *matK* sequences, including posterior probabilities (PP > 0.5) provided above each branch. The locations of *Tulipa* samples retrieved from the NCBI GenBank are indicated by capital letters: (KZ) Kazakhstan, (CN) China, (RU) Russia, (UZ) Uzbekistan. Tulip samples investigated in this study are marked with an asterisk (\*). Tulipa sections are represented by different colors on the tree.



**Figure S2.** ML phylogenetic tree based on a combined *matK* sequence set, including bootstrap values (BS > 50%) provided above each branch. The locations of *Tulipa* samples retrieved from the NCBI GenBank are indicated by capital letters: (KZ) Kazakhstan, (CN) China, (RU) Russia, (UZ) Uzbekistan. Tulip samples investigated in this study are marked with an asterisk (\*). Tulipa sections are represented by different colors on the tree.



**Figure S3.** Bayesian inference 50% majority rule consensus tree based on *rbcL* sequences, including posterior probabilities (PP > 0.5) provided above each branch. The locations of *Tulipa* samples retrieved from the NCBI GenBank are indicated by capital letters: (KZ) Kazakhstan, (CN) China, (RU) Russia, (UZ) Uzbekistan. Tulip samples investigated in this study are marked with an asterisk (\*). Tulipa sections are represented by different colors on the tree.



**Figure S4.** ML phylogenetic tree based on a combined *rbcL* sequence set, including bootstrap values (BS > 50%) provided above each branch. The locations of *Tulipa* samples retrieved from the NCBI GenBank are indicated by capital letters: (KZ) Kazakhstan, (CN) China, (RU) Russia, (UZ) Uzbekistan. Tulip samples investigated in this study are marked with an asterisk (\*). Tulipa sections are represented by different colors on the tree.