



N=MRCA-1Cx (pg)
(95% Confidence Interval)

Supplementary Fig. S1 - Fifty percent majority-rule consensus tree from Bayesian inference (ITS, trnS-C, matK) showing the phylogenetic relationships of the 23 investigated *Fabae* species. Posterior probabilities are indicated for each node. The ancestral genome sizes reconstructed (1Cx-values [pg]) for the most recent common ancestor (MRCA) of each clade are depicted together with the 95% confidence interval in brackets.