

Fig. S1. A maximum-likelihood tree based on 42 plastomes inferred from *trnV-rps12* region.

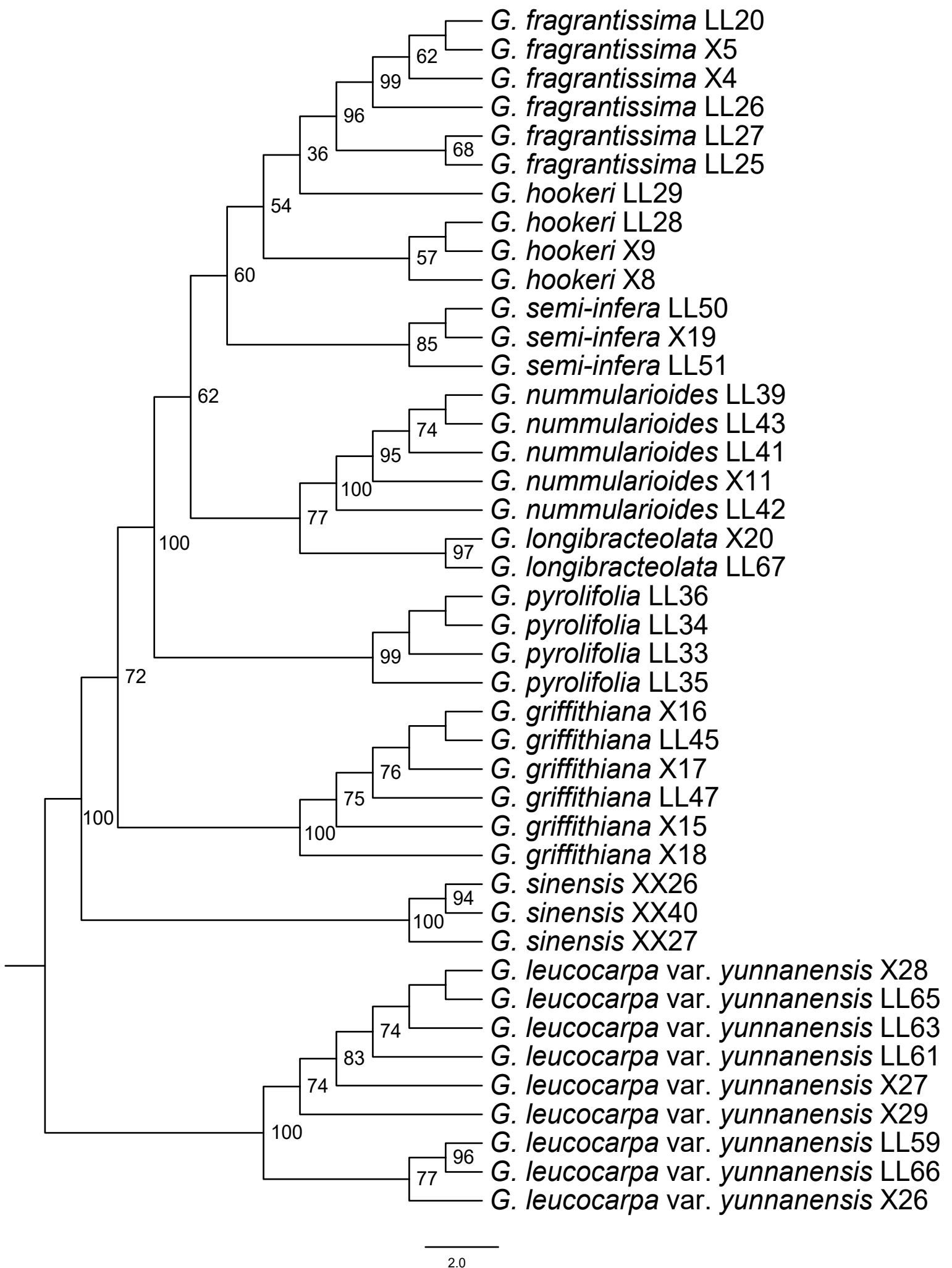


Fig. S2. A maximum-likelihood tree based on 42 plastomes inferred from *trnQ-psaA* region.

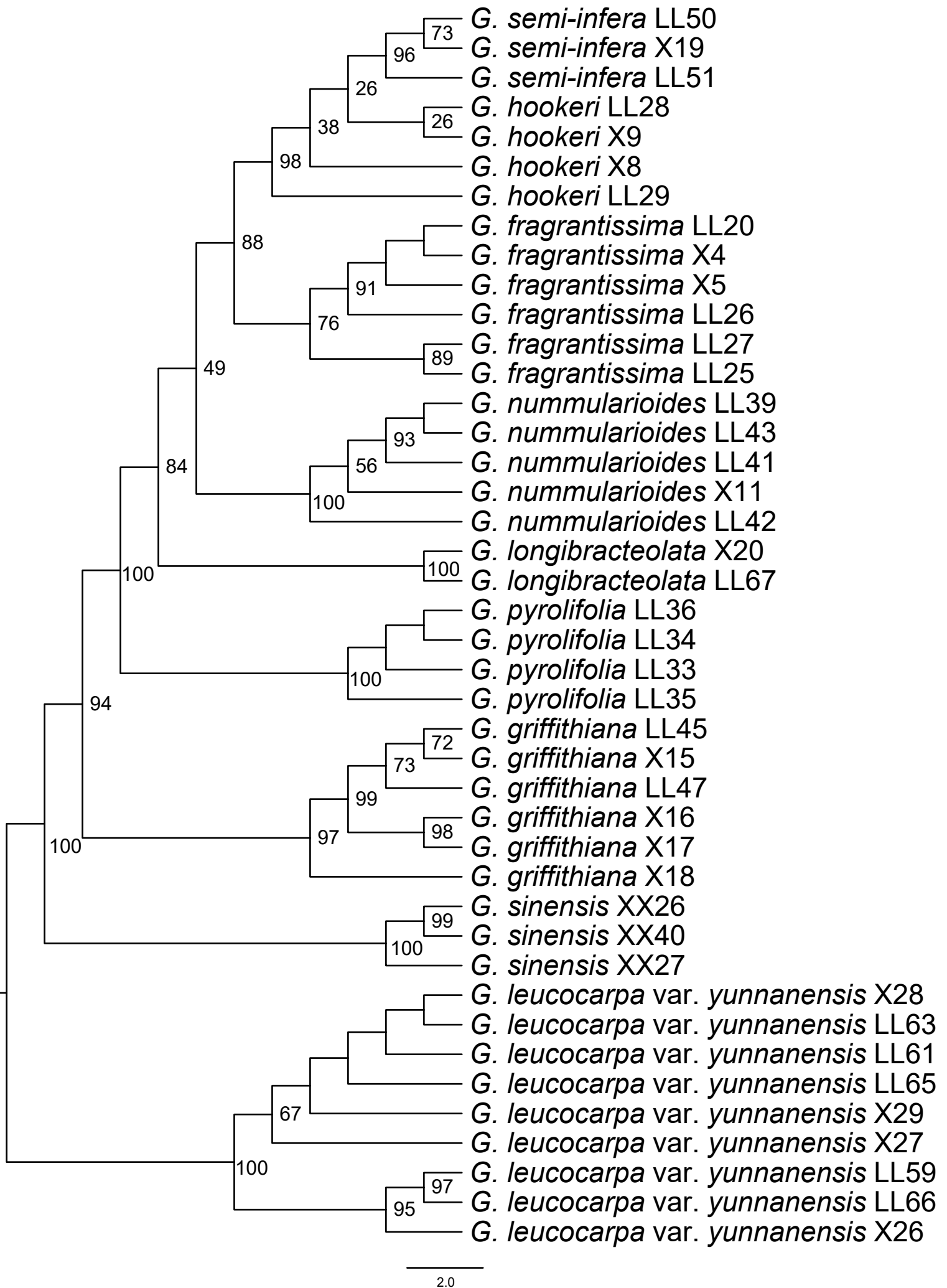
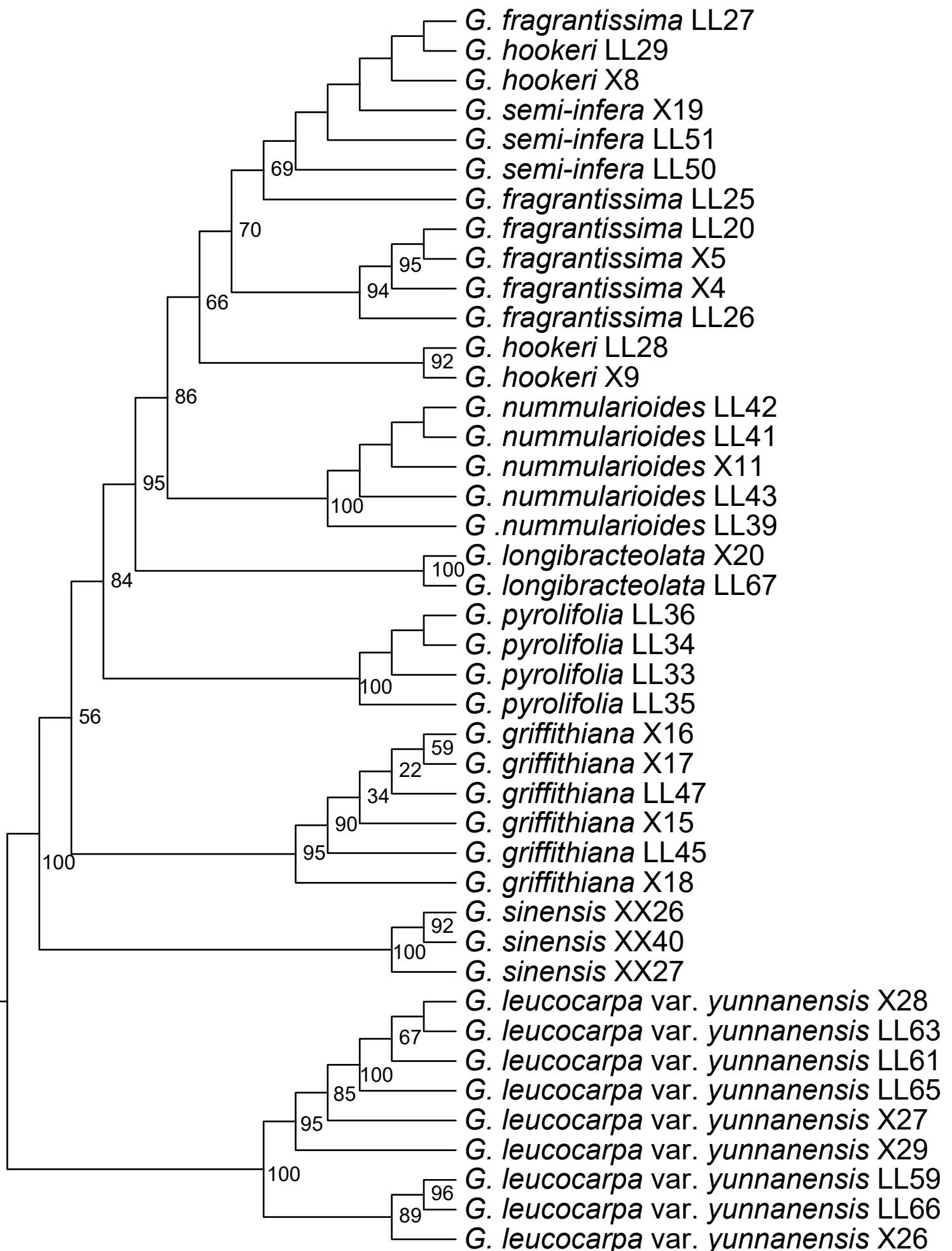
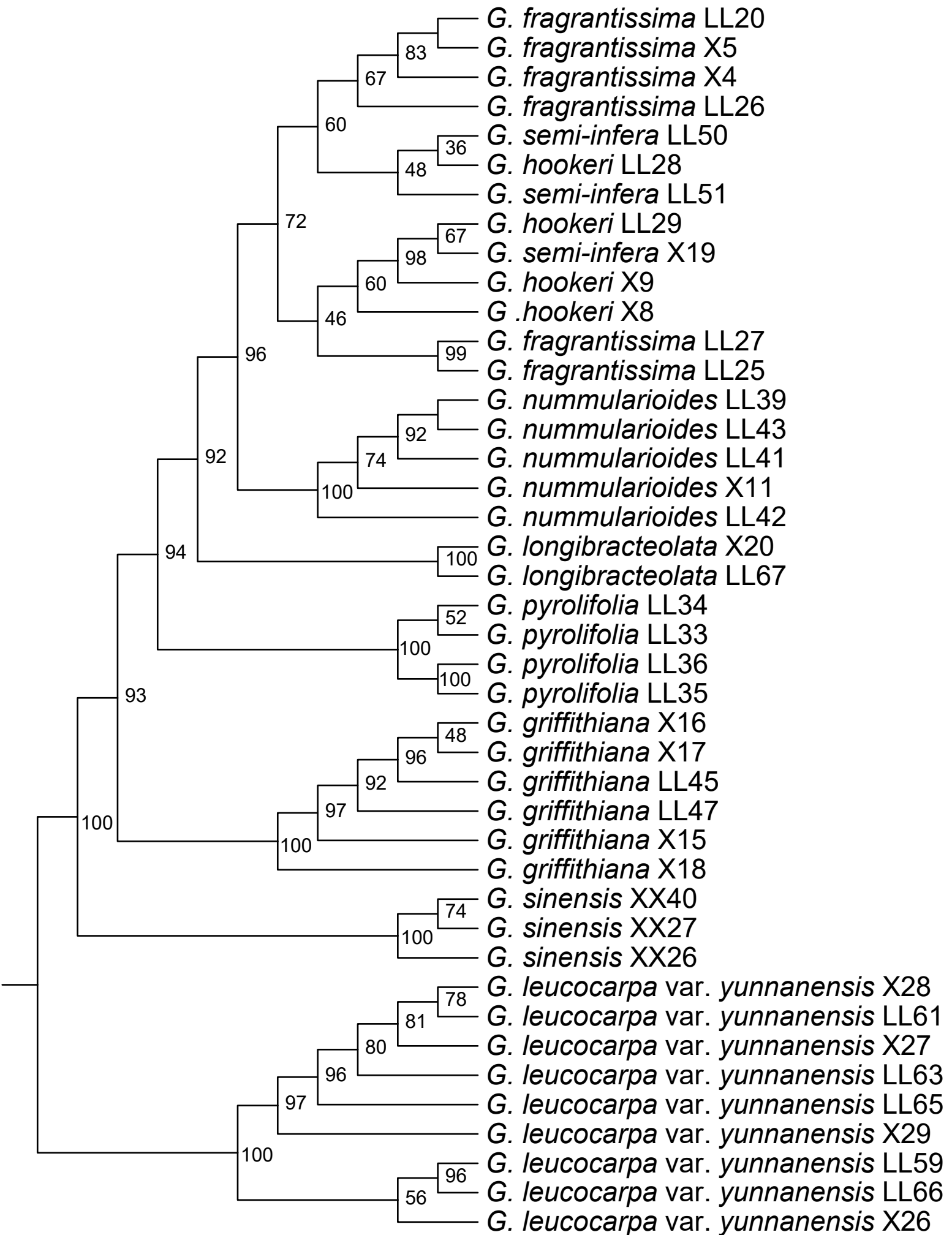


Fig. S3. A maximum-likelihood tree based on 42 plastomes inferred from *ndhF* region.



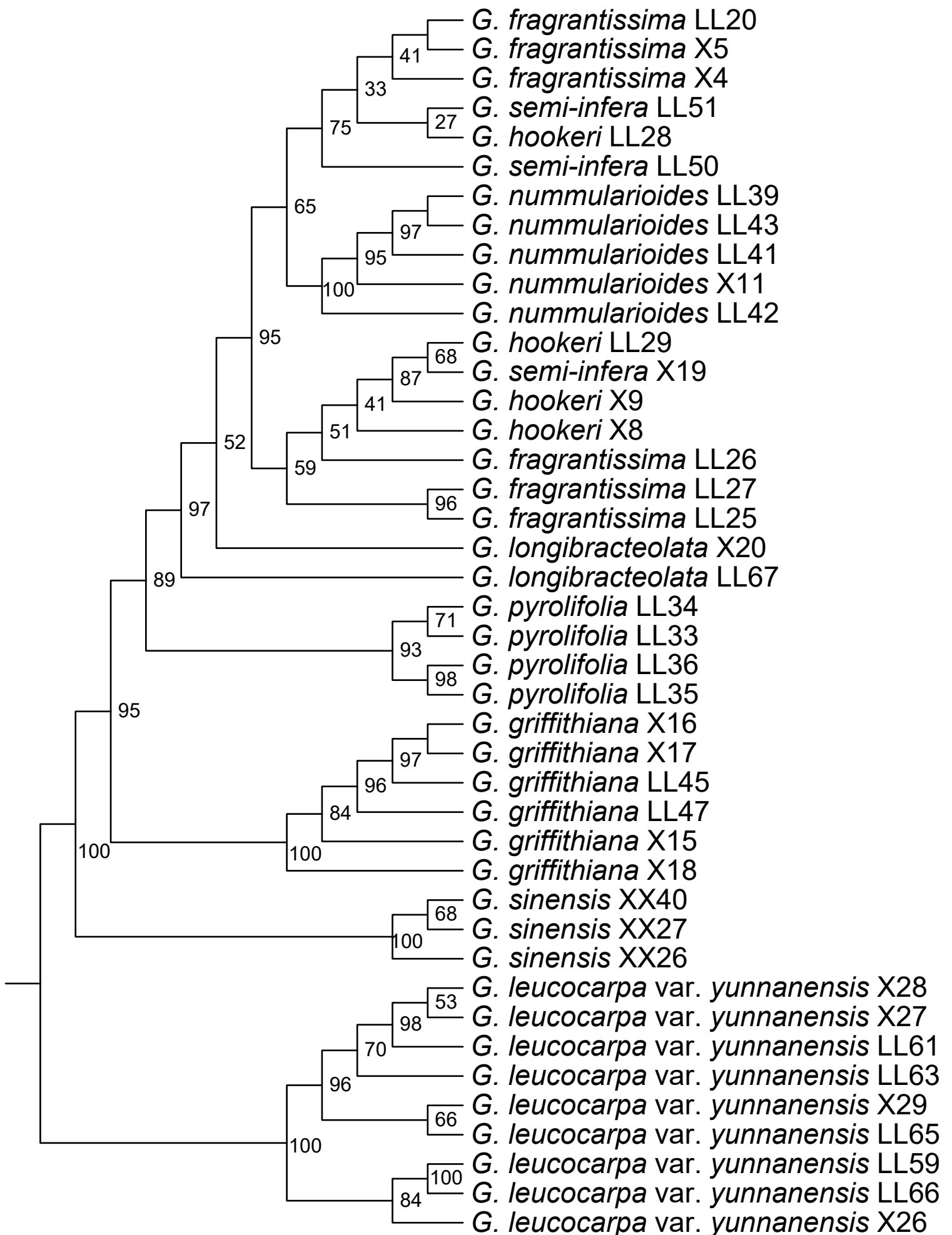
2.0

Fig. S4. A maximum-likelihood tree based on 42 plastomes inferred from *ycf3-trnK* region.



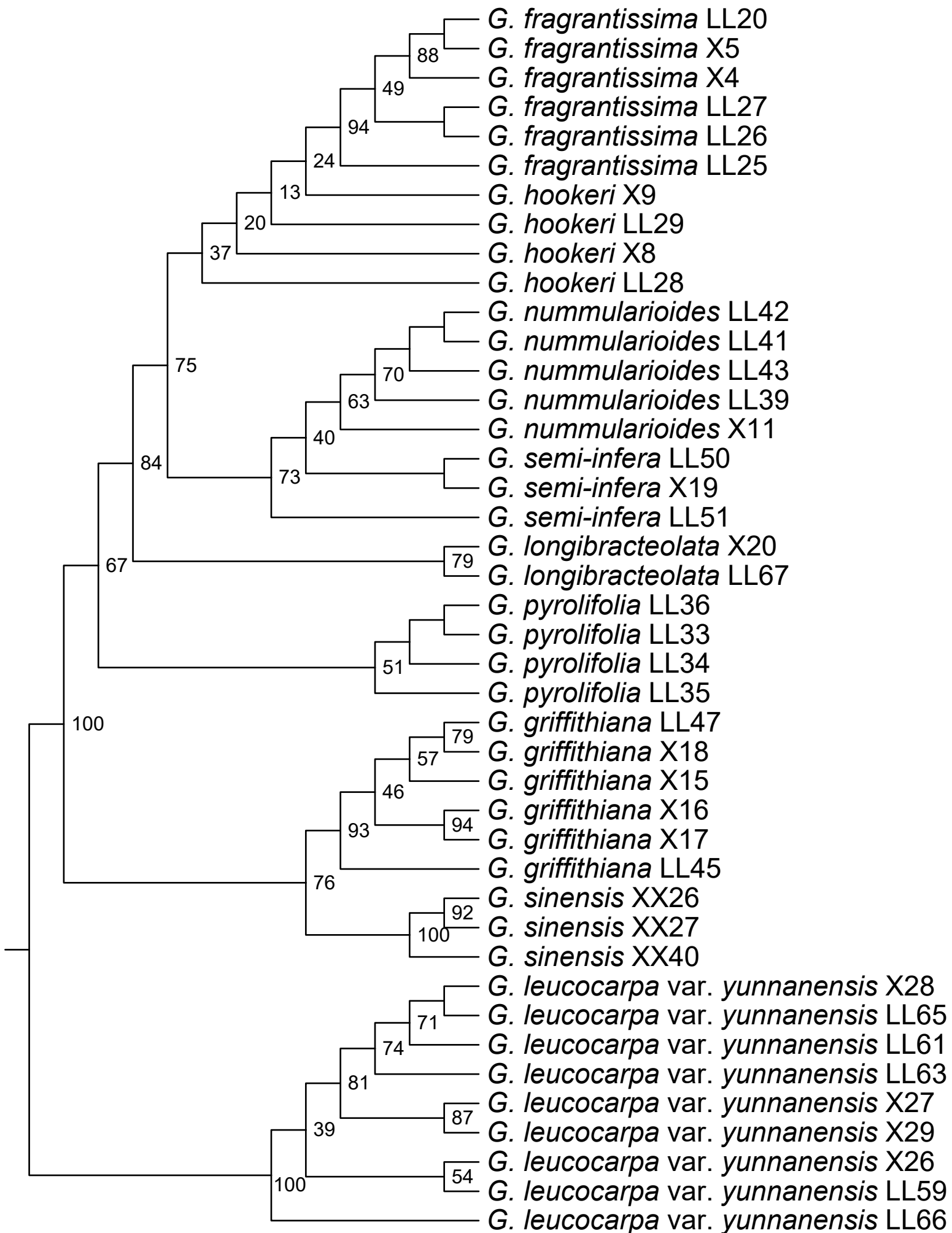
2.0

Fig. S5. A maximum-likelihood tree based on 42 plastomes inferred from *psal-trnM* region.



2.0

Fig. S6. A maximum-likelihood tree based on 42 plastomes inferred from *rps3-rpl16* region.



2.0

Fig. S7. A maximum-likelihood tree based on 42 plastomes inferred from *infA* region.