

Table S1. Contig names and lengths.

Contig	Length(bp)	Contig	Length(bp)
O1	68195	F1	152686
O2	60869	F2	53247
O3	54341	F3	48635
O4	50200	F4	19830
O5	36146	F5	9665
O6	15712	F6	8247
O7	5031	F7	4754
O8	1664	F8	836
O9	135		

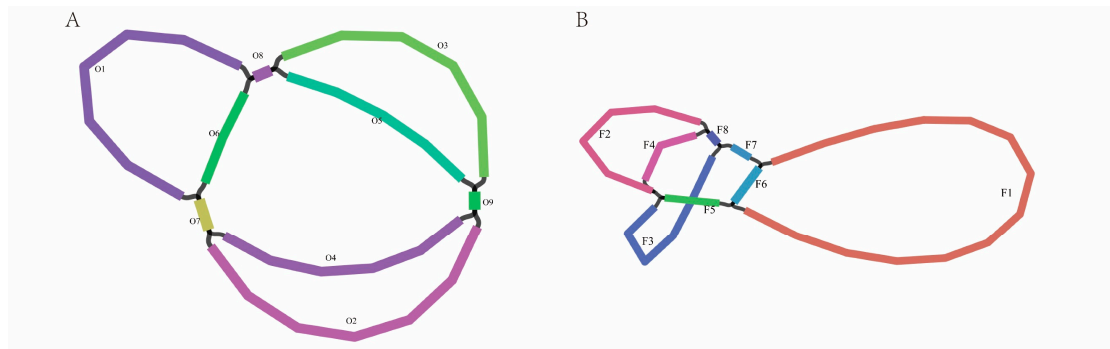


Figure S1. Mitochondrial genome bandage map. A. Zhongmu NO.1 mitochondrial genome. B. Zhongmu NO.4 mitochondrial genome.

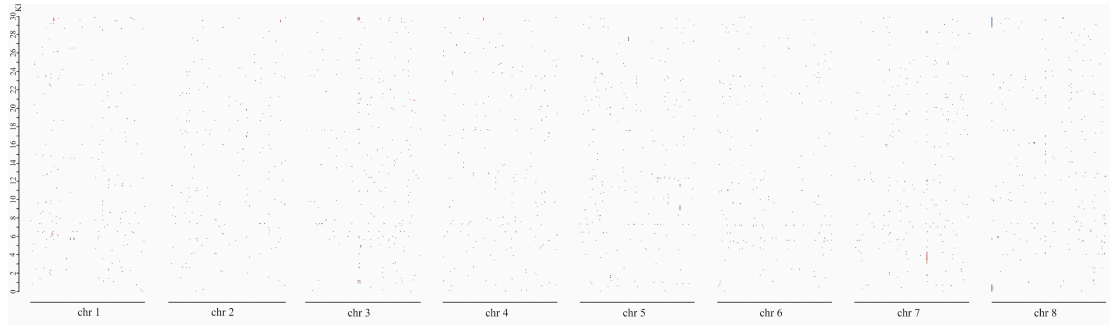


Figure S2. Distribution of mtDNA fragments on the nuclear chromosomes of *Medicago sativa*. The mtDNA fragments were plotted against the eight nuclear chromosomes of the *M. sativa* cultivar 'Zhongmu No.1' (x-axis) and Zhongmu NO.1 mitochondrial genome (y-axis). The red and blue colors indicate nupDNA fragments on the positive and negative strands of the nuclear chromosomes, respectively.

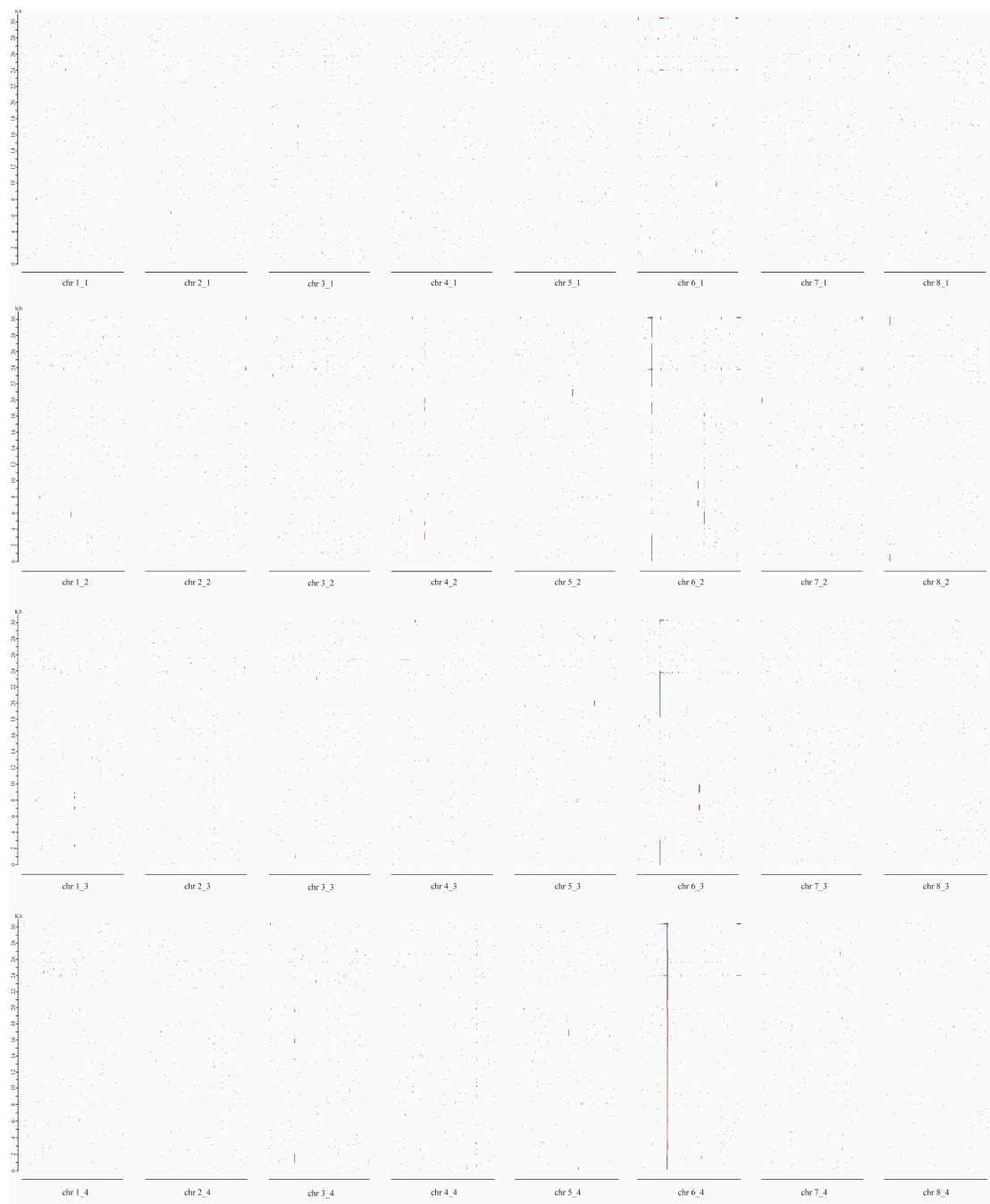


Figure S3. Distribution of mtDNA fragments on the nuclear chromosomes of *Medicago sativa*. The mtDNA fragments were plotted against the Thirty-two nuclear chromosomes of the *M. sativa* cultivar 'Zhongmu No.4' (x-axis) and Zhongmu NO.4 mitochondrial genome (y-axis). The red and blue colors indicate mtDNA fragments on the positive and negative strands of the nuclear chromosomes, respectively.

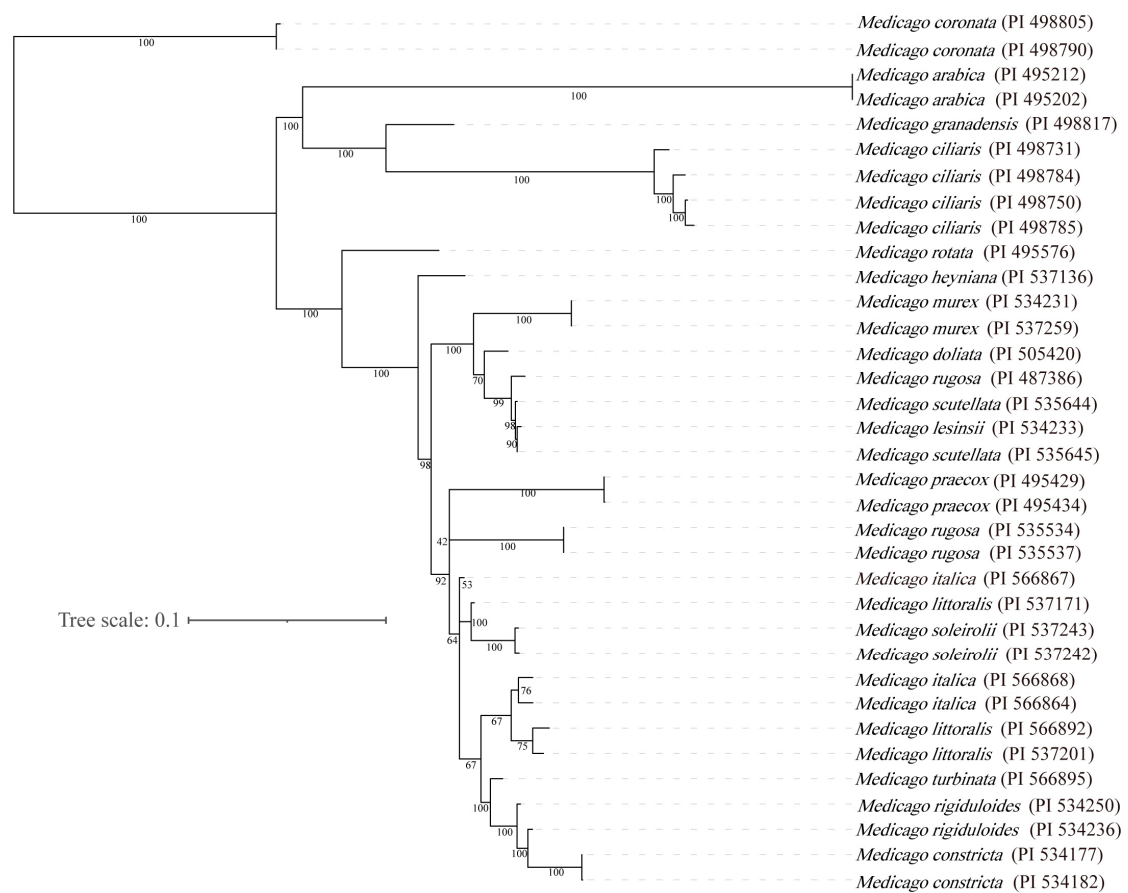


Figure S4. Maximum likelihood phylogenetic tree with bootstrap values.

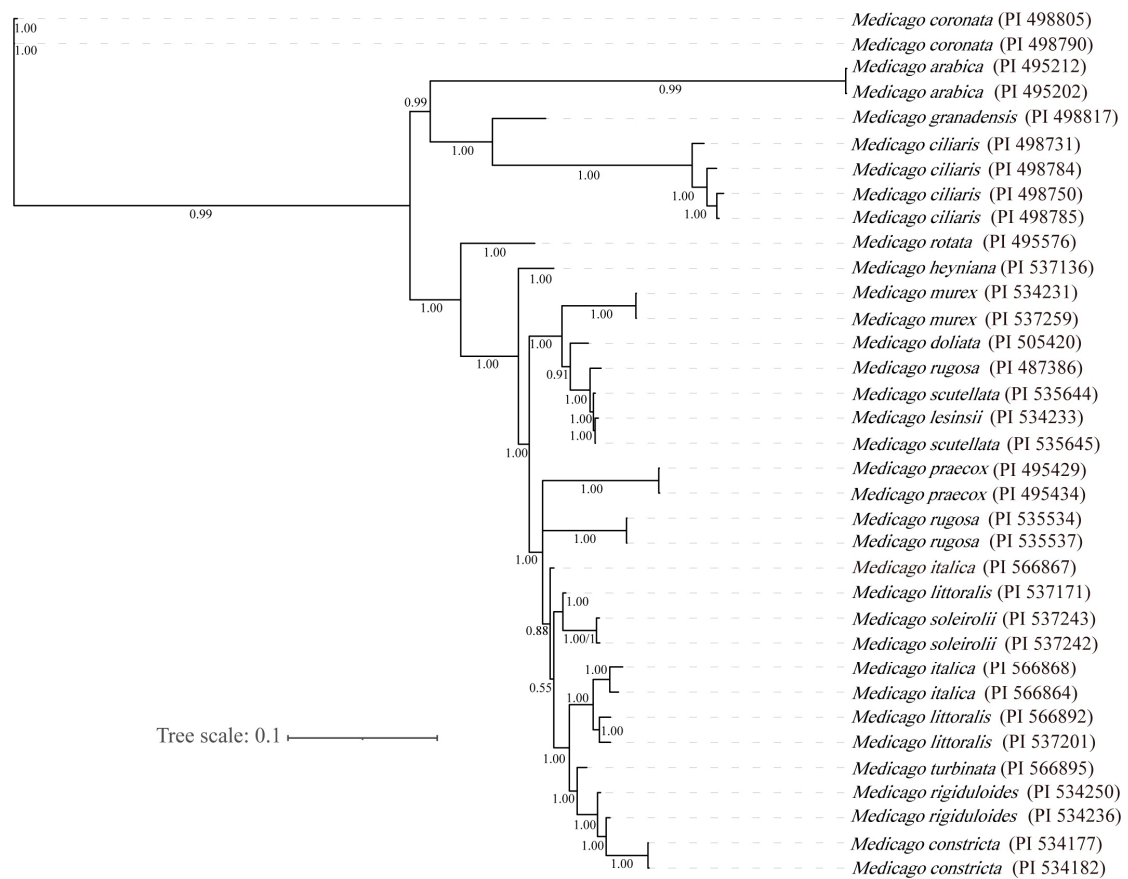


Figure S5. Bayesian phylogenetic tree with posterior probabilities.