Supplementary Material

Table A: reads per sample before and after adapter removal and quality trim (phred score threshold of 20)

sample	total reads	reads kept after quality trimming	% reads kept
Medicago italica	603490	529164	88%
Medicago sativa	852870	620087	73%
Medicago medicaginoides	689712	606195	88%
Melilotus neapolitanus	1107464	909632	82%
Melilotus sulcatus	1622968	1192313	73%

Methods A

Sequences of four additional species of *Medicago* (*M. littoralis*, *M. papillosa*, *M. marina* and *M. prostrata*) were produced following the protocol presented in the Methods section. Multiple individuals were sampled for *M. papillosa* and *M. prostrata,* in the latter case using mostly herbarium preserved specimens. Following sequence assembly, the program CLC-mapper (CLC Bio, Aarhus, Denmark) was used to map reads to the assembled sequence of genes 7 (Medtr2g038270.1), 9 (Medtr3g079830.1), 48 (Medtr3g113790.1) and 50 (Medtr3g113960.1). From the mapped reads, alleles were phased using the program Samtools phase (Li et al., 2009) and phased reads were re-assembled into contigs using CLC-assembler and aligned in Geneious Pro (v.5.3.6). Model testing was done using the reversible-jump

mcmc implemented in MrBayes v.3.1.2 (Huelsenbeck and Ronquist, 2005) and gene trees were reconstructed in BEAST v1.8.0. (Drummond and Rambaut, 2007).

Supplementary figure legends:

Calibrated BEAST trees of genes 7 (Figure A), 9 (Figure B), 48 (Figure C) and 50 (Figure D) showing posterior probability values for each node.

Supplementary figures:

Figure A

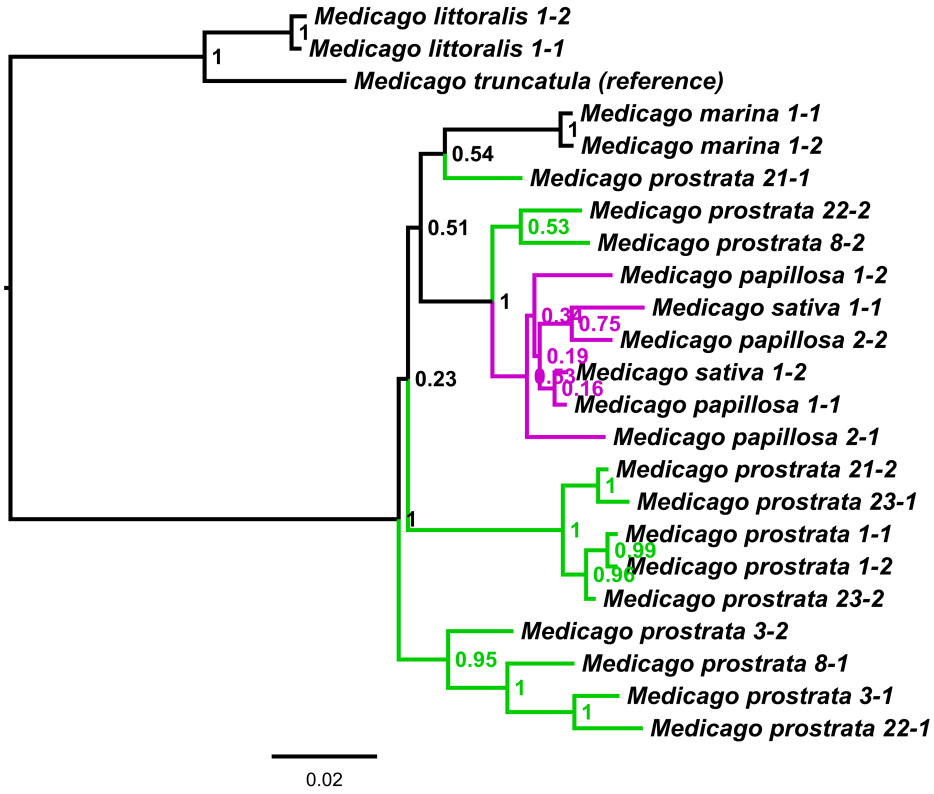


Figure B

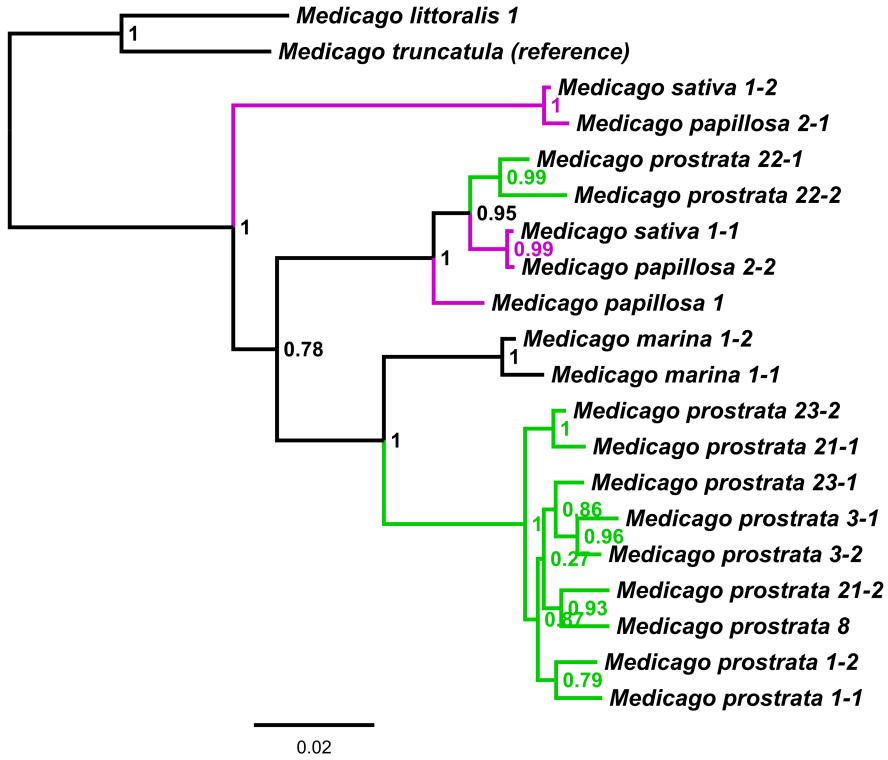


Figure C

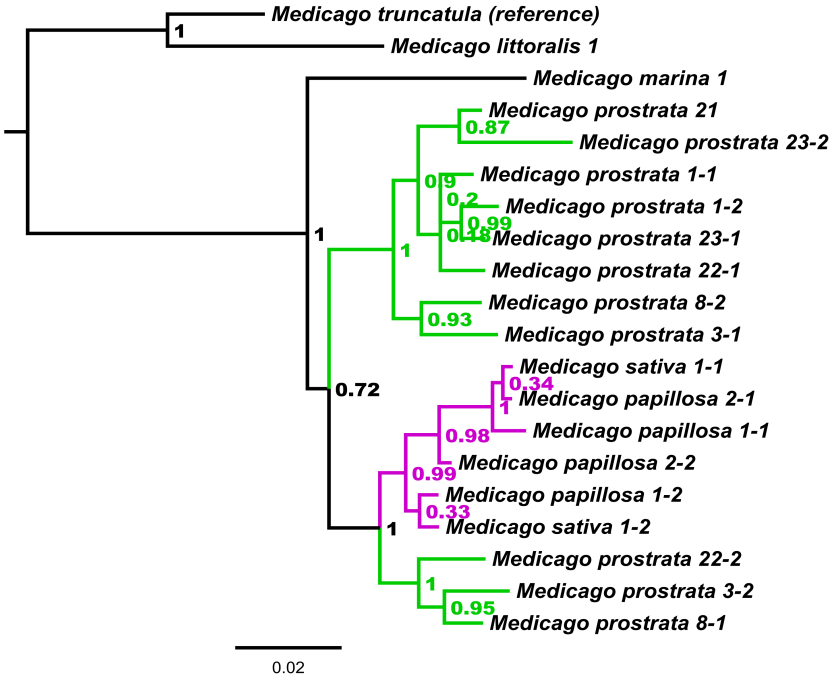
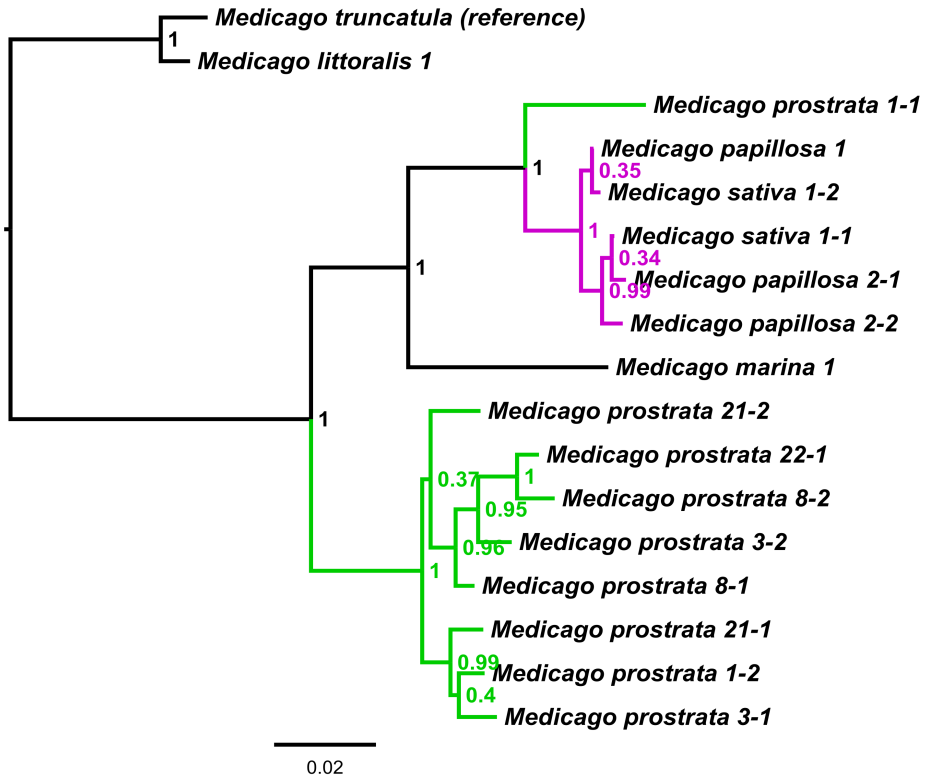


Figure D


Medicago truncatula (reference)
Medicago littoralis 1
Medicago prostrata 1-1
Medicago papillosa 1
Medicago sativa 1-2
Medicago sativa 1-1
Medicago papillosa 2-1
Medicago papillosa 2-2
Medicago marina 1
Medicago prostrata 21-2
Medicago prostrata 22-1
Medicago prostrata 8-2
Medicago prostrata 3-2
Medicago prostrata 8-1
Medicago prostrata 21-1
Medicago prostrata 1-2
Medicago prostrata 3-1
1
0.35
1
0.34
0.99
1
1
0.37
1
0.95
0.96
1
0.99
0.4
0.02