Genomic characterization of the LEED..PEEDs, a gene family unique to the *Medicago* lineage

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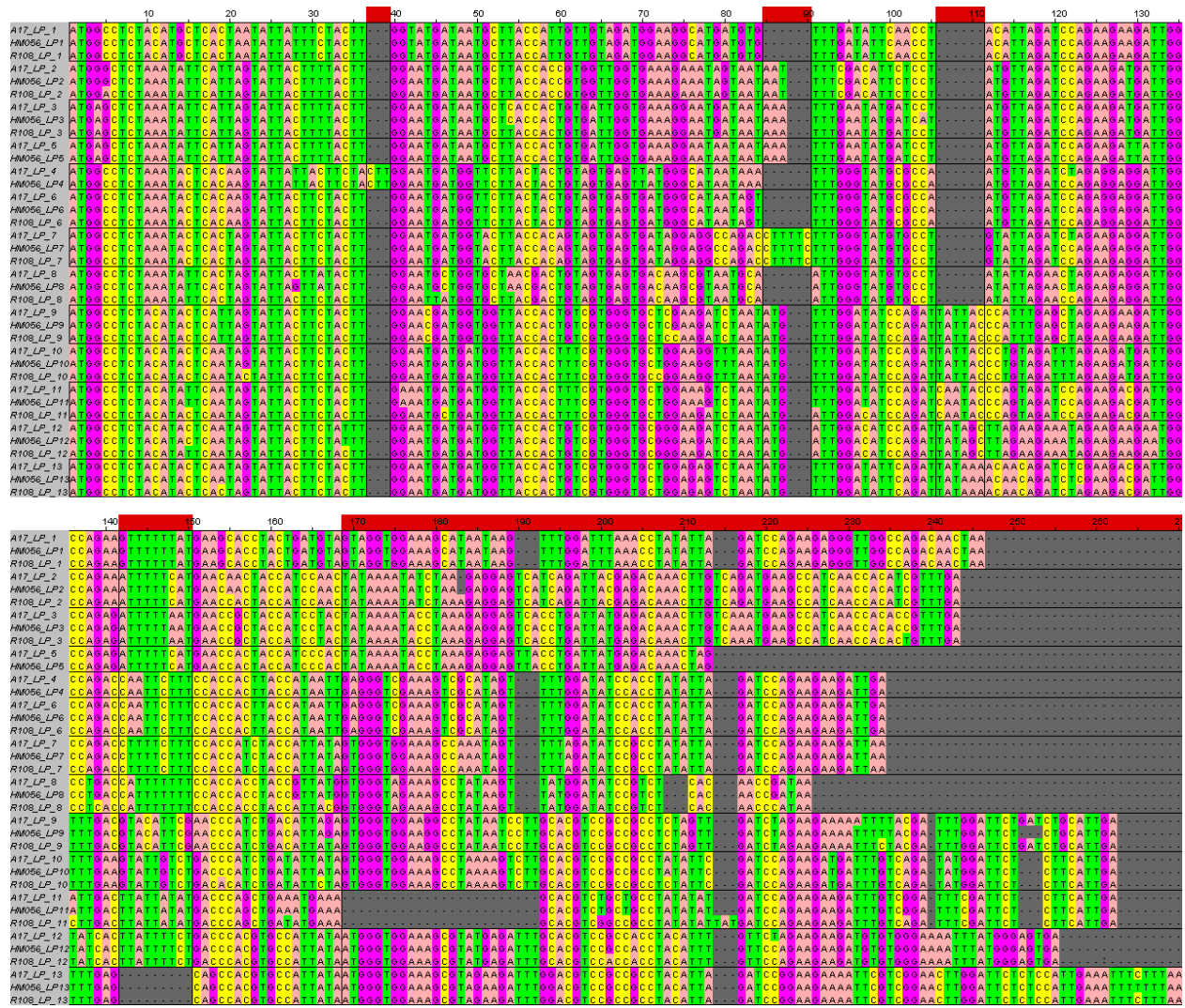[*]Department of Plant Biology, University of Minnesota, Saint Paul, MN 55108

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**Figure S1 Aligned LP DNA sequences from A17, HM056 and R108.** Columns that were omitted for the phylogenetic analysis are highlighted with red headers. Phylogenetic trees were based on the remaining 144 nucleotides.

D. I. Trujillo, K. A. T. Silverstein, and N. D. Young
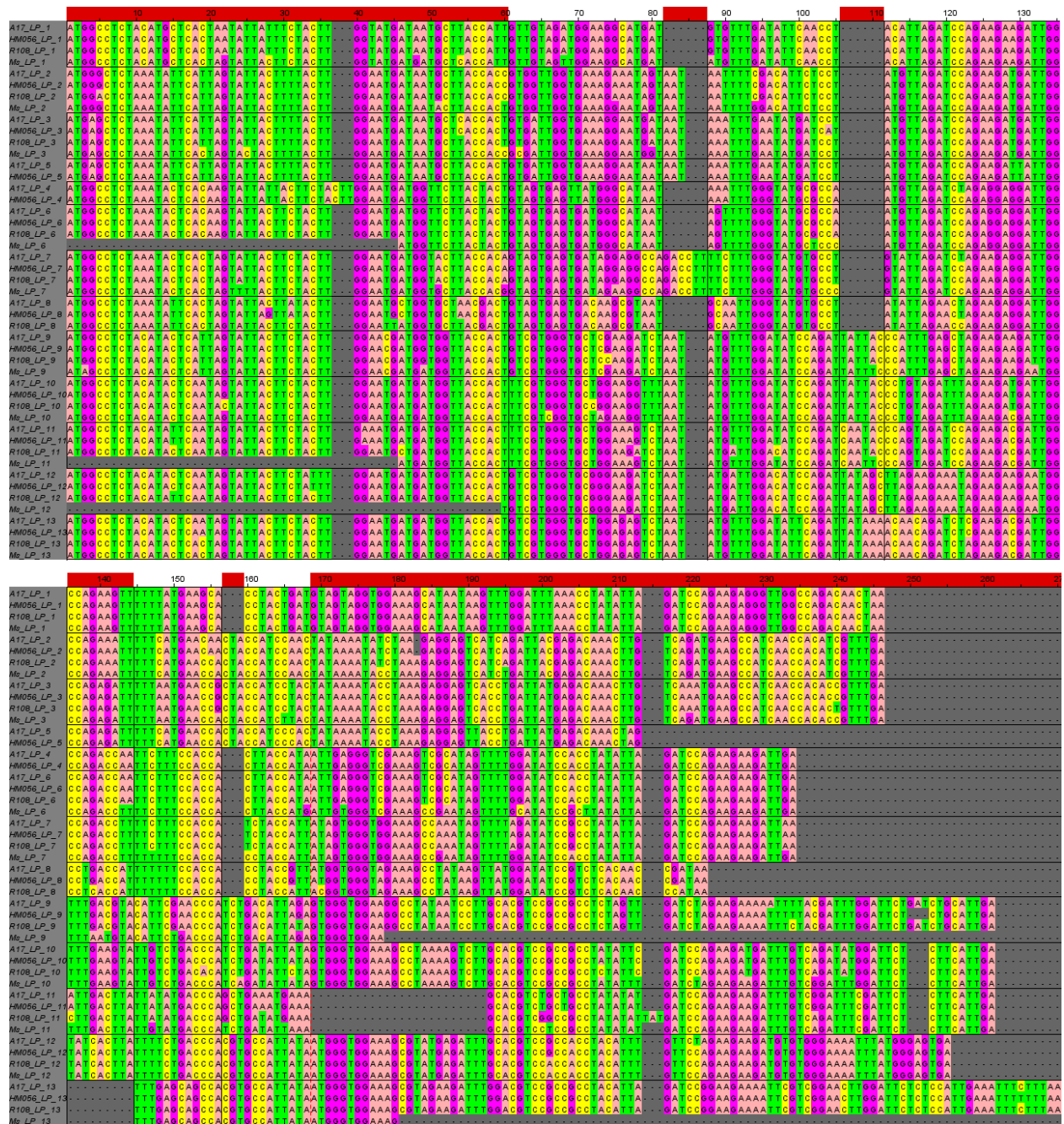
Figure S2   Aligned LP DNA sequences from A17, HM056, R108 and *M. sativa*. Columns that were omitted for the phylogenetic analysis are highlighted with red headers. Phylogenetic trees were based on the remaining 87 nucleotides.
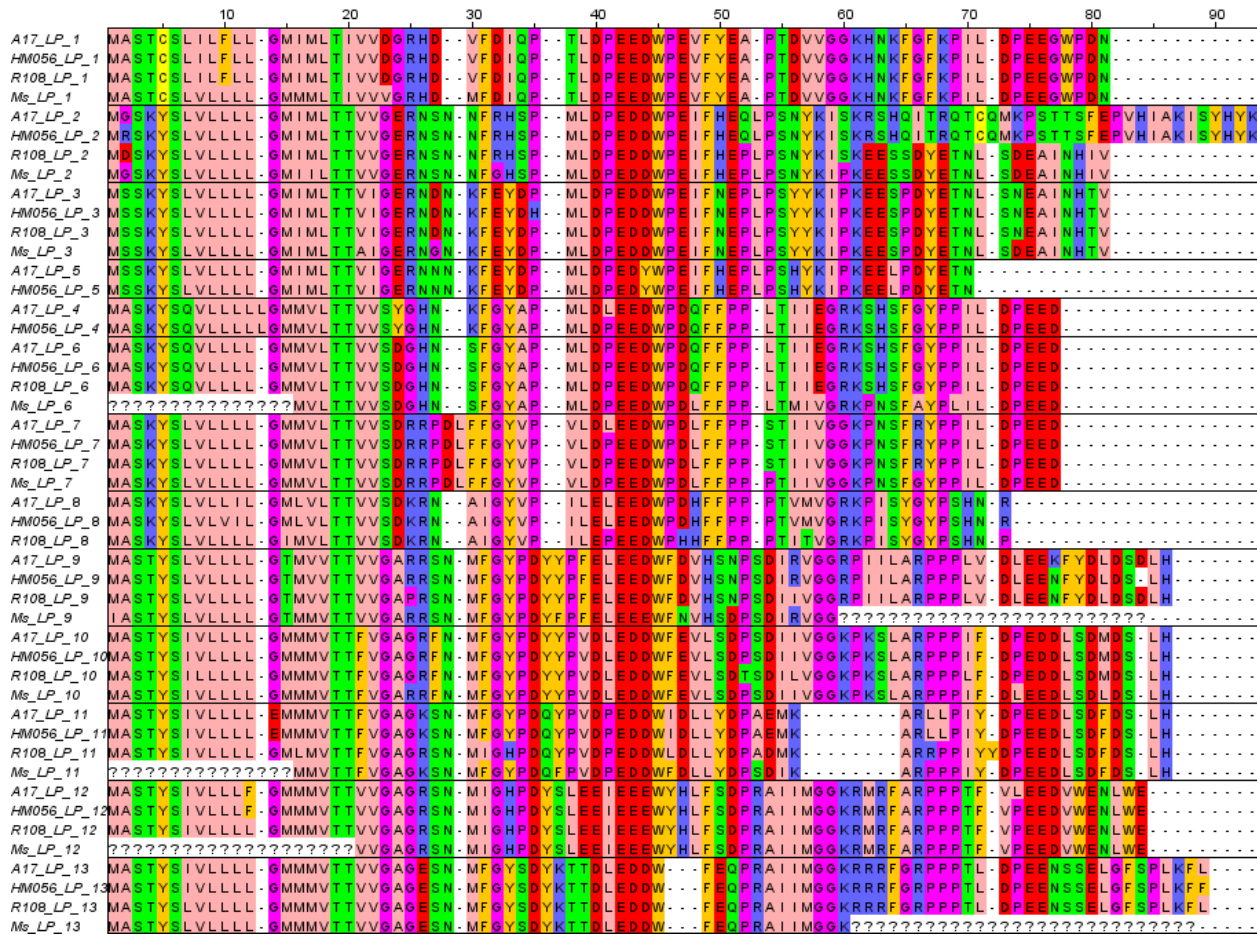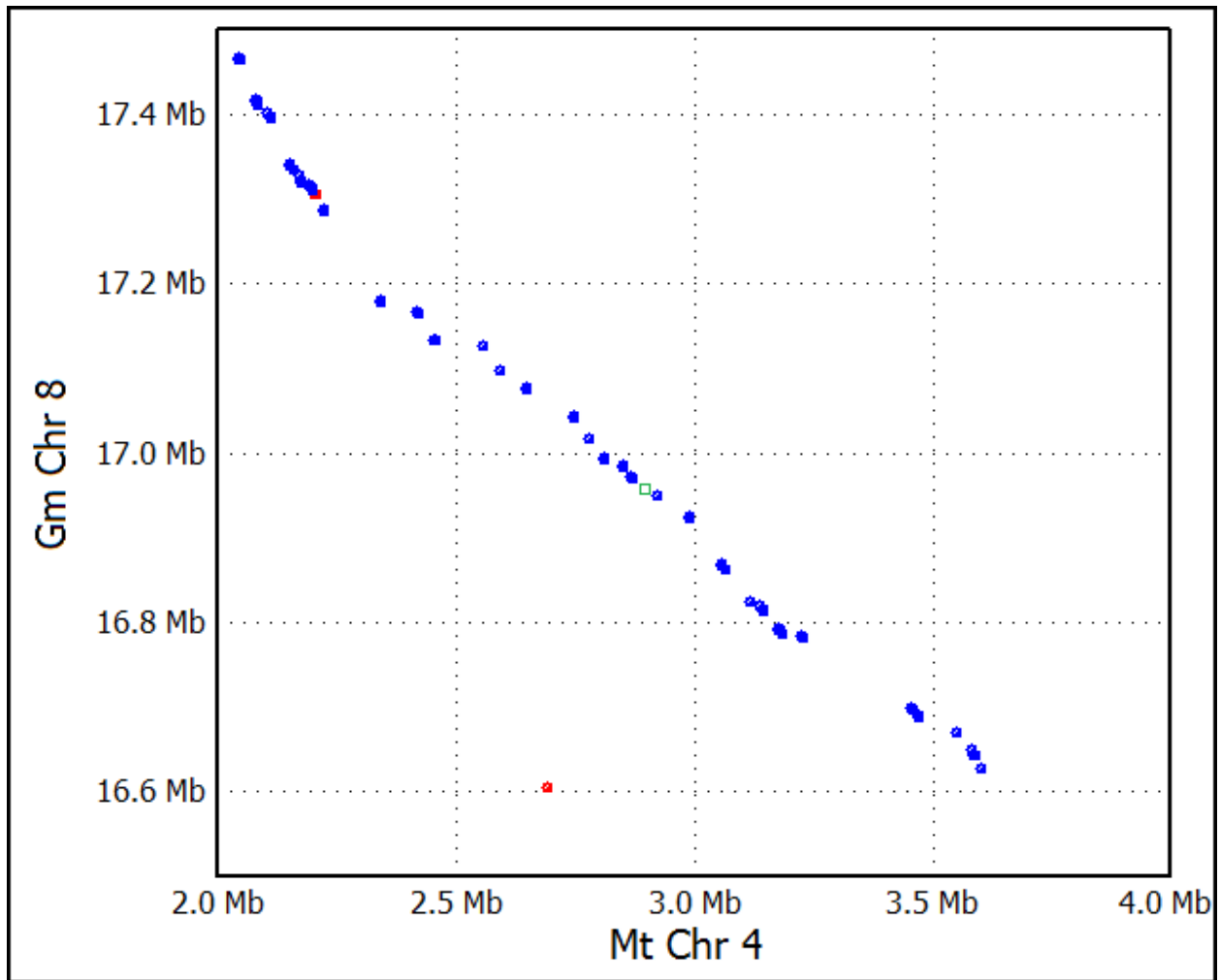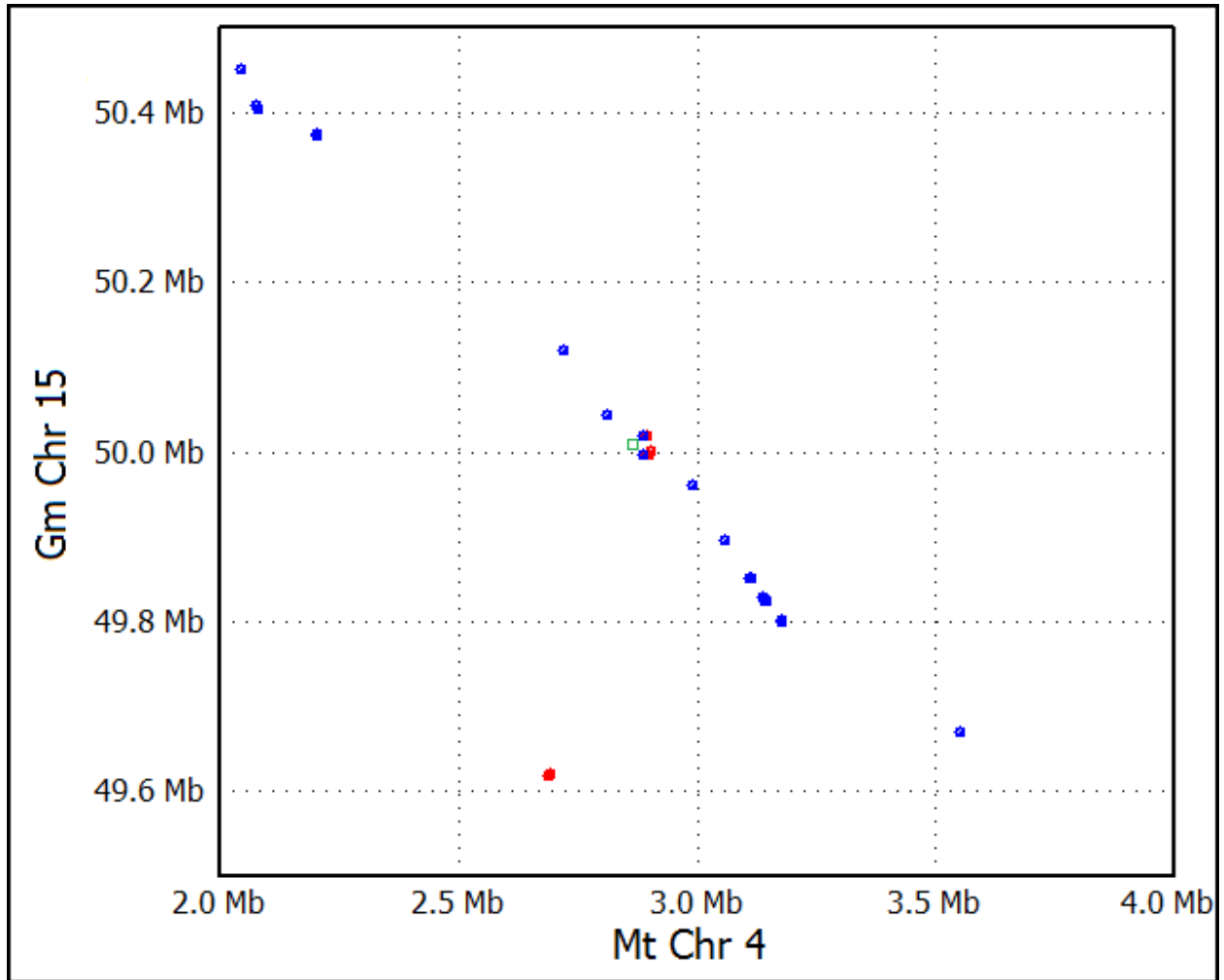
Figure S3   Multiple sequence alignment of LPs from *M. truncatula* accessions A17 and HM056, R108 and *M. sativa*. Unknown *M. sativa* residues are indicated with "?".
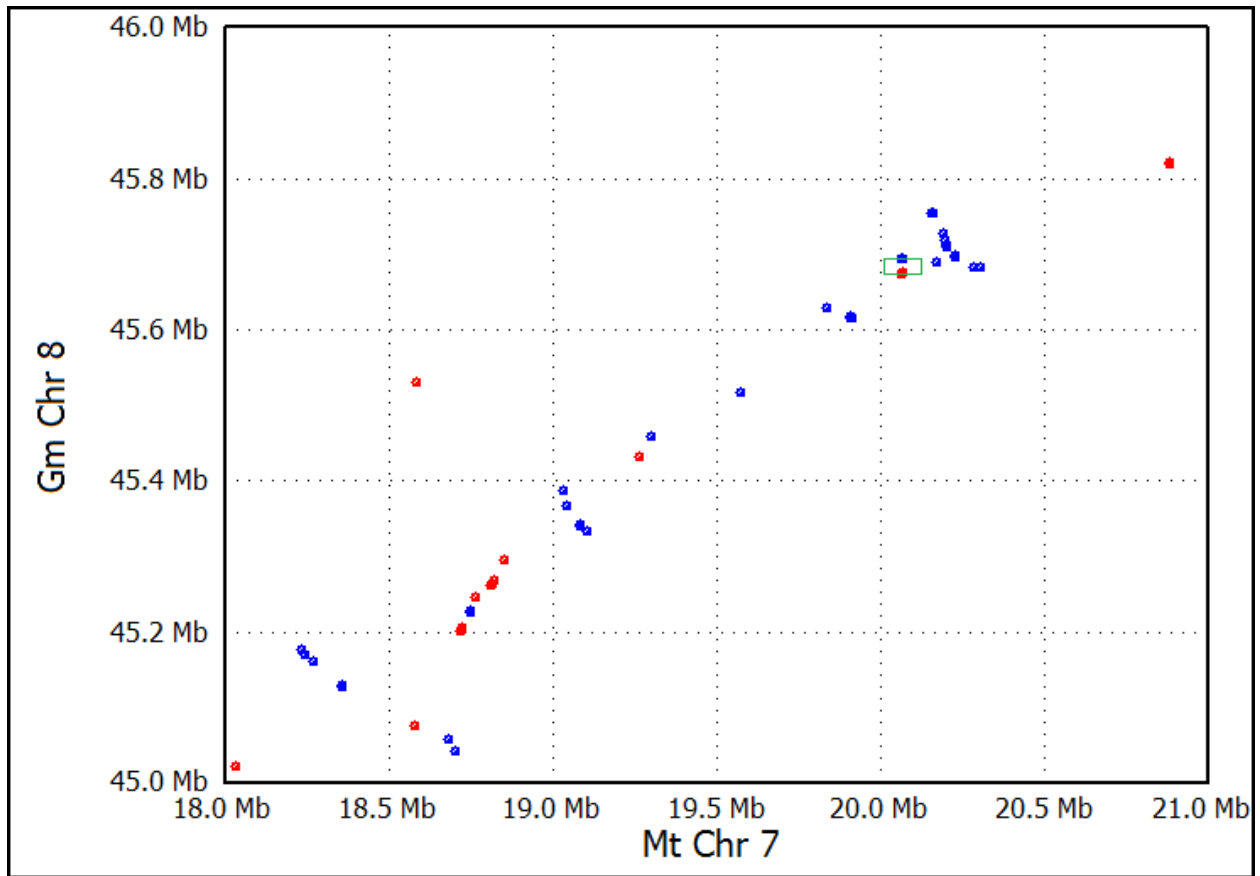
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A.

B.

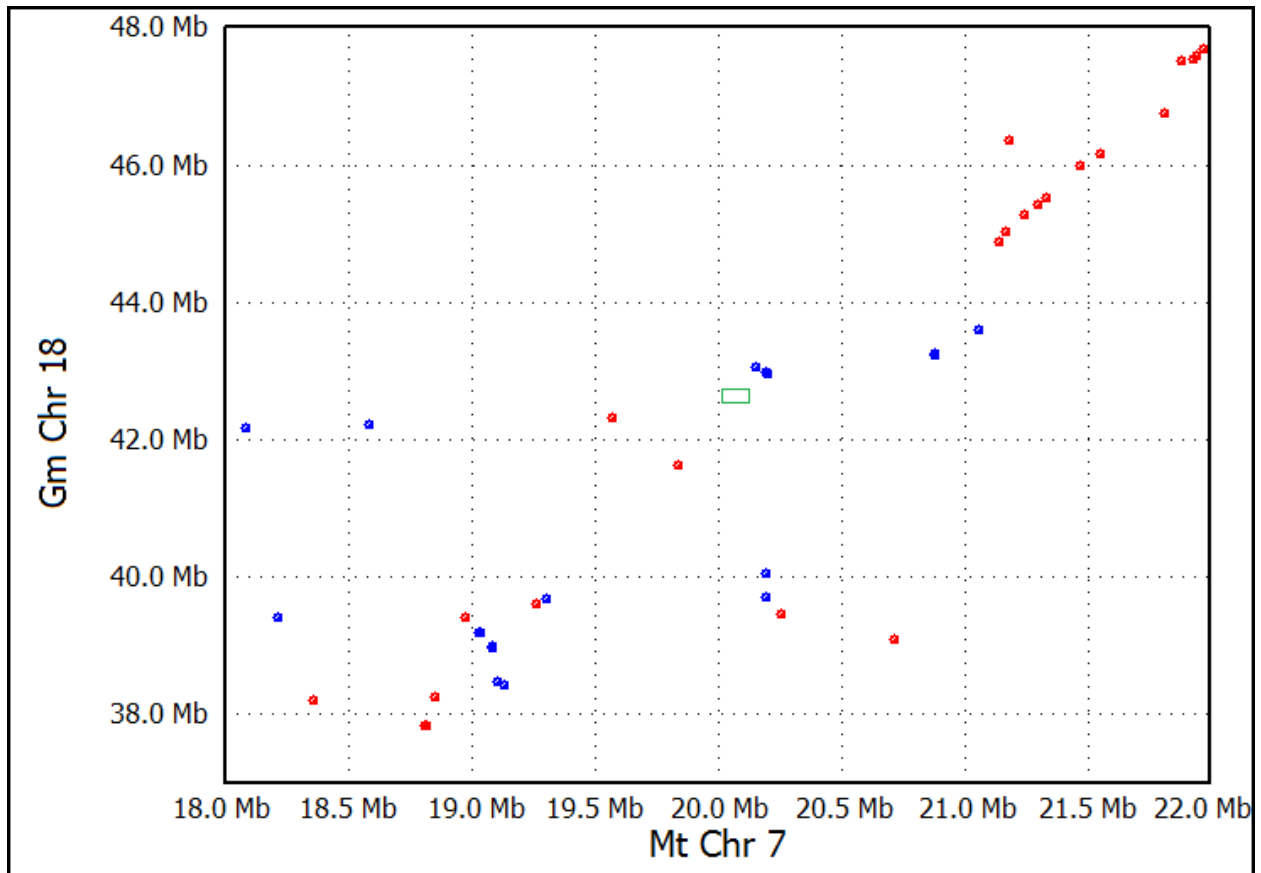D. I. Trujillo, K. A. T. Silverstein, and N. D. Young

C.

D.

Figure S4 Dotplot comparisons between *M. truncatula* and *G. max* in regions surrounding *M. truncatula* LPs. Panels show syntenic regions of *G. max* chromosomes 8 a) and 15 b) compared against a 2 Mb region in A17 chromosome 4, corresponding to 0.5% of the total *M. truncatula* genome. Syntenic regions of *G. max* chromosomes 8 c) and 18 d) are compared against a 3-4 Mb region of A17 chromosome 7. Red dots indicate regions of sequence similarity with a forward orientation, while blue dots indicate reverse matches. The LP region in *M. truncatula* is shown with green rectangles.

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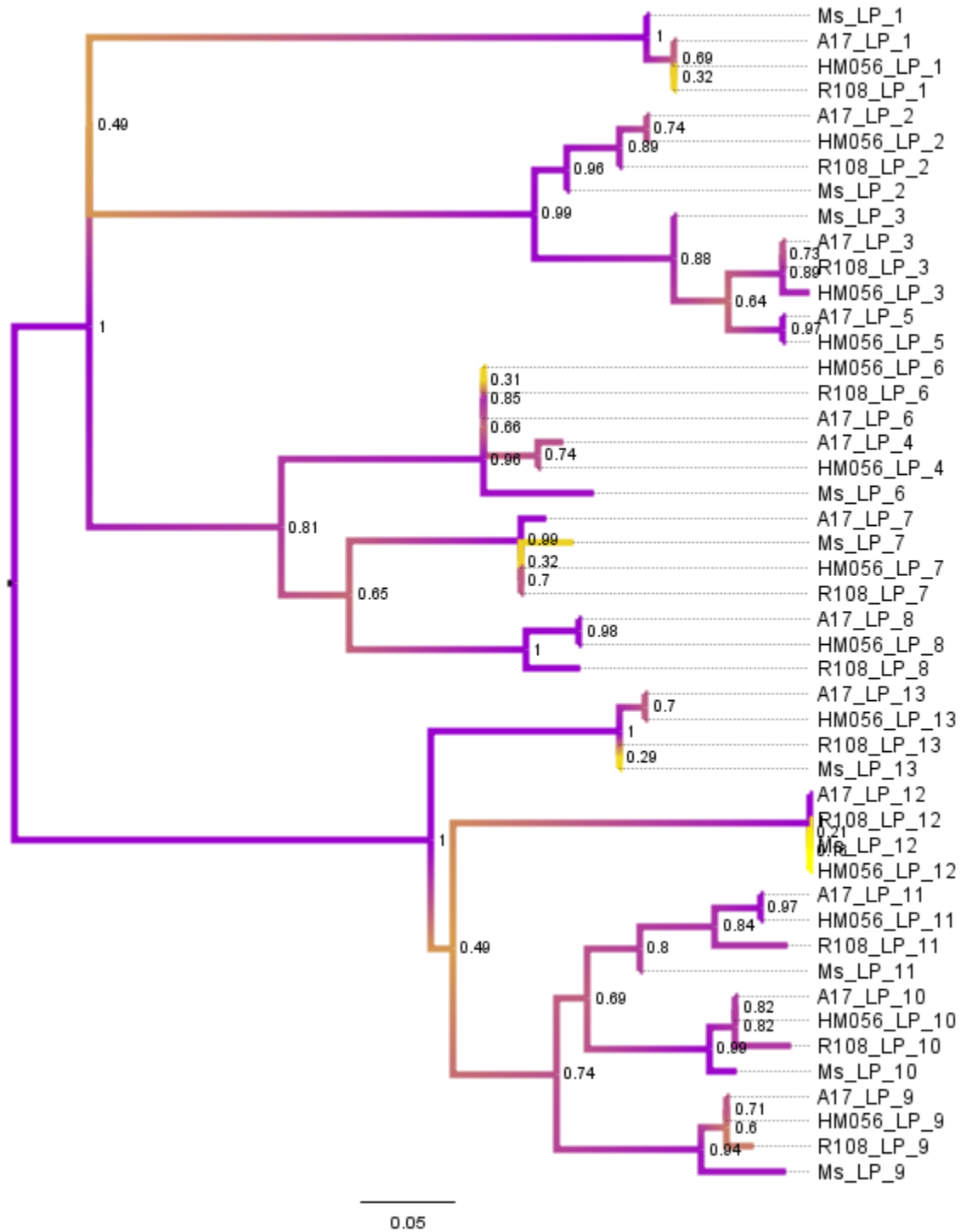
Figure S5 Phylogenetic tree of A17, HM056, R108 and *M. sativa* LP nucleotide sequences. The tree was generated through Bayesian Inference and visualized with FigTree software. Posterior probability values of the clades are indicated at the nodes.