Supplemental Table S1. Physical and genetic map positions of Bacterial Artificial Chromosomes (BACs) contributing to the Mt4.0, Mt3.5, and Mt3.0 genome assemblies, and flanking the inferred translocation breakpoint sites (highlighted) on chromosomes 4 (Chr4) and Chr8 in the A17 reference genotype.

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a Source for BACs contributing to contigs assigned to Chr4 and Chr8 in the Mt4.0 genome assembly:
ftp://ftp.jcvi.org/pub/data/m_truncatula/Mt4.0/Assembly/JCVI_Medr_v4.BAC.mapping.txt

b Source for linkage group (LG) and genetic map position (GMP) of BACs on the M. truncatula reference map:
http://tofu.cfans.umn.edu/downloads_genome/Mt_genetic_markers_Oct_2009.txt

c Source for BACs and their assigned chromosome in the Mt3.5 and Mt3.0 genome assemblies:
http://tofu.cfans.umn.edu/downloads_genome/Mt3.5/assembly_table.php
http://tofu.cfans.umn.edu/downloads_genome/Mt3.0/assembly_table.php

d Inferred translocation breakpoint sites based on BACs AC146651 and AC174329 (in bold) were located at 33.2
and 22.5 Mb on Chr 4 and 8, respectively, in the Mt3.5 assembly in agreement with Young et al. (2011).

Note: Both the Mt4.0 and Mt3.5 genome assemblies were generated via an optical mapping approach (Young et al.
2011), while the Mt3.0 assembly relied heavily on genetic mapping information.