Table 1 Suppl. Primers used in this study. Nucleotides corresponding to restriction enzyme cut sites and site-directed mutation sites are *underlined*.

Primer	Sequence(5′-3′)	Description
LEA3140F	GCGGATCCATGCTAGGAGGAGCAAAGAAAAC	ORF cloning and expression profiling
LEA3140R	GCGAGCTCTCACAGCCCAAACTGTCTCCT	
LEA3140MF	ACCAATTGGGGCAGGGTGGACA	Site-directed mutagenesis
LEA3140MR	TGTCCACCCTGCCCCAATTGGT	
LEA3160F	GCGGATCCATGCAAGGAGGAGCAAAGAA	ORF cloning and expression profiling
LEA3160R	GCGAGCTCCTATGCCCTATTTTGAGCAGC	
LEA3170F	GCGGATCCATGCAGGGAGCTAAGAAAGCT	ORF cloning and expression profiling
LEA3170R	GCGAGCTCTCATTTATAAGTACCACCAGTGGTGTA	
Medtr1g053970F	ATGCAGGCAGCAAGGAAAGCA	Expression profiling
Medtr1g053970R	CTAATTATTAGTAGTAGGTCC	
ActinF	TGCTTCTAACTGAGGCTCCACT	Internal control for expression profiling
ActinR	AAAGGACTTCTGGGCAACG	

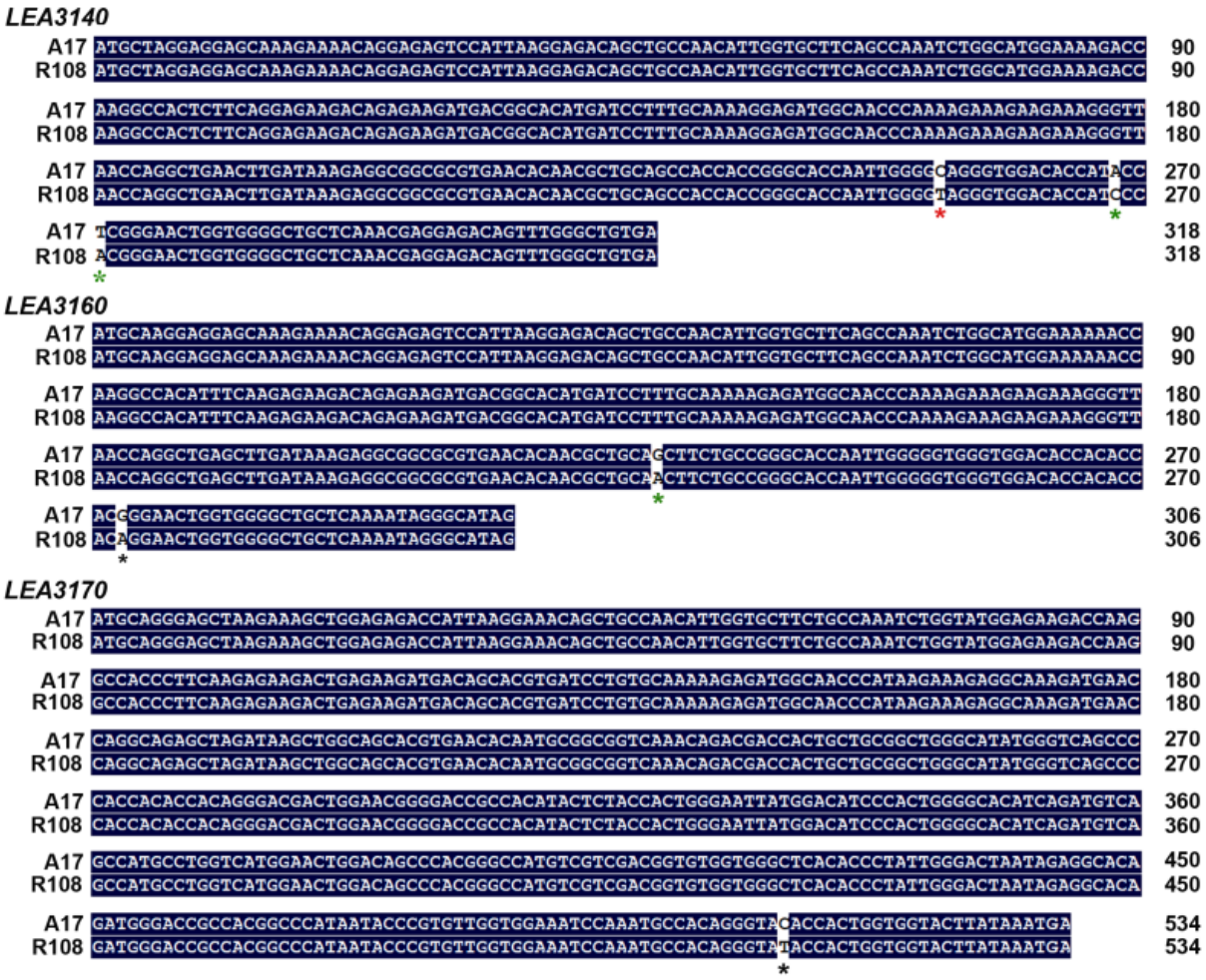

Fig. 1 Suppl. Alignments of *MtLEA* genes from *Medicago truncatula* genotypes A17 and R108. Single nucleotide polymorphisms responsible for the premature termination codon, amino acid substitutions, and synonymous substitutions are indicated by *red*, *green*, and *black asterisks*, respectively.

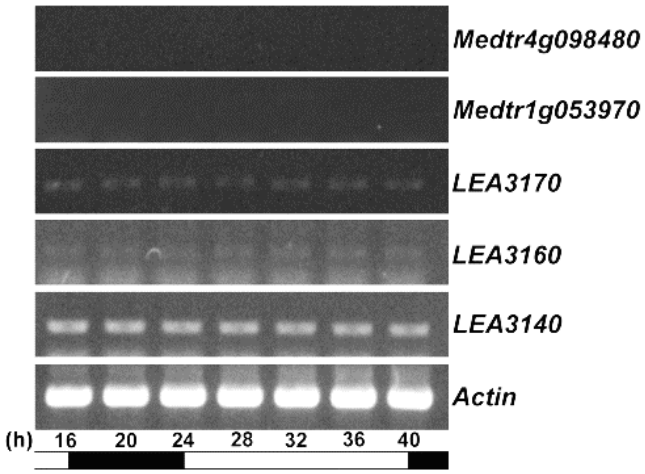

Fig. 2 Suppl. Reverse transcription PCR detection of the diurnal transcriptional patterns of *MtLEA* genes in *Medicago truncatula* genotype R108. The *black* and *white bars* indicate dark and light, respectively. Seedlings grown in *Vermiculite* for two weeks at 21 °C were collected at appropriate time points for transcription profiling.

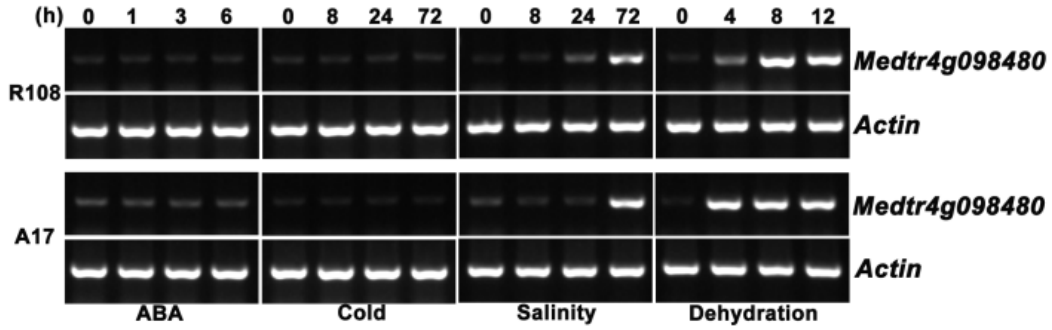

Fig. 3 Suppl. Reverse transcription PCR detection of abiotic stresses and abscisic acid induced transcriptional patterns of *Medtr4g098480*, which encodes a subgroup 4A LEA protein in *Medicago truncatula* genotypes A17 and R108. Specific primers for *Medtr4g098480* (LEA8480F: 5′-ATGCAATCTTCAATGGAGAAGCT-3′, LEA8480R: 5′-CTACATGCGATTGTTCTGTGGAA-3′) were used.