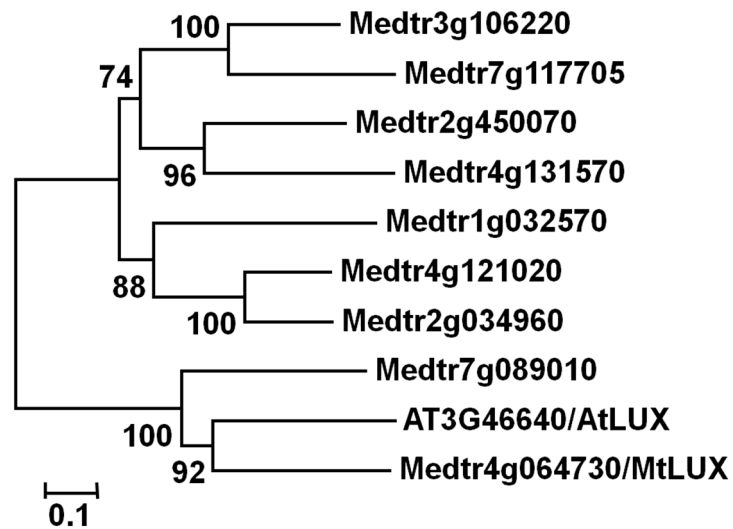**Supporting Informations**

Figure S1 | Phylogenetic analysis of AtLUX protein and MtLUX like proteins from *M. truncatula.* The most strongly related *M. truncatula* protein to AtLUX is the product of *Mt4g064730* (*MtLUX*). Bootstrap value supporting each node is shown.
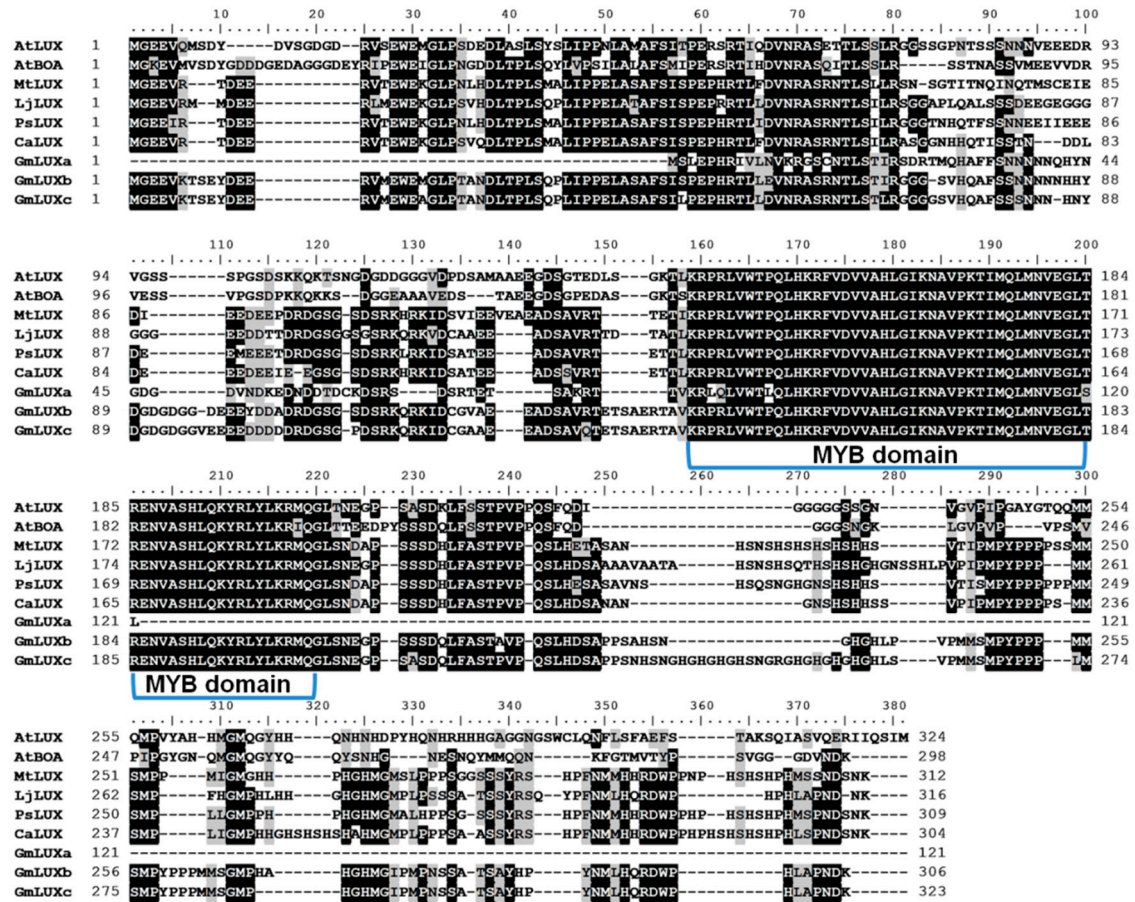
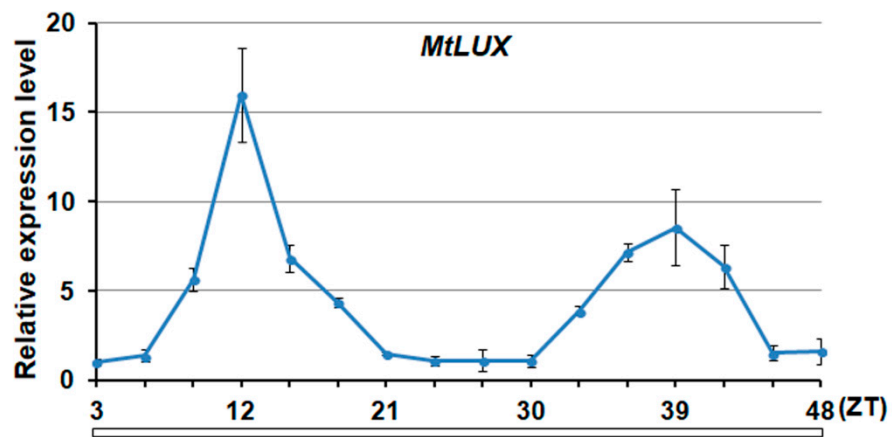**Figure S2 |** Amino acids alignment for LUX-Like proteins.

Figure S3 | The expression pattern of *MtLUX* in the leaves of 4-week-old WT under constant light condition. Values shown as means ± SD of three biological replicates. *MtUBIQUITIN* was used as the internal control. White bar at the bottom indicates period of constant light.
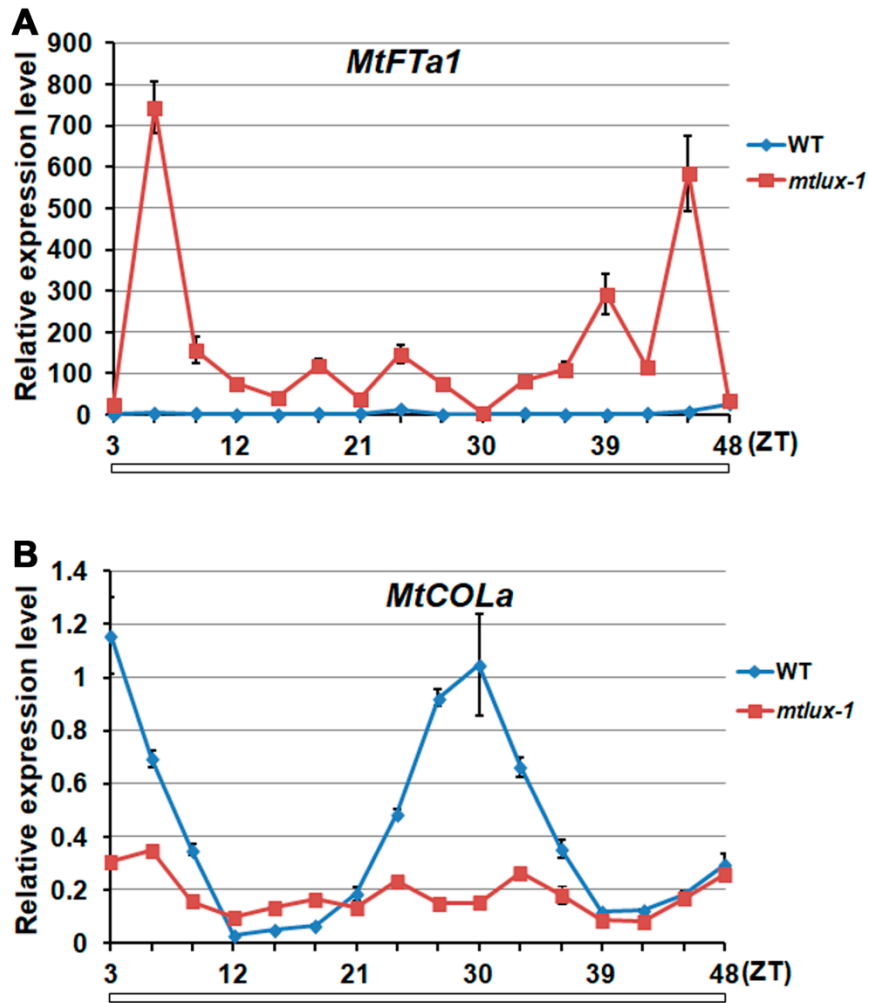
Figure S4 | The expression pattern of *MtFTa1* (A) and *MtCOLa* (B) in the leaves of 4-week-old WT under constant light condition. Values shown as means ± SD of three biological replicates. *MtUBIQUITIN* was used as the internal control. White bars at the bottom indicate periods of constant light.
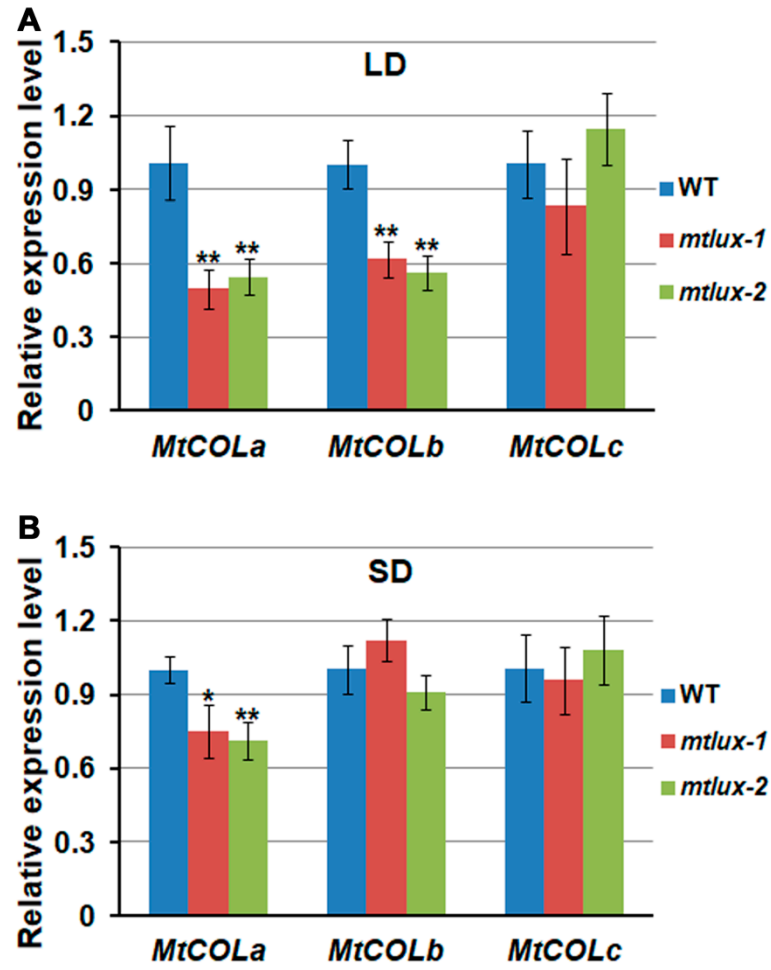
Figure S5 | Relative gene expression of three *Medicago COL* genes in long day (A) and short day (B) conditions in WT and *mtlux* mutant plants. Values shown as means ± SD of three biological replicates. *, **: means differ significantly ($P < 0.05$, $P < 0.01$).
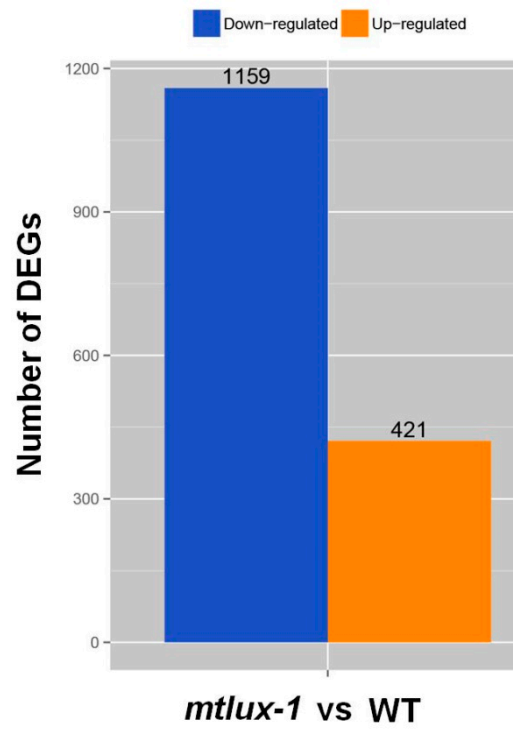
Figure S6 | Differentially expressed genes (DEGs) between *mtlux-1* and wild type.
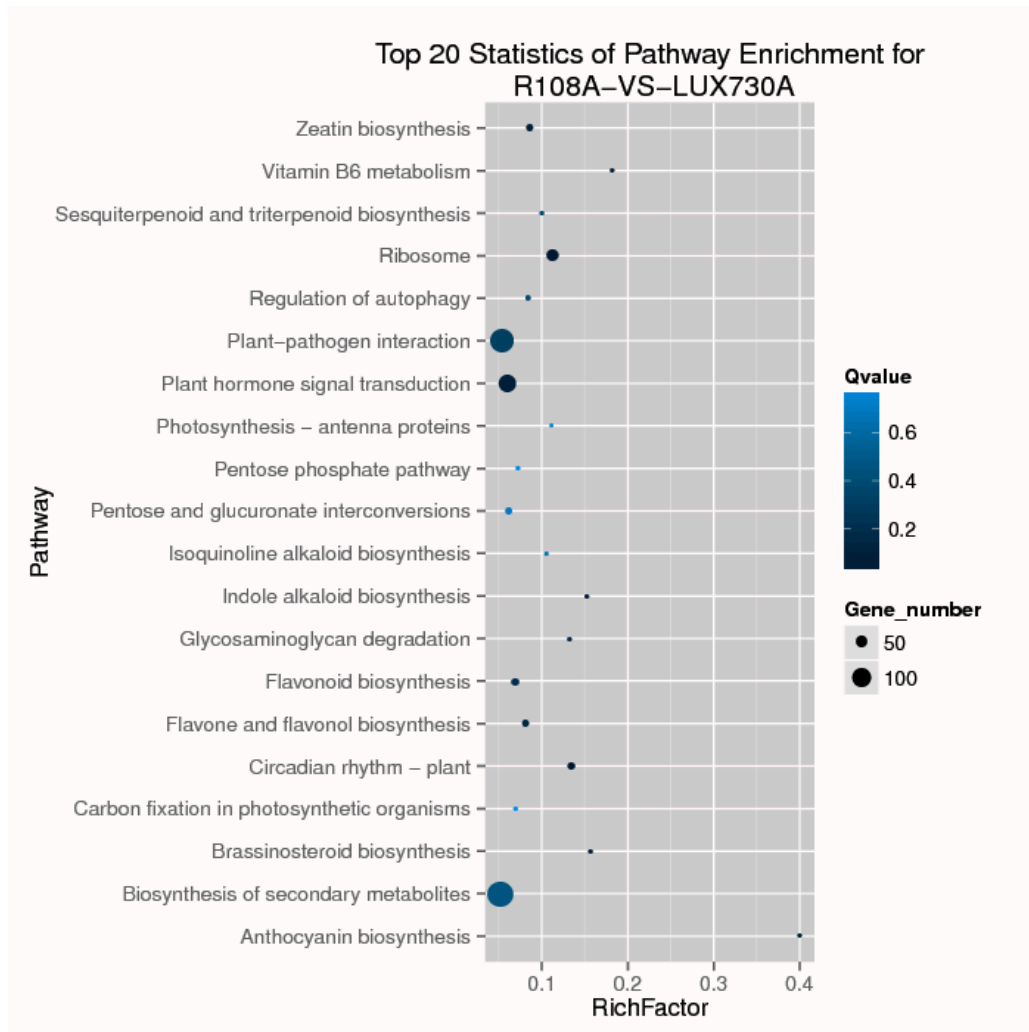
Figure S7 | Functional assignment of the differentially expressed genes (DEGs) by Gene Ontology (GO) analysis of top20 pathways. R108A as the wild type and LUX730A as the *mtlux-1* mutant. Scale represents *q* value.
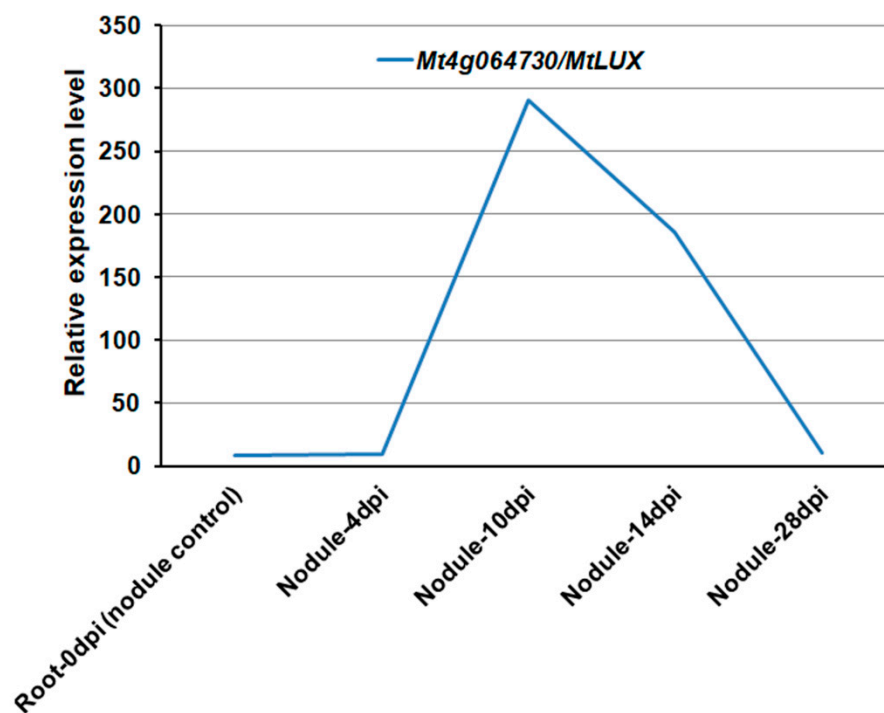
Figure S8 | Transcriptional profile of *MtLUX* in nodule. The transcriptional profile of *MtLUX* derived from the *M. truncatula* Gene Expression Atlas (https://mtgea.noble.org/v2/). The microarray probe set used is Mtr.32211.1.S1_at.