

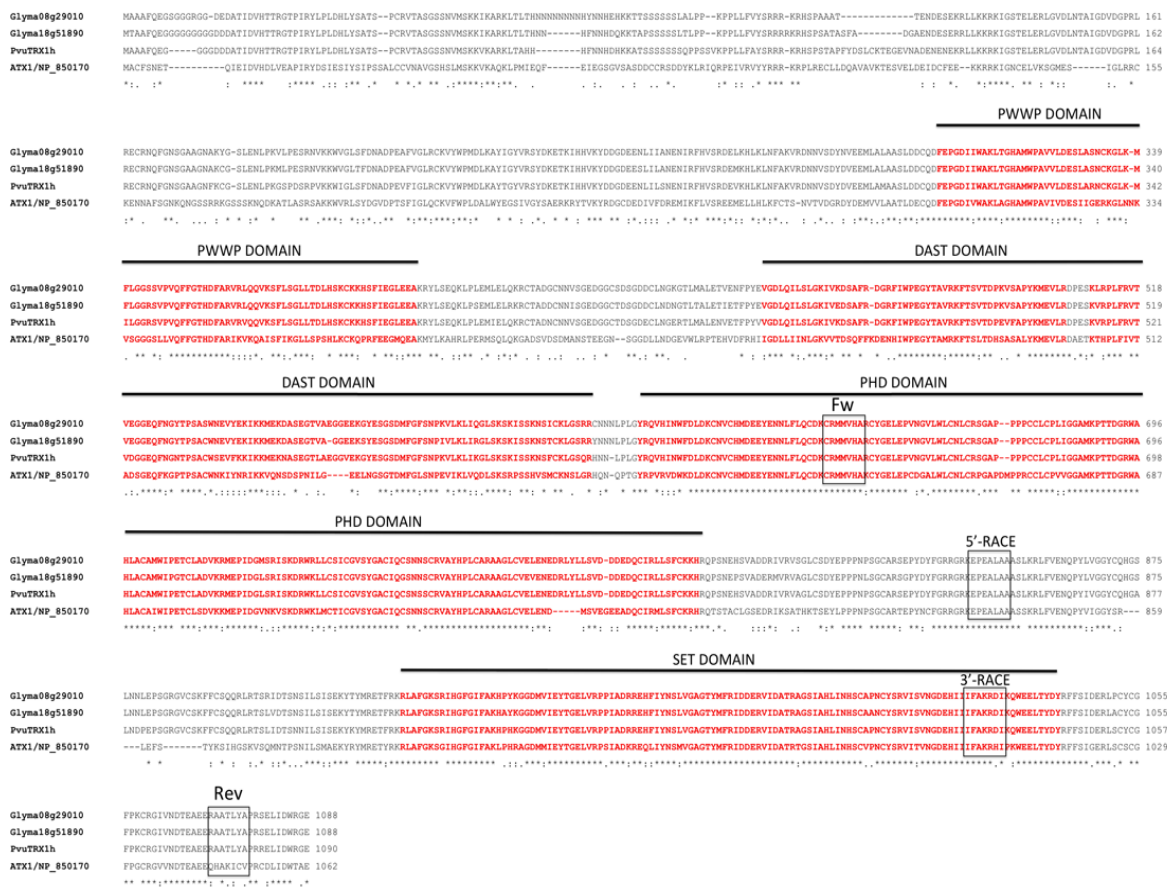
## Supplementary Data

Molecular cloning and characterization of two Trithorax-Group genes from *Phaseolus vulgaris* roots and symbiotic nodules.Juan Manuel Quiceno-Rico<sup>1</sup>, José Alberto Camas-Reyes<sup>1</sup> and Raúl Alvarez-Venegas<sup>1,2</sup>

## Supplementary figures.



**Fig S1.** Multiple sequence alignment of TRX proteins. Alignment of the Arabidopsis cDNA *ATX1* sequence (At2g31650) with two predicted soybean (*Glycine max*) Trithorax sequences (Glyma08g29010.1 and Glyma18g51890.1) and the *P. vulgaris* *PvuTRX1h* sequence. Consensus sequences used to design consensus primers to amplify an internal fragment from the *P. vulgaris* *PvuTRX1h* are shown inside rectangles as “Fw” and “Rev”. Protein domains are indicated in red letters with the name of the conserved domains above the sequences.



**Fig S2.** Multiple sequence alignment of Ash1 proteins. Alignment of the Arabidopsis ASH1 sequence with two homologous soybean sequences, Glyma20g30870.1 and Glyma10g36720.1, and the *P. vulgaris* *PvuASH1h* sequence. Consensus sequences used to design consensus primers to amplify an internal fragment from the *PvuASH1h* sequence are shown inside rectangles as “Fw” and “Rev”. Protein domains are indicated in red letters with the name of the conserved domains above the sequences.