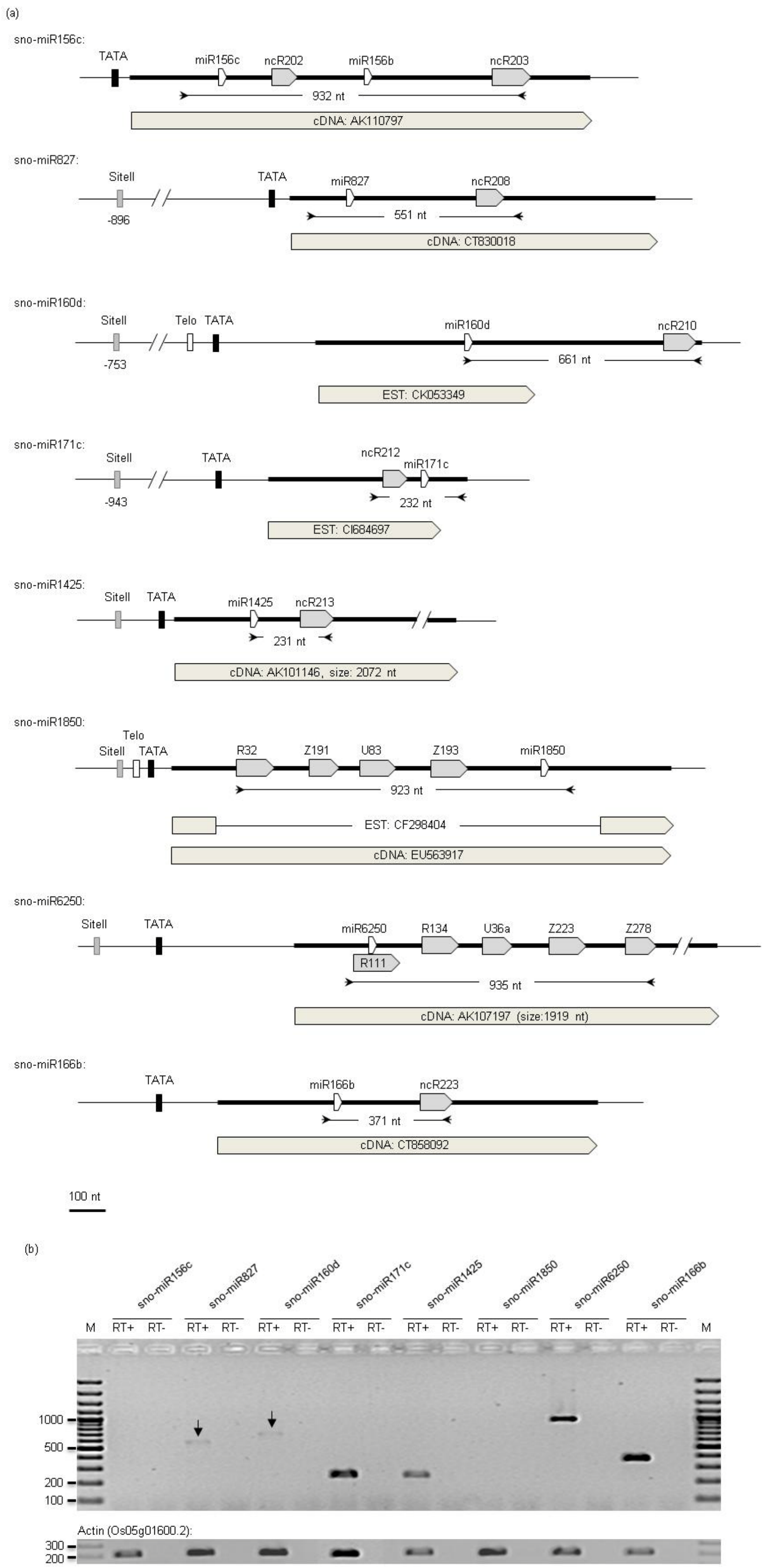

Figue S4. RT-PCR validation of sno-miRNA gene precursors in *Oryza sativa*

inflorescence tissue. (a) Schematic diagram of sno-miRNA genes. The snoRNA and the miRNA are denoted by a gray pentagon and an open pentagon, respectively. The TeloSII elements and TATA box are represented by different boxes: Telo-box (open box), Site II (gray box), and TATA box (black box). The primers designed for sno-miRNA precursors and the expected sizes are indicated by arrows and solid lines. (b) RT-PCR analysis of sno-miRNA precursors expression in inflorescence tissue. RT+ and RT- refer to the presence and absence of reverse transcriptase, respectively. Molecular markers are shown as M. Genomic DNA, G, was used as a positive control. Actin protein (Os05g01600.2) is used as loading control.