

FIGURE S4 Molecular analyses of α -MMC transgenic N. benthamiana plants. (a) Semiquantitative RT-PCR analysis of α -MMC expression in leaves of WT and transgenic lines OE-2 and OE-5. (b) Quantitative RT-PCR analysis of α -MMC expression in leaves of WT and transgenic lines OE-2 and OE-5. Bars represent mean and standard deviation of values obtained from three biological replicates. Asterisks represent significant difference determined by Student's t test (*** P < 0.001). (c) Western blotting analysis of α -MMC expression in leaves of WT and transgenic lines OE-2 and OE-5. Rubisco proteins were used as loading controls and were stained by Ponceau S. WT: nontransformed wild type N. benthamiana plants. OE-2 and OE-5: α -MMC -transgenic N. benthamiana lines