Fig. S1. Trehalose contents of 101MTSH and 105MTSH plants. (A) Typical chromatograms obtained by gas chromatography–mass spectrometry (GC-MS) for trehalose quantification. (B) Trehalose contents of 101MTSH, 105MTSH, untransformed controls (NT) plants obtained by GC-MS. Crude extracts were obtained from leaves of 101MTSH, 105MTSH and NT control plants according to Quero et al., 2013.
Fig. S2. Analysis of the transcript levels of genes related to ABA signaling and stress response in the leaves. The transcript levels of genes related to ABA signaling and response were analyzed by qRT-PCR. OsUbil was used as a reference gene, and ratios were normalized against the control. Data presented are means ± SE (n=3) of two independent experiments. *, p < 0.05; **, p < 0.005; ***, p < 0.001. Abi2 (NM_001049950), SAPK10 (NM_001057188), LEA3 (NM_001062730), Rab16 (NM_001074376), Wsi18 (NM_001050543), SalT (NM_001049511), Dip1 (NM_001054224), ASR1 (NM_001072373).
Fig. S3. Analysis of the transcript levels of genes related to ABA (A) and trehalose (B) biosynthesis in the leaves. The transcript levels of genes were analyzed by qRT-PCR. OsUbi1 was used as a reference gene, and ratios were normalized against the control. Data presented are means ± SE (n=3) of two independent experiments. *, p < 0.05; **, p < 0.005; ***, p < 0.001. ABA1 (Os04g0443900), ABA2 (Os03g0810800), ABA4 (Os01g0128300), OsNCED1 (Os02g0704000), OsTPS1 (AK067066), OsTPP1 (AK103391), OsTPP3 (AK069361), OsTPP5 (AK106316), OsTPP7 (AK121015).