Figure S1. Genetic background identification by RT-PCR and RT-qPCR. (A) Identification of strong expression suppression of *SlNCED1* and *SlAAO* in the knockout lines of *not* and *sit*, respectively, by RT-PCR. Three individual plants from each genetic background were examined (Left). Similar expression level of *SlEfa* in WT, *not*, and *sit* confirmed it as qualified reference gene for RT-qPCR test (Right). (B) RT-qPCR of (A, left). Three individual plants were included (mean ± s.d.). Each group of data is tested with the respective control sample by t-test, *, p<0.05, **, p<0.01, n=3.