



Supplemental Figure 7. Analysis of transgenic rice plants overexpressing *BERF1* and *BEIL1*

A) and **B)** Southern blot analyses on genomic DNA extracted from young leaves of 4-week-old transgenic T1 (left) and T2 (right) lines overexpressing *BERF1* and *BEIL1* genes respectively. The *hygromycin phosphotransferase* gene was used as probe.

C) Duplex RT-PCR analysis on total RNA isolated from T1 seedlings (pMO11). The preliminary screening was performed using rice Ubiquitin (*OsUBQ*) gene as internal amplification control and specific primers BAPL-725 forward/attB2-BAPL. **D)** RT-PCR analysis of total RNA isolated from T1 seedlings (pMO8). The preliminary screening was carried out with primers BEIL1-1385 f/attB2-BEIL1 and ACC oxidase1 (*OsACO1*) gene specific primers, and rice ubiquitin (*OsUBQ*) gene as internal amplification control.

Nipponbare (NB) plants were used as wild-type control,