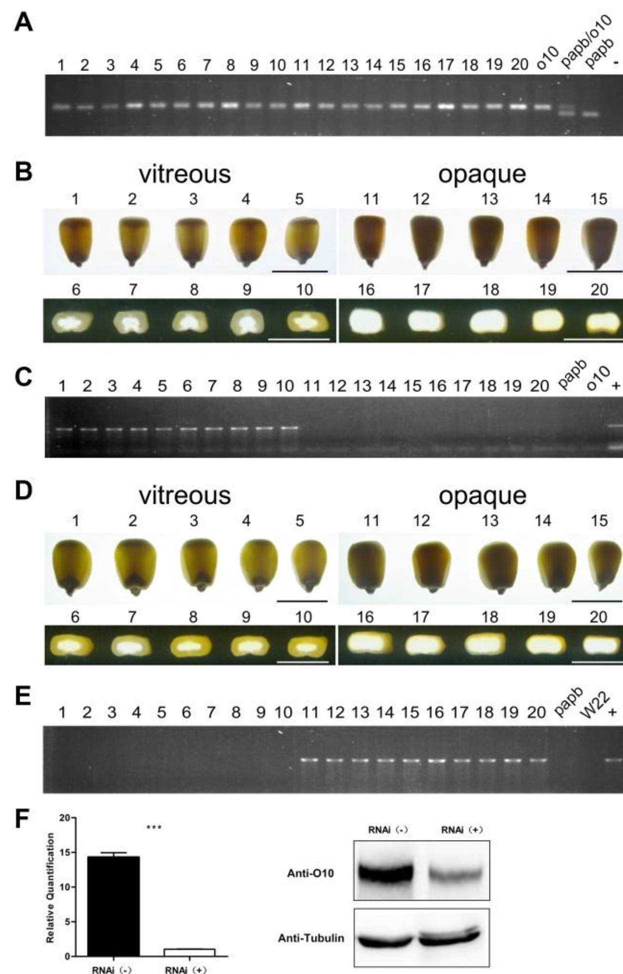

S2 Fig. Phenotyping and genotyping of transgenic kernels, the expression of *O10* and the accumulation of O10 in RNAi lines. (A) The transgenic events (T0 lines) were hybridized to the homozygous mutant (*o10*/*o10*) and self-pollinated (T2 lines). Using the molecular marker linked to the *o10* locus, ten vitreous and ten opaque homozygous mutant kernels were sorted out from T2 ears. -, H_2O control. (B) Light transmission and the transverse section of the ten vitreous and ten opaque homozygous mutant kernels were observed. Bars = 1 cm. (C) Using the primers of the *bar* gene to identify the transgenic negative and positive kernels. +, *PHB* vector. (D) The RNAi transgenic events (T0 lines) were hybridized to the W22 background and then self-pollinated (T2 lines), underwent light transmission and used to take transverse sections of the vitreous and opaque kernels from T2 ears. Bars = 1 cm. (E) Using the primers of the *bar* gene to identify the transgenic negative and positive kernels. +, *pFGC5941* vector. (F) Real-time quantitative PCR was used to analyze the RNA expression of *O10* at 21 DAP in the transgenic negative (RNAi (+)) and positive (RNAi (-)) mature kernels. An immunoblot analysis was performed to compare the accumulation of O10 in the transgenic negative and positive mature kernels. Anti-tubulin was used as a sample loading control.