



**Figure S4** Allele mining in a diverse wheat collection revealed a putative mutant at *TtLUX-A* in cultivar ‘Tsing Hua no. 559’. (A) ‘Tsing Hua no. 559’ (*T. turgidum* L.) was a relatively early heading (*red arrow*) genotype which flowered one week earlier than another Chinese cultivar ‘Fo Shou Mai’ (*T. turgidum* L., *blue arrow*), two plants per accession were evaluated in the field at IPK in Gatersleben in 2011. Deletion involving seven AA from the MYB domain of *TtLUX-A* could potentially impair function of the protein, Figure 2B. (B) Genome-specific primers were used to amplify both copies of *TtLUX*. In ‘Tsing Hua no. 559’, transcripts of *TtLUX-A* (A-genome copy of *LUX*, *red squares*) and *TtLUX-B* (B-genome copy of *LUX*, *black triangles*) were up-regulated when compared to ‘Fo Shou Mai’ (*TtLUX-A*, *blue diamonds*, *TtLUX-B*, *green triangles*). (C-E) Functional *TtLUX-B* most likely complemented missing function of *TtLUX-A* in ‘Tsing Hua no. 559’ (*red squares*, ‘Fo Shou Mai’; *blue diamonds*), no distortion was thus detected in the oscillation of central clock genes; *TtGI* (C), *TtPRR95* (D) and *TtCCA1* (E). (B-E) Transcript levels were measured from a one-day time-course RT-qPCR study. Sampling was performed on 31 days old plants starting at 6:00 am (ZT=0) of the second day under constant light and temperature. Leaves were harvested every three hours (LL conditions) from at least three plants per time point per genotype (biological replicates). Error bars indicate SEM