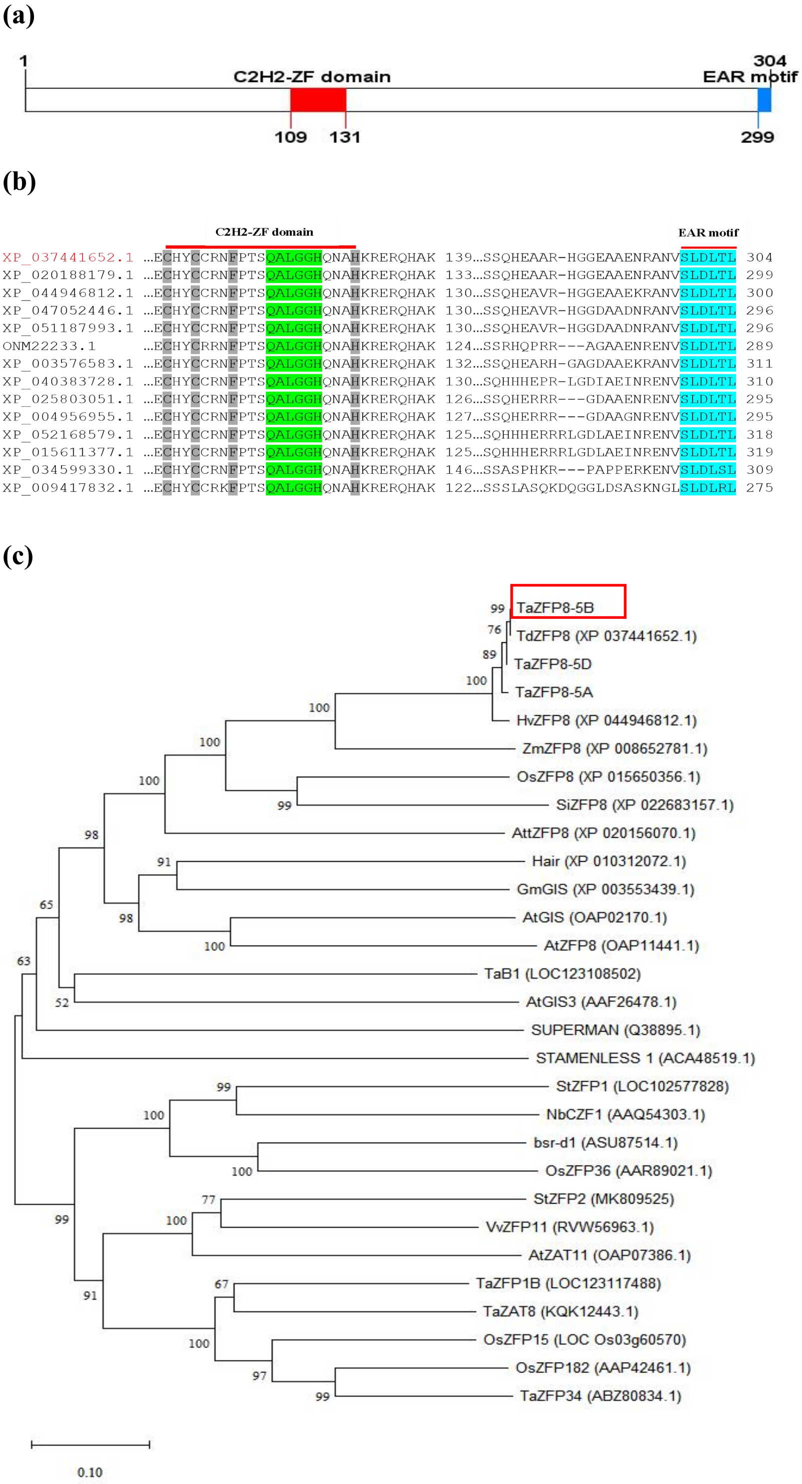

Fig. S1 Sequence analysis of TaZFP8. (**a**) Schematic diagram of TaZFP8 protein structure. (**b**) Sequence alignment of TaZFP8 with other C2H2-type ZFPs. The sequences were aligned with DNAMAN software. C2H2-ZF domain (gray), QALGGH conserved motif (green), and EAR motif (blue). (**c**) Phylogenetic analysis of TaZFP8. Different C2H2-ZFs from *T. aestivum* (Ta), *T. dicoccoides* (Td), Hordeum vulgare (Hv), Zea mays (Zm), *Oryza sativa* (Os), *Setaria italica* (Si), *Aegilops tauschii* (Att), *Arabidopsis thaliana* (At), *Solanum tuberosum* (St), *Nicotiana benthamiana* (Nb) and *Vitis vinifera* (Vv) were used for the phylogenetic analyses using MEGA11.