

**Figure S3 a** Phylogenetic tree of NAC proteins. The tree was constructed from the Rice and Arabidopsis sequences from the plnTFDB (Riano-Pachon et.al. 2007), with the addition of the maize genes ZmNRP1 (AY325313), ZmNAC4 (CAH56054), barley TA42485, TA42398, TA6584, TA40870, TA44577, TA41963, wheat TaGrab2 (AJ010832), and probe sets Ta11509.1.S1 (TA82591), Taaffy117676.1.S1 (CA734178), Ta25288.1.S1 (TA80395), Ta37139.1.S1 (TA93469), Ta12286.1.S1 (TA85008). The tree was generated using the maximum likelihood method PHYML (Guindon and Gascuel, 2003). Bootstrap values above 60% are indicated. The tree was constructed from the entire family but only the NAM and NAC1 subclades (Ooka et. al. 2003) are shown. **b.** Amino acid alignment of the five subdomains (A-E) of the NAC DNA binding domain (Ooka *et. al.* 2003). The alignment was generated using CLUSTAL X of the entire family but only sequences in the NAM and NAC1 subclades are shown. Gaps in the sequences and between subdomains are indicated by dashes. Shading is based on amino acid identities and properties.

**a**



