



Fig.S3. Phylogenetic relationships, conserved motifs, domains and gene structures of the *A. sinensis* AsNACs family. (A) A phylogenetic tree was constructed using the Neighbor Joining Method; different colors represent different motifs, and the X-axis represents amino acid length. (B) Comparison of conserved domains among AsNACs, with the X-axis representing amino acid length. (C) Gene structure of *AsNACs*, with the X-axis indicating base pair length (bp).