S1 Fig.
Phylogenetic analysis of the potato B-box family.
The trees shown are based on the alignments of the protein sequences of the B-box 1 domain (A), B-box 2 domain (B) and CCT domain (C). The 30 B-box members were aligned using MUSCLE in MEGA 6.06 software with default parameters [49]. The achieved alignment was used as a input to construct the phylogenetic tree with 1000 bootstrap replicates.