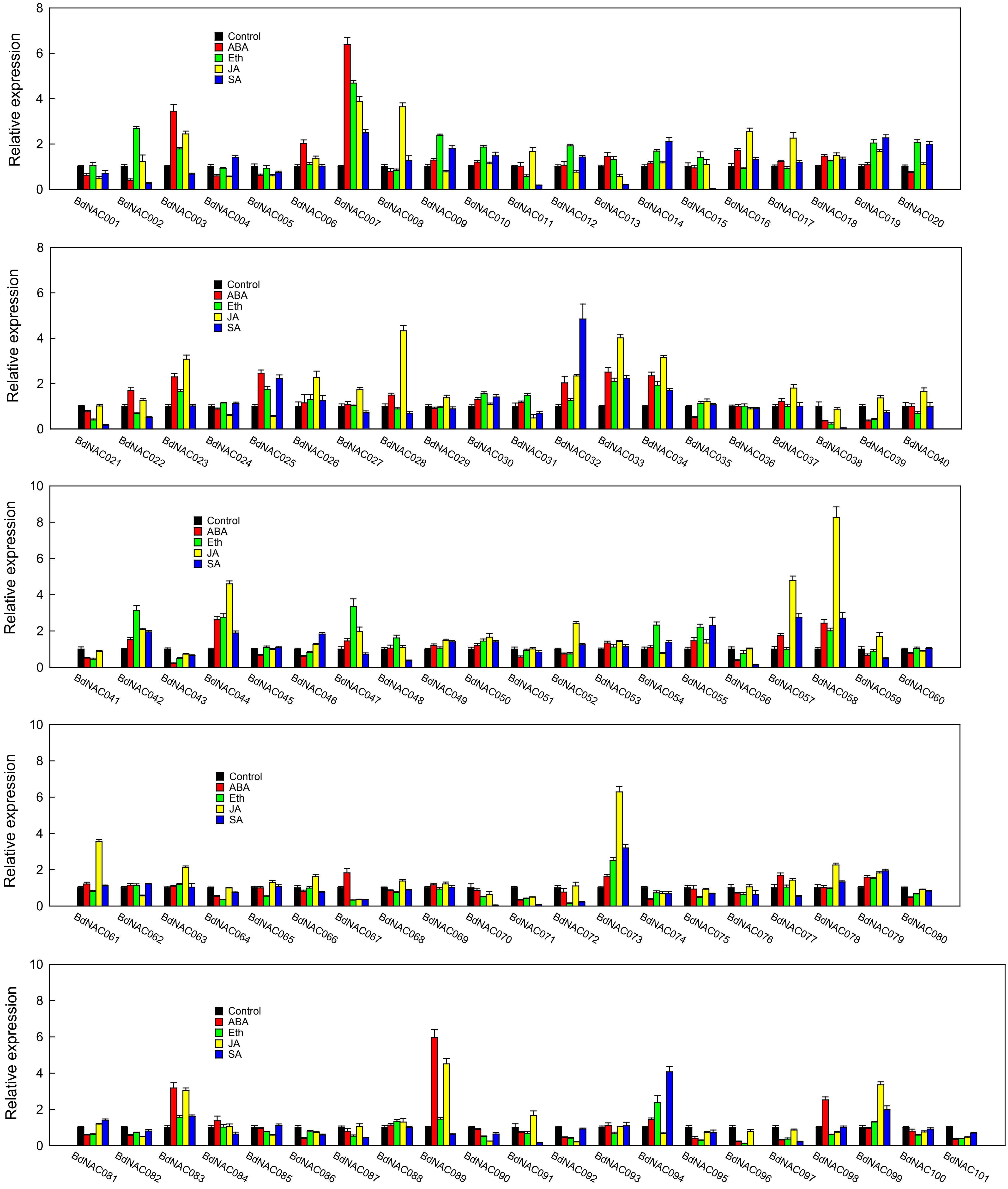

S8 Fig. Expression profile of *BdNAC* genes in response to various phytohormones. 3-week-old seedlings were treated with 100 µM ABA, 300 µM ethephon, 100 µM JA and 100 µM SA, respectively. Relative expression levels of *BdNAC* genes were analyzed by quantitative real-time RT-PCR (qPCR). The expression levels are normalized with respect to reference gene *UBC18* in different samples. Error bars indicate standard deviations (SD) based on three technical repeats.