Supplementary Materials

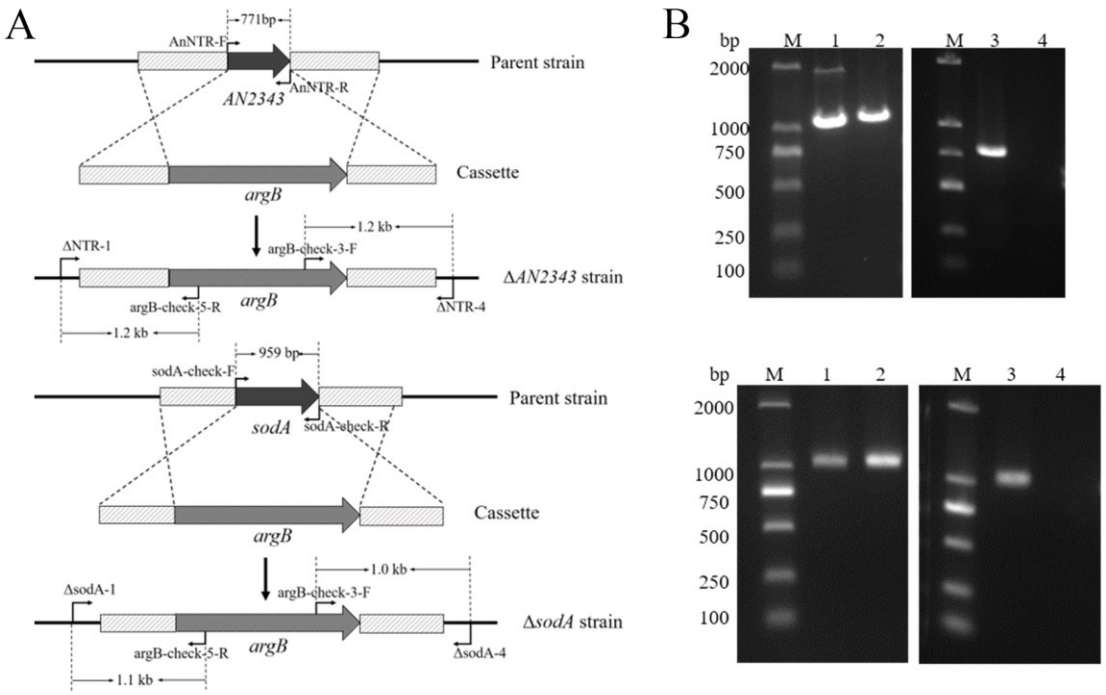

Fig S1. Disruption of *AN2343* and *sodA* genes in *A. nidulans*. (A) Strategy for homologous recombination to construct the *AN2343* gene disruptant (left). PCR analysis to verify the *AN2343* disruptant (right). M, marker. The *AN2343* disruptant was verified using the primer pairs ΔNTR-1 and *agrB*-check-5-R (lane 1), *agrB*-check-3-F and ΔNTR-4 (lane 2), respectively; Primer pairs AnNTR-F and AnNTR-R were used to amplify the *AN2343* encoding region in the parent strain (lane 3) and the disruptant strain (lane 4). (B) Strategy for *sodA* disruption (left) and the validation of the resulting disruptant (right). The method described above was used. The corresponding primers are listed in Table 3.

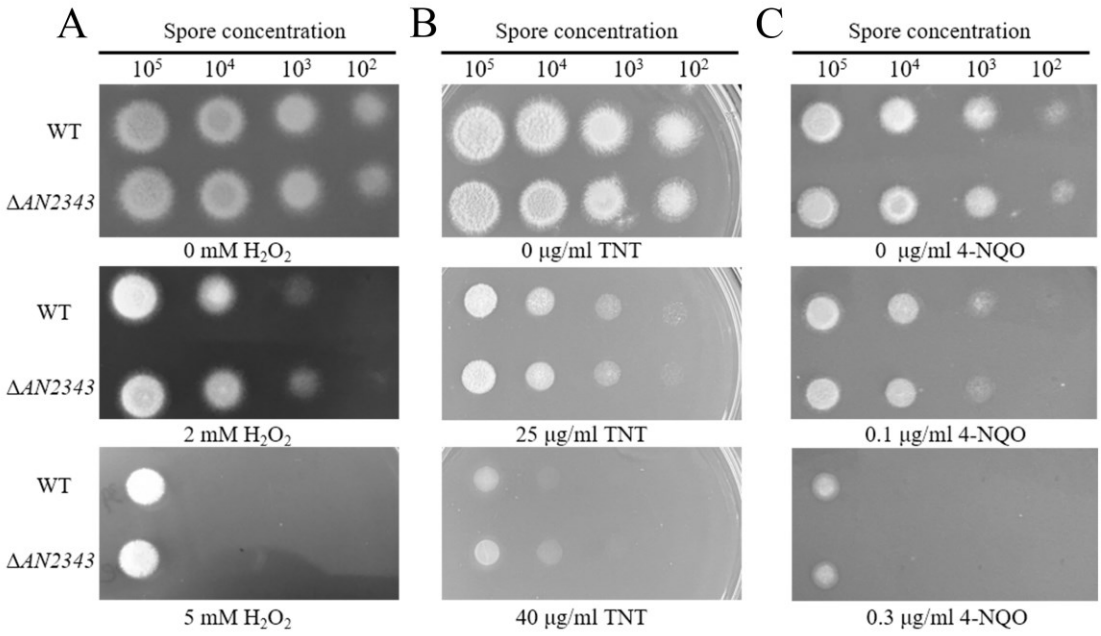

Fig S2. Effects of *AN2343* deletion on fungal sensitivities to H_2O_2, TNT, and 4-NQO. A series concentration of conidia of WT and Δ*AN2343* were spotted on MM plates containing 0, 2, and 5 mM H_2O_2 (A); 0, 25, and 40 μg/ml TNT (B); 0, 0.1, and 0.3 μg/ml 4-NQO (C) and cultivated at 37℃ for 48 h.

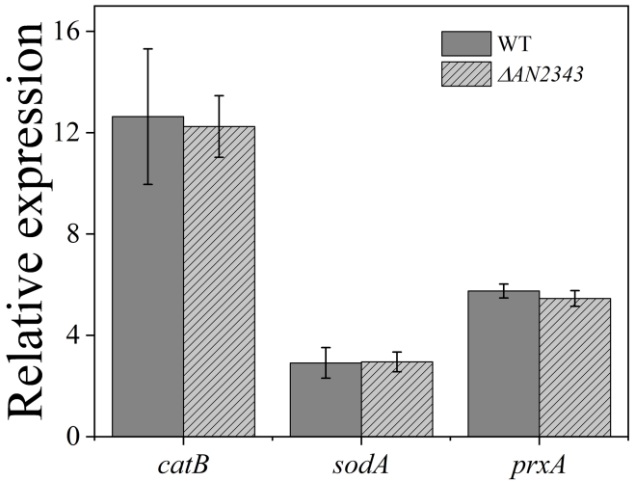

Fig S3. Q-RT-PCR analysis of transcription levels of the ROS resistant genes *catB*, *sodA*, and *prxA* in response to menadione in WT and Δ*AN2343* strains. After pre-culturing for 16 h, the WT and Δ*AN2343* strains were exposed to 0.8 mM menadione for 3 h. The relative mRNA levels were normalized to that of *actA*. Data are the means ± S.D. of three independent experiments.

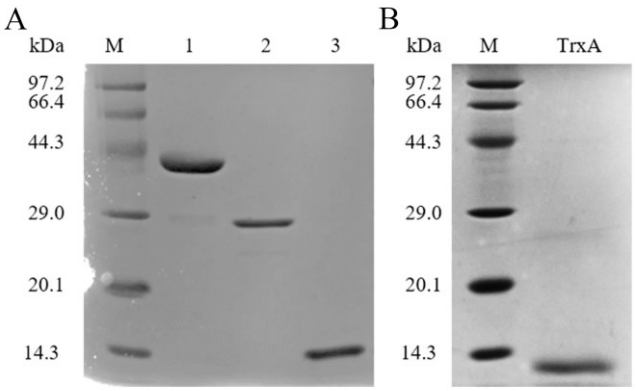

Fig S4. SDS-PAGE (10%) analysis of purified recombinant AnNTR (A) and TrxA (B). M, marker; Lane 1, Trx-tagged AnNTR; Lane 2, Trx-tag removed AnNTR (digested by thrombin); Lane 3, Trx-tag from tag removal of Trx-tagged AnNTR.

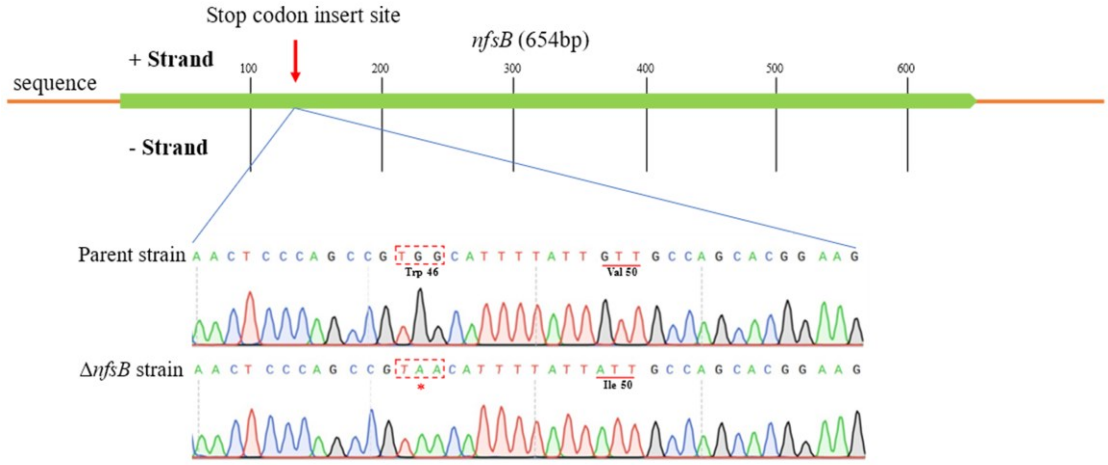

Fig S5. Sequence analysis of the *nfsB*-mutant strain revealed the successful insertion of a stop codon.