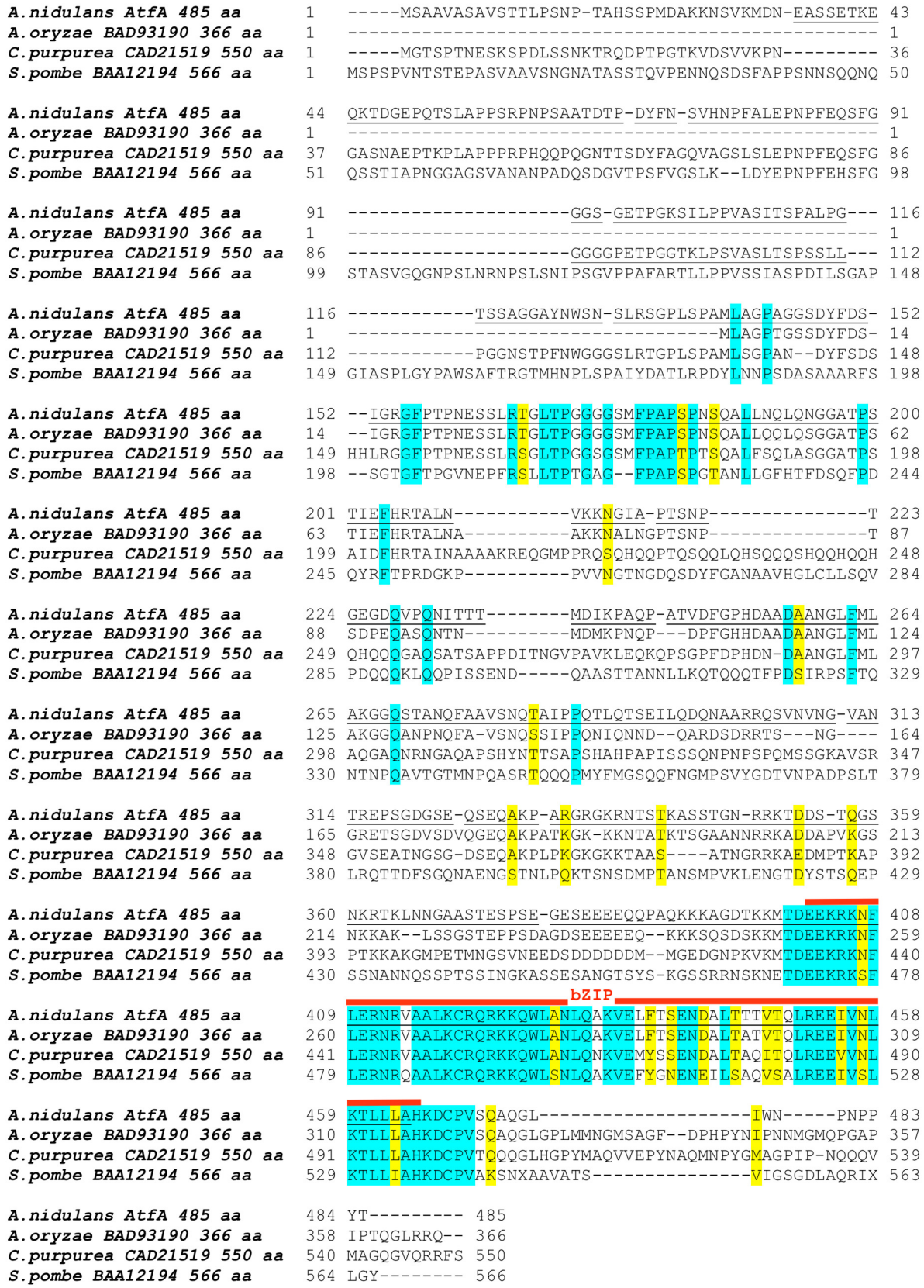

Fig. 1S. **The *atfA* gene encodes a putative transcription factor of ATF/CREB family.**
The amino acid sequence of *Aspergillus nidulans* AtfA is aligned with *Schizzosaccharomyces pombe* Atf1, *Claviceps purpurea* Cptf1 and *Aspergillus oryzae* AtfB. Secuences are identified by species name, GenBank accession number and protein size. Underlined sequence indicates the amino acids deleted in the Δ*atfA* mutant. The top red bar indicates the DNA binding domain as deduced from Expasy-Prosite database (http:://www.expasy.org/prosite/).

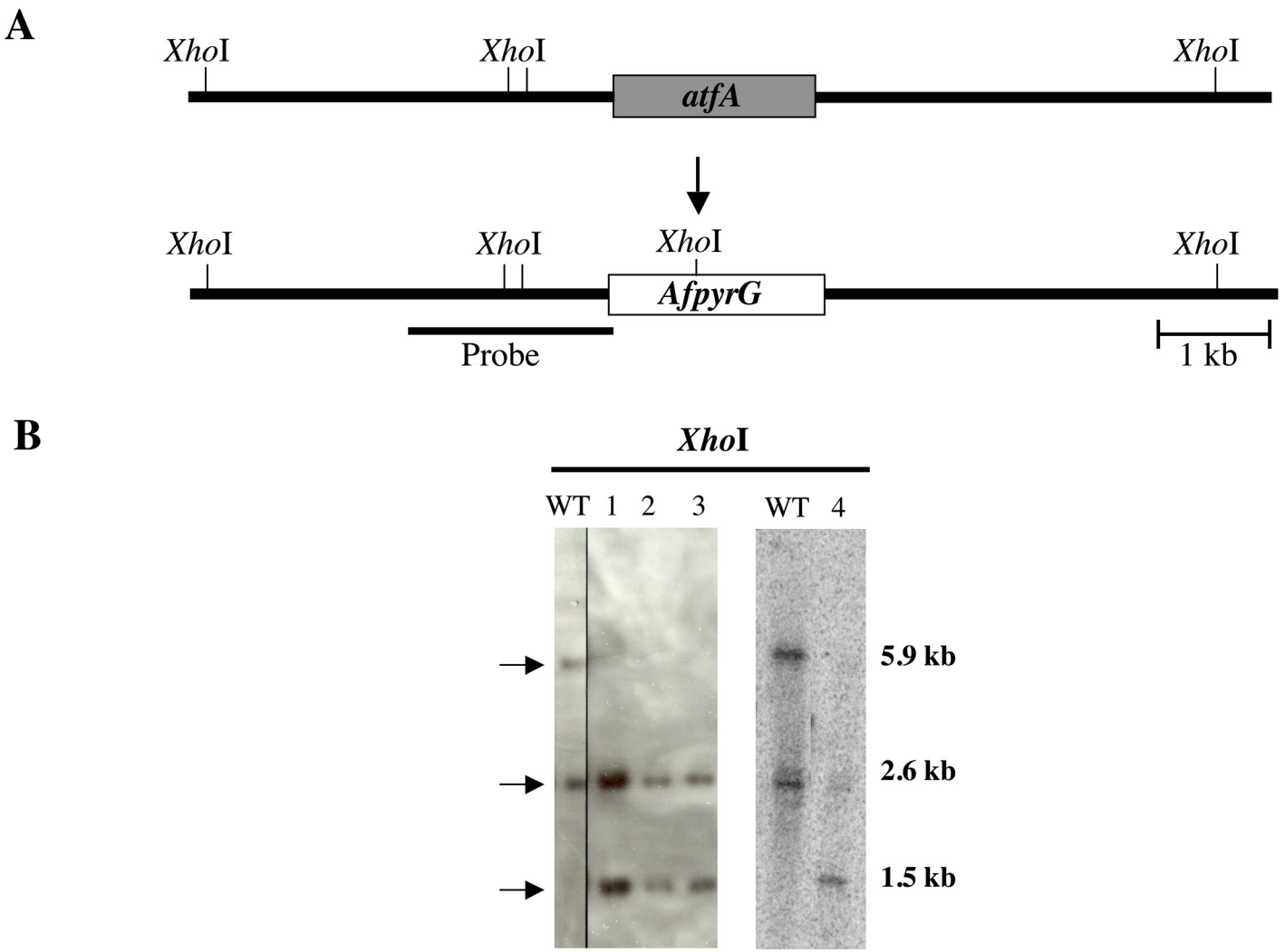

Fig. 2S. **Deletion of the *atfA* gene. (A)** The *atfA* deletion construct containing the *AfpyrG* gene as selective marker was generated by double-joint PCR and used to transform strains CFL3 and 11035. Double recombination results in the replacement of wild type *atfA* by the deletion construct. **(B)** DNA from WT and PyrG^{+} transformants from CFL3 (1-3) and 11035 (4) strains was digested with *Xho*I and used for Soutern blot analysis with the probe indicated in (A). The wild type *Xho*I pattern correspond to bands of 5.9 and 2.6 kb while Δ*atfA* pattern corresponds to bands of 2.6 and 1.5 kb.

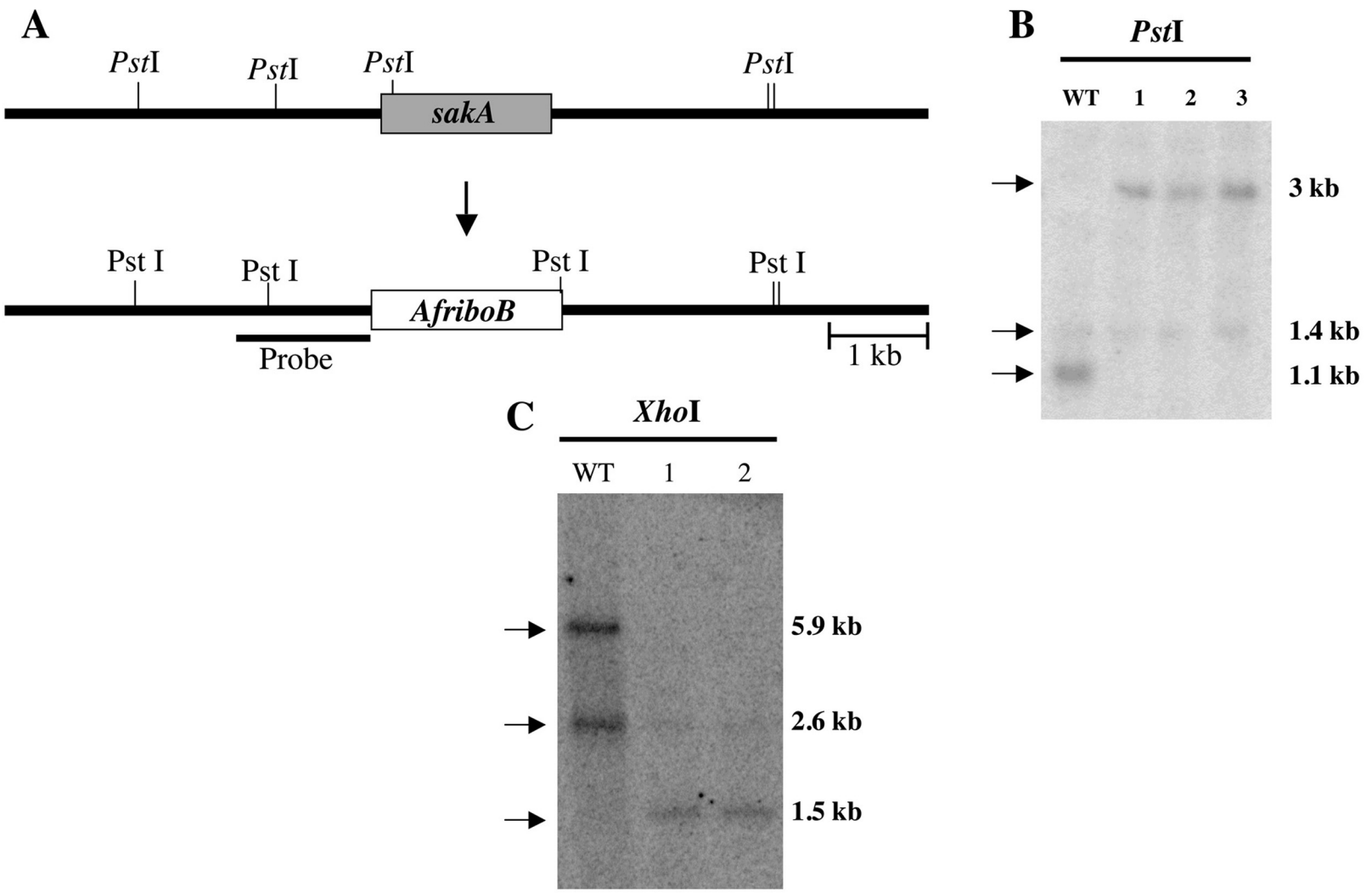

Fig. 3S. **Deletion of the *sakA* gene.** **(A)** A *sakA* deletion construct containing the *AfriboB* gene as selective marker was used to transform strain 11035. **(B)** To verify *sakA* deletion DNA of WT and RiboB$^+$ transformants (1-3) was digested with *Pst*I and used for Southern blot analysis with the indicated probe (A). Wild type *Pst*I pattern correspond to bands of 1.4 and 1.1 kb; Δ*sakA* pattern corresponds to bands of 1.4 and 1.1 kb. **(C)** Δ*sakA* Δ*atfA* double mutants were generated by transformation of Δ*sakA* strain TFLΔsakA-03 with the *atfA-AfpyrG* construct. *atfA* deletion was confirmed in PyrG$^+$ transformants 1 and 2, by Southern blot analysis as in Fig. 2S.

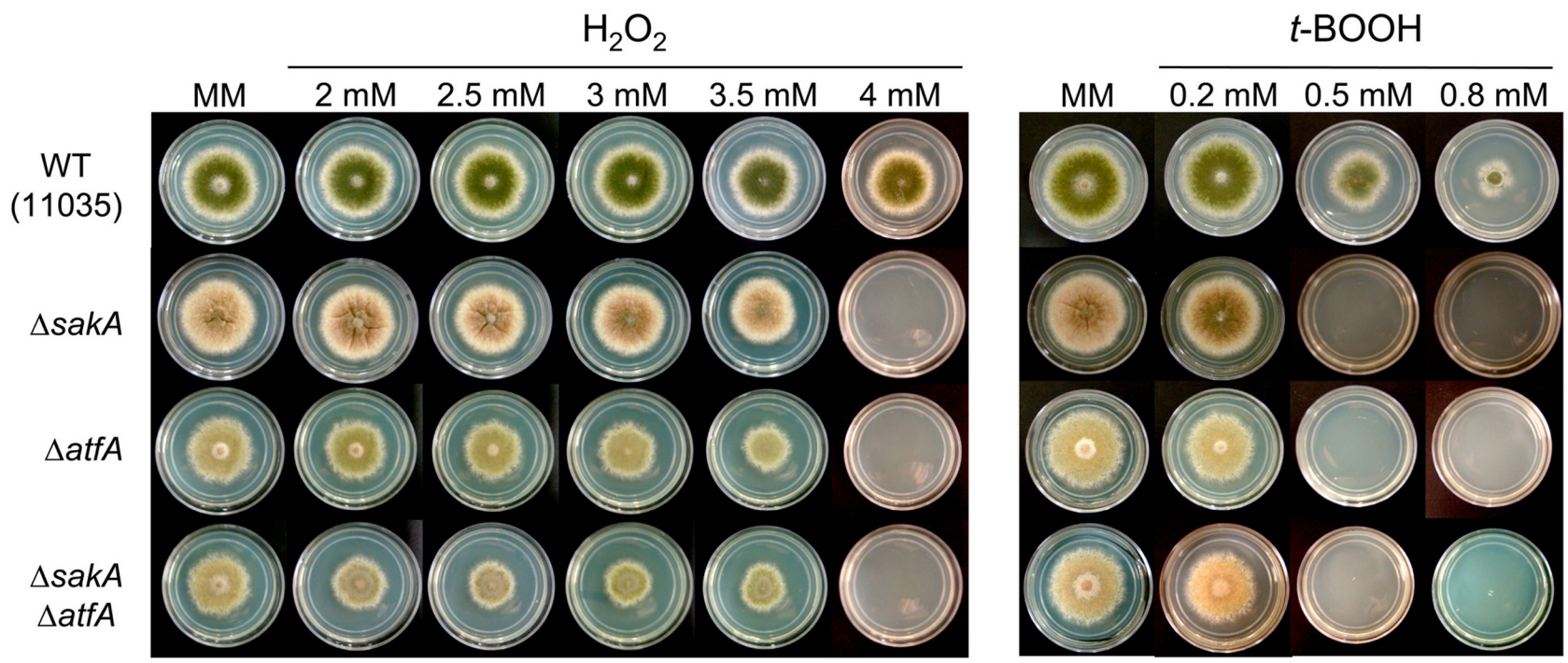

FIG. 4S. **Spores from single and double Δ*sakA* and Δ*atfA* mutants are equally sensitive to H_2O_2 and *t*-BOOH.** Conidia (10^4) from strains 11035 (WT), TFLΔsakA-03 (ΔsakA), TFLΔatfA-04 (ΔatfA) and TFL4 (Δ*sakA* Δ*atfA*) were inoculated on plates containing de indicated concentrations of H_2O_2 or *tert*-butyl hydroperoxide (*t*-BOOH) and incubated for 4 days at 37 ºC.

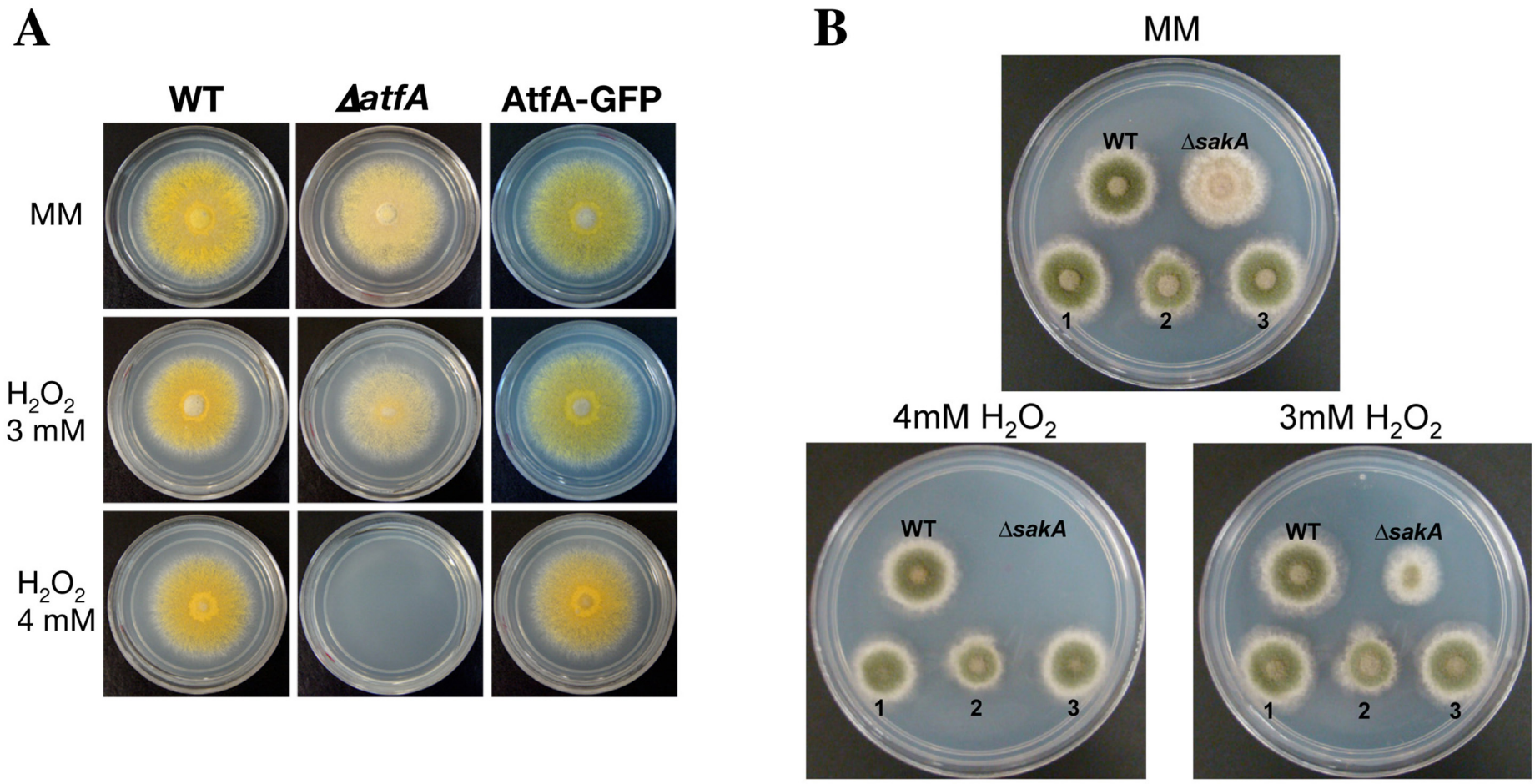

Fig. 5S. **GFP tagging does not interfer with *atfA* or *sakA* function. (A)** Conidiospores (10^4) from strains CLK43 (WT), CFLΔatfA-02 (Δ*atfA*) and TFL3 (*atfA-GFP*) were inoculated on plates containing 3 or 4 mM H_2O_2 and incubated at 37° C for 4 days. **(B)** Conidiospores from strains A1155 (WT), TFLΔsakA-03 (Δ*sakA*) and three *sakA-GFP* transformants were point inoculated on plates containing 3 or 4 mM H_2O_2 and incubated at 37° C for 3 days. Transformant 3 was named TFL6 and selected for further experiments.

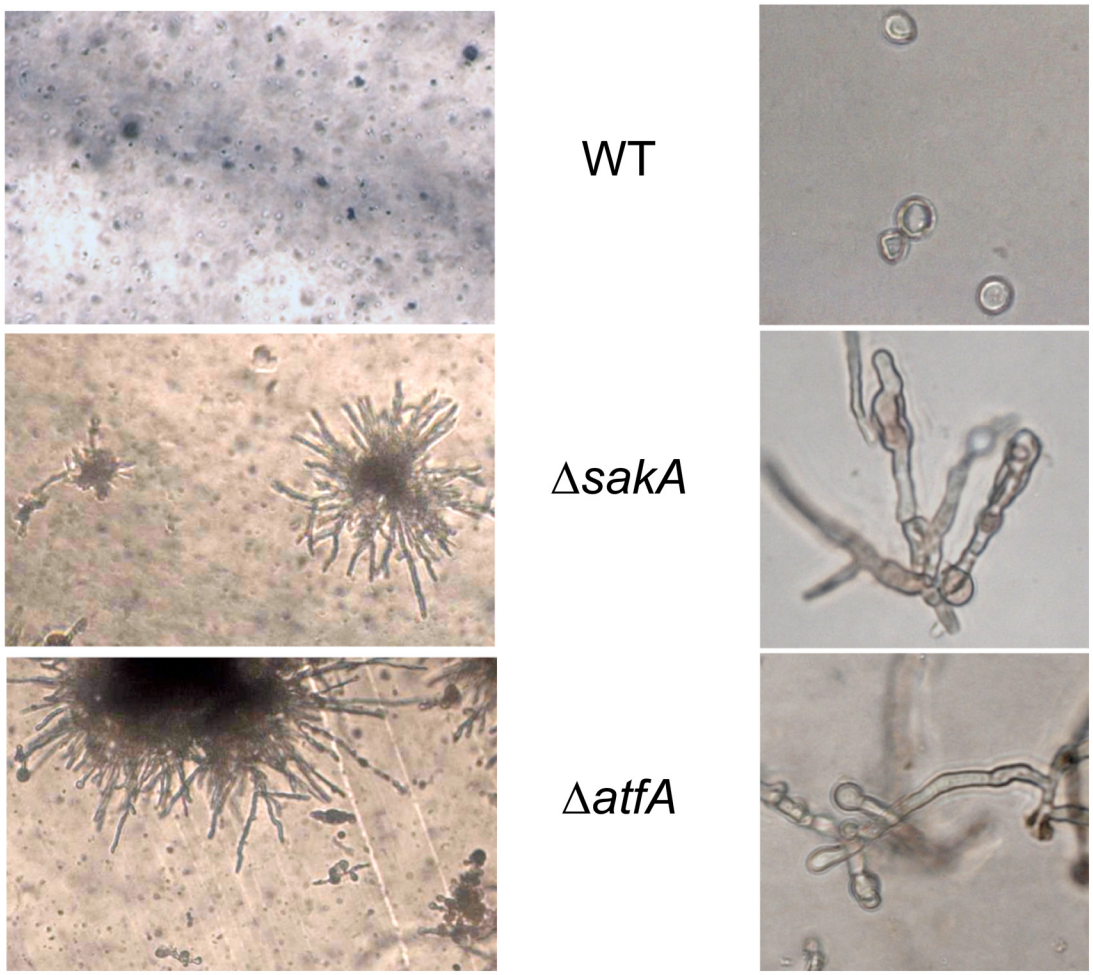

Fig. 6S. **Germination of WT, Δ *sakA* and Δ*atfA* conidia in the presence of fluidoxonil on solid medium**. Conidia from indicated strains were streaked on plates containing minimal solid medium plus 2 µg/ml of fludioxonil and incubated at 37 °C for 4 days. Pictures were taken under the microscope directly from inverted plates (left, 10X objective) or from samples scraped and transferred to a glass slide (right, 40X objective).

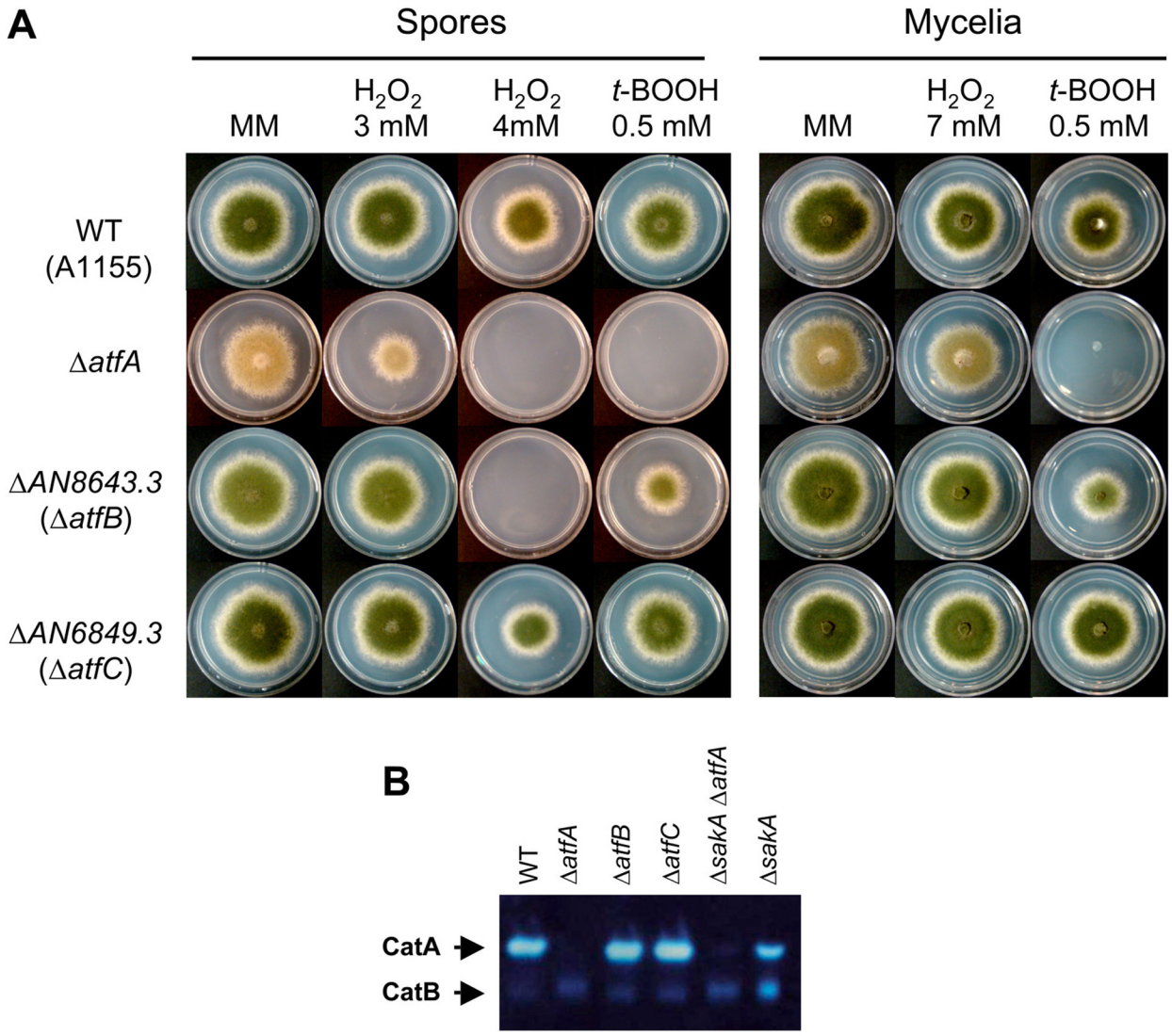

Fig 7S. **Oxidative stress sensitivity and spore catalase activity in mutants lacking putative transcription factors AtfA, AtfB and AtfC**. **(A)** Genes *AN8643.3* (*atfB*) and *AN6849.3* (*atfC*) were deleted in strain A1155, confirmed by Southern blot analysis and tested as in Fig. 1. **(B)** 30 µg of protein extract prepared from spores of the indicated strains were processed as in Fig. 2, to determine catalase activity.