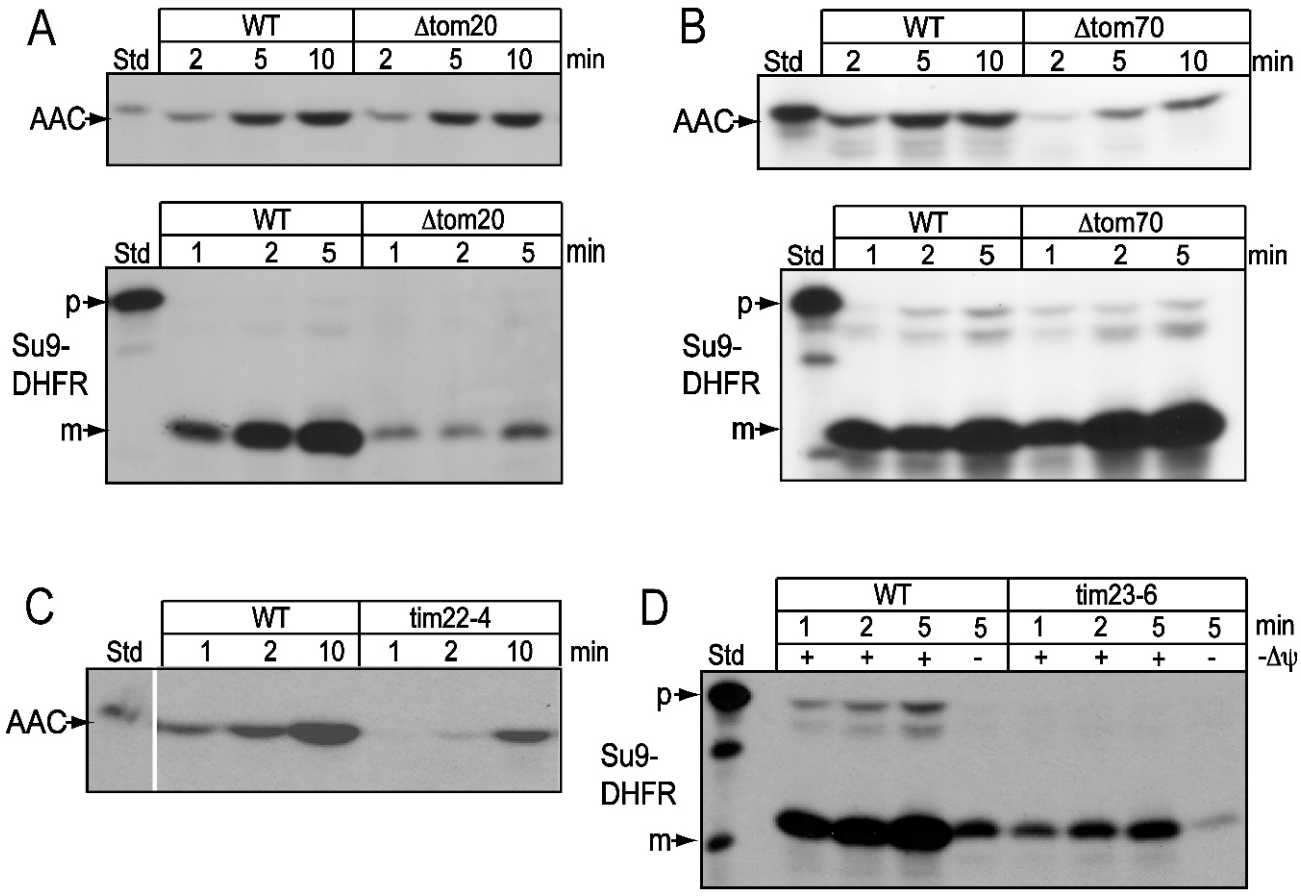
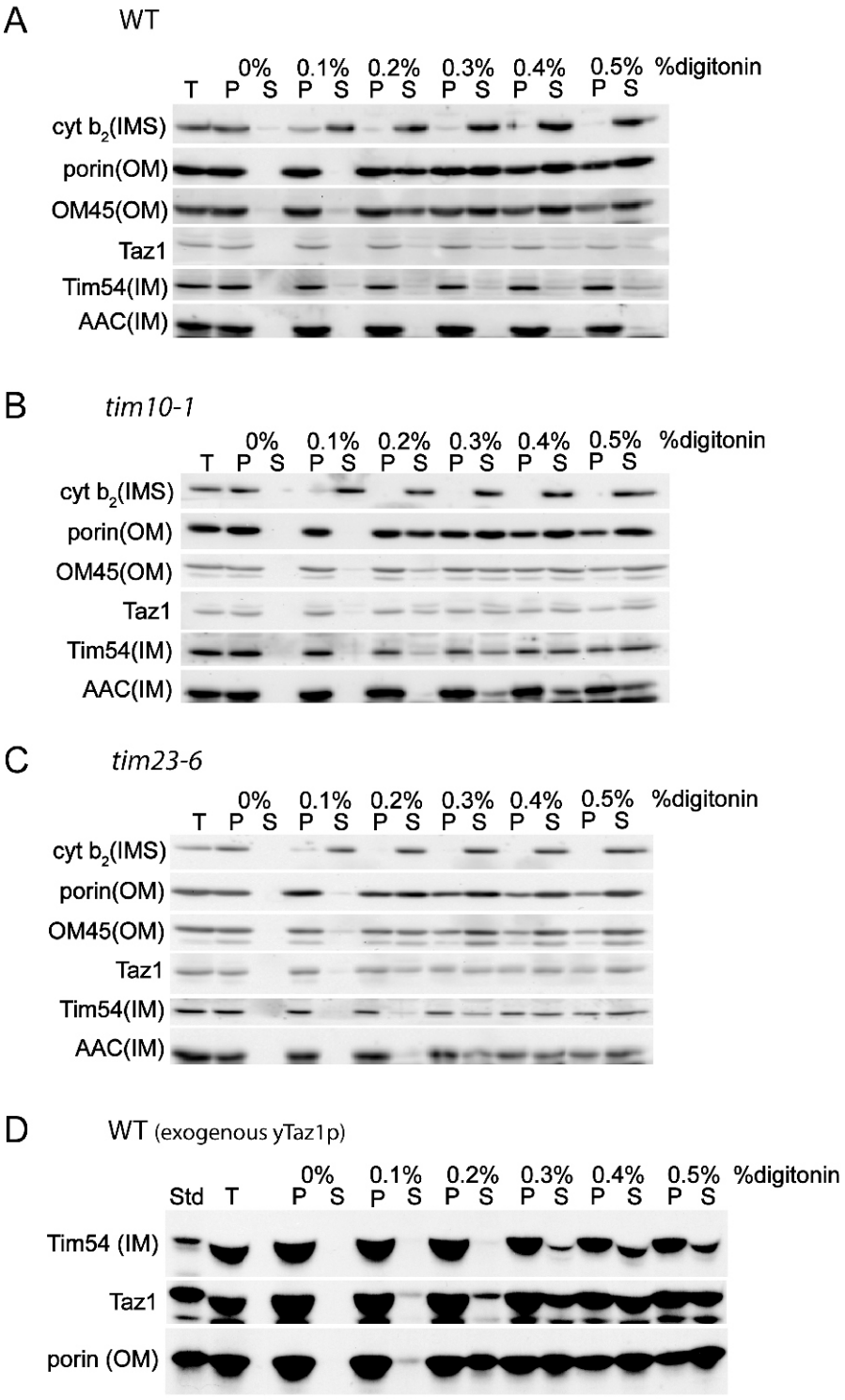
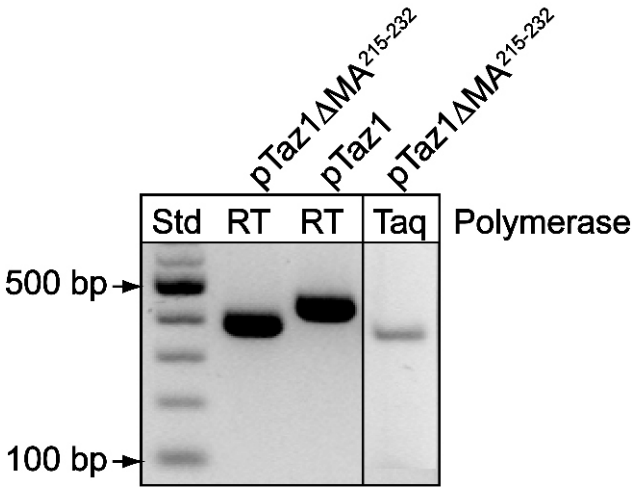


SUPPLEMENTAL FIG 1. The control precursors AAC and Su9-DHFR were imported into the following mutant mitochondria: (A) Δ*tom20*, (B) Δ*tom70*, (C) *tim22-4* and (D) *tim23-6*.



SUPPLEMENTAL FIG 2. (A-C) Immunoblot analysis for the digitonin solubilization experiments of Fig. 3. Purified mitochondria from each strain were solubilized in increasing amounts of digitonin, centrifuged at high speed, and analyzed as described in Fig. 3. 50 µg of mitochondria were used as a loading control for each marker (T). Images were captured with a BioRad Versadoc.



SUPPLEMENTAL FIG 3. To insure that the Taz1pΔMA$^{215-232}$ transcript was expressed (Fig. 5), total RNA from the Taz1pΔMA$^{215-232}$ strain was purified, treated with DNase, and subjected to RT-PCR using primers that amplified an internal sequence within the tafazzin open reading frame. The amplified products were visualized on an agarose gel stained with ethidium bromide. When Taq polymerase was used during the first amplification step, the signal was barely detected, indicating that there was minimal DNA contamination in the sample. As a control, RT-PCR analysis for the *TAZ1* transcript was also conducted on the WT strain.