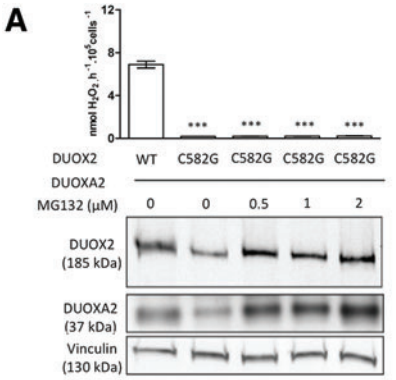
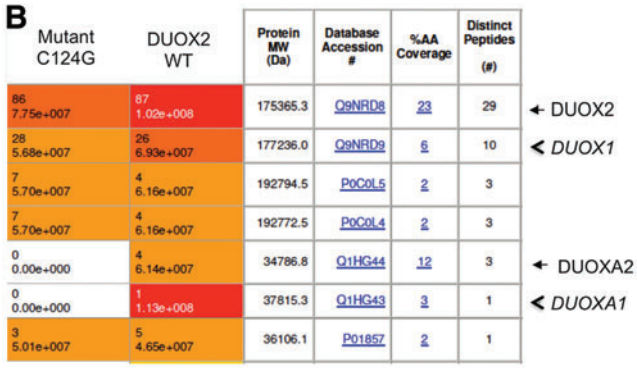
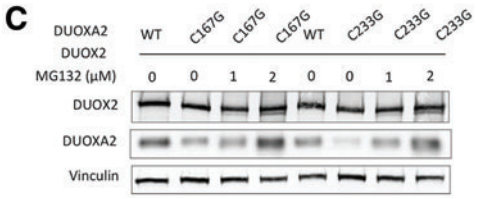
Supplementary Data







SUPPLEMENTARY FIG. S1. Oxidative folding of DUOX2 controls both stability and function of DUOXA2. **(A)** No extracellular H_2O_2 production of mutant DUOX2 C582G despite an increased DUOXA2 expression after treatment of cells with MG132. ***$P < 0.001$. **(B)** Table of data resulting from mass spectrometry analysis of high-molecular-weight complexes shown in Figure 3A. Note the total absence of detection of DUOXA2 peptides with mutant DUOX2 C124G. The Spectrum Mill score for the DUOX2 (Q9NRD8) is 461.7 and the respective score for DUOXA2 (Q1HG44) is 39.75. In addition, note that the Spectrum Mill score of 15 is sufficient for full confidence in the peptide identification. Peptides identified by the algorithm matching with DUOX1 and DUOXA1 sequences show 100% identity to DUOX2 and DUOXA2 protein sequences. Concerning the numbers in the *first two columns*, the number on the *top* corresponds to the number of times where the peptide has been identified and the *bottom* number is an average intensity of the peptides, which is illustrated with a gradient of color shade. **(C)** SDS-PAGE analysis of expression of wild-type (WT) DUOX2 and DUOXA2 WT or mutant proteins coexpressed in HEK293 cells pretreated for 12 h with increasing concentrations of MG132. DUOXA2, DUOX activator 2; SDS-PAGE, sodium dodecyl sulfate–polyacrylamide gel electrophoresis.