Figure S1. Comparative BN-PAGE analysis of the oligomeric structure of mTMEM16A(a), mTMEM16A(ac), and the concatenated mTMEM16A(a) homodimer. (A–D) Proteins labeled with $^{35}$S-methionine and Cy5 were purified and resolved by BN-PAGE in both their non-denatured and SDS-denatured states to determine their higher-order structure (A,B). The labeled proteins were also resolved in the fully SDS-denatured state with reducing SDS-urea-PAGE to determine their protomeric masses (C,D). The upper and lower panels refer to the $^{35}$S-methionine-labeled total form and the Cy5-labeled plasma membrane-bound form of the polypeptides. Note that the non-denatured mTMEM16A(a) and mTMEM16A(ac) migrate to the same position as the concatenated mTMEM16A(a) dimer (2mer), which as a covalently linked dimer is unaffected by the SDS pre-treatment. The orange double oval indicates the position of the concatenated mTMEM16A(a) homodimer.