Supplemental Data

SUPPLEMENTAL FIGURE LEGENDS

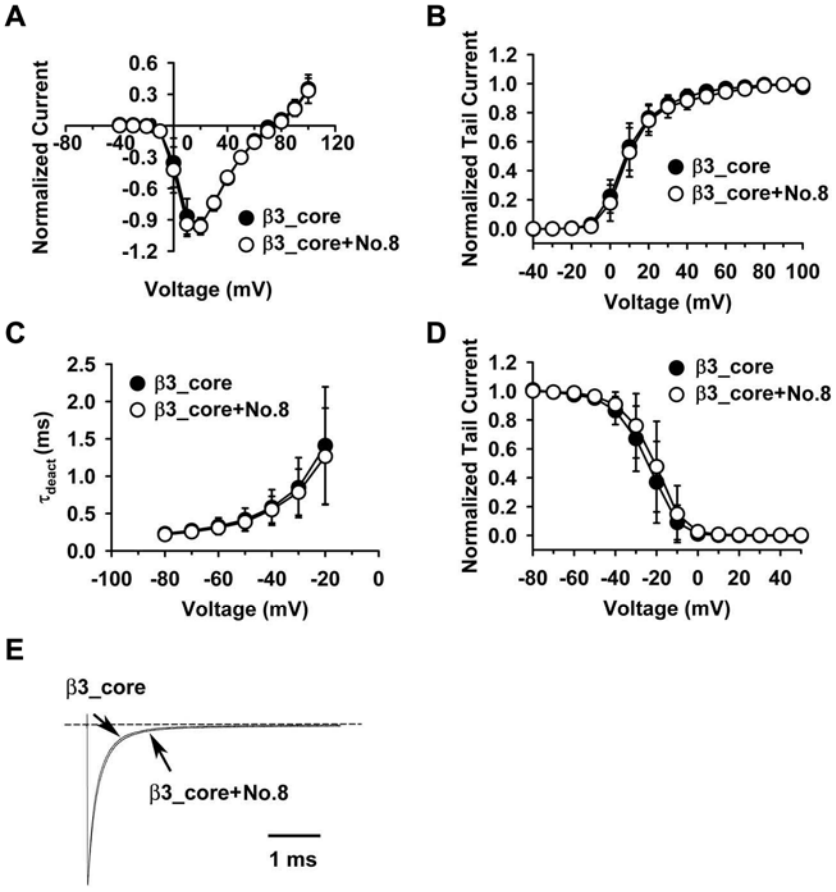
FIGURE S1. **Alignment of the amino acid sequence of the S Tail.** The predicted S tails from the indicated animal species were aligned with the human S tail using the ClustalW2 program. Amino acids different from those in the human S tail are in red. The length of each S tail is indicated on the right. Note that the predicted rabbit and mouse S tails are 14 and 22 amino acids shorter than the human S tail.

FIGURE S2. **Lack of effect of the S tail on Ca^{2+} channel properties.** cRNA of No.8 was co-injected into *Xenopus* oocytes with the channel complex cRNAs, and cell-attached patch clamps (*A*-*E*) were performed. β_3_core, amino acids G16-G366 of full length β_3, is as potent as β_3 to regulate channel activation and membrane targeting (5,45). *A,* current-voltage relationship. *B,* voltage-dependent activation. *C,* deactivation constant τ_{deact}. *D,* voltage-dependent inactivation. *E,* representative inactivation traces. N=5-6.

FIGURE S3. **Co-localization of overexpressed No.8 and β_3 in the nuclei of HEK 293T cells.** *A,* No.8 (fused with DsRed) and β_3 (fused with EGFP) were expressed separately. *B,* three individual examples, displayed in three rows, showing the co-localization of No.8 and β_3 in the nuclei when they were co-expressed. Note that the two proteins aggregate on the nuclear membrane. Bar, 10 μm.

Zhang et al., Figure S1

Zhang et al., Figure S2



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