SUPPLEMENTAL MATERIAL

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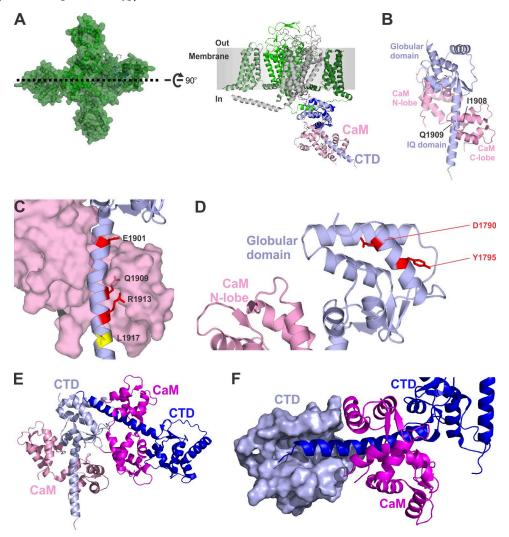


Figure S1. **CaM** interaction with the Na_V CTD. (A) CaM (pink) binds to the cytoplasmic CTD of Na_V channels (blue). Left panel shows the $Ca_V1.1$ $\alpha1$ subunit structure viewed from the top (PDB accession no. 5GJV; Wu et al., 2016). The right panel is rotated 90° and provides a possible orientation of the intracellular CTD ($Na_V1.5$) in complex with CaM (PDB accession no. 4OVN; Gabelli et al., 2014). (B) The isolated heterodimer of CaM associated with the $Na_V1.5$ CTD. The globular domain and the IQ domain are indicated, along with the location of its signature lle and Gln residues (Ile1908 and Gln1909). (C) Focus on LQT3 residues that interact with the CaM C-lobe, which wraps around the IQ domain to bury Gln1909 and Arg1913. Glu1901 interacts with the top of the CaM C-lobe. (D) Focus on LQT3 residues in the globular domain. (E and F) Proposed interaction between two $Na_V1.5$ CTD–CaM heterodimers based on arrangement of heterodimers observed in the crystal unit cell (PDB accession no. 4OVN).

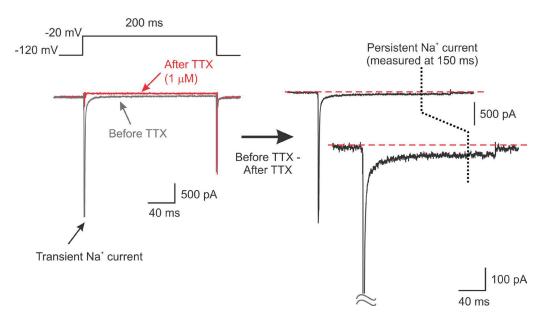


Figure S2. Measurement of persistent Na $^+$ current from Na $_V$ 1.5^{TTX-S}. (left) Exemplar traces of Na $_V$ 1.5^{TTX-S} expressed in HEK293T cells before and after application of 1 μ M TTX. (right) Subtraction of the TTX-sensitive background current leaves the TTX-resistant Na $^+$ channel current. (inset) At a magnified scale.

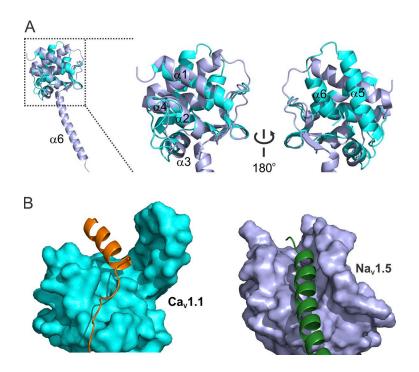


Figure S3. Structural parallels between the $Na_V1.5$ and $Ca_V1.1$ CTDs. (A) Overlay of the $Ca_V1.1$ (cyan) and $Na_V1.5$ (purple) CTDs. Note the structural homology from α helix $\alpha1$ to α helix $\alpha4$, but not for α helix $\alpha5$ and α helix $\alpha6$. (B) Structural homology showing the interaction of the III-IV linker (orange) with the globular domain of the $Ca_V1.1$ CTD; and a $Na_V1.5$ CTD IQ domain ($\alpha6$) with the globular domain of a second $Na_V1.5$ CTD (see also Fig. 3, A and B).

REFERENCES

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