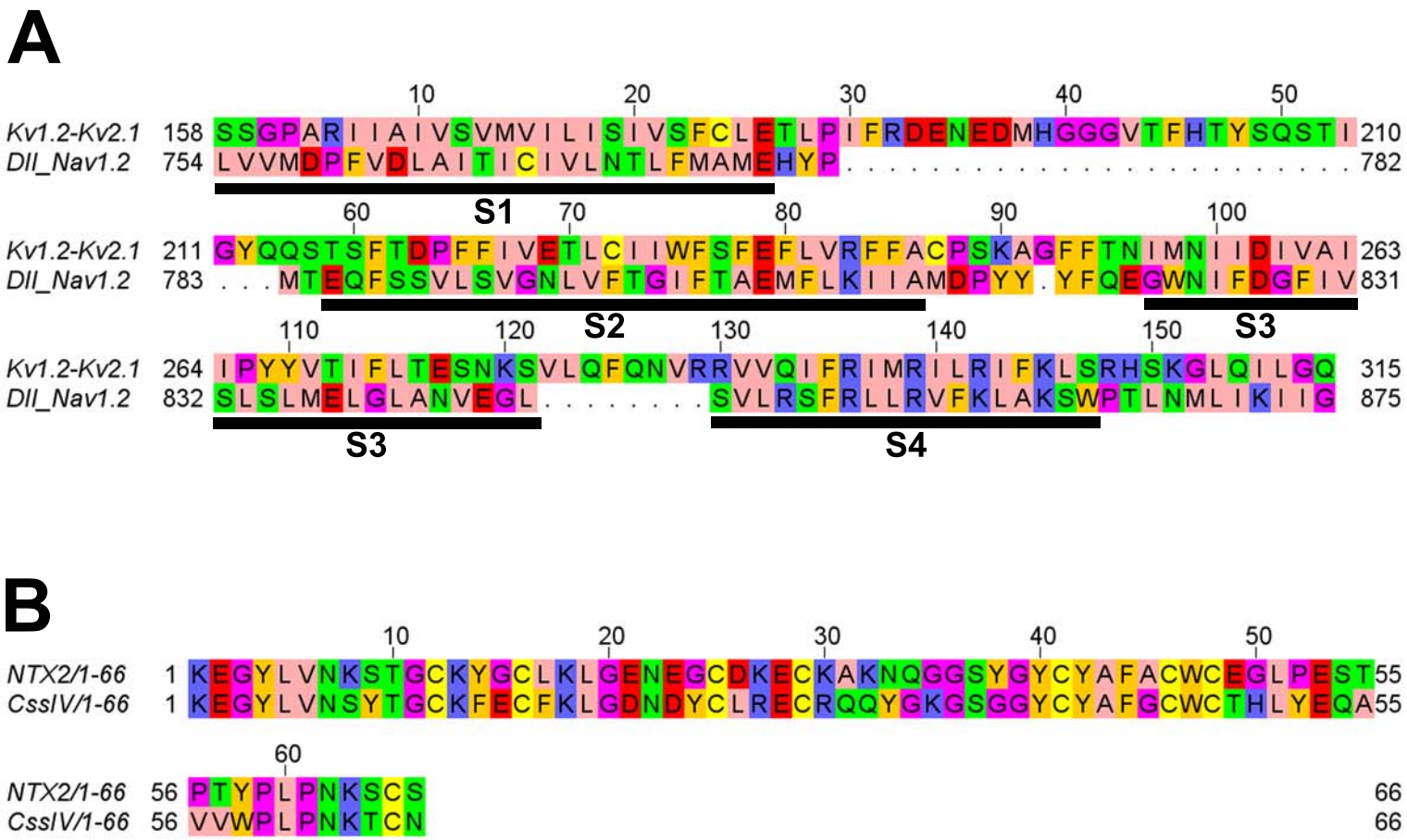
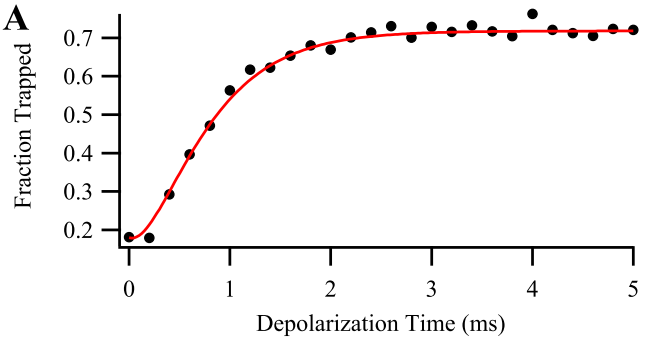
Supplementary Figures and Legends

SUPPLEMENTARY FIGURE 1. Amino acid sequence alignment. ***A***, sequence alignment between the voltage-sensing domain II of Nav1.2 and voltage-sensing domain of Kv1.2-Kv2.1 chimera channel. ***B***, sequence alignment between β-scorpion CssIV toxin and neurotoxin 2 (NTX2, pdb code: 1JZA). Residues were colored with Jalview program (Waterhouse et al., 2009) using the Zappo color scheme, where hydrophobic residues (I, L, V, A, and M) are colored pink, aromatic residues (F, W, and Y) are colored orange, positively charged residues (K, R, and H) are colored blue, negatively charged residues (D and E) are colored red, hydrophilic residues (S, T, N, and Q) are colored green, P and G colored magenta, and C is colored yellow.

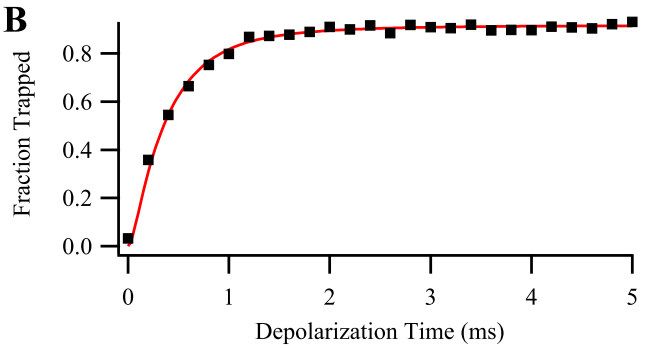
SUPPLEMENTARY FIGURE 2. Fitting a voltage-sensor trapping model to time courses of voltage sensor trapping for N842R, E884N and V843A. *A-C*, Fits of voltage-sensor trapping model to onset of voltage-sensor trapping data obtained from N842R (*A)*, E844N (*B*) and V843A (*C*). The trapping time course data were scaled by setting the 1 ms point equal to the fraction of current trapped at 1 ms obtained from current-voltage relationships recorded after 1 ms prepulses in Figs. *3C*, 5*B*, and *5D* and corrected for the amount of trapping that reversed during the 60 ms between the prepulse and the test pulse as measured from the trapping reversal time courses of Figs. 4*D* and 6*E*. These data were fit to the model shown in *D* with the parameters given in *E.* Every channel was assumed to have a bound toxin molecule at the concentration used for these mutant channels. The activation process was assumed to be irreversible at +50 mV with the rate controlled by parameter, *k1*.


A
10
20
30
40
50
Kv1.2-Kv2.1 158 SSGPARIIAIVSVMVILISIVSFCLETLPIFRDENEDMHGGGVTFHTYSQSTI 210
Dll_Nav1.2 754 LVVMDPFVDLAITICIVLNTLFMAMEHYP.....782
S1
60
70
80
90
100
Kv1.2-Kv2.1 211 GYQQSTSFTDPFFIVETLCIIWFSFEFLVRFFACPSKAGFFTNIMNIIDIVAI 263
Dll_Nav1.2 783 ...MTEQFSSVLSVGNLVFTGIFTAEMFLKIIAMDPYY.YFQEGWNIFDGFIV 831
S2
S3
110
120
130
140
150
Kv1.2-Kv2.1 264 IPYYVTIFLTESNKSVLQFQNVRRVVQIFRIMRILRIFKLSRHSKGLQILGQ 315
Dll_Nav1.2 832 SLSLMELGLANVEGL.....SVLRSFRLLRVFKLAKSWPTLNMLIKIIG 875
S3
S4
B
10
20
30
40
50
NTX2/1-66 1 KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPEST 55
CssIV/1-66 1 KEGYLVNSYTGCKFECFKLGDNDYCLRECRQQYGKGSGGYCYAFGCWCTHLYEQA 55
60
NTX2/1-66 56 PTYPLPNKSCS 66
CssIV/1-66 56 VVWPLPNKTCN 66

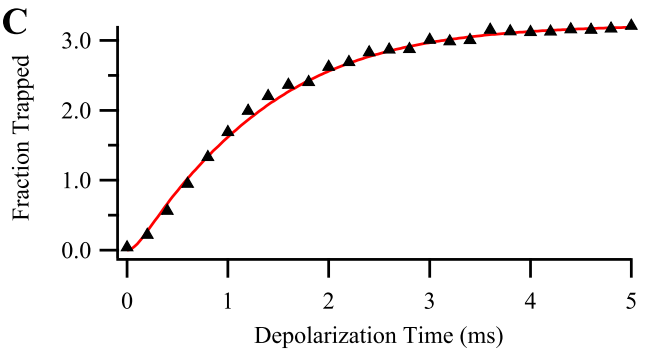
A



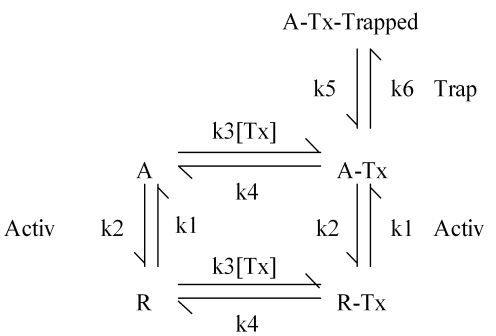
B



C



D



E

	N842R	E844N	V843A
Activation (k1, s^{-3})	3	25	5.3
Trapping (k5, s^{-3})	1.4	2.4	4.8
Untrapping (k6, s^{-3})	0.55	0.48	0.15