

### Supporting Information

**Figure S1.** Sequence alignments of human Kv7.1 (Swiss-Prot P51787), rat Kv1.2 (PDB ID 2A79, chain B) and *Streptomyces lividans* KcsA (PDB ID 1BL8). Multiple sequence alignment corresponding to S1, S2, S3, S4 and the S4-S5 linker was performed with ClustalW using all sequences provided in the web site <http://vkcdb.biology.ualberta.ca/> for the Kv1, 2, 3, 4 and 7 families. The alignment corresponding to the pore domain (S5-Pore helix-S6 segment) was performed with the program T-COFFEE (see Materials and methods). Black background indicates identical amino acids. Grey background indicates similarities according to size, hydrophobicity, aromaticity, charge and polarity. The letter “h” denotes alpha helix in the 3-D structural models of Kv7.1.

S1

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Kv7.1 120 WKCFVYHFAVFLIVLVCLIF  
Kv1.2 161 PARIIAIVSVMVILISIVSF

S2

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Kv7.1 153 TGTLEWMEIVLVVVEFGTEYVRLWS  
Kv1.2 219 TDPFEIVETLCIWFSEFLVRFFA

S3

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Kv7.1 198 ISTIDLIVVVASMVVLCVGSK  
Kv1.2 255 MNIIDIVAIIPYFITLGTELA

S4

S4-S5 linker

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Kv7.1 222 FATSARGIRFLQILRMLHVDROGGTWRLLGSVVF  
Kv1.2 288 MSLAILRVIRLVRFRIFKLSRHSKGLQILGQTLK

S5

Pore helix

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Kv7.1 257 -IHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVT  
Kv1.2 323 -ASMRELGLLIFFLFIGVILFSSAVYFAEADERDS---QFPSIPDAFWWAVVSM  
KcsA 23 ALHWRAAGAATVLLVIVLLAGSYLAVLAERGA---AQLITYPRALWWSVETAT

S6

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Kv7.1 312 TIGYGDKVPQTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQ 357  
Kv1.2 374 TVGYGDMVPTTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNFYHR 419  
KcsA 75 TVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWVFGREQ- 119