## **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.

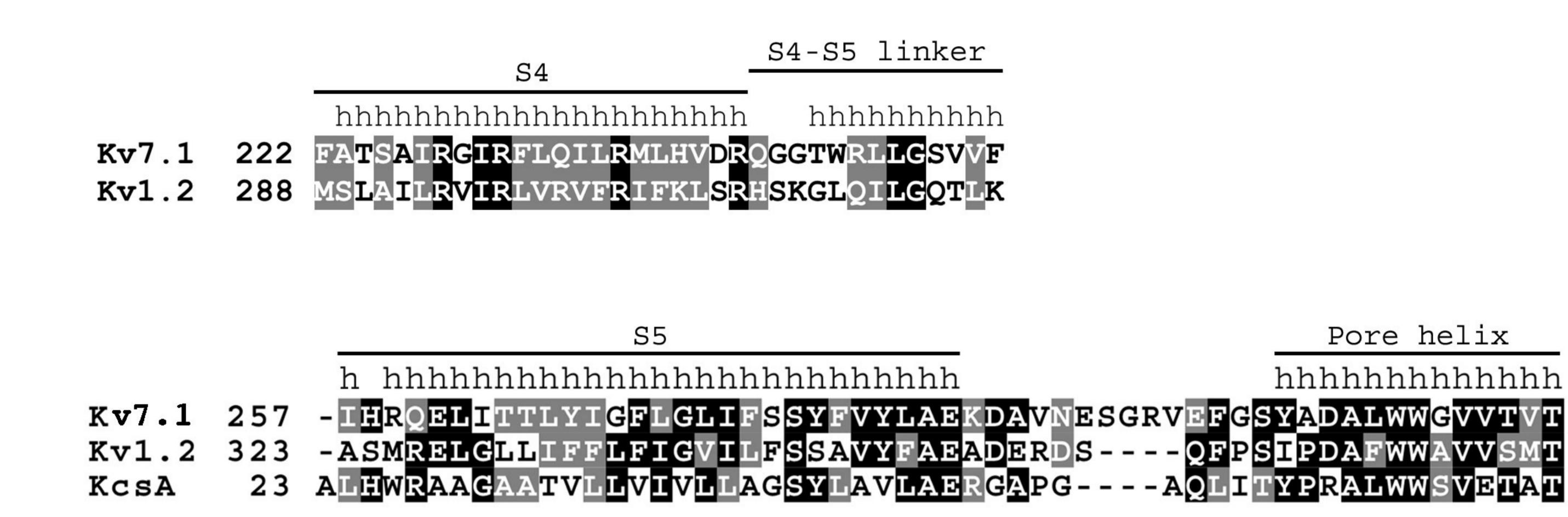


Kv1.2 161 PARIIAIVSVMVILISIVSF

## S2

## 





Kv7.1	312	TIGYGDKVPQTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQ TVGYGDMVPTTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHR TVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQ-	357
Kv1.2	374	TVGYGDMVPTTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHR	419
KcsA	75	TVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQ-	119