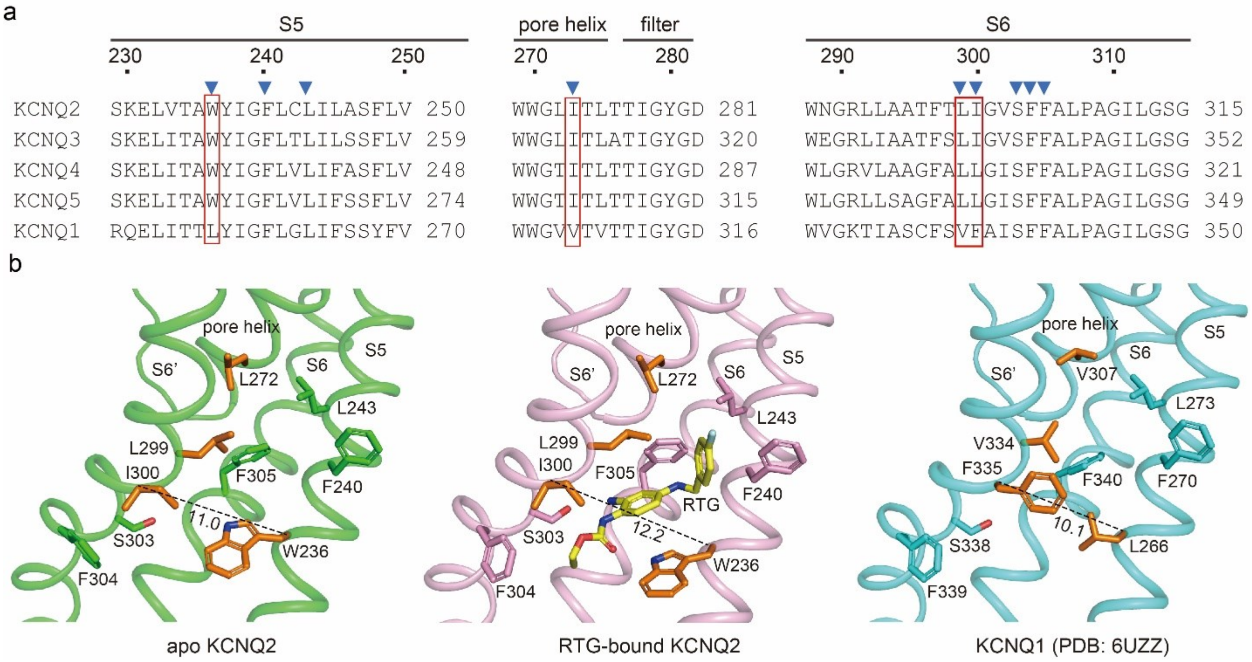

Fig. S10 The sequence and structure comparisons of pore domain among KCNQ family. a Sequence alignments of S5, pore helix and S6 in the KCNQ family. Secondary structures are assigned based on the apo KCNQ2 structure. Blue triangles indicate residues interacting with RTG in KCNQ2. Red boxes highlight the four residues that are not conserved in KCNQ1. **b** Structures of the RTG binding pocket in apo (green) and RTG-bound (pink) KCNQ2, and equivalent region in KCNQ1 (cyan). Side chains of residues (or equivalent residues in KCNQ1) interacting with RTG in KCNQ2 are shown as sticks. The four variable residues are shown in orange. Numbers show distances (in Å) between Cα atoms of Trp236 and Ile300 in KCNQ2 (or equivalent residues in KCNQ1).