Suppl. Information: Overview, preliminary & unpublished data (*Please keep confidential*).

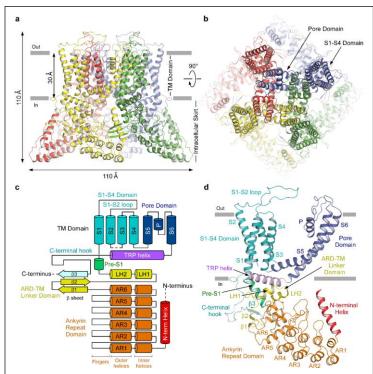


Figure 1. Architecture and domain organization of TRPV6. a-b. Side (a) and top (b) views of human TRPV6 structure. c. Domain organization diagram of the TRPV6 subunit. d. Single TRPV6 subunit, with domains colored as in c.

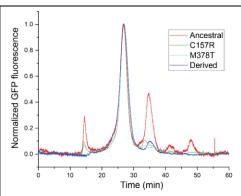


Figure 3. FSEC screening of nonsynonymous polymorphisms. Shown are normalized FSEC traces following eGFP fluorescence for two individual nonsynonymous polymorphisms as well as ancestral and derived TRPV6 variants. The main peak represents the prevailing tetrameric species.

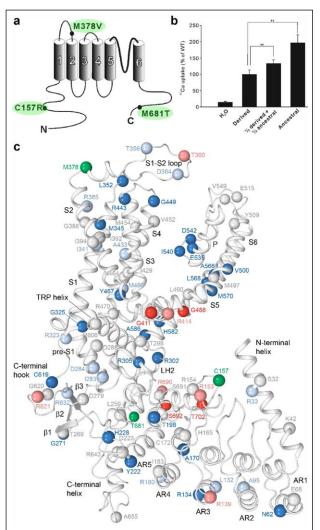


Figure 2. Genetic variability of TRPV6. a. Location of three major non-synonymous TRPV6 polymorphisms. **b.** Ca²⁺ uptake in *Xenopus* oocytes. **c.** Disease-associated mutations in hTRPV6. Spheres indicate mutations that result in <20% (blue), 20-90% (light blue), no change (grey), and 110-150% (light red) activity compared to wild type or toxic Ca²⁺ overload (red). Non-synonymous polymorphisms are in green.

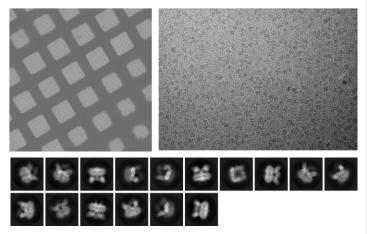


Figure 4. Example atlas (upper left panel) and micrograph (upper right panel) of a hTRPV6 screening and 2D class averages (lower panel).