



**Supplementary Figure S1. Whole exome sequencing (WES) and homozygosity mapping reveals 3 potential candidate genes for recessive distal renal tubular acidosis (dRTA).**

(A-F) Homozygosity maps across the genome were generated using nonparametric Lod scores based on WES variant data using Homozygosity Mapper. Homozygosity mapping identifies multiple recessive candidate loci (red circles) in dRTA families B1022 (A), F382 (B), B2673 (C, D) and F588 (E). WES identifies homozygous mutations in the gene *ATP6V1C2*, located within the maximum NPL peak on chromosome 2 in B1022 (arrowhead) (A), in the gene *WDR72*, located in the homozygosity peak on chromosome 15 in F382 (B), and B2673 (C, D) and in *SLC4A2*, located in a peak on chromosome 7 (E) in F588. Gene loci are indicated by arrowheads.