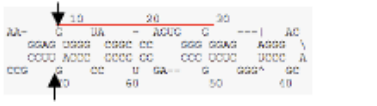
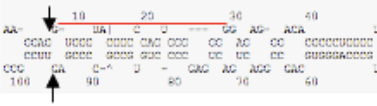
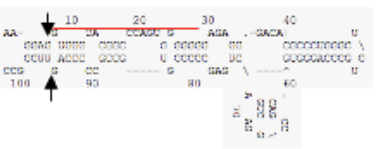


Variant	Structure	Pathogenicity	Mechanism
WT		N/A	N/A
IVS45+34_+47del14		Indeterminate	unknown
IVS45-36_-12del25		Highly likely pathogenic	Splice
IVS45-3C>G		Likely pathogenic	Splice
IVS45-14T>C		Highly likely pathogenic	miRNA*

Supplemental Figure 3. Documented intron 45 variants in *PKD1* that were analyzed in this study. Downward arrows indicate the 5' splice site, Up arrows indicate the 3' splice site. Mature miR-1225-5p sequence is highlighted by the red line. Pathogenicity and mechanisms of pathogenicity are based on the ADPKD variant database (<https://pkdb.mayo.edu/>) and/or published reports (19). *previously reported to alter splicing, our results suggest that it disrupts miR-1225. Variants that removed the miRNA, directly mutated or deleted the splice sites, or removed part of intron 45 and exon 46 simultaneously were not included.