

**Supplementary Figure 2**

The c.12608\_12635del mutation in the *PKD1* gene was predicted to change the open reading frame, cause the loss of the original stop codon UAG at position 4304, and introduce a new stop codon UAA at position 4348 (p.Arg4203Profs\*146), leading to a prolonged abnormal protein with 44 amino acid longer than the wildtype protein. The pink underline indicated the 28bp deletion from c.12608 to c.12635.