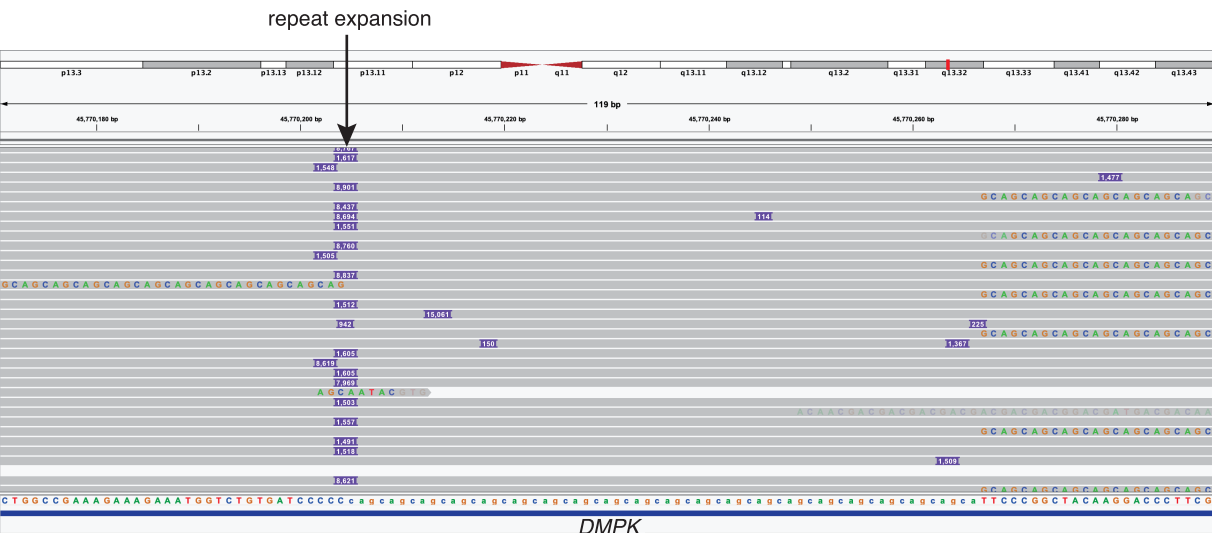




Supplementary Fig. S6 Validation of the 3 ' UTR repeat expansion in *DMPK* by long-read sequencing. A sample exhibiting *DMPK* repeat expansion was sequenced using Oxford Nanopore long-read sequencing. Sequencing was performed on the PromethION 2 Solo device, and the sequencing library was prepared using the Library Ligation Kit V14 according to the manufacturer' s protocol. Base calling was performed with Dorado v0.9.1, and the reads were mapped to the human reference genome (hg38) using Minimap2 (v.2.28). The figure visualizes the expanded region in the 3 ' -UTR of *DMPK* as viewed in IGV. The numbers enclosed in purple boxes indicate the number of expanded bases