Supplementary Figure 1: Evolutionary conservation of the locus affected by the missense mutation p.Leu277Pro. PhyloP conservation scores computed from pairwise alignment of orthologous COQ8A sequences from 100 vertebrate species across the KxGK motif are shown against genome and protein coordinates. Positive phyloP scores indicate conserved residues. The mutated residue is indicated in red. Bottom panel: Protein sequence alignments of representatives of major clades. Source: UCSC Genome browser, modified.