



Supplemental Figure 1: (A) Predicted structure of WT PPP1R35 protein using the RaptorX server (Källberg et al., 2012). Yellow circle contains just the WT C-terminus of PPP1R35 which is the pink alpha helix. **(B)** Predicted structure of mutant PPP1R35 protein using the RaptorX server (Källberg et al., 2012). Yellow circle encompasses the pink C-terminal alpha helix containing the frameshift variant and elongated protein. In contrast to the WT C-terminus in (A), the mutant C-terminus is elongated by 1 spiral and the overall protein is extended by 18 amino acids. **(C)** Genomic representation of *PPP1R35* and hypothesized models for deletion. Green circles show location of indel. The homozygous, frameshifting indel includes the canonical stop codon (TAG in red) in the last exon of *PPP1R35*. Two models predicated on hairpin formation between the complimentary CG rich segments flanking the stop codon are proposed to explain the mechanism of mutagenesis.