



Supplementary File 1. **Tolerance to variation of TRAPPC9 exons.** SubRVIS percentiles of all TRAPPC9 exons. Lower subRVIS percentiles correspond to more intolerant regions. The blue dot shows the location of the residue Leu178. Exon 2 has a subRVIS score of 1,56, meaning that only 1,56 % of all the other exons from the genome have a more intolerant score. The high subRVIS SDP (53%) indicates a high degree of variation in the intolerance scores across the gene's exons.[17]