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Supplemental Data

Heterozygous Variants in *KMT2E* Cause a Spectrum of Neurodevelopmental Disorders and Epilepsy

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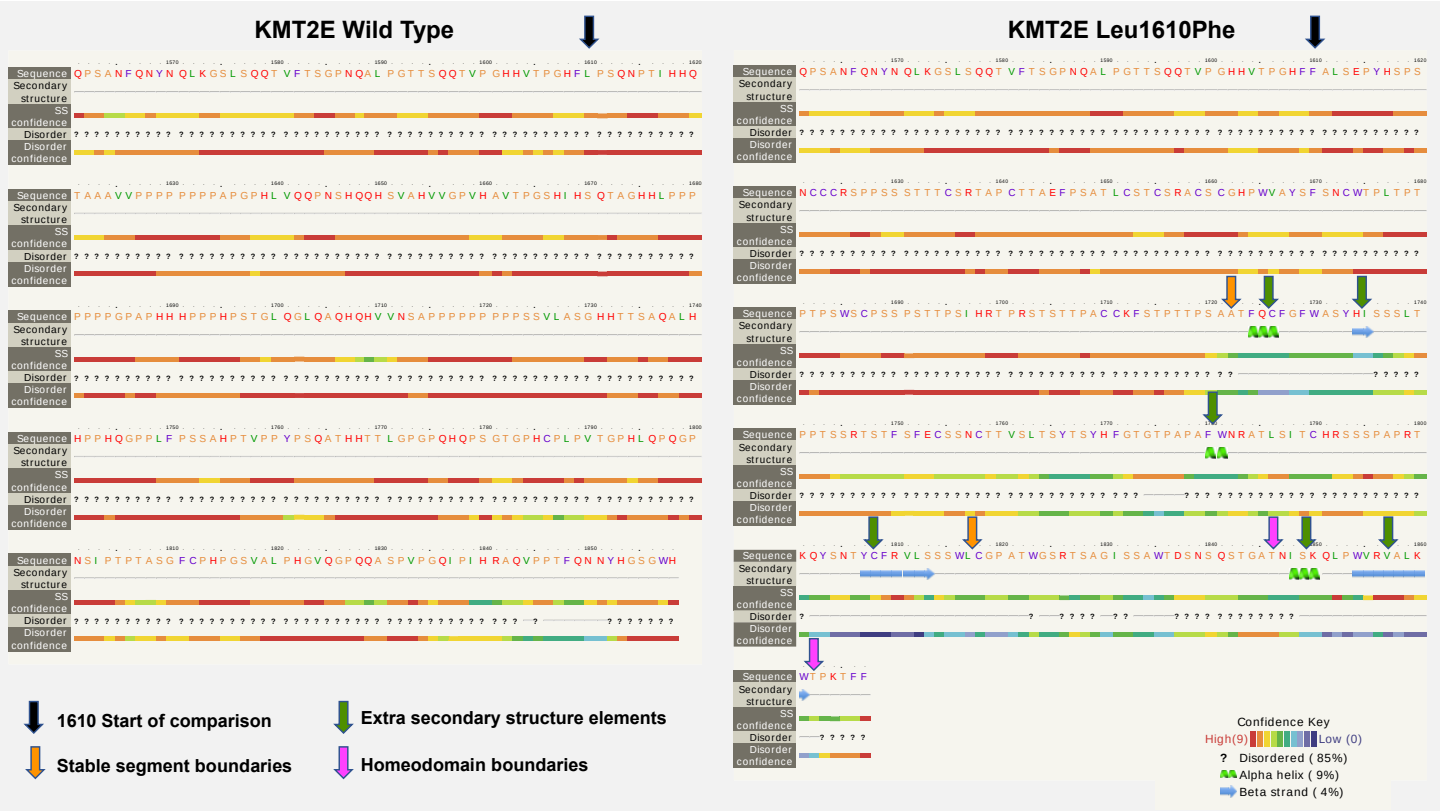

Figure S1. Frameshifting variants acquire stabilizing secondary structure elements. PHYRE[19] secondary structure report for the C-terminal fragments of KMT2E wild type (left panel, amino acids1560-1858) and KMT2E frameshifting variant Leu1610Phe (right panel, amino acids 1560-1867). Black arrows indicate the start of comparison at position 1610, after which the two variants are completely different due to a frameshift variant. The orange arrows indicate the boundaries of the stabilizing segment present in p.Leu1610Phefs*259 and p.Val1625Argfs*244 but not in wild type. The green arrows indicate the helices and strands not present in wild type. The pink arrows indicate the boundaries of the C-terminal predicted homeodomain present in p.Leu1610Phefs*259 and p.Val1625Argfs*244 but not in wild type. The confidence key (bottom right) indicates the reliability of secondary structure prediction (helix, strand, disorder) at each position.