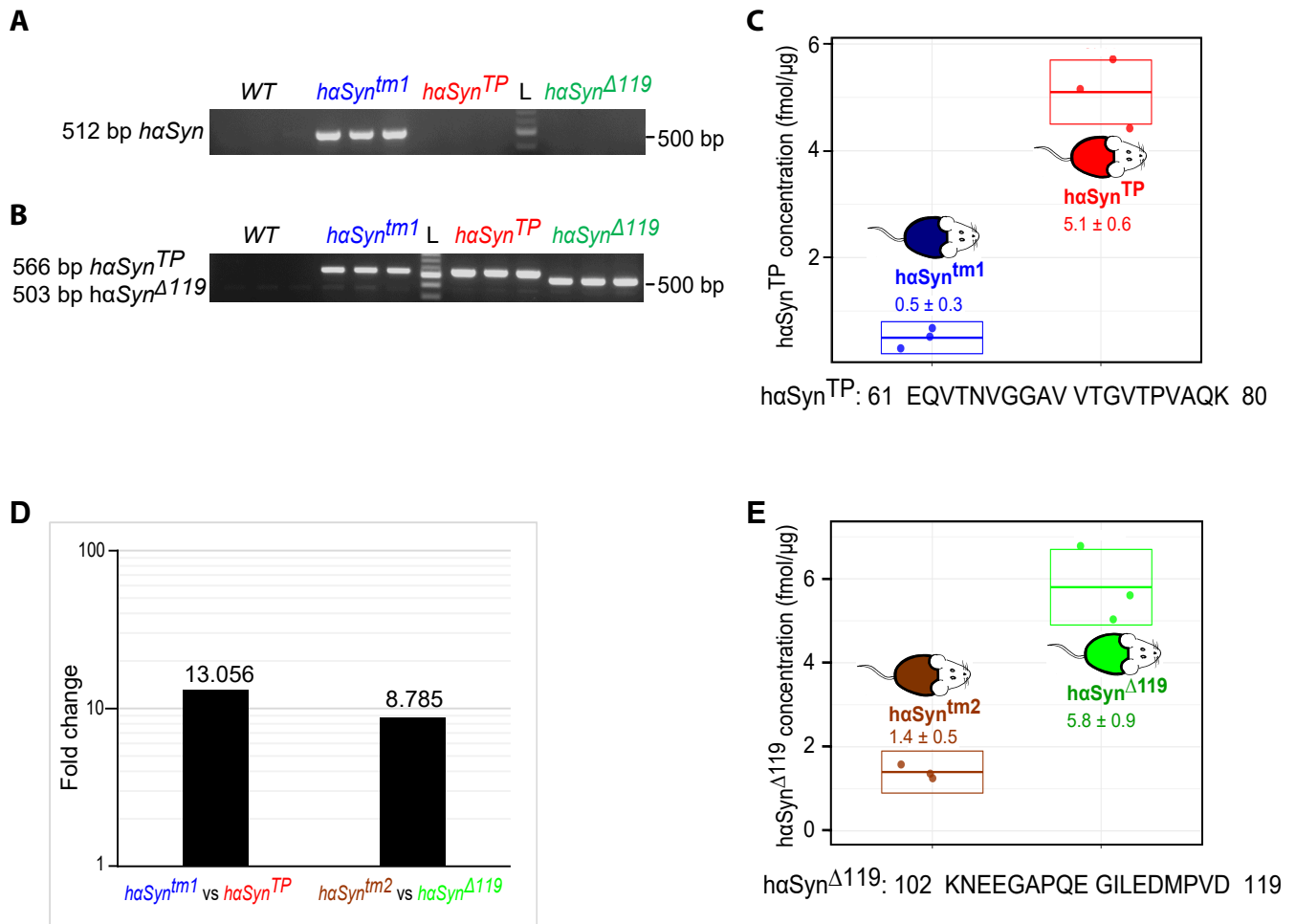


Supp. Fig. 4



**Supp. Fig. 4.** Analysis of *αSyn* transcripts (A, B, D) and proteins (C, E). **A.** RT-PCR using primers (sequence in Material and Methods) designed to identify *haSyn* produced the expected 512 bp band in *haSyn<sup>tm1</sup>* mice, but not in *haSyn<sup>TP</sup>* or *haSyn<sup>Δ119</sup>* mice. Data from cortical cDNA of 3 mice aged 1.5 years are shown. L: Ladder. **B.** RT-PCR using primers (Material and Methods) designed to identify *haSyn<sup>TP</sup>* produced the expected 566 bp amplicon in *haSyn<sup>TP</sup>* mice. This amplicon was also detected in *haSyn<sup>tm1</sup>* mice, and is the result of read-through transcription. Analogously, RT-PCR using primers identifying *haSyn<sup>Δ119</sup>* (sequence in Material and Methods) produced the expected 503 bp band in *haSyn<sup>Δ119</sup>* mice. Data from cortical cDNA of 3 mice aged 1.5 years are shown. L: Ladder. **C.** MS quantification of *haSyn<sup>TP</sup>* protein in 1.5 years old *haSyn<sup>tm1</sup>* mice using a *haSyn<sup>TP</sup>*-specific peptide (aa 61 - 80). We found an approximately 10-fold lower amount of *haSyn<sup>TP</sup>* protein in the parental strain when compared to age-matched *haSyn<sup>TP</sup>* mice. **D.** qPCR using *haSyn* pan-primers (recognizing wild type or mutant *haSyn*; sequence in Material and Methods) showed approximately 13 and 9 times more transgenic *haSyn* transcripts in the parental *haSyn<sup>tm1</sup>* and *haSyn<sup>tm2</sup>* strains than mutant transcripts in their corresponding *haSyn<sup>TP</sup>* or *haSyn<sup>Δ119</sup>* lines. Age of mice was 1.5 years. **E.** MS quantification of *haSyn<sup>Δ119</sup>* protein in 1.5 years old *haSyn<sup>tm2</sup>* mice using an *haSyn<sup>Δ119</sup>*-specific peptide (aa 102 – 119, full length *αSyn* would generate the aa 102 – 140 C-terminal peptide). We found *haSyn<sup>Δ119</sup>* protein in the parental strain but at approximately 4-fold lower level than in age-matched *haSyn<sup>Δ119</sup>* mice.