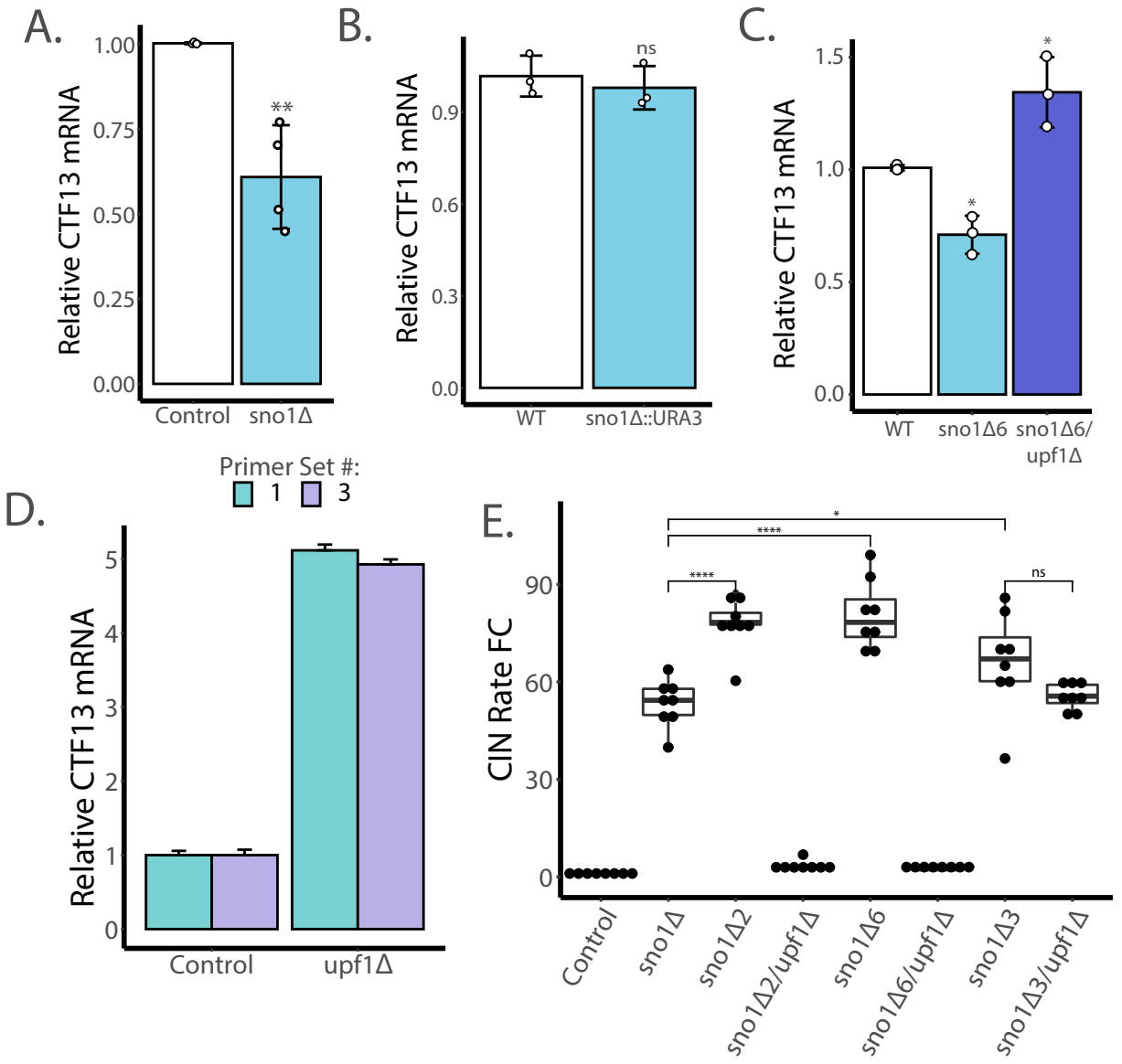

Figure S3. Analysis of *CTF13* mRNA abundance and length in KanMX insertion mutants in the presence and absence of NMD. A) qPCR analysis of *CTF13* mRNA levels expressed as fold changes performed on control and *sno1Δ* strains using a *CTF13* ORF primer set (set #1, see Supplemental Table S3). Six independent replicates were performed each including technical triplicates. Each values is normalized to the level of *ACT1* mRNA. Technical triplicates are averaged and pooled together and standard deviation is calculated for means of the independent strains. P-values are generated from a Tukey's post-hoc test. B) qPCR analysis (as described in section A) of *CTF13* mRNA levels expressed as fold changes performed on a wild-type strain and a *sno1Δ::URA3* strain using a *CTF13* ORF primer set (set #3). C) qPCR analysis (as described in section A) of *CTF13* mRNA levels expressed as fold changes performed on wild-type, *sno1Δ6*, and *sno1Δ6/upf1Δ* strains using a *CTF13* ORF primer set (set #3). D) qPCR analysis of the relative abundance of *CTF13* mRNA in a *upf1Δ* single mutant compared to a control strain. Only one independent isolate for each strain was used in this experiment and the standard deviation is measured from the technical triplicates. This result was validated using the same cDNA samples with two *CTF13* primer sets (#1 and #3). E) qCTF assay CIN rate measurements of control, *sno1Δ*, *sno1Δ2*, *sno1Δ3*, and *sno1Δ6* strains in the presence and absence of functional NMD. P-values are generated from a Tukey's post-hoc test.