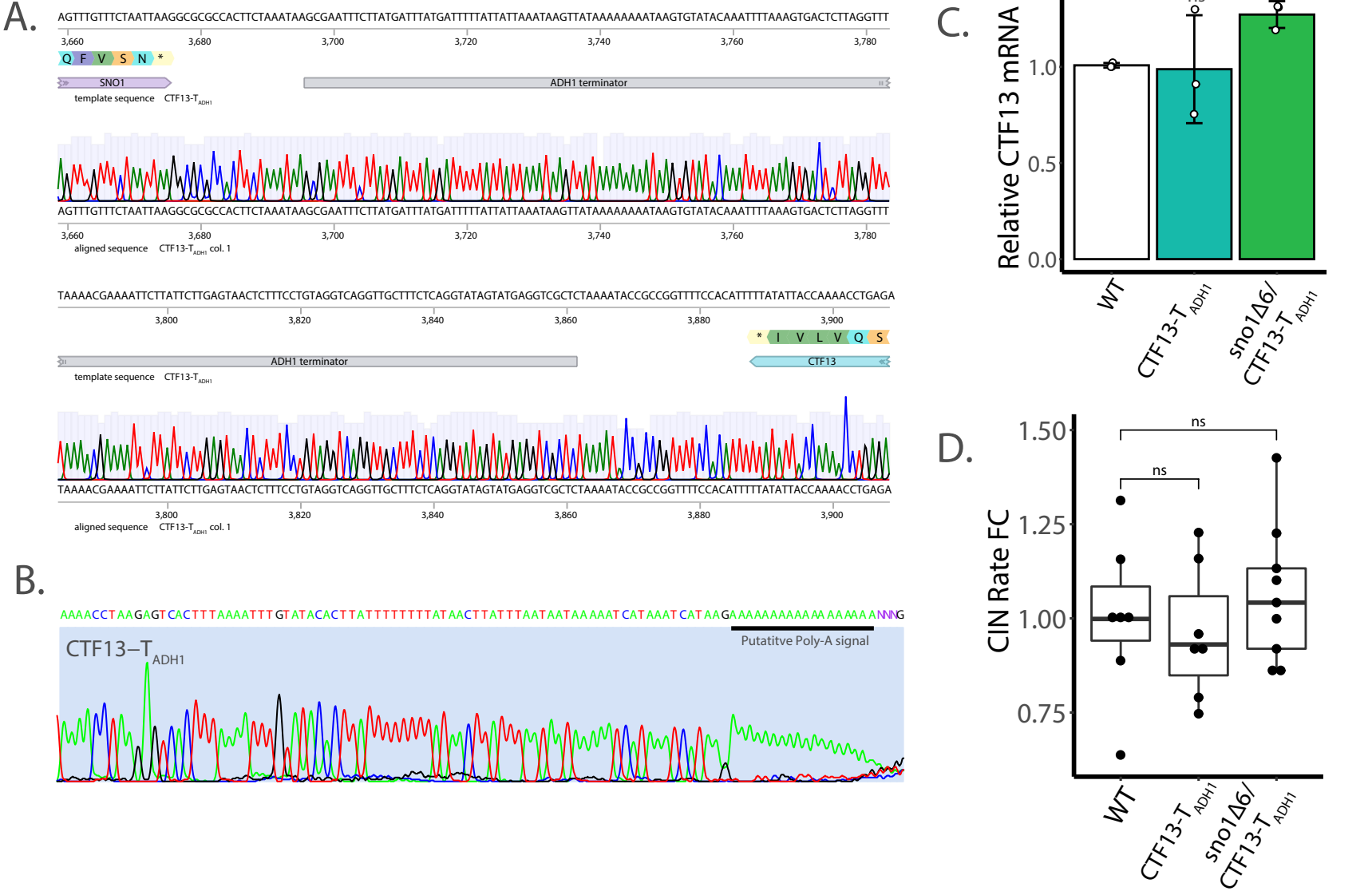


**Figure S4. Poly-adenylated *CTF13* mRNA suppresses CIN in the *sno1Δ6* mutant.** A) Graphical representation of the genotype of the *CTF13-T$_{ADH1}$* strain generated using Benchling software. T$_{ADH1}$ (grey box) is inserted at genomic coodinate chrXIII:457284 within the intergenic region between the stop codons of the *SNO1* ORF (Purple box shows last 5 codons) and the *CTF13* ORF (Blue box shows last 6 codons). DNA sequence alignment is from a single colony generated via negative selection. The DNA sequencing primer used was MRG316. B) Sanger sequencing of a 3'RACE product for the *CTF13* mRNA in the *CTF13-T$_{ADH1}$* strain trimmed to a 103 base pair window to confirm the presence of a poly-A tail. The putative poly-A tail signal is shown underlined in black. C) qPCR analysis of *CTF13* mRNA levels expressed as fold changes performed on wild-type (WT), *CTF13-T$_{ADH1}$*, and *sno1Δ6/CTF13-T$_{ADH1}$* strains using a *CTF13* ORF primer set (set #3). Each values is normalized to the level of *ACT1* mRNA. D) qCTF assay measuring CIN rates of the WT, *CTF13-T$_{ADH1}$* , and *sno1Δ6/CTF13-T$_{ADH1}$* strains. P-values are generated from a Tukey's post-hoc test.