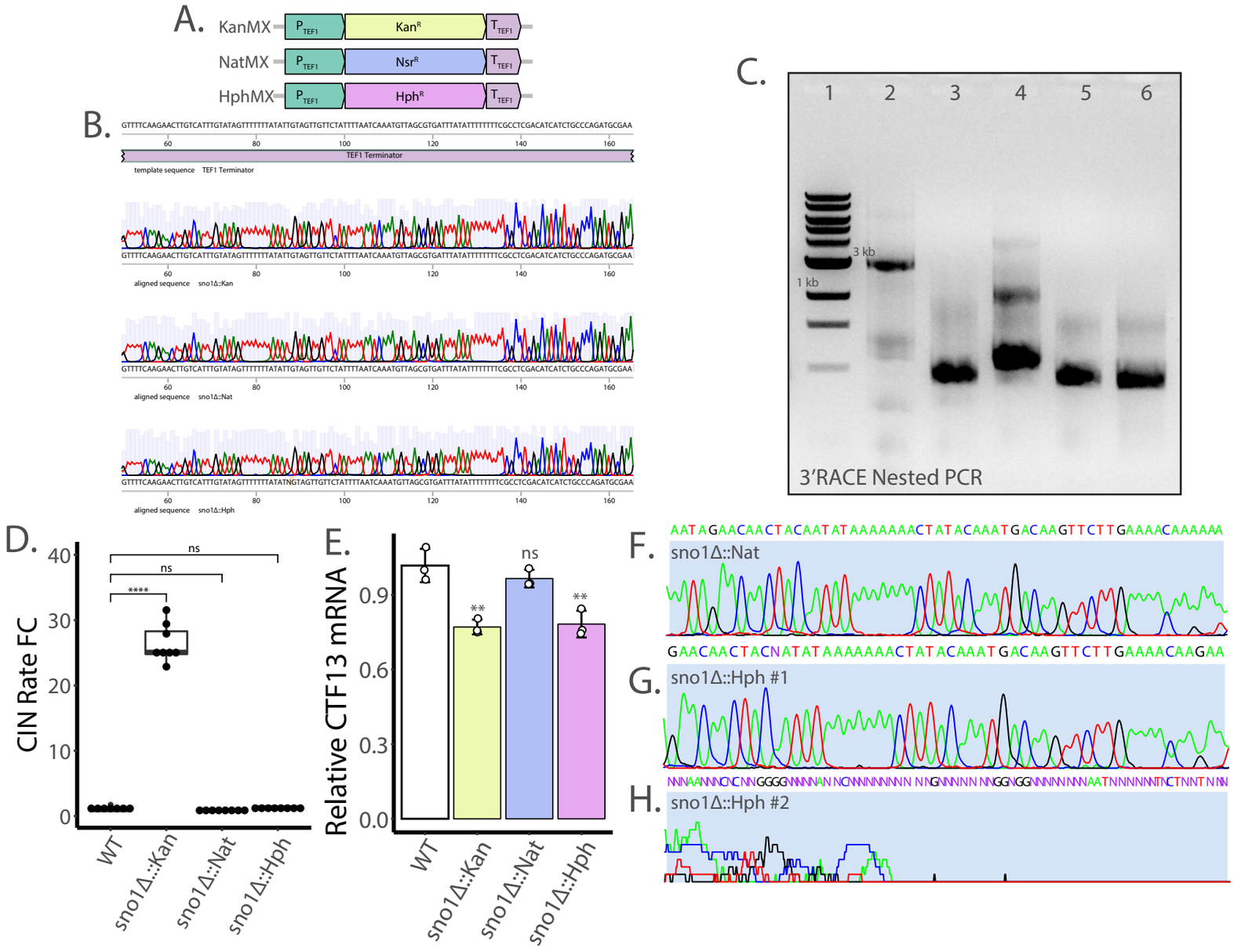

Figure S7. Determining the contribution of T_{TEF1} to increased CIN in *SNO1* null backgrounds. A) Graphical representation of cassettes used to delete *SNO1*, each cassette utilizing P_{TEF1} and T_{TEF1} from *Ashbya gossypii*. KanMX (KanR), NatMX (NsrR) and HphMX (HphR) confer resistance to the drugs geneticin, nourseothricin, and hygromycin, respectively. B) Sequence alignment of 3' RACE transcripts to the T_{TEF1} sequence to confirm each strain (*sno1Δ::Kan*, *sno1Δ::Nat*, and *sno1Δ::Hph*) contain the same genetic terminator sequences. C) Nested reverse transcriptase (RT)-PCR products from a 3' RACE assay using a *CTF13* gene specific primer (MRG577) and QI primer (see Supplemental Table S2) run on a 1% agarose gel stained with ethidium bromide. Lane 1: 8 µL 1 kb ladder (NEB # N3232L). Lane 2: Control strain, wild-type *SNO1-CTF13* locus. Lane 3: *sno1Δ::Kan*, Lane 4: *sno1Δ::URA3*, Lane 5: *sno1Δ::Nat*, Lane 3: *sno1Δ::Hph*. All strains were generated in the qCTF background. This image is a representative example of three biological replicates. D) qCTF assay measuring CIN rates of the *sno1Δ::Kan*, *sno1Δ::Nat*, and *sno1Δ::Hph* strains compared to a wild-type (WT) strain. P-values are generated from a Tukey's post-hoc test. E) qPCR analysis of *CTF13* mRNA levels expressed as fold changes performed on a wild-type strain and a *sno1Δ::Kan*, *sno1Δ::Nat*, and *sno1Δ::Hph* strains using a *CTF13* ORF primer set (set #3). F) Sanger sequencing of the 3' RACE product for the *CTF13* mRNA in the *sno1Δ::Nat* strain trimmed to a 61 base pair window within the *CTF13* 3' UTR containing the final sequencing read. 3/3 biological replicates contained the same 3' UTR sequence. G) Sanger sequencing of the 3' RACE product for the *CTF13* mRNA in the *sno1Δ::Hph* strain trimmed to a 54 base pair window within the *CTF13* 3' UTR containing the final sequencing read. 2/3 biological replicates contained the same 3' UTR sequence, which matched that of the *sno1Δ::Nat* strain. H) Sanger sequencing of the 3' RACE product for the *CTF13* mRNA in the *sno1Δ::Hph* strain trimmed to a 77 base pair window within the *CTF13* 3' UTR containing the final sequencing read. 1/3 bioloical replicates contained the a more heterogenous 3' UTR sequence.