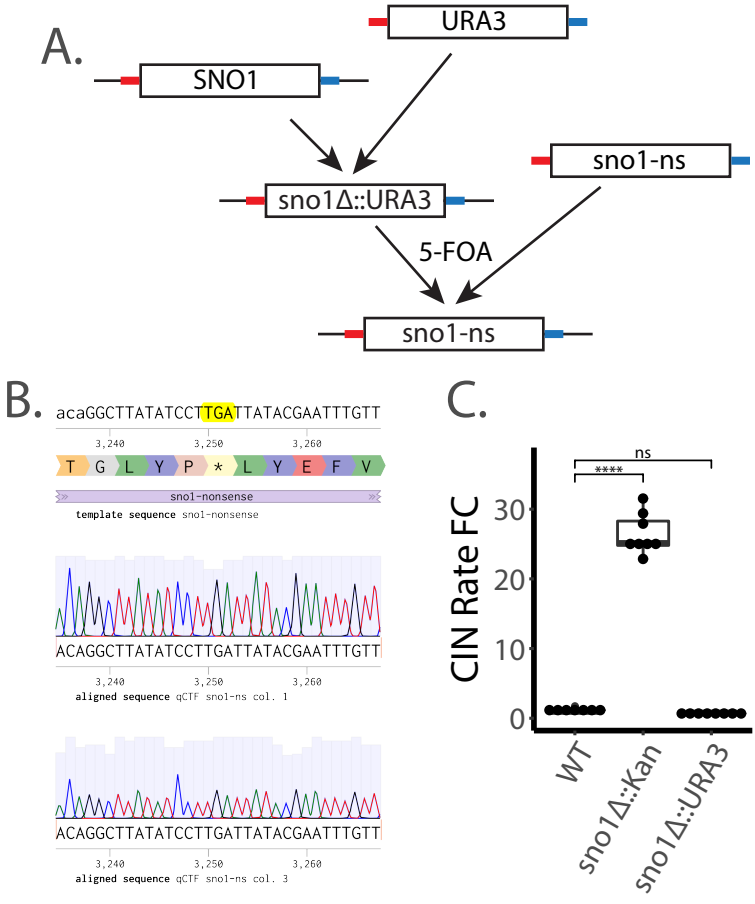

Figure S1. Generation of the *sno1-nonsense* point mutant using negative selection. A) Schematic representation of generating the *sno1-nonsense* point mutant. The *SNO1* ORF was replaced with a *URA3* selectable marker PCR amplified from the plasmid pRS316 containing 80 base pair homology up and downstream of the *SNO1* ORF (shown in red and blue, respectively). Following selection on Ura- dropout plates and subsequent PCR genotyping, we performed a transformation of the *sno1Δ::URA3* mutant using a PCR product containing the *sno1-nonsense* ORF from plasmid MG010 using the same 80 base pair homology sequence. Schematic adapted from (Gray et al. 2005). B) Sanger sequencing results from PCR products amplifying a portion of *SNO1* genomic DNA extracted from two independent isolates of the *sno1-nonsense* point mutation (Colony 1 and 3) aligned using Benchling software to the MG010 plasmid sequence. The DNA sequencing primer used was MRG420. The sequencing window was cropped to an area including the site of the nonsense mutation (Cys 84, shown as a yellow codon arrow marked with a "*" and highlighted in the template sequence), as well as 15 baepairs of sequencing reads up and downstream of this TGA stop codon. C) qCTF assay CIN rate measurements of the *sno1Δ::Kan* and the *sno1Δ::URA3* strain. P-values are generated from a Tukey's post-hoc test.