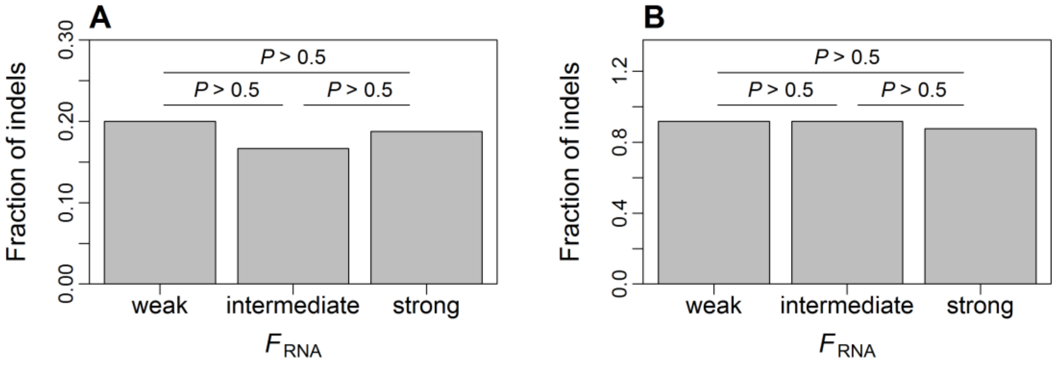

Figure S4. Fractions of mutations that are indels in the weak, intermediate (wild-type), and strong F_{RNA} versions of *CAN1* in (**A**) low-transcription and (**B**) high-transcription strains, determined by Sanger sequencing. The *P*-values are from two-tailed Fisher's exact test based on the numbers of indels and base substitutions in each pair of *CAN1* versions.