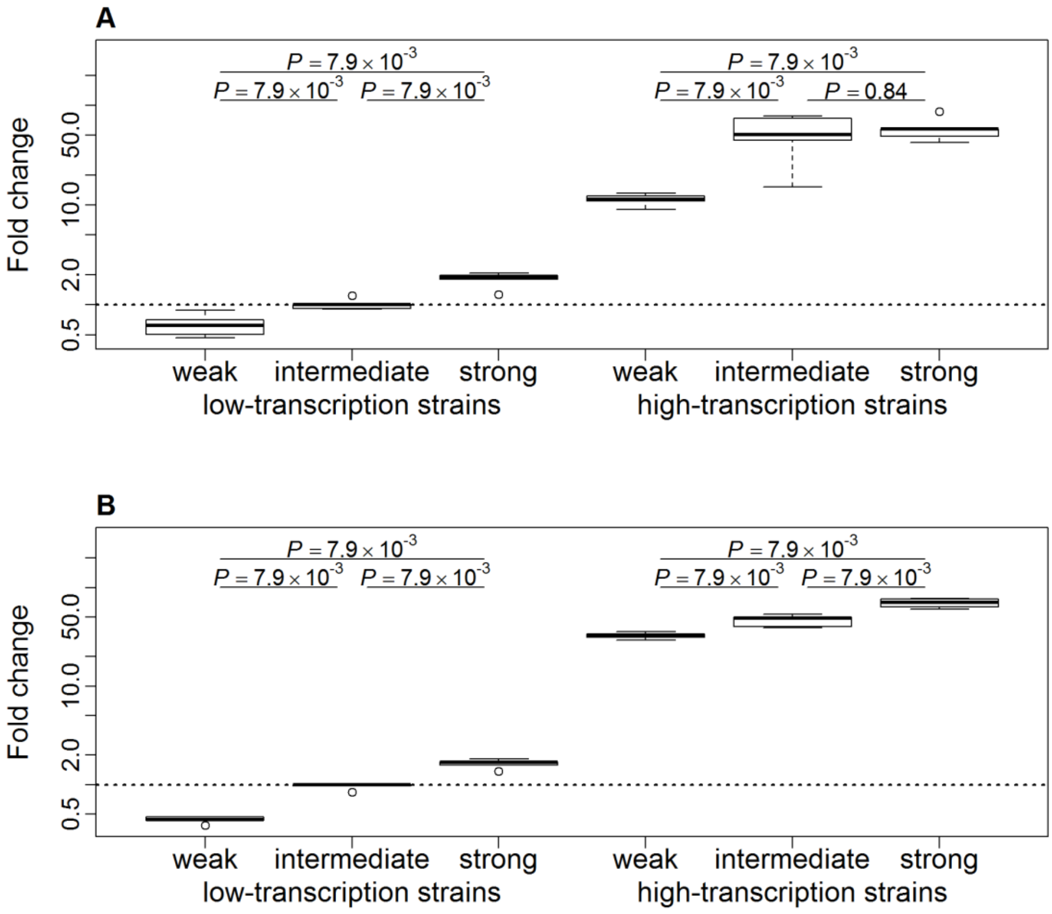

Figure S5. Relative expression levels of the weak, intermediate (wild-type), and strong F_{RNA} versions of *CAN1* in low-transcription and high-transcription strains determined by quantitative RT-PCR. (**A**) Results from biological replicate 1. (**B**) Results from biological replicate 2. Cells were grown independently in the two biological replicates. Expression levels are relative to that of the wild-type *CAN1* in the low-transcription strain. The bottom and top of each box are the first and third quartiles, and the band inside the box shows the median. The whiskers extend to the most extreme data point that is no more than 1.5 times the interquartile range from the box edges. Circles show outliers, which lie outside the range shown by the whiskers. The *P*-values are based on Mann-Whitney U tests.