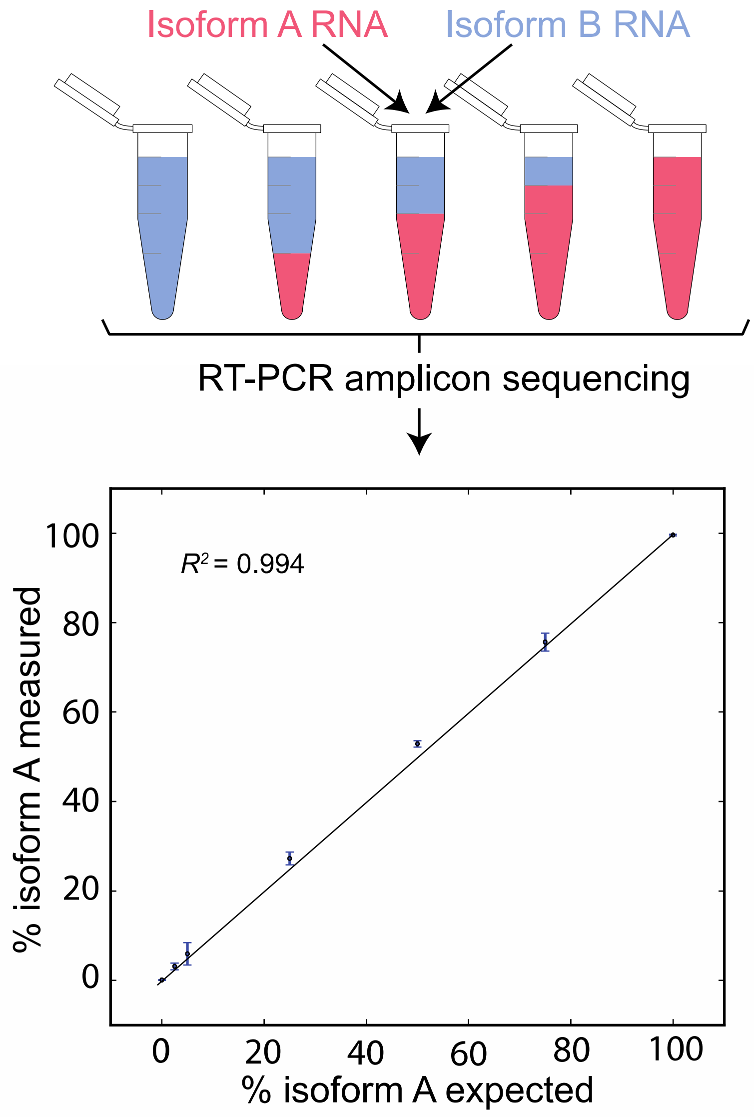

Figure S1: RT-PCR amplicon sequencing accurately and precisely measures splicing efficiency in complex mixtures containing known abundances of different spliced isoforms

Total cellular RNA was collected from two strains, each carrying a different splice isoform of the *pwi1* gene ORF in place of the native *pwi1* gene. Isoforms A and B differed by a length of 90 nucletotides. RNA from each strain was mixed in different proportions, and the relative abundance of each isoform was measured in each mixture by RT-PCR amplicon sequencing. Errorbars represent the standard deviation between three technical replicate RT-PCR reactions.