Figure S1. Prediction of mRNA secondary structures. Sequences of the transgenic *PSAD-, AR-*, and *AβSAP(i)-mCherry(i)* reporter transcripts and the native *PSAD*, *RBCS2*, and *βTUB2* transcripts were analyzed by the RNAfold program of the Vienna RNA package. We added a 50-nt poly-A tail after each polyadenylation signal. Shown are the positional entropies calculated by RNAfold for each nucleotide in the regions comprising 5'-UTRs and AUG start codons of the six transcripts and secondary structure predictions for the three transgene transcripts. The black box indicates a region within the *βTUB2-mCherry* transcript for which RNAfold predicts a stem-loop formed by sequences preceding the M10 AUG in the *mCherry* reporter and the *βTUB2*-5'-UTR.