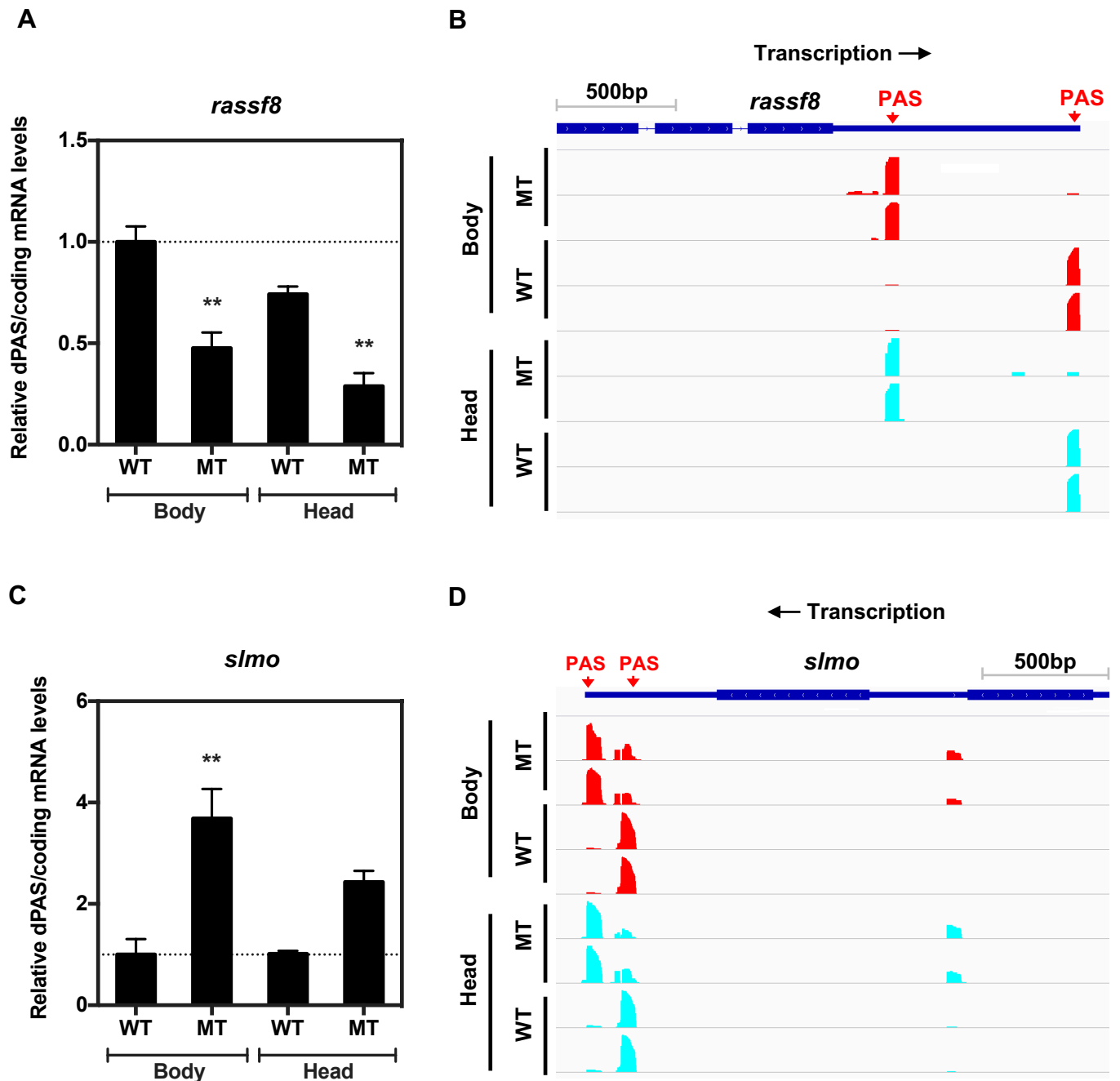


# Figure S3



**Figure S3. Expression analyses of *rassf8* and *slmo* 3'UTR-APA by RT-qPCR and 3'READS. (A)** Ratio of dPAS/coding relative mRNA expression levels for *rassf8* in wild-type (WT) and mutant (MT) bodies and heads, quantified by RT-qPCR. Data show the mean +/- standard deviation (SD) normalized to WT body, for at least three independent experiments. Comparisons were performed against WT body and head using an unpaired two-tailed t-test (\*\* $p < 0.001$ ). (B) UCSC genome browser tracks of 3'READS data for *rassf8*, showing a decrease in the dPAS isoform expression in both the body and head of mutant. Two replicates are shown. (C-D) Same as (A) and (B) except that data is for *slmo*, which shows an increase in the dPAS isoform expression in both the body and head of mutant.