

Supporting figure S1: Box plots of percentages of representative transcripts corresponding to putative UTR and putative retained introns.

Figure S1a: box plot of percentage of transcripts corresponding to UTRs as estimated by parsing of Blast alignments with *A. thaliana* orthologs. Data are shown for 1896 (*Ath*) and 2904 (*S.rexii*) "confidently annotated" representative transcripts from LSTCs

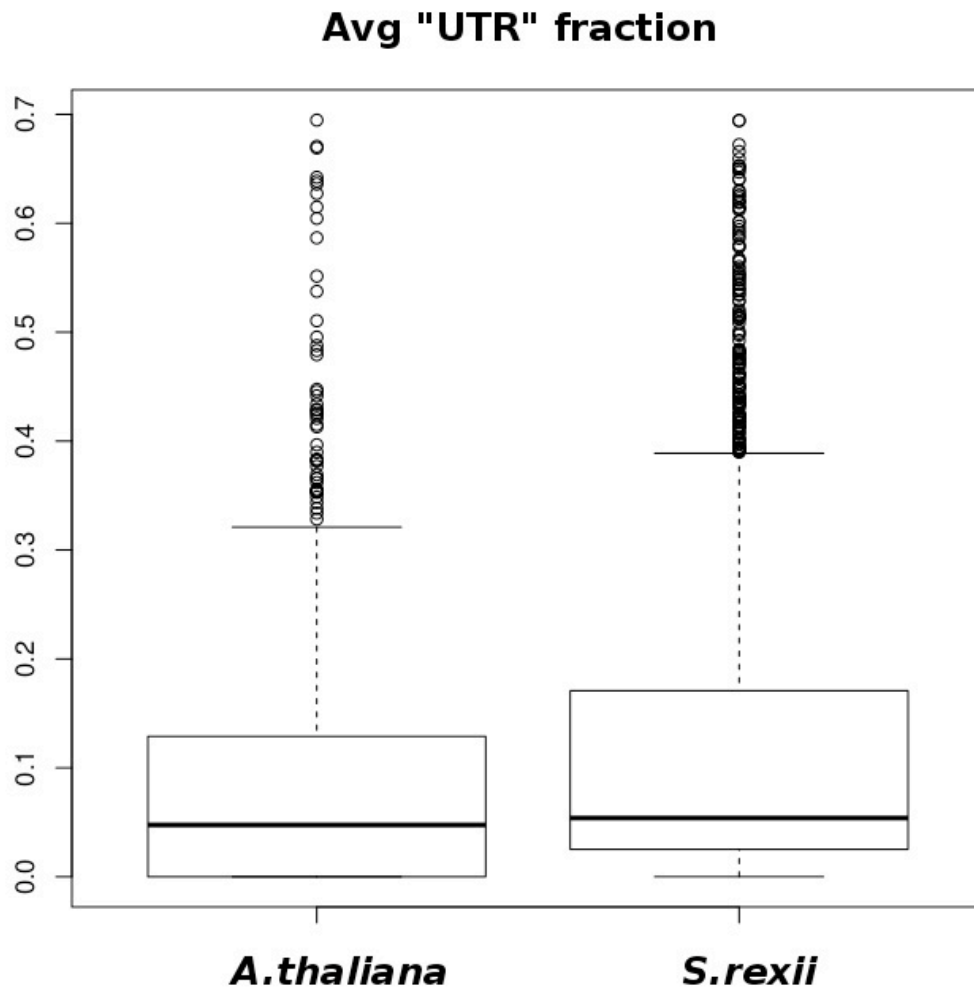


Figure S1b: box plot of percentage of transcripts corresponding to putative retained introns as estimated by parsing of Blast alignments with *A. thaliana* orthologs. Data are shown for 1896 (*Ath*) and 2904 (*S.rexii*) “confidently annotated” representative transcripts from LSTCs.

