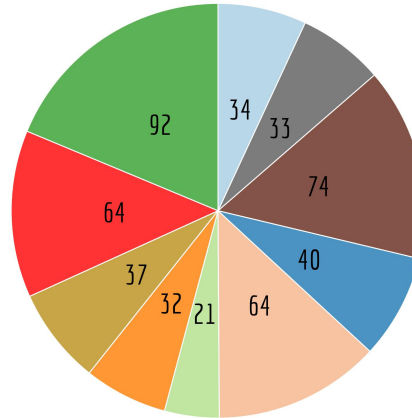
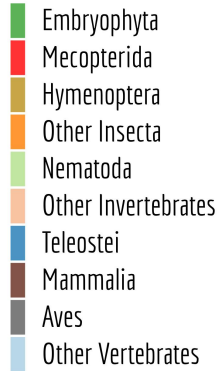
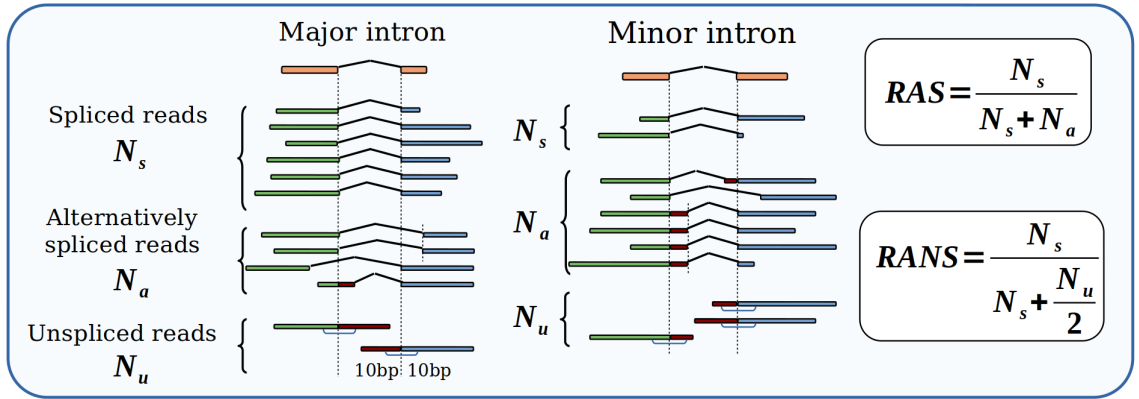


**A**

Transcriptomic data for Nspecies = 491

Clades

**B****C**

Variable	Definition
RAS	Relative abundance of a given spliced isoform compared to other overlapping spliced isoforms
RANS	Relative abundance of a given spliced isoform compared to unspliced transcripts overlapping its splice sites
Major intron	Intron corresponding to a major isoform ( <i>i.e</i> with $RAS > 0.5$ and $RANS > 0.5$ )
Minor intron / SV	Splice variant (SV) = intron corresponding to a minor isoform ( <i>i.e</i> with $RAS \leq 0.5$ or $RANS \leq 0.5$ )