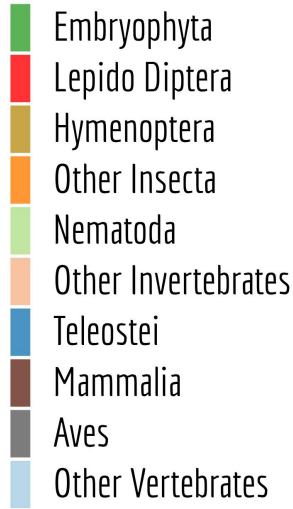
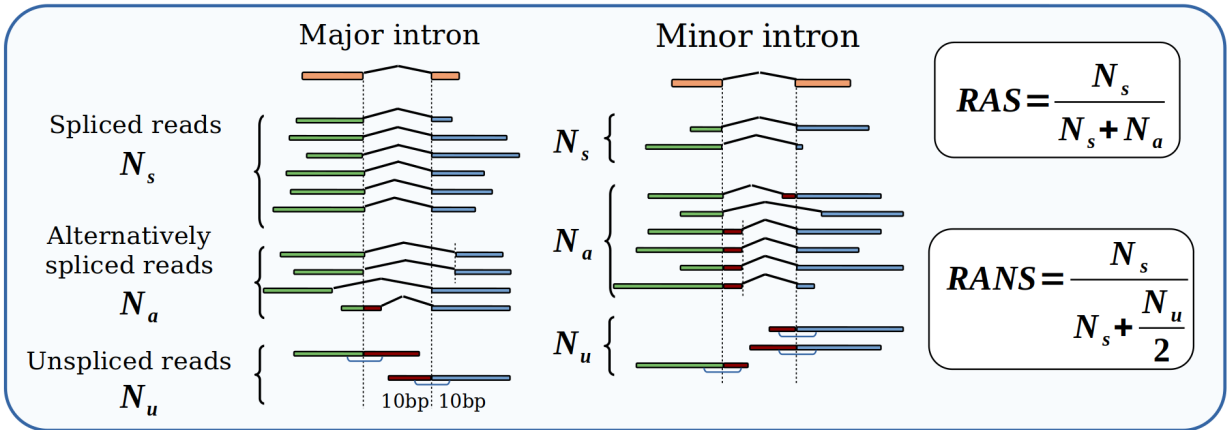


A

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 $RANS \leq 0.5$)
AS rate	Alternative splicing rate. For a given major intron, measures the rate at which SVs occur over its two boundaries.