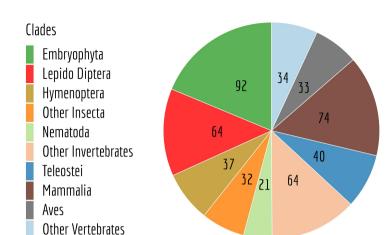
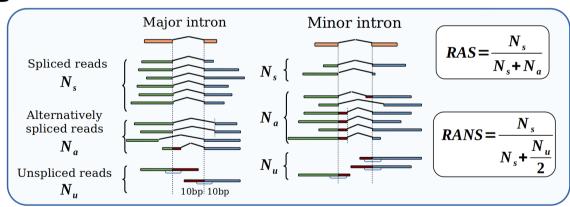
## Transcriptomic data for Nspecies=491







## 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 overlaping its splice sites
Major intron	Intron corresponding to a major isoform (i.e with RAS $> 0.5$ and RANS $> 0.5$ )
Minor intron / SV	Splice variant (SV) = intron corresponding to a minor isoform (i.e with RAS $\leq$ 0.5 or RANS $\leq$ 0.5)