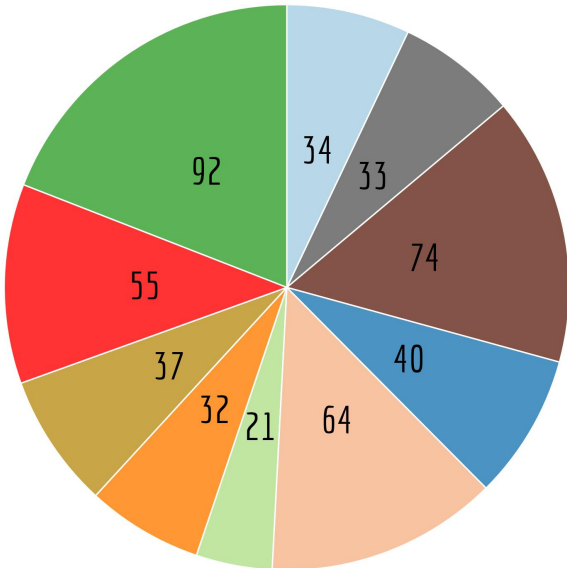


**A**

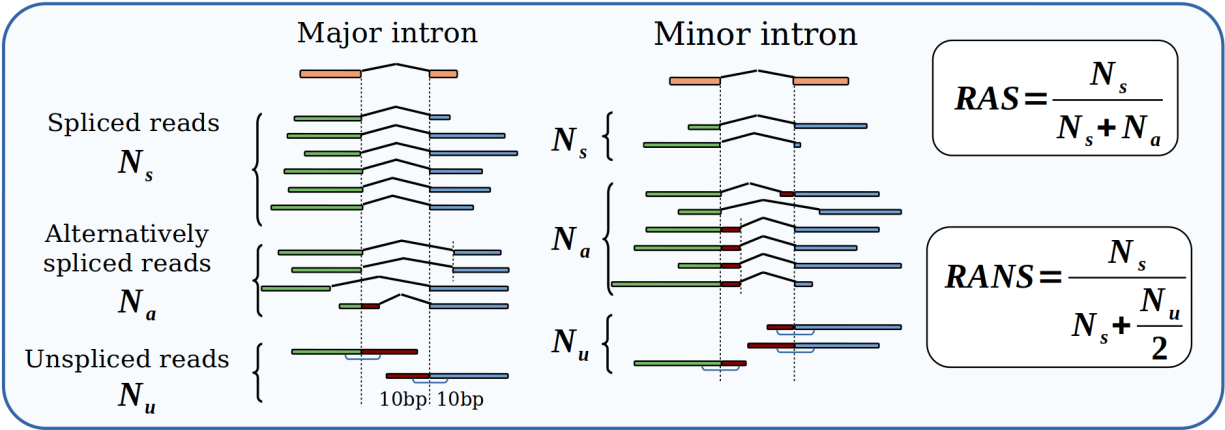
# Transcriptomic data for Nspecies=482

Clades

- Embryophyta
- Lepido Diptera
- Hymenoptera
- Other Insecta
- Nematoda
- Other Invertebrates
- Teleostei
- Mammalia
- Aves
- Other Vertebrates



**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.