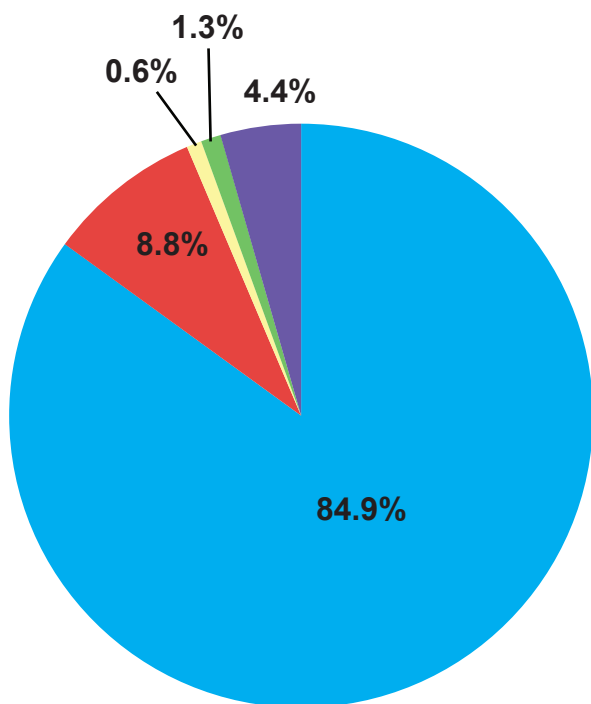
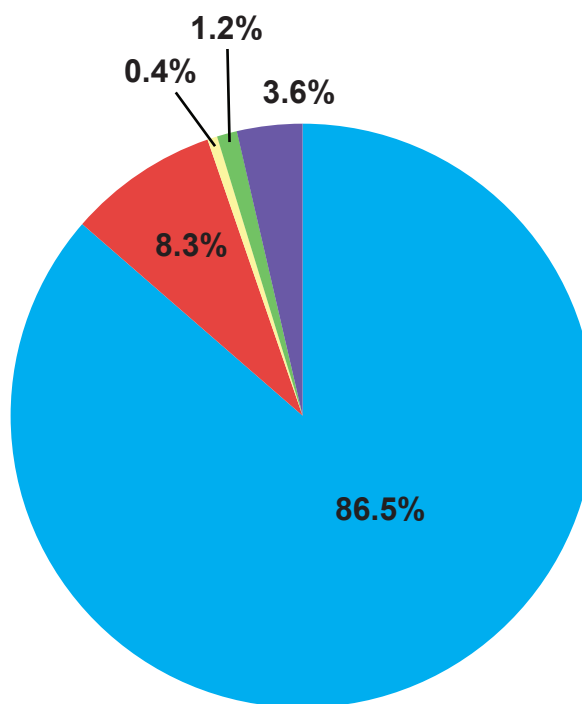


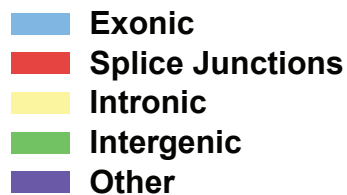
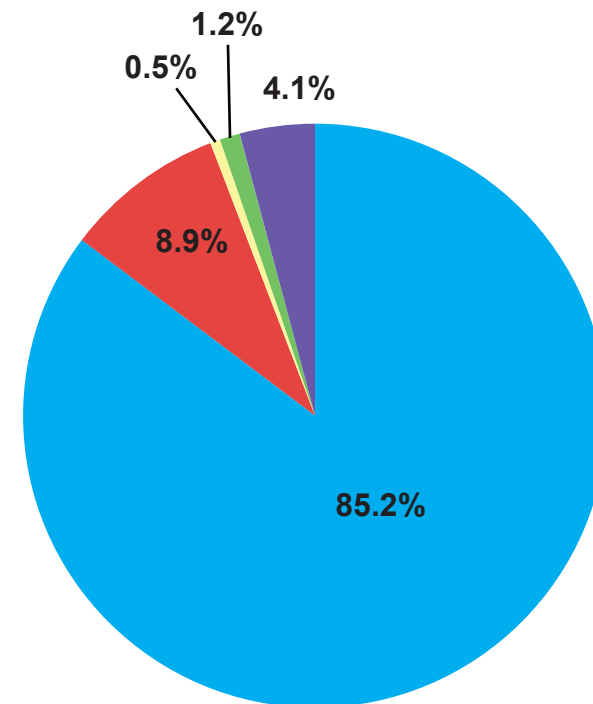
N2 Mixed Stage



N2 L4



N2 YA



**Figure S1. Distribution of mapped sequence reads.** Approximately 85% of the reads maps to known exonic regions while 9% of the reads map to exon junctions, indicating a high level of correlation in read mapping to existing gene annotations. Less than 5% of the sequenced reads map to novel regions in the genome.