

# 6.3 Intron Quantifications


List of features that are quantified by the Flux, and the corresponding attributes that are provided in the ouput.

## Transcripts

transcript_id	gene_id / locus_id	nr. reads	length	RPKM
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## Splice Junctions

gene_id/locus_id	nr.reads
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The coordinates (start,end) of splice junctions are located at the last/first nucleotide of the correspondinly joined exons. The stretch of the intron in genomic coordinates would correspondingly be located between [start+1;end-1]

## Introns ("all-intronic regions")

gene_id	locus_id	nr. reads	fraction cov.
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In the diagram above, the red box marks the all-intronic intersection of the two displayed introns. Read coverage of this region is expressed by the fraction of the intron that is covered by reads 10-bin resolution as a default). Intron parts outside of the red box are not considered for quantifying this feature, under the hypothesis that reads falling there could be assigned to the superimposed alternative exon boundaries.



So the coverage value reported for an intron is the fraction of the red box covered by reads (default resolution 0.1).