

Supplemental material to:

Multiple insert size paired-end sequencing for deconvolution of complex transcriptomes

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RNA Biology 2012; 9(5); DOI: 10.4161/rnabiol.19683

<http://www.landesbioscience.com/journal/rnabiology/article/19683>

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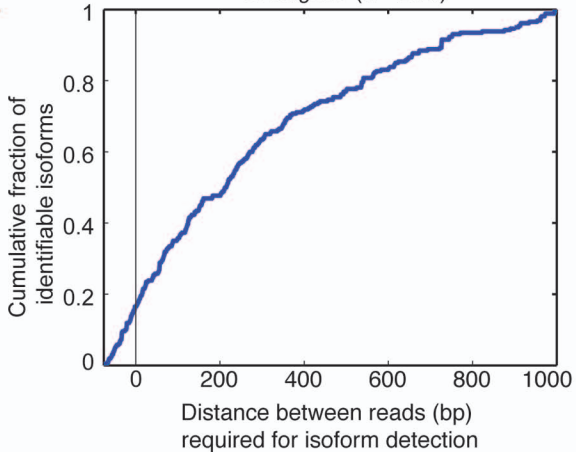
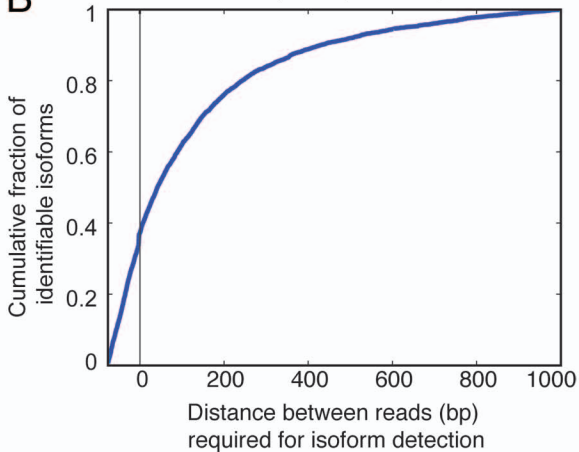
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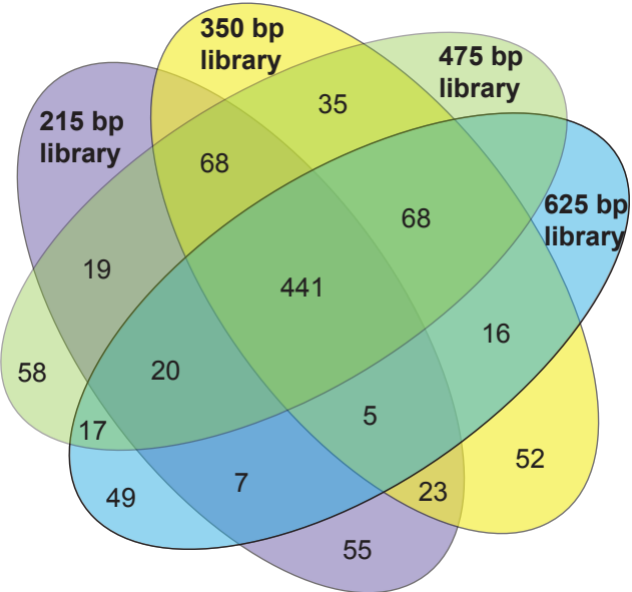
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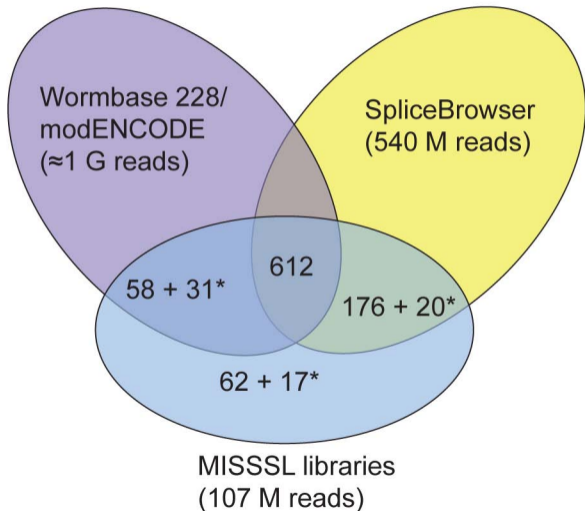
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A*C. elegans* (n = 260)**B***H. sapiens* (n = 5688)



Exon skips



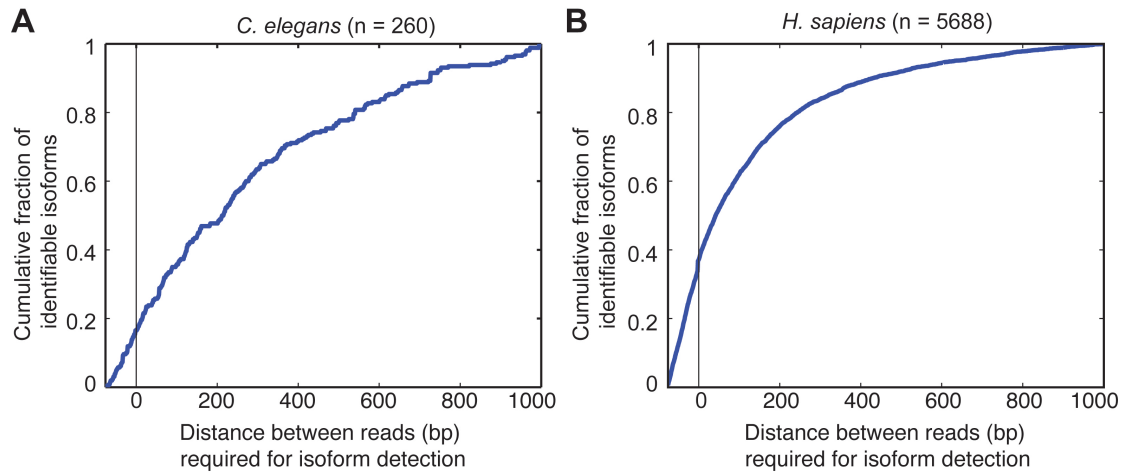


Figure S1: Cumulative fraction of identifiable isoforms for genes with three or more isoforms which can be identified only by paired-end sequencing. The cumulative fraction of isoforms, which can only be uniquely identified by paired-end sequencing with distance of less than 1 kb between the paired reads, is shown for isoforms of **(A)** *C. elegans* and **(B)** *H. sapiens* genes that generate three or more isoforms. Read length was defined as 76 bp and the utility of overlapping paired-end reads is indicated by the region between -76 and -1 bp, where overlapping reads were simulated as single reads of length 152 bp (2 x 76 bp) minus the length of overlap.

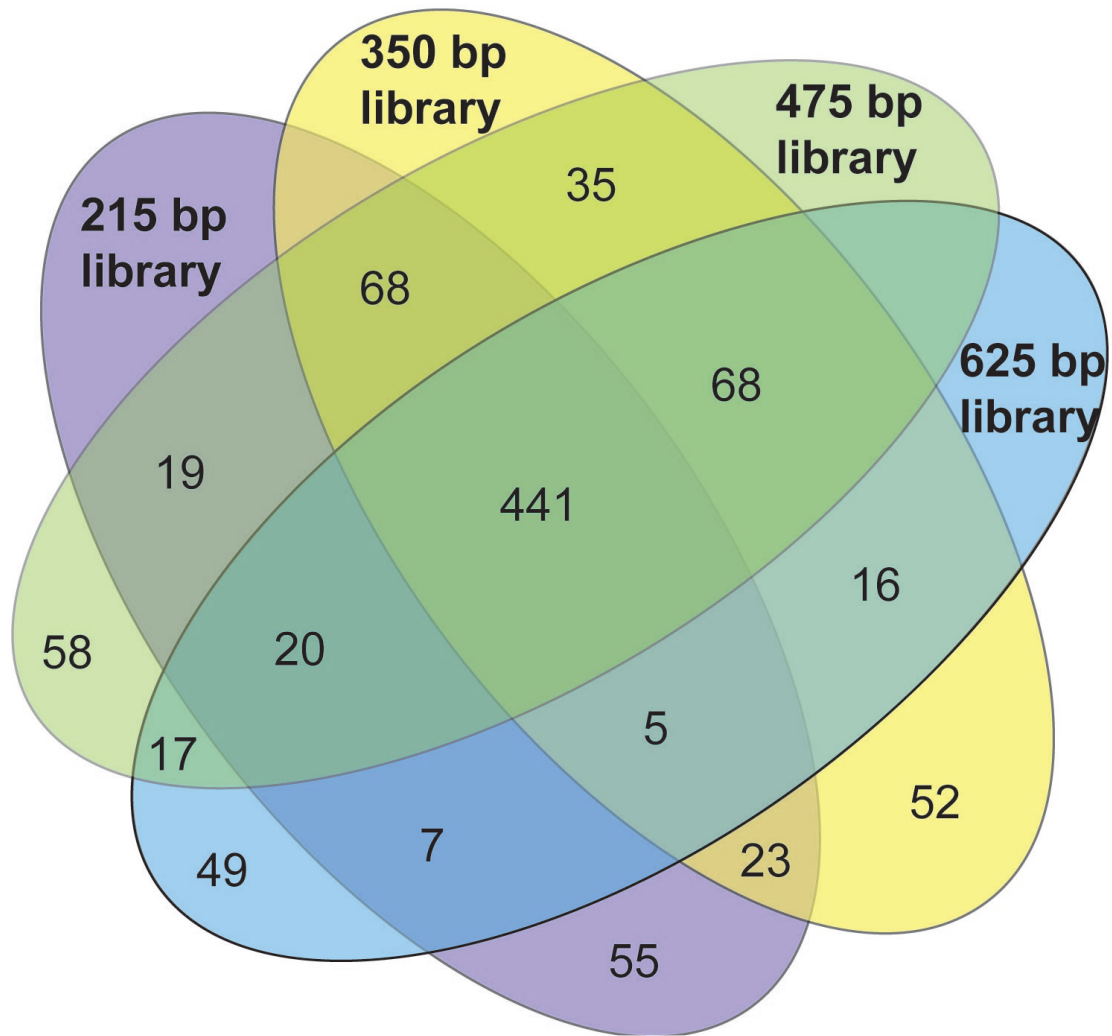


Figure S2: Support for novel splicing events from libraries with different insert sizes. For each library, paired-end read support for each predicted isoform was calculated, followed by computation of support for a novel isoform by at least 10 more paired-end reads than the annotated form. Overlap in novel isoform support between libraries for the total of 993 events is shown.

Exon skips

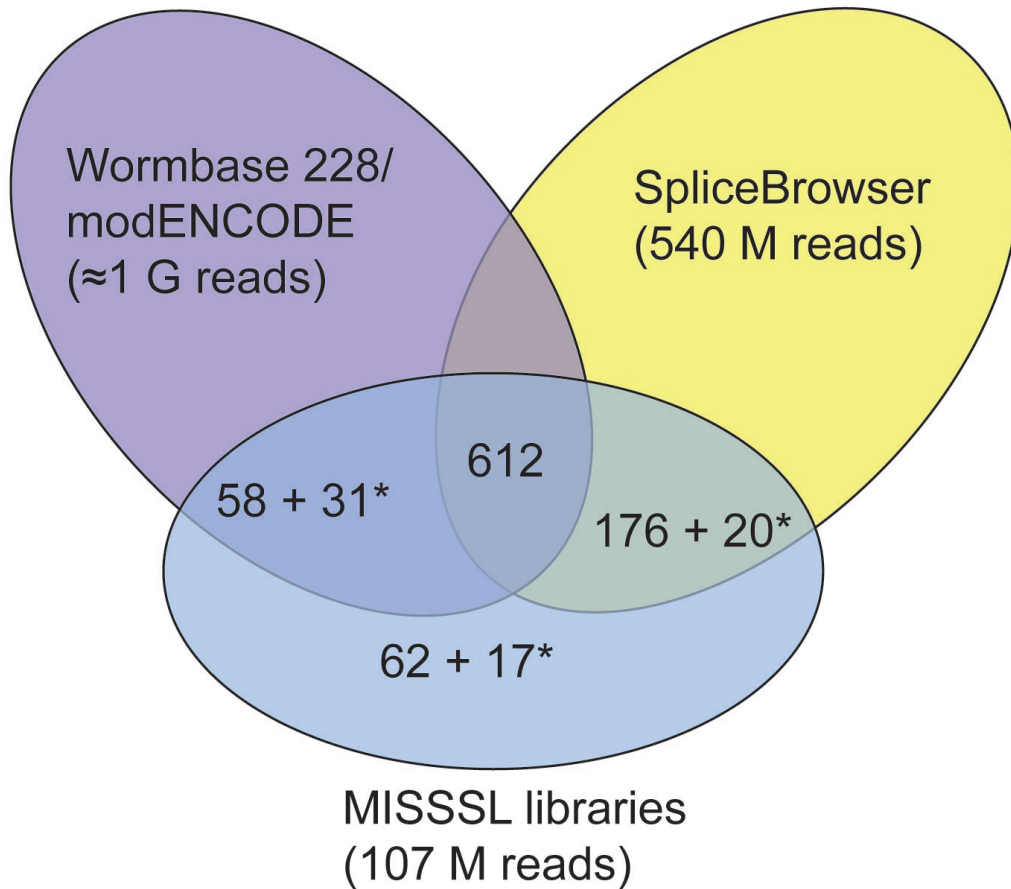


Figure S3: Comparison of MISSSL exon skipping events to two large RNA-seq datasets. The 976 MISSSL exon skipping events (blue) were compared to those annotated in SpliceBrowser (yellow; ²⁹) and Wormbase 228/the modENCODE project (purple; ^{23,30}). Asterisks indicate exon skipping events that were annotated as unconfirmed in one further dataset. Further details of all exon skipping events can be found in Table S1.