Supporting Information

Li *et al.* 10.1073/pnas.0807121105

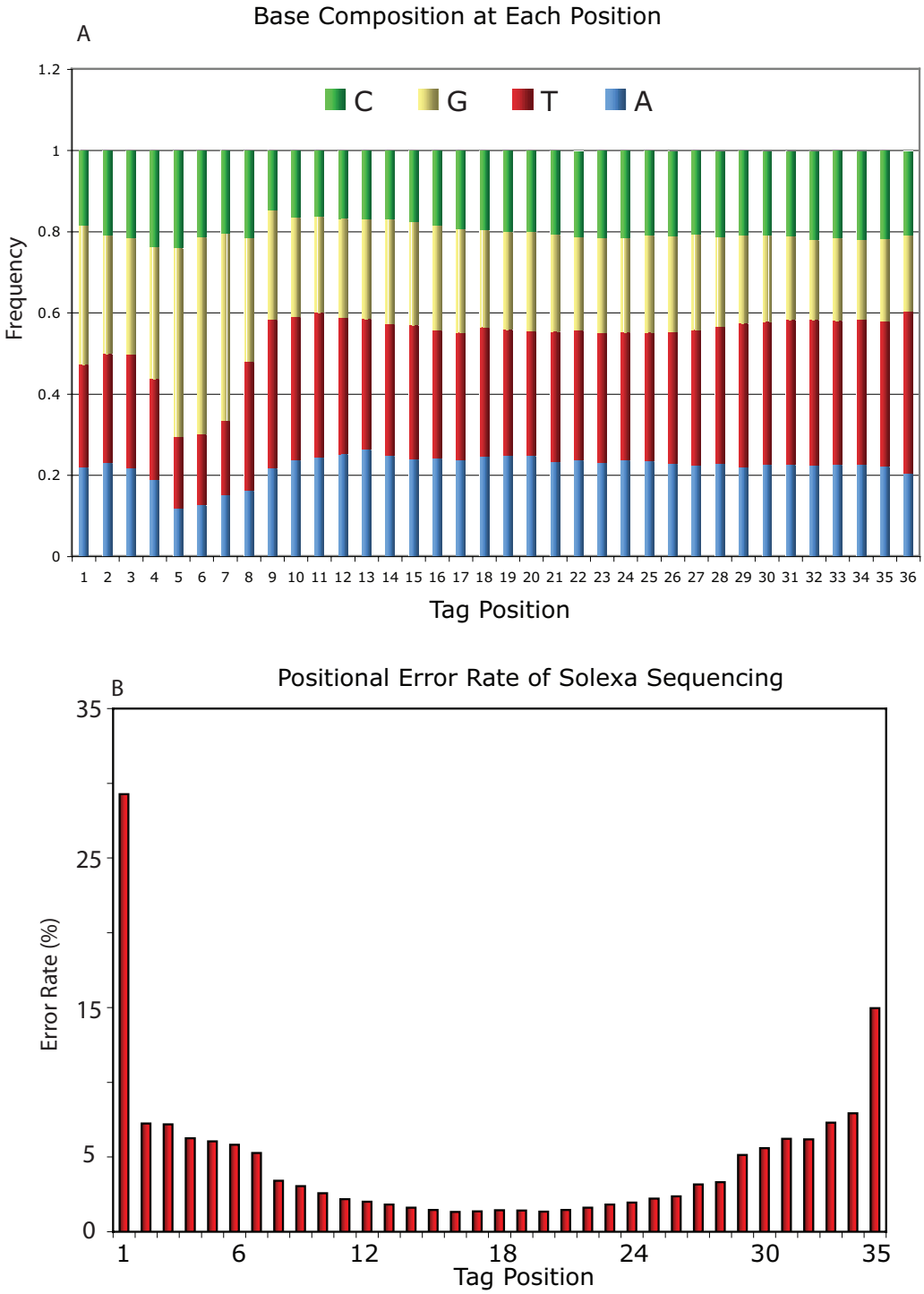

Fig. S1. Position dependent error rate and biases from random priming and sequencing. A. Sequence bias at positions 5 to 7 generated by random priming indicates a preference for higher GC content in the region hybridized. B. Error rate at individual sequence positions based on genomic alignment of uniquely mapped sequence tags, allowing 2 base mismatches.

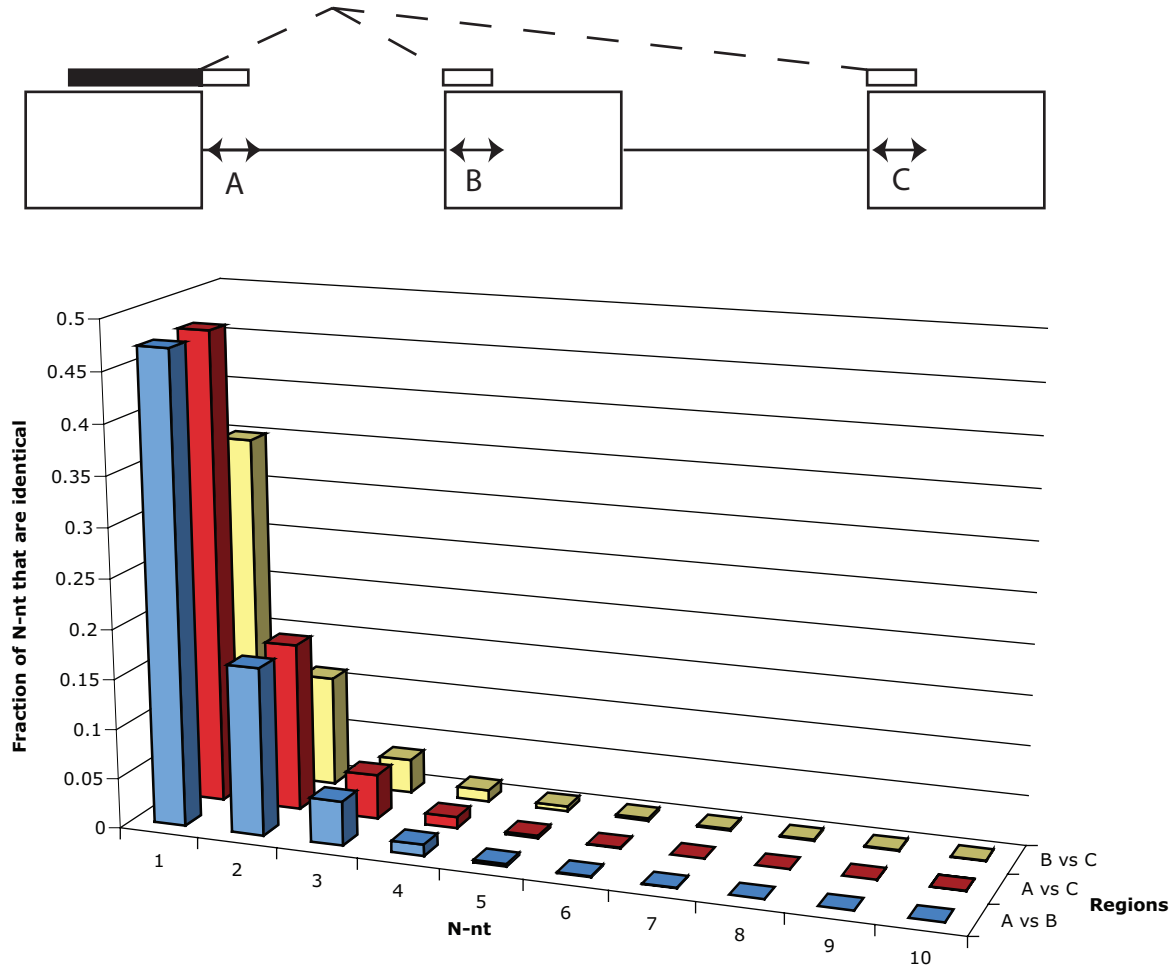

Fig. S2. Justification of requiring 4nt mapped across spliced junctions. The diagram above illustrates the strategy. N-mers at the regions A, B and C for all splice junctions were compared, and the fraction of N-mers that were indistinguishable between each of the comparisons was plotted against increasing levels of N. By requiring n = 4nt across splice junction, only 1% of the sequences are indistinguishable.

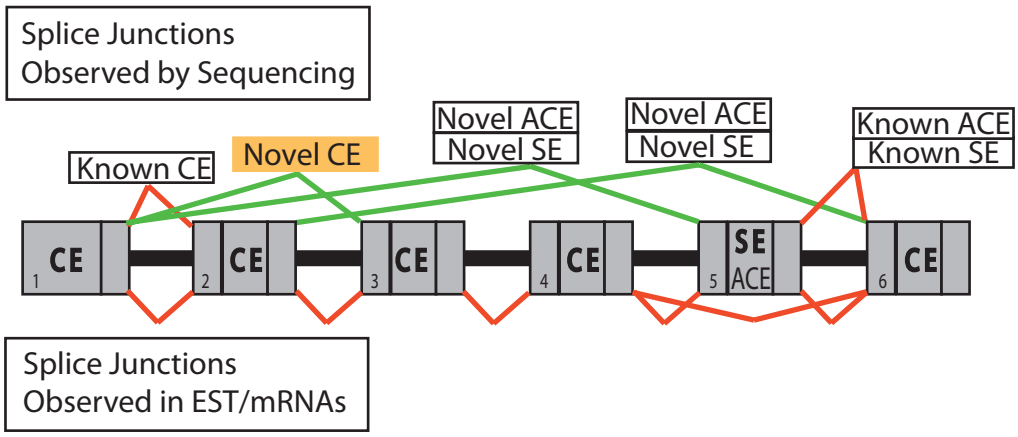

Fig. S3. Annotation of splice junctions. Splice junctions were annotated based on two criteria. First, mRNA/EST-verified junctions (red) were separated from potential novel junctions (green). Second, the junctions within each of these broad categories were further subdivided into CE, AS and ACE categories, based on the annotation of the exons within the span of each junction. Novel CE splice junctions (orange shaded box) indicate new evidence for alternative splicing between exons that were previously annotated as constitutive. Note that the overlap between AS and ACE databases is extensive, but not identical as AS database is much larger whereas ACE may contain splicing events that are not supported by the current mRNA/EST information.

Other Supporting Information Files

Table S1 (XLS)
Table S2 (XLS)
Table S3 (XLS)
Table S4 (XLS)
Table S5 (XLS)
Table S6 (PDF)