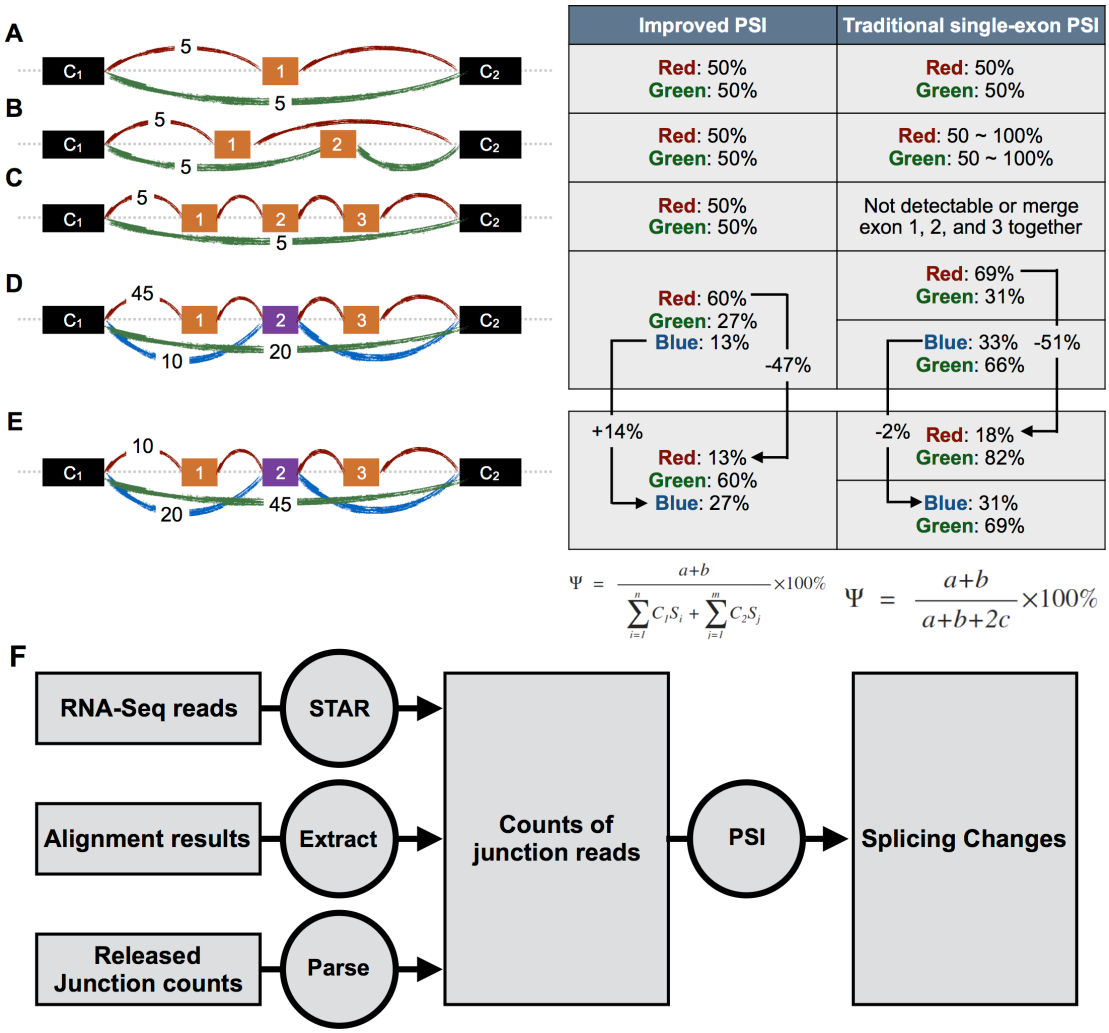

Figure S1. The improved PSI equation and flow chart of processing RNA-Seq datasets. (A, B, C, D) The diagrams on the left illustrate different types of splicing events such as **(A)** single-exon skipping, **(B)** mutually exclusive, **(C)** multiple-exon skipping, **(D)** complex splicing events. Black blocks are constitutive exons whereas orange and purple blocks are alternative exons. Purple blocks are the alternative exon used in multiple isoforms. Red, green, and blue arcs represent the junctions of different isoforms, and the numbers at the arcs are the number of junction reads supporting red, green, or blue isoforms. The box on the right shows the PSIs (%) calculated by using improved PSI equation or traditional PSI equation for each isoforms on the left. **(E)** The diagram illustrates a complex splicing event that is identical to the one at **(D)**, but the number of junction reads changed. Also, on the right, ΔPSIs of red and blue isoforms were shown in the arrow line. Traditional single-exon PSI index will split the complex events into two independent events: **(1)** Red versus Green and **(2)** Blue versus Green. **(F)** The flow chart shows three approaches used in the present study to obtain splicing changes in RNA-Seq datasets. The first approach started with RNA-Seq reads and used STAR to align the reads to obtain counts of junction reads. The second approach extracts the counts of junction reads from existing alignment files. The final approach is parsing released junction counts (e.g. GTEx) to obtain counts of junction reads for later PSI calculations.