We have provided the raw counts as supplementary files in GEO under accession ID GSE112037

Supplementary file	Size	Download	File type/resource
GSE112037_RASL_count.txt.gz	66.2 Kb	(ftp)(http)	TXT
GSE112037_darts_read_counts.txt.gz	2.9 Mb	(ftp)(http)	TXT
GSE112037_kallisto.tar.gz	16.7 Mb	(ftp)(http)	TAR

The first two files are junction counts for RASL-seq and RNA-seq, respectively.

In the RASL-seq count file, each column is a sample (e.g. PC3E_rep1), and each row is an event. Each entry represents the inclusion counts and skipping counts separated by a comma (e.g. 20,19 means inclusion counts I=20, skipping counts S=19). See the header snippet of RASL count file below.

```
ID      PC3E_rep1_RASL  PC3E_rep2_RASL  PC3E_rep3_RASL  GS689_rep1_RASL GS689_rep2_RASL GS689_rep3_RASL
chr6:+:130370538:130370900:130370975:130372393  20,19   11,18   23,18   30,24   28,27   15,13
chr13:+:96377506:96409897:96410050:96412293     1504,0  1215,2  1795,3  1960,2  2235,5  1193,2
chr3:+:66396832:66413283:66413353:66419901      70,1    86,4    77,1    80,2    72,0    46,1
chr6:+:43470087:43470325:43470355:43471138      0,475   0,629   2,502   0,439   0,416   5,314
```

RASL-PSI is calculated as I/(I+S). This is because only one inclusion junction is profiled in RASL-seq. Refer to the Method part in our paper (PubMed: 30923373) for the details in PSI calculation.

The RNA-seq count file follows the DARTS-BHT format. I1,S1 are inclusion and skipping junction counts from PC3E triplicates; I2,S2 are inclusion and skipping junction counts from GS689 triplicates. Last two columns are the effective lengths for inclusion and skipping counts.

```
ID      I1      S1      I2      S2      inc_len skp_len
chr16:+:19125446:19125962:19126257:19131428     2,8,9   0,0,0   0,5,3   0,1,0   202     101
chr12:+:118454697:118455494:118455620:118455799 23,28,24        1,3,0   20,13,10        4,2,0   202     101
chr12:+:118454697:118455494:118455620:118456876 31,36,30        618,392,679     35,21,10        408,330,374     202     101
chr12:+:118454697:118455494:118455657:118455799 25,23,24        1,3,0   20,14,7 4,2,0   202     101
chr12:+:118454697:118455494:118455657:118456876 23,23,24        618,392,679     18,13,7 408,330,374     202     101
```

In both files, the ID column is the unique identifiers for exon-skipping events in hg19 genome. The coordinates in the ID are joint by colons in the order of:

chromosome, strand, upstreamExonEnd, cassetteExonStart, cassetteExonEnd, downstreamExonStart.

The two count files can be inner-joint using the ID columns.