**Supplemental Materials**

**Supplementary figure legend**

**Figure S1. Identification of tissue-specific (TS) circRNAs.** **A,** Computational pipeline to identify and characterize tissue-specific circRNAs and, construct tissue-specific circRNA database TSCD. **B,** Algorithm to identify TS circRNAs. CircRNAs were identified by combination of three algorithms, CIRI, circRNA\_finder, and find\_circ. Then the donator and acceptor coordinates of each circRNA among tissues were compared to determine the tissues specificity of circRNAs.

**Figure S2. Tissue-specific circularization between human adult and fetal tissues. A,** CORIN in heart. **B,** ALB in liver.Donor and acceptor sites were connected and represented as dash line. Adult-specific circRNAs were represented in blue dash line, while fetal-specific circRNAs were represented in red dash line.

**Figure S3. Potential RNA binding proteins (RBP) in junction regions of tissue-specific circRNAs. A,** Potential RBP sites in TS circRNAs of human fetal tissues. **B,** Potential RBP sites in TS circRNAs of mouse tissues. Color depth represents the percentage of number of RBP sites.

**Figure S4. The concept of back splicing in the process of RNA circularization.**

CircRNAs are composed of one exon (I), two exons (II) or more than 3 exons (III), exon-intron (IV), and intron (V).