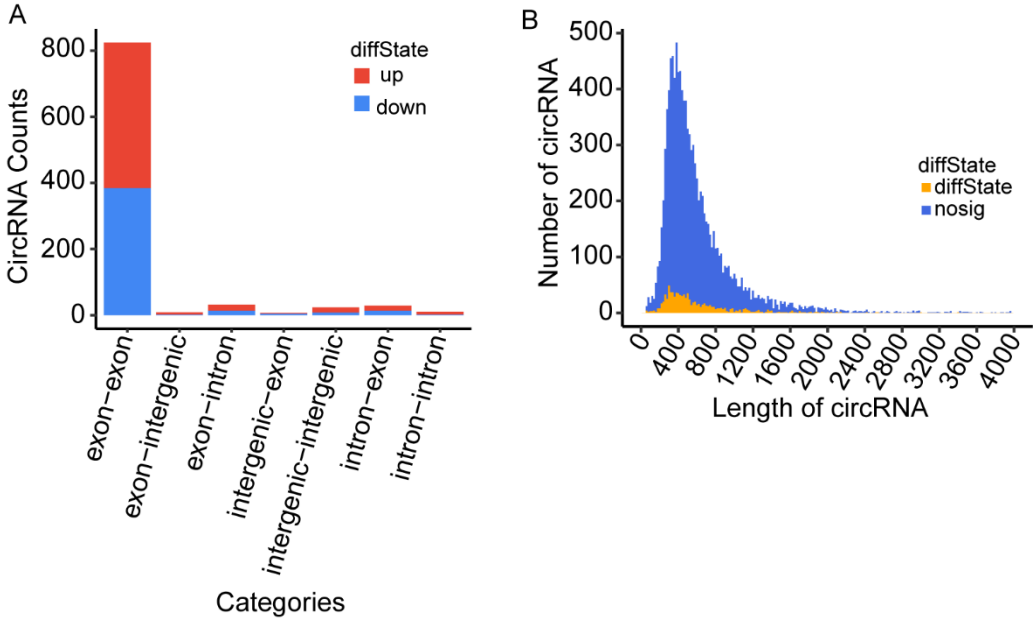


**Figure S1. Categories and length of differentially expressed circRNAs.** (A) categories of differentially expressed circRNAs in decidua between NP group and RPL group. (B) length of differentially expressed circRNAs in decidua between NP group and RPL group.



**Table S1. KEGG pathway of parental genes of circRNAs.**

databas eID	Description	geneRatio	bgRatio	pvalue	padj	enrichScore	overlapGeneList	overlap Gene Count
hsa003 10	Lysine degradation	9/109	63/2426	0.0016	0.0761	3.1795	ASH1L/PLOD2/PRDM2/SMYD2/ DOT1L/SETD2/NSD2/NSD1/EH MT1	9
hsa015 21	EGFR tyrosine kinase inhibitor resistance	10/109	79/2426	0.0023	0.0761	2.8173	AKT3/NF1/RPS6KB1/AKT2/PIK3 CA/PDGFR/RAF/PLCG2/STAT 3/MAP2K2	10
hsa005 32	Glycosamino glycan biosynthesis - chondroitin sulfate /	4/109	20/2426	0.0106	0.1738	4.4513	CSGALNACT1/CHSY1/XYLT1/C HST12	4

	dermatan sulfate							
hsa00670	One carbon pool by folate	4/109	20/2426	0.0106	0.1738	4.4513	GART/MTHFD1L/MTHFD1/MTHFD2L	4
hsa00562	Inositol phosphate metabolism	8/109	73/2426	0.0150	0.1960	2.4391	PIK3C3/PIK3CA/PIP5K1A/INPP5B/INPP5A/PI4K2A/PLCG2/PIKFYVE	8
hsa01522	Endocrine resistance	9/109	98/2426	0.0294	0.3194	2.0439	AKT3/RPS6KB1/AKT2/PIK3CA/BRAF/PTK2/NCOR1/MAP2K2/MAPK10	9
hsa01523	Antifolate resistance	4/109	31/2426	0.0476	0.3194	2.8718	CHUK/ABCC1/GART/ABCC5	4
hsa03015	mRNA surveillance pathway	8/109	98/2426	0.0700	0.5691	1.8168	PPP2R1B/PPP2R5C/PAPOLG/RNGTT/UPF2/DDX19A/PPP2R3A/NCBP1	8