

Supplementary material

Experimental procedures for CircRNA detection

1. Sample preprocessing

The peripheral blood (about 5 ml) collected from pregnant women using EDTA anticoagulant tubes was immediately stored at 4°C and processed within 2 h. These samples were centrifuged twice at 3000 rpm at 4°C and the supernatant (i.e. plasma) was retained and stored at -80°C until testing.

2. Total RNA

According to the manufacturer's instructions, the total RNAs of these samples were extracted using Trizol reagent (Invitrogen, Gaithersburg, MD, United States), and purified using a NucleoSpin RNA Clean-up kit (Macherey-Nagel, Germany). Then, a NanoDrop 2000 spectrophotometer (NanoDrop, USA) was used to quantify purified total RNA and an Agilent 2100 Bioanalyzer (Agilent Technologies, USA) was used to verify the RNA integrity.

3. RNase R treatment

For each sample, 5 µg of RNA, 2 µl of RNase R 10X Reaction Buffer, and 0.5 µl of RNase R were mixed in the 20 µl reaction system, followed by instantaneous centrifugation. The digestion reaction was performed at 37°C for 30 min. Then, RNA was purified using a NucleoSpin RNA Clean-up kit (Macherey-Nagel, Germany).

4. cDNA synthesis

4.1 First strand cDNA

Total RNA 100-500 ng was added to the 0.2 ml nuclease-free microcentrifuge tube and then the appropriate volume of spike-in controls was added (Agilent Technologies, USA) according to the table below.

Starting amount of RNA		Serial dilutions			Spike-in mix volume to be used in each labeling reaction [µl]
Total RNA [ng]	Maximum volume of RNA [µl]	First	Second	Third	
200	8.3	1 : 20	1 : 25	1 : 10	2
300	7.3	1 : 20	1 : 25	1 : 10	3
400	6.3	1 : 20	1 : 25	1 : 10	4
500	5.3	1 : 20	1 : 25	1 : 10	5

The reverse transcription Master Mix was prepared by gently mixing 4 µl of First Strand Buffer Mix and 1 µl of First Strand Enzyme Mix. It was instantaneously centrifuged and placed in an ice bath. The Master Mix (5 µl) was added to the previously prepared 0.2 ml nuclease-free microcentrifuge tube containing total RNA and spike-in controls.

The solution was gently mixed, instantaneously centrifuged, and then reacted at 42°C for 2 h. After the reaction, it was instantaneously centrifuged and ice-bathed in sequence, and then the subsequent steps were performed immediately.

4.2 Second strand cDNA

The Second Strand Master Mix was prepared by gently mixing 13 µl of Nuclease-free Water, 5 µl of Second Strand Buffer Mix, and 2 µl of Second Strand Enzyme Mix. It was instantaneously centrifuged and placed in an ice bath. Then, 20 µl of Second Strand Master Mix was added to the reacted system generated in step 4.1.

The solution was gently mixed and reacted at 16°C for 1 h, then at 65°C for 10 min.

5. cRNA synthesis

The In vitro Transcription Master Mix was prepared by gently mixing 4 µl of Nuclease-free Water, 20 µl of T7 Buffer Mix, and 6 µl of T7 Enzyme Mix. It was instantaneously centrifuged and added to the reacted system generated in step 4.2.

The solution was gently mixed and reacted at 40°C for 8–14 h. Following this, the cRNA was purified using a NucleoSpin RNA Clean-up kit (Macherey-Nagel, Germany).

6. cRNA reverse transcription

The purified cRNA (5 µg/7.5 µl) and Random Primer (4 µl) were added to a 0.2 ml nuclease-free centrifuge tube, mixed gently, and reacted at 65°C for 5 min, followed by an ice bath for 5 min.

The cRNA reverse transcription Master Mix was prepared by gently mixing 5 µl of 4X Script II Buffer, 2 µl of 0.1 M DTT, and 1.5 µl of CbcScript II. It was instantaneously centrifuged and transferred to the solution generated in the last step.

The mixture was gently mixed, instantaneously centrifuged, and then reacted at 25°C for 10 min and 37°C for 1.5 h.

After the reaction, Terminate Solution (5 µl) was added to the system and gently mixed. The mixture was reacted at 65°C for 10 min and stood at room temperature for 5 min. Neutralize Solution (1 µl) was added to this mixture and gently mixed.

The cDNA was purified using NucleoSpin Extract II (Macherey-Nagel, Germany) following the

manufacturer's instructions. The purified cDNA was quantified using the spectrophotometer ($1\text{OD}_{260} = 40\text{ }\mu\text{g}/\mu\text{l}$).

7. Fluorescence labeling

The volume of the purified cDNA was concentrated to $14\text{ }\mu\text{l}$. The Random Primer $4\text{ }\mu\text{l}$ was added to it, mixed well, instantaneously centrifuged, denatured at 95°C for 3 min, and ice-bathed for 5 min. Then, $5\text{ }\mu\text{l}$ of 5X Klenow Buffer, $1\text{ }\mu\text{l}$ of Cy5-dCTP (or Cy3-dCTP), and $1.2\text{ }\mu\text{l}$ of Klenow Fragment were added to it. The mixture was gently mixed, instantaneously centrifuged, and then reacted at 37°C for 1.5 h and 70°C for 5 min.

The labeled production of this step was purified using NucleoSpin Extract II (Macherey-Nagel, Germany) following the manufacturer's instructions and then quantified using the spectrophotometer ($1\text{OD}_{260} = 50\text{ }\mu\text{g}/\mu\text{l}$).

8. Microarray hybridization

The hybridization mixture was prepared according to the following table:

Reagent	Standard volume
2X GEx Hyb Buffer (HI-RPM)	$55.0\text{ }\mu\text{l}$
Formamide	$27.5\text{ }\mu\text{l}$
Sample	$27.5\text{ }\mu\text{l}$
Total volume prepared	$110\text{ }\mu\text{l}$

The hybridization mixture was added to the circRNA microarray (CapitalBio Corporation, Beijing, China), and hybridization was performed in the hybridization oven (Agilent Technologies, USA) at 20 rpm for 16 h.

9. Microarray washing and scanning

After hybridization, the circRNA microarray was washed in wash solution I containing 0.2% SDS and $2\times\text{SSC}$ at 42°C for 5 min and wash solution II containing $0.2\times\text{SSC}$ at room temperature for 5 min.

The washed microarray was scanned by a G2565CA Microarray Scanner (Agilent Technologies, USA) to obtain hybridization images.

10. Data extraction and analysis

Agilent Feature Extraction (v10.7) software was used to analyze the hybridization images and extract the data, which were then normalized using Agilent GeneSpring software.

All the processes of microarray analysis were conducted by the Bioassay Laboratory of CapitalBio Corporation (Beijing, China).

Supplementary Table SI. Clinical characteristics of pregnant women

Patients ID	Age	BMI	Primi-gravida	Primi-parity	Delivery modes	Delivery [gestational weeks]	Sampling 1 [gestational weeks]	Interval from sampling 1 to delivery [h]	Sampling 2 [hours after delivery]
L281	27	28.2	Yes	Yes	Vaginal	38.3	38.1	16	5
L284	28	32.4	No	No	Caesarean	39.9	39.7	26	44
L302	31	33.3	No	No	Vaginal	30.6	30.3	51	15
L317	28	23.7	No	Yes	Vaginal	29.6	29.1	108	30
L325	27	25.2	Yes	Yes	Vaginal	34.9	34.4	69	12
L328	27	29.0	Yes	Yes	Caesarean	34.3	34.1	16	42
L332	38	24.4	No	No	Caesarean	32.4	32.3	29	40

Sample	SRR376	SRR377	SRR378	SRR380	SRR381	SRR395	SRR396	SRR397	SRR398	SRR400	SRR405	SRR406	SRR379	SRR382	SRR383	SRR384	SRR385	SRR386	SRR387	SRR388	SRR389	SRR390	SRR391	SRR392	SRR393	SRR394	SRR399	SRR401	SRR402	SRR403	SRR404
Sex	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Female	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male	Male
chrY:22744476 22751461	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75,58338	0	0	42,64457	0	0	92,59081	0	156,6648	0	0	0	0	0	202,3707	0	49,22737
chrY:22749910 22751461	0	0	0	0	0	0	0	0	0	0	0	0	0	134,0695	0	0	0	0	0	101,3818	102,8787	41,08668	0	28,92499	0	0	0	0	0	86,1479	
chrY:22891809 22902966	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12,87685	0	0	0	0	0	0	
chrY:23300639 23314859	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20,57574	0	0	0	0	0	0	0	0	0	
chrY:23310428 23314859	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64,09015	0	0	0	0	0	0	0	
chrY:23359026 23360427	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30,8636	0	0	38,56665	0	0	0	62,26789	0	0	
chrY:23387378 23390345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20,57574	0	0	0	0	0	0	0	0	0	
chrY:23412200 23415079	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9,230132	
chrY:2661808 2682407	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15,4318	0	0	0	0	0	0	0	0	0	
chrY:2692622 2713784	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27,6904	
chrY:2819679 2822038	0	0	0	0	0	0	0	0	0	0	0	0	0	0	44,09031	0	0	0	0	0	56,58327	65,73869	92,57467	0	32,19211	0	30,69203	0	0	33,84382	
chrY:2821950 2829687	0	0	0	0	0	0	0	0	0	0	0	0	236,7641	150,8282	403,1114	224,1406	138,1242	245,2063	0	173,7973	154,318	205,4334	455,7522	318,1749	309,0443	72,72013	81,84541	126,2037	93,40184	182,428	187,6793
chrY:2821950 2843695	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12,30684	
chrY:2829115 2829687	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85,61835	0	0	
chrY:2947325 2970235	0	0	0	0	0	0	0	0	0	0	0	0	78,92138	0	37,79169	0	0	0	0	137,5895	77,15901	0	0	0	57,9458	155,8288	0	0	319,123	0	86,1479
chrY:7209156 7224271	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93,40184	0	0	