**Methods**

**Anesthesia, CPB and open-heart surgery**

For the patients, studies were performed beginning at the time of anesthesia, which was induced with midazolam (0.5 mg/kg), etomidate (0.3 mg/kg), fentanyl (5-10 µg/kg) and vecuronium (0.1 mg/kg), maintained with oxygen (100%), and supplemented with intravenous doses of fentanyl, midazolam, vecuronium and isoflurane. The right internal jugular vein was cannulated with 7.5 Fr triple-lumen central venous catheters for fluid, vasopressor/inotrope administration and central venous pressure measurement. Left radial artery was cannulated for invasive blood pressure monitoring and arterial blood pumped for gas analysis. The lungs were mechanically ventilated to maintain normocapnia and a pH of 7.35–7.45. Pulse oximetry, nasopharyngeal temperature, five-lead ECG and urine output were monitored. Volume replacement was conducted using hydroxyl ethyl starch (Voluven 6% Fresenius Kabi, Germany) or Ringer’s lactate as appropriate to maintain the CVP at 5 to 12 mmHg. Aortic and atrial cannulations were done after systemic heparin with intravenous heparin 400 IU/kg to achieve an activated clotting time of ＞ 480 sec. All patients underwent cardiac surgery with a standard CPB protocol: pump flow rates and perfusion pressures were maintained at 2.3 to 2.7 L/min/m2 and 50 to 80 mmHg, respectively; blood sugar was maintained 100 to 200 mg/dl during CPB. The hematocrit was maintained ≥ 20%. A 4:1 oxygenated blood: crystalloid cardioplegia solution was infused at a rate of 20 ml/kg every 30 minutes. After heart aortic surgery, dopamine was infused at a rate of 5 to 8 μg/kg/min.

**Quantification of miRNA Expressions**

Total RNA, including the small RNA fraction, was extracted from 400 µl plasma using the mirVana PARIS kit (Ambion, Warrington, United Kingdom) according to a modification of the manufacturer’s instructions, and subsequently eluted in 20 µl nuclease-free water. 5 µl RNA was reversed transcribed into cDNA with universal primers (TaKaRa), then measured (TaKaRa SYBR PrimeScript miRNA RT-PCR Kit #RR716) using specified miR primers for: miR-1, miR-21, miR-208a, miR-499, and snRNA U6 (Table S2). Quantitative reverse transcription polymerase chain reaction (qRT-PCR) was performed on an ABI 7500 real-time PCR instrument (Applied Biosystems, Foster City, USA). The 2× Universal PCR Master Mix (No AmpErase UNG) were used for quantification of miRNAs at 95°C for 10 min, followed by 95°C for 15 s then 60°C for 1 min (40 cycles). The Ct value was defined as the cycle number at which the fluorescence exceeded the threshold. In our experiment, the detection limit of a Ct value was defined as 40. The relative cycle threshold (Ct) values for U6 snRNA were used as endogenous controls for normalizing. miRNA expression values in each group were calculated by the mathematical delta-delta method. For each group, reactions were run three times.

Table S1. Characteristics of the patients

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| Characteristics | Mean ± SD |
| Age (years) | 48.47±11.10 |
| Sex (Male/Femal) | 9/6 |
| Aortic clamping time (min) | 75.80±14.81 |
| cardiopulmonary bypass time (min) | 119.40±17.07 |

Table S2. Primers used for quantitative real-time RT-PCR

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| Name | Sequence |
| miR-1 | TGGAATGTAAAGAAGTATGT |
| miR-21 | GCTTATCAGACTGATGTTG |
| miR-208a | ATAAGACGAGCAAAAAGCT |
| miR-499 | TTAAGACTTGCAGTGATGT |