**SUPPLEMENTARY METHODS**

**Patients and tissue samples collection**

All patients were interviewed about their medical history and underwent a careful physical examination, as well as laboratory studies, including test of serum electrolytes (sodium, potassium), hsCRP**,** glucose, total cholesterol, triglyceride, HDL, LDL, cardiac enzymes (CK, CK-MB, AST), hsTnT, urea, creatinine, uric acid, coagulation tests (PT, aPTT), blood count (hemoglobin, haematocrit, RBC, WBC and platelet count). Each patient underwent investigations such as clinical history, blood pressure, electrocardiography, hemodynamic studies, Doppler echocardiography and coronary angiography. The same basic medical treatment scheme was applied to all patients.

**RNA extraction, library preparation and sequencing**

The RNA integrity was evaluated through denaturing agarose gel electrophoresis and spectrophotometry [1,2]. RNA was quantified using a NanoDrop1000 spectrophotometer (Thermo Fisher Scientific, UK). All RNA samples displayed a 260/280-absorbance ratio ≤2.0. RNA quality was assessed by Experion System (Bio-Rad).

**Data validation by qRT-PCR and statistical analysis**

qRT-PCR was performed using a BioRad iQ iCycler Detection System (BioRad Laboratories, Ltd) with SYBR Premix Ex Taq (Tli RNaseH Plus) Takara (Clontech)protocol in a qRT-PCR System according to the manufacturer’s instructions (Biorad CLX-96).

**REFERENCES**

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2. Rienzo M, Schiano C, Casamassimi A, et al. Identification of valid reference housekeeping genes for gene expression analysis in tumor neovascularization studies. Clin Transl Oncol. 2013; 15:211-218. doi: 10.1007/s12094-012-0904-1.