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Working

Selection of a “housekeeping” miRNA to normalize qRT-PCR data

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ABSTRACT

The qRT-PCR expression analyses were performed on all the recruited patients (61 CAD, 38 AMI_T0 and 11 AMI_T1 patients respectively). Since the absence of a universally recognized miRNA with housekeeping properties, we have analyzed the amplification curve of 84 circulating microRNAs using the Human Serum & Plasma miScript miRNA PCR Array (MIHS-106ZA, QIAGEN).

EXTERNAL LINK

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MATERIALS TEXT

Human Serum & Plasma miScript miRNA PCR Array (MIHS-106ZA, QIAGEN). The Human Serum & Plasma miScript miRNA PCR Array profiles the expression of 84 miRNAs detectable and differentially expressed in serum, plasma, and other extracellular bodily fluids. These miRNAs have been selected based on results published. Data in literature suggest a correlation with these microRNAs in serum/plasma and specific diseases.

1 Identifcation of a "housekeeping" microRNA among the 84 circulating of the Human Serum & Plasma miScript miRNA PCR Array (MIHS-106ZA, QIAGEN):

Selection criteria:

2 • a Ct range <20 Ct

3 • a 0.5≤FC≥1.5 (GeneGlobe Data Analysis Center)

4 • evaluation of expression level by qRT-PCR in all the enrolled samples by using the comparative Ct method quantification (2-ΔCt method).

Result:

5 Based on the above criteria, miR-15b-5p did not show any significant differences in expression level among CAD, AMI_T0 and AMI_T1 patients and could be our internal control.