

## Erratum

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For the article entitled “Expression Profiling of Circular RNAs and Micrnas in Heart Tissue of Mice with Alcoholic Cardiomyopathy” [Cell Physiol Biochem 2018;46:2284-2296, DOI: 10.1159/000489596], the authors would like to correct some imprecise descriptions and one typographical error which happened due to negligence during manuscript preparation. The authors sincerely apologize for these mistakes. The corrections are as follows:

On page 2284 (Abstract), the sentence:

“After analyzing gene function and signaling pathways by bioinformatics software, we found that the differentially expressed mRNAs were associated with carbohydrate metabolism.”

should read as follows:

“After analyzing gene function and signaling pathways by bioinformatics software, we found that the target genes of differentially expressed miRNAs were associated with FoxO signaling pathway.”

On page 2289, the sentence:

“These results indicated that we had successfully established a chronic alcohol-induced ACM model.”

should read as follows:

“These results indicated that mice chronic alcohol consumption may have developed to be alcoholic cardiomyopathy.”

On page 2290, the following sentence should be regarded as deleted:

“A box plot was used to visualize the distribution of the miRNA profiles.”

On page 2292 in the legend of Fig. 6, the term “miR-3013-5p” should read as “miR-3103-5p”. The correct figure legend for Fig. 6 should thus read as follows:

**Fig. 6.** Comparison between the microarray data and qRT-PCR results for miRNAs. miR-467d-3p, miR-491-5p, and miR-3098-3p that were determined to be differentially expressed in alcohol-treated myocardium compared with control myocardium in 5 samples by microarray analysis were validated by qRT-PCR. Whereas, the validation results for miR-3103-5p indicated no significant difference in expression fold-change between the alcohol-treated and control groups. The heights of the columns in the chart represent fold change (alcohol/control) in expression across the 5 samples for each of the 4 validated miRNAs; the bars represent standard errors.