

Deep RNA sequencing identified a novel circular RNA, circ-RCAN2 in pig hearts with potential regulatory functions in acute myocardial infarction

Mester-Tonczar J., Einzinger P., Winkler J., Kastner N., Spannbaauer A., Zlabinger K., Traxler D., Lukovic D., Hasimbegovic E., Goliasch G., Pavo N., Gyöngyösi M.

In this study we used deep RNA-sequencing to identify cardiac circRNAs in infarcted and healthy pig hearts.

Results: Novel identified circ-C12orf29 and circ-RCAN2 were significantly downregulated in infarcted myocardium compared to healthy control (see Figure 1a and 1b). Interestingly, *in vitro* hypoxic porcine cardiac progenitor cells (pCPCs) did not show any significant changes in differential expression of circ-C12orf29. In contrast with the *in vivo* data, circ-RCAN2 exhibited significant ischemia-time-dependent upregulation in hypoxic pCPCs, validated by qPCR (see Figure 1c).

Conclusion: RNA-seq identified novel cardiac circRNAs in pig hearts associated with AMI. Our findings will advance our knowledge of circRNA regulation during AMI.

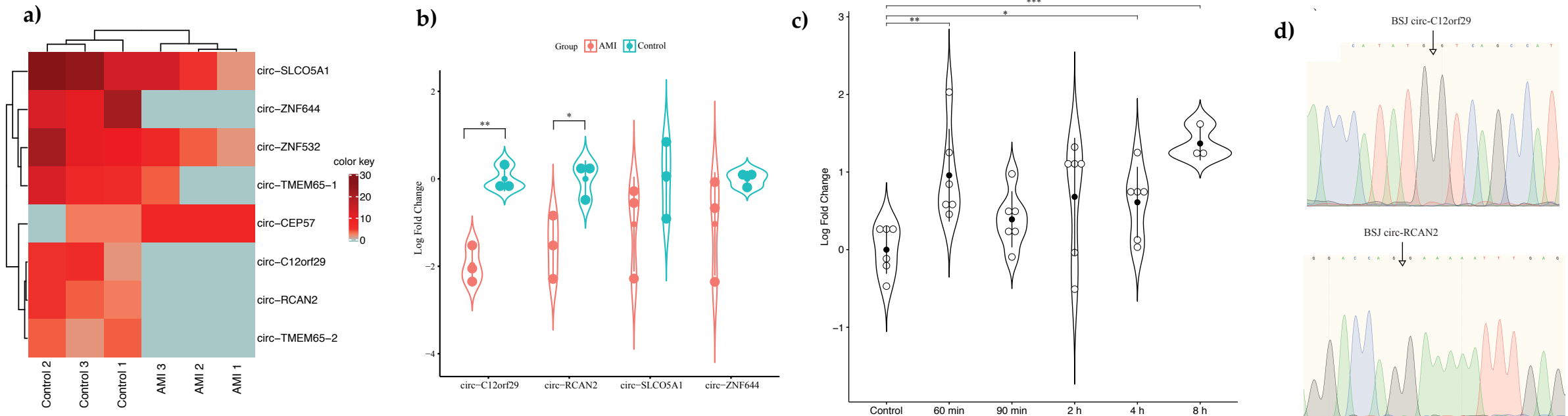


Figure: Identification of novel cardiac circRNA

RNA-seq identified novel cardiac circRNA, *in vivo* results were then validated using qPCR and *in vitro* experiments. Backsplice junction was confirmed using Sanger sequencing