



Category: Animal genomics

## A genome-wide map of circular RNAs in adult zebrafish

Disha Sharma<sup>1,3</sup>, Paras Sehgal<sup>2,3</sup>, Angom Ramcharan Singh<sup>2</sup>, Shamsudheen Karuthedath Vellarikkal<sup>2,3</sup>, Samatha Mathew<sup>2</sup>, Rijith Jayarajan<sup>2</sup>, Shruti Kapoor<sup>1,3</sup>, Vinod Scaria<sup>1,3\*</sup> and Sridhar Sivasubbu<sup>2,3\*</sup>

<sup>1</sup>GN Ramachandran Knowledge Center for Genome Informatics, CSIR Institute of Genomics and Integrative Biology (CSIR-IGIB), Mathura Road, Delhi 110025, INDIA

<sup>2</sup>Genomics and Molecular Medicine, CSIR Institute of Genomics and Integrative Biology, Mathura Road, Delhi 110025, INDIA

<sup>3</sup>Academy of Scientific and Innovative Research, CSIR Institute of Genomics and Integrative Biology South Campus, Mathura Road, Delhi 110025, INDIA

\*Corresponding author: Vinod Scaria ([vinods@igib.in](mailto:vinods@igib.in)) and Sridhar Sivasubbu ([s.sivasubbu@igib.res.in](mailto:s.sivasubbu@igib.res.in))

### Abstract

Circular RNAs are a new addition to the growing list of diverse species of RNAs that are formed by covalent linked 3' and 5' end forming a closed loop structure. Circular RNAs are characteristically resistant to exonuclease treatment and are relatively stable to linear transcripts. Circular RNAs are formed by alternate splicing mechanism but do not follow the canonical order of exons. Backsplice junctions are unique to circRNAs. CircRNAs are shown to possess potential to act as miRNA sponges and control transcription of mRNAs. CircRNAs are also reported as biomarkers for the disease like Alzheimer's, Parkinson's and cancer. A huge number of circRNA transcripts have been identified in model organisms including *C.elegans*, mouse, *Drosophila* as well as human. But there are no circular RNAs reported in zebrafish that is a very good model to study developmental stages, cardiovascular and blood-related disorders. In order to use zebrafish as a model organism and study the role of circRNAs in disease, we have used in-house generated RNA-sequencing data for five tissues including blood, brain, muscle, gills and heart. We discarded the reads mapped contiguously and full length over reference genome and identified back-splice junctions for putative circRNA transcripts. We identified a total of 3428 circRNA junctions out of which 78% were tissue specific. We validated 22 selected candidates for 5 tissues based on literature significance. We quantitatively analysed 5 tissue-enriched candidates using Real-time PCR. We also observed that major proportion of circRNAs is originating from protein coding loci. These circRNAs could be used to further study their role in hematopoietic and cardiovascular diseases.

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