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# **Subject Section**

# FUCHS - Full circle characterization RNAseq

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#### **Abstract**

**Motivation:** CircRNAs are a type of non-coding RNA neglected by many in the field of next-generation sequencing. Though the amount of circRNA detection tools quickly increased over the past two year, no tool is able to identify fully characterize the circle structure (e.g. exon usage and alternative splicing). **Results:** Here we present a new method tackling the ful characterization of circRNAs .... and more results about the data.

Availability: The method is written as a flexible python pipeline available as git-repository: ....

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Supplementary information: no supplementary data provided

# 1 Introduction

$$\sum x + y = Z \tag{1}$$

# 2 Approach

### 3 Methods

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2 Sample et al.

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Table 1. This is table caption

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row2	row2	row2	row2
row3	row3	row3	row3
row4	row4	row4	row4

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# FPO

Fig. 1. Caption, caption.

#### 3.2 Test1

### 4 Discussion

# **5 Conclusion**

4 Sample et al.

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- 3. this is item, use enumerate

#### **Acknowledgements**

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# **Funding**

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