OXFORD

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: ....
Contact: franziska.metge@age.mpg.de
Supplementary information: no supplementary data provided

1 Introduction

- circle research
- current programs to detect circles
- possible functions
- possible bio-genesis
- recent RNaseR treatment advances
- why it would be necessary to know about exon usage and coverage

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

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2 Approach

- RNaseR treated cells
- down stream program after circle detection
- python based pipeline

    Equation (1) Figure 2 Bofelli *et al*., 2000 .

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3 Methods

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3.1 CircRNA detection

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3.1.1 Mapping

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3.1.2 CircRNA detection

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3.2 FUCHS

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3.2.1 Input data

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3.2.2 Extracting reads

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3.2.3 Identifying skipped exons

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3.2.4 Mate pair information, indirect validation of circularity

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3.2.5 extract coverage

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3.2.6 Optional steps

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isoforms

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coverage profile

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cluster of circles with similar coverage profile

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3.3 Visualization

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3.3.1 picture from pipeline

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3.3.2 viusalization in genome browser

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3.4 Data

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3.4.1 Mouse heart and liver

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3.4.2 HEK293 cells

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4 Discussion

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Table 1. This is table caption

head1	head2	head3	head4
row1	row1	row1	row1
row2	row2	row2	row2
row3	row3	row3	row3
row4	row4	row4	row4

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Fig. 1. Caption, caption.

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5 Results

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6 Conclusion

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