

## RNA-DNA interactions in chromatin

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A majority of the eukaryotic genome is transcribed, including mRNAs, rRNAs, tRNAs and various kinds of non-coding RNAs. Non-coding RNAs are involved in many biological processes including regulation of transcription and spatial organization of chromosomes, but still little is known about mechanisms and principles of their functioning. For example, it is suggested that RNA interactions might be powerful organizers of chromatin topology, and multiple models are suggested [1]. There are methods to map RNA-DNA interactions (RNA Antisense Purification [2], ChIRP-seq [3] and CHART [4]), but they are restricted to single or few *a priori* known RNAs. This limitation leads to the problem that real amounts and kinds of chromatin-associated RNAs are still unknown, although a lot is known about cytoplasmic RNAs. Thus the methods of high-throughput analysis of RNA-DNA interactions have to be developed.

In current work, we developed a method for DNA-RNA proximity ligation with subsequent high-throughput sequencing. We performed various controls to validate the specificity of this method and assessed the quality of the results. We developed the pipeline for filtering and analysis of massive sequencing results, created the SQL-oriented database.

We provide primary analysis of datasets and compare them with other existing high-throughput RNA-chromatin interactions mapping techniques (MARGI [5] and ChAR-Seq [6]).

1. J.M. Engreitz et al. (2016) Long non-coding RNAs: spatial amplifiers that control nuclear structure and gene expression. *Nature Reviews Molecular Cell Biology*, **17**, 756–770.
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3. C. Chu et al. (2015) Technologies to probe functions and mechanisms of long

- noncoding RNAs. *Nature Structural & Molecular Biology*, **22**, 29–35.
4. M.D. Simon et al. (2011) The genomic binding sites of a noncoding RNA. *PNAS*, 108(51): 20497–20502.
  5. D. Sridhar et al. (2017) Systematic Mapping of RNA-Chromatin Interactions In Vivo. *Current Biology*, 27, 1–8.
  6. J.C.Bell et al. (2017) Chromatin-associated RNA sequencing (ChAR-seq) maps genome-wide RNA-to-DNA contacts. *bioRxiv*.