

Article Title

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2 ABSTRACT

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4 We introduce Single-cell Nanopore Spatial Transcriptomics (scNAST), a set of tools to facilitate
5 the analysis of spatial gene expression from short and long read sequencing of cDNA synthesized
6 *in situ* on tissue sections, allowing to generate a full-length single-cell transcriptional landscape
7 of the tissue microenvironment.

8 Taking advantage of the Visium Spatial platform, we adapted a strategy recently developed to
9 assign barcodes to long-read single-cell sequencing data for spatial capture technology.

10 **Keywords:** Spatial transcriptomics, Single-cell RNA sequencing, Oxford Nanopore, keyword, keyword

INTRODUCTION

MATERIAL AND METHODS

11 **Mouse heart samples**

12 **10X Genomics Visium experiments**

13 **Oxford Nanopore sequencing libraries**

14 **Cell barcode assignment**

RESULTS

DISCUSSION

DATA AVAILABILITY

15 The datasets [GENERATED/ANALYZED] for this study can be found in the [NAME OF REPOSITORY]
16 [LINK].

CODE AVAILABILITY

AUTHOR CONTRIBUTIONS

- 17 CD supervised the research. EB analyzed the data and wrote the manuscript. XX performed the experiments.
18 All authors contributed to review and editing.

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21 Heidelberg/Mannheim.

CONFLICT OF INTEREST

- 22 The authors declare that they have no conflict of interest.

SUPPLEMENTAL DATA

FIGURE CAPTIONS



Figure 1. Enter the caption for your figure here. Repeat as necessary for each of your figures



Figure 2. This is a figure with sub figures, (A) is one logo, (B) is a different logo.