

# A spatially resolved RNA map for the *Caenorhabditis elegans* germline

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A key question in development is how spatial distribution of RNAs shapes cell proliferation and differentiation. We address this question using the *Caenorhabditis elegans* germline as a powerful in vivo model. The basic molecular architecture of the *C. elegans* germline is similar to that of higher organisms (Nousch et al. 2015). However, despite many studies, the spatially resolved molecular makeup of the germline is largely unknown. To investigate the spatial distribution of RNAs we applied a new cryo-cut based method (Junker et al. Cell 2014) that allows spatially resolved transcriptomics at the scale of single cells. We extracted the germline and dissected it into at least 15 different sections. After RNA extraction from the individual sections, in vitro transcription for linear amplification of cDNA and high-throughput sequencing, we identify candidate genes expressed in specific patterns. We report how we will use this approach to determine genes and molecular mechanisms important for proliferation and differentiation during germline development.

## References

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