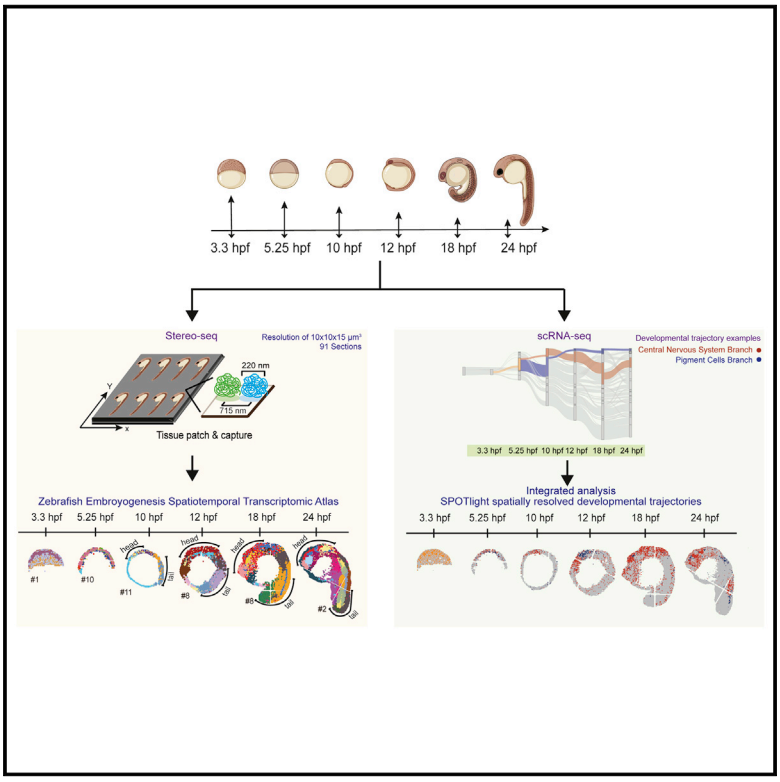
Resource

Developmental Cell

Spatiotemporal mapping of gene expression landscapes and developmental trajectories during zebrafish embryogenesis

Graphical abstract



Highlights

- Stereo-seq is used to generate a ZESTA
- Co-varying spatial gene modules reveal the interactions between functional regions
- Integration of Stereo-seq and scRNA-seq builds spatial developmental trajectories
- Spatiotemporal ligand-receptor dynamics provides insights to regulatory mechanisms

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In brief

Liu et al. employ Stereo-seq to dissect the spatiotemporal transcriptomic dynamics in developing zebrafish embryos. This study provides a spatially resolved resource for the research of vertebrate embryogenesis and also helps to uncover how molecular and cellular interactions contribute to zebrafish embryogenesis.

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