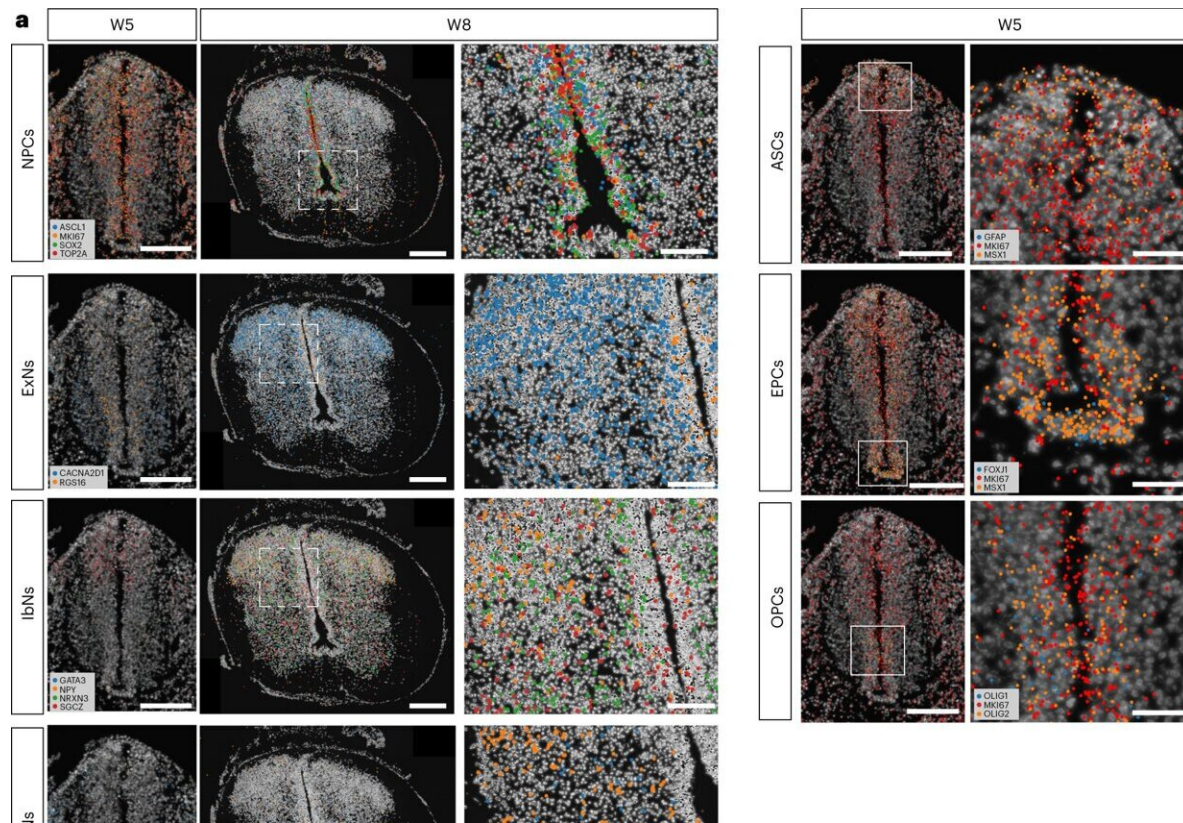


Map of spinal cord formation gives new knowledge on diseases of the nervous system

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Heterogenous neural cells in the human developing spinal cord. a, Representative images showing validation of newborn neurons and glial cells in the developing human spinal cord by HybISS. Scale bar, 200 μm . b, Representative confocal images showing immunostaining of newborn astrocytes (b) and ependymal cells (c) at W5, whereas OPCs are not born at W5 yet (d). Two independent experiments for each panel (a–d) were performed. Scale bars, 200 μm and 50 μm for low and high magnification, respectively. Rectangles indicate enlarged areas. e, UMAP illustrating the heterogenous cell types or cell states of different

neural cell populations. Credit: *Nature Neuroscience* (2023). DOI: 10.1038/s41593-023-01312-9

Researchers at Karolinska Institutet have mapped how cells in the human spinal cord are formed in the embryo and what genes control the process. Their findings can give rise to new knowledge on how injury to and diseases of the spinal cord arise and how they can be treated. The study has been published in the journal *Nature Neuroscience*.

The spinal cord is part of the central nervous system, serving as an important bridge for communication between the brain and the rest of the body. There are many different types of cells in the human spinal cord but much still remains to be understood about how these cells are formed from [stem cells](#) during embryonic development.

"Many [neurodegenerative diseases](#) and injuries of the spinal cord are incurable because of the poor regeneration of human spinal cord cells," says the study's first author Xiaofei Li, assistant professor at the Department of Neurobiology, Care Sciences and Society, Karolinska Institutet. "A better grasp of how the spinal cord is formed and how different genes control this development can lead to new therapies for [spinal cord injuries](#) and diseases such as ALS or cancer of the nervous system."

User-friendly online tool

The researchers have built up an extensive map of all the cell types of the human spinal cord, showing where the cells are and what genes they express during embryonic development. The information has been gathered in a [user-friendly](#) interactive online tool that researchers or other interested parties can use to search for genes that shape how the

spinal cord develops.

The study identified key genes that affect how the stem cells migrate when the spinal cord is formed and what specializations they have. A comparison with spinal cord development in mice revealed important differences between mice and humans.

"These findings are very important because much of what we already know is based on mouse studies," says Dr. Li.

The study was conducted using single-cell RNA sequencing and spatial transcriptomics, which enabled the researchers to map thousands of genes in each individual cell and analyze how they are expressed at different sites of the same tissue section.

Learning more about child cancer

The researchers also studied an unusual tumor type called ependymoma, which manifests as malignant brain tumors in children or benign [spinal cord](#) tumors in adults. On identifying [genes](#) that are specific to tumor development they were thus able to demonstrate how their findings can be used to increase understanding of diseases of the nervous system.

"We'll now be interrogating how stem cells form different cell types and change their properties both during [embryonic development](#) and later during maturity and aging, as well as in different kinds of pathological conditions," says the study's last author Erik Sundström, senior researcher at the Department of Neurobiology, Care Sciences and Society, Karolinska Institutet.

More information: Xiaofei Li et al, Profiling spatiotemporal gene expression of the developing human spinal cord and implications for ependymoma origin, *Nature Neuroscience* (2023). [DOI](#):

[10.1038/s41593-023-01312-9](https://doi.org/10.1038/s41593-023-01312-9)

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