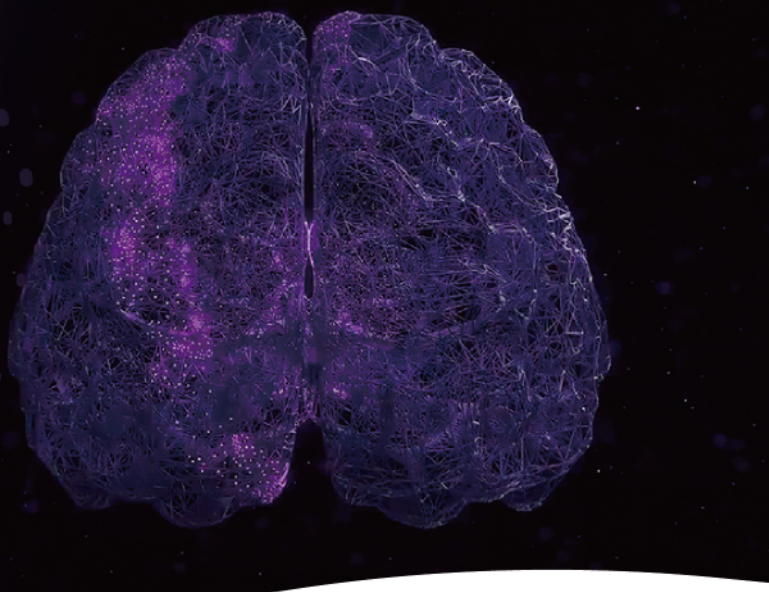
# STOmics

The brain is a complex and amazing organ, made up of distinct regions and diverse cell types. With spatial transcriptomics technology, scientists can now precisely map the brain, uncovering its intricate molecular workings. STOmics Stereo-seq solutions are now compatible with both fresh-frozen (FF) and formalin-fixed and paraffin-embedded (FFPE) samples with true single-cell resolution and centimeter-level field-of-view, which can significantly enhance our knowledge of the brain in both health and disease.



## Technology highlights

- Subcellular resolution allowing visualization of cellular heterogeneities and efficient cell type annotations

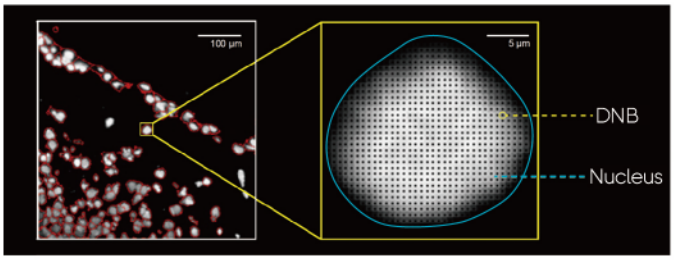



Figure 1. Stereo-seq capturing spots (DNBs) arranged down to single cell resolution, allowing mRNA within one cell to be captured with hundreds of coordinate ID containing DNBs

- Multiple chip sizes allowing various tissue types and scalable capture areas

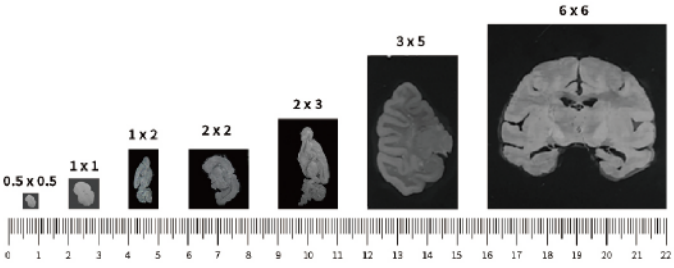
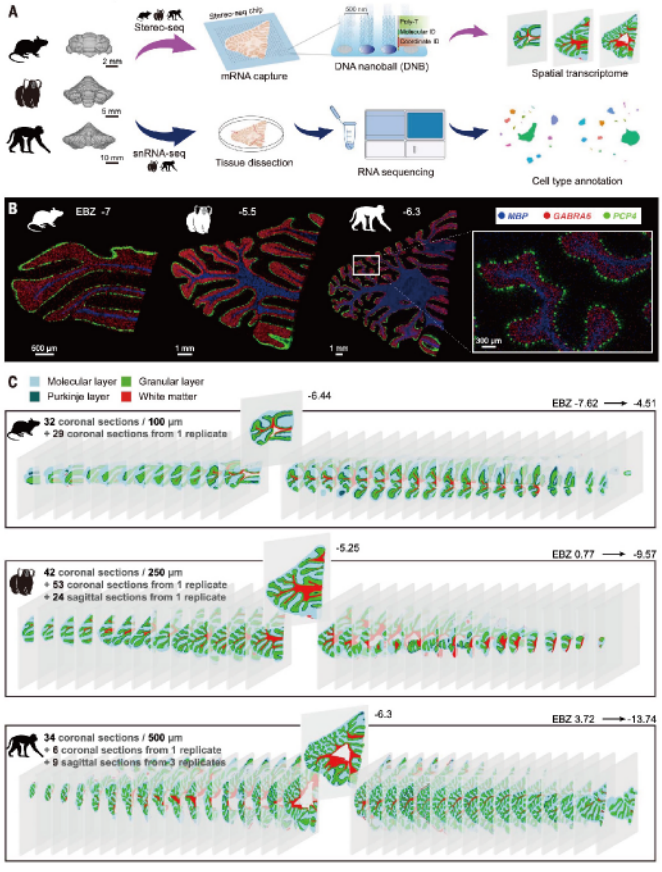



Figure 2. Demonstration of Stereo-seq chip at different sizes

## Featured publication

### Cross-species single-cell spatial transcriptomic atlases of the cerebellar cortex

Shijie Hao et al., *Science*, 2024



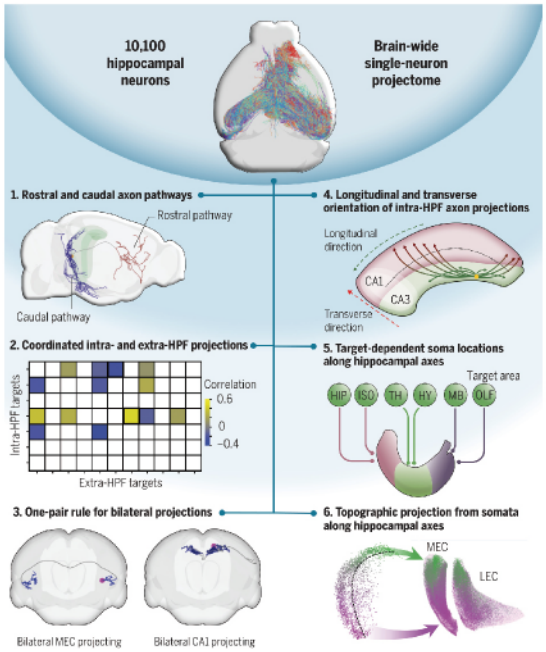
## Highlights

- The study provides comprehensive single-cell spatial transcriptomic atlases of the cerebellar cortex of macaques, marmosets, and mice, revealing primate-specific cell types and spatial gene expression patterns
- The research identified two primate-specific subtypes of Purkinje cells (the only output neurons of the cerebellar cortex) that expressed distinct levels of the gene GRID2, which encodes a delta2 glutamate receptor
- It elucidates the relationship of 3D gene expression patterns with functional connectivity of the cerebellar cortex across species

| STOmics product | Species | Sample type |
|---|---|---|
| Stereo-seq Large Chip Design (LCD)/Customized LCD | Macaques, marmosets, and mice | Fresh Frozen |

## Whole-brain spatial organization of hippocampal single-neuron projectomes

Ou et al., ***Advanced Science*** , 2022




## Highlights

- The researchers mapped the axon projections and their arborization patterns in both intra- and extra-HIP areas for 10,100 HIP neurons, with soma located throughout the entire HIP
- Spatial transcriptomic analysis of hippocampal sections was also performed to determine the correlations between soma location, transcriptome profile, and axonal projection

| | |
|---|---|
| STOmics product | Stereo-seq Transcriptomics Solution |
| Species | Mice |
| Sample type | Fresh Frozen |

# Additional publications

| Publication | Sample Info | Link |
|---|---|---|
| Spatially resolved gene regulatory and disease-related vulnerability map of the adult Macaque cortex<br>Ying Lei et al., ***Nature Communications*** ,2022 | Macaque cortex, Fresh Frozen | |
| Single-cell spatial transcriptome reveals cell-type organization in the macaque cortex<br>Ao Chen et al., ***Cell*** ,2023<br>Data access: https://macaque.digital-brain.cn/spatial-omics | Macaque cortex, Fresh Frozen | |
| Spatiotemporal transcriptome atlas reveals the regional specification of the developing human brain<br>Yanxin Li et al., ***Cell*** ,2023 | Human brain, Fresh Frozen | |