

Workflow of Our Spatial Transcriptome Sequencing Products



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With spatial transcriptome sequencing, the gene expression is brought into a morphological context. To combine gene expression with histological imaging data, the sample undergoes various steps, which are described here.

If you provide an FFPE tissue block, this block first needs to be sectioned. The resulting sections are placed on a 10x-approved standard glass slide. It is important that the section is placed within the allowable area of the slide. If you section the FFPE tissue block yourself and provide FFPE sections on slides, you may want to have a look at our [information flyer](#) about recommended slides and analyzable regions.



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www.cephor.com/spatial-transcriptome-sequencing

The tissue section on the glass slide is deparaffinized and undergoes H&E staining. The H&E-stained tissue is then imaged. This image is later used in the analysis and combined with the sequencing data to set the gene expression in context with the tissue's morphology. Additionally, this image can be used to determine the region to be analyzed if the tissue is larger than 6.5 mm x 6.5 mm. After imaging, crosslinks are removed, and probes are hybridized to the RNA within the tissue. In the next step, the standard glass slide is placed inside the Visium CytAssist together with the 10x Visium slide, bringing the tissue section in proximity to the Visium slide. The Visium CytAssist transfers the transcriptomic probes from the standard glass slide onto the Visium slide. Within the Visium CytAssist, the capture area is imaged. Subsequently, the probes are released from the tissue and captured by the oligonucleotides on the Visium slide. Outside the Visium CytAssist, the probes are extended, amplified, and released from the Visium slide. For the following library construction, indexes are added to the probes. The constructed library is then sequenced on one of our Illumina sequencing platforms. In the final data analysis, the sequencing data is combined with the H&E image to set the gene expression in its morphological context. The complete workflow is depicted in figure 1.

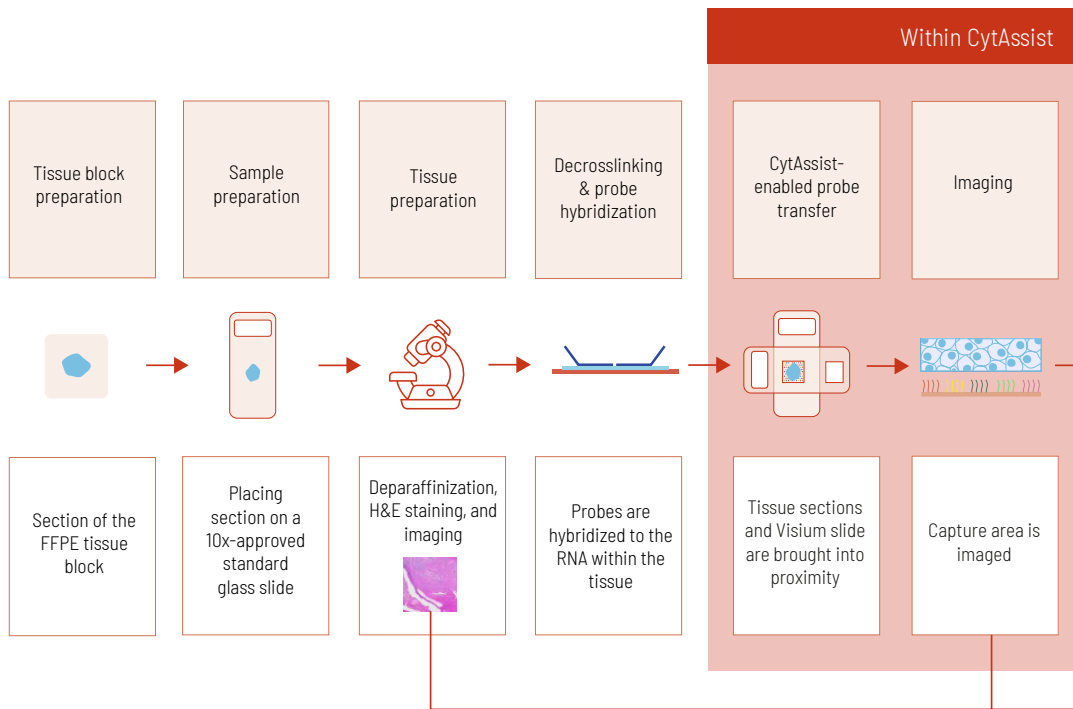


Figure 1 | Spatial Transcriptome Sequencing workflow. Multiple steps are required to bring gene expression into a morphological context.

