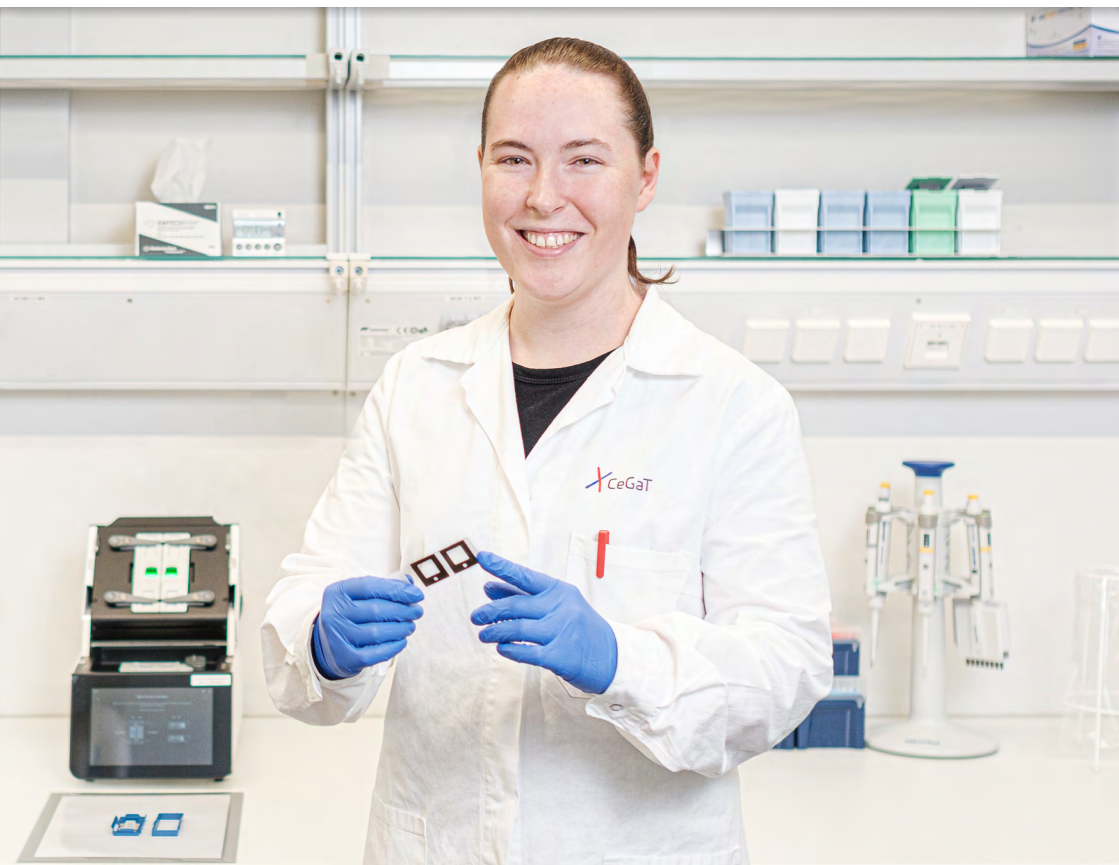


Spatial Transcriptome Sequencing



Combining Gene Expression with Its Tissue Morphology

Spatial Transcriptome Sequencing

Transcriptomic technologies provide crucial insights into cellular characteristics. Changes in a cell's surroundings can change its transcriptome. As cells cluster together to form tissues, the transcriptome of each individual cell is strongly affected by the surrounding tissue. Thus, bringing a cell's transcriptome in context with its tissue morphology can give valuable, novel insights. Spatial transcriptome sequencing combines conventional staining and imaging methods with RNA sequencing. With the resulting complex data, biological architectures can be disentangled. Furthermore, spatial transcriptome sequencing can unravel tissue heterogeneity, enable tissue classification based on expression profiles, and lead to the discovery of new biomarkers.

We offer various Spatial Transcriptome Sequencing products to discover novel insights into disease pathology, development, and translational research.



Want to Discover More?

We invite you to take a look at our website.

www.cegat.com/spatial-transcriptome-sequencing

Explore Our Product Portfolio for Spatial Transcriptome Sequencing

We offer different Spatial Transcriptome Sequencing (STS) products to address a variety of research questions. The products differ in their resolution and the sample type. You can choose between our standard (SD) products and the high-definition (HD) products, which are both suitable for FFPE tissue blocks and FFPE sections. If you want to learn more about the resolution differences between our SD and HD products, you might have a look at our [information flyer](#) concerning the SD vs. HD slide comparison. Each of our products can be supplemented with further services. We are happy to advise you.

	STS SD Block	STS SD Slide	STS HD Block	STS HD Slide
Species	Human, mouse			
Sample type	FFPE tissue block	FFPE section on slide	FFPE tissue block	FFPE section on slide
Target	Gene expression + spatial information			
Platform	Visium CytAssist (10x Genomics®) Illumina			
Resolution	~ 5,000 barcoded spots		~ 11 million continuous barcoded squares	
Output	125 million read pairs per fully covered capture area		275 million read pairs per fully covered capture area	
Included deliverables	Project report & files in FASTQ, BAM, H5, CLOUPE, HTML, TIFF, TSV, & CSV format			

STS: Spatial Transcriptome Sequencing



About Us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our sequencing service portfolio is complemented by analyses suited for microbiome, immunology, and translational oncology studies.

Our dedicated project management team of scientists and bio-informaticians works closely with you to develop the best strategy to realize your project. Depending on its scope, we select the most suitable library preparation and conditions on our sequencing platforms.

**We would be pleased to provide you with our excellent service.
Contact us today to start planning your next project.**



Accredited by DAKKS according to
DIN EN ISO/IEC 17025:2018



CLIA CERTIFIED ID: 99D2130225

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