CeGaT

Research &
Pharma Solutions

Quality Control Checkpoints for Spatial Transcriptome Sequencing

Quality Control Checkpoints for Spatial Transcriptome Sequencing

To ensure good quality results for your Spatial Transcriptome Sequencing project, we have three quality control checkpoints: the initial quality control, the library quality control, and the post-sequencing quality control.

Initial QC

During the initial quality control, we assess the provided material. Sections need to be placed on compatible and approved slides. We verify whether 10x-approved glass slides were used. Additionally, we validate the correct placement of the section on the slide, as sections are only allowed to be placed in the allowable area. If the tissue is placed outside the allowable area, it cannot be transferred to and subsequently analyzed with the Visium slide. For further information on approved glass slides and the correct placement of the tissue section, please have a look at our Slide-Guide for Spatial Transcriptome Sequencing flyer. Furthermore, we check for tissue detachment and sample integrity to avoid losing spatial information.

Library QC

The quality control during library preparation includes reviewing the qPCR performance of the samples. Specifically, the cycle threshold (Ct) value is determined to ensure the optimal number of cycles for the final library preparation step. Low Ct values suggest a high abundance of the target nucleic acid, while high Ct values indicate a low abundance. Ct values are influenced by sample quality, size, composition, and workflow steps. Very high values will likely lead to a drop in sensitivity and data quality. After the final library preparation step, we check for the correct library size and potential by-products. A fluorescence-based concentration measurement complements our library quality control. If the samples pass the quality control, we start the sequencing process.

Post-sequencing QC

After sequencing, the post-sequencing quality control includes examining the key metrics in the web summary generated by the Space Ranger software from 10x Genomics. We check the sequencing and mapping metrics, as well as the image alignments and UMI count distributions. Workflow errors, RNA degradation, or other irregularities would be visible in the key metrics of the post-sequencing quality.

With proper sample preparation, good sample quality, and continuous quality controls, Spatial Transcriptome Sequencing projects achieve good quality results.

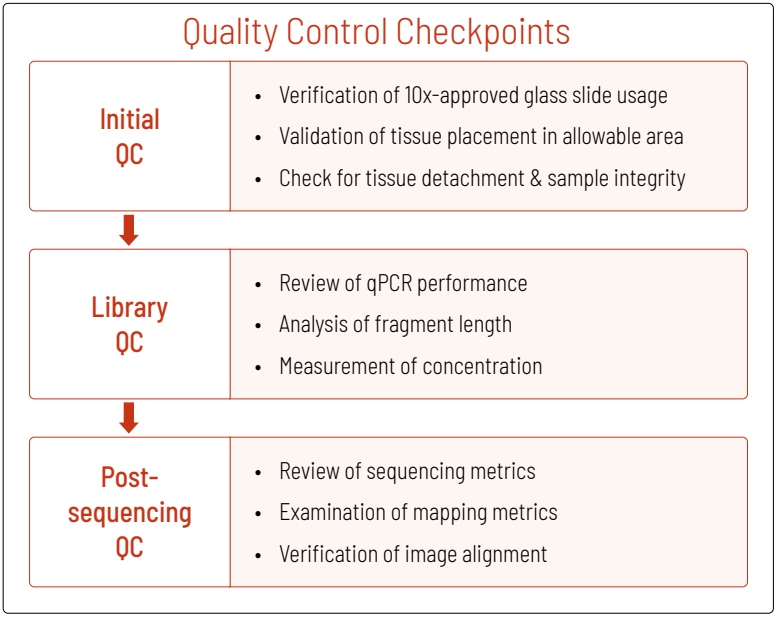

Figure 1| Quality control checkpoints.

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.

DAkkS
Deutsche Akkreditierungsstelle
D-PL-13206-01-00

Accredited according to DIN EN ISO/IEC 17025

CAP ACCREDITED
COLLEGE of AMERICAN PATHOLOGISTS

CLIA CERTIFIED ID: 99D2130225

CeGaT GmbH
Research & Pharma Solutions
Paul-Ehrlich-Str. 23
72076 Tübingen
Germany

Phone: +49 7071 56544-333
Fax: +49 7071 56544-56
Email: rps@cegat.com
Web: www.cegat.com/rps

2026/02