

Research & Comparing the Resolution of Our Standard Products with Our High-Definition Products for Spatial Transcriptome Sequencing



Comparing the Resolution of Our Standard Products with Our High-Definition Products for Spatial Transcriptome Sequencing

10x offers two different resolutions for Spatial Transcriptome Sequencing. On both the standard (SD) and the high-definition (HD) slide, two capture areas measuring 6.5 mm x 6.5 mm each are available.

The standard slide holds 5,000 barcoded spots per capture area. Each spot comprises millions of capture probes and has a diameter of 55 µm. The distance between two centers is 100 µm. Sequencing at least 25,000 read pairs per tissue-covered spot is recommended, resulting in 125 million read pairs per fully covered capture area.

The HD slide has a continuous lawn of oligonucleotides arrayed in approximately 11 million barcoded squares without gaps. The squares have a size of 2 μ m x 2 μ m. The following bin sizes are reported: 2 μ m x 2 μ m, 8 μ m x 8 μ m, and 16 x 16 μ m. 275 million read pairs are recommended per fully covered capture area. Thus, the high-definition products have a single cell-scale resolution and a continuous detection of gene expression.



Want to Discover More? We invite you to take a look at our website. www.cegat.com/spatial-transcriptome-sequencing Depending on your research question, it might be necessary to continuously map gene expression at a single-cell scale resolution. This might, for example, be beneficial for very small anatomical structures or highly heterogeneous tissues. If a single-cell scale resolution is not required, the standard slide might be sufficient. We have Spatial Transcriptome Sequencing products in our <u>portfolio</u> for both demands.



Figure 1| Difference between the Visium SD and the HD slide. While the standard slide holds 5,000 barcoded spots per capture area, the HD slide has a continuous lawn of barcoded oligonucleotides.