

EXHIBIT O

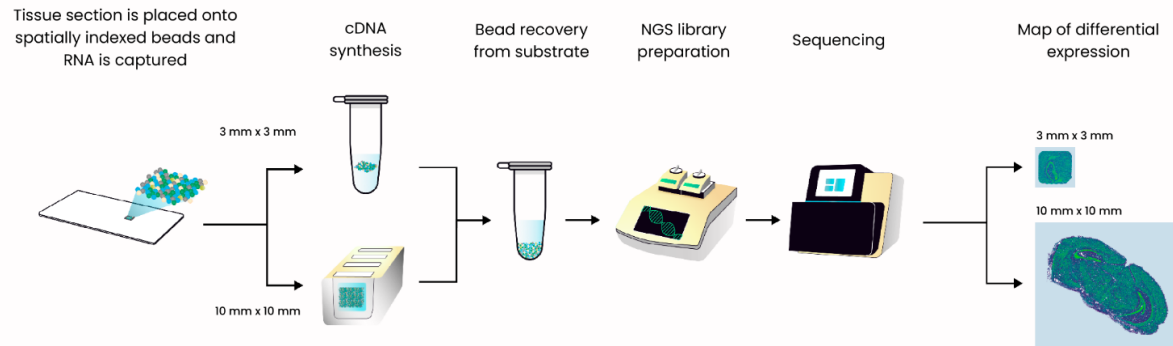
EXEMPLARY INFRINGEMENT CLAIM CHART
U.S. PATENT NO. 11,761,030

This chart is exemplary only and is based on information and belief that Plaintiffs have at this stage.

Claim Limitation	Curio Infringement
16. A composition comprising (i) an array comprising a substrate, a plurality of beads, and a plurality of capture probes, and (ii) a tissue section, wherein: the tissue section is disposed on the array: the plurality of beads are attached to the substrate;	A composition is formed when using the Curio Seeker kit and workflow, the composition comprising (i) an array comprising a substrate (Seeker tile), a plurality of beads (10-micron beads), and a plurality of capture probes (oligonucleotide comprising at least Poly(dT), UMI, bead barcode, and PCR handle), and (ii) a tissue section. The tissue section is disposed on the array, and the plurality of beads are attached to the substrate. Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 9:42.

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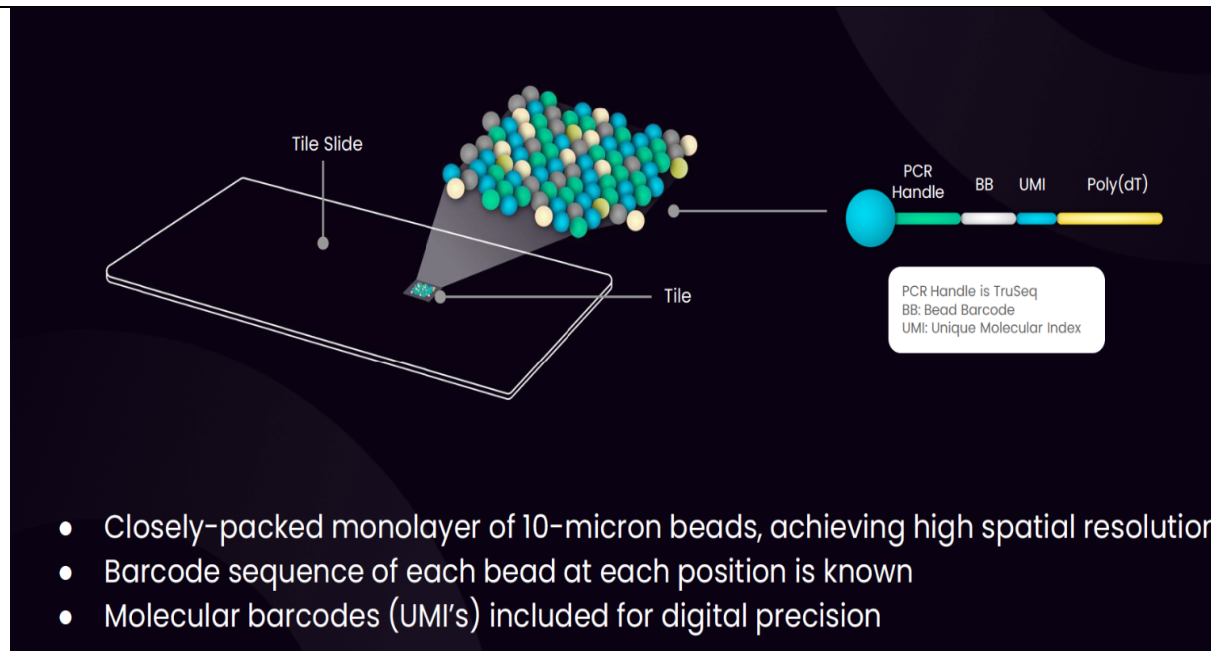
Curio Seeker workflow



Once your tissue section is placed on the Curio Seeker tile, mRNA is captured and hybridized on the spatially-indexed beads before reverse transcription. The indexed beads are then dissociated from the tile and the tissue digested, followed by second strand synthesis and cDNA amplification. After purification and quantification, the cDNA undergoes NGS library preparation and is sequenced on an Illumina sequencer. Lastly, the resulting FASTQ files are processed by the Curio Seeker bioinformatics pipeline to create a detailed spatial transcriptomic map of your tissue section.

Curio Bioscience, *Product*, <https://curiobioscience.com/product/>.

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“Intro to Curio Seeker,” Webinar by Cristin Douglas, Senior Account Executive, Curio Bioscience Houston Spatial Transcriptomics Webinar (Mar. 21, 2023), slide 8.

“These are some of the important features of the product. The resolution is 10 μm . And this is enabled by 10 μm beads, which are randomly placed on a tile, or an area that we call a tile. ... The plexity is whole transcriptome. We do have oligos on the surface of the beads that have poly(T) on the ends that will capture in an unbiased manner all the RNA with poly(A) tails.”

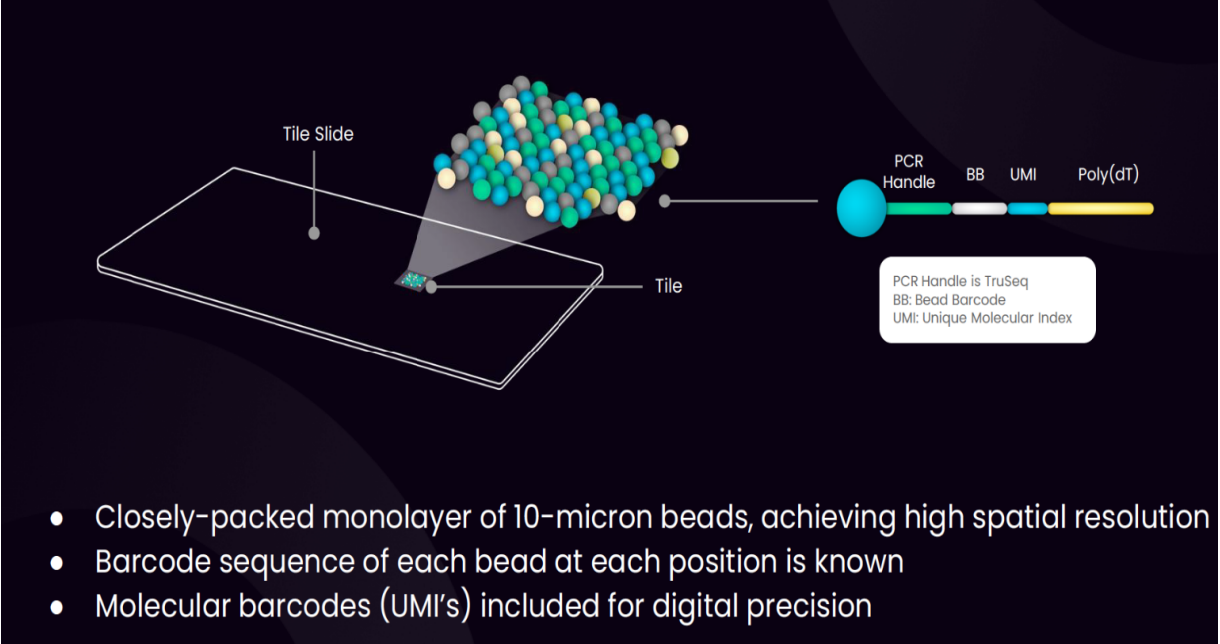
Curio Bioscience, *Single-cell RNA seq data analysis pipeline technology overview* (March 1, 2023), <https://www.youtube.com/watch?v=7gRsoqVUxb0>, at 5:01-5:35.

“On the right you’ll see the actual product. In the middle there is a white patch, which contains all the 10 μm beads in a 3x3 mm area. And there about 80,000 beads in that small patch. And those beads are mounted on a glass backing.”

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	Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 9:35-9:58. “And what you’ll do, is you’ll put that [Seeker tile] into the cryostat ahead of time to come to the same temperature as your tissue block. And I’m just going to show you an example of how to mount your tissue. This is a 10 µm section. For reference, this is a whole mouse brain. And it is larger than the actual tile area, which is not a big deal. All you’ll need to do is position it over the tile in whichever area you want to look at. And it’s easy because it’s at the same temperature as your tissue block. Your tile is at the same temperature, so it won’t melt pre-emptively. And so you just move it over the tile to wherever you want it within the tissue. And once it’s in position, you just pick it up and melt it with your finger.” Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 10:21-11:20.
each of the capture probes of the plurality of capture probes comprises a nucleic acid sequence comprising from the bead surface: (i) a primer binding site, (ii) a nucleic acid sequence that identifies a unique location on the substrate and is not configured to hybridize to a target nucleic acid that binds to a target nucleic acid binding domain, and (iii) the	Each of the capture probes comprises a nucleic acid sequence comprising from each bead surface: (i) a primer binding side (PCR handle); (ii) a nucleic acid sequence (bead barcode sequence) that identifies a unique location on the substrate and is not configured to hybridize to a nucleic acid that binds to the target-binding domain; and (iii) a target nucleic acid-binding domain (Poly(dT) sequence).

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target nucleic acid-binding domain;	 • Closely-packed monolayer of 10-micron beads, achieving high spatial resolution • Barcode sequence of each bead at each position is known • Molecular barcodes (UMI's) included for digital precision “Intro to Curio Seeker,” Webinar by Cristin Douglas, Senior Account Executive, Curio Bioscience Houston Spatial Transcriptomics Webinar (Mar. 21, 2023), slide 8. Each bead barcode comprises a nucleic acid sequence that identifies a unique location of the bead on the glass tile. <i>See</i> “Intro to Curio Seeker,” Webinar by Cristin Douglas, Senior Account Executive, Curio Bioscience, Houston Spatial Transcriptomics Webinar (Mar. 21, 2023), slide 8 (showing the barcode sequence of each bead at each position is known). “... the 10 μm beads are randomly placed on each tile. So what that means is that during our manufacturing process we actually have to index or sequence all those spatial barcodes up front so that the customer doesn’t have to. ... In the kit that we send you, you’ll get the spatially indexed tiles and the reagents, but we’ll also email you or send you the text files with the actual

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	bead barcodes and spatial locations. And you'll just use those text files as input into the primary analysis pipeline that we have.” Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 8:45-9:35.
the target nucleic acid-binding domain of each of the plurality of capture probes comprises a nucleic acid sequence capable of hybridizing to at least a portion of the target nucleic acid that binds to the target nucleic acid-binding domain; and	The target nucleic acid-binding domain (poly(dT) sequence) of each capture probe comprises a nucleic acid sequence (sequence of Ts) capable of hybridizing to at least a portion of the target nucleic acid that binds to the target nucleic acid-binding domain (poly(A) tails of RNA). <i>See</i> Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 5:20-5:35. “These are some of the important features of the product. The resolution is 10 μm. And this is enabled by 10 μm beads, which are randomly placed on a tile, or an area that we call a tile. ... The plexity is whole transcriptome. We do have oligos on the surface of the beads that have poly(T) on the ends that will capture in an unbiased manner all the RNA with poly(A) tails.” Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 5:01-5:35.
the plurality of beads was previously positioned on the substrate in a random pattern.	The beads were positioned on the tile in a random pattern. “These are some of the important features of the product. The resolution is 10 μm. And this is enabled by 10 μm beads, which are randomly placed on a tile, or an area that we call a tile.” Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 5:01-5:35. “ ... the 10 μm beads are randomly placed on each tile. So what that means is that during our manufacturing process we actually have to index or sequence all those spatial barcodes up front so that the customer doesn't have to. ... In the kit that we send you, you'll get the spatially indexed tiles and the reagents, but we'll also email you or send you the text files with the actual

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