

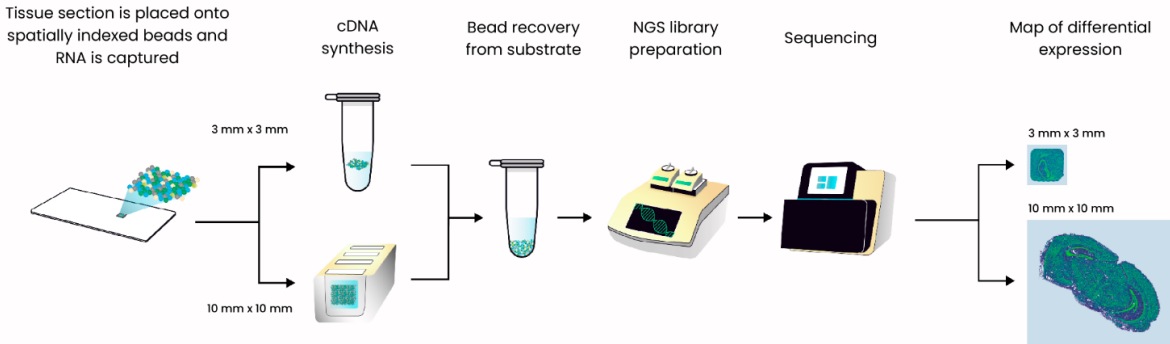
EXHIBIT L

EXEMPLARY INFRINGEMENT CLAIM CHART
U.S. PATENT NO. 10,662,468

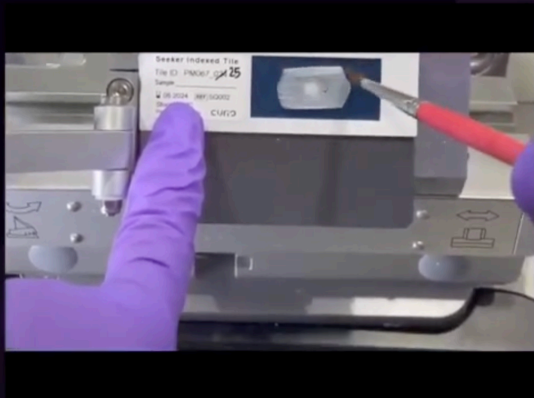
This chart is exemplary only and is based on information and belief that Plaintiffs have at this stage.

Claim Limitation	Curio Infringement
1. A method for determining the presence or abundance of a nucleic acid at a location in a tissue section comprising:	The Curio Seeker kits and workflow are used to determine the presence or abundance of a nucleic acid (e.g., an mRNA) at a location in a tissue section. 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.

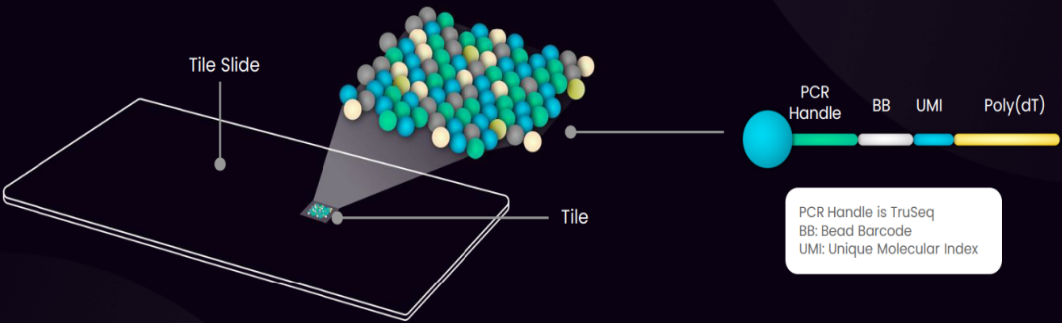
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Claim Limitation	Curio Infringement
	Curio Seeker workflow  The diagram illustrates the Curio Seeker workflow. It begins with a tissue section (10 mm x 10 mm) being placed on a Curio Seeker tile (3 mm x 3 mm). The workflow steps are: Tissue section is placed onto spatially indexed beads and RNA is captured; cDNA synthesis; Bead recovery from substrate; NGS library preparation; Sequencing; and Map of differential expression. The final output is a spatial transcriptomic map of the tissue section. 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, <i>Product</i>, https://curiobioscience.com/product/.
(a) contacting the tissue section with an array comprising a plurality of features, wherein a feature of the plurality of features comprises a capture agent, wherein the capture agent comprises: (i) a first sequence that specifically binds the	The Curio Seeker kits and workflow comprise contacting the tissue section with an array (e.g., a monolayer of 10-micron beads). A tissue section is mounted and melted on the Curio Seeker tile.

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nucleic acid, and (ii) a second sequence comprising a coding tag, wherein a sequence of the coding tag corresponds to a location of the capture agent on the array;	 Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 11:10. See also Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 0:53. The tile comprises an array (e.g., a monolayer of beads) comprising a plurality of features (beads), wherein each bead comprises a capture agent (oligonucleotide comprising at least Poly(dT), UMI, and bead barcode sequences):

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	 The diagram illustrates the Curio Seeker technology. It shows a 'Tile Slide' with a 'Tile' containing a 'Monolayer of 10-micron beads'. A 'Capture agent' is shown on a bead, consisting of a 'PCR Handle' (blue), 'BB' (Bead Barcode, green), 'UMI' (Unique Molecular Index, yellow), and 'Poly(dT)' (red) sequence. A legend box states: 'PCR Handle is TruSeq', 'BB: Bead Barcode', and 'UMI: Unique Molecular Index'. • 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 capture agent comprises a first sequence that specifically binds the nucleic acid. Specifically, the poly(dT) sequence of the capture agent specifically binds the poly(A) tails of mRNA of the tissue section. <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. Each capture agent comprises a second sequence comprising a coding tag (bead barcode), wherein a sequence of the coding tag corresponds to a location of the capture agent on the array. <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).

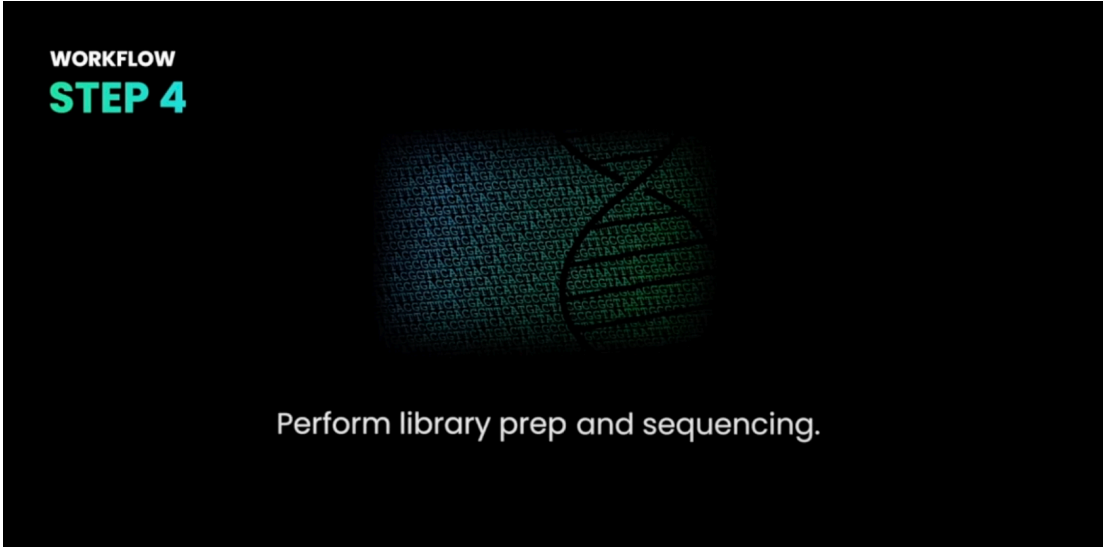
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(b) determining all or a portion of the sequence of the coding tag, or a complement thereof, and all or a portion of the sequence of the nucleic acid specifically bound to the capture agent, or a complement thereof, and using the determined sequences to determine presence or abundance of the nucleic acid at a location in the tissue section.	All or a portion of the sequence of the bead barcode and/or a complement thereof and all or a portion of the sequence of the captured mRNA are determined through sequencing. First, the Seeker tile with melted tissue is placed in a tube to hybridize and reverse transcribe the mRNA: Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 0:56-1:02.

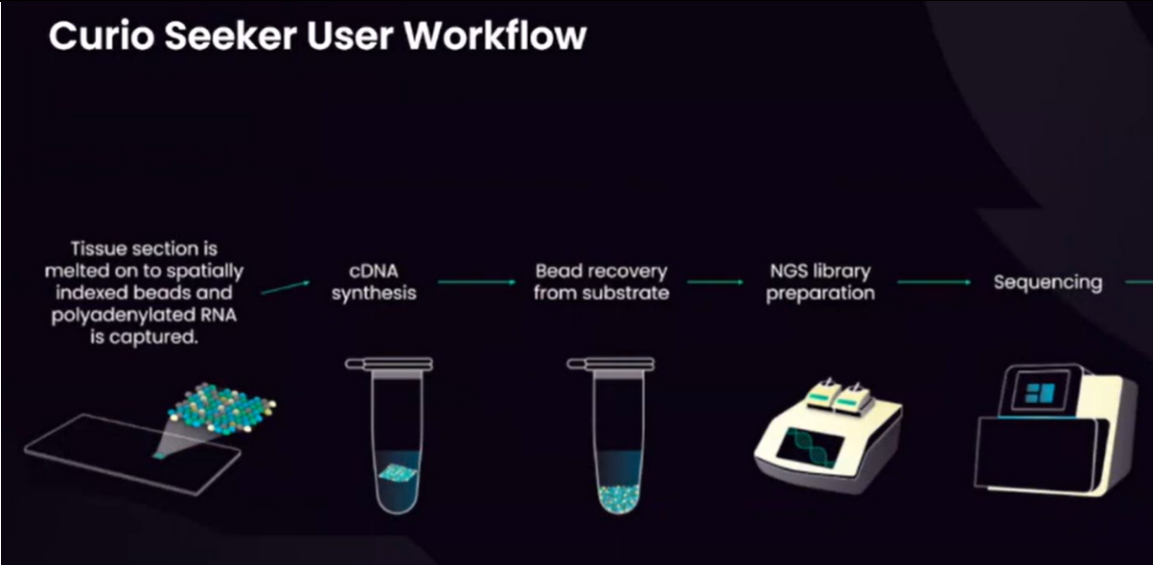
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	Next, the tissue is digested before taking the beads through second strand synthesis and cDNA amplification: WORKFLOW STEP 3  Clear the tissue and beads for second strand synthesis and cDNA amplification. Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 1:03-1:10.

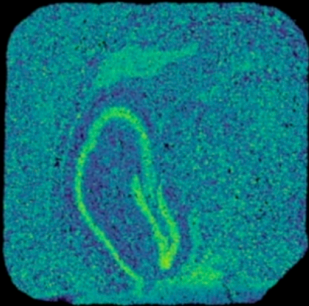
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	The sequencing libraries are then prepared and sequenced; sequencing determines the sequence of the bead barcode and the sequence of the captured mRNA:  WORKFLOW STEP 4 Perform library prep and sequencing. Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 1:18.

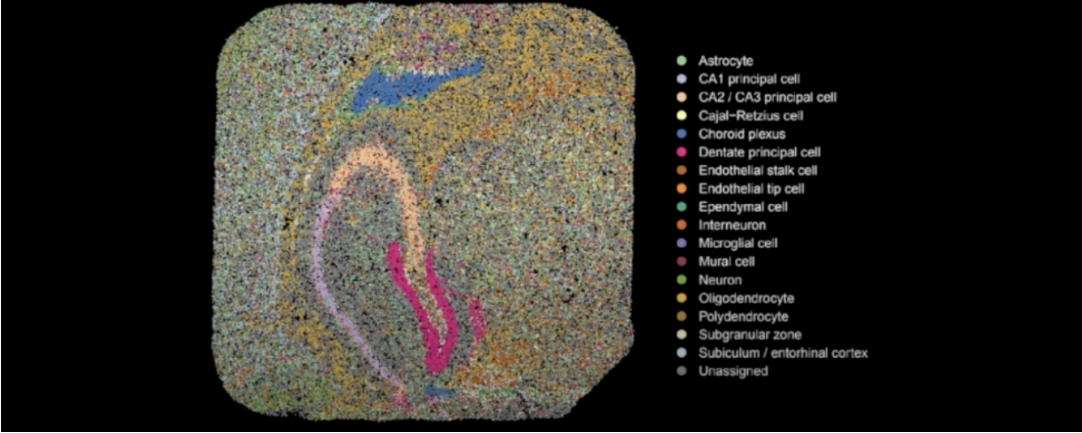
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Claim Limitation	Curio Infringement
	Curio Seeker User Workflow  Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview Curio Seeker by Curio Bioscience</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 12:00. The determined sequences of the bead barcode and the mRNA are used to determine presence or abundance of the nucleic acid at a location in the tissue section: “Our provided primary analysis pipeline will convert your sequencing FASTQ files to matrix files to enable reconstruction of the spatial whole transcriptome map of your tissue.”

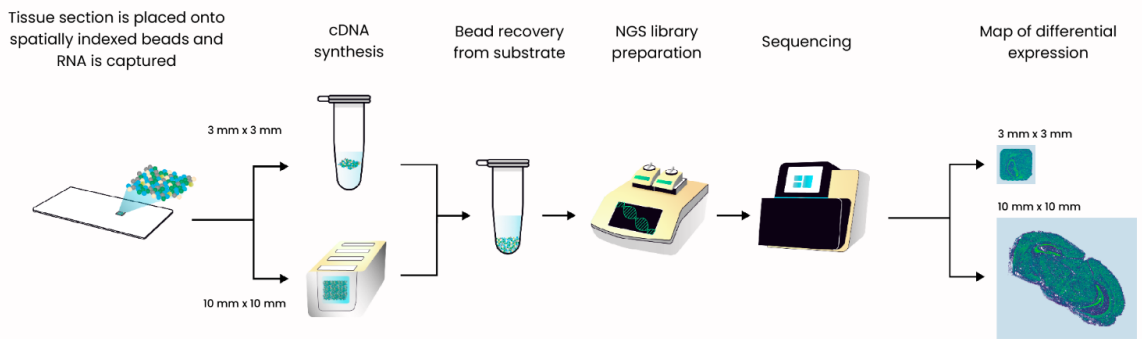
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Claim Limitation	Curio Infringement
	WORKFLOW STEP 5  Reconstruct the spatial whole-transcriptome map of the tissue by bioinformatics pipeline analysis. Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 1:15-1:29.

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	Identify localizations and interactions of distinct cell types by spatial gene expression patterns  Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 1:41.

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	Curio Seeker workflow  The diagram illustrates the Curio Seeker workflow. It begins with a tissue section (3 mm x 3 mm) being placed onto a spatially indexed bead array (10 mm x 10 mm). This is followed by cDNA synthesis, bead recovery from the substrate, NGS library preparation, and sequencing. The final output is a map of differential expression, showing a 3 mm x 3 mm area of the tissue section with a corresponding 10 mm x 10 mm spatial transcriptomic map. 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, <i>Product</i>, https://curiobioscience.com/product/.