

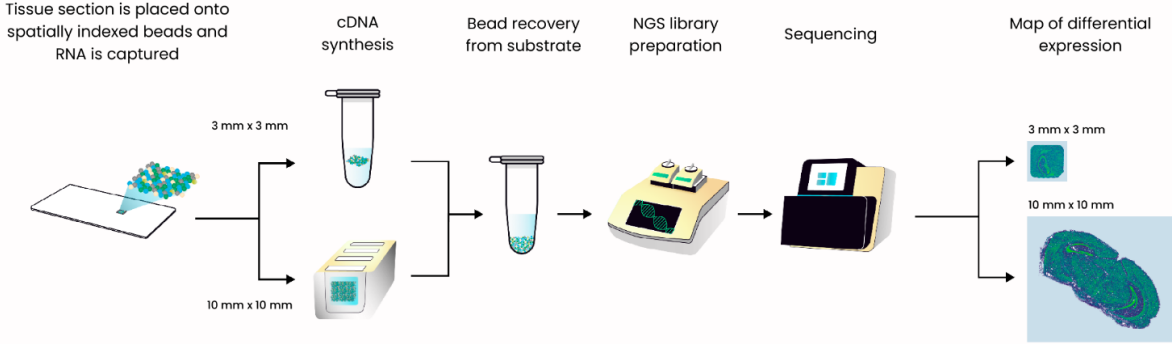
EXHIBIT K

EXEMPLARY INFRINGEMENT CLAIM CHART
U.S. PATENT NO. 10,480,022

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 a spatial location of a biological molecule of a tissue sample comprising:	The Curio Seeker kits and workflow are used to determine a spatial location of a biological molecule (e.g., an mRNA) of a tissue sample. 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.

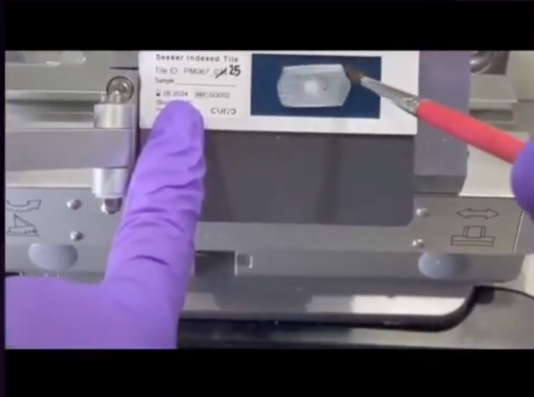
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Claim Limitation	Curio Infringement
	Curio Seeker workflow  The diagram illustrates the Curio Seeker workflow. It begins with a tissue section (10 mm x 10 mm) being placed onto a spatially indexed bead array (3 mm x 3 mm). This is followed by cDNA 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/.
(a) providing a plurality of beads, wherein the plurality of beads comprise a plurality of binding agents, wherein a binding agent of the plurality of binding agents (i) comprises a coding identifier having a nucleic acid sequence and (ii) is configured to	The Curio Seeker kits provide a plurality of beads, wherein each of the plurality of beads comprises a plurality of binding agents (oligonucleotides comprising at least Poly(dT), UMI, and bead barcode sequences).

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interact with a biological molecule of a tissue sample, wherein the coding identifier corresponds to a location at which the binding agent interacts with a biological molecule of a tissue sample	The diagram illustrates the Curio Infringement technology. It shows a 'Tile Slide' with a 'Tile' containing a 'Closely-packed monolayer of 10-micron beads'. A legend identifies the components of the bead barcode: PCR Handle (TruSeq), BB (Bead Barcode), UMI (Unique Molecular Index), and Poly(dT). Below the diagram, a list of features is provided: • 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 binding agent is configured to interact with a biological molecule of a tissue sample. Specifically, the poly(dT) sequence of the binding 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 binding agent of the plurality of binding agents comprises a coding identifier (bead barcode) having a nucleic acid sequence, wherein the coding identifier corresponds to a location at which the binding agent interacts with a biological molecule of a tissue sample. <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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	The plurality of binding agents for each bead is shown in the sample below, in which up to 5,238 genes were captured per bead. Spleen Treated <table><tr><th>Genes per bead</th><th>Min</th><th>25%</th><th>median</th><th>75%</th><th>max</th><th>mean</th></tr><tr><td>Curio</td><td>3</td><td>70</td><td>192</td><td>363</td><td>5238</td><td>244</td></tr><tr><td>Slide-seq</td><td>1</td><td>17</td><td>29</td><td>51</td><td>1767</td><td>40</td></tr></table> Curio Bioscience, <i>Implementation of Curio Seeker in a core facility setting</i> (March 1, 2023), https://www.youtube.com/watch?v=pXQVBHAKQ94, at 10:05.	Genes per bead	Min	25%	median	75%	max	mean	Curio	3	70	192	363	5238	244	Slide-seq	1	17	29	51	1767	40
Genes per bead	Min	25%	median	75%	max	mean																
Curio	3	70	192	363	5238	244																
Slide-seq	1	17	29	51	1767	40																
(b) contacting the plurality of beads with the tissue sample such that the binding agent interacts with the biological molecule; and	The Curio Seeker kits and workflow comprise contacting the plurality of beads with the tissue sample. A tissue section is mounted and melted on the Curio Seeker tile. Tissue mounting 																					

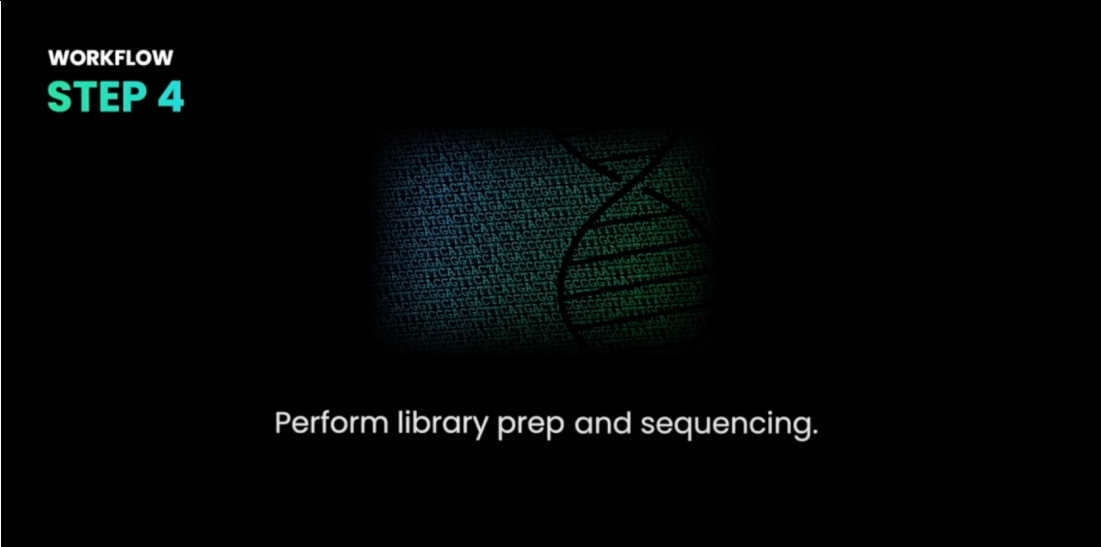
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	Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), https://www.youtube.com/watch?v=7gRsoqVUxb0, at 11:10. See also Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 0:53. The binding agent interacts with the biological molecule. Specifically, the poly(dT) sequence of the capture agent specifically binds the poly(A) tails of mRNA of the tissue section. See Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview</i> (March 1, 2023), <i>transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 5:20-5:35.
(c) using the coding identifier to identify the location where the binding agent interacted with the biological molecule, thereby determining a spatial location of the biological molecule of the tissue sample.	The coding identifier (bead barcode) is used to identify the location where the binding agent interacted with the molecule. First, the Seeker tile with melted tissue is placed in a tube to hybridize and reverse transcribe the mRNA:

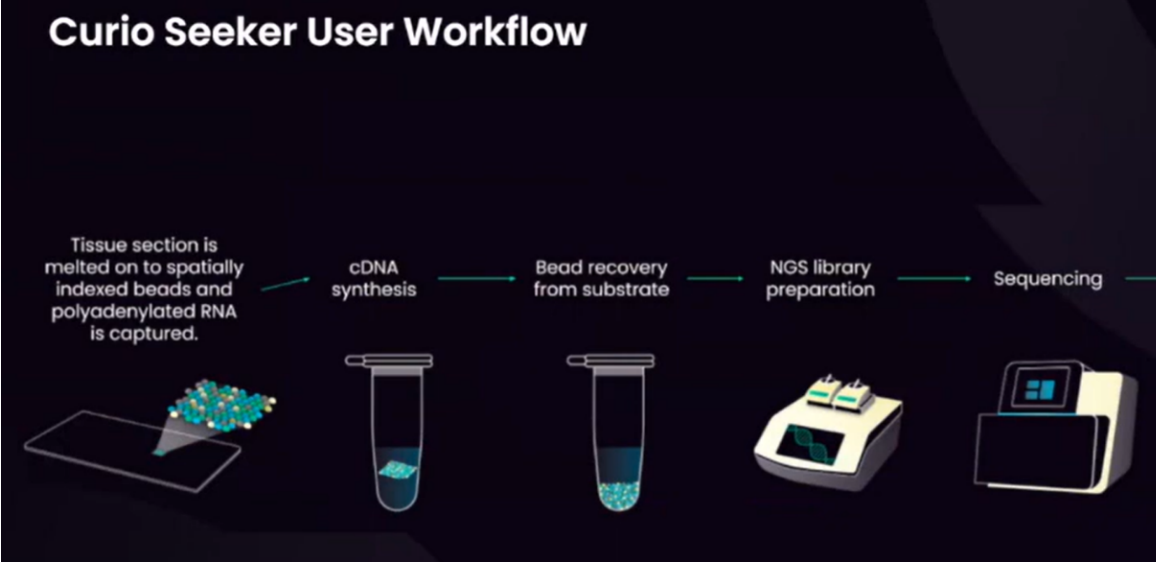
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	Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 0:56-1:02. Next, the tissue is digested before taking the beads through second strand synthesis 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. The sequencing libraries are then prepared and sequenced; sequencing determines the sequence of the coding identifier (bead barcode) and the sequence of the captured mRNA:

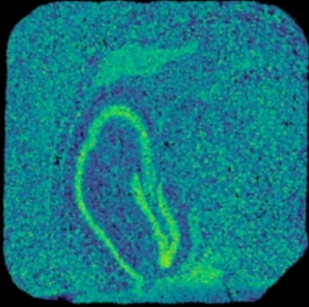
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Claim Limitation	Curio Infringement
	 Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, at 1:18.

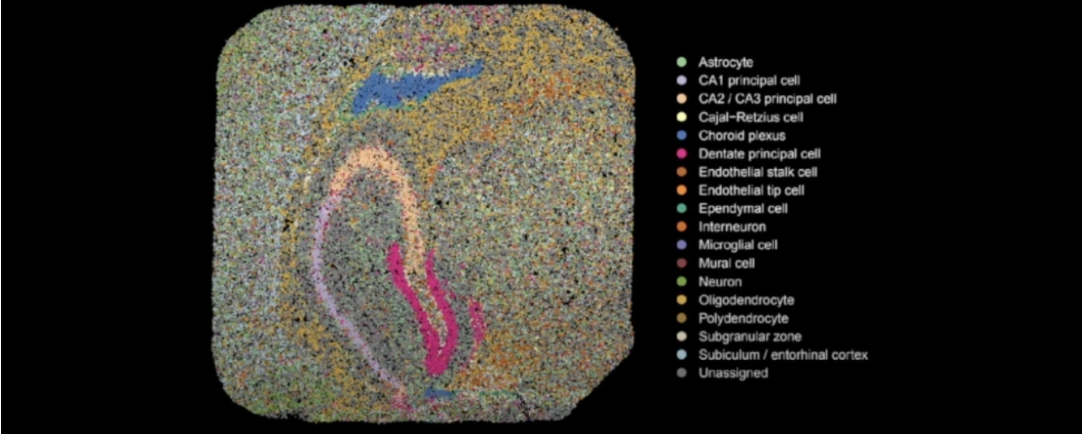
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Claim Limitation	Curio Infringement
	Curio Seeker User Workflow  The diagram illustrates the Curio Seeker User Workflow, a five-step process for single-cell RNA sequencing. Step 1: A tissue section is melted onto spatially indexed beads, and polyadenylated RNA is captured. Step 2: cDNA synthesis is performed. Step 3: Beads are recovered from the substrate. Step 4: NGS library preparation is completed. Step 5: Sequencing is performed. The workflow is represented by a series of icons: a tissue section, a test tube, a bead recovery setup, a library preparation machine, and a sequencing machine. Curio Bioscience, <i>Single-cell RNA seq data analysis pipeline technology overview Curio Seeker</i> by Curio Bioscience (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 the spatial location of the biological molecule (mRNA) of the tissue sample: “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.”

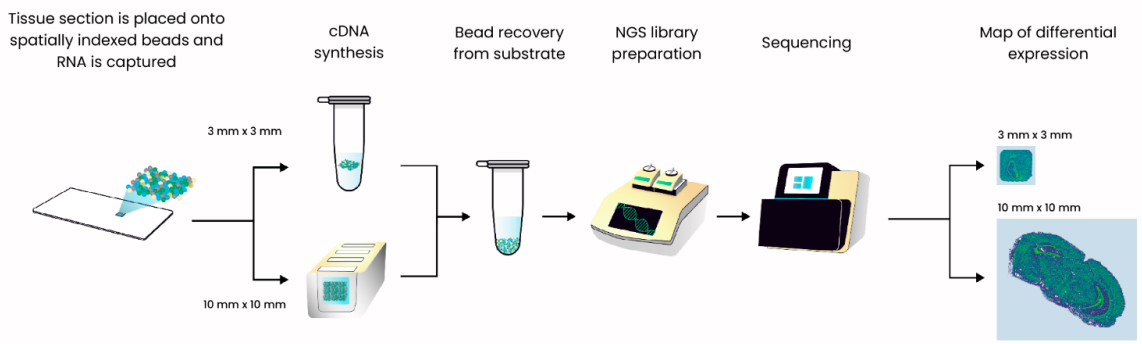
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	WORKFLOW STEP 5  Reconstruct the spatial whole-transcriptome map of the tissue by bioinformatics pipeline analysis. Curio Bioscience, <i>Introducing Curio Seeker: High-resolution spatial transcriptomics</i> (March 1, 2023), https://www.youtube.com/watch?v=Kh-qyQYiu48, 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 Curio Seeker tile (10 mm x 10 mm). The process involves capturing RNA on spatially indexed beads, 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/.