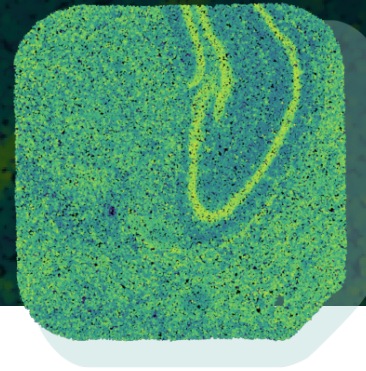# Curio Seeker 3x3 v1.1 tile

Increased sensitivity and performance with the same simple protocol

Introduction

Curio Bioscience is introducing an updated version of the Curio Seeker 3x3 tile for spatial transcriptomics analysis. As compared to the original version (v1), the next generation Curio Seeker tile (v1.1) offers improved sensitivity and performance.

Advantages of v1.1

- Improved sensitivity
- Increased detection of low expressing genes
- Improved clustering and sharper definition that better reflects biological relevance identified by potential regions of tumor immune evasion

Improved sensitivity

The Curio Seeker v1.1 tile provides higher sensitivity and improved transcript detection. When adjacent sections from an adult murine hippocampus block were analyzed with a v1 tile and a v1.1 tile, comparison of v1 (green) with v1.1 (yellow) showed a ~4X increase of the median number of UMIs per bead (left) and ~3X increase in median gene per bead (right) (Figure 1). A general 2X-4X increase in sensitivity was observed in a variety of tissue types tested (murine brain, spleen, and human breast tumor).
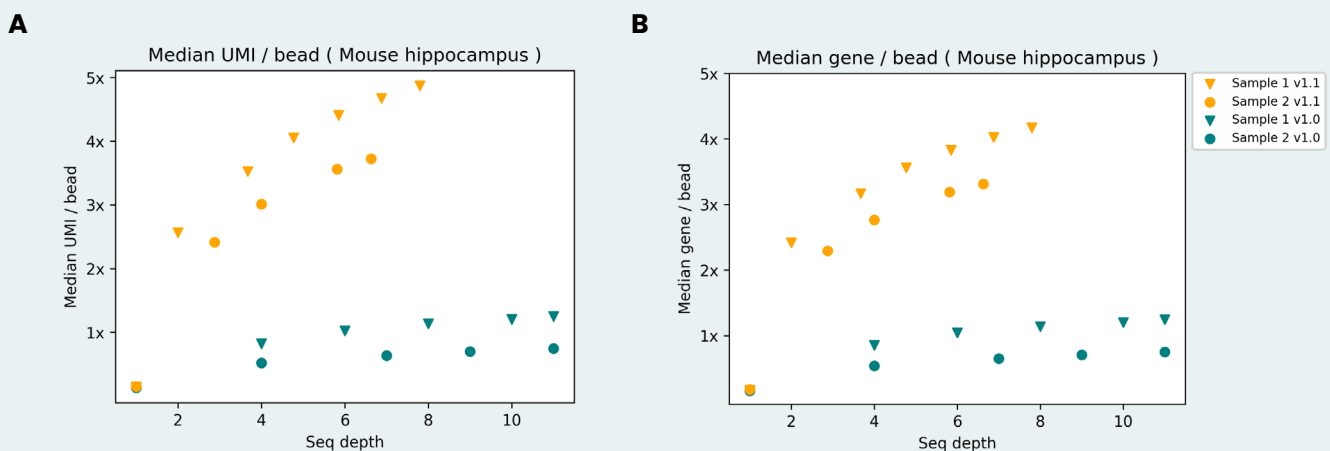

Figure 1: Curio Seeker v1.1 tile improves transcript detection as measured by median UMI (A) and gene (B) per bead. v1.1 in yellow and v1 in green. Data shown are from duplicate pairs of adjacent sections from a murine hippocampus block.

Increased detection of low expressing genes

With the improved sensitivity of the Curio Seeker v1.1 tile, low expressing genes are more readily detected, leading to more biological insights. Comparison of the median number of transcripts detected in only the Cornu Ammonis (CA) and dentate gyrus regions of the murine hippocampus on v1 or v1.1 demonstrates that v1.1 detects lower expressing genes that may not have been readily detected in v1. Overall, v1.1 outperforms v1 when detecting lower abundant transcripts (Figure 2A).
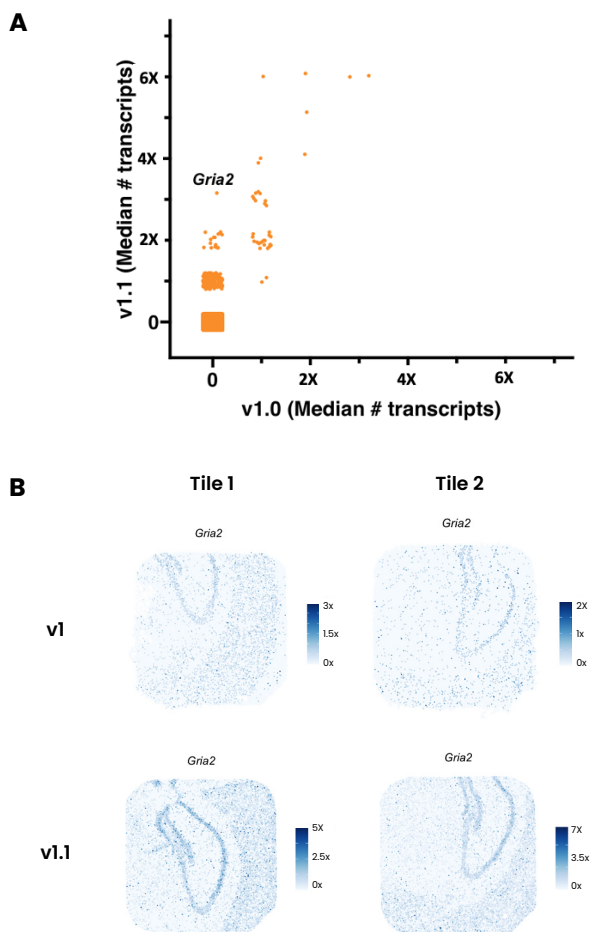
For example, gene Gria2 is more robustly detected in v1.1 as compared to v1 (Figure 2A), and is visually confirmed by the spatial map of the gene (Figure 2B). Overall, the improved detection of transcripts in v1.1 provides sharper definition of structural markers as defined by differential gene expression (Figure 3).
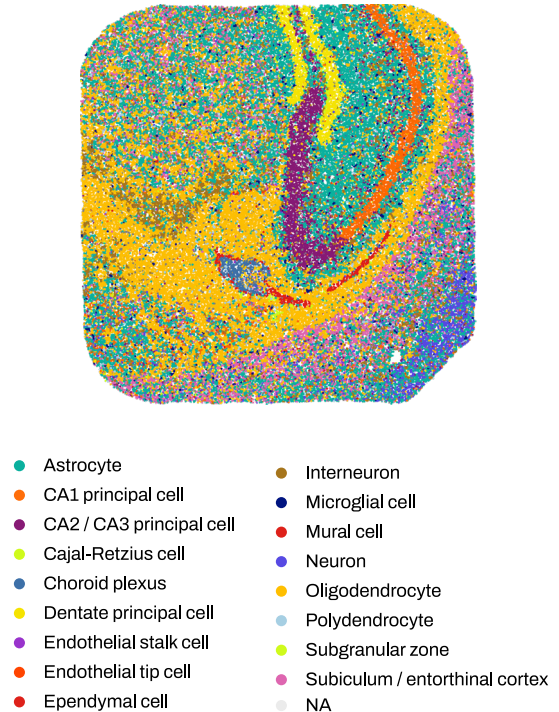

- ● Astrocyte
- ● CA1 principal cell
- ● CA2 / CA3 principal cell
- ● Cajal-Retzius cell
- ● Choroid plexus
- ● Dentate principal cell
- ● Endothelial stalk cell
- ● Endothelial tip cell
- ● Ependymal cell
- ● Interneuron
- ● Microglial cell
- ● Mural cell
- ● Neuron
- ● Oligodendrocyte
- ● Polydendrocyte
- ● Subgranular zone
- ● Subiculum / entorthinal cortex
- ● NA

Figure 3. Spatial mapping of an adult murine hippocampus on the Curio Seeker v1.1 tile with annotation from a single cell reference combined by RCTD.

Figure 2. Curio Seeker v1.1 tile improves detection of low expressing genes and better defines structures revealed by those genes. **A)** Comparison of number of transcripts detected per gene per bead in the CA and dentate gyrus region on v1.1 vs. v1.0 tiles. Each dot represents a gene, and dots are jittered in both X and Y to avoid overlap. The axes (e.g. 2X, 4X, and 6X) represent the number of UMI detected relative to a defined number of transcripts. **B)** Visual comparison of the spatial pattern of an example gene Gria2 in v1 (top row) versus v1.1 (bottom row) across the entire tile. Color bar represents the number of UMI detected relative to a defined number of transcripts.

Curio Seeker v1.1 tiles are now available. We do not recommend mixing v1 and v1.1 tiles within the same project. Please let us know if you have an existing project where you would prefer to continue using Curio Seeker v1 tiles.

Please note that the level of improvement may vary depending on tissue type, tissue preservation, and your individual run and tissue section.

If you have any questions or would like to learn more about Curio Seeker v1.1 tile, please contact us at techsupport@curiobioscience.com.