Sliding into Spatial Transcriptomics: Offering Slide-seqV2 as a Core Service

Genomics

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Understanding cellular organization and how it relates to cell function is crucial to answering many biological questions. Though some Next Generation Sequencing (NGS) applications have previously been used to understand cellular gene expression, it was not until spatial transcriptomics methods became available that researchers had the ability to map these expressions back to specific locations in an intact tissue sample. With the increasing demand for spatial transcriptomics technology, the Stowers Institute has implemented Slide-seqV2, a high-resolution and non-biased spatial transcriptomics method.

Slide-seqV2 developed as an updated method to Slide-seq that was created in the Chen and Macosko lab at the Broad Institute in Cambridge, MA. The improvements, which increase capture efficiency 10-fold, were first published in Nature Biotech by Stickels et al (2021). This spatial transcriptomics method utilizes a 3mm microarray, called a puck, arranged on a glass coverslip made by the Broad that is comprised of 10µm uniquely barcoded beads. After being densely packed in a single layer on the coverslip, the beads are sequenced using a monobase sequencing strategy to give the exact X and Y coordinates of each bead on the puck.

Slide-seq experiments require 10µm thick fresh frozen tissue sections which are carefully placed on the surface of the puck. Using oligo(dT), mRNA from the tissue is captured in its spatial position prior to cDNA synthesis. NGS libraries compatible with Illumina sequencers are then created for each sample. After sequencing is complete, downstream analysis is conducted to map the bead barcode sequence back to its location on the puck creating a spatial image of the cell arrangement and gene expression patterns found within the original intact tissue section. Here we present our cross-core collaborative workflow and showcase expected data generated from Slide-seq experiments.