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Nano-DESI Mass Spectrometry Imaging kidney characterization pipeline for tissues collected by Vanderbilt University

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Human BioMolecular Atlas Program (HuBMAP) Method Development Community

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ABSTRACT

Our goal is to map the biological tissues with Nano-DESI Mass Spectrometry Imaging and build an atlas of human kidney.

Scope:

Provide an overview of the sample preparation steps used by the Vanderbilt Tissue Mapping Center and Nano-DESI MSI workflow used by Julia Laskin's group as part of the Human Biomolecular Atlas Program (HuBMAP, NIH Common Fund).

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ABSTRACT

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Scope:

Provide an overview of the sample preparation steps used by the Vanderbilt Tissue Mapping Center and Nano-DESI MSI workflow used by Julia Laskin's group as part of the Human Biomolecular Atlas Program (HuBMAP, NIH Common Fund).

- 1 Collection of post-surgical tissue by Vanderbilt.
Collection: dx.doi.org/10.17504/protocols.io.7gehjte
- 2 Stabilize and freeze tissues by Vanderbilt
Freezing Tissue: dx.doi.org/10.17504/protocols.io.6wghfbw
- 3 Initial Rapid Pathology Assessment of Kidney Tissue by Vanderbilt.
Staining: dx.doi.org/10.17504/protocols.io.4qngvve
Assessment: dx.doi.org/10.17504/protocols.io.9dph25n
- 4 Cryosection tissues into micrometer thick sections, alternating between thaw mounting onto indium tin-oxide and positively charged glass slides (proceed to step 4), or collecting several tissue sections within a microcentrifuge tube for proteomics analysis by Vanderbilt.
Cryosectioning: dx.doi.org/10.17504/protocols.io.7ethjen
- 5 Perform autofluorescence microscopy on all tissue sections before IMS (step 5) by Vanderbilt.
Autofluorescence: dx.doi.org/10.17504/protocols.io.7e3hjgn
- 6 Perform high resolution IMS lipidomics and metabolomics analysis of tissue sections.
IMS: dx.doi.org/10.17504/protocols.io.bmw7k7de
- 7 Delipid the tissue section.
Sample preparation: dx.doi.org/10.17504/protocols.io.bmw6k7he
- 8 Perform high resolution IMS proteomics analysis of tissue sections.
IMS: dx.doi.org/10.17504/protocols.io.bm2nk8de
- 9 Annotation of Lipids from IMS Data
Annotation: dx.doi.org/10.17504/protocols.io.bm2qk8dw
- 10 Annotation of proteins from IMS data.
Annotation: dx.doi.org/10.17504/protocols.io.bm2rk8d6
- 11 Match the autofluorescence images from IMS sections with the ion images to visualize the correlation between molecules distribution and biological pathology.
- 12 Nano-DESI imaging mass spectrometry data processing.
Data processing: dx.doi.org/10.17504/protocols.io.bm2sk8ee