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High resolution Nano-DESI mass spectrometry imaging of lipidomics and motabolomics of tissue

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1 Works for me dx.doi.org/10.17504/protocols.io.bmwnk7de

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ABSTRACT

Scope:
Acquire imaging mass spectrometry (IMS) datasets of lipids and metabolites on human kidney tissue with ~12µm spatial resolution.

Expected Outcome:
Visualize the lipids distribution localizing to physiological regions within the human kidney by generating ion images of lipids precursor ions.

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Visualize the lipids distribution localizing to physiological regions within the human kidney by generating ion images of lipids precursor ions.

1 Scanned the tissue section with PathScan Enabler IV to visuslize the morphology in optical image.

2 Calibrate the instrument with Agilent tune mix.

3 Set up the appropriate method for lipids and metabolites.

4 Add lipid standards into 9/1 MeOH/H_2O solvent as the extracting solvent. Add extracting solvent into the syringe.

5 Place the slide on the slide holder and set up the primary capillary and secondary capillary and the solvent flow rate until there is liquid bridge between the two capillaries when land on the tissue surface. Direct the secondary capillary to the mass spectrometry inlet and clamp the capillary voltage on the syringe, adjust the positions of the capillaries untill there are stable and intensive signals in the spectrum.

6 Using the Labview software to train the shear force probe until it can appropriately recognize the sample surface from the air.

7 Place the shear force probe close to the liquid bridge so that it can lead the moving of the capillaries and enable the liquid bridge landing on the sample surface without scratching the tissue.

8 Set the start point and the end point of the scanning region.

9 Set up the worklist.

10 Start the acquisition.

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