ABSTRACT
Desorption Electrospray Ionization (DESI) mass spectrometry imaging (MSI) is utilized to map the distribution of metabolites, such as neurotransmitters, alongside lipids from brain tissue sections. Small molecules such as amino acids (e.g., taurine, glutamine, arachidonic acid) and neurotransmitters (e.g., GABA, serotonin) were simultaneously detected along with lipids (e.g., phosphatidylcholine, lysophosphatidylcholine). DESI-MSI data were collected and processed on a high definition mass spectrometer with ion mobility separation (SYNAPT HDMS G2-Si, QToF) using High Definition Imaging (HDI) 1.4 software. Mass accuracy of DESI-MSI analysis was improved by the elimination of systematic mass drift, using either in-line lock mass or other endogenous ions off tissue. This preliminary work indicated the utility of DESI imaging for clearly distinguishing localized metabolites and lipids to provide insights for neuromolecular research.

INTRODUCTION
- Spatial distribution of small molecules, such as neurotransmitters, alongside lipids, in brain improve our understanding of their biological functions
- Mass spectrometry imaging (MSI), such as Desorption Electrospray Ionization (DESI), can be used to map distributions of metabolites on tissue sections
- DESI is an ambient ionization technique that does not require any sample preparation steps, such as matrix deposition
- DESI often provides complementary information to matrix-assisted laser desorption ionization (MALDI), such as distribution of small metabolite and drug molecules that are amenable to electrospray ionization
- Here we show the utility of DESI imaging to detect neurotransmitters, such as serotonin, adenosine, and glutamine directly in brain tissue samples
- Ion mobility separation enhanced the detection of metabolite signal by discriminating from electrospray background species produced during the DESI analysis

RESULTS
- Coronal tissue sections of rat brain were mounted on microscope slides and imaged without any further sample preparation
- DESI imaging platform was coupled with a high definition mass spectrometer (HDMS) with ion mobility separation (SYNAPT G2-Si).
- DESI-MSI data were processed using High Definition Imaging (HDI) 1.4 software with MassLynx 4.1 data acquisition control.
- Molecular identification was done using high mass accuracy (low PPM) database searches against curated databases, such as METLIN; ID confidence was increased by high-fidelity isotopic distribution, collisional cross sections (CCS).

CONCLUSION
- Simultaneous MSI imaging of metabolites and lipids directly from tissue sections with no sample preparation by DESI-MSI.
- Molecular identification was aided by improved mass accuracy by the elimination of systematic mass drift, using either in-line lock mass or other endogenous ions off tissue. This preliminary work indicated the utility of DESI imaging for clearly distinguishing localized metabolites and lipids to provide insights for neuromolecular research.