**Characterizing commonalities and differences between the breast and prostate cancer metabotypes in African-American cohorts**

Aliquots of each de-identified sample were shipped to the NIH RTI-RCMRC on dry ice and immediately stored at -80 °C after being logged in for metabolomics analysis. A total of 48 study samples were weighed on dry ice to confirm weights and approximately 50 mg of the tissue was transferred to labeled MagNa Lyser bead tubes on ice and ice cold 50:50 acetonitrile:water was added, and samples were homogenized with two 30sec pulses at 3000rpm. Tubes were centrifuged at 16,000 rcf for 10 minutes at room temperature and supernatants were transferred to 1.5mL pre-labeled LoBind Eppendorf tubes. Aliquots of 500uL were then transferred into labeled 2.0mL LoBind Eppendorf tubes. Analytical quality control (QC) whole study pool samples were generated by transferring an additional 125µL aliquot of each study sample into a 10mL cyrovial and vortexed. To generate Total Pooled QC samples 500uL was transferred to 5 labeled 2.0mL LoBind Eppendorf tubes. All samples were lyophilized to complete dryness overnight, then reconstituted with 700uL of NMR Master Mix solution containing Chenomx ISTD: DSS-d6 and Phosphate Buffer at 7.4 pH. The tubes were vortexed for 4 min on a multi-tube vortexer and centrifuged at 16,000 rcf for 5 min. A 600uL aliquot of supernatants were transferred into a pre-labeled 5mm 4" NMR tubes for data acquisition on a 700 MHz spectrometer.

1H NMR spectra of tissue samples were acquired on a Bruker Avance 700 MHz NMR spectrometer (located at the David H. Murdock Research Institute) using a 5 mm cryogenically cooled ATMA inverse probe and ambient temperature of 25 ℃. A 1D NOESY pre-saturation pulse sequence (noesypr1d, [recycle delay (RD)-90°-t1-90°-tm-90°-acquire free induction decay (FID) was used for data acquisition. For each sample 128 transients were collected into 65k data points using a spectral width of 8.417 kHz (12.0227ppm), 2 s relaxation delay, 100 ms mixing time, and an acquisition time of 3.893 s per FID. The water resonance was suppressed using resonance irradiation during the relaxation delay and mixing time. NMR spectra were processed using TopSpin 3.2 software (Bruker-Biospin, Germany). Spectra were zero filled, and Fourier transformed after exponential multiplication with line broadening factor of 0.5 Hz. Phase and baseline of the spectra were manually corrected for each spectrum. Spectra were referenced internally to the DSS-d6 signal. The quality of each NMR spectrum was assessed for the level of noise and alignment of identified markers. Spectra were assessed for missing data and underwent quality checks. NMR bins (0.70-9.00ppm) were made after excluding water (4.78 – 4.90ppm), Imidazole (7.27-7.34ppm, and 8.25-8.33ppm), using intelligent bucket Integration with a 0.04 ppm bucket width using ACD NMR Processor (ACD Labs Inc, Toronto, Canada). Integrals of each of the bins were normalized to total integral of each of the spectrum.