**Utilizing Metabolomics to Understand Novel Anti-Desmoid Tumor Drugs**

Cell media was extracted with 50% acetonitrile:water, vortexed, and centrifuged. An analytical quality control (QC) total pool was generated from equal aliquots from all of the media samples, divided into three total pool aliquots, and processed identically to the media study samples. All study and pool samples were lyophilized to dryness and reconstituted in a 0.2M phosphate buffer, pH 7.4, in D2O with 10% Chenomx ISTD.

1H NMR spectra of cellular extracts were acquired on a Bruker Avance III 700 MHz spectrometer (located at the David H. Murdock Research Institute at Kannapolis, NC, USA) using a 5 mm cryogenically cooled ATMA inverse probe and ambient temperature of 25 °C. A noesypr-1d pulse sequence was used for data acquisition. For each sample 64 transients were collected into 65 k data points using a spectral width of 12.0227 ppm, 2s relaxation delay, 100 ms mixing time and an acquisition time of 3.89 s per FID. The water resonance was suppressed using resonance irradiation during the relaxation delay. Spectra were zero filled, and Fourier transformed after exponential multiplication with line broadening factor of 0.5. Phase and baseline of the spectra were manually corrected for each spectrum. Spectra were referenced internally to the DSS 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.