**NMR Metabolomics Methods for Blaser Serum samples**

Frozen serum study samples were thawed on ice and vortexed for 30 seconds. Aliquots of 50/100 µL (sub-study dependent) were transferred into BSI-labeled eppendorf tubes. Purchased mouse sera (Sigma #S7273) was also transferred into three BSI-labeled eppendorf tubes (50/100 µL) for QC samples during analysis. Freshly prepared 0.9% Saline (wt/v) solution in 10% D2O, was added to each tube (150/100 µL) and they were vortexed for 30 seconds. Freshly prepared 10 mM Formate solution containing 2% (wt/v) NaN3 was added to each tube (50 µL) to serve as internal standard and they were vortexed for 30 seconds again, then centrifuged at 12000 rcf for 5 minutes at 4 °C. A 200 µL aliquot of the supernatant was transferred into 3 mm NMR tubes (Bruker-Biospin, Switzerland), which were kept on ice until data acquisition.

1H NMR spectra of serum samples were acquired on a Bruker Avance 700 MHz NMR 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℃. A CPMG pulse sequence with presaturation (cpmgpr1d) was used for data acquisition. For each sample 512 transients were collected into 64k data points using a spectral width of 14.1 kHz (20.1 ppm), 2 s relaxation delay, 400 µs fixed echo time, loop for T2 filter (l4)=80, and an acquisition time of 2.324 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 Formate 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 spectra were processed using ACD NMR software (Advanced Chemistry Development, Toronto, ON, Canada). NMR bins (0.50-9.00 ppm) were made after excluding water (4.70-4.85 ppm) and formate (8.40-8.50 ppm) using Intelligent Bucketing Integration with a 0.04 ppm bucket width and a 50% looseness factor. Integrals of each of the bins were normalized to total integral of each of the spectrum.