**I. Supplementary Information**

***Metabolomic Profiling***

Metabolomic profiling was performed on serum samples in CAMP. Blood was shipped to the sample repository to the Broad Institute (Cambridge, MA, USA) on dry ice for metabolomic profiling. Samples were thawed on ice for sub-aliquoting for each of the metabolomic methods, and then re-frozen on dry ice and stored at -80C until analysis.

Four complimentary liquid chromatography tandem mass spectrometry (LC-MS) methods were used. (i) Hydrophilic interaction liquid chromatography (HILIC) analyses of water soluble metabolites in the negative ionization mode (HILIC-neg) were conducted using an LC-MS system comprised of an AQUITY UPLC system (Waters; Milford, MA and a 5500 QTRAP mass spectrometer (SCIEX; Framingham, MA)1. (ii) HILIC analyses of water soluble metabolites in the positive ionization mode (HILIC-pos) were conducted using an LC-MS system comprised of a Shimadzu Nexera X2 U-HPLC (Shimadzu Corp.; Marlborough, MA) coupled to a Q Exactive hybrid quadrupole orbitrap mass spectrometer (Thermo Fisher Scientific; Waltham, MA)2-5.(iii) Positive ion mode analyses of polar and non-polar plasma lipids (C8-pos) were conducted using an LC-MS system comprised of a Shimadzu Nexera X2 U-HPLC (Shimadzu Corp.; Marlborough, MA) coupled to a Exactive Plus orbitrap mass spectrometer (Thermo Fisher Scientific; Waltham, MA) (iv) Negative ion mode analyses of free fatty acids and bile acids (C18-neg) were conducted using an LC-MS system comprised of a Shimadzu Nexera X2 U-HPLC (Shimadzu Corp.; Marlborough, MA) coupled to a Q Exactive hybrid quadrupole orbitrap mass spectrometer (Thermo Fisher Scientific; Waltham, MA). Samples were prepared for analysis using solid phase extraction.

**References**

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