Supporting Information

LipPy software

A database of known lipid structures, fragmentation patterns, and neutral losses[2,3] was created *in silico* using Lipid MAPS nomenclature. Lipids were identified by matching the observed precursor/fragment mass pairs with entries in the database. LipPY® applied a set of filters to the data set to eliminate low abundance fragment signals with no analytical significance and to remove the isotopic contributions of lower mass peaks. With this approach, the number of false positive identifications was dramatically reduced. Identified lipids were normalized to their corresponding internal standard (i.e. each lipid of a specific class was normalized to its correspondent lipid class internal standard). When the appropriate internal standard was missing, identified lipids were normalized to cholesterol ester (CE) or PE for positive and negative ionization mode, respectively. Results were expressed in mean±standard error format.