



Supplemental Figure 3 : Result of S-Trap protein digestion on mouse podocyte lipid rafts prepared by three different methods. Left panel: Base peak chromatogram of fraction 2 after TCA precipitation and subsequent digestion by the S-Trap method. Central panel: Base peak chromatogram of fraction 2 after 5% SDS treatment followed by TCA precipitation and subsequent digestion by the S-Trap method. Right panel: Base peak chromatogram of fraction 2 subjected directly to S-Trap digestion. The number of identified proteins is indicated in each case. The extracted ion chromatograms (in blue) show the iodixanol ion (OptiprepTM, doubly charged ion m/z 775,47) in all cases.