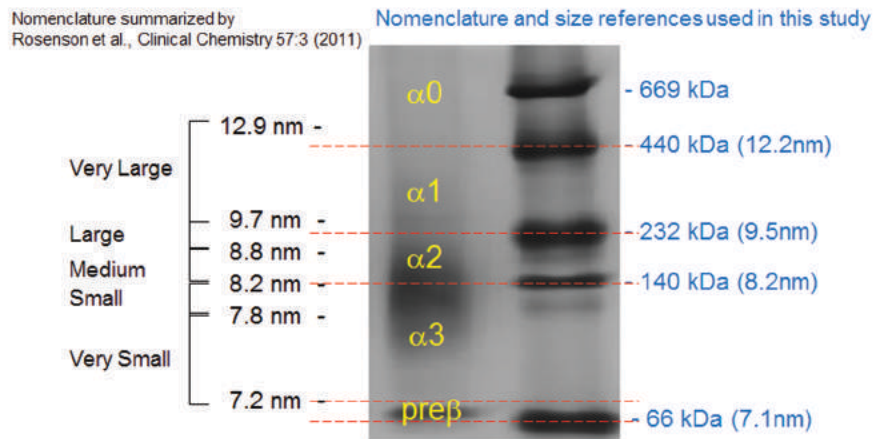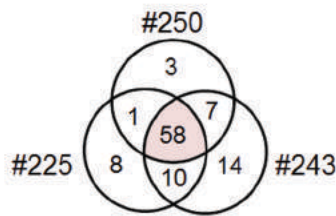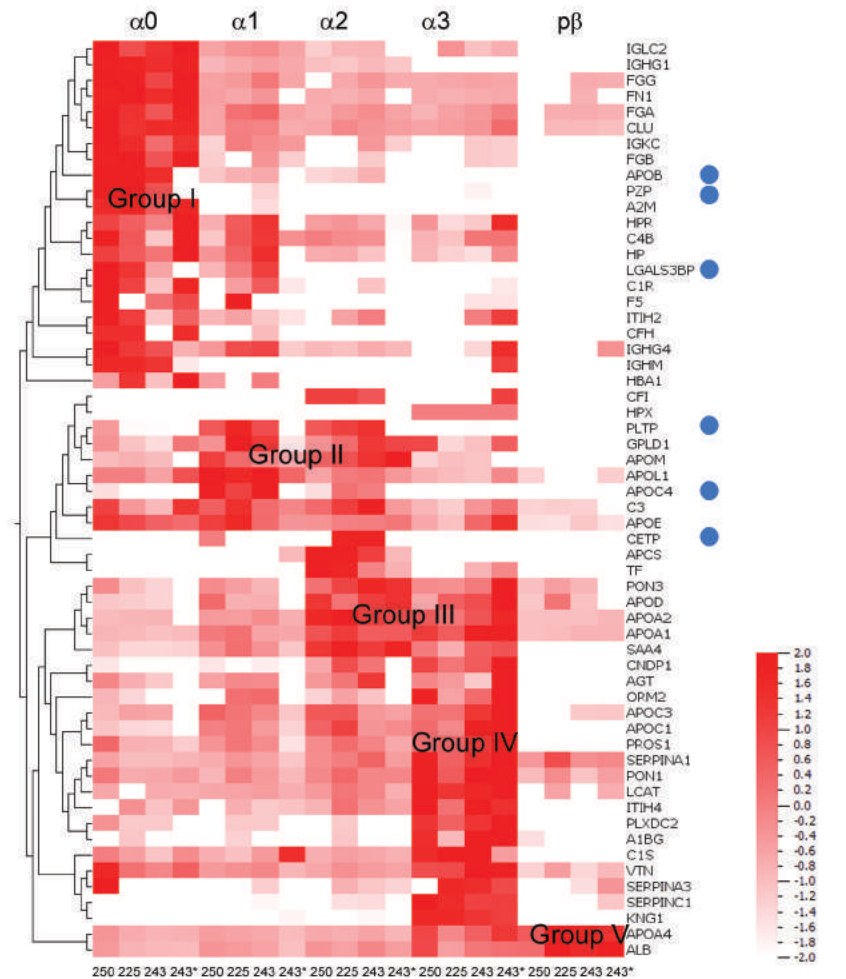**Supplementary Figure 1. Spectral counting based profiling of the HDL proteome.** (A) HDL size fraction windows and reference nomenclatures. The dashed lines indicate the molecular weight boundaries for in-gel trypsin digestion. (B) The HDL proteome intersect. Proteins with two or more unique peptides and in common (58) in participant samples 250, 225 and 243 were analyzed further. (C) Heat map of the HDL proteome intersect. The protein abundance profiles were normalized per participant dataset and clustered based on the similarity of the protein abundance profiles across the HDL size fractions. Scale: Red to white indicates highest to lowest (no signal). Size fractions are indicated on top. Participant IDs are indicated on the bottom - 243* indicates apoB (LDL and small chylomicron remnants)-depleted sample. Blue circles indicate proteins that were not detected in participant sample 243*.