Supplement

Title: The Effects of Apolipoprotein B Depletion on HDL Subspecies Composition and Function

Running Title: ApoB Depletion

Authors: W. Sean Davidson PhD¹, Anna Heink MS², Hannah Sexmith², John T Melchior PhD¹,

Scott M Gordon PhD³, Zsuzsanna Kuklenyik⁴, Laura Woolett PhD¹, John R Barr PhD⁴, Jeffrey I

Jones BS⁴, Christopher A Toth MS⁵, Amy S Shah MD MS²

¹Center for Lipid and Arteriosclerosis Science, Department of Pathology and Laboratory Medicine, University of Cincinnati, 2120 East Galbraith Road, Cincinnati, OH 45237-0507, USA

²Department of Pediatrics, Cincinnati Children's Hospital Research Foundation, 3333 Burnet Avenue, MLC 7012, Cincinnati, OH 45229-3039, USA

³National Heart, Lung and Blood Institute Lipoprotein Metabolism Section, 9000 Rockville Pike Building 10 Room 8N224 Bethesda, Maryland 20892

⁴ Division of Laboratory Sciences, National Center for Environmental Health, Centers for Disease Control and Prevention, Atlanta, GA 30341, USA.

⁵ Battelle Memorial Institute, Analytical Services, Atlanta, GA 30329, USA.

*Corresponding Author/Reprints: Amy S Shah MD MS. Cincinnati Children's Hospital Medical

Center, Division of Endocrinology. 3333 Burnet Ave ML 7012. Cincinnati OH 45229. Email:

amy.shah@cchmc.org. Phone: 513-636-4744. Fax: 513-696-7486.

Supplemental Methods

Trypsin digestion and LC-MS/MS analysis of apolipoproteins

To a 100 μ L aliquot of each of the 40 fractions, 50 μ L Perfinity digest buffer containing 0.45% Zwittergent 3-12 (EMD Millipore, Billerica, MA, USA) was added and spiked with 5 μ L isotopically labeled target peptide mix (~10 pmol/mL). The trypsin digestion coupled LC separation was performed on an on-line column switching system, Perfinity (Shimadzu Scientific Instruments/Perfinity Biosciences Inc.), equipped with a Perfinity trypsin column (2.1 x 50 mm), a trapping column and an analytical column (HALO C18 core shell 5 x 2.1 mm 2.7 μ m and 100 x 2.1 mm 2.7 μ m particle size, respectively). From each diluted and spiked fraction 50 μ L was injected on the on-line trypsin column at 25 μ L/min flow rate collecting peptide cleavage products for 8 min on the trapping column. After digestion/trapping, the cleavage products were eluted to the analytical column and separated using an acetonitrile/0.1% formic acid in water solvent gradient program (3-95% at 0-7 min, and equilibration to 3% at 7-10 min) with 350 μ L/min flow rate. The native peptide and the isotopically labeled peptide internal standard chromatograms were acquired in multiple reaction monitoring mode on a 6500 Qtrap instrument (AB Sciex, Foster City, CA, USA).

Supplementary Figures

Supplementary Figure 1: Overlay of phospholipid content from the triple Superdex Increase gel filtration chromatography separation of plasma (•) vs. ultracentrifugally-isolated LDL (\bigtriangledown) and HDL (\circ) from the same subject. Fractions 15-19 contain apoB and are comprised of LDL and VLDL. Fractions 20-29 are considered to be HDL-containing fractions because they are apoA-I rich and demonstrate particle diameters which are consistent with measurements for density-isolated HDL. Supplementary Figure 2: Phospholipid and cholesterol distribution across lipoprotein subspecies of ultracentrifugally-isolated HDL before and after PEG apoB depletion. 1 ml density-isolated HDL (lacking LDL/VLDL) containing 9 mg/ml protein was apoB depleted using 400 μ l 20% PEG (MW 6000). The resulting supernatant was collected and fractionated via triple Superdex Increase gel filtration chromatography. Comparison of volume-adjusted HDL control fractions (•) vs. PEG apoB depleted HDL fractions (\circ) in terms of a) phospholipid and b) cholesterol distribution. Supplementary Figure I:



