

Supplemental Material

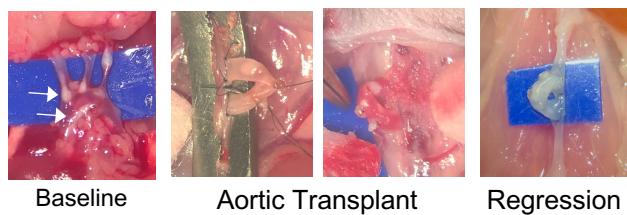
Expanded Materials & Methods

HDL analyses: Cholesterol efflux assays: Serum was reconstituted from freshly thawed plasma by addition of 2.5 M calcium chloride and incubated for 1 h. Polyethylene glycol (20% PEG8000, 2:5 v/v) was then added to precipitate apoB-containing lipoproteins. Cells were incubated in Dulbecco's modified Eagle medium supplemented with 0.1% (wt/vol) fatty acid-free albumin (Dulbecco's modified Eagle medium+fatty acid-free albumin), [³H]-cholesterol (0.5 μ Ci/mL), and an ACAT inhibitor (34.4 μ mol/L; Sandoz) for 24 hours at 37°C in a 5% CO₂ atmosphere with or without presence of 8CPTcAMP (0.3 mM). After 1 wash with PBS, the cells were incubated in Dulbecco's modified Eagle medium+fatty acid-free albumin supplemented with 8CPTcAMP (0.3 mM; Sigma) for 24 h. Cells were washed again with PBS and then incubated with serum HDL (1.6% v/v) for 4 h.

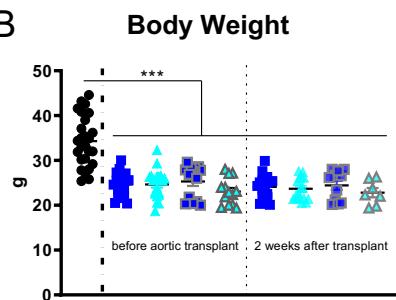
HDL particle concentration: Lipoproteins were rapidly isolated from plasma at density 1.21 g/ml, dialyzed into 20 mM ammonium acetate, pH 7 and analyzed on a electrospray differential ion mobility analyzed (TSI Inc., Shoreview, MN). HDL subspecies were fitted to the DMA profiles by an unsupervised, iterative curve-fitting.³⁵ Areas under the curve fitted for each subspecies were directly converted to HDL particle concentration using a glucose oxidase calibration curve. For total HDL particle concentration, intra-day and inter-day coefficients of variation were <10%. The %CVs were <10% for HDL subpopulations.

HDL proteomics: 10 μ g HDL protein was solubilized with 0.5% sodium deoxycholate (SDC) (Sigma-Aldrich, St Louis, MO) in 200 mM NH₄HCO₃, spiked with 0.5 μ g of [¹⁵N]APOA1 as internal standard³⁷, reduced with dithiothreitol, alkylated with iodoacetamide, and digested with two additions of trypsin (1:20, w/w HDL protein; sequencing grade; Promega, Fitchburg, WI) for 4 hours, and overnight. After precipitation of SDC with formic acid (1% final concentration), samples were frozen and stored at -20°C until analysis (less than a week). For the LC/MS analysis an equivalent of 200 ng of HDL protein was injected.³⁸ The DIA analysis was performed as follows: After desalting on a C18 trapping column (Reprosil-Pur 120 C18-AQ, 5 μ m, 0.1 x 40 mm, Dr. Maisch HPLC GmbH, Germany) (flow rate 4 μ L/min), the digested peptides were separated on an analytical column (Reprosil-Pur 120 C18-AQ, 5 μ m, 250x0.075 mm, Dr. Maisch HPLC GmbH). Following multi-step linear gradient was used: 1-5%B in 2 min, 5-25% in 50 min, 25-35% in 10 min. At the end of the gradient column was washed with a ramp to 80%B and re-equilibrated (A - 0.1% formic acid in water, B - acetonitrile, 0.1% formic acid, flow rate of 0.4 μ L/min). An LC-MSMS consisting of a nanoAquity UPLC (Waters, MA), and a Thermo Fusion Lumos (Thermo Fisher, San Jose, CA) tribrid mass spectrometer with electrospray ionization were used for the analysis. DIA parameters were: MS1 scan (395-1005 Da, resolution 120,000, maximum injection time 50 ms) followed with 60 MS/MS scans across 400-1000 Da range with 10 Da mass selection window each (resolution 15,000, maximum injection time 22 ms, loop time 3 sec). Fragmentation was induced by HCD activation at normalized collision energy 30%. Further data processing was accomplished using Skyline³⁹ to extract fragment ion chromatograms of the MS2 scans with 10 ppm accuracy windows. Chromatograms were integrated and chromatographic peak areas were exported for further analysis. Protein abundance was quantified after normalization of the representative peptides to 15N-APOA1 peptide VQPYLDDFQK. To quantify each protein, a response of at least 2 peptides specific to each protein was averaged. Peptide and protein abundance are therefore expressed in arbitrary units [a.u.].

A

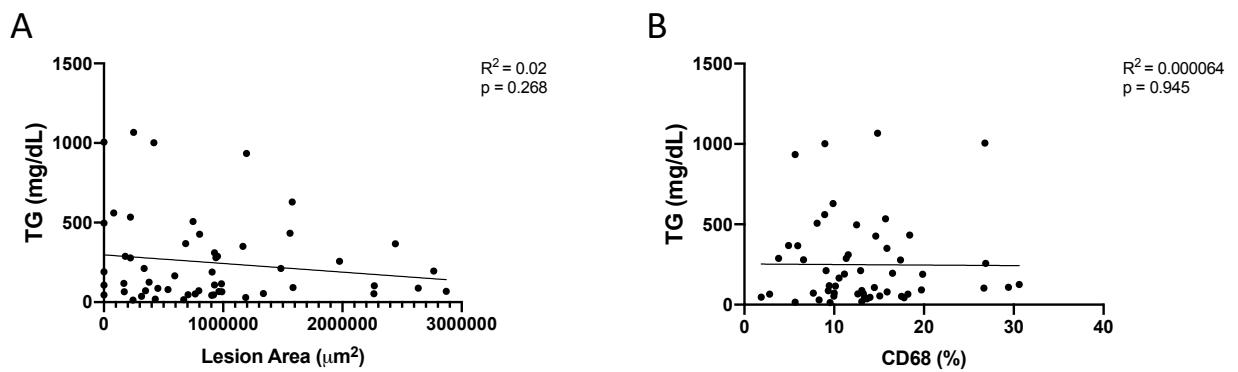


B



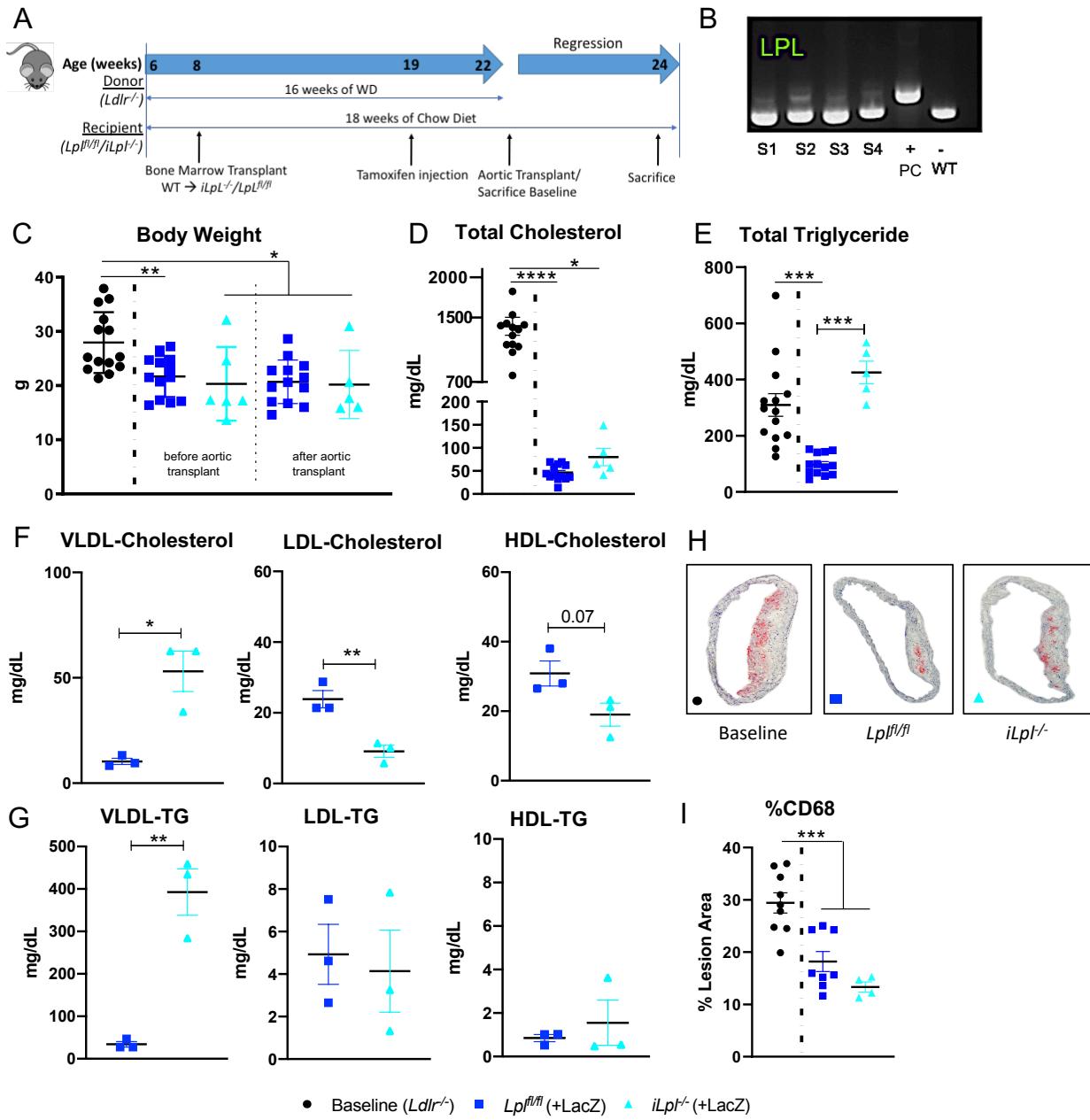
Supplemental Figure I

(A) Representative pictures of the aortic arch in the donor mouse (*left*), during aortic transplantation (*middle*) and after two weeks of atherosclerosis regression (*right*). Arrows indicate atherosclerotic lesions
(B) Body weight in baseline and regression groups before and after the 2 weeks atherosclerosis regression period. N= 5-24/group; data represented as mean \pm SEM, *** P < 0.0001, 2-way ANOVA with Tukey's multiple comparison test



Supplemental Figure II

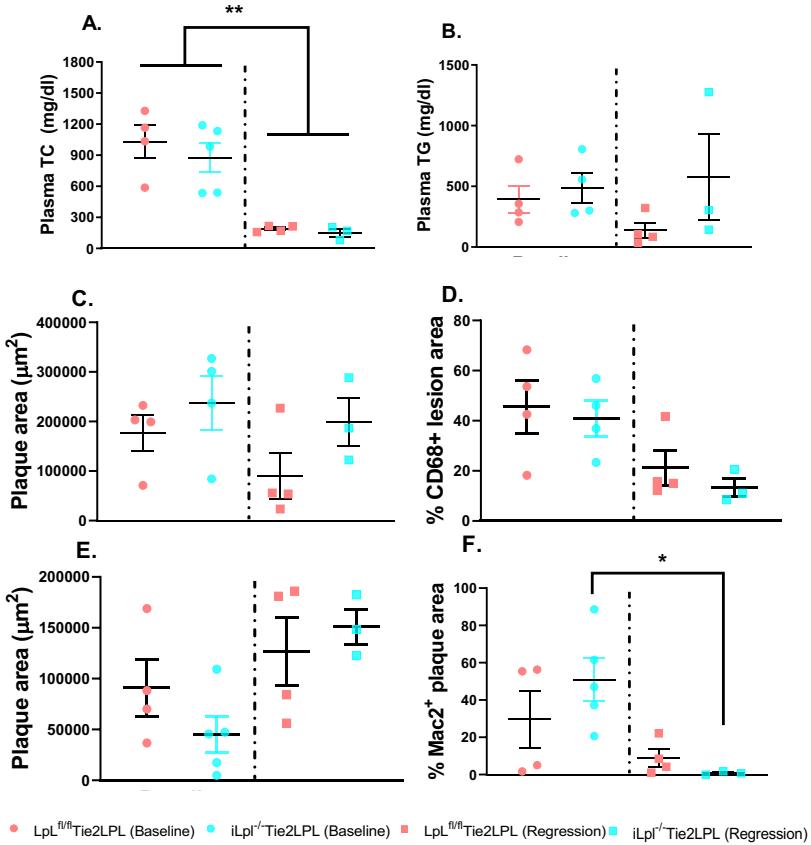
Correlation of plasma TG levels with (A) lesion size and (B) %CD68



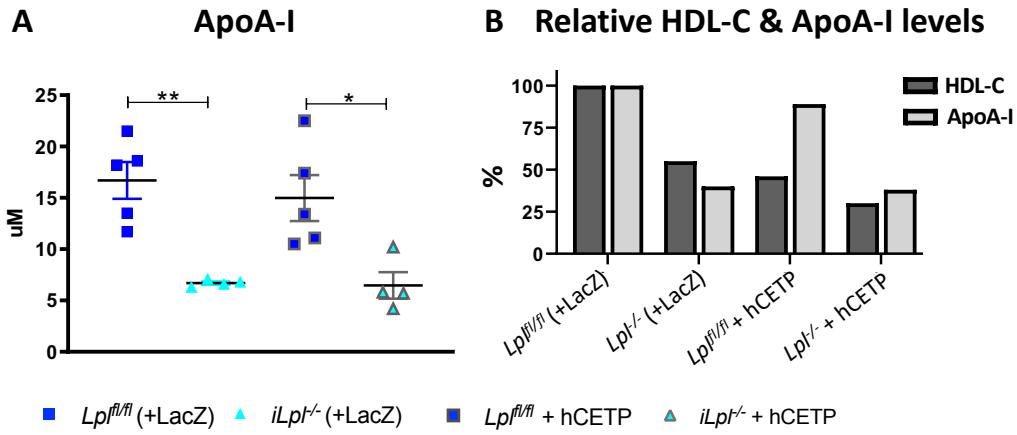
Supplemental Figure III

iLpL^{fl/fl} with LpL expressing macrophages do not impair atherosclerosis regression.

(A) Study setup (B) Genotyping using blood DNA confirming BMT (C) body weight in baseline and regression groups before and after the 2 weeks atherosclerosis regression period (D) Plasma Cholesterol (E) Plasma TG. Cholesterol (F) and triglyceride levels (G) of isolated lipoproteins (H) CD68 staining (I) CD68 area of lesion size (%). N= 4-14/group; data represented as mean ± SEM, *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001, 1-way ANOVA with Tukey's multiple comparison test (C,I), Kruskal-Wallis Test (D,E), students unpaired t-test (F-G).



Supplemental Figure IV. Hypertriglyceridemia and enhanced endothelial LPL expression does not alter atherosclerosis regression in a non-invasive model of regression. Atherosclerosis was created in *LpL^{fl/fl}* Tie2LPL and *iLpL^{-/-}* Tie2LPL mice with LDLR antisense oligonucleotides (ASO) and western diet feeding for 16 weeks. One set of mice were analyzed at 16 weeks as the baseline group and the rest of the mice were treated with SO to induce regression and were analyzed after 3 weeks. The mice in regression group were also treated with tamoxifen at Week 13 to induce hypertriglyceridemia in *iLpL^{-/-}* Tie2LPL mice. Plasma (A) total cholesterol (TC) and (B) triglyceride (TG) levels in baseline and regression groups. (C) Total plaque area, (D) % of macrophages (CD68⁺) within aortic root lesions, (E) total plaque area, (F) % of macrophage (Mac2⁺) in plaques within the BCA in the baseline and regression groups. N= Baseline *LpL^{fl/fl}* Tie2LPL 4, Regression *LpL^{fl/fl}* Tie2LPL 4 and Regression *iLpL^{-/-}* Tie2LPL 3. Results expressed as mean \pm SEM. *P < 0.05, **P < 0.01 using 1-way ANOVA with Tukey's multiple comparison test.



Supplemental Figure V. Circulating ApoA-I levels are reduced with HyperTG. (A) Plasma ApoA-I levels (uM) measured by mass spectrometry. (B) Comparison of HDL-C and ApoA-I reduction in HyperTG plasma +/- hCETP (% relative to $Lpl^{fl/fl} (+LacZ)$). N= $Lpl^{fl/fl}$ 5, $Lpl^{-/-}$ 4, $Lpl^{fl/fl} + hCETP$ 5, $Lpl^{-/-} + hCETP$ 4. * P < 0.05, ** P < 0.01, Kruskal-Wallis Test with Dunn's multiple comparison test.

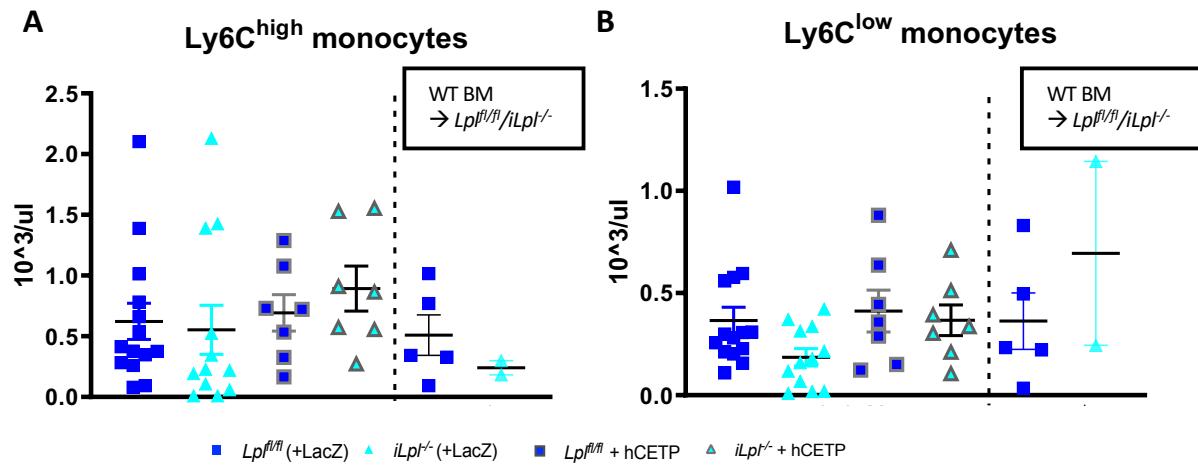


Figure VI. HyperTG does not change the ratio of circulating Ly6C^{hi}/Ly6C^{low} monocytes. (A) Ly6C^{hi} and (B) Ly6C^{low} monocytes assessed by flow cytometry and corrected by total white blood cell count ($10^3/\mu l$). N= (A) Lpl^{fl/fl} 14, Lpl^{-/-} 12, Lpl^{fl/fl} +hCETP 7, Lpl^{-/-} +hCETP 7; WT BM Lpl^{fl/fl} 5, Lpl^{-/-} 2 (B) Lpl^{fl/fl} 12, Lpl^{-/-} 13, Lpl^{fl/fl} +hCETP 7, Lpl^{-/-} + hCETP 7; WT BM Lpl^{fl/fl} 5, Lpl^{-/-} 2. Data shown as mean ± SEM.

Supplemental Table I

qPCR Primer

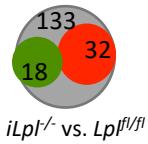
| Gene | Forward (5' - 3') | Reverse (5' - 3') |
|--------------|--------------------------|-----------------------|
| <i>Cetp</i> | GATGGGAGACGAGTTCAAGG | CTGGCGTGGAAAGAGGA |
| <i>LacZ</i> | TATCCGAACCATCCGCTGT | CTCCGCCGCCTTCATACT |
| <i>Lpl</i> | AGGTGGACATCGGAGAACTG | TCCCTAGCACAGAAGATGACC |
| <i>Plin2</i> | TCTGCGGCCATGACAAGTG | GCAGGCATAGGTATTGGCAAC |
| <i>Cpt1a</i> | TGCACTACGGAGTCCTGCAA | GGACAACCTCCATGGCTCAG |
| <i>Glut1</i> | TCGTAACGAGGGAGAACCG | GGCCGTGTTGACGATA |
| <i>Fasn</i> | TCTTCTAACAAACCACCCCTCTGG | CTTCACGACTCCATACGAATG |
| <i>Cd36</i> | CCTTAAAGGAATCCCCGTGT | TGCATTGCCAATGTCTAGC |
| <i>Tnf</i> | TGGAACTGGCAGAAGAGG | AGACAGAAGAGCGTGGTG |
| <i>Mcp1</i> | CCCAATGAGTAGGCTGGAGA | TCTGGACCCATTCCCTTCTG |
| <i>Nos2</i> | CAGCTGGCTGTACAAACCTT | CATTGGAAGTGAAGCGTTCG |
| <i>Fizz1</i> | CCAATCCAGCTAACTATCCCTCC | AAGCCACAAGCACACCCAGT |
| <i>Mrc1</i> | TGATTACGAGCAGTGGAAAGC | GTTCACCGTA-AGCCAATT |
| <i>Il10</i> | CTGGACAACATACTGCTAACCG | GGGCATCACTCTACCAGGTAA |

Supplemental Table II
Overview of detected Proteins

| Protein.Gene | Protein.Name | Protein.Accession | Protein.Description |
|--------------|--------------------------------|-----------------------|--|
| Actb | sp P60710 ACTB_MOUSE | P60710 | Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 |
| Agt | sp P11859 ANGT_MOUSE | P11859 | Angiotensinogen OS=Mus musculus GN=Agt PE=1 SV=1 |
| Ahsq | sp P29699 FETUA_MOUSE | P29699 | Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsq PE=1 SV=1 |
| Alb | sp P07724 ALBU_MOUSE | P07724 | Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 |
| Angptl3 | sp Q9R182 ANGL3_MOUSE | Q9R182 | Angiopoietin-related protein 3 OS=Mus musculus GN=Angptl3 PE=1 SV=1 |
| Antrx2 | sp Q6DFX2 ANTR2_MOUSE | Q6DFX2 | Anthrax toxin receptor 2 OS=Mus musculus GN=Antrx2 PE=1 SV=1 |
| Apoa2 | sp P09813 APOA2_MOUSE | P09813 | Apolipoprotein A-II OS=Mus musculus GN=Apoa2 PE=1 SV=2 |
| Apoa4 | sp P06728 APOA4_MOUSE | P06728 | Apolipoprotein A-IV OS=Mus musculus GN=Apoa4 PE=1 SV=3 |
| Apob | sp E9Q414 APOB_MOUSE | E9Q414 | Apolipoprotein B-100 OS=Mus musculus GN=Apob PE=1 SV=1 |
| Apoc1 | sp P349281 APOC1_MOUSE | P34928 | Apolipoprotein C-I OS=Mus musculus GN=Apoc1 PE=1 SV=1 |
| Apoc2 | sp Q50502 APOC2_MOUSE | Q50502 | Apolipoprotein C-II OS=Mus musculus GN=Apoc2 PE=2 SV=1 |
| Apoc3 | sp P33622 APOC3_MOUSE | P33622 | Apolipoprotein C-III OS=Mus musculus GN=Apoc3 PE=1 SV=2 |
| Apod | sp P51910 APOD_MOUSE | P51910 | Apolipoprotein D OS=Mus musculus GN=Apod PE=1 SV=1 |
| Apoe | sp P08226 APOE_MOUSE | P08226 | Apolipoprotein E OS=Mus musculus GN=Apoe PE=1 SV=2 |
| Apon | tr G3X9D6 G3X9D6_MOUSE | G3X9D6 | Apolipoprotein N OS=Mus musculus GN=Apon PE=1 SV=1 |
| Arhgdia | GD1R1_MOUSE | sp Q99PT1 GD1R1_MOUSE | Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3 |
| B2m | sp P01887 B2MG_MOUSE | P01887 | Beta-2-microglobulin OS=Mus musculus GN=B2m PE=1 SV=2 |
| BlvrB | sp Q9Z3D2 BLVRB_MOUSE | Q9Z3D2 | Flavin reductase (NADPH) OS=Mus musculus GN=BlvrB PE=1 SV=3 |
| Bpfa2 | sp P07743 BPFA2_MOUSE | P07743 | BPI fold-containing family A member 2 OS=Mus musculus GN=Bpfa2 PE=1 SV=1 |
| C3 | sp P01027 CO3_MOUSE | P01027 | Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3 |
| C4b | sp P01029 CO4B_MOUSE | P01029 | Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3 |
| Ca1 | sp P13634 CAH1_MOUSE | P13634 | Carbonic anhydrase 1 OS=Mus musculus GN=Ca1 PE=1 SV=4 |
| Ca2 | CAH2_MOUSE | sp P00920 CAH2_MOUSE | Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4 |
| Cd97 | sp Q9Z0M6 CD97_MOUSE | Q9Z0M6 | CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2 |
| Cfl1 | sp P18760 COF1_MOUSE | P18760 | Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3 |
| Clu | sp Q06890 CLUS_MOUSE | Q06890 | Custerin OS=Mus musculus GN=Clu PE=1 SV=1 |
| Cp | ceru_MOUSE | sp Q61147 ceru_MOUSE | Ceruloplasmin OS=Mus musculus GN=Cp PE=1 SV=2 |
| Ctsd | sp P18242 CATD_MOUSE | P18242 | Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1 |
| Dbi | sp P31786 ACBP_MOUSE | P31786 | Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2 |
| Dmnk | sp Q6P253 DMNK_MOUSE | Q6P253 | Dermokine OS=Mus musculus GN=Dmnk PE=2 SV=2 |
| Dsc3 | sp P55850 DSC3_MOUSE | P55850 | Desmocollin 3 OS=Mus musculus GN=Dsc3 PE=1 SV=3 |
| Dsp | DESP_MOUSE | sp E9Q557 DESP_MOUSE | Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1 |
| Fabp4 | sp P04117 FABP4_MOUSE | P04117 | Fatty acid-binding protein, adipocyte OS=Mus musculus GN=Fabp4 PE=1 SV=3 |
| Fga | sp E9PV24 FIBA_MOUSE | E9PV24 | Fibrinogen alpha chain OS=Mus musculus GN=Fga PE=1 SV=1 |
| Fgb | sp Q8K0E8 FIBB_MOUSE | Q8K0E8 | Fibrinogen beta chain OS=Mus musculus GN=Fgb PE=1 SV=1 |
| Gc | sp P21614 VTDB_MOUSE | P21614 | Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2 |
| Gm20425 | tr E9Q035 E9Q035_MOUSE | E9Q035 | Uncharacterized protein OS=Mus musculus GN=Gm20425 PE=4 SV=1 |
| Gm8909 | tr G3UXE9 G3UXE9_MOUSE | G3UXE9 | Uncharacterized protein OS=Mus musculus GN=Gm8909 PE=1 SV=1 |
| Gpld1 | sp P070362 PHLD_MOUSE | P070362 | Phosphatidylinositol-glycan-specific phospholipase D OS=Mus musculus GN=Gpld1 PE=1 SV=1 |
| Gpx3 | sp P46412 GPX3_MOUSE | P46412 | Glutathione peroxidase 3 OS=Mus musculus GN=Gpx3 PE=1 SV=2 |
| Gpx5 | GPX5_MOUSE | sp P21765 GPX5_MOUSE | Epididymal secretory glutathione peroxidase 5 OS=Mus musculus GN=Gpx5 PE=2 SV=3 |
| H2-L | sp P01897 HA1L_MOUSE | P01897 | H-2 class I histocompatibility antigen, L-alpha chain OS=Mus musculus GN=H2-L PE=1 SV=2 |
| H2-Q10 | sp P01898 HA10_MOUSE | P01898 | H-2 class I histocompatibility antigen, Q10 alpha chain OS=Mus musculus GN=H2-Q10 PE=1 SV=3 |
| H2-Q4 | tr Q8HWB2 Q8HWB2_MOUSE | Q8HWB2 | Histocompatibility, Q region locus 4 OS=Mus musculus GN=H2-Q4 PE=1 SV=1 |
| H2-Q7 | sp P14429 HA17_MOUSE | P14429 | H-2 class I histocompatibility antigen, Q7 alpha chain OS=Mus musculus GN=H2-Q7 PE=1 SV=1 |
| Hba | sp P01942 HBA_MOUSE | P01942 | Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2 |
| Hbbt1 | tr ABDUK4 ABDUK4_MOUSE | ABDUK4 | Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1 |
| Icam1 | sp P13597 ICAM1_MOUSE | P13597 | Intercellular adhesion molecule 1 OS=Mus musculus GN=Icam1 PE=1 SV=1 |
| Igfals | sp P70389 ALS_MOUSE | P70389 | Insulin-like growth factor-binding protein complex acid labile subunit OS=Mus musculus GN=Igfals PE=1 SV=1 |
| Ighm | sp P01872 IGHM_MOUSE | P01872 | Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2 |
| IGKC | IGKC_MOUSE | sp P01837 IGKC_MOUSE | Ig kappa chain C region OS=Mus musculus PE=1 SV=1 |
| Igkv14-126 | tr A0A075B5K0 A0A075B5K0_MOUSE | A0A075B5K0 | Uncaracterized protein (Fragment) OS=Mus musculus GN=Igkv14-126 PE=4 SV=7 |
| Itih4 | sp A6X935 ITIH4_MOUSE | A6X935 | Inter-alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=2 |
| K1C10_HUMAN | sp K1C10_HUMAN | K1C10_HUMAN | #N/A |
| K22E_HUMAN | sp K22E_HUMAN | K22E_HUMAN | #N/A |
| Kng1 | sp P08677 KNG1_MOUSE | P08677 | Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1 |
| Krt1 | sp P04104 K2C1_MOUSE | P04104 | Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4 |
| Krt10 | sp P02535 K1C10_MOUSE | P02535 | Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3 |
| Krt13 | sp P08730 K1C13_MOUSE | P08730 | Keratin, type I cytoskeletal 13 OS=Mus musculus GN=Krt13 PE=1 SV=2 |
| Krt14 | sp Q61781 K1C14_MOUSE | Q61781 | Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2 |
| Krt5 | sp Q92U2 K2C5_MOUSE | Q92U2 | Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1 |
| Krt72 | K2C72_MOUSE | sp Q6IME9 K2C72_MOUSE | Keratin, type II cytoskeletal 7 OS=Mus musculus GN=Krt72 PE=3 SV=1 |
| Krt9 | sp K1C9_HUMAN | P35527 | Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9) |
| Krt90 | tr E9Q1Z0 E9Q1Z0_MOUSE | E9Q1Z0 | Keratin 90 OS=Mus musculus GN=Krt90 PE=1 SV=1 |
| Lcat | sp P16301 LCAT_MOUSE | P16301 | Phosphatidylcholine-sterol acyltransferase OS=Mus musculus GN=Lcat PE=1 SV=2 |
| Mb | sp P04247 MYG_MOUSE | P04247 | Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3 |
| Mug1 | sp P28665 MUG1_MOUSE | P28665 | Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3 |
| Mup18 | sp A2BIM8 MUP18_MOUSE | A2BIM8 | Major urinary protein 18 OS=Mus musculus GN=Mup18 PE=3 SV=1 |
| Mup20 | sp QSFW60 MUP20_MOUSE | QSFW60 | Major urinary protein 20 OS=Mus musculus GN=Mup20 PE=1 SV=1 |
| Napsa | sp O09043 NAPSA_MOUSE | O09043 | Napsin A OS=Mus musculus GN=Napsa PE=1 SV=1 |
| Pcyox1 | sp Q9CQ9 PCYOX_MOUSE | Q9CQ9 | Prenylcysteine oxidase OS=Mus musculus GN=Pcyox1 PE=1 SV=1 |
| Pfn1 | sp P62962 PROF1_MOUSE | P62962 | Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2 |
| Pla2g7 | sp O60961 PAFA_MOUSE | O60963 | Platelet-activating factor acetylhydrolase OS=Mus musculus GN=Pla2g7 PE=2 SV=2 |
| Pltp | sp P55065 PLTP_MOUSE | P55065 | Phospholipid transfer protein OS=Mus musculus GN=Pltp PE=1 SV=1 |
| Pm20d1 | sp Q8C165 P20D1_MOUSE | Q8C165 | N-fatty-acyl-amino acid synthase/hydrolase PM20D1 OS=Mus musculus GN=Pm20d1 PE=1 SV=1 |
| Pon1 | sp P52430 PON1_MOUSE | P52430 | Serum paraoxonase/arylesterase 1 OS=Mus musculus GN=Pon1 PE=1 SV=2 |
| Ppia | PPIA_MOUSE | sp P17742 PPIA_MOUSE | Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 |
| Ppic | sp P30412 PRIC_MOUSE | P30412 | Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1 |
| Prdx2 | sp Q61171 PRDX2_MOUSE | Q61171 | Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3 |
| Pspap | sp Q61207 SAP_MOUSE | Q61207 | Proasparagin OS=Mus musculus GN=Psap PE=1 SV=2 |
| Pzp | sp Q16383 PZP_MOUSE | Q16383 | Pregnancy zone protein OS=Mus musculus GN=Pzp PE=1 SV=3 |
| Qsox1 | sp Q8RNDS QSOX1_MOUSE | Q8RNDS | Sulfhydryl oxidase 1 OS=Mus musculus GN=Qsox1 PE=1 SV=1 |
| Rbp4 | sp Q00724 RET4_MOUSE | Q00724 | Retinol-binding protein 4 OS=Mus musculus GN=Rbp4 PE=1 SV=2 |
| Saa1 | sp P05366 SAA1_MOUSE | P05366 | Serum amyloid A-1 protein OS=Mus musculus GN=Saa1 PE=1 SV=2 |
| Saa2 | sp P05367 SAA2_MOUSE | P05367 | Serum amyloid A-2 protein OS=Mus musculus GN=Saa2 PE=1 SV=1 |
| Saa4 | sp P31532 SAA4_MOUSE | P31532 | Serum amyloid A-4 protein OS=Mus musculus GN=Saa4 PE=1 SV=2 |
| Sell | sp P18337 LYAM1_MOUSE | P18337 | L-selectin OS=Mus musculus GN=Sell PE=1 SV=1 |
| Serpina1a | sp P07758 A1AT1_MOUSE | P07758 | Alpha-1-antitrypsin 1-1 OS=Mus musculus GN=Serpina1a PE=1 SV=4 |
| Serpina1b | sp P22599 A1AT2_MOUSE | P22599 | Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2 |
| Serpina1e | sp P00898 A1AT5_MOUSE | P00898 | Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e PE=1 SV=1 |
| Serpina3k | sp P07759 SPA3K_MOUSE | P07759 | Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2 |
| Serpinf2 | A2AP_MOUSE | sp Q61247 A2AP_MOUSE | Alpha-2-antiplasmin OS=Mus musculus GN=Serpinf2 PE=1 SV=1 |
| Tfrc | sp Q62351 TFR1_MOUSE | Q62351 | Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1 |
| Thbs1 | sp P35441 TSPI1_MOUSE | P35441 | Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1 |
| Ttr | sp P07309 ITRY_MOUSE | P07309 | Transthyretin OS=Mus musculus GN=Ttr PE=1 SV=1 |
| Vcam1 | sp P29533 VCAM1_MOUSE | P29533 | Vascular cell adhesion protein 1 OS=Mus musculus GN=Vcam1 PE=1 SV=1 |
| Vtn | sp P29788 VTNC_MOUSE | P29788 | Vitronectin OS=Mus musculus GN=Vtn PE=1 SV=2 |

Supplemental Table III

Detected Proteins in *iLpl*^{-/-} versus *Lpl*^{f/f}

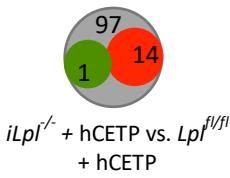


iLpl^{-/-} vs. *Lpl*^{f/f}

| Protein | Fold Change | P value |
|------------|-------------|---------|
| Dmtn | 0.229 | <0.001 |
| Apcoc3 | 0.207 | <0.001 |
| Apcoc2 | 0.176 | <0.001 |
| Apcoc4 | 0.129 | 0.001 |
| Rbp4 | 1.588 | 0.001 |
| Camp | 0.281 | 0.001 |
| Hpx | 4.842 | 0.001 |
| Apcoc1 | 0.125 | 0.001 |
| Pfn1 | 2.252 | 0.001 |
| Ctsd | 16.77 | 0.001 |
| Apoe | 0.362 | 0.001 |
| Prdx16 | 1.793 | 0.001 |
| Lig3 | 2.055 | 0.001 |
| Gm2160 | 3.343 | 0.002 |
| Pisap | 1.392 | 0.002 |
| Cst6 | 0.221 | 0.002 |
| Apcoc2 | 0.700 | 0.002 |
| Clec3b | 4.941 | 0.002 |
| Apcoc5 | 3.663 | 0.002 |
| Apod | 0.744 | 0.002 |
| Grn | 1.771 | 0.003 |
| Agt | 2.336 | 0.003 |
| Blvrb | 3.109 | 0.003 |
| Tmsb4x | 3.142 | 0.004 |
| Pipc | 0.717 | 0.004 |
| Apcoc1 | 0.797 | 0.004 |
| Ttr | 1.681 | 0.004 |
| Apmn | 0.703 | 0.007 |
| Fabp5 | 3.580 | 0.007 |
| Gc | 1.694 | 0.008 |
| Serpina1b | 1.607 | 0.009 |
| Ptp | 0.771 | 0.009 |
| Serpina1a | 1.467 | 0.011 |
| Cif1 | 2.214 | 0.011 |
| Ca1 | 3.043 | 0.012 |
| Igfbals | 1.627 | 0.013 |
| Vnn2 | 2.559 | 0.013 |
| Pm20d1 | 0.372 | 0.015 |
| Gm20425 | 4.585 | 0.017 |
| Itih4 | 1.963 | 0.017 |
| Serpina1d | 1.523 | 0.018 |
| Snca | 3.082 | 0.018 |
| Cd97 | 1.791 | 0.019 |
| Prdx2 | 2.318 | 0.019 |
| Thbs1 | 2.974 | 0.021 |
| Ces1b | 4.959 | 0.025 |
| Antx2 | 0.684 | 0.026 |
| Ahsq | 1.359 | 0.029 |
| Ihh | 0.783 | 0.031 |
| Pcyo1 | 0.825 | 0.032 |
| Angst13 | 0.383 | 0.035 |
| Pla2g7 | 0.643 | 0.038 |
| Kng1 | 1.775 | 0.040 |
| H2-Q1 | 0.809 | 0.049 |
| H2-Q10 | 0.810 | 0.052 |
| C3 | 1.533 | 0.055 |
| Saa1 | 0.503 | 0.061 |
| Krt10 | 2.176 | 0.064 |
| Pzp | 2.033 | 0.064 |
| Saa2 | 0.446 | 0.064 |
| Amcbp | 1.506 | 0.066 |
| Fg3 | 1.917 | 0.067 |
| Tfp1 | 0.833 | 0.068 |
| Krt13 | 2.159 | 0.078 |
| H2-L | 0.822 | 0.082 |
| B2m | 0.827 | 0.083 |
| K22E | 2.505 | 0.089 |
| Cst3 | 1.735 | 0.090 |
| Apcsc | 1.751 | 0.094 |
| Saa3 | 0.513 | 0.094 |
| Hbbt1 | 4.038 | 0.100 |
| Napsa | 0.500 | 0.101 |
| Hbs | 4.064 | 0.114 |
| Bpif2 | 1.390 | 0.115 |
| hHBA | 3.786 | 0.130 |
| Gm8909 | 0.847 | 0.140 |
| Dbi | 2.087 | 0.140 |
| Sgb11a1 | 1.767 | 0.147 |
| KIC10 | 1.786 | 0.149 |
| Gpx3 | 1.757 | 0.151 |
| Actb | 4.334 | 0.171 |
| Igkv14-126 | 0.333 | 0.175 |
| Fabp4 | 2.193 | 0.179 |
| Apcoc1 | 1.135 | 0.182 |
| F1b | 1.582 | 0.207 |
| Dsc3 | 1.521 | 0.222 |
| Saa4 | 0.809 | 0.239 |
| H2-K1 | 0.852 | 0.241 |
| Mup15 | 1.592 | 0.258 |
| Fgg | 1.474 | 0.263 |
| Gpld1 | 1.226 | 0.297 |
| Gsox1 | 1.304 | 0.302 |
| H2-Q7 | 0.877 | 0.334 |
| Mb | 1.566 | 0.348 |
| Ighm | 0.574 | 0.381 |
| Mup18 | 1.551 | 0.392 |
| Apcoc4 | 1.122 | 0.447 |
| Serpina3k | 1.229 | 0.480 |
| Hamp | 1.817 | 0.482 |
| Krt2 | 1.472 | 0.535 |
| Tfrc | 1.144 | 0.545 |
| C4b | 1.140 | 0.560 |
| Vcam1 | 0.869 | 0.562 |
| Mup17 | 1.560 | 0.592 |
| H2-Q4 | 0.946 | 0.594 |
| Mup3 | 1.222 | 0.596 |
| Mup2 | 1.252 | 0.604 |
| K2C1 | 0.592 | 0.652 |
| P00837 | 1.185 | 0.652 |
| Olu | 1.061 | 0.658 |
| Krt90 | 0.647 | 0.659 |
| CSN1S1 | 1.047 | 0.665 |
| Arg1 | 0.902 | 0.688 |
| Pon1 | 1.036 | 0.710 |
| Icam1 | 1.113 | 0.728 |
| Krt78 | 0.743 | 0.740 |
| Enpp7 | 1.040 | 0.776 |
| Lcat | 0.975 | 0.800 |
| Anxa2 | 1.129 | 0.801 |
| Krt1 | 0.613 | 0.809 |
| Serpina1e | 0.887 | 0.839 |
| Aph1 | 1.043 | 0.840 |
| Emc9 | 0.964 | 0.846 |
| Vtn | 1.043 | 0.855 |
| Krt5 | 1.125 | 0.860 |
| Fabp3 | 1.092 | 0.867 |
| Mup20 | 0.909 | 0.884 |
| TRY1 | 0.987 | 0.901 |
| Krt42 | 0.944 | 0.926 |
| Mug1 | 1.013 | 0.955 |
| Sell | 0.993 | 0.961 |
| Gm7298 | 1.003 | 0.990 |

Supplemental Table IV

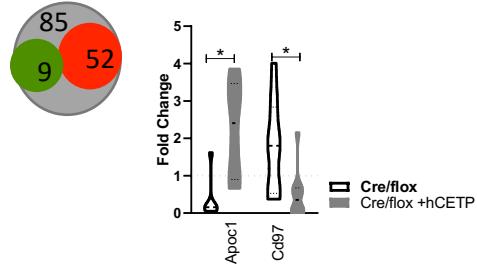
Detected Proteins in *iLpl^{-/-}* +hCETP versus *Lpl^{f/f}* +hCETP



| Protein | Fold Change | P value |
|-------------|-------------|---------|
| Pfn1 | 2.096 | 0.009 |
| Dbi | 1.926 | 0.010 |
| Arhgdia | 2.725 | 0.013 |
| Fga | 1.908 | 0.020 |
| Dsc3 | 2.094 | 0.024 |
| Hbbt1 | 3.166 | 0.024 |
| Kng1 | 3.343 | 0.025 |
| Blvrb | 2.449 | 0.032 |
| Serpinf2 | 2.864 | 0.032 |
| Prdx2 | 2.220 | 0.032 |
| Fabp4 | 2.209 | 0.033 |
| Ca1 | 2.462 | 0.040 |
| P2p | 4.669 | 0.043 |
| Apoa2 | 0.819 | 0.044 |
| Itih4 | 2.670 | 0.045 |
| Tbbs1 | 3.245 | 0.056 |
| Ppic | 1.415 | 0.061 |
| Cfl1 | 2.862 | 0.065 |
| Serpina3k | 2.132 | 0.077 |
| Serpina1b | 1.588 | 0.078 |
| IGKC | 2.200 | 0.082 |
| Hba | 2.408 | 0.088 |
| Apoa4 | 1.383 | 0.095 |
| Gpld1 | 0.584 | 0.104 |
| Apoa1 | 0.706 | 0.107 |
| Bpifaz2 | 0.324 | 0.110 |
| Ppia | 2.599 | 0.117 |
| Ttr | 1.405 | 0.120 |
| Tfrc | 0.177 | 0.122 |
| Gsox1 | 0.173 | 0.122 |
| Igfals | 0.125 | 0.129 |
| Pla2g7 | 0.288 | 0.130 |
| Fgb | 1.617 | 0.134 |
| Gm20425 | 2.948 | 0.134 |
| Vcam1 | 0.272 | 0.148 |
| Serpina1a | 1.469 | 0.152 |
| Ca2 | 2.596 | 0.159 |
| Cd97 | 0.168 | 0.187 |
| Pon1 | 0.658 | 0.192 |
| Gpx5 | 1.632 | 0.197 |
| Gpx3 | 1.581 | 0.201 |
| Mb | 1.693 | 0.222 |
| Cp | 2.750 | 0.235 |
| C4b | 0.554 | 0.237 |
| Apoc2 | 0.670 | 0.243 |
| Pm20d1 | 2.010 | 0.253 |
| Gc | 1.460 | 0.257 |
| Antxr2 | 0.494 | 0.310 |
| Apoe | 1.353 | 0.322 |
| B2m | 1.214 | 0.329 |
| Mup18 | 1.697 | 0.339 |
| Saa2 | 1.635 | 0.346 |
| Mup20 | 1.813 | 0.362 |
| Ighm | 1.564 | 0.370 |
| Apoc3 | 0.807 | 0.375 |
| Saa1 | 1.439 | 0.384 |
| Agt | 1.205 | 0.393 |
| Lcat | 0.793 | 0.409 |
| Dmkn | 0.713 | 0.427 |
| H2-Q7 | 1.388 | 0.430 |
| KRT9 | 1.307 | 0.438 |
| Napsa | 0.859 | 0.447 |
| Dsp | 0.000 | 0.451 |
| C3 | 0.805 | 0.459 |
| Icam1 | 0.477 | 0.474 |
| Krt14 | 0.310 | 0.479 |
| Serpina1e | 1.253 | 0.504 |
| Clu | 0.775 | 0.513 |
| Actb | 0.224 | 0.520 |
| H2-L | 1.179 | 0.569 |
| Ptp | 1.544 | 0.587 |
| Apon | 1.284 | 0.590 |
| Ahsg | 1.193 | 0.592 |
| H2-Q4 | 0.909 | 0.604 |
| Igkv14-126 | 1.357 | 0.605 |
| Gm8909 | 1.164 | 0.620 |
| Apod | 0.849 | 0.635 |
| Krt13 | 0.644 | 0.637 |
| Apoc1 | 1.110 | 0.640 |
| Pcyox1 | 0.908 | 0.641 |
| Krt72 | 0.650 | 0.650 |
| Krt5 | 0.603 | 0.651 |
| Mug1 | 1.226 | 0.719 |
| H2-Q10 | 1.102 | 0.730 |
| K1C10_HUMAN | 0.771 | 0.753 |
| Krt90 | 0.822 | 0.766 |
| Krt1 | 0.830 | 0.781 |
| Psap | 0.759 | 0.804 |
| TRYPS | 1.012 | 0.821 |
| Krt10 | 0.827 | 0.822 |
| Anptl3 | 1.156 | 0.826 |
| Rbp4 | 1.128 | 0.853 |
| Saa4 | 1.054 | 0.876 |
| K22E_HUMAN | 0.922 | 0.887 |
| Vtn | 0.939 | 0.932 |
| Sell | 0.953 | 0.936 |
| Ctsd | 1.025 | 0.947 |

Supplemental Table V

Overlapping Proteins Supplemental Table III and IV



Total of 85 proteins were detected in both proteomic data sets. 9 of them were significantly downregulated, 52 upregulated. They were associated with lipoprotein remodeling. Red bars: *iLpl*^{-/-} versus *Lpl*^{fl/fl}; Grey bars: *iLpl*^{-/-} + hCETP versus *Lpl*^{fl/fl}+hCETP.

Lpl^{fl/fl} n=8, *iLpl*^{-/-} n=8, *Lpl*^{fl/fl} + hCETP n=17,

iLpl^{-/-} + hCETP n=10

| Protein | Cre vs Flox Fold Change | Cre vs flox hCETP Fold Change | P value |
|------------|-------------------------|-------------------------------|---------|
| Qsox1 | 1.304 | 0.172 | 0.001 |
| Cd97 | 1.791 | 0.168 | 0.002 |
| Apoc1 | 0.125 | 1.110 | 0.019 |
| Thbs1 | 2.974 | 3.245 | 0.032 |
| Ppic | 0.717 | 1.414 | 0.047 |
| Apoc3 | 0.206 | 0.806 | 0.058 |
| Tfrc | 1.143 | 0.176 | 0.064 |
| H2-L | 0.821 | 1.178 | 0.088 |
| Serpina3k | 1.228 | 2.132 | 0.121 |
| Apon | 1.135 | 1.284 | 0.149 |
| Pltp | 0.771 | 1.544 | 0.163 |
| Serpina1a | 1.466 | 1.468 | 0.183 |
| Actb | 4.334 | 0.223 | 0.188 |
| Dmkn | 0.298 | 0.713 | 0.195 |
| Fgb | 1.581 | 1.616 | 0.197 |
| H2-Q10 | 0.810 | 1.102 | 0.198 |
| H2-Q4 | 0.946 | 0.899 | 0.200 |
| Gm8909 | 0.847 | 1.164 | 0.210 |
| Apoc2 | 0.176 | 0.669 | 0.211 |
| Rbp4 | 1.587 | 1.128 | 0.214 |
| Ahsg | 1.358 | 1.192 | 0.215 |
| Sell | 0.992 | 0.952 | 0.223 |
| Apod | 0.744 | 0.849 | 0.238 |
| Krt5 | 1.124 | 0.602 | 0.238 |
| Gc | 1.693 | 1.459 | 0.252 |
| Saa2 | 0.446 | 1.634 | 0.253 |
| Mup20 | 0.909 | 1.812 | 0.256 |
| Cfl1 | 2.214 | 2.861 | 0.274 |
| Bpifa2 | 1.389 | 0.324 | 0.286 |
| Dbi | 2.087 | 1.925 | 0.295 |
| Apoa4 | 1.128 | 1.383 | 0.300 |
| Krt10 | 2.175 | 0.826 | 0.303 |
| Saa1 | 0.503 | 1.438 | 0.304 |
| Mb | 1.566 | 1.692 | 0.305 |
| Pfn1 | 2.352 | 2.095 | 0.305 |
| Apoe | 0.362 | 1.352 | 0.326 |
| B2m | 0.827 | 1.214 | 0.328 |
| Ca1 | 3.042 | 2.462 | 0.328 |
| KRT9 | 0.320 | 1.306 | 0.330 |
| Mug1 | 1.012 | 1.226 | 0.334 |
| H2-Q7 | 0.876 | 1.388 | 0.338 |
| Serpina1e | 0.887 | 1.253 | 0.352 |
| Vtn | 1.043 | 0.939 | 0.359 |
| Napsa | 0.801 | 0.859 | 0.368 |
| Pzp | 2.033 | 4.668 | 0.383 |
| Krt1 | 0.813 | 0.829 | 0.397 |
| Dsc3 | 1.521 | 2.094 | 0.401 |
| Hba | 4.063 | 2.407 | 0.405 |
| Fga | 1.916 | 1.907 | 0.415 |
| Serpina1b | 1.607 | 1.587 | 0.426 |
| Gpld1 | 1.226 | 0.583 | 0.434 |
| Psap | 1.392 | 0.759 | 0.437 |
| Krt90 | 0.646 | 0.822 | 0.449 |
| Agt | 2.336 | 1.204 | 0.454 |
| Antxr2 | 0.684 | 0.494 | 0.456 |
| B1vrb | 3.108 | 2.448 | 0.463 |
| C3 | 1.533 | 0.805 | 0.466 |
| Igfa1s | 1.626 | 0.124 | 0.469 |
| Ctsd | 1.677 | 1.025 | 0.472 |
| Gm20425 | 4.584 | 2.947 | 0.486 |
| Kng1 | 1.774 | 3.343 | 0.488 |
| Krt13 | 2.158 | 0.644 | 0.504 |
| Pm20d1 | 0.372 | 2.010 | 0.507 |
| Vcam1 | 0.869 | 0.271 | 0.508 |
| Pcyox1 | 0.824 | 0.908 | 0.508 |
| Fabp4 | 2.192 | 2.208 | 0.515 |
| C4b | 1.140 | 0.554 | 0.526 |
| Apoa2 | 0.700 | 0.818 | 0.553 |
| Saa4 | 0.809 | 1.054 | 0.571 |
| Itih4 | 1.963 | 2.669 | 0.587 |
| Angptl3 | 0.383 | 1.155 | 0.629 |
| Icam1 | 1.112 | 0.476 | 0.642 |
| Ttr | 1.681 | 1.404 | 0.673 |
| Mup18 | 1.551 | 1.697 | 0.716 |
| Clu | 1.060 | 0.775 | 0.716 |
| Lcat | 0.974 | 0.792 | 0.752 |
| Gpx3 | 1.756 | 1.580 | 0.783 |
| Prdx2 | 2.318 | 2.220 | 0.802 |
| Hbbt1 | 4.038 | 3.166 | 0.820 |
| Igkv14-126 | 0.333 | 1.357 | 0.854 |
| Pon1 | 1.036 | 0.658 | 0.900 |
| Apoa1 | 0.797 | 0.705 | 0.914 |
| Pla2g7 | 0.643 | 0.288 | 0.925 |
| Ighm | 0.574 | 1.564 | 0.989 |

Supplemental Table VI

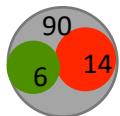
Patient characteristics

| Patient | Diagnosis | LpL deficient |
|---------|--|---------------|
| 1 | HyperTG, Pancreatitis | |
| 2 | LCAT Deficient | |
| 3 | HyperTG | |
| 4 | HyperTG | X |
| 5 | Hyperlipidemia | X |
| 6 | HyperTG, Pancreatitis, T1D, Ketoacidosis | |
| 7 | No Pancreatitis, Good TGs, On Meds | X |
| 8 | HyperTG | |
| 9 | Recurring Pancreatitis, DM | |

Supplemental Table VII

HyperTG versus Control

90 detected proteins in human samples, 6 being significantly downregulated, 14 upregulated with HyperTG.



HyperTG vs.
normal TG

| Protein | Fold change | P-value |
|----------|-------------|---------|
| ANTXR2 | 0.336 | <0.001 |
| ORM1 | 2.940 | 0.003 |
| GC | 4.023 | 0.003 |
| FGG | 3.300 | 0.004 |
| FGB | 3.164 | 0.004 |
| SERPINA1 | 3.128 | 0.007 |
| APOA1 | 0.586 | 0.007 |
| APOC2 | 2.509 | 0.008 |
| FGA | 3.798 | 0.009 |
| MENT | 0.476 | 0.010 |
| CD44 | 0.519 | 0.010 |
| PLTP | 0.494 | 0.011 |
| A1BG | 3.403 | 0.013 |
| SERPINF1 | 4.354 | 0.014 |
| APOH | 1.718 | 0.019 |
| AHSG | 3.104 | 0.021 |
| AZGP1 | 2.171 | 0.023 |
| ALB | 4.670 | 0.039 |
| APOC3 | 2.666 | 0.045 |
| PPBP | 2.769 | 0.046 |
| LPA | 0.065 | 0.048 |
| APOA2 | 0.669 | 0.063 |
| C1R | 4.764 | 0.064 |
| DIEF1 | 4.460 | 0.073 |
| APOC4 | 2.399 | 0.080 |
| IGHA1 | 1.696 | 0.080 |
| TTR | 1.927 | 0.083 |
| IGHG1 | 4.492 | 0.084 |
| IGKC | 3.779 | 0.091 |
| PLA2G7 | 3.085 | 0.095 |
| S100A8 | 2.797 | 0.098 |
| CST3 | 3.877 | 0.116 |
| APOE | 2.382 | 0.134 |
| RBPF4 | 3.897 | 0.143 |
| FGFBP2 | 0.638 | 0.147 |
| APOD | 0.831 | 0.152 |
| VTN | 0.761 | 0.162 |
| APOM | 0.798 | 0.164 |
| CA1 | 74.468 | 0.166 |
| CLU | 0.745 | 0.171 |
| APOA4 | 2.524 | 0.172 |
| KRT10 | 2.325 | 0.172 |
| APOA5 | 7.754 | 0.173 |
| C4BPA | 13.435 | 0.173 |
| SAA4 | 0.707 | 0.174 |
| APOL1 | 1.436 | 0.175 |
| APMAP | 1.608 | 0.192 |
| CA2 | 34.141 | 0.204 |
| A2M | 6.285 | 0.211 |
| KRT2 | 2.327 | 0.224 |
| SAA1 | 41.561 | 0.234 |
| CAMP | 1.832 | 0.249 |
| AMBp | 6.197 | 0.249 |
| KRT5 | 1.876 | 0.254 |
| KRT1 | 2.102 | 0.256 |
| IGHM | 8.624 | 0.257 |
| B2M | 7.417 | 0.262 |
| LCAT | 1.455 | 0.263 |
| KRT14 | 1.901 | 0.267 |
| APOC1 | 1.288 | 0.288 |
| TF | 9.556 | 0.294 |
| PCYOX1 | 0.847 | 0.301 |
| CD99 | 0.769 | 0.306 |
| MADCAM1 | 0.732 | 0.316 |
| S100A7 | 1.533 | 0.318 |
| SHH | 0.566 | 0.327 |
| PSAP | 0.697 | 0.335 |
| C3 | 1.170 | 0.335 |
| PON3 | 0.827 | 0.342 |
| IGHG2 | 2.638 | 0.374 |
| KRT9 | 1.953 | 0.384 |
| HBA1 | 175.992 | 0.415 |
| HBB | 365.166 | 0.417 |
| HBD | 119.098 | 0.420 |
| PON1 | 0.832 | 0.421 |
| HBZ | 58.339 | 0.422 |
| ANXA2P2 | 1.663 | 0.423 |
| KRT75 | 1.534 | 0.428 |
| HP | 1.392 | 0.456 |
| KRT6A | 1.532 | 0.470 |
| HLA-A | 2.551 | 0.473 |
| DCD | 1.321 | 0.486 |
| KRT16 | 1.724 | 0.510 |
| C4A | 1.251 | 0.528 |
| HPR | 1.282 | 0.549 |
| LTF | 0.806 | 0.643 |
| SFTPB | 0.768 | 0.657 |
| POTEF | 0.934 | 0.818 |
| KRT17 | 0.936 | 0.916 |
| PFN1 | 1.011 | 0.986 |
| C3orf85 | 0.998 | 0.996 |

Supplemental Table VIII

| Figure | | Comparison | P-value |
|---------------|---|---|-----------------------|
| Figure 1B | Total Cholesterol | Baseline versus Regression (Average) | 1.1x10 ⁻⁵ |
| Figure 1C | Total Triglycerides -Before aortic transplant | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 1.6x10 ⁻⁶ |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 6.6x10 ⁻⁷ |
| | Total Triglycerides -After aortic transplant | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 2.7x10 ⁻⁶ |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 1.3x10 ⁻⁶ |
| Figure 1D | CETP activity | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0021 |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 0.0010 |
| Figure 1E | VLDL Cholesterol | Baseline versus Regression (Average) | 1x10 ⁻¹⁵ |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0455 |
| | LDL Cholesterol | Baseline versus Regression | 2.4x10 ⁻¹³ |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0012 |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 0.0490 |
| | HDL Cholesterol | Baseline versus Regression (Average) | 0.0143 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0038 |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 0.0005 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-} + hCETP$ | 2.8x10 ⁻⁵ |
| | | $Lpl^{-/-}$ versus $Lpl^{-/-} + hCETP$ | 0.0198 |
| Figure 1F | VLDL Triglyceride | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 1.2x10 ⁻⁵ |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 0.0497 |
| | HDL Triglyceride | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0306 |
| Figure 2C | %CD68+ area (Aortic Arch) | Baseline versus Regression (Average) | 1.1x10 ⁻⁵ |
| Figure 3B | Total Cholesterol | Baseline versus $Lpl^{fl/fl}$ Regression | 1x10 ⁻¹⁵ |
| | | Baseline vs $iLpl^{-/-}$ Regression | 1x10 ⁻¹⁵ |
| Figure 3C | Triglycerides | $Lpl^{fl/fl}$ Regression versus $iLpl^{-/-}$ Regression | 1x10 ⁻¹⁵ |
| Figure 3D | %CD68+ area (Root) | Baseline versus $Lpl^{fl/fl}$ Regression | 1x10 ⁻¹⁵ |
| | | Baseline vs $iLpl^{-/-}$ Regression | 0.0466 |
| Figure 3F | %Mac+ area (BCA) | Baseline versus $Lpl^{fl/fl}$ Regression | 0.0018 |
| | | Baseline vs $iLpl^{-/-}$ Regression | 0.0121 |
| Figure 2E | Fibrous Cap | Baseline thin versus thick fibrous cap | 0.0444 |
| Figure 5A | Total HDL-P | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 2x10 ⁻⁸ |
| | | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0003 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-} + hCETP$ | 0.00042 |
| | Small HDL-P | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 6.4x10 ⁻⁶ |
| | | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0032 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-} + hCETP$ | 0.0066 |
| | Medium HDL-P | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0003 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0012 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-} + hCETP$ | 0.0105 |
| Figure 5B | Total Efflux | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0002 |
| | Total Efflux | $Lpl^{-/-}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0296 |
| Figure 5C | Total Efflux | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0181 |
| | ABCA1-mediated efflux | $Lpl^{fl/fl}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0139 |

| | | | |
|---------------------------|---------------------------------------|--|----------------------|
| | ABCA1-mediated efflux | $Lpl^{-/-}$ versus $Lpl^{fl/fl} + hCETP$ | 0.0432 |
| Figure 6B | Total HDL-P | Ctrl versus HyperTG | 3×10^{-6} |
| | Medium HDL-P | Ctrl versus HyperTG | 4.7×10^{-5} |
| | Large HDL-P | Ctrl versus HyperTG | 0.0007 |
| Figure 6C | ABCA1-mediated Efflux | Ctrl versus HyperTG | 0.0074 |
| Figure 6D | Total Efflux | Ctrl versus HyperTG | 0.0044 |
| | ABCA1-mediated Efflux | Ctrl versus HyperTG | 0.0077 |
| Supplemental Figure I | Body weight | Baseline versus Regression (Average) | 0.0040 |
| Supplemental Figure III C | Body weight -Before aortic transplant | Baseline versus $Lpl^{fl/fl}$ | 0.0046 |
| | | Baseline versus $Lpl^{-/-}$ | 0.0263 |
| | Body weight - After aortic transplant | Baseline versus $Lpl^{fl/fl}$ | 0.0187 |
| | | Baseline versus $Lpl^{-/-}$ | 0.0380 |
| Supplemental Figure III D | Total Cholesterol | Baseline versus $Lpl^{fl/fl}$ | 4.7×10^{-6} |
| | | Baseline versus $Lpl^{-/-}$ | 0.0316 |
| Supplemental Figure III E | Total Triglycerides | Baseline versus $Lpl^{fl/fl}$ | 0.0003 |
| | | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0006 |
| Supplemental Figure III F | VLDL Cholesterol | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0117 |
| | LDL Cholesterol | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0078 |
| Supplemental Figure III G | VLDL-TG | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0029 |
| Supplemental Figure III I | %CD68+ area (Aortic Arch) | Baseline versus Regression (Average) | 0.0006 |
| Supplemental Figure IV A | Total Cholesterol | Baseline $Lpl^{fl/fl}$ Tie2LPL versus Regression $Lpl^{fl/fl}$ Tie2LPL | 0.0019 |
| | | Baseline $iLpl^{-/-}$ Tie2LPL versus Regression $iLpl^{-/-}$ Tie2LPL | 0.0076 |
| Supplemental Figure IV F | %Mac+ area (BCA) | Baseline $iLpl^{-/-}$ Tie2LPL versus Regression $iLpl^{-/-}$ Tie2LPL | 0.0358 |
| Supplemental Figure V A | ApoA-I | $Lpl^{fl/fl}$ versus $Lpl^{-/-}$ | 0.0052 |
| | | $Lpl^{fl/fl} + hCETP$ versus $Lpl^{-/-} + hCETP$ | 0.0167 |