

Supplementary Table 1. HDL₃ proteins identified by mass spectrometric analysis.

IPI Number	Protein Name	Total Peptides Identified per Sample (SD)¹	Samples with Detectable Peptides²	% Amino Acid Coverage (SD)³	Average Protein Probability⁴
IPI00021841	Apolipoprotein AI	240.1 (42.7)	18	71.2 (13.7)	1.00
IPI00022434	Serum albumin	68.9 (36.4)	18	46.9 (11.4)	1.00
IPI00021854	Apolipoprotein A-II	44.3 (15.4)	18	68.9 (10.7)	1.00
IPI00019399	Serum amyloid A4	21.9 (5.2)	18	46.1 (11.9)	1.00
IPI00305457	Alpha-1-antitrypsin	14.3 (4.2)	18	21.5 (4.3)	1.00
IPI00030739	Apolipoprotein M	13.4 (3.5)	18	23.0 (11.2)	1.00
IPI00021857	Apolipoprotein C-III	12.7 (2.7)	18	27.8 (6.8)	1.00
IPI00021856	Apolipoprotein C-II	11.6 (5.0)	18	42.3 (4.5)	1.00
IPI00021842	Apolipoprotein E*	11.0 (4.0)	18	23.8 (8.5)	1.00
IPI00006662	Apolipoprotein D	7.9 (2.2)	18	23.8 (6.3)	1.00
IPI00478761	Apolipoprotein A-IV	7.1 (2.3)	18	16.5 (10.5)	1.00
IPI00218732	Paraoxonase 1	5.3 (2.8)	18	16.1 (7.6)	0.99
IPI00022331	Phosphatidylcholine-sterol acyltransferase	4.9 (2.8)	18	10.1 (3.8)	0.99
IPI00186903	Apolipoprotein L1	4.2 (1.7)	18	9.1 (3.1)	0.99
IPI00299435	Apolipoprotein F*	4.2 (1.6)	18	6.1 (2.2)	1.00
IPI00022368	Serum amyloid A	4.7 (3.8)	11	32.8 (10.2)	1.00
IPI00400826	Apolipoprotein J (Clusterin)*	3.5 (1.6)	11	6.1 (3.4)	0.99
IPI00022733	Phospholipid transfer protein*	5.0 (1.8)	6	8.0 (6.3)	0.98
IPI00452748	Serum amyloid A1	4.1 (2.1)	8	20.7 (7.6)	0.99
IPI00022431	Alpha-2-HS-glycoprotein	1.8 (0.4)	11	5.4 (0.0)	0.98
IPI00477597	Haptoglobin-related protein	2.8 (1.3)	5	11.0 (5.0)	0.99
IPI00418163	Complement component C4B	1.6 (0.8)	11	1.6 (0.5)	0.97
IPI00298971	Vitronectin	3.0 (1.9)	5	5.7 (2.7)	0.99
IPI00215894	Kininogen	2.0 (0.0)	4	2.1 (0.0)	0.98
IPI00298828	Beta-2-glycoprotein I	2.0 (0.0)	2	4.0 (0.1)	0.96
IPI00164623	Complement component C3	2.0 (1.4)	2	2.1 (0.8)	0.99
IPI00555812	Vitamin D-binding protein	1.5 (0.7)	2	4.9 (0.4)	0.96

Proteomic analysis of HDL₃ (d=1.10 to 1.21 g/mL) from six CAD subjects before and during niacin/statin therapy and six healthy control subjects (Table 1, Group 1).

*Proteins differentially expressed as assessed by spectral counting and Student's paired *t*-test or by XIC peak area and a two-way repeated measures analysis-of-variance between pre- and post-niacin/statin treatment.

¹ Average number of total peptides identified in each sample (SD) for samples in which at least one peptide was detected.

² Number of samples in which at least one peptide was detected and the protein identified. A total of 18 samples were analyzed.

³ Average percent of the total amino acid sequence of the protein detected by proteomic analysis.

⁴ Average Protein Probability Score from ProteinProphet.

Supplementary Table 2: Peptides quantified by peak areas of extracted ion chromatograms from HDL₃ of CAD subjects before and during niacin/statin (N/S) therapy.

Protein	Peptide Sequence	Precursor ion m/z	CAD AUCx10 ⁻⁶ (SD)	CAD+N/S AUCx10 ⁻⁶ (SD)
ApoE	LAVYQAGAR	474.767	20.8 (4.92)	15.9 (5.80)
	AATVGSLAGQPLQER	749.405	7.62 (2.74)	4.18 (2.39)
	GEVQAMLFQSTEELRVR ¹	665.011	8.30 (1.30)	4.41 (2.42)
	LKSWFEPLVEDMQR ¹	593.303	9.39 (4.06)	5.66 (2.67)
	LGPLVEQGR	484.770	42.4 (7.50)	33.1 (14.8)
	VQAAVGTSAAPVPSDNH	810.902	2.24 (2.21)	0.83 (0.47)
	AYKSELEEQLTPVAEETR ¹	698.351	1.96 (0.72)	1.10 (0.83)
ApoF	SGVQQLIQYYQDQK ¹	566.621	1.52 (0.79)	3.11 (1.41)
	SYDLDPGAGSLEI	668.817	11.2 (3.01)	18.73 (6.40)
ApoJ	LFSDPITVTVPVEVSR	937.499	0.89 (0.58)	2.49 (1.50)
	VTTVASHTSDSDVPSGVTEVVVK ¹	772.064	0.78 (0.57)	2.49 (1.79)
PLTP	TMLQIGVMPMLNER	816.917	0.06 (0.05)	0.31 (0.19)
	AGALQLLLVGDK ²	599.363	0.16 (0.11)	0.42 (0.30)
	SSVDELVGIDYSLMK ¹	552.611	0.15 (0.09)	0.51 (0.40)
	ATYFGSIVLLSPAVIDSPLK ¹	697.729	0.46 (0.34)	1.25 (1.19)
ApoC-II	TYLPAVDEKLRDLYSK	956.015	18.6 (2.60)	13.1 (5.02)
	STAAMSTYTGIFTDQVLSVLKGEE	1274.628	69.3 (18.3)	47.17 (21.0)
	TAAQNLYEK	519.267	1.18 (0.73)	0.56 (0.13)
ApoA-I	ATEHLSTLSEK	608.314	23.4 (20.8)	18.3 (17.2)
	DSGRDYVVSQFEGSALGK ¹	605.955	760 (345)	1079 (476)
	LLDNWDSVTSTFSK	806.896	1864 (729)	2669 (1226)
	DLATVYVDVLK ²	618.348	129 (54.5)	170 (37.9)
	DYVSQFEGSALGK	700.838	238 (122)	359 (173)
ApoAII	SKEQLTPLIK	578.850	19.5 (5.47)	18.8 (6.05)
	SYFEKSKEQLTPLIK ²	906.001	0.04 (0.03)	0.06 (0.05)
	EPCVESLVSQYFQTVTDYGK	1176.041	9.12 (4.00)	10.4 (2.73)
ApoCIII	TAKDALSSVQESQVAQQAR ²	1009.019	5.12 (0.88)	4.14 (1.16)
	DALSSVQESQVAQQAR	858.929	7.60 (2.40)	6.41 (3.30)
	GWVTDGFSSLK	598.801	0.24 (0.16)	0.31 (0.37)
Albumin	RHPDYSVLLLLR ¹	633.670	2.75 (1.67)	3.71 (2.58)
	RHPYFYAPELLFFAK ¹	489.953	1.46 (0.56)	2.08 (1.39)
	HPYFYAPELLFFAK ¹	581.636	0.20 (0.08)	0.32 (0.22)

¹The extracted ion chromatogram was calculated from the 3+ ion on indicated peptides. ² The extracted ion chromatogram was calculated from the sum of 2+ and 3+ ions with the precursor

m/z shown for the 2+ ion. For all other peptides, the extracted ion chromatogram was calculated from the 2+ ion.