

**Online Supplemental Materials**

**Supplementary Table 1.** Comparisons of HDL cholesterol (HDL-C) and ApoAI levels between diabetics and non-diabetics subjects, with and without adjustment for sex. Statistics presented as Pearson's correlation (95% CI).

Measure	Unadjusted Mean Difference (95% CI)	Unadjusted P-value	Adjusted Mean Difference (95% CI)	Adjusted P-value
HDL-C	-3.69(-16.91,9.52)	0.56	-3.76(-17.53,10.00)	0.57
ApoAI	4.42(-14.87,23.70)	0.63	4.04(-15.70,23.78)	0.67

**Supplementary Table 2.** Correlation of total and ABCA-independent cholesterol efflux with hyperglycemia (HbA<sub>1c</sub>) and ApoAI glycation at Lys-12 and Lys-133 residues. Statistics presented as Pearson's correlation (95% CI).

Cholesterol Efflux	<i>HbA<sub>1c</sub></i>		<i>Lys-12 Glycation</i>		<i>Lys-133 Glycation</i>	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
Total efflux	-0.28	0.03	-0.53	0.001	-0.13	0.16
ABCA1-independent	-0.07	0.31	-0.22	0.06	-0.01	0.70

HbA<sub>1c</sub>: glycated hemoglobin, ABCA1: ATP-binding cassette (ABC) family transporter.

**Supplementary Table 3.** Comparisons of the fractional catabolic rates (FCRs) of ApoAI, ApoAI glycation and HDL functions between T2DM patients and healthy controls with adjustment for HbA<sub>1c</sub>. The parameters that were not different after the adjustment for HbA<sub>1c</sub> are highlighted in bold.

Measure	Unadjusted Mean Difference (95% CI)	Unadjusted P-Value	Adjusted Mean Difference (95% CI)	Adjusted P-Value
<b>Fractional catabolic rate of ApoAI</b>				
ApoAI	0.01 (0.00,0.01)	<b>&lt;0.001</b>	0.01 (0.00,0.01)	<b>0.031</b>
<b>Glycation measures at different lysine sites of ApoAI</b>				
logApoA1K133	0.25 (-0.00,0.50)	<b>0.054</b>	0.39 (-0.09,0.88)	<b>0.100</b>
logApoA1K12	0.25 (0.15,0.36)	<b>&lt;0.001</b>	0.10 (-0.08,0.27)	<b>0.240</b>
logApoA1K205	0.71 (0.13,1.30)	<b>0.021</b>	0.88 (-0.26,2.01)	<b>0.120</b>
logApoA1K96	0.01 (-0.29,0.30)	0.960	-0.04 (-0.61,0.53)	0.880
<b>HDL function</b>				
PON1	-97.14 (-159.02,-35.27)	<b>0.005</b>	-55.76 (-173.58,62.06)	<b>0.33</b>
ABCA1-independent	-1.15 (-2.43,0.13)	0.074	-2.20 (-4.65,0.26)	0.075
Total efflux	-2.31 (-3.66,-0.95)	<b>0.002</b>	-2.98 (-5.64,-0.32)	<b>0.031</b>
ABCA1-dependent	-1.16 (-1.90,-0.43)	<b>0.004</b>	-0.81 (-2.26,0.64)	<b>0.250</b>

FCR: fractional catabolic rate, ApoA1K12: ApoAI glycation at lysine 12 site, ApoA1K96: ApoAI glycation at lysine 96 site ApoA1K133: ApoAI glycation at lysine 133 site, ApoA1K205: ApoAI glycation at lysine 205 site HbA<sub>1c</sub>: glycated hemoglobin; HDL: high density lipoprotein, PON1: paraoxonase 1.

**Supplementary Table 4.** List of the proteins associated with ApoAI. Two identical sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGEs) were performed for ApoAI-specific Western blotting and proteomics analysis. Based on the molecular weight markers and Western blot analysis matching, corresponding silver-stained gel bands containing ApoAI were analyzed by mass spectrometry. Proteins identified in each band are check marked.

Accession Number	Gene Name	Protein Name	Molecular Weight (kDa)	Control			T2DM		
				27 kDa	50 kDa	75 kDa	27 kDa	50 kDa	75 kDa
P01009	A1AT	Alpha-1-antitrypsin	47		√			√	√
P01008	ANT3	Antithrombin-III	53		√		√	√	√
P02647	APOA1	Apolipoprotein A-I	31	√	√	√	√	√	√
P04114	APOB	Apolipoprotein B-100	516		√		√	√	√
P02649	APOE	Apolipoprotein E	36			√		√	
P01857	IGHG1	Immunoglobulin heavy constant gamma 1	36		√			√	√
P01871	IGHM	Immunoglobulin heavy constant mu	49		√		√	√	√
Q14624	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	103			√	√	√	√
P02768	ALBU	Serum albumin	69		√	√	√	√	√
P04004	VTNC	Vitronectin	54		√		√	√	√
P02765	FETUA	Alpha-2-HS-glycoprotein	39		√				
P06727	APOA4	Apolipoprotein A-IV	45			√			
P05090	APOD	Apolipoprotein D	21			√			
O95445	APOM	Apolipoprotein M	21			√			
P04217	A1BG	Alpha-1B-glycoprotein	54						√
P08697	A2AP	Alpha-2-antiplasmin	55					√	√
P01023	A2MG	Alpha-2-macroglobulin	163					√	√
P04003	C4BPA	C4b-binding protein alpha chain	67				√	√	√
P09871	C1S	Complement C1s subcomponent	77					√	
P01024	CO3	Complement C3	187				√	√	√
P0C0L4	CO4A	Complement C4-A	193				√	√	√
P06396	GELS	Gelsolin	86					√	
P05546	HEP2	Heparin cofactor 2	57				√	√	√
P04196	HRG	Histidine-rich glycoprotein	60						√
P19823	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2	106						√
P55058	PLTP	Phospholipid transfer protein	55				√	√	√
P00747	PLMN	Plasminogen	91					√	
P00734	THRB	Prothrombin	70				√	√	√
P02787	TRFE	Serotransferrin	77					√	√

**Supplementary Figure 1.**  $^2\text{H}$ -labeling of native and glycosylated ApoAI analyzed by mass spectrometry. ApoB100-depleted plasma samples from a patient with type 2 diabetes at the baseline and after 4 days of  $^2\text{H}_2\text{O}$  labeling experiment were digested with trypsin and analyzed by high resolution mass spectrometry. To illustrate the changes in isotope distribution, the heavy isotopomers ( $M_1$ - $M_3$ ) were normalized relative to  $M_0$ . After 4 days of  $^2\text{H}_2\text{O}$  labeling, the intensities of heavy isotopomers, in particular  $M_1$ , were increased relative to monoisotopic peak in both non-glycosylated VSFLSALEEYTK (**A**) and glycosylated  $\text{Q}^{\text{Gly}}\text{KLHELQEK}$  (**B**) ApoAI peptides. However, the extent of the increase in the glycosylated peptide was substantially higher than in the non-glycosylated peptide, indicating that the glycosylated peptide has higher turnover rate and shorter half-life.

