

Supplemental Material

Data S1.

Supplemental Methods

Elastic Net Model after partial least squares discriminant analysis.

For proteins with $VIP > 1$, a logistic regression model with elastic net penalty²⁴ on each bootstrap dataset was further considered. The elastic net penalty shrinks some protein coefficients to zero in the logistic regression model so that proteins with zero coefficients can be deemed unimportant in discriminating cases and controls, and hence may be deleted. To select the elastic net regularization parameter, cross-validation using the *cv.glmnet* function in the R package *glmnet*⁴⁴ was used, and the elastic net parameter was set to $\alpha = 0.5$. PLSDA was carried out with the R package *Discriminer*.

Internal Validation via Bootstrap

In the absence of external validation data, we internally validated our findings using bootstrap. We repeated each step of the model development, from candidate protein biomarker selection to protein score development. We obtained 200 bootstrap samples and we kept the proportions of cases and controls similar to the proportions in the original data. For each bootstrap dataset, a two-component PLSDA model was fit, and proteins with $VIP > 1$ were kept. This step selected 31 proteins (compared to 29 proteins in the original [discovery] analysis). There were 27 overlapping proteins meeting this criterion in both the discovery and validation PLSDA models. As in the original analysis, logistic regression models with elastic net were fit on each bootstrap validation data for proteins with $VIP > 1$, and proteins with frequency of nonzero coefficients in the top 25th percentile were used to develop protein scores. We identified the same 8 proteins (FAM3B, ITGA11, IL6, HGF, CCL25, GT, PLA2G7, and SCGB3A2) that were found in the discovery analysis. We obtained 200 log-odds ratios for each protein using the bootstrap validation data, and a weighted mean (over 200 log-odds ratios) was ascertained. In the discovery analysis, the protein score and models were developed using the full dataset, but in order not to use the full dataset in

the validation step, we obtained a different set of bootstrap dataset (200 bootstrap datasets), and we developed protein scores for each bootstrap dataset. Then for each bootstrap data, we fit the two models: baseline, and baseline and protein score to obtain odds ratios and AUCs and their corresponding variances. A fixed-effect meta-analysis using inverse-variance method was used to obtain weighted averages and confidence intervals. The protein score from the validation analysis was statistically significant with an odds ratio of 2.78 (CI: 2.67-2.90) compared to an odds ratio of 2.17 (CI: 1.58 - 2.99) from the discovery set. The validation AUCs for the baseline and baseline plus protein score models were respectively 0.74 (CI: 0.73-0.75) and 0.79(CI: 0.78-0.80) (Table S12), representing an improvement in AUC above the baseline model of 6.8% compared to 5.8% in the discovery analyses.

Data S2. Appendix: Study Group Authors

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Table S1: Cause of CVD case status:

Cause of CVD	N
MI	26
Coronary Revascularization	64
Stroke	24
CVD Death or Unwitnessed Death and cause unknown	17
CVD Total	131

Table S2: Average variable importance in projection (VIP) for all 107 proteins. Some proteins were represented in more than one panel.

Protein	Average VIP	Protein	Average VIP	Protein	Average VIP	Protein	Average VIP	Protein	Average VIP
GT	2.24	PLA2G7	1.12	CCL19	0.94	CST5	0.84	PCSK9	0.79
ITGA11	1.43	EPHB4	1.11	KIM1	0.93	CCL3	0.83	COL18A1	0.79
ICAM1	1.39	CDCP1	1.11	IL10RB	0.93	LAMP3	0.83	REG3A	0.79
BTN3A2	1.30	TNFR1	1.06	TRAILR2	0.92	PGF	0.82	CPA1	0.79
SCGB3A2	1.28	IL6	1.06	MCP1	0.92	HNMT	0.82	PRSS2	0.78
TNFR2	1.28	UPAR	1.05	PRSS8	0.91	GAL4	0.82	KRT19	0.77
TNFRSF10A	1.28	CST3	1.04	CKAP4	0.90	IL8	0.82	ADM	0.77
CD83	1.28	CCL25	1.02	CDH1	0.89	TFF3	0.82	CCL11	0.77
GAS6	1.23	TCN2	1.01	CCL18	0.89	IL6	0.82	CCL20	0.76
EFEMP1	1.22	CHI3L1	1.00	SPON2	0.89	CCL14	0.810	MCP3	0.76
HOSCAR	1.20	UPA	1.00	MCP1	0.88	MMP10	0.81	CCL11	0.76
LILRB4	1.18	IL18R1	0.99	NTPROBNP	0.88	CXCL16	0.81	ST2	0.76
FAM3B	1.17	CX3CL1	0.97	LIFR	0.87	TNFSF13B	0.81	CPB1	0.75
GDF15	1.17	CTSZ	0.97	IL2RA	0.86	CTSL1	0.81	AREG	0.75

Table S3: Summary statistics for the number of times elastic net model had non-zero coefficients across the 200 bootstrap sets.

Protein	Counts	Proportions
HGF	199	0.995
IL6	193	0.965
FAM3B	187	0.935
SCGB3A2	187	0.935
GT	186	0.930
CCL25	180	0.900
ITGA11	179	0.895
PLA2G7	167	0.835
GDF15	159	0.795
ICAM1	146	0.730
TNFR1	140	0.700
GRN	138	0.690
EFEMP1	128	0.640
UPAR	127	0.635
CDCP1	123	0.615
CST3	123	0.615
LILRB4	119	0.595
CSF1	119	0.595
BTN3A2	116	0.580
TCN2	116	0.580
TIMP1	115	0.575
CD83	114	0.570
GAS6	114	0.570
IL18BP	113	0.565
TNFRSF9	112	0.560
HOSCAR	112	0.560
TNFRSF10A	111	0.555
TNFR2	109	0.545
EPHB4	109	0.545

Table S4: Conditional logistic regression model of CVD on standardized protein score. (This was used to generate forest plot in Figure 1. Here, n=375 as there were 15 samples with missing values.) OR for similar model with viral load categorized as: viral load (≥ 500 copies/ML) vs viral load (< 500 copies/ML) was 1.31 (CI: 0.60-2.84).

Variable	Odds Ratio	Std Error	Pr(> z)	LCI	UCI
CD4	1.00	0.00	0.95	1.00	1.00
RNA	1.00	0.00	0.85	1.00	1.00
Females vs Males	0.53	0.47	0.18	0.21	1.33
Age	1.20	0.05	<0.01	1.08	1.33
BMI	1.01	0.03	0.63	0.96	1.07
Diabetes	0.72	0.56	0.56	0.24	2.16
Black Race	1.19	0.40	0.67	0.54	2.59
Lipid-lowering medication	0.96	0.38	0.92	0.45	2.04
BP-lowering medication	1.46	0.39	0.33	0.68	3.15
CVD	3.22	0.71	0.10	0.81	12.90
Protein Score	2.17	0.16	<0.01	1.58	2.99

Table S5: Odds ratios and AUC from categorizing protein score

Protein Score	Case individuals (n)	Control individuals (n)	Odds ratio (95% CI)	AUC
Median				0.74
Below	38	157	1.00	
Above	93	102	3.15 (1.83- 5.41)	
Top 25% vs bottom 75%				0.69
1 (Top)	55	43	2.91 (1.65,5.12)	
2	76	216	1.00	
Above 0 vs below 0 protein score				0.75
Below	39	159	1.00	
Above	92	100	3.20 (1.86 to 5.49)	

Table S6: Incremental contribution of proteins and protein score to CVD risk when added to the baseline model. The baseline model includes the coagulation biomarker D-dimer. Here, n=364.

Model	AUC	LCI	UCI	Change in AUC from Baseline	NRI among cases	NRI among controls	Overall NRI
Baseline*	0.69	0.60	0.78	-	-	-	-
+ FAM3B	0.73	0.65	0.81	0.04	0.15(-0.03,0.32)	0.02(-0.10,0.15)	0.17(-0.04,0.39)
+ ITGA11	0.70	0.61	0.79	0.01	0.08(-0.09,0.26)	-0.01(-0.13,0.12)	0.07(-0.14,0.29)
+ IL6	0.70	0.61	0.78	0.01	0.15(-0.03,0.32)	0.12(-0.01,0.24)	0.26(0.05,0.48)
+ HGF	0.73	0.64	0.81	0.04	0.23(0.06,0.40)	0.11(-0.02,0.23)	0.34(0.12,0.55)
+ CCL25	0.69	0.60	0.78	0.00	0.02(-0.16,0.19)	0.15(0.02,0.27)	0.17(-0.05,0.38)
+ GT	0.73	0.65	0.82	0.05	0.28(0.11,0.45)	0.15(0.02,0.27)	0.43(0.22,0.64)
+ PLA2G7	0.72	0.64	0.80	0.03	0.16(-0.01,0.34)	0.12(0.00,0.25)	0.29(0.07,0.50)
+SCGB3A2	0.71	0.63	0.80	0.03	0.10(-0.08,0.27)	0.12(-0.01,0.24)	0.21(0.00,0.43)
+ Protein score from all 8 proteins	0.73	0.65	0.82	0.05	0.36 (0.20, 0.53)	0.24 (0.12,0.36)	0.60 (0.40,0.81)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, prior history of CVD, lipid lowering medication, blood pressure lowering medication and D-dimer (log2 transformed).

The proteins FAM3B, IL6, HGF, GT, and PLA2G7 were each statistically significant (p-value<0.05) when added to the baseline model.

Protein score was statistically significant ($p < 0.00001$) when added to the baseline model. Odds ratio for protein score: 2.09 (CI: 1.52, 2.88)

Of note, D-dimer was statistically significant (p-value =0.03) in the baseline model but not in the baseline + protein score model (p-value>0.05).

Integrated Discriminant Index when protein score was added to the baseline* model was 0.08 (0.05, 0.10).

Table S7: Incremental contribution of proteins and protein score to CVD risk when added to the baseline model. The baseline model includes the inflammatory biomarker hsCRP. Here, n=364.

Model	AUC	LCI	UCI	Change in AUC from Baseline	NRI among cases	NRI among controls	Overall NRI
Baseline*	0.73	0.65	0.81	-	-	-	-
+ FAM3B	0.72	0.63	0.80	-0.01	0.26(0.09,0.43)	0.02(-0.10,0.15)	0.29(0.07,0.50)
+ ITGA11	0.73	0.64	0.81	0.00	0.08(-0.09,0.26)	0.01(-0.12,0.13)	0.09(-0.13,0.31)
+ IL6	0.70	0.62	0.79	-0.03	0.03(-0.14,0.21)	0.13(0.01,0.26)	0.17(-0.05,0.38)
+ HGF	0.72	0.64	0.80	-0.01	0.21(0.04,0.39)	0.12(-0.01,0.24)	0.33(0.11,0.54)
+ CCL25	0.73	0.64	0.81	-0.01	0.05(-0.13,0.23)	0.12(0.00,0.25)	0.17(-0.04,0.39)
+ GT	0.73	0.65	0.81	0.00	0.30(0.13,0.46)	0.16(0.03,0.28)	0.45(0.24,0.66)
+ PLA2G7	0.72	0.63	0.80	-0.01	0.16(-0.01,0.34)	0.14(0.02,0.27)	0.30(0.09,0.52)
+SCGB3A2	0.72	0.62	0.79	-0.02	0.13(-0.04,0.31)	0.12(0.00,0.25)	0.26(0.04,0.47)
+ Protein score from all 8 proteins	0.75	0.66	0.83	0.02	0.37 (0.20, 0.53)	0.19 (0.07,0.31)	0.56 (0.35,0.76)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, prior history of CVD, lipid lowering medication, blood pressure lowering medication and hsCRP (log2 transformed).

The proteins FAM3B, IL6, HGF, GT, and PLA2G7 were each statistically significant (p-value<0.05) when added to the baseline model. SCGB3A2 was marginally significant (p-value=0.051).

Protein score was statistically significant ($p < 0.00001$) when added to the baseline model. Odds ratio for protein score: 2.14 (CI: 1.54, 2.97).

Of note, hsCRP was not statistically significant in both baseline and baseline + protein score models (p -value > 0.05).

Integrated Discriminant Index when protein score was added to the baseline* model was 0.08 (0.05, 0.10).

Table S8: Incremental contribution of protein factors to CVD risk when added to baseline model. Analyses restricted to PLWH on ART at baseline, n=269

Model	AUC	LCI	UCI	Change in AUC from Baseline	NRI among cases	NRI among controls	Overall NRI
Baseline*	0.70	0.60	0.80	-	-	-	-
+ FAM3B	0.69	0.59	0.79	-0.01	0.09 (-.12,.29)	0.01 (-.14,.15)	0.09 (-.16,.34)
+ ITGA11	0.69	0.59	0.79	-0.01	0.13 (-0.07,0.33)	-0.01 (-0.15,0.14)	0.12 (-0.13,0.38)
+ IL6	0.69	0.59	0.79	-0.01	0.35 (0.16,0.54)	0.18 (0.03,0.32)	0.523 (0.28,0.76)
+ HGF	0.69	0.59	0.79	-0.01	0.09 (-0.12,0.29)	0.09 (-0.06,0.23)	0.17 (-0.08,0.42)
+ CCL25	0.70	0.60	0.80	0.01	-0.02 (-0.23,0.18)	0.11 (-0.04,0.25)	0.09 (-0.17,0.34)
+ GT	0.71	0.61	0.81	0.01	0.30 (-0.11,0.50)	0.10 (-0.05,0.24)	0.40 (0.16,0.64)
+ PLA2G7	0.69	0.59	0.79	-0.01	0.17 (-0.03,0.38)	0.13 (-0.02,0.28)	0.30 (0.06,0.55)
+SCGB3A2	0.71	0.61	0.81	0.01	0.15 (-0.05,0.35)	0.11 (-0.04,0.25)	0.26 (0.01,0.51)
+ Protein score from all 8 proteins	0.74	0.64	0.83	0.04	0.28 (-0.09, 0.48)	0.16 (-0.02, 0.31)	0.45 (-0.20, 0.69)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, prior history of CVD, lipid lowering medication, and blood pressure lowering medication.

The proteins IL6, HGF, and GT were each statistically significant (p-value<0.05) when added to the baseline model. PLA2G7 was marginally significant (p-value =0.06).

Protein score was statistically significant ($p < 0.01$) when added to the baseline model. Odds ratio for protein score: 1.93 (CI: 1.35-2.77); Integrated Discriminant Index: 0.06 (0.04-0.09)

Table S9: Incremental contribution of protein factors to CVD risk when added to baseline model. Analyses restricted to individuals with no prior history of CVD (n=356)

Model	AUC	LCI	UCI	Change in AUC from Baseline	NRI among cases	NRI among controls	Overall NRI
Baseline*	0.66	0.56	0.75	-	-	-	-
+ FAM3B	0.67	0.58	0.76	0.01	0.24 (0.06, 0.42)	0.04 (-0.08, 0.16)	0.28 (0.06,0.50)
+ ITGA11	0.65	0.56	0.75	-0.01	0.05 (-0.13,0.24)	0.00 (-0.12,0.12)	0.05 (-0.17, 0.28)
+ IL6	0.67	0.58	0.77	0.01	0.33 (0.15, 0.50)	0.17 (0.05, 0.29)	0.50 (0.28, 0.71)
+ HGF	0.67	0.58	0.77	0.01	0.22 (0.04, 0.40)	0.11 (-0.01, 0.24)	0.33 (0.11, 0.55)
+ CCL25	0.67	0.57	0.76	0.01	0.11 (-0.08, 0.30)	0.12 (-0.00, 0.25)	0.23 (0.01, 0.45)
+ GT	0.68	0.59	0.77	0.02	0.24 (0.06,0.42)	0.08 (-0.04, 0.21)	0.32 (0.10, 0.54)
+ PLA2G7	0.70	0.61	0.79	0.04	0.22 (0.04, 0.40)	0.11 (-0.02, 0.23)	0.32 (0.10, 0.54)
+SCGB3A2	0.68	0.59	0.78	0.03	0.18 (-0.00, 0.37)	0.18 (0.06, 0.30)	0.36 (0.14, 0.58)
+ Protein score from all 8 proteins	0.70	0.61	0.79	0.04	0.46 (0.29, 0.62)	0.26 (0.14,0.38)	0.72 (0.51, 0.92)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, lipid lowering medication, and blood pressure lowering medication.

The proteins FAM3B, IL6, HGF, CCL25, GT, PLA2G7 and SCGB3A2 were each statistically significant (p-value<0.05) when added to the baseline model.

Protein score was statistically significant ($p < 0.00001$) when added to the baseline model. Odds ratio for protein score: 2.16 (CI: 1.57-2.96)

Integrated Discriminant Index when protein score was added to baseline model: 0.010 (0.07-0.12)

Table S10: Conditional logistic regression model of CVD on standardized protein score restricted to patients with smoking status reported at baseline. The sample size is 149 (50 CVD cases and 99 CVD controls). Here, we adjust for smoking status at baseline.

Variable	Odds Ratio	Std Error	Pr(> z)	LCI	UCI
CD4	1.00	0.00	0.62	1.00	1.00
RNA	1.00	0.00	0.56	1.00	1.00
Females vs Males	0.26	0.78	0.09	0.06	1.21
Age	1.25	0.11	0.04	1.01	1.53
BMI	1.06	0.06	0.34	0.95	1.18
Diabetes	0.63	0.93	0.62	0.10	3.90
Black Race	1.93	0.61	0.28	0.58	6.43
Lipid-lowering medication	1.42	0.71	0.63	0.35	5.71
BP-lowering medication	1.02	0.55	0.97	0.35	2.98
CVD	2.55	0.96	0.33	0.39	16.62
Smoking status (Yes vs No)	2.11	0.62	0.23	0.63	7.10
Protein Score	2.85	0.35	<0.01	1.45	5.63

Table S11: Incremental contribution of protein factors to CVD risk when added to baseline model that includes smoking status. The sample size is 149 (50 CVD cases and 99 CVD controls).

Model	AUC	LCI	UCI	Change in AUC from Baseline	NRI among cases	NRI among controls	Overall NRI
Baseline* (includes smoking status)	0.79	0.68	0.91	-	-	-	-
+ FAM3B	0.84	0.73	0.94	0.04	0.48(0.24,0.72)	0.07(-0.12,0.27)	0.55(0.24,0.86)
+ ITGA11	0.77	0.65	0.90	-0.02	0.24(-0.03,0.51)	0.05(-0.14,0.25)	0.29(-0.04,0.62)
+ IL6	0.77	0.65	0.90	-0.02	0.12(-0.16,0.40)	0.09(-0.10,0.29)	0.21(-0.13,0.55)
+ HGF	0.76	0.64	0.89	-0.03	0.28(0.01,0.55)	0.15(-0.04,0.34)	0.43(0.10,0.76)
+ CCL25	0.81	0.70	0.93	0.02	0.12(-0.16,0.40)	0.13(-0.06,0.32)	0.25(-0.08,0.59)
+ GT	0.81	0.70	0.93	0.02	0.08(-0.20,0.36)	0.11(-0.08,0.30)	0.19(-0.15,0.53)
+ PLA2G7	0.82	0.71	0.94	0.03	0.20(-0.07,0.47)	0.09(-0.10,0.29)	0.29(-0.04,0.62)
+SCGB3A2	0.77	0.65	0.89	-0.02	-0.12(-0.40,0.16)	0.13(-0.06,0.32)	0.01(-0.32,0.35)
+ Protein score from all 8 proteins	0.81	0.69	0.94	0.02	0.44(0.19,0.69)	0.19(0.00,0.38)	0.63 (0.32,0.95)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, prior history of CVD, lipid lowering medication, blood pressure lowering medication, and smoking status.

No individual protein was statistically significant ($p\text{-value} > 0.05$) when added to the baseline model that included smoking status.

Protein score was statistically significant ($p = 0.0025$) when added to the baseline model that included smoking status. Odds ratio for protein score: 2.56(CI: 1.39 – 4.70)

Integrated Discriminant Index when protein score was added to baseline model: 0.10 (0.05-0.14)

Table S12: Odds ratios and AUCs for discovery and validation sets.

Model	Discovery	Internal Validation
Baseline	0.69 (95% CI:0.60-0.78)	0.74 (95% CI: 0.73-0.74)
Baseline + Protein Score	0.73 (95% CI:0.65-0.81)	0.79 (95% CI: 0.78- 0.80)

Odds ratios for protein score in validation set is 2.78 (CI: 2.67, 2.90) and discovery set is 2.17 (CI: 1.58-2.99)

Baseline* is a model with the following variables: CD4, RNA, sex, age, BMI, diabetes status at baseline, prior history of CVD, lipid lowering medication, and blood pressure lowering medication,

Figure S1: Schematic representation of statistical approach

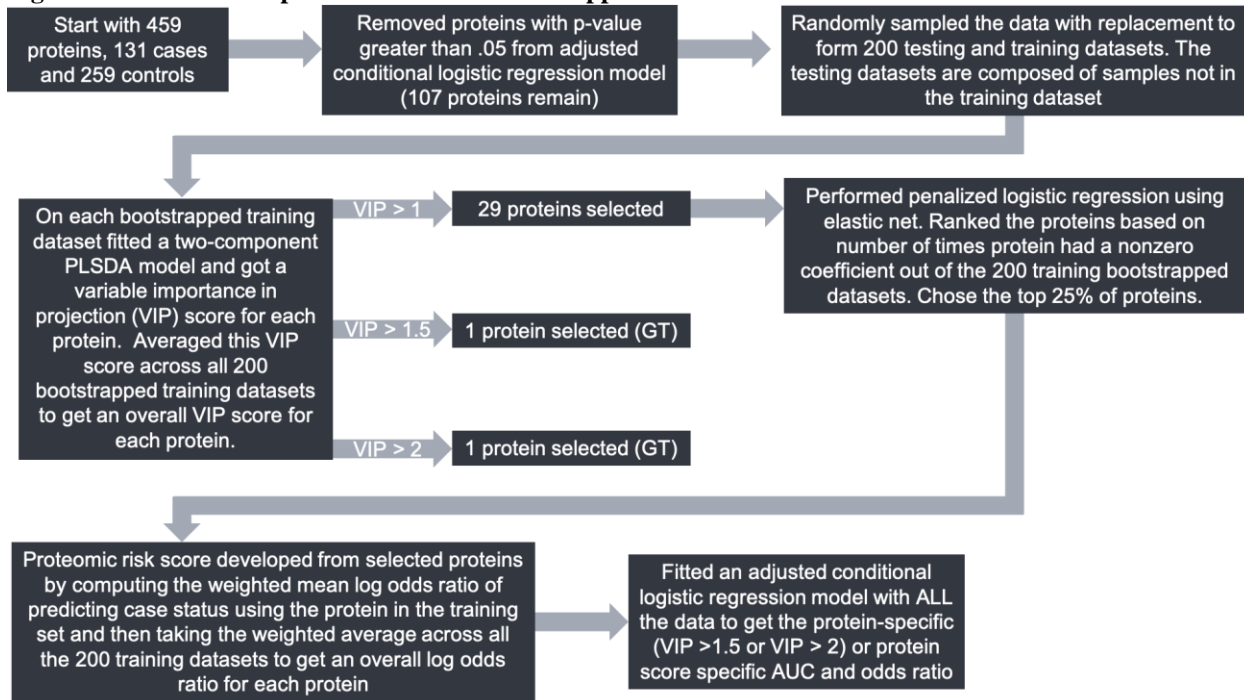
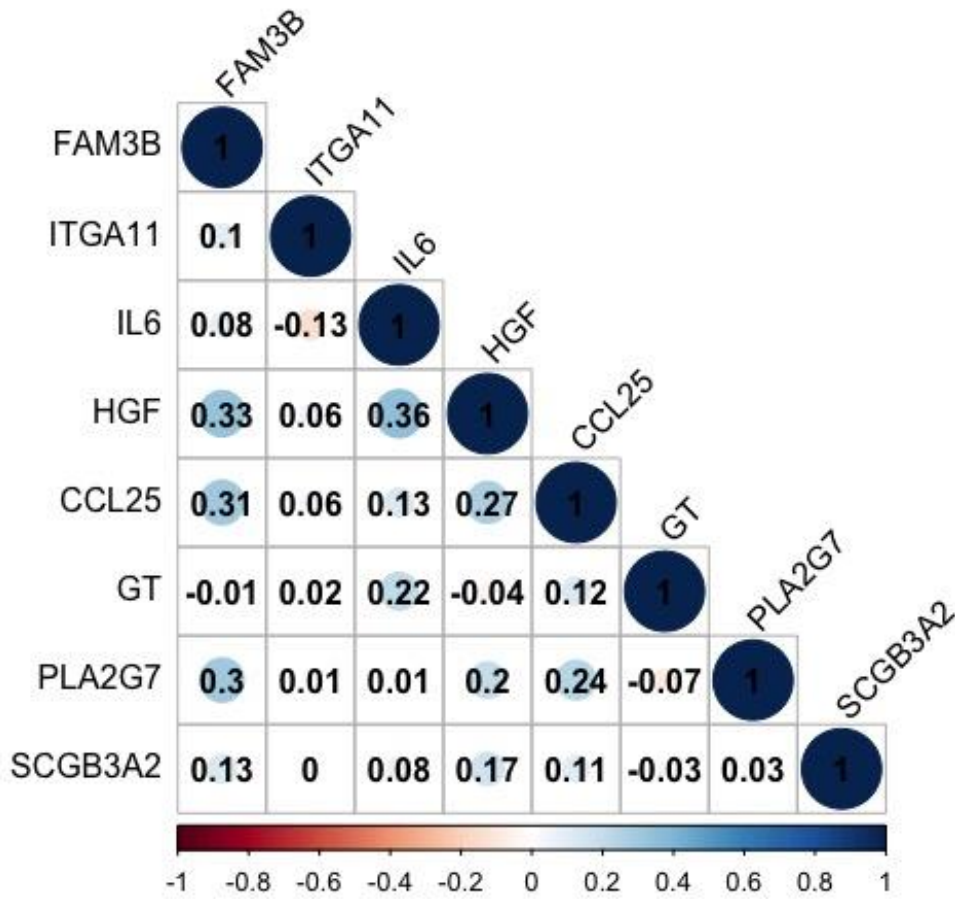


Figure S2: Correlation between pairs of proteins used in the protein score.



C. Description of Proteins Used in the Protein Score

Inflammation Panel:

Hepatocyte Growth Factor (HGF):

The protein HGF and its receptor c-MET are involved in tissue repair and respond to tissue injury. HGF has been proposed as a potential clinical biomarker for CVD⁴⁵ HGF has already been shown to be associated with stroke, CHD, atherosclerosis, and the progression of atherosclerosis in an ethnically diverse, general population.^{31,32}

C-C motif chemokine 25 (CCL25):

CCL-25 is involved in T-cell development. T-cells are involved in the development and progression of CVDs, including atherosclerosis.³⁶

Immune Response Panel:

Protein FAM3B (FAM3B):

Vascular smooth muscle cells (VSMCs) play an important role in the development of CVDs.³⁵ FAM3B is secreted with insulin and regulates glucose homeostasis. As such, dysregulation of FAM3B is associated with diabetes, which is a risk factor known to be associated with CVD.³⁵

Integrin α 11 (ITGA11):

Integrins have two functions: 1) extracellular matrix cell attachment and 2) signal transduction from the extracellular matrix.³⁷ In mouse models, overexpression of integrin α 11 induces cardiac fibrosis and left ventricular hypertrophy.³⁸

Interleukin-6 (IL6):

IL6 has been extensively studied in both healthy and HIV positive populations. IL6 is a marker of inflammation and coagulation. Increased levels of plasma IL6 has been shown to associated with increased risk of CVD, atherosclerosis, and mortality in an HIV positive population even when treated with ART^{17,29,30}

Cardiovascular 2 Panel:

Gastrotropin (GT):

Gastrotropin, also known as the ileal fatty acid binding protein, (FABP6) is a member of the fatty acid-binding protein (FABPs) family, which regulates general metabolic function via FABPs central role in fatty acid transport, metabolism, and storage. FABPs have been associated with a number of diseases including cardiovascular disease and are thought to serve an integral role in metabolic function.³⁹ FABP6 is more specifically known to be involved in bile acid metabolism. There has been shown to be a protective association between FABP6 Thr79Met polymorphism and incident type 2 diabetes.⁴⁰

Cardiovascular 3 Panel

Platelet-activating factor acetylhydrolase (PLA2G7):

PLA2G7 is found in both high-density lipoprotein (HDL) and low-density lipoprotein (LDL). In population studies it has been shown that overexpression of PLA2G7 is associated with increased coronary heart disease (CHD).^{33,34} It is thought that with individuals with low LDL cholesterol levels it can help predict CHD risk.^{33,34}

Cardiometabolic Panel

Secretoglobin Family 3A Member (SCGB3A2):

A case-control study in a Korean population on SNPs in the SCGB3A2 gene potentially contributes to susceptibility to asthma.⁴¹ The SCGB3A2 gene is also known as the uterus globulin associated protein 1 (UGRP1) found that UGRP1 may be able to predict graves' disease patients who develop hypothyroidism.⁴²

D. Sensitivity and Subgroup Analyses

When we added the inflammatory biomarkers D-dimer and hsCRP individually (as log₂-transformed measures) to the baseline model and we considered the protein score + baseline model, the protein score was again statistically significant ($p < 0.0001$) [Tables S6-S7]. Further, the AUCs and NRIs estimates from the baseline + protein score model were again higher than those from the baseline + individual proteins models. With the exception of the protein SCGB3A2, the proteins FAM3B, IL-6, HGF, GT, and PLA2G7 were each statistically significant (p -value < 0.05) when added to the baseline model.

Considering the 269 participants with complete data (92 cases and 177 controls) who were on ART at baseline, we observed that a one standard deviation increase in the protein score was associated with an odds ratio for CVD of 1.93 (CI: 1.35 - 2.78) [Table S8] compared to 2.17 (CI: 1.58 - 2.99) [Figure 1] in the combined data (i.e. data on those with ART and no ART at baseline). Unlike in the combined data where IL6 was likely driving the effect of the protein score, in this subpopulation, no individual protein had an AUC that was comparable to the protein score (Table S8). Further, the AUC for the baseline model was 0.70 (CI: 0.60- 0.80), and the AUC for the baseline + protein score model was 0.74 (CI: 0.64 - 0.83). There was a 16.7% increase in prediction when the analysis was restricted to those on ART at baseline, compared to a 17.4% increase in prediction for the full population. The NRI for the protein score + baseline model was 0.45 (CI: 0.20 - 0.69) in this subgroup as compared to 0.66 (CI: 0.46 - 0.86) in the combined data. Table S8 gives the NRI and IDI estimate for the protein score + baseline model restricted to individuals on ART at baseline as well as the incremental contributions of each protein.

When we restricted our analyses to individuals with no history of CVD ($n=356$, 110 cases and 246 controls), the protein score was again statistically significant (Table S9). A one standard deviation increase in the protein score was associated with an odds ratio for CVD of 2.16 (CI: 1.57-2.96) compared to 2.17 (CI: 1.58 - 2.99) in the combined data. The AUC for the baseline model was 0.66 (CI: 0.56-0.75). The AUC when PLA2G7 was added to the baseline model was the same as the AUC when the protein score was added to the baseline model (0.70) but the protein score + baseline model had a higher NRI (0.72 vs 0.32); the NRI for the full population was 0.66 (CI: 0.46 - 0.86).

We considered a sensitivity analysis that included individuals with smoking status. Here, the sample size was 149 with 50 CVD cases and 99 CVD controls. When we added smoking status to the baseline model, the protein score from the protein score + baseline model was statistically significant (p -value = 0.0024) [Table S10]. On the other hand, no individual protein achieved statistical significance when each was added to the baseline model that included smoking status as a covariate. A one standard deviation increase in the protein score was associated with an odds ratio for CVD of 2.85 (CI: 1.45- 5.63). The AUC for the baseline model was 0.79 (CI: 0.68- 0.91), and the AUC for the baseline + protein score model was 0.81 (CI: 0.69 - 0.94). This corresponded to a 6.8% increase in prediction compared to a 17.4% increase for the full population. Further, FAM3B, CCL25, GT, and PLA2G7 had AUC values that were similar or slightly higher than the AUC from the protein score + baseline model (Table S11). However, the NRI for these individual proteins were lower than the NRI from the baseline + protein score model.