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**Supplemental Methods**

**Measurement of Candidate Predictor Variables**

Candidate predictor variables considered for inclusion in the prediction models are displayed in eFigure 1. Candidate variables included those in the ACC/AHA PCEs1: age, sex, race/ethnicity, total cholesterol, high-density lipoprotein (HDL) cholesterol, systolic blood pressure (BP), use of BP-lowering medications, history of diabetes, and current smoking. Additional candidate variables were chosen based on associations with ASCVD among patients with CKD identified in prior reports, and included: metabolic factors (body mass index, hemoglobin A1c [HbA1c], use of glucose-lowering medications, insulin, uric acid, homocysteine); kidney disease factors (eGFR [cystatin C-based CKD-EPI equation], urinary albumin-to-creatinine ratio [ACR], hemoglobin, urea nitrogen, serum albumin, bicarbonate, urinary neutrophil gelatinase-associated lipocalin [NGAL]); lipid metabolism factors (low-density lipoprotein [LDL] cholesterol, very-LDL cholesterol, triglycerides, use of statin medications, apolipoprotein A1, apolipoprotein B); vascular factors (diastolic BP, ankle-brachial index [ABI]); mineral metabolism factors (calcium, phosphate, fibroblast growth factor-23); inflammation factors (white blood cell count, high-sensitivity c-reactive protein, fibrinogen, tumor necrosis factor-α, interleukin-6, interleukin-1 receptor antagonist, interleukin-1 β); and cardiac biomarkers (high-sensitivity troponin-T, troponin-I, N-terminal prohormone of brain natriuretic peptide [NT-proBNP]). We considered two sets of variables for development of the prediction models: one set including only readily clinically available variables (eFigure 1; black text) and another set containing all candidate predictor variables, including biomarkers that are less likely to be measured in routine clinical practice (eFigure 1; blue text). In a secondary analysis, we evaluated the performance of the “CKD Patch”, which incorporates eGFR and urinary albumin-to-creatinine ratio (ACR) measurements into the ACC/AHA PCEs.2 Specifically, the ACC/AHA PCEs were recalibrated to the CRIC Study sample by fitting a new Cox model with the log-transformed PCEs predicted risk as the only independent variable.3 Then, the published CKD Patch equations were applied to the recalibrated PCEs, with expected eGFR and urinary ACR centered at CRIC Study-specific averages.

Demographic information, medical history, and medication use were collected via self-reported questionnaire. We defined history of cardiovascular disease as self-reported prior coronary artery disease, heart failure, stroke, or peripheral artery disease. Body weight, height, and blood pressure (BP) were measured using standard protocols.4 Body mass index was quantified as weight in kilograms divided by height in meters squared. Ankle-brachial index (ABI) was measured using a standard protocol and the leg-specific ABI was calculated by dividing the higher systolic BP in the posterior tibial or dorsalis pedis by the higher of the right or left brachial systolic BP.5

Cholesterol, glucose, hemoglobin A1c (HbA1c), insulin, uric acid, serum creatinine, hemoglobin, urea nitrogen, serum albumin, bicarbonate, calcium, and phosphate were measured using standard laboratory methods. Urinary albumin was measured by radioimmunoassay. Apolipoprotein A1 and apolipoprotein B were measured using immunoturbidimetric assays. High-sensitive C-reactive protein (hsCRP), interleukin-6 (IL-6), tumor necrosis factor-α (TNF-α), homocysteine, and cystatin C were measured using the particle enhanced immunonephelometry method. Fibrinogen was measured using the immunochemical reaction method. Fibroblast growth factor-23 was measured by a second-generation C-terminal assay (Immutopics). Sandwich ELISAs (Quantikine HS; R&D Systems) were used to quantify interleukin-1 β and interleukin-1 receptor antagonist. Urinary neutrophil gelatinase-associated lipocalin (NGAL) was measured with a 2-step assay using chemiluminescent microparticle immunoassay technology on an ARCHITECT i2000SR (Abbott Laboratories). High-sensitivity troponin-T, troponin-I, and N-terminal prohormone of brain natriuretic peptide (NT-proBNP) were measured using chemiluminescent microparticle immunoassay technology on an Elecsys 2010 at the University of Maryland.

**Model Development**

 A priori, we evaluated the ACC/AHA PCEs in the CRIC sample using 2 approaches: 1) predicted risk from the published model coefficients1; and 2) variables included in the ACC/AHA PCEs with coefficients recalculated using the CRIC sample. Additionally, we evaluated several modeling algorithms and selection procedures to develop the final models. Our primary approach used Cox proportional hazards regression models to predict the probability of having an incident ASCVD event within 10 years of baseline.1 As a secondary approach, we used the Fine & Gray subdistribution hazards model to account for the competing risk of death.6 Within both modeling algorithms, we evaluated 3 predictor selection procedures. The first two procedures used 1) backward elimination with a *P*<0.05 criterion; and 2) backward elimination with an AIC criterion. The third procedure employed LASSO (“least absolute shrinkage and selection operator”).7 We tuned the LASSO model using cross-validation, and identified the regularization penalty that minimized cross-validated error (i.e., λ=minimum). To select parsimonious models with similar predictive performance to models utilizing λ=minimum, we used a regularization penalty one standard error higher than that which minimized cross-validated error, as recommended.8

**Model Validation**

All modeling strategies were internally validated using 10x10-fold cross-validation, similar to the ACC/AHA PCEs.1 Cross-validation is an extension of split sample testing, which divides available data into training and testing sets, then fits a model to the training data and evaluates the model in the testing data. Cross-validation extends split sample testing by dividing available data into at least 2 non-overlapping subsets, then using each subset once as a testing set and remaining subsets for training. Repeating the cross-validation procedure with different subsets enhances the precision of model performance estimates. The best-performing modeling procedure was used on the full CRIC sample to develop final clinical and biomarker-enriched models. In a sensitivity analysis, we evaluated the best-performing modeling procedure from the 10x10-fold cross-validation using an internal-external validation approach. In this approach, one clinical center is used as testing data while the others are training data, which provides additional information on the potential performance of the models in external datasets similar in composition to the CRIC Study sample.9

We validated our models externally using data from two independent, community-based prospective cohort studies. The Atherosclerosis Risk in Communities (ARIC) study is an ongoing population-based prospective study of 15,792 mostly white and black participants aged 45-64 years recruited from four US communities during 1987-1989. We included participants who attended Visit 4 (1996-1998) to maximize available data on novel predictors. The participants were through 2019 for validated incident CVD events and deaths.8 A total of 875 individuals with CKD, based on an eGFR <60 mL/min/1.73 m2 or urinary ACR ≥30 mg/g, were included in the external validation analyses. Incident CVD events and deaths were adjudicated by the Morbidity and Mortality Classification Committee.10

The Multi-Ethnic Study of Atherosclerosis (MESA) is a prospective cohort study of 6,814 persons aged 45-84 years without known CVD at baseline from six US communities.11 Participants were recruited during 2000-2002. A total of 1,347 individuals with CKD, based on an eGFR <60 mL/min/1.73 m2 or urinary ACR ≥30 mg/g, were included in the external validation analyses. Incident CVD events and deaths were independently classified by two physicians who were members of the MESA mortality and morbidity review committee.12

**Performance Metrics**

We evaluated the performance of developed models using measures of discrimination, calibration, and overall goodness of fit.13 Discrimination refers to the ability of a model to correctly identify those who will or will not experience an ASCVD event in a specific time interval (i.e., 10 years) and was assessed using the time-dependent area under the receive operating characteristic curve (AUC).14 Calibration refers to the agreement between observed outcomes and predictions provided by a given model and was assessed by plotting the observed vs. predicted risk across deciles of predicted risk. Observed risk was estimated using the cumulative incidence function accounting for the competing risk of death. The scaled Brier score, or index of prediction accuracy [IPA], incorporates information on both discrimination and calibration and is analogous to the proportion of explained variance in linear regression. An IPA of 0 indicates model accuracy is equivalent to that of a Kaplan-Meier curve, whereas an IPA of 1 indicates perfect risk prediction.15 We used the net reclassification improvement (NRI) statistic to evaluate the clinical utility of the developed models,16 using predicted risk thresholds used in current clinical practice guidelines (i.e., 7.5% and 20% per the ACC/AHA Primary Prevention Guideline).17 Bootstrapping with 1000 replicates was used to generate 95% confidence intervals [CIs] for the NRI.

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**Supplemental Figure 1.** Candidate Predictor Variables Considered for Inclusion in Prediction Models



Predictors highlighted in blue indicate biomarkers included for development of the biomarker-enriched model

**Supplemental Figure 2.** Calibration Slope Plots of Cox Proportional Hazards and Fine-Gray Subdistribution Hazards Modeling Algorithms

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\*The Aalen-Johansen estimator calculates cumulative incidence taking into consideration the competing risk of death. Results were obtained by aggregating predicted probabilities from 10x10 fold cross-validation and then assessing their calibration versus observed events.

**Supplemental Figure 3.** Calibration of the ACC/AHA Pooled Cohort Equations in the CRIC Study

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Observed probability was estimated using the cumulative incidence function accounting for the competing risk of death. Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; CRIC = Chronic Renal Insufficiency Cohort Study

**Supplemental Figure 4.** Prediction Performance of the CKD Patch in the CRIC Study

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Observed probability was estimated using the cumulative incidence function accounting for the competing risk of death. The CKD Patch was applied as recommended (Matsushita K, et al. EClinicalMedicine. 2020 Oct;27:100552): the ACC/AHA PCEs were recalibrated to the CRIC Study sample by fitting a new Cox model with the log-transformed PCEs predicted risk as the only independent variable (Steyerberg EW. Clinical Prediction Models. New York: Springer, 2019). Then, the published CKD Patch equations were applied to the recalibrated PCEs, with expected estimated glomerular filtration rate and urinary albumin-to-creatinine ratio centered at CRIC Study-specific averages. Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; AUC = area under the ROC curve; CKD = chronic kidney disease; CRIC = Chronic Renal Insufficiency Cohort Study; IPA = index of prediction accuracy

**Supplemental Figure 5.** Prediction Performance of Novel CRIC Study Models by CKD Stage

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Observed probability was estimated using the cumulative incidence function accounting for the competing risk of death. Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; AUC = area under the ROC curve; CKD = chronic kidney disease; CRIC = Chronic Renal Insufficiency Cohort Study; IPA = index of prediction accuracy

**Supplemental Figure 6.** Prediction Performance of Novel CRIC Study Models in External Validation Data

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Observed probability was estimated using the cumulative incidence function accounting for the competing risk of death. Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; ARIC, Atherosclerosis Risk in Communities Study; ASCVD, atherosclerotic cardiovascular disease; AUC = area under the ROC curve; CKD = chronic kidney disease; CRIC = Chronic Renal Insufficiency Cohort Study; IPA = index of prediction accuracy; MESA, Multi-Ethnic Study of Atherosclerosis

**Supplemental Table 1**. Discrimination and Index of Prediction Accuracy for 10-year Risk Prediction of Atherosclerotic Cardiovascular Disease

|  |  |  |
| --- | --- | --- |
| **Candidate Variables andSelection Procedures** | **Cox ProportionalHazards Regression** | **Fine & Gray SubdistributionHazards Model** |
| **AUC (95% CI) \*** | **IPA (95% CI) \*** | **AUC (95% CI) \*** | **IPA (95% CI) \*** |
| **ACC/AHA PCEs (CRIC Coefficients)** | 0.736 (0.649, 0.826) | 0.072 (-0.016, 0.137) | 0.732 (0.635, 0.821) | 0.060 (-0.003, 0.107) |
| **Traditional Candidate Variables** |  |  |  |  |
| *Backward Elimination, P<0.05* | 0.760 (0.678, 0.851) | 0.095 (0.013, 0.173) | 0.743 (0.645, 0.837) | 0.068 (0.011, 0.119) |
| *Backward Elimination, AIC* | 0.753 (0.656, 0.835) | 0.089 (0.007, 0.164) | 0.740 (0.630, 0.831) | 0.067 (0.011, 0.123) |
| *LASSO, λ=1 SE* | 0.748 (0.662, 0.848) | 0.060 (0.024, 0.109) | 0.731 (0.627, 0.833) | 0.063 (0.009, 0.119) |
| **All Candidate Variables** |  |  |  |  |
| *Backward Elimination, P<0.05* | 0.771 (0.674, 0.853) | 0.105 (0.033, 0.168) | 0.754 (0.664, 0.832) | 0.072 (0.022, 0.118) |
| *Backward Elimination, AIC* | 0.768 (0.664, 0.847) | 0.099 (0.015, 0.172) | 0.754 (0.651, 0.828) | 0.074 (0.023, 0.127) |
| *LASSO, λ=1 SE* | 0.760 (0.659, 0.845) | 0.075 (0.032, 0.121) | 0.751 (0.652, 0.839) | 0.070 (0.017, 0.123) |

Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; AIC = Akaike information criterion; AUC = area under the ROC curve; CI = confidence interval; IPA = index of prediction accuracy; LASSO = least absolute shrinkage and selection operator; NRI = net reclassification improvement (compared with published ACC/AHA PCEs); SE = standard error

\* AUC and IPA point and interval estimates were obtained using 10x10 fold cross-validation. Higher values for the AUC and IPA indicate better performing models. NRI is in comparison to the published ACC/AHA PCEs as the base model.

**Supplemental Table 2**. Internal-External Validation of 10-year Risk Prediction of Atherosclerotic Cardiovascular Disease in the CRIC Study

|  |  |  |
| --- | --- | --- |
| **Candidate Variables andSelection Procedures** | **10x10-fold Internal Cross-validation** | **Internal-external Validation** |
| **AUC (95% CI) \*** | **IPA (95% CI) \*** | **AUC (95% CI) \*** | **IPA (95% CI) \*** |
| **ACC/AHA PCEs (CRIC Coefficients)** | 0.736 (0.649, 0.826) | 0.072 (-0.016, 0.137) | 0.738 (0.655, 0.839) | 0.068 (0.010, 0.116) |
| **Traditional Candidate Variables** | 0.760 (0.678, 0.851) | 0.095 (0.013, 0.173) | 0.762 (0.705, 0.861) | 0.089 (0.035, 0.137) |
| **All Candidate Variables** | 0.771 (0.674, 0.853) | 0.105 (0.033, 0.168) | 0.776 (0.701, 0.868) | 0.102 (0.019, 0.142) |

Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; AUC = area under the ROC curve; CI = confidence interval; IPA = index of prediction accuracy

\* Models were fit using Cox proportional hazards regression and variables selected using backward elimination with a criterion of *P*<0.05. Higher values for the AUC and IPA indicate better performing models.

**Supplemental Table 3.** Example Calculations of Predicted 10-year Risk of ASCVD (ACC/AHA PCEs Variables)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variables** | **ModelCoefficients** | **Example Patient 1** | **Example Patient 2** | **Example Patient 3** |
| **Patient Values** | **Coefficients** **× Values\*** | **PatientValues** | **Coefficients × Values\*** | **PatientValues** | **Coefficients × Values\*** |
| Age (years) | 0.0275 | 65 | 1.7875 | 47 | 1.2925 | 54 | 1.4850 |
| Sex (1 if male) | 0.0900 | 1 | 0.0900 | 1 | 0.0900 | 1 | 0.0900 |
| Race (1 if black) | 0.1885 | 1 | 0.1885 | 0 | 0 | 0 | 0 |
| Total cholesterol (mg/dL) | 0.0020 | 202 | 0.4040 | 208 | 0.4160 | 149 | 0.2980 |
| HDL cholesterol (mg/dL) | -0.0134 | 47 | -0.6298 | 60 | -0.8040 | 34 | -0.4556 |
| Systolic BP (mm Hg) | 0.0126 | 173.33 | 2.1840 | 121.33 | 1.5288 | 148.67 | 1.8732 |
| BP-lowering medications (1 if yes) | 0.4342 | 1 | 0.4342 | 1 | 0.4342 | 1 | 0.4342 |
| History of diabetes (1 if yes) | 0.6300 | 1 | 0.6300 | 0 | 0 | 1 | 0.6300 |
| Current smoking (1 if yes) | 0.7382 | 0 | 0 | 0 | 0 | 1 | 0.7382 |
| **Risk Calculation** |
| Sum |   |   | 5.0884 |   | 2.9575 |   | 5.0930 |
| Probability (ASCVD event) |   |   | 0.3322 |   | 0.0468 |   | 0.3335 |
| 10-year risk, % |   |   | 33.22% |   | 4.68% |   | 33.35% |

ASCVD = atherosclerotic cardiovascular disease; BP = blood pressure; HDL = high density lipoprotein; LDL = low density lipoprotein

\* The 10-year risk can be calculated as 1–0.9045exp(ΣbX–3.6963) where b is the regression coefficient (beta) and X is the level for each risk factor.

**Supplemental Table 4.** Example Calculations of Predicted 10-year Risk of ASCVD (CRIC Clinical Model)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variables** | **ModelCoefficients** | **Example Patient 1** | **Example Patient 2** | **Example Patient 3** |
| **Patient Values** | **Coefficients × Values\*** | **PatientValues** | **Coefficients × Values\*** | **PatientValues** | **Coefficients × Values\*** |
| Age (years) | 0.0420 | 65 | 2.7300 | 47 | 1.9740 | 54 | 2.2680 |
| HDL cholesterol (mg/dL) | -0.0127 | 47 | -0.5969 | 60 | -0.7620 | 34 | -0.4318 |
| Systolic BP (mm Hg) | 0.0077 | 173.33 | 1.3346 | 121.33 | 0.9342 | 148.67 | 1.1448 |
| Current smoking (1 if yes) | 0.7086 | 0 | 0 | 0 | 0 | 1 | 0.7086 |
| Log (urine ACR) (mg/g) | 0.1553 | Log (33.83) | 0.5469 | Log (49.22) | 0.6051 | Log (2151.5) | 1.1918 |
| Hemoglobin A1c (%) | 0.1634 | 6.1 | 0.9967 | 5.1 | 0.8333 | 6 | 0.9804 |
| Hemoglobin (g/dL) | -0.0903 | 10.8 | -0.9752 | 14.2 | -1.2823 | 9.6 | -0.8669 |
| **Risk Calculation** |
| Sum |   |   | 4.0361 |   | 2.3024 |   | 4.9948 |
| Probability (ASCVD event) |   |   | 0.1788 |   | 0.0342 |   | 0.4018 |
| 10-year risk, % |   |   | 17.88% |   | 3.42% |   | 40.18% |

ACR = albumin-to-creatinine ratio; ASCVD = atherosclerotic cardiovascular disease; BP = blood pressure; HDL = high density lipoprotein

\* The 10-year risk can be calculated as 1–0.9075exp(ΣbX–3.3283) where b is the regression coefficient (beta) and X is the level for each risk factor.

**Supplemental Table 5.** Example Calculations of Predicted 10-year Risk of ASCVD (CRIC Enriched Model)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variables** | **ModelCoefficients** | **Example Patient 1** | **Example Patient 2** | **Example Patient 3** |
| **Patient Values** | **Coefficients × Values\*** | **PatientValues** | **Coefficients × Values\*** | **PatientValues** | **Coefficients × Values\*** |
| Age (years) | 0.0347 | 65 | 2.2555 | 47 | 1.6309 | 54 | 1.8738 |
| Total cholesterol (mg/dL) | 0.0073 | 202 | 1.4746 | 208 | 1.5184 | 149 | 1.0877 |
| HDL cholesterol (mg/dL) | -0.0164 | 47 | -0.7708 | 60 | -0.9840 | 34 | -0.5576 |
| Current smoking (1 if yes) | 0.6615 | 0 | 0 | 0 | 0 | 1 | 0.6615 |
| Log (urine ACR) (mg/g) | 0.1127 | Log (33.83) | 0.3969 | Log (49.22) | 0.4391 | Log (2151.5) | 0.8649 |
| Hemoglobin A1c (%) | 0.1616 | 6.1 | 0.9858 | 5.1 | 0.8242 | 6 | 0.9696 |
| Apolipoprotein B (mg/dL) | -0.0121 | 101 | -1.2221 | 76 | -0.9196 | 82 | -0.9922 |
| Log (hsCRP) (pg/mL) | 0.1045 | Log (6.23) | 0.1912 | Log (1.42) | 0.0366 | Log (0.92) | -0.0087 |
| Log (troponin-T) (pg/mL) | 0.2090 | Log (15.40) | 0.5715 | Log (11.33) | 0.5073 | Log (13.21) | 0.5394 |
| Log (NT-proBNP) (pg/mL) | 0.2011 | Log (460.7) | 1.2333 | Log (29.55) | 0.6809 | Log (259.2) | 1.1176 |
| **Risk Calculation** |
| Sum |   |   | 5.1158 |   | 3.7339 |   | 5.5560 |
| Probability (ASCVD event) |   |   | 0.1519 |   | 0.0405 |   | 0.2257 |
| 10-year risk, % |   |   | 15.19% |   | 4.05% |   | 22.57% |

ACR = albumin-to-creatinine ratio; ASCVD = atherosclerotic cardiovascular disease; eGFR = estimated glomerular filtration rate; HDL = high density lipoprotein; hsCRP, high-sensitivity C-reactive protein; NT-proBNP = N-terminal prohormone of brain natriuretic peptide

\* The 10-year risk can be calculated as 1–0.9100exp(ΣbX–4.5580) where b is the regression coefficient (beta) and X is the level for each risk factor.

**Supplemental Table 6.** Baseline Characteristics of Development (CRIC Study) and External Validation (ARIC and MESA) Cohort Participants

|  |  |  |
| --- | --- | --- |
| **Variables** | **CRIC Study(n=2,604)** | **ARIC + MESA(n=2,222)** |
| Age, mean (SD), years | 55.8 (11.7) | 67.2 (8.5) |
| Male, No. (%) | 1354 (52.0) | 993 (44.7) |
| Black race, No. (%) | 1013 (38.9) | 686 (30.9) |
| Body mass index, mean (SD), kg/m2 | 31.7 (7.8) | 29.3 (6.0) |
| Current smoking, No. (%) | 314 (12.1) | 307 (13.9) |
| Hemoglobin A1c, mean (SD), % | 6.4 (1.5) | 6.1 (1.5) |
| Diabetes mellitus, No. (%) | 1082 (41.6) | 615 (27.8) |
| Use of glucose-lowering medications, No. (%) | 620 (24.0) | 466 (21.2) |
| Systolic blood pressure, mean (SD), mm Hg | 127.0 (21.0) | 137.7 (23.2) |
| Diastolic blood pressure, mean (SD), mm Hg | 72.7 (12.4) | 73.1 (11.7) |
| Use of blood pressure-lowering medications, No. (%) | 2282 (87.6) | 1314 (59.4) |
| Total cholesterol, mean (SD), mg/dL | 188.4 (44.5) | 197.6 (40.2) |
| LDL cholesterol, mean (SD), mg/dL | 106.6 (35.3) | 118.5 (34.6) |
| HDL cholesterol, mean (SD), mg/dL | 48.8 (16.1) | 49.6 (15.7) |
| Apolipoprotein B, mean (SD), mg/dL | 85.6 (24.4) | 89.7 (27.0) |
| Use of statin medications, No. (%) | 1184 (45.8) | 411 (18.5) |
| Estimated glomerular filtration rate, mean (SD), mL/min/1.73 m2 \* | 56.0 (24.7) | 70.1 (24.3) |
| Urine ACR, median [IQR], mg/g | 39.1 [7.3, 391.2] | 38.4 [7.0, 100.0] |
| Hemoglobin, mean (SD), g/dL | 12.7 (1.8) | 13.3 (1.6) |
| High-sensitivity C-reactive protein, median [IQR], mg/L | 2.4 [1.0, 6.1] | 2.8 [1.2, 6.2] |
| Troponin-T, median [IQR], pg/mL | 9.7 [4.5, 18.9] | 9.0 [9.0, 9.0] |
| NT-proBNP, median [IQR], pg/mL | 106.5 [49.3, 249.7] | 98.2 [44.6, 213.1] |
| ASCVD Events within 10 years, No. (%) | 252 | 337 |
| Deaths within 10 years, No. (%) | 411 | 354 |
| Observed 10-year Risk of ASCVD, % | 10.5% | 15.5% |

Abbreviations: ACR, albumin-to-creatinine ratio; ARIC, Atherosclerosis Risk in Communities Study; ASCVD, atherosclerotic cardiovascular disease; CRIC, Chronic Renal Insufficiency Cohort; HDL, high density lipoprotein; IQR, interquartile range; LDL, low density lipoprotein; SD, standard deviation; MESA, Multi-Ethnic Study of Atherosclerosis; NT-proBNP, N-terminal prohormone of brain natriuretic peptide

\* Calculated using the CKD-EPI equation for comparison across the CRIC Study and external validation cohorts

**Supplemental Table 7.** Reclassification of Events for Risk Prediction Models for ASCVD in CKD

|  |  |  |
| --- | --- | --- |
|  |  | **No. of Participants Reclassified** |
|  |  | **Model 1** | **Model 2** | **Model 3** |
|  | *Cut Points* | *<7.5%* | *7.5-19.9%* | *≥20.0%* | *<7.5%* | *7.5-19.9%* | *≥20.0%* | *<7.5%* | *7.5-19.9%* | *≥20.0%* |
| **ACC/AHAPCEs** | *<7.5%* | 30 | 17 | 0 | 27 | 14 | 6 | 24 | 14 | 9 |
| *7.5-19.9%* | 1 | 82 | 7 | 6 | 63 | 21 | 6 | 58 | 26 |
| *≥20.0%* | 0 | 48 | 67 | 3 | 43 | 69 | 0 | 45 | 70 |
| **Model 1** | *<7.5%* |  |  |  | 23 | 8 | 0 | 20 | 10 | 1 |
| *7.5-19.9%* |  |  |  | 12 | 99 | 36 | 10 | 85 | 52 |
| *≥20.0%* |  |  |  | 1 | 13 | 60 | 0 | 22 | 52 |
| **Model 2** | *<7.5%* |  |  |  |  |  |  | 25 | 11 | 0 |
| *7.5-19.9%* |  |  |  |  |  |  | 5 | 89 | 26 |
| *≥20.0%* |  |  |  |  |  |  | 0 | 17 | 79 |

Models specified in the columns are compared to models specified in the rows for reclassification of events using cut points of 7.5% and 20%.

Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; ASCVD = atherosclerotic cardiovascular disease; CKD = chronic kidney disease

**Supplemental Table 8.** Reclassification of Non-events for Risk Prediction Models for ASCVD in CKD

|  |  |  |
| --- | --- | --- |
|  |  | **No. of Participants Reclassified** |
|  |  | **Model 1** | **Model 2** | **Model 3** |
|  | ***Cut Points*** | *<7.5%* | *7.5-19.9%* | *≥20.0%* | *<7.5%* | *7.5-19.9%* | *≥20.0%* | *<7.5%* | *7.5-19.9%* | *≥20.0%* |
| **ACC/AHAPCEs** | *<7.5%* | 621 | 159 | 0 | 614 | 161 | 5 | 610 | 159 | 11 |
| *7.5-19.9%* | 74 | 462 | 13 | 169 | 334 | 46 | 205 | 296 | 48 |
| *≥20.0%* | 0 | 122 | 114 | 6 | 140 | 90 | 17 | 152 | 67 |
| **Model 1** | *<7.5%* |  |  |  | 598 | 96 | 1 | 584 | 109 | 2 |
| *7.5-19.9%* |  |  |  | 191 | 488 | 64 | 245 | 427 | 71 |
| *≥20.0%* |  |  |  | 0 | 51 | 76 | 3 | 71 | 53 |
| **Model 2** | *<7.5%* |  |  |  |  |  |  | 697 | 92 | 0 |
| *7.5-19.9%* |  |  |  |  |  |  | 135 | 464 | 36 |
| *≥20.0%* |  |  |  |  |  |  | 0 | 51 | 90 |

Models specified in the columns are compared to models specified in the rows for reclassification of non-events using cut points of 7.5% and 20%.

Abbreviations: ACC/AHA PCEs = American College of Cardiology/American Heart Association Pooled Cohort Equations; ASCVD = atherosclerotic cardiovascular disease; CKD = chronic kidney disease