SUPPLEMENTARY MATERIAL

Hijazi et al.

A biomarker-based risk score to predict risk of death in patients with atrial fibrillation: The ABC (Age, Biomarkers, Clinical history) risk score

TABLE OF CONTENTS

Supplementary Table I
C-indices for all-cause mortality according to the different ABC-risk scores; ABC-death, ABC-stroke, and ABC-bleeding

Supplementary Table II
C-indices for all-cause mortality according to the different ABC-risk scores; ABC-death, ABC-stroke, and ABC-bleeding

Supplementary Table III
Event rates and hazard ratios between ABC-death risk classes for the derivation and the validation cohorts

Supplementary Table IV
C-indices for the contemporary ABC-death score without GDF-15 in the full cohorts and in subgroups for (A) all-cause mortality and (B) cardiovascular mortality

Supplementary Figure I
Calibration of the ABC-death model for all-cause mortality

Supplementary Figure II
Kaplan–Meier estimated cumulative event rate by randomized treatment (colour) by predicted ABC-death risk classes (panel): 0-1%, 1–2%, and ≥2%

Supplementary Figure III
Nomogram for the ABC-death for cardiovascular mortality

Supplementary Figure IV
Cumulative risk of cardiovascular death by predicted 1-year ABC-death risk group for the derivation (dashed lines, n=14,611) and the validation (solid lines, n=8,548) data

Supplementary Figure V
Decision curve analysis for cardiovascular mortality

Supplementary Figure VI
Nomogram for the ABC-death score using cTnI (instead of cTnT)
**Supplementary Figure VII**
Nomogram for the ABC-death without GDF-15 for cardiovascular mortality

**Supplementary Figure VIII**
Nomogram for the ABC-death without GDF-15 for all-cause mortality

**Supplementary Figure IX**
Exemplified application of the nomogram

**Summary of the derivation and validation cohorts and Statistical methods (detailed)**

**ABC-death score equations**
**Supplementary Table I**

C-indices for all-cause mortality according to the different ABC-risk scores; ABC-death, ABC-stroke, and ABC-bleeding

<table>
<thead>
<tr>
<th></th>
<th>Full cohort</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Derivation cohort</strong></td>
<td></td>
</tr>
<tr>
<td>ABC-death</td>
<td>0.74 [0.73, 0.76]</td>
</tr>
<tr>
<td>ABC-stroke</td>
<td>0.68 [0.67, 0.70]</td>
</tr>
<tr>
<td>ABC-bleeding</td>
<td>0.70 [0.68, 0.72]</td>
</tr>
<tr>
<td>CHA$_2$DS$_2$-VASc</td>
<td>0.59 [0.57, 0.61]</td>
</tr>
</tbody>
</table>

| **Validation cohort** |          |
| ABC-death             | 0.74 [0.72, 0.76] |
| ABC-stroke            | 0.67 [0.65, 0.69] |
| ABC-bleeding          | 0.70 [0.68, 0.73] |
| CHA$_2$DS$_2$-VASc    | 0.58 [0.56, 0.61] |
Supplementary Table II
C-indices for all-cause mortality according to the different ABC-risk scores; ABC-death, ABC-stroke, and ABC-bleeding

<table>
<thead>
<tr>
<th></th>
<th>Derivation cohort</th>
<th>Validation cohort</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABC-death score</td>
<td>0.74 [0.73, 0.76]</td>
<td>0.74 [0.72, 0.76]</td>
</tr>
<tr>
<td>ABC-stroke score</td>
<td>0.68 [0.67, 0.70]</td>
<td>0.67 [0.65, 0.69]</td>
</tr>
<tr>
<td>ABC-bleeding score</td>
<td>0.70 [0.68, 0.72]</td>
<td>0.70 [0.68, 0.73]</td>
</tr>
</tbody>
</table>
# Supplementary Table III

Event rates and hazard ratios between ABC-death risk classes for the derivation and the validation cohorts

<table>
<thead>
<tr>
<th>Risk class</th>
<th>N</th>
<th>Events</th>
<th>Incidence rate*</th>
<th>Hazard ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Derivation cohort</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low (0 - 2 %)</td>
<td>6488</td>
<td>183</td>
<td>1.39 [1.20, 1.61]</td>
<td>1.00 (ref)</td>
</tr>
<tr>
<td>Intermediate (2 - 5 %)</td>
<td>5556</td>
<td>368</td>
<td>3.44 [3.10, 3.81]</td>
<td>2.49 [2.09, 2.97]</td>
</tr>
<tr>
<td>High (5 - 10 %)</td>
<td>1872</td>
<td>286</td>
<td>8.37 [7.43, 9.40]</td>
<td>6.07 [5.45, 7.31]</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Validation cohort</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Low (0 - 2 %)</td>
<td>3642</td>
<td>84</td>
<td>1.14 [0.91, 1.42]</td>
<td>1.00 (ref)</td>
</tr>
<tr>
<td>Intermediate (2 - 5 %)</td>
<td>3262</td>
<td>225</td>
<td>3.51 [3.06, 4.00]</td>
<td>3.07 [2.39, 3.95]</td>
</tr>
<tr>
<td>High (5 - 10 %)</td>
<td>1161</td>
<td>166</td>
<td>7.55 [6.45, 8.79]</td>
<td>6.63 [5.10, 8.62]</td>
</tr>
<tr>
<td>Very high (&gt; 10 %)</td>
<td>483</td>
<td>119</td>
<td>14.25 [11.81, 17.05]</td>
<td>12.60 [9.53, 16.66]</td>
</tr>
</tbody>
</table>

* per 100 person-years
### Supplementary Table IV
C-indices for the contemporary ABC-death score without GDF-15 in the full cohorts and in subgroups

**A. All-cause mortality**

<table>
<thead>
<tr>
<th></th>
<th>Full cohort</th>
<th>No prior stroke/TIA</th>
<th>No prior heart failure</th>
<th>TTR &lt;65%</th>
<th>NOAC*</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Derivation cohort; Events/N</strong></td>
<td>1047/14611</td>
<td>816/11858</td>
<td>575/10080</td>
<td>354/4165</td>
<td>506/7319</td>
</tr>
<tr>
<td>ABC-death (cTnT)</td>
<td>0.74 [0.72, 0.76]</td>
<td>0.74 [0.72, 0.76]</td>
<td>0.72 [0.70, 0.74]</td>
<td>0.75 [0.72, 0.77]</td>
<td>0.74 [0.71, 0.76]</td>
</tr>
<tr>
<td>ABC-death (cTnI)</td>
<td>0.74 [0.73, 0.76]</td>
<td>0.75 [0.73, 0.76]</td>
<td>0.73 [0.71, 0.75]</td>
<td>0.74 [0.71, 0.77]</td>
<td>0.74 [0.72, 0.77]</td>
</tr>
<tr>
<td><strong>Validation cohort; Events/N</strong></td>
<td>594/8548</td>
<td>474/6893</td>
<td>324/6095</td>
<td>101/1119</td>
<td>391/5697</td>
</tr>
<tr>
<td>ABC-death (cTnT)</td>
<td>0.73 [0.71, 0.76]</td>
<td>0.73 [0.71, 0.76]</td>
<td>0.70 [0.68, 0.73]</td>
<td>0.74 [0.69, 0.79]</td>
<td>0.74 [0.72, 0.77]</td>
</tr>
<tr>
<td>ABC-death (cTnI)</td>
<td>0.71 [0.69, 0.73]</td>
<td>0.71 [0.69, 0.73]</td>
<td>0.68 [0.65, 0.70]</td>
<td>0.70 [0.64, 0.75]</td>
<td>0.72 [0.70, 0.75]</td>
</tr>
</tbody>
</table>

**B. Cardiovascular mortality**

<table>
<thead>
<tr>
<th></th>
<th>Full cohort</th>
<th>No prior stroke/TIA</th>
<th>No prior heart failure</th>
<th>TTR &lt;65%</th>
<th>NOAC*</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Derivation cohort; Events/N</strong></td>
<td>532/14611</td>
<td>406/11858</td>
<td>268/10080</td>
<td>196/4165</td>
<td>506/7319</td>
</tr>
<tr>
<td>ABC-death (cTnT)</td>
<td>0.76 [0.74, 0.78]</td>
<td>0.76 [0.73, 0.78]</td>
<td>0.74 [0.71, 0.77]</td>
<td>0.78 [0.74, 0.81]</td>
<td>0.74 [0.71, 0.77]</td>
</tr>
<tr>
<td>ABC-death (cTnI)</td>
<td>0.74 [0.72, 0.75]</td>
<td>0.76 [0.74, 0.78]</td>
<td>0.75 [0.72, 0.78]</td>
<td>0.77 [0.74, 0.81]</td>
<td>0.75 [0.72, 0.78]</td>
</tr>
<tr>
<td><strong>Validation cohort; Events/N</strong></td>
<td>385/8548</td>
<td>306/6893</td>
<td>182/6095</td>
<td>76/1119</td>
<td>391/5697</td>
</tr>
<tr>
<td>ABC-death (cTnT)</td>
<td>0.76 [0.74, 0.79]</td>
<td>0.76 [0.73, 0.79]</td>
<td>0.71 [0.67, 0.75]</td>
<td>0.77 [0.72, 0.82]</td>
<td>0.76 [0.73, 0.79]</td>
</tr>
<tr>
<td>ABC-death (cTnI)</td>
<td>0.74 [0.72, 0.77]</td>
<td>0.74 [0.71, 0.77]</td>
<td>0.68 [0.64, 0.72]</td>
<td>0.73 [0.67, 0.79]</td>
<td>0.75 [0.67, 0.78]</td>
</tr>
</tbody>
</table>

TTR - Time in therapeutic range (INR 2.0-3.0)
Contemporary ABC-death - Age, Biomarkers (cardiac troponin and NT-proBNP), Clinical history of heart failure
NOAC - non-vitamin K antagonist oral anticoagulation
*Apixaban in the derivation cohort and dabigatran in the validation cohort
Supplementary Figure I

Calibration of the ABC-death model for all-cause mortality
Supplementary Figure II

Kaplan–Meier estimated cumulative event rate by randomized treatment (colour) by predicted ABC-death risk classes (panel): 0-1%, 1–2%, and ≥2% for all-cause mortality
Supplementary Figure III

Nomogram for the ABC-death for cardiovascular mortality

For each predictor, read the points assigned on the 0-10 scale at the top and then sum these points. Find the number on the “Total Points” scale and then read the corresponding predictions of 1-year risk of death below it. Continuous variables are represented from the 1st to the 99th percentiles. The prediction model is preferably used as a web-based calculator or app.
Supplementary Figure IV

Cumulative risk of cardiovascular death by predicted 1-year ABC-death risk group for the derivation (dashed lines, n=14,611) and the validation (solid lines, n=8,548) data

![Graph showing cumulative risk of cardiovascular death over time for different risk groups.](graph.png)
Supplementary Figure VI

Decision curve analysis for cardiovascular mortality

Net benefit of using a model to predict one-year event of cardiovascular death as compared with strategies of "assume high risk to all" or "assume low risk to all" for different thresholds. A multivariable model based on all clinical information was used for comparison. The analysis is based on 24,348 patients from the ARISTOTLE and RE-LY trials.

ABC-death - Age, Biomarkers (cardiac troponin, NT-proBNP, and GDF-15), Clinical history of heart failure

All clinical information - a model solely consisting of clinical variables (age, gender, smoking, alcohol, prior stroke/TIA, diabetes, hypertension, heart failure, prior myocardial infarction, peripheral arterial disease, vascular disease, AF-type, and prior bleeding)
Supplementary Figure VI

Nomogram for the ABC-death score using cTnI-hs (instead of cTnT-hs)

For each predictor, read the points assigned on the 0-10 scale at the top and then sum these points. Find the number on the “Total Points” scale and then read the corresponding predictions of 1-year risk of death below it.
Continuous variables are represented from the 1st to the 99th percentiles.
The prediction model is preferably used as a web-based calculator or app.
For each predictor, read the points assigned on the 0-10 scale at the top and then sum these points. Find the number on the “Total Points” scale and then read the corresponding predictions of 1-year risk of death below it.
Continuous variables are represented from the 1st to the 99th percentiles.
The prediction model is preferably used as a web-based calculator or app.
Supplementary Figure VIII

Nomogram for the ABC-death score without GDF-15 for cardiovascular mortality

For each predictor, read the points assigned on the 0-10 scale at the top and then sum these points. Find the number on the “Total Points” scale and then read the corresponding predictions of 1-year risk of death below it.

Continuous variables are represented from the 1st to the 99th percentiles.

The prediction model is preferably used as a web-based calculator or app.
**Supplementary Figure IX**

Exemplified application of the nomogram

Example: A 64-year old man with atrial fibrillation, hypertension, chronic heart failure, NT-proBNP level of 5000 ng/L, GDF-15 2500 ng/L, and troponin T (high sensitivity) of 40 ng/L. By using the ABC-death score nomogram receives 0p for age, 1.5p for heart failure, 4.75p for NT-proBNP, 5.25p for GDF-15, and 6.75p for troponin levels. A total of 18.25p would equal a predicted 1-year risk of all-cause mortality of approximately 14%.

For the same patient, by using the ABC-death score nomogram for cardiovascular mortality, receives 0p for age, 1.5p for heart failure, 4.25p for NT-proBNP, 2p for GDF-15, and 7p for troponin levels. A total of 14.75p would equal a predicted 1-year risk of cardiovascular mortality of approximately 8%.
Summary of the derivation and validation cohorts

**Derivation cohort**

ARISTOTLE was a double blind, randomised clinical trial that enrolled 18,201 patients with AF at increased risk for stroke at 1034 clinical sites in 39 countries between December 2006 and April 2010. Patients included had paroxysmal, persistent or permanent AF, or atrial flutter, and one or more of the following risk factors; age ≥75 years, prior stroke, transient ischemic attack (TIA), or systemic embolus, heart failure, diabetes mellitus, or hypertension requiring pharmacologic treatment. Among the exclusion criteria were; clinically significant mitral stenosis, mechanical heart valve, recent stroke, previous intracranial haemorrhage, creatinine clearance less than 25 mL/min, or active alcohol or drug abuse. Participants were randomised to warfarin (n=9,081) or apixaban (n=9,120). The median length of follow-up was 1.7 years for the 14,537 participants with biomarker samples available at randomisation after exclusion of 45 (0.3%) patients with missing data.

**External validation cohort**

RE-LY was a prospective, multicentre, randomized trial comparing two blinded doses of dabigatran with open label warfarin that enrolled 18,113 patients with AF at 951 clinical sites in 44 countries between December 2005 and March 2009. Inclusion criteria were documented atrial fibrillation and at least one of the following risk factors for stroke: previous stroke or TIA; congestive heart failure or reduced left ventricular ejection fraction (<40%); at least 75 years of age; or at least 65 years of age with diabetes mellitus, hypertension, or coronary artery disease. Exclusion criteria included severe heart valve disorder, recent stroke, creatinine clearance less than 30 mL/min, or active liver disease. The median length of follow-up was 1.9 years for the 8,548 participants with biomarker samples available at randomisation.
**Statistical methods (detailed)**

In the first step a model including all candidate predictors (listed in Figure 1 in the main article) was fitted in 14,611 patients from the ARISTOTLE trial. The full model was then approximated, blinded for the outcome to avoid overfitting, by a smaller model including the most predictive variables. The approximation was done in the following way. First an ordinary least squares model was fitted with the estimated linear predictor from the full model as outcome and including the same predictors as in the full model. This model had, by definition, an $R^2$ of 1.0. A fast backward elimination algorithm was then applied to the model removing the least important variables until a good enough approximation was achieved with as few variables kept as possible. An alternative model was created in the same manner but replacing cTnT-hs with cTnl-hs. Similarly, a model was developed for cardiovascular mortality. In a subset of patients with additional biomarkers available, an extended biomarker model was developed which also incorporated D-dimer and IL-6 among the candidate variables. The final models were presented as nomograms. Risk categories were created according to 0-2%, 2-5%, 5-10%, and >10% risk for death within one year and 0-1%, 1-2%, 2-5%, and >5% for cardiovascular death within one year. The reason for choosing different class limits is that the incidence rate for cardiovascular death is lower than for total death.

*Internal and external model validation*

The model was internally validated using 150 bootstrap samples. External validation was conducted in 8,548 patients from the RE-LY trial. In the validation the predicted risk for each subject in the validation cohort was estimated by applying the model using the model coefficients derived in the derivation cohort. Thus, the model was not refitted in the validation data. In order to thoroughly compare the prognostication of death, the new
A biomarker-based risk model was evaluated against a multivariable model solely based on clinical variables and the widely used CHA\textsubscript{2}DS\textsubscript{2}-VASc score, although originally created for stroke prediction.

Discrimination was assessed by Harrell’s c-index\textsuperscript{26} and by comparing Kaplan-Meier curves and hazard ratios between the predefined risk categories. Calibration was assessed by comparing observed one-year event rates with predictions from the final model. Clinical usefulness and net benefit were estimated with decision curve analysis.\textsuperscript{27} The decision curve analysis estimate the net benefit of using the model for assigning subjects to either low or high risk for each possible threshold in comparison to not using the model and thus assuming either that everyone is at low risk or that everyone is at high risk. The net benefit at a given threshold gives the increased true positive rate without an increase of the false positive rate as compared to the two naïve approaches of assuming all low or all high risk. At a given threshold, the model with the highest net benefit is the superior model. The final model was also evaluated in different subgroups; without a history of stroke, without heart failure diagnosis, low time in therapeutic range (TTR), and in the groups randomised to apixaban and dabigatran therapy, respectively.

The analyses followed the framework for derivation and validation of prediction models proposed by Harrell, Steyerberg and Vergouwe, and Royston and Altman.\textsuperscript{26,28,29} The reporting followed the recently published TRIPOD statement.\textsuperscript{30} All analyses were performed using R version 3.2.
ABC-death score equations

Models for all-cause mortality

Note that, in all models, before entering the variables in the equations, Age and NT-proBNP should be truncated as
Age = max(Age, 65)
NT-proBNP = max(NT-proBNP, 200)
and the biomarkers should be naturally log-transformed as
hs-cTnT = ln(hs-cTnT)
hs-cTnl = ln(hs-cTnl)
NT-proBNP = ln(NT-proBNP)
GDF15 = ln(GDF15)

with hs-cTnT:
Prob(death within one year) = 1 – 0.9763^exp{Xb}
where
Xb = −7.218 + 0.3416 Heart failure
− 0.01305 Age + 0.0001723 (Age − 66)^3 − 0.0003446(Age − 74)^3 + 0.0001723(Age − 82)^3
+ 0.04248 NT-proBNP + 0.04728 (NT-proBNP − 5.303)^3
− 0.1139 (NT-proBNP − 6.708)^3 + 0.0666 (NT-proBNP − 7.705)^3
+ 0.7963 GDF15 − 0.1923(GDF15 − 6.608)^3
+ 0.3410 (GDF15 − 7.231)^3 − 0.1487 (GDF15 − 8.037)^3
+ 0.6875 (hs-cTnT − 0.07336 (hs-cTnT − 1.705)^3
+ 0.1344 (hs-cTnT − 2.389)^3 − 0.06104(hs-cTnT − 3.211)^3

with hs-cTnl:
Prob(death within one year) = 1 – 0.9770^exp{Xb}
where
Xb = −7.525 + 0.2902 Heart failure
− 0.006738 Age + 0.0001651 (Age − 66)^3 − 0.0003303 (Age − 74)^3 + 0.0001651 (Age − 82)^3
+ 0.009926 l + 0.04911 (NT-proBNP − 5.303)^3
− 0.1183 (NT-proBNP − 6.708)^3 + 0.06919(NT-proBNP − 7.705)^3
+0.8850 GDF15 − 0.2036 (GDF15 − 6.608)^3
+ 0.3611 (GDF15 − 7.231)^3 − 0.1575 (GDF15 − 8.037)^3
+0.6761 hs-cTnl − 0.07783 (hs-cTnl − 0.8329)^3
+ 0.1262(hs-cTnl − 1.686)^3 − 0.04841 (hs-cTnl − 3.059)^3
Models for cardiovascular death

Note that, in all models, before entering the variables in the equations, Age and NT-proBNP should be truncated as
Age = max(Age, 70)
NT-proBNP = max(NT-proBNP, 200)
and the biomarkers should be naturally log-transformed as
hs-cTnT = ln(hs-cTnT)
hs-cTnl = ln(hs-cTnl)
NT-proBNP = ln(NT-proBNP)
GDF15 = ln(GDF15)

with hs-cTnT:
Prob(death within one year) = 1 − 0.9876^exp{Xb}
where
Xb = −5.952 + 0.4635 Heart failure
− 0.01244 Age + 0.0003442 (Age − 71)^3 − 0.0006393 (Age − 77)^3 + 0.0002951 (Age − 84)^3
+ 0.05166 NT-proBNP + 0.05677 (NT-proBNP − 5.303)^3
− 0.1367 (NT-proBNP − 6.708)^3 + 0.07998 (NT-proBNP − 7.705)^3
+ 0.4796 GDF15 − 0.1769 (GDF15 − 6.608)^3
+ 0.3137(GDF15 − 7.231)^3 − 0.1368 (GDF15 − 8.037)^3
+ 1.026 hs-cTnT − 0.1508 (hs-cTnT − 1.705)^3
+ 0.2763(hs-cTnT − 2.389)^3 − 0.1255 (hs-cTnT − 3.211)^3

with hs-cTnl:
Prob(death within one year) = 1 − 0.9881^exp{Xb}
where
Xb = −6.723 + 0.3977 Heart failure
− 0.001642 Age + 0.0003115 (Age − 71)^3 − 0.0005785 (Age − 77)^3 + 0.000267 (Age − 84)^3
+ 0.01869NT-proBNP + 0.05777(NT-proBNP − 5.303)^3
− 0.1391 (NT-proBNP − 6.708)^3 + 0.08138 (NT-proBNP − 7.705)^3
+ 0.6364 GDF15 − 0.2133 (GDF15 − 6.608)^3
+ 0.3782 (GDF15 − 7.231)^3 −0.1649(GDF15 − 8.037)^3
+ 0.9549 hs-cTnl − 0.1157 (hs-cTnl − 0.8329)^3
+ 0.1877 (hs-cTnl − 1.686)^3 − 0.07197 (hs-cTnl − 3.059)^3