1 **Biomarker-based prediction of sinus rhythm in atrial**

2 **fibrillation patients: the EAST-AFNET 4 biomolecule study**

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Abstract

 Background and Aims. In patients with atrial fibrillation (AF), recurrent AF and sinus rhythm during follow-up are determined by interactions between cardiovascular disease processes and rhythm-control therapy. Predictors of attaining sinus rhythm at follow-up are not well known.

 Methods: To quantify the interaction between cardiovascular disease processes and rhythm outcomes, 14 biomarkers reflecting AF-related cardiovascular disease processes in 1586 patients in the EAST-AFNET 4 biomolecule study (71 years old, 46% women) were quantified at baseline. Mixed logistic regression models including clinical features were constructed for each biomarker. Biomarkers were interrogated for interaction with early rhythm control. Outcome was sinus rhythm at 12 months. Results were validated at 24 months and in external datasets.

 Results: Higher baseline concentrations of three biomarkers were independently associated with a lower chance of sinus rhythm at 12 months: angiopoietin 2 (ANGPT2) (odds ratio [OR] 0.76 [95% confidence interval 0.65-0.89], p=0.001), bone morphogenetic protein 10 (BMP10) (OR 0.83 [0.71-0.97], p=0.017) and N-terminal pro-B-type natriuretic peptide (NT- proBNP) (OR 0.73 [0.60–0.88], p=0.001). Analysis of rhythm at 24 months confirmed the results. Early rhythm control interacted with the predictive potential of NT-proBNP (pinteraction=0.033). The predictive effect of NT-proBNP was reduced in patients randomized to early rhythm control (usual care: OR 0.64 [0.51-0.80], p<0.001; early rhythm control: OR 0.90 [0.69-1.18], p=0.453). External validation confirmed that low concentrations of ANGPT2, BMP10 and NT-proBNP predict sinus rhythm during follow-up. 5 not well known.

6 **Methods:** To quantify the interaction between cardiovascular disease processes and

7 rhythm outcomes, 14 biomarkers reflecting AF-related cardiovascular disease processes in

1586 patients in the EA

 Conclusions: Low concentrations of ANGPT2, BMP10 and NT-proBNP identify patients with AF who are likely to attain sinus rhythm during follow-up. The predictive ability of NT-proBNP is attenuated in patients receiving rhythm control.

Key words: atrial fibrillation; blood biomarker; sinus rhythm; rhythm control; natriuretic

peptides; bone morphogenetic protein 10; angiopoietin 2; risk prediction; risk score

1

2 **Introduction**

3 $\;$ In addition to improving atrial fibrillation (AF)-related symptoms1, rhythm control therapy 2 4 can prevent AF-related cardiovascular events such as stroke, heart failure hospitalizations, 5 and cardiovascular death³. The cardiovascular complication-reducing effect of early rhythm 6 control therapy shown in the EAST-AFNET 4 study is mainly mediated by attaining sinus 7 hythm at 12-month follow-up⁴. This potentially reflects a reduced AF burden⁵ and lack of 8 progression to non-paroxysmal patterns of $AF^{6,7}$. Predicting sinus rhythm at 12 months 9 could therefore help to identify patients requiring intensive rhythm control, e.g. with AF 10 ablation^{3, 8}. Knowledge of treatable processes contributing to AF at 12-month follow-up can 11 help to develop adjunct therapies aimed at maintaining sinus rhythm and preventing AF 12 progression⁶. Several chronic, interdependent disease processes^{9, 10} contribute to AF. Such 13 processes can be aggravated by presence of AF, attenuated by rhythm control, or exist 14 independent of $AF^{1,11}$. Circulating biomarkers provide quantitative proxies for cardiomyocyte 15 death or injury (troponin [TnT]); atrial metabolic dysfunction and stress (bone 16 morphogenetic protein 10 [BMP10], fatty acid binding protein 3 [FABP3] and insulin-like 17 growth factor binding protein 7 [IGFBP7])^{12, 13}; thrombo-inflammation (D-dimer, C-reactive 18 protein [CRP], interleukin-6 [IL-6])^{14, 15}; vascular and endothelial dysfunction (angiopoietin 2 [ANGPT2], endothelial specific molecule 1 [ESM1])^{14, 15}; frailty (growth differentiation 20 factor 15 [GDF-15]); and cardiac load estimated (natriuretic peptides like N-terminal pro-B-21 type natriuretic peptide [NT-proBNP])¹⁶. Quantification of biomarkers selected to reflect 22 these disease processes in a single blood draw identifies patient clusters with different risk of 23 **Cardiovascular events¹⁷**. Whether the disease processes reflected by the molecules modify 24 future rhythm in patients with AF has not been investigated. 5 and cardiovascular death? The cardiovascular complication-reducing effect of early flythm
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25 This analysis of the EAST-AFNET 4 biomolecule study embedded into the **E**arly 26 treatment of Atrial fibrillation for **ST**roke prevention (EAST-AFNET 4) trial² quantified 14 biomarkers reflecting different disease processes in AF that were defined *a priori*⁹ 27 . The

 ability of each biomarker to predict sinus rhythm at 12-month follow-up in patients with and without early rhythm control therapy was evaluated.

 Validation was performed internally at 24 months, by comparing biomarker-based clusters at baseline by association with sinus rhythm at 12-and 24-month follow-up and by machine learning integrating biomarkers and clinical parameters. Clinical utility was assessed by defining and testing threshold values and by comparison with a clinical score. External validation was performed in two independent datasets of patients with AF.

Methods

 Details of the prespecified analysis plan of the EAST-AFNET 4 biomolecule study can be found in a separate supplementary material file (**Supplementary file Statistical analysis plan SAP**). Post-hoc exploratory analyses were added to gain more insight into the main findings.

14 Derivation dataset (EAST-AFNET 4). EAST-AFNET 4 randomized patients with recently diagnosed AF and stroke risk factors to systematic early rhythm control or usual care 16 including symptom-based rhythm control². All patients were followed-up for a median of 5.1 years. The EAST-AFNET 4 biomolecule study collected a baseline blood sample in 1586 18 patients enrolled in the EAST-AFNET 4 trial^{17, 18}. In brief, all consenting patients provided a blood sample at baseline. Samples were shipped to the core biostorage facility at UKE Hamburg, spun, shock-frozen and stored at -80°C. EAST-AFNET 4 and its biomolecule study were approved at all participating study sites. Written informed consent was obtained from all patients. 5 machine learning integrating biomarkers and clinical parameters. Clinical utility was

6 assessed by defining and testing threshold values and by comparison with a clinical score.

7 External validation was performed in

Validation datasets.

AXAFA-AFNET 5. The Anticoagulation using the direct factor Xa inhibitor apixaban during

Atrial Fibrillation catheter Ablation: Comparison to vitamin K antagonist therapy (AXAFA-

26 AFNET 5^{19}) trial was a randomized, investigator-initiated trial comparing continuous

 vitamin K antagonist therapy to apixaban in 633 patients undergoing a first AF ablation in 49 European and US American study sites. The same 14 biomarkers quantified in the derivation dataset were quantified in the AXAFA-AFNET 5 blood samples using the same 4 assays.²⁰ The outcome of interest was rhythm at the final follow-up visit, 120 days after 5 enrolment.¹⁹

 BBC-AF atrial fibrillation snapshot. Details of the BBC-AF cohort have been described before ²¹ . In brief, consecutive patients eligible for recruitment had ECG-diagnosed AF or presented with at least two cardiovascular conditions (congestive heart failure, hypertension, diabetes, prior stroke, or vascular disease) to a large teaching hospital (Sandwell and West Birmingham NHS Trust). Patients who did not have a diagnosis of AF underwent 7-day ambulatory ECG monitoring to rule out undiagnosed ECG-documented AF. For this analysis, only patients with ECG-documented AF were included. Follow-up data were collected by assessing local hospital records corroborated against Hospital Episode Statistics data, general practitioner (GP) records, and mortality data from NHS Digital, up to 2.5 years after 15 the final patient was recruited²². This study complied with the Declaration of Helsinki, was approved by the National Research Ethics Service Committee (IRAS ID 97753) and was sponsored by the University of Birmingham. All patients provided written informed consent. *TRUST snapshot.* A snapshot of patients enrolled in the Long-term Outcome and Predictors for Recurrence after Medical and Interventional Treatment of Arrhythmias study (TRUST; NCT05521451), with biomarker concentrations and 12-month rhythm status was created. All patients provided written informed consent. A snapshot of all patients with biomarker concentrations and ECG follow-up at 12-18 months was obtained in June 2024 for validation. 5 enrolment.⁹

6 *BHC-AF arrial fibrillation snapshot.* Details of the BBC-AF cohort have been described

7 before *n*. In brief, consecutive patients eligible for recruitment had ECG-diagnosed AF or

8 presented with a

1 Selection of biomarkers and their quantification. Circulating biomarkers were selected by scientists from the EU-funded CATCH-ME consortium based on relevant disease processes 3 and available high precision high throughput assays⁹. Biomarkers were selected in four steps: 1) Members of the consortium identified candidate biomarkers reflecting disease processes known to contribute to AF and its complications, 2) Deep literature and patent searches for candidate biomarkers and additional novel biomarkers were performed, 3) Expert discussion and Delphi-like votes by the consortium defined most promising candidates, and 4) Availability and feasibility checks to perform measurements of thousands of samples with high precision. Fourteen biomarkers were selected (**Table 1** following clinical characteristics); ANGPT2, BMP10, cancer antigen 125 (CA125), CRP, D-dimer, ESM1, FABP3, fibroblast growth factor 23 (FGF23), GDF15, IGFBP7, IL-6, NT-proBNP, TnT and serum creatinine (sCr). Blood samples were collected at all participating sites and shipped to the core lab at University Heart and Vascular Center (UHZ) Hamburg by courier at ambient temperatures (24-48 hours transport time). Upon arrival at UHZ, samples were spun, shock-frozen and stored at -80C for analysis. Biomarkers were centrally quantified using pre-commercial and commercial high-throughput, high-precision platforms (Roche, Penzberg, Germany) in EDTA plasma. The biomarker quantification was provided as an in-kind contribution of Roche to the CATCH ME consortium. Blood samples were shipped to, and quantifications 5 processes known to contribute to AF and its complications, 2) Deep literature and patent
searches for candidate biomarkers and additional novel biomarkers were performed, 3)
Expert discussion and Delphi-like votes by th

were conducted at the Roche biomarker research facility in Penzberg, Germany.

21 Statistical methods. As this is a secondary outcome analysis of the EAST-AFNET 4 trial, all 22 results are exploratory. Biomarker concentrations were one-percent winsorized²³ from above 23 and logarithmically-transformed (log base e) to normalize skewed concentration ranges for 24 all datasets. Concentrations below the detection limit for CA-125 and D-dimer were replaced with the lowest available value. For the initial testing of prespecified hypotheses, all fourteen biomarkers were used. Validations were done with predictive biomarkers. This analysis does not take into account the probability of chance findings because of performance of multiple

comparisons with 14 biomarkers. As a consequence, results should be interpreted as

explorative/hypothesis generating and call for further validation.

 Patients in AF at the time of blood sampling showed higher concentrations in most biomarkers (**Supplementary Table S1**). Rhythm at time of blood sampling was included as a confounder in all subsequent analyses in addition to the features predicting rhythm at 12 6 months in the main EAST-AFNET 4 data set.⁴

 Mixed logistic regression models were used to assess the predictive value of the 14 biomarkers on rhythm at 12 months, with study center as a random intercept. The lme4 R 9 package²⁴ was used. Each biomarker was assessed in a separate model adjusted for sex, age, body mass index, diastolic blood pressure, AF pattern (first-episode, paroxysmal, persistent), left ventricular ejection fraction, rhythm at baseline, and randomized group (usual care or early rhythm control). Those features are associated with rhythm at 12 months in the EAST-13 AFNET 4 trial⁴. Nested models with additional interaction terms between treatment type and the biomarker of interest were constructed. To obtain p-values for the interaction, each nested model pair was compared by ANOVA for their goodness of fit. Odds ratios and p- values for the biomarker effects under different treatment types were calculated by reference 17 cell coding²⁵. Missing values in heart rhythm and left ventricular ejection fraction were imputed in a 60-times multiple imputed dataset as described earlier², following the 19 recommendations of White, Royston and Wood^{26,27}. A sensitivity analysis constructed prediction models for recurrent AF at 12 and 24 month follow-up without imputation. To further explore the effect of rhythm on the biomarkers, mixed regression models were repeated in subgroups split by baseline rhythm (sinus rhythm or AF) and by rhythm control 23 therapy (early rhythm control or usual care) and odds ratios (OR) for the outcome sinus rhythm at 12 months were calculated using the methods described above. 5 as a confounder in all subsequent analyses in addition to the features predicting rhythmat 12

months in the main EAST-AFNET 4 data set.

7 Mixed logistic regression models were used to assess the predictive value of th

 As internal validation, analysis was repeated for sinus rhythm at 24-month follow-up. As sensitivity analysis, the analysis was repeated for recurrent AF up to 24 months.

 As additional internal validation, patient clusters formed using all biomarker 2 concentrations agnostic to clinical features¹⁷ were tested for prediction of presence of sinus rhythm at 12 and 24-month follow-up. The lowest-risk cluster was used as a reference.

 As another means of internal validation, we applied a random forest machine learning model (ML) and made use of a mixed effect random forest (MERF) wrapper to account for the center as a random effect. The ML model was fitted with the features used for confounding the generalized linear model as well as of all 14 biomarkers at once. To assess the variable importance we used the models' inherent Gini-based feature importance as well as the model agnostic SHapley Additive exPlanations (SHAP) values.

 Clinical utility. Cut-off values for clinically useful probabilities of sinus rhythm at 12 months (80%) and for AF at 12 months (40%) were determined for all biomarkers that predicted the main outcome. A clinical risk score was developed based on a recent meta - 13 analysis²⁸: Three accepted clinical features predicting recurrent AF, namely left atrial size, AF pattern, and age, were dichotomized with a point scored for persistent AF yes, anterior- posterior left atrial diameter > 50 mm, age >75 years (**Supplementary Table S2**). As many patients with one of these three features attain sinus rhythm at 12 months, the score was considered positively predictive of high risk of AF at 12 months if at least two of the three factors were present. Each of the biomarkers that were independently associated with sinus rhythm at 12 months were added to this clinical score separately, as well as in combination. If at least one biomarker was above the cut-off value, the patient was regarded as high risk of not attaining sinus rhythm. The confusion matrices for correctly and incorrectly classified patients at high-risk-classified of not attaining sinus rhythm were calculated for the reference clinical score alone and all additional, biomarker-enriched scores. 5 learning model (MI) and made use of a mixed effect random forest (MFRF) wrapper to
6 account for the center as a random effect. The ML model was fitted with the features used for
contounding the generalized linear model

 Biomarkers' predictive values were tested in the validation datasets using univariate and multivariate models restricted to the features that predicted sinus rhythm at 12 months in the derivation dataset. Python version 3.8.13 was employed for data preprocessing and

1 visualization, R version 4.2.2 for statistical computations²⁹. Relevant code will be made publicly available [\(https://github.com/UCCSHH](https://github.com/UCCSHH)).

Results

5 Derivation analysis dataset. The 1586 patients with a recent history of AF and stroke risk factors (age 71 years, 45% women) with clinical features, biomarker concentrations and cardiovascular outcomes were equally assigned to both randomized treatment groups.

(**Table 1**, **Supplementary Figure S1**).

 Association of biomarker concentrations with attaining sinus rhythm at 12 months. Three biomarkers (ANGPT2, BMP10 and NT-proBNP) showed lower concentrations at baseline in patients who were in sinus rhythm at the 12-month follow-up (**Figure 1A**). These three biomarkers were independently associated with sinus rhythm at the 12-month follow-up after multiple corrections for clinical features, early rhythm control, and baseline rhythm (**Figure 1A**). NT-proBNP interacted with early rhythm control therapy at 12-month follow- up (p=0.033) and low NT-proBNP concentrations only predicted sinus rhythm at 12 months in patients randomized to usual care (**Figure 1B**). Early rhythm control impacted on the rhythm-predicting effect of NT-proBNP and dampened its predictive value in this group. There was no significant interaction detected between early rhythm control and any of the other 13 biomarkers in this dataset (**Figure 1B**). **EXECUTE:**
 ACCENTE ACCENT THENT THEN THEND IS DEFINITION OF A BOOD MONDRIAL STRESS (THENT THEN SURVEY THEN SURVEY THEN THEN DETENDING THEN THEN DETENDING THEN DETENDING THEN MONDRIAL STRESS (Table **1.** Supplementary Fi

 Biomarker concentrations distributions depicted in violin plots after log transformation (**Figure 2**) show lower concentrations in sinus rhythm versus AF at 12 months. Numbers of mean biomarker concentrations by rhythm at 12-month follow-up and by randomized treatment group are given (**Table 2**).

Baseline biomarker concentrations depending on baseline rhythm in the derivation dataset

and clinical features are shown in **Table 3,** extended information shown in

Supplementary Table S1. Post-hoc subgroup analyses by rhythm at the time of baseline

 assessment (sinus rhythm or AF) and by randomized group (early rhythm control or usual care) find NT-proBNP mainly associated with sinus rhythm at 12 months in patients under usual care. BMP10 and ANGPT2 retained their predictive ability shown in the joint group of all patients also if only the subgroup patients in AF at the time of blood sampling were analysed (**Figure 3**).

 Internal validations. As a first internal validation, the same analysis was performed for the 24-month follow-up. The same biomarkers, ANGPT2, BMP10, and NT-proBNP, were consistently associated with sinus rhythm at 24-month follow-up (**Figure 4**).

 Repeating the analysis for recurrent AF up to 24 months showed similar results (**Supplementary Table S3**). As further internal validation analysis, unsupervised biomarker-based clustering of EAST patients previously performed was applied to sinus rhythm at 12-month follow-up. Clusters separated by risk of cardiovascular complications, with patients assigned to the high-risk cardiovascular outcome cluster showing a lower likelihood of sinus rhythm at 12 months, patients in the two intermediate cardiovascular risk biomarker clusters showing an intermediate likelihood of sinus rhythm, all tested against the low cardiovascular risk cluster, with the low-risk outcome patient cluster showing the highest likelihood of sinus rhythm at 12 months (**Figure 5A**). These findings were consistent for the high-risk biomarker-based clusters at 24-month follow-up (**Figure 5B**). As further internal validation, a random forest classifier was trained on the EAST-AFNET 4 dataset. Its feature performance evaluation confirmed the importance of the three biomarkers alongside AF pattern, rhythm at baseline, and early rhythm control for the outcome of sinus rhythm (**Figure 6**). 5 analysed (Figure 3).

6 Internal validations. As a first internal validation, the same analysis was performed for

the 24-month follow-up. The same biomarkers, ANGPT2, BMP10, and NT-proBNP, were

20 consistently associa

 Clinical utility. Thresholds to predict a high probability of attaining sinus rhythm (>80%, low risk of AF) or a high probability of recurrent AF at follow-up (>40%, high risk of AF) were determined for each biomarker (**Table 4, Supplementary Figures S2, S3, S4**). To compare them to clinical features predicting sinus rhythm, a score combining clinical features predicting recurrent AF was created²⁸ (**Supplementary Table S2**). Adding

 sinus rhythm at 12-month follow-up (**Table 5, Supplementary Table S4**). **External validation.** Several separate validation datasets (AXAFA-AFNET 5 trial, BBC-AF and TRUST cohort snapshot **Supplementary Tables S5, S6, S7**) were used. The biomarkers NT-proBNP, BMP10, and ANGPT2 were confirmed as predictive of sinus rhythm in the final follow-up in AXAFA-AFNET 5 (**Figure 7**). The clinical utility of adding the biomolecules to clinical predictors was validated in both cohorts using the thresholds derived in EAST-AFNET 4 (**Supplementary Table S8 and S9**).

biomarkers using these thresholds improved identification of patients at risk of not attaining

Discussion

 Main findings. Three out of fourteen candidate biomarkers, BMP10, ANGPT2 and NT- proBNP, are associated with sinus rhythm at 12-month and 24-month follow-up after correcting for clinical features. Low NT-proBNP, low ANGPT2 and low BMP10 concentrations independently predict sinus rhythm in patients at follow-up. NT-proBNP is less predictive of rhythm in patients receiving rhythm control therapy. Adding these biomarkers to a clinical score identifying patients with a low probability of sinus rhythm at 12 months (positive with two out of three features: left atrial size >50 mm, persistent AF, or age >75 years) refined risk prediction (Structured Graphical Abstract). 5 biomarkers NT-proBNP, BMP10, and ANGPT2 were confirmed as predictive of sinus rhythm

in the final follow-up in AXAFA-AFNET 5 (Figure 7). The clinical utility of adding the

16 in the final follow-up in AXAFA-AFNET 5 (F

20 Relevance for clinical care and research. In view of the growing choice of medical^{2, 30}, 21 interventional^{2, 31}, and surgical³² treatment options for patients with AF, selecting the best 22 strategy and the patients most benefitting from rhythm control therapy gains importance. Biomarker-based risk estimators have so far mainly been developed to refine anticoagulation 24 decisions in patients with AF33-35. Actionable biomarkers to guide rhythm control therapy are lacking. Similar to stroke prevention estimators, rhythm estimators face the challenge of random factors determining a binary outcome (AF or sinus rhythm). The present results suggest that NT-proBNP, BMP10, and ANGPT2 can stratify patients at high and low risk of

 attaining sinus rhythm alone and in combination. These biomarkers reflect and identify diseases processes that promote future AF, pointing to potential therapeutic targets for adjunct therapy supporting rhythm control. While a simple clinical score combining enlarged left atrial size, persistent AF, and older age predicted future sinus rhythm reasonably well, adding biomarkers reclassifies a clinically relevant number of patients at high risk of not attaining sinus rhythm at the price of also classifying more patients in sinus rhythm as high-risk.

 Effect of baseline rhythm on biomarker concentrations. This study shows that ANGPT2 and BMP10 provide additional information on future sinus rhythm when combined with NT-proBNP, especially in patients who are in AF at the time of blood sampling. Most biomarkers studied were elevated when the blood sample was taken in AF. Furthermore, NT- proBNP lost its ability to predict sinus rhythm in patients on rhythm control therapy, and the predictive ability of BMP10 decreased in the subgroup of patients who were in sinus rhythm, but not in the subgroup of patients who were in AF, similar to rhythm-dependent decrease of 15 predictive ability of NT-proBNP^{20, 36}. The effects of baseline rhythm on the concentrations and predictive ability of biomarkers should be further investigated in patients with AF undergoing rhythm control therapy. 5 reasonably well, adding biomarkers reclassifies a clinically relevant number of patients at thigh risk of not attaining sinus rhythm at the price of also classifying more patients in sinus rhythm as high-risk.

7 rhythm

 Interpretation of NT-proBNP. NT-proBNP is released by atrial cardiomyocytes in response to stretch and strain, thereby acutely regulating fluid balance in the body, resulting in high 20 concentrations during AF37. In heart failure, NT-proBNP is also released by ventricular cardiomyocytes, further enhancing its concentrations. Atrial stretch has proarrhythmic 22 effects including shortening of the atrial effective refractory period³⁸ and conduction slowing³⁹ , partially explaining its prediction of sinus rhythm in this study. NT-proBNP reflects short- and mid-term processes in patients with AF, probably explaining its interaction with rhythm. The possibility that elevated NT-proBNP concentrations predict 26 rhythm during follow-up have been reported before.⁴⁰⁻⁴⁷ NT-proBNP is also associated with 27 incident AF^{48-51} and with cardiovascular events in patients with and without AF and heart 1 failure.²² This analysis demonstrates that the rhythm-predicting ability of NT-proBNP is 2 reduced in patients treated with rhythm control therapy.

3 The NT-proBNP thresholds associated with a high risk of AF at 12 months in this 4 study (>1500 pg/ml) are comparable to the thresholds associated with cardiovascular events, 5 but higher than currently used thresholds e.g. for AF screening 52 or for diagnosing heart 6 failure with AF and heart failure with preserved ejection fraction⁵³. Based on the present 7 analysis, higher thresholds may have better clinical utility. This warrants further analysis.

 Interpretation of BMP10 and ANGPT2. BMP10 and ANGPT2 are tightly regulated circulating biomarkers, illustrating their signaling roles in regulating disease processes 10 contributing to AF³. Mechanistic studies of their role in AF are needed to define more precise clinical use cases for these biomarkers in patients with AF.

12 ANGPT2 is a vascular growth factor required for angiogenic remodeling ⁵⁴. 13 Overexpression of ANGPT2 in murine models promotes perivascular cardiac inflammation 14 and fibrosis⁵⁵. Pro-inflammatory molecules such as thrombin increase ANGPT2 expression 15 *in vitro*⁵⁶ and inhibition of thrombin in animals with persistent AF improves atrial 16 cardiomyopathy¹⁵. Thus, ANGPT2 mediates the inflammatory communication between 17 endothelial cells and myocardium in AF. Low ANGPT2 might reflect preserved vascular 18 integrity, reducing the inflammatory burden in atrial vascular beds and thereby slowing AF 19 progression. 5 but higher than currently used thresholds e.g. for AF screening ²⁵ or for diagnosing freart failure with AF and heart failure with preserved ejection fraction⁵¹. Based on the present analysis, higher thresholds may

ANGPT2 is associated with recurrent AF in patients after AF ablation²⁰ and with 21 prevalent AF in unselected hospitalized patients ⁵⁷. ANGPT2 is elevated in patients with 22 kidney disease⁵⁸, acute lung injury⁵⁹ and sepsis⁶⁰, conditions associated with AF. ANGPT2 23 \degree can also predict heart failure hospitalization in patients with AF⁶¹, similar to NT-proBNP.²² 24 This study is the first to suggest that ANGPT2 can predict sinus rhythm in patients with AF 25 with and without rhythm control therapy. Further research into treatable atrial disease 26 processes regulated by ANGPT2 is warranted.

1 BMP10 is selectively expressed in and released by atrial cardiomyocytes^{16, 62}. BMP10 2 is part of the TGFß growth factor family and regulates vascular smooth muscle cell tone ⁶³. Its 3 function in the atria is not well known. BMP10 concentrations are reduced in hereditary 4 forms of pulmonary arterial hypertension⁶⁴, possibly reflecting reduced left atrial 5 metabolism. Its inverse correlation and possible repression by PITX2 in atrial 6 cardiomyocytes^{16, 65} may suggest that elevated BMP10 concentrations could identify a 7 reversible atrial metabolic defect^{13, 17} that may be aggravated by the genomic basis of AF on 8 chromosome $4q25^{13}$.

9 High concentrations of BMP10 are associated with recurrent AF^{57,66}, and with 10 cardiovascular events^{17, 67} and stroke in patients with AF. BMP10 may also be associated with 11 atrial fibrosis⁶⁸. Lower BMP10 concentrations in patients in sinus rhythm²⁰, combined with 12 its prediction of future sinus rhythm (**Figure 1**) suggest that a possible BMP10-mediated 13 metabolic defect could partially be secondary to the metabolic demands of AF. Taken 14 together, these results suggest that BMP10 is a potentially actionable biomarker indicative of 15 atrial myopathy and atrial metabolic dysfunction. Further research into the atrial effects of 16 BMP10 and its relation to AF burden⁵ are warranted. 5 metabolism. Its inverse correlation and possible repression by PITX2 in attial
6 cardiomyocytes ^{a, es} may suggest that elevated BMP10 concentrations could identify a
7 reversible attial metabolic defects.¹¹ that may

 Biomolecule-based clustering of patients agnostic to clinical features previously identified four subgroups of patients with AF with a gradual increase in cardiovascular 19 events.¹⁷ The three biomarkers associated with sinus rhythm at 12 months in this study are 20 among the six dominant biomarkers previously defining these patient clusters.¹⁷ The biomarker-based clusters show a certain risk gradient for sinus rhythm at 12 months (**Figure 5**). At difference to the prior study that defined patient clusters based on 14 biomarker concentrations agnostic to clinical information, this analysis shows that the three biomarkers NT-proBNP, ANGPT2 and BMP10 predict sinus rhythm in context with clinical parameters. Of note, a simple clinical score was already quite useful in identifying patients who will attain sinus rhythm. This information can help clinicians to select different intensities of rhythm control therapy depending on the likelihood of attaining sinus rhythm.

 NT-proBNP, ANGPT2 and BMP10 can refine that selection. The present result and the biomarker-clustering also identify potentially treatable drivers of recurrent AF and or cardiovascular events in patients with AF. Based on the known atrial effects of BMP10 and ANGPT2, antihypertensive therapy and metabolic interventions such as SGLT2 inhibitor 5 therapy⁶⁹ could have beneficial effects in patients with elevated BMP10 and ANGPT2 6 concentrations. $16, 67, 70$ The underlying disease processes suggest that the same biomarkers could also be useful to identify patients at risk of AF. The present analysis identifies potentially actionable biomarkers suitable to select the intensity of rhythm control therapy. Further research into the mechanistic links between these biomarkers with baseline and future rhythm, and further evaluations of their clinical utility in different scenarios are warranted.

 Strengths and limitations. Central quantification of the biomarkers using high-precision assays combined with the rigorous, near-complete follow-up at 12 and 24 months in a controlled clinical trial is a strength of this analysis. The consistent findings at both time points may suggest that the effects can be extrapolated to even longer follow-up, but this would require validation. Another strength of the analysis is the collection of samples in a broad range of care settings in adequately treated patients with AF, and external validation both in a controlled clinical trial and in cohorts of patients with AF enrolled in routine care settings. Validation of the findings using the same assays in different clinical datasets is a strength, but also limits the findings to the assays provided for this study. 5 therapy% could have beneficial effects in patients with elevated BMP10 and ANGP12 concentrations.^{14,67,75} The underlying disease processes suggest that the same biomarkers
concentrations.^{14,67,75} The underlying dise

 The study has important limitations. Although the statistical analysis plan was prespecified and validation was possible in different datasets, all results are explorative. This study is limited to 14 preselected biomarkers. Selected biomarkers intentionally reflect overlapping disease processes, creating redundancy that enables robust definition of disease pathways. Collinearity of biomarkers was more deeply investigated in a previous study defining 26 biomarker-based patient clusters agnostic to clinical features¹⁷.

Additional biomarkers in AF may emerge from hypothesis-free quantification of many

2 molecules at once e.g. by RNA-sequencing of cardiac tissue^{71}, quantification of circulating

3 RNAs, and by proteomics^{72, 73}. Repeat blood samples were not obtained and no information

on changes over time is available. Some data on the changes of BMP10 and NT-proBNP over

5 time have been published $20, 36$.

 While NT-proBNP can be measured in clinical routine as *in-vitro* diagnostic devices with regulatory approval, the assays for ANGPT2 and BMP10 are not approved for clinical use, restricting them to research settings. Only the consenting portion of the total EAST-AFNET study participants was included in the biomarker study (two thirds), hence there could be a considerable selection bias. Due to time required to setup the biobank, the first 400 patients were not invited to participate in the biomarker study.

 The present study used serum creatinine rather than estimated glomerular filtration rate in the analyses as the formulas used to estimate kidney function rely on clinical parameters that are used in the regression model, including age, sex, and body mass index. Serum creatinine was not a major predictor of sinus rhythm. Whether estimated kidney function is a better predictor of sinus rhythm was not studied.

 Validation datasets were smaller than the derivation dataset and therefore did not allow for multiple confounding. Post-hoc subgroup analysis by baseline rhythm in EAST-AFNET 4 may have underestimated effects due to smaller group sizes. Almost all patients received guideline-recommended anticoagulation, rate and rhythm control, and often effective treatment of concomitant conditions. 24-hour blood pressure may provide more granular prognostic information than office-based blood pressure, but 24-hour blood pressure 23 readings were not available for this analysis. 5 time have been published ^{20,26}.

6 While NT-proBNP can be measured in clinical routine as *in-utro* diagnostic devices with

7 regulatory approval, the assays for ANGPI¹2 and BMP10 are not approved for eliginal use,

 Left atrial size was used in the clinical score rather than left atrial volume. Indexed left atrial volume can provide more detailed information on left atrial size compared to left atrial diameter, but the predictive value of left atrial volume for recurrent AF is less well 27 established than left atrial size²⁸. Indexed left atrial volume was not available in sufficient patients to be assessed in this study. The predictive ability of the different biomarker-based models is only valid for the specific AF prevalences in the cohorts studied. Further research into the clinical utility of the biomarkers identified here is warranted.

The blood samples studied here stem from patients with predominantly Caucasian ethnicity,

which may limit the generalizability of the findings to other ethnic groups. Validation in

other ethnicities is therefore needed.

Testing the relationship between specific blood biomarker levels and a remote outcome

observed 12 months later is challenging. In order to limit acute effects of the specific

biomarker levels at baseline, we corrected for the acute rhythm at baseline, among other

clinical parameters. Prediction of future rhythm by biomarkers depends on several factors,

including the underlying biology of each biomarker, spontaneous variations in

concentrations, and assay quality. Lack of predictive ability in this study does not rule out

relevant biological function of a given molecule. The proposed interventions countering the

disease processes associated with biomarkers require further testing.

Conclusion

 In conclusion, these findings suggest that NT-proBNP, ANGPT2 and BMP10 can be combined to identify patients with AF at high risk of not attaining sinus rhythm. The disease processes related to ANGPT2 and BMP10 emerge as likely contributors to future rhythm in patients with and without rhythm control therapy. NT-proBNP elevations interact with early rhythm control, potentially suggesting repeat assessment of NT-proBNP to monitor the effectiveness of rhythm control. 5 which may limit the generalizability of the findings to other ethnic groups. Validation in

6 other ethnicities is therefore needed.

7 Testing the relationship between specific blood biomarker levels and a remote outco

Acknowledgement: We thank AFNET staff.

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Figure legends

 Graphical Abstract. In patients diagnosed with atrial fibrillation, low concentrations of NT-proBNP, BMP10 and ANGPT2 at baseline predict sinus rhythm at 12-month follow-up in context with clinical features. This was validated in additional datasets, of which AXAFA- AFNET 5 is depicted here. A treatment interaction shows that NT-proBNP's predictive value is impacted by early rhythm control treatment.

AF, atrial fibrillation; ANGPT2, angiopoietin 2; BMP10, bone morphogenetic protein 10; NT-

proBNP, N-terminal pro-B-type natriuretic peptide

 Figure 1. Low concentrations of the biomarkers NT-proBNP, Angiopoietin 2 and Bone morphogenetic protein 10 predict sinus rhythm at 12-month follow-up in the derivation dataset (EAST-AFNET 4). Odds ratios for sinus rhythm at 12-month follow-up (A) and odds ratios by randomized treatment group (B). Forest plot showing odds ratios for each biomarker for the outcome sinus rhythm at 12-month follow-up and 95% confidence intervals. The odds ratio for NT-proBNP shows an interaction between NT-proBNP concentrations and randomized treatment group (early rhythm control or usual care). All odds ratios are corrected for clinical features, age, sex, EAST study center, rhythm at baseline, atrial fibrillation type, randomized treatment group, body mass index, diastolic blood pressure, and left ventricular ejection fraction. Even after multiple confounding, high biomarker concentrations indicate lower odds of sinus rhythm at 12-month follow-up. Low concentrations of NT-proBNP predict sinus rhythm at 12-month follow-up in patients with 23 usual care (only symptomatic rhythm control). High concentrations of NT-proBNP do not necessarily predict lack of sinus rhythm at 12 months if patients receive early rhythm control. *Angiopoietin 2 (ANGPT2), bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C- reactive protein (CRP), D-dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3* 5 context with clinical features. This was validated in additional datasets, of which AXAFA-AFNET 5 is depicted here. A treatment interaction shows that NT-proBNP's predictive value

2 is impacted by early rhythm control

(FABP3), fibroblast growth factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like

- *growth factor binding protein 7 (IGFBP7), interleukin-6 (IL-6), N-terminal pro–B-type natriuretic*
- *peptide (NT-proBNP), cardiac troponin (TnT) and serum creatinine (sCr).*
-

 Figure 2. Biomarker concentration distributions at baseline in patients with sinus rhythm (teal) or atrial fibrillation (orange) at 12-month follow-up. Violin plot of the distribution of log-transformed biomarker concentrations for each of 14 biomarkers at baseline, split by the outcome of rhythm at 12-month follow-up. Log-transformed biomarker concentrations are shown on the y-axis and the kernel estimated frequency on the x-axis. Central thick horizontal lines are the median and the thinner lines represent interquartile range. N-terminal pro B-type Natriuretic Peptide, Angiopoietin 2 and Bone Morphogenetic Protein 11 10 show an association with sinus rhythm at 12-month follow-up based on the acceptance of a Type 1 error of 5%. P-values were calculated using mixed logistic regression model with site as random effect, adjusted for age, sex, study site, rhythm at baseline, randomized group (early rhythm control or usual care), body mass index, diastolic blood pressure, and left 5 (teal) or atrial fibrillation (orange) at 12-month follow-up. Violin plot of the distribution of
6 log-transformed biomarker concentrations for each of 14 biomarkers at baseline. Split by the
6 outcome of rhythm at 12-m

 ventricular ejection fraction, those clinical features that were associated with outcomes including sinus rhythm in the main EAST-AFNET 4 trial.

 Angiopoietin 2 (ANGPT2), bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C- reactive protein (CRP), D-dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3 (FABP3), fibroblast growth factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like growth factor binding protein 7 (IGFBP7), interleukin-6 (IL-6), N-terminal pro–B-type natriuretic peptide (NT-proBNP), cardiac troponin (TnT) and serum creatinine (sCr).

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 Figure 3. Biomarkers measured at baseline predicting sinus rhythm at 12-month follow-up in all participants of the biomarker study, separately analysed by rhythm at baseline (atrial fibrillation at baseline or sinus rhythm at baseline) and randomized treatment group (early rhythm control or usual care), respectively, in a post-hoc analysis.

 Of the three biomarkers identified to be predictive of sinus rhythm in the whole cohort, NT- proBNP, ANGPT2 and BMP10, all three biomarkers retained their predictive value in the subgroup of patients randomized to usual care. All three biomarkers also retained their predictive value in the subgroup of patients in atrial fibrillation during blood draw at baseline.

 Angiopoietin 2 (ANGPT2), bone morphogenetic protein 10 (BMP10), N-terminal pro–B-type natriuretic peptide (NT-proBNP)

 Figure 4. Internal validation: Angiopoietin 2, Bone morphogenetic protein 10 and NT- proBNP biomarkers at baseline predict Sinus Rhythm at 24-month follow-up even after correction for multiple confounders. Odds ratios for sinus rhythm at 24-month follow-up. This analysis provides an internal validation of the biomarkers predicting sinus rhythm at 12-month follow-up (**Figure 1**). All Odds ratios are corrected for clinical age, sex, study site, rhythm at baseline, randomized treatment group (early rhythm control or usual care), body mass index, diastolic blood pressure, and left ventricular ejection fraction, those clinical features that were associated with outcomes including sinus rhythm in the main EAST-17 AFNET 4 trial⁴. Low concentrations of NT-proBNP, ANGPT2 and BMP10 predict sinus rhythm at 24-month follow-up in patients. Accordingly, high concentrations predict lack of sinus rhythm at 24-month follow-up. 5 baseline.

6 Angiopoietin 2 (ANGP12), bone marphogenetic protein 10 (184P10), N-terminal pro- μ Enger

7 notriuretic peptide (NT-proBNP)

8 **Figure 4.** Internal validation: Angiopoietin 2, Bone morphogenetic protein 10

 Angiopoietin 2 (ANGPT2), bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C- reactive protein (CRP), D-dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3 (FABP3), fibroblast growth factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like growth factor binding protein 7 (IGFBP7), interleukin-6 (IL-6), N-terminal pro–B-type natriuretic peptide (NT-proBNP), cardiac troponin (TnT) and serum creatinine (sCr).

 Figure 5. Validation applying biomarker based clusters indicating cardiovascular outcome risk: Patients at high risk of cardiovascular complications as estimated by biomarker-based

 clusters have reduced odds of sinus rhythm at 12-month and 24-month follow-up. Odds ratio for the high cardiovascular outcome risk (red) and intermediate cardiovascular outcome risk biomarker clusters (orange and green) for sinus rhythm at 12-months follow-up (A above) and at 24-month follow-up (B bottom) tested against the low cardiovascular risk cluster (not depicted as used as reference). All odds ratios are corrected for age, sex, study center, rhythm at baseline, atrial fibrillation type (depicted) randomized treatment group (early rhythm control or usual care), as well as body mass index, diastolic blood pressure, and left ventricular ejection fraction, the clinical features that were associated with outcomes 9 including sinus rhythm in the main EAST-FNET 4 trial⁴. *AF (atrial fibrillation)* **Figure 6**. Validation by Random forest analyses identified highest importance for similar biomarkers, alongside rhythm at baseline and AF pattern, as predictors of sinus rhythm at 12-month follow-up (Figure 6A – importance, Figure 6B – SHAP value). *Atrial fibrillation (AF), Angiopoietin 2 (ANGPT2), baseline (BL), body mass index (BMI), bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C-reactive protein (CRP), D-dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3 (FABP3), fibroblast growth factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like growth factor binding protein 7 (IGFBP7), interleukin-6 (IL-6), mixed-effects random forest (MERF), N-terminal pro–B- type natriuretic peptide (NT-proBNP), cardiac troponin (TnT), serum creatinine (sCr) and SHapley Additive exPlanations (SHAP)* 3 depicted as used as reference). All odds ratios are corrected for age, sex, study center, rhydim

23 Accelere, atrial fibrillation type (depicted) randomized treatment group (early rhydim

27 Centrol or usual care), as

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Figure 7. External validation of the prediction of sinus rhythm at the end of

follow-up by baseline biomarkers in AXAFA-AFNET 5. AXAFA –AFNET 5 enrolled

- 674 patients undergoing a first AF ablation with at least one stroke risk factor. Patients were
- randomized to apixaban or vitamin K antagonist therapy without affecting rhythm.
- Individual models with rhythm at baseline, age, and sex were constructed to determine 5 Individual models with rhythm at baseline, age, and sex were constructed to determine

6 whether each biomarker predicts sinus rhythm at the end of follow-up 120 days after >

7 randomization, 549 putients with sinus rh
- whether each biomarker predicts sinus rhythm at the end of follow-up 120 days after
- randomization, 549 patients with sinus rhythm, 71 patients with atrial fibrillation.
- ** p-values were calculated using logistic regression, adjusted for sex, age, rhythm at baseline and*
- *treatment group. Abbreviations: Angiopoietin 2 (ANGPT2), bone morphogenetic protein 10*
- *(BMP10), N-terminal pro–B-type natriuretic peptide (NT-proBNP).*

1 **Table 1:** Baseline characteristics and biomarkers in the EAST-AFNET 4 biomolecule study.

** p-values were calculated on the unimputed dataset using mixed logistic regression model with site*

2 as random effect, for biomarkers additionally adjusted for sex, age, body mass index, diastolic blood
3 pressure, left ventricular ejection fraction and AF-type. Distributions are shown as mean and SD for
4 normally dist *pressure, left ventricular ejection fraction and AF-type. Distributions are shown as mean and SD for*

normally distributed values, as median and IQR for non-normally distributed values and

biomarkers, and as frequency (percentage) for nominal features.

Abbreviations: Atrial Fibrillation (AF), sinus rhythm (SR), early rhythm control (ERC), usual care

(UC), body mass index (BMI), left ventricular ejection fraction (LVEF), left atrium (LA), New York

Heart Association Functional Classification of heart failure (NYHA), European Heart Rhythm

Association score (EHRA), angiopoietin 2 (ANGPT2), bone morphogenetic protein 10 (BMP10),

cancer antigen 125 (CA125), C-reactive protein (CRP), D-dimer, endothelial specific molecule 1

(ESM1), fatty acid binding protein 3 (FABP3), fibroblast growth factor 23 (FGF23), growth

 *differentiation factor 15 (GDF15), insulin-like growth factor binding protein 7 (IGFBP7), interleukin-*4 from the signification value of the state and ON Review and the state and the s

6 (IL-6), N-terminal pro–B-type natriuretic peptide (NT-proBNP), cardiac troponin (TnT) and

 serum creatinine (sCr). Estimated Glomerular Filtration (eGFR) rate was calculated as CKD EPI, Chronic Kidney Disease Epidemiology Collaboration

- 1 **Table 2.** Baseline biomarker concentrations are shown split by patient rhythm at 12-month
- 2 follow-up (sinus rhythm or atrial fibrillation) and by randomized group (early rhythm
- control or usual care).

	Randomisation	Early rhythm control		Usual care		SR vs. AF	
	group					12 month	
	Rhythm at 12-	Sinus rhythm	AF 12-month	Sinus rhythm	AF 12-month	p-value*	
	month follow-up	12-month FU	FU	12-month FU	FU		
	NT-proBNP	377	750	294	782	0.001	
	(pg/ml)	$[164 - 859]$	$[376 - 1351]$	$[127 - 700]$	$[437 - 1454]$		
	ANGPT2 (ng/ml)	2.34	3.45	2.24	3.31	0.001	
		$[1.78 - 3.41]$	$[2.43 - 5.62]$	$[1.7 - 3.09]$	$[2.15 - 4.62]$		
	BMP10 (ng/ml)	2.08	2.21	2.04	2.24	0.010	
		$[1.8 - 2.39]$	$[1.96 - 2.58]$	$[1.79 - 2.34]$	$[1.94 - 2.66]$		
	FGF23 (pg/ml)	151	179	141	168	0.429	
		$[112 - 209]$	$[125 - 238]$	$[108 - 197]$	[129 - 226]		
	ESM1 (ng/ml)	2.01	2.17	1.98	2.09	0.218	
		$[1.61 - 2.52]$	$[1.75 - 2.88]$	$[1.57 - 2.52]$	$[1.73 - 2.66]$		
	GDF15 (pg/ml)	1304	1441	1254	1589	0.461	
		$[958 - 1934]$	$[997 - 2008]$	$[911 - 1782]$	$[1071 - 2347]$		
	IGFBP7 (ng/ml)	100	108	98.8	104	0.487	
		$[89 - 114]$	$[93 - 126]$	$[88.5 - 110]$	$[94.7 - 119]$		
	IL-6 (pg/ml)	2.47	2.6	2.37	3.02	0.417	
		$[1.57 - 3.88]$	$[1.76 - 4.62]$	$[1.56 - 3.6]$	$[1.98 - 4.65]$		
	FABP3 (ng/ml)	31.4	35.3	30.4	33.5	0.151	
		$[25.6 - 39]$	$[28.3 - 43.4]$	$[25.7 - 37.8]$	$[28.0 - 42.0]$		
	D-dimer $(\mu g/ml)$	0.17	0.19	0.16	0.16	0.638	
		$[0.08 - 0.33]$	$[0.1 - 0.36]$	$[0.08 - 0.32]$	$[0.08 - 0.32]$		
	TnT (ng/l)	10.6 [°]	13.0	10.3	12.5	0.415	
		$[7.81 - 15.7]$	$[9 - 17.6]$	$[7.53 - 15.5]$	$[8.68 - 17.7]$		
	CRP (mg/l)	$\overline{2}$	1.97	2.07	2.52	0.910	
		$[0.95 - 4.65]$	$[0.9 - 4.63]$	$[0.93 - 4.37]$	$[1.12 - 4.87]$		
	sCr (µmol/l)	81.3	83	79.5	84.4	0.541	
		$[70 - 95]$	$[72.7 - 94.8]$	$[68.0 - 91.9]$	$[72 - 97.2]$		
	CA125 (U/ml)	11.4	12.3	10.8	11.4	0.779	
		$[8.0 - 15.8]$	$[8.3 - 17.1]$	$[7.8 - 15.7]$	$[7.96 - 15.9]$		
$\overline{4}$ 5		$*$ p-values were calculated using mixed logistic regression model with site as random effect, adjusted for sex, age, body mass index, diastolic blood pressure, left ventricular ejection fraction and					
6	randomization group. Values are shown as median [IQR].						
7							
8 Abbreviations: Atrial fibrillation (AF), sinus rhythm (SR), follow-up (FU), angiopoietin 2 (ANGPT2),							
9 bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C-reactive protein (CRP), D-							
1 በ	dimer, endothelial specific molecule $I(FSM1)$ fattu acid binding protein $2(FARP2)$ fibroblast						

binding protein 7 (IGFBP7), interleukin-6 (IL-6), N-terminal pro-B-type natriuretic peptide (NT-

13 proBNP), cardiac troponin (TnT) and serum creatinine (sCr). 13 *proBNP), cardiac troponin (TnT) and serum creatinine (sCr).*

15

^{*} *p*-values were calculated using mixed logistic regression model with site as random effect, adjusted for sex, age, body mass index, diastolic blood pressure, left ventricular ejection fraction and randomization group. 5 *for sex, age, body mass index, diastolic blood pressure, left ventricular ejection fraction and*

⁷

⁸ *Abbreviations: Atrial fibrillation (AF), sinus rhythm (SR), follow-up (FU), angiopoietin 2 (ANGPT2),*

⁹ *bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C-reactive protein (CRP), D-*

¹⁰ *dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3 (FABP3), fibroblast*

¹¹ *growth factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like growth factor*

¹⁴

1 **Table 3:** Baseline clinical characteristics used as confounders and biomarker concentrations

2 in the derivation data set (EAST-AFNET 4 biomolecule study) at baseline by randomized

3 group and by baseline rhythm. Rhythm at time of blood sampling was included as a fix factor

4 in the analyses of outcome.

1 ** p-values were calculated in the unimputed, pooled dataset (ERC and UC combined) using mixed* 2 *logistic regression model with site as random effect, for the biomarkers additionally adjusted for sex,* 3 age, body mass index, diastolic blood pressure, left ventricular ejection fraction and AF-type, the clinical features that were associated with outcomes including sinus rhythm in the main EAST-AFNET 4 dataset4. 4 *clinical features that were associated with outcomes including sinus rhythm in the main EAST-AFNET 4 dataset4.*

 Distributions are shown as mean and SD for normally distributed values, as median and IQR for non- normal distributed values and biomarkers, and as frequency (percentage) for nominal features. For biomarker concentrations there were no differences between the randomized groups, but differences between Sinus rhythm or AF during the baseline visit. 4 Cutton genuine state were associated with outcomes including sinus ringinal in the main Encyclopter 4 did the Distribution variables and biomorkers, and as frequency (percentage) for nominal fighters are shown as followi

10 *Abbreviations: Atrial fibrillation (AF), Early rhythm control (ERC), usual care (UC), body mass index* 11 *(BMI), atrial fibrillation (AF), left ventricular ejection fraction (LVEF), Angiopoietin 2 (ANGPT2),*

12 *bone morphogenetic protein 10 (BMP10), cancer antigen 125 (CA125), C-reactive protein (CRP), D-*

13 *dimer, endothelial specific molecule 1 (ESM1), fatty acid binding protein 3 (FABP3), fibroblast growth*

14 *factor 23 (FGF23), growth differentiation factor 15 (GDF15), insulin-like growth factor binding*

15 *protein 7 (IGFBP7), interleukin-6 (IL-6), N-terminal pro–B-type natriuretic peptide (NT-proBNP),* cardiac troponin (TnT) and serum creatinine (sCr).

1 **Table 4** Threshold concentrations for NT-proBNP, BMP10, and ANGPT2 determined in the derivation dataset (EAST-AFNET 4 biomolecule study). The lower threshold was defined as

2 derivation dataset (EAST-AFNET 4 biomolecule study). The lower threshold was defined as
3 the nearest round concentration below which 80% of patients attained sinus rhythm at 12

3 the nearest round concentration below which 80% of patients attained sinus rhythm at 12
4 months. The higher threshold was defined as the nearest rounded concentration above which

4 months. The higher threshold was defined as the nearest rounded concentration above which
5 40% of patients were in AF at 12 months.

5 40% of patients were in AF at 12 months.

6

- 7 *Abbreviations: Atrial Fibrillation (AF), angiopoietin 2 (ANGPT2), bone morphogenetic protein 10*
- 8 *(BMP10), N-terminal pro–B-type natriuretic peptide (NT-proBNP)*

1 **Table 5. Estimated clinical utility of adding NT-proBNP, BMP10, and ANGPT2**

2 **alone or in combination to a clinical risk score to predict sinus rhythm at 12**

months. Sinus rhythm at 12 months was initially predicted by a clinical risk score based on three validated clinical features (LA size > 50mm, persistent AF, age > 75 years) alone. This three validated clinical features (LA size >50mm, persistent AF, age >75 years) alone. This

5 reference score was then combined with one, a combination of two or all three binarized

6 predictive biomarkers (see Table 3 on biomarker thresholds: NT-proBNP <1000 pg/ml or

 $7 > 1500 \text{ pg/ml}$, ANGPT2 <3.5 ng/ml or >3.5 ng/ml, BMP10 <2 ng/ml or >3 ng/ml). If either

- 8 the clinical risk score is ≥ 2 or any of the biomarkers added to the model surpasses its
- 9 threshold, the model predicts failure to attain sinus rhythm at 12-month follow-up and
- 10 predicts AF instead. By definition, there was no reclassification into low-risk groups. All 11 numbers indicate number of patients with percentages of the predicted class in brackets.
- 12
- 13
- 14

15

16 *Abbreviations: Atrial Fibrillation (AF), angiopoietin 2 (ANGPT2), bone morphogenetic protein 10* 17 *(BMP10), N-terminal pro–B-type natriuretic peptide (NT-proBNP), Sinus Rhythm (SR), 12-month* 18 *Follow-up (12M)*

19 There were 140 missing values in outcomes and 225 missing values in LA size. The

20 additional use of biomarkers for prediction can lead to differing missing values in

21 predictions made for participants with available outcome data.

22

23

A

Each Biomarker at Baseline and Sinus Rhythm at 12-month Follow-up

2 *Figure 1* 3 *159x227 mm (x DPI)*

Biomarker Concentrations at Baseline in Patients with Sinus Rhythm or Atrial Fibrillation at 12-month Follow-up

Each Biomarker at Baseline and Sinus Rhythm at 12-month Follow-up

Each Biomarker at Baseline and Sinus Rhythm at 24-month Follow-up

\mathbf{A} Cardiovascular Risk Clusters and Sinus Rhythm at 12-month Follow-up

Structured Graphical Abstract

- Key Question
- Can clinical features or circulating biomarkers measured at baseline predict sinus rhythm
- during mid-term follow-up in patients with atrial fibrillation (AF)? Which biomarkers
- interact with early rhythm control therapy?

Key Finding

- Low baseline concentrations of angiopoietin 2 (ANGPT2), bone morphogenetic protein 10
- (BMP10), and N-terminal pro-B-type natriuretic peptide (NT-proBNP) predicted sinus
- rhythm at follow-up in the EAST-AFNET 4 trial and in two external validation datasets. NT-
- proBNP had reduced predictive value in patients treated with early rhythm control. ANGPT2
- and BMP10 added most information in patients who were in AF when blood samples were
- taken. The three biomarkers refined prediction of sinus rhythm compared to a clinical risk
- score.
- Take Home Message
- Low concentrations of NT-proBNP (<1000 pg/ml), ANGPT2 (<3.5 ng/ml) and BMP10 (<2
- ng/ml) identified patients with a high chance of attaining sinus rhythm during follow-up
- when added to a clinical risk score. Combining NT-proBNP with ANGPT2 and BMP10 is
- particularly useful in patients in AF at the time of blood sampling and in patients on rhythm
- control.

