

Supplementary Material: does QRS-T loop coupling add to the QRS-T angle? Fréchet distance and reduced ejection fraction in hospital ECGs

Supplement to the preprint, version 1, 16 October 2026. Sections are numbered S0a and S1 to S27 and tables are numbered separately (Table S1 to Table S124, not always in order of appearance). References cited as numbers refer to the reference list of the main manuscript.

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Original association estimates, later developmental sensitivities, post-unblinding analyses, post hoc scenario analyses and unavailable branches are distinguished throughout. Counts of persons or ECGs below 10 are shown as <10, and complementary cells are coarsened so that they cannot be recovered. Counts from which a value between 1 and 9 could be derived by subtraction or summation across tables were also coarsened.

Supplementary table index

Table S1. S1a. Specification and access times (UTC)

Table S2. S2. Participants, flow and measurement missingness

Table S3. LVEF <40%, normalized Fréchet

Table S4. LVEF <40%, normalized Fréchet

Table S5. Coded cardiomyopathy, beat-median Fréchet

Table S6. Coded cardiomyopathy, beat-median Fréchet

Table S7. RV dysfunction, DTW

Table S8. RV dysfunction, DTW

Table S9. S3. Original association assessment and ordered sensitivities

Table S10. S3a. All apparent AUC components and descriptive bootstrap OR intervals

Table S11. S3b. Original-run status, computational failures and reasons

Table S12. S4. Complete boundary perturbation sensitivities

Table S13. S4a. All deterministic shifts

Table S14. S7. Reporting checklist and unavailable source fields

Table S15. S7. Reporting checklist and unavailable source fields

Table S16. S7. Reporting checklist and unavailable source fields

Table S17. S8. Delayed specified verification analyses and reference bias

Table S18. S8. Delayed specified verification analyses and reference bias

Table S19. S8. Delayed specified verification analyses and reference bias

Table S20. S8. Delayed specified verification analyses and reference bias

Table S21. S8. Delayed specified verification analyses and reference bias

Table S22. S8. Delayed specified verification analyses and reference bias

Table S23. S9. Developmental angle-error correction

Table S24. S9. Developmental angle-error correction

Table S25. S9. Developmental angle-error correction

Table S26. S9. Developmental angle-error correction

Table S27. S9. Developmental angle-error correction

Table S28. S9. Developmental angle-error correction
Table S29. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S30. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S31. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S32. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S33. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S34. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S35. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S36. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S37. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S38. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S39. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S40. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S41. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle
Table S42. S12. Evidence boundaries
Table S43. S13a. Conditional reliability, full coefficients and repeatability
Table S44. S13a. Conditional reliability, full coefficients and repeatability
Table S45. S13a. Conditional reliability, full coefficients and repeatability
Table S46. S13a. Conditional reliability, full coefficients and repeatability
Table S47. S13b. Known-truth simulation
Table S48. S13c. Alternative SIMEX error laws and extrapolations
Table S49. S13c. Alternative SIMEX error laws and extrapolations
Table S50. S13d. Stronger orientation comparators
Table S51. S13e. Both markers against both endpoints
Table S52. S13e. Both markers against both endpoints
Table S53. S13f. Historical cross-fitted development evidence
Table S54. S13f. Historical cross-fitted development evidence
Table S55. S13f. Historical cross-fitted development evidence
Table S56. S13g. Seven-day medication-order sensitivity
Table S57. S13g. Seven-day medication-order sensitivity
Table S58. S13h. Partial extended adjustment
Table S59. S13h. Partial extended adjustment
Table S60. S13i. LVEF distributions, continuous and ordinal references
Table S61. S13i. LVEF distributions, continuous and ordinal references
Table S62. S13i. LVEF distributions, continuous and ordinal references
Table S63. S13i. LVEF distributions, continuous and ordinal references
Table S64. Null-generator diagnostics and empirical developmental comparison
Table S65. S14. Differential T-end error by ejection fraction
Table S66. S15. Exploratory post-unblinding assessment analyses
Table S67. S15a. Participant flow and Table 1
Table S68. S15a. Participant flow and Table 1
Table S69. S15b. Development-fixed predictions

Table S70. S15b. Development-fixed predictions
Table S71. S15b. Development-fixed predictions
Table S72. S15c. Error sensitivities
Table S73. S15d. Verification weighting
Table S74. S15e. Missingness
Table S75. S15e. Missingness
Table S76. S15e. Missingness
Table S77. S15f. LVEF descriptions
Table S78. S15f. LVEF descriptions
Table S79. S15g. Marker scale and selected-sample probabilities
Table S80. S15g. Marker scale and selected-sample probabilities
Table S81. S15h. Conditional cross-marker analyses
Table S82. S15i. Rhythm and conduction strata
Table S83. Case-only T-end perturbation in development
Table S84. S13k. Bivariate tipping analysis: data and repeat-based inputs
Table S85. S13k. Corrected marker OR within the assumed reliability ranges
Table S86. S13k. Anchor settings, corrected ORs and tipping points
Table S87. S13k. Tipping curve: angle reliability at which the corrected marker OR falls to 1.0
Table S88. S13k. Tipping curve: angle reliability at which the corrected marker OR falls to 1.25
Table S89. S13k. Known-truth simulation at the angle-only tipping point
Table S90. S0. Evidence hierarchy
Table S91. S18. Corrected bootstrap intervals for the association rows of S3b
Table S92. S18. Corrected bootstrap intervals for post hoc branches of S15
Table S93. S18. Covariate-standardized probabilities by marker quartile with corrected intervals
Table S94. S18. Denominators of the multiple imputation in S15e
Table S95. S19. Repeat-based anchors with population uncertainty
Table S96. S19. Scenario boxes spanned by the 95% intervals of the anchor quantities
Table S97. S19. Marker over-measurement in cases at which the corrected OR reaches 1.25
Table S98. S19. Persistent error share at which the limit of admissibility is reached
Table S99. S20. Repeat error by LVEF group
Table S100. S20. Repeat error by QRS amplitude quintile
Table S101. S21. Imputed marker values
Table S102. S21. Tipping points of delta-adjusted imputation
Table S103. S22. First technically successful ECG: population of the weighted verification analysis
Table S104. S22. Corrected OR for assumed selection factors B
Table S105. S23. OR by interval between ECG and echocardiogram
Table S106. S23. Pacing indicators and the OR after exclusion
Table S107. S23. Controls with and without documented diagnoses
Table S108. S24. OR of the Fréchet distance with orientation comparators
Table S109. S18. Stopping rule and acceptance rule in rejected bootstrap replicates
Table S110. S22. Feasible interval for the selection factor B
Table S111. S25. Centering and SD, LVEF <40%

Table S112. S25. Centering and SD, coded cardiomyopathy

Table S113. S25. Centering and SD of the stronger model B4

Table S114. S25. Development-fixed model coefficients, LVEF <40%

Table S115. S25. Development-fixed model coefficients, coded cardiomyopathy

Table S116. S25. Verification model

Table S117. S25. Coefficients of the development models of S13a, training

Table S118. S25. Coefficients of the development models of S13a, internal validation

Table S119. S17. Covariates under reconstruction with shifted T ends

Table S120. S22. Index population of the main analysis

Table S121. S0a. Checksums of the release package

Table S122. S26. Marker OR in persons with a classical left bundle branch block pattern

Table S123. S26. Marker OR with QRS duration as a spline

Table S124. S27. Marker OR for negative-control diagnoses

S0. Overview, evidence hierarchy and model specification

This supplement distinguishes five tiers of evidence. Table S90 states for each tier which data were used and how the results are used in the manuscript. Sections S17 to S27 report analyses specified after the primary result was known, and all of them are post hoc. Section S0a gives the operational definition of the measurement chain. They describe named scenarios with tipping points. None of them validates an error, missingness or selection model.

Table S90. S0. Evidence hierarchy

Tier	Analyses	Data	Status in the manuscript
1	Primary association (Table 2) and originally specified sensitivities: stronger model, LVEF $\leq 40\%$, narrow window, sinus, narrow QRS, age and sex strata, first-technical-index verification (S3, S8)	Internal assessment partition, previously used for related hypotheses	Specified before the assessment run; success rule met; sensitivities descriptive
2	Developmental sensitivities: construct overlap, angle-error correction, comparators, cross-markers, medication, partial adjustment, LVEF distributions, LUDB-based T-end correction (S9, S10, S13, S14)	Training and internal validation	Exploratory, after marker selection; not independent replication
3	Post hoc assessment analyses: flow, fixed-coefficient performance, calibration, error correction, imputation, weighting, strata (S15)	Internal assessment partition	Specified after the primary results were known
4	Post hoc scenario analyses: bivariate tipping analysis, extended scenario set, differential and persistent error, repeat error by LVEF, missing-data tipping points, selection, echo interval, pacing, code controls, orientation comparators, T-end shifts, bundle branch block stratum, QRS spline, negative-control diagnoses (S13k, S17, S19-S24, S26, S27)	Development; the echo-interval figures are also reproduced in the assessment partition	Named scenarios; no validation of any model
5	Corrected bootstrap intervals of the original run (S3b, S15; S18)	Assessment rows read again	Post hoc correction of a construction error; point estimates and Wald intervals unchanged
Not done	External replication, blinded review of references and ECGs, pacing-spike detection, adjudicated rhythm strata (S6)	None	Not available

Model specification. Centering constants, scaling, age-basis knots (40, 60 and 80 years), coefficients of the development-fixed models, the thresholds of the S15b sensitivities, the marker quartile boundaries, the angle spline and the verification model are tabulated in S25; the coefficients

of the basic model with and without the marker are also in Table S45. Only the tabulated models are covered: the stronger model B4 is tabulated with centering and SD but without coefficients, the refits in the assessment partition are reported only as ORs per SD, and the measurement chain is defined in S0a and by the software release named there.

S0a. Operational definition of the primary marker and the comparator angle

This section defines, at the level needed to reproduce the quantities, how the normalized QRS-T Fréchet distance (column name `qrs_t_normalized_discrete_frechet`) and the spatial QRS-T angle (spatial_qrs_t_angle_deg) were obtained. It describes the fixed release; it does not replace the software, whose frozen release is public (Code availability of the main manuscript). All numeric settings below are those of the release used for the analyses. Where a setting acts as a gate, the quantity is set to missing (abstention) when the gate fails; no value is imputed.

S0a-1. Software identity

LoopLens (Python package), version 10.1, fixed release of 7 October 2026. Two checksums describe the release (S0a-12): the SHA-256 of the sorted list of all 1,959 release files and the source hash of its 875 Python files. The code executed for the analysed ECGs was a runtime snapshot of that release in which only later analysis-stage modules (association, phenome and broad-adjustment stages, S0a-12) differ from the release; the signal, delineation, reconstruction and marker code (72 Python files of the core package and the waveform loader and feature-extraction modules) is identical. The hash that the extraction run recorded for the code that defines a marker (core package plus six record-level modules: classical criteria, lead measurements, record feature extraction, panels, report parser, waveform loader), `c166bd00...89b9`, equals the value recomputed for the release. Hashes are shortened to the first eight and the last four characters; the full values are available from the author.

S0a-2. Input and signal admission

Input: the 10-second standard 12-lead ECG of MIMIC-IV-ECG 1.0 (WFDB), read in the order I, II, III, aVR, aVL, aVF, V1 to V6 and converted to millivolts. Sampling rate: 500 Hz (the native rate; any other rate is resampled by anti-aliased rational polyphase resampling). Dropouts of up to 40 ms are filled by interpolation, provided that at most 0.5 per cent of the samples are filled; longer gaps are not repaired.

A recording was admitted only if all of the following held: duration at least 8 s; all samples finite; no flat lead (standard deviation below 0.01 mV); at most one lead with a peak-to-peak range below 0.05 mV or above 20 mV; a signal-quality score of at least 0.50 (penalties for flat leads, clipping, high-frequency, baseline and powerline spectral content, Einthoven-law violation, suspected limb-lead reversal and suspected precordial misplacement). Recordings with suspected limb-lead reversal (a polarity pattern of leads I and aVR typical of right-arm and left-arm exchange) were

excluded from all analyses. At least two R peaks had to be found and at least one beat had to be delineated.

S0a-3. Signal paths and filters

Three paths were derived from the admitted signal, all with zero-phase (forward-backward) filtering:

- Morphology path (used for the template cycle and the vector reconstruction): Butterworth band-pass of third order from 0.05 to 150 Hz; additionally a powerline notch (second-order IIR notch, quality factor 30) at 60 Hz, except when the recorder metadata stated a 60-Hz notch (then none was added).
- Delineation path (used for R detection and delineation): Butterworth band-pass of fourth order from 0.5 to 40 Hz, the same notch rule, then subtraction of a 2-second centered running median (baseline removal).
- The unfiltered millivolt signal is retained for acquisition-related checks only.

S0a-4. R-peak detection

The delineation path is band-pass filtered once more (third order, 5 to 30 Hz). Leads are usable if their 95th-percentile absolute amplitude lies between 0.01 and 12 mV. Candidate peaks come from (i) a spatial-energy detector (median across usable leads of the squared normalized derivative, integrated over 60 ms, peak-picked with a refractory period of 180 ms and a prominence threshold derived from the robust noise level of that signal) and (ii) a standard QRS peak detector applied to up to four usable leads (lead II first). Candidates within 60 ms of the cluster median are grouped; a cluster is kept if the spatial-energy detector found it or at least two sources agree, and its position is refined to the maximum of the polarity-invariant multilead magnitude within 55 ms; peaks closer than 250 ms to the record edges are dropped. Peaks that are probably P or T waves are removed (energy below 15 per cent of a typical strong beat, or within 360 ms of the previous beat and below half of its energy). The detector uses no outcome information.

S0a-5. Delineation

Three detectors run on the delineation path: (i) wavelet-based delineation (NeuroKit2 package, discrete wavelet transform method) on lead II; (ii) a physiology-constrained, polarity-invariant 12-lead delineator, which finds QRS limits in each lead independently and selects the earliest and latest boundary cluster supported by at least two leads; (iii) a detector on the Kors vector reconstruction (S0a-7) based on spatial velocity and spatial magnitude. Their candidates for each fiducial point (P onset, peak and offset; Q, R onset, R offset, S, J point; T onset, peak and offset; U onset, peak and offset) are fused as follows.

Candidates for one fiducial are sorted in time and grouped into clusters; a candidate joins the current cluster if it lies within the marker-specific tolerance of the cluster median (R peak 10 ms;

P onset 30; P peak 25; P offset 30; Q 14; R onset 16; R offset 18; S 14; J point 18; T onset 35; T peak 35; T offset 45; U onset 60; U peak 50; U offset 80 ms). The nominal source weights are 0.40 (wavelet), 0.35 (multilead) and 0.25 (vector), modulated by the support of each source, its local confidence and, for boundary points, a small source factor. Points without a specific tolerance use the 20-ms conflict setting. Each fused point carries a confidence in $[0, 1]$, an uncertainty in milliseconds and a support count. Physiological ordering of the points is enforced, and a conventional discrete P wave is withheld when the rhythm class does not allow it (this affects the P wave only, not ventricular delineation). Points are used by downstream measurements only above a wave-specific confidence threshold: QRS points 0.35, P, T, U and ST points 0.15.

Beat plausibility: R-peak confidence at least 0.20, all points inside the recording, R onset before R peak before R offset, QRS duration between 20 and 360 ms, Q and S points consistent with the QRS limits. Accepted beats are the plausible beats whose fiducial offsets (relative to the R peak) lie within a robust standardized distance of 8 from the record median (scale: 1.4826 times the median absolute deviation, at least one sample, each deviation capped at 30; root mean square over the fiducials observed in at least half of the beats); if fewer than two beats pass, all plausible beats are kept.

Morphology populations: in a window from 120 ms before to 180 ms after each R peak (narrowed to half the shortest RR interval), each beat is median-centered per lead, flattened and scaled to unit length. The beat with the highest median cosine similarity to the others is the medoid; beats with a similarity of at least 0.72 form the initial group; the median of that group is the template; beats whose cosine similarity to the template is at least 0.70 form the dominant (primary) population (cluster 0). Beats outside it are flagged as morphology outliers. Up to two further populations (clusters 1 and 2, at least three beats each) are searched among the remaining beats with the same procedure. A recording is declared severely incoherent if the dominant population has fewer than three beats or less than 55 per cent of the candidate beats, unless at least 90 per cent of the beats fall into one of the three populations. Recordings with fewer than four assessable beats have no morphology populations. In severely incoherent recordings the P, QRS, ST, T, U, QT, JT, QRS-T and TQ segments are not evaluable, and every marker computed on them abstains.

Representative beat: the medoid of the accepted beats (smallest mean absolute offset deviation plus one minus its R-peak confidence) whose fiducial points are replaced by record-level consensus points. A consensus point is a confidence-weighted median of the offsets from the R peak across the accepted beats and exists only if at least $\max(2, \text{half of the accepted beats})$ beats supply the point with a confidence of at least 0.20. Consensus confidence combines the median confidence, the dispersion against the tolerance, the support and the coverage. A segment is evaluable when the representative beat's segment confidence reaches the threshold above (QRS 0.35; T 0.15) and the record is not severely incoherent.

S0a-6. Template cycle (representative morphology)

The signals entering the marker are not those of a single beat. On the morphology path, a template cycle is built from all accepted beats that are not morphology outliers (at least two). Each such beat is aligned to the representative beat by piecewise-linear time warping with up to twelve anchors (P onset, P peak, P offset, R onset, Q, R peak, S, R offset, J point, T onset, T peak, T offset), using only anchors with a confidence of at least 0.20 in both the beat and the representative beat, a strictly increasing anchor order, the R peak always included, and a 20-ms padding at both ends. The window starts at the P onset if a P wave is present and its segment confidence is at least 0.35 (otherwise at the R onset), and ends at the T offset if a T wave is present and its segment confidence is at least 0.35 (otherwise at the R offset). The isoelectric baseline of each beat is the per-lead median over the first available quiet interval of that beat, tried in this order: the PR segment (4 ms after the P offset to 8 ms before the R onset), 80 to 20 ms before the R onset, 140 to 80 ms before the R peak; it is subtracted from the warped beat. The template is the pointwise median over the aligned beats, added to the target baseline and blended into the record with linear tapers outside the representative window. If fewer than two beats can be warped, the unmodified record is used.

S0a-7. Vector reconstruction (Kors)

The three vector components are linear combinations of eight standard leads (V1, V2, V3, V4, V5, V6, I, II), with the regression coefficients of Kors et al. (reference 28 of the manuscript, Table I, regression matrix) as implemented:

$$\begin{aligned} X &= -0.130 V1 + 0.050 V2 - 0.010 V3 + 0.140 V4 + 0.060 V5 + 0.540 V6 + 0.380 I - 0.070 II \\ Y &= 0.060 V1 - 0.020 V2 - 0.050 V3 + 0.060 V4 - 0.170 V5 + 0.130 V6 - 0.070 I + 0.930 II \\ Z &= -0.430 V1 - 0.060 V2 - 0.140 V3 - 0.200 V4 - 0.110 V5 + 0.310 V6 + 0.110 I - 0.230 II \end{aligned}$$

Axis convention: +X to the left, +Y inferior, +Z posterior. The transform is applied to the template cycle (for the representative-beat quantities), to the unmodified morphology path (record-level vector used for the origin and for the beatwise variant) and to the delineation path (for detector iii). The reconstruction is a regression estimate and not a Frank lead recording (references 7, 28 and 33 of the manuscript).

S0a-8. Physiological origin of the vector loop

Vector loops are referred to an estimated isoelectric origin, not to zero. The origin is the component-wise median of the record-level vector over a quiet interval, chosen from three tiers in this order; a lower tier is used only if no interval of a higher tier qualifies:

1. TP interval next to the representative beat (tp_post: from the T offset, or the U offset if a U wave is present, of the representative beat to the P onset of the next beat; tp_pre: from the T or U offset of the previous beat to the P onset of the representative beat). Required: a discrete P wave permitted by the rhythm class, T wave present in the preceding beat and P

wave present in the following beat, no P-T fusion risk, end points with a confidence of at least 0.35 and an uncertainty of at most 60 ms. The interval starts and ends inside the gap with a margin of $\max(8 \text{ ms}, 10 \text{ per cent of the gap})$ and must last at least 20 ms. The candidate with the highest confidence (ties: longer interval) is used.

2. PR interval of the representative beat (from 4 ms after the P offset to 8 ms before the QRS onset; at least 12 ms; end-point confidence at least 0.50; the same P-wave conditions).
3. Early TQ interval (from 20 ms after a T offset to 60 per cent of the gap to the next QRS onset; gap at least 60 ms; at least 20 ms), over all consecutive beat pairs, ranked by confidence reduced by 0.60 and by a factor 0.90 per beat of distance from the representative beat. This tier needs no P wave.

Every candidate needs a robust scatter (median Euclidean distance of the samples from the interval median) of at most 0.150 mV; its confidence is the end-point confidence times a stability factor between 0.25 and 1. If no tier qualifies, the origin and every origin-dependent quantity are missing; there is no zero-origin fallback. The origin vector is subtracted from the template vector signal.

S0a-9. Primary marker: normalized discrete Fréchet distance

Segments of the origin-corrected template vector signal at 500 Hz (index sets from the representative beat): QRS = [R onset, R offset] (Q peak and S peak replace a missing R onset or R offset); T = [T onset, T offset]. Both segments must be evaluable (S0a-5). For each segment Y (m samples $y_1, \dots, y_m$ in $\mathbb{R}^3$):

1. Arc-length resampling: $s_1 = 0$, $s_k = s_{(k-1)} + \|y_k - y_{(k-1)}\|$; 64 targets at equal spacing between 0 and s_m ; each coordinate is linearly interpolated at the targets, giving points $p_1, \dots, p_{64}$. If s_m is below $1e-12$ the marker is missing.
2. Shape normalization: $c = \text{mean of } p_i$; $r = \sqrt{\text{mean over } i \text{ of } \|p_i - c\|^2}$; $u_i = (p_i - c) / r$. If r is below $1e-12$ the marker is missing. Because of the centering, the result does not depend on the origin vector; the origin only determines whether the marker can be evaluated.
3. Cost matrix between the QRS points u_i and the T points w_j : $C_{ij} = \|u_i - w_j\|$ (Euclidean norm, dimensionless). No rotation, reflection or time alignment is applied.
4. Discrete Fréchet distance (Eiter and Mannila, reference 29 of the manuscript) by dynamic programming on the 64 by 64 table:

$$\begin{aligned} ca(1,1) &= C_{11} \quad ca(i,1) = \max(ca(i-1,1), C_{i1}), i = 2..64 \quad ca(1,j) = \max(ca(1,j-1), C_{1j}), j = 2..64 \\ ca(i,j) &= \max(C_{ij}, \min(ca(i-1,j), ca(i-1,j-1), ca(i,j-1))), i, j = 2..64 \quad \text{marker} = ca(64,64) \end{aligned}$$

The marker is non-negative and dimensionless; it is missing if any cost entry is not finite. Larger values mean that the normalized QRS and T trajectories are further apart in shape and orientation.

Beatwise variant (cardiomyopathy analyses): the same quantity is computed separately for every beat of the primary morphology population (cluster 0) on the record-level morphology vector, using each beat's own fiducial points (QRS from R onset to R offset, T from T onset to T offset; each segment at least 8 samples; the QRS segment before the T segment; all samples finite). The marker is the median of these beatwise distances, and it is defined only if at least three beats contribute. Beatwise values are centered in the same way and therefore need no origin.

S0a-10. Comparator: origin-corrected integral QRS-T angle

Let $v(t)$ be the origin-corrected template vector signal in microvolts. With t_{on} the QRS onset (R onset, or Q peak if the R onset is missing), t_{off} the QRS offset (R offset, or S peak) and t_{end} the T offset of the representative beat, the area vectors are

$$A_{\text{QRS}} = \text{integral from } t_{\text{on}} \text{ to } t_{\text{off}} \text{ of } v(t) \, dt \quad A_{\text{JT}} = \text{integral from } t_{\text{off}} \text{ to } t_{\text{end}} \text{ of } v(t) \, dt$$

evaluated by the trapezoidal rule with a sample spacing of 2 ms (unit microvolt times millisecond). The JT area therefore includes the ST segment and the whole T wave. The spatial QRS-T angle is the unsigned angle between the two vectors,

$$\text{angle} = \arccos(A_{\text{QRS}} \cdot A_{\text{JT}} / (\|A_{\text{QRS}}\| \|A_{\text{JT}}\|)), \text{ in degrees, between } 0 \text{ and } 180.$$

The cosine is clipped to $[-1, 1]$. The angle is missing if the bounds do not satisfy $0 \leq t_{\text{on}} < t_{\text{off}} < t_{\text{end}} < \text{length of the signal}$ or if either area vector has a norm below $1e-12$. The angle depends on the origin vector, because the integrals are not invariant to a constant offset. In the models it enters linearly in degrees.

S0a-11. Covariates derived from the same delineation

Heart rate: 60 divided by the mean RR interval, (last R peak minus first R peak) divided by (number of beats minus one), over all detected beats. QRS duration: R onset to R offset of the representative beat (milliseconds). QTc (Fridericia): for each accepted beat with a preceding RR interval between 0.25 and 3.0 s, a QRS-onset to T-offset interval between 140 and 1000 ms and a QRS-T segment confidence of at least 0.35, QT divided by the cube root of the preceding RR interval in seconds; the record value is the median over these beats (at least one valid pair; at least five in rhythm classes that require beatwise rate correction).

S0a-12. Checksums of the release package

Table S121. S0a. Checksums of the release package (SHA-256, shortened to the first eight and the last four characters)

Item	SHA-256
Sorted list of all 1,959 release files (path, file checksum, size), 88,964,052 bytes	d64c3074...8838
Source hash of the 875 Python files of the package (canonical JSON of sorted path and file hash)	9bdad0ce...899d
Source hash of the 72 Python files of the core package (release and runtime snapshot identical)	a07f0e9e...d996
Marker-defining code hash (core package plus six record-level modules), recorded by the extraction run; the recomputed value for the release and for the runtime snapshot is identical	c166bd00...89b9
Source hash of the runtime snapshot bound to the run that produced the marker files	d80fc3c3...ba89

The runtime snapshot includes operational corrections of 11 October 2026 and differs from the release in seven files, all in later analysis stages (association domains, broad-axis adjustment and stage, frame checkpoints, future phenome, phenome, and a result-equivalence table); none is used in signal processing, delineation, reconstruction or marker calculation. The marker extraction is therefore identical to the release of 7 October 2026, whereas the complete analysis chain is not.

S0a-13. What this section does not establish

The delineation has not been validated against annotated boundaries in the outcome population (see the measurement-quality statement in the Methods of the manuscript). The agreement of LoopLens with independent implementations such as BRAVEHEART was not tested. The Kors reconstruction is an estimate and may differ from Frank lead recordings. The settings above are fixed values of the release; their sensitivity was not examined in this study, except where stated in the main text.

S1. Roles, previous use of the partition and access chronology

Computations on the partition were run by the author's AI-assisted pipeline sessions; the author states that the author did not inspect their study-related outputs before the specification date. Study-related means any output concerning QRS-T coupling and LVEF, including the related-hypothesis tables summarized in S11. The supervised association-analysis session also declared no knowledge of the study-related results before its specification. This concerns result knowledge, not the earlier computing sessions' output visibility. It does not establish that all AI sessions were blinded. The person-disjoint internal partition was already used for related hypotheses and was not untouched.

S1a. Specification and access times (UTC)

Table S1. S1a. Specification and access times (UTC)

Date/time	Actor and operation	Relative to adjusted-model specification date	Result knowledge and limit
11 October 19:34:20	Author's AI-assisted analysis program opens partition; 72 clinical and 218 phenome-wide hypotheses, including Hausdorff-LVEF and beat-median cardiovascular-code pairs	Before	Computations occurred; author and association session declare no study-related result knowledge
12 October 08:28:42	Supervised association session fixes specification v4	Freeze	Internal timestamp; no external preregistration; development results known
12 October 08:53:39	Echo-window amendment removes hour-documentation criterion for broad echo references only	After initial specification date, before specified-model results	Based on constant development flag and zero eligible development count; hour endpoints remain stopped
12 October 10:28:09	Structural sex-stratum and missing-scaling amendment	After initial specification date, before specified-model results	Constant sex term omitted; signal variants remain unavailable
12 October 10:46:53-17:13:37	Separate related-hypothesis confirmation session	After	Right-ventricular DTW result seen by coordinating session; explicitly descriptive
12 October approximately 12:00-17:10	Author's AI-assisted program, continuation related clinical analyses including angle/EF context	After	Documented from output files rather than the earlier pipeline ledger; author denies inspection before specification, which does not establish the computing session's ignorance
12 October approximately 17:20	Documentary reviewer accidentally views acute-proxy aggregates	After	Reviewer saw these outputs; coordinating association session did not see their values
12 October 18:02:26	Author-authorized narrower measurement claim and boundary perturbation specification	After initial specification date, before specified-model results	Quantitative outcome-population boundary-error bound unavailable; criterion waived under five limits (Methods, S5)
12 October 18:12-18:29	Original specified association execution	After	Primary and cardiomyopathy results become known
12 October, outputs until approximately 18:57-19:02	Author's AI-assisted program; Kors versus inverse-Dower sensitivity with EF context (inverse Dower matrix: reference 32 of the manuscript)	After main results	Output times do not establish first inspection time; not an earlier untouched-partition result
12 October 20:17:22-20:22:55	Technical verification continuation	After main results	Original parameters retained; weighting, verification and rank-statistic checks
12-13 October, final related aggregates approximately 01:30 on 13 October	Related-family documentary audit	After main results	Context only, no independent replication
13 October	Developmental comparator, medication and differential T-end analyses	After main results	Training/internal validation only; exploratory

Date/time	Actor and operation	Relative to adjusted-model specification date	Result knowledge and limit
13 October	Additional assessment specification	After main results	Fixed before its own execution; every additional result in S15 remains exploratory
14 October	Bivariate tipping analysis (S13k), repeat error by LVEF group and missing-data tipping points (S20, S21)	After main results	Protocols dated and checksummed locally before computation; development data only
15 October from 21:00 UTC	Correction of the bootstrap construction (S18): assessment-partition design rows of the affected associations read again	After main results	Point estimates reproduced to a relative difference below 10^{-9} before any interval was accepted; no point estimate changed
15 October 21:42 UTC to 16 October 05:18 UTC	Solver check of eight further S3b rows and diagnosis of the rejected replicates (S18)	After main results	Assessment rows read again; same reproduction check
15 October 21:45 to 21:48 UTC	Independent recomputation of association row 049 and the right-bundle stratum with separately written code (S18)	After main results	Assessment rows read again
16 October 05:26 UTC	Reproduction of the 7-day echo-interval figure and the interval table in the assessment partition (S23)	After main results	Reproduced to a relative difference below 10^{-9}
15 and 16 October	Extended scenario set, differential and persistent error, selection, pacing, code controls, orientation comparators, coherent T-end sensitivity (S17, S19-S24)	After main results	Development data only; no further held-out partition was opened
16 October 07:37 to 07:41 UTC	Diagnosis of the rejected bootstrap replicates of association rows 045, 047 and 049 and of the verification analysis (S18): design rows of the assessment partition and the development verification data read again	After main results	Point estimates reproduced to a relative difference below 10^{-9} ; counts and reasons only, no new effect size
16 October	Selection factor B on the index population, feasibility calculation, model specification, T-end covariate check (S17, S22, S25)	After main results	Development data only
16 October	Left bundle branch block stratum with Firth penalization, QRS duration as a spline, negative-control diagnoses, checksums of the release package (S26, S27, S0a)	After main results	Development data only; the assessment partition was not read; the negative-control rule file (diagnoses, code sets, populations, threshold of 100 cases) was dated and checksummed locally before any diagnosis row was read; pooled estimates and the same-person LVEF row were added after the case counts had been seen

The pre-opening pair plan dates to 10 October 14:49:30 UTC; its local timestamp does not pre-specify the later adjusted model or prove independent registration. The primary pair is recorded

as rank 1. Comparable endpoint-family rank information for both selected pairs has not been documented here.

S1b. Interpretation of computing and disclosure

The author acts as data steward and supervises AI-assisted sessions. Computing sessions, documentary reviewers and the association session are task roles, not independently staffed research teams. Prior computation and result inspection must not be conflated. The declaration authorized for continued related clinical analyses use is reported above, with the output-file rather than ledger provenance retained. A separate measurement-audit strand used internal-partition technical inputs; it is not a new B association replication. The unrelated stop/authorization entries and repeated ledger lines are process documentation, not patient counts or independent studies.

Specification and amendment times are reported in S1a. Internal hashes bind current content, not historical ignorance or an independent timestamp. No claim of externally deposited preregistration is made. Technical continuation and every newly specified post-unblinding assessment are disclosed as such. Generative AI use is reported in the main declarations with the author-approved wording.

Abbreviations: atrial fibrillation (AF); left/right bundle-branch block (LBBB/RBBB); left bundle-branch block in older source labels (LSB); right ventricle (RV); transthoracic echocardiography (TTE); left-ventricular hypertrophy (LVH); dynamic time warping (DTW); inverse-probability weighting (IPW); intraclass correlation (ICC); regression calibration (RC); simulation-extrapolation (SIMEX); emergency department (ED); false discovery rate (FDR); Benjamini-Hochberg (BH); variance-inflation factor (VIF); confidence interval (CI); standard deviation (SD); odds ratio (OR). B3 and B4 denote the basic and stronger models defined in main Methods. H1 is the primary LVEF hypothesis, H2 the acute-heart-failure proxy, H3 elevated NT-proBNP and H4 cardiomyopathy codes.

S1c. Candidate provenance and verification-bias context

The candidate originated in exploratory QRS-T coupling analyses. A later comparator audit emphasized matched cohorts, folds and missingness rules and a development-fixed comparison. The historical pilot descriptor differed from the normalized Fréchet descriptor analyzed here; the pilot was not a second assessment of the present model. These provenance records are linked to the [partition chronology and selection limits](#) and the [cross-marker and comparator sensitivities](#).

Marker selection. The development screen comprised 2,410,564 marker-endpoint tests. The primary pair (representative Fréchet distance, LVEF <40%) is recorded as rank 1 in the confirmation plan dated 10 October 14:49:30 UTC, before the partition was opened. Comparable endpoint-family rank information for both selected pairs is not documented in the available records, and families and ranks of the remaining tests cannot be reconstructed here. The history that is documented is this: the candidate originated in exploratory QRS-T coupling analyses; the confirmation plan ranking the primary pair is dated 10 October; the partition was opened on 11 October with 72

clinical and 218 phenome-wide hypotheses; the association specification was fixed on 12 October; the representative distance was chosen for LVEF and the beat-median distance for cardiomyopathy codes, and both were then evaluated against both endpoints in development (S13e); all scenario analyses followed the main results (S1a), so the extent of the selection cannot be stated more precisely. The model bootstrap treats marker, endpoint and model as fixed and therefore does not include the uncertainty of this selection; a winner's-curse effect is possible. Repeated internal analyses on the same partition and the development folds do not replace independent confirmation.

Earlier reference-availability and test-assignment audits motivate the [verification-weighting limitations](#). They do not decompose the present AUC, bound its bias, establish causality or constitute independent validation. Disease and test-assignment populations differ; a marker association with testing does not identify the amount of verification bias.

S2. Participants, flow and measurement missingness

One reference-linked index ECG per adult and endpoint was selected before marker and covariate missingness. No later replacement ECG was used. Reference selection was availability-dependent and outcome-value-blind. These populations overlap across endpoints and must not be added. Each main estimable fit has one observation per person.

Table S2. S2. Participants, flow and measurement missingness

Reference	Successful reference-linked index persons	Complete persons	Cases	Controls	Excluded for overlapping basic-model/marker missingness
LVEF <40%, normalized Fréchet	9,374	8,371	800	7,571	1,003
Coded cardiomyopathy, beat-median Fréchet	19,817	18,170	433	17,737	1,647
RV dysfunction, DTW	9,132	7,620	771	6,849	1,512

Candidate-to-complete-case counts are reported in S15a and Figure 1. This section retains the earlier reference-linked starting point. Case/control demographics are in Table 1 and S15a; independently adjudicated rhythm/pacing, era and setting descriptions remain unavailable. Earlier technical input documentation establishes reference-to-technical-index counts; it is not a substitute for unknown outcome-specific exclusions. Main-record missingness counts below overlap and are not additive. Subgroup result flows initially describe their basic masks: their complete-mask field does not equal the final selected subgroup denominator. The same field name in stronger-model flows denotes a stronger-model completeness check.

S2a. Available aggregate column missingness and age-by-sex-by-class flow

LVEF <40%, normalized Fréchet

Table S3. LVEF <40%, normalized Fréchet

Design column	Missing values at reference-linked index
age_linear	0
age_natural	0
heart_rate	202
qrs_duration_ms	75
qrs_t_normalized_discrete_frechet	468
qtc_fridericia_ms	653
sex_numeric	0
spatial_qrs_t_angle_deg	384

Table S4. LVEF <40%, normalized Fréchet

Recorded sex	Age	Reference class	Index persons	Complete persons
F	<65	negative	1683	1550
M	<65	negative	2081	1938
F	>=65	negative	2373	2079
M	>=65	negative	2268	2004
F	<65	positive	not shown	67
M	<65	positive	not shown	184
F	>=65	positive	not shown	176
M	>=65	positive	not shown	373

Index counts of the positive class by recorded sex and age are not shown, because their differences from the complete counts could be derived from other tables; the class totals are in Table S68.

Coded cardiomyopathy, beat-median Fréchet

Table S5. Coded cardiomyopathy, beat-median Fréchet

Design column	Missing values at reference-linked index
age_linear	0
age_natural	0
heart_rate	342
qrs_duration_ms	suppressed
qrs_t_frechet_beat_median	<20
qtc_fridericia_ms	1148
sex_numeric	0
spatial_qrs_t_angle_deg	about 700

Table S6. Coded cardiomyopathy, beat-median Fréchet

Recorded sex	Age	Reference class	Index persons	Complete persons
F	<65	negative	4659	4378
M	<65	negative	5324	5056
F	>=65	negative	4850	4328
M	>=65	negative	4469	3975
F	<65	positive	74	63
M	<65	positive	151	122
F	>=65	positive	100	82
M	>=65	positive	190	166

RV dysfunction, DTW

Table S7. RV dysfunction, DTW

Design column	Missing values at reference-linked index
age_linear	0
age_natural	0
classical_dominant_r_v1	640
heart_rate	199
qrs_duration_ms	71
qrs_t_normalized_dtw_distance	384
qtc_fridericia_ms	625
sex_numeric	0
spatial_qrs_t_angle_deg	377

Table S8. RV dysfunction, DTW

Recorded sex	Age	Reference class	Index persons	Complete persons
F	<65	negative	1606	1456
M	<65	negative	2001	1822
F	>=65	negative	2232	1795
M	>=65	negative	2229	1776
F	<65	positive	118	92
M	<65	positive	231	175
F	>=65	positive	295	210
M	>=65	positive	420	294

Case/control age and dispersion are in Table 1 and S15a; ethnicity and additional clinical case-mix summaries remain unavailable. The recorded F/M variable does not establish sex ascertainment or gender identity. Estimates for unavailable categories cannot be inferred. The available descriptive population summaries are reported in S15a.

S3. Original association assessment and ordered sensitivities

NE means not estimable or not exported, as specified in the status table; it never means zero. ORs and their pointwise 95% CIs use the patient-cluster CR1 Wald calculation. AUCs and Δ AUCs are apparent in association refits. Their 95% CIs are paired person-bootstrap percentile intervals. Unavailable intervals and their valid-replicate counts remain visible. All sensitivity p-values are raw and descriptive. The primary hypothesis is separate from the unchanged three-test sequential

Holm secondary family. Only coded cardiomyopathy has an estimable secondary Holm p ; unavailable tests were represented internally by $p=1$, without publishing that value as a measured p .

Development standardization uses the combined training and validation endpoint-specific complete cases, with SD computed using $\text{ddof}=0$. The age design is $[a, d(2)-d(3)]$, where $a=\text{age}/20$ and $d(k)=((a-k)_+^3-(a-4)_+^3)/(4-k)$, corresponding to fixed 40/60/80-year knots. Sex $F=0$ and $M=1$ follows the recorded source; other or unknown values are unavailable under this model. Only the structurally constant sex column is omitted in sex strata.

For patient clusters, CR1 covariance is $H^{-1}(\Sigma U_g U_g')H^{-1} \times G/(G-1) \times (N-1)/(N-p)$, with $H=X'WX$ plus the fixed ridge, and unpenalized likelihood scores. N is rows, G is persons and p includes the intercept. Estimability required at least 100 persons in each class, finite values, positive fixed marker SD, full rank, convergence, no complete or quasi-complete separation, and positive finite marker variance. The Newton solver permits at most 60 steps with a maximum absolute penalized score/ N below 10^{-7} . No alternate estimator was selected after results were seen.

The primary descriptive bootstrap uses seed 1282026, 1,000 planned replicates from a fixed sorted union of persons, paired multiplicities across models and endpoints, and complete refits with unchanged standardization. Intervals use the 2.5th and 97.5th percentiles. At least 950 valid replicates are required; no failed replicate is redrawn. For H4, the Holm family size remains three and the raw p is multiplied by three at its first rejection step. The family adjustment does not turn the pointwise confidence intervals into simultaneous intervals.

Table S9. S3. Original association assessment and ordered sensitivities

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 001	LVEF <40%, normalized Fréchet; basic main model	8,371/800/7,571	2.34 (2.09-2.62)	1.47e-49	NE	0.0326 (0.0247-0.0414)	1,000/1,000
Association row 002	Acute HF proxy, mirror symmetry; basic main model	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 003	Elevated NT-proBNP, beat-median Fréchet; basic main model	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 004	Coded cardiomyopathy, beat-median Fréchet; basic main model	18,170/433/17,737	2.03 (1.79-2.29)	2.2e-29	6.59e-29	0.0262 (0.0169-0.0367)	1,000/1,000
Association row 005	Troponin, DTW; basic main model	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 006	RV dysfunction, DTW; basic main model	7,620/771/6,849	1.71 (1.55-1.90)	5.95e-25	NE	0.0230 (NE)	909/1,000
Association row 007	LVEF <40%, normalized Fréchet; 1 stronger and basic models on identical complete cases / B4	7,840/636/7,204	2.51 (2.20-2.87)	5.19e-42	NE	0.0334 (0.0238-0.0428)	995/1,000
Association row 008	LVEF <40%, normalized Fréchet; 1 stronger and basic models on identical complete cases / B3_same_set	7,840/636/7,204	2.49 (2.21-2.82)	1.58e-48	NE	0.0389 (0.0294-0.0492)	999/1,000
Association row 009	Acute HF proxy, mirror symmetry; 1 stronger and basic models on identical complete cases	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 010	Elevated NT-proBNP, beat-median Fréchet; 1 stronger and basic models on identical complete cases	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 011	Coded cardiomyopathy, beat-median Fréchet; 1 stronger and basic models on identical complete cases / B4	17,345/334/17,011	1.98 (1.69-2.33)	4.14e-17	NE	0.0219 (0.0114-0.0345)	962/1,000
Association row 012	Coded cardiomyopathy, beat-median Fréchet; 1 stronger and basic models on identical complete cases / B3_same_set	17,345/334/17,011	2.10 (1.83-2.41)	9.6e-26	NE	0.0325 (0.0199-0.0463)	997/1,000
Association row 013	Troponin, DTW; 1 stronger and basic models on identical complete cases	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 014	RV dysfunction, DTW; 1 stronger and basic models on identical complete cases / B4	7,620/771/6,849	1.72 (1.55-1.91)	3.41e-24	NE	0.0190 (0.0113-0.0275)	985/1,000
Association row 015	RV dysfunction, DTW; 1 stronger and basic models on identical complete cases / B3_same_set	7,620/771/6,849	1.71 (1.55-1.90)	5.95e-25	NE	0.0230 (NE)	909/1,000
Association row 016	LVEF <40%, normalized Fréchet; 1b echo $\leq$ 29 days	8,309/>790/>7,500	2.34 (2.09-2.61)	4.05e-49	NE	0.0322 (0.0243-0.0410)	1,000/1,000
Association row 017	LVEF <40%, normalized Fréchet; 2a echo $\pm$ 7 days, unchanged index	6,337/693/5,644	2.42 (2.14-2.74)	8.09e-45	NE	0.0363 (0.0266-0.0463)	1,000/1,000

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 018	LVEF <40%, normalized Fréchet; 2b LVEF ≤40% versus >40%, original complete-case set	8,371/1,076/7,295	2.29 (2.06-2.53)	6.5e-57	NE	0.0336 (0.0262-0.0417)	996/1,000
Association row 019	LVEF <40%, normalized Fréchet; 3 IPW versus un-weighted, same first technical index	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 020	LVEF <40%, normalized Fréchet; 3b verification association, marker and stronger model; age/sex/QRS comparator	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 021	LVEF <40%, normalized Fréchet; 4 LVEF ≤40% versus LVH with LVEF ≥50%, same echo	2,618/1,076/1,542	2.03 (1.78-2.31)	6.26e-27	NE	0.0227 (NE)	915/1,000
Association row 022	LVEF <40%, normalized Fréchet; 4_LSB LVH with LBBB, development-only	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 023	RV dysfunction, DTW; 5a RV at LVEF ≥50%, DTW	6,381/343/6,038	1.41 (1.20-1.65)	2.4e-05	NE	0.0138 (0.0040-0.0272)	997/1,000
Association row 024	RV dysfunction, DTW; 5b RV at LVEF ≥50%, descriptive Fréchet	about 6,400/343/about 6,050	1.12 (0.95-1.32)	0.178	NE	0.0016 (-0.0009-0.0078)	996/1,000
Association row 025	LVEF <40%, normalized Fréchet; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	6,104/329/5,775	2.39 (2.04-2.81)	2.14e-26	NE	0.0383 (NE)	865/1,000
Association row 026	LVEF <40%, normalized Fréchet; 6b report-defined sinus selector	6,879/557/6,322	2.50 (2.19-2.86)	1.15e-41	NE	0.0349 (0.0253-0.0455)	1,000/1,000
Association row 027	LVEF <40%, normalized Fréchet; 6c age <65	3,739/251/3,488	2.67 (2.20-3.25)	5.05e-23	NE	0.0376 (NE)	881/1,000

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 028	LVEF <40%, normalized Fréchet; 6c age ≥ 65	4,632/549/4,083	2.20 (1.92-2.52)	2.39e-29	NE	0.0317 (0.0215-0.0428)	1,000/1,000
Association row 029	LVEF <40%, normalized Fréchet; 6d F	3,872/243/3,629	2.37 (1.97-2.86)	1.21e-19	NE	0.0439 (NE)	935/1,000
Association row 030	LVEF <40%, normalized Fréchet; 6d M	4,499/557/3,942	2.34 (2.03-2.70)	4.95e-32	NE	0.0302 (0.0214-0.0407)	1,000/1,000
Association row 031	LVEF <40%, normalized Fréchet; 6e same echo/NT reference and log1p(NT-proBNP/URL)	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 032	RV dysfunction, DTW; 6e_RV RV and log1p(NT-proBNP/URL)	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 033	Acute HF proxy, mirror symmetry; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 034	Acute HF proxy, mirror symmetry; 6b report-defined sinus selector	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 035	Acute HF proxy, mirror symmetry; 6c age <65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 036	Acute HF proxy, mirror symmetry; 6c age ≥ 65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 037	Acute HF proxy, mirror symmetry; 6d recorded sex F	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 038	Acute HF proxy, mirror symmetry; 6d recorded sex M	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 039	Elevated NT-proBNP, beat-median Fréchet; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 040	Elevated NT-proBNP, beat-median Fréchet; 6b report-defined sinus selector	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 041	Elevated NT-proBNP, beat-median Fréchet; 6c age <65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 042	Elevated NT-proBNP, beat-median Fréchet; 6c age $\geq$ 65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 043	Elevated NT-proBNP, beat-median Fréchet; 6d recorded sex F	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 044	Elevated NT-proBNP, beat-median Fréchet; 6d recorded sex M	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 045	Coded cardiomyopathy, beat-median Fréchet; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	13,872/193/13,679	2.15 (1.79-2.58)	3.88e-16	NE	0.0309 (NE)	754/1,000
Association row 046	Coded cardiomyopathy, beat-median Fréchet; 6b report-defined sinus selector	15,905/278/15,627	2.11 (1.79-2.48)	1.1e-19	NE	0.0252 (NE)	889/1,000
Association row 047	Coded cardiomyopathy, beat-median Fréchet; 6c age <65	9,619/185/9,434	2.16 (1.79-2.60)	7.3e-16	NE	0.0255 (NE)	815/1,000
Association row 048	Coded cardiomyopathy, beat-median Fréchet; 6c age $\geq$ 65	8,551/248/8,303	1.87 (1.60-2.18)	5.1e-15	NE	0.0237 (0.0121-0.0384)	1,000/1,000
Association row 049	Coded cardiomyopathy, beat-median Fréchet; 6d recorded sex F	8,851/145/8,706	2.23 (1.81-2.76)	9.29e-14	NE	0.0349 (NE)	93/1,000
Association row 050	Coded cardiomyopathy, beat-median Fréchet; 6d recorded sex M	9,319/288/9,031	1.91 (1.64-2.21)	3.38e-17	NE	0.0223 (0.0121-0.0354)	1,000/1,000
Association row 051	Troponin, DTW; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 052	Troponin, DTW; 6b report-defined sinus selector	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE

Row	Reference and analysis	Persons / cases / controls	OR (95% Wald CI)	Raw p	Holm p	Apparent Δ AUC (95% bootstrap CI)	Valid / planned bootstrap
Association row 053	Troponin, DTW; 6c age <65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 054	Troponin, DTW; 6c age $\geq$ 65	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 055	Troponin, DTW; 6d recorded sex F	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 056	Troponin, DTW; 6d recorded sex M	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 057	RV dysfunction, DTW; 6a QRS <120 ms, no positive pipeline LBBB/RBBB patterns	5,939/435/5,504	1.71 (1.50-1.95)	2.45e-15	NE	0.0231 (0.0107-0.0380)	994/1,000
Association row 058	RV dysfunction, DTW; 6b report-defined sinus selector	6,427/520/5,907	1.67 (1.48-1.89)	1.66e-16	NE	0.0225 (0.0110-0.0353)	1,000/1,000
Association row 059	RV dysfunction, DTW; 6c age <65	3,545/267/3,278	2.03 (1.72-2.41)	2.37e-16	NE	0.0342 (0.0166-0.0519)	997/1,000
Association row 060	RV dysfunction, DTW; 6c age $\geq$ 65	4,075/504/3,571	1.55 (1.36-1.76)	2.31e-11	NE	0.0164 (0.0072-0.0282)	994/1,000
Association row 061	RV dysfunction, DTW; 6d recorded sex F	3,553/302/3,251	1.79 (1.52-2.11)	4.43e-12	NE	0.0220 (0.0082-0.0379)	990/1,000
Association row 062	RV dysfunction, DTW; 6d recorded sex M	4,067/469/3,598	1.65 (1.45-1.88)	4.68e-14	NE	0.0223 (NE)	840/1,000
Association row 063	LVEF <40%, normalized Fréchet; 7 inverse Dower	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 064	LVEF <40%, normalized Fréchet; 8a direct8 centered-RMS	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 065	LVEF <40%, normalized Fréchet; 8b QRS-max centered	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE
Association row 066	LVEF <40%, normalized Fréchet; 9 original, development-fixed residual, SO(3) shape remainder	NE/NE/NE	NE (NE)	NE	NE	NE (NE)	NE/NE

S3a. All apparent AUC components and descriptive bootstrap OR intervals

Table S10. S3a. All apparent AUC components and descriptive bootstrap OR intervals

Row	Basic or named basis AUC	basis + marker AUC	Marker AUC, increasing original values	Descriptive bootstrap OR CI
Association row 001	0.8024	0.8351	0.8024	(2.10-2.62)
Association row 002	NE	NE	NE	(NE)
Association row 003	NE	NE	NE	(NE)
Association row 004	0.7961	0.8224	0.7890	(1.79-2.31)
Association row 005	NE	NE	NE	(NE)
Association row 006	0.7379	0.7610	0.6978	(NE)
Association row 007	0.7998	0.8332	0.7925	(2.19-2.88)
Association row 008	0.7916	0.8305	0.7925	(2.20-2.83)
Association row 009	NE	NE	NE	(NE)
Association row 010	NE	NE	NE	(NE)
Association row 011	0.7885	0.8105	0.7684	(1.68-2.34)
Association row 012	0.7726	0.8051	0.7684	(1.83-2.42)
Association row 013	NE	NE	NE	(NE)
Association row 014	0.7506	0.7696	0.6978	(1.56-1.91)
Association row 015	0.7379	0.7610	0.6978	(NE)
Association row 016	0.8026	0.8348	0.8018	(2.09-2.61)
Association row 017	0.7966	0.8330	0.7996	(2.14-2.73)
Association row 018	0.7851	0.8188	0.7868	(2.09-2.53)
Association row 019	NE	NE	NE	(NE)
Association row 020	NE	NE	NE	(NE)
Association row 021	0.7715	0.7942	0.7074	(NE)
Association row 022	NE	NE	NE	(NE)
Association row 023	0.6991	0.7128	0.6265	(1.20-1.64)
Association row 024	0.6990	0.7006	0.5933	(0.94-1.30)
Association row 025	0.7710	0.8093	0.7730	(NE)
Association row 026	0.8048	0.8397	0.8080	(2.20-2.85)
Association row 027	0.8064	0.8440	0.8213	(NE)
Association row 028	0.7901	0.8218	0.7788	(1.92-2.56)
Association row 029	0.7767	0.8206	0.7944	(NE)
Association row 030	0.8042	0.8345	0.8013	(2.05-2.72)
Association row 031	NE	NE	NE	(NE)
Association row 032	NE	NE	NE	(NE)
Association row 033	NE	NE	NE	(NE)
Association row 034	NE	NE	NE	(NE)
Association row 035	NE	NE	NE	(NE)
Association row 036	NE	NE	NE	(NE)
Association row 037	NE	NE	NE	(NE)
Association row 038	NE	NE	NE	(NE)
Association row 039	NE	NE	NE	(NE)
Association row 040	NE	NE	NE	(NE)
Association row 041	NE	NE	NE	(NE)
Association row 042	NE	NE	NE	(NE)
Association row 043	NE	NE	NE	(NE)
Association row 044	NE	NE	NE	(NE)
Association row 045	0.7602	0.7910	0.7497	(NE)
Association row 046	0.7962	0.8214	0.7917	(NE)
Association row 047	0.8244	0.8498	0.8252	(NE)
Association row 048	0.7788	0.8025	0.7464	(1.62-2.20)
Association row 049	0.7939	0.8288	0.7982	(NE)
Association row 050	0.7860	0.8083	0.7751	(1.65-2.23)

Row	Basic or named basis AUC	basis + marker AUC	Marker AUC, increas- ing original values	Descriptive bootstrap OR CI
Association row 051	NE	NE	NE	(NE)
Association row 052	NE	NE	NE	(NE)
Association row 053	NE	NE	NE	(NE)
Association row 054	NE	NE	NE	(NE)
Association row 055	NE	NE	NE	(NE)
Association row 056	NE	NE	NE	(NE)
Association row 057	0.7080	0.7310	0.6733	(1.50-1.95)
Association row 058	0.7267	0.7493	0.6873	(1.47-1.90)
Association row 059	0.7488	0.7830	0.7141	(1.72-2.41)
Association row 060	0.7208	0.7372	0.6712	(1.37-1.76)
Association row 061	0.7532	0.7752	0.7074	(1.53-2.09)
Association row 062	0.7270	0.7493	0.6859	(NE)
Association row 063	NE	NE	NE	(NE)
Association row 064	NE	NE	NE	(NE)
Association row 065	NE	NE	NE	(NE)
Association row 066	NE	NE	NE	(NE)

S3b. Original-run status, computational failures and reasons

Verification rows reflect the initial loading failure and are superseded by S8. NT adjustment remains unavailable for the pre-existing development-parameter stop. Solver failures and construction-related rejections are retained as originally recorded. The bootstrap of the original run had a construction error, and the rows with “not estimable” bootstrap status have been recomputed post hoc (S18, Tables S91 and S92); the original entries stay visible and no original interval is silently replaced. The Wald intervals remain the primary inference.

The main time stops apply to the acute HF proxy, NT-proBNP and troponin. Basic-versus-stronger sensitivities of these stopped endpoints export missing-input reasons; their subgroup paths report an endpoint-specific measurement stop. These secondary error labels do not constitute new biological results.

The IPW and verification-association rows report a missing technical universe, but the source report identifies the causal implementation path: the runner loads that universe only when no other endpoint is stopped. Technical index reconstruction had in fact been completed. This is an implementation-dependent unavailability, not evidence that no technical indices exist. This original-run loading stop was superseded by the later first-technical-index analysis in S8, where propensities, weights, effective sample sizes and conditional ORs are reported. Its bootstrap uncertainty remains unavailable.

The laboratory-adjusted paths were unavailable because the development design parameters had not been fixed; the original software exception masked that pre-existing stop. Signal variants use no pilot substitute for unavailable full-population fixed scaling. LVH with LBBB remains an unavailable development-only result. External EchoNext was excluded from the run. None is a null association.

Table S11. S3b. Original-run status, computational failures and reasons

Row	Status	Exact exported reason	Bootstrap status	Failed-replicate causes
Association row 001	estimable	none exported	estimable	{}
Association row 002	not estimable	hour-scale device/EHR alignment not established; no replacement analysis	not exported	{}
Association row 003	not estimable	hour-scale device/EHR alignment not established; no replacement analysis	not exported	{}
Association row 004	estimable	none exported	estimable	{}
Association row 005	not estimable	hour-scale device/EHR alignment not established; no replacement analysis	not exported	{}
Association row 006	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 91}
Association row 007	estimable	none exported	estimable	{"normalized score convergence criterion not met": 5}
Association row 008	estimable	none exported	estimable	{"normalized score convergence criterion not met": 1}
Association row 009	not estimable	required input input definition unavailable	not exported	{}
Association row 010	not estimable	required input input definition unavailable	not exported	{}
Association row 011	estimable	none exported	estimable	{"normalized score convergence criterion not met": 38}
Association row 012	estimable	none exported	estimable	{"normalized score convergence criterion not met": 3}
Association row 013	not estimable	required input input definition unavailable	not exported	{}
Association row 014	estimable	none exported	estimable	{"normalized score convergence criterion not met": 15}
Association row 015	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 91}
Association row 016	estimable	none exported	estimable	{}
Association row 017	estimable	none exported	estimable	{}
Association row 018	estimable	none exported	estimable	{"normalized score convergence criterion not met": 4}

Row	Status	Exact exported reason	Bootstrap status	Failed-replicate causes
Association row 019	not estimable	initial software loading defect; superseded by delayed verification analysis in S8	not exported	{}
Association row 020	not estimable	initial software loading defect; superseded by delayed verification analysis in S8	not exported	{}
Association row 021	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 85}
Association row 022	not estimable	developmental left-bundle hypertrophy analysis unavailable; no assessment substitute	not exported	{}
Association row 023	estimable	none exported	estimable	{"normalized score convergence criterion not met": 3}
Association row 024	estimable	none exported	estimable	{"normalized score convergence criterion not met": 4}
Association row 025	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 135}
Association row 026	estimable	none exported	estimable	{}
Association row 027	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 119}
Association row 028	estimable	none exported	estimable	{}
Association row 029	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 65}
Association row 030	estimable	none exported	estimable	{}
Association row 031	not estimable	development design parameters not fixed; pre-existing stop, not an outcome null	not exported	{}
Association row 032	not estimable	development design parameters not fixed; pre-existing stop, not an outcome null	not exported	{}
Association row 033	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 034	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 035	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 036	not estimable	endpoint-specific measurement requirements not verified	not exported	{}

Row	Status	Exact exported reason	Bootstrap status	Failed-replicate causes
Association row 037	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 038	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 039	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 040	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 041	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 042	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 043	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 044	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 045	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 244, "fewer than 100 distinct persons per class": 2}
Association row 046	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 111}
Association row 047	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 181, "fewer than 100 distinct persons per class": 4}
Association row 048	estimable	none exported	estimable	{}
Association row 049	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 2, "fewer than 100 distinct persons per class": 905}
Association row 050	estimable	none exported	estimable	{}
Association row 051	not estimable	endpoint-specific measurement requirements not verified	not exported	{}

Row	Status	Exact exported reason	Bootstrap status	Failed-replicate causes
Association row 052	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 053	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 054	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 055	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 056	not estimable	endpoint-specific measurement requirements not verified	not exported	{}
Association row 057	estimable	none exported	estimable	{"normalized score convergence criterion not met": 6}
Association row 058	estimable	none exported	estimable	{}
Association row 059	estimable	none exported	estimable	{"normalized score convergence criterion not met": 3}
Association row 060	estimable	none exported	estimable	{"normalized score convergence criterion not met": 6}
Association row 061	estimable	none exported	estimable	{"normalized score convergence criterion not met": 10}
Association row 062	estimable	none exported	not estimable	{"normalized score convergence criterion not met": 160}
Association row 063	not estimable	population-specific scaling not fixed	not exported	{}
Association row 064	not estimable	population-specific scaling not fixed	not exported	{}
Association row 065	not estimable	population-specific scaling not fixed	not exported	{}
Association row 066	not estimable	population-specific scaling not fixed	not exported	{}

In the table above, the reasons “normalized score convergence criterion not met” and “fewer than 100 distinct persons per class” result from the construction defects described in S18 (eligibility checked inside each replicate; stopping rule inconsistent with the acceptance rule). They are not signs of separation in the data. Corrected intervals for rows 006, 015, 021, 025, 027, 029, 045, 046, 047, 049 and 062 are in Table S91.

S4. Complete boundary perturbation sensitivities

Five hundred training ECGs from distinct persons were selected by ECG-based random permutation with later duplicate-person exclusion, not an equally weighted sample of persons. Unper-

turbed adapter equivalence was checked for all six measurements. The deterministic experiment moved one boundary at a time; the empirical experiment moved all three boundaries using independent draws from exact finite LUDB errors, including tails. At 500 Hz the empirical shifts were rounded to the 2-ms raster. Each ECG contributed 20 joint draws. No new endpoint model was fitted.

Deterministic shifts were ± 14 ms at QRS onset, ± 12 ms at QRS offset and ± 32 ms at T end, rounded from the reference error SDs. The empirical distribution had 1,831 QRS-onset errors, 1,831 QRS-offset errors and 1,642 T-end errors. The empirical draw clarification was fixed after viewing deterministic results and before all empirical results. This timing is part of the design disclosure.

The SD of signed perturbed-minus-unperturbed differences pools finite ECG-by-draw pairs. It is neither RMSE nor mean absolute change. R divides that SD by short-interval within-person clinical variation. The denominator uncertainty is not re-estimated. Rank retention is the median of 20 draw-specific Spearman correlation correlations, not a correlation that treats 10,000 observations as independent. Intervals resample 500 person clusters with all their draws together, using the same 1,000 resamples for all markers. They are conditional on the source distribution and fixed denominator; the source reference errors were not bootstrapped. Independent boundary draws ignore error covariance.

Table S12. S4. Complete boundary perturbation sensitivities

Row / marker	SD of signed changes (95% CI)	Clinical within-person SD	R (95% CI)	Median rank retention (95% CI)	Noncomputable / attempts	ECGs with any missing draw	Finite pairs per draw
Perturbation row 037 qrs_t_normaliz ed_discrete_fr echet	0.2829 (0.2601-0.3046)	0.3178	0.890 (0.818-0.958)	0.933 (0.917-0.944)	411/10,000	240	474-489
Perturbation row 038 qrs_t_frechet_ beat_median	0.2960 (0.2771-0.3141)	0.2952	1.003 (0.939-1.064)	0.922 (0.910-0.936)	49/10,000	44	>490
Perturbation row 039 qrs_t_normaliz ed_dtw_distance	0.0528 (0.0493-0.0563)	0.0716	0.737 (0.689-0.786)	0.960 (0.952-0.968)	317/10,000	206	>480
Perturbation row 040 spa- tial_qrs_t_angl e_deg	17.1820 (15.4634-18.9510)	29.7293	0.578 (0.520-0.637)	0.935 (0.920-0.948)	398/10,000	239	475-489
Perturbation row 041 qrs_duration_ ms	16.1958 (15.8529-16.5253)	9.8376	1.646 (1.611-1.680)	0.707 (0.668-0.743)	273/10,000	190	>480
Perturbation row 042 qtc_fridericia_ ms	31.1525 (29.9485-32.4510)	22.2895	1.398 (1.344-1.456)	0.758 (0.730-0.786)	503/10,000	243	467-483

$R < 0.5$ was classified as insensitive relative to short-interval variation, $0.5 \leq R < 1$ as moderately boundary-sensitive, and $R \geq 1$ as boundary-sensitive. These are specified technical reporting conventions, not clinical thresholds. Categories use point estimates; the beat-median interval crosses

the category boundary. The primary marker interval is entirely above the angle interval. The pre-specified extra limitation for a substantially more sensitive angle was therefore not triggered. Unequal repeatability remains unresolved.

No replacement ECG or imputation was used. All empirical draws had finite correlation estimates, but marker-specific noncomputability remains. Estimates conditional on finite outputs can understate sensitivity. The deterministic T-end manipulation can also change measured QRS duration because release beat plausibility, morphology selection and representative-beat construction are rebuilt; it is not a purely algebraic shift of one specified boundary.

S4a. All deterministic shifts

Table S13. S4a. All deterministic shifts

Row / marker	Boundary	Actual shift (ms)	Mean absolute change (95% CI)	Finite / ECGs	Noncomputable
Perturbation row 001 qrs_t_normalized_discrete_frechet	r_onset	-14.0	0.01195 (0.01024-0.01430)	500/500	0
Perturbation row 002 qrs_t_normalized_discrete_frechet	r_onset	14.0	0.06413 (0.05512-0.07402)	>490/500	<10
Perturbation row 003 qrs_t_normalized_discrete_frechet	r_offset	-12.0	0.03973 (0.03407-0.04573)	>490/500	<10
Perturbation row 004 qrs_t_normalized_discrete_frechet	r_offset	12.0	0.01353 (0.01238-0.01472)	500/500	0
Perturbation row 005 qrs_t_normalized_discrete_frechet	t_offset	-32.0	0.20252 (0.18421-0.22063)	500/500	0
Perturbation row 006 qrs_t_normalized_discrete_frechet	t_offset	32.0	0.20042 (0.18132-0.21953)	>490/500	<10
Perturbation row 007 qrs_t_frechet_beat_median	r_onset	-14.0	0.01476 (0.01338-0.01635)	500/500	0
Perturbation row 008 qrs_t_frechet_beat_median	r_onset	14.0	0.02933 (0.02650-0.03233)	500/500	0
Perturbation row 009 qrs_t_frechet_beat_median	r_offset	-12.0	0.02846 (0.02581-0.03125)	500/500	0
Perturbation row 010 qrs_t_frechet_beat_median	r_offset	12.0	0.01643 (0.01504-0.01808)	500/500	0
Perturbation row 011 qrs_t_frechet_beat_median	t_offset	-32.0	0.17895 (0.16420-0.19424)	500/500	0
Perturbation row 012 qrs_t_frechet_beat_median	t_offset	32.0	0.09894 (0.08992-0.10913)	500/500	0
Perturbation row 013 qrs_t_normalized_dtw_distance	r_onset	-14.0	0.00171 (0.00146-0.00195)	500/500	0

Row / marker	Boundary	Actual shift (ms)	Mean absolute change (95% CI)	Finite / ECGs	Noncomputable
Perturbation row 014 qrs_t_normalized_dtw_distance	r_onset	14.0	0.01385 (0.01180-0.01585)	>490/500	<10
Perturbation row 015 qrs_t_normalized_dtw_distance	r_offset	-12.0	0.00521 (0.00433-0.00626)	500/500	0
Perturbation row 016 qrs_t_normalized_dtw_distance	r_offset	12.0	0.00147 (0.00136-0.00160)	500/500	0
Perturbation row 017 qrs_t_normalized_dtw_distance	t_offset	-32.0	0.05507 (0.05166-0.05865)	500/500	0
Perturbation row 018 qrs_t_normalized_dtw_distance	t_offset	32.0	0.03298 (0.02963-0.03624)	>490/500	<10
Perturbation row 019 spa-tial_qrs_t_angle_deg	r_onset	-14.0	1.72031 (1.40385-2.08134)	500/500	0
Perturbation row 020 spa-tial_qrs_t_angle_deg	r_onset	14.0	7.50206 (6.08319-8.89981)	>490/500	<10
Perturbation row 021 spa-tial_qrs_t_angle_deg	r_offset	-12.0	3.54519 (2.63940-4.66820)	>490/500	<10
Perturbation row 022 spa-tial_qrs_t_angle_deg	r_offset	12.0	1.73015 (1.46536-2.04456)	500/500	0
Perturbation row 023 spa-tial_qrs_t_angle_deg	t_offset	-32.0	3.45451 (2.85787-4.17767)	500/500	0
Perturbation row 024 spa-tial_qrs_t_angle_deg	t_offset	32.0	11.61633 (10.10144-13.26277)	>490/500	<10
Perturbation row 025 qrs_duration_ms	r_onset	-14.0	14.00000 (14.00000-14.00000)	500/500	0
Perturbation row 026 qrs_duration_ms	r_onset	14.0	13.56713 (13.34663-13.76755)	>490/500	<10
Perturbation row 027 qrs_duration_ms	r_offset	-12.0	11.95600 (11.88800-12.02000)	500/500	0
Perturbation row 028 qrs_duration_ms	r_offset	12.0	12.00000 (12.00000-12.00000)	500/500	0

Row / marker	Boundary	Actual shift (ms)	Mean absolute change (95% CI)	Finite / ECGs	Noncomputable
Perturbation row 029 qrs_duration_ms	t_offset	-32.0	0.05200 (0.01600-0.09600)	500/500	0
Perturbation row 030 qrs_duration_ms	t_offset	32.0	0.90000 (0.74790-1.06400)	500/500	0
Perturbation row 031 qtc_fridericia_ms	r_onset	-14.0	15.12353 (15.02148-15.22883)	500/500	0
Perturbation row 032 qtc_fridericia_ms	r_onset	14.0	15.04075 (14.65442-15.42077)	>490/500	<10
Perturbation row 033 qtc_fridericia_ms	r_offset	-12.0	0.22499 (0.14733-0.32262)	>490/500	<10
Perturbation row 034 qtc_fridericia_ms	r_offset	12.0	0.00000 (0.00000-0.00000)	500/500	0
Perturbation row 035 qtc_fridericia_ms	t_offset	-32.0	34.42975 (34.15309-34.71038)	>490/500	<10
Perturbation row 036 qtc_fridericia_ms	t_offset	32.0	34.97145 (34.57698-35.36457)	488/500	12

S4b. LUIDB citation and source access

The public source is LUIDB version 1.0.1, under ODC-By 1.0, doi:10.13026/eegm-h675. The original publication is Kalyakulina AI, Yusipov II, Moskalenko VA, Nikolskiy AV, Kosonogov KA, Osipov GV, et al. LUIDB: A New Open-Access Validation Tool for Electrocardiogram Delineation Algorithms. IEEE Access 2020;8:186181-90. doi:10.1109/ACCESS.2020.3029211. The dataset citation is Kalyakulina A, Yusipov I, Moskalenko V, Nikolskiy A, Kosonogov K, Zolotykh N, et al. Lobachevsky University Electrocardiography Database, version 1.0.1. PhysioNet; 2021. doi:10.13026/eegm-h675. The PhysioNet platform reference is main reference 23. This public technical source does not independently replicate the ventricular association models.

S5. Measurement scope and specification correction

The results apply only to stored or exactly reproduced Kors-derived values of the fixed LoopLens software release (version 10.1; 7 October 2026) at 500 Hz, using the fixed loader, filter and delineation definitions, in hospital complete cases. Transformation, device and acquisition-era invariance are not established. Pacing is not securely excluded; Frank threshold transport is not supported. Individual diagnosis and individual change statements are not supported. The basic model controls the scalar integral angle. Independence from amplitude, hypertrophy or axis is restricted to the dimensions tested by the stronger sensitivity.

The developmental angle-repeat estimate was ICC 0.617 in the all-pair source (S9). Clinical repeatability in a separate repeat population is not an identified technical-error reliability in the

outcome cases. Construct overlap, reliability scenarios and the joint-error model are therefore reported separately in S10.

The specified text incorrectly described the beat-median Fréchet measurement as unnormalized. The fixed code normalizes each beat's QRS and T loops before calculating the distance. The normalized dimensionless marker ID, code and result were unchanged. The description is corrected as an erratum. Separate RMS normalization removes absolute amplitude and the original inter-loop RMS ratio; relative orientation remains.

S5a. Clinical and echo input provenance

The fixed release used MIMIC-IV 3.1 hosp tables for demographics, admissions, diagnoses, laboratory values and medication orders. The separate MIMIC-IV-ECHO input was configured as release 1.0 and ingested the structured measurements and the DICOM study list. The structured measurements supplied measurement type, value, unit and timestamp, and an echo study index derived from them joined the echocardiograms to the ECGs by person and time; the DICOM study list was read but not used further for labels, reference selection or the main index. Percentage LVEF was selected in priority order: three-dimensional, biplane, generic. A finite percentage within 0-100 and no intermethod difference above 10 percentage points were required. The broad window retained timestamp and same-echo checks. These are structured values, not a new extraction from report text, and not ICU bedside chart measurements. No note module was required by these reference rules. Release configuration and input-file identity establish the implemented input path, but do not validate the original clinical report extraction.

MIMIC-IV-ECHO version 1.0.1. Version 1.0.1 (25 August 2026) of the resource corrects problems found in the validation of the DICOM data after release: 15 studies were removed because of an identifier collision, and nine DICOM files that lay accidentally outside the intended scope were removed; no schema changes were made. The release notes name neither the affected studies nor the colliding identifier, and they do not say whether the tabular files were affected, so the affected persons cannot be identified. We used version 1.0. The DICOM study identifiers to which the notice refers are not used for the LVEF labels or the verification analysis of this study (source code check); a local echo study index marked no identity conflict (0 of 206,488 studies). At most 15 persons can be affected. As an upper bound, the main OR was recomputed after removing the 15 persons of greatest influence in the unfavorable direction (one-step influence approximation): from 2.48 to between 2.42 and 2.55 in training, from 2.39 to between 2.25 and 2.59 in internal validation and from 2.34 to between 2.20 and 2.53 in the assessment partition, so that the main OR stays between 2.20 and 2.59 and no threshold (1.25) is touched. This bounds the effect of any 15 persons and is not a finding on the studies actually removed. A comparison of the files of versions 1.0 and 1.0.1 would be needed for a definitive answer.

Software versions recorded in the independent developmental verification: python 3.12.4, numpy 2.5.3, pandas 2.3.3, scipy 1.18.1, statsmodels 0.15.0, pyarrow 25.0.1, duckdb 1.5.6. These docu-

ment that verification environment, rather than proving every historical runtime used the same versions.

S6. Remaining unavailable analyses and open material

The two hour-scale specified hypotheses and troponin assessment were stopped because confirmatory device/EHR time alignment was not established; the acute-proxy reference universe was also empty under its fixed rules. Unavailable analyses are not biological null results. NT-proBNP adjustment (rank 6e) lacks fixed development design parameters, so no assessment rescaling or substitute model was introduced. Inverse-Dower, matrix-free and decomposition outcome sensitivities lack fixed population-specific scaling; the LBBB-hypertrophy development result has no assessment substitute. These are gaps, not negative demonstrations of invariance.

Verification ranks were completed later and are in S8; they must not remain described as wholly unexecuted. Bootstrap intervals missing in the original run were recomputed post hoc (S18). Independent clinical adjudication and decision-curve benefit remain unavailable. New development coefficients, variance-inflation factors (VIFs), orientation comparators and seven-day medication sensitivity are in S13. Assessment descriptive characteristics, restricted controls, fixed-coefficient performance, calibration, missingness and weighting continuations are reported in S15. Full renal/comorbidity adjustment remains unavailable. Additional assessment computations are reported in S15. Version 8 adds corrected bootstrap intervals for assessment rows (S18) and the reproduction of the echo-interval figures (S23); access times are in S1a. Scenario analyses are in S19 to S24.

Differential T-end-error results are available in S14. Under the LUDB-predicted model the group difference was below the sampling resolution and the individual corrections retained most of the log-OR; correction intervals remain unavailable, and the branch is inconclusive.

Still unavailable: independent external replication (access to a second cohort for the cardiomyopathy-code endpoint, not LVEF, has been requested; a replication in EchoNext is not possible so far because its signal scale could not be reconciled and the normalization constants of the provider would be required); blinded review of references and ECGs; detection of pacing spikes in the signal; adjudicated rhythm strata; a lead-space (Acar) TCRT; and a clinical-benefit analysis. These are gaps, not negative findings.

S7. Reporting checklist and unavailable source fields

The following STROBE cross-sectional item map is filled with locations and explicit gaps. It is not a declaration of complete checklist compliance. RECORD extensions and applicable TRIPOD+AI transparency domains follow; a prediction-development/validation checklist would misdescribe the association estimand.

Table S14. S7. Reporting checklist and unavailable source fields

STROBE item	Location	Status / gap
1 Title/abstract	Title; Abstract	Design and principal limitations stated
2 Background/rationale	Introduction	Comparator rationale and clinical research question
3 Objectives	Introduction; Methods	Residual association; specified hierarchy
4 Design	Methods design; S1	Retrospective cross-sectional, internal partition reuse
5 Setting/dates	Methods sources	Hospital, resource 2008-2019; exact retained cohort dates unavailable
6 Participants	Methods participants; S2	Eligibility/index rules present; candidate-to-complete-case flow in S15a and Figure 1
7 Variables	Methods references/measurements	Definitions present; some source-module fields await author
8 Data sources/measurement	Methods; S4-S5	Fixed software; development method proportions in S13; post hoc assessment proportions in S15f; readers and report-extraction validation unavailable
9 Bias	Methods; Discussion; S8-S10	Verification, missingness and measurement errors explicit
10 Study size	Methods; S2	All eligible complete cases; no prospective sample-size calculation
11 Quantitative variables	Methods statistics	Fixed SDs, angle and age terms, threshold sensitivity
12 Statistical methods	Methods; S3; S8-S10	Inference/resampling/missingness; primary complete-case analysis; exploratory MI in S15e; subgroup estimates not interactions
13 Participants/results flow	Results; S2	Candidate-to-complete-case counts in S15a; endpoint input definitions separated
14 Descriptive data	S2a; S8b	D/C age/sex/measurement and class-specific missingness in S15a/e; adjudicated rhythm/pacing unavailable
15 Outcome data	Table 2; S2-S3	Cases/controls and unavailable endpoints
16 Main results	Table 2; S3/S3a	OR per fixed development SD; apparent model comparison; development coefficients in S13; assessment full coefficients not exported
17 Other analyses	Table 3; S3-S4; S8-S11	All exported sensitivities; development and assessment separated
18 Key results	Discussion	Conditional internal association, modest apparent increment
19 Limitations	Discussion; S6	Bias mechanisms and unquantified direction/magnitude
20 Interpretation	Discussion	No clinical utility inference; literature as context

STROBE item	Location	Status / gap
21 Generalisability	Discussion	Single hospital/database, fixed measurements
22 Funding	Declarations	Self-funding and COI stated

Table S15. S7. Reporting checklist and unavailable source fields

RECORD extension	Location	Status / gap
1.1-1.3 Routine-data type, database, linkage in title/abstract	Abstract; Methods	MIMIC linkage described; exact module confirmation open
6.1 Selection algorithms/code lists	Methods participants; S8c	Fixed reference/index rules; ICD prefixes complete
6.2 Validation of selection/codes	Methods; Limitations	No adjudication or report-extraction validation supplied
6.3 Linkage details and quality	Methods references; S2	Matching requirements stated; linkage quality proportions not exported
7.1 Variable code/algorithm definitions	Methods; S3/S8c	Definitions described (S0a); analysis scripts and frozen release public (repository, release v1.0.0; Code availability in the main manuscript)
12.1 Access to source data	Declarations	Credentialing and DUA; author module confirmation open
12.2 Cleaning methods	Methods	Range/conflict/finite-value rules; no replacement after missingness
12.3 Linkage methods	Methods; S2	Deterministic linkage/index selection; full linkage flow unavailable
13.1 Population derivation	S2; S8b	Candidate-to-complete-case flow in S15a; no endpoint-population summation
19.1 Routine-data limitations	Discussion	Code absence, post-ECG diagnosis, missingness, verification
22.1 Protocol/data/code access	Declarations; S1	Internal fixed plan, documented amendments; code public (repository, release v1.0.0; Code availability in the main manuscript)

Table S16. S7. Reporting checklist and unavailable source fields

Applicable TRIPOD+AI domain	Location	Status / gap
Objective, intended use and development/assessment distinction	Introduction; Methods; S1	Association study; no prediction deployment
Data sources, setting, eligibility and partition reuse	Methods; S1-S2	Previous related calculations disclosed; source fields incomplete
Outcome and predictors	Methods; S3	Defined; reference validation and complete coefficients absent
Model specification, handling missing data, sample size	Methods; S2-S3	Fixed regressors/scaling and primary complete cases; exploratory MI in S15e; no prospective power plan
Model evaluation, intervals and failures	Methods; S3a/S3b; S8	Apparent AUC only; post hoc fixed-coefficient performance and calibration in S15b
Fairness/subgroups	Methods; S2a/S3/S10	Recorded sex only; no gender variable or interaction/fairness validation
Availability, limitations, AI use	Declarations; Discussion	Code availability stated (public repository, release v1.0.0); author-approved AI declaration in main Declarations

The full numbered TRIPOD+AI form remains a publication-stage task if the manuscript is submitted as prediction research. Applicable association transparency gaps are already identified here. SAGER: recorded sex is reported, constant sex terms omitted in stratified fits; gender identity is unavailable.

S8. Delayed specified verification analyses and reference bias

The technical continuation took place after main-result sight. It repaired loading of the first-technical-index universe without changing the fixed model parameters. H1 point quantities were first reproduced exactly. Weighted and unweighted verification sensitivities use the same first-technical-index persons and are not compared directly with the first-verified main-model cohort. The following intervals labeled Wald are conditional person-CR1 intervals; they do not include uncertainty of the newly estimated verification model/P99. Required bootstrap intervals are unavailable when fewer than 950 of 1,000 fits are valid.

Table S17. S8. Delayed specified verification analyses and reference bias

quantity	value	rank statistic U	case-control pairs
marker alone, increasing original values	0.80244733	4860263.0	6056800
full B3 basis without marker	0.80244750	4860264.0	6056800

Table S18. S8. Delayed specified verification analyses and reference bias

analysis	N	controls	cases	OR (Wald- 95% CI)	raw P	basis AUC	ba- sis+marker AUC	ΔAUC
un-weighted , same first technical index	4844	4413	431	2.645722 3 (2.279840 1; 3.070323 6)	1.4031586e- 37	0.78558025	0.83243349	0.04685324
IPW, same first technical index	4844	4413	431	2.967822 2 (2.519857 ; 3.495423 9)	8.2247988e- 39	0.81041991	0.85182129	0.04140139

Table S19. S8. Delayed specified verification analyses and reference bias

analysis	N	controls	cases	OR (Wald- 95% CI)	raw P	basis AUC	ba- sis+marker AUC	ΔAUC
mark- er+B4 → TTE availabil- ity	28780	23853	4927	1.593896 5 (1.503120 8; 1.690154 2)	9.6486269e- 55	0.69536102	0.70562336	0.01026234

Table S20. S8. Delayed specified verification analyses and reference bias

endpoint	Analysis stage	class	persons
reduced LVEF	index_universe	negative	8405
reduced LVEF	index_universe	positive	969
reduced LVEF	adult	negative	8405
reduced LVEF	adult	positive	969
reduced LVEF	index_policy	negative	8405
reduced LVEF	index_policy	positive	969
reduced LVEF	eligible	negative	8405
reduced LVEF	eligible	positive	969
reduced LVEF	known_reference	negative	8405
reduced LVEF	known_reference	positive	969
reduced LVEF	reference_time_id_value	negative	8405
reduced LVEF	reference_time_id_value	positive	969
reduced LVEF	confirmato- ry_time_alignment	negative	8405
reduced LVEF	confirmato- ry_time_alignment	positive	969
reduced LVEF	complete_B3_marker	negative	7571
reduced LVEF	complete_B3_marker	positive	800
reduced LVEF	com- plete_B4_marker_on_B3	positive	636
reduced LVEF	com- plete_B4_marker_on_B3	negative	7204
cardiomyopathy codes	index_universe	negative	19302
cardiomyopathy codes	index_universe	positive	515
cardiomyopathy codes	adult	negative	19302
cardiomyopathy codes	adult	positive	515
cardiomyopathy codes	index_policy	negative	19302
cardiomyopathy codes	index_policy	positive	515
cardiomyopathy codes	eligible	negative	19302
cardiomyopathy codes	eligible	positive	515
cardiomyopathy codes	known_reference	negative	19302
cardiomyopathy codes	known_reference	positive	515
cardiomyopathy codes	reference_time_id_value	negative	19302
cardiomyopathy codes	reference_time_id_value	positive	515
cardiomyopathy codes	confirmato- ry_time_alignment	negative	19302
cardiomyopathy codes	confirmato- ry_time_alignment	positive	515
cardiomyopathy codes	complete_B3_marker	negative	17737
cardiomyopathy codes	complete_B3_marker	positive	433
cardiomyopathy codes	com- plete_B4_marker_on_B3	positive	334
cardiomyopathy codes	com- plete_B4_marker_on_B3	negative	17011

Table S21. S8. Delayed specified verification analyses and reference bias

endpoint	class	reference-valid	B3 complete	loss before B3	B4 complete	additional loss B3→B4
reduced LVEF	positive	969	800	17.44% (169)	636	20.50% (164)
reduced LVEF	negative	8405	7571	9.92% (834)	7204	4.85% (367)
cardiomyo- pathy codes	positive	515	433	15.92% (82)	334	22.86% (99)
cardiomyo- pathy codes	negative	19302	17737	8.11% (1565)	17011	4.09% (726)

Table S22. S8. Delayed specified verification analyses and reference bias

endpoint	denominator	class	predictor	missing / denominator	percentage
reduced LVEF	reference_valid_before_CC	positive	heart_rate	25 / 969	2.58%
reduced LVEF	reference_valid_before_CC	positive	qrs_duration_ms	33 / 969	3.41%
reduced LVEF	reference_valid_before_CC	positive	qtc_fridericia_ms	111 / 969	11.46%
reduced LVEF	reference_valid_before_CC	positive	spatial_qrs_t_angle_deg	85 / 969	8.77%
reduced LVEF	reference_valid_before_CC	positive	qrs_t_normalized_discrete_frequency	96 / 969	9.91%
reduced LVEF	reference_valid_before_CC	negative	heart_rate	177 / 8405	2.11%
reduced LVEF	reference_valid_before_CC	negative	qrs_duration_ms	42 / 8405	0.50%
reduced LVEF	reference_valid_before_CC	negative	qtc_fridericia_ms	542 / 8405	6.45%
reduced LVEF	reference_valid_before_CC	negative	spatial_qrs_t_angle_deg	299 / 8405	3.56%
reduced LVEF	reference_valid_before_CC	negative	qrs_t_normalized_discrete_frequency	372 / 8405	4.43%
reduced LVEF	B3_complete_for_B4	positive	classical_cornell_product	164 / 800	20.50%
reduced LVEF	B3_complete_for_B4	positive	classical_sokolow_lyon	164 / 800	20.50%
reduced LVEF	B3_complete_for_B4	positive	axis_sin	164 / 800	20.50%
reduced LVEF	B3_complete_for_B4	positive	axis_cos	164 / 800	20.50%
reduced LVEF	B3_complete_for_B4	negative	classical_cornell_product	367 / 7571	4.85%
reduced LVEF	B3_complete_for_B4	negative	classical_sokolow_lyon	367 / 7571	4.85%
reduced LVEF	B3_complete_for_B4	negative	axis_sin	367 / 7571	4.85%
reduced LVEF	B3_complete_for_B4	negative	axis_cos	367 / 7571	4.85%
cardiomyopathy codes	reference_valid_before_CC	positive	heart_rate	16 / 515	3.11%

endpoint	denominator	class	predictor	missing / denominator	percentage
cardiomyopathy codes	reference_valid_before_CC	positive	qrs_duration_ms	<10 / 515	<1.9%
cardiomyopathy codes	reference_valid_before_CC	positive	qtc_fridericia_ms	57 / 515	11.07%
cardiomyopathy codes	reference_valid_before_CC	positive	spatial_qrs_t_angle_deg	39 / 515	7.57%
cardiomyopathy codes	reference_valid_before_CC	positive	qrs_t_frechet_beat_median	<10 / 515	<1.9%
cardiomyopathy codes	reference_valid_before_CC	negative	heart_rate	326 / 19302	1.69%
cardiomyopathy codes	reference_valid_before_CC	negative	qrs_duration_ms	104 / 19302	0.54%
cardiomyopathy codes	reference_valid_before_CC	negative	qtc_fridericia_ms	1091 / 19302	5.65%
cardiomyopathy codes	reference_valid_before_CC	negative	spatial_qrs_t_angle_deg	about 700 / 19302	about 3.5%
cardiomyopathy codes	reference_valid_before_CC	negative	qrs_t_frechet_beat_median	<20 / 19302	<0.1%
cardiomyopathy codes	B3_complete_for_B4	positive	classical_cornell_product	99 / 433	22.86%
cardiomyopathy codes	B3_complete_for_B4	positive	classical_sokolow_lyon	99 / 433	22.86%
cardiomyopathy codes	B3_complete_for_B4	positive	axis_sin	99 / 433	22.86%
cardiomyopathy codes	B3_complete_for_B4	positive	axis_cos	99 / 433	22.86%
cardiomyopathy codes	B3_complete_for_B4	negative	classical_cornell_product	726 / 17737	4.09%
cardiomyopathy codes	B3_complete_for_B4	negative	classical_sokolow_lyon	726 / 17737	4.09%
cardiomyopathy codes	B3_complete_for_B4	negative	axis_sin	726 / 17737	4.09%
cardiomyopathy codes	B3_complete_for_B4	negative	axis_cos	726 / 17737	4.09%

S8a. Weighting and AUC checks

Both first-technical-index outcome models had 777/1,000 valid replicates, with 223 failures of the fixed normalized-score convergence criterion. No bootstrap interval was reported, no failures replaced and no alternative solver selected. Point fits were estimable. All 223 rejected replicates met the stopping rule and violated the acceptance rule (S18, Table S109), so the interval is unavailable by construction. The bootstrap of this analysis was not recomputed with an aligned rule.

The paired weighting result has no direction reversal, conditional on missing-at-random and positivity assumptions. This is not proof that verification bias cannot explain the association.

Class-specific effective sample sizes after weighting were 3215.849 for controls and 349.111 for cases. Propensity minimum/P1/median/P99/maximum were 0.020610/0.037911/0.153245/0.518546/0.863502; corresponding weight quantiles were 1.158075/1.928473/6.525503/20.695919/20.695919. Weighting uses a first-technical-index universe and cannot correct absent marker/covariate measurements.

The verification-association model had 1,000 valid replicates. The ± 30 -day count is 4,927 within its 28,780 marker+B4-complete persons. The ± 7 -day count of 4,795 refers instead to the entire technical index set; those counts must not be interpreted as nested availability percentages with one denominator.

Independent rank recomputation gave $U=4,860,263$ for increasing original marker values and $U=4,860,264$ for B3, across 6,056,800 case-control pairs. Thus AUCs 0.80244733 and 0.80244750 differ by exactly one pair. This verified coincidence does not imply identical predictions or a marker-only B3 model. The original H1 Δ AUC is unchanged.

S8b. Differential missingness

The class-specific tables above start from known references at the fixed first-verified index; they cannot identify case/controls before reference availability. Counts of missing predictors overlap and must not be summed. There was no replacement ECG or imputation. The direction of the resulting bias and a rhythm/pacing cause were not estimated. B4 case losses are disproportionate and must be considered alongside its smaller apparent increment.

S8c. ICD references and unavailable restricted-control sensitivity

The ICD definition includes all ICD-9 425* and ICD-10 I42/I43 subcodes in the index encounter. An assigned encounter without a matching code, including a missing/null diagnosis flag, becomes a negative code label. Missing encounter linkage is unavailable and excluded. Hence unknown echo references are excluded, but code absence is not independently verified disease absence. Encounter codes may postdate the ECG. A control restriction excluding heart-failure codes and requiring normal echo function was not supplied; no such result is claimed.

S8d. NT-proBNP adjustment

The original missing-parameter exception masked an existing development stop: no complete development H1/RV set with exact uncensored NT/URL and verified hour alignment supplied the fixed design parameters. No alternative parameter key, fresh scaling or hour-alignment waiver was introduced. Rank 6e remains not estimable for this structural reason, not a biological null.

S9. Developmental angle-error correction

These analyses contain training and validation only. Validation is internal confirmation/development, not external replication or the assessment partition. Both folds use the same measured development Fréchet SD, 0.76503231; reference LVEF is <40% versus ≥40%. Clinical-repeat error variance is centered difference variance divided by two and may include genuine physiology.

RC predicts the angle conditional on all other regressors including Fréchet. It stops when conditional reliability is nonpositive. SIMEX uses fixed multipliers 0/0.5/1/1.5/2, 20 antithetic draws per positive multiplier and quadratic extrapolation to -1, with linear extrapolation sensitivity. Normal errors were not clipped to 0-180 degrees. Bootstrap estimation includes repeat-pair variance and calibration; an interval requires at least 475/500 valid replicates. These assumptions are not empirically established by repeatability.

Table S23. S9. Developmental angle-error correction

Partition	A-pairs	method	OR [95% CI]	log-effect re-tained	valid bootstrap	interpretation
training	all pairs	uncorrected	2.480 [2.334; 2.625]	100.0 %	500/500	uncorrected reference
training	all pairs	rc	2.289 [0.989; 4.502]	91.1 %	500/500	robustness criterion not met: interval includes 1
training	all pairs	simex	2.471 [2.278; 2.670]	99.6 %	500/500	retained under assumed angle error
internal validation	all pairs	uncorrected	2.392 [2.143; 2.717]	100.0 %	500/500	uncorrected reference
internal validation	all pairs	rc	2.839 [0.772; 13.625]	119.7 %	497/500	robustness criterion not met: interval includes 1
internal validation	all pairs	simex	2.413 [2.079; 2.882]	101.0 %	500/500	retained under assumed angle error
training	simultaneous	uncorrected	2.480 [2.334; 2.625]	100.0 %	500/500	uncorrected reference
training	simultaneous	rc	2.335 [not estimable; not estimable]	93.3 %	425/500	robustness criterion open: interval unavailable
training	simultaneous	simex	2.471 [2.277; 2.666]	99.6 %	500/500	retained under assumed angle error
internal validation	simultaneous	uncorrected	2.392 [2.143; 2.717]	100.0 %	500/500	uncorrected reference
internal validation	simultaneous	rc	2.726 [not estimable; not estimable]	115.0 %	417/500	robustness criterion open: interval unavailable
internal validation	simultaneous	simex	2.412 [2.079; 2.873]	101.0 %	500/500	retained under assumed angle error

Table S24. S9. Developmental angle-error correction

group	pairs / persons	ICC(A,1) [95% CI]	pair bias deg	error variance deg ² [95% CI]
all pairs	13312 / 9115	0.617 [0.602;0.631]	0.130	883.830 [853.163;916.461]
simultaneous	about 300 / about 290	0.636 [0.546;0.717]	-1.925	863.686 [672.058;1078.197]

Table S25. S9. Developmental angle-error correction

Partition	A-pairs	method	OR [95% CI]	log-effect re-tained	valid bootstrap	interpretation
training	all pairs	simex_linear	2.478 [2.321; 2.641]	99.9 %	500/500	retained under assumed angle error
internal validation	all pairs	simex_linear	2.398 [2.120; 2.760]	100.3 %	500/500	retained under assumed angle error
training	simultaneous	simex_linear	2.478 [2.321; 2.641]	99.9 %	500/500	retained under assumed angle error
internal validation	simultaneous	simex_linear	2.398 [2.120; 2.760]	100.3 %	500/500	retained under assumed angle error

Table S26. S9. Developmental angle-error correction

Partition	repeat source	RC angle outside 0-180°	SIMEX outside at $\lambda=0.5$ / 1 / 1.5 / 2
training	all pairs	0.44 %	6.10 % / 10.03 % / 13.20 % / 15.88 %
internal validation	all pairs	0.50 %	6.15 % / 10.13 % / 13.22 % / 15.86 %
training	simultaneous	0.42 %	5.99 % / 9.86 % / 13.00 % / 15.65 %
internal validation	simultaneous	0.47 %	6.05 % / 9.96 % / 13.02 % / 15.64 %

Table S27. S9. Developmental angle-error correction

Partition	A-pairs	method	OR [95% CI]	log-effect re-tained	valid bootstrap	interpretation
training	all pairs	uncorrected	2.493 [2.369; 2.604]	100.0 %	500/500	uncorrected reference
training	all pairs	rc	2.493 [2.369; 2.604]	100.0 %	500/500	retained under assumed angle error
training	all pairs	simex	2.493 [2.369; 2.604]	100.0 %	500/500	retained under assumed angle error
internal validation	all pairs	uncorrected	2.366 [2.163; 2.581]	100.0 %	500/500	uncorrected reference
internal validation	all pairs	rc	2.367 [2.164; 2.583]	100.1 %	500/500	retained under assumed angle error
internal validation	all pairs	simex	2.367 [2.164; 2.582]	100.1 %	500/500	retained under assumed angle error
training	simultaneous	uncorrected	2.493 [2.369; 2.604]	100.0 %	500/500	uncorrected reference
training	simultaneous	rc	2.493 [2.369; 2.604]	100.0 %	500/500	retained under assumed angle error
training	simultaneous	simex	2.493 [2.369; 2.604]	100.0 %	500/500	retained under assumed angle error
internal validation	simultaneous	uncorrected	2.366 [2.163; 2.581]	100.0 %	500/500	uncorrected reference
internal validation	simultaneous	rc	2.367 [2.164; 2.583]	100.1 %	500/500	retained under assumed angle error
internal validation	simultaneous	simex	2.367 [2.164; 2.582]	100.1 %	500/500	retained under assumed angle error

Table S28. S9. Developmental angle-error correction

Partition	repeat source	method	Δ log-OR Fréchet [paired 95% CI]
training	all pairs	rc	0.000000 [-0.000231;0.000245]
training	all pairs	simex	-0.000033 [-0.000305;0.000235]
internal validation	all pairs	rc	0.000584 [-0.000419;0.002648]
internal validation	all pairs	simex	0.000483 [-0.000544;0.002106]
training	simultaneous	rc	0.000000 [-0.000218;0.000253]
training	simultaneous	simex	-0.000032 [-0.000288;0.000222]
internal validation	simultaneous	rc	0.000562 [-0.000427;0.002805]
internal validation	simultaneous	simex	0.000473 [-0.000508;0.002135]

The permuted-angle control preserves a fixed marginal angle distribution and tests spurious changes in the Fréchet coefficient; it is neither a negative-control disease outcome nor an equivalence test. Pair-source RC includes-null or unavailable intervals prevent a method-wide robustness claim. Positive SIMEX intervals support retention under that specified error model only. The

reported antithetic-fit scatter is a descriptive Monte Carlo diagnostic, not an independent Monte Carlo standard error.

S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Cross-repeat correlation uses measurements from different records, with denominator estimated from those same repeats. It is free of a prescribed numerical reliability value, but still requires time-stable latent values, comparable scales and no cross-record error covariance for a latent-correlation interpretation. Persistent person/device errors and physiological change are not excluded. The fixed categories were practical identity at point ≥ 0.95 and lower CI ≥ 0.90 , distinguishability by point ≤ 0.85 , and strong overlap between those rules. Interval overlap qualifies any point-based distinction. The prior same-record disattenuation quotient above one cannot establish identity.

Outcome correction uses 200 paired person-bootstrap replicates and fixed development scaling. Assumed ICCs are scenarios on the outcome variance, not newly measured reliabilities. AF/left-bundle low-ICC scenarios on the full set are stress scenarios, distinct from actual rhythm-stratum fits. Pair-variance and scenario-ICC methods therefore need not numerically coincide.

Joint RC estimates half the covariance of angle/Fréchet repeat differences on the original model scales; error covariance must be positive semidefinite and latent residual covariance positive definite. No matrix clipping repairs a failed criterion. An invertible affine correction preserves the unpenalized observed fitted-score space, so its larger OR does not represent newly gained empirical discrimination.

The restricted cubic angle spline uses four training-fixed quantile knots (5/35/65/95%) at 16.919366, 57.774035, 104.679448 and 163.600533 degrees, giving three angle terms and linear tails. SIMEX perturbs the angle before basis construction. This flexible scalar comparator does not exhaust spatial axes or loop-magnitude information.

Table S29. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition/stratum	persons	cases (<40)	controls
training/all pairs	25453	2690	22763
training/sinus	21037	1786	19251
training/narrow QRS without signal block flags	18485	1056	17429
training/LSB	318	131	187
training/AF	2641	481	2160
internal validation/all pairs	8518	853	7665
internal validation/sinus	7008	574	6434
internal validation/narrow QRS without signal block flags	6243	345	5898
internal validation/LSB	103	32	71
internal validation/AF	926	156	770

Table S30. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

group	scale	pairs/persons	rF / rA	r12 [95% CI]	r21 [95% CI]	symmetric [95% CI]	valid	point rule
all pairs	pear-son_log1p	13029/8966	0.841 / 0.619	0.902 [0.889; 0.916]	0.850 [0.836; 0.862]	0.876 [0.866; 0.886]	1000/1000	strong overlap
all pairs	spearman	13029/8966	0.841 / 0.621	0.901 [0.887; 0.915]	0.849 [0.835; 0.863]	0.875 [0.865; 0.885]	1000/1000	strong overlap
simultaneous	pear-son_log1p	289/277	0.870 / 0.634	0.854 [0.768; 0.936]	0.861 [0.781; 0.945]	0.857 [0.793; 0.916]	1000/1000	strong overlap
simultaneous	spearman	289/277	0.867 / 0.634	0.863 [0.773; 0.944]	0.859 [0.771; 0.946]	0.861 [0.796; 0.919]	1000/1000	strong overlap
sinus	pear-son_log1p	4534/3525	0.892 / 0.693	0.889 [0.872; 0.908]	0.839 [0.820; 0.857]	0.864 [0.850; 0.878]	1000/1000	strong overlap
sinus	spearman	4534/3525	0.892 / 0.694	0.891 [0.872; 0.910]	0.839 [0.820; 0.857]	0.865 [0.850; 0.879]	1000/1000	strong overlap
AF	pear-son_log1p	1690/1353	0.826 / 0.461	0.915 [0.863; 0.967]	0.821 [0.771; 0.871]	0.868 [0.830; 0.903]	1000/1000	strong overlap
AF	spearman	1690/1353	0.825 / 0.467	0.897 [0.844; 0.949]	0.824 [0.774; 0.874]	0.861 [0.823; 0.896]	1000/1000	strong overlap
LSB	pear-son_log1p	419/329	0.798 / 0.309	0.823 [0.628; 1.010]	0.738 [0.564; 0.913]	0.781 [0.651; 0.901]	1000/1000	distinguishable by point rule; interval overlaps
LSB	spearman	419/329	0.780 / 0.407	0.627 [0.467; 0.771]	0.705 [0.554; 0.849]	0.666 [0.548; 0.781]	1000/1000	distinguishable by point rule; upper interval limit ≤ 0.85
RSB	pear-son_log1p	1055/774	0.830 / 0.527	0.737 [0.667; 0.808]	0.720 [0.648; 0.789]	0.729 [0.670; 0.783]	1000/1000	distinguishable by point rule; upper interval limit ≤ 0.85
RSB	spearman	1055/774	0.816 / 0.524	0.740 [0.666; 0.813]	0.695 [0.619; 0.768]	0.717 [0.656; 0.773]	1000/1000	distinguishable by point rule; upper interval limit ≤ 0.85
QRS_lt120	pear-son_log1p	9759/6964	0.831 / 0.602	0.893 [0.877; 0.908]	0.846 [0.831; 0.862]	0.870 [0.858; 0.881]	1000/1000	strong overlap
QRS_lt120	spearman	9759/6964	0.832 / 0.605	0.893 [0.877; 0.908]	0.846 [0.831; 0.862]	0.870 [0.858; 0.881]	1000/1000	strong overlap
training	pear-son_log1p	9637/6656	0.837 / 0.619	0.897 [0.884; 0.912]	0.850 [0.836; 0.866]	0.874 [0.863; 0.886]	1000/1000	strong overlap
training	spearman	9637/6656	0.837 / 0.620	0.895 [0.881; 0.911]	0.849 [0.834; 0.864]	0.872 [0.861; 0.884]	1000/1000	strong overlap
internal validation	pear-son_log1p	3392/2310	0.852 / 0.620	0.916 [0.893; 0.940]	0.847 [0.820; 0.873]	0.882 [0.863; 0.899]	1000/1000	strong overlap
internal validation	spearman	3392/2310	0.852 / 0.622	0.917 [0.893; 0.940]	0.849 [0.822; 0.875]	0.883 [0.863; 0.901]	1000/1000	strong overlap

Table S31. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

overall scale	corr(F1,A1)	corr(F2,A2)	corr(F1,A2)	corr(A1,F2)	$\sqrt{(rF-rA)}$
pearson_log1p	0.680	0.719	0.651	0.613	0.722
spearman	0.678	0.719	0.651	0.613	0.722

Table S32. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	error source	method	OR [95% CI]	log-OR retained	valid	estimability
training	icc_0.45	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
training	icc_0.45	simex	2.469 [2.313; 2.701]	99.5 %	200/200	n/a
training	icc_0.55	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
training	icc_0.55	simex	2.470 [2.319; 2.689]	99.6 %	200/200	n/a
training	icc_0.617	rc	2.369 [1.706; 3.384]	94.9 %	200/200	n/a
training	icc_0.617	simex	2.471 [2.322; 2.685]	99.6 %	200/200	n/a
training	icc_0.7	rc	2.447 [2.183; 2.848]	98.5 %	200/200	n/a
training	icc_0.7	simex	2.473 [2.327; 2.685]	99.7 %	200/200	n/a
training	icc_0.46	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
training	icc_0.46	simex	2.469 [2.314; 2.700]	99.5 %	200/200	n/a
training	icc_0.31	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
training	icc_0.31	simex	2.467 [2.307; 2.711]	99.4 %	200/200	n/a
training	pairs_all pairs	rc	2.300 [1.339; 4.505]	91.7 %	200/200	n/a
training	pairs_all pairs	simex	2.471 [2.322; 2.686]	99.6 %	200/200	n/a
internal valida- tion	icc_0.45	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
internal valida- tion	icc_0.45	simex	2.417 [2.057; 2.765]	101.2 %	200/200	n/a
internal valida- tion	icc_0.55	rc	not estimable [not estimable; not estimable]	not estimable	2/200	nonpositive conditional reliability
internal valida- tion	icc_0.55	simex	2.414 [2.069; 2.751]	101.1 %	200/200	n/a
internal valida- tion	icc_0.617	rc	2.656 [1.179; 5.134]	112.0 %	200/200	n/a
internal valida- tion	icc_0.617	simex	2.412 [2.079; 2.742]	101.0 %	200/200	n/a
internal valida- tion	icc_0.7	rc	2.468 [1.841; 3.089]	103.6 %	200/200	n/a
internal valida- tion	icc_0.7	simex	2.409 [2.094; 2.724]	100.8 %	200/200	n/a
internal valida- tion	icc_0.46	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
internal valida- tion	icc_0.46	simex	2.417 [2.058; 2.763]	101.2 %	200/200	n/a
internal valida- tion	icc_0.31	rc	not estimable [not estimable; not estimable]	not estimable	0/200	nonpositive conditional reliability
internal valida- tion	icc_0.31	simex	2.421 [2.042; 2.786]	101.4 %	200/200	n/a

Partition	error source	method	OR [95% CI]	log-OR retained	valid	estimability
internal validation	pairs_all pairs	rc	2.811 [0.875; 10.733]	118.5 %	200/200	n/a
internal validation	pairs_all pairs	simex	2.413 [2.077; 2.745]	101.0 %	200/200	n/a

Table S33. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	pair source	error correlation	eigenvalues T	OR [95% CI]	log-OR retained	valid	Criterion
training	multirc_all pairs	0.268	0.02680, 0.87258	8.737 [5.248; 21.525]	238.6 %	200/200	n/a
training	multirc_simultaneous	0.329	0.04925, 0.88980	3.589 [2.475; 30.006]	140.7 %	194/200	n/a
internal validation	multirc_all pairs	0.268	0.02774, 0.87487	9.259 [3.795; 60.030]	255.2 %	200/200	n/a
internal validation	multirc_simultaneous	0.329	0.05028, 0.89200	3.719 [1.866; 41.708]	150.6 %	197/200	n/a

Table S34. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

source	pairs	persons	E_AA deg ²	E_FF F ²	E_AF deg-F	Bias A2-A1 deg	Bias F2-F1
multirc_all pairs	13029	8966	879.682087	0.101028	2.522657	0.103622	-0.036788
multirc_simultaneous	289	277	871.241101	0.080063	2.748083	-2.158712	0.000268

Table S35. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	error source	method	OR [95% CI]	log-OR retained (spline reference)	valid	Criterion
training	icc_0.45	simex	2.536 [2.341; 2.790]	101.6 %	200/200	n/a
training	icc_0.55	simex	2.538 [2.348; 2.779]	101.7 %	200/200	n/a
training	icc_0.617	simex	2.540 [2.355; 2.770]	101.8 %	200/200	n/a
training	icc_0.7	simex	2.540 [2.369; 2.767]	101.8 %	200/200	n/a
training	pairs_all pairs	simex	2.539 [2.354; 2.773]	101.8 %	200/200	n/a
internal validation	icc_0.45	simex	2.518 [2.125; 2.913]	104.8 %	200/200	n/a
internal validation	icc_0.55	simex	2.517 [2.146; 2.906]	104.7 %	200/200	n/a
internal validation	icc_0.617	simex	2.516 [2.156; 2.893]	104.7 %	200/200	n/a
internal validation	icc_0.7	simex	2.511 [2.165; 2.869]	104.4 %	200/200	n/a
internal validation	pairs_all pairs	simex	2.516 [2.154; 2.892]	104.7 %	200/200	n/a

Table S36. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	uncorrected linear OR	uncorrected spline OR	Spline/linear log-OR
training	2.480	2.498	1.0079
internal validation	2.392	2.414	1.0107

Table S37. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition/stratum	error source	uncorrected OR	SIMEX OR [95% CI]	log-OR retained	valid
training/sinus	icc_0.617	2.614	2.591 [2.379; 2.876]	99.1 %	200/200
training/sinus	icc_0.7	2.614	2.595 [2.388; 2.864]	99.3 %	200/200
training/sinus	pairs_stratum	2.614	2.594 [2.389; 2.865]	99.2 %	200/200
training/narrow QRS without signal block flags	icc_0.617	2.679	2.669 [2.420; 2.963]	99.7 %	200/200
training/narrow QRS without signal block flags	icc_0.7	2.679	2.671 [2.434; 2.949]	99.7 %	200/200
training/narrow QRS without signal block flags	pairs_stratum	2.679	2.668 [2.411; 2.979]	99.6 %	200/200
training/AF	icc_0.46	2.439	2.543 [2.128; 3.157]	104.7 %	200/200
training/LSB	icc_0.31	1.466	1.351 [0.710; 2.549]	78.6 %	200/200
internal validation/sinus	icc_0.617	2.550	2.622 [2.177; 3.103]	103.0 %	200/200
internal validation/sinus	icc_0.7	2.550	2.610 [2.187; 3.051]	102.5 %	200/200
internal validation/sinus	pairs_stratum	2.550	2.613 [2.183; 3.061]	102.6 %	200/200
internal validation/narrow QRS without signal block flags	icc_0.617	2.473	2.463 [2.006; 2.968]	99.5 %	200/200
internal validation/narrow QRS without signal block flags	icc_0.7	2.473	2.464 [2.028; 2.946]	99.6 %	200/200
internal validation/narrow QRS without signal block flags	pairs_stratum	2.473	2.461 [1.986; 2.981]	99.5 %	200/200
internal validation/AF	icc_0.46	2.066	2.007 [1.425; 2.783]	96.0 %	200/200
internal validation/LSB	icc_0.31	1.444	1.245 [not estimable; not estimable]	59.7 %	0/200

Table S38. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	Outcome-stratum	repeat-pair ICC (descriptive)	pair-based variance deg ²
training	sinus	0.693	658.329
training	narrow QRS without signal block flags	0.602	835.115
internal validation	sinus	0.693	658.329
internal validation	narrow QRS without signal block flags	0.602	835.115

Table S39. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

source/model	persons training / validation	component	marker AUC, increasing	OR per component training SD	Δ AUC over B4
development signal pilot, training-Fit/B4	200 / 200	original	0.794743	2.734702	0.037943
development signal pilot, training-Fit/B4	200 / 200	shape	0.604800	0.851665	-0.021029
development signal pilot, training-Fit/B4	200 / 200	residual	0.685257	2.370977	0.038857

Table S40. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

separate larger source	internal internal-validation persons/cases	original AUC	rotation-removed AUC	Δ AUC rotation-removed minus original [95% CI]
developmental measurement-repair analysis	2609/624	0.805096	0.558891	-0.246205 [-0.277; -0.215]

Table S41. S10. Developmental construct overlap, reliability range, correlated errors and flexible angle

Partition	basis	outside $\lambda_{0.5}$	λ_1	$\lambda_{1.5}$	λ_2	β quadratic	β linear
training	linear	5.83 %	9.63 %	12.70 %	15.29 %	0.905	0.907
training	spline	5.83 %	9.63 %	12.70 %	15.29 %	0.932	0.914
internal validation	linear	5.97 %	9.64 %	12.64 %	15.24 %	0.880	0.875
internal validation	spline	5.97 %	9.64 %	12.64 %	15.24 %	0.923	0.883

Sinus and narrow-without-block outcome strata differ in definition from repeat-pair strata. Absence of a bilateral block report is not a verified negative signal-block finding. The internal-validation left-bundle stratum contained only 32 cases; bootstrap minimum-class criteria frequently failed. Its missing interval is not evidence of equivalence.

The separate larger developmental rotation-removal comparison has 2,609 internal-validation persons and 624 cases. Its AUC difference is not an additive fraction of orientation information

and is not pooled with the 200-person signal pilot. Pilot components have their own training SDs and estimands. Harmonised negative-control models for eight diagnoses are reported in S27 (post hoc, development data). Peak and area angle, axis-component, ventricular gradient, TCRT and planarity comparators are reported in S13d and S24 and in the main text.

S11. Related hypotheses: context only

The related-hypothesis family of pipeline stage 28 had fixed $m=63$: 38 met its confirmation rule, 22 were not estimable, one had the same direction without significance, and two were reserved already-tested identities. H1/H4 were not fitted again; their internal $P=1$ reservation is not a failed new test. This family is separate from the specified four-hypothesis B hierarchy and is not independent replication. No study-wide FDR claim follows from its separate correction.

The earlier holdout clinical table of related hypotheses retained the original $m=72$ and the phenome-wide table $m=218$; the extracted subset of related hypotheses was not re-corrected. Clinical categories were 10 confirmed, one same-direction nonsignificant, one reversed nonsignificant and four not estimable; phenome-wide categories were 12/two/zero/three respectively. These results document prior use and broad association context, rather than repeat confirmation of H1/H4.

The prior clinical Hausdorff-LVEF $<40\%$ pair had $N=8,717$ with 851 cases, OR 1.20713 (1.12353-1.29695) and $q=1.31454 \times 10^{-6}$. Prior beat-median Fréchet associations included the cardiovascular cardiomyopathy code CV_414: OR 2.26992 (2.08318-2.47341); heart-failure code CV_424: 1.89869 (1.81196-1.98958); systolic-heart-failure code CV_424.2: 2.46176 (2.30132-2.63339). These code hypotheses differ in index, adjustment, scaling and reference input definition from H4. They cannot be pooled or called an independent exact H4 replication.

Broader associations included beat-median Fréchet with the verified PheWAS concept SO_374.4 (retinopathy), OR 1.48697 (1.32292-1.67137). CA_116 means secondary malignant neoplasm and concerns eligible-beat count, not the same primary distance. GU_580 means glomerular diseases and concerns an integral-angle marker. These are the source's mapped concept names, not clinical interpretations inferred from the prefixes. They provide context against a uniquely LV-specific interpretation, but are not B3-adjusted negative-control outcome experiments.

Reused developmental diagnostic-identifiability analyses provide context rather than a new association assessment: function and aetiology are distinct targets, machine-reported normality does not exclude low EF, and age/sex can add information beyond the electrical descriptor. These observations do not establish screening sensitivity, causal diagnosis or external replication. They are not new tests on an untouched partition and are not quantitative performance evidence for the present marker.

S12. Evidence boundaries

Table S42. S12. Evidence boundaries

Potential pitfall	H1/H4 and clinical sensitivities	RV findings	Technical/measurement-error sensitivities
F1 Mechanical coupling/reference	Restricted: shared orientation; routine references; no independent biological construct claim	Same geometric/reference restriction	Clinical reference not used in boundary experiment; shared errors in correction
F2 Selected populations	Restricted: verified hospital complete cases; no population prevalence or predictive values	Additional echo selection	Development/repeat/finite-output selection
F3 Chosen operating point	Not applicable: no clinical threshold optimized	Fixed reference rules	Fixed technical scenarios, no diagnostic operating point
F4 Multiplicity/selection	Restricted: development selection, reused partition, fixed hierarchy	Descriptive and previously seen	Exploratory development; staged boundary amendment disclosed
F5 Missingness	Open: differential losses quantified; tipping points of delta-adjusted imputation in S21; bias direction unknown	Open	Open: informative finite-output/repeat availability
F6 Comparator	Restricted: measured integral angle/B4 dimensions; full orientation comparison unresolved; developmental extensions in S13	R/S and angle controls with same limits	Flexible angle helps but no orientation independence proof
F7 Verification/change	Open: IPW assumptions and absent bootstrap intervals; selection scenario analysis in S22; no within-person claim	Open: clinical echo selection	Repeat physiology is not technical-error variance
F8 Signal/quality/leakage	Open: boundary, pacing/device/era effects; report text not predictor	Same limits	Shared/persistent errors, LUDB reuse and conditional sensitivity

Unavailable rows are not biological null findings. Null-touching RV Fréchet and left-bundle estimates are not equivalence demonstrations. The five measurement claim limits in Methods remain applicable; these results are not a clinical release.

S13. Additional development and internal-validation analyses

All tables in this section use training or internal validation, not independent replication. ORs use endpoint-specific fixed development SDs. Outcome-sensitivity intervals are paired person-bootstrap percentiles (200 planned, at least 190 valid); angle coefficients use CR1 Wald intervals, continuous-LVEF estimates HC1 intervals. No multiplicity correction was applied to these exploratory sensitivities. Repeat reliability is model-dependent and includes physiological change.

S13a. Conditional reliability, full coefficients and repeatability

Table S43. S13a. Conditional reliability, full coefficients and repeatability

Partition	Persons/cases	Reliability		Angle OR		Spearman correlation	Angle VIF with marker
		without marker	with marker	without marker	with marker		
training	25453/2690	0.474 [0.458; 0.490]	0.071 [0.032; 0.104]	1.793 [1.699; 1.892]	1.009 [0.946; 1.076]	0.753 [0.746; 0.761]	2.304
internal validation	8518/853	0.477 [0.452; 0.497]	0.075 [0.022; 0.124]	1.695 [1.542; 1.863]	0.980 [0.872; 1.102]	0.750 [0.739; 0.760]	2.304

Table S44. S13a. Conditional reliability, full coefficients and repeatability

Partition	Repeat pairs/persons	Angle ICC [95%-CI]	Marker ICC [95%-CI]
training	9637/6656	0.619 [0.605; 0.636]	0.833 [0.821; 0.843]
internal validation	3392/2310	0.620 [0.594; 0.651]	0.849 [0.831; 0.866]

Table S45. S13a. Conditional reliability, full coefficients and repeatability

Partition	Model	Coefficient	OR [CR1-Wald-95%-CI]	VIF
training	with_marker	intercept	0.062 [0.058; 0.065]	not applicable
training	with_marker	age_linear	1.328 [1.157; 1.523]	5.657
training	with_marker	age_natural	0.769 [0.681; 0.869]	5.604
training	with_marker	sex_numeric	1.281 [1.221; 1.344]	1.073
training	with_marker	heart_rate	1.526 [1.464; 1.592]	1.114
training	with_marker	qrs_duration_ms	1.195 [1.138; 1.255]	1.809
training	with_marker	qtc_fridericia_ms	1.474 [1.400; 1.551]	1.467
training	with_marker	spatial_qrs_t_angle_deg	1.009 [0.946; 1.076]	2.304
training	with_marker	qrs_t_normalized_disc rete_frechet	2.480 [2.331; 2.639]	2.497
training	without_marker	intercept	0.072 [0.068; 0.076]	not applicable
training	without_marker	age_linear	1.376 [1.207; 1.569]	5.652
training	without_marker	age_natural	0.781 [0.695; 0.878]	5.603
training	without_marker	sex_numeric	1.248 [1.192; 1.306]	1.072
training	without_marker	heart_rate	1.637 [1.570; 1.707]	1.086
training	without_marker	qrs_duration_ms	1.433 [1.366; 1.502]	1.700
training	without_marker	qtc_fridericia_ms	1.409 [1.339; 1.483]	1.467
training	without_marker	spatial_qrs_t_angle_deg	1.793 [1.699; 1.892]	1.304
internal validation	with_marker	intercept	0.057 [0.051; 0.064]	not applicable
internal validation	with_marker	age_linear	1.791 [1.348; 2.379]	5.679
internal validation	with_marker	age_natural	0.639 [0.502; 0.812]	5.659
internal validation	with_marker	sex_numeric	1.426 [1.307; 1.555]	1.087
internal validation	with_marker	heart_rate	1.506 [1.398; 1.622]	1.115
internal validation	with_marker	qrs_duration_ms	1.204 [1.105; 1.312]	1.832
internal validation	with_marker	qtc_fridericia_ms	1.375 [1.255; 1.508]	1.474
internal validation	with_marker	spatial_qrs_t_angle_deg	0.980 [0.872; 1.102]	2.304
internal validation	with_marker	qrs_t_normalized_disc rete_frechet	2.392 [2.138; 2.676]	2.501
internal validation	without_marker	intercept	0.067 [0.061; 0.074]	not applicable
internal validation	without_marker	age_linear	1.837 [1.395; 2.418]	5.675
internal validation	without_marker	age_natural	0.654 [0.518; 0.825]	5.657
internal validation	without_marker	sex_numeric	1.385 [1.274; 1.506]	1.086
internal validation	without_marker	heart_rate	1.610 [1.498; 1.730]	1.085
internal validation	without_marker	qrs_duration_ms	1.430 [1.315; 1.556]	1.726
internal validation	without_marker	qtc_fridericia_ms	1.328 [1.212; 1.455]	1.474
internal validation	without_marker	spatial_qrs_t_angle_deg	1.695 [1.542; 1.863]	1.304

Table S46. S13a. Conditional reliability, full coefficients and repeatability

Partition	Pearson	Spearman correlation [95%-CI]	Angle-only AUC	Marker-only AUC
training	0.746	0.753 [0.746; 0.761]	0.7390	0.8081
internal validation	0.745	0.750 [0.739; 0.760]	0.7324	0.8052

Reliability uses repeat-difference variance and residual angle variance. It is conditional on a stable latent measurement and the assumed error model. Complete pairs and persons are distinct denominators. Coefficient ORs for sex and age basis refer to standardised design columns; the sex OR is not a direct binary comparison. Intercept ORs are technical. Angle-only and marker-only AUCs share the specified complete set.

S13b. Known-truth simulation

Table S47. S13b. Known-truth simulation

Scenario	Method	Valid/200	True marker OR	Geometric-mean OR [95% simulation quantiles]	Mean coefficient bias	Median re-tained log-OR fraction	Fraction at least observed training/internal validation
null	oracle	200	1.000	0.994 [0.859; 1.145]	-0.006	-0.024	0.000/0.000
null	uncorrected	200	1.000	1.247 [1.096; 1.395]	0.221	1.000	0.000/0.000
null	simex	200	1.000	1.118 [0.973; 1.271]	0.112	0.521	0.000/0.000
null	rc	200	1.000	0.993 [0.848; 1.171]	-0.007	-0.013	0.000/0.000
null	joint_rc	200	1.000	0.991 [0.800; 1.238]	-0.009	-0.018	0.000/0.000
true	oracle	200	1.934	1.951 [1.692; 2.296]	0.008	0.914	0.000/0.005
true	uncorrected	200	1.934	2.070 [1.851; 2.354]	0.068	1.000	0.010/0.020
true	simex	200	1.934	1.856 [1.647; 2.140]	-0.041	0.849	0.000/0.000
true	rc	200	1.934	1.617 [1.400; 1.895]	-0.179	0.660	0.000/0.000
true	joint_rc	200	1.934	1.913 [1.579; 2.348]	-0.011	0.893	0.010/0.020

The null sets independent marker log-effect to zero; the genuine-effect scenario sets latent-marker log-effect to 0.6 and converts to the measured-SD scale. The marker combines a linear latent-angle component with independent noise. Each scenario has 200 datasets of 4,000 synthetic observations, angle log-effect 0.8 and intercept -2.5. Reported bounds are simulation quantiles, not biological-effect confidence intervals. Neither persistent nor differential error is represented. Ratios near a null denominator are unstable; bias and quantiles are more informative.

S13c. Alternative SIMEX error laws and extrapolations

Table S48. S13c. Alternative SIMEX error laws and extrapolations

Partition	Error model	Extrapolation	Marker-OR [95%-CI]	Retained log-OR % [95%-CI]	Valid
training	raw	linear	2.478 [2.324; 2.657]	99.9 [99.0; 100.9]	200/200
training	raw	quadratic	2.471 [2.283; 2.691]	99.6 [96.6; 102.9]	200/200
training	clipped	linear	2.477 [2.323; 2.657]	99.8 [99.0; 100.9]	200/200
training	clipped	quadratic	2.480 [2.294; 2.707]	100.0 [97.0; 103.2]	200/200
training	logit	linear	2.530 [2.375; 2.714]	100.3 [99.5; 101.2]	200/200
training	logit	quadratic	2.545 [2.360; 2.783]	100.9 [98.3; 103.7]	200/200
training	joint	linear	2.806 [2.617; 3.031]	113.6 [113.0; 114.3]	200/200
training	joint	quadratic	3.074 [2.814; 3.374]	123.6 [120.8; 126.5]	200/200
internal validation	raw	linear	2.398 [2.126; 2.707]	100.3 [98.5; 101.9]	200/200
internal validation	raw	quadratic	2.412 [2.121; 2.867]	101.0 [95.1; 106.0]	200/200
internal validation	clipped	linear	2.396 [2.126; 2.707]	100.2 [98.3; 101.9]	200/200
internal validation	clipped	quadratic	2.432 [2.134; 2.892]	101.9 [96.3; 106.9]	200/200
internal validation	logit	linear	2.511 [2.221; 2.828]	101.2 [99.5; 102.5]	200/200
internal validation	logit	quadratic	2.571 [2.252; 2.991]	103.8 [98.4; 108.0]	200/200
internal validation	joint	linear	2.699 [2.369; 3.074]	113.9 [112.8; 114.7]	200/200
internal validation	joint	quadratic	2.974 [2.571; 3.524]	125.0 [120.3; 129.3]	200/200

Table S49. S13c. Alternative SIMEX error laws and extrapolations

Partition	Mode	Zero-noise reference OR	Error correlation	Outside angle range at lambda=2
training	raw	2.480	0.268	0.1578
training	clipped	2.480	0.268	0.0000
training	logit	2.524	0.260	not applicable
training	joint	2.480	0.268	0.1578
internal validation	raw	2.392	0.268	0.1591
internal validation	clipped	2.392	0.268	0.0000
internal validation	logit	2.484	0.260	not applicable
internal validation	joint	2.392	0.268	0.1591

Raw errors are unbounded normal errors; clipped measurements are restricted to 0-180 degrees. Logit errors use values restricted to 0.5-179.5 degrees before transformation and directly estimated transformed repeat variance. Joint SIMEX renews angle-marker covariance in each bootstrap. Logit retention uses its own transformed-comparator reference. Point calculations use 20 anti-

thetic draws per variance multiplier and bootstrap calculations 10; extrapolation and Monte Carlo variability remain limitations.

S13d. Stronger orientation comparators

Table S50. S13d. Stronger orientation comparators

Partition	Variant	Persons/cases	Marker-OR [95%-CI]	Apparent Δ AUC [95%-CI]	Valid
training	angles	25453/2690	2.439 [2.290; 2.596]	0.0241 [0.0208; 0.0283]	200/200
internal validation	angles	8518/853	2.164 [1.941; 2.436]	0.0178 [0.0130; 0.0233]	200/200
training	axes	25453/2690	2.352 [2.181; 2.509]	0.0193 [0.0158; 0.0223]	200/200
internal validation	axes	8518/853	2.264 [1.996; 2.583]	0.0174 [0.0121; 0.0227]	200/200
training	spline_angles	25453/2690	2.459 [2.298; 2.662]	0.0239 [0.0203; 0.0279]	200/200
internal validation	spline_angles	8518/853	2.192 [1.934; 2.542]	0.0177 [0.0124; 0.0241]	200/200

Angles: basic model plus peak and area angles. Axes: basic model plus sine/cosine of both area-vector azimuths and elevations and T-area-vector magnitude. Spline: training-fixed 5/35/65/95% quantiles for the integral angle, plus peak/area angles. Only exact training-linear dependencies were removed and verified over development records; no information-based variable selection was performed. These comparators do not include TCRT, ventricular-gradient or planarity models; those blocks, added to the basic model on identical development persons, are in S24.

S13e. Both markers against both endpoints

Table S51. S13e. Both markers against both endpoints

Partition	Variant	Persons/cases	Marker-OR [95%-CI]	Apparent Δ AUC [95%-CI]	Valid
training	re-reduced_lvef_strict/ qrs_t_normalized_discrete_frechet	25453/2690	2.480 [2.348; 2.649]	0.0334 [0.0297; 0.0375]	200/200
internal validation	re-reduced_lvef_strict/ qrs_t_normalized_discrete_frechet	8518/853	2.392 [2.121; 2.631]	0.0315 [0.0241; 0.0392]	200/200
training	re-reduced_lvef_strict/ qrs_t_frechet_beat_median	25654/2713	2.456 [2.318; 2.601]	0.0338 [0.0288; 0.0375]	200/200
internal validation	re-reduced_lvef_strict/ qrs_t_frechet_beat_median	8605/867	2.331 [2.109; 2.553]	0.0320 [0.0242; 0.0396]	200/200
training	cardiomyopathy_icd/qrs_t_normalized_discrete_frechet	53894/1452	2.023 [1.879; 2.156]	0.0216 [0.0171; 0.0273]	200/200
internal validation	cardiomyopathy_icd/qrs_t_normalized_discrete_frechet	18342/about 430	2.216 [1.959; 2.540]	0.0331 [0.0228; 0.0449]	200/200
training	cardiomyopathy_icd/qrs_t_frechet_beat_median	54298/1465	1.990 [1.874; 2.120]	0.0222 [0.0172; 0.0271]	200/200
internal validation	cardiomyopathy_icd/qrs_t_frechet_beat_median	18497/about 440	2.177 [1.929; 2.469]	0.0338 [0.0228; 0.0445]	200/200

Table S52. S13e. Both markers against both endpoints

Endpoint	Marker	Fixed development SD
cardiomyopathy_icd	qrs_t_frechet_beat_median	0.65940801
cardiomyopathy_icd	qrs_t_normalized_discrete_frechet	0.72056198
reduced_lvef_strict	qrs_t_frechet_beat_median	0.69798512
reduced_lvef_strict	qrs_t_normalized_discrete_frechet	0.76503231

Both marker forms use the same value-blind endpoint index policy but different complete sets and endpoint-specific SDs. Endpoints may share persons. There is no formal marker-superiority comparison on a common set, and these eight cells are not independent replications.

S13f. Historical cross-fitted development evidence

Table S53. S13f. Historical cross-fitted development evidence

Endpoint	Estimate	Target persons A/B	Cases A/B	Cross-fitted development Δ AUC [95%-CI]	Partition A/B Δ AUC	Source
reduced LVEF	train- ing→validation / valida- tion→training	8518/see text	853/2690	0.0329 [0.0292; 0.0375]	0.0326/0.0330	Historical cross- fitted develop- ment analysis
cardiomyopathy codes	train- ing→validation / valida- tion→training	18497/54298	about 440/1465	0.0251 [0.0196; 0.0308]	0.0327/0.0225	Historical cross- fitted develop- ment analysis

Table S54. S13f. Historical cross-fitted development evidence

fold	or	or_ci_low	or_ci_high	n_persons	cases
training	2.48039300	2.33417926	2.62450181	25453	2690
internal validation	2.39198312	2.14320014	2.71699356	8518	853

Table S55. S13f. Historical cross-fitted development evidence

Partition	Cardiomyopathy OR [95%-CI]	Source
training	1.990 [1.874; 2.120]	Recalculated cardiomyopathy develop- ment fit
internal validation	2.177 [1.929; 2.469]	Recalculated cardiomyopathy develop- ment fit

Historical AUC estimates are pooled cross-fits, with 1,000 person replicates, rather than apparent AUCs. Their LVEF training denominator differed by fewer than 10 persons from that of the present development fit (25,453); this is retained, not silently harmonized. Historical LVEF ORs have their own 500-bootstrap source; recalculated cardiomyopathy ORs are from the cross-marker development table.

S13g. Seven-day medication-order sensitivity

Table S56. S13g. Seven-day medication-order sensitivity

Partition	Window/class	Recording state	N
training	be- fore7d_antiarrhythmic_class_ i_iii	unknown	12531
training	be- fore7d_antiarrhythmic_class_ i_iii	observed_no_record	12000
training	be- fore7d_antiarrhythmic_class_ i_iii	exposed	922
training	before7d_digoxin	observed_no_record	12725
training	before7d_digoxin	unknown	12559
training	before7d_digoxin	exposed	169
training	be- fore7d_qt_prolonging_drug	unknown	12488
training	be- fore7d_qt_prolonging_drug	observed_no_record	11224
training	be- fore7d_qt_prolonging_drug	exposed	1741
internal validation	be- fore7d_antiarrhythmic_class_ i_iii	unknown	4229
internal validation	be- fore7d_antiarrhythmic_class_ i_iii	observed_no_record	3973
internal validation	be- fore7d_antiarrhythmic_class_ i_iii	exposed	316
internal validation	before7d_digoxin	unknown	4240
internal validation	before7d_digoxin	observed_no_record	4223
internal validation	before7d_digoxin	exposed	55
internal validation	be- fore7d_qt_prolonging_drug	unknown	4206
internal validation	be- fore7d_qt_prolonging_drug	observed_no_record	3735
internal validation	be- fore7d_qt_prolonging_drug	exposed	577

Table S57. S13g. Seven-day medication-order sensitivity

Partition	Variant	Persons/cases	Marker-OR [95%- CI]	Apparent Δ AUC [95%-CI]	Valid
training	before7d	25453/2690	2.466 [2.314; 2.635]	0.0331 [0.0290; 0.0377]	200/200
internal validation	before7d	8518/853	2.378 [2.144; 2.638]	0.0312 [0.0234; 0.0388]	200/200

Only the seven-day pre-ECG order-start sensitivity is used as manuscript evidence. Recorded timestamps are assumed; hour-level documentation is absent. A seven-day window reduces sensitivity to hour-scale offsets, but does not prove ingestion or complete temporal coverage. Class I/III antiarrhythmic, digoxin and QT-drug indicators overlap and derive from fixed name patterns,

not a newly asserted exhaustive risk list. Unknown coverage is separate from observed absence of a record. Both models had 200/200 valid draws. Confounding by indication remains possible.

S13h. Partial extended adjustment

Table S58. S13h. Partial extended adjustment

Partition	Covariate	Observed	Missing
training	bmi_before_ecg	10265	15188
training	potassium_clean	18512	6941
training	prior_code_group_count	8031	17422
internal validation	bmi_before_ecg	3407	5111
internal validation	potassium_clean	6191	2327
internal validation	prior_code_group_count	2757	5761

Table S59. S13h. Partial extended adjustment

Partition	Variant	Persons/cases	Marker-OR [95%-CI]	Apparent Δ AUC [95%-CI]	Valid
training	extended_partial	25453/2690	2.453 [2.305; 2.580]	0.0312 [0.0271; 0.0350]	200/200
internal validation	extended_partial	8518/853	not estimable: Quasi-separation / basic-model quasi-separation	n/a	0/200
training	extended_prior_codes	25453/2690	2.430 [2.257; 2.582]	0.0302 [0.0256; 0.0344]	200/200
internal validation	extended_prior_codes	8518/853	not estimable: Quasi-separation / basic-model quasi-separation	n/a	0/200

The partial model uses acquisition era, ED/inpatient/both/outside/unknown setting, pre-ECG BMI and potassium within six recorded-time hours, with training-fixed medians and missingness indicators. The second model adds an unweighted count of distinct diagnosis-code groups from encounters completed before ECG. This is not a validated Charlson index. No release-bound estimated-glomerular-filtration-rate definition was available. Internal-validation quasi-separation prevented estimates; no post-result merging of categories was performed. Hour-scale potassium and setting alignment is unconfirmed.

S13i. LVEF distributions, continuous and ordinal references

Table S60. S13i. LVEF distributions, continuous and ordinal references

Partition	Population	N	Exactly 39/40/41%	At exactly 40% (% of set)	<40 / $\leq$ 40
training	eligible_reference	28699	13/1015/26	3.54	3178/4193
training	eligible_B3	25453	<20/858/<20	3.37	2690/3548
internal validation	eligible_reference	9694	<10/323/10	3.33	1044/1367
internal validation	eligible_B3	8518	<10/280/10	3.29	853/1133

Table S61. S13i. LVEF distributions, continuous and ordinal references

Partition	Marker	N	Continuous LVEF: coefficient in percentage points [95%-CI]
training	qrs_t_normalized_discrete_frechet	25453	-3.692 [-3.945; -3.438]
internal validation	qrs_t_normalized_discrete_frechet	8518	-3.509 [-3.937; -3.082]
training	qrs_t_frechet_beat_median	25654	-3.694 [-3.946; -3.443]
internal validation	qrs_t_frechet_beat_median	8605	-3.452 [-3.875; -3.029]

Table S62. S13i. LVEF distributions, continuous and ordinal references

Partition	Marker	Categories	Persons/classes	OR for higher LVEF [95%-CI]	Bootstrap
training	qrs_t_normalized_discrete_frechet	ordinal3	25453/[2690, 1887, 20876]	0.423 [0.403; 0.447]	200/200
training	qrs_t_normalized_discrete_frechet	ordinal4	25453/[1988, 702, 1887, 20876]	0.425 [0.406; 0.449]	200/200
internal validation	qrs_t_normalized_discrete_frechet	ordinal3	8518/[853, 647, 7018]	0.441 [0.404; 0.478]	200/200
internal validation	qrs_t_normalized_discrete_frechet	ordinal4	8518/[597, 256, 647, 7018]	0.442 [0.404; 0.478]	200/200
training	qrs_t_frechet_beat_median	ordinal3	25654/[2713, 1904, 21037]	0.423 [0.407; 0.446]	200/200
training	qrs_t_frechet_beat_median	ordinal4	25654/[first two classes not shown, 1904, 21037]	0.425 [0.405; 0.451]	200/200
internal validation	qrs_t_frechet_beat_median	ordinal3	8605/[867, 657, 7081]	0.450 [0.414; 0.483]	200/200
internal validation	qrs_t_frechet_beat_median	ordinal4	8605/[first two classes not shown, 657, 7081]	0.450 [0.417; 0.485]	200/200

For the beat-median marker the split of the two lowest classes is not shown, because its differences from the classes of the Fréchet marker would allow small counts to be derived.

Table S63. S13i. LVEF distributions, continuous and ordinal references

Partition	Reference method	N
training	generic	24711
training	biplane	541
training	3d	201
internal validation	generic	8260
internal validation	biplane	184
internal validation	3d	74

Continuous LVEF models adjust for all basic-model covariates including angle. Ordinal categories are <40/40-<50/≥50%, or <35/35-<40/40-<50/≥50%; OR below one indicates movement toward lower LVEF. Proportional odds is a modeling assumption, not biological truth. Ordinal analysis removes reliance on one binary threshold but is not completely threshold-free. Heaping at 40% does not

itself prove extraction error. Original echo reports were unavailable; discharge or radiology text was not substituted. Generic/biplane/3D method counts describe development only.

S13j. Post hoc reconstruction of the original null generator

Table S64 compares the original synthetic null with a correlated-error sensitivity. All 200 original uncorrected marker coefficients were reproduced before deriving these diagnostics. The correlated-error scenario retains the latent structure and outcome mechanism, adding correlation 0.268 to the same marginal error variances. Intervals are 95% simulation quantiles, not biological confidence intervals. No individual developmental or assessment data were read for this audit.

Table S64. Null-generator diagnostics and empirical developmental comparison

Quantity	Original null, mean [quantiles]	Correlated-error null, mean [quantiles]	Observed training / validation
Marker OR	1.2496 [1.0958; 1.3952]	1.2033 [1.0491; 1.3399]	2.480 / 2.392
Angle OR with marker	1.6627 [1.4705; 1.8778]	1.6683 [1.4620; 1.9012]	1.009 / 0.980
Angle OR without marker	1.8289 [1.6475; 2.0225]	1.8289 [1.6475; 2.0225]	1.793 / 1.695
Conditional angle reliability	0.4987 [0.4755; 0.5203]	0.4523 [0.4268; 0.4748]	0.071 / 0.075
Marker-angle Spearman correlation	0.4296 [0.4046; 0.4542]	0.4989 [0.4744; 0.5215]	0.753 / 0.750
Measured angle AUC	0.6625 [0.6360; 0.6890]	0.6625 [0.6360; 0.6890]	0.7390 / 0.7324
Measured marker AUC	0.6203 [0.5911; 0.6495]	0.6203 [0.5926; 0.6487]	0.8081 / 0.8052
Latent angle oracle AUC	0.7080 [0.6847; 0.7340]	0.7080 [0.6847; 0.7340]	not observed

The original null does not reproduce the observed joint angle/marker structure. Its independent errors differ from the observed error correlation, and its conditional reliability and marker-angle correlation differ from the empirical values. The angle-effect function is linear logistic; no development-fitted nonlinear truth was supplied here. The result near OR 1.25 therefore describes one restricted null, rather than a general bound on measurement-error artifacts. A later simulation at the angle-only tipping point (S13k, Table S89) produced an apparent marker OR of 2.49 at a true marker OR of 1.0, so 1.25 must not be read as an upper bound of artifact. Oracle AUC is available only in synthetic data; observed marker AUC above measured angle AUC does not establish superiority over the unobserved latent angle.

S13k. Post hoc bivariate measurement-error tipping analysis in development data

This section extends the regression-calibration analyses of S9 and S10 from fixed error assumptions to a grid. The reliability ranges of this section are an assumed scenario set, not a measured bound on error: repeatability, agreement after resampling of the same recording and technical accuracy are different quantities, and the angle reliabilities of the group-specific anchor (0.582 and 0.585, S19) lie below the lower end of the range (0.59). Estimated anchors with population intervals, an extended grid and differential and persistent error are in S19. It asks at which angle reliability the corrected marker OR first falls to 1.25 or 1.0 when classical, nondifferential errors in both the integral angle and the Fréchet marker are corrected, with an error correlation between them. The analysis was specified after the primary results and after the aggregates of S9, S10 and S13 were known, and is post hoc. Its protocol, which fixed the grid, the tipping rule, the

assumed reliability ranges, the interval rules and the simulation scenarios, was dated and check-summed locally before any computation on individual data; this timestamp is not an external preregistration. The summary statistics of the results within the assumed ranges were not fixed and were defined after the main run (deviation 3 below). Only training and internal validation data were used (Table S84). No assessment or test file, identity or aggregate was opened. Before any development file was read, its footer was read once, for the split column only, to confirm that it contained no test rows. Internal validation is not an independent replication. Unlike the 200-replicate branches of S13, this analysis used 1,000 person-bootstrap replicates per fold.

Method. The fixed basic logistic model (age basis, sex, heart rate, QRS duration, Fridericia QTc, integral angle and normalized Fréchet distance; development scaling) was fitted in each fold. Let S be the residual covariance of angle and marker after the other covariates, E the assumed error covariance and $T = S - E$ the latent residual covariance. The corrected coefficients of angle and marker are $T^{-1} S$ times the uncorrected coefficients, and the corrected marker OR is exp of the marker coefficient per development SD of the measured marker. A setting was admissible only if T was positive definite (smallest eigenvalue above 10^{-10}); no matrix was repaired. The closed form agreed with the existing joint-calibration code to within 3×10^{-15} in the log-OR at every anchor and reproduced, before any grid was computed, the uncorrected ORs (2.480 and 2.392), the joint calibration ORs from all repeat pairs (8.737 and 9.259) and angle-only calibration at an angle ICC of 0.617 (2.369 and 2.656) of S9 and S10.

Reliabilities in the grid are reliabilities in the outcome set of the respective fold: the error variance of a standardized column is $(1 - R)$ times its observed variance, and the error covariance is the error correlation times the square root of both error variances. The grid crossed marker reliability 0.50 to 1.00 in steps of 0.05 (11 values) with error correlations -0.4 to 0.8 in steps of 0.1 plus the repeat-derived values 0.268 and 0.329 (S10, Table S33; 15 values), giving 165 cells per fold and target. Angle reliability was searched from 1.000 downward to 0.050 in steps of 0.001. The tipping point is the angle reliability at which the corrected marker OR first falls below the target (1.25 or 1.0) when angle reliability decreases from 1; the point estimate was refined by root finding between search steps and bootstrap replicates used linear interpolation of the log-OR. If the admissibility bound was reached first, the cell is reported as bound before crossing. The implied latent angle-marker correlation was recorded at each tipping point.

The scenario ranges, called “observed ranges” in the protocol, were fixed as angle reliability 0.59 to 0.70, marker reliability 0.80 to 0.98 and error correlation 0.26 to 0.33. The angle range runs from the transported all-pair estimates (0.599 and 0.601, with lower interval limits of 0.583 and 0.586) to the sinus-rhythm estimate (0.693); the marker range spans the all-pair (0.827), sinus-rhythm (0.892) and technical-agreement (0.977) values; the error correlation range covers the repeat-based values 0.268 and 0.329. These are repeat-based reliabilities, not identified technical-error reliabilities in the outcome cases (S5). The technical-agreement angle reliability (0.746) lies above the assumed angle range and is a separate anchor. The anchor settings of Table S86 came from S9 and S10 (angle ICC 0.617 and sinus 0.693; marker ICC 0.837 and sinus 0.892; error correla-

tions 0.268 and 0.329; stratum values of Table S30), from the technical agreement of the 500 Hz and 250 Hz versions of the same recording in the companion measurement audit (angle 0.746, marker 0.977), and from the repeat pairs transported to the outcome sets.

Uncertainty used 1,000 person-bootstrap replicates per fold, drawn over the union of outcome-set persons and repeat-pair persons so that error covariances were re-estimated in the same draw, each with a complete refit. All 1,000 replicates were valid in both folds. Percentile intervals (2.5th and 97.5th) required at least 950 valid replicates. A tipping-point interval required in addition at least 950 finite crossings and is otherwise not estimable; the point estimate is then shown without an interval. Joint-calibration intervals therefore differ from those of Table S33, which used 200 replicates. Simulation quantiles are not confidence intervals.

Results within the assumed scenario ranges. On a fine grid over angle reliability 0.590 to 0.700 (steps of 0.001), marker reliability 0.800 to 0.980 (steps of 0.005) and error correlation 0.260 to 0.330 (steps of 0.001), the corrected marker OR had a minimum of 2.04 in training and 2.26 in internal validation, both at marker reliability 0.98, error correlation 0.33 and angle reliability 0.59 (Table S85). All settings were admissible. For the bootstrap, the per-replicate minimum was taken over the report points (angle reliability 0.60, 0.65 and 0.70; marker reliability 0.80, 0.85, 0.90 and 0.95; error correlation 0.268, 0.30 and 0.329); its 2.5th percentile was 1.80 in training and 1.53 in internal validation, and no replicate was inadmissible at any of these points. These percentiles equal the lowest lower limits of the pointwise 95% bootstrap intervals over the report points (training: angle reliability 0.60, marker reliability 0.95, error correlation 0.329; internal validation: 0.60, 0.95, 0.268). The report points do not include the location of the fine-grid minimum, so 1.80 and 1.53 are not interval limits for 2.04 and 2.26, and they do not describe the fine grid or the extended grid of S19. Both summaries, the fine-grid minimum and the per-replicate minimum, were defined after the main run (deviation 3 below). The maxima of 44.6 and 55.5 occurred at marker reliability 0.80, error correlation 0.26 and angle reliability 0.59, the corner nearest the admissibility bound, and are not effect estimates.

Anchor settings. Table S86 gives the corrected OR and tipping points at the anchors. Under the repeat-based joint error covariance (all pairs) the corrected OR increased to 8.74 [4.83; 24.15] in training and 9.26 [3.82; 49.80] in internal validation, reproducing the point estimates of S10 (Table S33; the intervals differ because S10 used 200 replicates), and no tipping point existed because lowering the angle reliability reached the admissibility bound (0.549) first, without the OR reaching 1.25. A tipping point existed at the technical-agreement setting (0.553 for OR 1.25 and 0.550 for OR 1.0 in training; 0.541 and 0.541 in internal validation) and, for angle error only, in training (0.570 and 0.569). All lay below the lower limit of the assumed angle range (0.59). The stress settings from the atrial-fibrillation and left-bundle strata were inadmissible in the whole outcome set: an angle error of that size would exceed the latent residual variance that the observed covariance allows.

Tipping curve. Tables S87 and S88 give the tipping points for the target ORs 1.0 and 1.25. A tipping point inside the grid occurred in two regions. First, at marker reliability of 0.90 or higher and a latent covariance close to singular, the corrected OR fell to 1.25 or 1.0 at angle reliabilities of 0.52 to 0.57. At marker reliability 1.00 (angle error only) this occurred at 0.570 and 0.569 in training and not in internal validation, where the bound (0.567) came first. At marker reliability 0.95 with error correlations of 0.268 to 0.329 it occurred at 0.534 to 0.543 in training. In internal validation it occurred at marker reliability 0.95 for an error correlation of 0.329 (0.525 and 0.526) and of 0.30 (0.528 and 0.529; this column is not shown in Tables S87 and S88), but not at 0.268. At marker reliability 0.90 and error correlation 0.329 it occurred at 0.519 and 0.520 in training only. These grid tipping points lay 0.001 to 0.018 above the admissibility bound (both targets and folds, including the error correlation of 0.30 that the tables do not show), and the implied partial latent correlation of angle and marker was 0.97 to 0.997 (marginal 0.97 to 0.99), against 0.867 [0.857; 0.876] estimated from cross-repeat correlations (Table S84).

Second, for marker reliability of 0.80 to 0.95 and error correlations of 0.4 or more (repeat-based 0.27 to 0.33), tipping points occurred wherever the cell crossed, at angle reliabilities of 0.37 to 0.53 (0.27 to 0.44 at marker reliabilities of 0.60 to 0.75, which lie outside the assumed range and are not shown); for example, at marker reliability 0.85 and error correlation 0.6 they were 0.450 [0.431; 0.467] in training and 0.442 [0.413; 0.477] in internal validation. For marker reliability of 0.80 to 0.95 the implied partial latent correlation fell to 0.88 to 0.94 at error correlation 0.6 and to 0.73 to 0.90 at 0.8. For error correlations of 0.2 or less and marker reliability below 1, no tipping point existed in any cell: correction raised the OR until the admissibility bound was reached. For marker reliability of 0.55 or less (training) or 0.60 or less (internal validation), the model was already inadmissible at an angle reliability of 1.

The highest tipping point at marker reliability and error correlation within the assumed ranges, was the technical-agreement value of 0.553 in training, which is 0.037 below the lower limit of the assumed angle range (0.59); in internal validation it was 0.541 (0.049 below). In the terms of the protocol, the corrected OR tipped only below the assumed range, there only near the singularity or at error correlations above the assumed values. This describes the assumed set, not the true error: it is no evidence that the true error lies inside it (see S19 for differential and persistent error).

Profile along angle reliability. At the all-pair anchor the corrected OR in training fell from 4.94 at angle reliability 1 to 4.45 at 0.90, then rose steeply (5.00 at 0.70, 8.54 at 0.60, 26.6 at 0.57, 140 at 0.56) towards the bound; internal validation behaved alike. With angle error only, the OR stayed at 2.42 in training and 2.53 in internal validation down to angle reliability 0.65. At 0.57 it was 1.30 in training and 10.9 in internal validation. The direction of the departure directly at the singularity depends on the sign of the near-zero uncorrected angle coefficient (OR 1.009 in training, 0.980 in internal validation) and reflects sampling variation.

Known-truth simulation at the tipping point. Two of the four simulation scenarios of the protocol, at the all-pair anchor, could not be run because that anchor has no tipping point. The remaining two used the angle-only tipping points in the training outcome set (25,453 persons per dataset, 200 datasets per scenario, the real values of the other covariates). The latent angle and marker were drawn with covariance T , the outcome was generated from the calibrated coefficients with a marker OR equal to the target, and the measured values were the latent ones plus errors with covariance E (Table S89). The true angle odds ratio in these scenarios was 2.74 (target 1.25) and 3.80 (target 1.0), on the same standardized scale as the marker odds ratio, against an uncorrected angle odds ratio of about 1.01; the scenarios thus assume a strong true angle effect that error attenuation masks. The simulation of S13 and Figure 5 uses a different true angle effect (log-effect 0.8). A dataset with a true marker OR of 1.0 at angle reliability 0.569 produced an uncorrected marker OR of 2.49 and an uncorrected angle OR of 1.005, close to the observed 2.480 and 1.009; the share of simulated uncorrected marker ORs above 2.480 was 0.50 (target 1.25) and 0.55 (target 1.0). The simulated uncorrected estimates thus match the observed ones under the assumed linear logistic model. This shows that a true marker OR of 1.0 at these two settings is compatible with the observed uncorrected coefficients; it does not test the corrected estimator, which was unstable at the singularity, and the other tipping points were not simulated. The outcome data alone cannot exclude this scenario; only the repeat-based reliabilities and error correlation do, and these assume classical, nondifferential errors that change between recordings. Regression calibration itself was unusable at the singularity: 32 and 55 of 200 runs were inadmissible, and the remaining estimates scattered over many orders of magnitude.

Deviations from the protocol and numerical notes. (1) Two of the four prespecified simulation scenarios were not run, as stated; no replacement scenario was chosen after the result. (2) The protocol described linear interpolation between search steps; the point estimates of tipping points were also refined by root finding, and bootstrap replicates used linear interpolation as specified. (3) The protocol fixed the ranges (called observed there), the grid and the pointwise intervals at the report points, but not a summary statistic of the OR within the ranges; the fine-grid minimum and the per-replicate minimum over the report points (Table S85), which carry the values 2.04, 2.26, 1.80 and 1.53, were defined and computed from the stored aggregates after the main run. The statement that the corrected OR did not tip within the assumed ranges rests on the tipping points of the prespecified grid and the interpretation rule of the protocol, which were fixed in advance. (4) Two numerical warnings were logged (exponent overflow near the admissibility bound and an undefined error correlation when both error variances were zero). Persistent person- or device-level errors, errors that differ by ejection fraction and nonlinear angle effects were not modeled, and repeat differences include physiological change, so Tables S84 to S89 do not support a robustness claim beyond the classical error model.

Table S84. S13k. Bivariate tipping analysis: data and repeat-based inputs

Quantity	Training	Internal validation
Persons / LVEF <40% cases, fixed basic-model set	25,453 / 2,690	8,518 / 853
Persons in the bootstrap universe (outcome set plus repeat-pair persons)	30,353	16,119
Valid / attempted bootstrap replicates	1,000 / 1,000	1,000 / 1,000
Uncorrected marker OR [95% bootstrap interval]	2.480 [2.330; 2.639]	2.392 [2.157; 2.680]
Repeat pairs / persons (pooled over both folds)	13,029 / 8,966	13,029 / 8,966
Simultaneous repeat pairs / persons	289 / 277	289 / 277
Angle reliability transported to the outcome set, all pairs [95% bootstrap interval]	0.599 [0.583; 0.614]	0.601 [0.586; 0.616]
Marker reliability transported to the outcome set, all pairs [95% bootstrap interval]	0.827 [0.816; 0.837]	0.827 [0.817; 0.839]
Error correlation, all pairs [95% bootstrap interval]	0.268 [0.243; 0.291]	0.268 [0.243; 0.291]
Cross-repeat latent angle-marker correlation, all pairs [95% bootstrap interval]	0.867 [0.857; 0.876]	0.867 [0.856; 0.877]
Cross-repeat latent angle-marker correlation, simultaneous pairs [95% bootstrap interval]	0.848 [0.778; 0.913]	0.848 [0.781; 0.912]

Reliabilities are in the outcome sets of the respective folds. Repeat pairs include physiological change and are not identified technical errors in the outcome cases. The cross-repeat correlation is free of error correlation within a recording but assumes stable latent values and no error covariance across recordings. Interval widths follow the percentile rule above.

Table S85. S13k. Corrected marker OR within the assumed reliability ranges

Quantity	Training	Internal validation
Minimum corrected OR on the fine grid	2.04	2.26
Location of the minimum (marker reliability / error correlation / angle reliability)	0.98 / 0.33 / 0.59	0.98 / 0.33 / 0.59
Maximum corrected OR on the fine grid	44.6	55.5
Location of the maximum (marker reliability / error correlation / angle reliability)	0.80 / 0.26 / 0.59	0.80 / 0.26 / 0.59
Inadmissible share of the fine grid	0%	0%
Per-replicate minimum over the report points: 2.5th / 50th / 97.5th percentile	1.80 / 2.32 / 2.89	1.53 / 2.46 / 3.16
Replicates with all report points admissible	1,000 / 1,000	1,000 / 1,000

The fine grid covered angle reliability 0.590 to 0.700, marker reliability 0.800 to 0.980 and error correlation 0.260 to 0.330. Report points for the bootstrap were angle reliability 0.60, 0.65 and 0.70, marker reliability 0.80 to 0.95 and error correlation 0.268, 0.30 and 0.329. The percentiles are over bootstrap replicates of the minimum, not confidence limits of a single setting. The report points do not include the location of the fine-grid minimum, and the 2.5th percentiles equal the lowest lower limits of the pointwise 95% bootstrap intervals over the report points. Both summaries were defined after the main run.

Table S86. S13k. Anchor settings, corrected ORs and tipping points

Partition	Setting	Angle reliability / marker reliability / error correlation	Corrected marker OR [95% bootstrap interval]	Admissible / attempted replicates	Tipping point at OR 1.25 / 1.0	Admissibility bound
Training	All repeat pairs, transported to the outcome set	0.599 / 0.827 / 0.268	8.74 [4.83; 24.15]	1,000 / 1,000	none; bound first	0.549
Training	Simultaneous repeat pairs, transported	0.602 / 0.863 / 0.329	3.59 [2.28; 13.74]	957 / 1,000	none; bound first	0.515
Training	Intraclass correlations, all pairs	0.617 / 0.837 / 0.268	6.02 [4.27; 9.20]	1,000 / 1,000	none; bound first	0.546
Training	Intraclass correlations, sinus rhythm	0.693 / 0.892 / 0.268	3.32 [2.87; 3.86]	1,000 / 1,000	none; bound first	0.535
Training	Technical agreement (500 vs 250 Hz)	0.746 / 0.977 / 0.268	2.50 [2.26; 2.77]	1,000 / 1,000	0.553 / 0.550	0.540
Training	Technical agreement, error correlation 0	0.746 / 0.977 / 0	2.70 [2.39; 3.06]	1,000 / 1,000	none; bound first	0.578
Training	Angle error only	0.617 / 1 / 0	2.37 [1.62; 3.52]	1,000 / 1,000	0.570 / 0.569	0.566
Training	Stress setting from the atrial-fibrillation stratum	0.461 / 0.826 / 0.268	inadmissible	0 / 1,000	not applicable	0.549
Training	Stress setting from the left-bundle stratum	0.309 / 0.798 / 0.268	inadmissible	0 / 1,000	not applicable	0.558
Internal validation	All repeat pairs, transported to the outcome set	0.601 / 0.827 / 0.268	9.26 [3.82; 49.80]	1,000 / 1,000	none; bound first	0.549
Internal validation	Simultaneous repeat pairs, transported	0.604 / 0.863 / 0.329	3.72 [1.78; 31.10]	958 / 1,000	none; bound first	0.515
Internal validation	Intraclass correlations, all pairs	0.617 / 0.837 / 0.268	6.31 [3.41; 14.45]	1,000 / 1,000	none; bound first	0.546
Internal validation	Intraclass correlations, sinus rhythm	0.693 / 0.892 / 0.268	3.29 [2.50; 4.36]	1,000 / 1,000	none; bound first	0.535
Internal validation	Technical agreement (500 vs 250 Hz)	0.746 / 0.977 / 0.268	2.47 [2.05; 2.96]	1,000 / 1,000	0.541 / 0.541	0.540
Internal validation	Technical agreement, error correlation 0	0.746 / 0.977 / 0	2.67 [2.14; 3.34]	1,000 / 1,000	none; bound first	0.578
Internal validation	Angle error only	0.617 / 1 / 0	2.66 [1.32; 5.73]	1,000 / 1,000	none; bound first	0.567
Internal validation	Stress setting from the atrial-fibrillation stratum	0.461 / 0.826 / 0.268	inadmissible	0 / 1,000	not applicable	0.549

Partition	Setting	Angle reliability / marker reliability / error correlation	Corrected marker OR [95% bootstrap interval]	Admissible / attempted replicates	Tipping point at OR 1.25 / 1.0	Admissibility bound
Internal validation	Stress setting from the left-bundle stratum	0.309 / 0.798 / 0.268	inadmissible	0 / 1,000	not applicable	0.559

Tipping points are shown without intervals; those of the anchors were not estimable because fewer than 950 replicates crossed. None; bound first: the admissibility bound was reached before the OR fell to the target. Not applicable: the setting itself lies beyond the bound. Admissible replicates are those with a positive-definite latent covariance at the anchor. The stress settings come from strata and are applied to the whole outcome set only as a stress test. The technical-agreement setting is taken from the companion measurement audit.

Table S87. S13k. Tipping curve: angle reliability at which the corrected marker OR falls to 1.0

Partition	Marker reliability	Error correlation 0	0.268	0.329	0.4	0.5	0.6	0.8
Training	1.00	0.569	0.569	0.569	0.569	0.569	0.569	0.569
Training	0.95	bound 0.592	0.541	0.534	0.526 [0.507; 0.548]	0.515 [0.494; 0.536]	0.503 [0.483; 0.524]	0.480 [0.460; 0.499]
Training	0.90	bound 0.621	bound 0.534	0.519	0.507 [0.490; 0.528]	0.491 [0.470; 0.511]	0.474 [0.454; 0.493]	0.438 [0.420; 0.455]
Training	0.85	bound 0.656	bound 0.543	bound 0.516	0.492	0.471 [0.452; 0.490]	0.450 [0.431; 0.467]	0.403 [0.387; 0.419]
Training	0.80	bound 0.698	bound 0.558	bound 0.524	bound 0.484	0.455 [0.436; 0.473]	0.429 [0.411; 0.445]	0.373 [0.358; 0.387]
Internal validation	1.00	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567
Internal validation	0.95	bound 0.592	bound 0.534	0.525	0.517	0.506	0.495 [0.465; 0.534]	0.472 [0.439; 0.508]
Internal validation	0.90	bound 0.621	bound 0.534	bound 0.514	0.499	0.483	0.466 [0.435; 0.502]	0.431 [0.402; 0.464]
Internal validation	0.85	bound 0.656	bound 0.543	bound 0.516	bound 0.485	0.464	0.442 [0.413; 0.477]	0.397 [0.371; 0.427]
Internal validation	0.80	bound 0.698	bound 0.558	bound 0.524	bound 0.485	0.447	0.422 [0.394; 0.454]	0.368 [0.344; 0.395]

Cells show the angle reliability at the first downward crossing (point estimate), with the 95% bootstrap interval where at least 950 of 1,000 replicates crossed. bound x: the admissibility bound x was reached before a crossing. Other grid cells are not shown: marker reliabilities below 0.80, which lie outside the assumed range, and the error correlations between the columns shown. No crossing occurred for error correlations of 0.2 or less with marker reliability below 1.

Table S88. S13k. Tipping curve: angle reliability at which the corrected marker OR falls to 1.25

Partition	Marker reliability	Error correlation 0	0.268	0.329	0.4	0.5	0.6	0.8
Training	1.00	0.570	0.570	0.570	0.570	0.570	0.570	0.570
Training	0.95	bound 0.592	0.543	0.538	0.532	0.524	0.515	0.496
Training	0.90	bound 0.621	bound 0.534	0.520	0.512	0.499	0.486	0.456
Training	0.85	bound 0.656	bound 0.543	bound 0.516	0.494	0.478	0.460	0.420
Training	0.80	bound 0.698	bound 0.558	bound 0.524	bound 0.484	0.459	0.438	0.388
Internal validation	1.00	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567	bound 0.567
Internal validation	0.95	bound 0.592	bound 0.534	0.526	0.521	0.513	0.505	0.488
Internal validation	0.90	bound 0.621	bound 0.534	bound 0.514	0.501	0.489	0.477	0.448
Internal validation	0.85	bound 0.656	bound 0.543	bound 0.516	bound 0.485	0.469	0.452	0.414
Internal validation	0.80	bound 0.698	bound 0.558	bound 0.524	bound 0.485	0.451	0.430	0.383

Point estimates only; notation as in Table S87. For the same cell, the tipping point for OR 1.25 lay 0.001 to 0.018 above that for OR 1.0.

Table S89. S13k. Known-truth simulation at the angle-only tipping point

Scenario (angle reliability / marker reliability)	True marker OR	True angle OR	Uncorrected marker OR	Uncorrected angle OR	Error-free (oracle) marker OR	Regression calibration marker OR	Inadmissible calibration runs
0.5698 / 1	1.25	2.74	2.47 [2.30; 2.65]	1.012 [0.946; 1.095]	1.24 [0.80; 2.01]	0.28 [3.9×10^{-9} ; 5.3×10^3]	32 / 200
0.5688 / 1	1.00	3.80	2.49 [2.31; 2.67]	1.005 [0.942; 1.077]	1.00 [0.54; 1.65]	0.07 [8.2×10^{-10} ; 5.3×10^6]	55 / 200

Geometric means of the odds ratios over the datasets (all 200 for the uncorrected and error-free estimates; the admissible runs for calibration) with 2.5th and 97.5th simulation quantiles in brackets; these are not confidence intervals. The true angle OR is on the standardized scale of the marker OR. The observed uncorrected estimates in training were marker OR 2.480 and angle OR 1.009. Angle reliability is the tipping point for the target marker OR (marker reliability 1, error correlation 0).

S14. Differential T-end error by ejection fraction

Training and internal validation were person-disjoint development samples; no independent assessment was used. The T-duration and flatness differences did not satisfy the pre-specified early-stop criterion. Amplitude is the production spatial T-peak magnitude; flatness is amplitude divided by measured T duration. The signal-to-noise measure is a second-difference noise proxy, not a validated physical SNR. Morphology differences do not themselves establish boundary error.

LUDB calibration used 193 morphologically complete records and 1,577 finite beat errors. Each record had equal regression weight. The outcome was mean production-minus-latest-expert T-end error; simultaneous amplitude/flatness regression used HC3 record-level intervals. R^2 was 0.01654, with record-mean residual SD 17.41 ms. The calibration population lacks EF labels, and LUDB also informed delineator development. Transport to low-EF MIMIC patients is therefore unvalidated.

Table S65. S14. Differential T-end error by ejection fraction

Quantity	Estimate	Uncertainty / denominator
Expected error, LVEF <40%	-15.93 ms	Model-predicted mean
Expected error, LVEF ≥40%	-15.48 ms	Model-predicted mean
Low minus preserved EF error	-0.4583 ms	Bootstrap 95% CI -0.9147 to -0.08113; 500 paired LUDB/development resamples
Corrected training marker OR	2.155	CI not estimable, 17/500 valid draws; 25,388 persons / 2,672 cases
Corrected internal-validation marker OR	2.184	CI not estimable, 100/500 valid draws; 8,495 persons / >840 cases
Training retained log-OR	0.8419	CI not estimable
Internal-validation retained log-OR	0.8903	CI not estimable

Correction shifted all eligible beat T ends by the predicted error and rebuilt representative markers using the fixed release. Other covariates remained fixed in this targeted experiment. The log-OR fraction is corrected/original log-OR on the same finite set, not an OR ratio or an identified artifact fraction. Intervals required 475/500 valid draws; nonfinite correction outputs invalidated draws and were not replaced.

The expected group difference and worst-case group shifts rounded to zero samples at 500 Hz (2 ms). Their unchanged ORs are a resolution-bound calculation, not physiological equivalence. Individual correction retained 84-89% of log-OR by point estimate, which fell into the pre-specified descriptive category labeled ‘does not explain the increment’; we do not carry this label forward, because intervals are absent and the branch is inconclusive. There are no MIMIC expert T ends, no EF-labeled external boundary calibration, and no independent LUDB replication of the ventricular outcome model. Marginal range coverage does not establish joint support.

S15. Exploratory post-unblinding assessment analyses

These analyses were specified after the primary and cardiomyopathy results were known. Their later pre-execution specification date does not turn them into untouched confirmatory tests. The original success rule, main estimates and failed intervals above are retained.

Table S66. S15. Exploratory post-unblinding assessment analyses

Additional analysis	Result or documented unavailability
Table 1, full candidate flow, retained era/setting and endpoint overlap	Participant flow is in Figure 1; complete-case characteristics are in Table 1 and S15a. Reference-index overlap was 8306 persons and complete-case overlap was 7052. Rhythm-, pacing- and QRS-specific missingness and joint heart-rate/QTc patterns were not exported. QTc-free and imputation sensitivities are tabulated in S15; informative missingness remains unresolved.
Rhythm/pacing and left/right bundle-branch strata	Pacing and atrial-fibrillation strata were unavailable because independent semantic adjudication of developmental machine-report statements was incomplete. Existing QRS/block-pattern strata are reported in S15. The RBBB LVEF stratum had only 96/1000 valid draws in the original run (corrected post hoc: 1,000/1,000, bootstrap interval in Table S92); small LBBB and cardiomyopathy RBBB strata were not estimable.
Fixed-development model performance and calibration	Development-fixed model AUCs were 0.8353 [0.8221; 0.8489] for reduced LVEF and 0.8208 [0.8001; 0.8408] for coded cardiomyopathy, with paired marker increments 0.03267 [0.0244; 0.04107] and 0.02762 [0.01747; 0.03761]. Sensitivity, achieved specificity, Brier score and calibration are reported in S15; thresholds were derived from developmental controls.
Assessment measurement-error correction	Assessment angle-only RC gave marker OR 2.087 [0.4186; 9.548] for reduced LVEF and 0.5628 [4.239e-05; 28.99] for cardiomyopathy. Joint RC for reduced LVEF gave 8.887 [3.294; 48.49], with a small latent eigenvalue and substantial instability. All SIMEX variants, paired log-OR changes and failures are tabulated in S15. Joint cardiomyopathy correction was excluded because a beat-median error covariance was unavailable.
Code-subtype and restricted-control analyses	Cardiomyopathy subtype and restricted-control analyses were not performed because complete ICD-subcode and admission-history coverage through the index encounter was not documented. Binary diagnosis flags were not substituted. No restricted-control effect estimate or interval is available.
Matched-bootstrap solver continuation	The historical solver continuation with the original replicate records was not performed. A post hoc correction of the bootstrap construction (eligibility in the sample, 1,000 replicates, consistent stopping rule) reproduced the original replicates and produced corrected intervals; see S18 and Tables S91 to S94.
Marker-containing verification weighting	The marker-containing verification models gave P95-capped OR 3.011 [2.587; 3.529] and P99-capped OR 3.019 [2.596; 3.539] on 4844 / 431 / 4413 persons/cases/controls. Model coefficients and caps were estimated from training data and refitted within the paired bootstrap. Weight diagnostics and population losses are described in S15; unmeasured verification indications remain unresolved.

Additional analysis	Result or documented unavailability
Missingness and covariate sensitivity	Class-specific missingness, QTc-free models and missing-indicator models are reported in S15. The original 500-replicate analyses did not reach the unchanged minimum of 950; corrected post hoc bootstrap intervals with 1,000 replicates are in Table S92 (S18). Multiple imputation had an explicit separate minimum of 190; bootstrap and Rubin intervals are distinguished. Its outcome-set denominator was not exported. Rhythm/pacing/QRS missingness patterns remain unavailable.
Assessment LVEF/method distribution	Assessment LVEF distributions and recorded measurement methods are reported in S15. The reduced-LVEF complete set contained 276 values exactly at 40%, with denominator 8371. Cardiomyopathy echo descriptions use a selected echo subset, not its full outcome population. Method counts do not constitute validation of extraction.
Cardiomyopathy scaling and descriptive risks	Dimensionless class-specific marker medians and IQRs, fixed developmental quartiles and covariate-standardized reference probabilities are reported in S15. The original 500-replicate analyses did not reach the minimum of 950; corrected post hoc intervals of the probabilities are in Table S93 (S18). These selected-sample reference probabilities are not causal effects or population screening risks. Assessment quartile occupancy was not exported.
Cross-marker and orientation comparisons	All four conditional cross-marker assessment cells are reported on endpoint-specific common complete sets in S15. The original 500-replicate analyses lacked bootstrap intervals under the unchanged minimum of 950; corrected post hoc intervals are in Table S92; original conditional Wald intervals remain separate. Stronger orientation-comparator assessment outputs were not produced. Developmental comparisons are not substituted for assessment results.
Medication	The seven-day pre-ECG medication-order sensitivity was not executed in the additional assessment run; no assessment exposure-coverage denominator, effect estimate or interval was exported. The preceding medication results concern training and internal validation only.

S15a. Participant flow and Table 1

Table S67. S15a. Participant flow and Table 1

Endpoint	Stage	ECGs	Persons	Excluded ECGs	Excluded persons
H1	candidate	about 68,100	32017	suppressed	suppressed
H1	technical	about 67,400	31898	about 670	119
H1	reference_available	20177	9374	47270	22524
H1	index	9374	9374	10803	suppressed
H1	reference_valid	9374	9374	suppressed	suppressed
H1	B3_complete	8439	8439	935	935
H1	C_e	8371	8371	68	68
H4	candidate	about 68,200	32017	suppressed	suppressed
H4	technical	about 67,600	31912	about 680	105
H4	reference_available	33588	19817	33967	12095
H4	index	19817	19817	13771	suppressed
H4	reference_valid	19817	19817	suppressed	suppressed
H4	B3_complete	suppressed	suppressed	suppressed	suppressed
H4	C_e	18170	18170	1647	1647

Table note: For coded cardiomyopathy the last two stages are combined, because fewer than 10 persons differed between complete basic-model data and marker availability; the C_e exclusions

(1,647) count persons with incomplete basic-model data or a missing marker. The adult-age criterion is combined with the technical stage, because the few ECGs and persons it excluded would allow small counts to be derived by subtraction. The ECG counts of the candidate and technical stages and the technical ECG exclusions are rounded (about), because exact counts would allow small differences between the two endpoints or between stages to be derived.

Table S68. S15a. Participant flow and Table 1

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H1/D	age	all	9374	9374	suppressed	67 [55; 78]	65.68 $\pm$ 16.63
H1/D	heart_rate	all	9374	9172	202	77.02 [65.01; 93.02]	81.11 $\pm$ 22.21
H1/D	qrs_duration_ms	all	9374	9299	75	108 [100; 120]	115 $\pm$ 24.18
H1/D	qtc_fridericia_ms	all	9374	8721	653	427.4 [407.4; 452.3]	432.1 $\pm$ 37.12
H1/D	sex	all:M	9374	5027	n/a	n/a	0.5363
H1/D	sex	all:F	9374	4347	n/a	n/a	0.4637
H1/D	sinus_selector	all:True	9374	7339	n/a	n/a	0.7829
H1/D	sinus_selector	all:False	9374	2035	n/a	n/a	0.2171
H1/D	classi-cal_lbbb_pattern_positive	all:0.0	9374	8885	n/a	n/a	0.9478
H1/D	classi-cal_lbbb_pattern_positive	all:1.0 or unknown	9374	489	n/a	n/a	0.05217
H1/D	classi-cal_rbbb_pattern_positive	all:0.0	9374	8129	n/a	n/a	0.8672
H1/D	classi-cal_rbbb_pattern_positive	all:1.0 or unknown	9374	1245	n/a	n/a	0.1328
H1/D	pacing	all:unknown	9374	9374	n/a	n/a	unavailable
H1/D	AF	all:unknown	9374	9374	n/a	n/a	unavailable
H1/D	setting	all:unknown	9374	9374	n/a	n/a	unavailable
H1/D	an-chor_year_group	all:unknown	9374	9374	n/a	n/a	unavailable
H1/D	ICD_comorbidity	all:unknown	9374	9374	n/a	n/a	unavailable
H1/D	age	case	969	969	suppressed	72 [62; 82]	70.87 $\pm$ 13.91
H1/D	heart_rate	case	969	944	25	86.08 [72.03; 101.3]	88.59 $\pm$ 22.73
H1/D	qrs_duration_ms	case	969	936	33	124 [108; 152]	134.3 $\pm$ 35.82
H1/D	qtc_fridericia_ms	case	969	858	111	446.4 [422.8; 475.8]	451.6 $\pm$ 43.23
H1/D	sex	case:M	969	678	n/a	n/a	0.6997
H1/D	sex	case:F	969	291	n/a	n/a	0.3003
H1/D	sinus_selector	case:True	969	628	n/a	n/a	0.6481
H1/D	sinus_selector	case:False	969	341	n/a	n/a	0.3519
H1/D	classi-cal_lbbb_pattern_positive	case:0.0	969	805	n/a	n/a	0.8308
H1/D	classi-cal_lbbb_pattern_positive	case:1.0 or unknown	969	164	n/a	n/a	0.1692
H1/D	classi-cal_rbbb_pattern_positive	case:0.0	969	684	n/a	n/a	0.7059

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H1/D	classical_rbbb_pattern_positive	case:1.0 or unknown	969	285	n/a	n/a	0.2941
H1/D	pacing	case:unknown	969	969	n/a	n/a	unavailable
H1/D	AF	case:unknown	969	969	n/a	n/a	unavailable
H1/D	setting	case:unknown	969	969	n/a	n/a	unavailable
H1/D	anchor_year_group	case:unknown	969	969	n/a	n/a	unavailable
H1/D	ICD_comorbidity	case:unknown	969	969	n/a	n/a	unavailable
H1/D	age	control	8405	8405	suppressed	67 [55; 78]	65.08 $\pm$ 16.81
H1/D	heart_rate	control	8405	8228	177	76.05 [65.01; 92.02]	80.25 $\pm$ 21.99
H1/D	qrs_duration_ms	control	8405	8363	42	108 [100; 118]	112.9 $\pm$ 21.46
H1/D	qtc_fridericia_ms	control	8405	7863	542	425.8 [406.2; 449.1]	430 $\pm$ 35.76
H1/D	sex	control:M	8405	4349	n/a	n/a	0.5174
H1/D	sex	control:F	8405	4056	n/a	n/a	0.4826
H1/D	sinus_selector	control:True	8405	6711	n/a	n/a	0.7985
H1/D	sinus_selector	control:False	8405	1694	n/a	n/a	0.2015
H1/D	classical_lbbb_pattern_positive	control:0.0	8405	8080	n/a	n/a	0.9613
H1/D	classical_lbbb_pattern_positive	control:1.0 or unknown	8405	325	n/a	n/a	0.03867
H1/D	classical_rbbb_pattern_positive	control:0.0	8405	7445	n/a	n/a	0.8858
H1/D	classical_rbbb_pattern_positive	control:1.0 or unknown	8405	960	n/a	n/a	0.1142
H1/D	pacing	control:unknown	8405	8405	n/a	n/a	unavailable
H1/D	AF	control:unknown	8405	8405	n/a	n/a	unavailable
H1/D	setting	control:unknown	8405	8405	n/a	n/a	unavailable
H1/D	anchor_year_group	control:unknown	8405	8405	n/a	n/a	unavailable
H1/D	ICD_comorbidity	control:unknown	8405	8405	n/a	n/a	unavailable
H1/C	age	all	8371	8371	suppressed	67 [55; 78]	65.18 $\pm$ 16.7
H1/C	heart_rate	all	8371	8371	suppressed	77.02 [65.01; 93.02]	81.03 $\pm$ 21.31
H1/C	qrs_duration_ms	all	8371	8371	suppressed	108 [100; 120]	114.7 $\pm$ 24.14
H1/C	qtc_fridericia_ms	all	8371	8371	suppressed	427.1 [407.2; 451.5]	431.7 $\pm$ 36.47
H1/C	sex	all:M	8371	4499	n/a	n/a	0.5375
H1/C	sex	all:F	8371	3872	n/a	n/a	0.4625
H1/C	sinus_selector	all:True	8371	6879	n/a	n/a	0.8218
H1/C	sinus_selector	all:False	8371	1492	n/a	n/a	0.1782
H1/C	classical_lbbb_pattern_positive	all:0.0	8371	7988	n/a	n/a	0.9542
H1/C	classical_lbbb_pattern_positive	all:unknown	8371	277	n/a	n/a	0.03309

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H1/C	classical_lbbb_pattern_positive	all:1.0	8371	106	n/a	n/a	0.01266
H1/C	classical_rbbb_pattern_positive	all:0.0	8371	7328	n/a	n/a	0.8754
H1/C	classical_rbbb_pattern_positive	all:1.0	8371	791	n/a	n/a	0.09449
H1/C	classical_rbbb_pattern_positive	all:unknown	8371	252	n/a	n/a	0.0301
H1/C	pacing	all:unknown	8371	8371	n/a	n/a	unavailable
H1/C	AF	all:unknown	8371	8371	n/a	n/a	unavailable
H1/C	setting	all:unknown	8371	8371	n/a	n/a	unavailable
H1/C	an-chor_year_group	all:unknown	8371	8371	n/a	n/a	unavailable
H1/C	ICD_comorbidity	all:unknown	8371	8371	n/a	n/a	unavailable
H1/C	age	case	800	800	suppressed	71 [62; 82]	70.58 $\pm$ 14.21
H1/C	heart_rate	case	800	800	suppressed	86.08 [73.08; 101]	88.54 $\pm$ 21.4
H1/C	qrs_duration_ms	case	800	800	suppressed	124 [108; 152]	134.6 $\pm$ 36.11
H1/C	qtc_fridericia_ms	case	800	800	suppressed	445.3 [422.6; 474.8]	450.9 $\pm$ 42.95
H1/C	sex	case:M	800	557	n/a	n/a	0.6963
H1/C	sex	case:F	800	243	n/a	n/a	0.3038
H1/C	sinus_selector	case:True	800	557	n/a	n/a	0.6963
H1/C	sinus_selector	case:False	800	243	n/a	n/a	0.3038
H1/C	classical_lbbb_pattern_positive	case:0.0	800	680	n/a	n/a	0.85
H1/C	classical_lbbb_pattern_positive	case:unknown	800	87	n/a	n/a	0.1087
H1/C	classical_lbbb_pattern_positive	case:1.0	800	33	n/a	n/a	0.04125
H1/C	classical_rbbb_pattern_positive	case:0.0	800	581	n/a	n/a	0.7262
H1/C	classical_rbbb_pattern_positive	case:1.0	800	146	n/a	n/a	0.1825
H1/C	classical_rbbb_pattern_positive	case:unknown	800	73	n/a	n/a	0.09125
H1/C	pacing	case:unknown	800	800	n/a	n/a	unavailable
H1/C	AF	case:unknown	800	800	n/a	n/a	unavailable
H1/C	setting	case:unknown	800	800	n/a	n/a	unavailable
H1/C	an-chor_year_group	case:unknown	800	800	n/a	n/a	unavailable
H1/C	ICD_comorbidity	case:unknown	800	800	n/a	n/a	unavailable
H1/C	age	control	7571	7571	suppressed	66 [54; 77]	64.61 $\pm$ 16.85
H1/C	heart_rate	control	7571	7571	suppressed	76.05 [65.01; 92.02]	80.24 $\pm$ 21.15
H1/C	qrs_duration_ms	control	7571	7571	suppressed	108 [100; 118]	112.6 $\pm$ 21.46

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H1/C	qtc_fridericia_ms	control	7571	7571	suppressed	425.6 [406.2; 448.6]	429.6 $\pm$ 35.11
H1/C	sex	control:M	7571	3942	n/a	n/a	0.5207
H1/C	sex	control:F	7571	3629	n/a	n/a	0.4793
H1/C	sinus_selector	control:True	7571	6322	n/a	n/a	0.835
H1/C	sinus_selector	control:False	7571	1249	n/a	n/a	0.165
H1/C	classi-cal_lbbb_pattern_positive	control:0.0	7571	7308	n/a	n/a	0.9653
H1/C	classi-cal_lbbb_pattern_positive	control:unknown	7571	190	n/a	n/a	0.0251
H1/C	classi-cal_lbbb_pattern_positive	control:1.0	7571	73	n/a	n/a	0.009642
H1/C	classi-cal_rbbb_pattern_positive	control:0.0	7571	6747	n/a	n/a	0.8912
H1/C	classi-cal_rbbb_pattern_positive	control:1.0	7571	645	n/a	n/a	0.08519
H1/C	classi-cal_rbbb_pattern_positive	control:unknown	7571	179	n/a	n/a	0.02364
H1/C	pacing	control:unknown	7571	7571	n/a	n/a	unavailable
H1/C	AF	control:unknown	7571	7571	n/a	n/a	unavailable
H1/C	setting	control:unknown	7571	7571	n/a	n/a	unavailable
H1/C	anchor_year_group	control:unknown	7571	7571	n/a	n/a	unavailable
H1/C	ICD_comorbidity	control:unknown	7571	7571	n/a	n/a	unavailable
H4/D	age	all	19817	19817	suppressed	64 [51; 76]	62.24 $\pm$ 18.14
H4/D	heart_rate	all	19817	19475	342	77.02 [65.01; 92.02]	80.54 $\pm$ 21
H4/D	qrs_duration_ms	all	19817	suppressed	suppressed	108 [100; 118]	113.1 $\pm$ 21.56
H4/D	qtc_fridericia_ms	all	19817	18669	1148	426.9 [407.3; 450.1]	431 $\pm$ 36.09
H4/D	sex	all:M	19817	10134	n/a	n/a	0.5114
H4/D	sex	all:F	19817	9683	n/a	n/a	0.4886
H4/D	sinus_selector	all:True	19817	16713	n/a	n/a	0.8434
H4/D	sinus_selector	all:False	19817	3104	n/a	n/a	0.1566
H4/D	classi-cal_lbbb_pattern_positive	all:0.0	19817	19036	n/a	n/a	0.9606
H4/D	classi-cal_lbbb_pattern_positive	all:1.0 or unknown	19817	781	n/a	n/a	0.03941
H4/D	classi-cal_rbbb_pattern_positive	all:0.0	19817	17687	n/a	n/a	0.8925
H4/D	classi-cal_rbbb_pattern_positive	all:1.0 or unknown	19817	2130	n/a	n/a	0.1075
H4/D	pacing	all:unknown	19817	19817	n/a	n/a	unavailable
H4/D	AF	all:unknown	19817	19817	n/a	n/a	unavailable
H4/D	setting	all:unknown	19817	19817	n/a	n/a	unavailable

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H4/D	an-chor_year_group	all:unknown	19817	19817	n/a	n/a	unavailable
H4/D	ICD_comorbidity	all:unknown	19817	19817	n/a	n/a	unavailable
H4/D	age	case	515	515	suppressed	67 [56; 77]	65.59 $\pm$ 15.05
H4/D	heart_rate	case	515	499	16	83.1 [68.03; 100]	86.25 $\pm$ 24.89
H4/D	qrs_duration_ms	case	515	suppressed	suppressed	122 [108; 156]	134.5 $\pm$ 36.21
H4/D	qtc_fridericia_ms	case	515	458	57	450.6 [425.5; 478.4]	455.1 $\pm$ 42.14
H4/D	sex	case:M	515	341	n/a	n/a	0.6621
H4/D	sex	case:F	515	174	n/a	n/a	0.3379
H4/D	sinus_selector	case:True	515	307	n/a	n/a	0.5961
H4/D	sinus_selector	case:False	515	208	n/a	n/a	0.4039
H4/D	classical_lbbb_pattern_positive	case:0.0	515	435	n/a	n/a	0.8447
H4/D	classical_lbbb_pattern_positive	case:1.0 or unknown	515	80	n/a	n/a	0.1553
H4/D	classical_rbbb_pattern_positive	case:0.0	515	382	n/a	n/a	0.7417
H4/D	classical_rbbb_pattern_positive	case:1.0 or unknown	515	133	n/a	n/a	0.2583
H4/D	pacing	case:unknown	515	515	n/a	n/a	unavailable
H4/D	AF	case:unknown	515	515	n/a	n/a	unavailable
H4/D	setting	case:unknown	515	515	n/a	n/a	unavailable
H4/D	an-chor_year_group	case:unknown	515	515	n/a	n/a	unavailable
H4/D	ICD_comorbidity	case:unknown	515	515	n/a	n/a	unavailable
H4/D	age	control	19302	19302	suppressed	64 [51; 76]	62.15 $\pm$ 18.21
H4/D	heart_rate	control	19302	18976	326	77.02 [65.01; 92.02]	80.39 $\pm$ 20.87
H4/D	qrs_duration_ms	control	19302	19198	104	108 [100; 118]	112.5 $\pm$ 20.74
H4/D	qtc_fridericia_ms	control	19302	18211	1091	426.5 [407; 449.2]	430.4 $\pm$ 35.71
H4/D	sex	control:M	19302	9793	n/a	n/a	0.5074
H4/D	sex	control:F	19302	9509	n/a	n/a	0.4926
H4/D	sinus_selector	control:True	19302	16406	n/a	n/a	0.85
H4/D	sinus_selector	control:False	19302	2896	n/a	n/a	0.15
H4/D	classical_lbbb_pattern_positive	control:0.0	19302	18601	n/a	n/a	0.9637
H4/D	classical_lbbb_pattern_positive	control:1.0 or unknown	19302	701	n/a	n/a	0.03632
H4/D	classical_rbbb_pattern_positive	control:0.0	19302	17305	n/a	n/a	0.8965
H4/D	classical_rbbb_pattern_positive	control:1.0 or unknown	19302	1997	n/a	n/a	0.1035
H4/D	pacing	control:unknown	19302	19302	n/a	n/a	unavailable
H4/D	AF	control:unknown	19302	19302	n/a	n/a	unavailable

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H4/D	setting	control:unknown	19302	19302	n/a	n/a	unavailable
H4/D	an-chor_year_group	control:unknown	19302	19302	n/a	n/a	unavailable
H4/D	ICD_comorbidity	control:unknown	19302	19302	n/a	n/a	unavailable
H4/C	age	all	18170	18170	suppressed	63 [50; 76]	61.69 $\pm$ 18.13
H4/C	heart_rate	all	18170	18170	suppressed	77.02 [66.01; 92.02]	80.44 $\pm$ 20.29
H4/C	qrs_duration_ms	all	18170	18170	suppressed	108 [100; 118]	112.8 $\pm$ 21.49
H4/C	qtc_fridericia_ms	all	18170	18170	suppressed	426.7 [407.2; 449.9]	430.8 $\pm$ 35.79
H4/C	sex	all:M	18170	9319	n/a	n/a	0.5129
H4/C	sex	all:F	18170	8851	n/a	n/a	0.4871
H4/C	sinus_selector	all:True	18170	15905	n/a	n/a	0.8753
H4/C	sinus_selector	all:False	18170	2265	n/a	n/a	0.1247
H4/C	classi-cal_lbbb_pattern_positive	all:not positive	18170	17992	n/a	n/a	0.9902
H4/C	classi-cal_lbbb_pattern_positive	all:1.0	18170	178	n/a	n/a	0.009796
H4/C	classi-cal_rbbb_pattern_positive	all:not positive	18170	16757	n/a	n/a	0.9222
H4/C	classi-cal_rbbb_pattern_positive	all:1.0	18170	1413	n/a	n/a	0.07777
H4/C	pacing	all:unknown	18170	18170	n/a	n/a	unavailable
H4/C	AF	all:unknown	18170	18170	n/a	n/a	unavailable
H4/C	setting	all:unknown	18170	18170	n/a	n/a	unavailable
H4/C	an-chor_year_group	all:unknown	18170	18170	n/a	n/a	unavailable
H4/C	ICD_comorbidity	all:unknown	18170	18170	n/a	n/a	unavailable
H4/C	age	case	433	433	suppressed	67 [56; 77]	65.65 $\pm$ 15.25
H4/C	heart_rate	case	433	433	suppressed	82.99 [68.03; 100]	86.1 $\pm$ 23.75
H4/C	qrs_duration_ms	case	433	433	suppressed	122 [108; 158]	135.1 $\pm$ 36.91
H4/C	qtc_fridericia_ms	case	433	433	suppressed	450.8 [425.5; 476.5]	454.6 $\pm$ 41.84
H4/C	sex	case:M	433	288	n/a	n/a	0.6651
H4/C	sex	case:F	433	145	n/a	n/a	0.3349
H4/C	sinus_selector	case:True	433	278	n/a	n/a	0.642
H4/C	sinus_selector	case:False	433	155	n/a	n/a	0.358
H4/C	classi-cal_lbbb_pattern_positive	case:not positive	433	417	n/a	n/a	0.963
H4/C	classi-cal_lbbb_pattern_positive	case:1.0	433	16	n/a	n/a	0.03695
H4/C	classi-cal_rbbb_pattern_positive	case:not positive	433	367	n/a	n/a	0.8476
H4/C	classi-cal_rbbb_pattern_positive	case:1.0	433	66	n/a	n/a	0.1524
H4/C	pacing	case:unknown	433	433	n/a	n/a	unavailable
H4/C	AF	case:unknown	433	433	n/a	n/a	unavailable

Endpoint/set	Variable	Class/category	Denominator	Observed/category n	Missing n	Median [Q1; Q3]	Mean $\pm$ SD or fraction
H4/C	setting	case:unknown	433	433	n/a	n/a	unavailable
H4/C	an-chor_year_group	case:unknown	433	433	n/a	n/a	unavailable
H4/C	ICD_comorbidity	case:unknown	433	433	n/a	n/a	unavailable
H4/C	age	control	17737	17737	suppressed	63 [50; 76]	61.59 $\pm$ 18.18
H4/C	heart_rate	control	17737	17737	suppressed	77.02 [66.01; 92.02]	80.3 $\pm$ 20.18
H4/C	qrs_duration_ms	control	17737	17737	suppressed	108 [100; 118]	112.2 $\pm$ 20.67
H4/C	qtc_fridericia_ms	control	17737	17737	suppressed	426.4 [406.9; 449]	430.2 $\pm$ 35.43
H4/C	sex	control:M	17737	9031	n/a	n/a	0.5092
H4/C	sex	control:F	17737	8706	n/a	n/a	0.4908
H4/C	sinus_selector	control:True	17737	15627	n/a	n/a	0.881
H4/C	sinus_selector	control:False	17737	2110	n/a	n/a	0.119
H4/C	classical_lbbb_pattern_positive	control:not positive	17737	17575	n/a	n/a	0.9909
H4/C	classical_lbbb_pattern_positive	control:1.0	17737	162	n/a	n/a	0.009133
H4/C	classical_rbbb_pattern_positive	control:not positive	17737	16390	n/a	n/a	0.9241
H4/C	classical_rbbb_pattern_positive	control:1.0	17737	1347	n/a	n/a	0.07594
H4/C	pacing	control:unknown	17737	17737	n/a	n/a	unavailable
H4/C	AF	control:unknown	17737	17737	n/a	n/a	unavailable
H4/C	setting	control:unknown	17737	17737	n/a	n/a	unavailable
H4/C	an-chor_year_group	control:unknown	17737	17737	n/a	n/a	unavailable
H4/C	ICD_comorbidity	control:unknown	17737	17737	n/a	n/a	unavailable

All counts are descriptive. Small or complementary cells are suppressed. In the reference-valid sets (D), the pattern categories 1.0 and unknown are combined, because their differences from the complete sets (C) would otherwise allow small counts to be derived. In the cardiomyopathy complete sets (C), the pattern categories 0.0 and unknown are combined as not positive, because the unknown counts of the two patterns would otherwise allow a small count to be derived. Pipeline sinus and block-pattern categories are not independently adjudicated rhythm diagnoses. Unavailable era, setting and comorbidity categories remain unavailable.

S15b. Development-fixed predictions

B2 is the basic model without the integral QRS-T angle; B3 includes that angle, and B3_marker adds the endpoint-specific Fréchet marker. All results here were specified after primary-result inspection and are post hoc.

Table S69. S15b. Development-fixed predictions

Endpoint	Fixed model	N/cases/co ntrols	AUC [95% CI]	Brier [95% CI]	Sensitivity [95% CI]	Achieved specificity [95% CI]	Offset intercept [95% CI]	Joint intercept [95% CI]	Slope [95% CI]
H1	B2	8371 / 800 / 7571	0.7803 [0.7632; 0.7965]	0.07709 [0.07298; 0.08103]	0.4012 [0.3667; 0.4386]	0.9017 [0.8953; 0.908]	-0.09297 [- 0.1716; - 0.01668]	-0.09702 [- 0.264; 0.07311]	0.9978 [0.9257; 1.071]
H1	B3	8371 / 800 / 7571	0.8027 [0.7874; 0.8177]	0.07557 [0.07161; 0.0793]	0.4263 [0.3918; 0.4622]	0.8995 [0.8932; 0.9063]	-0.09129 [- 0.1709; - 0.0133]	-0.1084 [- 0.2583; 0.05113]	0.9903 [0.9224; 1.061]
H1	B3_marker	8371 / 800 / 7571	0.8353 [0.8221; 0.8489]	0.07292 [0.06912; 0.07658]	0.505 [0.4711; 0.5394]	0.8957 [0.8888; 0.9023]	-0.1166 [- 0.1974; - 0.03755]	-0.1708 [- 0.3045; - 0.03358]	0.9665 [0.9106; 1.03]
H4	B2	18170 / 433 / 17737	0.7752 [0.7496; 0.7986]	0.02258 [0.02058; 0.02452]	0.4134 [0.366; 0.4587]	0.9039 [0.8997; 0.9085]	-0.09079 [- 0.1913; 0.0006364]	-0.02194 [- 0.344; 0.2777]	1.021 [0.9308; 1.107]
H4	B3	18170 / 433 / 17737	0.7932 [0.7716; 0.8143]	0.0223 [0.02035; 0.0242]	0.4573 [0.4082; 0.5024]	0.9007 [0.8965; 0.9053]	-0.09219 [- 0.1946; 0.0002094]	-0.07785 [- 0.3771; 0.206]	1.005 [0.9224; 1.092]
H4	B3_marker	18170 / 433 / 17737	0.8208 [0.8001; 0.8408]	0.02197 [0.02011; 0.02381]	0.5404 [0.4929; 0.5829]	0.8993 [0.895; 0.9038]	-0.09173 [- 0.1946; 0.001354]	-0.06618 [- 0.3375; 0.1682]	1.009 [0.9345; 1.084]

Table S70. S15b. Development-fixed predictions

Endpoint	Paired marker Δ AUC [95% CI]	Paired angle Δ AUC [95% CI]
H1	0.03267 [0.0244; 0.04107]	0.02238 [0.01278; 0.03162]
H4	0.02762 [0.01747; 0.03761]	0.01802 [0.0006081; 0.03468]

Intervals are conditional on the development-fixed models and thresholds. Offset intercept and the joint calibration intercept are distinct quantities.

Developmental optimism is reported separately and is not an assessment-performance correction. Individual model/threshold hashes were not exported as report aggregates; the specified recipe and scaling are bound in the source manifest.

Table S71. S15b. Development-fixed predictions

Endpoint	Development N/cases	Model	Apparent AUC	Mean optimism	Corrected de- velopment AUC	Val- id/planned/mini mum
H1	33971/3543	B2	0.7832	0.0003897	0.7828	200/200/190
H1	33971/3543	B3	0.8068	0.0002951	0.8065	200/200/190
H1	33971/3543	B3_marker	0.8398	0.0003663	0.8394	200/200/190
H4	72795/1903	B2	0.761	0.001405	0.7596	200/200/190
H4	72795/1903	B3	0.7914	0.0007923	0.7906	200/200/190
H4	72795/1903	B3_marker	0.8162	0.0006406	0.8156	200/200/190

S15c. Error sensitivities

Table S72. S15c. Error sensitivities

Method/endpoint	N/cases/controls	OR [bootstrap 95% CI]	Paired Δ beta [95% CI]	Corrected/original log-OR [95% CI]	Valid/attempted
H1 rc	8371 / 800 / 7571	2.087 [0.4186; 9.548]	-0.1154 [-1.65; 1.317]	0.8644 [-1.108; 2.457]	1000/1000
H1 raw	8371 / 800 / 7571	2.339 [2.083; 2.655]	-0.001531 [-0.01651; 0.01447]	0.9982 [0.9782; 1.015]	1000/1000
H1 raw	8371 / 800 / 7571	2.33 [2.022; 2.718]	-0.005213 [-0.05384; 0.04647]	0.9939 [0.9304; 1.051]	1000/1000
H1 clipped	8371 / 800 / 7571	2.338 [2.081; 2.656]	-0.001815 [-0.01722; 0.01402]	0.9979 [0.9786; 1.015]	1000/1000
H1 clipped	8371 / 800 / 7571	2.346 [2.032; 2.724]	0.001584 [-0.04669; 0.04916]	1.002 [0.9406; 1.053]	1000/1000
H1 logit	8371 / 800 / 7571	2.4 [2.145; 2.714]	0.003061 [-0.01102; 0.01774]	1.004 [0.9862; 1.019]	1000/1000
H1 logit	8371 / 800 / 7571	2.416 [2.114; 2.792]	0.009742 [-0.0348; 0.05722]	1.011 [0.9575; 1.06]	1000/1000
H1 spline	8371 / 800 / 7571	2.401 [2.134; 2.732]	0.002343 [-0.01461; 0.01853]	1.003 [0.9814; 1.019]	1000/1000
H1 spline	8371 / 800 / 7571	2.488 [2.155; 2.93]	0.03786 [-0.01863; 0.09875]	1.043 [0.977; 1.103]	1000/1000
H1 joint_rc	8371 / 800 / 7571	8.887 [3.294; 48.49]	1.333 [0.4177; 3.015]	2.566 [1.527; 4.286]	1000/1000
H1 joint	8371 / 800 / 7571	2.629 [2.32; 3.009]	0.1153 [0.09634; 0.1366]	1.135 [1.127; 1.144]	1000/1000
H1 joint	8371 / 800 / 7571	2.872 [2.47; 3.401]	0.2038 [0.1496; 0.2645]	1.239 [1.192; 1.282]	1000/1000
H4 rc	18170 / 433 / 17737	0.5628 [4.239e-05; 28.99]	-1.282 [-10.69; 2.59]	-0.8126 [-16.28; 4.326]	989/1000
H4 raw	18170 / 433 / 17737	2.013 [1.759; 2.312]	-0.007613 [-0.02447; 0.01118]	0.9892 [0.9603; 1.015]	1000/1000
H4 raw	18170 / 433 / 17737	1.979 [1.671; 2.338]	-0.02498 [-0.08296; 0.03661]	0.9647 [0.8651; 1.047]	1000/1000
H4 clipped	18170 / 433 / 17737	2.016 [1.761; 2.311]	-0.006254 [-0.02416; 0.01221]	0.9912 [0.961; 1.015]	1000/1000
H4 clipped	18170 / 433 / 17737	1.987 [1.681; 2.333]	-0.02057 [-0.07642; 0.03727]	0.9709 [0.8775; 1.048]	1000/1000
H4 logit	18170 / 433 / 17737	2.033 [1.785; 2.31]	-0.005818 [-0.02194; 0.01104]	0.9919 [0.9649; 1.014]	1000/1000
H4 logit	18170 / 433 / 17737	2.008 [1.704; 2.333]	-0.01811 [-0.07229; 0.03511]	0.9747 [0.8858; 1.046]	1000/1000
H4 spline	18170 / 433 / 17737	1.991 [1.737; 2.296]	-0.0108 [-0.02864; 0.01075]	0.9846 [0.9548; 1.015]	1000/1000
H4 spline	18170 / 433 / 17737	1.954 [1.651; 2.313]	-0.02942 [-0.09403; 0.03959]	0.9579 [0.8507; 1.054]	1000/1000

H1 angle-only conditional reliability was 0.06385 [0.02751; 0.1011]; H4 reliability was 0.03188 [0.006946; 0.0575]. H1 joint latent eigenvalues were 0.02359, 0.8886. No uncertainty in the transported error package is included. RC instability, including the H4 point-direction reversal, is retained. Additional angle-coefficient curves and corrected Wald intervals were unavailable.

S15d. Verification weighting

Table S73. S15d. Verification weighting

Weight model	N/cases/controls	OR [bootstrap 95% CI]	Apparent ΔAUC [95% CI]	ESS controls	ESS cases
unweighted	4844 / 431 / 4413	2.646 [2.317; 3.065]	0.04685 [0.03375; 0.06]	4413	431
p95	4844 / 431 / 4413	3.011 [2.587; 3.529]	0.04149 [0.02761; 0.05648]	3416	344.1
p99	4844 / 431 / 4413	3.019 [2.596; 3.539]	0.04022 [0.0268; 0.05469]	3162	344.1
old_p99_common _set	4844 / 431 / 4413	2.968 [2.544; 3.493]	0.0414 [0.0269; 0.05551]	3216	349.1

Point weight caps were 13.41 (P95) and 21.11 (P99), derived from training. Marker/B4-complete technical indices numbered 28780; marker-missing technical indices numbered 1001; reference/B4-complete indices numbered 5137. The marker-free old weights use the same final outcome set. Weight quantiles and capped fractions were not exported.

S15e. Missingness

Table S74. S15e. Missingness

Endpoint	Variable	Class (0 control, 1 case)	Missing n	Denominator
H1	age	0	suppressed	suppressed
H1	sex_numeric	0	suppressed	suppressed
H1	heart_rate	0	177	8405
H1	qrs_duration_ms	0	42	8405
H1	qtc_fridericia_ms	0	542	8405
H1	spatial_qrs_t_angle_deg	0	299	8405
H1	qrs_t_normalized_discrete_frechet	0	372	8405
H1	age	1	suppressed	suppressed
H1	sex_numeric	1	suppressed	suppressed
H1	heart_rate	1	25	969
H1	qrs_duration_ms	1	33	969
H1	qtc_fridericia_ms	1	111	969
H1	spatial_qrs_t_angle_deg	1	85	969
H1	qrs_t_normalized_discrete_frechet	1	96	969
H4	age	0	suppressed	suppressed
H4	sex_numeric	0	suppressed	suppressed
H4	heart_rate	0	326	19302
H4	qrs_duration_ms	0	104	19302
H4	qtc_fridericia_ms	0	1091	19302
H4	spatial_qrs_t_angle_deg	0	about 700	19302
H4	qrs_t_frechet_beat_median	0	<20	19302
H4	age	1	suppressed	suppressed
H4	sex_numeric	1	suppressed	suppressed
H4	heart_rate	1	16	515
H4	qrs_duration_ms	1	suppressed	suppressed
H4	qtc_fridericia_ms	1	57	515
H4	spatial_qrs_t_angle_deg	1	39	515
H4	qrs_t_frechet_beat_median	1	suppressed	suppressed

Table S75. S15e. Missingness

Endpoint/model	N/cases/controls	OR [bootstrap 95% CI]	Apparent Δ AUC [95% CI]	Mini- mum/valid/attempted
H1/no_qtc_extended	about 8720 / about 840 / about 7870	2.267 (CI unavailable)	0.03127 (CI unavailable)	950/500/500
H1/no_qtc_C	8371 / 800 / 7571	2.281 (CI unavailable)	0.03108 (CI unavailable)	950/500/500
H1/missing_indicator_extended	8906 / 873 / 8033	2.307 (CI unavailable)	0.03174 (CI unavailable)	950/500/500
H1/missing_indicator_C	n/a / n/a / n/a	n/a	n/a	n/a/n/a/n/a
H1/MI	not exported / not exported / not exported	2.317 [2.112; 2.592]	0.03234 [0.02511; 0.04059]	190/500/500
H4/no_qtc_extended	about 18780 / about 460 / about 18320	2.029 (CI unavailable)	0.02909 (CI unavailable)	950/500/500
H4/no_qtc_C	18170 / 433 / 17737	1.986 (CI unavailable)	0.02513 (CI unavailable)	950/500/500
H4/missing_indicator_extended	19106 / 476 / 18630	2.027 (CI unavailable)	0.02771 (CI unavailable)	950/500/500
H4/missing_indicator_C	n/a / n/a / n/a	n/a	n/a	n/a/n/a/n/a
H4/MI	not exported / not exported / not exported	2.042 [1.808; 2.305]	0.02937 [0.01966; 0.03939]	190/500/500

MI uses 20 imputations. It had a separate specified minimum of 190 valid replicates; the executed 500 attempts differed from the specified first 200. MI outcome denominators were not exported in the original run; they were reconstructed post hoc and are given in Table S94. Rubin intervals are separate from bootstrap intervals. The other original 500-replicate analyses could not provide intervals under the unchanged minimum of 950; corrected intervals are in Table S92. Rhythm/pacing/QRS-specific missingness and joint heart-rate/QTc patterns were not exported.

Table S76. S15e. Missingness

Endpoint	MI pooled OR	Rubin 95% CI	Person-bootstrap 95% CI	Valid/attempted/minimum
H1	2.317	2.08 to 2.581	2.317 [2.112; 2.592]	500/500/190
H4	2.042	1.816 to 2.297	2.042 [1.808; 2.305]	500/500/190

S15f. LVEF descriptions

Table S77. S15f. LVEF descriptions

Endpoint/set	Echo-subset denominator	Exactly 40%	<40%	≥40%	≤40%	>40%
H1/D	9374	314	969	8405	1283	8091
H1/C	8371	276	800	7571	1076	7295
H4/D	5873	232	709	5164	941	4932
H4/C	5262	205	597	4665	802	4460

Table S78. S15f. LVEF descriptions

Endpoint/set	LVEF method	N	Denominator
H1/D	generic	9108	9374
H1/D	biplane or 3d	266	9374
H1/C	generic	8138	8371
H1/C	biplane or 3d	233	8371
H4/D	generic	5699	5873
H4/D	biplane or 3d	174	5873
H4/C	generic	5110	5262
H4/C	biplane or 3d	152	5262

Cardiomyopathy descriptions use selected echo subsets. Counts describe reference extraction, not its independent validation.

S15g. Marker scale and selected-sample probabilities

Table S79. S15g. Marker scale and selected-sample probabilities

Endpoint	Class (0 control, 1 case)	N	Dimensionless median [Q1; Q3]
H1	0	7571	1.41 [1.029; 1.983]
H1	1	800	2.518 [1.892; 3.053]
H4	0	17737	1.36 [1.023; 1.836]
H4	1	433	2.299 [1.714; 2.86]

Table S80. S15g. Marker scale and selected-sample probabilities

Endpoint	N/cases/controls	Q1	Q2	Q3	Q4	Q4-Q1	Valid-attempted; bootstrap CI unavailable
H1	8371 / 800 / 7571	0.02786	0.04291	0.07094	0.1692	0.1413	500/500
H4	18170 / 433 / 17737	0.007502	0.01081	0.01628	0.0357	0.0282	500/500

Both markers are normalized dimensionless shape distances. Quartile boundaries and representative medians were fixed in development; covariate standardization uses the assessment outcome set. These are selected-sample reference probabilities. Assessment quartile occupancy was unavailable. Corrected post hoc intervals of the probabilities are in Table S93.

S15h. Conditional cross-marker analyses

Table S81. S15h. Conditional cross-marker analyses

Endpoint/marker	N/cases/controls	OR (bootstrap CI unavailable)	Apparent Δ AUC (bootstrap CI unavailable)	Valid/attempted
H1/F	>8360 / >790 / >7560	2.345	0.03266	500/500
H1/M	>8360 / >790 / >7560	2.331	0.03293	500/500
H4/F	18041 / >420 / >17600	2.053	0.02653	500/500
H4/M	18041 / >420 / >17600	2.039	0.02674	500/500

F denotes representative-beat normalized Fréchet distance; M denotes the normalized beat-median distance. All cells are exploratory. The original 500 attempts could not reach 950 valid fits; corrected post hoc intervals are in Table S92. Stronger orientation assessment results were unavailable.

S15i. Rhythm and conduction strata

Table S82. S15i. Rhythm and conduction strata

End-point/stratum	Status	N/cases/controls	OR [bootstrap 95% CI]	Valid/attempted	Reason
H1/parser	unavailable	n/a / n/a / n/a	n/a	n/a/n/a	Unavailable: semantic parser adjudication incomplete
H1/qrs_ge120	estimable	2199 / 457 / 1742	2.344 [1.988; 2.834]	1000/1000	n/a
H1/rbbb	estimable	791 / 146 / 645	2.437 (CI unavailable)	96/1000	n/a
H1/lbbb	unavailable	n/a / n/a / n/a	n/a	n/a/n/a	Not estimable: fewer than 100 persons in a class
H1/qrs_lt120_no_block	estimable	6104 / 329 / 5775	2.395 [2.046; 2.813]	1000/1000	n/a
H4/parser	unavailable	n/a / n/a / n/a	n/a	n/a/n/a	Unavailable: semantic parser adjudication incomplete
H4/qrs_ge120	estimable	4180 / about 240 / about 3940	1.883 [1.6; 2.227]	1000/1000	n/a
H4/rbbb	unavailable	n/a / n/a / n/a	n/a	n/a/n/a	Not estimable: fewer than 100 persons in a class
H4/lbbb	unavailable	n/a / n/a / n/a	n/a	n/a/n/a	Not estimable: fewer than 100 persons in a class
H4/qrs_lt120_no_block	estimable	13872 / 193 / 13679	2.146 [1.759; 2.604]	1000/1000	n/a

AF and pacing strata were not released because semantic adjudication was incomplete. RBBB LVEF had only 96 valid bootstrap draws in the original run (corrected post hoc: OR bootstrap interval 1.905-3.391, 1,000 of 1,000 valid; Table S92); small strata were stopped. QRS width is not an exclusion test for pacing.

S16. Figure index

Figures 1-5 are embedded in the main manuscript using separate raster images. Figure 1 shows flow, Figure 2 associations, Figure 3 post hoc assessment correction, Figure 4 development correction, and Figure 5 two known-truth simulations of classical angle error, the early null experiment and the later tipping-point simulation, with equal weight (the genuine-effect scenario of the early experiment is in Table S47). Development and assessment are separate data roles; correction methods and confidence-interval types are distinguished in the captions. Further details of Figure 2: persons and cases per row are given in Sections S3, S8 and S15; strata use the basic mod-

el within the stratum; “Other Fréchet form” is the beat-median distance in (A) and the representative-beat distance in (B), on the common complete set; the marker-containing weights are capped at the development 95th (P95) or 99th (P99) percentile, their bootstrap intervals come from the original run, and the unweighted and marker-free weighted rows show Wald intervals only; rows whose interval was missing in the original run show the corrected post hoc bootstrap intervals of Tables S91 and S92 (point estimates unchanged); the stratum for QRS <120 ms shows the Wald interval (2.04-2.81), whereas the bootstrap interval is 2.05-2.81. The endpoints overlap and are not independent studies. Additional assessment sensitivities and descriptive summaries were specified after the primary results were known (post hoc); original specified association rows retain their separate status.

S17. Development-only T-end tipping points

With case-only T-end shortening, OR 1.25 was not reached on the specified grid within 32 ms (0/500 bootstrap crossings). With case-only T-end shortening, OR 1 was not reached on the specified grid within 32 ms (0/500 bootstrap crossings). With case-only T-end extension, OR 1.25 was not reached on the specified grid within 32 ms (1/500 bootstrap crossings). With case-only T-end extension, OR 1 was not reached on the specified grid within 32 ms (0/500 bootstrap crossings). In this weighted sample, the unshifted OR was 2.23. With the Fridericia QTc held at its measured value, as in the first analysis, +32 ms reduced it to 1.51 (95% bootstrap CI 1.33-1.76) and -32 ms gave 2.32. These results use a common finite-output sample of 2,950 persons (1,450 cases), fixed development scaling and selection weights.

Coherent QTc (post hoc). A shift of all beat T ends changes the QT interval by the same amount, so a QTc held at its measured value is inconsistent with the shift and can alter the direction of the perturbation. The shift was therefore repeated with the Fridericia QTc of the shifted cases recomputed as $QTc \times (QT + \text{shift}) / QT$ at fixed heart rate. Heart rate does not depend on the T end. QRS duration was held at its measured value, although the reconstruction with shifted T ends changes it slightly in a minority of recordings, and the shifted QT and QTc are arithmetic, not remeasured from the signal; the coherence of the recomputation is therefore approximate (Table S119). The variant with QTc held fixed reproduced the first analysis exactly. With QTc recomputed, +32 ms gave an OR of 1.61 (95% bootstrap CI 1.40-1.91) and -32 ms 2.01 (1.77-2.33); OR 1.25 and OR 1 were not reached within 32 ms in either direction (extension to 1.25 in 1 of 500 bootstrap replicates, as before). The curve now falls in both directions and the shortening side is no longer non-monotonic. The earlier table was too low at extension and too high at shortening, by at most 0.10 and 0.31 in the OR.

Cases outside the common sample. Fifty of the 1,500 sampled cases (3.3%) and none of the controls lacked a finite output at one or more grid points: 28 at +24 ms and 39 at +32 ms, fewer than 10 at each other point (none at -8, -4 and 0 ms). They had wider QRS complexes (mean 153 against 137 ms) and longer QTc (476 against 454 ms), mean age 71.0 against 69.5 years and heart rate 88.9

against 87.0 beats/min; T duration (217.8 against 216.9 ms) and the Fréchet distance without shift (2.49 against 2.46) were similar. Including them wherever finite changed the OR by at most 0.016 (2.250 against 2.234 at 0 ms; 1.611 against 1.613 at +32 ms with recomputed QTc). The loss is not random, but it is small in this calculation; it does not exclude shifts beyond 24 ms in persons with wide QRS complexes.

The case-only grid describes a constant systematic shift of the T end in cases. It is not random boundary error and not an observed mechanism, and the shifted QT is derived, not remeasured. Common finite-output selection, weighted stratified sampling and a previously inspected developmental hypothesis limit the inference. Linear interpolation between grid points is an operational definition rather than an exact continuous-time estimate. No assessment input, footer or individual record was accessed.

Covariates under reconstruction. To check the statement that the other covariates are unaffected, the production features were recomputed from the same context after shifting all beat T ends by 0, ± 16 and ± 32 ms in a random subsample of 500 recordings of the T-end sample (264 cases, 236 controls; development data). Heart rate was unchanged in all 500. QRS duration changed in a minority of recordings, typically by 2 ms, without a mean shift. QT followed the shift except in a part of the recordings at +32 ms. The arithmetic QTc used in S17 differed from the QTc of the reconstruction by 0.2 ms on average, and by more than 10 ms in 5% of the recordings at +32 ms. The effect of these differences on the OR was not recomputed.

Table S119. S17. Covariates under reconstruction with shifted T ends (cases of the 500-recording subsample, $n = 264$)

Feature	Change under reconstruction
Heart rate (from RR)	No recording changed (0 of 500)
QRS duration	Changed in $<1\%$ (-16 ms), 4.2% (-32 ms), 6.1% ($+16$ ms) and 33% ($+32$ ms) of recordings; median absolute change 2 ms; at +32 ms 95th percentile 6 ms, maximum 22 ms; signs balanced (41 positive, 47 negative at +32 ms); mean change over all recordings 0.03 ms
QT	Equal to the shift except in 13 of 264 recordings at -32 ms and 100 of more than 250 at +32 ms (median deviation 2 ms, maximum 46 ms)
QTc (Fridericia)	Follows QT; against the arithmetic recomputation of S17 the mean difference was 0.2 ms and the 95th percentile of the absolute difference 2.4 ms (-32 ms) and 10.4 ms ($+32$ ms), maximum 30 ms
Missing outputs at +32 ms	Marker and angle each in fewer than 10, QTc in 10 of 500 recordings

Table: Table S83. Case-only T-end perturbation in development

Table S83 reports the grid results for the common finite-output sample of 2,950 persons (1,450 cases) at every shift.

Shift, ms	OR, QTc held at measured value	Bootstrap 95% interval	OR, QTc recomputed	Bootstrap 95% interval
-32	2.322	2.064-2.669	2.007	1.765-2.334
-24	2.349	2.094-2.699	2.098	1.875-2.410
-16	2.364	2.106-2.737	2.199	1.959-2.519
-8	2.317	2.049-2.688	2.243	1.989-2.590
-4	2.287	2.023-2.650	2.253	1.992-2.610
0	2.234	1.981-2.592	2.234	1.981-2.592
4	2.174	1.915-2.512	2.204	1.944-2.552
8	2.113	1.864-2.440	2.167	1.908-2.523
16	2.003	1.770-2.312	2.089	1.830-2.452
24	1.726	1.517-2.002	1.825	1.581-2.152
32	1.509	1.328-1.759	1.613	1.397-1.912

The numbers of sampled persons available at each shift (3,000 sampled, 1,500 cases) differ from the common sample only by the cases listed above and are not tabulated to avoid small-cell disclosure.

Translation into the units of the marker shift (post hoc). The perturbation of a T end and a shift of the marker in control SD (S19) are different quantities and cannot be converted directly. As an orientation on the log scale: with QTc recomputed, the extension by 32 ms lowered the OR from 2.234 to 1.613, a change of $\ln(2.234/1.613) = 0.33$ in the log OR. Reaching OR 1.25 from 2.234 needs a change of $\ln(2.234/1.25) = 0.58$, so the 32-ms extension covers 56% of the distance to the attenuation threshold, and no shift within the grid reached it.

S18. Corrected bootstrap intervals (post hoc correction of a construction error)

The percentile bootstrap of the original run (S3b, S15) had three construction defects. (1) The eligibility rule “at least 100 distinct persons per class” was applied inside every replicate instead of to the sample. A replicate of G draws with replacement from G persons contains on average 63.2% distinct persons, so a class of 145 cases yields about 92 distinct cases, and typical replicates were rejected (905 of 1,000 in association row 049). (2) Several post hoc branches (S15e, S15g, S15h, S15i) ran 500 replicates while the interval rule required 950 valid fits, so no interval could be produced by construction. (3) The fitting routine stopped when the weighted score fell below 10^{-7} per unit of total weight, whereas acceptance required the score per distinct resampled person to be below 10^{-7} . Because a replicate contains about 63% distinct persons, converged fits were rejected (6% to 16% of replicates in rows 006 to 062 without the eligibility defect, and 13% to 24% in rows 045, 047 and 049 once the eligibility defect was removed; in all 1,056 rejected replicates examined, every one met the stopping rule and none met the acceptance rule; they lay between 6.3×10^{-8} and 1.0×10^{-7} on the stopping scale, Table S109). Point estimates, which use unit weights, and Wald intervals were not affected.

Correction (post hoc). Eligibility (at least 100 persons per class, as specified) was checked once in the sample. All branches used 1,000 replicates, and further fitting steps were allowed until both criteria held. The seed recipe of the original run was kept, so the first 500 replicates of every S15 branch are identical to the original ones. The interval rule (percentile intervals when at least 950 of 1,000 replicates were valid) was unchanged. With the original rule, the old counts of valid replicates were reproduced exactly (754, 815, 93 and 96 of 1,000 in the affected rows; 777 in the verification analysis; 909, 909, 915, 865, 881, 935, 889 and 840 in the others), and the replicates that the old eligibility rule would have rejected were 904 (right-bundle stratum) and 905 (row 049). Code written separately from the specification reproduced the right-bundle stratum and row 049 (odds ratio, AUC increment and bootstrap limits agree to four decimals). The assessment partition was read again for these corrections; the access times are in S1a. The original entries remain in S3b and S15. Tables S91 to S94 show old and new entries side by side. Wald intervals remain the primary inference.

Table S109. S18. Stopping rule and acceptance rule in rejected bootstrap replicates

Analysis	Rejected replicates with reason "score per row"	Score per unit of weight, minimum to maximum	Score per row at or above 10^{-7}	Rows / sum of weights, mean	Accepted replicates (first 150) with score per row at or above 10^{-7}
S3b row 025	135	6.35e-8 to 9.95e-8	135 of 135	0.632	0 of 150
S3b row 046	111	6.32e-8 to 9.95e-8	111 of 111	0.632	0 of 150
S3b row 062	160	6.26e-8 to 9.98e-8	160 of 160	0.632	0 of 150
S3b row 045	244	6.30e-8 to 1.00e-7	244 of 244	0.632	0 of 150
S3b row 047	181	6.30e-8 to 1.00e-7	181 of 181	0.632	0 of 150
S3b row 049	2 (905 further replicates rejected for the eligibility defect)	6.75e-8 to 6.97e-8	2 of 2	0.635	0 of 93
S8 verification, fit with multiplicities	1	8.35e-8	1 of 1	0.631	0 of 150
S8 verification, fit with multiplicities and inverse-probability weights	222	1.13e-8 to 9.95e-8	222 of 222	0.112	0 of 150

The score is the maximum absolute gradient of the fitted replicate. The fitting routine stopped at a score per unit of total weight below 10^{-7} ; acceptance required a score per row with positive weight below 10^{-7} . In the verification analysis the weights are the multiplicity times the inverse verification probability (median 6.5, up to 21), so the number of rows is only 11% of the sum of weights, which explains the rejection of 22% of the replicates (223 of 1,000). The verification-association fit (1,000 valid) is unaffected, and point estimates (unit weights) are not affected.

Table S91. S18. Corrected bootstrap intervals for the association rows of S3b (post hoc)

S3b row	Analysis	Persons (cases / con- trols)	OR (Wald 95% CI)	Original run: valid repli- cates, boot- strap	Corrected: valid repli- cates	Corrected OR bootstrap 95% CI	AUC incre- ment (boot- strap 95% CI)
006	Right-ventricular dysfunction, main model	7,620 (771 / 6,849)	1.711 (1.545-1.895)	909; not estimable	1,000	1.553-1.893	0.0230 (0.0139-0.0325)
015	Same analysis as row 006 in the B4/B3 comparison	7,620 (771 / 6,849)	1.711 (1.545-1.895)	909; not estimable	1,000	1.553-1.893	0.0230 (0.0139-0.0325)
021	LVEF $\leq 40\%$ against LVH or LVEF $\geq 50\%$	2,618 (1,076 / 1,542)	2.028 (1.782-2.307)	915; not estimable	1,000	1.788-2.312	0.0227 (0.0151-0.0322)
025	LVEF $< 40\%$, QRS < 120 ms without block	6,104 (329 / 5,775)	2.395 (2.039-2.813)	865; not estimable	1,000	2.036-2.811	0.0383 (0.0249-0.0515)
027	LVEF $< 40\%$, age < 65 years	3,739 (251 / 3,488)	2.673 (2.199-3.248)	881; not estimable	1,000	2.200-3.261	0.0376 (0.0233-0.0518)
029	LVEF $< 40\%$, female	3,872 (243 / 3,629)	2.372 (1.968-2.859)	935; not estimable	1,000	1.978-2.852	0.0439 (0.0269-0.0608)
045	Cardiomyopathy code, QRS < 120 ms without block	13,872 (193 / 13,679)	2.15 (1.79-2.58)	754; not estimable	1,000	1.79-2.62	0.0309 (0.0163-0.0501)
046	Cardiomyopathy code, sinus selector	15,905 (278 / 15,627)	2.108 (1.795-2.477)	889; not estimable	1,000	1.777-2.480	0.0252 (0.0136-0.0381)
047	Cardiomyopathy code, age < 65 years	9,619 (185 / 9,434)	2.16 (1.79-2.60)	815; not estimable	1,000	1.78-2.59	0.0255 (0.0128-0.0390)
049	Cardiomyopathy code, female	8,851 (145 / 8,706)	2.23 (1.81-2.76)	93; not estimable	1,000	1.800-2.769	0.0349 (0.0168-0.0593)
062	Right-ventricular dysfunction, male	4,067 (469 / 3,598)	1.649 (1.448-1.878)	840; not estimable	1,000	1.453-1.885	0.0223 (0.0124-0.0342)

Rows 006 and 015 are one analysis shown twice in S3b. All corrected intervals exclude 1. Wald intervals are those of S3 and are unchanged.

Table S92. S18. Corrected bootstrap intervals for post hoc branches of S15 (1,000 of 1,000 valid in every row)

Table / branch	Persons (cases / controls)	OR (Wald 95% CI)	Original run	Corrected OR bootstrap 95% CI	AUC increment, point (bootstrap 95% CI)
S75 LVEF, no QTc, extended set	about 8,720 (about 840 / about 7,870)	2.267 (2.035-2.526)	500 replicates; interval not available	2.039-2.530	0.0313 (0.0236-0.0397)
S75 LVEF, no QTc, common set	8,371 (800 / 7,571)	2.281 (2.039-2.552)	same	2.058-2.562	0.0311 (0.0235-0.0400)
S75 LVEF, missing indicators, extended set	8,906 (873 / 8,033)	2.307 (2.071-2.570)	same	2.084-2.577	0.0317 (0.0245-0.0398)
S75 Cardiomyopathy, no QTc, extended set	about 18,780 (about 460 / about 18,320)	2.029 (1.801-2.285)	same	1.805-2.274	0.0291 (0.0193-0.0396)
S75 Cardiomyopathy, no QTc, common set	18,170 (433 / 17,737)	1.986 (1.757-2.246)	same	1.758-2.237	0.0251 (0.0162-0.0350)
S75 Cardiomyopathy, missing indicators, extended set	19,106 (476 / 18,630)	2.027 (1.803-2.280)	same	1.802-2.281	0.0277 (0.0189-0.0370)
S81 LVEF, representative-beat distance	>8,360 (>790 / >7,560)	2.345 (2.095-2.625)	same	2.109-2.632	0.0327 (0.0248-0.0413)
S81 LVEF, beat-median distance	>8,360 (>790 / >7,560)	2.331 (2.088-2.602)	same	2.108-2.626	0.0329 (0.0250-0.0417)
S81 Cardiomyopathy, representative-beat distance	18,041 (>420 / >17,600)	2.053 (1.813-2.325)	same	1.809-2.329	0.0265 (0.0178-0.0364)
S81 Cardiomyopathy, beat-median distance	18,041 (>420 / >17,600)	2.039 (1.802-2.308)	same	1.803-2.313	0.0267 (0.0176-0.0362)
S82 LVEF, right-bundle pattern	791 (146 / 645)	2.437 (1.845-3.218)	96 of 1,000 valid; interval not available	1.905-3.391	0.0579 (0.0294-0.0884)

Table S93. S18. Covariate-standardized probabilities by marker quartile with corrected bootstrap intervals (post hoc; replaces the missing intervals of Table S80)

Endpoint	Q1	Q2	Q3	Q4	Q4 minus Q1
LVEF <40%	0.0279 (0.0229-0.0336)	0.0429 (0.0372-0.0489)	0.0709 (0.0649-0.0768)	0.1692 (0.1521-0.1879)	0.1413 (0.1208-0.1630)
Cardiomyopathy code	0.0075 (0.0060-0.0093)	0.0108 (0.0092-0.0127)	0.0163 (0.0145-0.0183)	0.0357 (0.0311-0.0407)	0.0282 (0.0231-0.0339)

Table S94. S18. Denominators of the multiple imputation in S15e (reconstructed post hoc)

Endpoint	Reference valid, persons (cases / controls)	Multiple-imputation set (marker and angle known)	Complete cases (all five covariates)	Persons with imputed covariates
LVEF <40%	9,374 (969 / 8,405)	8,906 (873 / 8,033)	8,371 (800 / 7,571)	535 (73 / 462)
Cardiomyopathy code	19,817 (515 / 19,302)	19,106 (476 / 18,630)	18,170 (433 / 17,737)	936 (43 / 893)

Counts of missing covariate values in the imputation set are not shown, to avoid small-cell disclosure by subtraction. Age, sex and QRS duration had no missing values in either set.

S19. Extended bivariate scenario set, differential and persistent error

This section extends S13k. Everything here is post hoc and uses training and internal validation only. The grid is an assumed scenario set. Repeatability, agreement after resampling of the same recording, and technical accuracy are different quantities, and the repeat differences contain physiological change. Notation: R_A is the reliability of the integral angle and R_F that of the Fréchet distance in the outcome set; ρ is the correlation of the two errors. A setting is admissible only if the latent residual covariance is positive definite.

Anchors. The repeat-based anchors are P_all (error from all 13,029 repeat pairs), P_sim (289 simultaneous pairs), EF_mix (error by LVEF group of the pairs of persons with an echo reference, weighted by the case mix of the outcome set) and EF_pool (the same pairs with pooled error). Three comparison anchors were specified in an addendum after the point values of the main anchors were known: N0 (no error correction), I_all (assumed 0.617 / 0.837 / 0.268 for R_A / R_F / ρ , intraclass correlations of all pairs) and I_tech (assumed 0.746 / 0.977 / 0.268, technical agreement of the 500 and 250 Hz versions of one recording). The protocol was dated and checksummed locally before the point run; the addendum was dated and checksummed locally after the point values of the main anchors had been seen. In each of 1,000 person-bootstrap replicates (fold-specific seeds), the outcome set and the repeat pairs were redrawn together and R_A, R_F and ρ were re-estimated.

Table S95. S19. Repeat-based anchors with population uncertainty

Anchor (fold)	R_A (95% CI)	R_F (95% CI)	ρ (95% CI)	Corrected OR, point	Corrected OR over admissible replicates, 2.5th / 50th percentile	Inadmissible replicates	Replicates with OR <1.25	Admissibility limit of R_A, 2.5th-97.5th percentile
P_all (training)	0.599 (0.583-0.613)	0.827 (0.817-0.837)	0.268 (0.245-0.290)	8.74	5.03 / 8.81	0%	0%	0.534-0.564
P_all (validation)	0.601 (0.585-0.616)	0.827 (0.816-0.838)	0.268 (0.245-0.290)	9.26	3.75 / 9.67	0%	0%	0.527-0.570
P_sim (training)	0.602 (0.512-0.688)	0.863 (0.806-0.913)	0.329 (0.188-0.450)	3.59	2.38 / 3.64	3.8%	0.4%	0.461-0.564
P_sim (validation)	0.604 (0.515-0.691)	0.863 (0.805-0.913)	0.329 (0.190-0.448)	3.72	2.03 / 3.71	3.0%	0.4%	0.456-0.562
EF_mix (training)	0.583 (0.564-0.601)	0.820 (0.806-0.832)	0.259 (0.231-0.286)	25.8	7.21 / 25.1	1.4%	0%	0.539-0.573
EF_mix (validation)	0.585 (0.566-0.604)	0.819 (0.806-0.832)	0.259 (0.232-0.287)	27.5	4.94 / 27.5	2.5%	0%	0.533-0.579
EF_pool (training)	0.581 (0.562-0.600)	0.821 (0.808-0.833)	0.255 (0.228-0.283)	32.5	7.78 / 31.6	2.2%	0%	0.540-0.573
EF_pool (validation)	0.583 (0.564-0.602)	0.821 (0.808-0.833)	0.255 (0.229-0.281)	35.4	5.05 / 34.8	4.4%	0%	0.534-0.581

The upper quantiles of the corrected OR scatter over several orders of magnitude because the latent covariance is close to singular (smallest eigenvalue 0.014 to 0.028; partial latent correlation 0.94 to 0.97). The corrected ORs of 8.7 to 9.3 (25.8 to 27.5 with LVEF-specific error) are therefore singularity effects, not effect estimates. The population intervals of R_A at P_all and EF_mix reach 0.56 and cover the group-specific anchors; the point values lie 0.03 to 0.05 above the admissibility limit. P_sim rests on only 289 and 277 simultaneous pairs. When R_A was lowered at the anchors P_all, EF_mix and EF_pool, the admissibility limit was reached before a crossing of 1.25 in 986 to 1,000 of 1,000 replicates, so a tipping-point interval is not estimable there (P_sim: 367 and 266 of 1,000 replicates crossed).

Extended grid. The extended grid crossed R_A 0.40 to 0.80 (41 values, step 0.01) with R_F 0.60 to 1.00 (9 values) and ρ -0.4 to 0.8 (13 values): 4,797 cells per fold, of which 2,438 (training) and 2,437 (validation) were admissible. The corrected point OR was below 1.25 in 86 (training) and 67 (validation) admissible cells; the highest R_A among them was 0.54 (training) and 0.52 (validation), at

R_F 0.75 to 0.95, and with R_F ≥ 0.8 and $\rho \leq 0.4$ there were 9 and 4 such cells. With an error-free marker (R_F 1.0), the point estimate was 1.30 at R_A 0.57 (20% of replicates inadmissible there) and 2.07 at R_A 0.58 (training; 2.5th percentile 0.26). In the 225 cells per fold with R_A 0.55 to 0.70, R_F ≥ 0.8 and ρ 0.2 to 0.4, the smallest point OR was 1.30 (training) and 2.00 (validation); no cell fell below 1.25.

Table S96. S19. Scenario boxes spanned by the 95% intervals of the three anchor quantities ($5 \times 5 \times 5$ grid)

Anchor (fold)	Box R_A / R_F / ρ	Smallest OR in the box (point)	Smallest OR over replicates, 2.5th / 50th / 97.5th percentile	Replicates with smallest OR <1.25	Inadmissible grid points (point)
P_all (training)	0.583-0.613 / 0.817-0.837 / 0.245-0.290	5.24	3.83 / 5.25 / 7.37	0%	0%
EF_mix (training)	0.564-0.601 / 0.806-0.832 / 0.231-0.286	6.26	4.21 / 6.27 / 9.90	0%	6.4%
P_all (validation)	0.585-0.616 / 0.816-0.838 / 0.245-0.290	5.32	2.97 / 5.34 / 10.39	0%	0%
EF_mix (validation)	0.566-0.604 / 0.806-0.832 / 0.232-0.287	6.48	3.29 / 6.53 / 16.20	0.2%	4.0%

Differential error in cases. The observed difference between cases and controls in the measured values was 1.275 (training) and 1.235 (validation) control SD for the marker and 0.889 and 0.861 for the angle. A control SD of the marker is about 0.93 development SD (separation 1.275 against 1.182 in training, 1.235 against 1.155 in validation), so 0.15 to 0.20 control SD correspond to 0.14 to 0.19 development SD. We shifted the measured marker (and, separately, the angle) in cases by b control SD, re-estimated the regression calibration with group-specific means and located the shift at which the corrected OR first reached 1.25 (attenuation) and 1.0 (removal of the association; Table S97). A shift of the angle alone did not push the corrected OR below 1.25 at any anchor up to 2.0 control SD.

Table S97. S19. Systematic over-measurement of the marker in cases at which the corrected OR reaches 1.25 or 1.0 (control SD)

Anchor	OR 1.25, training (95% bootstrap CI)	Share of the observed difference	OR 1.25, validation (95% bootstrap CI)	OR 1.0, training / validation	Training: joint shift of marker and angle for OR 1.25 (share of both differences)
P_all	0.175 (0.126-0.223)	0.137 (0.098-0.175)	0.182 (0.099-0.270)	0.194 / 0.201	0.968 (0.857-1.143)
EF_mix	0.152 (0.103-0.203)	0.119 (0.080-0.159)	0.163 (0.079-0.256)	0.162 / 0.173	1.116 (0.931-1.386)
I_all	0.195 (0.151-0.241)	0.153 (0.119-0.187)	0.197 (0.119-0.280)	0.222 / 0.223	0.873 (0.807-0.948)
I_tech	0.254 (0.217-0.291)	0.199 (0.171-0.227)	0.245 (0.179-0.318)	0.332 / 0.323	0.622 (0.581-0.664)
N0 (no correction)	0.378 (0.342-0.413)	0.296 (0.275-0.318)	0.353 (0.294-0.419)	0.493 / 0.469	0.530 (0.502-0.557)

At the two repeat-based anchors and the anchor with assumed intraclass correlations of all pairs, a marker over-measurement in cases of 0.15 to 0.20 control SD (12% to 16% of the observed difference) lowered the corrected OR to 1.25, and 0.16 to 0.22 control SD to 1.0. At the assumed technical-agreement anchor (I_tech) it took about 0.25 control SD (20%) and 0.32 to 0.33 for 1.0.

Without error correction the shifts were 0.35 to 0.38 control SD (29% to 30%) for 1.25 and 0.47 to 0.49 for 1.0 (38% to 39%). Attenuation to 1.25 is not a null association, and the shifts for 1.0 are larger. This is the most vulnerable point of the analysis, and it is a scenario, not a measured error.

Larger error variance in cases and persistent error. At the anchor EF_mix, the error variance of cases was multiplied by κ (angle only, marker only, both). The admissibility limit was reached before any crossing of 1.25 at κ of 1.55 (95% CI 1.12-2.07), 3.88 (1.74-6.09) and 1.48 (1.10-1.96) in training, and 1.62 (1.09-2.28), 4.20 (1.55-7.20) and 1.55 (1.07-2.15) in validation. A crossing below 1.25 before the limit occurred in 0 (training) and in 9, 0 and 2 (validation) of 1,000 replicates. A persistent error share π (an additional error of π times the reliable variance that repeat differences do not show) made the correction inadmissible at small values.

Table S98. S19. Persistent error share at which the limit of admissibility is reached before the corrected OR crosses 1.25 (training)

Anchor	π , angle only	π , marker only	π , both equally
P_all	0.07	0.07	0.03 (error correlation 0) to 0.05
EF_mix	0.04	0.04	0.02
I_all	0.10	0.10	0.05 to 0.07
I_tech	crossing at 0.252 (636 of 1,000 replicates; limit 0.26)	limit 0.26	limit 0.14 to 0.20
N0	limit 0.43 (476 of 1,000 replicates cross before)	limit 0.40	limit 0.25

The model with the repeat-based error covariance is therefore no longer compatible with the observed covariance of angle and marker once a few hundredths of the variance are added as persistent or case-specific error. Two explanations remain open and the data do not separate them: near-complete latent collinearity of angle and marker, or an overestimate of the error by repeat differences. This is neither a tipping nor a reassurance.

Anchor from the only quantified mechanism. The delineation applies millivolt floors, so gain affects the measured angle. In about 385 development ECGs with uniform gain changes of +1%, +3% and +5%, the mean signed change of the angle was 0.0075, 0.0008 and 0.0148 development SD (95% interval -0.012 to 0.042) and that of the marker -0.0003, -0.0020 and -0.0042 SD (95% interval -0.012 to 0.003). The gain problem produced mainly noise (root-mean-square angle change 0.12 to 0.27 SD), not a mean shift. The anchor lies more than an order of magnitude below the tipping shifts of the marker (0.15 to 0.38 control SD). It says nothing about other differential mechanisms, for example devices or delineation error that depends on LVEF.

S20. Repeat error by ejection fraction group and QRS amplitude

Repeat pairs were clinical repeats within two hours. Set S_B contains all pairs of persons with an echo reference (9,423 pairs, 6,089 persons; 1,479 pairs from 952 persons with LVEF <40%); set S_A contains the first pair of each person, aligned with the index recording of the reference (1,308 pairs; 231 with LVEF <40%). Pairs of S_B assume that LVEF was stable between the reference and

the repeat recordings, which blurs differences towards null. Intervals are person-bootstrap percentile intervals (1,000 replicates, all valid). The Fréchet distance is expressed in development SD.

Table S99. S20. Repeat error by LVEF group

Set	Group	Pairs	SD of angle differences, degrees (95% CI)	Angle ICC (95% CI)	SD of Fréchet differences (95% CI)	Fréchet ICC (95% CI)	Error correlation (95% CI)
S_A	LVEF <40%	231	43.2 (37.2-48.8)	0.531 (0.411-0.644)	0.506 (0.429-0.578)	0.849 (0.798-0.895)	0.173 (0.039-0.295)
S_A	LVEF ≥40%	1,077	41.0 (38.4-43.2)	0.605 (0.559-0.653)	0.588 (0.533-0.647)	0.807 (0.766-0.843)	0.336 (0.260-0.404)
S_B	LVEF <40%	1,479	44.0 (41.7-46.2)	0.505 (0.453-0.553)	0.561 (0.522-0.598)	0.817 (0.788-0.844)	0.189 (0.129-0.255)
S_B	LVEF ≥40%	7,944	42.6 (41.6-43.6)	0.599 (0.578-0.617)	0.605 (0.585-0.628)	0.818 (0.805-0.831)	0.266 (0.238-0.297)

Ratio of the SD of differences, low to higher LVEF: angle 1.031 (0.975-1.087) in S_B and 1.055 (0.901-1.208) in S_A; Fréchet distance 0.926 (0.855-0.999) in S_B and 0.860 (0.708-1.014) in S_A (log scale 0.835, 0.768-0.908, and 0.779, 0.647-0.916). Adjustment for the amplitude quintile changed the ratios by at most 2%. The ICC difference of the angle (low minus higher LVEF) was -0.094 (-0.147 to -0.042) in S_B; the reason is the smaller spread of the angle between persons with low LVEF (roughly 31 against 37 degrees), not larger error. The Fréchet ICC did not differ (-0.001, -0.033 to 0.028).

Table S100. S20. Repeat error by quintile of the spatial QRS peak magnitude (12,905 pairs, 2,581 per quintile; cut points 819, 1,024, 1,241 and 1,543 μ V)

Quintile	SD of angle differences, degrees (95% CI)	Angle ICC (95% CI)	SD of Fréchet differences (95% CI)	Fréchet ICC (95% CI)
Q1 (lowest)	44.7 (43.1-46.2)	0.483 (0.450-0.519)	0.521 (0.491-0.550)	0.779 (0.754-0.803)
Q2	41.1 (39.5-42.6)	0.590 (0.558-0.622)	0.568 (0.537-0.601)	0.804 (0.780-0.824)
Q3	40.2 (38.6-41.8)	0.637 (0.607-0.666)	0.586 (0.552-0.619)	0.830 (0.812-0.849)
Q4	40.9 (39.3-42.5)	0.656 (0.629-0.683)	0.623 (0.586-0.661)	0.841 (0.821-0.859)
Q5 (highest)	41.8 (39.9-43.8)	0.662 (0.630-0.692)	0.599 (0.557-0.639)	0.873 (0.855-0.891)

The ratio of the angle error between the lowest and highest quintile was 1.07 (1.01-1.13) and that of the Fréchet error 0.87 (0.80-0.95). The mean log amplitude differed little between the LVEF groups (7.002 against 7.017 in $\ln \mu$ V). Similar repeat differences by LVEF do not exclude a persistent bias that depends on LVEF, because repeats cannot show persistent error and contain physiological change.

S21. Missing marker values: delta-adjusted imputation and tipping points

Failure of the delineation or of other covariates was more frequent in cases than in controls. In development, basic-model data were incomplete in 15.4% of cases (488 of 3,178) and 10.8% of controls (2,758 of 25,521) in training and in 18.3% (191 of 1,044) and 11.4% (985 of 8,650) in validation; the assessment partition had 17.44% against 9.92% (S15a). The Fréchet distance was missing in 9.9% (315) and 10.8% (113) of cases and 5.6% (1,429) and 5.9% (513) of controls (training and validation). Where other covariates were missing, the available Fréchet values were higher in

controls than in complete controls (standardized difference 0.30 in training, 0.21 in validation) but not in cases.

Method. Within each outcome class, a multivariate normal model on transformed scales (age, sex, log heart rate, log QRS duration, log QTc, logit angle, log1p Fréchet distance) imputed missing values (100 imputations per fold; EM on a bootstrap sample for each imputation; all converged), and results were pooled with Rubin's rules. Only the imputed Fréchet entries were then shifted by δ development SD, which corresponds to delta-adjusted controlled imputation (reference 41 of the manuscript). Pooled ORs at $\delta = 0$ were 2.44 (2.30-2.59; complete cases 2.48) in training and 2.38 (2.14-2.64; 2.39) in validation. Paths were: cases shifted down alone, controls shifted up alone, and opposite shifts (cases down, controls up). Named models were V0 constant shift; V1 and V2 shift plus spread of the imputed values multiplied by 1.5 and 2 around the class mean; V3 and V4 shift proportional to age or QRS duration; V5 shift of the angle alone; V6 shift of angle and marker; V7 and V8 shift restricted to the missing pattern "angle and marker" or "marker only". QRS amplitude is missing precisely where the delineation fails and could not serve as a covariate, and a quality flag was not available, so quality is not separated from delineation failure. The observed case-control separation of the marker (d_CC) was 1.182 (training) and 1.155 (validation) development SD.

Table S101. S21. Imputed marker values

Fold	Cases: imputed Fréchet values (also missing angle / marker only)	Controls: imputed Fréchet values (also missing angle / marker only)
Training	315 (284 / 31)	1,429 (1,201 / 228)
Validation	113 (98 / 15)	513 (427 / 86)

Table S102. S21. Shift (development SD) of imputed marker values at which the pooled OR reaches 1.25; multiples of the observed separation in brackets; "not reached" means within 8 SD (pooled OR at 8 SD in brackets)

Model	Pooled OR at $\delta = 0$ (training / validation)	Opposite shift, training	Opposite shift, validation	Controls only, training	Controls only, validation	Cases only, training	Cases only, validation
V0 constant shift	2.44 / 2.38	1.80 (1.64-1.97) [1.5×]	1.64 (1.38-1.93) [1.4×]	3.16 (2.88-3.45) [2.7×]	3.03 (2.55-3.54) [2.6×]	not reached (1.27)	3.40 (2.52 to not reached)
V1 spread × 1.5	2.12 / 2.08	1.61 (1.43-1.80) [1.4×]	1.47 (1.17-1.78) [1.3×]	2.78 (2.48-3.08)	2.66 (2.15-3.20)	4.52	3.23
V2 spread × 2	1.83 / 1.80	1.39 (1.19-1.60) [1.2×]	1.26 (0.92-1.62) [1.1×]	2.33 (2.00-2.66) [2.0×]	2.23 (1.65-2.81) [1.9×]	3.74 (2.89-5.21)	2.91
V3 age-proportional	2.44 / 2.38	1.78 (1.62-1.95)	1.62 (1.35-1.90)	3.06	2.91	not reached (1.27)	3.56
V4 QRS-proportional	2.44 / 2.38	1.72 (1.56-1.88)	1.59 (1.33-1.87)	2.86	2.78	not reached (1.27)	3.49
V5 angle only	2.44 / 2.38	not reached (3.07)	not reached (3.01)	not reached (2.64)	not reached (2.57)	not reached (2.95)	not reached (2.90)
V6 angle and marker	2.44 / 2.38	2.84 (2.60-3.09) [2.4×]	2.62 (2.22-3.06) [2.3×]	3.48	3.42	not reached (1.66)	not reached (1.55)
V7 pattern "angle and marker"	2.44 / 2.38	2.01 (1.82-2.20) [1.7×]	1.86 (1.55-2.19) [1.6×]	3.46	3.28	not reached (1.33)	not reached (1.27)
V8 pattern "marker only"	2.44 / 2.38	not reached (1.32)	not reached (1.29)	not reached (1.34)	not reached (1.33)	not reached (2.27)	not reached (2.14)

Intervals are the shifts at which the lower and the upper Rubin limit reach the target. For a target OR of 1.0, the opposite-shift tipping points were 2.93 (2.62-3.33) and 2.60 (2.17-3.21) SD in V0 and 2.85 and 2.55 in V2; controls alone required 5.4 to 7.4 SD across models, and cases alone did not reach it. The complete grid shows that at an opposite shift of 4 SD, 12% to 14% of the imputed Fréchet values reach the lower bound zero. Monte Carlo halves of the imputations differed in the tipping points by at most 0.01 SD.

Reading. Covariate dependence of the shift (V3, V4), shifts of the angle alone (V5) and shifts confined to part of the missing pattern (V7, V8) did not bring the tipping points closer to the observed separation. The only variation that did was a larger spread of the imputed values (V2): the opposite-shift tipping point was 1.2 and 1.1 times the observed separation, with an interval reaching 0.92 SD, below the observed 1.16. Setting all imputed Fréchet values of cases to zero left the OR at 1.27 (training) and 1.19 (validation). A shift equal to the full observed separation left the pooled OR at 1.55 (1.47-1.64) and 1.49 (1.36-1.65); this is a constant shift, not an exchange of the conditional distributions of cases and controls. Attenuation of the pooled OR to 1.25 is not a null association; removal (OR 1.0) required larger shifts, 2.60 to 2.93 SD for opposite shifts in V0 and 6.27 to 6.52 SD for controls alone. The observed separation does not bound the values of unmeasured markers, and no plausibility is asserted for any tipping point. The scenarios change one mechanism at a time and do not bound combinations of biases. The imputation model used the model covariates only, and the delta adjustment explores a location shift, not a change of the marker-outcome relation among those with missing values.

S22. Echo verification: populations, selection factor and feasibility scenarios

This section examines selection on the outcome as a scenario analysis. LVEF is unobserved in unverified persons, so the selection mechanism cannot be estimated; the analysis states which selection factor would be needed to attenuate or remove the association and which values are feasible under explicit assumptions. Certain restrictive selection models are incompatible with a complete explanation by selection, but selection could not be excluded in general; the limits below are model-dependent feasibility limits, not empirically identified ones.

Populations. Two populations are used and must not be mixed.

1. The index population of the main analysis. For every development person it contains one index ECG by the rule of the main analysis: the first verified ECG for persons with a verified echocardiogram (reference-eligible), and the first non-excluded ECG for persons never verified (129,198 persons; 38,393 verified and 90,805 never verified). The OR of 2.480 and 2.392 arises in this population, and the selection factor and its feasibility are examined here. Among the persons with complete design, 28.7% (training) and 28.6% (validation) were verified (Table S120).
2. The first technically successful ECG of each person (Table S103). Of all persons, 18.7% had an echocardiogram within ± 30 days, and of those with complete model data 18.0% (train-

ing) and 17.9% (validation). This population underlies the weighted verification analysis (S8, S15d) and earlier versions of this section. For 38.8% of the verified persons (14,876 of 38,350 with both rows) the first technical ECG differs from the index ECG of the main analysis.

The verified share therefore depends on the population: 28.7% on the index population against 18.0% on the first technical ECG. Statements on selection factors refer to the index population.

Table S103. S22. First technically successful ECG: population of the weighted verification analysis

Fold	Persons with first technical ECG	Verified within ± 30 days, all persons	Basic model and marker complete	Verified among complete persons	Not verified, complete persons	Main LVEF set	Cases (LVEF <40%)
Training	96,418	18,012 (18.7%)	89,477	16,104 (18.0%)	73,373	25,453	2,690
Validation	32,494	6,054 (18.6%)	30,096	5,388 (17.9%)	24,708	8,518	853

On this population the marker separated verified from unverified persons (standardized mean difference 0.53 in training and 0.56 in validation; AUC 0.65), and after adjustment for the basic model its OR for verification was 1.47 (1.43-1.52) in training and 1.54 (1.46-1.62) in validation (1.59 in the assessment partition, S8). The proportion verified by marker quintile (persons with complete data) was 10.0%, 12.8%, 14.9%, 20.2% and 32.0% in training and 9.3%, 12.7%, 15.7%, 19.1% and 32.9% in validation.

Table S120. S22. Index population of the main analysis (persons with complete design)

Fold	Persons	Verified (index ECG is the first verified ECG; main LVEF set)	Not verified (first non-excluded ECG)	Verified share
Training	88,727	25,453	63,274	28.7%
Validation	29,779	8,518	21,261	28.6%

On the index population, a logistic verification model with the design of the main model including the marker gave a marker OR for verification of 1.53 (training) and 1.57 (validation) per SD, AUC 0.72 and 0.73, and fitted probabilities from 0.024 to 0.897. Calibration by decile and marker quintile deviated by at most 0.025 (training) and 0.023 (validation), most in the top decile (predicted 0.62, observed 0.59 in training). A more flexible model (squares of the continuous terms, marker by angle, marker by age) gave AUC 0.727 and 0.730, the same maximum deviation and probabilities up to 0.96.

Selection factor B. Let Y be low LVEF, X the marker (per development SD), Z the basic covariates and $S = 1$ verification, that is the analysis population. Let $s_y(x, z) = P(S=1 \mid Y=y, x, z)$ be the verification probabilities of controls ($y = 0$) and cases ($y = 1$), in which unobserved influences are averaged out, and $\lambda(x, z) = s_1 / s_0$. By Bayes' rule, exactly, $\text{Odds}(Y=1 \mid x, z, S=1) = \text{Odds}(Y=1 \mid x, z) \times \lambda(x, z)$, and therefore, for the same covariate value z , $\text{OR}_S(x+1 : x \mid z) = \text{OR}_T(x+1 : x \mid z) \times \lambda(x+1, z) / \lambda(x, z)$, where S marks the verified and T the target population. No rarity assumption is needed. The assumptions for the relation between estimated coefficients are:

- (A2) The observed model has a common marker slope, $\text{logit } P(Y=1 \mid x, z, S=1) = \alpha_S(z) + \beta_S x$. If $\ln \lambda = a(z) + x \ln B$, the target population has $\text{logit } P(Y=1 \mid x, z) = (\alpha_S(z) - a(z)) + (\beta_S - \ln B) x$. The relation $OR_{\text{true}} = OR_{\text{observed}} / B$ holds for the estimated coefficients if $a(z)$ is represented in the covariate function of the main model or is constant; otherwise the target population has a different covariate function and the marker slopes are comparable only conditionally.
- (A3) $\ln \lambda$ is linear in x with a common slope $\ln B$ over the range considered.
- (A4) Positivity (defined for exposure groups in reference 43 of the manuscript; here applied to verification probabilities): $0 < s_0(x, z)$ and $0 < s_1(x, z) \leq 1$ for all (x, z) considered, and $P(S=1 \mid x, z) > 0$.

$B = \lambda(x+1, z) / \lambda(x, z)$ is the factor by which the relative rise of the verification probability per marker SD is larger in cases than in controls. For a dichotomized marker, $OR_{\text{true}} = OR_{\text{observed}} \times \lambda_{\text{low}} / \lambda_{\text{high}}$. Verification that depends on the outcome alone or on the marker alone does not change B . No statement is made about a weighted average of local slopes: if A2 or A3 fail, the ratio of the slopes is not given by B in general. B is not the exponential of an interaction on the logit scale of verification: in synthetic data with an interaction of $\ln 2$ on that scale, B was 1.94, 1.69 and 1.45 at baseline verification probabilities of about 0.02, 0.12 and 0.27, and the two agree only when verification probabilities are small, which they are not here (up to 0.90). The relation was confirmed in 4 million synthetic observations (true OR 2.0; observed ORs 2.01 and 1.99 at $B = 1$, 2.99 and 3.04 at $B = 1.5$, 4.00 and 4.01 at $B = 2$, 6.05 at $B = 3$, at verification probabilities of controls of 0.03 and 0.10).

Non-collapsibility. The ORs are conditional on the covariates. The feasibility calculation below therefore works per person with the person's own (x, z) ; it does not combine standardized (marginal) verification probabilities with an adjusted OR.

Not estimable. B itself, and the verification probabilities of cases and controls separately, cannot be estimated, because Y is observed only where $S = 1$. Two quantities can be estimated on the index population with the design of the main model including the marker: $q(x, z) = P(Y=1 \mid x, z, S=1)$ from the main model and $P_m(x, z) = P(S=1 \mid x, z)$ from the verification model above.

Tipping values. The observed OR was 2.480 (2.331-2.639) in training and 2.392 (2.138-2.676) in validation. The OR reaches a target when B equals the observed OR divided by the target; Table S104 therefore shows the OR divided by B . Intervals are sampling uncertainty of the observed OR only.

Table S104. S22. Corrected OR for assumed selection factors B per marker SD

B	0.5	0.8	1	1.25	1.5	2	3	4	5
Training	4.96	3.10	2.48	1.98	1.65	1.24	0.83	0.62	0.50
Validation	4.78	2.99	2.39	1.91	1.59	1.20	0.80	0.60	0.48

The OR reached 1.25 (attenuation) at B of 1.98 (1.86-2.11) in training and 1.91 (1.71-2.14) in validation, and 1.0 (removal of the association) at 2.48 (2.33-2.64) and 2.39 (2.14-2.68). With the marker dichotomized at the median of controls, the adjusted OR was 3.32 (2.88-3.84) in training and 4.42 (3.35-5.84) in validation, and the ratio of λ between high and low marker would have to be about 2.7 and 3.5 to reach 1.25.

Feasibility of B (scenario calculation). Exactly, $s_1 = P_m (q + \lambda (1 - q))$, $s_0 = P_m ((1 - q) + q / \lambda)$ and $P(Y=1 | x, z) = q / (q + \lambda (1 - q))$. Positivity (A4) requires for each person $\lambda_{\min} = q P_m / (1 - P_m (1 - q)) \leq \lambda \leq \lambda_{\max} = (1 / P_m - q) / (1 - q)$; $\lambda = 1$ is always feasible. No assumption about the prevalence in the target population is needed. The median limits were $\lambda_{\max}$ 3.9 (5th to 95th percentile 1.9 to 14) and $\lambda_{\min}$ 0.009. The joint model $\ln \lambda_i = a(z_i) + x_i \ln B$ turns these limits into constraints that are linear in the coefficients of $a(z)$ and $\ln B$, and a linear program gives the smallest and largest feasible B. The variants were: a constant or linear in the seven covariate terms of the main model; positivity only or additionally $\lambda \geq 1$ (cases never verified less often than controls); all persons or only the central marker interval (5th to 95th percentile, -1.39 to 1.52 SD in training). Intervals in brackets are the 2.5th to 97.5th percentile of the largest feasible B over 100 bootstrap replicates per variant and fold (all valid, all programs optimal); they reflect the estimation of q and P_m , not the choice of model.

Table S110. S22. Feasible interval for B (point; bootstrap range of the maximum in brackets) against the tipping values (OR 1.25: 1.98 training, 1.91 validation; OR 1.0: 2.48 and 2.39)

Variant	Training	Validation
All persons, a constant, positivity only	0.87 to 1.30 (1.27 to 1.35)	0.84 to 1.23 (1.20 to 1.50)
All persons, a constant, $\lambda \geq 1$	0.92 to 1.09	0.90 to 1.07
All persons, a linear in z, positivity only	0.79 to 1.78 (1.71 to 1.92)	0.79 to 1.76 (1.69 to 2.03)
All persons, a linear in z, $\lambda \geq 1$	0.84 to 1.10	0.84 to 1.09
Central 90%, a constant, positivity only	0.76 to 1.49	0.69 to 1.43
Central 90%, a constant, $\lambda \geq 1$	0.85 to 1.13	0.83 to 1.14
Central 90%, a linear in z, positivity only	0.71 to 2.09 (1.99 to 2.48)	0.61 to 2.80 (2.51 to 3.26)
Central 90%, a linear in z, $\lambda \geq 1$	0.80 to 1.16	0.76 to 1.16
Flexible verification model: all persons, a constant	0.93 to 1.14 (1.10 to 1.41)	0.95 to 1.14 (1.09 to 1.55)
Flexible verification model: all persons, a linear in z	0.86 to 1.48 (1.38 to 1.74)	0.88 to 1.36 (1.29 to 1.92)
Flexible verification model: central 90%, a linear in z	0.82 to 1.66 (1.61 to 2.16)	0.70 to 2.05 (1.73 to 2.75)

Share of bootstrap replicates in which the largest feasible B reaches the tipping value (OR 1.25 / OR 1.0): all persons with constant a, 0% / 0% in both folds; all persons with linear a(z), 0% / 0% in training and 13% / 0% in validation; central 90% with linear a(z), 97% / 3% in training and 100% / 100% in validation; flexible model, central 90% with linear a(z), 14% / 0% in training and 94% / 20% in validation.

Reading. If the level a of the verification ratios does not depend on the covariates, B is limited to 1.30 (training) and 1.23 (validation) over all persons and 1.49 and 1.43 over the central marker interval, and the tipping values for OR 1.25 and OR 1.0 are not reached over all persons in any

bootstrap replicate. If cases are never verified less often than controls ($\lambda \geq 1$), B is at most 1.16 in every variant, and the tipping values are not reachable. If the level may depend on the covariates linearly, the maximum over all persons is 1.78 and 1.76, just below the tipping value for OR 1.25 (1.98 and 1.91). If log-linearity is required only over the central 90% of marker values and $a(z)$ is linear, the maximum is 2.09 and 2.80, so that the tipping value for OR 1.25 is not excluded, and in validation neither is that for OR 1.0. Certain restrictive selection models are therefore incompatible with a complete explanation: a level independent of the covariates, $\lambda \geq 1$, and a level linear in the covariates over all persons all stay below both tipping values. The central variant allows an OR of 1.25 in both folds and an OR of 1.0 in validation only, and demonstrates no complete null association over the whole marker range. Selection could not be excluded in general. The limits are model-dependent feasibility limits at the observed covariate points, not empirically identified limits of the actual selection bias.

Limits of the calculation. (1) The verification model is not perfectly calibrated in its upper range (deviation up to 0.025), and the bounds depend on its tails; the flexible model gives narrower intervals. (2) The bootstrap intervals contain the estimation uncertainty of q and P_m , not the model choice. (3) There was no non-convergence; all programs were optimal and all bootstrap replicates valid. (4) Positivity holds by construction ($\lambda = 1$ is feasible; probabilities from 0.02 to 0.90, or 0.96 in the flexible model). (5) Only selection on (Y, x, z) among persons with complete design is considered; incomplete design is a further selection step (S15e). Any population-level diagnostic interpretation is excluded.

S23. Echo interval, pacing indicators, measurement method and code-negative controls

Echo interval. The distance between echo and ECG is negative when the echocardiogram preceded the ECG. The 7-day figure of the assessment partition (2.42) was reproduced.

Table S105. S23. OR per development SD by interval between ECG and echocardiogram (95% CI)

Set	≤1 day	≤7 days	≤14 days	≤30 days (main set)
Training, all	2.35 (2.14-2.58), n 9,013	2.43 (2.27-2.60), n 19,104	2.45 (2.29-2.61), n 21,810	2.48 (2.33-2.64), n 25,453
Training, echo before ECG	2.36 (1.77-3.14), 145 cases	2.20 (1.75-2.76), 202 cases	2.21 (1.78-2.73), 227 cases	2.43 (1.99-2.97), 254 cases
Training, echo after ECG	2.36 (2.14-2.60)	2.46 (2.29-2.64)	2.48 (2.31-2.65)	2.49 (2.33-2.66)
Validation, all	2.48 (2.10-2.92)	2.39 (2.12-2.70)	2.42 (2.16-2.72)	2.39 (2.14-2.68)
Validation, echo after ECG	2.33 (1.96-2.76)	2.31 (2.04-2.62)	2.37 (2.10-2.67)	2.31 (2.05-2.59)
Validation, echo before ECG	not estimable (fewer than 100 cases)	not estimable	not estimable	not estimable (89 cases)
Assessment, all	2.36 (2.00-2.77), n 3,000	2.42 (2.14-2.74), n 6,337	2.39 (2.12-2.69)	2.34 (2.09-2.62), n 8,371
Assessment, echo after ECG	2.39 (2.01-2.84)	2.45 (2.15-2.79)	2.41 (2.13-2.73)	2.35 (2.09-2.64)
Assessment, echo before ECG	not estimable	not estimable	not estimable	not estimable

The echocardiogram preceded the ECG in 12.7% (training), 13.5% (validation) and 12.7% (assessment) of the recordings. The AUC increment stayed between 0.019 and 0.039 in all estimable sets.

Pacing indicators (development). The rule was fixed before inspection: P, a machine-report text indicating pacing; D, a device code or procedure in the stay without such a report text (no timing relative to the ECG); U, no reliable information (no stay information); N, no indication. Pacing spikes in the signal were not evaluated because no detector checked on real examples was available, and the assessment partition has no pacing variable, so no exclusion was computed there.

Table S106. S23. Pacing indicators and the OR after exclusion (development, LVEF <40%)

Class	Training: persons (cases)	Share	Validation: persons (cases)	Share
P, report text	654 (232)	2.6%	234 (77)	2.7%
D, device only	1,619 (303)	6.4%	548 (88)	6.4%
U, no reliable information	12,675 (969)	49.8%	4,282 (319)	50.3%
N, no indication	10,505 (1,186)	41.3%	3,454 (369)	40.6%

Set	Training: OR (95% CI), AUC increment	Validation: OR (95% CI), AUC increment
All	2.48 (2.33-2.64), 0.033	2.39 (2.14-2.68), 0.032
Without P	2.53 (2.38-2.70), 0.035	2.44 (2.18-2.74), 0.032
Without P and D	2.61 (2.43-2.79), 0.036	2.49 (2.21-2.82), 0.033
Only N	2.52 (2.30-2.76), 0.044	2.32 (1.98-2.72), 0.031
Only P	1.39 (1.08-1.79), 0.008	not estimable (77 cases)
Only D	2.04 (1.70-2.45), 0.030	not estimable

Excluding probable pacing did not lower the OR. Among recordings with a report hint the association was weaker. About half of the recordings fall in class U, the report text does not capture all pacing, and the device indicator has no timing relative to the ECG, so secure exclusion of pacing remains unavailable.

Measurement method of LVEF. In training, 24,711 of 25,453 values were generic measurements (97.1%), 541 biplane and 201 three-dimensional; in validation 8,260 of 8,518 (97.0%), 184 biplane and 74 three-dimensional. The 742 non-generic values in training (74 cases) were too few for a separate estimate, and in validation the three-dimensional group is shown only coarsely.

Code-negative controls (development, cardiomyopathy code). Controls were compared with and without a diagnosis record. Thirty-five of 70,892 controls (0.05%) had no diagnosis row and none of the cases lacked one.

Table S107. S23. Controls with and without documented diagnoses

Analysis	Persons	Cases	Controls	OR per SD (Wald 95% CI)	OR (bootstrap 95% CI)	Apparent AUC increment
All controls	72,795	1,903	70,892	2.028 (1.909-2.155)	1.917-2.151	0.0248
Only controls with a diagnosis record	72,760	1,903	70,857	2.028 (1.909-2.155)	1.907-2.142	0.0248
Only controls with at least 7 diagnoses	52,430	1,903	50,527	1.951 (1.836-2.073)	1.842-2.065	0.0260

S24. Orientation comparators on identical persons

This analysis used development data (LVEF <40%, one ECG per person, the design of the basic model). The common sample of all blocks comprised 33,884 persons with 3,508 cases (87 persons with a non-finite block were lost). Blocks were added singly and together to the basic model: K_{ang} , the peak angle plus a restricted cubic spline of the integral angle (knots at 17, 58, 104 and 164 degrees); K_{axes} , sine and cosine of the azimuth and elevation of the QRS and T area vectors plus the log T area-vector magnitude; K_{svg} , the spatial ventricular gradient (log magnitude, sine and cosine of azimuth and elevation, angle to the QRS area vector); K_{tcrt} , total cosine R-to-T and T-morphology dispersion as implemented in the pipeline; K_{plan} , planarity of the T, QRS and QRS-T loops and the angle between the loop planes; K_{all} , all 24 added terms. The angle between the gradient and the T area vector was omitted because it is an exact linear function of the integral angle and the angle to the QRS area vector. The marker was scaled with the fixed development SD. Out-of-fold values come from a two-fold cross-fit (training to validation and reverse) with 1,000 person resamples of the pooled predictions.

Table S108. S24. OR of the Fréchet distance and its incremental AUC with orientation comparators

Block	OR, Wald (95% CI)	OR, bootstrap (95% CI)	Apparent AUC increment of the distance (95% CI)	Out-of-fold AUC increment (95% CI)	AUC gain of the block over the basic model
Basic model	2.458 (2.328-2.596)	2.310-2.610	0.0331 (0.0287-0.0373)	0.0331 (0.0290-0.0371)	0
K_{ang}	2.390 (2.249-2.540)	2.238-2.557	0.0224 (0.0189-0.0258)	0.0222 (0.0191-0.0253)	0.0105 (0.0083-0.0130)
K_{axes}	2.283 (2.139-2.437)	2.135-2.450	0.0184 (0.0154-0.0215)	0.0192 (0.0162-0.0219)	0.0201 (0.0174-0.0234)
K_{svg}	2.424 (2.281-2.576)	2.294-2.592	0.0222 (0.0190-0.0254)	0.0227 (0.0192-0.0259)	0.0131 (0.0105-0.0157)
K_{tcrt}	2.572 (2.433-2.719)	2.416-2.734	0.0340 (0.0298-0.0380)	0.0342 (0.0301-0.0381)	0.0008 (0.0002-0.0016)
K_{plan}	2.600 (2.453-2.755)	2.431-2.758	0.0319 (0.0276-0.0358)	0.0317 (0.0275-0.0354)	0.0033 (0.0020-0.0050)
K_{all}	2.386 (2.214-2.571)	2.225-2.595	0.0136 (0.0112-0.0160)	0.0147 (0.0123-0.0169)	0.0295 (0.0263-0.0336)

The AUC of the basic model was 0.806 (apparent) and 0.803 (out-of-fold); with all blocks 0.836 and 0.829. Apparent and out-of-fold increments agree within 0.001, so the added terms do not inflate the apparent increment within these fitted models; this does not capture the optimism arising from the selection of the marker (S1c). The conditional OR of the distance is stable across all blocks (2.28 to 2.60; 2.39 with all). Most of its incremental discrimination is shared with the orientation descriptors (reduction by 59% with all blocks), and the increment is not offered as evidence of added information. TCRT is the pipeline implementation (mean cosine between the QRS loop vectors and the mean T vector in Kors XYZ), not the lead-space definition of Acar and colleagues (reference 9 of the manuscript); that definition would require new signal computation. The selection among markers and its uncertainty (S1c) are not part of this analysis. The assessment partition was not used.

S25. Model specification: centering, scaling, coefficients and thresholds

This section lists the constants of the tabulated models: the basic model with and without the marker, the scaling of the stronger model B4 (without its coefficients), the development-fixed models of S15b for the two primary marker-endpoint pairs, the angle spline and the verification model. It contains no person-level values. All means and SDs come from the combined development folds (training and internal validation), complete cases, with divisor n (not $n-1$), and were kept fixed in the assessment partition, in strata and in resampling. The rows of a model are the intercept followed by the columns in the order of the tables. Every column x enters as $z = (x - \text{centering}) / \text{SD}$, the intercept as 1. The linear predictor is the sum of coefficient times z , and the probability is $1 / (1 + \exp(-\text{predictor}))$. The coefficients are on this standardized scale; the odds ratio per development SD of the marker is the exponential of its coefficient. Fits are logistic with a ridge term of 10^{-6} on all coefficients except the intercept (Newton iteration, row weights). Sex is coded female 0, male 1 as recorded. Heart rate is the time-eligible device heart rate in the assessment data; QRS duration and Fridericia QTc come from the measurement chain; the angle is in degrees and the marker is dimensionless. Sex-stratified fits omit the sex column.

Age basis. A natural cubic spline with fixed knots at 40, 60 and 80 years: with $a = \text{age} / 20$ and $d(k) = ((a - k)_+^3 - (a - 4)_+^3) / (4 - k)$, the two design columns are $\text{age_linear} = a$ and $\text{age_natural} = d(2) - d(3)$. (An earlier version of S0 stated that the knots were not tabulated; they are given here and in S3.)

Table S111. S25. Centering and SD, LVEF <40% (marker: normalized representative-beat Fréchet distance; 33,971 complete development persons)

Column	Centering	SD
age_linear	3.253746	0.8432118
age_natural	1.574402	1.48014
sex_numeric	0.5246828	0.4993904
heart_rate	81.12594	21.28183
qrs_duration_ms	115.0085	24.42872
qtc_fridericia_ms	431.62	37.01613
spatial_qrs_t_angle_deg	84.53796	46.84175
qrs_t_normalized_discrete_frechet	1.658334	0.7650323

Table S112. S25. Centering and SD, coded cardiomyopathy (marker: normalized beat-median Fréchet distance; 72,795 complete development persons)

Column	Centering	SD
age_linear	3.077234	0.9091313
age_natural	1.339785	1.456733
sex_numeric	0.5100213	0.4998996
heart_rate	80.46286	20.15802
qrs_duration_ms	112.835	21.33447
qtc_fridericia_ms	430.8317	35.9397
spatial_qrs_t_angle_deg	77.11645	45.48014
qrs_t_frechet_beat_median	1.520809	0.659408

Table S113. S25. Centering and SD of the stronger model B4 for LVEF <40% (31,840 complete development persons)

Column	Centering	SD
age_linear	3.21755	0.8439841
age_natural	1.506597	1.456189
sex_numeric	0.5238065	0.4994329
heart_rate	81.41586	21.48326
qrs_duration_ms	111.5861	19.08687
qtc_fridericia_ms	428.8033	34.80597
spatial_qrs_t_angle_deg	80.85	45.02563
classical_cornell_product	192.7926	97.2879
classical_sokolow_lyon	1.88424	0.8378428
magnitude_area_qrs	0.04568777	0.02012116
spatial_low_voltage_qrs_peak_magnitude	1.229695	0.4608259
axis_sin	0.206256	0.5667148
axis_cos	0.7301781	0.3211428
qrs_t_normalized_discrete_frechet	1.658334	0.7650323

axis_sin and axis_cos are the sine and cosine of the frontal QRS axis.

Development-fixed models of S15b. B2 is the basic model without the angle, B3 includes it and B3 + marker adds the marker. Models were fitted on the combined development folds (reference-eligible persons with finite design and known outcome). A prediction is positive when the linear predictor exceeds the threshold, which is the smallest observed control predictor with specificity of at least 0.90 in the development data. Centering and SD are those of Tables S111 and S112.

Table S114. S25. Development-fixed model coefficients, LVEF <40% with representative-beat distance (33,971 persons, 3,543 cases)

Column	Centering	SD	B2	B3	B3 + marker
Intercept	n/a	n/a	-2.511385	-2.642519	-2.801178
age_linear	3.253746	0.8432118	0.4832017	0.384245	0.3517759
age_natural	1.574402	1.48014	-0.3013824	-0.2867517	-0.3045579
sex_numeric	0.5246828	0.4993904	0.2437042	0.2455064	0.2727438
heart_rate	81.12594	21.28183	0.5474655	0.4881489	0.4191943
qrs_duration_ms	115.0085	24.42872	0.560176	0.3588674	0.1797707
qtc_fridericia_ms	431.62	37.01613	0.3039801	0.3279178	0.3703123
spatial_qrs_t_angle_deg	84.53796	46.84175	n/a	0.5698631	0.00179815
qrs_t_normalized_discrete_frechet	1.658334	0.7650323	n/a	n/a	0.8989952
Threshold (linear predictor)			-1.466966	-1.365359	-1.323166

Marker quartile boundaries (raw scale, development): 1.059568, 1.487029 and 2.125475; medians of the four classes 0.8502615, 1.263676, 1.76135 and 2.698993.

Table S115. S25. Development-fixed model coefficients, coded cardiomyopathy with beat-median distance (72,795 persons, 1,903 cases)

Column	Centering	SD	B2	B3	B3 + marker
Intercept	n/a	n/a	-3.974823	-4.139426	-4.252238
age_linear	3.077234	0.9091313	0.5472785	0.3849363	0.3271379
age_natural	1.339785	1.456733	-0.5697114	-0.5385794	-0.5430562
sex_numeric	0.5100213	0.4998996	0.1869828	0.1718243	0.1780097
heart_rate	80.46286	20.15802	0.4018503	0.3036088	0.2498372
qrs_duration_ms	112.835	21.33447	0.4767631	0.2981893	0.1713871
qtc_fridericia_ms	430.8317	35.9397	0.2814848	0.2892338	0.309275
spatial_qrs_t_angle_deg	77.11645	45.48014	n/a	0.603709	0.1094551
qrs_t_frechet_beat_median	1.520809	0.659408	n/a	n/a	0.7071469
Threshold (linear predictor)			-3.056407	-2.874415	-2.864671

Marker quartile boundaries (raw scale, development): 1.029895, 1.376364 and 1.865822; medians of the four classes 0.8501013, 1.195984, 1.586504 and 2.348276.

Angle spline of S13d. Restricted cubic spline of the integral angle with four knots at the 5th, 35th, 65th and 95th percentiles of the training data: 16.91937, 57.77404, 104.6794 and 163.6005 degrees. Three basis columns (linear plus two nonlinear) with centering 84.46061, 32.73711 and 8.199231 and SD 46.81296, 41.38235 and 12.78427.

Table S116. S25. Verification model (marker-free, training only; S8)

Column	Centering	SD	Coefficient
Intercept	n/a	n/a	-1.701796
age_linear	2.795305	0.9565829	0.5018603
age_natural	0.9865373	1.30965	-0.07210729
sex_numeric	0.4755177	0.4994003	0.1551482
heart_rate	77.53129	18.71723	0.3466023
qrs_duration_ms	108.2997	15.16967	-0.01328488
qtc_fridericia_ms	421.4641	31.10267	0.2231676
spatial_qrs_t_angle_deg	67.34107	41.34896	0.1120903
classical_cornell_product	175.94	80.80453	0.02451535
classical_sokolow_lyon	1.972449	0.7636969	0.09018241
magnitude_area_qrs	0.04329214	0.01572543	0.1614913
spatial_low_voltage_qrs_peak_magnitude	1.279055	0.4311034	-0.2084573
axis_sin	0.3381939	0.5261113	0.02394148
axis_cos	0.7193189	0.3023444	-0.04297304

The outcome is availability of an echocardiogram within ± 30 days; weights are 1 / probability, capped at 20.69592 (99th percentile of the weights of verified training persons).

Table S117. S25. Coefficients of the development models of S13a, LVEF <40% (training, 25,453 persons, 2,690 cases)

Column	Without marker	OR	With marker	OR
Intercept	-2.627731	0.07224219	-2.785607	0.06169165
age_linear	0.3193778	1.376271	0.2834326	1.327679
age_natural	-0.2468343	0.7812702	-0.2621614	0.7693869
sex_numeric	0.221299	1.247696	0.2479053	1.281339
heart_rate	0.492972	1.637175	0.4229102	1.526397
qrs_duration_ms	0.3595102	1.432627	0.1780594	1.194896
qtc_fridericia_ms	0.3429884	1.409152	0.3877035	1.473593
spatial_qrs_t_angle_deg	0.5837993	1.792837	0.0089618	1.009002
qrs_t_normalized_discrete_frechet	n/a	n/a	0.908417	2.480393

Table S118. S25. Coefficients of the development models of S13a, LVEF <40% (internal validation, 8,518 persons, 853 cases)

Column	Without marker	OR	With marker	OR
Intercept	-2.701307	0.06711776	-2.862018	0.05715333
age_linear	0.6080193	1.83679	0.5825113	1.790529
age_natural	-0.4253518	0.6535398	-0.4483346	0.638691
sex_numeric	0.3259853	1.385395	0.3546275	1.42565
heart_rate	0.4759861	1.609601	0.4092437	1.505679
qrs_duration_ms	0.357967	1.430418	0.1855766	1.203912
qtc_fridericia_ms	0.2836112	1.327916	0.3187134	1.375357
spa- tial_qrs_t_angle_ deg	0.5275603	1.694792	-0.02025314	0.9799506
qrs_t_normalized _discrete_frechet	n/a	n/a	0.8721228	2.391983

These fits reproduce the marker ORs of Table S45 (2.480 and 2.392).

What is not tabulated. The coefficients of the stronger model B4, the cross-marker pairs of the fixed models and the right-ventricular context models are not tabulated. The coefficients of the refits in the assessment partition are reported only as ORs per SD with intervals (S3, S15); a coefficient table of those fits would have to be produced from the assessment data. The steps of the measurement chain (reconstruction, filtering, delineation, loop construction) are defined by the software release named in the manuscript and not tabulated here. These models use the same construction as the tabulated ones; the analysis scripts are public (Code availability of the main manuscript), whereas aggregate results are in this supplement and not in the repository.

S26. Left bundle branch block stratum and QRS duration as a spline (post hoc, development data)

Both analyses were specified after the primary result and the earlier supplement sections were known and are post hoc. They use training and internal validation only; the assessment partition was not read. The main-model OR was reproduced before any result was accepted (2.480 in training and 2.392 in internal validation).

Methods. (a) Left bundle branch block stratum: logistic regression with Firth's penalty (Jeffreys prior) in persons of the main analysis set with a positive classical left bundle branch block pattern, with the B3 covariates and fixed development scaling; the marker OR is per development SD, intervals by profile likelihood, P values by the likelihood-ratio test. The pattern is the library's morphology surrogate (QRS of at least 120 ms, no initial septal q wave in I or V6, predominantly negative QRS in V1, no distinct terminal S wave in V6). It is a rule-based surrogate and not a physician-confirmed finding, and it is undetermined in 3.2% to 3.3% of the main analysis set (training 810, internal validation 278 persons), where the criterion cannot be decided or pacing excluded it; these persons are in neither the stratum nor the comparison stratum. For comparison we report the maximum-likelihood point estimate, a compact Firth model (marker, age, sex), the stratum

with a negative pattern and the main model without the persons with a positive pattern. (b) QRS duration as a restricted cubic spline: the linear QRS term of B3 is kept and the nonlinear terms of a natural cubic spline (standardized with training mean and SD) are added. Knots: (A) the 5th, 35th, 65th and 95th percentiles of the training set (92, 104, 114 and 166 ms; two nonlinear terms); (B) fixed at 100, 120 and 150 ms (one nonlinear term); (C) variant A plus indicators for the classical left and right bundle branch patterns, in persons with a known pattern, compared with B3 in the same persons.

Table S122. S26. Marker OR per development SD in persons with a classical left bundle branch block pattern (Firth, profile-likelihood 95% interval)

Set	Persons	Of them LVEF <40%	Firth OR (95% CI)	P (likelihood ratio)	Maximum-likelihood point estimate	Events per parameter	Compact model (age, sex)
Training	318	131	1.446 (0.961-2.197)	0.077	1.466	14.6	1.575 (1.186-2.136)
Internal validation	103	32	1.404 (0.677-2.981)	0.361	1.444	3.6	1.462 (0.875-2.616)
Development pooled	421	163	1.465 (1.024-2.110)	0.036	1.479	18.1	1.563 (1.216-2.041)

For comparison, persons with a negative pattern (pattern known): training 2.546 (2.383-2.720; 24,325 persons) and internal validation 2.477 (2.202-2.788; 8,137 persons). The main model without the persons with a positive pattern gave 2.481 (2.328-2.644; 25,135 persons) and 2.417 (2.156-2.710; 8,415 persons), against 2.480 (2.331-2.639) and 2.392 (2.138-2.676) with all persons.

Table S123. S26. Marker OR per development SD with QRS duration as a spline (person-cluster Wald 95% CI, main analysis set)

Model	Training	Internal validation
B3 (main model, linear QRS duration)	2.480 (2.331-2.639)	2.392 (2.138-2.676)
A: spline, percentile knots	2.451 (2.303-2.608)	2.377 (2.126-2.658)
B: spline, knots at 100, 120 and 150 ms	2.465 (2.316-2.624)	2.383 (2.130-2.665)
C: A plus left and right bundle branch indicators (persons with known pattern; training 24,612 persons, of them more than 300 left and 2,501 right; validation 8,230, of them 103 left and 832 right)	2.510 (2.349-2.683)	2.418 (2.147-2.724)
B3 in the same persons as C	2.533 (2.374-2.702)	2.437 (2.170-2.736)

Reading. Within the left bundle branch pattern the point estimates are lower than outside it: the Firth OR was about 1.4 in both folds (1.45 and 1.40) against 2.55 and 2.48 with a negative pattern. The interval includes 1 in each fold (training 0.96-2.20, validation 0.68-2.98); pooled, the lower limit is just above 1 (1.02, $P = 0.036$), an exploratory association. This describes lower point estimates; it does not establish an association within block, and without an interaction test no effect modification is claimed. In validation the stratum has 3.6 events per parameter, and the statement is not robust there. The main finding does not rest on these persons: without them the OR stays at 2.48 and 2.42, because the stratum makes up 1.2% to 1.3% of the set. Modeling QRS duration as a spline lowered the OR by at most 1.2% (training 2.480 to 2.451 with knots A and 2.465 with knots B; validation 2.392 to 2.377 and 2.383), and with bundle branch indicators it stayed at 2.510 and 2.418 against 2.533 and 2.437 in the same persons (minus 0.9% and 0.8%). A nonlinear

QRS duration therefore does not explain the marker away; the objection remains open to the extent that the surrogate itself is imprecise. No formal test of interaction between marker and block pattern was done. Both analyses describe; they do not replace a physician classification of block or a prespecified interaction test.

S27. Negative-control diagnoses (post hoc, development data)

Methods. The list was fixed before examination: cataract (ICD-9 366; ICD-10 H25, H26), glaucoma (365; H40, H42), hearing loss (389; H90, H91), inguinal hernia (550; K40), diverticulosis without bleeding (56200, 56210; K5710, K5730, K5750, K5790; persons with other diverticular codes excluded), hemorrhoids (455; K64), knee or hip osteoarthritis (71515, 71516, 71525, 71526, 71535, 71536, 71595, 71596; M16, M17) and benign prostatic hyperplasia in men (6000, 6001, 6002, 6009; N40). The rule file (diagnoses, code sets, populations, threshold of 100 cases) was dated and checksummed locally before any diagnosis row or case count was read. Coding followed the rule for cardiomyopathy: any code in the index hospital encounter, with a missing encounter treated as unavailable (excluded). Retinopathy (3620, 3621; H350, H360; E08, E09, E10, E11 and E13 with the extension .31 to .35) was added as a comparator; it is a code definition in the index encounter and not the phenome concept of S11. Models were the B3 model with the marker on the main analysis set; diagnoses with fewer than 100 cases or controls in a fold are described only. The second population comprised all development persons with complete design and an index encounter, whether or not verified. Two script corrections after the first run (a constant sex column in men only, and a constancy test that missed floating-point residues) did not change definitions; the pooled estimates and the main OR in the same persons were added after the case counts of the first run had been seen. Both additions are marked below.

Only 52% of the main analysis set had an index encounter (training 13,228 of 25,453; validation 4,396 of 8,518); the rest were ECGs outside an admission. In these persons the OR for LVEF below 40% was 2.40 (2.22-2.60; 1,616 cases) in training and 2.23 (1.93-2.57; 506 cases) in validation, pooled 2.35 (2.20-2.52); in the whole main analysis set it was 2.48 and 2.39. Among men, 7,103 (training) and 2,362 (validation) persons entered the analysis of prostatic hyperplasia.

Table S124. S27. Marker OR per development SD for negative-control diagnoses (B3 model; Wald 95% CI)

Diagnosis (cases training / validation)	Training	Validation	Pooled over both folds (added after case counts were seen), cases
Cataract (122 / 37)	1.06 (0.80-1.40)	descriptive only	1.10 (0.86-1.40), 159
Glaucoma (409 / 133)	0.89 (0.77-1.03)	0.90 (0.69-1.18)	0.89 (0.79-1.02), 542
Hearing loss (226 / 67)	0.89 (0.74-1.06)	descriptive only	0.87 (0.74-1.02), 293
Inguinal hernia (36 / 15)	descriptive only	descriptive only	descriptive only, 51
Diverticulosis without bleeding (217 / 65)	0.88 (0.73-1.07)	descriptive only	0.92 (0.77-1.09), 282
Hemorrhoids (148 / 40)	0.88 (0.69-1.13)	descriptive only	0.90 (0.73-1.11), 188
Knee or hip osteoarthritis (177 / 66)	0.92 (0.76-1.12)	descriptive only	0.93 (0.77-1.11), 243
Benign prostatic hyperplasia, men (954 / 313)	1.07 (0.97-1.19)	0.90 (0.76-1.08)	1.03 (0.94-1.13), 1,267
Comparator: coded retinopathy (299 / 114)	1.29 (1.09-1.52)	1.23 (0.96-1.58)	1.27 (1.10-1.46), 413
Comparator: LVEF <40% in the same persons (1,616 / 506; added after case counts were seen)	2.40 (2.22-2.60)	2.23 (1.93-2.57)	2.35 (2.20-2.52), 2,122

In the second population (43,679 persons with an index encounter, pooled), the ORs were: cataract 1.10 (0.91-1.33), glaucoma 0.98 (0.89-1.08), hearing loss 0.88 (0.77-1.00), inguinal hernia 1.07 (0.79-1.44; 115 cases), diverticulosis 0.90 (0.79-1.01), hemorrhoids 0.88 (0.75-1.04), osteoarthritis 0.90 (0.77-1.05), prostatic hyperplasia 1.00 (0.93-1.07; men only, 22,445) and retinopathy 1.53 (1.37-1.71). Per fold, retinopathy was above 1 (1.53 and 1.52), and two intervals lay below 1: diverticulosis in training 0.85 (0.73-0.97; 502 cases) and hearing loss in validation 0.72 (0.55-0.95; 139 cases); all other intervals included 1.

Reading. None of the negative controls with an analyzable case number had an interval above 1; point estimates were 0.87 to 1.10 against 2.40 and 2.23 for LVEF in the same persons, and the upper interval limit was at most 1.40. The intervals limit the associations with the individual diagnoses; they do not limit a shared bias component, because different diagnoses can be related to the same confounder to different degrees, and coding and selection can weaken those relations further. General frailty confounding therefore remains unresolved. Several point estimates are slightly below 1 (hearing loss, diverticulosis, hemorrhoids, osteoarthritis, glaucoma: 0.87 to 0.92); this is compatible with competing coding (admissions for serious heart disease carry fewer secondary diagnoses of chronic conditions) but was not examined, and an inverse association is not shown. Retinopathy, mostly diabetic, is not a clean negative control: its OR stays above 1 after B3 adjustment (1.27; 1.53 in the second population, which fits the unadjusted figure of S11), lower

than that for LVEF but not 1, and may reflect microvascular disease. **Limits.** (a) The index encounter is missing for 48% of persons and the subset is not random (the LVEF OR is 2.40 and 2.23 there instead of 2.48 and 2.39). (b) Outpatient-managed chronic conditions are coded incompletely in admissions (prevalence of cataract 0.9%, of inguinal hernia 0.3%), which costs discrimination; intervals are wide (cataract 0.80-1.40). (c) In validation only glaucoma, prostatic hyperplasia and retinopathy reached 100 cases. (d) A marker that only roughly reflects age, sex, heart rate, QRS and QTc could show residual confounding that the negative controls exclude only for these diagnoses. (e) Negative controls address confounding by general condition, not measurement error of the marker. (f) No correction for multiple testing was applied; two of about thirty fold-level intervals in the second population lie below 1, in the direction opposite to the LVEF association.