SUPPLEMENTARY DATA

Supplementary methods

All supplementary analyses were performed in the study cohort (n = 77 with available LGE data). Genotype was classified as genotype-positive (pathogenic/likely pathogenic variant) or genotype-negative and, among genotype-positive individuals, as desmosomal (*DSP, DSG2,* and *DSC2*) vs nondesmosomal. The discriminative capacity of univariable models for predicting LGE was compared using DeLong's test for 2 correlated ROC curves. To account for the modest sample size and limited number of events, the primary multivariable model (LGE ~ EI-RBBB-VE + indexed CMR LVEDD [z-score]) was additionally estimated using Firth's penalized logistic regression with profile-likelihood confidence intervals. EI-RBBB-VE was characterized by precordial transition, QRS duration, fragmentation, and coupling interval. An epicardial proxy was defined as QRS duration ≥ 140 ms combined with a late precordial transition (≥ V_4). Categorical variables were compared using the Fisher exact test, whereas continuous variables were compared using either the Student *t*-test or the Mann-Whitney U test, as appropriate.

Table S1. Morphological characteristics of RBBB ectopy by LGE status (48 morphologies in 37 patients)

Feature (RBBB morphologies, n = 48)	LGE(+)	LGE(-)	*P*
QRS duration, ms	130 [120-145]	130 [125-145]	.851
Precordial transition lead	3 [2-4]	4 [3-4]	.703
Coupling interval, ms	415 [380-478]	360 [330-425]	.082
Fragmented QRS	7/35 (20)	2/13 (15)	.999

IQR, interquartile range; LGE, late gadolinium enhancement; RBBB, right bundle branch block.
The data are presented as n/N (%) or median [interquartile range].

Table S2. Resting Holter ectopic burden by LGE status

Variable (n = 69)	LGE(+)	LGE(-)	*P*
PVC count / 24 h, median [IQR]	1167 [250-2360]	292 [26-1486]	.065
PVC %, median [IQR]	1 [0-3]	0 [0-1]	.058
NSVT on Holter, n (%)	8/38 (21)	5/31 (16)	.760

IQR, interquartile range; LGE, late gadolinium enhancement; NSVT, nonsustained ventricular tachycardia; PVC, premature ventricular complex.
The data are presented as n/N (%) or median [interquartile range].

Table S3. Genotype vs EI-RBBB-VE as predictors of LGE

Predictor/model	Estimate	95%CI	*P*
Desmosomal genotype and LGE (Fisher)	11/12 (92) vs 30/65 (46)	—	.004
AUC—EI-RBBB-VE (univariable)	0.638	—	—
AUC—Genotype-positive (univariable)	0.606	—	—
DeLong (EI-RBBB-VE vs genotype)	ΔAUC	—	.656
Genotype-positive (univariable)	3.60	1.12-11.53	.031
Genotype-positive — adjusted for EI-RBBB-VE + LVEDD-z	2.88	0.79-10.56	0.111

AUC, area under the ROC curve; CI, confidence interval; CMR, cardiac magnetic resonance; EI-RBBB-VE, exercise-induced right bundle branch block-pattern ventricular ectopy; LGE, late gadolinium enhancement; LVEDD, left ventricular end-diastolic diameter.
The data are presented as n/N (%) or odds ratios.

Univariable analyses and AUC comparison performed in the full cohort (n = 77); the multivariable model adjusted for CMR-derived LVEDD was restricted to patients with available CMR measurements (n = 66).

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Table S4. Association between EI-RBBB-VE and LGE according to genetic subgroup

Subgroup	n	LGE(+) among EI-RBBB-VE(+)	LGE(+) among EI-RBBB-VE(-)	*P*
Desmosomal	12	9/9 (100)	2/3 (67)	.250
Nondesmosomal	65	16/28 (57)	14/37 (38)	.140
Nondesmosomal P/LP	48	13/21 (62)	12/27 (44)	.259
Genotype-negative/inconclusive	17	3/7 (43)	2/10 (20)	.593

EI-RBBB-VE, exercise-induced right bundle branch block-pattern ventricular ectopy; LGE, late gadolinium enhancement; P/LP, pathogenic/likely pathogenic.

Table S5. Comparison of standard and Firth penalized logistic regression models for the association between EI-RBBB-VE and myocardial fibrosis

Model	EI-RBBB-VE OR (95%CI)	*P*	CMR LVEDD-z OR (95%CI)	*P*
Standard logistic regression (n = 66)	3.92 (1.28-12.00)	.017	0.53 (0.28-1.04)	.064
Firth penalized regression	3.59 (1.26-11.18)	.016	0.59 (0.28-0.99)	.047

CI, confidence interval; CMR, cardiac magnetic resonance; EI-RBBB-VE, exercise-induced right bundle branch block-pattern ventricular ectopy; LVEDD, left ventricular end-diastolic diameter; OR, odds ratio.
Both models included EI-RBBB-VE and CMR-derived LVEDD z-score as independent variables.