

La genetica nella stratificazione del rischio clinico della
cardiomiopatia dilatativa

La genetica nella stratificazione del rischio clinico della cardiomiopatia dilatativa

Marta Gigli, MD

**Cardiothoracovascular Department - Azienda Sanitaria Universitaria Giuliano
Isontina, Trieste (Italy)**



2023 ESC Guidelines for the management of cardiomyopathies

Developed by the task force on the management of cardiomyopathies of the European Society of Cardiology (ESC)

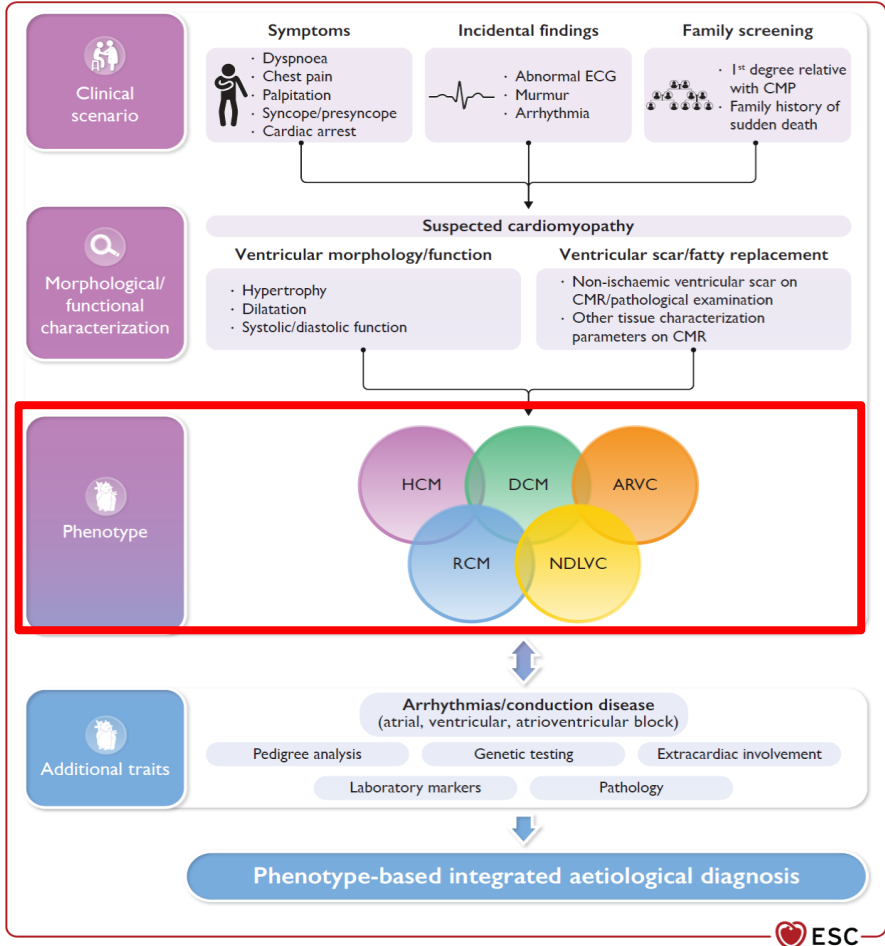
The cardiomyopathy mindset
Phenotype-centered diagnostic approach



ESC

European Society of Cardiology

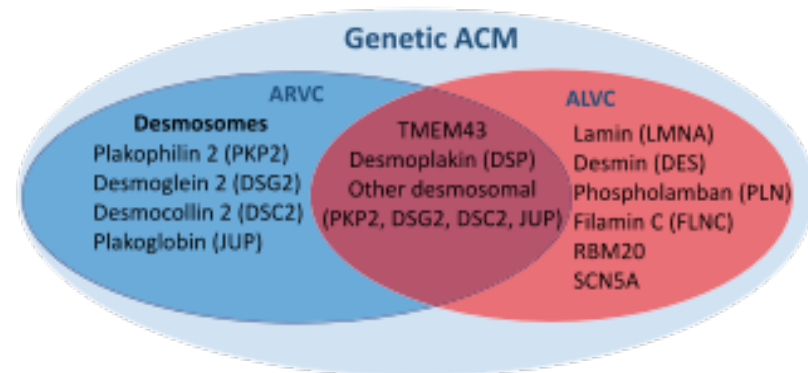
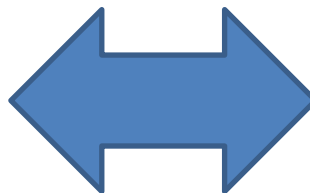
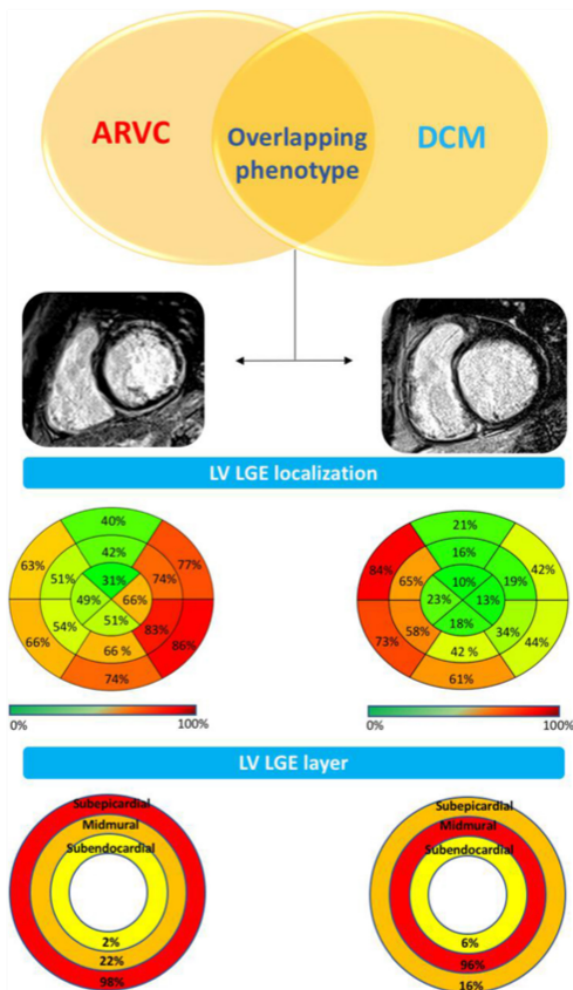
European Heart Journal (2023) 00, 1–124
<https://doi.org/10.1093/eurheartj/ehad194>



ESC

Arrhythmogenic left ventricular cardiomyopathy

Domenico Corrado , Cristina Basso



Corrado D, Basso C. *Heart* 2021;0:1–11. doi:10.1136/heartjnl-2020-316944

Panel A

Autosomal dominant complete penetrance

Low familial aggregation

Diagnosis

Individual approach

Therapy and lifestyle recommendation

Severity

Disease threshold

Disease susceptibility

● Rare pathogenic variant

● Intermediate penetrance

● Small effect size

● Non-genetic

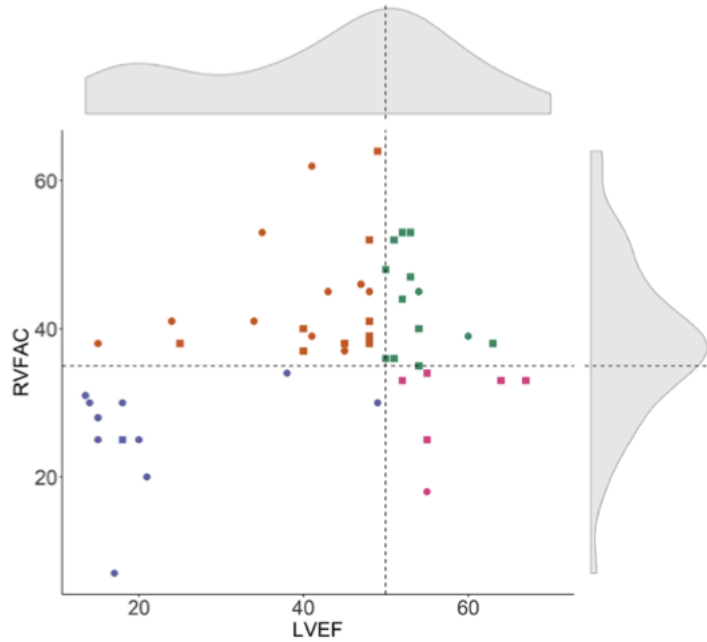
MAF > 1–5%

ESC

Cascade family screening

Genotype–phenotype correlations

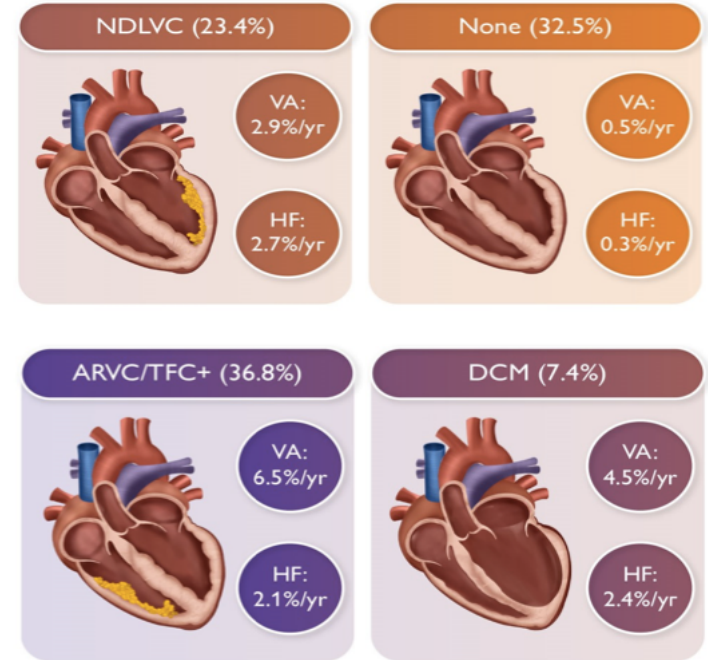
FLNC



LV vs. RV Dysfunction: ● No ● Left ● Biventricular ● Right

Proband: ■ No ● Yes

DSP



Gasperetti et al. European Heart Journal (202

Prognosis (and therapy)

Worse Outcomes
in Genotype-Positive
DCM



Major Adverse Cardiovascular Events
HR 1.51 (95% CI, 1.17-1.94; $P = 0.001$)



End-Stage Heart Failure
HR 1.67 (95% CI, 1.16-2.41; $P = 0.006$)

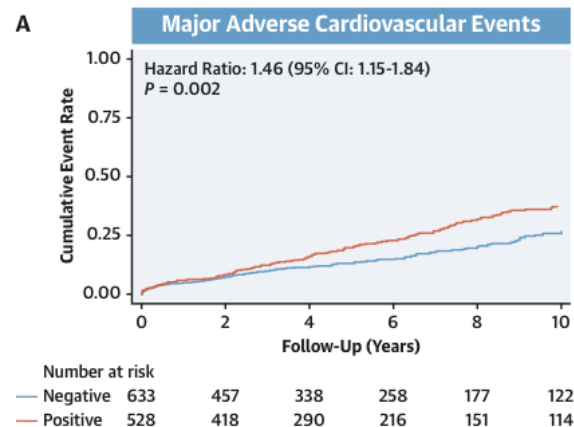


Malignant Ventricular Arrhythmia
HR 1.50 (95% CI, 1.09-2.07; $P = 0.013$)

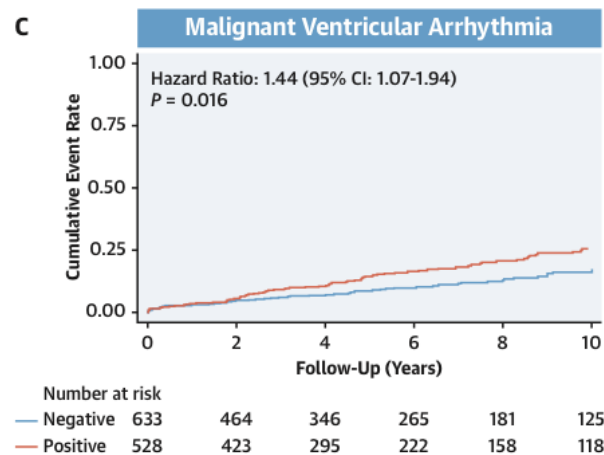


Left Ventricular Reverse Remodeling
OR 0.77 (95% CI, 0.59-0.99; $P = 0.047$)

A



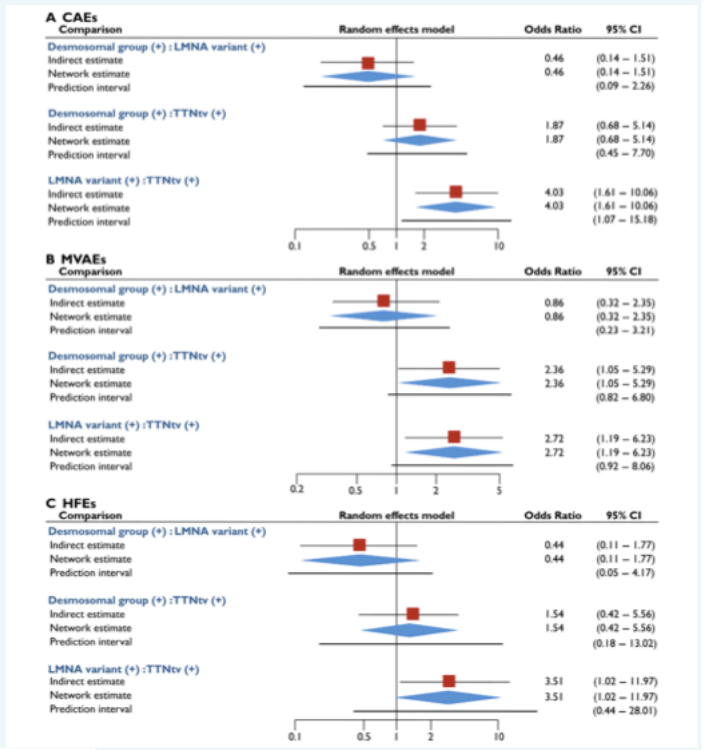
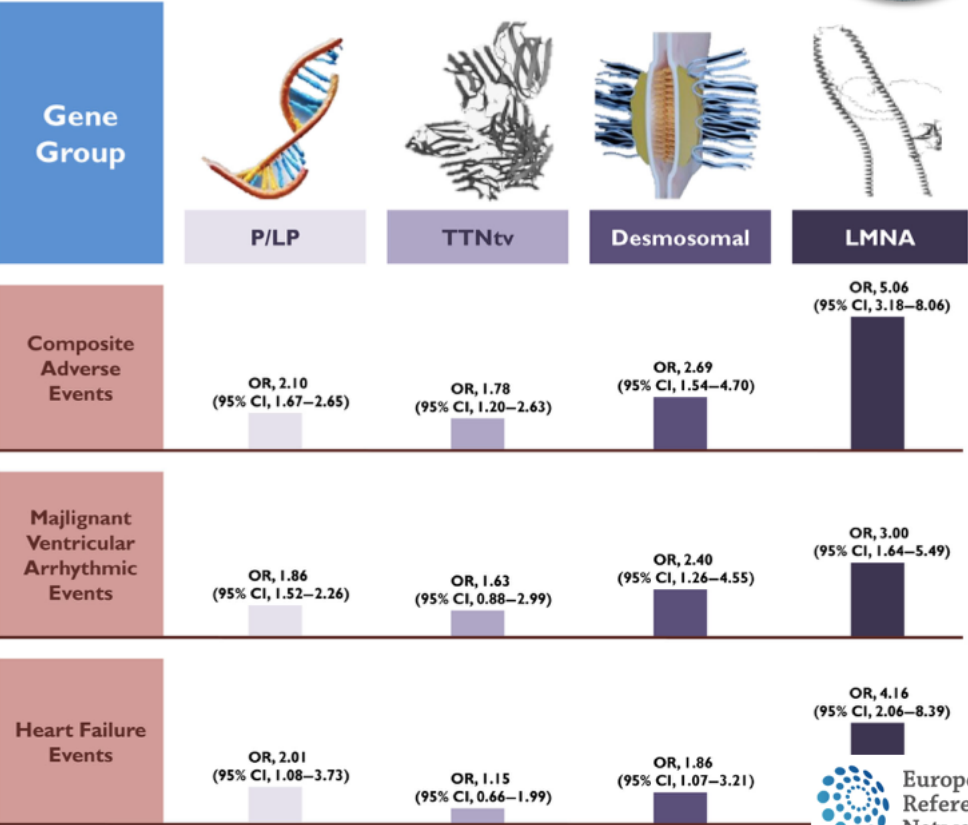
C



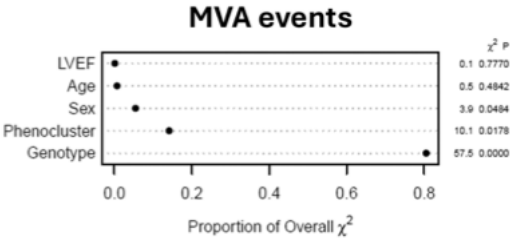
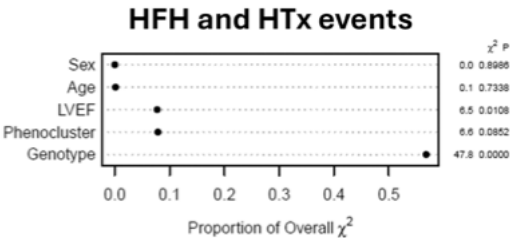
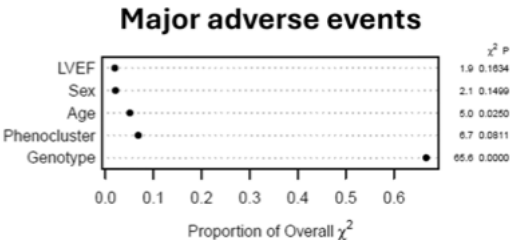
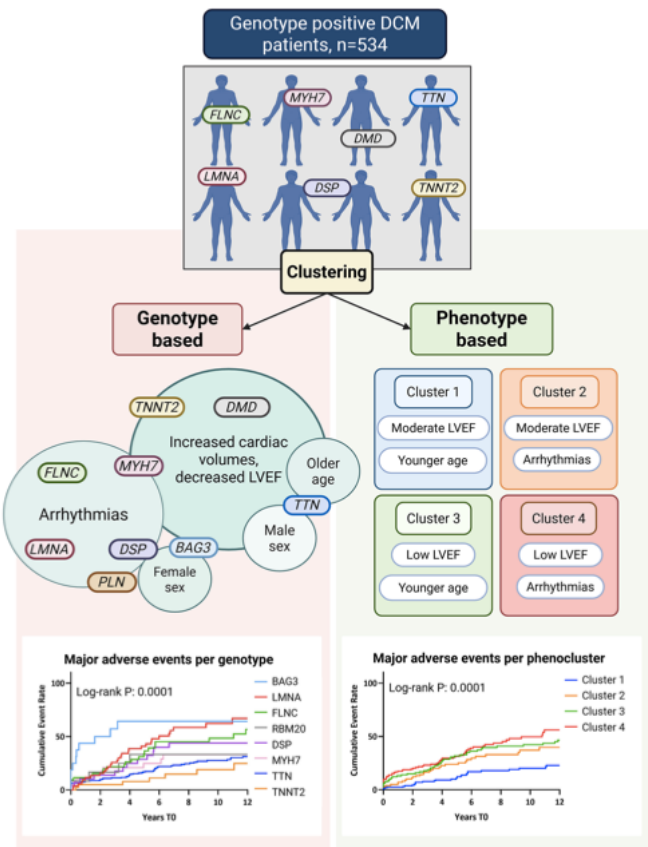
Prognostic implications of genotype findings in non-ischaemic dilated cardiomyopathy: A network meta-analysis

- 26 studies
 - 1,382 genotype positive (P/LP) patients
 - 645 truncating titin (TTNtv) patients
 - 62 desmosomal gene patients
 - 119 lamin A/C (LMNA) patients
 - No difference in LVEF between gene groups

Prognosis



Impact of genotype–phenotype associations on prognosis in dilated cardiomyopathy

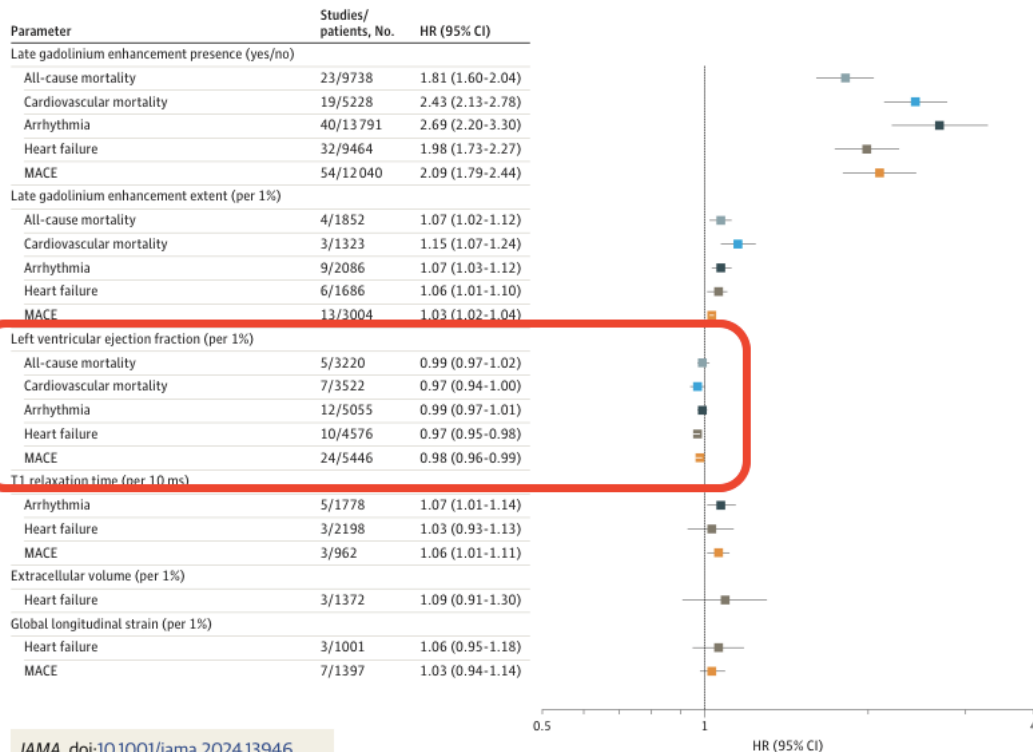


Stroeks et al. European Journal of Heart Failure 2025

Risk Stratification in Nonischemic Dilated Cardiomyopathy Using CMR Imaging A Systematic Review and Meta-Analysis

...the weakness of LVEF

Figure 1. Cardiac Magnetic Resonance (CMR) Imaging Parameters and Clinical Outcomes



JAMA. doi:10.1001/jama.2024.13946

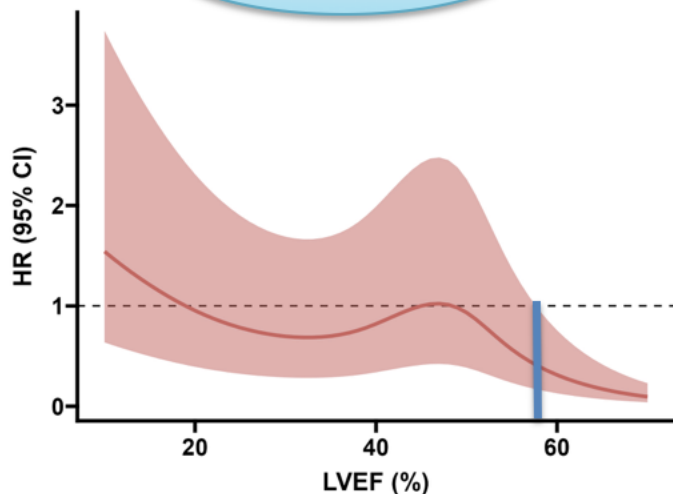
Published online September 19, 2024.

Stratify the genotypes...the weakness of LVEF

Prognosis

FLNC

DSP

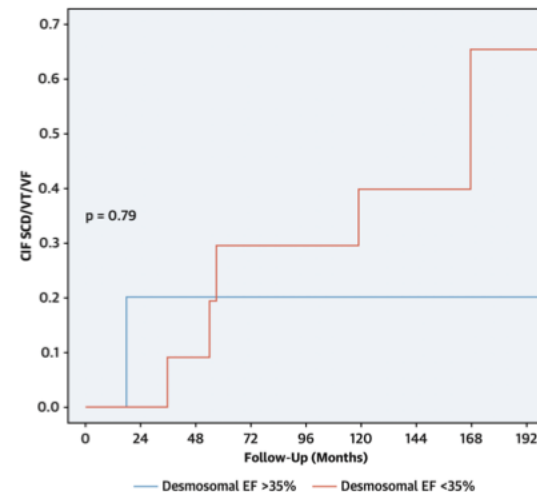


The patient's genotype should be considered in the estimation of SCD risk in DCM ^{185,186,869,886}

An ICD should be considered in patients with DCM with a genotype associated with high SCD risk and LVEF >35% in the presence of additional risk factors (see Table 21). ^{541,542,867,869,873,878,881,886}

An ICD may be considered in selected patients with DCM with a genotype associated with high SCD risk and LVEF >35% without additional risk factors (see Table 21). ^{869,873,881,886}

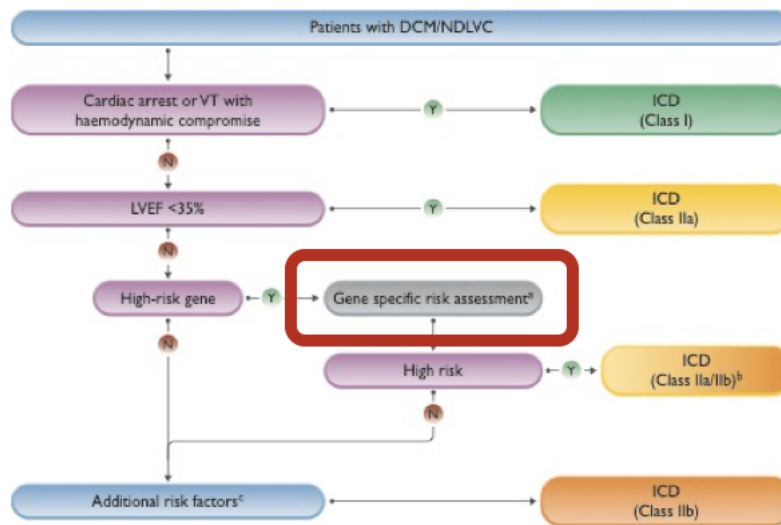
Ila	B
Ila	C
IIb	C



Gigli, Mestroni, Sinagra et al. JAMA Cardiology 2025

Gigli, Mestroni, Sinagra et al. JACC 2019

2023 CMP guidelines



The patient's genotype should be considered in the estimation of SCD risk in DCM. ^{185,186,869,886}

An ICD should be considered in patients with DCM with a genotype associated with high SCD risk and LVEF >35% in the presence of additional risk factors (see Table 21). ^{541,542,867,869,873,878,881,886}

An ICD may be considered in selected patients with DCM with a genotype associated with high SCD risk % without additional risk factors (see ^{185,186}

IIa

B

IIa

C

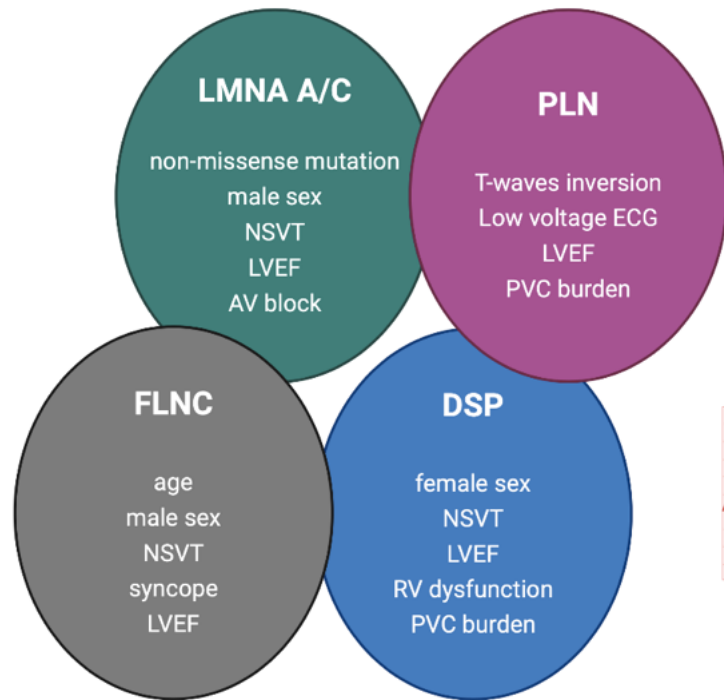
IIb

C

Gene	Annual SCD rate	Predictors of SCD
LMNA ^{185,186,438,541,865,878,879}	5–10%	Estimated 5-year risk of life-threatening arrhythmia using LMNA risk score (https://lmna-risk-vta.fr)
FLNC-truncating variants ^{866,867,880}	5–10%	LGE on CMR LVEF < 45%
TMEM43 ^{868,881}	5–10%	Male Female and any of the following: LVEF <45%, NSVT, LGE on CMR, >200 VE on 24h Holter ECG
PLN ^{542,882,883}	3–5%	Estimated 5-year risk of life-threatening arrhythmia using PLN risk score (https://plnriskcalculator.shinyapps.io/final_shiny) LVEF < 45% LGE on CMR NSVT
DSP ^{185,186}	3–5%	LGE on CMR LVFF < 45%
RBM20 ⁸⁶⁹	3–5%	LG LVI

Gene-specific personalized risk estimation

Prognosis



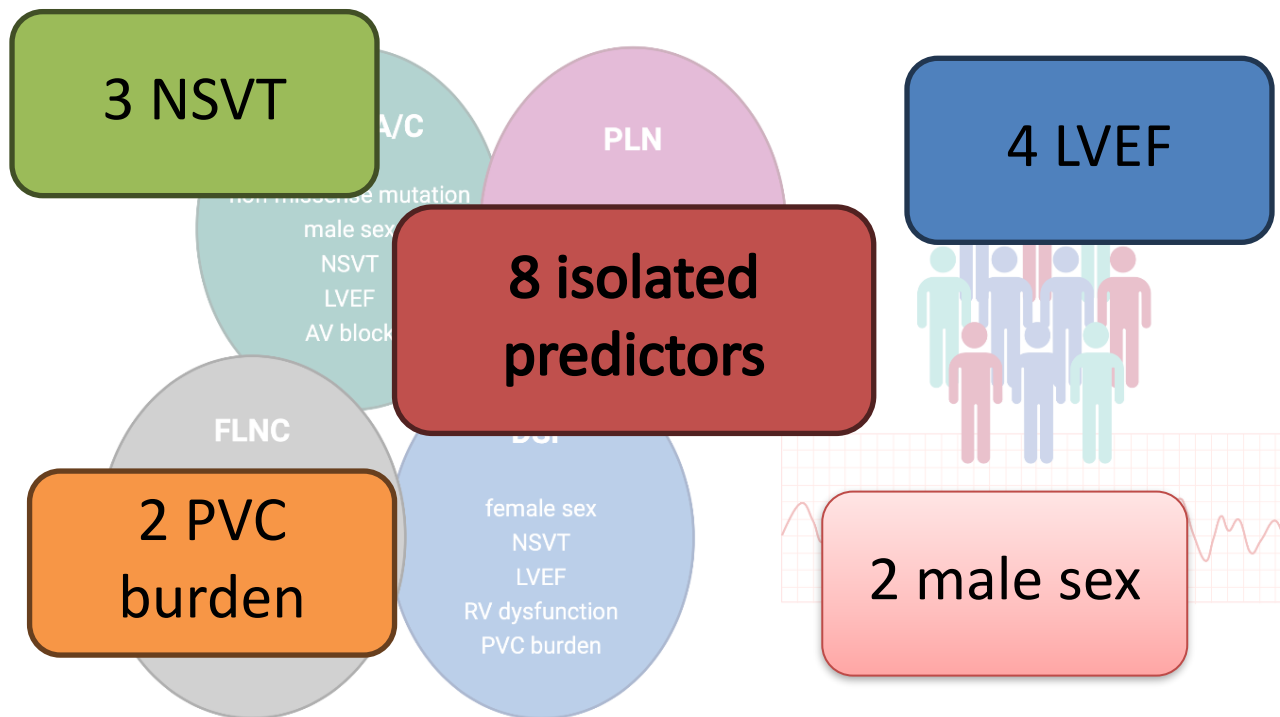
- <https://www.dsp-risk.com/>
- <https://flnctv.shinyapps.io/RiskCalculator/>
- <http://lmna-risk-vta.fr/>
- https://plnriskcalculator.shinyapps.io/final_shiny/

Gigli M, Sinagra G, et al. European Journal of Heart Failure 2025 – HFA consensus

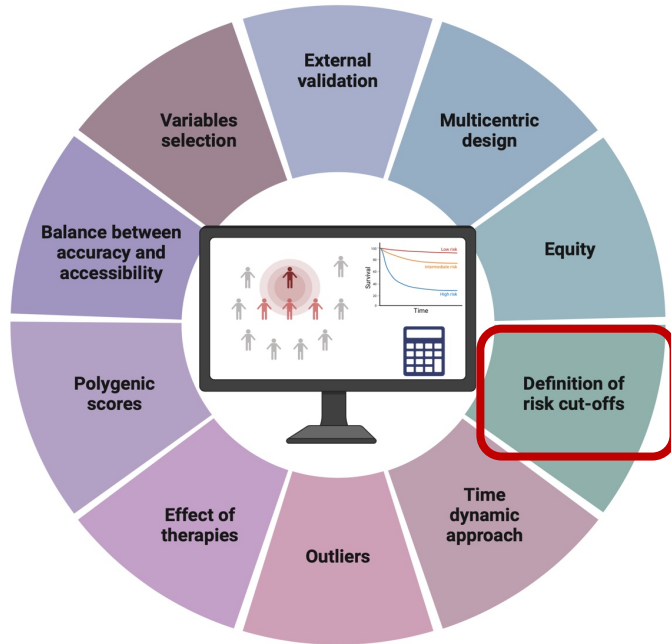
Gene-specific risk scores in DCM/NDLVC

Prognosis

Gene-specific personalized risk estimation



What is the reasonable threshold for ICD implantation?



...the Task Force acknowledges the **challenges associated with defining universal thresholds** for acceptable risk across different cardiomyopathy phenotypes, but is of the opinion that a **similar approach** to that taken in risk stratification for **HCM** is reasonable. **Although the 2022 ESC Guidelines** for the management of patients with ventricular arrhythmias and the prevention of sudden cardiac death have suggested a higher **threshold of 10%** risk at 5 years to guide primary prevention ICD implantation in patients with **DCM and LMNA variants**



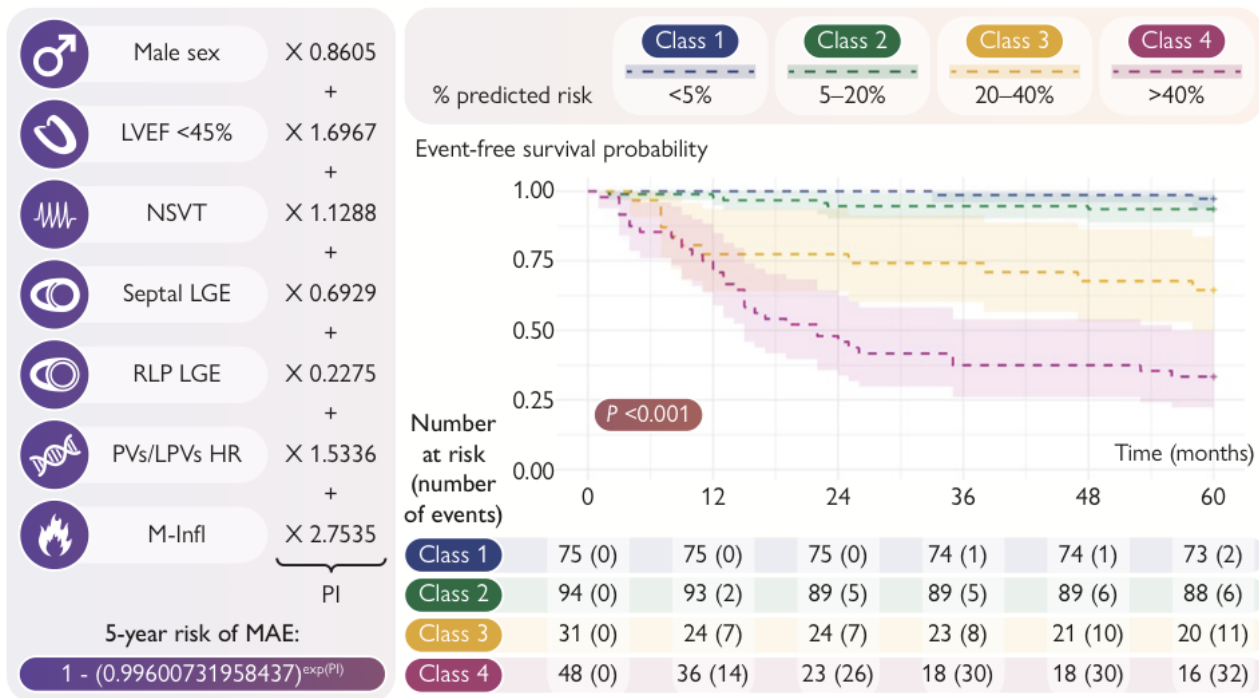
ESC

European Society
of CardiologyEuropean Heart Journal (2025) 00, 1–13
<https://doi.org/10.1093/eurheartj/ehaf477>

Major arrhythmias in non-dilated left ventricular cardiomyopathy: a novel prediction score

Prognosis

NDLVC-5y risk score for the prediction of 5-year MAE risk



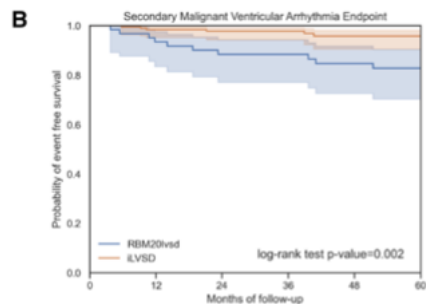
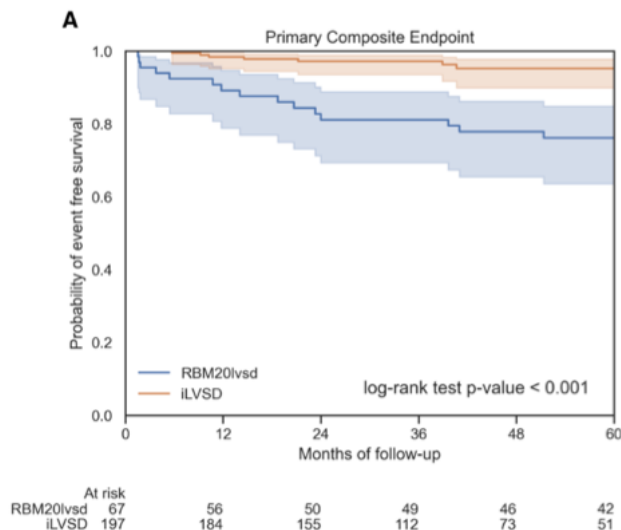
Arrhythmogenic genotypes – less frequent but not less dangerous

ORIGINAL ARTICLE

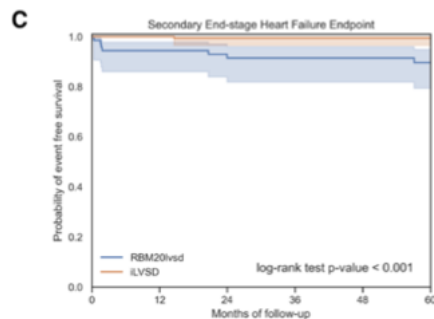
6

Risks of Ventricular Arrhythmia and Heart Failure in Carriers of RBM20 Variants

RBM20



At risk	0	12	24	36	48	60
RBM20lvsd	67	56	50	49	46	42
ILVSD	197	184	155	112	73	51



At risk	0	12	24	36	48	60
RBM20lvsd	72	63	59	57	54	49
ILVSD	221	207	175	125	86	64

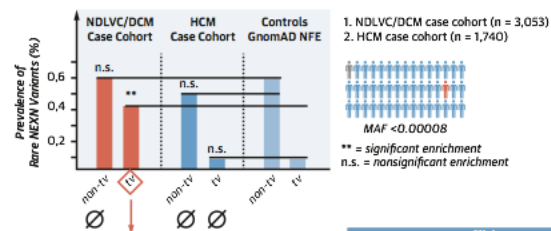
- 6-fold higher risk of composite outcome
- 40% MVA had EF>35%
- Similar risk of MVA in males vs females
- Higher risk of ESHF in males vs females

Genetic and Phenotypic Characterization of Nexilin (*NEXN*)-Related Cardiomyopathy

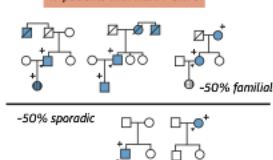
Results From a Multicentric Study



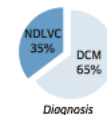
60 patients
with all CMPs phenotypes
and rare *NEXN* variant



17 patients with *NEXN*-CMPs



Clinics	
Age, y	45
Male, % (n)	53% (9)
Caucasian, % (n)	76% (13)
Probands, % (n)	88% (15)
Familial cardiomyopathy, % (n)	47% (8)
Familial sudden cardiac death, % (n)	35% (6)

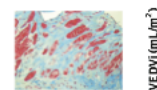


Symptoms	
Syncope-palpitations: 40%	
Dyspnea: 23%	
Chest pain: 17%	
Asymptomatic: 17%	



Phenotype

Nondilated/mildly dilated LV	
LVEF: 42% (median)	
Fibrosis in 64%	
PVC > 1,000 in 24 hours: 42%	
LBBS: 6%	



LVEDV (mL m⁻²)

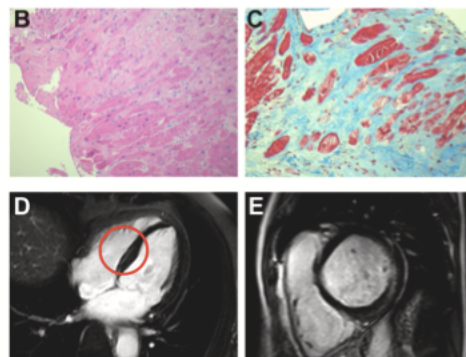
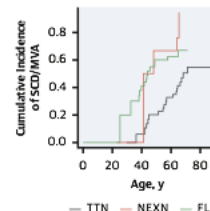
ULN male
ULN female
LLN male
LLN female

200
150
100
50
0

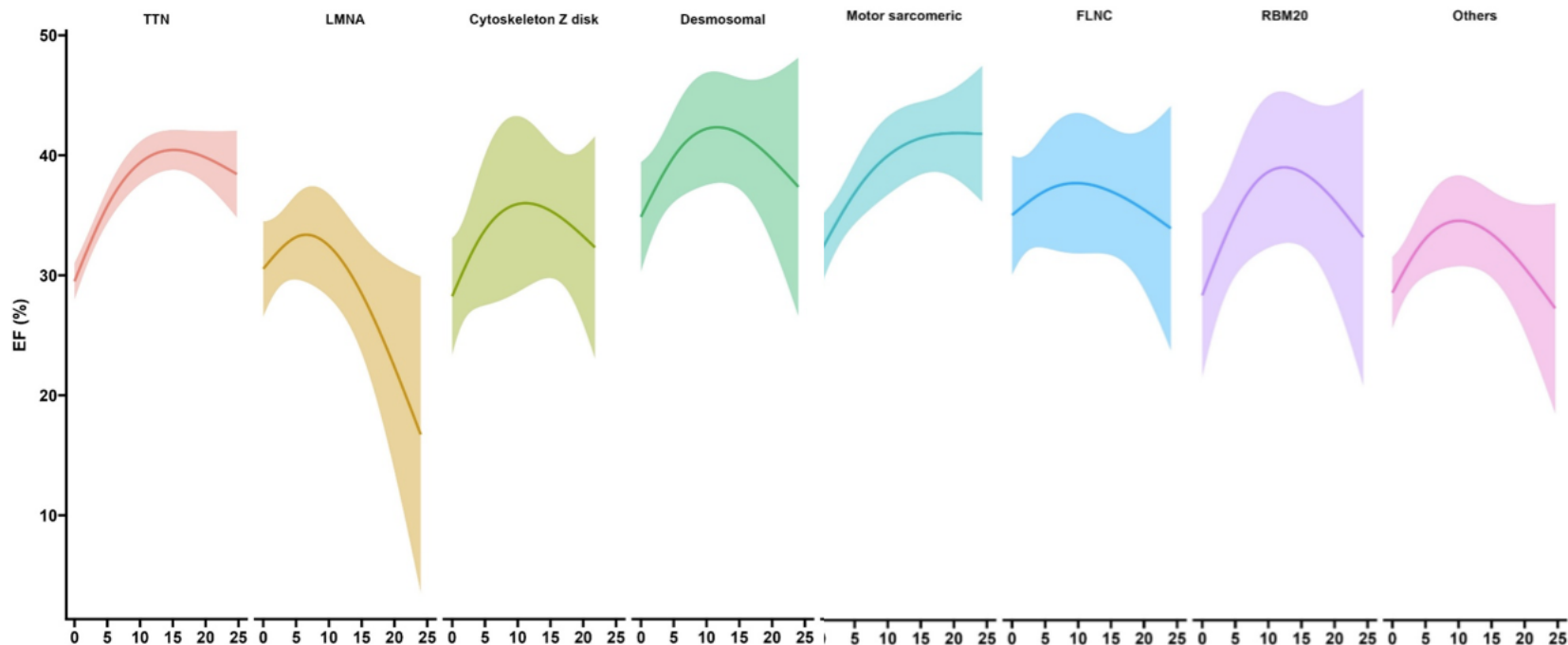
Male Female

Prognosis: 45 Months Follow-Up

MVA outcome: 25%	
HF outcome: 0%	
% ICD: 53%	
LVEF: 45%	
≠ TTN, = FLNC	

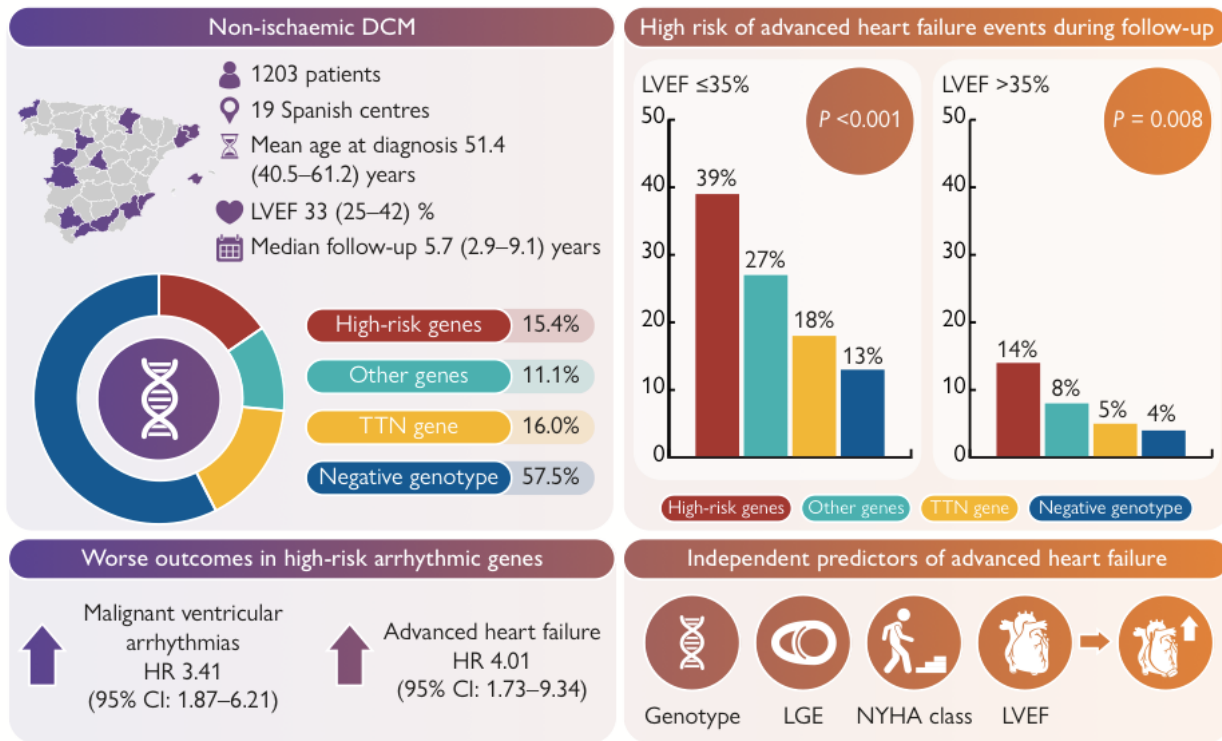


Gene-specific LVEF trajectory



Manca P, Stolfo D, Gigli M, et al. unpublished

Arrhythmic genotypes in dilated cardiomyopathy and risk of advanced heart failure



Mora-Ayestarán et al. European Heart Journal 2025

Laminopathies: natural history and risk prediction of heart failure

LMNA risk score for prediction of 5-year risk of major heart failure events

Analysis of registry data



Exclusion of patients with LVEF <30% at baseline



Derivation cohort
OPAL: nationwide registry on laminopathies
470 patients



Validation cohort
Tertiary cardiology referral centres
245 patients

Five independent risk factors



Male sex

Adjusted HR

1.86



LVEF <50%

2.18



Missense variants in head and rod domains

2.91



Complete left bundle branch block

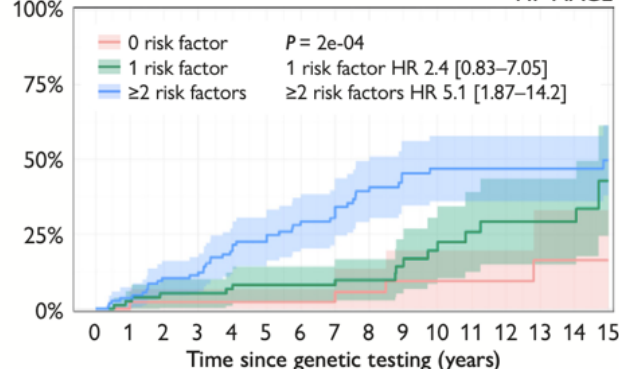
2.99

Good discrimination of the model with C-index of 0.750 and 0.758 in the derivation and validation cohorts

An additive effect of risk factors

Cumulative incidence (%)

HF-MACE



HF-MACE, heart failure-major adverse cardiac event; HR, hazard ratio; LMNA, lamin A/C gene; LVEF, left ventricular ejection fraction

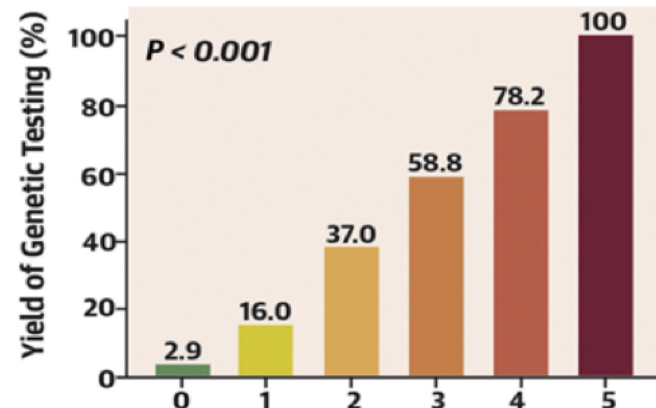
Charron P, et al. *European Heart Journal*.

Clinical Risk Score to Predict Pathogenic Genotypes in Patients With Dilated Cardiomyopathy



Predictors of a Positive Genetic Result	
Clinical Predictors	Points
Skeletal myopathy	1
Family history of DCM	1
Low voltage on ECG	1
Absence of hypertension	1
Absence of LBBB	1
Scoring Range: 0 to 5 Points	

Yield of Positive Genotype According to the Score Category (n = 1,015)



The yield and clinical impact of genetic testing in older patients with dilated cardiomyopathy

Douglas E. Cannie^{1,2,*}, Athanasios Bakalakos^{1,2}, Petros Syrris¹,
Alexandros Protonotarios^{1,2}, Massimiliano Lorenzini^{1,2}, Oliver Guttman^{1,2},
Constantinos O'Mahony^{1,2}, Konstantinos Savvatis^{1,2,3}, Neha Sekhri^{2,3},
Saidi Mohiddin^{2,3}, Luis R. Lopes^{1,2}, and Perry M. Elliott^{1,2}

The Yield and Clinical Impact of Genetic Testing in Older Patients with Dilated Cardiomyopathy

Single Centre DCM Cohort



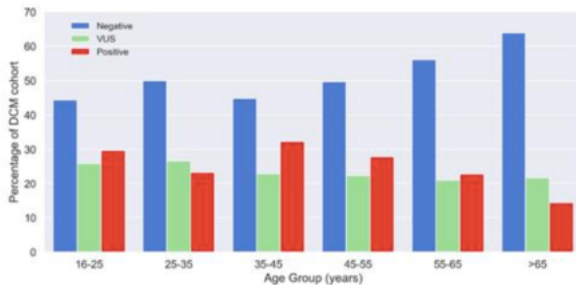
**686 patients
with DCM
undergoing
genetic testing**

62.1% male,
age 50 (37, 59)
years



**24% with LP/P
variants**

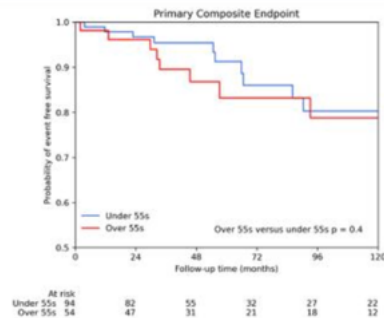
Yield of Genetic Testing by Age Group



One in five patients >55 years were genotype-positive.

**30% of genotype-positive patients >55 years had
high-risk genotypes.**

Genotype-Positive Outcomes by Age



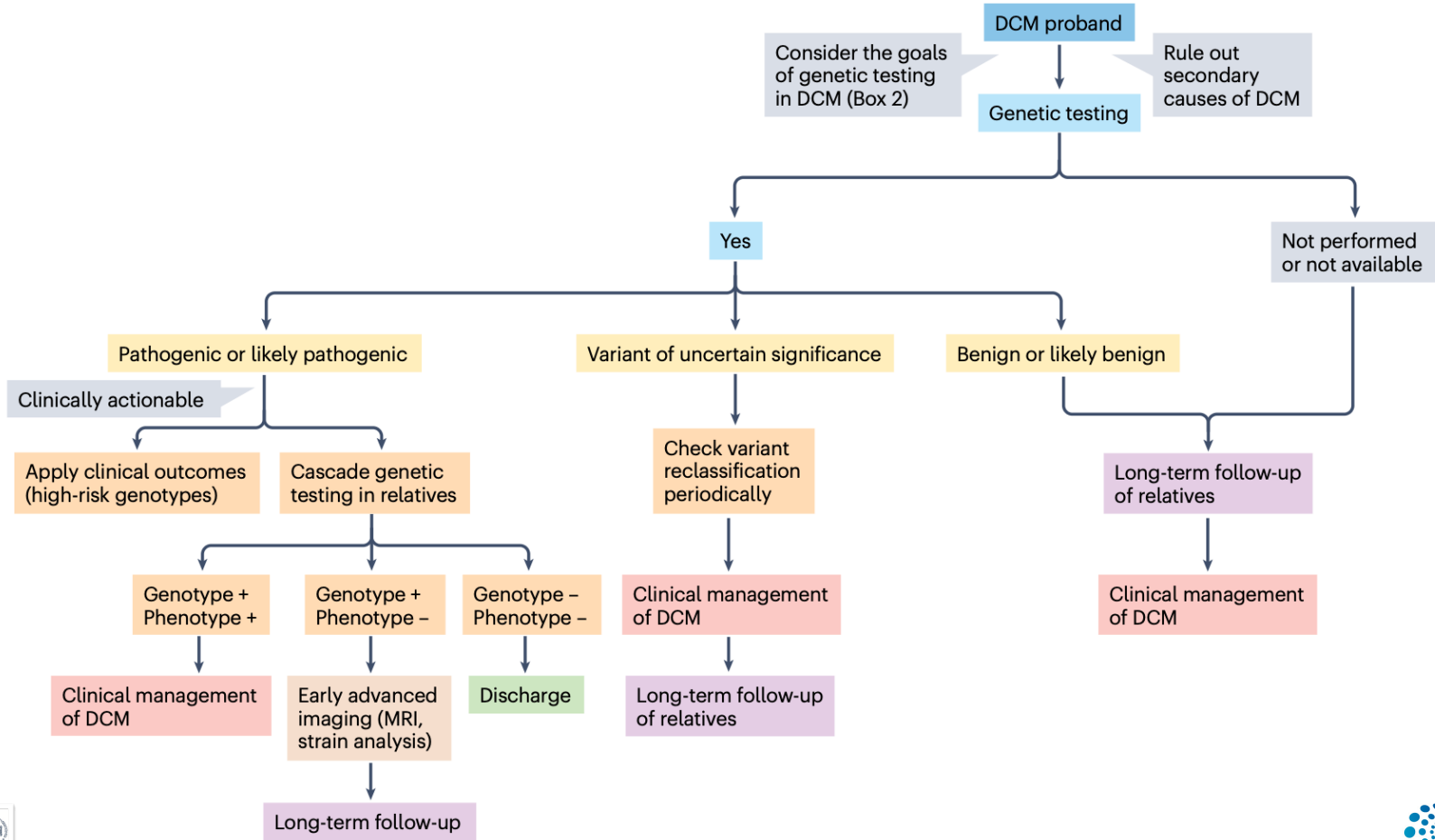
**Age
groups
<55 vs >55
years**

Similar risk of:

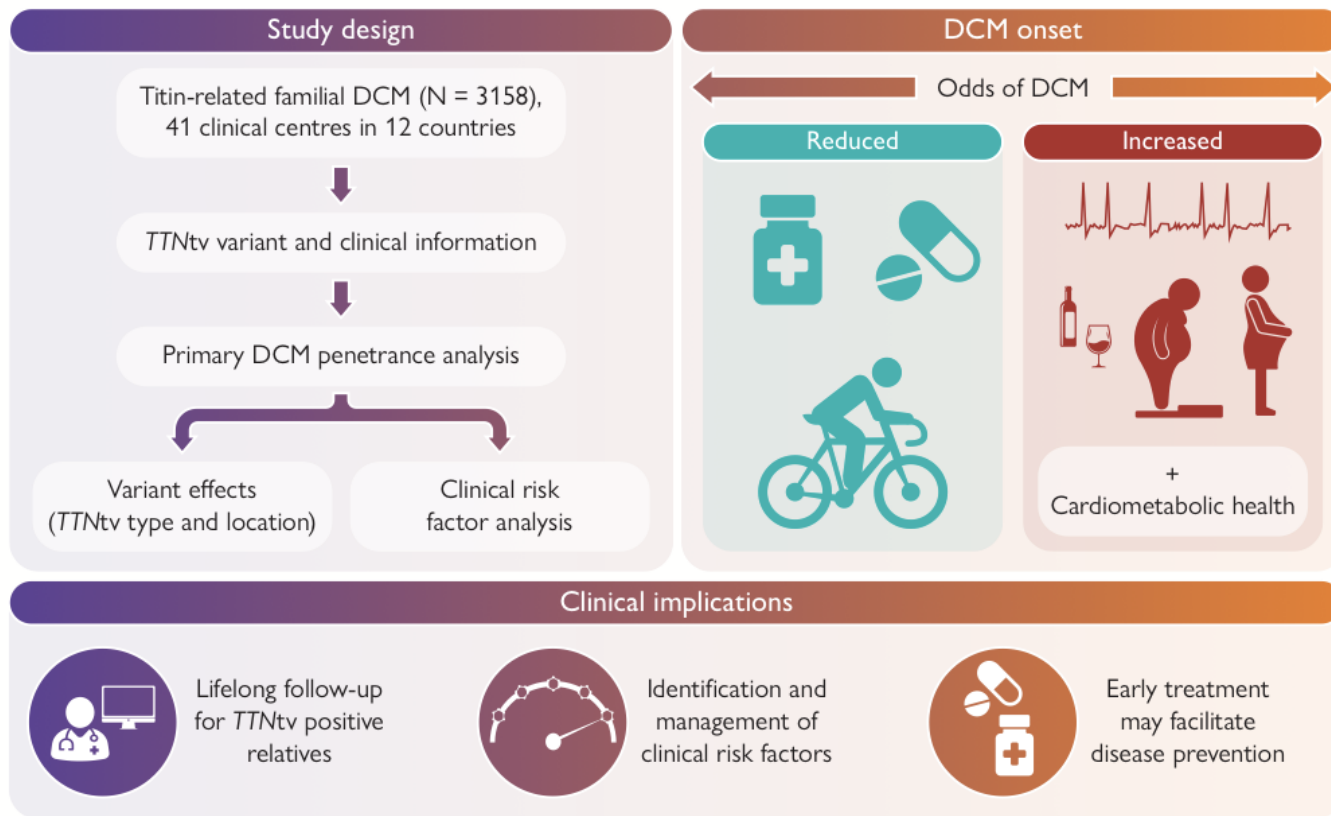
Ventricular arrhythmia

End-stage heart failure

Genetic testing: a rationale approach



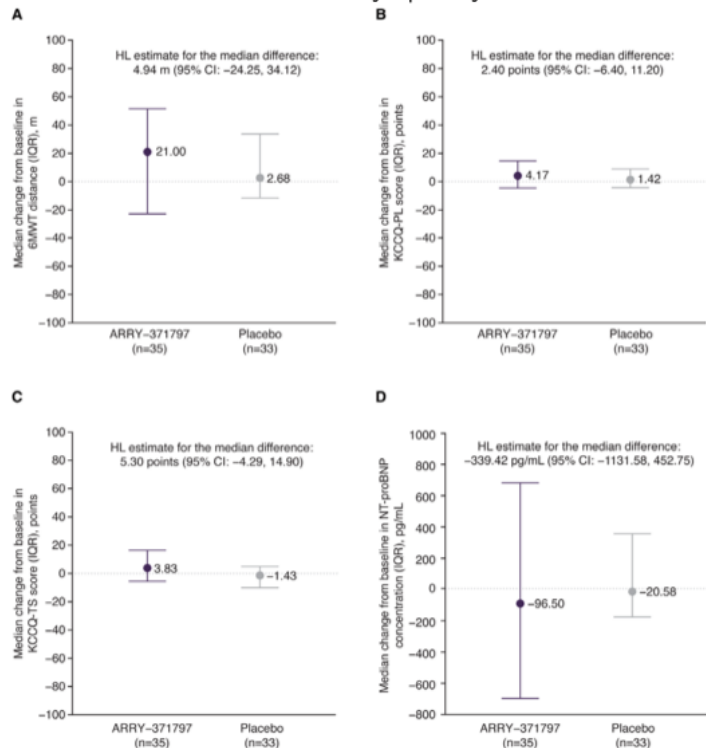
Titin-related familial dilated cardiomyopathy: factors associated with disease onset



Fatkin D. et al. European Heart Journal (2025) 00, 1–18

REALM-DCM: A Phase 3, Multinational, Randomized, Placebo-Controlled Trial of ARRY-371797 in Patients With Symptomatic *LMNA*-Related Dilated Cardiomyopathy

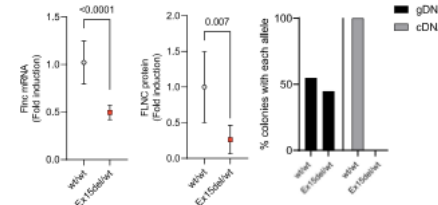
The Future
NEXT EXIT



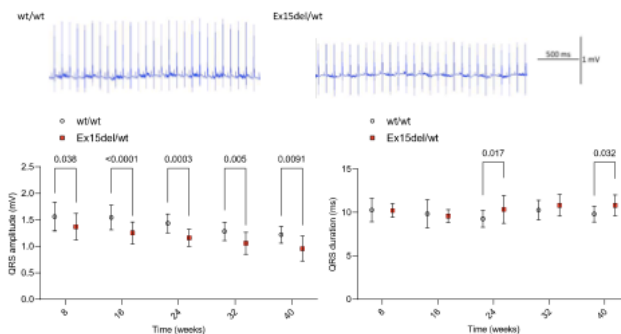
Garcia-Pavia P et al. Circ Heart Fail. 2024;17:e0111548

CRISPR activation to repair electrocardiogram abnormalities caused by a FLNC truncating variant in mice

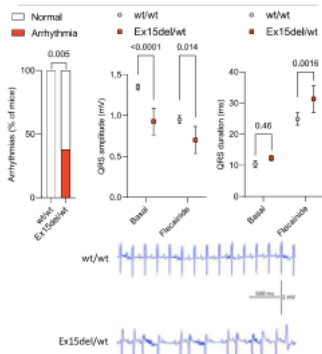
A Design and confirmation of new FLNCtv mouse model



B Electrical abnormalities in FLNCtv mice



C Flecainide-induced arrhythmias

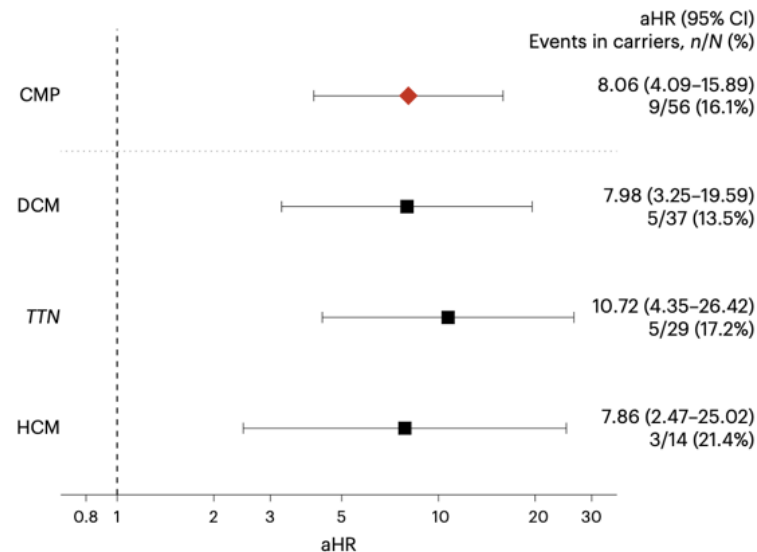
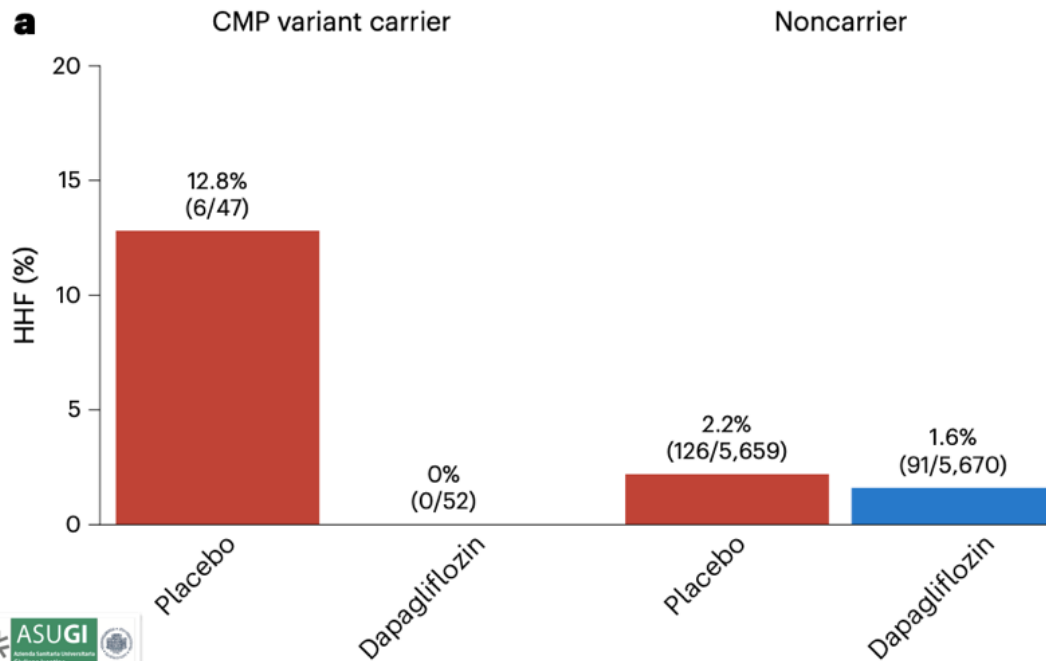


Cañas-Alvaro et al

European Heart Journal (2025) 00, 1–4

Effects of SGLT2 inhibition on incident heart failure in carriers of cardiomyopathy-associated genetic variants

The Future
NEXT EXIT



The Future
NEXT EXIT

Early Treatment With Candesartan vs Placebo in Genetic Carriers of Dilated Cardiomyopathy (EARLY-GENE Trial)

C Cristina Avendaño Solá

Status and phase

Enrolling

Phase 3

Conditions

Cardiomyopathy, Dilated

Treatments

Drug: Candesartan

Study type

Interventional ?

Funder types

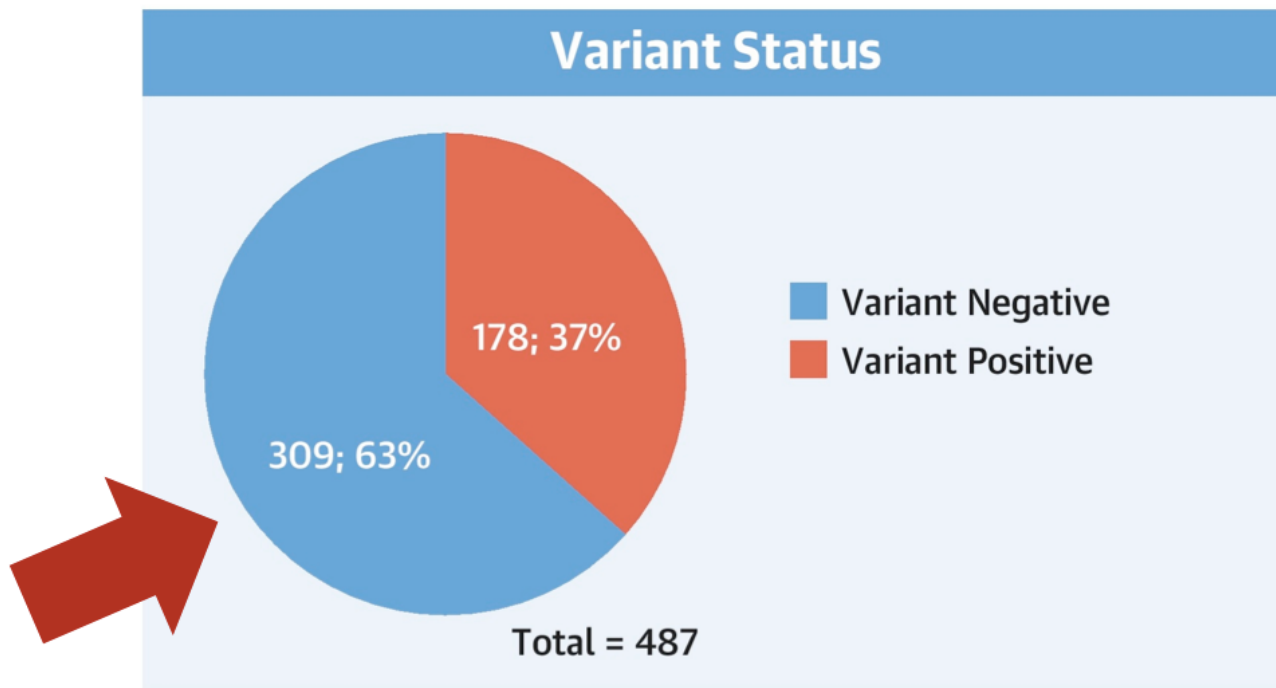
Other ?

Identifiers

[NCT05321875](#)

EARLY-GENE

But for gene elusive/not tested patients we still lack prognostic scores



Gigli, M. et al. J Am Coll Cardiol. 2019;74(11):1480-90.

