

1 **Supplementary Materials**

2

3 **Content**

4	Methods.....	2
5	Figure legends.....	3
6	Figure S1.....	6
7	Figure S2.....	7
8	Figure S3.....	8
9	Figure S4.....	9
10	Figure S5.....	10
11	Figure S6.....	11
12	Figure S7.....	12
13	Figure S8.....	13
14	Figure S9.....	14
15	Figure S10.....	15

1 **Methods**

2 *Data engineering strategy*

3 We developed a de novo data engineering pipeline for extracting outcome data from the UK
4 Biobank called “PhenotypeConstructor”. Its core functionality revolves around processing a
5 range of disease definitions to extract the earliest diagnosis dates for various conditions.
6 This includes interpreting ICD diagnosis codes, self-reported diagnoses, doctor-confirmed
7 conditions, as well as medication details, and family health history. The phenotypes,
8 corresponding UK Biobank field names, and codes considered in this study are described in
9 **Supplementary Table S2.**

Figure legends

Figure S1. Loadings of the eight principal components explaining 90% of the variance in the CMR measurements.

Abbreviations: EF = ejection fraction, EDV = end-diastolic volume, ESV = end-systolic volume, i = indexed, LA = left atrial, LV = left ventricular, MAPSE = mitral annular plane systolic excursion, PC = principal component, RA = right atrial, RV = right ventricular, SV = stroke volume, TAPSE = tricuspid annular plane systolic excursion, V = volume, 2Ch = in 2-chamber view.

Figure S2. Cumulative variance explained by the eight principal components explaining 90% of the CMR measurements.

Figure S3. Distribution of UK biobank participants carrying pathogenic and likely pathogenic variants in cardiomyopathy-associated genes.

Figure S4. Survival of incident atrial fibrillation based on CMR measurements.

The curves estimate cumulative incidence for atrial fibrillation categorising the CMR measurements into two groups: an 85% 'reference' group and a 15% 'risk increasing' group, based on either the 15th or 85th percentile of CMR measurements as the cut-off point. Each plot is annotated with the hazard ratio derived from univariable Cox regression, along with the corresponding confidence interval and p-value.

Abbreviations: EF = ejection fraction, EDV = end-diastolic volume, ESV = end-systolic volume, i = indexed, LA = left atrial, LV = left ventricular, RA = right atrial, RV = right ventricular, SV = stroke volume, TAPSE = tricuspid annular plane systolic excursion, V = volume, 4Ch = in 4-chamber view.

Figure S5. Survival of incident heart failure based on CMR measurements.

The curves estimate cumulative incidence for heart failure categorising the CMR measurements into two groups: an 85% 'reference' group and a 15% 'risk increasing' group, based on either the 15th or 85th percentile of CMR measurements as the cut-off point. Each plot is annotated with the hazard ratio derived from univariable Cox regression, along with the corresponding confidence interval and p-value.

Abbreviations: EF = ejection fraction, EDV = end-diastolic volume, ESV = end-systolic volume, i = indexed, LA = left atrial, LV = left ventricular, RA = right atrial, RV = right ventricular, SV = stroke volume, TAPSE = tricuspid annular plane systolic excursion, V = volume, 4Ch = in 4-chamber view.

Figure S6. Spearman correlation between the effect estimates of the analyses on complete-case and imputed data.

Figure S7. Association of CMR measurements with HCM G+ and the three most common HCM genes.

Associations are presented as $-\log_{10}(\text{p-value})$ multiplied by the effect direction. Results with a p-value smaller than 6.25×10^{-3} are indicated by a star and smaller than 0.05 are indicated with a diamond. Heterogeneity p-values did not reach statistical significance for any of the CMR measurements.

Abbreviations: CMR = cardiac magnetic resonance imaging, EF = ejection fraction, ESV = end-systolic volume, HCM = hypertrophic cardiomyopathy, i = indexed, RA = right atrial, RV = right ventricular, TAPSE = tricuspid annular plane systolic excursion, V = volume, 4Ch = in 4-chamber view.

Figure S8. Association of CMR measurements with DCM G+ and the three most common DCM genes.

Associations are presented as $-\log_{10}(\text{p-value})$ multiplied by the effect direction. Results with a p-value smaller than 6.25×10^{-3} are indicated by a star and smaller than 0.05 are indicated with a diamond. Heterogeneity p-values reached statistical significance for all of the CMR measurements.

Abbreviations: CMR = cardiac magnetic resonance imaging, DCM = dilated cardiomyopathy, EF = ejection fraction, ESV = end-systolic volume, i = indexed, LV = left ventricular.

Figure S9. Association of CMR measurements with the most common HCM genes.

None of the associations of CMR measurements with *MYH7* reached statistical significance.

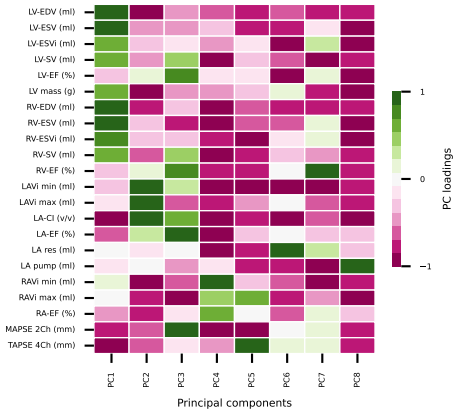
Abbreviations: CMR = cardiac magnetic resonance imaging, EF = ejection fraction, EDV = end-diastolic volume, ESV = end-systolic volume, HCM = hypertrophic cardiomyopathy, i = indexed, LV = left ventricular, MAPSE = mitral annular plane systolic excursion, OR = odds ratio, RV = right ventricular, TAPSE = tricuspid annular plane systolic excursion, 4Ch = in 4-chamber view, 95%CI = 95% confidence interval.

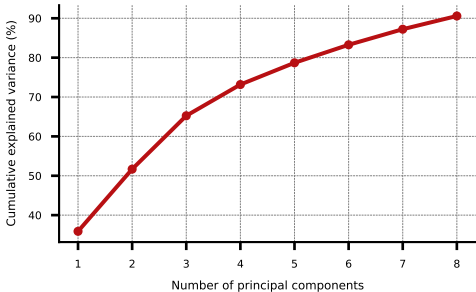
Figure S10. Association of CMR measurements with the most common DCM genes.

None of the associations of CMR measurements with *FLNC* reached statistical significance.

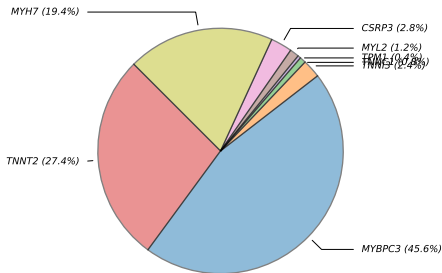
Abbreviations: CMR = cardiac magnetic resonance imaging, DCM = dilated cardiomyopathy, EF = ejection fraction, ESV = end-systolic volume, i = indexed, LV = left ventricular, MAPSE = mitral annular plane systolic excursion, OR = odds ratio, pump = pump volume, 2Ch = in 2-chamber view, 95%CI = 95% confidence interval.

Heatmap of loadings

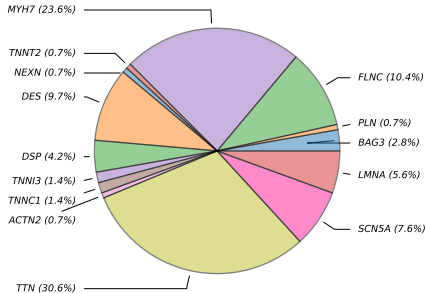


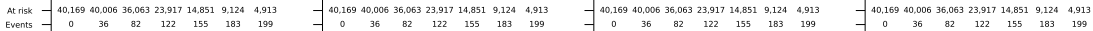
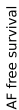


Gene distribution for HCM



Gene distribution for DCM

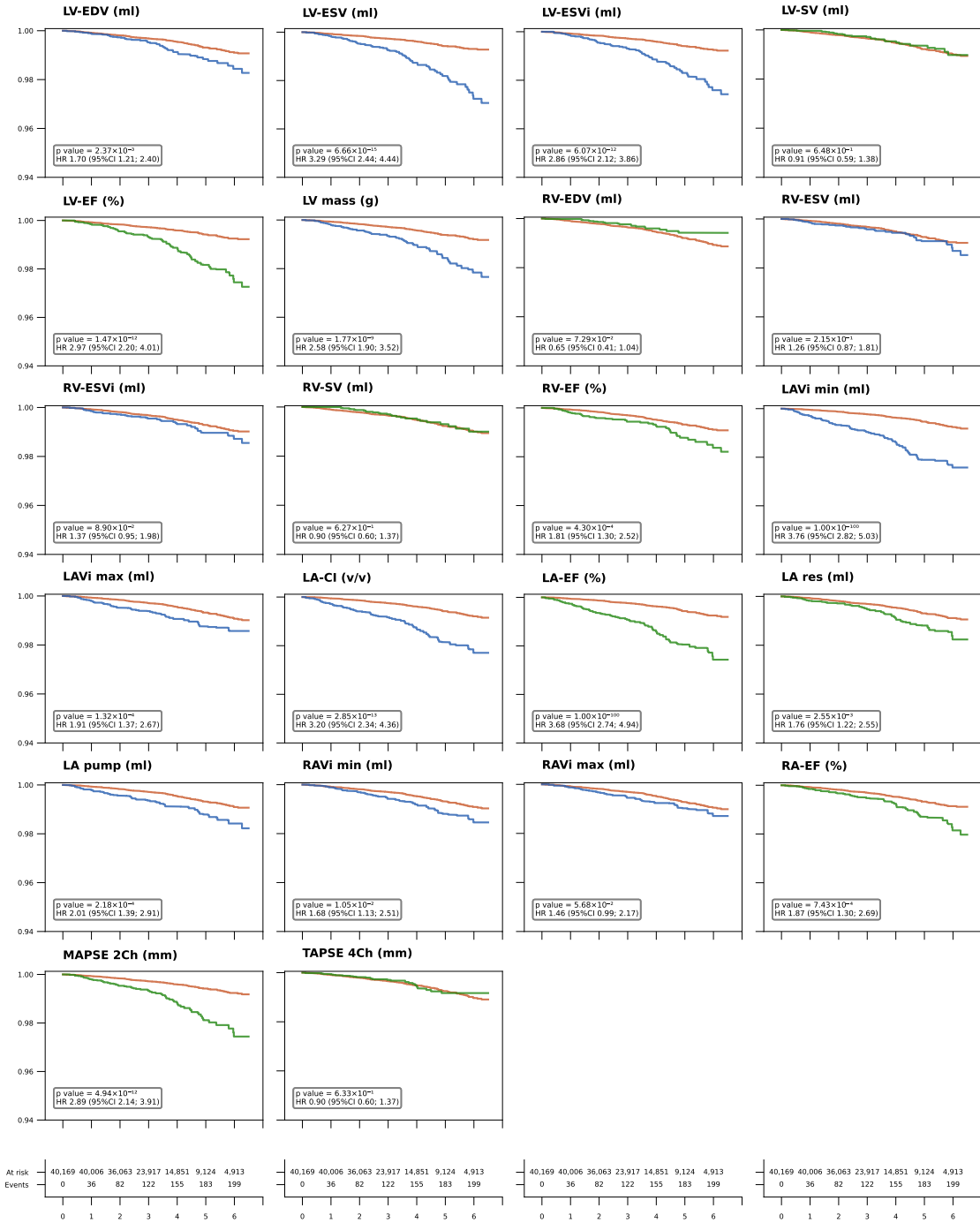




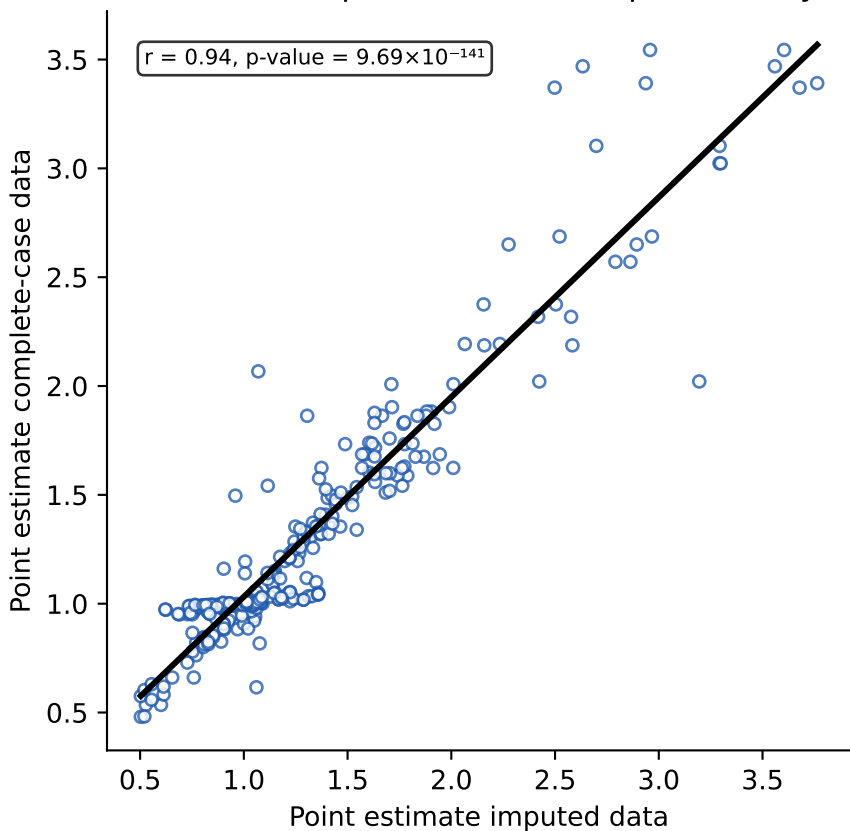
Year

■ Risk increase <15% ■ Reference ■ Risk increase >15%

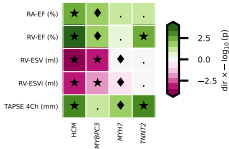
HF free survival



Correlation complete-case and imputed analyses



HCM



DCM

	DCM	MYH7	TTN
LV-EF (%)	★	.	★
LV-ESV (ml)	★	.	★



2.5
0.0
-2.5

$\text{dir } x - \log_{10}(p)$

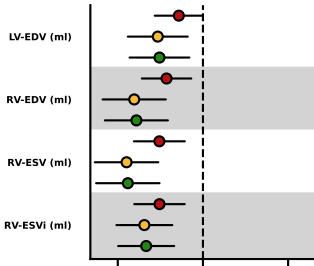
● Model 1 ● Model 2 ● Model 3

MYBPC3

Cases
(total sample)

OR
(95% CI)

p-value



113 (40,169)

0.82 (0.68; 1.00)

5.02×10^{-2}

0.69 (0.54; 0.88)

3.17×10^{-3}

0.70 (0.55; 0.90)

4.44×10^{-3}

0.74 (0.61; 0.91)

4.01×10^{-3}

113 (40,169)

0.57 (0.44; 0.74)

2.06×10^{-5}

0.58 (0.45; 0.75)

3.53×10^{-5}

0.70 (0.57; 0.86)

8.11×10^{-4}

113 (40,169)

0.54 (0.41; 0.70)

2.49×10^{-6}

0.54 (0.42; 0.70)

3.51×10^{-6}

0.70 (0.57; 0.86)

7.51×10^{-4}

113 (40,169)

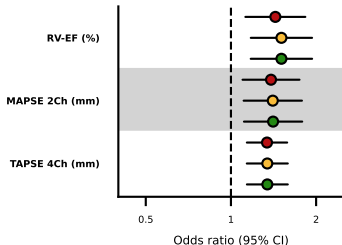
0.62 (0.49; 0.78)

4.07×10^{-5}

0.63 (0.50; 0.79)

7.36×10^{-5}

TNNT2



68 (40,169)

1.44 (1.12; 1.83)

3.72×10^{-3}

1.51 (1.18; 1.94)

1.25×10^{-3}

1.51 (1.17; 1.94)

1.27×10^{-3}

68 (40,169)

1.39 (1.10; 1.75)

5.84×10^{-3}

1.41 (1.11; 1.78)

4.94×10^{-3}

1.41 (1.11; 1.79)

4.59×10^{-3}

1.34 (1.14; 1.58)

4.58×10^{-4}

68 (40,169)

1.34 (1.14; 1.59)

5.15×10^{-4}

1.34 (1.14; 1.59)

4.88×10^{-4}

● Model 1 ● Model 2 ● Model 3

TTN

**Cases
(total sample)**

**OR
(95% CI)**

p-value

LV-ESV (ml)

44 (40,169)

1.43 (1.09; 1.87)

9.35×10^{-3}

LV-ESVi (ml)

44 (40,169)

1.68 (1.31; 2.16)

5.23×10^{-5}

LV-EF (%)

44 (40,169)

0.56 (0.44; 0.72)

2.96×10^{-6}

MAPSE 2Ch (mm)

44 (40,169)

0.60 (0.44; 0.84)

2.32×10^{-3}

MYH7

LA pump (ml)

34 (40,169)

1.57 (1.15; 2.14)

4.39×10^{-3}

RA-EF (%)

34 (40,169)

1.60 (1.16; 2.21)

4.27×10^{-3}

1.62 (1.17; 2.24)

3.77×10^{-3}

1.70 (1.21; 2.38)

1.96×10^{-3}

1.61 (1.16; 2.23)

4.45×10^{-3}

0.5

1

2

Odds ratio (95% CI)