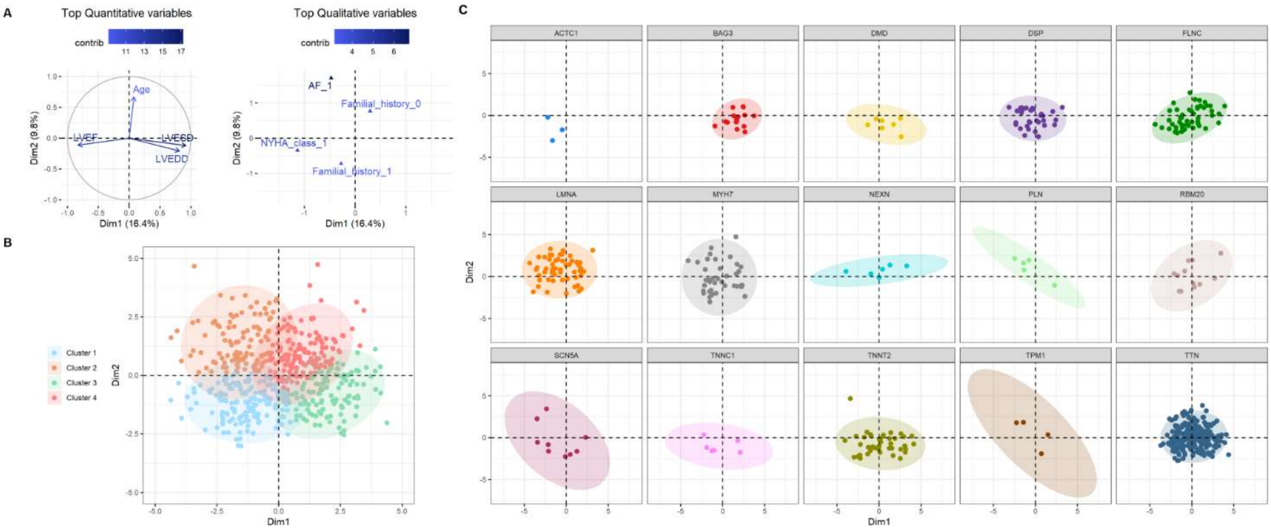
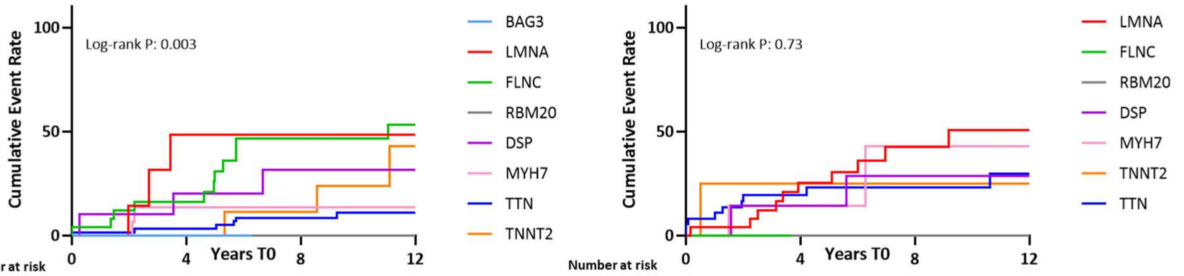
Supplemental figures and tables

Supplemental Figure 1: A. Top variables that gave the most contribution to the principle components, quantitative (continuous) and qualitative (categorical) variables respectively, are projected to the FAMD principle components. **B**. Cluster plot from factor map, individual samples coloured by pheno-clusters projected on the FAMD principle components. **C.** Factor map of genotype, individual samples of each genotype projected on the FAMD principle components are presented in own panel.



Supplemental Figure 2: Cumulative event rates per genotype in each of the four clusters. Event rates for major adverse events (all-cause mortality, heart failure hospitalization (HFH), heart transplantation (HTx), and malignant ventricular arrhythmias (MVA)), heart failure events (HFH and HTx) or arrhythmogenic event (MVA).

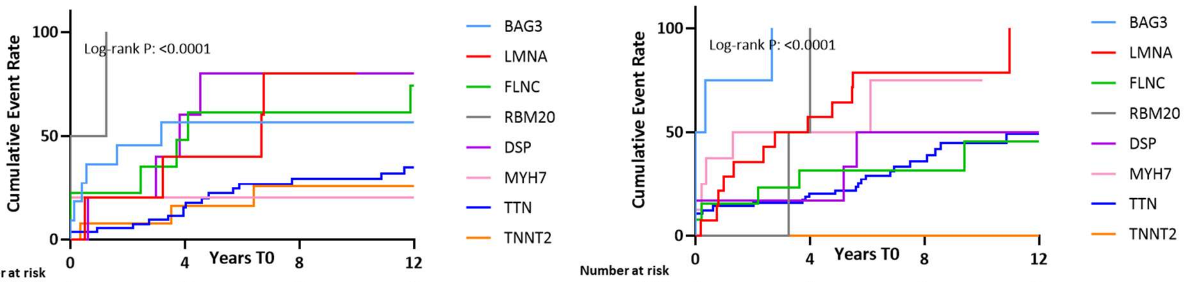


Major adverse events per genotype in cluster 1
All-cause mortality, HFH, HTx, MVA

Major adverse events per genotype in cluster 2
All-cause mortality, HFH, HTx, MVA

Number at risk	0	4	8	12
BAG3	1	1	0	0
LMNA	8	3	2	2
FLNC	26	20	10	7
RBM20	4	4	3	2
DSP	11	7	3	3
MYH7	17	10	8	4
TTN	66	58	40	29
TNNT2	16	11	7	2

Number at risk	0	4	8	12
LMNA	8	3	2	2
FLNC	26	20	10	7
RBM20	4	4	3	2
DSP	11	7	3	3
MYH7	17	10	8	4
TNNT2	16	11	7	2
TTN	66	58	40	29



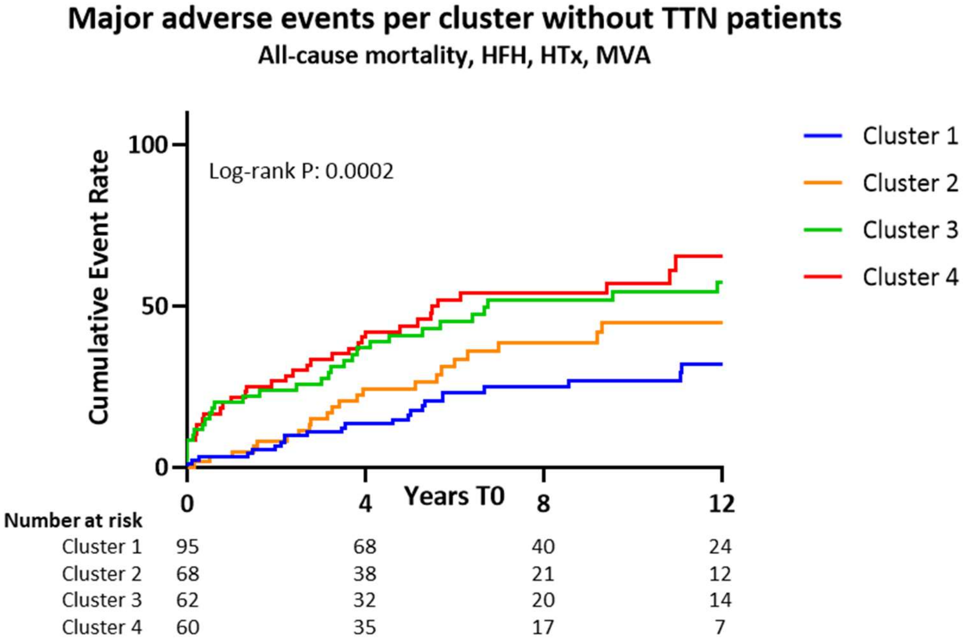
Major adverse events per genotype in cluster 3
All-cause mortality, HFH, HTx, MVA

Major adverse events per genotype in cluster 4
All-cause mortality, HFH, HTx, MVA

Number at risk	0	4	8	12
BAG3	11	3	3	1
LMNA	5	3	3	0
FLNC	9	4	3	2
RBM20	2	0	0	0
DSP	6	2	1	1
MYH7	6	3	2	2
TTN	57	41	27	23
TNNT2	14	10	7	6

Number at risk	0	4	8	12
BAG3	5	0	0	0
LMNA	15	7	3	0
FLNC	14	9	6	1
RBM20	2	1	0	0
DSP	7	6	3	1
MYH7	8	4	1	0
TTN	86	52	23	13
TNNT2	7	7	4	3

Supplemental Figure 3: Cumulative event rates per cluster after removing the *TTN* patients from each cluster. Event rates for major adverse events (all-cause mortality, heart failure hospitalization (HFH), heart transplantation (HTx), and malignant ventricular arrhythmias (MVA)), heart failure events (HFH and HTx) or arrhythmogenic event (MVA).

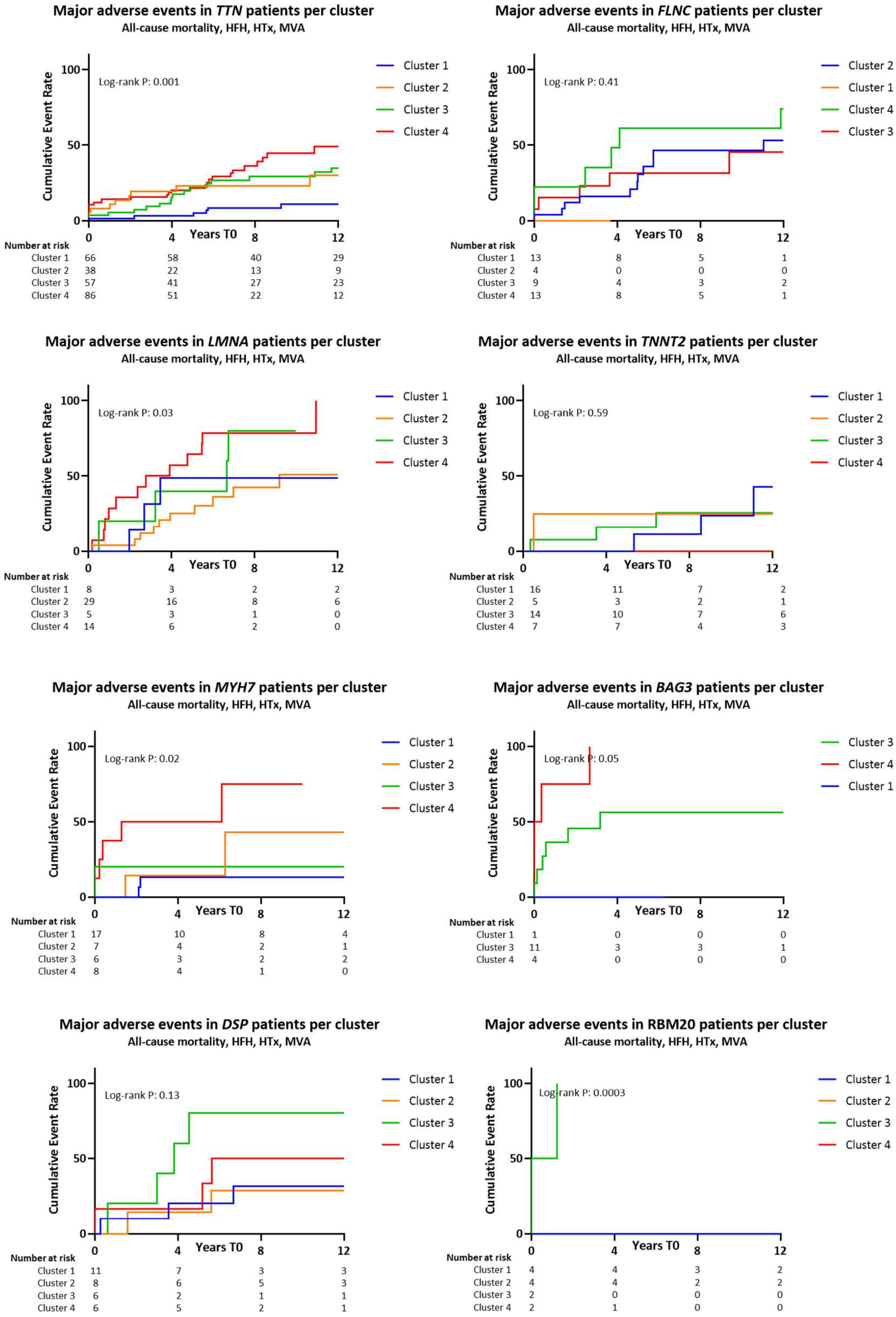


Major adverse events per cluster without TTN patients

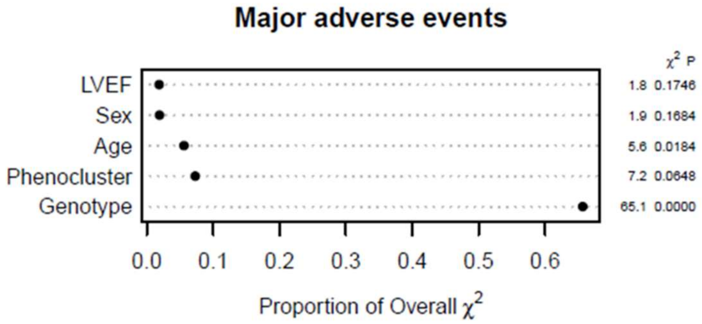
All-cause mortality, HFH, HTx, MVA

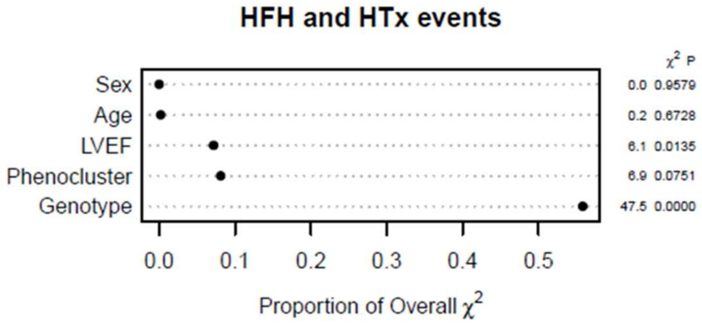
Number at risk	0	4	8	12
Cluster 1	95	68	40	24
Cluster 2	68	38	21	12
Cluster 3	62	32	20	14
Cluster 4	60	35	17	7

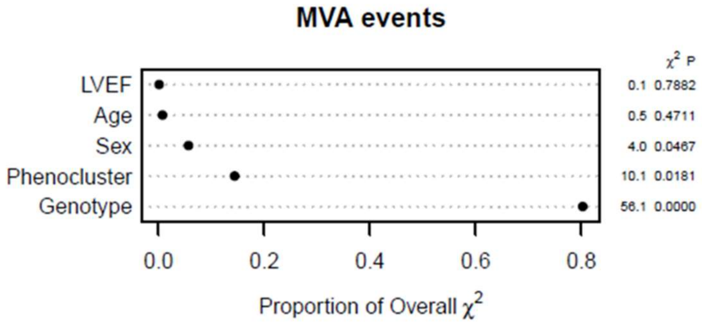
Supplemental Figure 4: Cumulative event rates per cluster in each of the genotypes. Event rates for major adverse events (all-cause mortality, heart failure hospitalization (HFH), heart transplantation (HTx), and malignant ventricular arrhythmias (MVA)), heart failure events (HFH and HTx) or arrhythmogenic event (MVA).



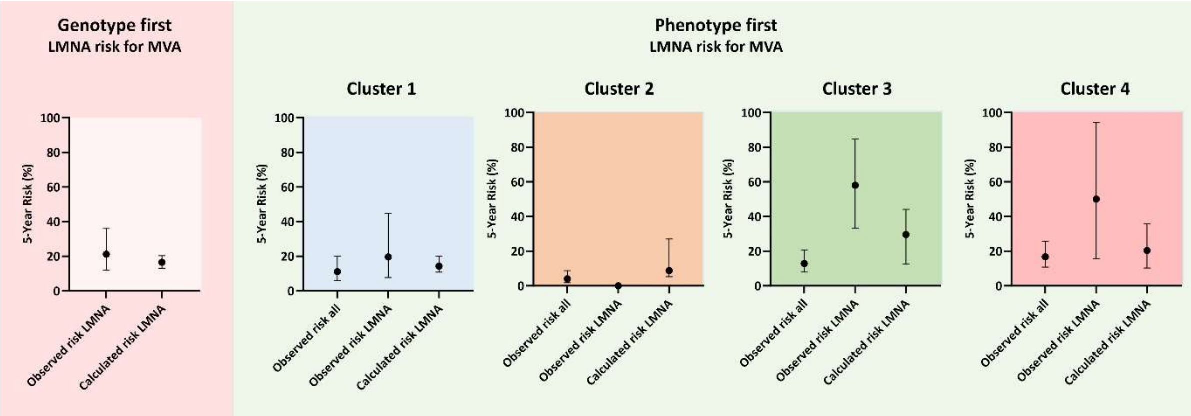
Supplemental figure 5: Relative contribution of genotype, phenocluster, and clinical variables to outcome prediction in genetic DCM patients using cox proportional hazards models. Plots showing non-imputated predictions for major adverse events (all-cause mortality, heart failure hospitalization (HFH), heart transplantation (HTx), and malignant ventricular arrhythmias (MVA)), heart failure events (HFH and HTx) or arrhythmogenic event (MVA).







Supplemental Figure 6: Comparing the genotype- and phenotype first approached for the five-year observed and calculated risk for malignant ventricular arrhythmias (MVA) in *LMNA* patients utilizing the *LMNA* risk score for MVA.



Supplemental Table 1: Number of events per cluster per genotype for major adverse events and malignant ventricular arrhythmias (MVA).

	Cluster 1		**Cluster 2**		**Cluster 3**		**Cluster 4**	
	Major adverse events	MVA	Major adverse events	MVA	Major adverse events	MVA	Major adverse events	MVA
Total	30	11	34	13	49	25	62	18
ACTC1	0	0	-	-	-	-	-	-
BAG3	0	0	-	-	6	3	4	1
DMD	0	0	-	-	3	2	1	0
DSP	3	2	2	1	5	5	3	1
FLNC	11	6	0	0	6	2	5	0
LMNA	4	0	13	7	4	2	12	7
MYH7	2	0	2	0	2	0	5	0
NEXN	-	-	1	1	-	-	2	0
PLN	-	-	4	1	1	1	-	-
RBM20	0	0	0	0	2	1	2	1
SCN5A	1	1	1	0	0	0	-	-
TNNTC1	0	0	0	0	0	0	-	-
TNNT2	3	0	1	0	3	0	0	0
TPM	-	-	1	0	0	0	0	0
TTN	6	2	9	3	17	9	28	8