Supplemental information:

Supplemental Table 1. Oligonucleotide primer sequences

Primers	Sequence (5' - 3')	Amino acid	Fragment (bp)
HRC_Exon1_1F	CCCTATTGGCTGGGGAATG	5’UTR, 1-14	281
HRC_Exon1_1R	CCCAGAGGACAGAAGCGTG		
HRC_Exon1_2F	CAGTGCTGCCTGTCCGTC	1-81	264
HRC_Exon1_2R	ATGATGCCCATTCTCTGTGG		
HRC_Exon1_3F	ATCAGCAGAGCTTCGCCAC	52-142	271
HRC_Exon1_3R	TTCCGTGTCTTCACTCCCG		
HRC_Exon1_4F	GTCGGAGATGAGGGTGTCTC	112-210	296
HRC_Exon1_4R	TGTCCATACTCAGTGGAGGC		
HRC_Exon1_5F	TCATATCCTCAGGCATGGAC	174-269	285
HRC_Exon1_5R	GCCTGGTGTCTATATTCAATGG		
HRC_Exon1_6F	TCTCAGATGGACACCATCATCA	226-327	304
HRC_Exon1_6R	TCTTCCTTTCTGTGGTCTTGGT		
HRC_Exon1_7F	AGGCACCGAAGCCATGAAG	295-392	292
HRC_Exon1_7R	TTGCAACATAGTGGCCGAAC		
HRC_Exon1_8F	GATGTGTCCACTGAACGTTGGC	355-445	270
HRC_Exon1_8R	GTGGCTTTGCCTGTGGCTG		
HRC_Exon1_9F	CCTCACCATCACCACCACAG	414-498	252
HRC_Exon1_9R	GTCTTCCTCATGGGAGCCG		
HRC_Exon1_10F	AAGGATAGAAGCCATTTGAGG	471-558	261
HRC_Exon1_10R	AACCTCAGCCCTCTCTTCC		
HRC_Exon1_11F	TCAGCCTGAACCAGGAGGAG	527-610	296
HRC_Exon1_11R	CAGGCTGACTCGGTTCCTTC		
HRC_Exon2F	GTGGGAAGGAACCGAGTCAG	611-633	174
HRC_Exon2R	GGGACAGATTCTGGGGACAC		
HRC_Exon3F	CCTCCCAAGTGGCGTTAGAG	634-656	165
HRC_Exon3R	ATCCTGAGGCCCAGTGGAG		
HRC_Exon4F	CCCATCCTAACTCCGCCC	657-674	185
HRC_Exon4R	ACCAGGATTCACCACGCTG		
HRC_Exon5F	GTGGCTGCCTAATTTTGCTC	675-686	138
HRC_Exon5R	CTAAACGGGGCTTTTACACG		
HRC_Exon6F	GGCTTTGAACACCAGCTGTC	687-699, 3’UTR	219
HRC_Exon6R	ATGCCCTGAGATTCCCAGAC		

Supplemental Table 2. Hardy-Weinberg Equilibrium Analysis

	Overall (n=219)					**DCM (n=123)**					**Controls (n=96)**				
HRC Variant	**χ^2**	**χ^2 *p*-value**	**LR**	**LR *p*-value**	**Exact *p*-value**	**χ^2**	**χ^2 *p*-value**	**LR**	**LR *p*-value**	**Exact *p*-value**	**χ^2**	**χ^2 *p*-value**	**LR**	**LR *p*-value**	**Exact *p*-value**
Leu35Leu (A→G)	0.371	0.542	0.372	0.542	0.565	0.191	0.662	0.192	0.662	0.683	0.181	0.670	0.182	0.670	0.832
Ser43Asn (G→A)	0.106	0.745	0.106	0.745	0.765	0.106	0.745	0.106	0.745	0.837	0.610	0.435	0.611	0.434	0.401
Ser96Ala (T→G)	0.342	0.558	0.342	0.558	0.591	0.647	0.421	0.648	0.421	0.549	0.005	0.945	0.005	0.945	1.000
Glu202_Glu203insGlu (-→GAG)	0.846	0.358	0.848	0.357	0.315	0.080	0.777	0.080	0.777	0.698	1.097	0.295	1.102	0.294	0.294
Asp261del (GAT→-)	2.512	0.113	2.514	0.113	0.119	1.568	0.211	1.568	0.210	0.238	0.948	0.330	0.949	0.330	0.429
His321ins51aa	0.065	0.799	0.127	0.721	1.000	0.042	0.838	0.082	0.775	0.039	0.024	0.876	0.048	0.827	1.000

LR, Likelihood Ratio

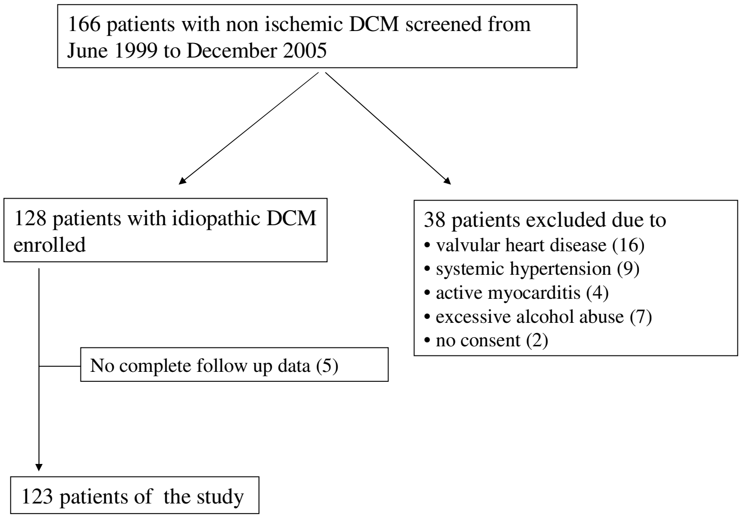
Supplemental Table 3. Statistical Analysis of Clinical Parameters and Genotypes (One Way ANOVA, χ^2, and Fisher Exact Test)

Genotype	**NYHA Classification**		**AF**		**LBBB**		**LVEF**		**LVEDD**		**LVESD**		**ICD (History of sustained VT or VF)**		**Unexplained Syncope**	
	χ^2 (DF)	***p***	**χ^2 (DF)**	***p***	**χ^2 (DF)**	***p***	**F-ratio**	***p***	**F-ratio**	***p***	**F-ratio**	***p***	**χ^2 (DF)**	***p***	**χ^2 (DF)**	***p***
Leu35Leu	4.596 (4)	0.331	3.662 (2)	0.160	0.409 (2)	0.815	0.352	0.788	0.747	0.526	0.541	0.659	0.818 (2)	0.664	0.850 (2)	0.654
Ser43Asn	7.726 (4)	0.102	0.170 (2)	0.919	0.235 (2)	0.889	0.066	0.978	0.337	0.798	0.408	0.748	0.152 (2)	0.927	1.295 (2)	0.523
Ser96Ala	1.314 (4)	0.859	0.915 (2)	0.633	1.617 (2)	0.449	1.088	0.340	1.740	0.180	0.367	0.693	**11.710 (2)**	**0.003**	3.131 (2)	0.209
Glu202_Glu203insGlu	1.657 (4)	0.798	2.923 (2)	0.232	1.627 (2)	0.443	0.028	0.994	0.335	0.800	0.198	0.898	0.517 (2)	0.772	0.521 (2)	0.771
Asp261del	6.612 (4)	0.158	2.797 (2)	0.247	0.253 (2)	0.881	0.445	0.721	1.508	0.216	1.074	0.363	0.972 (2)	0.615	1.629 (2)	0.443
His321ins51aa	4.269 (2)	0.118	Fisher Exact	1.000	Fisher Exact	0.102	0.146	0.865	0.528	0.591	0.254	0.776	Fisher Exact	1.000	Fisher Exact	1.000

DF, degrees of freedom; with bold statistical significant associations

Supplemental Figure 1

Diagrammatic presentation of the idiopathic DCM patients entered in this study, according to inclusion and exclusion criteria.



Supplemental Figure 2

Kaplan-Meier plots for freedom from a life-threatening arrhythmic event according to left ventricular ejection fraction (A), gender (B), administration of amiodarone (C), New York Heart Association status (D), and history of sustained VT or VF episodes prior to study entry. Each event is depicted as a step down. Each censored case (death from other causes, heart transplantation, and end due to study termination) is marked with a cross. The tables at the bottom of the plots indicate the number of DCM patients at risk for each year of the follow up study.