SUPPLEMENTARY INFORMATION

Supplementary Table 1. Clinical characteristics of the study population. Peripheral and total QRS score were calculated through the sum of Q, R, and S height, each taken as absolute value in mm (1 mm = 0.1 mV), in peripheral and total leads respectively.

Clinical Characteristics	
Age at diagnosis (years)	75±5
Body surface area (m^2)	1.8±0.2
Systolic blood pressure (mmHg)	125±19
Diastolic blood pressure (mmHg)	72±13
NTproBNP (pg/ml)	7193±9312
Electrocardiography	
Heart rate (beats per minute)	77±17
Total QRS score (mm)	110±35
Peripheral QRS score (mm)	34±27
Echocardiography	
Left ventricular end diastolic diameter (mm)	42±15
Left ventricular end systolic diameter (mm)	31±18
Interventricular septum thickness (mm)	16±5
Posterior wall thickness (mm)	15±5
Interatrial septum thickness (mm)	6±5
Left atrial diameter (mm)	47±4
Left ventricular end diastolic volume (ml)	93±26
Left ventricular end systolic volume (ml)	53±22
Left ventricular ejection fraction	43±15
BSA Indexed left ventricular mass (g/m^2)	211±40

Supplementary Table 2. Full sequences of all haplotypes represented in Figure 4, obtained including variants at all frequencies for finer dissection.

HAP1	CCGCCGAAGCGGGAGCGATC
HAP2	CCGCCGAGGCGGGGGCGACC
HAP3	CCGCCGAAGCGGGGGCGACC
VAR1	TCGCCGAAGCGGGGACGACC
HAP5	TCGCCGAAGCGGGGGCAACC
HAP6	CCGCCGAAGCGAGAGCGATC
HAP7	CCGCCGGGGCGGGGGCGACC
HAP8	CCGCCGAAGCGGGGGCGACA
HAP9	TCGCCGGAGCGGGGGCAACC
HAP10	CCGCCGAAACGGGGGCGATC
HAP11	CCGCCGAAGCAGGAGCGATC
HAP12	CCGCCGAAGCGGGAGTGATC
HAP13	CCGTCGAGGCGGGGGCGACC
HAP14	CCGCCGAAGCGGGGGCGATC
HAP15	CCGCCGAAGCGGGGGCGACC
HAP16	TCGCCGAAGCGGGGGCGACC
HAP17	CCACCGAAGCGGGAGCGATC
HAP18	CCGCCGAAACGGGGGCGATA
HAP19	TCGCTGAAGCGGGGGCGACC
HAP20	TCGCTGAAGCGGAAGCAACC
HAP21	CCGCCGAAGCGGGAGCGCTC
HAP22	CCGTCAAGGCGGGGGCGACC
HAP23	CCGTCGAGGCGGGGGCGACA
HAP24	CCGCCAAAGCGGGAGCGATC
HAP25	CCGCCGAAGCGGGGGTGATC
HAP26	CTGCCGGGGCGGGGGCGACC
VAR2	TTGCCGAAGCGGGGACGACC
HAP28	TCACTGGAGCGGGGGCAACC
HAP29	CTGCCGAAACGGGGGCGATA
HAP30	CCACCAAAGCGGGAGCGATC
HAP31	CCGCCAAAGCAGGAGCGATC
HAP32	CCATCGAGGCGGGGGCGACC
HAP33	CCGCCGAAACGGGGGTGATC

Supplementary Table 3. Details of all variants reported in the manuscript.

Genomic_variant (hg19)	rsID	Fig. 3	Fig. 4	Consequence (VEP v104)	RefSeq_transcript_variant	HGVS_Predicted_Protein
18-29165918-C-T	rs17740847	YES	YES	intergenic_variant	–	
18-29166726-C-T	rs117748556	NO	YES	upstream_gene_variant	–	–
18-29167669-G-A	rs76431866	NO	YES	upstream_gene_variant	–	–
18-29167905-A-G	rs1667244	YES	NO	upstream_gene_variant	–	–
18-29168029-C-T	rs142696368	NO	YES	upstream_gene_variant	–	–
18-29168467-C-T	rs72922938	NO	YES	upstream_gene_variant	–	–
18-29169387-G-A	rs150555470	NO	YES	upstream_gene_variant	–	–
18-29169825-A-G	rs3764479	YES	NO	upstream_gene_variant	–	–
18-29170483-G-T	rs3764478	YES	NO	upstream_gene_variant	–	–
18-29170617-A-G	rs112278416	YES	YES	upstream_gene_variant	–	–
18-29170698-A-G	rs72922940	YES	YES	upstream_gene_variant	–	–
18-29170709-G-A	rs3764477	NO	YES	upstream_gene_variant	–	–
18-29171033-C-T	rs116409170	NO	YES	upstream_gene_variant	–	–
18-29171123-A-T	rs3794885	YES	NO	upstream_gene_variant	–	–
18-29171184-G-A	rs79748512	NO	YES	upstream_gene_variant	–	–
18-29172476-G-T	rs723744	YES	NO	intron_variant	NM_000371.3:c.70-383G>T	NP_000362.1:p.?
18-29172865-G-A	rs1800458	YES	YES	missense_variant	NM_000371.3:c.76G>A	NP_000362.1:p.(Gly26Ser)
18-29173680-C-G	rs1080093	YES	NO	intron_variant	NM_000371.3:c.200+691C>G	NP_000362.1:p.?
18-29173784-G-A	rs72922947	NO	YES	intron_variant	NM_000371.3:c.200+795G>A	NP_000362.1:p.?
18-29173795-A-G	rs1080094	YES	YES	intron_variant	NM_000371.3:c.200+806A>G	NP_000362.1:p.?
18-29176460-C-A	rs3764476	YES	NO	intron_variant	NM_000371.3:c.336+1242C>A	NP_000362.1:p.?
18-29176873-G-C	rs7235277	YES	NO	intron_variant	NM_000371.3:c.336+1655G>C	NP_000362.1:p.?
18-29176971-T-G	rs3794884	YES	NO	intron_variant	NM_000371.3:c.337-1560T>G	NP_000362.1:p.?
18-29178618-G-A	rs76992529	NO	YES	missense_variant	NM_000371.3:c.424G>A	NP_000362.1:p.(Val142Ile)
18-29178899-C-T	rs62093482	NO	YES	3_prime_UTR_variant	NM_000371.3:c.*261C>T	NP_000362.1:p.?
18-29179040-C-T	rs1791228	YES	NO	downstream_gene_variant	–	–
18-29179228-G-A	rs75032823	YES	YES	downstream_gene_variant	–	–
18-29181885-A-C	rs117207032	NO	YES	downstream_gene_variant	–	–
18-29182352-T-G	rs1791229	YES	NO	downstream_gene_variant	–	–
18-29183587-A-C	rs4799583	YES	NO	downstream_gene_variant	–	–
18-29183812-T-C	rs1473342	YES	YES	downstream_gene_variant	–	–
18-29184386-C-A	rs144559530	NO	YES	intergenic_variant	–	–