Supplemental Material

Rare variants in the *FBN1* gene are associated with sporadic dilated cardiomyopathy in a Chinese Han population

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Table S1. Rare variants of *FBN1* identified in DCM cases and controls.

HGVS.c (NM_000138)	Consequence	MAF in gnomAD exome (EAS)	MAF in ExAC (EAS)	MAF in 1,000 Genomes (EAS)	VEST3 score	REVEL score	CADD phred	MutationTaster pred	ACMG	Pathogenicity	NO. in cases (*n* = 53)	NO. in controls (*n* = 9)
c. C13T	missense	5.82E-05	0.0001	ND	0.18	0.119	24.6	N	PM1+PM2+BP1	Uncertain significance	1	0
c. G100C	missense	5.80E-05	ND	ND	0.147	0.103	19.93	N	PM1+PM2+BP1	Uncertain significance	0	1
c. A149T	missense	ND	ND	ND	0.48	0.278	14.91	N	PM1+PM2+BP1	Uncertain significance	2	0
c. T605C	missense	0.0006	ND	ND	0.853	0.829	26.9	D	PM2+PP3+BP1	Uncertain significance	1	0
c. C657G	missense	0.0002	0.0001	ND	0.941	0.741	23.9	D	PM2+PP3+BP1	Uncertain significance	1	0
c. A913G	missense	0.0003	0.0001	ND	0.106	0.22	11	N	PM2+BP1	Uncertain significance	3	1
c. T1217A	missense	ND	ND	ND	0.195	0.132	11	N	PM2+BP1	Uncertain significance	5	0
c. T1841C	missense	0.0002	0.0002	ND	0.837	0.961	25.1	D	PM2+PP3+BP1	Uncertain significance	1	0
c. C1858T	missense	0.0001	ND	ND	0.402	0.224	20.1	D	PM2+BP1	Uncertain significance	1	1
c. A2011G	missense	ND	ND	ND	0.037	0.31	6.945	N	PM2+BP1	Uncertain significance	1	0
c. A2149T	missense	ND	ND	ND	0.386	0.405	16.23	D	PM2+BP1	Uncertain significance	0	1

HGVS.c (NM_000138)	Consequence	MAF in gnomAD exome (EAS)	MAF in ExAC (EAS)	MAF in 1,000 Genomes (EAS)	VEST3 score	REVEL score	CADD phred	MutationTaster pred	ACMG	Pathogenicity	NO. in cases (*n* = 53)	NO. in controls (*n* = 9)
c. G2269C	missense	ND	ND	ND	0.554	0.768	26.2	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G2290A	missense	0.0003	0.0002	ND	0.05	0.259	16.72	N	PM2+BP1	Uncertain significance	1	0
c. A2613C	missense	5.80E-05	ND	ND	0.588	0.652	24	D	PM2+PP3+PP5+BP1	Uncertain significance	1	0
c. 2793dupG	frameshift insertion	ND	ND	ND	NA	NA	NA		PVS1+PM2	Likely pathogenic	1	0
c. G2887C	missense	5.80E-05	0.0001	ND	0.192	0.344	19.9	D	PM2+PP3+BP1	Uncertain significance	1	1
c. A3142G	missense	0.0002	ND	ND	0.348	0.297	23	D	PM2+BP1	Uncertain significance	1	1
c. G3571A	missense	5.81E-05	0	ND	0.105	0.407	24.1	D	PM2+PP3+BP1	Uncertain significance	1	0
c. C3697G	missense	ND	ND	ND	0.35	0.431	20.2	D	PM2+PP3+BP1	Uncertain significance	1	0
c. A3971G	missense	0	0	ND	0.442	0.893	23.4	D	PM2+PP3+BP1	Uncertain significance	1	0
c. T3984G	missense	ND	ND	ND	0.259	0.607	23.1	D	PM2+BP1+BP4	Likely benign	0	1
c. A4325G	missense	ND	ND	ND	0.544	0.484	17.69	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G4406A	missense	0	0	ND	0.85	0.791	33	D	PM2+PM5+PP3+BP1	Uncertain significance	1	0
c. G4750A	missense	0.0002	0.0002	ND	0.71	0.659	28.2	D	PM2+PP3+BS2+BP1	Likely benign	1	0
c. C5210G	missense	ND	ND	ND	0.947	0.927	28.5	D	PM2+PP3+BP1	Uncertain significance	1	0
c. C5509T	missense	0	0	ND	0.803	0.719	21.6	D	PM2+PP3+BP1	Uncertain significance	1	0
c. A5596G	missense	0.0004	0.0004	ND	0.44	0.357	12.48	D	PM2+BP1	Uncertain significance	2	1
c. A5750G	missense	ND	ND	ND	0.186	0.292	15.09	D	PM2+BP1	Uncertain significance	1	0
c. G6174A	missense	ND	ND	ND	0.169	0.24	22.4	D	PM2+BP1	Uncertain significance	1	0
c. A6270C	missense	ND	ND	ND	0.324	0.507	19.47	D	PM2+PP3+BP1	Uncertain significance	1	0
c. A6301G	missense	ND	ND	ND	0.085	0.245	7.934	N	PM2+BP1	Uncertain significance	1	0

HGVS.c (NM_000138)	Consequence	MAF in gnomAD exome (EAS)	MAF in ExAC (EAS)	MAF in 1,000 Genomes (EAS)	VEST3 score	REVEL score	CADD phred	MutationTaster pred	ACMG	Pathogenicity	NO. in cases (*n* = 53)	NO. in controls (*n* = 9)
c. G6725A	missense	0.0001	0.0002	ND	0.432	0.518	28.2	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G6845A	missense	0.0001	0.0002	ND	0.687	0.543	24.1	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G6863C	missense	ND	ND	ND	0.097	0.304	19.8	D	PM2+BP1	Uncertain significance	1	0
c. C7082T	missense	0	ND	ND	0.601	0.611	33	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G7099A	missense	0	0	ND	0.531	0.644	27	D	PM2+PP3+BP1	Uncertain significance	1	0
c. C7193T	missense	0	ND	ND	0.616	0.584	26.2	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G7231A	missense	5.80E-05	0.0001	ND	0.029	0.493	22	D	PM2+BP1	Uncertain significance	1	0
c. G7241A	missense	0.0001	0	ND	0.665	0.45	22.9	D	PM2+BP1	Uncertain significance	1	0
c. C7559T	missense	0.0003	0.0001	ND	0.892	0.656	26.4	D	PM2+PP3+BP1	Uncertain significance	2	0
c. A7598G	missense	0	0	ND	0.042	0.37	11.61	D	PM2+BP1	Uncertain significance	1	0
c. A7807G	missense	ND	ND	ND	0.361	0.586	25.1	D	PM2+PP3+BP1	Uncertain significance	1	0
c. G7816A	missense	0	ND	ND	0.486	0.377	23.9	D	PM2+PP3+BP1	Uncertain significance	1	0
c. T8069G	missense	0.0005	0.0006	ND	0.525	0.373	20.4	D	PM2+BP1	Uncertain significance	1	1
c. G8081A	missense	0	ND	ND	0.801	0.422	23.2	D	PM2+BP1	Uncertain significance	1	0
c. C8306G	missense	ND	ND	ND	0.852	0.697	25.1	D	PM2+PP3+BP1	Uncertain significance	1	0
c. T8507A	missense	ND	ND	ND	0.931	0.732	25.4	D	PM2+PP3+BP1	Uncertain significance	1	0

Abbreviations: HGVS.c: variants using HGVS notation (DNA level); MAF, minor allele frequency; EAS, East Asian; NA, not available; ND, not detected; VEST3 score, VEST(variant effect scoring tool) version 3 score; REVEL score, rare exome variant ensemble learner score; CADD phred, CADD (combined annotation dependent depletion) phred-like score, the deleteriousness threshold recommended by the authors is greater than 20; MutationTaster pred, MutationTaster prediction, which evaluates the pathogenic potential of DNA sequence alterations, D: disease causing - i.e. probably deleterious, N: polymorphism - i.e. probably harmless; ACMG, the American College of Medical Genetics and Genomics; PVS1, PM1, PM2, PM5, PP3, BS2, BP1, and BP4 are part of the 28 criteria in the ACMG guidelines for the clinical interpretation of sequence variations.

Table S2. The deleteriousness prediction for rare missense variants of *FBN1* in DCM cases and controls.

HGVS.c (NM_000138)	HGVS.p	MAF in gnomAD exome (EAS)	VEST3 score	REVEL score	CADD phred	MutationTaster pred	NO. in cases	NO. in controls
c.T605C	p.I202T	0.0006	0.853	0.829	26.9	D	1	0
c.C657G	p.H219Q	0.0002	0.941	0.741	23.9	D	1	0
c.T1841C	p.I614T	0.0002	0.837	0.961	25.1	D	1	0
c.G2269C	p.D757H	ND	0.554	0.768	26.2	D	1	0
c.A2613C	p.L871F	5.80E-05	0.588	0.652	24	D	1	0
c.G4406A	p.R1469H	0	0.85	0.791	33	D	1	0
c.C5210G	P1737R	ND	0.947	0.927	28.5	D	1	0
c.C5509T	P1837S	0	0.803	0.719	21.6	D	1	0
c.G6845A	R2282Q	0.0001	0.687	0.543	24.1	D	1	0
c.C7082T	p.S2361L	0	0.601	0.611	33	D	1	0
c.G7099A	p.G2367R	0	0.531	0.644	27	D	1	0
c.C7193T	p.T2398I	0	0.616	0.584	26.2	D	1	0
c.G7241A	p.R2414Q	0.0001	0.665	0.45	22.9	D	1	0
c.C7559T	p.T2520M	0.0003	0.892	0.656	26.4	D	2	0
c.G8081A	p.R2694Q	0	0.801	0.422	23.2	D	1	0
c.C8306G	p.S2769C	ND	0.852	0.697	25.1	D	1	0
c.T8507A	p.L2836H	ND	0.931	0.732	25.4	D	1	0

Abbreviations: HGVS.c: variants using HGVS notation (DNA level); HGVS.p: HGVS notation (protein level); MAF, minor allele frequency; EAS, East Asian; VEST3 score, VEST(variant effect scoring tool) version 3 score; REVEL score, rare exome variant ensemble learner score; CADD phred, CADD (combined annotation dependent depletion) phred-like score, the deleteriousness threshold recommended by the authors is greater than 20; MutationTaster pred, MutationTaster prediction, which evaluates the pathogenic potential of DNA sequence alterations, D: disease causing - i.e. probably deleterious.

Table S3. Rare deleterious *FBN1* variants across the DCM cohort.

Subject	Exon	HGVS.c (NM_000138)	HGVS.p	SNP	MAF in gnomAD exome (EAS)	MAF in ExAC (EAS)	MAF in 1,000 Genomes (EAS)	ACMG	Pathogenicity
DCM1	7	c.T605C	p.I202T	rs1300991442	0.0006	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM2	7	c.C657G	p.H219Q	rs774754863	0.0002	0.0001	ND	PM2+PP3+BP1	Uncertain significance
DCM3	16	c.T1841C	p.I614T	rs762427180	0.0002	0.0002	ND	PM2+PP3+BP1	Uncertain significance
DCM4	19	c.G2269C	p.D757H	rs2043616147	ND	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM5	22	c.A2613C	p.L871F	rs770290542	5.80E-05	ND	ND	PM2+PP3+PP5+BP1	Uncertain significance
DCM6	24	c.2793dupG	p.S932fs	NA	ND	ND	ND	PVS1+PM2	Likely pathogenic
DCM7	36	c.G4406A	p.R1469H	rs397515808	0	0	ND	PM2+PM5+PP3+BP1	Uncertain significance
DCM8	42	c.C5210G	P1737R	NA	ND	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM9	45	c.C5509T	P1837S	rs755430984	0	0	ND	PM2+PP3+BP1	Uncertain significance
DCM10	56	c.G6845A	R2282Q	rs759696323	0.0001	0.0002	ND	PM2+PP3+BP1	Uncertain significance
DCM11	58	c.C7082T	p.S2361L	rs397515844	0	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM12	58	c.G7099A	p.G2367R	rs368978109	0	0	ND	PM2+PP3+BP1	Uncertain significance
DCM13	58	c.C7193T	p.T2398I	rs1169351376	0	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM14	59	c.G7241A	p.R2414Q	rs143863014	0.0001	0	ND	PM2+BP1	Uncertain significance
DCM15	61	c.C7559T	p.T2520M	rs763759308	0.0003	0.0001	ND	PM2+PP3+BP1	Uncertain significance
DCM16	61	c.C7559T	p.T2520M	rs763759308	0.0003	0.0001	ND	PM2+PP3+BP1	Uncertain significance
DCM17	65	c.G8081A	p.R2694Q	rs371375126	0	ND	ND	PM2+BP1	Uncertain significance
DCM18	66	c.C8306G	p.S2769C	NA	ND	ND	ND	PM2+PP3+BP1	Uncertain significance
DCM19	66	c.T8507A	p.L2836H	NA	ND	ND	ND	PM2+PP3+BP1	Uncertain significance

Abbreviations: HGVS.c: variants using HGVS notation (DNA level); HGVS.p: HGVS notation (protein level); DCM, dilated cardiomyopathy; MAF, minor allele frequency; EAS, East Asian; NA, not available; ND, not detected; ACMG, the American College of Medical Genetics and

Genomics; PVS1, PM2, PP3, PP5, and BP1 are part of the 28 criteria in the ACMG guidelines for the clinical interpretation of sequence variations.

Table S4. List of 44 DCM-associated genes evaluated by ClinGen and included in this study.

	ClinGen DCM gene-disease validity classification	Gene symbol
High evidence genes	Moderate	*ACTC1*
	Moderate	*ACTN2*
	Definitive	*BAG3*
	Definitive	*DES*
	Strong	*DSP*
	Definitive	*FLNC*
	Moderate	*JPH2*
	Definitive	*LMNA*
	Definitive	*MYH7*
	Moderate	*NEXN*
	Definitive	*PLN*
	Definitive	*RBM20*
	Definitive	*SCN5A*
	Definitive	*TNNC1*
	Moderate	*TNNI3*
	Definitive	*TNNT2*
	Moderate	*TPM1*
	Definitive	*TTN*
	Moderate	*VCL*
Low/variable evidence genes	Limited	*ABCC9*
	Limited	*ANKRD1*
	Limited	*CSRP3*
	Limited	*CTF1*
	Limited	*DSG2*
	Limited	*DTNA*
	Limited	*EYA4*
	Limited	*GATAD1*
	Limited	*ILK*
	Limited	*LAMA4*
	Limited	*LDB3*
	Limited	*MYBPC3*
	Limited	*MYH6*
	Limited	*MYL2*
	Limited	*MYPN*
	Limited	*NEBL*
	Limited	*NKX2-5*
	Limited	*OBSCN*
	Limited	*PLEKHM2*
	Limited	*PRDM16*

	ClinGen DCM gene-disease validity classification	Gene symbol
Low/variable evidence genes	Limited	*PSEN2*
	Limited	*SGCD*
	Limited	*TBX20*
	Limited	*TCAP*
	Limited	*TNNI3K*

Abbreviations: DCM, dilated cardiomyopathy; ClinGen: Clinical Genome Resource.

Table S5. Rare variants identified as pathogenic or likely pathogenic in DCM-associated genes according to ACMG guidelines.

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr10	121411252	TG	T	frameshift deletion	*BAG3*	PVS1+PM2	Likely pathogenic	1	0
chr10	121411299	T	TA	frameshift insertion	*BAG3*	PVS1+PM2	Likely pathogenic	1	0
chr10	121429549	C	T	stop gain	*BAG3*	PVS1+PP3+PP5	Pathogenic	1	0
chr6	7563990	C	T	stop gain	*DSP*	PVS1+PM2+PP3	Pathogenic	1	0
chr6	7568096	ACATG	A	frameshift deletion	*DSP*	PVS1+PM2	Likely pathogenic	1	0
chr6	7577219	C	T	stop gain	*DSP*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr6	7580621	C	T	stop gain	*DSP*	PVS1+PM2+PP5	Pathogenic	2	0
chr6	7581438	AG	A	frameshift deletion	*DSP*	PVS1+PM2	Likely pathogenic	1	0
chr6	7584541	CTT	C	frameshift deletion	*DSP*	PVS1+PM2	Likely pathogenic	1	0
chr6	7585369	CAG	C	frameshift deletion	*DSP*	PVS1+PM2	Likely pathogenic	1	0
chr6	7585826	C	CA	frameshift insertion	*DSP*	PVS1+PM2	Likely pathogenic	1	0
chr7	128470692	A	T	startloss	*FLNC*	PVS1+PM2	Likely pathogenic	1	0
chr7	128477557	C	T	stop gain	*FLNC*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr7	128477603	G	C	splicing	*FLNC*	PVS1+PM2+PP3	Pathogenic	1	0
chr7	128480139	A	T	stop gain	*FLNC*	PVS1+PM2+PP3	Pathogenic	1	0
chr7	128481226	TTC	T	frameshift deletion	*FLNC*	PVS1+PM2	Likely pathogenic	1	0
chr7	128482356	G	GC	frameshift insertion	*FLNC*	PVS1+PM2	Likely pathogenic	1	0
chr7	128484099	C	T	stop gain	*FLNC*	PVS1+PM2+PP3	Pathogenic	1	0
chr7	128488905	CTG	C	frameshift deletion	*FLNC*	PVS1+PM2	Likely pathogenic	1	0
chr7	128489402	C	T	stop gain	*FLNC*	PVS1+PM2+PP3+PP5	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr7	128491547	G	T	stop gain	*FLNC*	PVS1+PM2+PP3	Pathogenic	1	0
chr7	128494863	TG	T	frameshift deletion	*FLNC*	PVS1+PM2	Likely pathogenic	1	0
chr20	42788645	GC	G	frameshift deletion	*JPH2*	PVS1+PM2	Likely pathogenic	1	0
chr20	42788815	G	GCCGA	frameshift insertion	*JPH2*	PVS1+PM2	Likely pathogenic	1	0
chr1	156084729	GGC	G	frameshift deletion	*LMNA*	PVS1+PM2	Likely pathogenic	1	0
chr1	156084885	T	C	missense	*LMNA*	PM1+PM2+PM5+PP3	Likely pathogenic	1	0
chr1	156104248	C	T	missense	*LMNA*	PM1+PM2+PP3+PP5	Likely pathogenic	1	0
chr1	156104692	C	T	stop gain	*LMNA*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr1	156104767	G	C	splicing	*LMNA*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr1	156105758	C	T	missense	*LMNA*	PM1+PM2+PP3+PP5	Likely pathogenic	1	0
chr1	156105800	C	T	missense	*LMNA*	PM1+PM2+PP3+PP5	Likely pathogenic	1	0
chr1	156106903	G	GATCT	splicing	*LMNA*	PVS1+PM2	Likely pathogenic	1	0
chr1	156108541	G	GA	frameshift insertion	*LMNA*	PVS1+PM2	Likely pathogenic	1	0
chr14	23883069	G	A	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23884407	T	C	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23884879	G	C	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	0	1
chr14	23885010	C	T	missense	*MYH7*	PM1+PM2+PM5+PP2 +BP1	Likely pathogenic	1	0
chr14	23886132	C	T	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23886383	G	A	missense	*MYH7*	PM1+PM2+PP2+PP5+BP1	Likely pathogenic	1	0
chr14	23886440	G	A	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23887584	G	A	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr14	23888742	C	T	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	5	0
chr14	23891462	C	T	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23891500	C	T	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	0	2
chr14	23892874	T	C	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23894061	A	G	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr14	23894084	C	T	missense	*MYH7*	PM1+PM2+PM5+PP2+PP3+BP1	Likely pathogenic	0	1
chr14	23901959	G	C	missense	*MYH7*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr10	112404329	AG	A	frameshift deletion	*RBM20*	PVS1+PM2	Likely pathogenic	1	0
chr10	112540899	C	T	stop gain	*RBM20*	PVS1+PM2+PP3	Pathogenic	1	0
chr10	112581063	GA	G	frameshift deletion	*RBM20*	PVS1+PM2	Likely pathogenic	1	0
chr3	52486161	CA	C	frameshift deletion	*TNNC1*	PVS1+PM2	Likely pathogenic	0	1
chr1	201328764	C	T	missense	*TNNT2*	PM1+PM2+PP3+PP5+BP1	Likely pathogenic	1	0
chr1	201333497	G	A	missense	*TNNT2*	PM1+PM2+PP3+PP5+BP1	Likely pathogenic	1	0
chr15	63362083	C	T	stop gain	*TPM1*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179395540	CTG	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	2	0
chr2	179395588	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179396395	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179396467	TA	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179397088	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179399943	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179404263	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr2	179404296	G	GA	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179404375	T	TC	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179408130	AG	A	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179411050	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179411339	G	A	stop gain	*TTN*	PVS1+PM2+PP5	Pathogenic	1	0
chr2	179414134	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179414391	G	GT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179416930	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179417382	A	AT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179417474	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179418306	CG	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179418850	C	CT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179419260	ATG	A	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179419385	AC	A	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179421736	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179421743	CA	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179422374	C	CT	splicing	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179422963	C	A	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	2	0
chr2	179424695	CAT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	2	0
chr2	179424731	A	AT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179425592	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179426257	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr2	179426643	TA	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179427020	G	GA	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179427128	TC	T	stop gain	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179429822	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	4	0
chr2	179429903	TA	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179431835	CA	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	0	1
chr2	179431880	G	A	stop gain	*TTN*	PVS1+PM2+PP5	Pathogenic	1	0
chr2	179432127	GTTCT	G	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179432542	GT	G	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179432880	AG	A	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179433260	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179433839	T	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179434089	CTT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179434925	C	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179435045	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179435390	G	A	stop gain	*TTN*	PVS1+PM2+PP5	Pathogenic	1	0
chr2	179436280	G	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179436949	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179437013	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179437449	T	TAAAG	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179438698	G	C	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179439257	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr2	179439773	ACT	A	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179440577	CA	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179440643	T	TA	stop gain	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179440808	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179441449	A	T	stop gain	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179441550	CA	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179443655	G	GT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179447724	TG	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179449216	CTCCA	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179449972	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	2	0
chr2	179451478	TG	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	2	0
chr2	179452411	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179454531	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179454906	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179455623	T	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179456095	A	AATCTC	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179456620	C	T	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179457670	C	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179460312	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179464371	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179468602	C	T	splicing	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179468792	C	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr2	179468831	CACCAT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179468939	CTACTT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179468996	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179469000	C	CTCTG	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179469506	T	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179469581	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179470331	A	C	stop gain	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179472209	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179473331	AC	A	splicing	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179474016	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179474816	C	T	splicing	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179476662	C	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179477578	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	2	0
chr2	179480366	A	G	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179481235	G	A	stop gain	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179481609	G	GTACTT	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179481846	C	T	splicing	*TTN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr2	179482809	C	G	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179494967	C	T	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	2	0
chr2	179494977	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179495921	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179500166	C	A	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr2	179500879	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179501421	AG	A	stop gain	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179604536	TC	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179604706	C	T	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179604886	CT	C	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179606500	TG	T	frameshift deletion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179631340	C	A	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179634405	C	T	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179638282	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179647792	C	G	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179648832	C	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179650739	C	CA	frameshift insertion	*TTN*	PVS1+PM2	Likely pathogenic	1	0
chr2	179650808	G	A	stop gain	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr2	179659647	A	G	splicing	*TTN*	PVS1+PM2+PP3	Pathogenic	1	0
chr10	92679010	G	GT	frameshift insertion	*ANKRD1*	PVS1+PM2	Likely pathogenic	2	2
chr11	19207813	G	A	stop gain	*CSRP3*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr18	29099830	G	A	missense	*DSG2*	PM1+PM2+PP3+PP5+BP1	Likely pathogenic	0	1
chr18	29104430	T	A	stop gain	*DSG2*	PVS1+PM2+PP3	Pathogenic	1	0
chr18	29118742	GA	G	frameshift deletion	*DSG2*	PVS1+PM2	Likely pathogenic	1	0
chr18	32470299	CT	C	frameshift deletion	*DTNA*	PVS1+PM2	Likely pathogenic	1	0
chr6	112441484	A	C	splicing	*LAMA4*	PVS1+PM2+PP3	Pathogenic	0	1
chr6	112452303	A	ATC	frameshift insertion	*LAMA4*	PVS1+PM2	Likely pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr6	112496514	C	T	splicing	*LAMA4*	PVS1+PM2+PP3	Pathogenic	0	1
chr11	47353626	G	A	stop gain	*MYBPC3*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr11	47354119	TG	T	frameshift deletion	*MYBPC3*	PVS1+PM2	Likely pathogenic	3	0
chr11	47364572	C	T	missense	*MYBPC3*	PM1+PM2+PM5+PP3	Likely pathogenic	1	0
chr11	47374196	C	T	startloss	*MYBPC3*	PVS1+PM2	Likely pathogenic	1	0
chr14	23854251	C	A	splicing	*MYH6*	PVS1+PM2+PP3	Pathogenic	1	0
chr14	23863118	C	T	splicing	*MYH6*	PVS1+PM2+PP3	Pathogenic	1	0
chr12	111351128	C	T	missense	*MYL2*	PM1+PM2+PP2+PP3	Likely pathogenic	1	0
chr10	69957164	C	T	stop gain	*MYPN*	PVS1+PM2+PP3+PP5	Pathogenic	1	0
chr10	21120237	T	C	splicing	*NEBL*	PVS1+PM2+PP3	Pathogenic	1	0
chr10	21120430	GCT	G	frameshift deletion	*NEBL*	PVS1+PM2	Likely pathogenic	0	1
chr10	21129691	G	A	stop gain	*NEBL*	PVS1+PM2	Likely pathogenic	0	1
chr10	21139402	AT	A	frameshift deletion	*NEBL*	PVS1+PM2	Likely pathogenic	2	0
chr10	21177032	CTG	C	frameshift deletion	*NEBL*	PVS1+PM2	Likely pathogenic	0	1
chr5	172660415	CA	C	stop gain	*NKX2-5*	PVS1+PM2	Likely pathogenic	1	0
chr1	228412436	G	C	splicing	*OBSCN*	PVS1+PM2+PP3	Pathogenic	1	0
chr1	228431123	AG	A	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228433212	C	T	stop gain	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228464876	CGG	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	0	1
chr1	228467521	G	A	splicing	*OBSCN*	PVS1+PM2+PP3	Pathogenic	1	0
chr1	228469804	C	T	stop gain	*OBSCN*	PVS1+PM2+PP3	Pathogenic	1	0
chr1	228487176	CAT	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0

Chr	Pos	Ref	Alt	Consequence	Gene symbol	ACMG	Pathogenicity	NO. in cases	NO. in controls
chr1	228494102	CAG	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228495865	G	T	stop gain	*OBSCN*	PVS1+PM2+PP3	Pathogenic	1	0
chr1	228506894	CT	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228521482	G	A	splicing	*OBSCN*	PVS1+PM2+PP3	Pathogenic	0	1
chr1	228525020	C	G	stop gain	*OBSCN*	PVS1+PM2+PP3	Pathogenic	0	1
chr1	228525846	G	A	splicing	*OBSCN*	PVS1+PM2+PP3	Pathogenic	0	1
chr1	228539121	CA	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228547775	CAGAG	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228552733	AG	A	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	0	1
chr1	228553810	C	T	stop gain	*OBSCN*	PVS1+PM2+PP3	Pathogenic	0	1
chr1	228554527	CAG	C	frameshift deletion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228558395	G	T	stop gain	*OBSCN*	PVS1+PM2+PP3	Pathogenic	1	0
chr1	228559297	G	GC	frameshift insertion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr1	228560305	C	CAGGT	frameshift insertion	*OBSCN*	PVS1+PM2	Likely pathogenic	1	0
chr5	155771665	T	A	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr5	155935612	A	G	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	2	0
chr5	156016244	A	C	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	3	1
chr5	156016305	A	C	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr5	156184675	C	T	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	1
chr5	156186300	C	G	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	1	0
chr5	156186354	G	T	missense	*SGCD*	PM1+PM2+PP2+PP3+BP1	Likely pathogenic	0	1

Abbreviations: Chr, chromosome; Pos, position; Ref, reference allele; Alt, alternative allele.

Table S6. Baseline comparisons among *FBN1* carriers, patients positive for DCM-associated genes, and patients negative for DCM-associated genes.

	***FBN1*$^+$**	***FBN1*$^-$ / DCMGenes$^+$**	***FBN1*$^-$ / DCMGenes$^-$**	***P* value**	
	(n = 19)	**(n = 205)**	**(n = 835)**	***FBN1*$^+$ vs. *FBN1*$^-$/ DCMGenes$^+$**	***FBN1*$^+$ vs. *FBN1*$^-$/ DCMGenes$^-$**
Male (%)	12 (63.2)	160 (78.0)	604 (72.3)	0.141	0.378
Age of onset (years)	54.74 ± 19.57	51.12 ± 12.47	52.21 ± 13.95	0.254	0.439
Age at enrollment (years)	57.42 ± 18.63	54.23 ± 12.92	55.09 ± 14.32	0.324	0.486-
NYHA III/IV (%)	14 (73.7)	158 (77.1)	555 (66.5)	0.738	0.509
Smoke (%)	5 (26.3)	89 (43.4)	355 (42.5)	0.149	0.157
Alcohol intake (%)	0 (0.0)	26 (15.1)	112 (16.5)	0.105	0.086
Non-fatal stroke (%)	1 (5.3)	5 (2.4)	41 (4.9)	0.466	0.945
Hypertension (%)	10 (52.6)	72 (35.1)	444 (53.2)	0.13	0.963
Hyperlipidemia (%)	1 (5.3)	14 (6.8)	91 (10.9)	0.794	0.433
Diabetes mellitus (%)	4 (21.1)	34 (16.6)	138 (16.5)	0.62	0.6
Renal insufficiency (%)	6 (33.3)	8 (4.4)	71 (9.5)	<0.001	0.001
Body mass index (kg/m^2)	24.97 ± 3.36	23.73 ± 4.13	23.88 ± 4.59	0.419	0.506
TC (mmol/L)	3.89 ± 1.25	3.82 ± 0.87	3.93 ± 1.01	0.785	0.885
TG (mmol/L)	1.40 ± 0.75	1.39 ± 0.80	1.39 ± 0.98	0.96	0.988
HDL-C (mmol/L)	0.98 ± 0.25	0.93 ± 0.28	0.97 ± 0.34	0.53	0.935
LDL-C (mmol/L)	2.40 ± 1.15	2.43 ± 0.78	2.51 ± 0.83	0.891	0.619
NT-proBNP (pg/mL)	3368.00 [1533.00, 10404.00]	3804.00 [1655.00, 7459.50]	3841.00 [1722.00, 9000.00]	0.969	0.853
ALT (U/L)	30.00 [22.00, 45.50]	25.00 [16.25, 43.75]	26.00 [16.00, 48.00]	0.324	0.351

AST (U/L)	27.00 [22.00, 34.50]	27.00 [18.00, 39.00]	27.00 [20.00, 42.00]	0.754	0.935
Cr (μmol/L)	89.00 [73.00, 127.00]	87.00 [72.00, 102.00]	89.00 [74.00, 113.25]	0.617	0.85
Atrial fibrillation (%)	8 (42.1)	42 (20.5)	187 (22.4)	0.03	0.043
Non-sustained ventricular tachycardia (%)	2 (10.5)	34 (16.6)	109 (13.1)	0.491	0.746
Left bundle branch block (%)	4 (21.1)	12 (5.9)	96 (11.5)	0.014	0.2
Any arrhythmia (%)	12 (63.2)	85 (41.5)	353 (42.3)	0.068	0.069
IVS (mm)	9.44 ± 1.34	9.37 ± 1.22	9.61 ± 1.47	0.818	0.638
LVPW (mm)	9.44 ± 1.04	9.34 ± 1.13	9.60 ± 1.39	0.701	0.629
LVEDD (mm)	65.42 ± 9.44	66.24 ± 7.72	66.77 ± 8.37	0.666	0.488
LAD (mm)	46.16 ± 8.08	45.65 ± 7.87	45.66 ± 7.91	0.788	0.785
LVEF (%)	33.32 ± 8.35	29.80 ± 9.67	31.77 ± 10.08	0.127	0.506
E/A	1.45 ± 1.00	1.71 ± 0.90	1.75 ± 1.67	0.403	0.584
E/e′	24.75 ± 16.80	21.82 ± 11.29	22.67 ± 12.64	0.497	0.646
Aortic root diameter (mm)	27.88 ± 2.80	31.07 ± 28.56	29.26 ± 3.97	0.753	0.327
Proximal ascending aorta diameter (mm)	34.58 ± 4.46	31.71 ± 4.96	32.82 ± 4.78	0.057	0.207
Aortic root dilatation (%)	0 (0.0)	8 (6.2)	41 (7.9)	0.397	0.332
Proximal ascending aorta dilatation (%)	6 (42.9)	31 (25.4)	152 (30.9)	0.165	0.341
Any aorta dilatation (%)	6 (40.0)	37 (23.1)	169 (27.0)	0.147	0.266

Pacemaker implantation (%)	0 (0.0)	11 (5.4)	43 (5.2)	0.3	0.309
Implantable cardioverter-defibrillator (%)	2 (10.5)	4 (2.0)	13 (1.6)	0.027	0.003
Cardiotonic use (%)	10 (52.6)	102 (49.8)	395 (47.6)	0.81	0.664
Diuretic use (%)	16 (84.2)	173 (84.4)	680 (81.9)	0.984	0.798
ACE inhibitor use (%)	13 (68.4)	152 (74.1)	637 (76.7)	0.588	0.403
Beta-blocker use (%)	8 (42.1)	101 (49.3)	446 (53.7)	0.55	0.315
Aldactone use (%)	17 (89.5)	159 (77.6)	638 (76.9)	0.226	0.196

Abbreviations: DCM, dilated cardiomyopathy; *FBN1*$^{+}$, DCM cases carrying rare deleterious variants in *FBN1*; *FBN1*$^{-}$ / DCMGenes^{+}, DCM cases not carrying rare deleterious variants in *FBN1*, but carrying rare deleterious variants in other known DCM-associated genes; *FBN1*$^{-}$ / DCMGenes^{-}, DCM cases not carrying rare deleterious variants in either *FBN1* or other known DCM-associated genes; NYHA, New York Heart Association; NT-proBNP, N-terminal pro-B-type natriuretic peptide; TC: total cholesterol; TG: triglycerides; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; ALT: alanine aminotransferase; AST: aspartate aminotransferase; Cr: creatinine; IVS, interventricular septum; LVPW, left ventricular posterior wall; LVEDD, left ventricular end-diastolic diameter; LAD, left atrial diameter; LVEF, left ventricular ejection fraction.

For non-normally distributed data, values are presented as the median and interquartile range (IQR). All other numerical data, which are normally distributed, are represented as the mean ± standard deviation (SD). Categorical data are provided as counts (percentages).

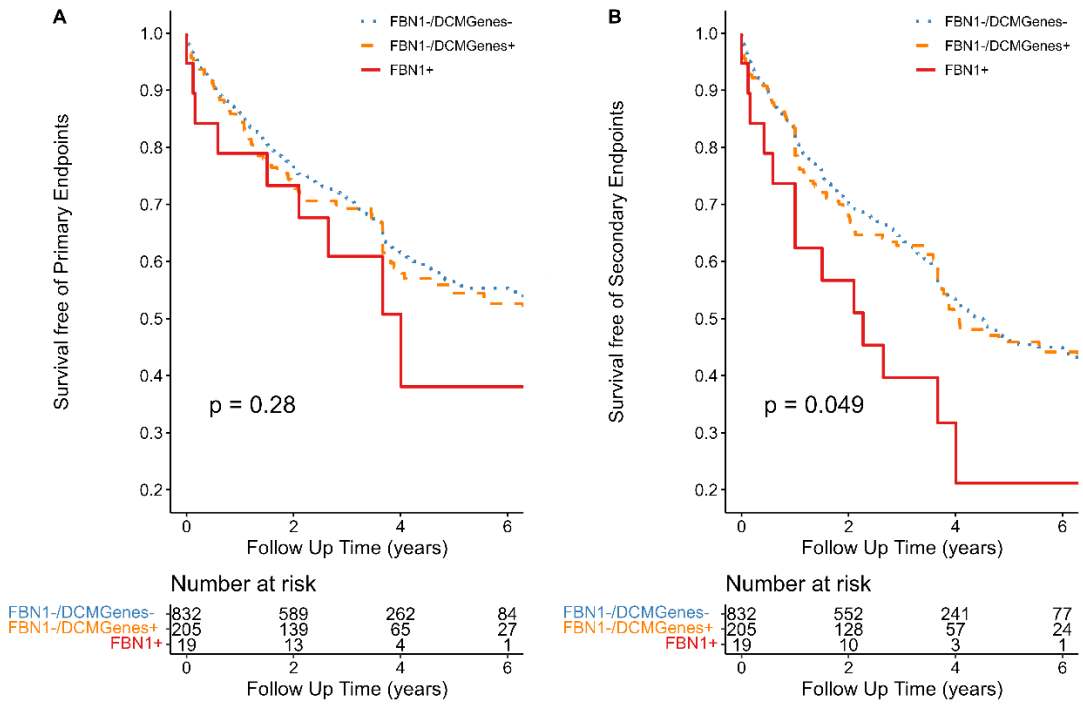

Figure S1. Clinical outcomes in different groups of DCM patients. (**A**) Kaplan-Meier curve illustrates survival free of primary endpoints, which include cardiac mortality or heart transplantation. (**B**) The curve represents survival free of secondary endpoints, comprising all-cause mortality or heart failure recurrence. Probability values were calculated using the log-rank test. *FBN1*$^{+}$, DCM cases carrying rare deleterious variants in *FBN1*; *FBN1*$^{-}$ / DCMGenes^{+}, DCM cases not carrying rare deleterious variants in *FBN1*, but carrying rare deleterious variants in other known DCM-associated genes; *FBN1*$^{-}$ / DCMGenes^{-}, DCM cases not carrying rare deleterious variants in either *FBN1* or other known DCM-associated genes.