SUPPLEMENTAL MATERIAL

Table S1. Cardiomyopathy gene testing panels.

Panel	DCM-pnlA	DCM-pnlB	PCM-pnlD	DCM-pnlC	PCM-pnlCv2	PCM-pnlA	PCM-pnlAv2	PCM-pnlCv3	PCM-pnlAv3
Genes	*MYBPC3*	*LDB3*	*CASQ2*	*ABCC9*	*ABCC9*	*ABCC9*	*ABCC9*	*ABCC9*	*ABCC9*
	MYH7	*LMNA*	*DSC2*	*ACTC1*	*ACTC1*	*ACTC1*	*ACTC1*	*ACTC1*	*ACTC1*
	TNNI3	*ACTC1*	*DSG2*	*ACTN2*	*ACTN2*	*ACTN2*	*ACTN2*	*ACTN2*	*ACTN2*
	TNNT2	*PLN*	*DSP*	*CSRP3*	*BAG3*	*ANKRD1*	*ANKRD1*	*BAG3*	*ANKRD1*
	TPM1	*TAZ*	*JUP*	*CTF1*	*CSRP3*	*CASQ2*	*BAG3*	*CASQ2*	*BAG3*
			PKP2	*DES*	*CTF1*	CAV3	*CASQ2*	*CHRM2*	*CASQ2*
			RYR2	*EMD*	*DES*	*CRYAB*	CAV3	*CRYAB*	CAV3
			TMEM43	*LDB3*	*EMD*	*CSRP3*	*CRYAB*	*CSRP3*	*CHRM2*
				LMNA	*GATAD1*	*CTF1*	*CSRP3*	*DES*	*CRYAB*
				MYBPC3	*LAMP2*	*DES*	*CTF1*	*DMD*	*CSRP3*
				MYH7	*LDB3*	*DSC2*	*DES*	*DOLK*	*DES*
				PLN	*LMNA*	*DSG2*	*DSC2*	*DSC2*	*DMD*
				SGCD	*MYBPC3*	*DSP*	*DSG2*	*DSG2*	*DOLK*
				TAZ	*MYH7*	*DTNA*	*DSP*	*DSP*	*DSC2*
				TCAP	*NEXN*	*EMD*	*DTNA*	*DTNA*	*DSG2*
				TNNI3	*PLN*	*FHL2*	*EMD*	*EMD*	*DSP*
				TNNT2	*RBM20*	*GLA*	*FHL2*	*GATAD1*	*DTNA*
				TPM1	*SCN5A*	*JUP*	*GATAD1*	*GLA*	*EMD*
				VCL	*SGCD*	*LAMA4*	*GLA*	*JUP*	*FHL2*
					TAZ	*LAMP2*	*JUP*	*LAMP2*	*GATAD1*
					TCAP	*LDB3*	*LAMA4*	*LDB3*	*GLA*
					TNNC1	*LMNA*	*LAMP2*	*LMNA*	*ILK*
					TNNI3	*MYBPC3*	*LDB3*	*MURC*	*JPH2*
					TNNT2	*MYH6*	*LMNA*	*MYBPC3*	*JUP*
					TPM1	*MYH7*	*MYBPC3*	*MYH6*	*LAMA4*
					TTN	*MYL2*	*MYH6*	*MYH7*	*LAMP2*
					VCL	*MYL3*	*MYH7*	*MYL2*	*LDB3*
						MYLK2	*MYL2*	*MYL3*	*LMNA*
						MYOZ2	*MYL3*	*MYOZ2*	*MURC*
						NEXN	*MYLK2*	*MYPN*	*MYBPC3*
						PKP2	*MYOZ2*	*NEBL*	*MYH6*
						PLN	*NEBL*	*NEXN*	*MYH7*
						PRKAG2	*NEXN*	*PKP2*	*MYL2*
						RBM20	*PKP2*	*PLN*	*MYL3*
						RYR2	*PLN*	*PRDM16*	*MYLK2*
						SGCD	*PRKAG2*	*PRKAG2*	*MYOM1*
						TAZ	*RBM20*	*PTPN11*	*MYOZ2*
						TCAP	*RYR2*	*RAF1*	*MYPN*
						TMEM43	*SCN5A*	*RBM20*	*NEBL*
						TNNC1	*SGCD*	*RYR2*	*NEXN*

						TNNI3	*TAZ*	*SCN5A*	*PDLIM3*
						TNNT2	*TCAP*	*SGCD*	*PKP2*
						TPM1	*TMEM43*	*TAZ*	*PLN*
						TTN	*TMPO*	*TCAP*	*PRDM16*
						TTR	*TNNC1*	*TMEM43*	*PRKAG2*
						VCL	*TNNI3*	*TNNC1*	*PTPN11*
							TNNT2	*TNNI3*	*RAF1*
							TPM1	*TNNT2*	*RBM20*
							TTN	*TPM1*	*RYR2*
							TTR	*TRDN*	*SCN5A*
							VCL	*TTN*	*SGCD*
								TTR	*TAZ*
								VCL	*TCAP*
									TMEM43
									TNNC1
									TNNI3
									TNNT2
									TPM1
									TRDN
									TTN
									TTR
									VCL

Genes included in cardiomyopathy sequencing panels. Testing panels expanded from 5 to 62 genes over the study period.

Table S2. Relationship between number of genes tested and test result.

Test Result		Positive		Inconclusive		Negative	
Re-classification status		Before	After	Before	After	Before	After
Number of genes tested	**<= 10**	1/6	3/6	3/6	1/6	2/6	1/6
	> 10 - 50	4/24	3/24	13/24	11/24	7/24	10/24
	> 50	11/33	9/33	22/33	20/33	0/33	4/33
	All	16/63	15/63	38/63	32/63	9/63	15/63

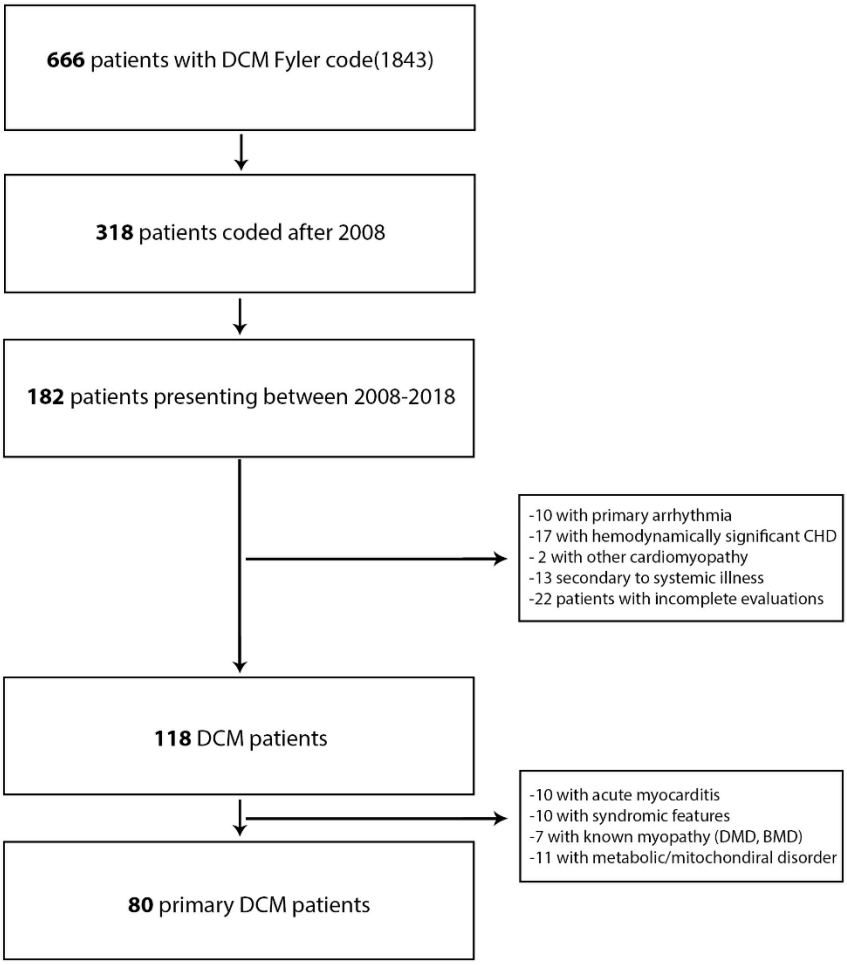
Test results before and after variant reclassification as a proportion of the total number of tests are shown. Tests are grouped by number of genes tested. Positive tests include those with pathogenic or likely pathogenic variants. Negative tests include those with benign or likely benign variants. Inconclusive tests include those with VUS's that do not meet positive test criteria. Variants that were ultimately determined to be disease causing at the discretion of the clinican are grouped with their original testing result as issued by the laboratory.

Table S3. Number of variants identified by genetic testing panel.

Panel(s) Tested	DCM-pnlA	DCM-pnlB	PCM-pnlD	DCM-pnlA, DCM-pnlB	DCM-pnlC	PCM-pnlCv2	PCM-pnlA	PCM-pnlAv2	PCM-pnlCv3	PCM-pnlAv3
Number of genes tested	5	5	8	10	19	27	46	51	53	62
Number of tests performed	1	1	1	3	18	5	1	9	1	23
Number of causal variants* identified	0	1	0	2	5	1	0	4	0	6

Genetic testing by gene panel. A list of genes for each panel can be found in Table S2. *includes Likely pathogenic and pathogenic variants as per ACMG/AMP classification criteria, as well as those classified as VUS favor pathogenic where clinical judgement was used to override the initial variant classification following clinical assessment

Figure S1. Patient selection scheme.



80 patients with primary DCM were identified within the study period. 73 patients were probands without prior genetic evaluations, and 63 probands that underwent genetic testing included in this study.