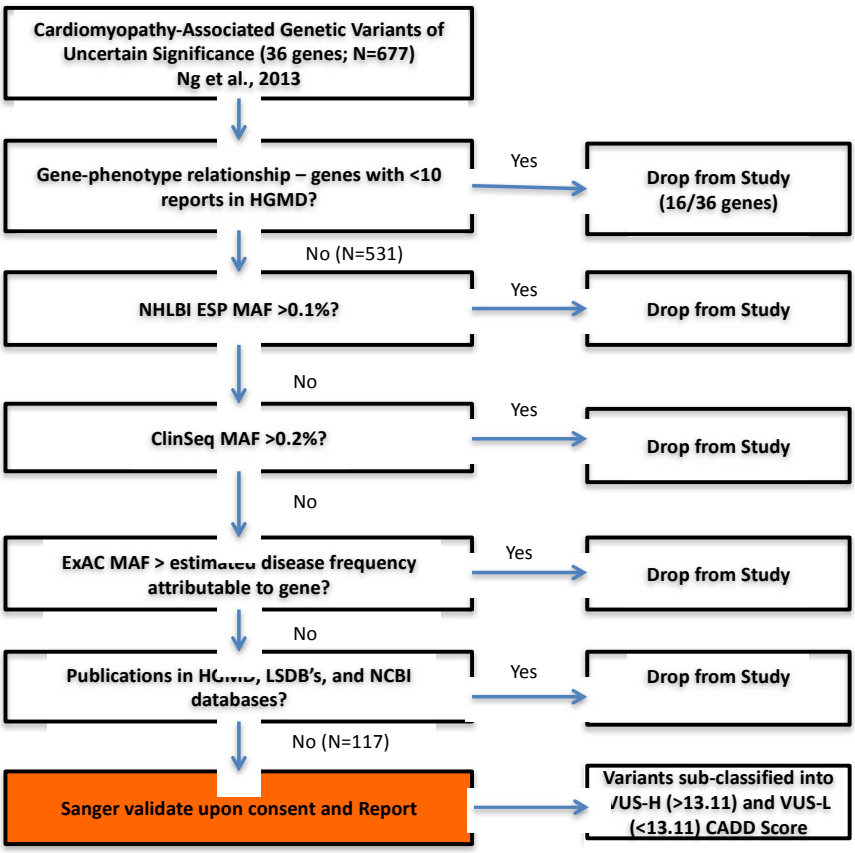
Supplementary Table 1: Cardiomyopathy-associated genes eligible for study

Gene	Cardiomyopathy[a]	Other Conditions[a]	Gene	Cardiomyopathy[a]	Other Conditions[a]
MYPN **(myopalladin)**	DCM=12; HCM=1; RCM=1		***TPM1*** **(tropomyosin 1 alpha)**	HCM=22; DCM=19; LNVC=5, RCM=1	
PKP2 **(plakophillin 2)**	ARVC=193; SCD=5; DCM=1	Brugada syndrome=4	***TMEM43*** **(transmembrane protein 43)**	ARVC=10;	Emery-Dreifuss muscular dystrophy-related myopathy=2
DSC2 **(desmocollin)**	ARVC=51; DCM=1; SCD=1		***ACTN2*** **(Actinin, alpha2)**	DCM=6; HCM=5	
JUP (junction plakoglobin)	ARVC=18;	Cutaneous disease=2; Naxos disease=2; Epidermolysis bullosa=1	***MYL2*** **(myosin, light chain 2)**	HCM=26; RCM=1	Muscle fibre disease, infantile, type1=2
DSP **(desmoplakin)**	ARVC=103; DCM=19;	Skin fragility and wooly hair=6; Epidermolysis bullosa=4	***VCL*** **(vinculin)**	DCM=11; HCM=2; SCD=1	
DSG2 **(desmoglein 2)**	ARVC=89; DCM=2		***MYH6*** **(myosin, heavy chain polypeptide 6, cardiac)**	DCM=9; HCM=4	Congenital heart defects=4; ASD=4; Cardiac dysrhythmia=1
MYBPC3 **(myosin binding protein C, cardiac)**	HCM=514; DCM=55; LVNC=4; Increased LV wall thickness=2		***BAG3*** **(BCL-associated athanogene 3)**	DCM=24	Myofibrillar myopathy=4
MYH7 **(myosin heavy polypeptide 7, cardiac muscle)**	HCM=421; DCM=98; LVNC=23	Myopathy, distal1=17	***TCAP*** **(titin cap)**	HCM=6; DCM=5	Muscular dystrophy, limb girdle=5; Intestinal pseudo-obstruction=1
TTN **(Titin)**	DCM, ARVC	Centronuclear myopathy, tibial muscular dystrophy	***TNNI3*** **(troponin I, cardiac)**	HCM=53; DCM=10; RCM=10; Increased LV wall thickness=2	
ANKRD1 **(ankyrin repeat domain1, cardiac)**	DCM=7; HCM=3	Neurodevelopmental d/o=6; Total anomalous pulmonary venous return =2	***TNNT2*** **(troponin T2, cardiac)**	HCM=63; DCM=37; RCM=2; Increased LV wall thickness=1	

HCM=hypertrophic cardiomyopathy; DCM=dilated cardiomyopathy; ARVC=arrhythmogenic right ventricular cardiomyopathy; RCM=restrictive cardiomyopathy; SCD=sudden cardiac death

[a] Number of reports/publications in Human Gene Mutation Database (HGMD) associating gene with listed phenotype.

Supplementary Figure 1: Variant Assessment Process



HGMD: Human Gene Mutation Database; MAF: minor allele frequency; NHLBI ESP: National Heart Lung & Blood Institute Exome Sequencing Project; ExAC: Exome Aggregation Consortium; LSDB: Locus Specific Database; NCBI: National Center for Biotechnology Information.

S1: VUS sub-classification disclosure to individuals with family history of cardiomyopathy

Nine individuals, 6 VUS-high and 3 VUS-low, with a family history of cardiomyopathy were included in the study. Four participants intended to share results (2 VUS-high and 2 VUS-low), 3 did not intend to share (3 VUS-high), 1 was unsure (VUS-high), and 1 did not complete the survey (VUS-low). There were no statistically significant differences in intentions between individuals with (mean=4.828, SD=0.582 [95% CI = 4.341 – 5.315]) and without (mean=4.636, SD=0.953 [95% CI = 4.410 – 4.861]) family history of cardiomyopathy (t=0.557, p=0.579).