Table S1: Prioritised noncoding DNVs within the human ventricular cardiomyocyte regulome. We used the ABC model to predict enhancer–gene connections in cardiomyocytes. Promoters were defined as 2 kb upstream or 1 kb downstream of TSSs. Promoter Capture Hi-C (pcHi-C) interactions were obtained from the 3DIV database. The Fathmm-MKL score indicates the pathogenic impact of individual SNVs. Predictions are given as p-values in the range 0 to 1; values > 0.5 are predicted to be deleterious.

| Family ID | Disease | Genomic position (GRCh38) | ABC predictions | -2kb/1kb of TSS | 3DIV pcHi-C | Fathmm-MKL score |
|-----------|---------|---------------------------|-----------------|----------------|-------------|-----------------|
| Fam000    | HCM     | chr8:140511298 A>C        | AGO2; TRAPPC9   | CHRAC1         | .           | 0.60893         |
| Fam087    | DCM     | chr2:227503696 G>C        | AGFG1          | .               | .           | 0.68879         |
| Fam108    | DCM     | chr19:44008139 A>T        | .              | .               | .           | 0.74361         |
| Fam126    | DCM     | chr6:144216524 C>CA       | UTRN; STX11; SF3B5 | . | . | NA |
| Fam306    | LVNC    | chr6:150196298 G>A        | PPP1R14C       | .               | .           | 0.84031         |
| Fam313    | DCM     | chr6:26189301 G>GTA       | .              | H4C4           | .           | NA              |
| Fam334    | DCM     | chr17:75784788 T>C        | UNC13D; WBP2; SAP30BP; TRIM65 | H3-3B; MIR4738; UNK | TRIM56; TMEM94 | 0.84602         |
| Fam338    | LVNC    | chr15:40953466 C>T        | .              | CHAC1          | DLL4        | 0.61755         |
| Fam468    | HCM     | chr1:116485382 A>T        | ATP1A1         | .               | .           | 0.8964          |
| Fam499    | HCM     | chr20:44116250 A>G        | JPH2           | .               | .           | 0.88391         |
| Fam499    | HCM     | chr5:140711461 A>G        | .              | VTRNA1-1       | .           | 0.99137         |
| Fam509    | HCM     | chr19:18557700 C>T        | ELL            | KXD1           | .           | 0.9407          |
| Fam539    | HCM     | chr10:68406789 C>T        | .              | RUFY2          | .           | 0.73967         |
| Fam571    | DCM     | chr2:189661420 AAAAG>A    | .              | ASNSD1; ASDURF | WDR17       | NA              |
| Fam599    | HCM     | chr20:298489 C>G          | SOX12          | ZCCHC3         | SOX12       | 0.94203         |
| Fam687    | LVNC    | chr4:18021878 A>G         | DCAF16         | LCORL          | LAP3        | 0.93949         |
| Fam733    | HCM     | chr9:131270697 A>G        | .              | FAM78A         | .           | 0.8224          |
| Fam737    | HCM     | chr2:96816570 G>C         | .              | CNNM3          | .           | 0.52844         |
| Fam791    | ARVC    | chr11:67317729 C>T        | GRK2; RHOD     | RAD9A          | .           | 0.76606         |
| Fam992    | ARVC    | chr8:15540211 C>A         | TUSC3          | .              | .           | 0.8979          |