**Table 1. Definite disease-causing genes for rare genetic variants and common genetic variants loci in inherited cardiac disease**

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| --- | --- | --- | --- | --- |
|  | Rare variants, high effect size | Ref. | Common variants, low effect size | Ref. |
| LQTS | *KCNQ1, KCNH2, SCN5A* (typical LQTS)*CALM1, CALM2, CALM3, TRDN* (atypical LQTS) | (30) | *NOS1AP*, *KCNQ1*, *KLF12* | (31) |
| BrS | *SCN5A* | (34) | *SCN5A, SCN10A, HEY2* | (35) |
| HCM | *MYBPC3, MYH7, TNNT2, TNNI3, TPM1, ACTC1, MYL2, MYL3* | (48) | *HSPB7, SLC35F1, BAG3, PKD1, NSF, FHOD3, FNDC3B, ACTBL2, DNAJC18, CDKN1A, CCDC136, SYNPO2L, VTI1A, ZNF592, PRKCA, SMARCB1, SLC6A6, PLN, TBX3, ADPRHL1, ALPK3, SPPL2C, MMP11* | (40, 41) |
| DCM | *BAG3*, *DES*, *FLNC*, *LMNA*, *MYH7*, *PLN*, *RBM20*, *SCN5A*, *TNNC1*, *TNNT2*, *TTN**DSP* (strong) | (42) | *HSPB7, BAG3, SLC6A6*, *SMARCB1* | (46) |

LQTS, long QT syndrome; BrS, Brugada syndrome; HCM, hypertrophic cardiomyopathy; DCM, dilated cardiomyopathy