Table 2. WES results of susceptible SNVs with a focus on cardiac disease-associated genes in SUD families

| Gene | Transcript | 1000G_ALL* | 1000G_EAS** | dbSNP141 | SIFT*** | PolyPhen2# | Mutation Assessor## | Samples |
|---|---|---|---|---|---|---|---|---|
| IRX4 | NM_001278633.1:p.Tyr77Cys/c.230A>G | 0.000599042 | 0.002 | rs201931586 | 0.04（D） | 0.995（D） | 2.17（M） | DP-2A, DP-4A, DP-18A, HP-24A |
| LDB3 | NM_001171610.1:p.Cys702Gly/c.2104T>G | _ | _ | _ | 0（D） | 0.998（D） | 4.475（H） | SGZ-42A, SGZ-43A |
| MYH6 | NM_002471.3:p.Tyr1310His/c.3928T>C | _ | _ | _ | 0.02（D） | 0.974（D） | 2.175（M） | TJ-15A, TJ-25A |
| MYH6 | NM_002471.3:p.Met1?/c.3G>A | _ | _ | _ | 0.01（D） | 0.968（D） | _ | HP-9A, HP-18A |
| SCN5A | NM_001099404.1:p.Arg1193Trp/c.3577C>T | 0.000399361 | 0.001 | rs192379242 | 0(D) | 0.964(D) | 1.93(M) | ALH-19A, ALH-21A |
| SCN5A | NM_001099404.1:p.Val1279Ile/c.3835G>A | _ | _ | rs199473341 | 0.02（D） | 0.995（D） | 3.375（M） | AJZ-1A |
| ACTN2 | NM_001103.3:p.Asp673Ala/c.2018A>C | _ | _ | _ | 0.03（D） | 0.995（D） | 2.485（M） | ALH-19A |
| ANK2 | NM_001148.4:p.Asp3707Asn/c.11119G>A | 0.000399361 | 0 | rs199549660 | 0.03（D） | 0.551（P） | 1.78（L） | TJ-8A |
| CSRP3 | NM_003476.4:p.Gly6Arg/c.16G>A | 0.000599042 | 0.002 | rs185980145 | 0.04（D） | 0.998（D） | 2.65（M） | SGZ-43A |
| DMPK | NM_001081562.2:p.Pro605Leu/c.1814C>T | _ | _ | _ | 0.03（D） | 0.998（D） | _ | GT-37A |
| LAMA4 | NM_001105206.2:p.Leu492His/c.1475T>A | 0.00259585 | 0.0099 | rs3752579 | 0（D） | 0.842（P） | 1.445（L） | DP-3A |
| LMNA | NM_170707.3:p.Arg527Cys/c.1579C>T | _ | _ | rs57318642 | 0（D） | 0.953（D） | 2.56（M） | GT-6A |
| MCTP2 | NM_018349.3:p.Pro398Leu/c.1193C>T | _ | _ | _ | 0（D） | 0.999（D） | 2.95（M） | ALH-20A |
| SLC8A1 | NM_021097.2:p.Ala327Thr/c.979G>A | _ | _ | _ | 0.01（D） | 0.965（D） | 2.105（M） | QS-10A |
| SLC8A1 | NM_021097.2:p.Ser70Tyr/c.209C>A | _ | _ | _ | 0（D） | 0.991（D） | 2.675（M） | GT-37A |
| SYNPO2L | NM_001114133.2:p.Glu26Lys/c.76G>A | _ | _ | _ | 0.01（D） | 0.7（P） | 3.02（M） | GT-6A |
| TTN | NM_001267550.2:p.Pro26996Leu/c.80987C>T | _ | _ | _ | 0（D） | 0.842（P） | 3.46（M） | HP-9A, HP-18A |
| TTN | NM_001267550.2:p.Thr2690Ile/c.8069C>T | 0.00179712 | 0.0079 | rs374620001 | 0（D） | 0.976（D） | 2.495（M） | HP-24A, TJ-15A, TJ-25A |
| TTN | NM_001267550.2:p.Arg29578His/c.88733G>A | 0.00139776 | 0.005 | rs374147064 | 0（D） | 0.999（D） | 2.175（M） | SGZ-42A, TJ-8A |
| TTN | NM_001267550.2:p.Glu32685Gly/c.98054A>G | _ | _ | _ | 0（D） | 0.998（D） | 2.805（M） | GT-6A |
| TTN | NM_001267550.2:p.Asp16118Gly/c.48353A>G | 0.000399361 | 0.002 | rs376273101 | 0（D） | 0.999（D） | 0.41（N） | GT-6A |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| TTN | NM_001267550.2:p.Gly7677Arg/c.23029G>A | 0.000399361 | 0.002 | rs367826445 | 0（D） | 0.993（D） | 4.685（H） | GT-6A |
| TTN | NM_001267550.2:p.Gly16881Ala/c.50642G>C | 0.000199681 | 0.001 | rs201302681 | 0（D） | 0.999（D） | 2.24（M） | GT-37A |
| TTN | NM_001267550.2:p.Arg18050Cys/c.54148C>T | 0.00139776 | 0.0069 | rs55734111 | 0（D） | 0.95（D） | 1.215（L） | GT-35A |
| TTN | NM_001267550.2:p.Val28895Met/c.86683G>A | 0.00299521 | 0 | rs201290358 | 0（D） | 0.568（P） | 2.345（M） | QS-10A |
| TTN | NM_001267550.2:p.Arg15731His/c.47192G>A | 0.000399361 | 0 | rs373613871 | 0（D） | 0.999（D） | 3.625（H） | QS-10A |
| TTN | NM_001267550.2:p.Pro6384Thr/c.19150C>A | 0.001597444 | 0.003 | rs72648953 | 0（D） | 0.997（D） | 3.215（M） | ALH-20A |
| TTN | NM_001267550.2:p.Tyr17441Asp/c.52321T>G | _ | _ | _ | 0（D） | 0.999（D） | 4.37（H） | HP-24A |
| TTN | NM_001267550.2:p.Pro13673Leu/c.41018C>T | _ | _ | _ | 0（D） | 0.47（P） | 1.955（M） | DP-20A |

*: The allele frequency of the mutated base at the site of the mutation was found in all population groups that gave data on the 1000-person genome project. (n=2504).

**: The allele frequency of the mutated base at the mutation site in an East Asian population with data from the 1000-person genome project. Samples were derived from the sum (n=405) of CDX (Chinese Dai in Xishuanbanna, China, n=93) , CHB (Han Chinese in Beijing, China, n=103) , CHS (Southern Han Chinese, n=105) , and JPT(Japanese in Tokyo, Japan, n=104).

***: Indicating the effect of this variation on the protein sequence. The comma before and after the SIFT _score and SIFT _pred：SIFT _score is SIFT scores, the smaller the score is, the more likely it is "harmful ", indicating that the SNP is likely to cause changes in protein structure or function. SIFT _pred is the predicted result with a value of T or D. When this variation affects multiple protein sequences at the same time, there is a SIFT value for each protein sequence, taking the minimum value. D：Deleterious (SIFT <=0.05); T：Tolerated (SIFT > 0.05)

#: Predict the effect of this variation on the protein sequence. The column contains two values, the first is the Polyphen2 score, the greater the value is "harmful ", indicating that the SNP is more likely to cause changes in protein structure or function; the second is D or P or B. (D: Probably damaging(>=0.957) ,P: Possibly damaging (0.453<=pp2<=0.956); B:Benign ( pp2<=0.452 ))

##: Indicating the effect of this variation on the protein sequence. The comma before and after the MutationAssessor _score and MutationAssessor _pred：MutationAssessor _score is MutationAssessor initial scores, the larger the more likely to be "harmful ", indicating that the SNP is likely to cause changes in protein structure or function. MutationAssessor _pred is H、M、L or N (H: High; M:Medium; L: Low; N: Neutral).H and M are functional, L and N are non-functional.