

Supplemental Table S6: Representative list of pathogenic and likely pathogenic variants by ancestry group.

Ancestry Group	Population (N)			
Overall	414,830			
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification
MYBPC3				
c.1504C>T (Arg502Trp)	88	0.0212	Nonsynonymous	Likely Pathogenic
c.1624G>C (Glu542Gln)	51	0.0123	Splice Region Missense	Likely Pathogenic
c.26-2A>G	44	0.0106	Splice Acceptor	Pathogenic
c.3330+5G>C	43	0.0104	Splice Donor (5th base)	Pathogenic
c.1591G>C (Gly531Arg)	29	0.0070	Nonsynonymous	Likely Pathogenic
TTN				
c.103945_103946insTTGGG (Arg34649LeufsTer25)	68	0.0164	Frameshift	Pathogenic
c.103943_103944del (Tyr34648SerfsTer3)	68	0.0164	Frameshift	Likely Pathogenic
c.61876C>T (Arg20626Ter)	46	0.0111	Stop Gain	Pathogenic
c.86821+2T>A	29	0.0070	Splice Donor	Pathogenic
c.103360del (Glu34454AsnfsTer3)	20	0.0048	Frameshift	Pathogenic
PKP2				
c.971_972insCT (p.Ala325TrpfsTer28)	62	0.0149	Frameshift	Pathogenic
c.2014-1G>C	46	0.0111	Splice Acceptor	Pathogenic
c.2066_2070del (His689ProfsTer8)	31	0.0075	Frameshift	Pathogenic
c.1237C>T (Arg413Ter)	31	0.0075	Stop Gain	Pathogenic
c.1511del (Gly504ValfsTer15)	30	0.0072	Frameshift	Pathogenic
MYH7				
c.2606G>A (Arg869His)	34	0.0082	Nonsynonymous	Likely Pathogenic
c.2389G>A (Ala797Thr)	26	0.0063	Nonsynonymous	Likely Pathogenic
c.3169G>A (Gly1057Ser)	20	0.0048	Nonsynonymous	Likely Pathogenic
SCN5A				
c.3214G>T (Glu1072Ter)	31	0.0075	Stop Gain	Likely Pathogenic
c.673C>T (Arg225Trp)	30	0.0072	Nonsynonymous	Likely Pathogenic
MYL3				
c.427G>A (Glu143Lys)	22	0.0053	Nonsynonymous	Likely Pathogenic

* indicate the variant is unique to this ancestry group

Ancestry Group		Population (N)		
South Asians		5,579		
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification
TTN				
c.77185A>T (Lys25729Ter) *	< 20	< 0.358	Stop Gain	Pathogenic

* indicate the variant is unique to this ancestry group

Ancestry Group		Population (N)			
East Asians		10,099			
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification	
MYH7					
c.4145G>A (Arg1382Gln)	< 20	< 0.198	Nonsynonymous	Likely Pathogenic	
c.3134G>A (Arg1045His)	< 20	< 0.198	Nonsynonymous	Likely Pathogenic	
SCN5A					
c.4279G>T (Ala1427Ser) *	< 20	< 0.198	Nonsynonymous	Likely Pathogenic	
c.674G>A (Arg225Gln)	< 20	< 0.198	Nonsynonymous	Likely Pathogenic	

* indicate the variant is unique to this ancestry group

Ancestry Group		Population (N)		
Admixed Americans		79,106		
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification
MYBPC3				
c.1800del(Lys600AsnfsTer2)	< 20	< 0.0253	Frameshift	Pathogenic
c.3811C>T(Arg1271Ter)	< 20	< 0.0253	Stop Gain	Pathogenic
c.3190+5G>A	< 20	< 0.0253	Splice Donor (5th base)	Pathogenic
c.1624G>C (Glu542Gln)	< 20	< 0.0253	Splice Region Missense	Likely Pathogenic
c.1591G>C (Gly531Arg)	< 20	< 0.0253	Nonsynonymous	Likely Pathogenic
c.1483C>G (Arg495Gly)	< 20	< 0.0253	Nonsynonymous	Likely Pathogenic
c.926+1G>C *	< 20	< 0.0253	Splice Donor	Pathogenic
TTN				
c.75469C>T (Arg25157Ter)	< 20	< 0.0253	Stop Gain	Pathogenic
c.103705A>T (Lys34569Ter) *	< 20	< 0.0253	Stop Gain	Likely Pathogenic
c.75138_75141del (Lys25046AsnfsTer8) *	< 20	< 0.0253	Frameshift	Pathogenic
c.52102+1G>A	< 20	< 0.0253	Splice Donor	Pathogenic
c.40963G>T (Glu13655Ter) *	< 20	< 0.0253	Stop Gain	Pathogenic
c.40723+1G>T	< 20	< 0.0253	Splice Donor	Pathogenic
c.13760del (Glu4587GlyfsTer5) *	< 20	< 0.0253	Frameshift	Likely Pathogenic
c.46855C>T (Gln15619Ter) *	< 20	< 0.0253	Stop Gain	Likely Pathogenic
PKP2				
c.1511del (Gly504ValfsTer15)	23	0.0291	Frameshift	Pathogenic
MYH7				
c.2389G>A (Ala797Thr)	< 20	< 0.0253	Nonsynonymous	Likely Pathogenic
c.611G>A (Arg204His)	< 20	< 0.0253	Nonsynonymous	Likely Pathogenic
SCN5A				
c.5461_5464del (Glu182HisfsTer10) *	< 20	< 0.0253	Frameshift	Likely Pathogenic
c.3214G>T (Glu1072Ter)	< 20	< 0.0253	Stop Gain	Likely Pathogenic
DSP				
c.126T>G (Tyr42Ter)	< 20	< 0.0253	Stop Gain	Pathogenic
MYL3				
c.427G>A (Glu143Lys) *	22	0.0278	Nonsynonymous	Likely Pathogenic

* indicate the variant is unique to this ancestry group

Ancestry Group	Population (N)			
Africans	84,148			
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification
MYBPC3				
c.3330+5G>C *	43	0.0511	Splice Donor (5th base)	Pathogenic
c.3286G>T (Glu1096Ter) *	< 20	< 0.0237	Stop Gain	Pathogenic
c.1624G>C (Glu542Gln)	< 20	< 0.0237	Splice Region Missense	Likely Pathogenic
c.3815-1G>A *	< 20	< 0.0237	Splice Acceptor	Pathogenic
c.1504C>T (Arg502Trp)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
TTN				
c.103945_103946insTTGGG (Arg34649LeufsTer25)	64	0.0761	Frameshift	Pathogenic
c.103943_103944del (Tyr34648SerfsTer3)	64	0.0761	Frameshift	Likely Pathogenic
c.9164-2A>T *	< 20	< 0.0237	Splice Acceptor	Pathogenic
c.6355G>T (Glu2119Ter)	< 20	< 0.0237	Stop Gain	Pathogenic
c.68224+2T>C	< 20	< 0.0237	Splice Donor	Likely Pathogenic
c.57127del (Val19043Ter) *	< 20	< 0.0237	Frameshift Stop Gain	Likely Pathogenic
PKP2				
c.971_972insCT (p.Ala325TrpfsTer28)	21	0.0250	Frameshift	Pathogenic
c.1237C>T (Arg413Ter)	< 20	< 0.0237	Stop Gain	Pathogenic
c.1557-1G>C *	< 20	< 0.0237	Splice Acceptor	Pathogenic
144_165del (Gln49SerfsTer56) *	< 20	< 0.0237	Frameshift	Pathogenic
c.2357+1G>A	< 20	< 0.0237	Splice Donor	Pathogenic
c.837_838del (Val280HsfsTer55)	< 20	< 0.0237	Frameshift	Pathogenic
c.1511del (Gly504ValfsTer15)	< 20	< 0.0237	Frameshift	Pathogenic
c.1379-2A>T *	< 20	< 0.0237	Splice Acceptor	Pathogenic
c.533dup (His179AlafsTer37) *	< 20	< 0.0237	Frameshift	Pathogenic
c.190dup (Leu64ProfsTer22) *	< 20	< 0.0237	Frameshift	Pathogenic
c.2066_2070del (His689ProfsTer8)	< 20	< 0.0237	Frameshift	Pathogenic
c.1171-2A>G *	< 20	< 0.0237	Splice Acceptor	Pathogenic
c.623del (Thr208LysfsTer55) *	< 20	< 0.0237	Frameshift	Pathogenic
MYH7				
c.2606G>A (Arg869His)	26	0.0309	Nonsynonymous	Likely Pathogenic
c.1324C>T (Arg442Cys)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.2389G>A (Ala797Thr)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
SCN5A				
c.3214G>T (Glu1072Ter)	22	0.0261	Stop Gain	Likely Pathogenic
c.673C>T (Arg225Trp)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.2533del (Val845CysfsTer2) *	< 20	< 0.0237	Frameshift	Pathogenic
c.1099C>T (Arg367Cys)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.3953G>T (Gly1318Val)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.4892G>A (Arg1631His)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
DES2				
c.1048C>T (Arg350Trp)	< 20	< 0.0237	Nonsynonymous	Pathogenic
DSP				
c.3865C>T (Gln1289Ter) *	< 20	< 0.0237	Stop Gain	Likely Pathogenic
FLNC				
c.3934_3937dup (Arg1313LeufsTer20) *	< 20	< 0.0237	Frameshift	Likely Pathogenic
TNNC1				
c.23C>T (Ala8Val)	< 20	< 0.0237	Splice Region Missense	Likely Pathogenic
TNNI3				
c.497C>T (Ser166Phe)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.586G>A (Asp196Asn)	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic
c.433C>T (Arg145Trp)	< 20	< 0.0237	Nonsynonymous	Pathogenic
TPM1				
c.842T>C (Met281Thr) *	< 20	< 0.0237	Nonsynonymous	Likely Pathogenic

* indicate the variant is unique to this ancestry group

Ancestry Group	Population (N)			
Europeans	234,353			
Variants by Gene	Carriers (n)	Prevalence (%)	Variant Type	Variant Classification
MYBPC3				
c.1504C>T (Arg502Trp)	79	0.0337	Nonsynonymous	Likely Pathogenic
c.26-2A	42	0.0179	Splice Acceptor	Pathogenic
c.1624G>C (Glu542Gln)	36	0.0154	Splice Region Missense	Likely Pathogenic
c.2373dup (Trp792ValfsTer41)	< 20	< 0.0085	Frameshift	Pathogenic
c.1591G>C (Gly531Arg)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.3330+2T>G *	< 20	< 0.0085	Splice Donor (5th base)	Pathogenic
c.2459G>A (Arg820Gln)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.1624+4A>T	< 20	< 0.0085	Splice Region Intron	Pathogenic
c.927-9G>A	< 20	< 0.0085	Intron	Likely Pathogenic
c.772G>A (Glu258Lys)	< 20	< 0.0085	Splice Region Missense	Pathogenic
c.2864_2865del (Pro955ArgfsTer95)	< 20	< 0.0085	Frameshift	Pathogenic
c.177_187del (Glu60AlafsTer49) *	< 20	< 0.0085	Frameshift	Pathogenic
c.1928-2A>G	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.833del (Gly278GlufsTer22)	< 20	< 0.0085	Frameshift	Pathogenic
c.821+1G>A	< 20	< 0.0085	Splice Donor	Pathogenic
TTN				
c.61876C>T (Arg20626Ter)	45	0.0192	Stop Gain	Pathogenic
c.86821+2T>A	26	0.0111	Splice Donor	Pathogenic
c.103360del (Glu34454AsnfsTer3) *	20	0.0085	Frameshift	Pathogenic
c.44816-1G>A *	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.49648+2del	< 20	< 0.0085	Splice Donor	Pathogenic
c.98299_98300del (Arg32767GlyfsTer2)	< 20	< 0.0085	Frameshift	Pathogenic
c.8902+1G>A	< 20	< 0.0085	Splice Donor	Pathogenic
c.105805del (Thr35269GlnfsTer24) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
c.12587C>A (Ser4196Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.67349-2A>C	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.45895+1G>T *	< 20	< 0.0085	Splice Donor	Likely Pathogenic
c.10303+2T>C	< 20	< 0.0085	Splice Donor	Pathogenic
c.4724_4728del (Met1575SerfsTer6) *	< 20	< 0.0085	Stop Gain	Pathogenic
c.98994del (Lys32998AsnfsTer63)	< 20	< 0.0085	Frameshift	Pathogenic
c.9220C>T (Arg3074Ter) *	< 20	< 0.0085	Stop Gain	Pathogenic
c.97050dup (Glu32351ArgfsTer6) *	< 20	< 0.0085	Frameshift	Pathogenic
c.92317C>T (Arg30773Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.89197+1G>C *	< 20	< 0.0085	Splice Donor	Pathogenic
c.88895-5_88895-2del	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.86335C>T (Arg28779Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.83064_83073del (Ala27689LeufsTer31) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
c.82036C>T (Gln27346Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.77652_77662del (Glu25884AspfsTer3) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
c.77648_77649del (Ile25883ArgfsTer7) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
c.77646del (Ile25883SerfsTer4) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
c.68224+1G>A *	< 20	< 0.0085	Splice Donor	Pathogenic
c.54112del (Glu18038ArgfsTer47) *	< 20	< 0.0085	Frameshift	Likely Pathogenic
PKP2				
c.2014-1G>C	44	0.0188	Splice Acceptor	Pathogenic
c.971_972insCT (Ala325TrpfsTer28)	40	0.0171	Frameshift	Pathogenic
c.2066_2070del (His689ProfsTer8)	26	0.0111	Frameshift	Pathogenic
c.235C>T (Arg79Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.1237C>T (Arg413Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.1481G>A (Trp494Ter) *	< 20	< 0.0085	Stop Gain	Pathogenic
c.148_151del (Thr50SerfsTer61)	< 20	< 0.0085	Frameshift	Pathogenic
c.2357+1G>A	< 20	< 0.0085	Splice Donor	Pathogenic
c.1780C>T (Gln594Ter) *	< 20	< 0.0085	Stop Gain	Pathogenic
MYH7				
c.3169G>A (Gly1057Ser)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.5135G>A (Arg1712Gln)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.3133C>T (Arg1045Cys) *	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.1727A>G (His576Arg)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2389G>A (Ala797Thr)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2167C>T (Arg723Cys)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.1325G>A (Arg442His)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.427C>T (Arg143Trp)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2717A>G (Asp906Gly)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2722C>G (Leu908Val)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.1988G>A (Arg663His)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2080C>T (Arg694Cys)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.1370T>C (Ile457Thr)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2608C>T (Arg870Cys)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.4498C>T (Arg1500Trp) *	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.4145G>A (Arg1382Gln)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2609G>A (Arg870His)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.1491G>T (Glu497Asp) *	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
SCN5A				
c.3953G>T (Gly1318Val)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.4842CTT[2];[1] (Phe1615[2];[1])	< 20	< 0.0085	Inframe Deletion	Likely Pathogenic
c.1338+2T>A	< 20	< 0.0085	Splice Donor	Pathogenic
c.673C>T (Arg225Trp)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.2441G>A (Arg814Gln)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.5347G>A (Glu1783Lys)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.1127G>A (Arg376His)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.4892G>A (Arg1631His)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
DSG2				
c.523+2T>C *	< 20	< 0.0085	Splice Donor	Pathogenic
DSP				
c.2436+2T>C *	< 20	< 0.0085	Splice Donor	Pathogenic
c.478C>T (Arg160Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.126T>G (Tyr42Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
c.3735_3741dup (Asp1248LysfsTer7)	< 20	< 0.0085	Frameshift	Pathogenic
c.4531C>T (Gln1511Ter) *	< 20	< 0.0085	Stop Gain	Likely Pathogenic
c.2437-1G>C	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.6496C>T (Arg2166Ter)	< 20	< 0.0085	Stop Gain	Pathogenic
FLNC				
c.3791-1G>C *	< 20	< 0.0085	Splice Acceptor	Pathogenic
c.5199+1G>T *	< 20	< 0.0085	Splice Donor	Pathogenic
LMNA				
c.1583C>T (Thr528Met) *	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.992G>A (Arg331Gln)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
TNNC1				
c.23C>T (Ala8Val)	< 20	< 0.0085	Splice Region Missense	Likely Pathogenic
TNNI3				
c.497C>T (Ser166Phe)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.485G>A (Arg162Gln)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.484C>T (Arg162Trp)	< 20	< 0.0085	Nonsynonymous	Likely Pathogenic
c.434G>A (Arg145Gln)	< 20	< 0.0085	Nonsynonymous	Pathogenic
TNNT2				
c.430C>T (Arg144Trp)	< 20	< 0.0085	Nonsynonymous	Pathogenic
c.452G>A (Arg151Gln)	< 20	< 0.0085	Nonsynonymous	Pathogenic