Supplementary Table S2. Assessment of the PM1 criterion in *SOD1* variants.

Coding change (NM_000454.5)	Protein change (NP_000445.1)	Variant ID	PM1_Strong	PM1_Moderate	PM1_Supporting
c.13G>A	p.Ala5Thr	rs121912444		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.13G>T	p.Ala5Ser	rs121912444		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.13_14delGCinsTT	p.Ala5Phe			13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.14C>T	p.Ala5Val	rs121912442		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.16G>T	p.Val6Leu	rs1568807314		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.19T>A	p.Cys7Ser	rs1312702973		15 missense/in-frame/non-synonymous variants (13 pathogenic, 2 uncertain, and 0 benign)	
c.19T>G	p.Cys7Gly	rs1312702973		15 missense/in-frame/non-synonymous variants (13 pathogenic, 2 uncertain, and 0 benign)	
c.20G>A	p.Cys7Tyr	rs121912448		15 missense/in-frame/non-synonymous variants (13 pathogenic, 2 uncertain, and 0 benign)	
c.21C>G	p.Cys7Trp			15 missense/in-frame/non-synonymous variants (13 pathogenic, 2 uncertain, and 0 benign)	
c.23T>A	p.Val8Glu	rs1568807330		15 missense/in-frame/non-synonymous variants (13 pathogenic, 2 uncertain, and 0 benign)	
c.25C>G	p.Leu9Val	rs1568807333	17 missense/in-frame/non-synonymous variants (15 pathogenic, 2 uncertain, and 0 benign)		
c.26T>A	p.Leu9Gln	rs1568807342	17 missense/in-frame/non-synonymous variants (15 pathogenic, 2 uncertain, and 0 benign)		
c.31G>C	p.Gly11Arg	rs1568807350	18 missense/in-frame/non-synonymous variants (15 pathogenic, 3 uncertain, and 0 benign)		

c.32G>C	p.Gly11Ala	rs1555836167	18 missense/in-frame/non-synonymous variants (15 pathogenic, 3 uncertain, and 0 benign)		
c.34G>T	p.Asp12Tyr	rs762628133	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.35A>C	p.Asp12Ala	rs1568807374	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.37G>C	p.Gly13Arg	rs121912456		19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)	
c.43G>A	p.Val15Met	rs1568807400		19 missense/in-frame/non-synonymous variants (14 pathogenic, 5 uncertain, and 0 benign)	
c.44T>C	p.Val15Ala	rs1202989817		19 missense/in-frame/non-synonymous variants (14 pathogenic, 5 uncertain, and 0 benign)	
c.44T>G	p.Val15Gly	rs1202989817		19 missense/in-frame/non-synonymous variants (14 pathogenic, 5 uncertain, and 0 benign)	
c.49G>A	p.Gly17Ser	rs121912453		17 missense/in-frame/non-synonymous variants (12 pathogenic, 5 uncertain, and 0 benign)	
c.50G>C	p.Gly17Ala	rs1200906022		17 missense/in-frame/non-synonymous variants (12 pathogenic, 5 uncertain, and 0 benign)	
c.56_58delTCA	p.Ile19del			16 missense/in-frame/non-synonymous variants (11 pathogenic, 5 uncertain, and 0 benign)	
c.59A>G	p.Asn20Ser	rs768029813		15 missense/in-frame/non-synonymous variants (10 pathogenic, 5 uncertain, and 0 benign),	
c.62T>G	p.Phe21Cys	rs1555836169		14 missense/in-frame/non-synonymous variants (9 pathogenic, 5 uncertain, and 0 benign)	
c.63C>G	p.Phe21Leu	rs1555836170		12 missense/in-frame/non-synonymous variants (8 pathogenic, 4 uncertain, and 0 benign)	
c.64G>A	p.Glu22Lys	rs121912450		12 missense/in-frame/non-synonymous variants (8 pathogenic, 4 uncertain, and 0 benign)	

c.65A>G	p.Glu22Gly	rs1568807435		11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.66G>C	p.Glu22Asp			11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.68A>T	p.Gln23Leu	rs1169198442		11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.68A>G	p.Gln23Arg	rs1169198442		11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.69G>C	p.Gln23His	rs1424217272		10 missense/in-frame/non-synonymous variants (7 pathogenic, 3 uncertain, and 0 benign)	
c.95T>C	p.Val32Ala	rs1428716759			8 missense/in-frame/non-synonymous variants (5 pathogenic, 3 uncertain, and 0 benign)
c.95T>G	p.Val32Gly	rs1428716759			8 missense/in-frame/non-synonymous variants (5 pathogenic, 3 uncertain, and 0 benign)
c.112G>A	p.Gly38Arg	rs121912431		13 missense/in-frame/non-synonymous variants (9 pathogenic, 4 uncertain, and 0 benign)	
c.112G>C	p.Gly38Arg	rs121912431		13 missense/in-frame/non-synonymous variants (9 pathogenic, 4 uncertain, and 0 benign)	
c.113G>T	p.Gly38Val	rs1555836517		12 missense/in-frame/non-synonymous variants (9 pathogenic, 3 uncertain, and 0 benign)	
c.115C>G	p.Leu39Val	rs121912432		13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	
c.116T>A	p.Leu39Gln	rs1555836520		13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	
c.116T>G	p.Leu39Arg	rs1555836520		13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	
c.116T>C	p.Leu39Pro			13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	

c.122A>G	p.Glu41Gly	rs1568809149		15 missense/in-frame/non-synonymous variants (11 pathogenic, 4 uncertain, and 0 benign)	
c.123A>T	p.Glu41Asp			15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.124G>A	p.Gly42Ser	rs121912433		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.125G>A	p.Gly42Asp	rs121912434		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.131A>G	p.His44Arg	rs121912435		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.137T>C	p.Phe46Ser	rs121912457		14 missense/in-frame/non-synonymous variants (12 pathogenic, 2 uncertain, and 0 benign)	
c.137T>G	p.Phe46Cys	rs121912457		14 missense/in-frame/non-synonymous variants (12 pathogenic, 2 uncertain, and 0 benign)	
c.139C>G	p.His47Asp	rs748897491		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.140A>G	p.His47Arg	rs121912443		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign),	
c.142G>T	p.Val48Phe	rs1555836523		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.143T>C	p.Val48Ala	rs1568809169		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.146A>G	p.His49Arg	rs1568809172		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.147T>G	p.His49Gln	rs1568809175		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.148G>A	p.Glu50Lys	rs1568809178		10 missense/in-frame/non-synonymous variants (9 pathogenic, 1 uncertain, and 0 benign)	

c.164C>G	p.Thr55Arg	rs986277034			6 missense/in-frame/non-synonymous variants (5 pathogenic, 1 uncertain, and 0 benign)
c.172T>C	p.Cys58Arg	rs1568810255			6 missense/in-frame/non-synonymous variants (5 pathogenic, 1 uncertain, and 0 benign)
c.172T>G	p.Cys58Gly				6 missense/in-frame/non-synonymous variants (5 pathogenic, 1 uncertain, and 0 benign)
c.179G>A	p.Ser60Asn	rs1413388444			6 missense/in-frame/non-synonymous variants (6 pathogenic, 0 uncertain, and 0 benign)
c.179G>T	p.Ser60Ile	rs1413388444			6 missense/in-frame/non-synonymous variants (6 pathogenic, 0 uncertain, and 0 benign)
c.184G>C	p.Gly62Arg	rs1568810268		7 missense/in-frame/non-synonymous variants (7 pathogenic, 0 uncertain, and 0 benign)	
c.193T>C	p.Phe65Leu	rs1030039318		10 missense/in-frame/non-synonymous variants (9 pathogenic, 1 uncertain, and 0 benign)	
c.197A>G	p.Asn66Ser	rs1568810275		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.199C>G	p.Pro67Ala	rs1356474292		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.199C>T	p.Pro67Ser	rs1356474292		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.199G>C	p.Pro67Ala	rs1356474292		17 amino-acids has 11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.200C>G	p.Pro67Arg	rs1568810284		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign),	
c.203T>C	p.Leu68Pro	rs1568810289		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	
c.203T>G	p.Leu68Arg	rs1568810289		11 missense/in-frame/non-synonymous variants (9 pathogenic, 2 uncertain, and 0 benign)	

c.215A>C	p.His72Pro			13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.217G>A	p.Gly73Ser	rs121912455		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.217G>T	p.Gly73Cys	rs121912455		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.218G>A	p.Gly73Asp			13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.223C>T	p.Pro75Ser			10 missense/in-frame/non-synonymous variants (8 pathogenic, 2 uncertain, and 0 benign)	
c.224C>G	p.Pro75Arg			10 missense/in-frame/non-synonymous variants (8 pathogenic, 2 uncertain, and 0 benign)	
c.229G>T	p.Asp77Tyr	rs1601157750			7 missense/in-frame/non-synonymous variants (5 pathogenic, 2 uncertain, and 0 benign)
c.230A>T	p.Asp77Val	rs1568810316			7 missense/in-frame/non-synonymous variants (5 pathogenic, 2 uncertain, and 0 benign)
c.230A>G	p.Asp77Gly				7 missense/in-frame/non-synonymous variants (5 pathogenic, 2 uncertain, and 0 benign)
c.241C>T	p.His81Tyr			10 missense/in-frame/non-synonymous variants (10 pathogenic, 0 uncertain, and 0 benign)	
c.242A>G	p.His81Arg	rs121912458		10 missense/in-frame/non-synonymous variants (10 pathogenic, 0 uncertain, and 0 benign)	
c.250G>A	p.Asp84Asn	rs1555836789		15 missense/in-frame/non-synonymous variants (14 pathogenic, 1 uncertain, and 0 benign)	
c.251A>T	p.Asp84Val		15 missense/in-frame/non-synonymous variants (14 pathogenic, 1 uncertain, and 0 benign)		
c.251A>G	p.Asp84Gly	rs1568810615		15 missense/in-frame/non-synonymous variants (14 pathogenic, 1 uncertain, and 0 benign)	

c.253T>G	p.Leu85Val	rs121912452		15 missense/in-frame/non-synonymous variants (14 pathogenic, 1 uncertain, and 0 benign)	
c.255G>C	p.Leu85Phe	rs1315541036	17 missense/in-frame/non-synonymous variants (16 pathogenic, 1 uncertain, and 0 benign)		
c.255G>T	p.Leu85Phe		17 missense/in-frame/non-synonymous variants (16 pathogenic, 1 uncertain, and 0 benign)		
c.256G>A	p.Gly86Ser	rs121912436	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.256G>C	p.Gly86Arg	rs121912436	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.259A>G	p.Asn87Asp	rs1555836792	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.260A>G	p.Asn87Ser	rs11556620	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.260A>T	p.Asn87Ile	rs11556620	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.261T>A	p.Asn87Lys	rs1555836793	20 missense/in-frame/non-synonymous variants (19 pathogenic, 1 uncertain, and 0 benign)		
c.262G>A	p.Val88Met	rs1568810641	21 missense/in-frame/non-synonymous variants (20 pathogenic, 1 uncertain, and 0 benign)		
c.263T>C	p.Val88Ala	rs1339283341	21 missense/in-frame/non-synonymous variants (20 pathogenic, 1 uncertain, and 0 benign)		
c.268G>A	p.Ala90Thr	rs1568810660	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		
c.269C>T	p.Ala90Val	rs1280042397	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		
c.271G>A	p.Asp91Asn	rs1343616996	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		

c.272A>C	p.Asp91Ala	rs80265967	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		
c.272A>T	p.Asp91Val	rs80265967	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		
c.272_274dupACA	p.Asp91_Lys92insAsn		23 missense/in-frame/non-synonymous variants (21 pathogenic, 2 uncertain, and 0 benign)		
c.280G>A	p.Gly94Ser	rs121912437	26 missense/in-frame/non-synonymous variants (24 pathogenic, 2 uncertain, and 0 benign)		
c.280G>T	p.Gly94Cys	rs121912437	26 missense/in-frame/non-synonymous variants (24 pathogenic, 2 uncertain, and 0 benign)		
c.280G>C	p.Gly94Arg	rs121912437	26 missense/in-frame/non-synonymous variants (24 pathogenic, 2 uncertain, and 0 benign)		
c.281G>A	p.Gly94Asp	rs121912438	24 missense/in-frame/non-synonymous variants (22 pathogenic, 2 uncertain, and 0 benign)		
c.281G>C	p.Gly94Ala	rs121912438	24 missense/in-frame/non-synonymous variants (22 pathogenic, 2 uncertain, and 0 benign)		
c.284T>C	p.Val95Ala	rs202198235	22 missense/in-frame/non-synonymous variants (20 pathogenic, 2 uncertain, and 0 benign)		
c.286G>A	p.Ala96Thr	rs1568810686	21 missense/in-frame/non-synonymous variants (19 pathogenic, 2 uncertain, and 0 benign)		
c.287C>G	p.Ala96Gly	rs1568810690	21 missense/in-frame/non-synonymous variants (19 pathogenic, 2 uncertain, and 0 benign)		
c.287C>T	p.Ala96Val	rs1568810690	21 missense/in-frame/non-synonymous variants (19 pathogenic, 2 uncertain, and 0 benign)		
c.289G>A	p.Asp97Asn	rs121912459	20 missense/in-frame/non-synonymous variants (18 pathogenic, 2 uncertain, and 0 benign)		
c.290A>T	p.Asp97Val	rs1555836803	20 missense/in-frame/non-synonymous variants (18 pathogenic, 2 uncertain, and 0 benign)		

c.292G>A	p.Val98Met	rs1555836806	21 missense/in-frame/non-synonymous variants (19 pathogenic, 2 uncertain, and 0 benign)		
c.292G>C	p.Val98Leu	rs1555836806	21 missense/in-frame/non-synonymous variants (19 pathogenic, 2 uncertain, and 0 benign)		
c.298A>G	p.Ile100Val	rs760740095	18 missense/in-frame/non-synonymous variants (16 pathogenic, 2 uncertain, and 0 benign)		
c.301G>A	p.Glu101Lys	rs76731700	20 missense/in-frame/non-synonymous variants (17 pathogenic, 3 uncertain, and 0 benign)		
c.301G>C	p.Glu101Gln		20 missense/in-frame/non-synonymous variants (17 pathogenic, 3 uncertain, and 0 benign)		
c.302A>G	p.Glu101Gly	rs121912439	20 missense/in-frame/non-synonymous variants (17 pathogenic, 3 uncertain, and 0 benign)		
c.304G>A	p.Asp102Asn	rs1568810715	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.304G>C	p.Asp102His	rs1568810715	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.304G>T	p.Asp102Ty	rs1568810715	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.305A>G	p.Asp102Gly	rs1568810721	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.313A>T	p.Ile105Phe	rs121912445		18 missense/in-frame/non-synonymous variants (13 pathogenic, 5 uncertain, and 0 benign)	
c.317C>T	p.Ser106Leu	rs1378590183		18 missense/in-frame/non-synonymous variants (14 pathogenic, 4 uncertain, and 0 benign)	
c.319C>G	p.Leu107Val	rs121912440	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.319C>T	p.Leu107Phe	rs121912440	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		

c.326G>A	p.Gly109Glu	rs1359299834	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.326G>T	p.Gly109Val	rs1359299834	21 missense/in-frame/non-synonymous variants (17 pathogenic, 4 uncertain, and 0 benign)		
c.328G>T	p.Asp110Tyr	rs567432143	20 missense/in-frame/non-synonymous variants (16 pathogenic, 4 uncertain, and 0 benign)		
c.335G>A	p.Cys112Tyr	rs1601158483	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.338T>C	p.Ile113Thr	rs74315452	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.339C>G	p.Ile113Met	rs1299542356		18 missense/in-frame/non-synonymous variants (14 pathogenic, 4 uncertain, and 0 benign)	
c.340A>T	p.Ile114Phe	rs1568810780		18 missense/in-frame/non-synonymous variants (14 pathogenic, 4 uncertain, and 0 benign)	
c.341T>C	p.Ile114Thr	rs121912441		18 missense/in-frame/non-synonymous variants (14 pathogenic, 4 uncertain, and 0 benign)	
c.344G>C	p.Gly115Ala	rs1568810789		17 missense/in-frame/non-synonymous variants (13 pathogenic, 4 uncertain, and 0 benign)	
c.346C>G	p.Arg116Gly	rs1301635320		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.346C>T	p.Arg116Cys	rs1301635320		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.350C>G	p.Thr117Arg	rs1568810800		15 missense/in-frame/non-synonymous variants (12 pathogenic, 3 uncertain, and 0 benign)	
c.352C>G	p.Leu118Val	rs199474723		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.355G>C	p.Val119Leu	rs1235629842		12 missense/in-frame/non-synonymous variants (11 pathogenic, 1 uncertain, and 0 benign)	

c.355G>T	p.Val119Leu	rs1235629842		12 missense/in-frame/non-synonymous variants (11 pathogenic, 1 uncertain, and 0 benign)	
c.355G>A	p.Val119Met			12 missense/in-frame/non-synonymous variants (11 pathogenic, 1 uncertain, and 0 benign)	
c.358G>T	p.Val120Phe			12 missense/in-frame/non-synonymous variants (11 pathogenic, 1 uncertain, and 0 benign)	
c.358G>C	p.Val120Leu	rs1457889952		9 missense/in-frame/non-synonymous variants (7 pathogenic, 2 uncertain, and 0 benign)	
c.361C>A	p.His121Asn			9 missense/in-frame/non-synonymous variants (7 pathogenic, 2 uncertain, and 0 benign)	
c.362A>T	p.His121Leu	rs1410925719		13 missense/in-frame/non-synonymous variants (11 pathogenic, 2 uncertain, and 0 benign)	
c.374A>C	p.Asp125Ala	rs1568811366		11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.374A>T	p.Asp125Val	rs1568811366		11 missense/in-frame/non-synonymous variants (8 pathogenic, 3 uncertain, and 0 benign)	
c.376G>C	p.Asp126His	rs1568811372		12 missense/in-frame/non-synonymous variants (9 pathogenic, 3 uncertain, and 0 benign)	
c.376G>A	p.Asp126Asn			12 missense/in-frame/non-synonymous variants (9 pathogenic, 3 uncertain, and 0 benign)	
c.377A>C		rs1164911383		12 missense/in-frame/non-synonymous variants (9 pathogenic, 3 uncertain, and 0 benign)	
c.380T>C	p.Leu127Ser	rs121912454		13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	
c.382G>C	p.Gly128Arg	rs1568811389		13 missense/in-frame/non-synonymous variants (10 pathogenic, 3 uncertain, and 0 benign)	
c.385A>G	p.Lys129Glu			12 missense/in-frame/non-synonymous variants (9 pathogenic, 3 uncertain, and 0 benign)	

c.400G>A	p.Glu134Lys			15 missense/in-frame/non-synonymous variants (11 pathogenic, 4 uncertain, and 0 benign)	
c.401A>T	p.Glu134Val	rs1568811426		15 missense/in-frame/non-synonymous variants (11 pathogenic, 4 uncertain, and 0 benign)	
c.403A>G	p.Ser135Gly	rs1555836932		12 missense/in-frame/non-synonymous variants (8 pathogenic, 4 uncertain, and 0 benign)	
c.404G>A	p.Ser135Asn	rs121912451		12 missense/in-frame/non-synonymous variants (8 pathogenic, 4 uncertain, and 0 benign)	
c.404G>C	p.Ser135Thr	rs121912451		12 missense/in-frame/non-synonymous variants (8 pathogenic, 4 uncertain, and 0 benign)	
c.412A>G	p.Thr138Ala	rs1568811445		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign)	
c.413C>G	p.Thr138Arg	rs1568811454		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign)	
c.416G>A	p.Gly139Glu	rs1568811464		17 missense/in-frame/non-synonymous variants (13 pathogenic, 4 uncertain, and 0 benign)	
c.418A>C	p.Asn140His	rs1568811471	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.418A>G	p.Asn140Asp	rs1568811471	19 missense/in-frame/non-synonymous variants (15 pathogenic, 4 uncertain, and 0 benign)		
c.420C>A	p.Asn140Lys	rs1804449	20 missense/in-frame/non-synonymous variants (16 pathogenic, 4 uncertain, and 0 benign)		
c.422C>G	p.Ala141Gly	rs1555836937	21 missense/in-frame/non-synonymous variants (16 pathogenic, 5 uncertain, and 0 benign)		
c.424G>A	p.Gly142Arg		23 missense/in-frame/non-synonymous variants (17 pathogenic, 6 uncertain, and 0 benign)		
c.425G>A	p.Gly142Glu	rs1568811489	22 missense/in-frame/non-synonymous variants (17 pathogenic, 5 uncertain, and 0 benign)		

c.425G>C	p.Gly142Ala	rs1568811489	22 missense/in-frame/non-synonymous variants (17 pathogenic, 5 uncertain, and 0 benign)		
c.434T>C	p.Leu145Ser	rs121912446	23 missense/in-frame/non-synonymous variants (16 pathogenic, 7 uncertain, and 0 benign)		
c.435G>C	p.Leu145Phe	rs1482760341	23 missense/in-frame/non-synonymous variants (16 pathogenic, 7 uncertain, and 0 benign)		
c.436G>A	p.Ala146Thr	rs121912447	23 missense/in-frame/non-synonymous variants (16 pathogenic, 7 uncertain, and 0 benign)		
c.437C>A	p.Ala146Asp	rs1131690781	23 missense/in-frame/non-synonymous variants (16 pathogenic, 7 uncertain, and 0 benign)		
c.437C>G	p.Ala146Gly	rs1131690781	23 missense/in-frame/non-synonymous variants (16 pathogenic, 7 uncertain, and 0 benign)		
c.439T>C	p.Cys147Arg	rs1568811515	21 missense/in-frame/non-synonymous variants (15 pathogenic, 6 uncertain, and 0 benign)		
c.442G>C	p.Gly148Arg	rs1568811520	20 missense/in-frame/non-synonymous variants (15 pathogenic, 5 uncertain, and 0 benign)		
c.442G>A	p.Gly148Ser		20 missense/in-frame/non-synonymous variants (15 pathogenic, 5 uncertain, and 0 benign)		
c.442G>T	p.Gly148Cys		20 missense/in-frame/non-synonymous variants (15 pathogenic, 5 uncertain, and 0 benign)		
c.443G>A	p.Gly148Asp	rs1555836950	20 missense/in-frame/non-synonymous variants (15 pathogenic, 5 uncertain, and 0 benign)		
c.445G>A	p.Val149Ile	rs567511139		19 missense/in-frame/non-synonymous variants (14 pathogenic, 5 uncertain, and 0 benign)	
c.446T>G	p.Val149Gly	rs1476760624		17 missense/in-frame/non-synonymous variants (12 pathogenic, 5 uncertain, and 0 benign)	
c.446T>C	p.Val149Ala			17 missense/in-frame/non-synonymous variants (12 pathogenic, 5 uncertain, and 0 benign)	

c.448A>G	p.Ile150Val	rs1169917994		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign),	
c.449T>C	p.Ile150Thr	rs1424014997		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign),	
c.455T>C	p.Ile152Thr	rs121912449		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign	
c.455T>G	p.Ile152Ser			16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign	
c.457G>A	p.Ala153Thr	rs747094021		16 missense/in-frame/non-synonymous variants (12 pathogenic, 4 uncertain, and 0 benign)	