Supp. Table S1: Expert-curated variants meeting functional criteria (PS3/BS3).

[a]Expert panel-curated variants that met either PS3 or BS3 functional criteria are listed by gene, cDNA, amino acid, and variant type. Variants were curated by expert panels using the following reference transcripts: *PTPN11* (NM_002834.3), *BRAF* (NM_004333.4), *MAP2K1* (NM_002755.3), *MYH7* (NM_000257.3), *HRAS* (NM_005343.2), *RAF1* (NM_002880.3), *KRAS* (NM_004985.4), *SOS1* (NM_005633.3), *SHOC2* (NM_007373.3), and *MAP2K2* (NM_030662.3). [b]Evidence Satisfied, as determined by expert panels in Gelb et al. (2018) and Kelly et al. (2018), displayed as the number satisfied in each abbreviated category described in Richards et al. (2015). The first letter of each code indicates support for a pathogenic (P) or benign (B) classification and the second letter indicates the assigned evidence strength: supporting (P), moderate (M), strong (S), very strong (VS), or stand-alone (A). [c,d] The final variant classification assessed according to categorical ACMG/AMP combining rules (Table 5 in Richards et al., 2015), with Expert Panel (EP) variant classifications considering only evidence satisfied in (b). Variant class according to the categorical combining rules if PS3 had not been met is shown as "-PS3" in (c), and if BS3 had not been met in shown as "-BS3" is (d). [e]Variant class according to the quantitative, Bayesian-adapted framework was determined by posterior probability of pathogenicity (Post_P). Post_P was calculated by entering evidence totals by strength in Supplemental Table 1 from Tavtigian et al. (2018), using the default settings: Prior Probability (Prior_P) = 0.100; Odds Path Very Strong = 350; Exponential progression (X) = 2.000. Each Post_P was then assigned a variant classification as follows: benign <0.001; 0.001 ≤ likely benign < 0.1; 0.1 ≤ VUS < 0.90; 0.90 ≤ likely pathogenic < 0.99; 0.99 ≤ pathogenic. ACMG/AMP, American College of Medical Genetics and Genomics/Association for Molecular Pathology; BS3, well-established functional studies show no deleterious effect; EP, Expert Panel; LB, likely benign; LP, likely pathogenic; P, pathogenic; Post_P, posterior probability of pathogenicity; PS3, well established functional studies show a deleterious effect; VUS, variant of uncertain significance.

EP classified as pathogenic, met PS3[a]				**Evidence Satisfied (MET PS3)[b]**							**Categorical[c]**		**Quantitative[e]**	
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**-PS3**	**Class**	**Post_P**
PTPN11	c.794G>A	p.Arg265Gln	Missense	2	2	2	1	0	0	0	P	P	P	1.000
BRAF	c.770A>G	p.Gln257Arg	Missense	2	2	1	1	0	0	0	P	P	P	1.000
BRAF	c.1406G>A	p.Gly469Glu	Missense	2	2	1	1	0	0	0	P	P	P	1.000
MAP2K1	c.389A>G	p.Tyr130Cys	Missense	2	2	1	1	0	0	0	P	P	P	1.000
MYH7	c.2155C>T	p.Arg719Trp	Missense	1	3	4	0	0	0	0	P	P	P	1.000
MYH7	c.1357C>T	p.Arg453Cys	Missense	1	2	4	0	0	0	0	P	P	P	1.000
PTPN11	c.922A>G	p.Asn308Asp	Missense	2	1	4	0	0	0	0	P	P	P	1.000
HRAS	c.34G>A	p.Gly12Ser	Missense	2	3	3	0	0	0	0	P	P	P	1.000

MYH7	c.1208G>A	p.Arg403Gln	Missense	1	3	3	0	0	0	0	P	P	P	1.000
RAF1	c.775T>A	p.Ser259Thr	Missense	4	2	3	0	0	0	0	P	P	P	1.000
KRAS	c.40G>A	p.Val14Ile	Missense	2	2	3	0	0	0	0	P	P	P	1.000
PTPN11	c.1403C>T	p.Thr468Met	Missense	2	2	3	0	0	0	0	P	P	P	1.000
SOS1	c.1642A>C	p.Ser548Arg	Missense	2	2	3	0	0	0	0	P	P	P	1.000
SHOC2	c.4A>G	p.Ser2Gly	Missense	1	2	3	0	0	0	0	P	P	P	1.000
BRAF	c.736G>C	p.Ala246Pro	Missense	2	3	2	0	0	0	0	P	P	P	1.000
BRAF	c.1741A>G	p.Asn581Asp	Missense	2	2	2	0	0	0	0	P	P	P	1.000
BRAF	c.1787G>T	p.Gly596Val	Missense	2	2	2	0	0	0	0	P	P	P	1.000
KRAS	c.173C>T	p.Thr58Ile	Missense	2	2	2	0	0	0	0	P	P	P	1.000
KRAS	c.178G>C	p.Gly60Arg	Missense	2	2	2	0	0	0	0	P	P	P	1.000
KRAS	c.65A>G	p.Gln22Arg	Missense	2	2	2	0	0	0	0	P	P	P	1.000
MAP2K2	c.383C>A	p.Pro128Gln	Missense	2	2	2	0	0	0	0	P	P	P	1.000
PTPN11	c.188A>G	p.Tyr63Cys	Missense	2	2	2	0	0	0	0	P	P	P	1.000
SOS1	c.322G>A	p.Glu108Lys	Missense	2	2	2	0	0	0	0	P	P	P	1.000
MYH7	c.1594T>C	p.Ser532Pro	Missense	2	2	2	0	0	0	0	P	LP	P	1.000
HRAS	c.350A>G	p.Lys117Arg	Missense	1	2	2	0	0	0	0	P	LP	P	0.999
RAF1	c.770C>T	p.Ser257Leu	Missense	1	2	2	0	0	0	0	P	LP	P	0.999
MAP2K1	c.199G>A	p.Asp67Asn	Missense	2	1	2	0	0	0	0	P	LP	P	0.999
PTPN11	c.1510A>G	p.Met504Val	Missense	2	1	2	0	0	0	0	P	LP	P	0.999
RAF1	c.1837C>G	p.Leu613Val	Missense	1	1	2	0	0	0	0	P	LP	P	0.997
KRAS	c.458A>T	p.Asp153Val	Missense	0	1	2	0	0	0	0	P	LP	P	0.994
MAP2K1	c.158T>C	p.Phe53Ser	Missense	2	3	1	0	0	0	0	P	LP	P	0.999
MAP2K2	c.170T>G	p.Phe57Cys	Missense	2	3	1	0	0	0	0	P	LP	P	0.999
SOS1	c.508A>G	p.Lys170Glu	Missense	2	3	1	0	0	0	0	P	LP	P	0.999
SOS1	c.2536G>A	p.Glu846Lys	Missense	2	3	1	0	0	0	0	P	LP	P	0.999
MAP2K2	c.401A>G	p.Tyr134Cys	Missense	2	2	1	0	0	0	0	P	LP	P	0.994
PTPN11	c.417G>C	p.Glu139Asp	Missense	2	2	1	0	0	0	0	P	LP	P	0.994
RAF1	c.768G>T	p.Arg256Ser	Missense	2	2	1	0	0	0	0	P	LP	P	0.994

RAF1	c.1472C>T	p.Thr491Ile	Missense	2	2	1	0	0	0	0	P	LP	P	0.994
RAF1	c.781C>T	p.Pro261Ser	Missense	1	2	1	0	0	0	0	P	LP	LP	0.988
EP classified as likely benign with BS3[a]				**Evidence Satisfied (MET BS3)[b]**							**Categorical[d]**		**Quantitative[e]**	
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**-BS3**	**Class**	**Post_P**
PTPN11	c.1678C>T	p.Leu560Phe	Missense	0	0	0	0	1	1	0	LB	VUS	LB	0.0028

Supp. Table S2: Expert-curated variants not meeting functional criteria (PS3/BS3).

[a]Expert panel (EP)-curated variants that met neither PS3 or BS3 functional criteria are listed by gene, cDNA, protein, and variant type and are grouped by EP classification. Variants were curated by expert panels using the following reference transcripts: *PTPN11* (LRG_614t1, intronic variants; NM_002834.3, all others), *BRAF* (LRG_299t1, intronic variants; NM_004333.4, all others), *MAP2K1* (LRG_725t1, intronic variants; NM_002755.3, all others), *MYH7* (LRG_384t1, intronic and splice variants; NM_000257.3, all others), *HRAS* (NM_005343.2), *RAF1* (LRG_413t1, intronic variants; NM_002880.3, all others), *KRAS* (NC_000012.12, intronic variants; NM_004985.4, all others), *SOS1* (NM_005633.3), *SHOC2* (LRG_753t1, 5' UTR variants; NM_007373.3, all others), and *MAP2K2* (LRG_750t1, 3' UTR variants; NM_030662.3, all others). [b]Evidence Satisfied, as determined by expert panels in Gelb et al. (2018) and Kelly et al. (2018), displayed as the number satisfied in each abbreviated category described in Richards et al. (2015). The first letter of each code indicates support for a pathogenic (P) or benign (B) classification and the second letter indicates the assigned evidence strength: supporting (P), moderate (M), strong (S), very strong (VS), or stand-alone (A). [c]The final variant classification assessed according to categorical ACMG/AMP combining rules (Table 5 in Richards et al., 2015), with EP classifications considering only evidence satisfied in (b). [d]Variant class with the addition of either PS3 or BS3 criteria in the categorical interpretation framework (Table 5 in Richards et al.). [e]Variant class according to the quantitative, Bayesian-adapted framework was determined by posterior probability of pathogenicity (Post_P). Post_P was calculated by entering evidence totals by strength in Supplemental Table 1 from Tavtigian et al. (2018), using the default settings: Prior Probability (Prior_P) = 0.100; Odds Path Very Strong = 350; Exponential progression (X) = 2.000. Each Post_P was then assigned a variant classification as follows: benign <0.001; 0.001 ≤ likely benign < 0.1; 0.1 ≤ VUS < 0.90; 0.90 ≤ likely pathogenic < 0.99; 0.99 ≤ pathogenic. The last four columns show the variant classification according to Post_P if strong pathogenic criteria (PS3) or strong benign criteria (BS3) were to be added within the quantitative framework (see manuscript text for details). ACMG/AMP, American College of Medical Genetics and Genomics/Association for Molecular Pathology; B, benign; BS3, well-established functional studies show no deleterious effect; CON, conflicting; EP, Expert Panel; LB, likely benign; LP, likely pathogenic; n/a, not available; P, pathogenic; Post_P, posterior probability of pathogenicity; PS3, well established functional studies show a deleterious effect; Synonym., synonymous; VUS, variant of uncertain significance.

EP classified as benign[a]				Evidence Satisfied (no PS3/BS3)[b]							Categorical[c]			Quantitative[e]					
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**+PS3[d]**	**+BS3[d]**	**Class**	**Post_P**	**+PS3**	**Post_P**	**+BS3**	**Post-P**
RAF1	c.119G>A	p.Arg40His	Missense	0	0	0	0	1	1	1	B	CON	B	All of these meet BA1, which is not included in Bayesian framework described by Tavtigian et al. (2018).					
BRAF	c.1227A>G	p.Ser409=	Synonym.	0	0	0	0	3	0	1	B	CON	B						
SHOC2	c.1302C>T	p.Asn434=	Synonym.	0	0	0	0	3	0	1	B	CON	B						
SOS1	c.1230G>A	p.Gln410=	Synonym.	0	0	0	0	3	0	1	B	CON	B						
BRAF	c.1433-19A>G	n/a	Intronic	1	0	0	0	2	0	1	B	CON	CON						
RAF1	c.1108+9_1108+21delGGGGCCCTCCCTT	n/a	Intronic	0	0	0	0	2	0	1	B	CON	B						
HRAS	c.257A>C	p.Asn86Thr	Missense	0	0	0	0	1	0	1	B	CON	B						
KRAS	c.531_533delGAA	p.Lys180del	Deletion	0	0	0	0	1	0	1	B	CON	B						
MAP2K1	c.848C>T	p.Ala283Val	Missense	0	0	0	0	1	0	1	B	CON	B						
MAP2K1	c.694-8_694-7dupTC	n/a	Intronic	0	0	0	0	1	0	1	B	CON	B						
MAP2K2	c.844C>T	p.Pro282Ser	Missense	0	0	0	0	1	0	1	B	CON	B						
PTPN11	c.1658C>T	p.Thr553Met	Missense	0	0	0	0	1	0	1	B	CON	B						
SHOC2	c.10A>C	p.Ser4Arg	Missense	0	0	0	0	1	0	1	B	CON	B						
MYH7	c.327C>T	p.Tyr109=	Synonym.	0	0	0	0	1	0	1	B	CON	B						
MYH7	c.3036C>T	p.Ala1012=	Synonym.	0	0	0	0	1	0	1	B	CON	B						
MYH7	c.2162+4G>A	n/a	Intronic	0	0	0	0	1	0	1	B	CON	B						
BRAF	c.968C>T	p.Ser323Leu	Missense	0	0	0	0	0	0	1	B	CON	B						
HRAS	c.81T>C	p.His27=	Synonym.	0	0	0	0	0	0	1	B	CON	B						
KRAS	c.519T>C	p.Asp173=	Synonym.	0	0	0	0	0	0	1	B	CON	B						
MAP2K2	c.1162C>T	p.Arg388Trp	Missense	0	0	0	0	0	0	1	B	CON	B						
PTPN11	c.525+12G>C	n/a	Intronic	0	0	0	0	0	0	1	B	CON	B						
PTPN11	c.854-32A>C	n/a	Intronic	0	0	0	0	0	0	1	B	CON	B						
PTPN11	c.925A>G	p.Ile309Val	Missense	0	0	0	0	0	0	1	B	CON	B						

RAF1	c.212A>G	p.Asn71Ser	Missense	0	0	0	0	0	0	1	B	CON	B							
SHOC2	c.38A>C	p.Glu13Ala	Missense	0	0	0	0	0	0	1	B	CON	B							
SOS1	c.749T>C	p.Val250Ala	Missense	0	0	0	0	0	0	1	B	CON	B							
SOS1	c.2122G>A	p.Ala708Thr	Missense	0	0	0	0	0	0	1	B	CON	B							
SOS1	c.73C>T	p.Pro25Ser	Missense	0	0	0	0	0	0	1	B	CON	B							
SOS1	c.2371C>A	p.Leu791Ile	Missense	0	0	0	0	0	0	1	B	CON	B							
SOS1	c.3032A>G	p.Asn1011Ser	Missense	0	0	0	0	0	0	1	B	CON	B							
BRAF	c.64G>A	p.Asp22Asn	Missense	0	0	0	0	0	2	0	B	CON	B	B	0.0003	LB	0.0059	B	0.00002
EP classified as likely benign[a]				**Evidence Satisfied (no PS3/BS3)[b]**							**Categorical[c]**			**Quantitative[e]**					
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**+PS3[d]**	**+BS3[d]**	**Class**	**Post_P**	**+PS3**	**Post_P**	**+BS3**	**Post_P**
SOS1	c.350T>G	p.Val117Gly	Missense	1	0	0	0	1	1	0	LB	CON	CON	LB	0.006	VUS	0.100	B	0.0003
MYH7	c.4377G>T	p.Lys1459Asn	Missense	1	0	0	0	0	1	0	LB	CON	CON	LB	0.012	VUS	0.188	B	0.0007
SOS1	c.109A>G	p.Thr37Ala	Missense	0	0	0	0	2	1	0	LB	CON	B	LB	0.001	LB	0.025	B	0.0001
BRAF	c.92C>G	p.Ala31Gly	Missense	0	0	0	0	1	1	0	LB	CON	B	LB	0.003	LB	0.051	B	0.0002
RAF1	c.66T>G	p.Phe22Leu	Missense	0	0	0	0	1	1	0	LB	CON	B	LB	0.003	LB	0.051	B	0.0002
HRAS	c.510G>A	p.Lys170=	Synonym.	0	0	0	0	3	0	0	LB	CON	LB	LB	0.012	VUS	0.188	B	0.0007
BRAF	c.111G>A	p.Ser37=	Synonym.	0	0	0	0	2	0	0	LB	CON	LB	LB	0.025	VUS	0.325	LB	0.0014
KRAS	c.451-14T>C	n/a	Intronic	0	0	0	0	2	0	0	LB	CON	LB	LB	0.025	VUS	0.325	LB	0.0014
MAP2K2	c.*8C>T	n/a	3' UTR	0	0	0	0	2	0	0	LB	CON	LB	LB	0.025	VUS	0.325	LB	0.0014
EP classified as likely pathogenic[a]				**Evidence Satisfied (no PS3/BS3)[b]**							**Categorical[c]**			**Quantitative[e]**					
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**+PS3[d]**	**+BS3[d]**	**Class**	**Post_P**	**+PS3**	**Post_P**	**+BS3**	**Post_P**
MYH7	c.2539_2541delAAG	p.Lys847del	Deletion	1	2	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MYH7	c.2539A>G	p.Lys847Glu	Missense	1	2	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MYH7	c.3158G>A	p.Arg1053Gln	Missense	1	2	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MYH7	c.4066G>A	p.Glu1356Lys	Missense	1	2	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MAP2K1	c.275T>G	p.Leu92Arg	Missense	3	1	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MAP2K2	c.619G>A	p.Glu207Lys	Missense	3	1	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812

RAF1	c.1082G>C	p.Gly361Ala	Missense	3	1	1	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MYH7	c.5135G>A	p.Arg1712Gln	Missense	2	1	1	0	0	0	0	LP	P	CON	LP	0.975	P	0.999	VUS	0.675
MYH7	c.428G>A	p.Arg143Gln	Missense	1	1	1	0	0	0	0	LP	P	CON	LP	0.949	P	0.997	VUS	0.500
MYH7	c.3133C>T	p.Arg1045Cys	Missense	1	1	1	0	0	0	0	LP	P	CON	LP	0.949	P	0.997	VUS	0.500
MYH7	c.4130C>T	p.Thr1377Met	Missense	1	1	1	0	0	0	0	LP	P	CON	LP	0.949	P	0.997	VUS	0.500
MAP2K1	c.388T>C	p.Tyr130His	Missense	2	3	0	0	0	0	0	LP	P	CON	LP	0.975	P	0.999	VUS	0.675
RAF1	c.769T>C	p.Ser257Pro	Missense	2	4	0	0	0	0	0	LP	P	CON	P	0.994	P	1.000	VUS	0.900
RAF1	c.788T>G	p.Val263Gly	Missense	2	4	0	0	0	0	0	LP	P	CON	P	0.994	P	1.000	VUS	0.900
MYH7	c.1106G>A	p.Arg369Gln	Missense	0	4	0	0	0	0	0	LP	P	CON	LP	0.975	P	0.999	VUS	0.675
MAP2K2	c.400T>C	p.Tyr134His	Missense	3	3	0	0	0	0	0	LP	P	CON	LP	0.988	P	0.999	VUS	0.812
MYH7	c.2608C>T	p.Arg870Cys	Missense	2	3	0	0	0	0	0	LP	P	CON	LP	0.975	P	0.999	VUS	0.675
MYH7	c.2678C>T	p.Ala893Val	Missense	1	3	0	0	0	1	0	LP	CON	CON	VUS	0.500	LP	0.949	LB	0.051
MYH7	c.2791_2793delGAG	p.Glu931del	Deletion	1	3	0	0	0	0	0	LP	P	CON	LP	0.949	P	0.997	VUS	0.500
MYH7	c.1157A>G	p.Tyr386Cys	Missense	1	3	0	0	0	0	0	LP	P	CON	LP	0.949	P	0.997	VUS	0.500
HRAS	c.175G>A	p.Ala59Thr	Missense	4	2	0	0	0	0	0	LP	P	CON	LP	0.975	P	0.999	VUS	0.675
BRAF	c.1595G>A	p.Cys532Tyr	Missense	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
MAP2K1	c.169A>C	p.Lys57Gln	Missense	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
MYH7	c.3658_3660delGAG	p.Glu1220del	Deletion	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
MYH7	c.5401G>A	p.Glu1801Lys	Missense	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
MYH7	c.5740G>A	p.Glu1914Lys	Missense	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
PTPN11	c.155C>T	p.Thr52Ile	Missense	2	2	0	0	0	0	0	LP	P	CON	LP	0.900	P	0.994	VUS	0.325
MYH7	c.4258C>T	p.Arg1420Trp	Missense	1	2	0	0	0	0	0	LP	LP	CON	VUS	0.812	LP	0.988	VUS	0.188
MYH7	c.5726G>C	p.Arg1909Pro	Missense	1	2	0	0	0	0	0	LP	LP	CON	VUS	0.812	LP	0.988	VUS	0.188
EP classified as pathogenic[a]				**Evidence Satisfied (no PS3/BS3)[b]**							**Categorical[c]**			**Quantitative[e]**					
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**EP Class**	**+PS3[d]**	**+BS3[d]**	**Class**	**Post_P**	**+PS3**	**Post_P**	**+BS3**	**Post_P**
MAP2K2	c.169T>G	p.Phe57Val	Missense	2	2	0	1	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.994
MYH7	c.2167C>T	p.Arg723Cys	Missense	1	4	2	0	1	0	0	P	CON	CON	P	1.000	P	1.000	P	0.999

MYH7	c.1207C>T	p.Arg403Trp	Missense	1	3	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
MYH7	c.2146G>A	p.Gly716Arg	Missense	1	3	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
MYH7	c.2156G>A	p.Arg719Gln	Missense	1	3	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
MYH7	c.2167C>G	p.Arg723Gly	Missense	1	3	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
BRAF	c.1785T>G	p.Phe595Leu	Missense	3	2	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
PTPN11	c.1529A>C	p.Gln510Pro	Missense	3	2	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.997
HRAS	c.37G>T	p.Gly13Cys	Missense	2	2	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.994
SOS1	c.806T>C	p.Met269Thr	Missense	2	2	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.994
SOS1	c.1654A>G	p.Arg552Gly	Missense	2	2	2	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.994
MYH7	c.788T>C	p.Ile263Thr	Missense	1	2	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.988
MYH7	c.2722C>G	p.Leu908Val	Missense	1	2	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.988
MYH7	c.1988G>A	p.Arg663His	Missense	0	2	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.975
MYH7	c.2609G>A	p.Arg870His	Missense	0	2	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.975
MYH7	c.2717A>G	p.Asp906Gly	Missense	0	2	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.975
PTPN11	c.1530G>C	p.Gln510His	Missense	2	1	2	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.975
MYH7	c.2221G>C	p.Gly741Arg	Missense	2	4	1	0	0	0	0	P	P	CON	P	1.000	P	1.000	P	0.994
MYH7	c.1358G>A	p.Arg453His	Missense	1	4	1	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.988
MYH7	c.2221G>T	p.Gly741Trp	Missense	1	4	1	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.988
HRAS	c.173C>T	p.Thr58Ile	Missense	3	3	1	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.988
BRAF	c.730A>C	p.Thr244Pro	Missense	2	3	1	0	0	0	0	P	P	CON	P	0.999	P	1.000	LP	0.975
PTPN11	c.781C>T	p.Leu261Phe	Missense	1	3	1	0	0	0	0	P	P	CON	P	0.997	P	1.000	LP	0.949
MYH7	c.1750G>C	p.Gly584Arg	Missense	1	3	1	0	0	0	0	P	P	CON	P	0.997	P	1.000	LP	0.949
MYH7	c.2681A>G	p.Glu894Gly	Missense	1	3	1	0	0	0	0	P	P	CON	P	0.997	P	1.000	LP	0.949
MYH7	c.2207T>C	p.Ile736Thr	Missense	0	3	1	0	0	0	0	P	P	CON	P	0.994	P	1.000	LP	0.900
KRAS	c.101C>T	p.Pro34Leu	Missense	2	2	1	0	0	0	0	P	P	CON	P	0.994	P	1.000	LP	0.900
MYH7	c.2513C>T	p.Pro838Leu	Missense	2	2	1	0	0	0	0	P	P	CON	P	0.994	P	1.000	LP	0.900
KRAS	c.15A>T	p.Lys5Asn	Missense	2	2	1	0	0	0	0	P	P	CON	P	0.994	P	1.000	LP	0.900
EP classified as VUS[a]				**Evidence Satisfied (no PS3/BS3)[b]**							**Categorical[c]**			**Quantitative[e]**					
Gene	**cDNA**	**Amino Acid**	**Variant Type**	**PP**	**PM**	**PS**	**PVS**	**BP**	**BS**	**BA**	**Class**	**+PS3[d]**	**+BS3[d]**	**Class**	**Post_P**	**+PS3**	**Post_P**	**+BS3**	**Post_P**

MYH7	c.732+1G>A	n/a	Splice donor	1	2	0	0	0	0	0	VUS	LP	CON	VUS	0.812	LP	0.988	VUS	0.188
MYH7	c.3169G>A	p.Gly1057Ser	Missense	1	2	0	0	0	0	0	VUS	LP	CON	VUS	0.812	LP	0.988	VUS	0.188
MYH7	c.1477_1478delAT	p.Met493fs	Frameshift	0	2	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.4588C>T	p.Arg1530*	Nonsense	0	2	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
RAF1	c.1193G>T	p.Arg398Leu	Missense	2	1	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.4276G>A	p.Glu1426Lys	Missense	2	1	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.5302G>A	p.Glu1768Lys	Missense	2	1	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.5329G>A	p.Ala1777Thr	Missense	2	1	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.5588G>A	p.Arg1863Gln	Missense	2	1	0	0	0	0	0	VUS	LP	CON	VUS	0.675	LP	0.975	VUS	0.100
MYH7	c.4354-7C>T	n/a	Intronic	1	1	0	0	1	0	0	VUS	CON	CON	VUS	0.325	LP	0.900	LB	0.025
HRAS	c.277A>G	p.Ile93Val	Missense	1	1	0	0	0	0	0	VUS	LP	CON	VUS	0.500	LP	0.949	LB	0.051
MYH7	c.2360G>A	p.Arg787His	Missense	0	1	0	0	1	0	0	VUS	CON	CON	VUS	0.188	VUS	0.812	LB	0.012
SHOC2	c.519G>A	p.Met173Ile	Missense	0	1	0	0	0	0	0	VUS	LP	CON	VUS	0.325	LP	0.900	LB	0.025
PTPN11	c.244A>G	p.Met82Val	Missense	1	0	0	0	1	0	0	VUS	CON	CON	VUS	0.100	VUS	0.675	LB	0.006
MYH7	c.3981C>A	p.Asn1327Lys	Missense	1	0	0	0	0	1	0	VUS	CON	CON	LB	0.012	VUS	0.188	B	0.0007
MAP2K2	c.281C>T	p.Ser94Leu	Missense	1	0	0	0	0	0	0	VUS	VUS	CON	VUS	0.188	VUS	0.812	LB	0.012
MYH7	c.3286G>T	p.Asp1096Tyr	Missense	1	0	0	0	0	0	0	VUS	VUS	CON	VUS	0.188	VUS	0.812	LB	0.012
MYH7	c.3578G>A	p.Arg1193His	Missense	1	0	0	0	0	0	0	VUS	VUS	CON	VUS	0.188	VUS	0.812	LB	0.012
MYH7	c.5326A>G	p.Ser1776Gly	Missense	1	0	0	0	0	0	0	VUS	VUS	CON	VUS	0.188	VUS	0.812	LB	0.012
MAP2K2	c.784G>A	p.Val262Ile	Missense	0	0	0	0	1	0	0	VUS	CON	LB	LB	0.051	VUS	0.500	LB	0.003
RAF1	c.935T>C	p.Val312Ala	Missense	0	0	0	0	1	0	0	VUS	CON	LB	LB	0.051	VUS	0.500	LB	0.003
MYH7	c.3382G>A	p.Ala1128Thr	Missense	0	0	0	0	0	0	0	VUS	VUS	VUS	VUS	0.100	VUS	0.675	LB	0.006
MYH7	c.4909G>A	p.Ala1637Thr	Missense	0	0	0	0	0	0	0	VUS	VUS	VUS	VUS	0.100	VUS	0.675	LB	0.006
MYH7	c.5704G>C	p.Glu1902Gln	Missense	0	0	0	0	0	0	0	VUS	VUS	VUS	VUS	0.100	VUS	0.675	LB	0.006
SHOC2	c.-1C>T	n/a	5' UTR	0	0	0	0	0	0	0	VUS	VUS	VUS	VUS	0.100	VUS	0.675	LB	0.006