Table S2. A list of causative variants identified in each family during this study along with their pathogenicity predictions.

Pedigree ID	Phenotype	Gene	c. DNA	Protein Change	Intervar_ 20180118	CADD_ PHRED	GERP++ _NR	GNOMAD FQ	Reference
MA0315	ar LCA	*LCA5 (NM_001122769)*	c.1151del	p.(Pro384GlnfsTer18)	-	-	-	-	[14]
MA0320	arRP	*TULP1 (NM_ 001289395.2)*	c.417del	p. (Lys140Arg fsTer2)	-	-	-	-	This study
MA0324	arRP	*CRB1 (NM_201253)*	c.107C>G	p.(Ser36Ter)	Pathogenic	36	5.52	-	[48]
MA0328	arRP	*CERKL(NM_201548)*	c.967_ 968del	p.(Met323ValfsTer20)	-	-	-	-	[49]
MA0334	arRP	*CNGA1 (NM_000087)*	c.1270C>T	p.(Arg424Ter)	Uncertain Significance	39	5.31	0.00002644599	This study
MA0337 MA0371	arRP	*CERKL (NM_201548)*	c.769C>T	p.(Arg257Ter)	Pathogenic	26.4	5.93	0.0003173	[50]
MA0341 MA0503	arRP arLCA	*CRB1 (NM_ 001193640.2)*	c.3007_ 3016del	p.(Gly1003Ile) fsTer23	-	-	-	-	[51]
MA0353	arRP	*RPE65 (NM_000329)*	c. 74C>T	(p.Pro25Leu)	Uncertain significance	25.7	5.33	0.0000037	[52]
MA0356	arRP	*CRB1 (NM_ 001193640.2)*	c.3626G>C >C	p.(Cys1209Ser)	Uncertain significance	26.2	5.36	-	Variant not published
MA0366	arRP	*AIPL1 (NM_014336)*	c.834G>A	p.(Trp278Ter)	Uncertain significance	44	5.14	0.0004155	[52]
MA0380	arRP	*CRB1 (NM_201253)*	c.601T>C	p.(Cys201Arg)	Uncertain significance	24.6	5.53	-	Variant not Published
MA0383	arMC	*CLCN1 (NM_000083)*	c.2647C>A	p.(Pro883Thr)	Uncertain significance	24.5	4.52	-	[53]
MA0392 MA0435	arLCA	*AIPL1 (NM_014336)*	c.834G>A	p.(Trp278Ter)	Uncertain significance	44	5.14	0.0004155	[54]
MA0396	arRP	*RPGRIP1 (NM_020366)*	c.2480G>T	p.(Arg827Leu)	Likely pathogenic	24.6	4.71	-	[55]
MA0400	arRP	*LRP5 (NM_002335)*	c.2173G>A	p.(Val725Ile)	Uncertain significance	23.9	4.41	-	Variant not published
MA0406	arRP	*CRB1 (NM_201253)*	c.1459T>C	p.(Ser487Pro)	Uncertain significance	24.2	5.82	-	[20]
MA0410	arRP	*EYS (NM_001142800)*	c.5928-2A>T	N/A	-	33	4.73	-	[56]
MA0413 MA0430	arRP	*PDE6A (NM_000440)*	c.650_ 651dup	p.(Ala218LeufsTer4)	-	-	-	-	This study
MA0422	RP	*CHM (NM_000390)*	c.1584_ 1587del	p.(Val529HisfsTer7)	-	-	-	-	[57]

Table 2. *Cont.*

Pedigree ID	Phenotype	Gene	c. DNA	Protein Change	Intervar_ 20180118	CADD_ PHRED	GERP++ _NR	GNOMAD FQ	Reference
MA0425	arACHM	*CNGA3 (NM_001298)*	c.1774C>G	p. (Pro592Ala)	Uncertain significance	24.2	5.42	-	This study
MA0443	arRP	*RLBP1 (NM_000326)*	c.256G>T	p.(Glu86Ter)	Uncertain significance	36	5.03	-	This study
MA0449	arLCA	*GUCY2D (NM_000180)*	c.1171T>C	p.(Cys391Arg)	Uncertain significance	25.8	4.95	-	This study
MA0454	arLCA	*PRPH2 (NM_000322*	c.626T>G	p.Val209Gly	Uncertain significance	29.4	5.1	-	This study
MA0461	arLCA	*GUCY2D (NM_000180)*	c.3056A>C	p.(His1019Pro)	Uncertain significance	32	4.22	-	[58]
MA0468	arKNO1	*COL18A1 (NM_030582.4)*	c.3559_3577del	p. (Ser1187AlafsTer18)	-	-	-	0.000022668	This study
MA0472	arCRD	*GUCY2D (NM_000180)*	c.3138+1G>A	N/A	-	35	4.21	-	This study
MA0477	arHPS-8	*BLOC1S3 (NM_ 212550)*	c.499C>T	p.(Leu167Phe)	Uncertain significance	25.2	3.61	0.000015	Variant not published
MA0484	arSTGD	*ABCA4 (NM_000350)*	c.5196+1G>A	N/A	-	33	5.38	0.000015	[59]
MA0489	arCC.OAGS	*FOXE3 (NM_012186)*	c.720C>A	p.(Cys240Ter)	Uncertain significance	36	3.09	-	[60]
MA0494	arRA	*GALK1 (NM_000154)*	c.593C>T	p.(Ala198Val)	Uncertain significance	24.3	5.53	0.00073	[61]
MA0499	arRDEG+GLU	*CYP1B1 (NM_000104)*	c.1310C>T	p.(Pro437Leu)	Uncertain significance	25.9	5.95	0.0000793	[62]
MA0507	arLCA	*AIPL1 (NM_014336)*	c.664T>C	p.(Trp222Arg)	Uncertain Significance	28.2	5.15	-	This Study
MA0510	arCRD	*GUCY2D (NM_000180)*	c.2965dup	p.(Val989GlyfsTer83)	-	-	-	-	This study
MA0515	arCG	*CYP1B1 (NM_000104)*	c.1063C>T	p. (Arg355Ter)	-	47	5.65	0.0000151	[63]
MA0524	arCODAS	*LONP1 (NM_001276480)*	c.1448G>A	p. (Arg483His)	Uncertain significance	22.5	3,72	0.00006800	[64]
MA0530	ar Anophth	*FOXE3 (NM_012186)*	c.289A>G	p.(Ile97Val)	Uncertain significance	24.9	3.24	-	[59]
MA0534	ar USH	*MYO7A (NM_000260)*	c.5743-2A>G	N/A	-	35	5.01	-	[65]
MA0537	ar STL Type-IV	*COL9A1 (NM_078485.4)*	c.851_852insCAAT	p.(Pro285AsnfsTer20)	-	-	-	-	This study

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