

**Table S2. Primer information mutation verification.**

Family ID	Gene	Variation (nucleotide change)	Forward primer (5'→3')	Reverse primer (5'→3')	Amplicon length (bp)
ARRP07	<i>EYS</i>	c.6557G>A	TCAGTCTTTTCCTCTGTACTGGT	TGTCTTGTCAGCTCAGATCCT	583
	<i>PLXNA</i>	c.2824C>T	CCTGTGGAGAGCGAGTACAT	CACCCTCTCAGAGCAGCAG	286
	<i>CDH23</i>	c.8944C>T	CTAGATGTGCCACCTACCC	TATACTGCCTTTCACGCCCT	464
	<i>RP1L1</i>	c.5677C>G	GGTGACCAAGATCCAGGACA	GGTCTGCCCTTCTGCCTC	399
	<i>RP1L1</i>	c.3026C>T	GTGTGTCACCCAGCTCTCT	GGCCTCTCTGTCTGCTCC	368
	<i>SPATA7</i>	c.1562A>T	CCTGCTGCATGTCCTGAAAG	CGCCTTTGACACTGGAGAAC	494
	<i>USH1C</i>	c.2375G>A	GCTGCGTTTTCTCCAGATGG	GGCAGTCGGATGGATGGAC	389
ARRP08	<i>EYS</i>	c.5093T>C	ACAGAAGTGCCATCTTTATTTCC	TCCAGAGAACTATCACTTGGGT	365
	<i>EYS</i>	c.9248G>A	AGAATCTCTGTGCCTATGAGCT	CAGTTGATTCCCCGTAAGCA	448
	<i>EYS</i>	c.6416G>A	CTCTGTTGCAGCACCCCTCT	TGTTTGTGCTAGTACCCATCAC	247
	<i>RP1</i>	c.5585G>T	GGAAGTACTCAACCCCTTG	TTCTGAAGTGTACCATGAATCA	292
	<i>CDH23</i>	c.9359T>C	AGGTGAGAAGGCAGTGGG	GTTTCTGAGGGTGGAGGGAG	400
	<i>ALMS1</i>	c.11402C>T	TCAGAGGAGAGTGAGCTGC	AGTCCATGAAGAGGGCAGTC	381
	<i>CEP164</i>	c.3931A>C	TTGAGTCCCTTCCCACCATC	CAGAGTGGGGCTTACATGGA	400
	<i>PLA2G5</i>	c.1T>C	TCTGGCTGGACTCATCTTGT	GATTCAAACCCAAGTCTCTACGA	298
	<i>BBS4</i>	c.1209T>A	ACCATTTGTTGCAGAGCCC	CAGAACAGCCATGAACGTGT	300
	ARRP09	<i>ALMS1</i>	c.203T>C	CAGAGCGAGACACCAACATG	GTCTGGGCCGCCTACTAG
<i>ALMS1</i>		c.2993C>T	CAGACCCTGCCAGACTTTCT	TCCAGGGAAGGCTGAAACTT	486
<i>EYS</i>		c.7228+1G>A	GCCAGTTTGCAAGTTGTGAA	TGATCAGTCAAGTGCTATCCTTG	217

	<i>EYS</i>	c.6557G>A	TCAGTCTTTTCCTCTGTACTGGT	TGTCTTGTCAGCTCAGATCCT	583
	<i>ABCA4</i>	c.6398C>G	GCTGAGCTTAATCCCCAAAATT	AGAGGAGGAGCTGGAAGATC	297
	<i>COL2A1</i>	c.1109+3G>A	CTCAGATGCAGAGGAGGCC	GGAACAAGACAGACACCGAT	300
	<i>DMD</i>	c.2096C>G	TTTCCTTTGCCACTCCAAGC	TGACATTACAGGTACCCGAGG	373
ARRP10	<i>GPR179</i>	c.6125_6129del	TGCAGGTGTGTATAAATCTGACA	TGCCTCAGAACTGCCTCT	298
	<i>HMCN1</i>	c.3585A>G	TGGCTGCCTGTTGATAAGGA	TCACCTTGGACATGTAGCGT	369
	<i>EYS</i>	c.7228+1G>A	GCCAGTTTGCAAGTTGTGAA	TGATCAGTCAAGTGCTATCCTTG	217
	<i>EYS</i>	c.4957dupA	GGGCATTCATTTTCTTCTGCT	TGGGTGAAGTTTGAACAGTGT	400
	<i>NRL</i>	c.17G>C	TTGGGCTTTGAGGGAAGAGG	TGAGCTGTAAGGTGTGGAGC	249
	<i>PDE6A</i>	c.1728+2T>C	GTGTCCTGCCTCACTGATGT	GCCCGTACTGCTTTCACATA	282
	<i>RIMS1</i>	c.2894C>T	TCTTCATAGATCAATGGCTGCT	GATTAAACAACAGACTGCCACA	443
	<i>TLR3</i>	c.1160C>T	TTGCCTCACTCCCCAAGATT	GGCCCAGGTCAAGTACTTCT	300
	<i>TLR3</i>	c.1175G>A	TTGCCTCACTCCCCAAGATT	GGCCCAGGTCAAGTACTTCT	300
	<i>USH2A</i>	c.6998T>C	GAGGTGTGCTTTGATCCTGC	CACATTCTGAGAACCGTCGG	497
	<i>USP39</i>	c.1013A>G	AGCTTCAACGTTTTCCACCC	TAATCCACCCACCTCGGC	231

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**Abbreviations:** bp: base pair.

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