Utility and acceptability of remote 6-lead electrocardiographic monitoring in children with inherited cardiac conditions

Supplementary Table 1. Genetic variants in included children with Long QT Syndrome

Affected gene*	Nucleotide change	Amino acid change
KCNQ1	c.604G>A	p.Asp202Asn
KCNQ1	c.1513C>T	p.Gln505*
KCNH2	c.2481C>G	p.Tyr827*
KCNH2	c.2755_2764del	p.Ser919fs
KCNH2	c.2755_2764del	p.Ser919fs
KCNQ1	c.805G>A	p.Gly269Ser
KCNH2	c.142T>C	p.Phe48Leu
KCNH2	c.142T>C	p.Phe48Leu
KCNH2	c.1327_1333del	p.Thr443ValfsTer76
KCNQ1	c.742G>A	p.Asp242Asn
KCNQ1	c.1096C>T	p.Arg366Trp
KCNH2	c.2766del	p.Pro923fs
KCNQ1	c.683+5G>A	
KCNH2	c.1969G>A	p.Gly657Ser
KCNQ1	c.1175G>A	p.Trp392*
KCNQ1	c.797T>G	p.Leu266Arg
KCNQ1	c.604G>A	p.Asp202Asn
KCNE1	c.50G>A	p.Trp17*
KCNQ1	c.1664G>A	p.Arg555His
KCNH2	c.452dupC	p.Thr152fs

* Each row represents a sperate child. Children heterozygous for listed variants. N=2 children had a clinical phenotype of Long QT 2 syndrome with no pathogenic or likely pathogenic variants identified.

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