

Family ID	Exon Number	Nucleotide Change	Amino Acid Change	Polyphen-2 Prediction	Polyphen-2 Score
CHOP-AG <sup>6</sup>	2	c.175T>C	p.W59R	Probably damaging	1.000
FG-CI <sup>5</sup>	8	c.784T>C	p.S262P	Probably damaging	1.000
FG-HW	4	c.457T>C	p.F153L	Probably damaging	1.000
FG-HX	2	c.214G>C	p.E72Q	Possibly damaging	0.911
FS-A <sup>5</sup>	8	c.763A>G	p.K255E	Possibly damaging	0.719
FS-X <sup>5</sup>	8	c.776C>T	p.T259I	Probably damaging	1.000
FS-XL <sup>6</sup>	4	c.445-447delATC	p.I149del	N/A	N/A

Supplementary Table 1. List of *ACTN4* heterozygous missense mutations by family and *in silico* protein function prediction according to Polyphen-2 software. Alterations in nucleotide and amino acid sequence are reported using the following NCBI RefSeq accession numbers: ACTN4 – NM\_004924 and NP\_004915.

Family ID	Exon Number	Nucleotide Change	Amino Acid Change	Polyphen-2 Prediction	Polyphen-2 Score
FG-BN <sup>7</sup>	2	c.808T>A	p.S270T	Probably damaging	0.999
FG-FQ <sup>7</sup>	13	c.2683C>T	p.R895C	Probably damaging	1.000
FG-MM	2	c.328T>G	p.N110H	Probably damaging	1.000
FS-XR <sup>7</sup>	13	c.2689G>A	p.E897K	Probably damaging	0.998
FS-Z <sup>7</sup>	12	c.2455A>T	p.K874-	N/A	N/A

Supplementary Table 2. List of *TRPC6* heterozygous missense mutations by family and *in silico* protein function prediction according to Polyphen-2 software. Alterations in nucleotide and amino acid sequence are reported using the following NCBI RefSeq accession numbers: TRPC6 – NM\_004621 and NP\_004612.