Statistical analysis and experimental parameters for sanger validation

Categorical variables are represented as numbers and percentages. Categorical variables were compared using the two-tailed Fisher's exact test and the Kruskal-Wallis analysis of variance test. Statistical analyses were conducted using Statistica 10.0 (StatSoft, Tulsa, OK, United States), MedCalc 23.0.2 (MedCalc Software Ltd, Ostend, Belgium); $P < 0.05$ was considered statistically significant.

Supplementary Table 1 Primer Sequences

№ Patient	Gene	Exon number	Primer Sequences, 5' to 3' direction	Type	Length	GC%	Tm	Product length
1	TRPM4	19	ATGGGGCGTGTTTTTGGGAT	F	20	50	60	425
			AGAGACCCAGAGAGATGATGATGG	R	24	50	60	
2	TRPM4	22	TTCTCGAATCACCAGGGGCT	F	20	55	61	481
			TTCAGGCGCTGTTCGTACTC	R	20	55	61	
2	MYPN	18	TGTGAGGCATGAACCTCAAAGTA	F	23	43,48	60	656
			GTAAGCCAGACTCAAATAGCAGC	R	23	47,83	60	

Abbreviation: Type – orientation: F – Forward, R - Reverse; Length - number of nucleotide bases in primer; GC- GC content in percent; TM - melting temperature of primer in degree Celsius.

Following sequencing platforms were used: NGS Platform – MiSeq System Illumina, Inc; Sanger Sequencing Platform — Genetic Analyzer 3500 Applied Biosystems.