SUPPLEMENTARY TABLE S1. OTHER VARIANTS IDENTIFIED IN CAMEROONIAN FAMILIES USING OTOSCOPE AND RELATED GENE-SPECIFIC VARIANT FREQUENCY IN EXOME DATA 105 CAMEROONIAN CONTROL, ALL AFRICAN, EUROPEAN, AND EAST ASIAN FROM 1000 GENOME PROJECT PHASE 3

Gene	*95% CI frequency Cameroonian*	*95% CI frequency in African from 1000G*	*95% CI frequency in European from 1000G*	*95% CI frequency in East Asian from 1000G*	*Gene name*	*Location*	*Inheritance*
MYO3A	0.21 (0.004–0.46)	0.12 (0.0008–0.71)	0.19 (0.001–0.72)	0.14 (0.001–0.63)	Myosin IIIA DFNB30	10p11.1	Recessive
COL11A2	0.14 (0.004–0.48)	0.18 (0.0008–0.91)	0.18 (0.001–0.72)	0.22 (0.001–0.97)	‘‘collagen type XI alpha 2’’ DFNB53/DFNA13	6p21.3	Both
MYO1A	0.06 (0.002–0.36)	0.052 (0.0008–0.15)	0.06 (0.001–0.15)	0.11 (0.001–0.28)	Myosin IA DFNA48	12q13-q15	Dominant
LOXHD1	0.18 (0.004–0.47)	0.095 (0.0008–0.64)	0.18 (0.001–0.86)	0.20 (0.001–0.88)	Lipoxygenase homology domains 1 DFNB77	18q21.1	Recessive
ADGRV1	0.19 (0.0–0.47)	0.126 (0.0008–0.86)	0.14 (0.001–0.76)	0.25 (0.001–0.90)	G protein-coupled receptor v1 USH2C	5q14.3	Recessive
GIPC3	0.14 (0.004–0.45)	0.11 (0.0008–0.64)	0.12 (0.001–0.54)	0.06 (0.001–0.23)	GAIP C-terminus-interacting protein 3 DFNB15/DFNB95	19p13.3	Recessive
OTOF	0.16 (0.004–0.47)	0.12 (0.0008–0.8)	0.16 (0.001–0.94)	0.24 (0.001–0.99)	Otoferlin DFNB6/9	2p23.1	Recessive
CLDN14	0.23 (0.004–0.49)	0.17 (0.0008–0.8)	0.29 (0.001–0.90)	0.28 (0.001–0.68)	Claudin 14 DFNB29	21q22	Recessive
WFS1	0.21 (0.004–0.5)	0.17 (0.0008–0.8)	0.25 (0.001–0.83)	0.451 (0.001–0.99)	Wolfram syndrome 1 (wolframin) DFNA6/DFNA14	4p16.3	Dominant

The frequency was obtained by aggregating the frequencies from all SNPs in LD (>0.75) within each gene.

95% CI, 95% confidence interval; LD, linkage disequilibrium; SNPs, single nucleotide polymorphisms.