Table S1. Molecular Modeling Results for Novel Variants Identified in Cameroonian Families*

Protein	Variant	Domain	Template	PDB #	Ref.	Predicted Effect on Protein
MYO7A	p.Leu1935del	αA helix of F1 lobe of FERM2	MYO7A MyTH4-FERM1-SH3 in complex with SANS CEN1	3PVL	[8]	Disrupts folding of FERM2 domain, which is predicted to result in poor contact of F1 lobe residues with the CEN1/central domain of SANS protein
CDH23	p.Asp2133Glu	EC20	CDH23 EC2	2WD0	[9]	Loss of Ca^{++}-binding site, which would likely affect tip link rigidity, unfolding and *trans*-EC binding
CDH23	p.Met2907Thr	EC27	CDH8 EC3	2A62	[10]	H-bond change is expected to result in structural changes in linker regions
LOXHD1	p.Arg1124His	β8 strand of PLAT 8	11R-lipoxygenase	3VF1	[11]	Longer β9 strand and malpositioned residues in the linker region between strands β8-β9, limiting access to β8 strand residues that might be involved in binding
LOXHD1	p.Phe1327Ile	β2 strand of PLAT 10	11R-lipoxygenase	3VF1	[11]	Might affect gating of the β-sandwich or binding of other proteins

PDB, RCSB Protein Data Bank; Ref, reference number; CDH, cadherin; EC, extracellular domain.

* For the five novel variants identified in Cameroonian families, molecular modeling was performed using SWISS-MODEL [6] and Phyre2 [7].

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Table S2: Description of Study Subjects

Characteristics	Categories	*n* (%)
Sex	Male	14 (53.8)
	Female	12 (46.2%)
Genetics	Autosomal Recessive	10[1] (100)
	Nonsyndromic	26 (100)
	GJB2-, GJB6-negative	26 (100)
Age of Onset of Hearing Impairment	Congenital / Prelingual	26 (100)
Type of Hearing Impairment	Profound I (91-100dB)	12 (46.2)
	Profound II (101-110dB)	11 (42.3)
	Profound III (111-119dB)	3 (11.5)
	Bilateral Symmetric	26 (100)
	Sensorineural	26 (100)
Audiogram Shape	Flat	9 (34.6)
	Sloping	17 (65.4%)

[1] Number of families

Supplementary Table S3: Genes included on the targeted genomic enrichment panel used in this study

Gene Name	Gene Name		Location	REFSEQ IDs	Inheritance
ACTG1	actin, gamma 1	DFNA20/26	*17q25*	NM_001614	dominant
ADGRV1	G protein-coupled receptor v1	USH2C	*5q14.3*	NM_032119	recessive
CCDC50	coiled-coil domain containing 50	DFNA44	*3q28-q29*	NM_178335	dominant
CDH23	cadherin-related 23	DFNB12, USH1D	*10q21-q22*	NM_022124	recessive
CLDN14	claudin 14	DFNB29	*21q22*	NM_012130	recessive
CLRN1	clarin 1	USH3	*3q25.1*	NM_174878	recessive
COCH	coagulation factor C homolog, cochlin	DFNA9	*14q12-q13*	NM_004086	dominant
COL11A2	collagen, type XI, alpha 2	DFNB53/DFNA13	*6p21.3*	NM_080680	both
CRYM	crystallin, mu	…	*16p12.2*	NM_001888	dominant
DFNA5	deafness, autosomal dominant 5	DFNA5	*7p15*	NM_004403	dominant
DFNB31/WHRN	whirlin/autosomal recessive deafness type 31 protein	USH2D	*9q32*	NM_015404	recessive
DFNB59/PJVK	pejvakin/autosomal recessive deafness type 59 protein		*2q31.2*	NM_001042702	recessive
DIAPH1	diaphanous homolog 1	DFNA1	*5q31*	NM_005219	dominant
DSPP	dentin sialophosphoprotein	DFNA39	*4q21.3*	NM_014208	dominant
ESPN	espin	DFNB36	*1p36.3*	NM_031475	recessive
ESRRB	estrogen-related receptor beta	DFNB35	*14q24.1-24.3*	NM_004452	recessive
EYA4	eyes absent homolog 4	DFNA10	*6q22-q23*	NM_004100	dominant
GIPC3	GAIP C-terminus interacting protein 3	DFNB15/DFNB95	*19p13.3*	NM_133261	recessive
GJB2	gap junction protein, beta 2	DFNB1/DFNA3	*13q12*	NM_004004	both
GJB3	gap junction protein, beta 3	DFNA2	*1p34*	NM_024009	both
GJB6	gap junction protein, beta 6	DFNB1/DFNA3	*13q12*	NM_006783	both
GPSM2	g-protein signalling modulator 2	DFNB82	*1p13.3-22.1*	NM_013296	recessive
GRHL2	grainyhead-like 2	DFNA28	*8q22*	NM_024915	recessive
GRXCR1	glutaredoxin cysteine-rich 1	DFNB25	*4p13*	NM_001080476	recessive
HGF	hepatocyte growth factor	DFNB39	*7q21.1*	NM_000601	recessive

ILDR1	immunoglobulin-like domain containing receptor 1	DFNB42	*3q21.1*	NM_175924	recessive
KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	DFNA2	*1p34*	NM_004700	dominant
LHFPL5	lipoma HMGIC fusion partner-like 5	DFNB66/67	*6p21.2-p22.3*	NM_182548	recessive
LOXHD1	lipoxygenase homology domains 1	DFNB77	*18q21.1*	NM_144612	recessive
LRTOMT	leucine rich transmembrane and O-methyltransferase	DFNB63	*11q13.4*	NM_145309	recessive
MARVELD2	MARVEL domain containing 2	DFNB49	*5q12.3-q14.1*	NM_001038603	recessive
miR-96	microRNA 96	DFNA50	*7q32.2*	NR_029512	microRNA
miR-182	microRNA 182	…	*7q32.2*	NR_029614	microRNA
miR-183	microRNA 183	…	*7q32.2*	NR_029615	
MTRNR1	mitochondrially encoded 12S RNA	…	*chrM*		
MTTS1	mitochondrially encoded tRNA serine 1	…	*chrM*		
MYH14	myosin, heavy chain 14, non-muscle	DFNA4	*19q13.33*	NM_024729	dominant
MYH9	myosin, heavy chain 9, non-muscle	DFNA17	*22q13.1*	NM_002473	dominant
MYO15A	myosin XVA	DFNB3	*17p11.2*	NM_016239	recessive
MYO1A	myosin IA	DFNA48	*12q13-q15*	NM_005379	dominant
MYO3A	myosin IIIA	DFNB30	*10p11.1*	NM_017433	recessive
MYO6	myosin VI	DFNA22, DFNB37	*6q14.1*	NM_004999	both
MYO7A	myosin VIIA	DFNA11, DFNB2	*11q13.5*	NM_000260	both
OTOA	otoancorin	DFNB22	*16p12.2*	NM_144672	recessive
OTOF	otoferlin	DFNB6/9	*2p23.1*	NM_194248	recessive
PCDH15	protocadherin-related 15	DFNB12, USH1F	*10q21.1*	NM_033056	recessive
POU3F4	POU class 3 homeobox 4	DFN3	*Xq21.1*	NM_000307	x-linked recessive
POU4F3	POU class 4 homeobox 3	DFNA15	*5q31*	NM_002700	dominant
PRPS1	phosphoribosylpyrophosphate synthetase 1	DFN2	*Xq22*	NM_002764	recessive

PTPRQ	protein-tyrosine phosphatase receptor, type Q	DFNB84	*12q21.2*	NM_001145026	recessive
RDX	radixin	DFNB24	*11q23*	NM_002906	recessive
SLC17A8	solute carrier family 17, member 3	DFNA25	*12q21-24*	NM_01098486	recessive
SLC26A4	solute carrier family 26, member 4	DFNB4	*7q31*	NM_000441	recessive
SLC26A5	solute carrier family 26, member 4	…	*7q22.1*	NM_198999	recessive
STRC	stereocilin	DFNB16	*15q21-q22*	NM_153700	recessive
TECTA	tectorin alpha	DFNB21/DFNA8/DFNA12	*11q*	NM_005422	both
TJP2	tight junction protein 2	DFNA51	*9q21*	NM_001170416	recessive
TMC1	transmembrane channel-like 1	DFNB7/DFNB11/DFNA36	*9q13-q21*	NM_138691	both
TMIE	transmembrane inner ear	DFNB6	*3p14-p21*	NM_147196	recessive
TMPRSS3	transmembrane protease, serine 3	DFNB8/DFNB10	*21q22*	NM_024022	recessive
TPRN	taperin	DFNB79	*9q34.3*	NM_001128228	recessive
TRIOBP	TRIO and F-actin binding protein	DFNB28	*22q13*	NM_001039141	recessive
USH1C	Usher syndrome 1C homolog	DFNB18/USH1C	*11p14-p15.1*	NM_153676	recessive
USH1G	Usher syndrome 1G	USH1G	*17q25.1*	NM_173477	recessive
USH2A	Usher syndrome 2A	USH2A	*1q41*	NM_206933	recessive
WFS1	Wolfram syndrome 1 (wolframin)	DFNA6/DFNA14	*4p16.3*	NM_006005	dominant

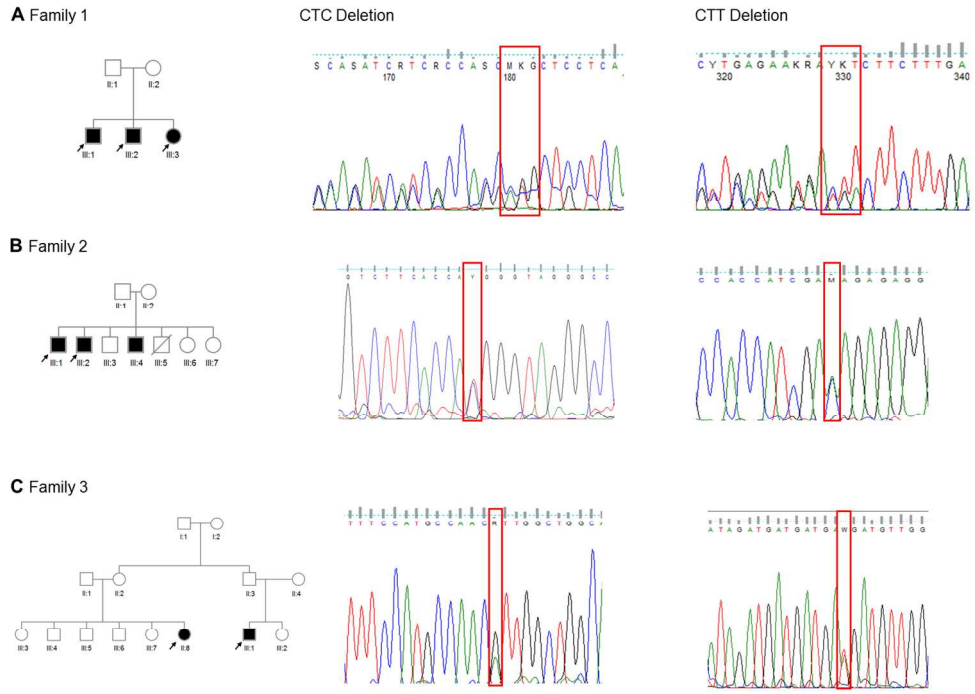

Fig. S1

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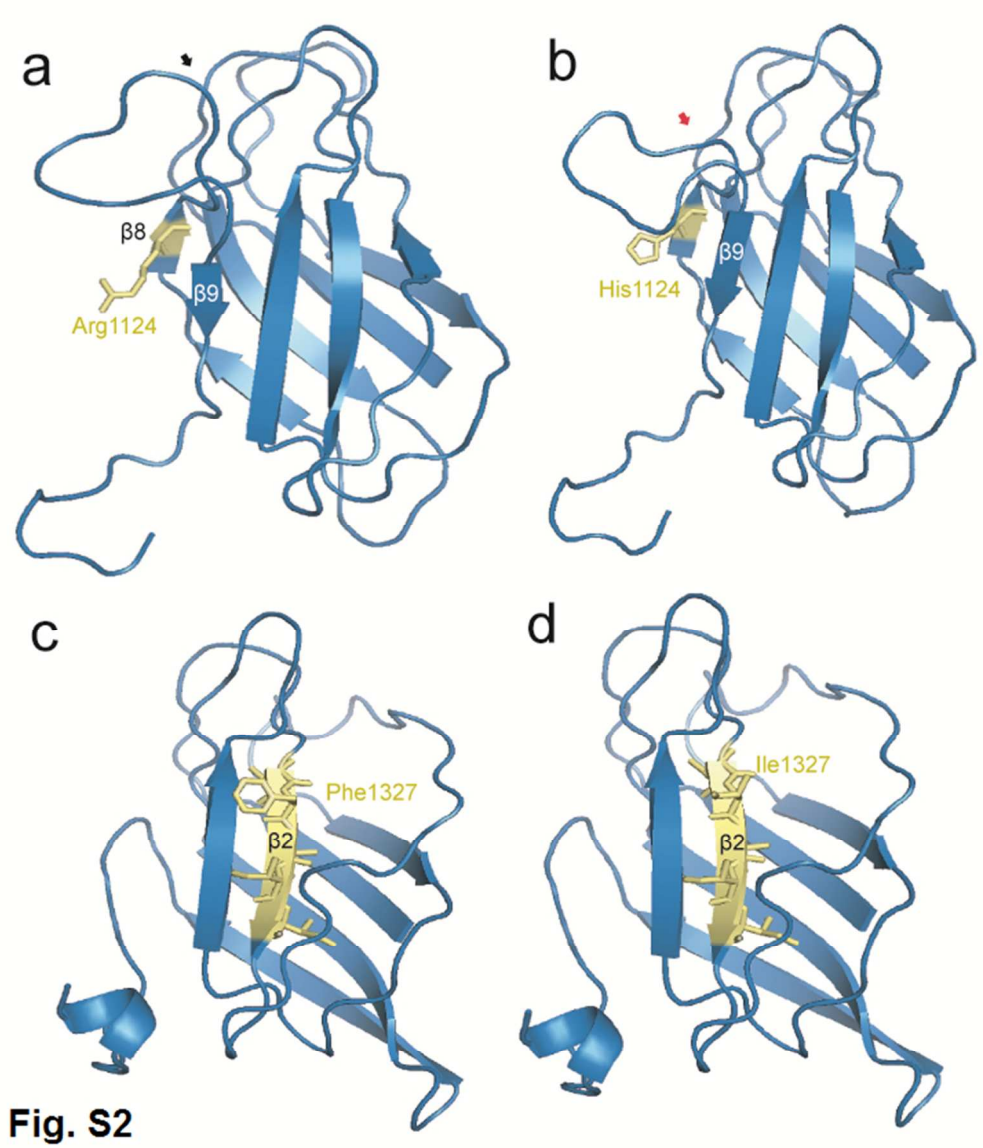

Fig. S2

61x71mm (300 x 300 DPI)