Supplementary Information for:

Genomic Analysis of Inherited Hearing Loss in the Palestinian Population

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Table S1. Genes on the sequencing panel

Gene (OMIM)	SureDesign input	Inherit	Locus (OMIM)	Syndrome and notes
ACTG1	*ACTG1*	AD	DFNA20/26	
ADCY1	*NM_021116*	AR	DFNB44	
ADGRV1	*ADGRV1*	AR		Usher syndrome, type 2C
AIFM1	*AIFM1*	XR	DFNX5	Auditory neuropathy
ALMS1	*ALMS1*	AR		Alstrom syndrome
ATP2B2	*ATP2B2*	AR		DFNB12 modifier
ATP6B1	*ATP6V1B1*	AR		Renal tubular acidosis with deafness
ATP6V1B2	*ATP6V1B2*	AD		Deafness with onychodystrophy
BCS1L	*BCS1L*	AR		Bjornstad syndrome
BDP1	*BDP1*	AR	DFNB49	
BSND	*BSND*	AR	DFNB73	
CABP2	*CABP2*	AR	DFNB93	
CACNA1D	*CACNA1D*	AR		Sinoatrial node dysfunction and deafness
CATSPER2	*CATSPER2*	AR		Deafness-infertility syndrome
CCDC50	*CCDC50*	AD	DFNA44	
CD151	*CD151*	AR		Nephropathy, pretibial epidermolysis bullosa, deafness
CD164	*CD164*	AD	DFNA66	
CDC14A	*CDC14A*	AR	DFNB105	Deafness-infertility syndrome
CDH23	*CDH23*	AR		Usher syndrome, type 1D
CEACAM16	*CEACAM16*	AD		
CHD7	*NM_017780*	AD		CHARGE syndrome
CIB2	*CIB2*	AR	DFNB48	
CISD2	*CISD2*	AR		Wolfram syndrome
CLDN14	*CLDN14*	AR	DFNB29	
CLIC5	*CLIC5*	AR	DFNB103	
CLPP	*CLPP*	AR	DFNB81	Perrault syndrome 3
CLRN1	*CLRN1*	AR		Usher syndrome, type 3A
COCH	*COCH*	AD	DFNA9	
COL11A1	*COL11A1*	AD		Stickler syndrome, type II
COL11A2	*COL11A2*	AD,AR	DFNB53	Otospondylomegaepiphyseal dysplasia, Stickler syndrome
COL2A1	*COL2A1*	AD		Stickler syndrome, type I
COL4A3	*NM_000091*	AD,AR		Alport syndrome
COL4A4	*COL4A4*	AR		Alport syndrome
COL4A5	*COL4A5*	XR		Alport syndrome
COL4A6	*COL4A6*	XR	DFNX6	
COL9A1	*COL9A1*	AD		Stickler syndrome, type IV
COL9A2	*COL9A2*	AR		Stickler syndrome, type V
CRYL1	*CRYL1*	AR		large connexin deletion
CRYM	*CRYM*	AD		
DCDC2	*DCDC2*	AR	DFNB66	
DFNA5	*DFNA5*	AD	DFNA5	
DIAPH1	*DIAPH1*	AD	DFNA1	
DIAPH3	*DIAPH3*	AD		Auditory Neuropathy
DMXL2	*DMXL2*	AD		
DNMT1	*DNMT1*	AD		Cerebellar ataxia, deafness, and narcolepsy
DSPP	*DSPP*	AD	DFNA39	Deafness with dentinogenesis
EDN3	*EDN3*	AD,AR		Waardenburg syndrome, type 4B
EDNRB	*EDNRB*	AD,AR		Waardenburg syndrome, type 4A
ELMOD3	*ELMOD3*	AR	DFNB88	
EPS8	*EPS8*	AR	DFNB102	
EPS8L2	*EPS8L2*	AR		
ERAL1	*ERAL1*	AR		Perrault syndrome 6
ERCC2	*ERCC2*	AR		Cerebrooculofacioskeletal syndrome 2
ESPN	*ESPN*	AR	DFNB36	
ESRP1	*ESRP1*	AR		
ESRRB	*ESRRB*	AR	DFNB35	
EYA1	*EYA1*	AD		Branchio-oto-renal syndrome
EYA4	*EYA4*	AD	DFNA10	
FAM65B	*FAM65B*	AR		
FGF3	*FGF3*	AR		Deafness with inner ear agenesis, microtia, and microdontia
FGFR1	*FGFR1*	AD		Pfieffer syndrome
FGFR2	*FGFR2*	AD		Pfieffer syndrome/ Crouzon syndrome
FOXI1	*FOXI1*	AR		Pendred syndrome
GATA3	*GATA3*	AD		Hypoparathyroidism, deafness, renal (HDR) syndrome
GIPC3	*NM_133261*	AR	DFNB15/72/95	Audiogenic Seizures
GJB2	*GJB2*	AR	DFNB1	

Gene (OMIM)	SureDesign input	Inherit	Locus (OMIM)	Syndrome and notes
GJB2 exon 1	chr13:20,766,864-20,767,146	AR		
GJB3	*NM_001005752*	AD	DFNA2B	
GJB6	*GJB6*			Includes regions regulating GJB2
GPSM2	*GPSM2*	AR	DFNB82	Chudly-McCullough syndrome
GREB1L	*GREB1L*			
GRHL2	*NM_024915*	AD	DFNA28	
GRXCR1	*GRXCR1*	AR	DFNB25	
GRXCR2	*GRXCR2*	AR	DFNB101	
HARS	*HARS*	AR		Usher syndrome type 3B
HARS2	*HARS2*	AR		Perrault syndrome 2
HGF	*HGF*	AR	DFNB39	
HOMER2	*HOMER2*	AD		
HSD17B4	*HSD17B4*	AR		Perrault syndrome 1
ILDR1	*ILDR1*	AR	DFNB42	
KARS	*KARS*	AR	DFNB89	
KCNE1	*KCNE1*	AR		Jervell and Lange-Nielsen syndrome 2
KCNJ10	*KCNJ10*	AR		Pendred syndrome
KCNQ1	*KCNQ1*	AD		Long QT syndrome 1
KCNQ4	*KCNQ4*	AD	DFNA2A	
KITLG	*KITLG*	AD		Waardenburg syndrom, type 2
LARS2	*LARS2*	AR		Perrault syndrome 4
LHFPL5	*LHFPL5*	AR	DFNB66/67	
LMX1A	*LMX1A*			
LOC653786		-		OTOA Pseudogene
LOXHD1	*LOXHD1*	AR	DFNB77	
LOXL3	*LOXL3*	AR		possible Stickler syndrome
LRTOMT	*LRTOMT*	AR	DFNB63	
MARVELD2	*MARVELD2*	AR	DFNB49	
MCM2	*MCM2*	AD		
MET	*MET*	AR	DFNB97	
MIRN96	chr7:129,414,493-129,414,651	AD	DFNA50	
MITF	*MITF*	AD		Waardenburg syndrome, type 2A
MPZL2	*MPZL2*	AR	DFNB111	
MSRB3	*MSRB3*	AR	DFNB74	
MTRNR1	chrM:650-1603	M		
MTTE	chrM:14675-14743	M		Maternally inherited diabetes and deafness (MIDD)
MTTK	chrM:8296-8365	M		MERFF, MTTK
MTTL1	chrM:3231-3305	M		MERRF syndrome
MTTS1	chrM:7447-7515	M		
MYH14	*MYH14*	AD	DFNA4	
MYH9	*MYH9*	AD	DFNA17	
MYO15A	*MYO15A*	AR	DFNB3	
MYO15A	chr17:18026518-18026747	AR		MYO15A exon 1A
MYO1A	*MYO1A*	AD	DFNA48 ?	
MYO3A	*MYO3A*	AR	DFNB30	
MYO6	*MYO6*	AR	DFNB37; DFNA22	
MYO7A	*MYO7A*	AR,AD	DFNB2; DFNA11	Usher syndrome, type 1B
NARS2	*NARS2*	AR	DFNB94	
NDP	*NDP*	XLR		Norrie disease
NLRP3	*NLRP3*	AD		Muckle-Wells syndrome
OPA1	*OPA1*	AD		Optic atrophy plus syndrome
OSBPL2	*OSBPL2*	AD	DFNA67	
OTOA	*OTOA*	AR	DFNB22	
OTOF	*OTOF*	AR	DFNB9	Auditory neuropathy
OTOG	*OTOG*	AR	DFNB18B	
OTOGL	*OTOGL*	AR	DFNB84	
P2RX2	*P2RX2*	AD	DFNA41	
PAX3	*PAX3*	AD,AR		Waardenburg syndrome, type 1 and type 3
PCDH15	*PCDH15*	AR		Usher syndrome, type 1F
PDE1C	*PDE1C*	AD	DFNA74 ?	
PDZD7	*PDZD7*	AR		Usher syndrome, type IIC
PEX1	*PEX1*	AR		Heimler syndrome
PEX6	*PEX6*	AR		Heimler syndrome
PJVK	*DFNB59*	AR	DFNB59	Auditory neuropathy
PNPT1	*PNPT1*	AR	DFNB70	
POLR1C	*POLR1C*	AR		Treacher Collins syndrome 3
POLR1D	*POLR1D*	AD		Treacher Collins syndrome 2

Gene (OMIM)	SureDesign input	Inherit	Locus (OMIM)	Syndrome and notes
POU3F4	*POU3F4*	XR	DFNX2	
POU4F3	*POU4F3*	AD	DFNA15	
PRPS1	*PRPS1*	XR	DFNX1	
PTPRQ	*PTPRQ*	AR	DFNB84	
PTRH2	*PTRH2*	AR		IMNEPD syndrome
RDX	*RDX*	AR	DFNB24	
ROR1	*NM_005012*	AR		
S1PR2	*S1PR2*	AR	DFNB68	
SEMA3E	*SEMA3E*	AD		CHARGE syndrome
SERPINB6	*SERPINB6*	AR	DFNB91	
SIX1	*SIX1*	AD	DFNA23	Branchio-oto-renal syndrome
SIX5	*SIX5*			Branchio-oto-renal syndrome
SLC17A8	*SLC17A8*	AD	DFNA25	
SLC22A4	*SLC22A4*	AR		
SLC26A4	*SLC26A4*	AR		Pendred syndrome
SLC26A5	*SLC26A5*	AR	DFNB61	
SLITRK6	*SLITRK6*	AR		Deafness and myopia
SMAC/DIABLO	*DIABLO*	AD	DFNA64	
SMPX	*SMPX*	XR	DFNX4	
SNAI2	*SNAI2*	AR		Waardenburg syndrome, type 2D
SOX10	*SOX10*	AD		Waardenburg syndrome, type 4C
STRC	*STRC*	AR	DFNB16	
STRCP1		-		STRC pseudogene
SYNE4	*SYNE4*	AR	DFNB76	
TBC1D24	*TBC1D24*	AR,AD	DFNA65	
TBX1	*TBX1*	AD		Velocardiofacial syndrome
TCOF1	*TCOF1*	AD		Treacher Collins syndrome 1
TECTA	*TECTA*	AR,AD	DFNB21	
TECTB	*TECTB*			mouse model
TIMM8A	*TIMM8A*	XR		Mohr-Tranebjaerg syndrome
TJP2	*TJP2*	AD	DFNA51	
TMC1	*TMC1*	AR,AD	DFNB7/11	
TMEM132E	*TMEM132E*	AR	DFNB99	
TMIE	*TMIE*	AR	DFNB6	
TMPRSS3	*TMPRSS3*	AR	DFNB8/10	
TNC	*TNC*	AD	DFNA56	
TPRN	*TPRN*	AR	DFNB79	
TRIOBP	*TRIOBP*	AR	DFNB28	
TSPEAR	*TSPEAR*	AR	DFNB98	
TWNK	*NM_021830*	AR		Perrault syndrome 5
USH1C	*USH1C*	AR	DFNB18	Usher syndrome, type 1C
USH1G	*USH1G*	AR		Usher syndrome, type 1G
USH2A	*USH2A*	AR		Usher syndrome, type 2A
WBP2	*WBP2*	AR		
WFS1	*WFS1*	AD	DFNA6/14/38	Wolfram syndrome
WHRN	*DFNB31*	AR	DFNB31	Usher syndrome, type 2D

Table S2A. Genes responsible for hearing loss in Palestinian families

Gene	Number of families	Number of different mutations	Phenotype
ADGRV1	4	3	Usher 2C
CACNA1D	4	1	SANDD
CDC14A	1	1	DFNB32
CDH23	17	10	DFNB12 / Usher 1D
CLDN14	8	2	DFNB29
CLPP	1	1	Perrault syn
COCH	1	1	DFNA9
COL11A2	1	1	DFNB53
COL4A6	1	1	DFNX6
DFNA5	1	1	DFNA5
EDNRB	2	2	Waardenburg syn
EPS8L2	2	2	DFNB106
ESPN	2	2	DFNB36
ESRRB	3	2	DFNB35
GIPC3	1	1	DFNB15 /JAMS
GJB2	74	7	DFNB1A
GPSM2	5	4	DFNB82 / CMCS
HSD17B4	1	1	Perrault syn
ILDR1	3	2	DFNB42
LARS2	4	1	Perrault syn
LHFPL5	2	2	DFNB67
LOXHD1	2	2	DFNB77
LRTOMT	1	1	DFNB63
MARVELD2	1	1	DFNB49
MYO3A	1	1	DFNB30
MYO6	5	2	DFNB37 / DFNA22
MYO7A	28	15	DFNB2 / DFNA11
MYO15A	37	15	DFNB3
OTOA	8	5	DFNB22
OTOF	3	3	AUNB1
PAX3	6	3	Waardenburg syn
PCDH15	7	2	DFNB23
PJVK	2	1	DFNB59
POU3F4	2	1	DFNX2
POU4F3	2	2	DFNA15
PTPRQ	3	2	DFNB84A
PTRH2	2	1	IMNEPED
RDX	1	1	DFNB24
SLC26A4	30	14	DFNB4 / Pendred syn
STRC	1	1	DFNB16
TBC1D24	1	1	DFNB86 / DOORS
TECTA	9	3	DFNB21
TMC1	4	4	DFNB7
TMPRSS3	15	6	DFNB8/10
TRIOBP	21	4	DFNB28
USH1C	2	1	Usher 1C / DFNB18A
USH1G	2	2	Usher 1G
USH2A	3	1	Usher 2A
Total	337	143	

Abbreviations:
AUNB1: Auditory neuropathy
CMCS: Chudley-McCullough syndrome
DOORS: Deafness, onychodystrophy, osteodystrophy, MR, and seizures
IMNEPED: Infantile-onset multisystem neurologic, endocrine, pancreatic disease
JAMS1: Juvenile audiogenic monogenic seizures
SANDD: Synoatrial node dysfunction

Table S2B. Phenotypes and genotypes of all families with genetic diagnoses for their hearing loss

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre- post-lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
CX	Ramallah	yes	multi	2	AR	pre		moderate to severe	new	homoz	*ADGRV1*	c.2898G>A	p.(Glu966Glu)	chr5:89940686
JO	Ramallah	yes	multi	2	AR	pre		moderate	new	homoz	*ADGRV1*	c.2898G>A	p.(Glu966Glu)	chr5:89940686
EI	Bethlehem	yes	multi	3	AR	pre		moderate to severe	new	homoz	*ADGRV1*	c.10426 G>A	p.(Gly3476Arg)	chr5:90024750
IJ	Bethlehem	yes	multi	2	AR	pre	yes	moderate to severe	new	homoz	*ADGRV1*	c.14315C>A	p.(Ser4772*)	chr5:90086961
CT	Bethlehem	yes	multi	4	AR	pre	yes	moderate; cardiac signs	new	homoz	*CACNA1D*	c.1127C>T	p.(Ala376Val)	chr3:53707750
HN	Jersualem	yes	sing	1	AR	pre	yes	moderate; prolonged AV conduc	new	homoz	*CACNA1D*	c.1127C>T	p.(Ala376Val)	chr3:53707750
QS051-052	Qalqilia	yes	sing	1	AR	pre			new	homoz	*CACNA1D*	c.1127C>T	p.(Ala376Val)	chr3:53707750
X16-17	Jersualem	yes	multi	2	AR	pre			new	homoz	*CACNA1D*	c.1127C>T	p.(Ala376Val)	chr3:53707750
Q-N	Tulkarm	yes	multi	4	AR	pre		severe	new	homoz	*CDC14A*	c.51-1G>T	p.(?)	chr1:100819317
FO	Nablus	yes	multi	2	AR	pre		profound	known	homoz	*CDH23*	c.683A>T	p.(Asp228Val)	chr10:73330605
AS-KK	Jenin	yes	sing	1	AR	pre			known	homoz	*CDH23*	c.1036C>T	p.(Pro346Ser)	chr10:73377052
DW	Ramallah	yes	multi	2	AR	pre		severe to profound	known	homoz	*CDH23*	c.1036C>T	p.(Pro346Ser)	chr10:73377052
G	Hebron	yes	multi	5	AR	pre		severe to profound	known	homoz	*CDH23*	c.1036C>T	p.(Pro346Ser)	chr10:73377052
DA (EP5-7)	Ramallah	yes	multi	3	AR	pre		moderate	known	homoz	*CDH23*	c.1037C>T	p.(Pro346Ser)	chr10:73377053
AA-N	Jenin	yes	multi	4	AR	pre		severe to profound	known	homoz	*CDH23*	c.1675C>T	p.(Pro559Ser)	chr10:73437373
GA-D	Gaza	yes	multi	2	AR	pre		moderate	known	homoz	*CDH23*	c.1675C>T	p.(Pro559Ser)	chr10:73437373
AB	Ramallah	no	multi	6	AR	pre		moderate	known	cpd het	*CDH23*	c.[(1675C>T);(3211G>A)]	p.[(Pro559Ser);(Glu1071Lys)]	chr10:73437373; chr10:73468959
EE	Ramallah	yes	multi	2	AR	pre		moderate	known	homoz	*CDH23*	c.3211G>A	p.(Glu1071Lys)	chr10:73468959
HS8	Ramallah	yes	sing	1	AR	pre			known	homoz	*CDH23*	c.3211G>A	p.(Glu1071Lys)	chr10:73468959
EG	Hebron	yes	multi	3	AR	pre		profound	new	homoz	*CDH23*	c.4562A>G	p.(Asn1521Ser)	chr10:73500652
EPIC	Bethlehem	yes	multi	3	AR	pre	yes	profound, RP, epilepsy	new	homoz	*CDH23*	c.5749G>A	p.(Glu1917Lys)	chr10:73545424
A151	Jersualem	yes	sing	1	AR	pre		moderate	known	homoz	*CDH23*	c.6614C>T	p.(Pro2205Leu)	chr10:73553299
IP	Nablus	yes	sing	1	AR	pre		moderate to severe	known	homoz	*CDH23*	c.6614C>T	p.(Pro2205Leu)	chr10:73553299
DF (EP10-12)	Bethlehem	yes	multi	2	AR	pre			new	homoz	*CDH23*	c.8140G>T	p.(Asp2714Tyr)	chr10:73566000
BV3 (EP23-24)	Jersualem	yes	multi	3	AR	pre		profound	new	homoz	*CDH23*	c.8204T>C	p.(Leu2735Pro)	chr10:73567059
EP25	Bethlehem	yes	sing	1	AR	pre		severe to profound	new	homoz	*CDH23*	c.8204T>C	p.(Leu2735Pro)	chr10:73567059
X13	Jersualem	yes	sing	1	AR	pre			new	homoz	*CLDN14*	c.664delG	p.(Ala222Profs*4)	chr21:37833330
AA-G	Jenin	yes	multi	3	AR	pre		severe to profound	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
AA-K	Jenin	yes	multi	3	AR	pre		severe to profound	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
AA-O	Jenin	yes	sing	1	AR	pre		severe to profound	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
AS-X	Jenin	yes	multi	5	AR	pre			known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
DB	Hebron	yes	multi	3	AR	pre		severe to profound	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
QS039	Qalqilia	yes	sing	1	AR	pre		severe to profound	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
FN	Jenin	yes	multi	3	AR	pre		profound w/mild MR, DD	known	homoz	*CLDN14*	c.83C>T	p.(Pro28Leu)	chr21:37833911
GA-H	Gaza	yes	multi	3	AR	pre		severe to profound	new	homoz	*CLPP*	c.270+3G>T	p.(?)	chr19:6361954
CO	Jenin	no	multi	9	AD	post		progressive, onset 20-30y	new	het	*COCH*	c.1625G>C	p.(Cys542Ser)	chr14:31358969
Q-U	Tulkarm	yes	multi	4	AR	pre	yes	severe with joint problems	new	homoz	*COL11A2*	c.3080G>A	p.(Gly1027Glu)	chr6:33139560
AS-CC	Jenin	yes	sing	1	XR	pre		any cochlear malformation?	new	hemiz	*COL4A6*	c.1549C>T	p.(Arg517*)	chrX:107431785
BL	Nablus	no	multi	5	AD	post		progressive, onset ~17y	known	het	*DFNA5*	c.991-15_991-13del	p.(?)	chr7:24746008
Q-R	Tulkarm	yes	sing	1	AD	pre	yes	severe w/ Waardenberg	new	het	*EDNRB*	c.1071+2T>C	p.(?)	chr13:78477289
JS	Tulkarm	yes	sing	1	AR	pre	yes	Waardenberg syndrome	new	homoz	*EDNRB*	c.823G>A	p.(Val275Met)	chr13:78477673
IW	Nablus	yes	multi	3	AR	pre		profound	new	homoz	*EPS8L2*	c.148insGGACA	p.(Ser50Trpfs*34)	chr11:710469
GX	Nablus	yes	multi	4	AR	post		progressive, onset ~6y	new	homoz	*EPS8L2*	c.1430dup	p.(Val478Serfs*25)	chr11:723327
AA-E	Jenin	yes	sing	1	AR	pre		profound	new	homoz	*ESPN*	c.2081_2082del	p.(Ser694Cysfs*51)	chr1:6511911
Q-S	Tulkarm	yes	sing	1	AD	post		progressive, moderate	known	het	*ESPN*	c.2155A>C	p.(Ser719Arg)	chr1:6511986
BP	Jersualem	yes	multi	3	AR	pre		severe to profound	new	homoz	*ESRRB*	c.545G>A	p.(Arg182His)	chr14:76948389
AS-S	Jenin	yes	multi	2	AR	pre			new	homoz	*ESRRB*	c.787G>A	p.(Gly263Ser)	chr14:76949102
FT	Jenin	yes	multi	3	AR	pre		profound	new	homoz	*ESRRB*	c.787G>A	p.(Gly263Ser)	chr14:76949102
AA-F	Jenin	yes	multi	2	AR	pre	yes	severe to profound w/ epilepsy	known	homoz	*GIPC3*	c.122C>A	p.(Thr41Lys)	chr19:3585717
AS-C	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.358_360delGAG	p.(Glu120del)	chr13:20763361
GV	Jenin	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.358_360delGAG	p.(Glu120del)	chr13:20763361
DG	Jersualem	yes	multi	3	AR	pre		severe to profound	known	homoz	*GJB2*	c.235delC	p.(Leu79Cysfs*3)	chr13:20763486
FM	Hebron	yes	multi	2	AR	pre		severe to profound	known	homoz	*GJB2*	c.235delC	p.(Leu79Cysfs*3)	chr13:20763486
IZ	Hebron	yes	sing	1	AR	pre		moderate to severe	known	homoz	*GJB2*	c.235delC	p.(Leu79Cysfs*3)	chr13:20763486
X33	Jersualem	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.235delC	p.(Leu79Cysfs*3)	chr13:20763486
X18	Jersualem	no	sing	1	AR	pre			known	cpd het	*GJB2*	c.[(235delC);(290insA)]	p.[(Leu79Cysfs*3);(Arg98Thrfs*15]	chr13:20763486; chr10:20763430
X23	Jersualem	no	sing	1	AR	pre			known	cpd het	*GJB2*	c.[(235delC);(290insA)]	p.[(Leu79Cysfs*3);(Arg98Thrfs*15]	chr13:20763486; chr10:20763430
B6-7	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.229T>C	p.(Trp77Arg)	chr13:20763492
AF	Hebron	yes	multi	3	AR	pre			known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554
L	Hebron	yes	multi	6	AR	pre			known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554
S	Hebron	yes	multi	17	AR	pre		severe to profound	known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554
X6	Jersualem	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554
α16	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre- post- lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
α31	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.167delT	p.(Leu56Argfs*26)	chr13:20763554
GI	Hebron	yes	multi	2	AR	pre		severe to profound	known	cpd het	*GJB2*	c.[(167delT);(c.235delC)]	p.[(Leu56Argfs*26); (Leu79Cysfs*3)]	chr13:20763554; chr10:20763486
D	Hebron	yes	multi	8	AR	pre		severe to profound	known	cpd het	*GJB2*	c.[(167delT);(c.235delC)]	p.[(Leu56Argfs*26); (Leu79Cysfs*3)]	chr13:20763554; chr10:20763486
A127-129	Jersualem	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-C	Jenin	yes	multi	3	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-I	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-J	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-M	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-P	Jenin	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-R	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-Y	Jenin	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AA-Z	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AC	Hebron	yes	sing	1	AR	pre		profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AQ	Tulkarem	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS	Hebron	yes	multi	2	AR	pre		profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS-D	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS-DD	Jenin	yes	multi	4	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS-G	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS-U	Jenin	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
AS-Y	Jenin	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
B3-5	Hebron	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
BN	Bethlehem	yes	multi	4	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
BO	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
BS	Bethlehem	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
CE	Jenin	yes	multi	5	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
CP	Hebron	yes	multi	2	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
CW	Jenin	yes	multi	2	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
DM	Hebron	yes	multi	3	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
EP1-4	Bethlehem	yes	multi	4	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
FI	Jersualem	no	multi	3	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
FJ	Jersualem	yes	multi	6	AR	pre		severe	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
FR	Hebron	yes	multi	5	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
FS	Salfeet	yes	multi	3	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
GA-L	Gaza	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
GC	Hebron	yes	multi	6	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
GG	Qalqilia	yes	multi	2	AR	pre		moderate	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
GK	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
HE	Nablus	no	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
HO	Jenin	yes	multi	2	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
HS1	Ramallah	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
HS4	Ramallah	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
IN	Nablus	yes	sing	1	AR	pre		profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
JD	Ramallah	yes	multi	2	AR	pre		moderate	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
JG	Bethlehem	yes	sing	1	AR	pre		moderate	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
JI	Bethlehem	yes	multi	3	AR	pre		moderate to severe	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
Q-A	Tulkarm	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
Q-E	Tulkarm	yes	multi	4	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
Q-M	Tulkarm	yes	multi	2	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
QS036-037	Qalqilia	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
X29	Jersualem	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
α36	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*GJB2*	c.35delG	p.(Gly12Valfs*2)	chr13:20763686
FP	Ramallah	no	sing	1	AR	pre		severe to profound	known	cpd het	*GJB2*	c.[(35delG);(c.235delC)]	p.[(Gly12Valfs*2);(Leu79Cysfs*3)]	chr13:20763686; chr13:20763486
HV	Hebron	yes	multi	2	AR	pre		severe to profound	known	cpd het	*GJB2*	c.[(35delG);(c.235delC)]	p.[(Gly12Valfs*2);(Leu79Cysfs*3)]	chr13:20763686; chr13:20763486
J1-2	Hebron	yes	sing	1	AR	pre			known	cpd het	*GJB2*	c.[(35delG);(c.235delC)]	p.[(Gly12Valfs*2);(Leu79Cysfs*3)]	chr13:20763686; chr13:20763486
X37-38	Jersualem	no	multi	2	AR	pre			known	cpd het	*GJB2*	c.[(35delG);(c.235delC)]	p.[(Gly12Valfs*2);(Leu79Cysfs*3)]	chr13:20763686; chr13:20763486
GO	Jenin	no	multi	2	AR	pre		severe to profound	known	cpd het	*GJB2*	c.[(35delG);(c.-23+1G>A)]	p.[(Gly12Valfs*2);(?)]	chr13:20763686; chr13:20766921
IK	Bethlehem	no	multi	2	AR	pre		moderate to severe	known	cpd het	*GJB2*	c.[(35delG);(c.-23+1G>A)]	p.[(Gly12Valfs*2);(?)]	chr13:20763686; chr13:20766921
J3-5	Hebron	yes	multi	2	AR	pre			known	cpd het	*GJB2*	c.[(35delG);(c.-23+1G>A)]	p.[(Gly12Valfs*2);(?)]	chr13:20763686; chr13:20766921
X12	Jersualem	yes	sing	1	AR	pre			known	homoz	*GJB2*	c.-23+1G>A	p.(?)	chr13:20766921
GZ	Hebron	yes	sing	1	AR	pre		severe	known	homoz	*GPSM2*	c.832C>T	p.(Arg278*)	chr1:109444446
GA-N	Gaza	yes	sing	1	AR	pre		severe to profound	known	homoz	*GPSM2*	c.977G>A	p.(Trp326*)	chr1:109445771
α33	Hebron	yes	multi	6	AR	pre		severe to profound	known	homoz	*GPSM2*	c.977G>A	p.(Trp326*)	chr1:109445771
CC	Bethlehem	yes	sing	1	AR	pre			known	homoz	*GPSM2*	c.1492C>T	p.(Arg498*)	chr1:109465090
CG	Qalqilia	yes	multi	13	AR	pre	yes	severe to profound w/ID	known	homoz	*GPSM2*	c.379C>T	p.(Arg127*)	chr1:109440214
EY	Nablus	yes	sing	1	AR	pre		severe to profound	new	homoz	*HSD17B4*	c.1842G>A at splice	p.(?)	chr5:118862914

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre- post- lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
AS-BB	Jenin	yes	multi	4	AR	pre		severe to profound	new	homoz	*ILDR1*	c.820C>T	p.(Gln274*)	chr3:121712776
II	Jenin	yes	multi	3	AR	pre		severe to profound	new	homoz	*ILDR1*	c.C820T	p.(Gln274*)	chr3:121712776
GA-O	Gaza	yes	multi	2	AR	pre		profound	new	homoz	*ILDR1*	c.294delA	p.(Val99Phefs*3)	chr3:121724176
BB	Bethlehem	yes	multi	3	AR	pre		severe	new	homoz	*LARS2*	c.457A>C	p.(Asn153His)	chr3:45461162
GA-A	Gaza	yes	multi	2	AR	pre		profound	new	homoz	*LARS2*	c.457A>C	p.(Asn153His)	chr3:45461162
HS	Gaza	yes	multi	2	AR	pre		profound	new	homoz	*LARS2*	c.457A>C	p.(Asn153His)	chr3:45461162
Q-F	Tulkarm	yes	multi	2	AR	pre	yes	severe to profound	new	homoz	*LARS2*	c.457A>C	p.(Asn153His)	chr3:45461162
DD	Bethlehem	yes	multi	5	AR	pre		severe to profound	known	homoz	*LHFPL5*	c.1A>G	p.(Met1Val)	chr6:35773448
CK	Salfeet	yes	multi	1	AR	pre		severe to profound	new	homoz	*LHFPL5*	c.676+1G>A	p.(?)	chr6:35787241
AH	Bethlehem	yes	multi	6	AR	pre		profound	new	homoz	*LOXHD1*	del ex 22-25 out of frame	p.(?)	chr18:44118336_44136525
QS044-047	Qalqilia	no	multi	2	AR	pre		profound	new	cpd het	*LOXHD1*	c.[(3404_3407dup);(c.4843G>C)]	p.[(Arg1137Valfs*9);(Gly1615Arg)]	chr18:44126967; chr18:44104462
GA-R	Gaza	yes	multi	3	AR	pre		profound	new	homoz	*LRTOMT*	c.327C>T	p.(Cys109Cys)	chr11:71817225
X39	Jersualem	yes	sing	1	AR	pre			new	homoz	*MARVELD2*	c.608dupT	p.(Leu203Phefs*18)	chr5:68715820
BA	Hebron	yes	multi	7	AR	pre		profound	new	cpd het	*MYO15A*	c.[(1223C>T);(4240G>A)]	p.[(Ala408Val);(Glu1414Lys)]	chr17:18023337; chr17:18035800
C	Hebron	yes	multi	11	AR	pre		severe to profound	new	homoz	*MYO15A*	c.3609+985G>A	p.(?)	chr17:18026708
FG	Hebron	yes	multi	4	AR	pre		severe to profound	new	homoz	*MYO15A*	c.3609+985G>A	p.(?)	chr17:18026708
GJ	Hebron	yes	multi	8	AR	pre		severe	new	homoz	*MYO15A*	c.3609+985G>A	p.(?)	chr17:18026708
GL	Hebron	yes	multi	4	AR	pre		severe to profound	new	homoz	*MYO15A*	c.3609+985G>A	p.(?)	chr17:18026708
HG	Hebron	yes	multi	2	AR	pre		moderate mixed	new	homoz	*MYO15A*	c.3609+985G>A	p.(?)	chr17:18026708
IG	Hebron	yes	multi	2	AR	pre		moderate	new	cpd het	*MYO15A*	c.[(3609+985G>A);(7207G>T)]	p.[(?);(Asp2403Tyr)]	chr17:18026708; chr17:18052889
E	Hebron	no	multi	5	AR	pre		moderate to severe	new	cpd het	*MYO15A*	c.[(3609+985G>A);(9572G>A)]	p.[(?);(Arg3191His)]	chr17:18026708; chr17:18065953
AR	Hebron	no	sing	1	AR	pre			new	cpd het	*MYO15A*	c.[(3609+985G>A);(9572G>A)]	p.[(?);(Arg3191His)]	chr17:18026708; chr17:18065953
EP28	Bethlehem	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO15A*	c.3866+1G>A	p.(?)	chr17:18029771
IO	Salfeet	yes	multi	2	AR	pre		severe to profound	new	homoz	*MYO15A*	c.4142+5G>A	p.(?)	chr17:18034661
QS027	Qalqilia	yes	multi	3	AR	pre			new	homoz	*MYO15A*	c.4142+5G>A	p.(?)	chr17:18034661
CI	Hebron	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO15A*	c.4240G>A	p.(Glu1414Lys)	chr17:18035800
DC (α15-α25)	Hebron	yes	multi	3	AR	pre		profound	new	homoz	*MYO15A*	c.4240G>A	p.(Glu1414Lys)	chr17:18035800
X3	Jersualem	yes	sing	1	AR	pre			known	homoz	*MYO15A*	c.6340G>A	p.(Val2114Met)	chr17:18049252
X24	Jersualem	no	sing	1	AR	pre			new	cpd het	*MYO15A*	c.[(6499T>C);(8767C>T)]	p.[(Tyr2167His);(Arg2923*)]	chr17:18049411; chr17:18060523
IE	Hebron	yes	multi	4	AR	pre		HL and cleft palate (IE3 only)	known	homoz	*MYO15A*	c.6893G>A	p.(Arg2298Gln)	chr17:18052203
AL	Hebron	yes	multi	3	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
AN	Hebron	yes	multi	4	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
BW	Hebron	yes	multi	5	AR	pre		moderate to severe	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
CF	Hebron	yes	multi	2	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
DX	Bethlehem	yes	multi	3	AR	pre		severe	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
HH	Hebron	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
HI	Bethlehem	yes	multi	2	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
M	Hebron	yes	multi	2	AR	pre		profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
P	Hebron	yes	multi	9	AR	pre			new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
α18	Hebron	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
α19-α20	Hebron	yes	multi	2	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
α8-α9	Hebron	yes	multi	3	AR	pre		severe to profound	new	homoz	*MYO15A*	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889
GP	Hebron	no	sing	1	AR	pre			new	cpd het	*MYO15A*	c.[(7207G>T);(8183G>A)]	p.[(Asp2403Tyr);(Arg2728His)]	chr17:18052889; chr17:18058028
FY	Hebron	yes	multi	2	AR	pre			known	homoz	*MYO15A*	c.8183G>A	p.(Arg2728His)	chr17:18058028
HJ	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*MYO15A*	c.8183G>A	p.(Arg2728His)	chr17:18058028
Z	Hebron	yes	multi	3	AR	pre			known	homoz	*MYO15A*	c.8183G>A	p.(Arg2728His)	chr17:18058028
BZ	Bethlehem	yes	multi	8	AR	pre		severe to profound	new	homoz	*MYO15A*	c.8309_8311del	p.(Glu2770del)	chr17:18058506
JQ	Tubas	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO15A*	c.8788+5G>T	p.(?)	chr17:18060549
AI	Ramallah	yes	multi	3	AR	pre		moderate to severe	new	homoz	*MYO15A*	c.9572G>A	p.(Arg3191His)	chr17:18065953
CQ	Ramallah	yes	multi	2	AR	pre		severe to profound	new	cpd het	*MYO15A*	c.[(9572G>A);(8309_8311del)]	p.[(Arg3191His);(Glu2770del)]	chr17:18065953; chr17:18058506
A132	Jersualem	yes	sing	1	AR	pre			check	homoz	*MYO3A*	c.1370_1371del	p.(Arg457Asnfs*25)	chr10:26377142
AV	Nablus	yes	multi	6	AR	post		profound	known	homoz	*MYO6*	c.897G>T	p.(Glu299Asp)	chr6:76554694
X36	Jersualem	yes	sing	1	AR	pre				homoz	*MYO6*	c.897G>T	p.(Glu299Asp)	chr6:76554694
AS-V	Jenin	yes	sing	1	AR	pre			known	homoz	*MYO6*	c.2777T>A	p.(Leu926Gln)	chr6:76599892
AS-W	Jenin	yes	multi	5	AR	pre			known	homoz	*MYO6*	c.2777T>A	p.(Leu926Gln)	chr6:76599892
QS009	Qalqilia	yes	multi	3	AR	pre		profound	known	homoz	*MYO6*	c.2777T>A	p.(Leu926Gln)	chr6:76599892
AS-R	Jenin	yes	sing	1	AR	pre			new	homoz	*MYO7A*	c.4951G>A	p.(Gly1651Ser)	chr11:72912591
X5	Jersualem	yes	sing	1	AR	pre			known	homoz	*MYO7A*	c.700C>T	p.(Gln234*)	chr11:76868015
QS017	Qalqilia	yes	multi	8	AR	pre		severe to profound	known	homoz	*MYO7A*	c.1117C>T	p.(Arg373Cys)	chr11:76871245
JH	Salfeet	no	multi	3	AR	pre	yes	moderate to severe, w/ Usher	known	cpd het	*MYO7A*	c.[(1583T>G);(6229dup)]	p.[(Leu528Pro);(Trp2077Leufs*51)]	chr11:76873927; chr11:76922374
X40	Jersualem	yes	sing	1	AR	pre			known	homoz	*MYO7A*	c.2187+1G>T	p.(?)	chr11:76886511
GU	Jenin	yes	multi	2	AR	pre	yes	severe to profound, balance	known	homoz	*MYO7A*	c.2307del	p.(Asn769Lysfs*5)	chr11:76890115
AA-A	Jenin	yes	multi	3	AR	pre		severe to profound	new	homoz	*MYO7A*	c.2683C>T	p.(Arg895Cys)	chr11:76891516
X19	Jersualem	yes	sing	1	AR	pre			known	homoz	*MYO7A*	c.3892G>A	p.(Gly1298Arg)	chr11:76901883
QS004	Qalqilia	yes	multi	3	AR	pre		profound	known	homoz	*MYO7A*	c.4153-2A>G	p.(?)	chr11:76905397
QS013	Qalqilia	yes	multi	2	AR	pre		profound	known	homoz	*MYO7A*	c.4153-2A>G	p.(?)	chr11:76905397

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre-post-lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
QS042-043	Qalqilia	yes	sing	1	AR	pre			known	homoz	*MYO7A*	c.4153-2A>G	p.(?)	chr11:76905397
AP	Hebron	yes	sing	1	AR	pre		severe to profound	new	homoz	*MYO7A*	c.4297C>T	p.(Gln1433*)	chr11:76905543
IT	Jersualem	no	multi	6	AR	pre		profound	known	cpd het	*MYO7A*	c.[(5095C>T);(700C>T)]	p.[(Gln1699*);(Gln234*)]	chr11:76913396; chr11:76868015
Q-Q	Tulkarm	yes	sing	1	AR	pre				homoz	*MYO7A*	c.5101C>T	p.(Arg1701*)	chr11:76913402
AO	Hebron	yes	multi	5	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6196C>T	p.(Gln2066*)	chr11:76922341
BV6	Jersualem	yes	multi	3	AR	pre		profound	known	homoz	*MYO7A*	c.6196C>T	p.(Gln2066*)	chr11:76922341
DT	Hebron	yes	multi	2	AR	pre			known	homoz	*MYO7A*	c.6196C>T	p.(Gln2066*)	chr11:76922341
GB	Hebron	yes	multi	3	AR	pre			known	homoz	*MYO7A*	c.6196C>T	p.(Gln2066*)	chr11:76922341
α12	Hebron	yes	multi	3	AR	pre			known	homoz	*MYO7A*	c.6196C>T	p.(Gln2066*)	chr11:76922341
DI	Nablus	yes	sing	1	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6211C>T	p.(Gln2071*)	chr11:76922356
HY	Ramallah	yes	sing	1	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6211C>T	p.(Gln2071*)	chr11:76922356
QS025-026	Qalqilia	yes	sing	1	AR	pre		profound	known	homoz	*MYO7A*	c.6211C>T	p.(Gln2071*)	chr11:76922356
A118-119	Jersualem	yes	sing	1	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
FD	Ramallah	yes	sing	1	AR	pre		moderate	known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
J9-17	Hebron	yes	multi	7	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
QS014-015	Qalqilia	yes	multi	2	AR	pre			known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
QS023-024	Qalqilia	yes	sing	1	AR	pre			known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
X31	Jersualem	yes	sing	1	AR	pre		severe to profound	known	homoz	*MYO7A*	c.6487G>A	p.(Gly2163Ser)	chr11:76924953
DO	Hebron	yes	multi	5	AR	pre		severe to profound	new	homoz	*OTOA*	del 320-550 kb, complete gene		chr16:21675289_21772050 or larger
GQ	Hebron	yes	multi	7	AR	pre		moderate	new	homoz	*OTOA*	del 162-373 kb, complete gene		chr16:21675289_21772050 or larger
X10	Jersualem	yes	multi	2	AR	pre			known	homoz	*OTOA*	del >86kb, complete gene		chr16:21687467_21773938 or larger
X30	Jersualem	yes	multi	2	AR	pre			known	homoz	*OTOA*	del >86kb, complete gene		chr16:21687467_21773938 or larger
BR	Bethlehem	yes	multi	7	AR	pre		severe to profound	new	homoz	*OTOA*	c.1025A>T	p.(Asp342Val)	chr16:21716534
HT	Hebron	yes	sing	1	AR	pre		moderate to severe	new	homoz	*OTOA*	c.1025A>T	p.(Asp342Val)	chr16:21716534
X1	Hebron	yes	sing	1	AR	pre			new	homoz	*OTOA*	c.2017-2A>G	p.(?)	chr16:21739560
X8-9	Jersualem	yes	multi	2	AR	pre			new	homoz	*OTOA*	c.2017-2A>G	p.(?)	chr16:21739560
AM	Bethlehem	yes	multi	3	AR	pre		severe to profound	known	homoz	*OTOF*	c.4030C>T	p.(Arg1344*)	chr2:26691336
IM	Jersualem	yes	multi	2	AR	pre		profound	known	homoz	*OTOF*	c.2239G>T	p.(Glu747*)	chr2:26700593
FH	Hebron	yes	multi	3	AR	pre		profound	new	homoz	*OTOF*	c.1477C>T	p.(Arg1583Cys)	chr2:26688592
DL	Bethlehem	yes	multi	2	AD	pre	yes	Waardenberg syn type I	known	het	*PAX3*	c.812G>A	p.(Arg271His)	chr2:223086087
BK	Jersualem	yes	multi	2	AD	pre	yes	Waardenburg syn type I	known	het	*PAX3*	c.251C>T	p.(Ser84Phe)	chr2:223161767
DH	Hebron	yes	multi	14	AD	pre	yes	Waardenberg syn type I	known	het	*PAX3*	c.251C>T	p.(Ser84Phe)	chr2:223161767
EP26	Bethlehem	no	multi	2	AD	pre	yes	Waardenberg syn type I	known	het	*PAX3*	c.251C>T	p.(Ser84Phe)	chr2:223161767
EP41	Bethlehem	no	sing	1	AD	pre	yes	Waardenberg syn type I	known	het	*PAX3*	c.218C>T	p.(Ser84Phe)	chr2:223161800
JM	Hebron	yes	sing	2	AD	pre	yes	Waardenberg syn type I	new	het	*PAX3*	c.202C>T	p.(Arg68Trp)	chr2:223161816
A161	Jersualem	yes	sing	1	AR	pre		moderate	new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
AS-T	Jenin	yes	multi	3	AR	pre			new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
CA	Salfeet	yes	sing	1	AR	pre		severe to profound	new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
EX	Qalqilia	yes	multi	3	AR	pre		severe to profound	new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
GY	Salfeet	yes	multi	3	AR	pre		severe to profound	new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
X21	Jersualem	yes	sing	1	AR	pre			new	homoz	*PCDH15*	c.4726C>T	p.(Gln1576*)	chr10:55569099
GA-U	Gaza	yes	multi	2	AR	pre			new	homoz	*PCDH15*	c.432C>G	p.(Asp144Glu)	chr10:56128937
A	Hebron	yes	multi	12	AR	pre		severe to profound	known	homoz	*PJVK*	c.406C>T	p.(Arg136*)	chr2:179319253
B1-2	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*PJVK*	c.406C>T	p.(Arg136*)	chr2:179319253
GW	Nablus	yes	multi	6	XR	pre		severe to profound	known	hemiz	*POU3F4*	c.G845T	p.(Arg282Leu)	chrX:82764177
JE	Tubas	no	multi	5	XR	pre		moderate	known	hemiz	*POU3F4*	c.G845T	p.(Arg282Leu)	chrX:82764177
GA-G	Gaza	yes	sing	1	AR	pre		severe to profound	known	homoz	*POU4F3*	c.54delA	p.(Glu18Aspfs*66)	chr5:145718729
X32	Jersualem	yes	sing	1	AR	pre			new	homoz	*POU4F3*	c.694G>T	p.(Glu232*)	chr5:145719684
CN	Bethlehem	yes	multi	3	AR	pre		moderate	known	homoz	*PTPRQ*	c.769G>T	p.(Glu257*)	chr12:80878248
DP	Bethlehem	yes	multi	3	AR	pre		moderate, vestibular problems	known	homoz	*PTPRQ*	c.769G>T	p.(Glu257*)	chr12:80878248
AS-EE	Jenin	yes	multi	3	AR	pre		severe to profound	new	homoz	*PTPRQ*	c.6730C>T	p.(Gln2244*)	chr12:81067075
EC	Hebron	yes	multi	2	AR	pre	yes	severe w/mild MR, DD	known	homoz	*PTRH2*	c.254A>C	p.(Gln85Pro)	chr17:57775086
FF	Hebron	yes	multi	2	AR	pre	yes	severe w/mild MR, DD	known	homoz	*PTRH2*	c.254A>C	p.(Gln85Pro)	chr17:57775086
IH	Hebron	yes	sing	1	AR	pre		severe to profound	new	homoz	*RDX*	c.513_514delAA	p.(Arg171Serfs*6)	chr11:110128868
AS-P	Jenin	yes	sing	1	AR	pre		severe to profound	new	homoz	*SLC26A4*	c.284G>A	p.(Gly95Glu)	chr7:107303860
GA-Q	Gaza	yes	multi	2	AR	pre		severe to profound	new	homoz	*SLC26A4*	c.304G>A	p.(Gly102Arg)	chr7:107303880
JF1	Ramallah	yes	multi	4	AR	pre		moderate to severe	new	homoz	*SLC26A4*	c.304G>A	p.(Gly102Arg)	chr7:107303880
EZ	Nablus	yes	multi	3	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.397T>A	p.(Ser133Thr)	chr7:107312675
Y	Hebron	yes	multi	10	AR	pre			known	homoz	*SLC26A4*	c.716T>A	p.(Val239Asp)	chr7:107315505
AA-L	Jenin	yes	multi	4	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
BF	Bethlehem	yes	multi	3	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
C5/C8	Hebron	yes	multi	2	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
DY	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
EP13-14	Bethlehem	yes	multi	2	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
EP35	Bethlehem	yes	sing	1	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
HQ	Gaza	yes	multi	3	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre-post-lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
JF2	Ramallah	yes	sing	1	AR	pre		moderate to severe	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
X4	Bethlehem	yes	multi	5	AR	pre		profound	known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
α22	Hebron	yes	sing	1	AR	pre			known	homoz	*SLC26A4*	c.1001G>T	p.(Gly334Val)	chr7:107323982
EO	Ramallah	yes	sing	1	AR	pre			new	cpd het	*SLC26A4*	c.[(1054delG);(334C>T)]	p.[(Ala352Hisfs*16);(Pro112Ser)]	chr7:107329550; chr7:107312612
EM	Hebron	yes	multi	4	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1061T>C	p.(Phe354Ser)	chr7:107329557
CS	Jenin	yes	multi	6	AR	pre		severe	known	homoz	*SLC26A4*	c.1198delT	p.(Cys400Valfs*32)	chr7:107330617
FB	Hebron	yes	multi	3	AR	pre	yes	moderate w/Pendred syn	known	homoz	*SLC26A4*	c.1198delT	p.(Cys400Valfs*32)	chr7:107330617
J6-8	Hebron	yes	multi	2	AR	pre			known	homoz	*SLC26A4*	c.1198delT	p.(Cys400Valfs*32)	chr7:107330617
GR	Nablus	no	multi	2	AR	pre			known	cpd het	*SLC26A4*	c.[(1198delT);(1001G>T)]	p.[(Cys400Valfs*32);(Gly334Val)]	chr7:107330617; chr7:107323982
CB	Bethlehem	yes	multi	4	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1341+1delG	p.(?)	chr7:107334926
FU4	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1341+1delG	p.(?)	chr7:107334926
HB	Hebron	yes	multi	3	AR	pre		severe to profound	known	homoz	*SLC26A4*	c.1341+1delG	p.(?)	chr7:107334926
X2	Jersualem	yes	sing	1	AR	pre			known	homoz	*SLC26A4*	c.1341+1delG	p.(?)	chr7:107334926
α21	Hebron	yes	sing	1	AR	pre			known	homoz	*SLC26A4*	c.1341+1delG	p.(?)	chr7:107334926
HF	Nablus	no	multi	4	AR	pre	yes	severe to profound w/EVA	new	cpd het	*SLC26A4*	c.[(1341+1delG);(1149_1149+5)]	p.[(?);(?)]	chr7:107334926; chr7:107329645
Q-B	Tulkarm	yes	multi	3	AR	pre			known	homoz	*SLC26A4*	c.1489G>A	p.(Gly497Ser)	chr7:107336429
QS002	Qalqilia	yes	multi	2	AR	pre		moderate	known	homoz	*SLC26A4*	c.2048T>C	p.(Phe683Ser)	chr7:107344789
QS058-059	Qalqilia	yes	multi	4	AR	pre			known	homoz	*SLC26A4*	c.2048T>C	p.(Phe683Ser)	chr7:107344789
GA-T	Gaza	yes	multi	4	AR	pre			known	homoz	*STRC*	complete gene deletion		chr15:43891761_43910998 or larger
CZ9-10 (α6-α7)	Hebron	yes	multi	2	AR	pre		severe to profound	new	homoz	*TBC1D24*	c.1114_1116del	p.(Ser372del)	chr16:2548369
HD	Hebron	yes	multi	2	AR	pre		moderate to severe	known	homoz	*TECTA*	c.1705C>T	p.(Gln569*)	chr11:120996512
BI	Hebron	yes	multi	5	AR	pre		moderate	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
BQ	Bethlehem	yes	multi	5	AR	pre		moderate	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
CH	Bethlehem	yes	multi	7	AR	pre		moderate to severe	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
CV	Hebron	yes	multi	11	AR	pre		moderate	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
EP40	Bethlehem	yes	multi	2	AR	pre		moderate to severe	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
HM	Bethlehem	yes	multi	4	AR	pre		moderate to severe	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
HP	Bethlehem	yes	multi	7	AR	pre		moderate	known	homoz	*TECTA*	c.4857C>A	p.(Cys1619*)	chr11:121031011
JA	Hebron	no	multi	7	AD	pre		moderate to severe	known	het	*TECTA*	c.5609A>G	p.(Tyr1870Cys)	chr11:121038785
GA-P	Gaza	yes	multi	3	AR	pre		profound	known	homoz	*TMC1*	c.100C>T	p.(Arg34*)	chr9:75309494
FA	Nablus	no	multi	2	AR	pre		moderate to profound	known	cpd het	*TMC1*	c.[(100C>T);(1532C>A)]	p.[(Arg34*);(Pro511His)]	chr9:75309494; chr9:75407234
GA-F	Gaza	yes	multi	3	AR	pre		severe to profound	new	homoz	*TMC1*	c.1184delA	p.(Gln395Argfs*15)	chr9:75404193
DN	Hebron	yes	multi	2	AR	pre		severe to profound	new	homoz	*TMC1*	c.1763+1G>T	p.(?)	chr9:75431127
AU	Hebron	yes	multi	3	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
BG-B	Hebron	yes	multi	9	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
BG-G	Hebron	yes	multi	7	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
CU	Hebron	yes	multi	4	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
EP45	Bethlehem	yes	sing	1	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
IX	Hebron	yes	multi	4	AR	pre		moderate	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
JC	Hebron	yes	multi	2	AR	pre		moderate	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
R	Hebron	yes	sing	1	AR	pre		moderate to severe	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
W	Hebron	yes	multi	15	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1193delA	p.(Gln398Argfs*18)	chr21:43796651
CL	Ramallah	yes	multi	4	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.1176del8ins~1224	p.(?)	chr21:43796665
EP36	Bethlehem	yes	sing	1	AR	pre			known	homoz	*TMPRSS3*	c.989delA	p.(Glu330Glyfs*28)	chr21:43800285
GT	Hebron	yes	sing	1	AR	pre		moderate to severe	known	homoz	*TMPRSS3*	c.989delA	p.(Glu330Glyfs*28)	chr21:43800285
JB	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.989delA	p.(Glu330Glyfs*28)	chr21:43800285
I	Hebron	yes	multi	3	AR	pre			known	homoz	*TMPRSS3*	c.582T>A	p.(Cys194*)	chr21:43804113
AA-X	Jenin	yes	multi	3	AR	pre		severe to profound	known	homoz	*TMPRSS3*	c.323-6G>A	p.(?)	chr21:43808641
AE	Hebron	yes	sing	1	AR	pre		moderate to severe	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
AK	Bethlehem	yes	multi	6	AR	pre		moderate to severe	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
AX	Bethlehem	yes	multi	4	AR	pre		moderate	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
AZ	Bethlehem	yes	multi	6	AR	pre		moderate	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
DU	Hebron	yes	sing	1	AR	pre		severe	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
EP30	Bethlehem	yes	sing	1	AR	pre		profound	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
FV	Hebron	yes	multi	2	AR	pre		severe	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
ID	Bethlehem	yes	multi	3	AR	pre			known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
K	Bethlehem	yes	multi	11	AR	pre		severe to profound	known	homoz	*TRIOBP*	c.1039C>T	p.(Arg347*)	chr22:38119602
HA	Jersualem	yes	multi	8	AR	pre		severe to profound	known	cpd het	*TRIOBP*	c.[(1039C>T);(1741C>T)]	p.[(Arg347*);(Gln581*)]	chr22:38119602; chr22:38120304
X7-X25	Jersualem	yes	multi	2	AR	pre		severe to profound	known	cpd het	*TRIOBP*	c.[(1039C>T);(1741C>T)]	p.[(Arg347*);(Gln581*)]	chr22:38119602; chr22:38120304
AY	Bethlehem	yes	multi	9	AR	pre		moderate	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
BD	Bethlehem	yes	multi	2	AR	pre		severe to profound	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
DR	Bethlehem	yes	multi	4	AR	pre		profound	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
EP44	Bethlehem	yes	sing	1	AR	pre		moderate to severe	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
FK	Hebron	yes	sing	1	AR	pre		severe to profound	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
GE	Hebron	yes	sing	1	AR	pre			known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
GN	Hebron	yes	multi	5	AR	pre		severe	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304

Family	City	Consang	Single / multi HL	Aff in family	Inherit	Onset pre- post- lingual	Synd	Hearing loss	New / known allele	Geno type	Gene	cDNA	Protein	hg19 position
QS033	Qalqilia	yes	multi	3	AR	pre		severe	known	homoz	*TRIOBP*	c.1741C>T	p.(Gln581*)	chr22:38120304
CM	Hebron	yes	multi	3	AR	pre			new	homoz	*TRIOBP*	c.2202_2203delTC	p.(Arg735Glnfs*25)	chr22:38120765
GM	Jersualem	yes	multi	4	AR	pre		severe to profound	new	homoz	*TRIOBP*	c.3232dup	p.(Arg1078Profs*6)	chr22:38121795
DV	Hebron	yes	multi	2	AR	pre		severe to profound, onset 1.5y	new	homoz	*USH1C*	c.104+5G>C	p.(?)	chr11:17554797
FL	Jersualem	yes	multi	2	AR	pre	yes	profound w/ Usher syndrome	new	homoz	*USH1C*	c.104+5G>C	p.(?)	chr11:17554797
BG-R	Hebron	yes	multi	3	AR	pre	yes	profound w/ Usher syndrome	known	homoz	*USH1G*	c.832_851del	p.(Ser278Profs*71)	chr17:72916080_72916099
α14	Hebron	yes	sing	1	AR	pre			known	homoz	*USH1G*	c.469dup	p.(His157Profs*199)	chr17:72916461
C32	Hebron	yes	multi	2	AR	pre		moderate, no other signs	new	homoz	*USH2A*	c.9685delG	p.(Glu3229Argfs*72)	chr1:215987132
IR	Hebron	yes	multi	3	AR	pre	yes	moderate to severe w/RP	new	homoz	*USH2A*	c.9685delG	p.(Glu3229Argfs*72)	chr1:215987132
JJ	Hebron	yes	multi	4	AR	pre		moderate, no other signs	new	homoz	*USH2A*	c.9685delG	p.(Glu3229Argfs*72)	chr1:215987132

Table S3. Hearing loss in consanguineous and non-consanguineous families

Hearing loss	Consanguineous families	Non consanguineous families	Total
Autosomal recessive, homozygous	293	2	295
AR compound heterozygous	11	17	28
Autosomal dominant	6	5	11
X-linked	2	1	3
No genetic diagnosis	128	26	154
Total	440	51	491

Table S4. Missense mutations in Palestinian families with hearing loss

Gene	Protein	cDNA	zygosity	hg19 position	Hearing loss phenotype	Pal families with mutation	co-seg P	Pal control exomes (2618)	gnomad exomes (246366)	Our suggestion for ClinVar	Evidence for interpretation in addition to co-segregation P-values and control allele frequencies
A. Missense mutations not reported elsewhere: private or Palestinian founder mutations											
CACNA1D	p.(Ala376Val)	c.1127C>T	homoz	chr3:53707750	congenital, moderate w/cardiac signs (prolonged AV conduction on EEG)	4	2.58E-05	0	4	LP	Good fit to syndromic recessive phenotype; co-seg in multiple families, completely consserved residue, TM domain
CDH23	p.(Asp228Val)	c.683A>T	homoz	chr10:73330605	congenital, profound	1	0.047	0	0	LP	Completely conserved residue
CDH23	p.(Asn1521Ser)	c.4562A>G	homoz	chr10:73500652	congenital, profound	1	6.50E-03	0	5	LP	Completely conserved residue
CDH23	p.(Glu1917Lys)	c.5749G>A	homoz	chr10:73545424	congenital with RP	1	0.012	0	0	LP	Completely conserved residue; Usher 1D mutation region
CDH23	p.(Asp2714Tyr)	c.8140G>T	homoz	chr10:73566000	congenital, severe to profound	1	0.047	0	0	LP	Completely conserved residue
CDH23	p.(Leu2735Pro)	c.8204T>C	homoz	chr10:73567059	congenital, severe to profound	2	1.53E-05	0	0	LP	Completely conserved residue
COL11A2	p.(Gly1027Glu)	c.3080G>A	homoz	chr6:33139560	HL and joint problems	1	5.00E-04	0	0	LP	Good fit to syndromic phenotype; completely conserved residue
DNAH11	p.(Thr3824Pro)	c.11470A>C	homoz	chr7:21904249	severe to profound, recurrent ear infections, conductive?	1	0.026	0	0	LP	Good fit to syn phenotype (Primary ciliary dyskinesia); polyphen 0.99, gerp 5.2
EDNRB	p.(Val275Met)	c.823G>A	homoz	chr13:78477673	Waardenburg syn	1	0.011	0	33	LP	Good fit to recessive syndromic phenotype; completely conserved residue
ESRRB	p.(Arg182His)	c.545G>A	homoz	chr14:76948389	congenital, severe to profound	1	6.50E-03	1	0	LP	Co-seg in very large family; gerp 4.9; R179H pathogenic per RJSmith
LHFPLS	p.(Met1Val)	c.1A>G	homoz	chr6:35773448	congenital, severe to profound	1	2.44E-04	0	28	LP	Translation start
MYO15A	p.(Ala408Val)	c.1223C>T	cpd het	chr17:18023337	congenital profound	1	0.063	9	5	VUS	Compound het with MYO15A c.4240G>A enhancer mutaton
MYO6	p.(Leu926Gln)	c.2777T>A	homoz	chr6:76599892	congenital, profound	3	3.83E-06	0	0	LP	
MYO7A	p.(Arg895Cys)	c.2683C>T	homoz	chr11:76891516	congenital, severe to profound	1	6.50E-04	0	4	LP	
OTOA	p.(Asp342Val)	c.1025A>T	homoz	chr16:21716534	moderate to profound	2	2.50E-08	2	0	LP	Polyphen 1.0, gerp 5.3; very large family
OTOF	p.(Arg1583Cys)	c.1477C>T	homoz	chr2:26688592	congenital, profound	1	0.036	0	5	LP	R1583H pathogenic on ClinVar as cpd het w/nonsense
PAX3	p.(Arg68Trp)	c.202C>T	het	chr2:223161816	Waardenburg syn	1	sing	0	0	LP	Good fit to syn phenotype in proband and mother; completely conserved residue
PCDH15	p.(Asp144Glu)	c.432C>G	homoz	chr10:56128937	congenital, severe to profound	1	0.047	0	0	LP	Completely conserved residue; cadherin domain; R134G causes HL in Pakistani family
B. Missense mutations suggested to be reclassified from VUS or benign to likely pathogenic											
CDH23	p.(Pro2205Leu)	c.6614C>T	homoz	chr10:73553299	congenital, moderate to severe	2	0.063	0	0	LP	Arab allele; VUS by Expert Panel due to few Arab popn controls; suggest reclassification given 2 more
CLDN14	p.(Pro28Leu)	c.83C>T	homoz	chr21:37833911	congenital, severe to profound	7	2.50E-10	0	3	LP	Pal allele, now with convincing family data and popn controls
GIPC3	p.(Thr41Lys)	c.122C>A	homoz	chr19:3585717	severe to profound w/ epilepsy	1	0.02	0	2	LP	Additional family to add to observation in Saudi family (PMID:23510777)
MYO7A	p.(Arg373Cys)	c.1117C>T	homoz	chr11:76871245	congenital, severe to profound	1	1.72E-05	0	0	LP	Completely conserved site, now another, very large family, still 0 in controls
POU3F4	p.(Arg282Leu)	c.845G>T	hemiz	chrX:82764177	congenital, moderate to severe	2	0.001	0	0	LP	Two additional families, absent in popn controls
SLC26A4	p.(Phe354Ser)	c.1061T>C	homoz	chr7:107329557	congenital, severe to profound	3	6.50E-03	5	184	LP	Common but all gnomad and popn controls are hets; suggest reclassification based on 3 additional families; mutation predicted to weaken TM domain

Gene	Protein	cDNA	zygosity	hg19 position	Hearing loss phenotype	Pal families with mutation	co-seg P	Pal control exomes (2618)	gnomad exomes (246366)	Our suggestion for ClinVar	Evidence for interpretation in addition to co-segregation P-values and control allele frequencies
C. Missense mutations previously reported from multiple sources as pathogenic or likely pathogenic											
CDH23	p.(Pro346Ser)	c.1036C>T	homoz	chr10:73377052	congenital, severe to profound	3		0	0	P	
CDH23	p.(Pro346Ser)	c.1037C>T	homoz	chr10:73377053	congenital, moderate	1		0	5	P	
CDH23	p.(Pro559Ser)	c.1675C>T	homoz	chr10:73437373	congenital, moderate to severe	2		0	0	P	
CDH23	p.(Glu1071Lys)	c.3211G>A	homoz	chr10:73468959	congenital, moderate	2		0	0	P	
COCH	p.(Cys542Ser)	c.1625G>C	het	chr14:31358969	onset ~age 20, moderate, progressive	1		0	0	P	
ESPN	p.(Ser719Arg)	c.2155A>C	het	chr1:6511986		1		0	1	P	
GJB2	p.(Trp77Arg)	c.229T>C	homoz	chr13:20763492	congenital, severe to profound	1		0	10	P	Disulfide bond region, disrupts channel fcn
LARS2	p.(Asn153His)	c.457A>C	homoz	chr3:45461162	severe to profound with ovarian dys and neurological problems	4		1	0	LP	
MYO6	p.(Glu299Asp)	c.897G>T	homoz	chr6:76554694	congenital, profound	1		0	0	P	
MYO7A	p.(Gly1298Arg)	c.3892G>A	homoz	chr11:76901883		1		2	0	LP	
MYO7A	p.(Gly2163Ser)	c.6487G>A	homoz	chr11:76924953	congenital, moderate to profound	6		0	7	P/LP	
MYO15A	p.(Val2114Met)	c.6340G>A	homoz	chr17:18049252	congenital, severe to profound	1		1	1	P	Also Yang 2013 (compound het with frameshift); no splice effect
MYO15A	p.(Arg2728His)	c.8183G>A	homoz	chr17:18058028	congenital, severe to profound	3		1	48	LP	Completely conserved site; compound het w/fs on ClinVar and in our cohort; no splice effect
PAX3	p.(Arg271His)	c.812G>A	het	chr2:223086087	Waardenburg syn type I	1		0	0	P	
PAX3	p.(Ser84Phe)	c.251C>T	het	chr2:223161767	Waardenburg syn type I	3		0	0	P	
PTRH2	p.(Gln86Pro)	c.254T>G	homoz	chr17: 57775086	severe HL w/mild DD	2		0	0	P/LP	
SLC26A4	p.(Ser133Thr)	c.397T>A	homoz	chr7:107312675	congenital, severe to profound	1		0	1	LP	Missense on ClinVar; we predict enhancer effect
SLC26A4	p.(Val239Asp)	c.716T>A	homoz	chr7:107315505	congenital, severe to profound	1		1	51	P	Damages protein fcn
SLC26A4	p.(Gly497Ser)	c.1489G>A	homoz	chr7:107336429	congenital, severe to profound	1		0	7	P	Damages protein fcn
SLC26A4	p.(Phe683Ser)	c.2048T>C	homoz	chr7:107344789	congenital, moderate	2		0	2	P	
TECTA	p.(Tyr1870Cys)	c.5609A>G	het	chr11:121038785	congenital, moderate to severe	1		0	0	P/LP	Original DFNA8/12 mutation

Table S5. Mutations with transcript effects. Predictions using approach of Casadei et al 2019. Effects were experimentally validated for genes expressed in available tissues

				NNSPLICE			MaxEnt							Expt		Families	
Gene	cDNA	Protein	hg19 position	ref	mutant	cryptic	ref	mutant	cryptic	distance to splice sites	Mutation effect(s)	Transcript effect	Protein effect	confirm in RNA	Co-seg P	with mutation	gnomad
ADGRV1	c.2898G>A	p.(Glu966Glu)	chr5:89940686	1.00	0.88		8.39	3.59		El164Il1	disrupt splice donor exon 15	del 164 bp	stop codon 931	yes	0.002	2	0
ADGRV1	c.10426 G>A	p.(Gly3476Arg)	chr5:90024750	0.96	0.26	0.58	6.95	2.17	5.35	El265Il1	cryptic splice donor c.10216, exon 49 (chr5:90,024,540)	del 210 bp	del aa 3407-3476 in EAR4 domain	yes	0.012	1	0
CDC14A	c.51-1G>T	p.(?)	chr1:100819317	0.87	0.00		11.01	2.41			disrupt splice acceptor exon 2	del 91 bp	stop codon 25	yes	sing	1	0
CLPP	c.270+3G>T	p.(?)	chr19:6361954	0.96	0.54		8.69	1.83			disrupt splice donor exon 2; retain intron 2	del 72 bp; ins 505 bp	del aa 67-90 Clp protease proteolytic subunit; stop cdn 128	na	0.105	1	0
DFNA5	c.991-15_991-13del	p.(?)	chr7:24746008						-		weaken polypyrimidine tract at exon 8 acceptor	del 193 bp	stop codon 372	yes	to do	1	
EDNRB	c.1071+2T>C	p.(?)	chr13:78477289	0.90	0.00		8.76	1.01			disrupt splice donor exon 4	del 205 bp	stop codon 317	yes	sing	1	0
ESRRB	c.787G>A	p.(Gly263Ser)	chr14:76949102	1.00	0.91		9.60	6.39		El162Il1	disrupt splice donor exon 7	del 162 bp	del aa 209-262 in transactivation domain	yes	0.001	2	1
GJB2	c.-23+1G>A	p.(?)	chr13:20766921	0.99	0.00		9.60	1.42			disrupt splice donor exon 1	loss of transcript	no protein	yes		4	
HSD17B4	c.1842G>A	p.(Lys614Lys)	chr5:118862914	0.99	0.56	0.95	9.11	3.87	4.82	El87Il1	disrupt splice donor exon 21; cryptic splice donor c.1842+70	del 87 bp	del aa 586-614 in hydratase domain; stop codon 616	yes	0.141	1	5
LHFPL5	c.*16+1G>A	p.(?)	chr6:35787241	0.98	0.00		11.11	2.93			disrupt splice donor exon 3 (3'UTR)	del 12 bp	extend 32 codons (PMID:30177809)	known allele	sing	1	0
LRTOMT	c.327C>T	p.(Cys109Cys)	chr11:71817225	0.94		0.83	8.68		7.39	El244Il32	cryptic splice donor at c.326 in exon 7	del 33 bp	del aa 110-120 in tramsmembrane domain	ne	0.011	1	0
MYO6	c.897G>T	p.(Glu299Asp)	chr6:76554694	0.36	0.00		7.13	-2.49		El81Il1	disrupt splice donor exon 10	del 81 bp	del aa 275-301 in ATPase domain	yes	9.77E-04	2	0
MYO7A	c.4951G>A	p.(Gly1651Ser)	chr11:72912591							El99Il93	ESE loss and ESS gain exon 36	del 191 bp	stop codon 1656	yes	0.079	1	0
MYO7A	c.4153-2A>G	p.(?)	chr11:76905397	0.88	0.00		5.93	-2.02			disrupt splice acceptor exon 32	del 171 bp	del aa 1385-1441 in FERM1 domain	known allele		3	
MYO15A	c.3609+985G>A	p.(?)	chr17:18026708	0.96	0.00		7.77	-0.41			disrupt splice donor exon 1	comp loss	cochlear and pituitary-specific isoform	ne		9	0
MYO15A	c.3866+1G>A	p.(?)	chr17:18029771	0.93	0.00		8.40	0.22			disrupt splice donor exon 5	110 bp	stop codon 1277	ne	sing	1	2
MYO15A	c.4142+5G>A	p.(?)	chr17:18034661	0.97	0.09	0.54	9.25	2.65	6.42		disrupt splice donor exon 9; cryptic donor splice exon 9	106 bp; del 70 bp	stop codon 1360	ne	0.016	2	0
MYO15A	c.4240G>A	p.(Glu1414Lys)	chr17:18035800							El34Il81	ESS gain exon 11	del 114 bp	del aa 1403-1440 in motor domain	ne	7.32E-04	3	1
MYO15A	c.6499T>C)	p.(Tyr2167His)	chr17:18049411							El226Il11	ESE loss exon 30	del 236 bp	stop codon 2095	ne	sing	1	7
MYO15A	c.6893G>A	p.(Arg2298Gln)	chr17:18052203							El129Il64	ESE loss, ESS gain, exon 33	del 192 bp	del aa 2256-2319 in tail domain	ne	0.002	1	2
MYO15A	c.7207G>T	p.(Asp2403Tyr)	chr17:18052889	0.00	0.87		0.08	7.73		El90Il6	cryptic splice donor c.7206, exon 35 (chr17:18,052,888)	del 7 bp	stop codon 2414	ne	4.67E-17	13	0
MYO15A	c.8309_8311del	p.(Glu2770del)	chr17:18058506							El84Il31	ESE loss exon 46	del 116 bp	stop codon 2803	ne	0.026	1	0
MYO15A	c.8788+5G>T	p.(?)	chr17:18060549	0.38	0.00		3.29	-3.85			disrupt splice donor exon 50	del 75 bp	del aa 2906-2930 in SH3 domain	ne	0.105	1	0
MYO15A	c.9572G>A	p.(Arg3191His)	chr17:18065953							El55Il41	ESE loss, ESS gain, exon 58	del 95 bp	stop codon 3189	ne	0.008	2	10
OTOA	c.2017-2A>G	p.(?)	chr16:21739560	0.71	0.00	0.30	7.47	-0.48	5.22		disrupt splice acceptor exon 20; cryptic splice acceptor c.2017-72	del 191 bp; ins 71 bp	stop codon 696; stop codon 751	yes	0.016	2	0
SLC26A4	c.284G>A	p.(Gly95Glu)	chr7:107303860							El120Il21	ESE loss; ESS gain exon 3	del 140 bp	stop codon 134	yes	0.105	1	0
SLC26A4	c.304G>A	p.(Gly102Arg)	chr7:107303880	0.99	0.82		10.57	6.91		El140Il1	disrupt splice donor exon 3	del 140 bp	stop codon 134	yes	0.002	1	0
SLC26A4	c.397T>A	p.(Ser133Thr)	chr7:107312675							El93Il19	ESE loss exon 4	del 111 bp	del aa 102-138 in TM domain	yes	0.016	1	0
SLC26A4	c.1001G>T	p.(Gly334Val)	chr7:107323982	0.98	0.45	0.94	7.93	6.05	9.14	El83Il1	(1) disrupt splice donor exon 8; (2) cryptic splice donor	(1) del 83 bp; (2) ins 40 bp	(1) stop codon 311; (2) stop codon 355	yes	6.86E-11	10	2
SLC26A4	c.1341+1delG	p.(?)	chr7:107334926				7.08	-5.81		El1Il78	disrupt splice donor exon 11	del 78 bp	del aa 422-446, complete TM domain	yes		5	4
TBC1D24	c.1114_1116del	p.(Ser372del)	chr16:2548369							El131Il27	ESE loss exon 4	del 159 bp	del aa 328-380 in TBC domain	yes	0.047	1	0
TMC1	c.1763+1G>T	p.(?)	chr9:75431127	0.52	0.00		6.99	-1.51			disrupt splice donor exon 19	del 68 bp	stop codon 600	known allele	sing	1	0
USH1C	c.104+5G>C	p.(?)	chr11:17554797	0.99	0.23		9.09	1.17			disrupt splice donor exon 2	del 68 bp	stop codon 29	ne	0.004	2	0

ne: not expressed in available tissue
na: family not available

Table S6. Unpaired heterozygous mutations in probands with apparently recessive hearing loss

Gene		cDNA	Chr	position (hg19)	Type	Family	Family type	Consang	Gene solving family
A. Families with no genetic diagnosis									
GJB2	p.(Thr8Met)	c.23C>T (exon2)	13	20,763,698	missense	JM	sing	yes	not solved
GJB2	p.(Gly12Valfs*2)	c.35delG (exon2)	13	20,763,686	delFS	A158	sing	no	not solved
GJB2	p.(Gly12Valfs*2)	c.35delG (exon2)	13	20,763,686	delFS	AS-HH	sing	no	not solved
GJB2	p.(Gly12Val)	c.35G>T (exon2)	13	20,763,686	missense	AS-II	sing	no	not solved
GJB2	p.(Tyr65Ser)	c.194A>C (exon2)	13	20,763,527	missense	HZ	sing	yes	not solved
GJB2	p.(Arg98Trp)	c.292C>T (exon2)	13	20,763,429	missense	HW	sing	yes	not solved
GJB2	p.(Met163Val)	c.487A>G (exon2)	13	20,763,234	missense	H	sing	yes	not solved
MYO15A	p.(Arg2728His)	c.8183G>A (exon44)	17	18,058,028	missense	GD	sing	no	not solved
OTOG	p.(Arg2485fs*)	c.7454delG (exon43)	11	17,655,766	delFS	A173	sing	yes	not solved
SLC26A5	-	c.971+2T>C (exon9)	7	103,038,377	splice	A173	sing	yes	not solved
TECTA	p.(Cys1619*)	c.4857C>A (exon14)	11	121,031,011	nonsense	FC14	multi	yes	not solved
USH2A	p.(Gly2313Cys)	c.6937G>T (exon36)	1	216,143,987	missense	GA-M	sing	yes	not solved
B. Families with hearing loss solved by a different gene									
GJB2		c.-23+1A>C	13	20,763,744	splice	IW	multi	yes	*EPS8L2*
GJB2	p.(Gly12Valfs*2)	c.35delG (exon2)	13	20,763,686	delFS	AS-T	multi	yes	*PCDH15*
GJB2	p.(Gly12Valfs*2)	c.35delG (exon2)	13	20,763,686	delFS	QS059	multi	yes	*SLC26A4*
GJB2	p.(Gly12Val)	c.35G>T (exon2)	13	20,763,686	missense	JF	multi	yes	*SLC26A4*
GJB2	p.(Leu79Cysfs*3)	c.235delC (exon2)	13	20,763,486	delFS	GR	multi	yes	*SLC26A4*
GJB2	p.(Leu90Pro)	c.269T>C (exon2)	13	20,763,452	missense	AA-N	multi	yes	*CDH23*
GJB2	p.(Tyr97*)	c.290dupA (exon2)	13	20,763,430	nonsense	AS-R	sing	yes	*MYO7A*
GJB2	p.(Met163Val)	c.487A>G (exon2)	13	20,763,234	missense	JH	multi	no	*MYO7A*
GJB2	p.(Met163Val)	c.487A>G (exon2)	13	20,763,234	missense	QS043	sing	yes	*MYO7A*