Supplementary materials

Diagnostic yield of whole exome sequencing with targeted gene analysis in prelingual sensorineural hearing loss in Thailand

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Table S1. Demographic data of 100 patients based on type of hearing loss

Probands	Non-syndromic group (N=94)		Syndromic group (N=6)	
	All (N=94)	Positive result (N=41)	All (N=6)	Positive result (N=5)
Sex				
Male	47 (50.0%)	27 (65.9%)	1 (16.7%)	1 (20.0%)
Female	47 (50.0%)	14 (34.1%)	5 (83.3%)	4 (80.0%)
Family history of hearing loss				
Yes	32 (34.0%)	18 (43.9%)	4 (66.7%)	3 (60.0%)
No	62 (66.0%)	23 (56.1%)	2 (33.3%)	2 (40.0%)
Consanguinity				
Yes	4 (4.3%)	1 (2.4%)	0 (0.0%)	0 (0.0%)
No	86 (91.5%)	38 (92.7%)	6 (100.0%)	5 (100.0%)
Unknown	4 (4.3%)	2 (4.9%)	0 (0.0%)	0 (0.0%)
Hearing screening (n=38)				
Pass	7 (18.4%)	4 (10.5%)	0 (0.0%)	0 (0.0%)
Refer	30 (79.0%)	12 (31.6%)	1 (2.6%)	0 (0.0%)
Severity of hearing loss [a]				
Moderate	8 (8.5%)	4 (9.8%)	1 (16.7%)	0 (0.0%)
Severe	11 (11.7%)	6 (14.6%)	0 (0.0%)	0 (0.0%)
Profound	47 (50.0%)	16 (39.0%)	2 (33.3%)	2 (40.0%)
Moderate-to-severe	20 (21.3%)	9 (22.0%)	1 (16.7%)	1 (20.0%)
Severe-to-profound	8 (8.5%)	6 (14.6%)	2 (33.3%)	2 (40.0%)
CT/MRI temporal bone (n=28)				
Normal	21 (75.0%)	5 (17.8%)	1 (3.6%)	1 (3.6%)
Abnormal	6 (21.4%)	3 (10.7%)	0 (0.0%)	0 (0.0%)
Non-audiological symptoms and/or inner ear abnormalities				
Yes	23 (24.5%)	11 (26.8%)	6 (100.0%)	5 (100.0%)
No	71 (75.5%)	30 (73.2%)	0 (0.0%)	0 (0.0%)

[a] the severity of hearing loss: moderate 41-70 dB; severe 71-90 dB; profound >90 dB or having cochlear implant; those with unavailable audiological reports, moderate-to-severe was assigned for patients who could hear some sound and speak some words, severe-to-profound for those who did not hear any sound and had no words

Table S2. Demographic data of each 100 individual patients

Patient ID	Recruitment site	Sex	Enrolled age	Severity	OAEs screening	Fam. Hx.	Family relatives	Consanguinity	Non-audiological symptoms		sSNHL/ nsSNHL	CT/MRI	Other genetic testing	WES result
									Other symptoms	DD				
1 [g]	Hosp.	F	12	P	No record	Y	Sister ID 2	Y	Abnormal (tandem) gait; Hx GM delay	Y	nsSNHL	Normal		Neg
2 [g]	Hosp.	F	13	P	No record	Y	Sister ID 1	Y	Hx GM delay	Y	nsSNHL	Normal	GJB2, Pendrin gene-negative; Normal chromosome	Neg
3	Hosp.	F	9	MS	R	N	-	N	-	N	nsSNHL	NA		Neg
4	Hosp.	F	8	MS	No record	N	-	N	-	N	nsSNHL	NA		Neg
5	Hosp.	F	11	P	No record	N	-	N	-	N	nsSNHL	Normal		Neg
7	Hosp.	F	7	Mo	P	N	-	N	-	N	nsSNHL	NA		Neg
8	Hosp.	F	4	P	No record	N	-	N	-	N	nsSNHL	NA		Neg
9	Hosp.	M	4	P	R	N	-	N	-	N	nsSNHL	NA		Neg
10 [a]	Hosp.	M	6	P	R	Y	Twin ID 11	N	Abnormal gait (valgus knee)	N	nsSNHL	NA		Pos
11 [a]	Hosp.	M	6	P	R	Y	Twin ID 10	N	Abnormal gait (valgus knee)	N	nsSNHL	NA		Pos
12 [h]	Hosp.	F	12	P	No record	Y	Brother ID 20	N	-	N	nsSNHL	NA		Neg
13	Hosp.	M	3	P	P	N	-	N	-	N	nsSNHL	Normal		Pos
14	Hosp.	F	4	P	No record	N	-	N	-	N	nsSNHL	Normal		Neg
15	Hosp.	F	6	MS	R	N	-	N	-	N	nsSNHL	EVA		Pos
16	Hosp.	M	10	S	No record	N	-	N	-	N	nsSNHL	NA		Pos
17	Hosp.	F	8	MS	R	N	-	N	-	N	nsSNHL	NA		Neg
18	Hosp.	F	10	MS	No record	N	-	N	-	N	nsSNHL	NA		Neg
20 [h]	Hosp.	M	9	P	R	Y	Sister ID 12	N	-	N	nsSNHL	NA		Neg
21	Hosp.	F	11	P	No record	N	-	N	Epilepsy	N	nsSNHL	Normal		Neg
22	Hosp.	F	8	P	No record	Y	3 Siblings	Y	-	N	nsSNHL	NA	GJB2 gene-negative	Neg
23	Hosp.	F	4	P	R	N	-	N	-	N	nsSNHL	Normal		Neg
24	Hosp.	M	2	P	R	N	-	N	-	N	nsSNHL	NA		Neg
26	Hosp.	M	4	P	R	N	-	N		N	nsSNHL	NA		Neg
27	Hosp.	M	4	S	No record	N	-	N	-	N	nsSNHL	NA		Pos

28	Hosp.	F	5	P	No record	N	-	N	-	N	nsSNHL	EVA (Right)		Neg
29	Hosp.	F	2	P	R	N	-	N	-	N	nsSNHL	Normal		Neg
30	Hosp.	M	9	S	No record	N	-	N	-	N	nsSNHL	Normal	GJB2 gene, Pendrin gene - negative	Pos
31	Hosp.	M	3	P	P	N	-	N	-	N	nsSNHL	Normal	-	Neg
32	Hosp.	F	8	S	No record	N	-	N	-	N	nsSNHL	NA	-	Pos
33	Hosp.	M	12	P	No record	N	-	N	-	N	nsSNHL	Normal	-	Pos
34	Hosp.	M	7	P	No record	N	-	N	-	N	nsSNHL	Normal	-	Pos
35	Hosp.	M	4	Mo	P	N	-	N	-	N	nsSNHL	NA	-	Pos
36	Hosp.	M	6	P	No record	Y	Grandfather	N	-	N	nsSNHL	Normal	-	Pos
37 [b]	School	F	7	Mo	No record	Y	Mother ID 65, Father ID 66	N	-	N	nsSNHL	NA	-	Pos
38	School	M	8	P	R	N	-	N	-	N	nsSNHL	NA	-	Pos
39 [i]	School	M	15	P	No record	Y	Mother ID 71, Father ID 72	N	-	N	nsSNHL	NA	-	Neg
40 [c]	School	F	16	P	No record	Y	Mother ID 67, Father ID 68, Grandmother	N	blue iris, light/grey colored hair, and skin since birth	N	sSNHL (Tietz albinism)	NA	-	Pos
41	School	F	6	P	No record	N	-	N	Preauricular skin tags on the right (0.5 cm) and left ear (0.3 cm)	N	nsSNHL	NA	-	Neg
42	Hosp.	M	11	S	No record	N	-	N	-	N	nsSNHL	NA	-	Neg
44	School	F	9	MS	No record	N	-	N	-	N	nsSNHL	NA	-	Pos
45	School	F	11	MS	No record	N	-	Unkown	-	N	nsSNHL	NA	-	Neg
46	School	F	16	MS	No record	N	-	N	-	N	nsSNHL	Normal	-	Neg
47	School	F	11	MS	No record	N	-	N	-	N	nsSNHL	Absent/ hypoplastic cochlear	-	Neg
48	School	M	16	MS	No record	Y	Brother	N	-	N	nsSNHL	NA	Normal chromosome	Pos
49	School	M	5	MS	P	N	-	N	-	N	nsSNHL	NA	-	Pos
50	School	F	4	MS	No record	N	-	N	-	N	nsSNHL	Normal	-	Neg
51	School	F	18	P	No record	N	-	N	Cleft palate S/P closure at age 1.5 y, flat malar	N	nsSNHL	NA	-	Neg
52	School	F	13	MS	No record	N	-	N	-	N	nsSNHL	NA	-	Neg

53	School	M	8	MS	No record	N	-	N	Hx GM delay	Y	nsSNHL	NA	-	Neg
54	School	F	9	MS	No record	N	-	N		N	nsSNHL	NA	-	Pos
56	School	M	20	MS	No record	N	-	N	Hx GM delay	Y	nsSNHL	NA	-	Neg
58	School	F	15	MS	No record	N	-	N	Hyperpigmented spot on left leg	N	nsSNHL	NA	-	Pos
59	Hosp.	M	8	P	No record	N	-	N	Hx of GM delay, Blue pigment macule at left buttock, flat foot ± wide base gait	Y	nsSNHL	NA	-	Pos
60	Hosp.	M	17	P	No record	N	-	N		N	nsSNHL	NA	-	Pos
61	School	M	7	MS	No record	N	-	N	Blue iris bilateral, no white forelock	N	sSNHL (Waardenburg)	NA	-	Pos
62	School	F	19	P	R	N	-	N	Pre-auricular skin tag 1 cm at Left ear	N	nsSNHL	Normal	-	Neg
63 [d]	School	F	8	MS	R	Y	Brother, Mother ID 69, Father ID 70	N	-	N	nsSNHL	NA	-	Pos
64	Hosp.	M	5	P	R	N	-	N	Hyperpigmented patch 6 x 4 cm at left side of neck	N	nsSNHL	Normal	-	Neg
65 [b]	School	F	34	SP	No record	Y	Daughter ID 37	N	Goiter S/P thyroidectomy	N	sSNHL (Pendred)	NA	-	Pos
66 [b]	School	M	39	SP	No record	Y	Daughter ID 37	N	-	N	nsSNHL	NA	-	Pos
67 [c]	School	F	43	SP	No record	Y	Daughter ID 40, Sister	N	blue iris, light/grey colored hair, and skin since birth	N	sSNHL (Tietz albinism)	NA	-	Pos
68 [c]	School	M	44	SP	No record	Y	Daughter ID 40	N	-	N	nsSNHL	NA	-	Pos
69 [d]	School	F	37	SP	No record	Y	Daughter ID 63	N	-	N	nsSNHL	NA	-	Pos
70 [d]	School	M	40	SP	No record	Y	Daughter ID 63	N	-	N	nsSNHL	NA	-	Pos
71 [i]	School	F	42	SP	No record	Y	Son ID 39	N	-	N	nsSNHL	NA	-	Neg
72 [i]	School	M	45	SP	No record	Y	Son ID 39	N	-	N	nsSNHL	NA	-	Neg
73	Hosp.	M	14	P	R	N	-	N	-	N	nsSNHL	NA	-	Neg
74	Hosp.	M	6	P	No record	Y	Father	N	-	N	nsSNHL	NA	GJB2 gene-negative	Pos
75	Hosp.	M	0	P	R	N	-	N	-	N	nsSNHL	NA	-	Pos

76 [e]	Hosp.	M	1	P	R	Y	Sister ID 77, Aunt	N	-	N	nsSNHL	NA	-	Pos
77 [e]	Hosp.	F	6	Mo	P	Y	Brother ID 76, Aunt	N	-	N	nsSNHLnsSHL	NA	-	Pos
78	Hosp.	F	1	P	R	N	-	N	-	N	nsSHL	Normal	Normal chromosome	Neg
79	Hosp.	F	1	P	R	N	-	N	-	N	nsSHL	1 ½ turned cochlear with cyst apex (bilateral)		Pos
80	Hosp.	F	4	Mo	R	Y	Father	N	Heterochromia, telecanthus,no white forelock	N	sSNHL (Waardenburg)	NA	PAX3 gene deletion exon 5-8	Neg
81	Hosp.	F	36	P	No record	N	-	N	-	N	nsSNHL	NA	-	Neg
82	Hosp.	M	37	SP	No record	N	-	N	-	N	nsSNHL	NA	-	Pos
83	Hosp.	M	1	S	R	N	-	N	-	N	nsSNHL	NA	-	Pos
84	Hosp.	F	4	SP	No record	N	-	N	-	N	nsSNHL	NA	-	Pos
85	Hosp.	M	14	S	R	N	-	N	-	N	nsSNHL	Absent/ hypoplastic cochlear	GJB2, Pendrin gene - negative	Neg
86	Hosp.	F	3	P	No record	Y	-	N	-	N	nsSNHL	NA	-	Neg
87	Hosp.	F	5	P	No record	N	-	N	Lt eye heterochromia, Hx GM delay	Y	sSNHL (Waardenburg)	Normal	-	Pos
88 [f]	Hosp.	M	10	P	No record	Y	Brother ID 89	N	Hx GM delay	Y	nsSNHL	NA	-	Pos
89 [f]	Hosp.	M	17	S	No record	Y	Brother ID 88	N	Hx GM delay	Y	nsSNHL	NA	-	Pos
90	Hosp.	F	5	Mo	R	N	-	N	light skin, epicanthal fold	N	nsSNHL	NA	Normal chromosome	Pos
91 [j]	Hosp.	M	9	P	No record	Y	Brother 92	N	-	N	nsSNHL	NA	-	Neg
92 [j]	Hosp.	M	5	P	R	Y	Brother 91	N	-	N	nsSNHL	Normal	-	Neg
93	Hosp.	F	11	P	No record	N	-	N	-	N	nsSNHL	NA	-	Neg
94	Hosp.	M	2	S	R	N	-	N	-	N	nsSNHL	NA	-	Neg
95	Hosp.	F	1	Mo	No record	N	-	N	-	N	nsSNHL	NA	-	Neg
96	Hosp.	F	2	S	R	N	-	N	-	N	nsSNHL	NA	-	Neg
97	Hosp.	M	5	P	R	N	-	N	-	N	nsSNHL	Normal	-	Neg
98	Hosp.	F	2	Mo	R	N	-	N	-	N	nsSNHL	Normal	GJB2 gene-negative	Neg

99	Hosp.	M	2	P	R	Y	Brother	Y	-	N	nsSNHL	NA	-	Pos
100	Hosp.	M	0	P	R	Y	Mother	N	Cup-shaped ear, AF 2x2, truncal hypotonia, micrognathia	Y	nsSNHL	Hypoplasia of bilateral internal acoustic canal and semicircular canal; enlarged vestibules; normal cochlear	Normal chromosome; FISH 22q11-no deletion	Pos
101 [k]	Hosp.	M	8	Mo	No record	Y	Brother ID 102	N	-	N	nsSNHL	NA	-	Neg
102 [k]	Hosp.	M	2	P	P	Y	Brother 101	N	-	N	nsSNHL	NA	-	Neg
103	Hosp.	F	6	MS	No record	Y	Mother, Father	unknown	ADHD	N	nsSNHL	NA	GJB2 gene-negative	Pos
104	Hosp.	M	4	S	No record	Y	1 Sister (out of 4 siblings)	N	-	N	nsSNHL	NA	-	Neg
105	Hosp.	F	14	P	No record	N	-	unknown	-	N	nsSNHL	NA	-	Neg
106	Hosp.	F	8	MS	No record	N	-	unknown	-	N	nsSNHL	NA	-	Pos

[a] male twins; of a normal hearing couple; [b] Patient 37 is the child of Patients 65 (mother) and 66 (father); [c] Patient 40 is a daughter of Patients 67 (mother) and 68 (father); [d] Patient 63 is the child of Patients 69 (mother) and 70 (father); [e] Patients 76 and 77 are son and daughter of a normal hearing couple; [f] Patients 88 and 89 are sons of a normal hearing parents; [g] Patients 1 and 2 are daughter of a normal hearing couple; [h] Patients 12 and 20 are daughter and son of a normal hearing couple; [i] Patient 39 is the child of Patients 71 (mother) and 72 (father); [j] Patients 91 and 92 are sons of normal hearing parents; [k] Patients 101 and 102 are sons of normal hearing parents.

CT/MRI, computed tomography and/or magnetic resonance imaging of temporal bone or inner ear; DD, developmental delay; EVA, enlarged vestibular aqueduct; F, female; Fam.Hx,, family history of hearing loss; Hosp.,Ramathibodi Hospital; Hx of GM delay, history of gross motor delay; M, male; Mo, moderate; MS, moderate-to-severe; N, no; NA, not available or not done; Neg, negative; nsSHL, non-syndromic sensorineural hearing loss; OAEs, otoacoustic emission hearing screening; P, profound; Pos, positive; S, severe; SP, severe-to-profound; sSHL, syndromic sensorineural hearing loss; WES, whole exome sequencing; Y, yes

Table S3. Detailed genetic variants identified in each 46 individual patients

Patient ID	Gene; Ref sequence	Variant 1						Variant 2					
		Nucleotide; Protein	ACMG	Score	Clinvar Accession	GenomAD	ThaiGeR	Nucleotide	ACMG	Score	Clinvar Accession	GenomAD	ThaiGeR
10 [a]	MYO7A; NM_000260.4	c.1915A>G; p.Asn639Asp	VUS	PM2, PP3	N/A	N/A	N/A	c.6051+2T>C; Splicing defect	VUS	PVS1, PM2, PP5	RCV001955084	1/31394	N/A
11 [a]	MYO7A; NM_000260.4	c.1915A>G; p.Asn639Asp	VUS	PM2, PP3	N/A	N/A	N/A	c.6051+2T>C; Splicing defect	VUS	PVS1, PM2, PP5	RCV001955084	1/31394	N/A
13	SLC26A4; NM_000441.2	c.706C>G; p.Leu236Val	P	PM1, PM2, PM3, PM5, PP1, PP2	RCV000411990.5	12/251474	1/ 2184	c.706C>G; p.Leu236Val	P	PM1, PM2, PM3, PM5, PP1, PP2	RCV000411990.5	12/251474	1/ 2184
15	SLC26A4; NM_000441.2	c.349del; p.Leu117SerfsTer9	P	PVS1, PM2, PM3	RCV000667022	1/31318	N/A	c.1229C>T; p.Thr410Met	P	PS3, PM1, PM2, PM3, PM5, PP2, PP3	RCV000576483	48/282236	3/2184
16	SLC26A4; NM_000441.2	c.290T>A; p.Val97Glu	P	PM1, PM2, PM3, PP2, PP3	RCV003037251	N/A	N/A	c.1708G>T; p.Val570Phe	LP	PM2, PM5, PP2, PP3	N/A	N/A	N/A
27	GJB2; NM_004004.6	c.71G>A; p.Trp24Ter	P	PVS1, PS4, PM2	RCV000211778	147/281436	2/2184	c.235del; p.Leu79CysfsTer3	P	PVS1, PS3, PM2,PM3, PP1	RCV000211768	134/282792	N/A
30	MYO15A; NM_016239.4	c.5964+3G>A; splicing defect	LP	PS4_Mo, PM2	RCV000224977	5/174324	N/A	c.6371G>A; p.Arg2124Gln	LP	PM1, PM2, PM3, PP3	RCV002491675	2/280080	N/A
32	SLC26A4; NM_000441.2	c.1547dup; p.Ser517PhefsTer10	P	PVS1, PM2, PM3	RCV000169076	5/251180	3/2184	c.1547dup; p.Ser517PhefsTer10	P	PVS1, PM2, PM3	RCV000169076	5/251180	3/2184
33	TMPRSS3; NM_001256317.3	c.572+2T>G; splicing defect	LP	PVS1, PM2, PP3	N/A	N/A	N/A	c.1193G>A; p.Gly398Glu	VUS	PM2, PP2, PP3	N/A	1/251186	N/A
34	PCDH15; NM_001384140.1	c.981del; p.Val328LeufsTer26	LP	PVS1, PM2	-	N/A	N/A	NA (another unidentified variant)					
35	OTOF; NM_194248.3	c.1273C>T; p.Arg425Ter	P	PVS1, PM2, PP5	VCV000065776.5	3/282132	N/A	c.1273C>T; p.Arg425Ter	P	PVS1, PM2, PP5	VCV000065776.5	3/282132	N/A
36	POU3F4; NM_000307.5	c.688dup; p.Thr230AsnfsTer41	LP	PVS1, PM2, PP3	N/A	N/A	N/A	NA (XR inheritance)					
37 [b]	SLC26A4; NM_000441.2	c.919-2A>G; splicing defect	P	PVS1, PM2, PM3, PP1	VCV000004840.52	103/282410	40/29404	c.1971C>A; p.Ser657Arg	LP	PM1, PM2, PM3, PP2, PP3	-	N/A	N/A
38	PCDH15; NM_001384140.1	c.299del; p.Gly100GlufsTer10	P	PVS1, PM2, PP5	VCV000550507.1	N/A	N/A	c.1997+1G>A; Splicing defect	P	PVS1, PM2, PM3	VCV000379720.11 (P, LP)	2/250238	N/A
40 [c]	MITF; NM_001354604.2	c.971G>A; p.Arg324Lys	P	PM1, PM2,PM5, PP3	-	N/A	N/A	NA (AD inheritance)					
	GSDME;	c.781C>T; p.Arg261Ter	P	PVS1, PM2, PP5	RCV002221705.2	12/251492	N/A	NA (AD inheritance)					

	NM_001127453.2													
44	ACTG1; NM_001614.5	c.547C>T; p.Arg183Trp	LP	PM1, PM2, PM5, PP2, PP3, PP5	VCV000808333.30	N/A	N/A	NA (AD inheritance)						
48	GJB2; NM_004004.6	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	
49	OTOF; NM_194248.3	c.1046-1G>C; splicing defect	LP	PVS1, PM2	-	N/A	N/A	c.5567G>A; p.Arg1856Gln	P	PM2, PM3, PM5, PP3	VCV000065811.6 (P, LP)	2/250872	N/A	
54	GJB2; NM_004004.6	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	
58	GJB2	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	
59	PTEN; NM_000314.8	c.19G>T; p.Glu7Ter	P	PVS1, PS4, PM2	VCV000493079.29	N/A	N/A	NA (AD inheritance)						
60	GJB2; NM_004004.6	c.35del; p.Gly12ValfsTer2	P	PVS1, PS3, PM2, PP5	VCV000017004.130	1737/280696	N/A	c.235del; p.Lys79CysfsTer3	P	PVS1, PS3, PM2,PM3, PP1	VCV000017014.57	134/282792	89/29398	
61	SOX10; NM_006941.4	c.448A>G; p.Lys150Glu	P	PS2, PM2, PM5,PP3, PP5	RCV001729954.10	N/A	N/A	NA (AD inheritance)						
63 [d]	MYO15A; NM_016239.4	c.5603G>A; p.Arg1868His	VUS	PM2	RCV000339103.6	26/280918	464/29402	c.6728C>T; p.Thr2243Met	VUS	PM2, PP3	RCV000505627.2	11/188116	1/11312	
65 [b]	SLC26A4; NM_000441.2	c.1150-1G>A; splicing defect	P	PVS1, PM2, PM3	RCV000473991.2	N/A	N/A	c.1971C>A; p.Ser657Arg	LP	PM1, PM2, PM3, PP2, PP3	-	N/A	N/A	
66[b]	SLC26A4; NM_000441.2	c.919-2A>G; splicing defect	P	PVS1, PM2, PM3, PP1	VCV000004840.52	103/282410	40/29404	c.1716C>T p.Phe572Leu	LP	PM1, PM2, PM3, PP2, PP3	RCV002051741.1, RCV004770190.1	N/A	N/A	
67 [c]	MITF; NM_001354604.2	c.971G>A; p.Arg324Lys	LP	PM1, PM2,PM5, PP3	-	N/A	N/A	NA (AD inheritance)						
68 [c]	GSDME; NM_001127453.2	c.781C>T; p.Arg261Ter	P	PVS1, PM2, PP5	RCV002221705.2	12/251492	N/A	NA (AD inheritance)						
69 [d]	MYO15A	c.5603G>A; p.Arg1868His	LP	PM2	RCV000339103.6	26/280918	464/29402	NA (another unidentified variant)						
70 [d]	MYO15A	c.6728C>T; p.Thr2243Met	LP	PM2, PP3	RCV000505627.2	11/188116	1/11312	NA (another unidentified variant)						
74	SLC26A4; NM_000441.2	c.754T>C; p.Ser252Pro	P	PM1, PM2, PM3, PP2, PP3	VCV001065210.8	1/251,316	29/29,358	c.1229C>T; p.Thr410Met	P	PS3, PM1, PM2, PM3, PP1, PP2, PP3	VCV000043498.44	48/282,236	9/29,402	

75	MYO7A; NM_000260.4	c.2904G>A; p.Glu968Glu	LP	PS4, PM2, PP3	VCV000228280.8	N/A	2/17,520	c.3576G>A; p.Trp1192Ter	P	PVS1, PS4, PM2	VCV000550723.7 (P/LP)	N/A	2/18,064
76 [e]	MYO15A; NM_016239.4	c.3385C>T; p.Arg1129Ter	P	PVS1, PM2, PM3, PP5	RCV001824841.5	66/1613028	2/29392	c.3525dup; p.Ser1176ValfsTer14	LP	PVS1,PM2	-	N/A	N/A
77 [e]	MYO15A; NM_016239.4	c.3385C>T; p.Arg1129Ter	P	PVS1, PM2, PM3, PP5	RCV001824841.5	66/1613028	2/29392	c.3525dup; p.Ser1176ValfsTer14	LP	PVS1,PM2	-	N/A	N/A
79	SLC26A4; NM_000441.2	c.2162C>T; p.Thr721Met	P	PS3, PM1, PM2, PM3, PM5, PP1, PP2, PP3, PP5	VCV000004826.25	28/1607208	N/A	c.2162C>T; p.Thr721Met	P	PS3, PM1, PM2, PM3, PM5, PP1, PP2, PP3, PP5	VCV000004826.25	28/1607208	N/A
82	GJB2; NM_004004.6	c.235del; p.Leu79CysfsTer3	P	PVS1, PS3, PM2,PM3, PP1	RCV000211768	134/282792	N/A	c.235del; p.Leu79CysfsTer3	P	PVS1, PS3, PM2,PM3, PP1	RCV000211768	134/282792	N/A
83	GJB2; NM_004004.6	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402
84	GJB2; NM_004004.6	c.235del; p.Leu79CysfsTer3	P	PVS1, PS3, PM2,PM3, PP1	RCV000211768	134/282792	N/A	c.299_300del; p.His100ArgfsTer14	P	PVS1, PS3, PM2,PM3, PP5	VCV000044736.41	47/1613906	7/29402
87	PAX3; NM_181459.4	c.321+2T>C; splicing defect	LP	PVS1, PM2	-	N/A	N/A	NA (AD inheritance)					
88 [f]	POU3F4; NM_000307.5	c.731dup; p.Asn244LysfsTer27	LP	PVS1, PM2	-	N/A	N/A	NA (XR inheritance)					
89 [f]	POU3F4; NM_000307.5	c.731dup; p.Asn244LysfsTer27	LP	PVS1, PM2	-	N/A	N/A	NA (XR inheritance)					
90	MPZL2; NM_005797.3	c.220C>T; p.Gln74Ter	P	PVS1, PM2,PP5	VCV000585269.9	255/1613904	26/29400	c.220C>T; p.Gln74Ter	P	PVS1, PM2,PP5	VCV000585269.9	255/1613904	26/29400
99	SLC26A4; NM_000441.2	c.290T>A; p.Val97Glu	P	PM1, PM2, PM3, PP2, PP3, PP5		N/A	N/A	c.290T>A; p.Val97Gln	P	PM1, PM2, PM3, PP2, PP3, PP5		N/A	N/A
100	GJB2; NM_004004.6	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402
103	MITF	c.1209G>A; pThr404Thr	LP	PS4, PM2, PP1	RCV001290159.2	N/A	N/A	NA (another unidentified variant)					
106	GJB2	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402	c.109G>A; p.Val37Ile	P	PS4, PM1, PM3, PM5, PP1, PP3	RCV000211759	2132/282164	2784/29402

LP, likely pathogenic; N/A, not available; P, pathogenic; ThaiGeR, Thai Genome Reference Database; VUS, variant of unknown significance

Table S4. Clinical history suggesting acquired hearing loss

• gestational age 24-31 weeks
• birth weight <1500 gm
• low APGAR scores at 5 minutes
• congenital infection
• hyperbilirubinemia requiring exchange transfusion
• admission in NICU >12 days
• prolonged use of high-frequency mechanical ventilation >10 days
• on extracorporeal membrane oxygenation (ECMO)
• infantile exposure to ototoxic medication e.g., aminoglycosides, furosemide, and chemotherapy
• history of meningitis
• head trauma especially temporal bone
• maternal history of perinatal treatment with ototoxic drugs, such as aminoglycosides and quinine