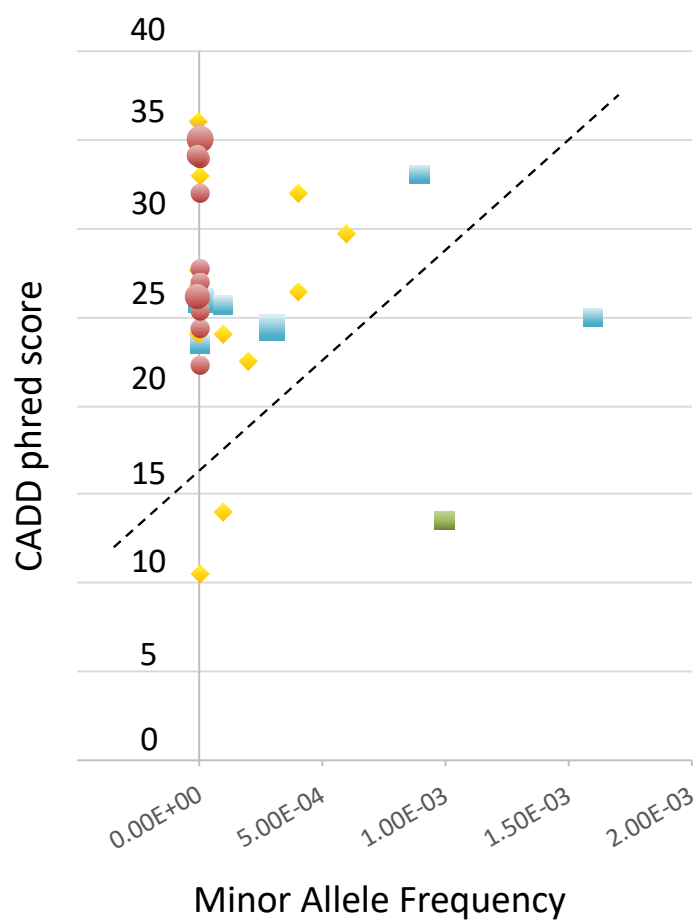1

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Figure S1. Scatter plot of each identified variant's CADD score and higher MAF values in ToMMo 3.5kJPN or
ExAC0.3. The color of each point corresponds to the interpretation based on the ACMG criteria in Table1. Red
indicates likely pathogenic variants. Yellow indicates candidate variants classified as VUS identified in this
study. Blue indicates the VUS variants we removed from the analysis. Green indicates a likely benign variant.
The dotted-line separates two groups; the putative benign variants with a high MAF and/or low CADD score,
and the candidate variants with a low MAF and/or high CADD score.

Table S1. The 68 target genes for hearing loss.

Number	Locus Symbol	Gene Symbol	Gene ID	Transcript Variant
1	DFNA1	*DIAPH1*	NM_005219	NM_001079812
2	DFNA2	*KCNQ4*	NM_004700	NM_172163
3	DFNA2	*GJB3*	NM_024009	NM_001005752
4	DFNA3	*GJB6*	NM_006783	NM_001110219
				NM_001110220
				NM_001110221
5	DFNA4	*MYH14*	NM_024729	NM_001145809.
				NM_001077186
6	DFNA5	*DFNA5*	NM_004403	NM_001127454
				NM_001127453
7	DFNA6/14/38	*WFS1*	NM_006005	NM_001145853
8	DFNA8/12/DFNB21	*TECTA*	NM_005422	-
9	DFNA9/31	*COCH*	NM_004086	NM_001135058
10	DFNA10	*EYA4*	NM_004100	NM_172103
				NM_172105
11	DFNA11/DFNB2/USH1B	*MYO7A*	NM_000260	NM_001127179
				NM_001127180
12	DFNA13/DFNB53/STL3	*COL11A2*	NM_080680	NM_080679
				NM_080681
				NM_001163771
13	DFNA15	*POU4F3*	NM_002700	-
14	DFNA17	*MYH9*	NM_002473	-
15	DFNA20/DFNA26	*ACTG1*	NM_001614	NM_001199954
16	DFNA22/DFNB37	*MYO6*	NM_004999	-
17	DFNA25	*SLC17A8*	NM_139319	NM_001145288
18	DFNA28	*GRHL2*	NM_024915	-
19	DFNA36/DFNB7/11	*TMC1*	NM_138691	-
20	DFNA40	*CRYM*	NM_001888	NM_001014444
21	DFNA44	*CCDC50*	NM_178335	NM_174908
22	DFNA48	*MYO1A*	NM_005379	-

23	DFNA50	*MIRN96*		
24	DFNA51	*TJP2*	NM_001170414	NM_004817
				NM_201629
				NM_001170630
				NM_001170415
				NM_001170416
25	DFNA64	*DIABLO*	NM_019887	NM_138929
26		*CEACAM16*	NM_001039213	-
27	DFNB1/DFNA3	*GJB2*	NM_004004	-
28	DFNB3	*MYO15A*	NM_016239	-
29	DFNB4/Pendred	*SLC26A4*	NM_000441	-
30	DFNB6	*TMIE*	NM_147196	-
31	DFNB8/10	*TMPRSS3*	NM_024022	NM_032405
32	DFNB9	*OTOF*	NM_194248	NM_194322
				NM_194323
				NM_004802
33	DFNB12/USH1D	*CDH23*	NM_022124	NM_001171930
				NM_001171931
				NM_001171932
				NM_001171933
				NM_001171934
				NM_001171936
				NM_052836
34	DFNB15/72/95	*GIPC3*	NM_133261	-
35	DFNB16	*STRC*	NM_153700	-
36	DFNB18/USH1C	*USH1C*	NM_153676	NM_005709
37	DFNB22	*OTOA*	NM_144672	NM_001161683
				NM_170664
38	DFNB23/USH1F	*PCDH15*	NM_033056	NM_001142763
				NM_001142764
				NM_001142765
				NM_001142766

				NM_001142767
				NM_001142769
				NM_001142770
				NM_001142771
				NM_001142772
				NM_001142773
39	DFNB24	*RDX*	NM_002906	-
40	DFNB25	*GRXCR1*	NM_001080476	-
41	DFNB28	*TRIOBP*	NM_007032	NM_138632
				NM_001039141
42	DFNB29	*CLDN14*	NM_144492	NM_001146077
				NM_001146078
				NM_001146079
				NM_012130
43	DFNB30	*MYO3A*	NM_017433	-
44	DFNB31/USH2D	*WHRN*	NM_015404	NM_001083885
				NM_001173425
45	DFNB35	*ESRRB*	NM_004452	-
46	DFNB36	*ESPN*	NM_031475	-
47	DFNB39	*HGF*	NM_000601	NM_001010931
				NM_001010932
				NM_001010933
				NM_001010934
48	DFNB42	*ILDR1*	NM_001199799	NM_001199800
				NM_175924
49	DFNB48	*CIB2*	NM_006383	NM_001271888
				NM_001271889
50	DFNB49	*MARVELD2*	NM_001038603	NM_001244734
51	DFNB59	*DFNB59*	NM_001042702	-
52	DFNB61	*SLC26A5*	NM_206883	NM_001167962

				NM_206884
				NM_206885
				NM_198999
53	DFNB63	*LRTOMT*	NM_001145307	NM_001145308
				NM_001205138
				NM_145309
54	DFNB66/67	*LHFPL5*	NM_182548	-
55	DFNB70	*PNPT1*	NM_033109	-
56	DFNB74	*MSRB3*	NM_198080	NM_001031679
				NM_001193460
				NM_001193461
57	DFNB77	*LOXHD1*	NM_144612	NM_001173129
				NM_001145472
				NM_001145473
58	DFNB79	*TPRN*	NM_001128228	-
59	DFNB82	*GPSM2*	NM_013296	-
60	DFNB84	*PTPRQ*	NM_001145026	-
61	DFNB89	*KARS*	NM_005548	NM_001130089
62	DFNB91	*SERPINB6*	NM_004568	NM_001195291
63	DFNB93	*CABP2*	NM_016366	-
64	USH2A	*USH2A*	NM_007123	NM_206933
65	DFNX1	*PRPS1*	NM_002764	NM_001204402
66	DFNX2	*POU3F4*	NM_000307	-
67	DFNX4	*SMPX*	NM_014332	-
68	DFNX6	*COL4A6*	NM_001847	NM_033641