Genetic Variation in *POU4F3* and *GRHL2* Associated with Noise-Induced Hearing Loss in Chinese Population: A Case-Control Study

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Table S1. Demographic and general characteristics of case and control subjects.

Variables	Case (*n* = 239)	Control (*n* = 239)	*p*
Age (yr), mean ± SD	40.4 ± 8.3	39.5 ± 8.2	0.264
Tenure (yr), mean ± SD	18.7 ± 9.2	18.1 ± 8.9	0.447
HL (dB), mean ± SD	51.4 ± 8.8	9.3 ± 9.1	**<0.001**
Height (cm),mean ± SD	171.2 ± 5.5	170.1 ± 5.4	**0.026**
Hypertension, n (%)			
yes	107 (44.8)	100 (41.8)	0.518
no	132 (55.2)	139 (58.2)	
Smoking, n (%)			
yes	161 (67.4)	118 (49.4)	**<0.001**
no	78 (32.6)	121 (50.6)	
Drinking (Alcohol), n (%)			
yes	170 (71.1)	166 (69.5)	0.689
no	69 (28.9)	73 (30.5)	
Protector (Eaeplug), n (%)			
yes	125 (52.3)	118 (49.4)	0.522
no	114 (47.7)	121 (50.6)	
Noise intensity exposure, dB(A)	86.1 ± 3.9	86.1 ± 3.9	0.930
CNE, dB(A)	98.2 ± 4.6	98.1 ± 4.5	0.856

Notes: HL: hearing level; CNE: cumulative noise exposure.

Table S2. Associations of candidate SNPs with the risk of NIHL.

Genes	SNPs	Genotypes	Case (*n* = 239)		Control (*n* = 239)		Adjusted *OR* (95% *CI*) *	*p* *
			N	%	N	%		
POU4F3	rs1368402	CC	12	5.0	14	5.9	1.00	
		CA	75	31.4	82	34.3	0.87 (0.37–2.07)	0.756
		AA	150	62.8	141	59.0	1.13 (0.49–2.57)	0.780
		CA/AA	225	94.1	223	93.3	1.13 (0.51–2.51)	0.762
		CC/CA/AA						0.304
	rs891969	AA	12	5.0	14	5.9	1.00	
		GA	74	31.0	81	33.9	0.91 (0.39–2.15)	0.837
		GG	153	64.0	142	59.4	1.14 (0.50–2.60)	0.759
		GA/GG	227	95.0	223	93.3	1.06 (0.47–2.38)	0.895
		AA/GA/GG						0.354
GRHL2	rs611419	AA	56	23.4	47	19.7	1.00	
		AT	101	42.3	108	45.2	0.77 (0.47–1.26)	0.301

Table S2. *Cont.*

Genes	SNPs	Genotypes	Case (n = 239)		Control (n = 239)		Adjusted *OR* (95% *CI*) *	p *
			N	%	N	%		
		TT	79	33.1	81	33.9	0.77 (0.46–1.31)	0.336
		AT/TT	180	75.3	189	79.1	0.77 (0.49–1.22)	0.265
		AA/AT/TT						0.365
	rs10955255	GG	14	5.9	14	5.9	1.00	
		AG	87	36.4	90	37.7	1.10 (0.48–2.53)	0.822
		AA	139	58.2	135	56.5	1.22 (0.55–2.71)	0.627
		AG/AA	226	94.6	225	94.1	1.18 (0.54–2.58)	0.684
		GG/AG/AA						0.524
	rs1981361	TT	20	8.4	16	6.7	1.00	
		CT	79	33.1	109	45.6	0.63 (0.30–1.34)	0.231
		CC	136	56.9	112	46.9	1.09 (0.53–2.24)	0.811
		CT/CC	215	90.0	221	92.5	0.90 (0.45–1.82)	0.774
		TT/CT/CC					1.30 (0.97–1.74)	0.085
	rs3779617	AA	0	0.0	6	2.5	1.00	
		GA	42	17.6	38	15.9	–	0.812
		GG	195	81.6	195	81.6	–	0.812
		GA/GG	237	99.2	233	97.5	–	0.976
		AA/GA/GG						0.324
	rs3735713	AA	19	7.9	14	5.9	1.00	
		GA	96	40.2	104	43.5	0.62 (0.27–1.44)	0.268
		GG	121	50.6	118	49.4	0.64 (0.27–1.52)	0.312
		GA/GG	217	90.8	222	92.9	0.64 (0.28–1.44)	0.273
		AA/GA/GG						0.645
	rs3824090	TT	6	2.5	5	2.1	1.00	
		CT	79	33.1	86	36.0	0.67 (0.17–2.66)	0.568
		CC	151	63.2	145	60.7	0.77 (0.20–3.03)	0.707
		CT/CC	230	96.2	231	96.7	0.73 (0.19–2.81)	0.642
		TT/CT/CC						0.684
	rs3735714	TT	28	11.7	24	10.0	1.00	
		CT	111	46.4	124	51.9	0.75 (0.39–1.44)	0.389
		CC	100	41.8	91	38.1	0.92 (0.47–1.80)	0.799
		CT/CC	211	88.3	215	90.0	0.81 (0.43–1.53)	0.521
		TT/TC/CC						0.769
	rs3735715	AA	52	21.8	49	20.5	1.00	
		GA	104	43.5	130	54.4	0.78 (0.49–1.25)	0.304
		GG	80	33.5	56	23.4	1.23 (0.73–2.09)	0.443
		GA/GG	184	77.0	186	77.8	0.91 (0.58–1.48)	0.678
		GG/GA/AA						0.265

Note: * Adjusted for smoking, drinking and CNE.

Table S3. Linkage disequilibrium test of GRHL2 gene.

SNPs	rs611419	rs10955255	rs1981361	rs3779617	rs3735713	rs3824090	rs3735714	rs3735715
rs611419	–	0.033	0.139	0.177	0.016	0.095	0.023	0.015
rs10955255	0.000	–	0.792	0.009	0.332	0.262	0.375	0.198
rs1981361	0.006	0.525	–	0.039	0.214	0.098	0.193	0.070
rs3779617	0.003	0.000	0.000	–	0.398	0.58	0.493	0.420
rs3735713	0.000	0.014	0.007	0.007	–	1.000	1.000	0.989
rs3824090	0.002	0.005	0.001	0.009	0.630	–	1.000	0.981
rs3735714	0.000	0.025	0.008	0.014	0.713	0.449	–	0.992
rs3735715	0.000	0.014	0.002	0.022	0.331	0.205	0.466	–

Notes: The upper triangle was D′ value and the lower triangle was r^2 value.