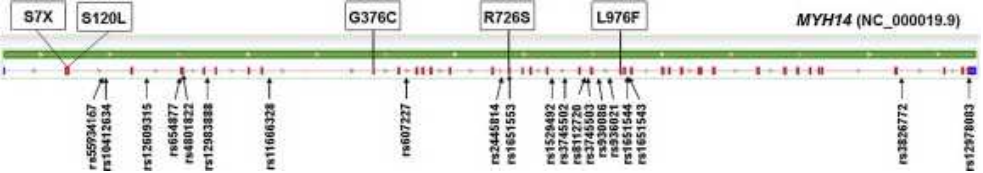


Type of file: figure

Label: Fig. S1

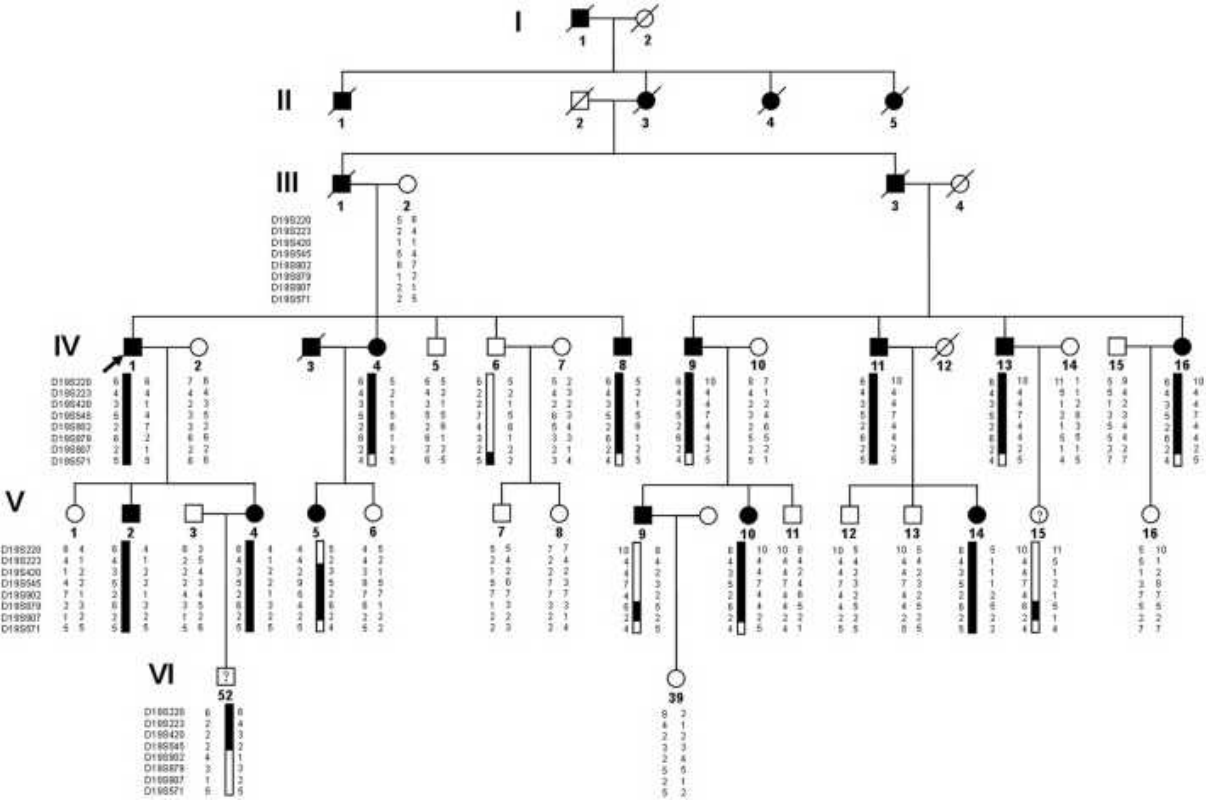
Filename: figs1.jpg



Type of file: figure

Label: Fig. S12

Filename: figs2.jpg



Type of file: table

Label: Table S1

Filename: mmc2.doc

Table S1. Summary of clinical data for hearing impaired members in family Z002

Subject	Sex	Age of test (year)	Age of onset (year)	PTA (dB HL)^a	Hearing impairment	Audiogram
IV:1	M	61	27	92.5	profound	downslope
IV:13	M	42	23	80.0	severe	flat
IV:8	M	50	25	76.3	severe	downslope
IV:9	M	52	20	72.5	severe	flat
IV:16	F	43	20	72.5	severe	flat
IV:11	M	47	40	58.8	moderate	downslope
IV:4	F	48	22	30.0	mild	downslope
V:9	M	30	23	76.3	severe	flat
V:4	F	29	24	56.3	moderate	downslope
V:10	F	26	20	35.0	mild	downslope
V:2	M	26	24	28.8	mild (2-8kHz)	flat
V:5	F	24	24 ^b	26.3	mild (2-8kHz)	downslope
V:14	F	25	25 ^b	25.5	mild	flat

^a PTA, pure-tone air-conduction averages (0.5, 1, 2 and 4 kHz) for the better-hearing ear of affected subjects in family Z002.

^b Diagnosed at the time of test.

Type of file: table

Label: Table S2

Filename: mmc3.doc

Table S2. Two-point LOD scores between 19q microsatellite markers for family Z002

Markers	Genetic distance (cM)	LOD score at $\theta=?$							
		0.00	0.01	0.05	0.1	0.2	0.3	0.4	0.5
D19S220	62.03	-infini	1.01	1.50	1.54	1.31	0.92	0.47	0.00
D19S223	64.16	-infini	1.20	1.19	1.10	0.83	0.49	0.16	0.00
D19S420	66.30	3.03	4.88	4.52	3.13	2.48	1.65	0.72	0.00
D19S545	71.46	-0.21	4.77	4.42	3.04	2.40	1.56	0.63	0.00
D19S902	72.72	3.54	2.94	2.69	2.36	1.69	1.00	0.38	0.00
D19S879	75.41	5.30	5.17	4.80	4.36	3.33	2.22	1.02	0.00
D19S907	78.08	1.16	1.13	1.04	0.93	0.70	0.47	0.23	0.00
D19S571	84.08	-infini	-4.80	-2.14	-0.50	-0.03	0.11	0.11	0.00

Type of file: table

Label: Table S3

Filename: mmc4.doc

Table S3. SNPs identified in candidate genes of family Z002 (partial results shown)

Candidate gene	SNP Site in mRNA	Nucleotide position*	dbSNP(rs#)
<i>CEACAM16</i>	1421C>T(p.T405T)	9516	rs61744497
<i>KCNA7</i>	922C>G(P189P)	2674	rs1611775
	2035G>A	3787(3'UTR)	rs3810186
	2500G>A	4252(3'UTR)	rs4802547
	3090T>C	4842(3'UTR)	rs11673003
	3495G>A	5247(3'UTR)	rs35203905
	4361G>A	6113(3'UTR)	rs4802546
<i>KPTN</i>	942C>T(P302P)	7924	rs2293424
<i>ERCC1</i>	IVS1-114G>T	851	rs3212924
	524T>C(N59N)	4125	rs17359303
	IVS4+86G>A	4282	rs3212955
	IVS5+33C>A	5455	rs3212961
	IVS9-110A>G	14685	rs1007616

*The position is relative to the gene sequence.

Type of file: table

Label: Table S4

Filename: mmc5.doc

**Table S4. PCR primer pairs for candidate genes screening
(partial results shown)**

Candidate gene	Screened region	Forward primer (5'-3')	Reverse primer (5'-3')	PCR products size (bp)
<i>CEACAM16</i>	Exon1	aaatggcaaatccccttct	ggcacctgtaatcccagcta	497
	Exon2	ctcgatccctccaaattcag	tgctcacaccttcctctct	284
	Exon3	cccgagcctgagtctctct	ttgagaaggagatgggaagg	487
	Exon4	caagatggcctccaggatta	catccatgaggttggacact	499
	Exon5	ctccactcctcctcctct	cttaaccttcgcagcctgat	399
	Exon6	gacaccatgccagatgcag	agcctgatggaggaagcaa	462
	Exon7	cctggtcctccatctctctg	gtgcacaccagactgagaa	385
<i>KCNN4</i>	Exon1	gggatactgcctgcttgcta	cagaccaagagtctgacc	794
	Exon2	tctcagaaccgacacatca	tcagatcaggaggaggagga	349
	Exon3	ggcacaccccacttatctca	gttctctcaccacagttga	712
	Exon4	gatgggagggtataga	gagaatggggctctgg	378
	Exon5、6	aactggggatggctc	gatccaggtgaga	646
	Exon7	ctctttcagctcttcg	gatctgtgccttcat	411
	Exon8	agtggtaggtggtaaa	gccacatagggtgctg	403
	Exon9	ttgtctggctgtccat	gtctgccagttaggag	794
<i>KCNA7</i>	Exon1-1	atgcttcccactgggtgtctc	ggcctcactctgtttccag	445
	Exon1-2	cctcagttccccgtctgta	agaccatctggctaacacg	550
	Exon1-3	aggttcatgccattctctg	gattgaggccaggagtcaa	558
	Exon1-4	gagtgacagtggtgcaatcat	cactcccattctcccetaca	553
	Exon1-5	tctctcccttgggtctctg	ctcataggccatgctgaat	543
	Exon1-6	tacatgatgcttcccactg	ggccatgtgggtcaagtta	547
	Exon1-7	gcccacagaaccctacaag	acgagtggggaacactgag	553
	Exon1-8	aaggctccatgagctttgc	gggtgactcccatttact	641
	Exon1-9	ctggcagggaaatagtcagc	tctgggataaccaggtcacg	758
	Exon2-1	gccttatgattggccaggt	cttcccggacactctgcta	541
	Exon2-2	tagaaggccacctctccag	tgaagcctgattctgacgaa	677
	Exon2-3	ctagcagagtgtccgggaag	tgaagcctgattctgacgaa	508
<i>KPTN</i>	Exon1	ccttggtccagaaatggaaa	cagtgacccccctaaaacca	589
	Exon2	tgagcctagggttcaggatt	ggctcagtggaactcacat	340

Exon3、 4	gtacctagagccccctccac	ttccagaaggggaaacaga	451
Exon5、 6	ccctgggtctagtgtctgga	gagggtgagtcacctctt	588
Exon7	atccaggaggaatcaagcag	cctcatcctcaaccact	358
Exon8	ggaaagtcgatggttcagg	ggatccaggagagaggact	288
Exon9	gtagaggcggggtttatca	tccagctctgggtaatcac	302
Exon10、 11	acccttgctgggtctatg	aggaactgcctcctgaaat	694
Exon12	aattcgcttaagccactcc	tgggttctaccctgggatct	766