

**Supplemental Data**

**Noncoding Mutations of *HGF* Are Associated**

**with Nonsyndromic Hearing Loss, DFNB39**

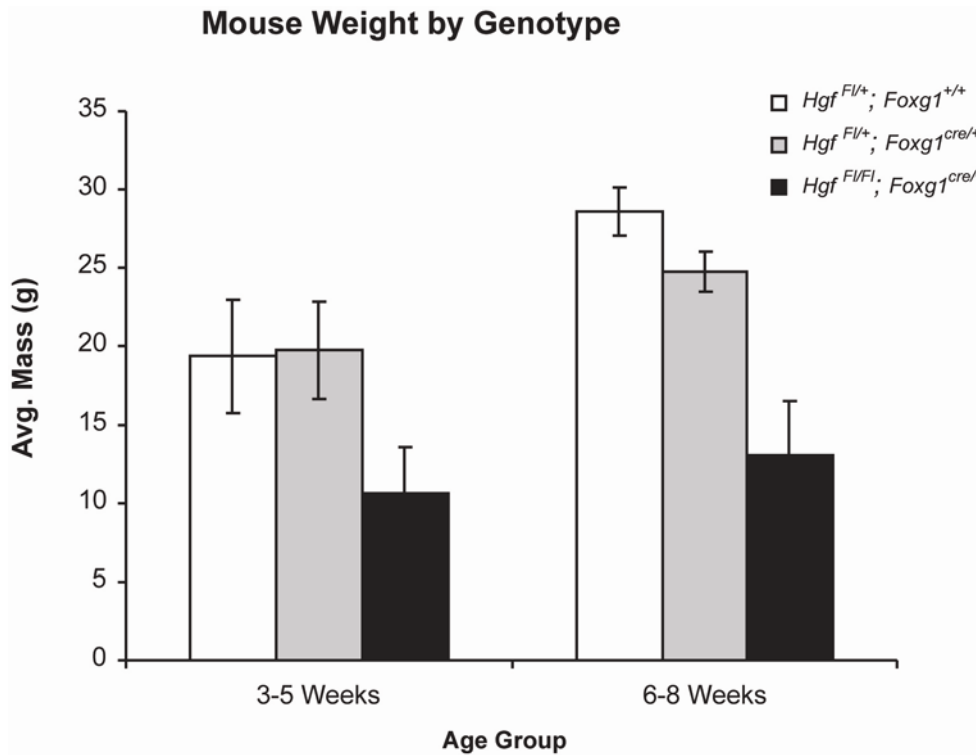
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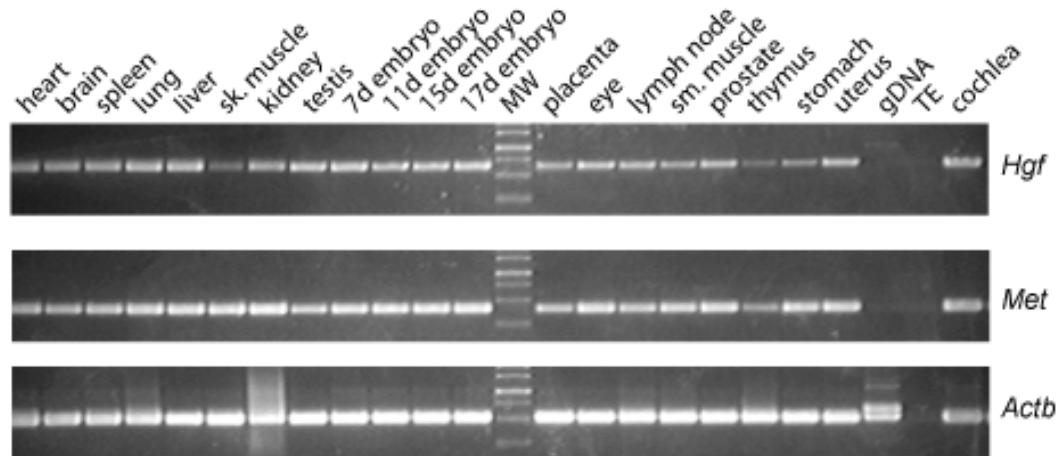
**Figure S1. Pedigrees of 36 Families Cosegregating Profound Deafness and c.482+1986\_1988delTGA within Intron 4 of *HGF***

Filled symbols represent individuals with prelingual, severe to profound, hearing loss. Asterisks indicate subjects enrolled in the protocol who contributed DNA samples. The pedigree for family DEM4011 was reported.<sup>16</sup> The exact relationship between families DEM4333A and DEM4333B was not determined at the time of family history interview.



**Figure S2. Differences in Weights of *Hgf* Conditional Knockout Mice and Littermate Controls Weighed before ABR Testing**

Conditional knockout mice were significantly smaller than littermate controls. Vertical bars indicate standard deviations.



**Figure S3. RT-PCR of *Hgf* and *Met* from Mouse cDNAs**

Mouse MTC panels I and III (Clontech) and cDNA from mouse cochlea were amplified with PCR primers for *Hgf* (forward 5'-cgacaaggcttgatgataa-3', reverse 5'-aggcaataatccaaggaa-3'), *Met* (forward 5'-tgcaaggttgctgattcg-3', reverse 5'-ggacgtagtgtcccaatg-3') and *Actb* (forward 5'-agtgtgacgttgacatccgta-3', reverse 5'-gttgctccaaccaactgct-3'). Mouse genomic DNA and TE are included as controls. *Hgf* and *Met* are ubiquitously expressed in all mesenchymal and epithelial tissues, respectively.

**Table S1. Primer Sequences Used to Amplify and Sequence *HGF* Genomic DNA**

Exon	Forward Primer	Reverse Primer	Product (bp) <sup>a</sup>
1	gttcagggatctgtttggt	gaggggagttgagggaaagt	582
2	gctcctaaccctggaaatc	ggtagcagttttgcgctct	508
3	tgcattgtttctatattgtcca	gagggaggaagggaaatcaag	461
4	acagcgactgctctctgga	aaacctgccgtaatacaattca	502
IVS4	gatgtttatggccgagagga	ggctttaagagagacaagtgagg	500
5	tcagcaaattcacaggctca	tagttgcattgcacgaaca	517
6	gcgctcgtggcctatagtaa	ccctgctgatgattttgtgtt	669
7	actcgattggaacctcagc	tccaaaaatgcaaagattgg	555
A (7b)	tgtgcagcatcacaaagtca	gccctgtattcaaagaatgaaa	471
8	tgaatgaaaggaaaattggaatg	ttgaggaccaaaccaga	558
9	aggccaatgtttgaaatgg	caaaaccagtgagcaagaa	580
10	tctcgatcctctgacctcgt	cttgagggttgaacaaaa	600
11	atctttgccatctgcttgc	ttgggaataaatgccagacc	583
12	aagtagctgggtgtggtggt	gcattgtgccccaaattaa	622
13	tgaggggtggtgagggattag	gggtacaacctcaggacca	514
14	gtgtgttcgggatggctatt	gcaaaatttccccaactga	598
15	tgctttacctgagcattttca	atcagactgttgcccaatg	654
16	catttggacattcccacctt	acctcacatggtctgatcc	518
17	tggatgcacaattctgaaa	ggagtccggctctacacac	571
18	cagttgcagttattctcttttctg	ccaacatcagaaagcagcttag	640

<sup>a</sup> All PCR products were amplified with 1.5 mM MgCl<sub>2</sub> and 57°C annealing temperature, except exons 5 and 8, where 2.5 mM MgCl<sub>2</sub> was used.

**Table S2. Control Chromosomes Screened for Mutations of *HGF***

Mutation <sup>a</sup>	Pakistani	Indian	Coriell Human Diversity Panel	Coriell Caucasian Panel	Total
Δ3	2/858	0/262	0/168	0/400	2/1688
Δ10	0/858	0/262	0/168	0/400	0/1688
c.495G>A (p.S165S)	0/474		0/172	0/394	0/1040

<sup>a</sup> Δ3 = c.482+1986\_1988delTGA; Δ10 = c.482+1991\_2000delGATGATGAAA

Table S3. SNP Genotypes in 221,150 bp Surrounding *HGF* Mutations

	rs4732399	rs10231299	rs5745752	rs2286194	B39 <sup>a</sup>	rs1558001	rs969705	rs12155338
~Mb <sup>b</sup>	81.12	81.12	81.17	81.19	81.22	81.25	81.26	81.34
PKDF002	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF084	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF121	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF157	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF204	TT	CC	GG	AA	Δ3	GG	CC	TT
PKDF239 <sup>c</sup>	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF351 <sup>c</sup>	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF352	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF402	CC	TT	GG	AA	Δ3	GG	TT	AA
PKDF711	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF841	CC	TT	GG	AA	Δ3	GG	CC	AA
PKDF847	CC	TT	GG	AA	Δ3	GG	CC	AA
PKDF879	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF1113	CC	TT	GG	AA	Δ3	GG	CC	TT
PKSR36a	CC	TT	GG	AA	Δ3	GG	CC	TT
PKSR53a	CC	TT	GG	AA	Δ3	GG	CC	TT
PKSR2b	CC	TT	GG	AA	Δ3	GG	CC	TT
IDM13	CC	TT	GG	AA	Δ3	GG	CC	TT
Kla2	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4011	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4017A	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4018	CC	TT	GG	AA	Δ3	GG	CC	AA
DEM4048	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4050	CC	CC	GG	AA	Δ3	GG	CC	TT
DEM4058	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4071	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4142	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4174	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4199	CC	CC	GG	AA	Δ3	GG	CC	TT
DEM4201	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4212	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4320	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4332	CC	TT	GG	AA	Δ3	GG	CC	TT
DEM4333 (A,B)	CC	TT	GG	AA	Δ3	GG	CC	TT
PKDF601	CC	TT	AA	AA	Δ10	AA	TT	TT
PKDF210	CC	CC	GG	TT	G>A	GG	CC	AA

<sup>a</sup> *HGF* mutations: Δ3=c.482+1986\_1988delTGA; Δ10=c.482+1991\_2000delGATGATGAAA; G>A=c.495G>A (p.S165S)

<sup>b</sup> Nucleotide location in megabases according to human genome reference sequence (NCBI build 36.1)

<sup>c</sup> Pedigrees that define the proximal and distal breakpoints for the minimal *DFNB39* interval