Supplemental Data

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Nonsense Mutations in *SMPX*, Encoding a Protein Responsive to Physical Force, Result in X-Chromosomal Hearing Loss (DFNX4)

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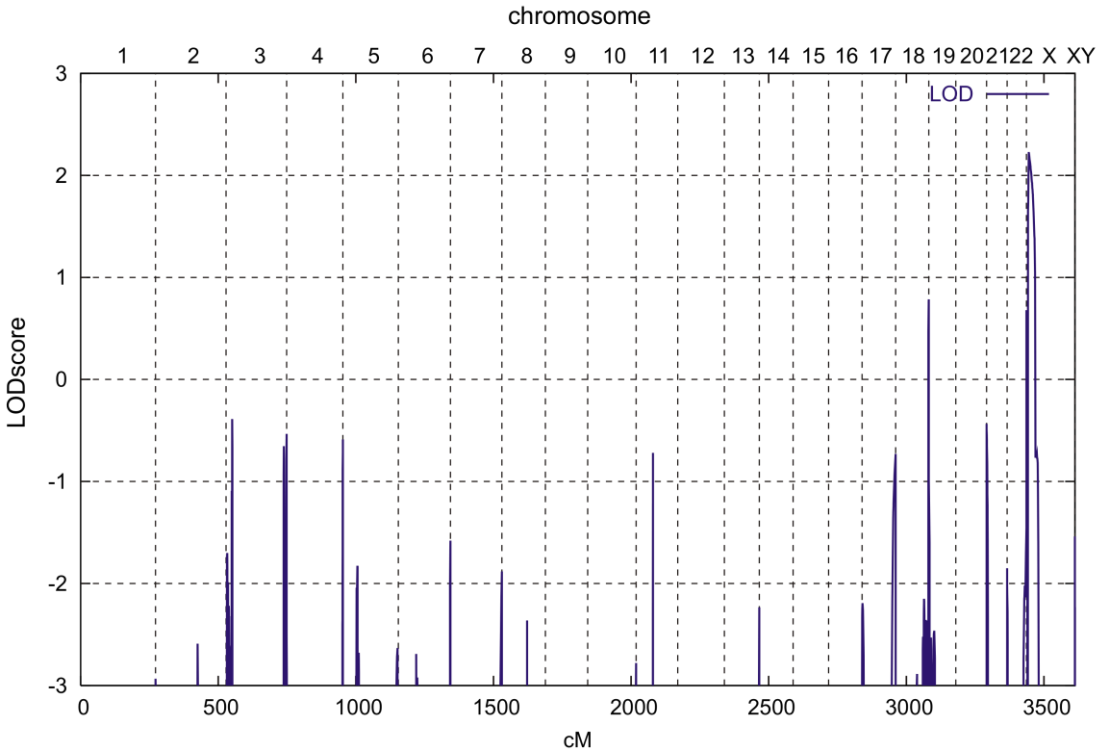

Figure S1. Schematic representation of genome-wide LOD score calculations in the German family. LOD scores calculated with ALLEGRO are given along the y-axis relative to genomic position in cM (centi Morgan) on the x-axis. Note the peak (LOD 2.23) on chromosome X.

Table S1. X-chromosomal variants identified by targeted resequencing in two individuals with hearing loss from the German family. 398 and 347 variants passed the filtering process and from the six variants considered two were predicted to be damaging according to *in-silico* analyses: p.Pro135Ala in *FIGF* (NM_004469.4), and p.Glu37X in *SMPX* (NM_014332.1). A full list of the filtered variants is given for individual III2 in Supplemental Table 2. No mutation was identified by direct sequencing of the *FIGF* coding region in the Spanish family reported.

	Individual 1 III-2	**Individual 2 III-5**
Total variants called	3858	3443
SNVs	3492	3121
Indels	366	322
Variants in the linkage interval	398	347
SNVs	356	300
Indels	42	47
Exonic + SpliceSite (+/- 2nts intronic)	14	14
Absent from the Ensembl human variation database	6	6
Probably damaging	**2**	**2**