



Supplementary Figure 1. Pedigrees of *DFNB59* families 700 and 710.

Figure 1. Mapping the *DFNB59* locus. **(a,b)** Pedigree and segregation analyses of families 705 **(a)** and 312 **(b)**. The complete family 705 consists of 60 members, but only those relevant to the study are shown. Haplotypes are represented as columns of numbers, with the ancestral, disease-associated haplotype boxed. The column on the extreme left indicates the physical distance of each microsatellite marker from the centrosome of chromosome 2. Filled and open symbols denote hearing-impaired and unaffected individuals, respectively. **(c)** Two-point LOD scores between 2q31.1-q31.3 polymorphic markers and the *DFNB59* locus in family 705. **(d)** Critical intervals for the three hearing impairment loci (*DFNA16*, *DFNB27*, and *DFNB59*) mapped to chromosomal region 2q31.