

Prevalence and clinical features of autosomal dominant and recessive *TMCI*-associated hearing loss.

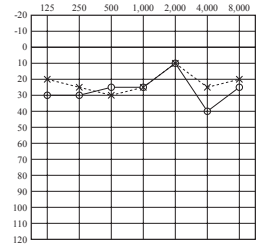
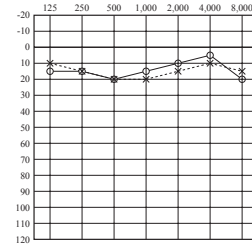
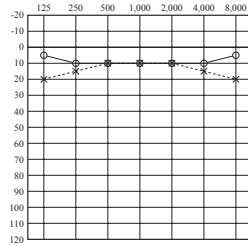
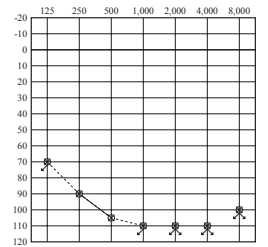
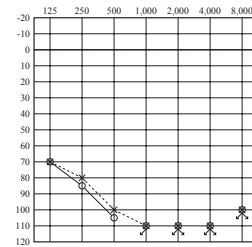
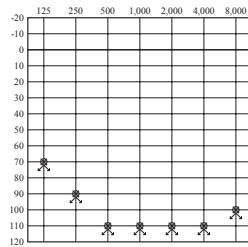
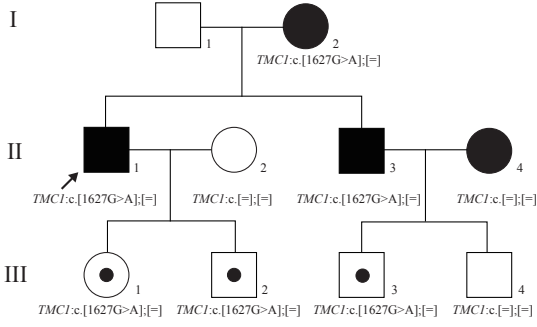
Shin-ya Nishio¹, Shin-ichi Usami¹.

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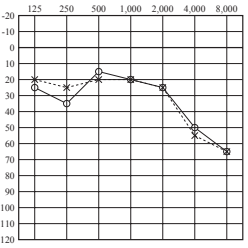
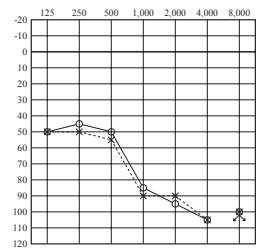
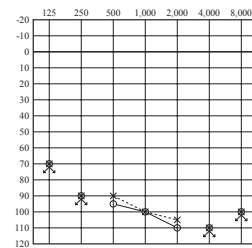
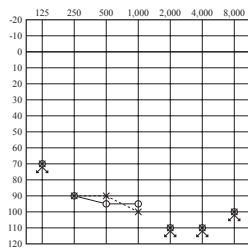
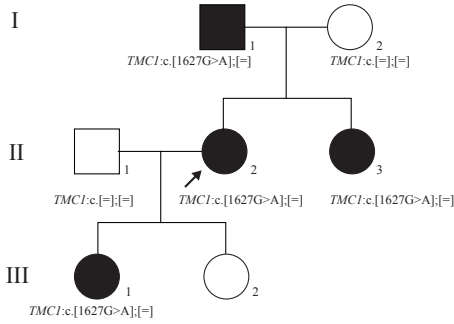
Supplemental Figure 1. Pedigree and audiograms for each family with *TMCI* variants. Arrows indicate the probands in each family. Genetic findings for each individual are shown in the pedigree. The age at audiometric testing is shown below the audiogram.

Supplemental Figure 2. Detailed progression analysis of each DFNA36 mutation. Hearing thresholds from audiograms (the better ear) of the patients of each DFNA36 mutation were plotted for each frequency. Estimated age-related typical audiogram (ARTA) demonstrating the progression of hearing loss for each DFNA36 mutation. For p.Gly417Arg mutation in previous reports did not indicate the hearing threshold for 125 Hz, so we excluded from analysis.

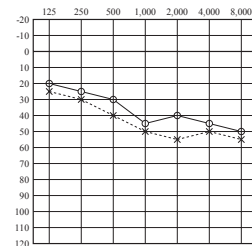
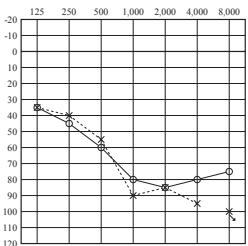
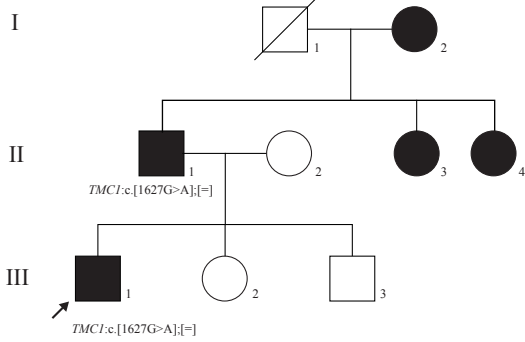
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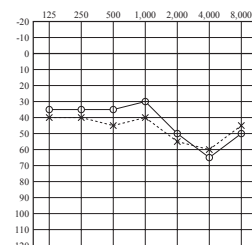
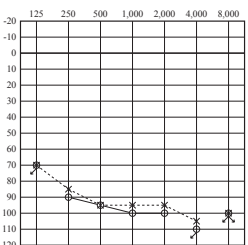
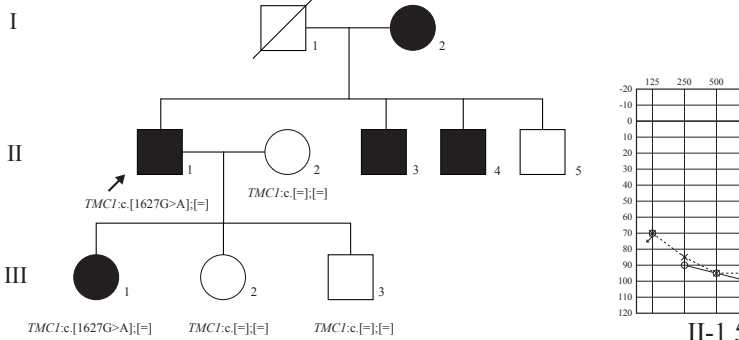
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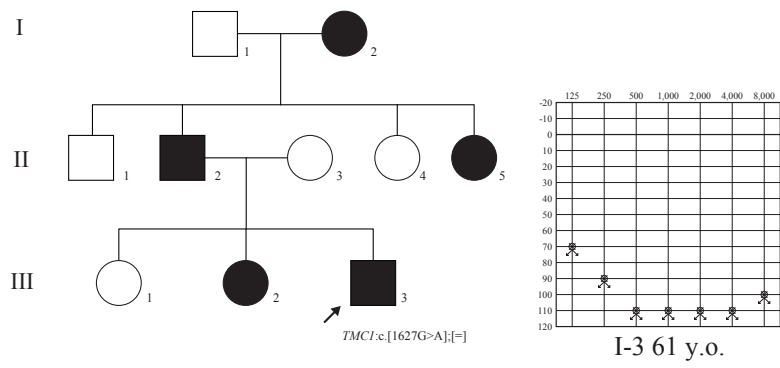
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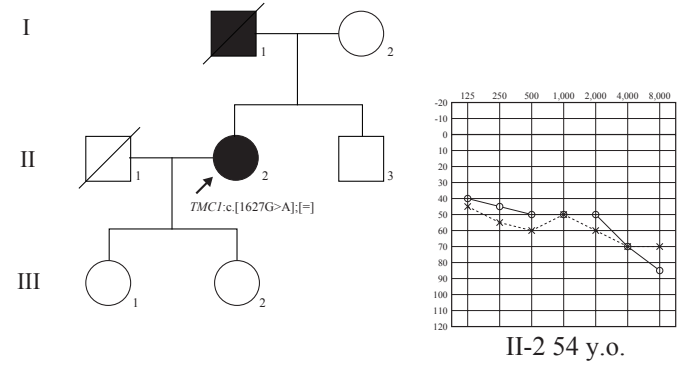
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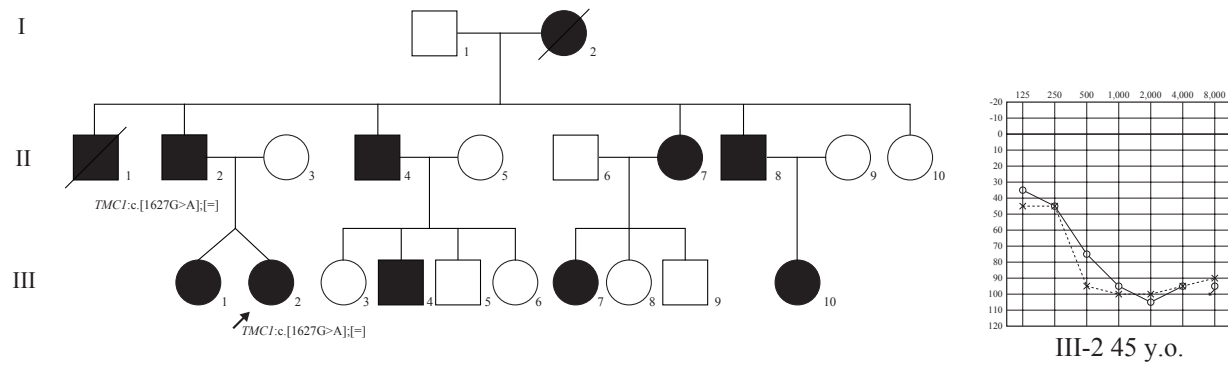
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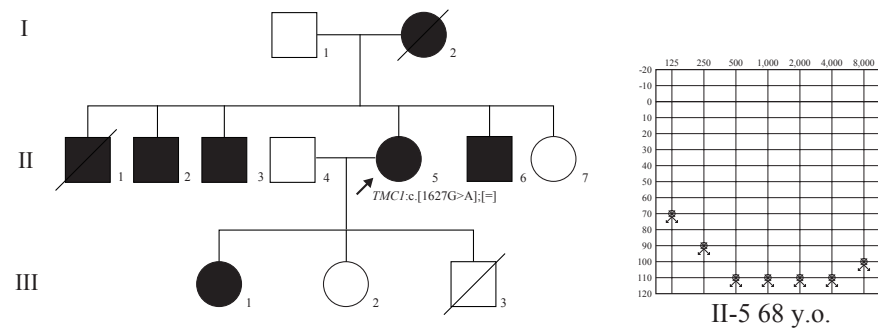
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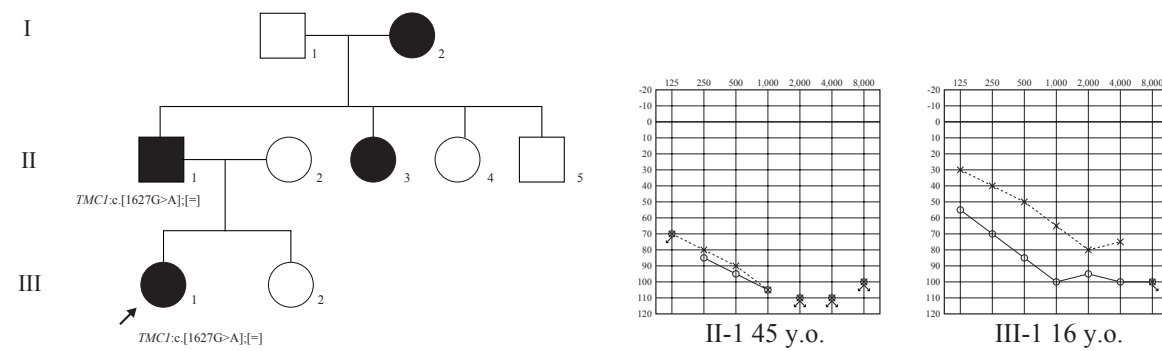
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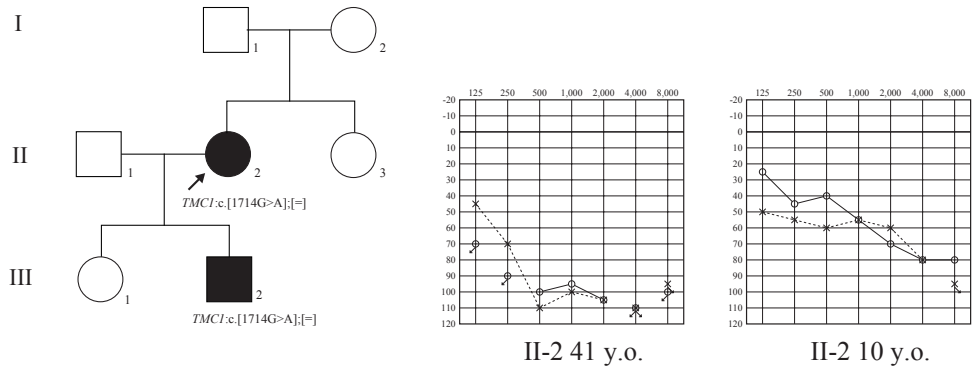


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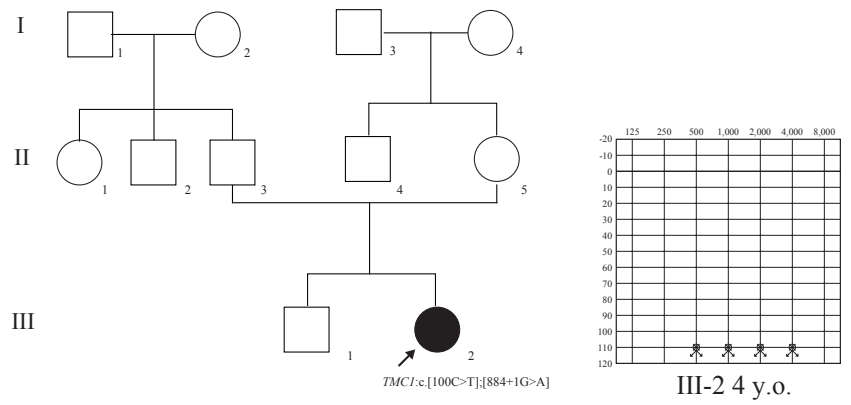


Detailed clinical information for HL4994, HL6717, HL4498, HL8588 and HL7492 were not available.

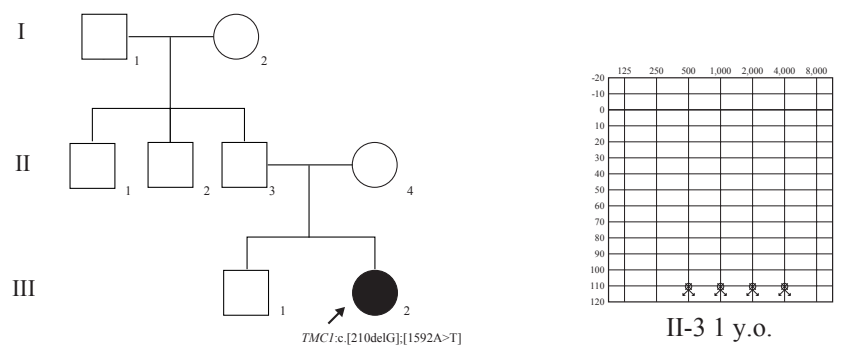
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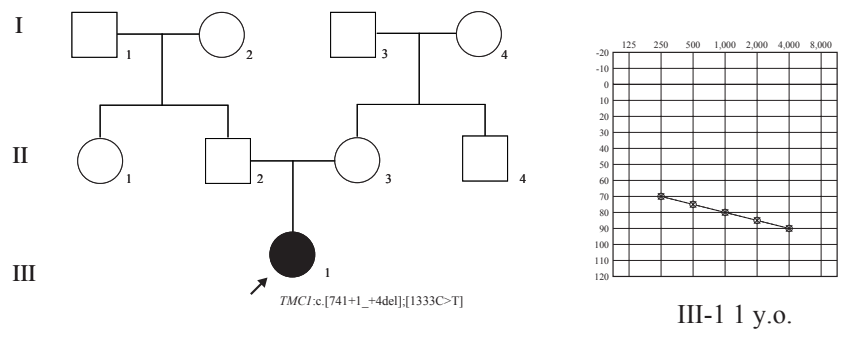
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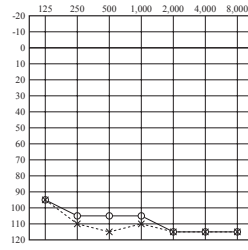
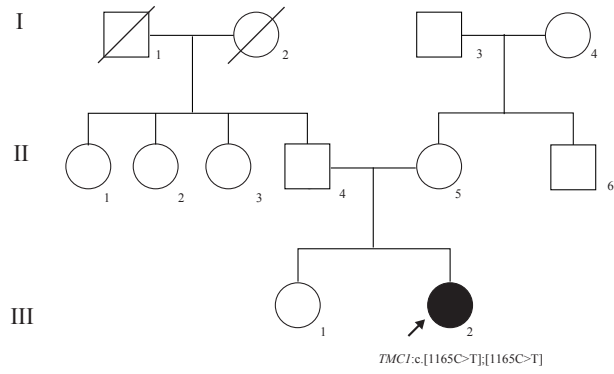
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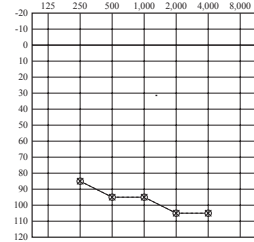
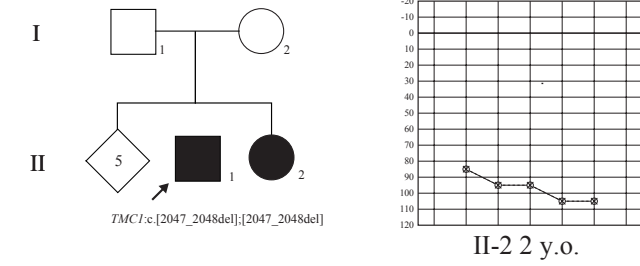
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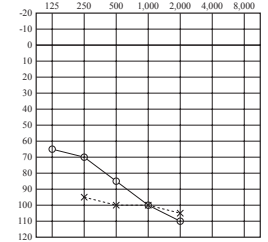
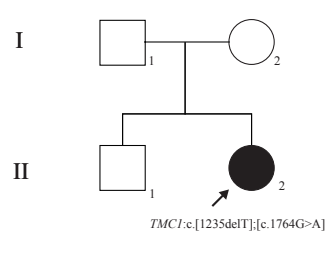
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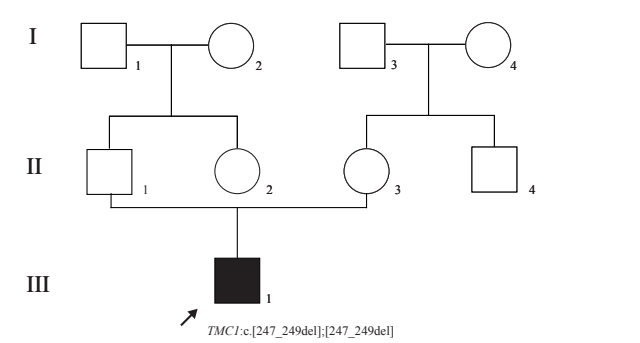
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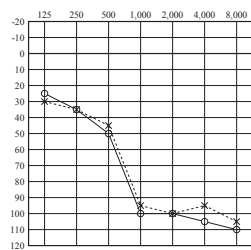
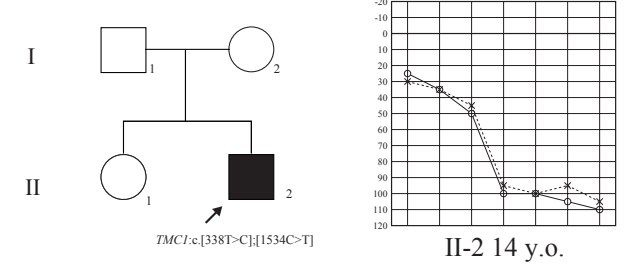


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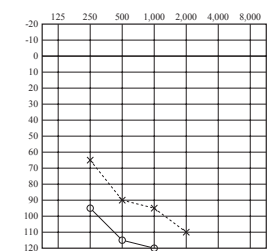
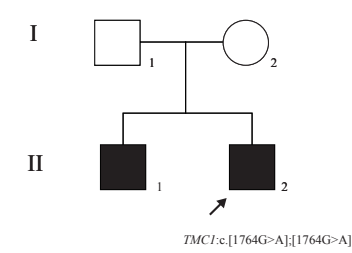


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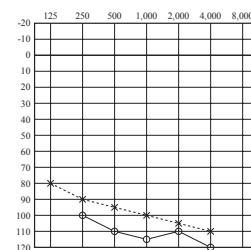
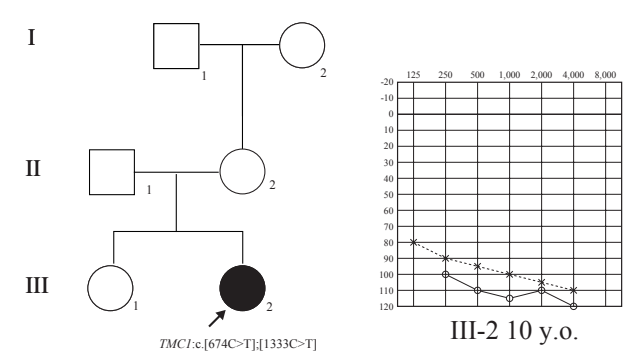
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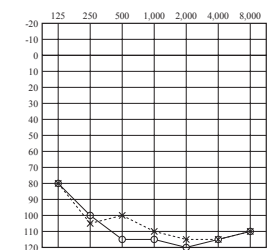
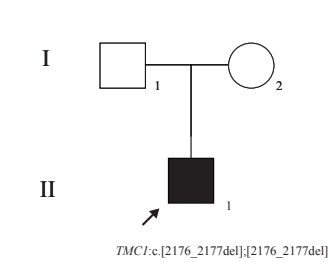
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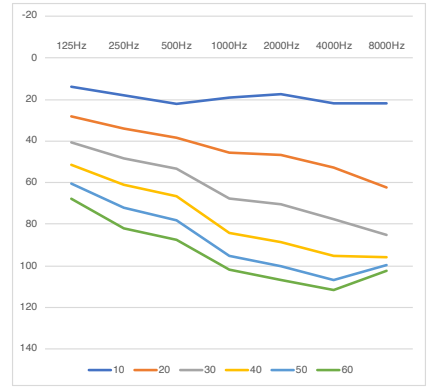
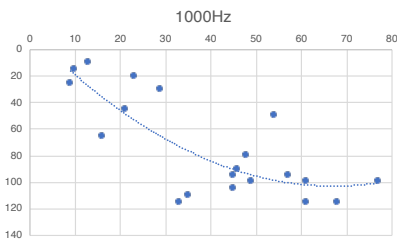
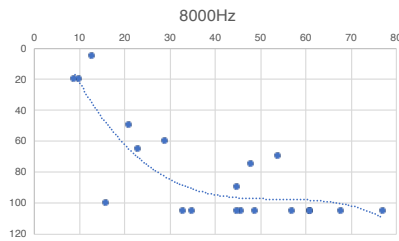
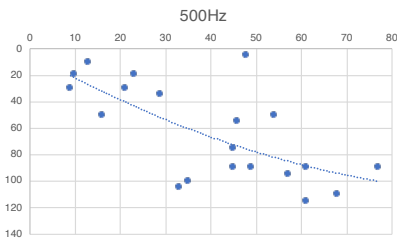
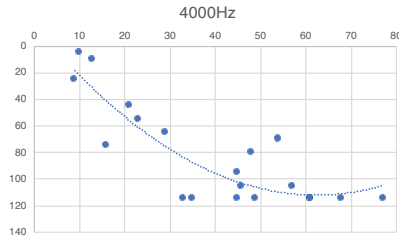
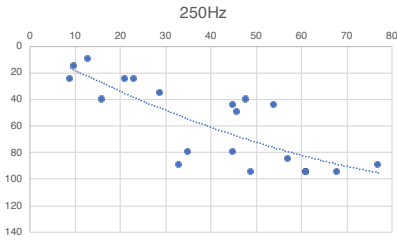
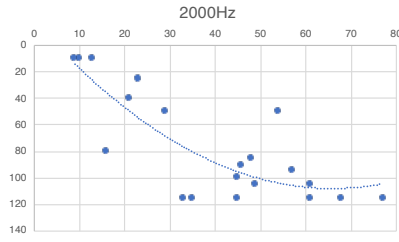
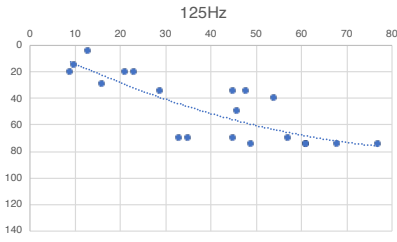
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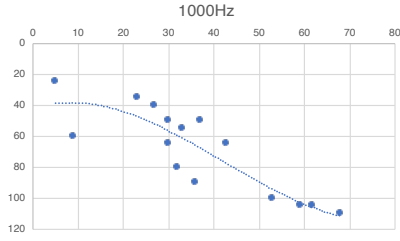
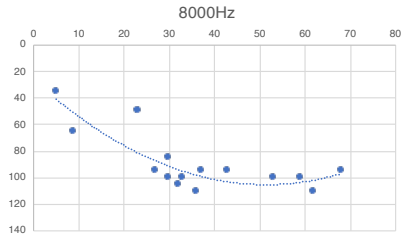
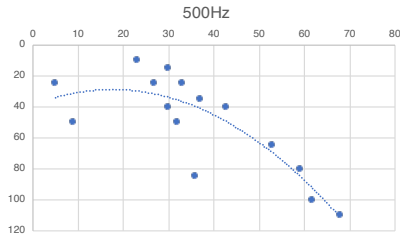
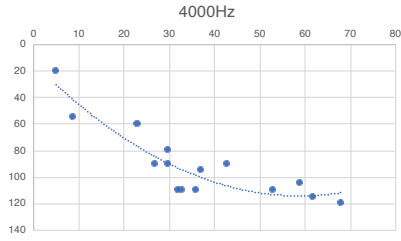
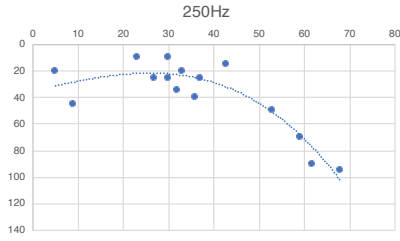
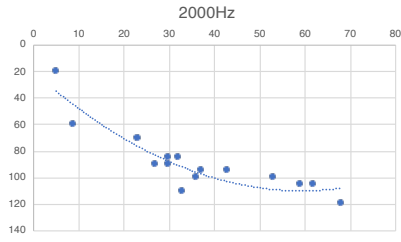
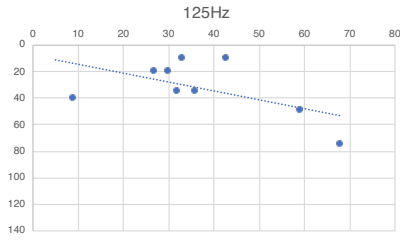
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p.Met418Lys



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