Prevalence of variant among hearing impaired is determined by checking all unsolved deaf probands. Control group of at least 100 hearing individuals of same ethnicity as proband tested to differentiate between polymorphism and mutation. Known variants present in databases (dbSNP, EVS) are excluded. Damage prediction web tools, including PolyPhen 2, SIFT, ConSurf allow assessment of the effect on the protein. Variants with low evolutionary conservation across 46 vertebrates (PhyloP score <1) are excluded. Variants with >1% frequency in 1000 Genomes Project excluded. Output data of sequencer is aligned to reference genome (hg19). Predicted causative variants are checked for segregation of HL in the family by Sanger sequencing. Carrier rate in specific population determined by checking additional hearing individuals. Prevalence of variant among hearing impaired is determined by checking all unsolved deaf probands. Functional validation and gene characterization tested through biological assays, mouse model.