

# GENETIC TESTING: HEARING LOSS

## OVERVIEW

Hereditary hearing loss can be classified as syndromic or nonsyndromic. Syndromic hearing loss refers to hearing loss associated with other medical or physical findings, including visible abnormalities of the external ear. Because syndromic hearing loss occurs as part of a syndrome of multiple clinical manifestations, it is often recognized more readily as hereditary. Nonsyndromic hearing loss is defined as hearing loss not associated with other physical signs or symptoms. Nonsyndromic hearing loss accounts for 70% to 80% of genetically determined deafness, and it is more difficult to determine whether the etiology is hereditary or acquired.

This policy primarily focuses on the use of genetic testing to identify a cause of suspected hereditary hearing loss. The diagnosis of syndromic hearing loss can be made on the basis of associated clinical findings. However, at the time of hearing loss presentation, associated clinical findings may not be apparent; furthermore, variants in certain genetic loci may cause both syndromic and nonsyndromic hearing loss. Given this overlap, the policy focuses on genetic testing for hereditary hearing loss more generally.

## POLICY REFERENCE TABLE

Below is a list of higher volume tests and the associated laboratories for each coverage criteria section. This list is not all inclusive.

<a href="#">Coverage Criteria Sections</a>	Example Tests (Labs)	Common CPT Codes	Common ICD Codes	<a href="#">Ref</a>
<b><a href="#">Hereditary Hearing Loss</a></b>				
<a href="#">Known Familial Variant Analysis</a>	Targeted Variants- <i>GJB2</i> (PreventionGenetics)	81253	H90-H90.8, H90.A-90.A3, H91.3- H91.93	1, 2
	Targeted Variants- <i>GJB6</i> (PreventionGenetics)	81479		
<a href="#">GJB2 and GJB6 Sequencing and/or Deletion Duplication</a>	<i>GJB2</i> Sequence Analysis (Baylor Miraca Genetics Laboratories)	81252		

<a href="#">Analysis or Multigene Panel Analysis</a>	<i>GJB2</i> Deletion/Duplication Analysis (Baylor Miraca Genetics Laboratories)	81479		
	<i>GJB6</i> Deletion/Duplication Analysis (Baylor Miraca Genetics Laboratories)	81254		
	<i>GJB6</i> Gene Sequencing (GeneDx)	81479		
	Hearing Loss Panel (GeneDx)	81430, 81431		

## OTHER RELATED POLICIES

This policy document provides coverage criteria for genetic testing for hereditary hearing loss. Please refer to:

- ***Genetic Testing: Prenatal and Preconception Carrier Screening*** for coverage criteria related to carrier screening for hereditary hearing loss.
- ***Genetic Testing: Multisystem Inherited Disorders, Intellectual Disability, and Developmental Delay*** for coverage criteria related to genetic disorders that affect multiple organ systems
- ***Genetic Testing: General Approach to Genetic Testing*** for coverage criteria related to genetic testing for hearing loss that is not specifically discussed in this or another non-general policy.

## COVERAGE CRITERIA

### HEREDITARY HEARING LOSS

#### Known Familial Variant Analysis

- I. Targeted variant analysis for known familial variant(s) to establish a diagnosis of hereditary hearing loss (81253, 81403) is considered **medically necessary** when:
  - A. The member has a [close relative](#) with pathogenic or likely pathogenic variant(s) in *GJB2*, *GJB6*, or another gene known to cause hereditary hearing loss.

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## **GJB2 and GJB6 Sequencing and/or Deletion Duplication Analysis or Multigene Panel Analysis**

- I. *GJB2* sequencing (81252) and/or deletion/duplication (81479) and/or *GJB6* sequencing (81479) and/or deletion/duplication analysis (81254) or multigene panel analysis (81430, 81431) to establish a diagnosis of hereditary hearing loss is considered **medically necessary** when:
  - A. The member has hearing loss, **AND**
  - B. There is no known acquired cause of the hearing loss (examples: TORCH infections [Toxoplasma gondii, other agents, rubella, cytomegalovirus, and herpes simplex virus], bacterial infection, age-related or noise-related hearing loss).
- II. *GJB2* sequencing (81252) and/or deletion/duplication (81479) and/or *GJB6* sequencing (81479) and/or deletion/duplication analysis (81254) or multigene panel analysis (81430, 81431) to establish a diagnosis of hereditary hearing loss is considered **investigational** for all other indications.

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## **NOTES AND DEFINITIONS**

1. Close relatives include first, second, and third degree blood relatives:
  - a. **First-degree relatives** are parents, siblings, and children
  - b. **Second-degree relatives** are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half siblings
  - c. **Third-degree relatives** are great grandparents, great aunts, great uncles, great grandchildren, and first cousins

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## CLINICAL CONSIDERATIONS

If there is not a high suspicion for a specific hearing loss etiology, ideally the evaluation should occur in a stepwise fashion. About 50% of individuals with autosomal recessive hereditary hearing loss have pathogenic variants in the *GJB2* gene, in the other 50% of patients with apparent autosomal recessive hereditary hearing loss, numerous other genes are implicated. There is no single identifiable gene responsible for most cases of autosomal dominant hereditary hearing loss.

If there is suspicion for autosomal recessive congenital hearing loss, it would be reasonable to begin with testing of *GJB2* and *GJB6* and if testing is negative, screening for the other genes associated with hearing loss with a multigene panel would be efficient. An alternative strategy for suspected autosomal recessive or autosomal dominant hearing loss would be to obtain a multigene panel that includes *GJB2* and *GJB6* as a first step.

Given the extreme heterogeneity in genetic causes of hearing loss, these 2 strategies may be considered reasonably equivalent.

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## BACKGROUND AND RATIONALE

### **GJB2 and GJB6 Sequencing and/or Deletion/Duplication Analysis or Multigene Panel Analysis**

*American College of Medical Genetics and Genomics (ACMG)*

The American College of Medical Genetics and Genomics (ACMG) published guidelines in 2022 to guide genetics evaluation for individuals with hearing loss: “For individuals lacking physical findings suggestive of a known syndrome, a tiered diagnostic approach should be implemented. Unless clinical and/or family history suggests a specific genetic etiology, comprehensive HL gene panel testing should be initiated.” (page 9) The guidelines state the following: “Although nonsyndromic HL [hearing loss] demonstrates high genetic heterogeneity, the *DFNB1* locus, which includes the *GJB2* gene encoding the gap junction protein connexin 26 and the *GJB6* gene encoding the gap junction protein connexin 30, accounts for an estimated 50% of all autosomal recessive nonsyndromic HL and 15% to 40% of all deaf individuals in a variety of populations.” (page 3)

### *GeneReviews: Hereditary Hearing Loss and Deafness Overview*

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The recommended evaluation for hearing loss is as follows:

Within the section of “Differential Diagnosis of Hereditary Hearing Loss and Deafness,” GeneReviews states: “Acquired hearing loss in children commonly results from prenatal infections from ‘TORCH’ organisms...or postnatal infections.”

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## REFERENCES

1. Li MM, Tayoun AA, DiStefano M, et al. Clinical evaluation and etiologic diagnosis of hearing loss: A clinical practice resource of the American College of Medical Genetics and Genomics (ACMG). *Genet Med*. 2022;24(7):1392-1406
2. Shearer AE, Hildebrand MS, Smith RJH. Hereditary Hearing Loss and Deafness Overview. 1999 Feb 14 [Updated 2017 Jul 27]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2020. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1434/>

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