Hearing loss can be categorized by type, onset, or severity. Sensorineural hearing loss is the result of impairment of the inner ear structures. Conductive hearing loss is the result of abnormalities of the external ear and/or the middle ear. Mixed hearing loss is a combination of sensorineural and conductive hearing loss. Central auditory dysfunction is the result of damage or dysfunction of the eighth cranial nerve, auditory brain stem, or cerebral cortex. Age of onset is characterized as prelingual (before speech develops) or postlingual (after speech develops). Severity ranges from mild to profound.

The prevalence of bilateral sensorineural hearing loss is 1 in 500 newborns and 3.5 per 1000 adolescents. While the causes of hearing loss are diverse, at least 50% (and possibly up to two-thirds) of prelingual hearing loss is genetic in origin. The remaining cases of hearing loss are thought to be due to environmental factors or unidentified genetic factors. Hearing loss can be associated with a particular genetic syndrome, such as Usher syndrome or Pendred syndrome; however, most cases of prelingual sensorineural hearing loss are the result of an autosomal recessive, nonsyndromic condition. Genetic loss can be inherited in many ways. Autosomal recessive causes account for approximately 80% of hearing loss cases and are typically prelingual in onset. Autosomal dominant causes account for approximately 20% of hearing loss cases and are typically postlingual in onset. Less than 1% of hearing loss cases are inherited through the mitochondria or the X chromosome. Approximately 50% of autosomal recessive nonsyndromic hearing loss cases are caused by mutations in the GJB2 and GJB6 genes.

In the presence of specific mitochondrial DNA (mtDNA) mutations, moderate to severe hearing loss can result from exposure to aminoglycoside antibiotics such as gentamycin, tobramycin, amikacin, kanamycin, or streptomycin [6]. Pathogenic variants in the mitochondrial MTRNR1, MTOC1, and MTTS1 genes have been associated with aminoglycoside ototoxicity in an estimated 2% of deaf individuals in the US [7-8]. The prevalence is higher, 15-30%, among deaf persons with a history of aminoglycoside exposure [9]. One of the most common mitochondrial pathogenic variants is the m.17443A>G substitution in the MTRNR1 gene which can be found in 0.6-2.5% of Caucasian, 3-5% of Asian and as high as 17% of the Spanish population with non-syndromic hearing loss [10].

The mitochondrial variants m.7445A>G/m.7444G>A/m.7443A>G in the tRNA serine gene (MTCO1 and MTTS1) have been found in patients with maternally inherited sensorineural hearing loss, but they are less likely to cause aminoglycoside hypersensitivity. Of individuals with mitochondrial nonsyndromic hearing loss, 14% have pathogenic variants m.7443A>G, m.7444G>A, or m.7445A>G. Most mitochondrial DNA mutations causing non-syndromic hearing loss are maternally inherited. However, heteroplasmic states (uneven distribution of mitochondrial DNA during cell division) and variable penetrance may be related to the level of mutant mitochondria present, and is not quantitated by this assay. The Hearing Loss Panel provides sequencing of genes in which pathogenic variants are known to cause hearing loss or have hearing loss as part of the clinical spectrum of disease. The vast majority of genes on this panel cause sensorineural hearing loss.

References:

- GeneReviews
- OMIM

**Genes**

- ABHD12, ABHD5, ACTG1, ADCY1, ADGRV1, AIFM1, ALMS1, ARSB, ATP6V1B1, BNSD, BTD, C4BP2, CACNA1D, CCDC50, CDH23, CEACAM16, CHD7, CIR2, CISO2, CLDN14, CLIC5, CLPP, CLRN1, COCH, COCH1L2, COL1A2, COL2A1, COL4A3, COL4A4, COL4A5, COL4A6, COL9A1, CRYM, DDCA2, DFNB5, DFNB9, DIABLO, DIAPH1, DNMT1, DSG2, EDN3, EDNRB, ELMOD3, EPS8, ESRNB, EYA1, EYA4, FAM65B, FG3, FGFR3, FOXC1, FOXI1, GIPC3, GJB2, GJB3, GJB6, GPSM2, GRHL2, GRXCR1, GRXCR2, HARS2, HGF, HOMER1, HSRD17B4, IGLR1, KARS, KCN1, KCNJ10, KCNJ1, KCNJ4, LARS2, LHFPL5, LOXHD1, LRTOMT, MARVEL2, MASP1, MIF, MSRB3, MTRNR1, MYH14, MYH9, MYO15A, MYO1A, MYO3A, MYO6, MYO7A, OPA1, OSBPL2, OTOF, OTOF, OTOML, P2RX2, PAX3, PCDH15, PITX2, POLR1C, POLR1D, POUJF4, PRPS1, RDX, RPS6KB3, SALL1, SALL4, SERPINB6, SIX1, SIX5, SLC17A8, SLC26A4, SLC26A5, SLC29A3, SLITRK6, SMXP, SOX10, SYNE4, TBC1D24, TCOF1, TECTA, TIMM8A, TJP2, TM1C1, TMEM132E, TMIE, TMPRSS3, TPRN, TRIOBP, TSPER, USH1C, USH1G, USH2A, WFS1, WHRN

**Indications**

This test is indicated for:

- **ABHD12, ABHD5, ACTG1, ADCY1, ADGRV1, AIFM1, ALMS1, ARSB, ATP6V1B1, BNSD, BTD, C4BP2, CACNA1D, CCDC50, CDH23, CEACAM16, CHD7, CIR2, CISO2, CLDN14, CLIC5, CLPP, CLRN1, COCH, COCH1L2, COL1A2, COL2A1, COL4A3, COL4A4, COL4A5, COL4A6, COL9A1, CRYM, DDCA2, DFNB5, DFNB9, DIABLO, DIAPH1, DNMT1, DSG2, EDN3, EDNRB, ELMOD3, EPS8, ESRNB, EYA1, EYA4, FAM65B, FG3, FGFR3, FOXC1, FOXI1, GIPC3, GJB2, GJB3, GJB6, GPSM2, GRHL2, GRXCR1, GRXCR2, HARS2, HGF, HOMER1, HSRD17B4, IGLR1, KARS, KCN1, KCNJ10, KCNJ1, KCNJ4, LARS2, LHFPL5, LOXHD1, LRTOMT, MARVEL2, MASP1, MIF, MSRB3, MTRNR1, MYH14, MYH9, MYO15A, MYO1A, MYO3A, MYO6, MYO7A, OPA1, OSBPL2, OTOF, OTOF, OTOML, P2RX2, PAX3, PCDH15, PITX2, POLR1C, POLR1D, POUJF4, PRPS1, RDX, RPS6KB3, SALL1, SALL4, SERPINB6, SIX1, SIX5, SLC17A8, SLC26A4, SLC26A5, SLC29A3, SLITRK6, SMXP, SOX10, SYNE4, TBC1D24, TCOF1, TECTA, TIMM8A, TJP2, TM1C1, TMEM132E, TMIE, TMPRSS3, TPRN, TRIOBP, TSPER, USH1C, USH1G, USH2A, WFS1, WHRN**

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Methodology

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members. The GJB6 gene 342kb deletion is detected by allele-specific amplification.

**Detection**

Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype. The GJB6 deletion component of this test will detect nearly all 342kb common deletion alleles in Connexin 30.

Analytical Sensitivity: ~99%.

**Specimen Requirements**

Submit only 1 of the following specimen types

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube:
- Infants (Children >2 years): 3-5 ml
- Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.

**Type: Isolated DNA**

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

**Related Tests**

- Hearing Loss Panel: GJB2 and GJB6 Sequencing, GJB6 Common Deletion, and Targeted Mitochondrial Analysis
- Hearing Loss: GJB2 & GJB6 Gene Sequencing Panel
- Hearing Loss: GJB2 Gene Sequencing
- Hearing Loss: GJB6 Gene Sequencing
- Hearing Loss: Deletion/Duplication Panel