Nonsyndromic Hearing Loss secondary to *GJB2* (connexin 26) mutations

Disorder: Hearing loss affects about 1 in 500 newborns and a genetic etiology is suspected in two thirds of these patients. Hearing loss can be caused by mutations in many different genes which can be inherited in an autosomal dominant, autosomal recessive, X-linked or mitochondrial (maternal inheritance) manner.

Mutations in the *GJB2* gene, which encodes for the connexin 26 protein, are the most frequent cause of autosomal recessive nonsyndromic hereditary hearing loss, known as DFNB1. Mutations in the *GJB2* gene are found in various populations, with carrier rates of approximately 1-in-30 in the United States Caucasian population and 1-in-20 in the Ashkenazi Jewish population.

Indications:

- Sensorineural hearing loss of unknown etiology
- Carrier testing in a relative of a patient with a proven *GJB2* mutation

Specimen: At least 2 mLs whole blood in a lavender top (EDTA) tube. Alternately, two cytobrushes (cheek swabs) may be collected.

Testing Methodology: PCR-based sequencing of the exon/intron boundaries and the entire coding sequence which is contained within exon 2 of the *GJB2* gene.

Analysis of *GJB2* is also offered as part of our **Hearing Loss Panel Tier 1 and OtoSeq® Hearing Loss Panel** which includes analyses for additional genes which cause hereditary hearing loss. Please refer to our web site for additional information.

Test Sensitivity: PCR-based sequencing detects 99% of the reported mutations in *GJB2*. Mutations in *GJB2* account for 18% of congenital sensorineural hearing loss in the U.S. population.

The sensitivity of DNA sequencing is over 99% for the detection of nucleotide base changes, small deletions and insertions in the regions analyzed. Mutations in regulatory regions or other untranslated regions are not detected by this test. Large deletions involving entire single exons or multiple exons, large insertions and other complex genetic events are not identified using this test methodology. Rare primer site variants may lead to erroneous results.