Lab Dept: Anatomic Pathology

Test Name: OTOGENOME TEST FOR HEARING LOSS

General Information

Lab Order Codes: OTOG

Synonyms: Hearing Loss Genes

CPT Codes: 81430 x1 – Hearing loss (eg, nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); genomic sequence analysis panel, must include at least 60 genes
81431 X1 – Hearing loss; deletion/duplication panel

Test Includes: Sequence testing for 70 genes known to cause nonsyndromic hearing loss and syndromes that can present as nonsyndromic.

Logistics

Test Indications: Evaluation of undiagnosed hearing loss.

Lab Testing Section: Anatomic Pathology - Sendouts

Referred to: Harvard Medical School Laboratory for Molecular Genetics

Phone Numbers: MIN Lab: 612-813-6280

STP Lab: 651-220-6550

Test Availability: Daily, 24 hours

Turnaround Time: 8 - 12 weeks

Special Instructions: Please send completed Harvard requisition and consent with the patient or specimen to the laboratory. The consent portion of the form is required. Please note that incomplete of missing paperwork may delay the start of testing.

Specimen

Specimen Type: Whole blood

Container: Lavender top (EDTA) tube

Draw Volume: 7 mL (Minimum 3-5 mL for an infant) blood

Processed Volume:	Same as Draw Volume
Collection:	Routine venipuncture
Special Processing:	Lab Staff: Send lavender tubes labeled with a minimum of Name, Date of Birth, and Age. The reference laboratory accepts samples Monday through Friday from 9am to 5pm. Labeled specimens and requisitions/consents should be sent overnight at room temperature. **Notice: Samples are NOT accepted on Saturdays, Sundays or holidays. Please keep blood samples collected on these days at refrigerated temperatures until the next business day.
Patient Preparation:	None
Sample Rejection:	Mislabeled or unlabeled specimens

Interpretive

Reference Range:	Benign for familial variants
Methodology:	Next generation sequencing using oligonucleotide-based target capture (Agilent SureSelect) followed by Illumina HiSeq sequencing of the coding regions and splice sites. Sanger sequencing is used to confirm all clinically significant variants and fill in regions with insufficient coverage.
References:	Harvard Medical School, Laboratory for Molecular Genetics, Partners Health Care Center for Personalized Genetic Medicine Phone: 617-768-8500 Fax: 617-768-8513 Email: lmm@partners.org
Updates:	1/21/2014: CPT update 3/5/2015: CPT update 6/9/2016: CPT update