MAYO CLINIC LABORATORIES

NEW TEST

Notification Date: April 13, 2021
Effective Date: April 27, 2021

Custom Gene Panel, Hereditary, Next-Generation Sequencing (NGS), Varies

Test ID: CGPH

Useful for:

- Customization of existing next-generation sequencing (NGS) panels offered through Mayo Clinic Laboratories
- Detection of single nucleotide and copy number variants in a custom gene panel
- Identification of a pathogenic variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for a hereditary condition

Reflex Tests:

Test ID	Reporting Name	Available Separately	Always Performed
G145	Hereditary Custom Gene Panel Tier 1	No (Bill Only)	No
G146	Hereditary Custom Gene Panel Tier 2	No (Bill Only)	No
G147	Hereditary Custom Gene Panel Tier 3	No (Bill Only)	No
G148	Hereditary Custom Gene Panel Tier 4	No (Bill Only)	No
G149	Hereditary Custom Gene Panel Tier 5	No (Bill Only)	No
G150	Hereditary Custom Gene Panel Tier 6	No (Bill Only)	No

Methods:

Custom Sequence Capture and Next-Generation Sequencing (NGS)/Polymerase Chain Reaction (PCR), Sanger Sequencing and/or Multiplex Ligation-Dependent Probe Amplification (MLPA)

Advisory Information:

This test can only be utilized to modify genetic testing panels for biochemical disease states at this time. The Custom Gene Ordering Tool must be used to create a unique Gene List ID that directs the laboratory to test the genes requested.

Reference Values:

An interpretive report will be provided.

Specimen Stability Information:

Specimen Type	Temperature	Time
Varies	Varies	

Specimen Requirements:

Specimen Type: Whole blood

Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.
Container/Tube:
Preferred: Lavender top (EDTA) or yellow top (ACD)
Acceptable: Any anticoagulant
Specimen Volume: 3 mL
Collection Instructions:
1. Invert several times to mix blood.
2. Send specimen in original tube.
Specimen Stability Information: Ambient / Refrigerated

Necessary Information:

Molecular Genetics: Hereditary Custom Gene Panel Patient Information **is required**.

Cautions:

Clinical Correlations:
Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.
To discuss the availability of further testing options or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted at 1-800-533-1710.

Technical Limitations:
Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively amplified for sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

The test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Insertions/deletions (indels) greater or equal to 40 bp, including mobile element insertions, may be less reliably detected than smaller indels.

Deletion/Duplication Analysis:
This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

For detailed information regarding gene specific performance and technical limitations, see Targeted Genes and Methodology Details for Inborn Errors of Metabolism Custom Gene Panel or contact a laboratory Genetic Counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent heterologous blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

Reclassification of Variants-Policy:
At this time it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages health care providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time.

Variant Evaluation:
Evaluation and categorization of variants is performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(1) Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.

CPT Code:

81223 (if appropriate)
81249 (if appropriate)
81286 (if appropriate)
81403 (if appropriate)
81404 (if appropriate)
81405 (if appropriate)
81406 (if appropriate)
81407 (if appropriate)
81408 (if appropriate)
81443 (if appropriate)
81479 (if appropriate)

Day(s) Setup: Varies **Analytic Time:** 4 weeks

Questions

Contact your Laboratory Technologist Resource Coordinators, Heather Flynn Gilmer or Melissa Lonzo Green, at 800-533-1710.