MAYO CLINIC LABORATORIES

Test Definition: CGPH

Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies

Overview

Useful For

Customization of existing next-generation sequencing panels offered through Mayo Clinic Laboratories

Detection 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

Genetics Test Information

For more information, see Method Description and the following:
-Targeted Genes and Methodology Details for Cardiovascular/Connective Tissue/Dyslipidemia/Cerebrovascular/Primary Ciliary Dyskinesia Custom Gene Panel
-Targeted Genes and Methodology Details for Epilepsy Custom Gene Panel
-Targeted Genes and Methodology Details for Hearing Loss Custom Gene Panel
-Targeted Genes and Methodology Details for Hereditary Cancer Custom Gene Panel
-Targeted Genes and Methodology Details for Inborn Errors of Metabolism Custom Gene Panel
-Targeted Genes and Methodology Details for Nephrology Custom Gene Panel
-Targeted Genes and Methodology Details for Neurologic Disorders Custom Gene Panel
-Targeted Genes and Methodology Details for the Nuclear Mitochondrial Disorders Custom Gene Panel

Testing Algorithm

Pricing for this test is based on the number of genes selected (1, 2-14, 15-49, 50-100, 101-500, and greater than 500) and their corresponding CPT codes. For more information see Custom Gene Ordering Pricing.

Special Instructions

- Informed Consent for Genetic Testing
- Custom Gene Panel Pricing
- Informed Consent for Genetic Testing (Spanish)
- Molecular Genetics: Hereditary Custom Gene Panel Patient Information
- Targeted Genes and Methodology Details for Inborn Errors of Metabolism Custom Gene Panel
- Targeted Genes and Methodology Details for Hereditary Cancer Custom Gene Panel
- Targeted Genes and Methodology Details for Epilepsy Custom Gene Panel
- Targeted Genes and Methodology Details for Nephrology Custom Gene Panel
- Targeted Genes and Methodology Details for Neurologic Disorders Custom Gene Panel
- Targeted Genes and Methodology Details for Cardiovascular/Connective Tissue/Dyslipidemia/Cerebrovascular/Primary Ciliary Dyskinesia Custom Gene Panel
- Targeted Genes and Methodology Details for Hearing Loss Custom Gene Panel

Method Name

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

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

This test **requires** the creation of a unique Gene List ID that directs the laboratory to test the genes requested.
To create the **required Gene List ID** for your Custom Gene Panel, navigate to:
-Custom Gene Ordering Tool
-Custom Gene Ordering Tutorial

For answers to frequently asked questions, see Custom gene ordering on MayoClinicLabs.com.

Targeted testing for familial variants (also called site-specific or known mutation testing) is available under FMTT / Familial Variant, Targeted Testing, Varies. Call 800-533-1710 to obtain more information about this testing option.

Shipping Instructions

Specimen preferred to arrive within 96 hours of collection.

Necessary Information

Molecular Genetics: Hereditary Custom Gene Panel Patient Information **is required**. Testing may proceed without the

patient information; however, it aids in providing a more thorough interpretation. Ordering providers are strongly encouraged to complete the form and send it with the specimen.

Specimen Required

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 whole blood specimen in original tube. **Do not aliquot.**
Specimen Stability Information: Ambient 4 days/Refrigerated

Forms

1. **Molecular Genetics: Hereditary Custom Gene Panel Patient Information is required**.
2. **New York Clients-Informed consent is required**. Document on the request form or electronic order that a copy of the consent is on file.
-Informed Consent for Genetic Testing (T576)
-Informed Consent for Genetic Testing (Spanish) (T826)
3. If not ordering electronically, complete, print, and send a Neurology Specialty Testing Client Test Request (T732) with the specimen.

Specimen Minimum Volume

See Specimen Required

Reject Due To

All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

Clinical & Interpretive

Clinical Information

This test can be used to customize genetic testing panels offered at Mayo Clinic Laboratories. Individual genes can be added or removed to an existing genetic testing panel. Additionally, this test can be used to create your own custom single gene or multi-gene panel or to combine existing panels within the same disease state.
Note: Any genes added to the custom panel must be from the same disease state. Only one Gene List ID may be

submitted per Custom Gene Panel, Hereditary order. The Gene List ID can be created using the Custom Gene Ordering tool (see Ordering Guidance).

Reference Values
An interpretive report will be provided.

Interpretation
All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

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 additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratories genetic counselors at 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 GC (guanine-cytosine) 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. Deletions-insertions (delins) greater or equal to 40 bp, including mobile element insertions, may be less reliably detected than smaller delins.

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 the appropriate Targeted Gene and Methodology details in Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent 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:
Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare 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 are 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.

Clinical Reference

1. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med. 2015 May;17(5):405-424. doi: 10.1038/gim.2015.30

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known disease-causing variants. The human genome reference GRCh37/hg19 build is used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for deletions less than 40 base pairs (bp), above 95% for deletions up to 75 bp, and insertions up to 47 bp. NGS and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed. 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 GC (guanine-cytosine) content, and repetitive sequences. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.(Unpublished Mayo method)

For details regarding the specific gene regions not routinely covered, see the appropriate information:
-Targeted Genes and Methodology Details for Cardiovascular/Connective Tissue/Dyslipidemia/Cerebrovascular/Primary Ciliary Dyskinesia Custom Gene Panel
-Targeted Genes and Methodology Details for Epilepsy Custom Gene Panel
-Targeted Genes and Methodology Details for Hearing Loss Custom Gene Panel
-Targeted Genes and Methodology Details for Hereditary Cancer Custom Gene Panel
-Targeted Genes and Methodology Details for Inborn Errors of Metabolism Custom Gene Panel
-Targeted Genes and Methodology Details for Nephrology Custom Gene Panel
-Targeted Genes and Methodology Details for Neurologic Disorders Custom Gene Panel
-Targeted Genes and Methodology Details for the Nuclear Mitochondrial Disorders Custom Gene Panel

PDF Report
Supplemental

Day(s) Performed
Varies

Report Available
28 to 35 days

Specimen Retention Time
Whole Blood: 2 weeks (if available); Extracted DNA: 3 months

Performing Laboratory Location
Rochester

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

Test Classification
This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
CPT codes are based on the gene content of the custom gene panel. Refer to the Custom Gene Ordering Tool for custom gene panel specific CPT code information.

81165 (if appropriate)
81166 (if appropriate)
81167 (if appropriate)
81162 (if appropriate)
81201 (if appropriate)
81216 (if appropriate)
81223 (if appropriate)
81249 (if appropriate)
81252 (if appropriate)
81286 (if appropriate)
81292 (if appropriate)
81295 (if appropriate)
81298 (if appropriate)
81307 (if appropriate)
81319 (if appropriate)
81321 (if appropriate)
81351 (if appropriate)
81403 (if appropriate)
81404 (if appropriate)
81405 (if appropriate)
81406 (if appropriate)
81407 (if appropriate)
81408 (if appropriate)
81430 (if appropriate)
81431 (if appropriate)
81440 (if appropriate)
81443 (if appropriate)
81448 (if appropriate)
81479 (if appropriate)
81189 (if appropriate)
81419 (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
CGPH	Custom Gene Panel, Hereditary	In Process

Result ID	Test Result Name	Result LOINC® Value
MG135	Gene List ID	48018-6
610422	Test Description	62364-5
606046	Specimen	31208-2
606047	Source	31208-2
606040	Result Summary	50397-9
606041	Result	82939-0

606042	Interpretation	69047-9
610423	Resources	99622-3
606043	Additional Information	48767-8
606044	Method	85069-3
610424	Genes Analyzed	48018-6
606045	Disclaimer	62364-5
606048	Released By	18771-6
620157	Additional Results	82939-0