

## Overview

### Useful For

Evaluating patients with a personal or family history suggestive of hereditary diffuse gastric cancer (HDGC) syndrome

Establishing a diagnosis of HDGC syndrome allowing for targeted cancer surveillance based on associated risks

Identifying genetic variants associated with increased risk for HDGC syndrome allowing for predictive testing of at-risk family members

### Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in the *CDH1* gene associated with hereditary diffuse gastric cancer (HDGC) syndrome. See Method Description for additional details.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for HDGC syndrome.

### Special Instructions

- [Molecular Genetics: Inherited Cancer Syndromes Patient Information](#)
- [Informed Consent for Genetic Testing](#)
- [Informed Consent for Genetic Testing \(Spanish\)](#)

### Method Name

Sequence Capture and Targeted Next-Generation Sequencing (NGS) followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing

### NY State Available

Yes

## Specimen

### Specimen Type

Varies

### Ordering Guidance

For a comprehensive hereditary cancer panel that includes the *CDH1* gene, consider ordering 1 of the following tests:

- CRCGP / Hereditary Gastrointestinal Cancer Panel, Varies
- BRGYP / Hereditary Breast/Gynecologic Cancer Panel, Varies

Testing for *CDH1* gene as part of a customized panel is available. For more information see CGPH / Custom Gene Panel,

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Hereditary, Next-Generation Sequencing, Varies.

Targeted testing for familial variants (also called site-specific or known mutations testing) is available for this gene. For more information see FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

**Specimen Required**

**Patient Preparation:** A previous bone marrow transplant from an allogenic donor will interfere with testing. For information about testing patients who have received a bone marrow transplant, call 800-533-1710.

**Specimen Type:** Whole blood

**Container/Tube:**

**Preferred:** Lavender top (EDTA) or yellow top (ACD)

**Acceptable:** Green top (Sodium heparin)

**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 4 days/Frozen 4 days

**Additional Information:**

1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA is met, the preferred volume of blood must be submitted. Testing may be canceled if DNA requirements are inadequate.

**Specimen Type:** Saliva

**Patient Preparation:** Patient **should not** eat, drink, smoke, or chew gum 30 minutes prior to collection.

**Supplies:** Saliva Collection Kit (T786)

**Specimen Volume:** 1 Swab

**Collection Instructions:** Collect and send specimen per kit instructions.

**Specimen Stability Information:** Ambient (preferred) 30 days/Refrigerated 30 days

**Additional information:** Due to lower quantity/quality of DNA yielded from saliva, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will be noted in the report. Alternatively, additional specimen may be required to complete testing.

**Forms**

1. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file. The following documents are available:

[-Informed Consent for Genetic Testing](#) (T576)

[-Informed Consent for Genetic Testing \(Spanish\)](#) (T826)

2. [Molecular Genetics: Inherited Cancer Syndromes Patient Information Sheet](#) (T519)

3. If not ordering electronically, complete, print, and send a [Oncology Test Request](#) (T729) with the specimen.

**Specimen Minimum Volume**

Whole blood: 1 mL; Saliva: 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**

Germline variants in the *CDH1* gene are associated with hereditary diffuse gastric cancer (HDGC) syndrome, a rare autosomal dominant hereditary cancer syndrome representing 30% to 50% of all diffuse gastric cancer cases. HDGC syndrome is characterized by increased risk to develop diffuse (signet ring cell) gastric cancer and lobular breast cancer, with overall penetrance of this condition approaching 80%.<sup>(1-5)</sup> Colorectal cancer has been reported in individuals with germline *CDH1* variants, however, the specific lifetime risk for colorectal cancer is unknown.<sup>(1,5)</sup>

The National Comprehensive Cancer Network and the International Gastric Cancer Linkage Consortium provide recommendations regarding the medical management of individuals with hereditary diffuse gastric cancer syndrome.<sup>(1,4-5)</sup>

**Reference Values**

An interpretive report will be provided.

**Interpretation**

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.<sup>(6)</sup> 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 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

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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 evaluated by 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.

This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more 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 Method Description 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:

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. Due to broadening genetic knowledge, it is possible that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

#### 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.<sup>(6)</sup> 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

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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.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. These findings will be carefully reviewed to determine whether they will be reported.

### Clinical Reference

1. Kaurah P, Huntsman DG. Hereditary diffuse gastric cancer. In: Adams MP, Everman DB, Mirzaa GM, et al, eds. GeneReviews (Internet). University of Washington, Seattle; 2002. Updated March 22, 2018. Accessed September 10, 2024. Available at [www.ncbi.nlm.nih.gov/books/NBK1139/](http://www.ncbi.nlm.nih.gov/books/NBK1139/)
2. Lindor NM, McMaster ML, Lindor CJ, Greene MH. Concise handbook of familial cancer susceptibility syndromes-second edition. J Natl Cancer Inst Monogr. 2008;(38):1-93. doi:10.1093/jncimonographs/IGN001
3. Siegel RL, Miller KD, Jemal A. Cancer statistics, 2020. CA Cancer J Clin. 2020;70(1):7-30
4. Blair VR, McLeod M, Carneiro F, et al. Hereditary diffuse gastric cancer: updated clinical practice guidelines. Lancet Oncol. 2020;21(8):e386-e397
5. Ajani JA, D'Amico TA, Almhanna K, et al. Gastric Cancer, Version 3.2016. NCCN clinical practice guidelines in Oncology. J Natl Compr Canc Netw. 2016;14(10):1286-1312
6. 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;17(5):405-424

### 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 *CDH1* gene, as well as some other regions that have known disease-causing variants. The human genome reference GRCh37/hg19 build was 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-insertions (delins) 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 *CDH1* gene.

There may be regions of the gene that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine content, and repetitive sequences. The reference transcript for the *CDH1* gene is NM\_004360.5. Reference transcript numbers may be updated due to transcript re-versioning. Always refer to the final patient report for gene transcript information referenced at the time of testing.(Unpublished Mayo method)

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

**PDF Report**

Supplemental

**Day(s) Performed**

Varies

**Report Available**

21 to 28 days

**Specimen Retention Time**

Whole blood: 2 weeks (if available); Extracted DNA: 3 months; Saliva: 1 month

**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**

81406

**LOINC® Information**

| Test ID | Test Order Name         | Order LOINC® Value |
|---------|-------------------------|--------------------|
| CDHZ    | CDH1 Full Gene Analysis | 94240-9            |

| Result ID | Test Result Name       | Result LOINC® Value |
|-----------|------------------------|---------------------|
| 614671    | Test Description       | 62364-5             |
| 614672    | Specimen               | 31208-2             |
| 614673    | Source                 | 31208-2             |
| 614674    | Result Summary         | 50397-9             |
| 614675    | Result                 | 82939-0             |
| 614676    | Interpretation         | 69047-9             |
| 614677    | Resources              | 99622-3             |
| 614678    | Additional Information | 48767-8             |

## Test Definition: CDHZ

Hereditary Diffuse Gastric Cancer Syndrome,  
CDH1, Full Gene Analysis, Varies

|        |                |         |
|--------|----------------|---------|
| 614679 | Method         | 85069-3 |
| 614680 | Genes Analyzed | 48018-6 |
| 614681 | Disclaimer     | 62364-5 |
| 614682 | Released By    | 18771-6 |