

Overview

Useful For

Evaluation for patients with a personal or family history suggestive of PTEN hamartoma tumor syndrome (PHTS)
Establishing a diagnosis of PHTS allowing for targeted cancer surveillance based on associated risks
Identifying variants within genes known to be associated with increased risk for PHTS 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 one gene associated with PTEN hamartoma tumor syndrome (PHTS): *PTEN* (including promoter). See Method Description for additional details.

Identification of a pathogenic variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for PTEN hamartoma tumor syndrome (PHTS).

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 *PTEN* gene, consider ordering 1 of the following tests:

- BRGYP / Hereditary Breast/Gynecologic Cancer Panel, Varies
- ENDCP / Hereditary Endocrine Cancer Panel, Varies
- HPGLP / Hereditary Paraganglioma/Pheochromocytoma Panel, Varies
- RENCN / Hereditary Renal Cancer Panel, Varies

Customization of this panel or single gene analysis for any gene present on this panel is available. For more information see CGPH / Custom Gene Panel, 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 Mutation, Targeted Testing, Varies.

Shipping Instructions

Specimen preferred to arrive within 96 hours of collection.

Specimen Required

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.

Specimen Type: Whole blood

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. **Do not** aliquot.

Specimen Stability Information: Ambient (preferred) 4 days/Refrigerated

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 in Special Instructions:

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

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

2. [Molecular Genetics: Inherited Cancer Syndromes Patient Information\(T519\)](#) in Special Instructions

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

Reject Due To

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

Specimen Minimum Volume

See Specimen Required

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies (preferred)		

Clinical & Interpretive**Clinical Information**

[Germline variants in the *PTEN* gene are associated with a rare group of overlapping clinical syndromes collectively referred to as PTEN hamartoma tumor syndrome \(PHTS\). This includes Cowden syndrome \(CS\), Bannayan-Riley-Ruvalcaba syndrome \(BRRS\), Proteus syndrome \(PS\), Proteus-like syndrome \(PLS\), and autism with macrocephaly.\(1,2\)](#)

PHTS is inherited in an autosomal dominant manner.(1) Between 10% to 48% of individuals with PHTS have a de novo *PTEN* variant.(3) Affected individuals have an increased risk of cancer, including cancers of the breast, endometrium, thyroid, kidney, and colon.(1) Individuals with PHTS also may present with macrocephaly, vascular lesions, trichilemmomas, mucocutaneous papillomatous papules, lipomatosis, hemangiomas, and pigmented macules on the glans penis.(1) Dysplastic gangliocytoma of the cerebellum, also known as Lhermitte-Duclos disease, is another hamartomatous tumor associated with PHTS.(1) Intellectual disability, developmental delay, and autism are commonly

seen in individuals with PHTS.(1)

Since it was reported that *PTEN* variants account for up to 10% to 20% of individuals with autism with macrocephaly, the American College of Medical Genetics and Genomics has recommended *PTEN* gene testing in individuals with both features.(4) The long-term clinical outcomes of individuals with *PTEN*-related autism with macrocephaly is not currently known.(1,2) As such, individuals with *PTEN*-related autism with macrocephaly should follow the same cancer screening recommendations provided for PHTS.(1,2)

[The National Comprehensive Cancer Network provides recommendations regarding the medical management of individuals with PTEN hamartoma tumor syndrome \(PHTS\).](#)(5)

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics (ACMG) recommendations.(6) 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 further testing options or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted at [800-533-1710](tel: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 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. Insertions/deletions (indels) of 40 or more 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 Method Description or

contact a laboratory genetic counselor at 800-533-1710.

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:

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. 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 judgement.

Clinical Reference

1. Yehia L, Eng C: PTEN hamartoma tumor syndrome. In: Adam MP, Ardinger HH, Pagon RA, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2001. Updated February 11, 2021. Accessed July 7, 2021. Available at www.ncbi.nlm.nih.gov/books/NBK1488/
2. Yehia L, Keel E, Eng C: The clinical spectrum of *PTEN* mutations. *Annu Rev Med*. 2020 Jan 27;71:103-116
3. Mester J, Eng C: Estimate of de novo mutation frequency in probands with PTEN hamartoma tumor syndrome. *Genet Med*. 2012 Sep;14(9):819-22
4. Schaefer BG, Mendelsohn NJ, et al: Clinical genetics evaluation in identifying the etiology of autism spectrum disorders: 2013 guideline revisions. *Genet Med*. 2013 May;15(5):399-407
5. Daly MB, Pal T, Berry MP, et al: Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic, Version 2.2021, NCCN Clinical Practice Guidelines in Oncology. *J Natl Compr Canc Netw*. 2021 Jan 6;19(1):77-102
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 May;17(5):405-424

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing is performed to test for the presence of variants in coding regions and intron/exon boundaries of the *PTEN* gene analyzed, as well as some other regions that have known pathogenic 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 insertions/deletions (indels) 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 (PCR)-based quantitative method is performed to test for the presence of deletions and duplications in the gene analyzed.

There may be regions of 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 (GC) content, and repetitive sequences.

The reference transcript for *PTEN* gene is NM_000314.8. 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.

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.(Unpublished Mayo method)

PDF Report

Supplemental

Specimen Retention Time

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

Performing Laboratory Location

Rochester

Fees & Codes**Test Classification**

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

CPT Code Information

81321