Test Definition: GNBLC

Bleeding Disorders, Comprehensive Gene Panel, Next-Generation Sequencing, Varies

Overview

Useful For

Evaluating hereditary bleeding in patients with a personal or family history suggestive of a hereditary bleeding disorder

Confirming a hereditary bleeding disorder diagnosis with the identification of a known or suspected disease-causing alteration in one or more of 25 genes associated with a variety of hereditary bleeding disorders

Determining the disease-causing alterations within one or more of these 25 genes to delineate the underlying molecular defect in a patient with a laboratory diagnosis of a bleeding disorder

Identifying the causative alteration for genetic counseling purposes

Prognosis and risk assessment based on genotype-phenotype correlations

Carrier testing for close family members of an individual with a hereditary bleeding disorder diagnosis

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
_STR1	Comp Analysis using STR (Bill only)	No, (Bill only)	No
_STR2	Add'l comp analysis w/STR (Bill Only)	No, (Bill only)	No
CULFB	Fibroblast Culture for Genetic Test	Yes	No
CULAF	Amniotic Fluid Culture/Genetic Test	Yes	No
MATCC	Maternal Cell Contamination, B	Yes	No

Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 25 genes associated with a variety of hereditary bleeding disorders: *F2*, *F5*, *F7*, *F8*, *F9*, *F10*, *F11*, *F13A1*, *F13B*, *FGA*, *FGB*, *FGG*, *GGCX*, *GP1BA*, *KLKB1*, *KNG1*, *LMAN1*, *MCFD2*, *PLAT*, *SERPINA1* c.1145T>G only, *SERPINE1*, *SERPINF2*, *THBD*, *VKORC1*, and *VWF*. See Targeted Genes and Methodology Details for Bleeding Disorders, Comprehensive Gene Panel and Method Description for additional details.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, recurrence risk assessment, familial screening, and genetic counseling for a variety of hereditary bleeding disorders.

Testing Algorithm

A systematic diagnosis through conventional coagulation testing is recommended prior to considering genetic testing for any suspected bleeding disorder.

Genetic testing for a hereditary bleeding disorder is indicated if:
-Coagulation tests indicate a deficiency or functional abnormality (note these tests are best performed in medically stable patients who are not receiving particular anticoagulants)
-There is a clinical suspicion for a hereditary bleeding disorder due to family history or atypical clinical presentation
-Acquired causes of deficiencies associated with bleeding have been excluded (eg, multiple myeloma, liver disease, warfarin therapy, vitamin K deficiency, systemic amyloidosis, or inhibitors)

However, no screening test exists for detecting defects in a subset of genes on this panel, such as *THBD*. If the bleeding tendency is a concern, sets of clinical guidelines on testing for heritable bleeding disorders, both common and rare, are freely available.(1-5)

Prenatal specimens:
Prenatal genetic testing is not routinely performed without the prior identification of familial alterations. Requests for this prenatal testing without a known familial alteration are performed at the discretion of the Molecular Hematopathology Laboratory Director.

If an amniotic fluid specimen is received, an amniotic fluid culture will be performed at an additional charge.
If a chorionic villi specimen or cultured chorionic villi are received, a fibroblast culture will be performed at an additional charge.

For any prenatal specimen that is received, maternal cell contamination testing will be performed at an additional charge.

Special Instructions

- Informed Consent for Genetic Testing
- Informed Consent for Genetic Testing (Spanish)
- Rare Coagulation Disorder Patient Information
- Targeted Genes and Methodology Details for Bleeding Disorders, Comprehensive Gene Panel

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

Special coagulation testing for evaluating patients with bleeding or hypocoagulability states should be performed prior to genetic testing. For more information see ALBLD / Bleeding Diathesis Profile, Limited, Plasma.

This test is designed to evaluate a variety of clotting factor-related hereditary bleeding disorders.

If testing for hereditary bleeding disorders using a smaller panel is desired, a six-gene bleeding panel is available; order GNBLF / Bleeding Disorders, Focused Gene Panel, Next-Generation Sequencing, Varies

This test is not designed to evaluate for a single common hereditary bleeding disorder, such as when an individual has a known family history of hemophilia A or B or von Willebrand disease, specifically. If testing for a particular common hereditary bleeding disorder is desired, single gene tests are available for the *F8*, *F9*, and *VWF* genes. See GNHMA / Hemophilia A, *F8* Gene, Next-Generation Sequencing, Varies; GNHMB / Hemophilia B, *F9* Gene, Next-Generation Sequencing, Varies; or GNVWD / von Willebrand Disease, *VWF* and *GP1BA* Genes, Next-Generation Sequencing, Varies.

This test does not evaluate for the presence of inversions in the *F8* gene that can cause hemophilia A. If testing for possible inversions in the *F8* gene is desired, order F8INV / Hemophilia A *F8* Gene, Intron 1 and 22 Inversion Mutation Analysis, Whole Blood

This test is not designed to evaluate hereditary thrombosis disorders. If thrombosis is the indication for testing and testing for hereditary thrombosis disorders is desired, order GNTHR / Thrombosis Disorders, Comprehensive Gene Panel, Next-Generation Sequencing, Varies

This test is not designed to evaluate inherited platelet disorders. If a platelet disorder is suspected and comprehensive testing for platelet disorders is desired, order GNPLT / Platelet Disorders, Comprehensive Gene Panel, Next-Generation Sequencing, Varies

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

Additional Testing Requirements

All prenatal specimens must be accompanied by a maternal blood specimen; order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on the maternal specimen as this must be a different order number than the prenatal specimen.

Necessary Information

Rare Coagulation Disorder Patient Information is required. Testing may proceed without the patient information; however, the information aids in providing a more thorough interpretation. Ordering providers are strongly encouraged to fill out the form and send with the specimen.

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.

Submit only 1 of the following specimens:

Specimen Type: Whole blood
Container/Tube:
Preferred: Lavender top (EDTA)
Acceptable: Yellow top (ACD)
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 (preferred) 4 days/Refrigerated 4 days
Additional Information:
1. To ensure minimum volume and concentration of DNA are met, the requested volume must be submitted. Testing may be canceled if DNA requirements are inadequate.

Prenatal Specimens
Due to its complexity, consultation with the laboratory is required for all prenatal testing; call 800-533-1710 to speak to a genetic counselor.

Specimen Type: Amniotic fluid
Container/Tube: Amniotic fluid container
Specimen Volume: 20 mL
Specimen Stability Information: Refrigerated (preferred) 24 hours/Ambient 24 hours
Additional information:
1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULAF / Culture for Genetic Testing, Amniotic Fluid. An additional 2 to 3 weeks are required to culture amniotic fluid before genetic testing can occur.
3. All prenatal specimens must be accompanied by a maternal blood specimen; order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on the maternal specimen.

Specimen Type: Chorionic villi
Container/Tube: 15-mL Tube containing 15 mL of transport media
Specimen Volume: 20 mg
Specimen Stability Information: Refrigerated 24 hours
Additional Information:
1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks are required to culture fibroblasts before genetic testing can occur.
3. All prenatal specimens must be accompanied by a maternal blood specimen; order MATCC / Maternal Cell

Contamination, Molecular Analysis, Varies on the maternal specimen.

Acceptable:
Specimen Type: Confluent cultured cells
Container/Tube: T-25 flask
Specimen Volume: 2 Full flasks
Collection Instructions: Submit confluent cultured cells from another laboratory.
Specimen Stability Information: Ambient (preferred) 24 hours/Refrigerated 24 hours
Additional Information:
1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing.
3. All prenatal specimens must be accompanied by a maternal blood specimen; order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on the maternal specimen.

Forms

1. Rare Coagulation Disorder Patient Information (T824) is required.
2. **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)
3. If not ordering electronically, complete, print, and send an Coagulation Test Request (T753) with the specimen.

Specimen Minimum Volume

Blood: 1 mL; Amniotic fluid: 10 mL; Other specimen types: 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

Congenital or acquired bleeding diatheses are caused by a wide variety of coagulation abnormalities. The clinical presentation of an underlying bleeding disorder may include epistaxis, easy bruising, ecchymoses, umbilical stump bleeding, subcutaneous and muscle hematomas, prolonged post-injury or post-operative bleeding, bleeding into joint spaces, mucosal tract bleeds, intracranial bleeding, or gastrointestinal bleeding. Affected women may have an increased risk for bleeding during menstrual periods, pregnancy, and after childbirth, as well as recurrent pregnancy loss.

Determination of a hereditary bleeding disorder contributing to bleeding events in an individual or family can be useful

for prognosis and risk assessment. Identification of an alteration that is known or suspected to cause disease can also be useful for determining the risk for bleeding for family members.

This panel evaluates 25 genes associated with a variety of hereditary bleeding disorders or abnormal coagulation laboratory results such as prolonged clotting times, including prothrombin deficiency; factor V deficiency; factor VII deficiency; hemophilia A; hemophilia B; factor X deficiency; factor XI deficiency; factor XIII deficiency; fibrinogen deficiencies (afibrinogenemia, hypofibrinogenemia, dysfibrinogenemia, and hypodysfibrinogenemia); vitamin K-dependent clotting factors deficiencies 1 and 2; platelet-type von Willebrand disease; fletcher factor (prekallikrein) deficiency; kininogen deficiency; combined factor V and VIII deficiency; familial hyperfibrinolysis; hemorrhagic diathesis due to antithrombin Pittsburgh; plasminogen activator inhibitor 1 deficiency; alpha 2 antiplasmin deficiency; bleeding due to high soluble thrombomodulin; and von Willebrand disease.

The risk for developing bleeding associated with these syndromes varies. For example, intracranial bleeding was reported in 5% of cases with afibrinogenemia and hypofibrinogenemia, 7% of cases with prothrombin deficiency, 8% of cases with factor V deficiency, 21% of symptomatic cases with factor X deficiency, and is considered very uncommon in cases with factor XI deficiency or combined factor V and factor VIII deficiency.(1) Several of the genes on this panel have established bleeding risk or expert group guidelines.(1-7)

Indications for testing include, but are not limited to:
-Individuals with a suspected bleeding disorder for which there is no specific coagulation assay readily available
-Individuals who are at risk of being a carrier of a bleeding disorder, especially those bleeding disorders where carrier status cannot be easily determined by available coagulation assays
-Individuals whose personal or family history indicate coinheritance of multiple hereditary bleeding disorders

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(8) 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 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.

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.

Deletion/duplication events that extend past the genes included on the panel may occur. In these instances, genes included in the ordered test are provided on the report and interpreted, and genomic breakpoints are reported if they are confirmed. However, copy number variants for genes not listed in the Method Description are typically not reported or interpreted for haploinsufficiency/triplosensitivity. CMACB / Chromosomal Microarray, Congenital, Blood; WESPR / Panel to Whole Exome Sequencing Reflex Test, Varies; or WGSDX / Whole Genome Sequencing for Hereditary Disorders, Varies is recommended for a full interpretation of deletions/duplications predicted to extend past the genes included on the panel.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic mutations 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 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 professionals 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.(8) 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.

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. Mumford AD, Ackroyd S, Alikhan R, et al. Guideline for the diagnosis and management of the rare coagulation disorders: a United Kingdom Haemophilia Centre Doctors' Organization guideline on behalf of the British Committee for Standards in Haematology. Brit J Haematol. 2014;167(3):304-326
2. Pruthi RK. Hemophilia: a practical approach to genetic testing. Mayo Clin Proc. 2005;80(11):1485-1499
3. Srivastava A, Santagostino E, Dougall A, et al. WFH Guidelines for the Management of Hemophilia, 3rd edition. Haemophilia. 2020;26 Suppl 6:1-158. doi:10.1111/hae.14046
4. Laffan MA, Lester W, O'Donnell JS, et al. The diagnosis and management of von Willebrand disease: a United Kingdom Haemophilia Centre Doctors Organization guideline approved by the British Committee for Standards in Haematology. Brit J Haematol. 2014;167(4):453-465
5. James PD, Connell NT, Ameer B, et al. ASH ISTH NHF WFH 2021 guidelines on the diagnosis of von Willebrand disease. Blood Adv. 2021;5(1):280-300
6. International Society on Thrombosis and Haemostasis: Bleeding Thrombotic and Platelet Disorder TIER1 genes. ISTH; 2018. Updated July 26, 2024. Accessed March 2, 2026. Available at:www.isth.org/page/GinTh_GeneLists
7. Megy K, Downes K, Simeoni I, et al. Curated disease-causing genes for bleeding, thrombotic, and platelet disorders: Communication from the SSC of the ISTH. J Thromb Haemost. 2019;17(8):1253-1260
8. Richards S, Aziz N, Bale S, et al. ACMG Laboratory Quality Assurance Committee: 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 genes analyzed, 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 deletion-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 genes analyzed.

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. See Targeted Genes and Methodology Details for Bleeding Disorders, Comprehensive Gene Panel and Methodology Details for details regarding the targeted genes analyzed for each test and specific gene regions not routinely covered.(Unpublished Mayo method)

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.

Genes analyzed: *F2*, *F5*, *F7*, *F8*, *F9*, *F10*, *F11*, *F13A1*, *F13B*, *FGA*, *FGB*, *FGG*, *GGCX*, *GP1BA*, *KLKB1*, *KNG1*, *LMAN1*, *MCFD2*, *PLAT*, *SERPINA1* c.1145T>G only, *SERPINE1*, *SERPINF2*, *THBD*, *VKORC1*, and *VWF*

PDF Report
Supplemental

Day(s) Performed
Varies

Report Available
28 to 42 days

Specimen Retention Time
Whole blood: 2 weeks (if available); Amniotic fluid, chorionic villi, cultured chorionic villi: 1 month; Extracted DNA: 3 months

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

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

81443
88233-Tissue culture, skin, solid tissue biopsy (if appropriate)
88240-Cryopreservation (if appropriate)
88235-Amniotic fluid culture (if appropriate)
81265-Maternal cell contamination (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
GNBLC	Bleeding Comprehensive Panel, NGS	105330-5

Result ID	Test Result Name	Result LOINC® Value
619258	Test Description	62364-5
619259	Specimen	31208-2
619260	Source	31208-2
619261	Result Summary	50397-9
619262	Result	82939-0
619263	Interpretation	59465-5
619264	Additional Results	82939-0
619265	Resources	99622-3
619266	Additional Information	48767-8
619267	Method	85069-3
619268	Genes Analyzed	82939-0
619269	Disclaimer	62364-5
619270	Released By	18771-6