Coagulation Factor Deficiency Panel

Test code: HE0501

The Blueprint Genetics Coagulation Factor Deficiency Panel is a 16 gene test for genetic diagnostics of patients with clinical suspicion of hemophilia A, hemophilia B, rare bleeding disorder or Von Willebrand disease.

Inheritance pattern in these coagulation factor deficiencies may be autosomal recessive, autosomal dominant or X-linked. This panel is included in the Bleeding Disorder/Coagulopathy Panel and Comprehensive Hematology Panel.

About Coagulation Factor Deficiency

Coagulation Factor Deficiencies refers to a heterogenous group of inherited bleeding disorders. The most common coagulation factor deficiencies are hemophilias (A and B), and von Willebrand disease (VWD), accounting together for 95% of bleeding disorders. The clinical presentation of inherited bleeding disorders can be highly variable and the severity of the clinical manifestations depends on the biological activity of the coagulation factor. The diseases are characterized by abnormal bleeding of variable severity occurring either spontaneously or in association with an invasive procedure. Age of onset in hemophilia is in infancy. In VWD, the symptoms can begin at any age. Hemophilia A and B and are inherited in an X-linked recessive manner through mutations in the \( F8 \) and \( F9 \) genes, respectively. The diseases primarily affect males, but female carriers of the disease-causing mutations may also manifest generally milder forms of the disease. VWD is inherited in both autosomal dominant and recessive manners and the causative gene is \( VWF \). Rare bleeding disorders (RBDs) include inherited deficiencies of coagulation factors fibrinogen, factor (F)II, FV, combined FV and FVIII, FVII, FX, FXI, FXIII, and congenital deficiency of vitamin K-dependent factors (VKCFDs). RBDs are autosomal recessive conditions and deficiencies in FVII and FXI together account for 64% of cases (PMID: 25712993). The associated genes are \( FGA, FGB, FGG, F2, F5, F7, F10, F11, F13A1, LMAN1 \) and \( VKORC1 \). The prevalence of hemophilia is estimated at 1:12,000 and the prevalence of symptomatic VWD that requires specific treatment is estimated at between 1:50,000 and 1:8,500.

Availability

Results in 3-4 weeks. We do not offer a maternal cell contamination (MCC) test at the moment. We offer prenatal testing only for cases where the maternal cell contamination studies (MCC) are done by a local genetic laboratory. Read more: http://blueprintgenetics.com/faqs/#prenatal

Gene set description

Genes in the Coagulation Factor Deficiency Panel and their clinical significance

<table>
<thead>
<tr>
<th>Gene</th>
<th>Associated phenotypes</th>
<th>Inheritance</th>
<th>ClinVar</th>
<th>HGMD</th>
</tr>
</thead>
<tbody>
<tr>
<td>F2</td>
<td>Thrombophilia due to thrombin defect, Prothrombin deficiency, congenital</td>
<td>AD/AR</td>
<td>14</td>
<td>66</td>
</tr>
<tr>
<td>F5</td>
<td>Factor V deficiency, Thrombophilia due to activated protein C resistance</td>
<td>AD/AR</td>
<td>18</td>
<td>162</td>
</tr>
<tr>
<td>F7</td>
<td>Factor VII deficiency</td>
<td>AR</td>
<td>23</td>
<td>304</td>
</tr>
<tr>
<td>F8*</td>
<td>Hemophilia A</td>
<td>XL</td>
<td>276</td>
<td>3074</td>
</tr>
<tr>
<td>F9</td>
<td>Hemophilia B, Warfarin sensitivity, Thrombophilia, due to factor IX defect</td>
<td>XL</td>
<td>109</td>
<td>1260</td>
</tr>
<tr>
<td>F10</td>
<td>Factor X deficiency</td>
<td>AR</td>
<td>15</td>
<td>147</td>
</tr>
<tr>
<td>F11</td>
<td>Factor XI deficiency</td>
<td>AD/AR</td>
<td>35</td>
<td>250</td>
</tr>
<tr>
<td>F12</td>
<td>Angioedema</td>
<td>AD/AR</td>
<td>5</td>
<td>53</td>
</tr>
<tr>
<td>F13A1</td>
<td>Factor XIII deficiency</td>
<td>AR</td>
<td>20</td>
<td>165</td>
</tr>
<tr>
<td>FGA</td>
<td>Afibrinogenemia, congenital, Dysfibrinogenemia, congenital, Hypodysfibrinogenemia, congenital, Familial visceral amyloidosis</td>
<td>AD/AR</td>
<td>9</td>
<td>140</td>
</tr>
</tbody>
</table>
**Gene** | **Genomic location HG19** | **HGVS** | **RefSeq** | **RS-number** | **Comment** | **Reference**
---|---|---|---|---|---|---
F13A1 | Chr6:6320808 | c.-19+12A>T | NM_000129.3 | rs2815822 | | |
F2 | Chr11:46761055 | c.*97G>A | NM_000506.4 | rs1799963 | | |
F8 | ChrX:154219579 | c.601+1632G>A | NM_000132.3 | rs387906429 | | |
FGG | Chr4:155530122 | c.667-320A>T | NM_021870.2 | | | |

**Non-coding disease causing variants covered by the panel**

**Test performance**

Blueprint Genetics offers a comprehensive Coagulation Factor Deficiency Panel that covers classical genes associated with congenital factor II deficiency, congenital factor V deficiency, congenital factor VII deficiency, congenital factor X deficiency, congenital factor XI deficiency, hemophilia A, hemophilia B, hereditary combined deficiency of vitamin K-dependent clotting factors, rare bleeding disorder, severe hemophilia A, severe hemophilia B, Von Willebrand disease and Von Willebrand disease type 1. The genes are carefully selected based on the existing scientific evidence, our experience and most current mutation databases. Candidate genes are excluded from this first-line diagnostic test. The test does not recognise balanced translocations or complex inversions, and it may not detect low-level mosaicism. The test should not be used for analysis of sequence repeats or for diagnosis of disorders caused by mutations in the mitochondrial DNA.

Analytical validation is a continuous process at Blueprint Genetics. Our mission is to improve the quality of the sequencing process and each modification is followed by our standardized validation process. Average sensitivity and specificity in Blueprint NGS Panels is 99.3% and 99.9% for detecting SNPs. Sensitivity to for indels vary depending on the size of the alteration: 1-10bps (96.0%), 11-20 bps (88.4%) and 21-30 bps (66.7%). The longest detected indel was 46 bps by sequence analysis. Detection limit for Del/Dup (CNV) analysis varies through the genome depending on exon size, sequencing coverage and sequence content. The sensitivity is 71.5% for single exon deletions and duplications and 99% for three exons’ deletions and duplications. We have validated the assays for different starting materials including EDTA-blood, isolated DNA (no FFPE) and saliva that all provide high-quality results. The diagnostic yield varies substantially depending on the used assay, referring healthcare professional, hospital and country. Blueprint Genetics’ Plus Analysis (Seq+Del/Dup) maximizes the chance to find
molecular genetic diagnosis for your patient although Sequence Analysis or Del/Dup Analysis may be cost-effective first line test if your patient’s phenotype is suggestive for a specific mutation profile.

**Bioinformatics**

The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. The highest relevance in the reported variants is achieved through elimination of false positive findings based on variability data for thousands of publicly available human reference sequences and validation against our in-house curated mutation database as well as the most current and relevant human mutation databases. Reference databases currently used are the 1000 Genomes Project (http://www.1000genomes.org), the NHLBI GO Exome Sequencing Project (ESP; http://evs.gs.washington.edu/EVS), the Exome Aggregation Consortium (ExAC; http://exac.broadinstitute.org), ClinVar database of genotype-phenotype associations (http://www.ncbi.nlm.nih.gov/clinvar) and the Human Gene Mutation Database (http://www.hgmd.cf.ac.uk). The consequence of variants in coding and splice regions are estimated using the following *in silico* variant prediction tools: SIFT (http://sift.jcvi.org), Polyphen (http://genetics.bwh.harvard.edu/pph2/), and Mutation Taster (http://www.mutationtaster.org).

Through our online ordering and statement reporting system, Nucleus, the customer can access specific details of the analysis of the patient. This includes coverage and quality specifications and other relevant information on the analysis. This represents our mission to build fully transparent diagnostics where the customer gains easy access to crucial details of the analysis process.

**Clinical interpretation**

In addition to our cutting-edge patented sequencing technology and proprietary bioinformatics pipeline, we also provide the customers with the best-informed clinical report on the market. Clinical interpretation requires fundamental clinical and genetic understanding. At Blueprint Genetics our geneticists and clinicians, who together evaluate the results from the sequence analysis pipeline in the context of phenotype information provided in the requisition form, prepare the clinical statement. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals, even without training in genetics.

Variants reported in the statement are always classified using the Blueprint Genetics Variant Classification Scheme modified from the ACMG guidelines (Richards et al. 2015), which has been developed by evaluating existing literature, databases and with thousands of clinical cases analyzed in our laboratory. Variant classification forms the corner stone of clinical interpretation and following patient management decisions. Our statement also includes allele frequencies in reference populations and in silico predictions. We also provide PubMed IDs to the articles or submission numbers to public databases that have been used in the interpretation of the detected variants. In our conclusion, we summarize all the existing information and provide our rationale for the classification of the variant.

A final component of the analysis is the Sanger confirmation of the variants classified as likely pathogenic or pathogenic. This does not only bring confidence to the results obtained by our NGS solution but establishes the mutation specific test for family members. Sanger sequencing is also used occasionally with other variants reported in the statement. In the case of variant of uncertain significance (VUS) we do not recommend risk stratification based on the genetic finding. Furthermore, in the case VUS we do not recommend use of genetic information in patient management or genetic counseling. For some cases Blueprint Genetics offers a special free of charge service to investigate the role of identified VUS.

We constantly follow genetic literature adapting new relevant information and findings to our diagnostics. Relevant novel discoveries can be rapidly translated and adopted into our diagnostics without delay. These processes ensure that our diagnostic panels and clinical statements remain the most up-to-date on the market.

**CPT codes**

SEQ 81479
DEL/DUP 81479
ICD codes

Commonly used ICD-10 codes when ordering the Coagulation Factor Deficiency Panel

<table>
<thead>
<tr>
<th>ICD-10</th>
<th>Disease</th>
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<tbody>
<tr>
<td>D68.0</td>
<td>Von Willebrand disease</td>
</tr>
<tr>
<td>D66</td>
<td>Hemophilia A</td>
</tr>
<tr>
<td>D67</td>
<td>Hemophilia B</td>
</tr>
</tbody>
</table>

Accepted sample types

- EDTA blood, min. 1 ml
- Purified DNA, min. 5μg
- Saliva (Oragene DNA OG-500 kit)

Label the sample tube with your patient's name, date of birth and the date of sample collection.

Note that we do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue.

Resources

- World Federation of Hemophilia
- National Hemophilia Foundation
- Hemophilia & Rare Bleeding Disorders
- Hemophilia Federation of America
- Canadian Hemophilia Society
- Haemophilia Society UK
- Irish Haemophilia Society
- Suomen Hemofiliayhdistys
- NORD - Von Willebrand Disease
- NORD - Hemophilia A
- NORD - Hemophilia B
- NORD - Factor XI Deficiency
- Gene Reviews - Von Willebrand Disease
- Gene Reviews - Hemophilia A
- Gene Reviews - Hemophilia B