Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	Unknown
Gender:	Unknown
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Factor V Leiden (F5) R506Q Mutation

ARUP test code 0097720

FACV Specimen	Whole Blood
Factor V Leiden (F5) R506Q Mutation	Negative

Indication for testing: Assess genetic risk for thrombosis.

NEGATIVE: The factor V Leiden variant, c.1601G>A; p.Arg534Gln, was not detected. This does not exclude a genetic cause for thrombophilia. If this individual has had a previous venous thromboembolism, this negative result is unlikely to significantly reduce the risk for recurrence; thus, future clinical management to reduce recurrence should not be altered.

This result has been reviewed and approved by [redacted]

H=High, L=Low, *=Abnormal, C=Critical

BACKGROUND INFORMATION: Factor V Leiden (F5) R506Q Mutation

CHARACTERISTICS: Venous thromboembolism (VTE) is multifactorial caused by a combination of genetic and environmental factors. The Factor V Leiden (FVL) variant is the most common cause of inherited VTEs, accounting for over 90 percent of activated protein C (APC) resistance. Because the FVL variant eliminates the APC cleavage site, factor V is inactivated slower, thus persisting longer in blood circulation, leading to more thrombin production. Other genetic risk factors for VTE include, male sex and variants in antithrombin, protein C, protein S, or factor XIII. Non-genetic risk factors include, age, smoking, prolonged immobilization, malignant neoplasms, surgery, pregnancy, oral contraceptives, estrogen replacement therapy, tamoxifen and raloxifene therapy.
INCIDENCE OF FACTOR V LEIDEN VARIANT: Approximately 5 percent of Caucasians, 2 percent of Hispanics, 1 percent of African Americans and 0.5 percent of Asians are heterozygous; homozygosity occurs in 1 in 1500 Caucasians.
INHERITANCE: Semi-dominant; both heterozygotes and homozygotes are at increased risk for VTE.
PENETRANCE: Lifetime risk of VTE is 10 percent for heterozygotes and 80 percent of homozygotes.
CAUSE: The pathogenic gain of function in the F5 gene variant c.1601G>A (p.Arg534Gln). Legacy nomenclature: R506Q (1691G>A)
CLINICAL SENSITIVITY: 20-50 percent of individuals with an isolated VTE have the FVL variant.
METHODOLOGY: Polymerase chain reaction and fluorescence monitoring.
ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. F5 gene mutations, other than p.Arg534Gln, will not be detected.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

Prothrombin (F2) c.*97G>A (G20210A) Pathogenic Variant

ARUP test code 0056060

PT PCR Specimen	Whole Blood
Prothrombin (F2) G20210A Variant	Negative

H=High, L=Low, *=Abnormal, C=Critical

Indication for testing: Assess genetic risk for thrombosis.

NEGATIVE: The Factor II, prothrombin G20210A mutation, was not detected. Other causes of elevated prothrombin levels and hereditary forms of venous thrombosis have not been excluded.

Recommendations: If clinically indicated, testing for other inherited or acquired thrombophilic disorders is recommended including DNA testing for the factor V Leiden mutation, measurement of total plasma homocysteine concentration, serological assays for anticardiolipin antibodies, multiple phospholipid-dependent coagulation assays for lupus inhibitor, protein C activity, protein S activity or free protein S antigen, and antithrombin activity.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Prothrombin (F2) c.*97G>A (G20210A) Pathogenic Variant
CHARACTERISTICS: The Factor II, c.*97G>A (G20210A) pathogenic variant is a common genetic risk factor for venous thrombosis associated with elevated prothrombin levels leading to increased rates of thrombin generation and excessive growth of fibrin clots. The expression of Factor II thrombophilia is impacted by coexisting genetic thrombophilic disorders, acquired thrombophilic disorders (eg, malignancy, hyperhomocysteinemia, high factor VIII levels), and circumstances including: pregnancy, oral contraceptive use, hormone replacement therapy, selective estrogen receptor modulators, travel, central venous catheters, surgery, and organ transplantation.
INCIDENCE: Approximately 2 percent of Caucasians and 0.3 percent of African Americans are heterozygous; homozygosity occurs in 1 in 10,000 individuals.
INHERITANCE: Incomplete autosomal dominant.
PENETRANCE: The risk of thrombosis is increased 2-4 fold for heterozygotes and further increased for homozygotes.
CAUSE: Homozygosity or heterozygosity for F2 c.*97G>A (G20210A).
PATHOGENIC VARIANT TESTED: F2 c.*97G>A (G20210A).
CLINICAL SENSITIVITY FOR VENOUS THROMBOSIS: Approximately 10 percent.
METHODOLOGY: Polymerase chain reaction and fluorescence monitoring.
ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. F2 gene variants, other than c.*97G>A (G20210A), will not be detected.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

Methylenetetrahydrofolate Reductase (MTHFR) 2 Variants

ARUP test code 0055655

MTHFR PCR Specimen	Whole Blood
MTHFR Variant: c.665C>T	Negative

H=High, L=Low, *=Abnormal, C=Critical

MTHFR Variant: c.1286A>C	Negative
MTHFR Interpretation	See Note

Indication for testing: Determine genetic contribution to hyperhomocysteinemia.

Negative: Neither of the common MTHFR gene variants tested, c.665C>T (previously designated C677T) and c.1286A>C (previously designated A1298C), were detected. Other causes of elevated homocysteine levels were not evaluated.

This result has been reviewed and approved by [redacted]

Background Information: Methylenetetrahydrofolate Reductase (MTHFR) 2 Variants
Characteristics: Variants in the MTHFR gene may reduce enzyme activity contributing to hyperhomocysteinemia. Although hyperhomocysteinemia was previously reported to be a risk factor for many conditions, especially venous thrombosis and cardiovascular disease, recent meta-analysis casts doubt on whether lifelong moderate homocysteine elevation has an effect on cardiovascular disease. The American College of Medical Genetics Practice Guidelines indicate that individuals with elevated homocysteine and two copies of the c.665C>T variant have an odds ratio of 1.27 for venous thromboembolism. Thus, they recommend MTHFR genotyping not be ordered as part of a routine evaluation for recurrent pregnancy loss or thromobophilia due to questionable clinical significance.
Incidence: The allele frequency of the c.665C>T variant is 0.35 in European Caucasians, 0.5 in Hispanics, and 0.12 in African Americans.
Inheritance: Autosomal recessive; two copies of the c.665C>T variant may be a contributing factor to hyperhomocysteinemia.
Variants Tested: c.665C>T(p.Ala222Val) and c.1286A>C(p.Glu429Ala). (legacy names C677T and A1298C, respectively).
Clinical Sensitivity: Undefined; hyperhomocysteinemia is caused by genetic, physiologic and environmental factors. MTHFR variants are only one contributing factor.
Methodology: Polymerase chain reaction (PCR) and fluorescence monitoring.
Analytical Sensitivity & Specificity: 99 percent.
Limitations: Only two MTHFR gene variants (c.665C>T and c.1286A>C) are tested. Diagnostic errors can occur due to rare sequence variations.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

H=High, L=Low, *=Abnormal, C=Critical

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
FACV Specimen	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Factor V Leiden (F5) R506Q Mutation	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
PT PCR Specimen	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Prothrombin (F2) G20210A Variant	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR PCR Specimen	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Variant: c.665C>T	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Variant: c.1286A>C	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Interpretation	22-125-105238	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

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