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*****Example Report*****

Patient Age/Gender: 19 years Female
Printed: 28-Dec-18 07:49:03

Procedure	Result	Units	Ref Interval	Accession	Collected	Received	Reported/ Verified
FACV Specimen	Whole Blood			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
Factor V Leiden (F5) R506Q Mutation	**Homozygous *f**			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
PT PCR Specimen	Whole Blood			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
Prothrombin (F2) G20210A Variant	Negative f			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
MTHFR PCR Specimen	Whole Blood			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
MTHFR Mutation: c.665C>T	**Heterozygous ***			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
MTHFR Mutation: c.1286A>C	**Heterozygous ***			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15
MTHFR Interpretation	See Note f			18-352-900100	18-Dec-18 12:44:00	18-Dec-18 12:44:00	18-Dec-18 12:52:15

18-Dec-18 12:44:00 Factor V Leiden (F5) R506Q Mutation:

Indication for testing: Assess genetic risk for thrombosis.

HOMOZYGOUS: Two copies of the factor V Leiden variant, c.1601G>A; p.Arg534Gln, were detected. This is associated with activated protein C resistance and an 80 fold increased risk for venous thrombosis in comparison to individuals without this variant. Genetic consultation is recommended.

This result has been reviewed and approved by Rong Mao, M.D.

18-Dec-18 12:44:00 Prothrombin (F2) G20210A Variant:

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 Rong Mao, M.D.

18-Dec-18 12:44:00 MTHFR Interpretation:

Indication for testing: Determine genetic contribution to hyperhomocysteinemia.

Compound Heterozygous MTHFR c.665C>T/c.1286A>C: One copy each of the two MTHFR variants tested, c.665C>T (previously designated C677T) and c.1286A>C (previously designated A1298C), were detected. This genotype may be associated with a mild but clinically insignificant decrease in MTHFR enzyme activity.

This result has been reviewed and approved by Rong Mao, M.D.

18-Dec-18 12:44:00 Factor V Leiden (F5) R506Q Mutation:
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.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

18-Dec-18 12:44:00 Prothrombin (F2) G20210A Variant:
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.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

18-Dec-18 12:44:00 MTHFR Interpretation:
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.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS