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

Physician: Doctor, Example

Patient: Patient, Example

DOB	10/26/2018
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Methylenetetrahydrofolate Reductase (MTHFR) 2 Variants

ARUP test code 0055655

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

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

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 and 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.

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
MTHFR PCR Specimen	24-054-401875	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Variant: c.665C>T	24-054-401875	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Variant: c.1286A>C	24-054-401875	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MTHFR Interpretation	24-054-401875	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

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