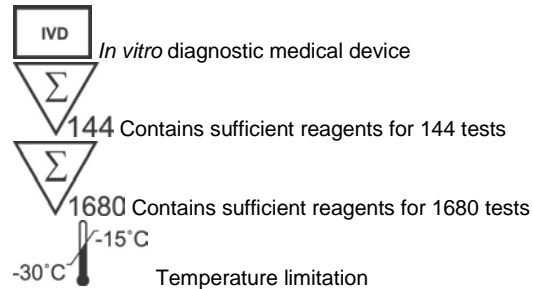


Invader® MTHFR 677

REF 95-454: 144 tests or REF 95-458: 1680 tests



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I. INDICATIONS AND USE

A. Intended Use

The Invader® MTHFR 677 test is an *in vitro* diagnostic test intended for the detection and genotyping of a single point mutation (C to T at position 677) of the human 5,10-methylenetetrahydrofolate reductase (MTHFR) gene in isolated genomic DNA obtained from whole blood potassium EDTA samples from patients with suspected thrombophilia.

B. Clinical Significance

MTHFR is the metabolic enzyme involved in the conversion of homocysteine to methionine via the remethylation pathway. The MTHFR C677T mutation is a base change of a cytosine (C) with a thymine (T) at nucleotide position 677 giving rise to an amino acid replacement of valine for alanine at codon 222.^{1,2} The MTHFR C677T mutation renders the resultant enzyme more thermolabile, decreasing enzymatic activity by 30% in heterozygous individuals and by 70% in homozygous individuals, and is associated with increased plasma homocysteine levels¹. The prevalence of the MTHFR C677T mutation varies widely with ethnicity but not between sexes in the same ethnic group.³ Frequency of the mutant T allele is generally between 30% and 40% in Caucasians,^{4,5-7} Chinese,^{8,9} and Japanese,^{10,11} — higher in American Hispanics¹² — and below 5% in South African Blacks.¹³ Patients with classic homocystinuria are at extremely elevated risk of venous thromboembolism (VTE). Homozygosity of this mutation accounts for about a third of cases of hyperhomocysteinemia.¹⁴ Hyperhomocysteinemia interacts synergistically with coexisting Factor V Leiden to increase the relative risk of VTE to 20-fold greater than individuals without either risk factor.¹⁴ Elevated plasma homocysteine has also been associated with an increased risk of cardiovascular disease and neural tube defects in fetuses of pregnant women.^{4,15,16}

Principles and Procedures

The Invader® MTHFR 677 test utilizes the Invader Plus® chemistry with DNA isolated from human whole blood for the detection of the targeted sequence polymorphism. Specifically, the Invader Plus® chemistry utilizes a single-tube, two phase reaction, including target amplification and signal generation (mediated by Invader® chemistry). Invader Plus® reaction mixes are assembled by combining the MTHFR 677 Oligo Mix, Universal Enzyme Mix, and Universal Buffer. In a 96-well plate, reaction mix is combined with purified genomic DNA samples, as well as four (4) controls included with the test. The No DNA Control is used by the interpretive software to set the "noise" component of the run for "signal-to-noise" calculations. The genotype-specific controls (WT, HET, MUT) ensure reagents were assembled correctly and perform according to the specifications. The 96-well plate is transferred to an appropriately programmed thermal cycler for target amplification and signal generation. In the target amplification phase of the reaction, amplification is carried out using "two-step" cycling conditions (i.e., denaturation & annealing/extension). Following amplification, Taq polymerase is inactivated by a 10 minute incubation at 99°C, after which the thermal cycler proceeds to 63°C to initiate the signal generation (Invader®) phase of the reaction (see Figure 1).

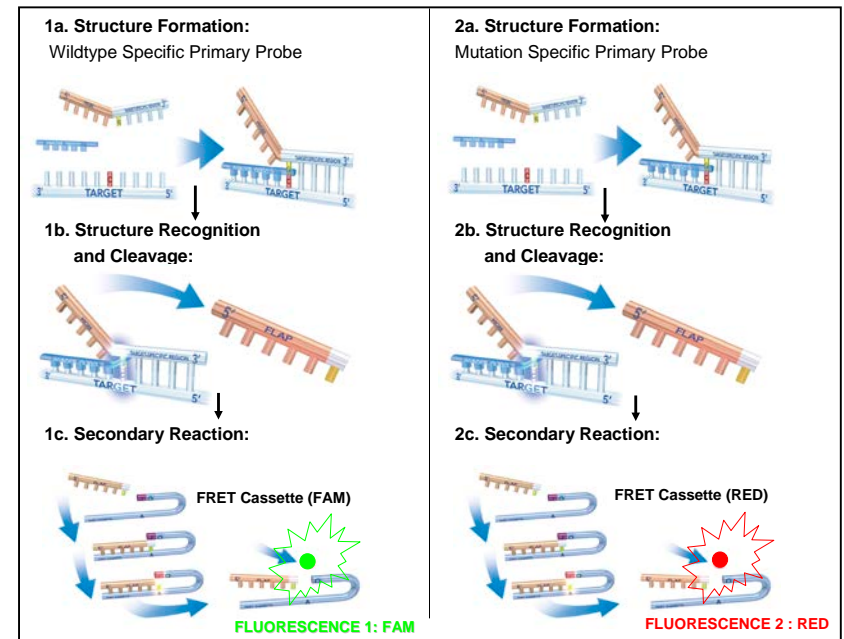


Figure 1: Invader Plus® Signal Generation Phase

During the signal generation phase, a discriminatory Primary Probe transiently hybridizes to the amplified target sequence along with an Invader[®] oligonucleotide, to form an overlapping structure. The 5'-end of the Primary Probe includes a 5'-flap that does not hybridize to the target DNA. The 3'-nucleotide of the bound Invader[®] oligonucleotide overlaps the Primary Probe, and does not hybridize to the target DNA. The Cleavase[®] enzyme recognizes this overlapping structure and cleaves off the unpaired 5'-flap of the Primary Probe, releasing it as a target-specific product. The Primary Probe is designed to have a melting temperature aligned with the Invader[®] reaction temperature so that under the isothermal reaction conditions (~63°C) the Primary Probes cycle on and off the target DNA. This allows for multiple rounds of Primary Probe cleavage for each DNA target resulting in an accumulation of the number of released 5'-flaps. The released 5'-flap transiently hybridizes with a corresponding FRET cassette forming an overlapping structure that is recognized and the fluorophore is cleaved from the FRET cassette by the Cleavase[®] enzyme. The 5'-flap is designed to have a melting temperature aligned with the Invader[®] reaction temperature, so that the 5'-flaps cycle on and off of the corresponding FRET cassettes. This allows for multiple rounds of FRET cassette cleavage for each 5'-flap, and an accumulation of released fluorophore. When the FRET cassette is cleaved, a fluorophore and quencher are separated, generating detectable fluorescence signal. The format uses two different discriminatory Primary Probes, one for the mutant allele and one for the wild type allele (Figure 1). Each Primary Probe is assigned a unique 5'-flap, and distinct FRET cassette, with a spectrally distinct fluorophore. By design, the released 5'-flaps will bind only to their respective FRET cassettes to generate a target-specific signal, linking the wild type allele with one fluorophore (Fluorescence 1: FAM) and the mutant allele with the second fluorophore (Fluorescence 2: RED).

II. MATERIALS AND METHODS

A. Reagents Provided

Note: For information on any hazard and precautionary statements that may be associated with reagents, refer to the Safety Data Sheet Library at www.hologic.com/sds.

Reagent	Vial Label Abbreviation
MTHFR 677 Oligo Mix	None
Universal Buffer	B
Universal Enzyme Mix	E
Invader [®] MTHFR 677 WT	None
Invader [®] MTHFR 677 HET	None
Invader [®] MTHFR 677 MUT	None
No DNA Control	C4

B. Reaction Mix

All of the Invader[®] MTHFR 677 reagents are supplied in concentrations ready for use. The amount of reagents required for each reaction is summarized in Table 2. Make sure to mix reagents well prior to use.

C. Other Materials Provided

Invader Call Reporter[®] software and Invader[®] MTHFR 677 software
 Software User Manual for Invader[®] MTHFR 677 (MAN-01689)

Both software programs are provided along with the first order/shipment of the Invader[®] MTHFR 677 test. Contact Hologic Technical Support (1 888 484 4747) if an additional copy is needed.

D. Materials and Reagents Needed But Not Provided

- Thermal cycler with heated lid capable of holding set temperatures within +/- 1°C.
- Multi-well Fluorometer (see Software User Manual for Invader[®] MTHFR 677, MAN-01689, for fluorometer software specifications)
- Computer (see Software User Manual for Invader[®] MTHFR 677, MAN-01689, for computer specifications)
- Pipette tips, filter barrier
- 96-well plates
- Optically Clear Adhesive Plate sealers
- Nuclease-free water
- Mineral oil
- Microcentrifuge tubes
- Commercially Available DNA Extraction kit (or validated in-house laboratory method)
- General laboratory equipment as needed (tube racks, micropipettors, multichannel pipette, microcentrifuge, vortex mixer).

E. Storage and Handling

NOTE: Product requires multiple storage temperatures for reagents.



Immediately upon receipt, genotype-specific controls are to be stored at +2°C to +8°C. All other components of the kit should be stored between -30°C to -15°C in a non-frost-free freezer.

Prior to use, allow reagents to equilibrate to room temperature, excluding the Universal Enzyme Mix which should remain between -30°C to -15°C until just prior to use. Minimize reagent exposure to light. Do not subject the reagents to more than 15 freeze-thaw cycles.

F. Indications of Instability

When properly stored, the reagents are stable through the dating indicated on the label. There are no obvious signs to indicate instability of this product. However, genotype-specific controls should be run simultaneously with unknown specimens. Increase in non-specific fluorescence signal may indicate reagent instability. If this is observed, contact Hologic Technical Support (1 888 484 4747).

G. Specimen Collection and Preparation for Analysis

Clinical Specimens: Human whole blood samples should be anti-coagulated with potassium EDTA. DNA extraction may be accomplished using commercially available DNA extraction chemistries, capable of obtaining DNA concentrations greater than 5 ng/μL for use in the Invader[®] MTHFR 677 test.

Genotype-Specific Control Samples: Genotype-specific (i.e., WT, HET, MUT) controls are provided with the test. Genotype-specific controls consist of synthetic DNA in a blood-like matrix, and are not infectious. Genotype-specific controls must be extracted prior to use, and can serve as a DNA extraction control as well if prepared using the same method as the blood samples. Prior to extraction, genotype-specific controls should be vortexed (30-60 seconds) to re-suspend the contents.

DNA Storage: The purified DNA from samples and genotype-specific controls can be used immediately or safely stored in elution buffer as per the DNA Extraction Kit manufacturer's recommendation.

DNA Preparation: Extracted clinical specimen and genotype-specific control DNA must be diluted 1:20 in nuclease-free water just prior to running the Invader[®] MTHFR 677 test (see Section IV A. 3). The level of DNA present in the extracted genotype-specific controls may not be detectable with certain quantitation methods and is not quantifiable by spectrophotometer measurements.

III. SAFETY ISSUES

A. Safety and Handling Precautions

1. Universal safety precautions should be used when handling any human whole blood samples. Specimens should be disposed of according to local requirements.
2. Product components (product residuals and packaging) can be considered laboratory waste. Dispose of unused reagents and waste in accordance with applicable federal, state, and local regulations.

B. Precautions

1. The Invader[®] MTHFR 677 test is intended for *in vitro* diagnostic use.
2. These components have been tested as a unit. Do not interchange components from their sources or from different lots. Do not pool reagents from different lots or from different vials of the same lot.
3. Take reasonable precautions when handling reagents. Use disposable gloves when handling suspected carcinogens or toxic materials.
4. Do not smoke, eat or drink in areas where specimens or reagents are being handled.
5. Avoid contact of eyes and mucous membranes with reagents. If reagents come in contact with sensitive areas, wash with copious amounts of water.
6. Patient specimens and all materials coming into contact with them should be handled as if capable of transmitting infection and disposed of with proper precautions. Never pipette by mouth and avoid contact of reagents and specimens with skin and mucous membranes.
7. Avoid microbial contamination of reagents as this could produce incorrect results.
8. Incubation times and temperatures other than those specified may give erroneous results.
9. The reagents have been optimally formulated and further dilution may result in loss of performance.
10. Do not use reagents after their expiration date.
11. Use fresh mineral oil for each reaction set-up (do not transfer these reagents back to the original container once they have been dispensed).
12. Provided genotype-specific controls are in a blood-like matrix and are not infectious. Material can be used in a Bio-Safety Level 1 laboratory.
13. **IMPORTANT CONTAMINATION PRECAUTIONS: This product generates amplified DNA targets. When performing the test, caution must be taken to prevent amplicon contamination of work areas. Always use barrier pipette tips for pipetting procedures. Perform the amplification set up in an isolated area with dedicated pipettes. Use tips and tubes that are DNase/RNase free.**



C. Toxicity of Invader[®] Reagents

The Invader[®] MTHFR 677 test reagents are not controlled as dangerous substances and no toxicity has been determined.

IV. INSTRUCTIONS FOR USE

A. Invader[®] Test Step by Step Procedure

Software Set up

1. Open the Invader Call Reporter[®] software and complete the testing information. Details for using the software can be found in the software user manual (Software User Manual for Invader[®] MTHFR 677, MAN-01689).
 - a. Enter the name of the operator.
 - b. In the dropdown "Menu Selection" select the MTHFR 677 test.
 - c. Enter the number of samples to be tested in the space provided.
 - d. Click the "Proceed to Mix Preparation" button located in the lower right corner of the window.

- e. On the Mix Preparation tab, fill in the green shaded boxes for Lot Numbers and Expiration Dates for the reagents used during the testing.
 - f. If desired, click the "View/Save PDF" button located in the upper right corner of the window. Print the PDF and then close the PDF window.
 - g. On the Sample Placement tab, enter the Sample IDs into the list on the left side of window. The sample ID list runs down columns (i.e., wells E1 through H1, followed by A2 through H2, and then A3 through H3...).
 - h. Verify all samples are entered in the list and are in correct position of the sample grid.
 - i. If desired, click the "View/Save PDF" button located in the upper right corner of the window. Print the PDF and then close the PDF window.
 - j. Close the Invader Call Reporter[®] software.
2. Confirm the thermal cycler is programmed as stated in Figure 3.

Sample Preparation (1:20 Dilution)

3. Dilute extracted genotype-specific controls and all extracted sample DNAs (1:20) using 5 μ L of genotype-specific control/sample and 95 μ L nuclease-free water in a 0.5 mL tube or similar consumable. Mix the diluted genotype-specific controls/samples thoroughly. Do not dilute the No DNA Control (Control 4) prior to use.

Mix Preparation

4. Remove the reagents (Oligo Mix, Universal Buffer, No DNA Control) from their respective storage locations and allow them to equilibrate to room temperature for approximately 30 minutes. Do not remove the Universal Enzyme Mix from the -30°C to -15°C freezer until just prior to use.
5. Vortex the components of the reaction mix thoroughly and spin down the contents in a microcentrifuge for 3 – 5 seconds.
6. Combine the components of the reaction mix as shown in Table 2 in a microcentrifuge tube.



Note: The prepared reaction mixture must be used within 30 minutes.

Note: Controls must be placed in the correct wells for proper data interpretation. Refer to Figure 2.

Table 2: Invader[®] MTHFR 677 Reaction Mix

Component	μ L/well	Number of Rxns	25% Overage	Total Volume (μ L)
MTHFR 677 Oligo Mix	7.5 μ L	<i>k</i>	1.25	=7.5 <i>k</i> (1.25)
Universal Buffer	2.0 μ L	<i>k</i>	1.25	=2.0 <i>k</i> (1.25)
Universal Enzyme Mix	0.5 μ L	<i>k</i>	1.25	=0.5 <i>k</i> (1.25)
Total Mix Volume	10 μL	<i>k</i>	1.25	=10<i>k</i>(1.25)

7. Vortex the reaction mix thoroughly and spin down the contents in a microcentrifuge for 3-5 seconds.

Plate Set up

- Reaction mix may be aliquoted into a 96-well plate to facilitate the use of a multi-channel pipettor.
- Add 10 μL of reaction mix to the bottom of each control and sample well of the reaction plate.
- Dispense 10 μL of the appropriate control or sample (genotype-specific controls and all samples are diluted (See Step 3) Control 4 (NDC) is undiluted) to bottom of the appropriate well of the reaction plate (See Figure 2). Mix by pipetting up and down 3 – 5 times upon addition to ensure reaction homogeneity. Change pipette tips between every addition.

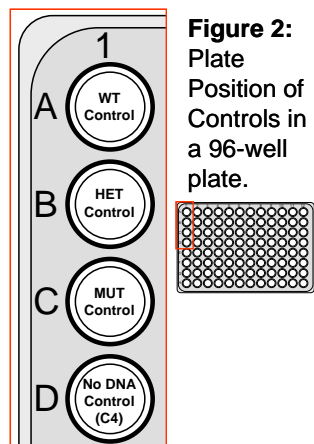


Figure 2:
Plate
Position of
Controls in
a 96-well
plate.

- Overlay all control and sample wells with 20 μL of mineral oil by dispensing along the side of the wells. Change pipette tips between every addition.
- Cover the reaction plate with optically clear adhesive film. Thoroughly secure the film to the surface of the plate.
- Visually confirm no bubbles exist in the reaction wells. If bubbles are visible, remove bubbles (e.g., centrifuge plate briefly).
- Place the reaction plate in the thermal cycler.

Step	Description	Temperature ($^{\circ}\text{C}$)	Time	Cycles
1	Denaturation	95	2 Minutes	2
2	Anneal / Extend	72	2 Minutes	
3	Denaturation	94	0.5 Minutes	28
4	Anneal / Extend	72	1.5 Minutes	
5	Heat Inactivate Polymerase	99	10 Minutes	1
6	Invader [®] Reaction	63	1 Minute	
7	Hold	10	Hold	

Figure 3: Invader Reaction Program

- Start the Invader reaction program.
- When the reaction profile is complete, the reaction plate can be held in the thermal cycler at $+10^{\circ}\text{C}$ or stored in a refrigerator ($+2^{\circ}\text{C}$ to $+8^{\circ}\text{C}$) protected from light, overnight.

Data Collection

- Allow the reaction plate to equilibrate to room temperature on the bench top at least 1 minute prior to reading the plate.

- Visually confirm no bubbles exist in the reaction wells. If bubbles are visible, remove bubbles (e.g., centrifuge plate briefly).
- Read the reaction plate on a multi-well fluorometer according to manufacturer's instructions. Verify parameters match Table 3.

Table 3: Recommended Multi-well Fluorometer Settings		
Setting Category	Measurement 1 (FAM)	Measurement 2 (Red)
Mode:	Fluorescence Top Reading	Fluorescence Top Reading
Do not use "Plate with cover" option		
Excitation Wavelength (Bandwidth):	485 (20) nm	560 (20) nm
Emission Wavelength (Bandwidth):	535 (25) nm	612 (10) nm
Number of Reads:	10	10
Integration Time:	20 μs	20 μs
Lag Time:	0 μs	0 μs
Settle Time:	0 ms	0 ms
Multiple Reads per Well:	Not selected	Not selected
Label Name:	Label 1	Label 2

- Place the 96-well plate to be analyzed onto the plate carrier with the A1-well oriented to the upper left corner of the plate carrier. Do not remove the optically clear adhesive film from the surface of the plate. Read the entire plate according to manufacturer's instructions.



NOTE: If the No DNA Control (NDC) signal is not greater than 600 counts for FAM or Red fluorescence, re-read the plate adjusting the gain setting(s) accordingly so that each value is greater than 600 counts and the reader is in the linear dynamic range according to the manufacturer's instructions.

Data Analysis

- Open the Invader Call Reporter[®] software.
- Select the plate(s) to be analyzed by highlighting the appropriate row in the blue "Active Assay" field.
- Click the "Load Selected" button in lower left area of the window. This should allow the "Results" tab to be selected.
- Click on the "Results" tab.
- Select the Raw Data File by clicking on the "Select File" button and select the appropriate file in the browser.
- Select the appropriate Worksheet from the available choices in the dropdown menu.
- Click the "Import Raw Data" button to populate data fields.
- If desired, click the "View/Save PDF" button located in the upper right corner of window. Print the PDF, then close the PDF window.
- Click on "Summary" tab to view sample validity and genotype results.

30. If desired, click “View/Save PDF” button located in the upper right corner of window. Print the PDF and then close the PDF window.
31. If desired, click the “Finish Active Assay” button to delete run information when testing and analysis is completed.

B. Quality Control Procedures

Differences in blood processing and technical procedures in the user’s laboratory may produce variability in results, necessitating regular evaluation of laboratory designated controls in addition to the following procedures.

Prior to initial use of this test in the user’s laboratory, the performance of the test may be verified by testing a number of positive and negative samples with known characteristics. These quality control tests should be repeated for each new lot or a change in test parameters.

Test verification on a daily basis may be accomplished through the proper use of the above-mentioned laboratory designated controls, as described in this section.

The No DNA Control (C4) is used to establish the amount of signal generated in the absence of target.

Test runs are valid when the genotype-specific controls yield the appropriate genotype results (Table 4). If any of the genotype-specific controls are called incorrectly or EQ (equivocal), the run is invalid and must be repeated. A test run with invalid control results will fail to provide sample results. In the event of a control failure, all samples in the run should be re-tested.

Unexplained discrepancies in control results should be referred to Hologic Technical Support (1 888 484 4747). See the Troubleshooting section of this package insert for additional information.

All quality control requirements should be performed in conformance with local, state, and/or federal regulations or accreditation requirements.

C. Interpretation of the Results

Results from the Invader® MTHFR 677 test are reported to the user as a genotype “call”, indicating which genotype was detected in the sample (WT, HET, MUT). The results also report sample validity and run validity. Genotype call and corresponding nucleotides are shown in Table 4.

Genotype	Invader® MTHFR 677 Genotype	Nucleotides
Homozygous Wild Type	WT	GG
Heterozygous	HET	GA
Homozygous Mutant	MUT	AA

The Results in the Invader Call Reporter® software display sample and control data. If results are invalid or not displayed, refer to the Troubleshooting section of this package insert and the Software User Manual for Invader® MTHFR 677 (MAN-01689).

The “Summary” tab in the Invader Call Reporter® software displays results for all samples and controls in a condensed format. If results are invalid or not displayed, refer to the Troubleshooting section of this package insert or in the Software User Manual for Invader® MTHFR 677 (MAN-01689).

If any of the controls are invalid, sample results will not be displayed.

D. Limitations

General Limitations:

Reagents may demonstrate unexpected performance in previously untested samples. The possibility of unexpected performance even in tested blood samples cannot be completely eliminated due to the biological variability of sample matrices. Contact Hologic Technical Support (1 888 484 4747) with any documented unexpected result(s).

Specific Limitations:

It is recommended that the laboratory assess the possibility of any additional rare mutations that may generate false MTHFR 677 results and report this as a limitation, if applicable.

E. Summary of Expected Results

1. Accuracy compared to bi-directional DNA Sequencing

Human whole blood samples (n = 361) underwent DNA extraction and subsequent bi-directional DNA sequence analysis. The same DNA samples were then analyzed using the Invader® MTHFR 677 test. The observed agreement between the Invader® MTHFR 677 test and bi-directional DNA sequencing was 100% (359/359). The first run agreement with bi-directional DNA sequencing was 99.45% (359/361) with 98.01%, one-sided lower 95% confidence limit (see Table 5).

Table 5: Agreement between the Invader® MTHFR 677 Test and Bi-directional DNA Sequencing

MTHFR 677 Genotype*	Number Tested	Number of Valid Results on 1 st Run	Number of Correct Genotype Calls on 1 st Run	1 st Run Agreement
Homozygous Wild Type (GG)	180	178**	178**	98.89%
Heterozygous (GA)	104	104	104	100%
Homozygous Mutant (AA)	77	77	77	100%
Total	361	359**	359**	99.45%

* Genotype determined through bi-directional DNA sequencing
 ** Two samples failed to generate valid results. These samples were reported as invalid (EQ) and no genotype calls were assigned by the interpretive software. The EQ result was used to determine the First Run Agreement.

2. Reproducibility

- a. Inter-laboratory Reproducibility: A multi-center external study was conducted to determine the reproducibility of the Invader® MTHFR 677 test. A single lot of the Invader® MTHFR 677 test was used to compare the test performance at three different study sites. Aliquots of whole blood samples for each genotype were extracted at each site. DNA from the samples underwent subsequent Invader® analysis at each site on each of five (5) non-consecutive days. Results were obtained using the MTHFR 677 Invader Call Reporter® software (see Tables 6 and 7).

Table 6: Inter-laboratory Reproducibility of Invader® MTHFR 677 Test

Site	Operator	Samples Tested	First Pass			Final (Following Single Retest)			Final % Agreement <small>Final Correct Calls Samples Tested</small>
			Correct Calls	No Calls (Invalid, EQ)	Miscalls	Correct Calls	No Calls (Invalid, EQ)	Miscalls	
Site 001	1	90	90	0	0	90	0	0	100%
	2	90	90	0	0	90	0	0	100%
Site 002	1	90	90	0	0	90	0	0	100%
	2	90	90	0	0	90	0	0	100%
Site 003	1	90	90	0	0	90	0	0	100%
	2	90	90	0	0	90	0	0	100%
All	All	540	540	0	0	540	0	0	100%

Analyses	Number of Comparisons	Number of Agreements	Percent Agreement	One-Sided Lower 95% Confidence Limit
Within Operator (Within-day)	9 (samples) x 2 (operators) x 5 (days) x 3 (sites) = 270	270	100%	99.0%
Between-days (Within-Operator)	9 (samples) x 10 (day pairs) x 4 (2 reps per day) x 2 (operators) x 3 (sites) = 2160	2160	100%	99.5%
Between-operator (within-site)	9 (samples) x 4 (2 reps per operator) x 25 (day pairs between 2 operators) x 3 (sites) = 2700	2700	100%	99.5%
Between-Sites	9 (samples) x 20 (tests at site a) x 20 (tests at site b) x 3 (site pairs) = 10800	10800	100%	99.5%

b. Lot-to-Lot Reproducibility: Whole blood samples were extracted and subjected to bi-directional DNA sequencing. The same DNA samples were then analyzed using the Invader® MTHFR 677 test with three different lots of the reagents. The observed agreement between all three lots of the Invader® MTHFR 677 test and bi-directional DNA sequencing was 100% (108/108) (see Table 8). Across all genotypes tested, across all three (3) lots, the overall agreement with bi-directional sequencing was 100% (108/108), with 97.26%, one sided lower 95% confidence limit.

MTHFR 677 Genotype (bi-directional sequencing)	Number of Genotypes Tested	Replicates per Sample	Correct Genotype Calls in 1 st Run			Invalid Calls in 1 st Run			Percent Agreement
			GG	GA	AA	GG	GA	AA	
Homozygous Wild type (GG)	3	4	12	12	12	0	0	0	100%
Heterozygous (GA)	3	4	12	12	12	0	0	0	100%
Homozygous Mutant (AA)	3	4	12	12	12	0	0	0	100%
Total	9	4	36	36	36	0	0	0	100%

3. Upper and Lower Limits of Detection

Forty (40) replicates of genomic DNA samples representing the wildtype, heterozygous and mutant MTHFR 677 genotypes were tested at concentrations of both 5 ng/μL and 80 ng/μL, prior to 1:20 dilution for the Invader reaction, and the Invader results compared to bi-directional sequencing. For each concentration, there was 100% (120/120) agreement with bi-directional sequencing. Across all genotypes tested, for a given DNA concentration, the one sided lower 95% confidence limit was 97.53%. Samples were also tested beyond the recommended concentrations of DNA, at 10-fold extremes of the recommended range (e.g., 0.5 ng/μL and 800 ng/μL). At these extreme concentrations, there was 100% (120/120) agreement at 0.5 ng/μL and 100% (120/120) agreement at 800 ng/μL concentrations.

4. Interfering Substances

Heparin (1500 U/dL human whole blood), bilirubin (10 mg/dL human whole blood), cholesterol (300 mg/dL human whole blood), potassium EDTA (1.8 mg/mL human whole blood), hemoglobin (up to 0.2% in human whole blood), and ethanol-based wash buffer (5% in DNA sample) had no impact on Invader® MTHFR 677 performance.

F. Troubleshooting

Observation	Probable Cause	Solution
Errors occur during data import: "Check FAM & Red gain settings and read the whole plate again. (Partial plate reads are not allowed.)" "Check FAM gain setting and read the whole plate again. (Partial plate reads are not allowed.)" "Check Red gain setting and read the whole plate again. (Partial plate reads are not allowed.)"	Fluorometer issues.	See Invader Call Reporter® Invader® MTHFR 677 Software User Manual troubleshooting guide.
	Incubation period was longer than specified length of time recommended.	Verify that the Invader Reaction Program is as specified (Section IV.A. Figure 3).
High No DNA Control FAM or Red Signal	Contamination	Re-run test taking care not to contaminate samples or reagents.
	Bubbles in reaction well.	Remove bubbles (e.g., centrifuge plate briefly) and re-read.
Bubbles in reaction well.	Over-mixing	Remove bubbles (e.g., centrifuge plate briefly).
No DNA Control is Invalid-Result for one or more Control is Invalid	Incorrect sample volume or no sample added to well.	Vortex each reagent before adding to reaction mix.
		Verify correct reagent volumes were added to the reaction mix.
		Verify all reagents were added to the reaction mix.
Evaporation of reaction mix/sample during run.	Evaporation of reaction mix/sample during run.	Vortex reaction mix before adding to the 96-well plate.
		Visually confirm that no volume discrepancies exist in the 96-well plate by viewing the bottom side of the plate.
Evaporation of reaction mix/sample during run.	Evaporation of reaction mix/sample during run.	Verify reactions are covered by 20 μL of mineral oil.

Table 9: Troubleshooting Guide		
Observation	Probable Cause	Solution
No DNA Control is Invalid- Result for one or more Control is Invalid	Evidence of contamination during genotype-specific control preparation or reaction mix preparation.	Use DNase/RNase-free aerosol barrier tips at all times.
		Do not allow pipette tips to touch any surface except the solution being pipetted.
		Use sterile tubes for preparing reaction mixes.
No DNA Control is Invalid- Result for one or more Genotype-specific Control is Invalid	Evidence of contamination during genotype-specific control preparation or reaction mix preparation.	Wear gloves at all times
	Controls in wrong location on plate	Verify control well location (Section IV.A. Figure 2)
	Gain setting too low (NDC value <600 counts).	Adjust gain setting so NDC is above 600 counts.
	Genotype-specific controls not extracted	Extract genotype-specific controls using standard laboratory method.
Result for sample is "Low Signal", "EQ" or "Invalid"	Insufficient sample DNA used in the reaction.	Verify concentration of at least 5 ng/μL prior to dilution and reaction set up.
		Verify 1:20 dilution made correctly (Sample Preparation section IV.A).
		If the DNA concentration is <5 ng/μL pre-dilution, repeat the DNA extraction and purification protocol to obtain purified DNA at a higher concentration.
		Repeat sample with Invader® MTHFR 677 test.
	Bubbles in reaction well.	Remove bubbles (e.g., centrifuge plate briefly) and re-read.
	DNA sample inhibition	Repeat DNA extraction from specimen.
		Refer to package insert performance characteristics, (Interfering substances Section IV.E.4).
		Verify 1:20 dilution made correctly (Sample Preparation section IV.A).
	Incorrect sample volume or no sample added to well.	Verify that no volume discrepancies exist in the 96-well plate by viewing the bottom side of the plate.
	Improper preparation of reaction mix	Vortex each reagent before adding to reaction mix.
Verify correct reagent volumes were added to the reaction mix.		

Table 9: Troubleshooting Guide		
Observation	Probable Cause	Solution
Result for sample is "Low Signal", "EQ" or "Invalid"		Verify all reagents were added to the reaction mix.
		Vortex reaction mix before adding to the 96-well plate.
		Visually confirm that no volume discrepancies exist in the 96-well plate by viewing the bottom side of the plate.
Result for sample is "Low Signal", "EQ" or "Invalid"	Evaporation of reaction mix/sample during run.	Verify reactions are covered by 20 μL of mineral oil.
	Evaporation of reaction mix/sample during run.	Verify the 96-well plate is firmly sealed with optical clear adhesive cover before incubating.
		Verify thermal cycler heated lid is firmly closed.
		If the thermal cycler requires a compression pad, verify that the compression pad is seated properly on top of the 96-well plate.
	Insufficient DNA amplification.	Verify the correct Invader Reaction Program was used (Section IV.A. Figure 3). Repeat sample test.
		Verify all reagents have been added to reaction.
96-well plate incompatible with thermal cycler or positioned incorrectly within thermal cycler.	Verify the 96-well plate is compatible with the thermal cycler, is firmly seated in the thermal cycler and secured properly.	
Sample DNA degradation (DNA may degrade if stored at room temperature).	Store extracted DNA as indicated in the DNA extraction and purification protocol prior to the Invader® test.	

Troubleshooting Re-test Procedure

If the established criteria for an acceptable genotype call (i.e., WT, HET, or MUT) are not met by a given sample, it is identified as either "Low Signal" or "EQ" and the sample(s) must be re-tested. A given extraction of a sample that has two EQ (equivocal) results in a row cannot be called by the Invader® MTHFR 677 test. If a sample fails to produce the minimum fold-over-zero then the Invader test gives a "Low Signal" result, and the sample must be re-tested. Figure 4 illustrates the sample re-test process for samples with "Low Signal", "EQ" or "Invalid" results.

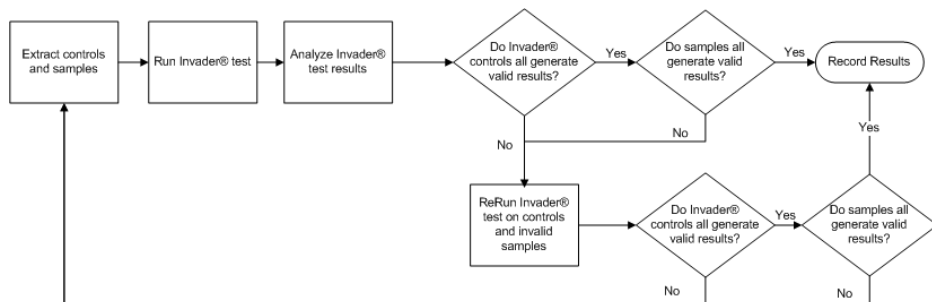


Figure 4: Recommended testing process for samples producing “Low Signal”, “EQ” or “Invalid” results with the Invader® MTHFR 677 test.

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VI. CONTACT INFORMATION

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