TEST CHANGE

Fragile X (FMR1) with Reflex to Methylation Analysis, Fetal

2009034, FX PCR FE

Specimen Requirements:	
Patient Preparation:	
Collect:	Fetal Cultured Amniocytes ~~or Cultured CVS~~ AND Maternal Whole Blood Specimen : Lavender (EDTA), pink (K2EDTA), or yellow (ACD solution A or B).
Specimen Preparation:	Cultured Amniocytes ~~or Cultured CVS~~: Transfer cultured amniocytes ~~or cultured CVS~~ to two T-25 flasks at 80 percent confluence (Min: one T-25 flask at 80 percent confluence). Backup cultures must be retained at the client's institution until testing is complete. If ARUP receives a sample below the minimum confluence, Cytogenetics Grow and Send (ARUP test code 0040182) will be added on by ARUP, and additional charges will apply. If clients are unable to culture specimens, Cytogenetics Grow and Send should be added to initial order. Maternal Whole Blood Specimen: Transport 2 mL whole blood. (Min: 1 mL)
Transport Temperature:	Cultured Amniocytes ~~or Cultured CVS~~: CRITICAL ROOM TEMPERATURE. Must be received within 48 hours of collection due to viability of cells. Maternal Whole Blood Specimen: Room temperature.
Unacceptable Conditions:	
Remarks:	Methylation patterns may not be fully established in early gestation; thus, methylation testing performed on chorionic villus samples may not distinguish between premutation and full mutation alleles.
Stability:	Cultured Amniocytes ~~or Cultured CVS~~: Room temperature: 48 hours; Refrigerated: Unacceptable; Frozen: Unacceptable Maternal Whole Blood Specimen: Room temperature: 7 days; Refrigerated: 1 month; Frozen: Unacceptable
Methodology:	Polymerase Chain Reaction (PCR)/Capillary Electrophoresis
Performed:	Varies~~Sun-Sat~~
Reported:	9-10 days
Note:	If a CGG repeat of 55 or greater is detected by PCR and capillary electrophoresis, methylation analysis will be added.

Additional charges apply.

CPT Codes:	81243; 81265 Fetal Cell Contamination (FCC); if reflexed, add 81244
New York DOH Approval Status:	This test is New York DOH approved.

Interpretive Data:

Refer to report. ~~Background information for Fragile X (FMR1) with Reflex to Methylation Analysis, Fetal~~

~~Characteristics of Fragile X syndrome (FXS): Affected males have moderate intellectual disability, hyperactivity, perseverative speech, social anxiety, poor eye contact, hand flapping or biting, autism spectrum disorders, and connective tissue anomalies. Females are usually less severely affected than males.~~

~~Characteristics of Fragile X tremor ataxia syndrome (FXTAS): Onset of progressive ataxia and intention tremor typically after the fourth decade of life. Females also have a 21 percent risk for primary ovarian insufficiency.~~

~~Incidence of FXS: 1 in 4,000 White males and 1 in 8,000 White females.~~

~~Inheritance: X-linked.~~

~~Penetrance of FXS: Complete in males; 50 percent in females.~~

~~Penetrance of FXTAS: 47 percent in males and 17 percent in females >50 years of age.~~

~~Cause: Expansion of the FMR1 gene CGG triplet repeat.~~

~~- Full mutation: typically >200 CGG repeats (methylated).~~

~~- Premutation: 55 to approx. 200 CGG repeats (unmethylated).~~

~~- Intermediate: 45-54 CGG repeats (unmethylated).~~

~~- Normal: 5-44 CGG repeats (unmethylated).~~

~~Clinical Sensitivity: 99 percent.~~

~~Methodology: Triplet repeat-primed polymerase chain reaction (PCR) followed by size analysis using capillary electrophoresis. Methylation-specific PCR analysis is performed for CGG repeat lengths of 55 or greater to distinguish between premutation and full mutation alleles.~~

~~Analytic Sensitivity and Specificity: 99 percent; estimated precision of sizing for intermediate and premutation alleles is within 2-3 CGG repeats.~~

~~Limitations: Methylation patterns may not be fully established in early gestation; thus, diagnostic testing on chorionic villus samples is not recommended. Diagnostic errors can occur due to rare sequence variations. Rare FMR1 variants unrelated to trinucleotide expansion will not be detected. A specific CGG repeat size estimate is not provided for full mutation alleles. AGG trinucleotide interruptions within the FMR1 CGG repeat tract are not assessed.~~

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

Phenotype	Number of CGG Repeats
Unaffected	< 45
Intermediate	45-54
Premutation	55-200
Affected	>200

Reference Interval:

By report