Ordered Items
Fragile X, PCR reflex Southern

**TESTS**          **RESULT**  **FLAG**  **UNITS**  **REFERENCE INTERVAL**  **LAB**
Fragile X, PCR reflex Southern

**RESULTS:** PCR: 27 and 34 CGG repeats

**INTERPRETATION:**
Negative: not a carrier of a fragile X expansion mutation. This result is not associated with fragile X syndrome.

**COMMENTS:**
Southern blot analysis is not indicated when PCR results are negative or intermediate and there is no family history of unexplained intellectual disability, ovarian dysfunction or ataxia tremor. Routine chromosome analysis is recommended in the diagnostic work-up for other causes of mental retardation.

Fragile X syndrome is caused by an expansion of CGG repeat sequences in the FMR1 gene in 99% of cases. There are rare FMR1 mutations including missense mutations and gene deletions which cause fragile X syndrome. The interpretation is based on the following ranges of repeat sequences:

- **Negative:** less than 45 repeats
- **Intermediate:** 45-54 repeats
- **Premutation:** 55-200 repeats with normal methylation pattern
- **Full Mutation:** greater than 200 repeats with abnormal methylation pattern

Reported CGG repeat sizes may vary as follows: +/- one for repeats less than 60, and +/- two to four for repeats in the 60-120 range respectively. For repeats greater than 120, the accuracy is +/- 10%.
This interpretation is based on the clinical and family relationship information provided and the current understanding of the molecular genetics of this condition. Genetic counseling is recommended for any individual seeking additional information regarding interpretation of genetic test results.

**METHODS/LIMITATIONS:**
Isolated DNA is tested by the polymerase chain reaction (PCR) to determine the size of the CGG repeats within the FMR1 gene. PCR products are generated using a fluorescence labeled primer and sized by capillary gel electrophoresis. If indicated, Southern blot analysis is performed by hybridizing the probe StB12.3 to EcoRI- and Eagl-digested DNA. The analytical sensitivity of both Southern blot and PCR analyses is 99% for expansion mutations in the FMR1 gene. False positive or negative results may occur for reasons that include somatic or tissue-specific mosaicism, rare genetic variants, blood transfusions, bone marrow transplantation, or erroneous representation of family history.

**REFERENCES:**

Results Released By: Hongli Zhan, Ph.D., Director
Report Released By: Jordan D. Dix, MS, CGC, Genetic Counselor

**Comment:**
This test was developed and its performance characteristics determined by LabCorp. It has not been cleared or approved by the Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary.

Fragile X Syndrome, PDF

---

<table>
<thead>
<tr>
<th>TESTS</th>
<th>RESULT</th>
<th>FLAG</th>
<th>UNITS</th>
<th>REFERENCE INTERVAL</th>
<th>LAB</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

LabCorp RTP
1912 TW Alexander Drive, RTP, NC 27709-0150
Dir: Arundhati Chatterjee, MD

For inquiries, the physician may contact Branch: 800-222-7566 Lab: 800-735-4087
Test Results of: NORMAL, 511919
DOB: 01/11/1990  Age: 29.0 Y  Sex: F
Collected on: 01/26/2019
Received on: 01/26/2019
Reported on: 01/30/2019

Patient ID#: 

Test: Fragile X, PCR reflex Southern

RESULTS: PCR: 27 and 34 CGG repeats

INTERPRETATION:
Negative: not a carrier of a fragile X expansion mutation. This result is not associated with fragile X syndrome.

COMMENTS:
Southern blot analysis is not indicated when PCR results are negative or intermediate and there is no family history of unexplained intellectual disability, ovarian dysfunction or ataxia tremor. Routine chromosome analysis is recommended in the diagnostic work-up for other causes of mental retardation.

Fragile X syndrome is caused by an expansion of CGG repeat sequences in the FMR1 gene in 99% of cases. There are rare FMR1 mutations including missense mutations and gene deletions which cause fragile X syndrome. The interpretation is based on the following ranges of repeat sequences:

- Negative: <45 repeats
- Intermediate: 45-54 repeats
- Premutation: 55-200 repeats with normal methylation pattern
- Full Mutation: >200 repeats with abnormal methylation pattern

Reported CGG repeat sizes may vary as follows: +/- one for repeats less than 60, and +/- two to four for repeats in the 60-120 range respectively. For repeats greater than 120, the accuracy is +/- 10%.

This interpretation is based on the clinical and family relationship information provided and the current understanding of the molecular genetics of this condition. Genetic counseling is recommended for any individual seeking additional information regarding interpretation of genetic test results.

METHODS/LIMITATIONS:
Isolated DNA is tested by the polymerase chain reaction (PCR) to determine the size of the CGG repeat within the FMR1 gene. PCR products are generated using a fluorescence labeled primer and sized by capillary gel electrophoresis. If indicated, Southern blot analysis is performed by hybridizing the probe StB12.3 to EcoRI- and EagI-digested DNA. The analytical sensitivity of both Southern blot and PCR analyses is 99% for expansion mutations in the FMR1 gene. False positive or negative results may occur for reasons that include somatic or tissue-specific mosaicism, rare genetic variants, blood transfusions, bone marrow transplantation, or erroneous representation of family history.

This test was developed and its performance characteristics determined by Laboratory Corporation of America Holdings (LabCorp). It has not been cleared or approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. This test is used for clinical purposes. It should not be regarded as investigational research.

REFERENCES:

This document contains private and confidential health information protected by state and federal law.
**Ordered Items**

<table>
<thead>
<tr>
<th>Fragile X, PCR reflex Southern</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>TESTS</strong></td>
</tr>
<tr>
<td>Fragile X DNA</td>
</tr>
<tr>
<td>Final report will follow under separate cover.</td>
</tr>
<tr>
<td>Fragile X Southern Blot</td>
</tr>
<tr>
<td>Comment:</td>
</tr>
</tbody>
</table>

**RESULTS:** PCR and Southern Blot: 141 CGG repeats.

**INTERPRETATION:**
Premutation carrier of fragile X syndrome. This individual is at risk for late-onset fragile X-associated tremor/ataxia syndrome (FXTAS). There is an increased risk of fragile X syndrome in future generations. See comments.

**COMMENTS:**
The diagnosis of fragile X syndrome is not confirmed by this analysis. Other causes of fragile X syndrome include rare point mutations and deletions in the FMR1 gene, or mutations in other genes such as FXE (fragile X E). Further diagnostic work-up is recommended. Routine chromosome analysis is recommended in the diagnostic work-up for other causes of mental retardation. Males with premutation alleles are at risk for developing fragile-X-associated tremor/ataxia syndrome (FXTAS). The risk correlates with increasing age and larger repeat size. In males with greater than 80-90 repeats FXTAS is present greater than 33% after the age of 50 and in greater than 50% after the age of 70 (Jaquemont, S et al. Lancet Neurol 2007;6:45-55). Men with premutations pass them to all of their daughters. Usually the daughters are unaffected with fragile X syndrome, but are at risk for primary ovarian insufficiency (POI), late-onset fragile X-associated tremor/ataxia syndrome (FXTAS), and for having children with fragile X syndrome. Genetic counseling is recommended for discussion of the clinical implications of this result for this individual and for at-risk family members.

Fragile X syndrome is caused by an expansion of CGG repeat sequences in the FMR1 gene in 99% of cases. There are
rare FMR1 mutations including missense mutations and gene deletions which cause fragile X syndrome. The interpretation is based on the following ranges of repeat sequences:

- **Negative:** less than 45 repeats
- **Intermediate:** 45-54 repeats
- **Premutation:** 55-200 repeats with normal methylation pattern
- **Full Mutation:** greater than 200 repeats with abnormal methylation pattern

Reported CGG repeat sizes may vary as follows: +/- one for repeats less than 60, and +/- two to four for repeats in the 60-120 range respectively. For repeats greater than 120, the accuracy is +/- 10%.

This interpretation is based on the clinical and family relationship information provided and the current understanding of the molecular genetics of this condition. Genetic counseling is recommended for any individual seeking additional information regarding interpretation of genetic test results.

**METHODS/LIMITATIONS:**
Isolated DNA is tested by the polymerase chain reaction (PCR) to determine the size of the CGG repeats within the FMR1 gene. PCR products are generated using a fluorescence labeled primer and sized by capillary gel electrophoresis. If indicated, Southern blot analysis is performed by hybridizing the probe StB12.3 to EcoRI- and Eagl-digested DNA. The analytical sensitivity of both Southern blot and PCR analyses is 99% for expansion mutations in the FMR1 gene. False positive or negative results may occur for reasons that include somatic or tissue-specific mosaicism, rare genetic variants, blood transfusions, bone marrow transplantation, or erroneous representation of family history.

**REFERENCES:**

Results Released By: Joseph B. Kearney, Ph.D., Director
Report Released By: Christine Vaughan, MS, CGC, Genetic
Counselor

Comment:
This test was developed and its performance characteristics determined by LabCorp. It has not been cleared or approved by the Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary.

Fragile X Syndrome, PDF 01

<table>
<thead>
<tr>
<th>TESTS</th>
<th>RESULT</th>
<th>FLAG</th>
<th>UNITS</th>
<th>REFERENCE INTERVAL</th>
<th>LAB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fragile X Syndrome, PDF</td>
<td>01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

For inquiries, the physician may contact Branch: 800-222-7566 Lab: 800-735-4087
RESULTS: PCR and Southern Blot: 141 CGG repeats.

INTERPRETATION:
Premutation carrier of fragile X syndrome. This individual is at risk for late-onset fragile X-associated tremor/ataxia syndrome (FXTAS). There is an increased risk of fragile X syndrome in future generations. See comments.

COMMENTS:
The diagnosis of fragile X syndrome is not confirmed by this analysis. Other causes of fragile X syndrome include rare point mutations and deletions in the FMR1 gene, or mutations in other genes such as FXE (fragile X E). Further diagnostic work-up is recommended. Routine chromosome analysis is recommended in the diagnostic work-up for other causes of mental retardation. Males with premutation alleles are at risk for developing fragile-X-associated tremor/ataxia syndrome (FXTAS). The risk correlates with increasing age and larger repeat size. In males with >80-90 repeats FXTAS is present in >33% after the age 50 and in >50% after the age of 70 (Jaquemont, S et al. Lancet Neurol 2007;6:45-55). Men with premutations pass them to all of their daughters. Usually the daughters are unaffected with fragile X syndrome, but are at risk for primary ovarian insufficiency (POI), late-onset fragile X-associated tremor/ataxia syndrome (FXTAS), and for having children with fragile X syndrome. Genetic counseling is recommended for discussion of the clinical implications of this result for this individual and for at-risk family members.

Fragile X syndrome is caused by an expansion of CGG repeat sequences in the FMR1 gene in 99% of cases. There are rare FMR1 mutations including missense mutations and gene deletions which cause fragile X syndrome. The interpretation is based on the following ranges of repeat sequences:

- **Negative:** <45 repeats
- **Intermediate:** 45-54 repeats
- **Premutation:** 55-200 repeats with normal methylation pattern
- **Full Mutation:** >200 repeats with abnormal methylation pattern

Reported CGG repeat sizes may vary as follows: +/- one for repeats less than 60, and +/- two to four for repeats in the 60-120 range respectively. For repeats greater than 120, the accuracy is +/- 10%.

This interpretation is based on the clinical and family relationship information provided and the current understanding of the molecular genetics of this condition. Genetic counseling is recommended for any individual seeking additional information regarding interpretation of genetic test results.

METHODS/LIMITATIONS:
Isolated DNA is tested by the polymerase chain reaction (PCR) to determine the size of the CGG repeat within the FMR1 gene. PCR products are generated using a fluorescence labeled primer and sized by capillary gel electrophoresis. If indicated, Southern blot analysis is performed by hybridizing the probe Sib12.3 to EcoRI- and EagI-digested DNA. The analytical sensitivity of both Southern blot and PCR analyses is 99% for expansion mutations in the FMR1 gene. False positive or negative results may occur for reasons that include somatic or tissue-specific mosaicism, rare genetic variants, blood transfusions, bone marrow transplantation, or erroneous representation of family history.

This test was developed and its performance characteristics determined by Laboratory Corporation of America Holdings (LabCorp). It has not been cleared or approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. This test is used for clinical purposes. It should not be regarded as investigational research.

REFERENCES:

Results Released By: Joseph B. Kearney, Ph.D., Director
Report Released By: Christine Vaughan, MS, CGC, Genetic Counselor

LabCorp
1912 Alexander Drive, RTP, NC, 27709
(800) 345-4363

This document contains private and confidential health information protected by state and federal law.