

NY Informed Consent – Fragile X Syndrome Analysis

NOTE: Please obtain patient signature on consent form and provide a signed copy to EGL Genetics to permit testing and processing.

I, (name) _____, voluntarily request of EGL Genetics to perform DNA-based testing for Fragile X in myself/my child (child's name _____) in an attempt to determine whether I/my child am a carrier of a disease gene or at increased risk to be affected by a genetic condition. The following points were explained and I understand that:

- The purpose of this analysis is to test for Fragile X syndrome, a hereditary (X-linked) form of intellectual disability. This test can identify affected individuals, female premutation carriers and females at risk for Premature Ovarian Insufficiency, and individuals at risk for Fragile X-associated tremor/ataxia syndrome.
- This is a genetic (DNA-based) test performed by PCR and Southern Blotting. These methods are used to quantify the size of the CGG repeats in the 5' untranslated region of the *FMR1* gene.
- DNA testing requires a blood sample, cheek or mouth swab, muscle or skin biopsy, all of which have risks associated with obtaining the sample. Additional samples may be needed if the sample is damaged in shipment or inaccurately submitted. In order to perform accurate prenatal testing, samples from the affected individual, parents, or additional family members may be required.
- DNA-based studies performed are specific to the condition indicated above. The accuracy of genetic testing is limited by the methods employed, the clinical diagnosis, and the nature of the specific condition for which testing is requested. In some cases, the test will detect an abnormality, called a mutation, in the gene. In other cases the test is unable to identify an abnormality although an abnormality may still exist. This event may be due to the current lack of knowledge of the complete gene structure or an inability of the current technology to identify certain types of changes (mutations) in a gene. These tests are currently available for clinical laboratory testing; however, improvements will be made as scientific knowledge advances. As with any complex genetic test, there is always a small possibility of a failure or error in sample analysis. Extensive measures are taken to try to avoid these errors. The methods are not 100% accurate due to the possibility of rare genetic variations in the DNA of an individual or due to the complexity of the testing itself. A low error rate, approximately 1 in 1000 samples, is generally estimated to exist in a laboratory.
- Possible diagnostic errors include sample mix-ups, genotyping errors, rare genetic variants that interfere with analysis, and other sources. These analyses may not detect pathogenic variants in the promoter or other regulatory regions. Sequence analysis will not detect large deletions and duplications. Deletion/duplication analysis will not detect point mutations or some intronic mutations.
- It is the responsibility of the referring physician or health care provider to understand the specific use and limitations of the testing ordered, and to educate the patient regarding these limitations. Additional information describing indications, methodology and detection can be found on the EGL website at: <https://www.egl-eurofins.com/>
- Accurate interpretation of test results is dependent upon the patient's clinical diagnosis or family medical history and upon reported family relationships being true biological relationships. An erroneous clinical diagnosis in the patient or family member can lead to an incorrect interpretation in the laboratory result. Genetic testing in family members can sometimes reveal that true biological relationships are not consistent with the reported biological relationships. For example, non-paternity may be detected, which means that the stated or assumed father of an individual is not the true biological father.
- This analysis can have the following outcomes:
 - Positive:
 - When a full mutation (>200 repeats) is found in a woman, there is a 50% chance of her having an affected male offspring.
 - When a full mutation is found in a male, there is an almost 100% chance of Fragile X syndrome.
 - A woman with an allele with 55-200 repeats ("premutation") has an increased risk for having affected male children with greater than 200 repeats.
 - Women with "premutation" alleles have a higher risk for premature ovarian insufficiency.
 - Negative:
 - A woman with an allele in the intermediate region (45-54 repeats), has an increased risk for having children with a premutation allele. These children are not at risk for Fragile X syndrome.
 - A female or male with <45 repeats is considered to not be at risk and is negative for the disease.

