

## NY Informed Consent – Cystic Fibrosis 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 cystic fibrosis in myself/my child (child's name \_\_\_\_\_) in an attempt to determine whether I/my child am a carrier of a pathogenic (disease causing) variant in the cystic fibrosis gene or are at increased risk to be affected by the condition.

The following points were explained and I understand that:

- Cystic fibrosis (CF) is a chronic genetic condition involving multiple organ systems. Classical CF primarily involves the respiratory and digestive systems, and may have a range of clinical severity. Pulmonary symptoms often include lower airway inflammation, chronic cough, chronic sinusitis, and recurrent infections. Digestive symptoms often include meconium ileus, pancreatic insufficiency resulting in malabsorption and/or failure to thrive, diabetes mellitus, and hepatobiliary disease. Congenital bilateral absence of the vas deferens (CBAVD) is seen in men without pulmonary or digestive symptoms of CF, and results in azoospermia. CBAVD is a significant cause of male infertility. CF is caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Individuals with mutations in the *CFTR* gene may also present with milder or atypical symptoms such as pancreatitis or chronic sinusitis. 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. This test is indicated for the following individuals: Individuals with a diagnosis of CF, or atypical presentations of CF (chronic pancreatitis, sinusitis); Males with congenital bilateral absence of the vas deferens (CBAVD); carrier screening for individuals of Caucasian or Ashkenazi Jewish background; or family members of an affected individual at risk to be carriers of CF.
- 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. The targeted testing options involve analysis of specific disease-causing changes listed on the EGL Genetics website, while full gene sequencing and deletion/duplication will analyze the entire gene sequence for potentially disease-causing changes.
- 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:
  - a. **Positive:** A pathogenic (disease-causing) variant could be identified in the *CFTR* gene and the person is identified as being a carrier OR two pathogenic variants could be identified in the *CFTR* gene and the person is identified as likely affected.
  - b. **Negative:** No pathogenic variant is identified. This reduces the risk of the person carrying a pathogenic variant in *CFTR*, but does not eliminate it completely.

