

NY Informed Consent – Cholestasis Panel

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 Neonatal and Adult Cholestasis in myself or my child (child's name _____) in an attempt to determine whether I/my child am a carrier of a Neonatal and Adult Cholestasis disease gene or are at increased risk to be affected by the condition. The following points were explained and I understand that:

- Neonatal and Adult Cholestasis testing analyzes a specific set of genes that are causes of cholestasis. The incidence of neonatal cholestasis is estimated to be 1 in 2500 live births. Genetic and metabolic causes account for at least 25-30% of all cases of neonatal cholestasis, generally due to impairments of hepatobiliary transport, intermediary metabolism, storage disorders, or bile duct dysgenesis. Several of these disorders are life-threatening and benefit from early diagnosis and intervention, yet diagnosing the specific cause via routine serum chemistries or by evaluation of liver biopsies is not as definitive as direct genetic testing. Moreover, several cholestatic entities develop in adults that are caused by variants in these same genes. This test is indicated for the following individuals: Newborns and adults with chronic liver disease.
- 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:** A pathogenic variant (disease-causing) could be identified in one or more of the genes being tested for and the person is identified as being affected.
 - **Negative:** No pathogenic variant is identified. This reduces the risk of being affected by the diseases specifically tested for, but does not eliminate it completely.
 - **Inconclusive:** Due to technical issues the results were inconclusive and the test might need repeating. Results may also be inconclusive due to the identification of a variant of unknown significance.
- Due to the complexity of DNA testing and potential implications of test results, results will be reported directly to the patient's ordering provider, who will then review and discuss the test results with me. Patient-identifying results and information at EGL will remain confidential and may only be released to other parties with my expressed written consent or as permitted or required by applicable law.

