Neonatal and Adult Cholestasis Panel: Sequencing and CNV Analysis

**Test Code:** MM340  
**Turnaround time:** 3 weeks  
**CPT Codes:** 81223 x1, 81330 x1, 81332 x1, 81404 x1, 81405 x1, 81406 x1

### Condition Description

Neonatal cholestasis is often clinically defined as the prolonged occurrence of conjugated hyperbilirubinemia in the newborn period, due to impairments in the flow of bile. It is caused by a diverse group of hepatobiliary diseases with overlapping clinical presentations, supporting a need for multi-gene diagnostic panel.

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.

Highlights for pediatricians, internists, gastroenterologists, and hepatologists include:

- PFICs, Alagille syndrome, A1AT, bile acid synthetic disorders, CF, etc., all on one platform
- Extremely rare cholangiopathies, (nephronphthises, ARPKD) as well as causes of neonatal liver failure (DGUOK and others)
- Opportunities to diagnose adult-onset cholestatic syndromes, including BRIC, LPAC, and ICP
- Evaluation of hyperbilirubinemia: Crigler-Najjar and Dubin-Johnson syndromes

Reference:


### Genes

| ABCB11, ABCB4, ABCG2, ABCG5, ABCG8, ACOX2, AKR1C4, AKR1D1, ALDOB, AMACR, ATP8B1, BAAT, CC2D2A, CFTR, CLDN1, CYP27A1, CYP7A1, CYP2R1, DCD2, DGUK, DHCR7, EHHAH, FAH, GNAT, GPBAR1, HNF1B, HSD17B4, HSD3B7, INVS, JAG1, KMT2D, LIPA, MKS1, MPV17, MYOB5, NOTCH2, NPC1, NPC2, NPHP1, NPHP3, NPHP4, NR1H4, PEX1, PEX10, PEX11B, PEX12, PEX13, PEX14, PEX16, PEX19, PEX2, PEX6, PEX8, PEX9, PEX15, PEX6, PEX7, PKD1L1, PKHD1, POLC, SCP2, SERPINA1, SLC10A1, SLC10A2, SLC25A13, SLC27A5, SLC51A, SLC51B, SMPD1, TALDO1, TJP2, TMEM216, TRMU, UGT1A1, UTP4, VIPAS39, VPS33B |

### Indications

This test is indicated for:

- Newborns and adults with chronic liver disease.

### Methodology

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient’s genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

**Copy Number Analysis:** Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

### Detection

**Next Generation Sequencing:** Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

**Copy Number Analysis:** The sensitivity and specificity of this method for CNV detection is highly dependent on the size of the event, sequence
context and depth of coverage for the region involved. The assay is highly sensitive for CNVs of 500 base pairs or larger and those containing at least 3 exons. Smaller (< 500 base pairs) CNVs and those that involving only 1 or 2 exons may or may not be detected depending on the sequence context, size of exon(s) involved and depth of coverage.

**Specimen Requirements**

*Submit only 1 of the following specimen types*

**Type: Saliva**

**Specimen Requirements:**
Oragene™ Saliva Collection Kit
Oragene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

**Specimen Collection and Shipping:**
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

**Type: DNA, Isolated**

**Specimen Requirements:**
Microtainer
8µg
Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

**Specimen Collection and Shipping:**
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

**Type: Whole Blood (EDTA)**

**Specimen Requirements:**
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

**Specimen Collection and Shipping:**
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

**Related Tests**

- Neonatal and Adult Cholestasis: Deletion/Duplication Panel

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