Congenital Hypothyroidism: \textit{FOXE1} Gene Deletion/Duplication

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\textbf{Test Code:} JR  \\
\textbf{Turnaround time:} 2 weeks  \\
\textbf{CPT Codes:} 81228 x1  \\
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\textbf{Condition Description}

Congenital hypothyroidism occurs when the thyroid gland fails to develop or function properly. In 80-85\% of cases, the thyroid gland is absent (agenesis), ectopically located, and/or severely reduced in size (hypoplasia) [1]. In the remaining cases, a normal-sized or enlarged thyroid gland is present, but production of thyroid hormones is decreased or absent. If treatment begins in the first month after birth, infants usually develop normally. When thyroid hormone therapy is not initiated within the first two months of life, however, congenital hypothyroidism can cause severe neurologic, mental, and motor damage (cretinism). In the United States and many other countries, all newborns are tested for congenital hypothyroidism.

Mutations in the \textit{FOXE1} (9q22) gene have been associated with Bamforth Lazarus syndrome (BLS). In addition to congenital hypothyroidism, other characteristics of BLS can include bilateral choanal atresia, cleft palate, bifid epiglottis, and spiky or curly hair. Hypothyroidism can be due to athyreosis or a nonfunctional eutopic thyroid. Sequencing of the \textit{FOXE1} gene is recommended after a biochemical diagnosis of congenital hypothyroidism that presents with the characteristics listed above. It can be used to confirm the presence of mutations in a proband, identify carriers among the proband's relatives, and provide prenatal diagnosis in families with known mutations.

Please click here for the OMIM summary on this condition.

\textbf{Genes}

\textit{FOXE1}

\textbf{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of congenital hypothyroidism presenting with choanal atresia, cleft palate, and spiky hair in individuals who have tested negative for sequence analysis

\textbf{Methodology}

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

\textbf{Detection}

Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

\textbf{Specimen Requirements}

\textit{Submit only 1 of the following specimen types}

\textbf{Type: DNA, Isolated}

\textbf{Specimen Requirements:}

- Microtainer
- 3µg
- Isolation using the Perkin Elmer™Chemagen™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

\textbf{Specimen Collection and Shipping:}

Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

\textbf{Type: Whole Blood (EDTA)}

\textbf{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

\textbf{Specimen Collection and Shipping:}

Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

\textbf{Special Instructions}

Submit copies of diagnostic biochemical test results with the sample, if appropriate. Contact the laboratory if further information is needed.
Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of EGL Genetics, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Sequence analysis of the *FOXE1* gene is available and is required before deletion/duplication analysis.
- Prenatal testing is available to couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.