Fanconi Anemia Type B: \textit{FANCB} Gene Sequencing

\textbf{Test Code:} SFANB  \\
\textbf{Turnaround time:} 6 weeks  \\
\textbf{CPT Codes:} 81479 x1

\textbf{Condition Description}

Fanconi anemia (FA) is characterized by physical abnormalities. Approximately 60-75\% of affected individuals have variable physical abnormalities which may include short stature, abnormal skin pigmentation, skeletal anomalies, and ear or eye abnormalities. Other features include heart defects, hearing loss, developmental delay, hypogonadism, and genitourinary tract abnormalities.

FA is diagnosed by the detection of chromosomal aberrations in cells that have been cultured with a DNA interstrand cross-linking agent. There are at least 15 genes that are responsible for the known FA complementation groups. Mutations in the \textit{FANCB} gene (Xp22.31) (\textit{OMIM}\# 300515), which are responsible for FA complementation group B (FA-B) (\textit{OMIM}\# 300514), account for 2\% of FA cases. FA-B cases are the only X-linked form of FA and mainly affect males. Females can be heterozygote carriers at risk for having a child with X-linked FA. Carriers are found to have 100\% skewing of X inactivation.

This testing is for sequence analysis of the \textit{FANCB} gene only.

For patients with suspected FA-B, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

\textbf{References:}

- GeneReviews
- \textit{OMIM}\# 300514: Fanconi anemia complementation group B
- \textit{OMIM}\# 300515: \textit{FANCB} gene

\textbf{Methodology}

PCR amplification of 8 exons contained in the \textit{FANCB} gene is performed on the patient's genomic DNA. Direct sequencing of amplification products is performed in both forward and reverse directions, using automated fluorescence dideoxy sequencing methods. The patient's gene sequences are then compared to a normal reference sequence. Sequence variations are classified as mutations, benign variants unrelated to disease, or variations of unknown clinical significance. Variants of unknown clinical significance may require further studies of the patient and/or family members. This assay does not interrogate the promoter region, deep intronic regions, or other regulatory elements, and does not detect large deletions.

\textbf{Detection}

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

Analytical Sensitivity: \textasciitilde 99\%

\textbf{Specimen Requirements}

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

\textbf{Type: Whole Blood}

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube:
- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml
Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

### Related Tests

- Deletion/duplication analysis of the **FANCB** gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available only for known familial mutations to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.
- X-Linked Intellectual Disability panels are available for 30, 60, and 90 genes.