Isolated Nonsyndromic Congenital Heart Disease: \textit{NKX2-5} Gene Deletion/Duplication

\textbf{Test Code:} KP  
\textbf{Turnaround time:} 2 weeks  
\textbf{CPT Codes:} 81228 x1

\section*{Condition Description}

Mutations in the \textit{NKX2-5} gene have been associated with atrioventricular (AV) conduction block, septal defects, conotruncal abnormalities (particularly Tetrology of Fallot), and AV valve formation defects. Mutations in \textit{NKX2-5} have been observed in autosomal dominant pedigrees and isolated cases of congenital heart disease. Studies suggest that \textit{NKX2-5} mutation may be a frequent cause (up to 4\%) of sporadic and familial congenital heart defects.

\textit{NKX2-5} mutation analysis is appropriate for patients with an atrioventricular conduction block or structural heart defects with or without a family history of congenital heart defects. Analysis includes sequencing the entire \textit{NKX2-5} coding region (2 exons) and immediate exon/intron boundaries. Mutations in other regulatory regions and large deletions will not be detected by this assay. Variants of unknown clinical significance may be detected. Custom mutation detection is available for known familial mutations.

\section*{Genes}

\textit{NKX2-5}

\section*{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of \textit{NKX2-5}-related congenital heart disease in an individual in whom sequence analysis was negative.
- Carrier testing in adults with a family history of \textit{NKX2-5}-related congenital heart disease in whom sequence analysis was negative.

\section*{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.

Please note that a “backbone” of probes across the entire genome are included on the array for analytical and quality control purposes. Rarely, off-target copy number variants causative of disease may be identified that may or may not be related to the patient’s phenotype. Only known pathogenic off-target copy number variants will be reported. Off-target copy number variants of unknown clinical significance will not be reported.

\section*{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.

\section*{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.

\textbf{Type: Saliva}

Specimen Requirements:

Oragene \textsuperscript{TM} 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.

\section*{Special Instructions}

\textbf{Disclaimer:} This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Please submit copies of diagnostic biochemical test results along with the sample. 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 Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition.