Speech-Language Disorder 1: \textit{FOXP2} Gene Sequencing

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

\begin{table}[h]
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\begin{tabular}{|l|}
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\textbf{Condition Description} \\
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Mutations of the \textit{FOXP2} gene (7q31) cause a severe form of speech and language disorder. In a large multi-generational family, a heterozygous missense mutation segregates with family members who have verbal dyspraxia or a deficit in sequencing the complex coordinated orofacial movements required for speech. It is also accompanied by a wide range of linguistic and grammatical deficits. Additionally, the \textit{FOXP2} gene was found to be disrupted by a de novo balanced translocation in a patient with speech and language disorder. \\
\textit{FOXP2} encodes a transcription factor which likely regulates gene expression in the developing lung, cardiovascular, intestinal, and neural tissue. \\
\textbf{References:} \\
\begin{itemize}
\item MacDermot et al. (2005). Am J Hum Genet, 76:1074-1080. \\
\item OMIM \#605317: \textit{FOXP2} gene \\
\item OMIM \#602081: Speech-Language Disorder 1
\end{itemize}
\end{tabular}
\end{table}

\textbf{Genes}

\textit{FOXP2}

\textbf{Indications}

This test is indicated for:

\begin{itemize}
\item Confirmation of a clinical diagnosis of speech-language disorder 1. \\
\item Carrier testing in adults with a family history of speech-language disorder 1.
\end{itemize}

\textbf{Methodology}

\textbf{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.

\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: \textasciitilde99\%

\textbf{Specimen Requirements}

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

\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{Type: Saliva}

\textbf{Specimen Requirements:}

Orangene™ Saliva Collection Kit  
Orangene™ 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™ 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.

**Related Tests**
- Deletion/duplication analysis of the *FOXP2* 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.