Lissencephaly 2: \textit{RELN} Gene Sequencing

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

\section*{Condition Description}

Lissencephaly refers to a “smooth brain” with absent gyri or abnormally wide gyri. This is due to impairment in neuronal migration which leads to a thickened cerebral cortex. Mutations in the \textit{RELN} gene (7q22) cause an autosomal recessive form of lissencephaly that is associated with severe abnormalities of the hippocampus, brainstem, and cerebellum. Additionally, individuals with mutations in the \textit{RELN} gene can have abnormal neuromuscular connectivity, congenital lymphedema, seizures, and developmental delays.

For patients with suspected Lissencephaly 2, 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.

\section*{References}

- Hong et al. (2000). Nature Genetics, 26:93-96.  \\
- OMIM \#257320: Lissencephaly 2  \\
- OMIM \#600514: \textit{RELN} gene

\section*{Genes}

\textit{RELN}

\section*{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of lissencephaly 2.
- Carrier testing in adults with a family history of lissencephaly 2.

\section*{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.

\section*{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%

\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) 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.

**Related Tests**

- Deletion/duplication analysis of the *RELN* gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Sequencing and deletion/duplication analysis of the *DCX* and *PAFAH1B1* genes is available.
- 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.