**Kabuki Syndrome: KDM6A Gene Sequencing**

**Condition Description**

Kabuki syndrome is a rare condition that affects multiple organ systems. It is characterized by five cardinal features: (1) characteristic facies, (2) skeletal anomalies, (3) dermatolyphic abnormalities, (4) mild to moderate intellectual disability, and (5) postnatal growth deficiency. Additional manifestations include a broad and depressed nasal tip, large prominent earlobes, a cleft or high-arched palate, immunological defects, such as recurrent ear infections in infancy, and cardiac anomalies. The estimated prevalence is 1 in 32,000 with 400 cases reported worldwide. The majority of cases are de novo; however, parent-to-child transmission has been described.

Pathogenic variants in the KMT2D (formerly MLL2) (12q13.12) or KDM6A (Xp11.3) gene cause Kabuki syndrome. Ng et al. reports loss-of-function mutations in KMT2D in 9 of the 10 individuals in their discovery population with Kabuki syndrome. KMT2D-related Kabuki syndrome is inherited in an autosomal dominant manner. A small number of cases of Kabuki syndrome caused by pathogenic variants in KDM6A have been described. All pathogenic variants reported in the KDM6A gene have apparently been de novo; however, X-linked inheritance is possible.

Please note that this test is for the KDM6A gene only.


**References:**

- GeneReviews
- Ng et al. (2010). Nat Genet, 42(9): 790-794.

**Genes**

- **KDM6A**

**Indications**

This test is indicated for:

- Confirmation of a clinical diagnosis of Kabuki syndrome.
- Carrier testing in adults with a family history of Kabuki syndrome.

**Methodology**

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.

**Detection**

Next Generation Sequencing: Clinical Sensitivity: Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype. Analytical Sensitivity: ~99%.

**Specimen Requirements**

**Type: Whole Blood**

Specimen Requirements:

- In EDTA (purple top) tube:
  - Infants (2 years): 3-5 ml
  - Older Children & Adults: 5-10 ml

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Specimen Collection and Shipping: Store sample at room temperature. 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:** Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

**Special Instructions**

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**

- Deletion/duplication analysis of the *KDM6A* gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Sequencing and deletion/duplication analysis of the *KMT2D* gene (formerly *MLL2*) is available.
- Kabuki syndrome sequencing panel and deletion/duplication analysis panel of the *KMT2D* and *KDM6A* genes are also 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.