## Jalili Syndrome: CNNM4 Gene Deletion/Duplication

**Test Code:** DCNNM  
**Turnaround time:** 2 weeks  
**CPT Codes:** 81228 x1

### Condition Description

Jalili syndrome is an autosomal recessive condition characterized by visual impairment and amelogenesis imperfecta (abnormal enamel). In families with Jalili syndrome, all affected individuals had significant visual impairment, starting in infancy or early childhood and progressing with age, and abnormal enamel of the primary and secondary dentitions and were susceptible to rapid post eruptive failure due to hypomineralization. The first clinical sign of visual impairment is often nystagmus. Photophobia and achronatopsia are also present in individuals with Jalili syndrome. Pathogenic variants in the CNNM4 gene (2q11.2) cause Jalili syndrome.

For patients with suspected Jalili syndrome, sequence analysis is recommended as the first step in pathogenic variant identification. For patients in whom pathogenic variants are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

### References:
- OMIM #607805: CNNM4 gene  
- OMIM #217080: Jalili syndrome  
- Doucette et al. (2013), Ophthalmic Genet, 34:19-29.  
- Parry et al. (2009), Am J Hum Genet, 84:266-273.

### Genes

**CNNM4**

### Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of Jalili syndrome in an individual in whom sequence analysis was negative.  
- Carrier testing in adults with a family history of Jalili syndrome in whom sequence analysis was negative.

### 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.

### Detection

Detection is limited to duplications and deletions. The CGH array will not detect point or intronic pathogenic variants. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

### Specimen Requirements

#### 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.

#### Type: Saliva

Specimen Requirements:

OrageneTM 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

- Sequence analysis of the CNNM4 gene is available and is required before deletion/duplication analysis.
- 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.