Connective Tissue Disorders Panel: Sequencing and CNV Analysis

**Test Code:** MM270  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81405 x1, 81406 x1, 81407 x1

### Condition Description

Connective tissues provide a framework and structural support for the body, protect organs, connect body tissues, and store energy. Connective tissue disorders are a heterogeneous group of more than 200 conditions that often involve the joints, muscles, and skin. Heritable connective tissue disorders include both soft tissue disorders, characterized by excessive skin laxity, joint hypermobility, and easy bruising, as well as skeletal dysplasias that affect bone development.

Diagnosis of heritable connective tissue disorders may be challenging due to extensive clinical variability, phenotypic overlap, or atypical presentation. However, making a specific diagnosis is important given that some of these disorders feature life-threatening complications, such as aortic root rupture, that require careful medical surveillance and monitoring. In addition, treatment options are available for some connective tissue disease.

Reference:

### Genes

ACTA2, ACVR1, ADAMTS2, ATP6V0A2, CBS, CHST14, COL11A1, COL1A1, COL1A2, COL2A1, COL3A1, COL5A1, COL5A2, ELN, FBLN5, FBN1, FBN2, FKBP14, MYLK, NOTCH1, PKD2, PLD1, PRDM5, SLC2A10, SLC39A13, SMAD3, TGFBR1, TGFBR2, ZNF469

### Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of connective tissue disorder.

### 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.

**Copy Number Analysis:** Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

### 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. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

**Copy Number Analysis:** The sensitivity and specificity of this method for CNV detection is highly dependent on the size of the event, sequence context and depth of coverage for the region involved. The assay is highly sensitive for CNVs of 500 base pairs or larger and those containing at least 3 exons. Smaller (< 500 base pairs) CNVs and those that involving only 1 or 2 exons may or may not be detected depending on the sequence context, size of exon(s) involved and depth of coverage.

### Specimen Requirements

**Submit only 1 of the following specimen types**

**Type:** Whole Blood (EDTA)

**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 uncotted cord or cardiac blood

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Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Type: DNA, Isolated

Specimen Requirements:
Microtainer
8µg
Isolation using the Perkin Elmer™ 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.

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Oragene™ 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.

Related Tests

- Connective Tissue Disorders: Deletion/Duplication Panel