**Arrhythmias: Sequencing Panel**

**Test Code:** MM093  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81403 x1, 81404 x1, 81479 x1

### Condition Description

Arrhythmia is any change from the normal sequence of electrical impulses of the heart. These impulses may happen too fast (tachycardia), too slowly (bradycardia), or erratically. Types of arrhythmias include atrial fibrillation, conduction disorders, premature contraction, ventricular fibrillation, tachycardia, and bradycardia. Arrhythmias can present with a broad spectrum of symptoms including palpitation, a fluttering sensation, fatigue, dizziness, lightheadedness, syncope, rapid heartbeat, shortness of breath, chest pain, and sudden cardiac arrest.

References:
- American Heart Association
- OMIM

### Genes

- AKAP9, ANK2, CACNA1C, CACNB2, CALM1, CASQ2, CTNNA3, DSC2, DSG2, DSP, GJA5, GPD1L, HCN4, JUP, KCNA5, KCND3, KCNE1, KCNE2, KCNE3, KCNH2, KCNN2, KCNJ5, KCNJ8, KCNQ1, NKX2-5, NPPA, PKP2, RANGRF, RYR2, SCN1B, SCN3B, SCN4B, SCN5A, SNTA1, TMEM43, TRDN, TRPM4

### Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of arrhythmia.
- Carrier testing in adults with a family history of arrhythmia.

### 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

**Clinical Sensitivity:** Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants 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:** ~99%

### Specimen Requirements

Submit only 1 of the following specimen types

#### 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: Ship sample at room temperature with overnight delivery.

#### Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight
Related Tests

- Comprehensive Cardiovascular: Sequencing Panel (MCAR1)
- Arrhythmias: Deletion/Duplication Panel