Familial Atrial Fibrillation (FAF) Panel Sequencing

CPT Code(s): 81406

Service Code (IU Health): 53025532

Ordering Recommendation: Information about the KCNQ1, SCN5A, KCNE2, KCNA5, LMNA, and KCNJ2 genes sequence may be used as an aid to clinicians in confirming the clinical diagnosis in symptomatic subjects, determining the risk assessment for asymptomatic first degree relatives, and establishing the most appropriate therapeutic strategy and treatment

Synonyms: KCNQ1, SCN5A, KCNE2, KCNA5, LMNA, KCNJ2, familial atrial fibrillation, arrhythmia, syncope

Methodology: Sanger sequencing analysis

Performed: weekly

Reported: 21-28 days

Specimen Requirements

Patient Preparation: None required for whole blood

Collect: Preferred: Lavender (EDTA); Acceptable: Yellow (ACD Solution A or B), DNA extracted from leukocytes, muscle, or fibroblasts eluted in sterile DNAse/RNAse free water or TE and with A260:A280 ratio should of 1.8-2.0

Specimen Volume/Amount: Blood: 7mL whole blood (minimum 2mL), Extracted DNA: 3 micrograms

Storage/Transport: Refrigerated/Room temperature

Unacceptable Conditions: Grossly hemolyzed or clotted

Remarks:

Stability: 2 weeks refrigerated; 1 month frozen

Reference Interval: N/A
Interpretive Data

**Characteristics:** Pathogenic variants in the KCNQ1, SCN5A, KCNE2, KCNA5, LMNA, and KCNJ2 genes cause abnormal function of cardiac voltage-gated potassium and sodium channels, channel-interacting proteins and proteins of the perinuclear lamina leading to various forms of cardiac rhythm disturbances in some cases associated with congenital profound bilateral sensorineural hearing loss or with Andersen-Tawil syndrome (ATS)

**Inheritance:** autosomal dominant

**Cause:** Pathogenic variants such as, but not limited to missense, nonsense, splicing, and insertions and deletions

**Incidence of Familial Atrial Fibrillation:** Atrial fibrillation is a pan ethnic disease with a estimated worldwide incidence of 1:168 people, while the incidence of the familial form of atrial fibrillation is unknown but estimate to account for 30% of the total of atrial fibrillation patients

**Penetrance:** Incomplete

**Clinical sensitivity:** Pathogenic variants in the KCNA5 gene have been identified in patients with atrial fibrillation (FAF)

**Analytical sensitivity and specificity:** 99%

**Limitations:** Only the coding and immediate flanking regions of the KCNQ1, SCN5A, KCNE2, KCNA5, LMNA, and KCNJ2 genes are analyzed by DNA sequencing. Changes in the promoter and other non-coding regions are not detected by this assay. In addition, the presence of a large intragenic deletion of the KCNQ1, SCN5A, KCNE2, KCNA5, LMNA, and KCNJ2 genes (such as the deletion of an exon or multiple exons) will not be detected by sequence analysis. Although rare, false positive or false negative results may occur. All results should be interpreted in context of clinical findings, relevant history, and other laboratory data

**References:** Genetic Testing Registry, Gene Reviews, OMIM, ACC/AHA/HRS Guidelines