Clinical Appropriateness Guidelines

Genetic Testing for Hereditary Cardiac Disease

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Scope

This document addresses genetic testing for inherited arrhythmias and cardiomyopathies. Aortopathies and other connective tissue disorders with cardiac manifestations as well as congenital heart defects are NOT included in this document; see Clinical Appropriateness Guidelines: Genetic Testing for Single-Gene and Multifactorial Conditions. All tests listed in this guideline may not require prior authorization; please refer to the health plan.

Genetic Counseling Requirement

Genetic testing included in these guidelines is covered when:

1. The patient meets coverage criteria outlined in the guidelines
2. A recommendation for genetic testing has been made by one of the following:
    - An independent board-certified or board-eligible medical geneticist not employed by a commercial genetic testing laboratory*
    - An American Board of Medical Genetics or American Board of Genetic Counseling-certified genetic counselor not employed by a commercial genetic testing laboratory*
    - A genetic nurse credentialed as either a Genetic Clinical Nurse (GCN) or an Advanced Practice Nurse in Genetics (APGN) by either the Genetic Nursing Credentialing Commission (GNCC) or the American Nurses Credentialing Center (ANCC) who is not employed by a commercial genetic testing laboratory*

    Who:

    - Has evaluated the case and performed pre-test genetic counseling with the patient or the patient's legal guardian
    - Has completed a three-generation pedigree
    - Intends to engage in post-test follow-up counseling with the patient or the patient's legal guardian

**A physician, genetic counselor or genetic nurse employed by a laboratory that operates within an integrated, comprehensive healthcare delivery system is not considered to be an employee of a commercial genetic testing laboratory for the purpose of these guidelines.*

Appropriate Use Criteria

Genetic testing is medically necessary when all of the following criteria are met:

- The test is clinically reasonable:
    - Symptoms and presentation are consistent with the suspected condition
    - Results are expected to lead to a change in medical management
    - If testing guidelines* exist, the clinical scenario falls within those recommendations
    - The test is customarily recognized as clinically and technically appropriate in the diagnosis and/or treatment of the suspected condition
- The clinical benefit of testing outweighs the potential risk of psychological or medical harm to the individual being tested
- The test is as targeted as possible for the clinical situation (e.g., familial pathogenic or likely pathogenic (P/LP) variant testing, common variants, genes related to phenotype)
- The clinical presentation warrants testing of multiple genes when a multi-gene panel is requested
- The testing methodology has been clinically validated and is the most accurate method unless technical limitations (e.g., poor sample quality) necessitate the need for alternate testing strategies

**See the Professional Society Guidelines section.*

Genetic Testing of Affected Individuals

In addition to the above appropriate use criteria, confirmatory or diagnostic genetic testing for hereditary arrhythmias (i.e., Brugada syndrome (BrS), catecholaminergic polymorphic ventricular tachycardia (CPVT), Long QT syndrome (LQTS)) and cardiomyopathies (i.e., arrhythmogenic right ventricular cardiomyopathy (ARVC), dilated cardiomyopathy (DCM), hypertrophic cardiomyopathy (HCM), left ventricular non-compaction cardiomyopathy (LVNC), restrictive cardiomyopathy (RCM)) is medically necessary when all of the following criteria are met:

- The individual has a clinical diagnosis of a hereditary cardiomyopathy or arrhythmia **OR** the individual has a suspected syndromic, metabolic or neuromuscular form of a hereditary cardiomyopathy or arrhythmia
- The requested testing is as targeted as possible to a specific subset of genes with a demonstrated gene/disease association with the individual's diagnosed or suspected condition

Single-site genetic testing of asymptomatic individuals for a known familial deleterious or suspected deleterious pathogenic or likely pathogenic (P/LP) variant is medically necessary.

Genetic Testing in the Evaluation of Unexplained Sudden Cardiac Arrest

Cardiac genetic testing of an individual with an unexplained sudden cardiac arrest is medically necessary in the following circumstances:

- Comprehensive clinical cardiac evaluation (heart rhythm monitoring, cardiac imaging, provocative testing, etc.) has not confirmed a diagnosis of a specific underlying heritable cardiac condition (e.g., ARVC, HCM, LQTS, etc.)
- Non-genetic causes of sudden cardiac arrest have been ruled out (toxicology, ischemic coronary artery disease, etc.)

Post-Mortem Genetic Testing

Post-mortem cardiac genetic testing of an individual with sudden unexplained death, whose first degree family member is a covered member, is medically necessary in the following circumstances:

- When the autopsy reveals evidence for a *specific* underlying heritable cardiac condition (e.g., ARVC, HCM, DCM, RCM) AND all of the following criteria are met:
    a. The corresponding targeted testing is ordered (e.g., HCM panel testing in cases where autopsy revealed evidence for HCM)
- In 'autopsy negative' cases when cause of death remains unknown after completion of autopsy and toxicology testing and one of the following criteria are met:
    a. Documented arrhythmic death is suggestive of an arrhythmia syndrome
    b. Deceased individual is less than 40 years old at time of death
    c. Sudden cardiac death event is preceded by specific triggers associated with familial arrhythmia syndromes

Tests Not Clinically Appropriate

- Broad "multi-condition" panel testing (e.g., pan-cardio panel, arrhythmia panel) is not medically necessary for routine cardiac genetic testing
- Genetic testing for short QT syndrome and atrial fibrillation is not medically necessary
- Genetic testing for isolated left ventricular noncompaction cardiomyopathy (LVNC) is not medically necessary

CPT Codes

The following codes are associated with the guidelines outlined in this document. This list is not all inclusive. Medical plans may have additional coverage policies that supersede these guidelines.

Covered when medical necessity criteria are met:

81403	Molecular Pathology Procedure Level 4
81404	Molecular Pathology Procedure Level 5
81405	Molecular Pathology Procedure Level 6
81406	Molecular Pathology Procedure Level 7
81407	Molecular Pathology Procedure Level 8
81408	Molecular Pathology Procedure Level 9
81413	Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, catecholaminergic polymorphic ventricular tachycardia); genomic sequence analysis panel, must include sequencing of at least 10 genes, including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A
81414	Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, catecholaminergic polymorphic ventricular tachycardia); duplication/deletion gene analysis panel, must include analysis of at least 2 genes, including KCNH2 and KCNQ1
81439	Hereditary cardiomyopathy (eg, hypertrophic cardiomyopathy, dilated cardiomyopathy, and arrhythmogenic right ventricular cardiomyopathy) genomic sequence analysis panel, must include sequencing of at least 5 cardiomyopathy-related genes (e.g., DSG2, MYBPC3, MYH7, PKP2, and TTN)

Background

Most forms of arrhythmias and cardiomyopathies are multifactorial. There are, however, several forms of Mendelian hereditary cardiac disease that cause severe and early-onset symptoms. The hereditary arrhythmias and cardiomyopathies are primarily diagnosed clinically and symptoms can be variable even within the same family. Although genetic test results may not guide medical management for those with a clinical diagnosis, identification of a P/LP variant can allow for detection of asymptomatic family members who might benefit from life-saving treatment. Most hereditary cardiac conditions are associated with multiple genes. Targeted panel testing is reasonable in most cases.

Rationale for Genetic Counseling for Hereditary Cardiac Conditions

Pre-test genetic counseling provides individuals seeking genetic testing the opportunity to make informed decisions about their genetic testing and subsequent medical management options. Genetic counseling combines expertise in obtaining and interpreting family history information, the ability to identify the most beneficial individual in a family to initiate testing, identification of the most appropriate

testing options, experience in obtaining informed consent for testing and proficiency in genetic variant interpretation, in order to maximize the genetic testing experience for patients and their healthcare providers. The genetic counseling informed consent process also educates and empowers patients to consider the psychological, financial, employment, disability, and insurance implications of genetic testing and results (Al-Khatib et al. 2018). Patients who receive genetic counseling report increased knowledge, understanding, and satisfaction regarding their genetic testing experience (Armstrong et al. 2015; Harvey et al. 2007).

The advent of multi-gene panels and genome-scale sequencing have increased the complexity of the genetic testing landscape. Misuse of genetic testing increases the risk for adverse events and patient harm, including missed opportunities for diagnosis and disease prevention (Bellcross et al. 2011; Plon et al. 2011). Genetic information requires expert interpretation and ongoing re-evaluation to ensure the most accurate interpretation is utilized to inform medical management decision making. The multitude of genetic testing options as well as the complex information revealed by genetic testing can make choosing the most appropriate test and interpretation of results difficult for non-genetics healthcare providers (Ray 2011). Involvement of a clinical genetics provider has been shown to ensure the correct test is ordered, limit result misinterpretation and allow patients to make informed, evidence-based medical decisions with their healthcare providers (Cragun et al. 2015).

Genetic counseling not only improves patient outcomes but also reduces unnecessary healthcare spending. Pre-test genetic counseling has been shown to reduce inappropriate test ordering and prevent unnecessary medical procedures and interventions that follow from inaccurate result interpretation (DHHS 2011). While genetic testing is now available for almost all clinical specialties, correct use and interpretation is necessary to prevent adverse outcomes. While genetic counseling may benefit any patient considering or undergoing genetic testing, tests that offer predictive information or have a higher chance of identifying variants of uncertain significance often carry stronger recommendations in the form of consensus guidelines and professional statements recommending genetic counseling by trained genetics professionals.

Both the joint consortium of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society (AHA/ACC/HRS) as well as the ACMG have issued strong recommendations for genetic counseling for individuals undergoing evaluation for inherited cardiac disease.

In their Task Force publication from 2017 (Al Khatib et al. 2018), the AHA/ACC/HRS provided this recommendation:

> *The decision to proceed with genetic testing requires discussion, regarding the clinical use of genetic information to be obtained for both the proband and family members, as well as consideration of the important psychological, financial, employment, disability, and life insurance implications of positive genotyping. Balancing privacy of health care information for the proband with the "right to know" for family members, and the ability to provide appropriate communication of information to all potentially affected family members can be challenging on many levels, including family dynamics, geographic proximity, and access to healthcare. For these reasons, genetic counseling generally occurs before proceeding with genetic testing, and, from a patient's perspective, is optimally provided by genetic counselors, if available, in collaboration with*

physicians. A combined approach of genetic counseling with medical guidance may appropriately balance the decision as to whether genetic testing would be beneficial on an individual basis.

In the joint statement put forth by the ACMG and Heart Failure Society (Hershberger et al. 2018), genetic counseling performed by a board-certified or board-eligible genetic specialist or specialized physician in the absence of a genetics professional is recommended as a key component of the evaluation of individuals with suspected familial cardiomyopathies with a level of evidence of A, their strongest recommendation. In addition, this recommendation includes specific guidance regarding genetic counseling which notes that genetics professionals are specially trained to provide: review of medical records essential for phenotyping, obtaining a pedigree, patient and family education, evaluating genetic testing options, obtaining consent for genetic testing, facilitating family communication, and ordering and interpreting genetic test results while addressing psychosocial issues.

Multi-Gene Panel Testing for Hereditary Cardiomyopathies and Arrhythmias

The current plethora of genes purported to be associated with hereditary cardiomyopathies and arrhythmias is the result of dedicated efforts to better elucidate the genetic architecture of hereditary cardiac disease. This has resulted in the availability of multi-gene panels which include genes with limited levels of disease association. Historically, the promise of identifying new genes to explain "current" gene-negative cases was the driver of numerous candidate gene studies. At that time a missense variant in a conserved region, absent in a small set of control alleles, and with some evidence of segregation, suggested a new gene association. The National Institutes of Health-funded Clinical Genome Resource (ClinGen) has more recently developed evaluation frameworks to assess both the strength of evidence supporting a relationship between a gene and disease (gene-disease validity), and whether loss or gain of function of individual genes or genomic regions is a mechanism for disease (dosage sensitivity). The genetic evidence required to establish gene-disease validity and dosage sensitivity of specific genes includes a robust demonstration of case-level data, segregation data, functional data, and model organisms. Disease specific frameworks across multiple domains have been made publicly available and can be utilized to inform pathogenicity of sequence variants, guide test development and inform genomic variant filtering pipelines (Thaxton et al. 2021).

We now recognize that clearly defined boundaries are needed for when candidate genes should be used for clinical testing. The historical approach is now widely viewed as insufficient; however, publication of gene-disease associations based on limited evidence have led to inclusion of such genes on clinical test panels even though it is unlikely these genes will be confirmed as monogenic causes of hereditary cardiovascular disease once sufficient numbers of people have been tested. Per the various ClinGen curation publications, analysis of the currently available evidence suggests that variation in these candidate genes is largely uninformative in isolation (Jordan et al. 2021). With the possible exception of a large family with ample opportunity for segregation analysis, variants in genes not classified as moderate, strong, or definitive evidence will seldom be clinically meaningful for hereditary cardiomyopathies and arrhythmias. Inclusion of such genes of uncertain significance on clinical testing panels for idiopathic/isolated phenotypes is likely to increase the VUS rate and contribute to uncertainty in clinical care for patients, family members and providers. Additionally, genetic testing limited to genes definitively or strongly associated with the hereditary cardiomyopathy or arrhythmia phenotypes has recently been endorsed by the American Heart Association as well as by several clinical publications (Musunuru et al. 2020; Landstrom et al., 2021; Mazzarotto et al., 2019, Alafares et al., 2015). For cases

of hereditary cardiomyopathies and/or arrhythmias suspected to be due to syndromic, metabolic or neuromuscular forms of disease, inclusion of additional genes on multi-gene panels may be warranted.

Arrhythmogenic Right Ventricular Cardiomyopathy

Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC) is heritable heart disease characterized by fibro-fatty replacement of heart cells predominantly in the right ventricle of the heart. ARVC typically presents in adolescence through early adulthood and is often asymptomatic prior to unanticipated cardiac events. When symptoms occur, they can include irregular heart rhythms, shortness of breath, and fainting episodes. Individuals with ARVC are at increased risk for sudden cardiac death, especially during strenuous exercise. The estimated prevalence of ARVC in the US is 1 in 1,000 to 1 in 2,000, with greater than 50% of cases being familial (Teo et al. 2015). The disease accounts for 5% of sudden cardiac deaths of young individuals in the US.

Clinical diagnosis of ARVC can be confirmed based on demonstration of characteristic ECG, arrhythmic, structural, and/or histological abnormalities. Diagnostic criteria, initially proposed by an international task force, were revised by Marcus et al. (2010) to incorporate new knowledge and technology to improve diagnostic sensitivity while maintaining diagnostic specificity. With this revised task force criteria (rTFC), individuals are classified as having a definite, borderline, or possible diagnosis of ARVC. Family history and genetic test results may also help to confirm a diagnosis (Ackerman et al. 2011). The most common genes associated with ARVC are the desmosomal genes *PKP2* (10-45%), *DSP* (10-15%), *DSG2* (7-10%), *DSC2* (2%) and *JUP* (Mattesi et al. 2020). For patients who meet the rTFC diagnostic criteria, the rate of a positive genetic testing result is approximately 50% (Corrado et al. 2020). Less commonly, ARVC can be inherited as an autosomal recessive condition when it is associated with palmoplantar keratoderma and wooly hair, namely Naxos disease and Carvajal syndrome (Teo et al. 2015). Specific medical management and lifestyle modifications are recommended for individuals with ARVC, and may depend on the specific gene involved. It is well established that desmosome gene P/LP variants (*PKP2*, *DSC2*, *DSG2*) are specifically associated with disease pathogenesis related to exercise, therefore, individuals with identified P/LP variants in these genes should avoid endurance and frequent exercise (James et al. 2013; Hershberger et al. 2018).

Multiple professional organizations have commented on the appropriateness of genetic testing for individuals and families with ARVC, including the Heart Rhythm Society, the European Heart Rhythm Association (HRS/EHRA), and the Heart Failure Society of America (HFSA). It is generally agreed that genetic testing panels are appropriate for patients who have been clinically diagnosed with ARVC or who are strongly suspected to have this diagnosis. Care in the utilization of genetic testing for ARVC is needed as up to 6% of healthy controls have been noted to have identified variants in ARVC associated genes (Kapplinger et al. 2011). If a syndromic cause of ARVC is suspected based on clinical examination and family history, relevant genetic testing panels are also appropriate. When a genetic cause of ARVC is identified, P/LP variant-specific testing in at-risk family members is also important given the benefits of screening and treatment for presymptomatic individuals (Ackerman et al. 2011; Hershberger et al. 2018; Towbin et al. 2019). It is recommended that first degree relatives of patients with ARVC receive regular cardiac screening, with frequency varying by age, unless they test negative for a known P/LP family variant (Hershberger et al. 2018).

In 2021, ClinGen evaluated 26 reported ARVC genes and found that only 6 were confirmed to have definitive or strong evidence of disease association (James et al. 2021). Definitive and strong evidence genes for ARVC include *PKP2*, *DSP*, *DSG2*, *DSC2*, *JUP* and *TMEM43*. There was moderate evidence for

DES and *PLN* while the remaining 18 genes had limited or no evidence of disease association. Of note, *RYR2* was refuted as an ARVC gene since clinical data and model systems exhibited a catecholaminergic polymorphic ventricular tachycardia phenotype. Per the findings of their work, this task force recommends caution in utilizing multigene panel testing outside of these confirmed 8 ARVC genes and stresses that use of larger panels is not routinely recommended.

Dilated Cardiomyopathy

Dilated cardiomyopathy (DCM) is characterized by enlargement of the left ventricle of the heart and systolic impairment, in the absence of abnormal loading conditions or coronary artery disease sufficient to cause global systolic dysfunction (Haas 2015; Rosenblaum et al. 2020). The symptoms of DCM include shortness of breath, chest pain/tightness, fainting episodes and cardiac arrhythmias. The most serious complication of DCM is sudden, irregular heart rhythms such as ventricular tachycardia/fibrillation that can lead to sudden cardiac arrest and death. Some individuals with DCM will have no symptoms throughout their lifetime.

DCM is a heterogeneous condition caused by ischemia, systemic disease (e.g., mitochondrial or muscular dystrophy), toxins, or infection. Twenty to 50 percent of cases of idiopathic DCM are inherited. DCM can be inherited as an X-linked, autosomal recessive or autosomal dominant condition. Autosomal dominant is the most common form of inherited DCM. Genetic testing is available for multiple DCM genes, typically in large multi-gene panels. Genetic testing identifies a P/LP variant in 25-40% of cases with an autosomal dominant family history, and 10-25% of isolated cases (Hershberger et al. 2018; Mazzarotto et al. 2020).

Multiple professional organizations have commented on the appropriateness of genetic testing for individuals and families with DCM, including the Heart Rhythm Society, the European Heart Rhythm Association (HRS/EHRA), and the Heart Failure Society of America (HFSA). It is generally agreed that genetic testing panels are appropriate for patients who have been clinically diagnosed with DCM, especially those with significant cardiac conduction disease and/or family history of premature unexpected death. When a genetic cause of DCM is identified, mutation-specific testing in at-risk family members is also important given the benefits of screening and treatment for presymptomatic individuals (Ackerman et al. 2011; Hershberger et al. 2018). It is recommended that first degree relatives of patients with DCM receive regular cardiac screening, with frequency varying by age, unless they test negative for a known pathogenic family mutation (Hershberger et al. 2018).

Although genetic testing is useful in differentiating between familial versus isolated DCM, and therefore facilitates identification of at-risk family members, management for the individual affected with DCM typically does not change once a diagnosis of familial DCM is established. One notable exception to this is when a *LMNA* P/LP variant is identified. In individuals identified with a *LMNA* P/LP variant requiring pacemaker placement (i.e., history of arrhythmia or known risk of arrhythmia), the use of a pacing ICD rather than a pacemaker has been recommended due to the risk of ventricular arrhythmias and sudden death (Meune 2006; Halliday et al. 2017; Kayvonpour et al. 2017).

In 2021, ClinGen evaluated 51 genes associated with DCM and identified 12 genes with definitive or strong evidence of disease causation (*BAG3*, *DES*, *DSP*, *FLNC*, *LMNA*, *MYH7*, *PLN*, *RBM20*, *SCN5A*, *TNNC1*, *TNNT2*, *TTN*) and another 7 genes with moderate evidence which are likely to emerge as strong or definitive with additional data (Jordan et al. 2021). Although clinical DCM genetic testing panels include an average of ~60 genes, only 19 genes emerged with high levels of evidence. This curation also

confirmed the overlap between definitive strong evidence genes that cause DCM as well as hypertrophic cardiomyopathy and arrhythmogenic right ventricular cardiomyopathy. As acknowledged by other ClinGen cardiovascular gene curation efforts, the rationale for commercial multi-gene DCM panels that include genes with limited, disputed or no known disease association is unclear and inclusion of these genes may contribute to uncertainty in clinical care for patients and providers (Musunuru et al. 2020). Additionally, DCM panels limited to genes with robust evidence for disease/gene association compared to extended DCM panels showed similar detection of pathogenic and likely pathogenic variants while also reducing the number of VUS (Stroeks et al. 2021).

Hypertrophic Cardiomyopathy

Hypertrophic cardiomyopathy (HCM) is characterized by increased size of the left ventricle of the heart, typically caused by thickening of the heart muscle tissue. The symptoms of HCM can be variable, ranging from no symptoms to shortness of breath or irregular heart rhythms, or sudden death. The irregular heart rhythms can occur without warning and may be life threatening. HCM has a prevalence of 1/500 individuals, making it one of the most common cardiac genetic diseases. It is inherited as an autosomal dominant trait with reduced penetrance.

HCM is typically diagnosed clinically with cardiac imaging, physical exam, electrocardiogram, or based on histopathologic features at autopsy. Risk stratification related to sudden cardiac death remains a clinical challenge (Geske et al. 2018). Family history focused on history of sudden death and age of onset in family members can be helpful in risk stratification. Genetic testing for nonsyndromic HCM is not always beneficial for risk stratification or prediction of sudden cardiac death. The major benefit of genetic testing in non-syndromic HCM lies in at-risk family member identification (Ackerman et al. 2011; Gersh et al. 2011; Hershberger et al. 2018). Once a P/LP variant has been identified, testing negative for a known familial variant allows at-risk family members to discontinue all screening (which can be both costly and time-consuming) (Gersh et al. 2011; Hershberger et al. 2018).

HCM is the most common cause of sudden death in athletes, accounting for 30% of cases of young sudden death during competition. Approximately 5%-10% of individuals with HCM progress to end-stage disease with impaired systolic function and, in some cases, left ventricular dilatation and regression of LVH. The annual mortality rate in individuals with end-stage disease is estimated at 11% and cardiac transplantation may be required. Disease-related mortality is most commonly caused by sudden cardiac death, heart failure, or embolic stroke, but with current management most individuals with HCM will not have a significantly reduced life-span (Sen-Chowdhry et al. 2016).

Multiple genes have been reported to be associated with HCM, most of which encode sarcomeric proteins that are involved with contraction of the heart muscle. Typically, P/LP variants in these genes are inherited in an autosomal dominant manner. The diagnostic yield of genetic testing panels for HCM is approximately 30-40% with another 20% of confirmed familial cases being gene elusive (Butters et al. 2020). *MYH7* and *MYBPC3* are the most common non-syndromic causes of HCM (Hershberger et al. 2018). Childhood onset conditions associated with HCM include inborn errors of metabolism (e.g., Pompe disease), mitochondrial disease (e.g., Friedreich Ataxia), RASopathies (e.g., Noonan syndrome), and rarely neuromuscular disorders (e.g., Limb girdle muscular dystrophy). Evaluation of the family history and presence of other clinical symptoms are often helpful in differentiating syndromic from non-syndromic HCM (Musunuru et al. 2020). When a syndromic cause of HCM is identified, additional medical management changes may be indicated based on other specific health risks. Therefore, a

diagnosis of HCM should prompt a thorough evaluation for associated conditions, especially in infants and children with HCM (Hershberger et al. 2018).

In 2019 ClinGen evaluated 57 genes associated with HCM and identified 8 causative genes with definitive evidence and 3 additional genes with moderate evidence. Another 12 syndromic genes were associated with isolated left ventricular hypertrophy with definitive evidence (Ingles et al. 2019; Musunuru et al. 2020). Importantly, many genes that are included on commercial HCM testing panels have only moderate or limited evidence of disease association, and the utility of variant detection in these genes is unclear (Ingles et al. 2019; Thomson et al. 2018). Approximately 5% of patients will have two or more P/LP variants identified (compound heterozygote); these patients often have an earlier age of onset and worse prognosis (Fourey et al. 2017).

Left Ventricular Non-Compaction Cardiomyopathy

Left ventricular noncompaction cardiomyopathy (LVNC) is a cardiac disorder involving the abnormal development of the left ventricle of the heart. This condition is typically diagnosed clinically with cardiac imaging when the left ventricle appears to be spongy and "non-compacted," having unusual and excessive trabeculations. Some individuals with LVNC are asymptomatic, but complications such as arrhythmia, palpitations, fatigue, shortness of breath, fainting, lymphedema, and blood clotting can occur. There is also a risk of sudden cardiac death for individuals with LVNC (van Waning et al. 2018).

P/LP variants in at least 15 genes have been reported in association with LVNC including *TNNT2*, *MYBPC3*, *ZASP* (*LBD3*), *MYH7*, and *TAZ* (van Waning et al. 2018). The majority of these genes are typically associated with additional syndromic phenotypes, such as Barth syndrome and Noonan syndrome (Arbustini et al. 2014). In a study of 128 individuals diagnosed with LVNC prior to age 21, 9% were found to have a syndromic or metabolic diagnosis, and 32% had a family history of cardiac disease. Among those with isolated LVNC, none had a genetic P/LP variant identified (Miller et al. 2017). Individuals with genetic P/LP variants and LVNC have higher rates of heart transplantation and higher risks of death, thus genetic testing may be useful in risk prediction (Li et al. 2018). However, limited data regarding detection rates, possible non-penetrant P/LP variants, genetic and epigenetic modifiers, environmental causes, and variants of uncertain significance all lend to the complexity of interpreting LVNC-related gene testing for both affected individuals and their at-risk relatives (Arbustini et al. 2015).

There is some debate as to whether LVNC on its own should be considered a primary cardiomyopathy, given that it may be present in 2-10% of the population when highly sensitive screening methodologies are used, and that LVNC has been observed to progress and regress when followed in athletes and pregnant women. Guidelines from the Heart Failure Society of America suggest considering LVNC to be a phenotype rather than a unique type of cardiomyopathy. When additional features of hypertrophic, dilated, or restrictive cardiomyopathy are present in an individual or family, guidelines for that type of cardiomyopathy should be followed. When isolated LVNC is detected incidentally in an asymptomatic individual with no apparent family history of cardiomyopathy, there is limited evidence to support genetic or family screening (Hershberger et al. 2018; Towbin et al. 2019; Ross et al. 2020). Therefore, genetic testing has limited clinical utility in diagnosing LVNC or establishing molecular confirmation for the purpose of testing at risk family members of individuals with a confirmed clinical diagnosis of LVNC, unless there are other phenotypic features suggestive of a known syndrome or other type of cardiomyopathy.

Restrictive Cardiomyopathy

Restrictive cardiomyopathy (RCM) is a rare heritable cardiac disorder in which the heart muscle is stiff and cannot fully relax after each contraction. The majority of acquired cases of RCM are idiopathic while a smaller number are caused by conditions such as sarcoidosis and endomyocardial fibrosis or as sequelae to radiation and chemotherapy for cancer treatment. RCM is characterized by the presence of impaired ventricular filling and diminished diastolic volume with normal or nearly normal LV wall thickness and ejection fraction.

The genetic spectrum of RCM remains largely unknown, and the diagnostic yield of currently available genetic testing panels may range from 10-60% (Hershberger et al. 2018). In patients with non-syndromic (idiopathic) RCM, RCM-specific P/LP variants have been described in over 18 of sarcomeric and cytoskeletal genes, including *TNNI3*, *MYH7*, *MYBPC3*, *BAG3*, and *ACTN2*. Many of these have also been implicated in dilated and hypertrophic cardiomyopathies and arrhythmias (Kostareva 2016). Familial RCM often occurs along with skeletal muscle involvement or abnormalities of other organ systems due to syndromic causes such as Noonan syndrome, hemochromatosis, or glycogen storage disorders. Familial *TTR* amyloidosis related to *TTR* gene variants is another common cause of RCM. Testing *TTR* is important given the prevalence of P/LP variants in elderly patients with severe heart failure, especially black patients, and available advances in treatment (Hershberger et al. 2018; Muchtar et al. 2017; Musunuru et al. 2020). Therefore, a diagnosis of RCM should prompt a thorough evaluation for associated conditions (Stollberger 2007). When a syndromic cause of RCM is identified, medical management changes may be indicated based on other specific health risks. For example, hemochromatosis is treated with therapeutic phlebotomy, while RCM due to sarcoidosis may be treated with antiarrhythmics or immunosuppressive agents (Brown and Diaz 2019).

Multiple professional organizations have commented on the appropriateness of genetic testing for individuals and families with RCM, including the Heart Rhythm Society, the European Heart Rhythm Association (HRS/EHRA), and the Heart Failure Society of America (HFSA). It is generally agreed that genetic testing panels are appropriate for patients who have been clinically diagnosed with RCM based on clinical evaluation. Genetic testing panels used in the initial workup may include those targeted to hypertrophic or dilated cardiomyopathies, given the overlap of causative genes among these conditions. If a syndromic form of RCM is suspected based on clinical examination and family history, relevant genetic testing panels are also appropriate. When a genetic cause of RCM is identified, P/LP variant-specific testing in at-risk family members is also important (Ackerman et al. 2011; Hershberger et al. 2018). It is recommended that first degree relatives of patients with RCM receive regular cardiac screening, with frequency varying by age, unless they test negative for the known P/LP family variant (Hershberger et al. 2018).

Brugada Syndrome

Brugada syndrome (BrS) is characterized by a specific pattern of ECG (ST segment elevation in leads V1-V3). This can be associated with right bundle branch block, a defect in the heart's conduction system that can also be seen on ECG. This pattern may be seen on resting ECG or may require an ECG while receiving a drug known as a sodium channel blocker. Symptoms of BrS can include arrhythmia or irregular heartbeats and fainting spells. BrS typically presents in males in their 30s or 40s and is the second most common cause of death in men from Southeast Asia under the age of 40 years. Implantable cardioverter defibrillators (ICDs) are the only therapy currently known to be effective in persons with BrS with syncope or cardiac arrest. Avoidance of certain medications is recommended for

persons with Brugada syndrome, as well as particular attention during a febrile state as this can be a risk factor for syncope (Hickey and Elzomor 2018). The diagnosis of Brugada Syndrome (BrS) is based on symptoms, electrocardiogram (ECG) and family history. A diagnosis can be made based on ECG results and clinical history in approximately 75% of persons. Genetic testing can also be helpful to make a diagnosis of BrS. In most cases, the primary value of genetic testing for Brugada syndrome is to benefit at-risk family members.

P/LP variants in the *SCN5A* gene are the most common genetic cause for Brugada syndrome (20-30%) and account for >75% of BrS genotype positive persons. Targeted testing of *SCN5A* can be useful among persons with clinical suspicion for BrS, according to HRS guidelines (2011). Genetic testing is not indicated among persons with an isolated type 2 or 3 Brugada pattern on ECG (Musunuru et al. 2020). In 2019 ClinGen evaluated 21 reported causative genes for Brugada syndrome and found the only gene with definitive evidence as causal for this condition was *SCN5A* (Hosseini et al. 2018; Musunuru et al. 2020).

Catecholaminergic Polymorphic Ventricular Tachycardia

Catecholaminergic polymorphic ventricular tachycardia (CPVT) is a rare form of cardiac arrhythmia in which emotional or physical stress triggers catecholamine release, which leads to abnormal heartbeat and symptoms such as dizziness, fainting, cardiac arrest, and even sudden death. The estimated prevalence of CPVT is 1 in 10,000, and symptoms tend to be earlier onset and more common among males than females (Fernández-Falgueras et al. 2017). The mean age of onset is between 7 and 12 years old, but onset can occur as late as 40. Mortality rate from sudden cardiac death may be as high as 30% (Hickey and Elzomor 2018).

RYR2 is the most common genetic cause of CPVT, with P/LP variants found in about 60% of individuals with this condition. Additional genes that have been associated with CPVT include *KCNJ2*, *CALM1*, *CALM2*, *CALM3*, *TRDN*, *CASQ2* and *ANK2* (Fernández-Falgueras et al. 2017; Baltogiannis et al. 2019). The majority of cases of CPVT are inherited in an autosomal dominant manner; however, *CASQ2* and *TRDN* P/LP variants cause autosomal recessive forms of CPVT. Genetic testing can confirm a diagnosis of CPVT, clarify risks to family members, and allow for family-specific testing. Guidelines from the Heart Rhythm Society recommend that at-risk relatives undergo genetic testing when a familial P/LP variant has been detected. Beta blockers are suggested for treatment in those with P/LP variants, even if they have had negative ECG findings (Ackerman et al. 2011).

Long QT syndrome

Long QT syndrome (LQTS) is characterized by prolongation of the QT interval on electrocardiogram (ECG). LQTS disorders are considered channelopathies, or diseases that affect cardiac ion channels. LQTS is diagnosed by considering the clinical features, family history, and ECG findings of the patient. LQTS may be diagnosed when the prolongation of the QTc interval is >470 msec (males) or >480 msec (females) (Alders and Christiaans 2015; Crotti 2008). Some individuals with LQTS are asymptomatic, but others may have symptoms including dizziness, ventricular tachycardia (specifically torsades de pointes), syncope, cardiac arrest or sudden cardiac death. Congenital LQTS will usually manifest before the age of 40 years, generally in childhood and adolescence with the age of onset associated with the genotype. Long-term management of LQTS may include lifestyle modification, beta-adrenergic blockers, and implantable cardioverter defibrillators.

LQTS is the most common inherited arrhythmia syndrome with a reported list of 17 associated genes; however, spurred by increased understanding of genomic variants the National Institutes of Health Clinical Genome Resource (ClinGen) completed a re-appraisal of purported published LQTS genes and found of the original 17, nine genes had limited/disputed evidence for disease causation. Definitive causal evidence was found for P/LP variants in only 3 genes: *KCNQ1*, *KCNH2*, and *SCN5A* (Adler et al. 2020). An additional 4 genes (*CAML1-3* and *TRDN*) are presumed causative for cases of LQTS with infantile/pediatric onset and atypical features (Adler et al. 2020). Not all patients meeting clinical criteria for LQTS have detectable P/LP variants in one of the known associated genes. The recommended testing approach includes either single gene sequencing or a targeted multi-gene sequencing panel, which may be more cost effective given the number of associated genes. Genetic testing for genes related to LQTS is recommended for any patients strongly suspected to have LQTS based on symptoms, family history and/or ECG findings if an acquired cause is unlikely. In addition, testing for a known familial P/LP variant is recommended for any at-risk family members, regardless of ECG findings, given the availability of prophylactic therapies (Akerman et al. 2011; Musunuru et al. 2020).

Genetic Testing in the Evaluation of Unexplained Sudden Cardiac Arrest

Sudden cardiac arrest (SCA) is the abrupt loss of cardiac function due to malfunction of the cardiac electrical activity. SCA is a distinct event from heart attack in which there is disrupted cardiac function due to loss of blood flow to cardiac tissue. The exact incidence of out-of-hospital cardiac arrest (OCHA) is unknown however, about 155,000 individuals have an EMS-treated all-rhythm OHCA per year in the United States (Rea et al., 2004). The causes of SCA are varied including structural and arrhythmic cardiac abnormalities, congenital and inherited heart diseases and recreational drug and alcohol use. Other non-cardiac causes of death should also be evaluated in the case of an unobserved OCHA including infection, thromboembolism, tumors, intracerebral lesions, and respiratory disease. The essential components of investigation into the cause of a resuscitated SCA include obtaining detailed personal and family history, witness accounts, physical examination, multiple electrocardiograms (ECGs), exercise testing and cardiac imaging. Additional evaluations may include provocative drug challenge testing and continuous heart rhythm monitoring. If inherited cardiac disease is thought to be a possible cause of SCA, genetic counseling and testing should also be considered. Consensus statements from both the Heart Rhythm Society (HRS) and the American Heart Association (AHA) agree on the importance of collaborative cariology and genetics services in this setting (Ackerman et al., 2011; Ahmad et al., 2019). Most SCAs experienced by individuals under age 35 are caused by potentially inherited heart diseases, including primary arrhythmogenic disorders (ex: LQTS, CPVT, HCM, ARVC and DCM) (Bagnall et al. 2016; Stecker et al. 2014).

If comprehensive evaluation into the cause of SCA identifies a specific underlying diagnosis for which genetic testing is available (ex: HCM), testing should be targeted toward that specific phenotype to maximize the chances of a clinically actionable result and minimize the risk of identifying variants of uncertain significance that may complicate result interpretation, medical management recommendations and familial screening and testing recommendations. If comprehensive evaluation does not elucidate a specific causative phenotype for the SCA, broad genetic evaluation may be recommended. In this setting, multi-condition panel testing is indicated and should include known genetic causes of sudden cardiac arrest (Stiles et al. 2021). Identification of the genetic cause of SCA may influence the medical management of both probands and affected family members. If a pathogenic variant is identified in the proband, cascade genetic testing and subsequent cardiac evaluations and interventions for family members can be facilitated. Genotype dependent medical management

recommendations for affected individuals include the use of beta blockers or sodium channel inhibitors in LQTS, decainide administration for patients with CPVT and exercise restrictions for patients with ARVC.

Post-Mortem Cardiac Genetic Testing

When plans cover genetic testing for the benefit of family members, post-mortem genetic testing should be considered to confirm a diagnosis and allow for early detection of other family members (cascade testing). Recent evidence suggests that genetic testing can help identify inherited cardiac disease in 25-45% of cases of sudden cardiac deaths and is significantly more likely to identify a pathogenic, causative variant in cases with identified structural heart disease at autopsy (Marey et al. 2020; Lahrouchi et al. 2020). Post-mortem cardiac genetic testing for SCD with a suspected genetic cause is a Class 1 recommendation from the 2020 APHRS/HRS expert consensus statement on the investigation of decedents with sudden unexplained death (Stiles et al. 2021).

Post-mortem investigation of sudden unexplained death or confirmed sudden cardiac death should begin with a comprehensive evaluation including but not limited to detailed autopsy, cardiac pathology/histology, toxicology evaluation and appropriate storage of blood and/or tissue for possible genetic analysis. Detailed family history and witness accounts can also help bring focus to the clinical and genetic investigation. Specific triggers occurring prior to the SCA may guide the investigation based on known associations with familial arrhythmia syndromes. Examples of triggers include competitive athletics participation, emotional or physical stress, swimming, drug use, acoustic triggers and seizures (Priori et al. 2013; Bagnall et al. 2016; Lahrouchi et al. 2017).

If post-mortem evaluations are able to identify a specific clinical diagnosis; genetic testing in the deceased is recommended to support the clinical diagnosis and to facilitate cascade genetic testing within the family. If a cardiac phenotype has been identified in the deceased proband, genetic testing should be targeted toward that specific phenotype to maximize the chances of a clinically actionable result and minimize the risk of identifying variants of uncertain significance that may complicate result interpretation and familial screening and testing recommendations. Targeted panels for hereditary cardiomyopathies and arrhythmias are preferable. However, given the limited clinical information and investigation, limited availability of proband DNA and potential financial implications, broader genetic testing may be considered. Wider panels and exome or genome scale sequencing share the high likelihood of identifying variants of uncertain/unknown significance. Given the complexities of test selection and result interpretation, post-mortem cardiac genetic testing is best conducted in centers of expertise.

Short QT Syndrome

Short QT syndrome (SQTS) is a rare, primary electrical disorder of the heart characterized by abnormally short QT intervals on the surface ECG (<360 ms) and an increased proclivity to develop atrial and/or ventricular tachyarrhythmias (Gussak 2005). HRS/EHRA guidelines regarding channelopathies and cardiomyopathies state that comprehensive or targeted SQTS genetic testing may be considered for any patient in whom a cardiologist has established a strong clinical index of suspicion for SQTS based on examination of the patient's clinical history, family history, and electrocardiographic phenotype (Class IIb-May be Useful) (HRS/EHRA 2011).

Variants in eight different genes have been reported with a potentially causative role in SQTS, however penetrance and genotype-phenotype correlations are not well described, making the utility of testing

uncertain for risk stratification (Ackerman et al. 2011; Wilde and Amin 2017). A recent exhaustive review of the 32 variants previously reported as P/LP for SQTS identified that only 21.8% had a definitively causal role in SQTS when reviewed against the 2015 ACMG/AMP guidelines for interpreting sequence variants (Hosseini et al., 2018). Additionally, the confirmed pathogenic variants were located only in the potassium-channel genes *KCNQ1*, *KCNH2*, or *KCNJ2*. Based on these data, routine testing for SQTS is not indicated.

Atrial Fibrillation

Atrial fibrillation is characterized by uncoordinated electrical activity in the atria. Symptoms include dizziness, chest pain, palpitations, shortness of breath, and an increased risk of stroke. Some individuals with atrial fibrillation do not experience any symptoms. While the majority of cases of AF are not hereditary, familial clustering does occur. Familial cases of AF are indistinguishable from acquired cases. Although a number of genes have been associated with an increased risk of AF, the role of these common genetic variants in risk stratification, assessment of disease progression, and determination of clinical outcomes is limited. Routine genetic testing related to AF is not indicated (January; ACC/AHA/HRS Practice Guidelines 2014).

Professional Society Guidelines

American College of Medical Genetics and Genomics (ACMG)

ACMG Technical Standard. Diagnostic Gene Sequencing Panels: From Design to Report.
Bean LJH, Funke B, Carlston CM, Gannon JL, Kantarci S, Krock BL, Zhang S, Bayrak-Toydemir P, on behalf of the ACMG Laboratory Quality Assurance Committee. Genet Med. 2019 Nov 16. PubMed PMID: 31732716.

ACMG Points to Consider Statement. DNA-Based Screening and Population Health.
Murray M, Giovanni M, Doyle D, et al. Genet Med. 2021 Jun;23(6):989-995. PubMed PMID: 33727704.

American Heart Association

AHA Scientific Statement. Genetic Testing for Inherited Cardiovascular Diseases.
Musunuru K, Hershberger RE, Day SM, et.al. AHA Council on Genomic and Precision Medicine; Council on Arteriosclerosis, Thrombosis and Vascular Biology; Council on Cardiovascular and Stroke Nursing; and Council on Clinical Cardiology. Circ Genom Precis Med. 2020 Aug;13(4):e000067. PubMed PMID: 32698598.

AHA Scientific Statement. Genetic Testing for Heritable Cardiovascular Diseases in Pediatric Patients.
Landstrom AP, Kim JJ, Gelb BD, et al. Circ Genom Precis Med. 2021 Oct;14(5):e000086. PubMed PMID: 34412507.

AHA Scientific Statement. Recommendations and Considerations Related to Preparticipation Screening for Cardiovascular Abnormalities in Competitive Athletes.
Maron BJ, Thompson PD, Ackerman MJ, et al. AHA Council on Nutrition, Physical Activity, and Metabolism: endorsed by the American College of Cardiology Foundation. Circulation. 2007 Mar 27;115(12):1643-455. PubMed PMID: 17353433.

Association for European Cardiovascular Pathology

Guidelines for Autopsy Investigation of Sudden Cardiac Death: 2017 update.
Basso C, Aguilera B, Banner J, et al. Virchows Arch. 2017 Dec;471(6):691-705. PubMed PMID: 28889247.

Clinical Genome Resource (ClinGen)

An International, Multicentered, Evidence-Based Reappraisal of Genes Reported to Cause Congenital Long QT Syndrome.
Adler A, Novelli V, Amin AS, et al. Circulation. 2020 Feb 11;141(6):418-428. PubMed PMID: 31983240.

Evaluating the Clinical Validity of Hypertrophic Cardiomyopathy Genes.
Ingles J, Goldstein J, Thaxton C, et al. Circ Genom Precis Med. 2019;12(2): e002460. PubMed PMID: 30681346.

Evidence-Based Assessment of Genes in Dilated Cardiomyopathy.
Jordan E, Peterson L, Ai T, et al. Circulation. 2021; 144:7-19. PubMed PMID: 33947203.

International Evidence Based Reappraisal of Genes Associated with Arrhythmogenic Right Ventricular Cardiomyopathy Using the Clinical Genome Resource Framework.
James CA, Jongbloed JDH, Hershberger RE, et al. Circ Genom Precis Med. 2021;14(3): e003273. PubMed ID: 33831308.

Reappraisal of Reported Genes for Sudden Arrhythmic Death: Evidence-based Evaluation of Gene Validity for Brugada Syndrome.
Hosseini SM, Kim R, Udupa S, et al; on behalf of NIH Clinical Genome Resource Consortium. Circulation. 2018;138:1195-1205. PubMed PMID: 29959160.

European Society of Cariology (ESC)

ESC Guidelines. Diagnosis and Management of Hypertrophic Cardiomyopathy.
Elliott PM, Anastasakis A, Borger MA, et al. The Task Force for the Diagnosis and Management of Hypertrophic Cardiomyopathy of the ESC. Eur Heart J. 2014 Oct 14;35(39):2733-79. PubMed PMID: 25173338.

Heart Rhythm Society (HRS)

HRS Expert Consensus Statement. Evaluation, Risk Stratification, and Management of Arrhythmogenic Cardiomyopathy.
Towbin JA, McKenna WJ, Abrams DJ, et al. Heart Rhythm. 2019 May 9.pii:S1547-5271. PubMed PMID: 31078652.

The International Task Force for Clinical Diagnosis of ARVC

Diagnosis of Arrhythmogenic Right Ventricular Cardiomyopathy/dysplasia: Proposed Modification of the Task Force Criteria.
Marcus FI, McKenna WJ, Sherrill D, et al. Circulation. 2010 Apr 6;121(13):1533-41. PubMed PMID: 20172911.

Joint Statements

2011 ACCF/AHA guideline for the diagnosis and treatment of hypertrophic cardiomyopathy: executive summary: a report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines.
Gersh BJ, Maron BJ, Bonow RO, et al. American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines; American Association for Thoracic Surgery; American Society of Echocardiography; American Society of Nuclear Cardiology; Heart Failure Society of America; Heart Rhythm Society; Society for Cardiovascular Angiography and Interventions; Society of Thoracic Surgeons. Circulation. 2011 Dec 13;124(24):2761-96. PubMed PMID: 22068435.

2019 AHA/ACC/HRS Focused Update of the 2014 AHA/ACC/HRS Guideline for the Management of Patients with Atrial Fibrillation: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society in Collaboration with the Society of Thoracic Surgeons.
January CT, Wann LS, Calkins H, et al. 2019 Jul 9;140(2):e125-e151. Erratum in: Circulation. 2019 Aug 6;140(6):e285. PubMed PMID: 30686041.

2020 APHRS/HRS Expert Consensus Statement on the Investigation of Descendents with Sudden Unexplained Death and Patients with Sudden Cardiac Arrest, and of Their Families.
Stiles MK, Wilde AAM, Abrams DJ, et al. Heart Rhythm. 2021 Jan;18(1):e1-e50. PubMed PMID: 33091602.

Cardiovascular Magnetic Resonance. American College of Cardiology Foundation (ACCF)/American College of Radiology (ACR)/AHA/ North American Society for Cardiac Imaging (NASCI)/Society for Cardiovascular Magnetic Resonance (SCMR) Expert Consensus Document.
Hundley WG, Bluemke DA, Finn JP, et al. J Am Coll Cardiol. 2010 Jun 8;55(23):2614-62. PubMed PMID: 20513610.

Genetic Evaluation of Cardiomyopathy. HFSA Practice Guideline in collaboration with ACMG.
Hershberger RE, Givertz MM, Ho CY, Judge DP, Kantor PF, McBride KL, Morales A, Taylor MRG, Vatta M, Ware SM. J Card Fail. 2018 May;24(5):281-302. PubMed PMID: 29567486.

Guideline for the Diagnosis and Treatment of Patients with Hypertrophic Cardiomyopathy: Executive Summary. ACC/AHA.
Ommen S, Mital S, Burke M, et al. Circulation. 2020 Dec. PubMed PMID: 33215938

Management of Patients with Ventricular Arrhythmias and the Prevention of Sudden Cardiac Death: Executive Summary. AHA/ACC/HRS Guideline.
Al-Khatib SM, Stevenson WG, Ackerman MJ, et al. Heart Rhythm. 2018 Oct;15(10):e190-e252. PubMed PMID: 29097320.

The Diagnosis and Management of Patients with Inherited Primary Arrhythmia Syndromes. EHRA/HRS/APHRS Expert Consensus Statement.
Priori SG, Wilde AA, Horie M. Endorsed by ACCF, AHA, PACES, and AEPC in June 2013. Heart Rhythm. 2013 Dec;10(12):1932-63. Epub 2013 Aug 30. PubMed PMID: 24011539.

The State of Genetic Testing for the Channelopathies and Cardiomyopathies. EHRA/HRS Expert Consensus Statement.
Ackerman MJ, Priori SG, Willems S, et al. Heart Rhythm. 2011 Aug;8(8):1308-39. PubMed PMID: 21787999.

Selected References

1 Adler A, Novelli V, Amin AS, Abiusi E, Care M, Nannenberg EA, et al. an international, multicentered, evidence-based reappraisal of genes reported to cause congenital long QT syndrome. Circulation. 2020 Feb 11;141(6):418-428. PubMed PMID: 31983240.

2 Ahmad F, McNally EM, Ackerman MJ, Baty LC, Day SM, Kullo IJ, Madueme PC, Maron MS, Martinez MW, Salberg L, Taylor MR, Wilcox JE. Establishment of Specialized Clinical Cardiovascular Genetics Programs: Recognizing the Need and Meeting Standards: A Scientific Statement From the American Heart Association. Circ Genom Precis Med. 2019 Jun;12(6):e000054. PubMed PMID: 31117808.

3 Alfares AA, Kelly MA, McDermott G, et al. Results of clinical genetic testing of 2,912 probands with hypertrophic cardiomyopathy: expanded panels offer limited additional sensitivity [published correction appears in Genet Med. 2015 Apr;17(4):319]. Genet Med. 2015;17(11):880-888. PubMed PMID: 25611685.

4 Alders M, Bikker H, Christiaans I. Long QT Syndrome. 2003 Feb 20 [Updated 2018 Feb 8]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1129/.

5 Antzelevitch C, Brugada P, Borggrefe M, et al. Brugada Syndrome: Report of the Second Consensus Conference. European Heart Rhythm Association (EHRA)/HRS Endorsement. Circulation. 2005 Feb 8;111(5):659-70. PubMed PMID: 15655131.

6 Arbustini E, Weidemann F, Hall JL. Left ventricular noncompaction: a distinct cardiomyopathy or a trait shared by different cardiac diseases? J Am Coll Cardiol. 2014 Oct 28;64(17):1840-50. PubMed PMID: 25443708.

7 Armstrong J, Toscano M, Kotchko N, et al.Utilization and Outcomes of BRCA Genetic Testing and Counseling in a National Commercially Insured Population: The ABOUT Study. JAMA Oncol. 2015 Dec;1(9):1251-60. PubMed PMID: 26426480.

8 Bagnall RD, Weintraub RG, Ingles J, Duflou J, Yeates L, Lam L, Davis AM, Thompson T, Connell V, Wallace J, Naylor C, Crawford J, Love DR, Hallam L, White J, Lawrence C, Lynch M, Morgan N, James P, du Sart D, Puranik R, Langlois N, Vohra J, Winship I, Atherton J, McGaughran J, Skinner JR, Semsarian C. A Prospective Study of Sudden Cardiac Death among Children and Young Adults. N Engl J Med. 2016 Jun 23;374(25):2441-52. PubMed PMID: 27332903.

9 Baltogiannis GG, Lysitsas DN, di Giovanni G, Ciconte G, Sieira J, Conte G, Kolettis TM, Chierchia GB, de Asmundis C, Brugada P. CPVT: Arrhythmogenesis, Therapeutic Management, and Future Perspectives. A Brief Review of the Literature. Front Cardiovasc Med. 2019 Jul 12; 6:92. PubMed PMID: 31380394.

10 Bean LJH, Funke B, Carlston CM, Gannon JL, Kantarci S, Krock BL, Zhang S, Bayrak-Toydemir P, on behalf of the ACMG Laboratory Quality Assurance Committee. Diagnostic gene sequencing panels: from design to report- a technical standard of the American College of Medical Genetics and Genomics (ACMG). Genet Med. 2019 Nov 16. PubMed PMID: 31732716.

11 Behr E, Wood DA, Wright M, et al. Cardiological assessment of first-degree relatives in sudden arrhythmic death syndrome. Lancet. 2003 Nov 1, 362(9394):1457-9. PubMed PMID: 14602442.

12 Bellcross CA, Kolor K, Goddard K, Coates RF, Reyes M, Khoury MJ. Awareness and utilization of BRCA1/2 testing among U.S. primary care physicians. Am J Prev Med. 2011;40:61–66. PubMed PMID: 21146769.

13 Bezzina CR, Lahrouchi N, Priori SG. Genetics of sudden cardiac death. Circ Res. 2015 Jun 5;116(12):1919-36. PubMed PMID: 26044248.

14 Bosman LP, Cadrin-Tourigny J, Bourfiss M, et al. Diagnosing arrhythmogenic right ventricular cardiomyopathy by 2010 Task Force Criteria: clinical performance and simplified practical implementation. Europace. 2020 May 1;22(5):787-796. PubMed PMID: 32294163.

15 Brown KN, Diaz RR. Restrictive (Infiltrative) Cardiomyopathy. [Updated 2019 Jan 17]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2019 Jan-. Available from: https://www-ncbi-nlm-nih-gov.proxy.lib.mcw.edu/books/NBK537234/.

16 Brugada R, Campuzano O, Sarquella-Brugada G, et al. Brugada Syndrome. 2005 Mar 31 [Updated 2016 Nov 17]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1517/.

17 Brugada R. Sudden death: managing the family, the role of genetics. Heart. 2011 Apr;97(8):676-81. PubMed PMID: 21421602.

18 Butters A, Bagnall RD, Ingles J. Revisiting the Diagnostic Yield of Hypertrophic Cardiomyopathy Genetic Testing. Circ Genom Precis Med. 2020;13(2). PubMed PMID: 32315220.

19 Charron P, Elliott PM, Gimeno JR, et al. The Cardiomyopathy Registry of the EURObservational Research Programme of the ESC. Baseline Data and Contemporary Management of Adult Patients with Cardiomyopathies. Eur Heart J. 2018 May 21;39(20):1784-1793. PubMed PMID: 29378019.

20 Cirino AL, Ho C. Hypertrophic Cardiomyopathy Overview. 2008 Aug 5 [Updated 2021 July 8]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1768/.

21 Clarke JL, Ladapo JL, Monane M, et al. The diagnosis of CAD in women: addressing the unmet need - a report from the national expert roundtable meeting. Popul Health Manag. 2015 Apr;18(2):86-92 Epub 2015 Feb 25. PubMed PMID: 25714757.

22 Corrado D, van Tintelen PJ, McKenna et al; International Experts. Arrhythmogenic right ventricular cardiomyopathy: evaluation of the current diagnostic criteria and differential diagnosis. Eur Heart J. 2020 Apr 7;41(14):1414-1429. PMID: 31637441.

23 Cragun D, Camperlango L, Robinson E, Caldwell M, Kim J, Phelan C, Monteiro AN, Vadaparampil ST, Sellers TA, Pal T. Differences in BRCA counseling and testing practices based on ordering provider type. Genet Med. 2015 Jan;17(1):51-7. PubMed PMID 24922460.

24 Crotti L, Celano G, Dagradi F, et al. Congenital long QT syndrome. Orphanet J Rare Dis. 2008 Jul 7; 3:18. PubMed PMID: 18606002.

25 Elliott PM, Anastasakis A, Asimaki A, Basso C, Bauce B, Brooke MA, Calkins H, Corrado D, Duru F, Green KJ, Judge DP, Kelsell D, Lambiase PD, McKenna WJ, Pilichou K, Protonotarios A, Saffitz JE, Syrris P, Tandri H, Te Riele A, Thiene G, Tsatsopoulou A, van Tintelen JP. Definition and treatment of arrhythmogenic cardiomyopathy: an updated expert panel report. Eur J Heart Fail. 2019 Aug;21(8):955-964. PubMed PMID: 31210398.

26 Fernández-Falgueras A, Sarquella-Brugada G, Brugada J, Brugada R, Campuzano O. Cardiac Channelopathies and Sudden Death: Recent Clinical and Genetic Advances. Franciolini F, Catacuzzeno L, eds. Biology. 2017;6(1):7. PubMed PMID: 28146053.

27 Fourey D, Care M, Siminovitch KA, et al. Prevalence and Clinical Implication of Double Mutations in Hypertrophic Cardiomyopathy: Revisiting the Gene-Dose Effect. Circ Cardiovasc Genet. 2017 Apr;10(2). PubMed PMID: 28420666.

28 Geske JB, Ommen SR, Gersh BJ. Hypertrophic Cardiomyopathy: Clinical Update. JACC Heart Fail. 2018 May;6(5):364-375. PubMed PMID: 29655825.

29 Goldenberg I, Horr S, Moss AJ, et al. Risk for life-threatening cardiac events in patients with genotype-confirmed long-QT syndrome and normal-range corrected QT intervals. J Am Coll Cardiol. 2011Jan 4;57(1):51–9. PubMed PMID: 21185501.
30 Gussak I, Bjerregaard P. Short QT syndrome: 5 years of progress. J Electrocardiol. 2005 Oct;38(4):375-7. PubMed PMID: 16216616.
31 Gussak I, Brugada P, Brugada J, et al. Idiopathic short QT interval: a new clinical syndrome? Cardiology. 2000;94(2):99-102. PubMed PMID: 11173780.
32 Haas J, Frese KS, Peil B, et al. Atlas of the clinical genetics of human dilated cardiomyopathy. Eur Heart J. 2015 May 7;36(18):1123-35a. Epub 2014 Aug 27. PubMed PMID: 25163546.
33 Halliday BP, Cleland JGF, Goldberger JJ, Prasad SK. Personalizing Risk Stratification for Sudden Death in Dilated Cardiomyopathy: The Past, Present and Future. Circulation 2017 Jul 11; 136(2): 215-231. PubMed PMID: 28696268.
34 Harvey EK, Fogel CE, Peyrot M, et al. Providers' knowledge of genetics: A survey of 5915 individuals and families with genetic conditions. Genet Med 2007. 9(5):259-267. PubMed PMID: 17505202.
35 Hershberger RE, Jordan E. Dilated Cardiomyopathy Overview. 2007 Jul 27 [Updated 2021 July 29]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1309/.
36 Hershberger RE, Morales A. LMNA-Related Dilated Cardiomyopathy. 2008 Jun 12 [Updated 2016 Jul 7]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1674/.
37 Hickey KT, Elzomor A. Cardiac Channelopathies: Recognition, Treatment, Management. AACN Adv Crit Care. 2018 Spring;29(1):43-57. PubMed PMID: 29496713.
38 Ingles J, et al. Evaluating the Clinical Validity of Hypertrophic Cardiomyopathy Genes. Circ Genom Precis Med. 2019 Jan 25;12(2):e002460. PubMed PMID: 30681346.
39 James CA, Bhonsale A, Tichnell C, Murray B, Russell SD, Tandri H, et al. Exercise increases age-related penetrance and arrhythmic risk in arrhythmogenic right ventricular dysplasia/cardiomyopathy-associated desmosomal mutation carriers. J Am Coll Cardiol 2013; 62:1290–1297. PubMed PMID: 23871885.
40 Kapplinger JD, Landstrom AP, Salisbury BA, Callis TE, Pollevick GD, Tester DJ, Cox MG, Bhuiyan Z, Bikker H, Wiesfeld AC, Hauer RN, van Tintelen JP, Jongbloed JD, Calkins H, Judge DP, Wilde AA, Ackerman MJ. Distinguishing arrhythmogenic right ventricular cardiomyopathy/dysplasia associated mutations from background genetic noise. J Am Coll Cardiol. 2011; 57:2317–2327. PubMed PMID: 2163032.
41 Kayvanpour E., Sedaghat-Hamedani F, Amr A, Lai, A, Haas J, Holzer DB, Frese KS, Keller A, Jensen K, Katus HA, Meder B. Genotype-phenotype associations in dilated cardiomyopathy: meta-analysis on more than 8000 individuals. Clin Res Cardiol. 2017 Feb; 106(2):127-139. PubMed PMID: 27576561.
42 Kostareva A, Kiselev A, Gudkova A, Frishman G, Ruepp A, Frishman D, et al. (2016) Genetic Spectrum of Idiopathic Restrictive Cardiomyopathy Uncovered by Next-Generation Sequencing. PLoS ONE. 2016 Sep 23;11(9)e0163362. PubMed PMID: 27662471.
43 Lahrouchi N, Raju H, Lodder EM, et al. Utility of Post-Mortem Genetic Testing in Cases of Sudden Arrhythmic Death Syndrome. J Am Coll Cardiol. 2017;69(17):2134-2145. PubMed PMID: 28449774.
44 Lahrouchi N, Raju H, Lodder EM, et al. The yield of postmortem genetic testing in sudden death cases with structural findings at autopsy. Eur J Hum Genet. 2020 Jan;28(1):17-22. PubMed PMID: 31534214.
45 Le Scouarnec S, Karakachoff M, Gourraud JB, et al. Testing the burden of rare variation in arrhythmia-susceptibility genes provides new insights into molecular diagnosis for Brugada syndrome. Hum Mol Genet. 2015 May 15;24(10):2757-63. Epub 2015 Feb 3. PubMed PMID: 25650408.
46 Lehnart SE, Ackerman MJ, Benson DW Jr, et al. Inherited Arrhythmias: Diagnosis, Phenotyping, Molecular Mechanisms, and Therapeutic Approaches for Primary Cardiomyopathies of Gene Mutations Affecting Ion Channel Function. NHLBI/ORD Consensus Report. National Heart, Lung, and Blood Institute and Office of Rare Diseases Workshop. Circulation. 2007 Nov 13;116(20):2325-45. PubMed PMID: 17998470.
47 Li S, Zhang C, Liu N, Bai H, Hou C, Wang J, Song L, Pu J. Genotype-Positive Status Is Associated with Poor Prognoses in Patients with Left Ventricular Noncompaction Cardiomyopathy. J Am Heart Assoc. 2018 Oct 16;7(20): e009910. PubMed PMID: 30371277.
48 Marcus FI, McKenna WJ, Sherrill D, et al. Diagnosis of Arrhythmogenic Right Ventricular Cardiomyopathy/dysplasia: Proposed Modification of the Task Force Criteria. Circulation. 2010 Apr 6;121(13):1533-41.PubMed PMID: 20172911.
49 Marey I, Fressart V, Rambaud C, Fornes P, Martin L, Grotto S, Alembik Y, Gorka H, Millat G, Gandjbakhch E, Bordet C, de la Grandmaison GL, Richard P, Charron P. Clinical impact of post-mortem genetic testing in cardiac death and cardiomyopathy. Open Med (Wars). 2020 May 19;15(1):435-446. PubMed PMID: 33336002.
50 Mattesi G, Zorzi A, Corrado D, Cipriani A. Natural History of Arrhythmogenic Cardiomyopathy. J Clin Med. 2020 Mar 23;9(3):878. PubMed. PMID: 32210158.
51 Mazzanti A, Kanthan A, Monteforte N, et al. Novel insight into the natural history of short QT syndrome. J Am Coll Cardiol. 2014 Apr 8;63(13):1300-8. Epub 2013 Nov 28. PubMed PMID: 24291113.
52 Mazzarotto F, Tayal U, Buchan RJ, et al. Reevaluating the Genetic Contribution of Monogenic Dilated Cardiomyopathy. Circulation. 2020 Feb 4;141(5):387-398. PubMed PMID: 31983221.
53 McNally E, MacLeod H, Dellefave-Castillo L. Arrhythmogenic Right Ventricular Cardiomyopathy. 2005 Apr 18 [Updated 2017 May 25]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1131/.

54 Mega JL, Stitziel NO, Smith JG et al. Genetic risk, coronary heart disease events, and the clinical benefit of statin therapy: an analysis of primary and secondary prevention trials. Lancet. 2015 Jun 6;385(9984):2264-71. Epub 2015 Mar 4. PubMed PMID: 25748612.
55 Meune C, Van Berlo JH, Anselme F, et al. Primary prevention of sudden death in patients with lamin A/C gene mutations. N Engl J Med. 2006 Jan 12;354(2):209-10. PubMed PMID: 16407522.
56 Middleton O, Baxter S, Demo E, et al. National Association of Medical Examiners position paper: retaining postmortem samples for genetic testing. Acad Forensic Pathol 2013;3(2):191-194.
57 Miller EM, Hinton RB, Czosek R, Lorts A, Parrott A, Shikany AR, Ittenbach RF, Ware SM. Genetic Testing in Pediatric Left Ventricular Noncompaction. Circ Cardiovasc Genet. 2017 Dec;10(6)e001735. PubMed PMID: 29212898.
58 Muchtar E, Blauwet LA, Gertz MA. Restrictive Cardiomyopathy: Genetics, Pathogenesis, Clinical Manifestations, Diagnosis, and Therapy. Circ Res. 2017 Sep 15;121(7):819-837. PubMed PMID: 28912185.
59 Napolitano C, Priori SG, Bloise R. Catecholaminergic Polymorphic Ventricular Tachycardia. 2004 Oct 14 [Updated 2016 Oct 13]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1289/.
60 Napolitano C, Splawski I, Timothy KW, et al. Timothy Syndrome. 2006 Feb 15 [Updated 2015 Jul 16]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1403/.
61 National Society of Genetic Counselors [Internet]. Chicago, IL: National Society of Genetic Counselors; c2017. Post mortem genetic testing. [updated 2017 Aug; cited 13 Sep. 2017]. Available at: http://www.nsgc.org/postmortem.
62 Olson TM, Michels VV, Ballew JD, et al. Sodium channel mutations and susceptibility to heart failure and atrial fibrillation. JAMA. 2005 Jan 26;293(4):447-54. PubMed PMID: 15671429.
63 Plon SE, Cooper HP, Parks B, Dhar SU, Kelly PA, Weinberg AD, Staggs S, Wang T, Hilsenbeck S. Genetic testing and cancer risk management recommendations by physicians for at-risk relatives. Genet Med. 2011;13:148–154. PubMed PMID: 21224735.
64 Ray T. "Cleveland Clinic Explores Issues Associated with Integrating Genomics into Healthcare." GenomeWeb. Mar 11, 2011. Accessed Nov 19, 2018.
65 Rea TD, Eisenberg MS, Sinibaldi G, White RD. Incidence of EMS-treated out-of-hospital cardiac arrest in the United States. Resuscitation. 2004 Oct;63(1):17-24. PubMed PMID: 15451582.
66 Rosenbaum AN, Agre KE, Pereira NL. Genetics of dilated cardiomyopathy: practical implications for heart failure management. Nat Rev Cardiol. 2020;17(5):286-297. PubMed PMID: 31605094.
67 Ross SB, Singer ES, Driscoll E, et al. Genetic architecture of left ventricular noncompaction in adults. Hum Genome Var. 2020 Oct 15;7:33. PMID: 33082984.
68 Schwartz PJ. The congenital long QT syndromes from genotype to phenotype: clinical implications. J Intern Med. 2006 Jan;259(1):39-47. PubMed PMID: 16336512.
69 Schwartz PJ, Crotti L. QTc behavior during exercise and genetic testing for the long-QT syndrome. Circulation. 2011 Nov 15;124(20):2181-4. PubMed PMID: 22083145.
70 Sen-Chowdhry S, Jacoby D, Moon JC, McKenna WJ. Update on hypertrophic cardiomyopathy and a guide to the guidelines. Nat Rev Cardiol. 2016 Nov; 13(11):651-675. PubMed PMID: 27671577.
71 Stecker EC, Reinier K, Marijon E, Narayanan K, Teodorescu C, Uy-Evanado A, Gunson K, Jui J, Chugh SS. Public health burden of sudden cardiac death in the United States. Circ Arrhythm Electrophysiol. 2014 Apr;7(2):212-7. PubMed PMID: 24610738.
72 Stollberger C and Finsterer J. Extracardiac medical and neuromuscular implications in restrictive cardiomyopathy. Clin. Cardiol. 2007 Aug;30(8):375-80. PubMed PMID: 17680617.
73 Stroeks SLVM, Hellebrekers DMEI, Claes GRF, Tayal U, Krapels IPC, Vanhoutte EK, van den Wijngaard A, Henkens MTHM, Ware JS, Heymans SRB, Brunner HG, Verdonschot JAJ. Clinical impact of re-evaluating genes and variants implicated in dilated cardiomyopathy. Genet Med. 2021 Nov;23(11):2186-2193. PubMed PMID: 34194005.
74 Tan HL, Hofman N, van Langen IM, et al. Sudden unexplained death: heritability and diagnostic yield of cardiological and genetic examination in surviving relatives. Circulation. 2005 Jul 12;112(2):207-13. Epub 2005 Jul 5. PubMed PMID: 15998675.
75 Teo LY, Moran RT, Tang WH. Evolving Approaches to Genetic Evaluation of Specific Cardiomyopathies. Curr Heart Fail Rep. 2015 Dec; 12(6):339-49. PubMed PMID: 26472190.
76 Thaxton C, Good ME, DiStefano MT, Luo X, Andersen EF, Thorland E, Berg J, Martin CL, Rehm HL, Riggs ER; ClinGen Gene Curation Working Group; ClinGen Dosage Sensitivity Working Group. Utilizing ClinGen gene-disease validity and dosage sensitivity curations to inform variant classification. Hum Mutat. 2021 Oct 25. PubMed PMID: 34694049.
77 Towbin JA, McKenna WJ, Abrams DJ, et al. 2019 HRS expert consensus statement on evaluation, risk stratification, and management of arrhythmogenic cardiomyopathy. Heart Rhythm. 2019 May 9. PubMed PMID: 31078652.
78 van Langen IM, Birnie E, Alders M, et al. The use of genotype-phenotype correlations in mutation analysis for the long QT syndrome. J Med Genet. 2003; 40:141–5. PubMed PMID: 12566525.
79 van Berlo JH, de Voogt WG, van der Kooi AJ, et al. Meta-analysis of clinical characteristics of 299 carriers of LMNA gene mutations: do lamin A/C mutations portend a high risk of sudden death? J Mol Med (Berl). 2005 Jan;83(1):79-83. Epub 2004 Nov 13. PubMed PMID: 15551023.
80 van Waning JI, Caliskan K, Hoedemaekers YM, van Spaendonck-Zwarts KY, Baas AF, Boekholdt SM, van Melle JP, Teske AJ, Asselbergs FW, Backx APCM, du Marchie Sarvaas GJ, Dalinghaus M, Breur JMPJ, Linschoten MPM, Verlooij LA, Kardys I, Dooijes D, Lekanne Deprez RH, IJpma AS, van den

Berg MP, Hofstra RMW, van Slegtenhorst MA, Jongbloed JDH, Majoor-Krakauer D. Genetics, Clinical Features, and Long-Term Outcome of Noncompaction Cardiomyopathy. J Am Coll Cardiol. 2018 Feb 20;71(7):711-722. PubMed PMID: 29447731.
81 Waldmüller S, Schroeder C, Sturm M, et al. Targeted 46-gene and clinical exome sequencing for mutations causing cardiomyopathies. Mol Cell Probes. 2015 Oct;29(5):308-14. Epub 2015 May 12. PubMed PMID: 25979592.
82 Ware SM, Bhatnagar S, Dexheimer PJ, Wilkinson JD, Sridhar A, Fan X, Shen Y, Tariq M, Schubert JA, Colan SD, Shi L, Canter CE, Hsu DT, Bansal N, Webber SA, Everitt MD, Kantor PF, Rossano JW, Pahl E, Rusconi P, Lee TM, Towbin JA, Lal AK, Chung WK, Miller EM, Aronow B, Martin LJ, Lipshultz SE; Pediatric Cardiomyopathy Registry Study Group. The genetic architecture of pediatric cardiomyopathy. Am J Hum Genet. 2022 Feb 3;109(2):282-298. PubMed PMID: 35026164.
83 Wilde AAM, Amin A. Channelopathies, genetic testing and risk stratification. Int J Cardiol. 2017 Jun 15;237:53-55. PubMed PMID: 28343764.

Revision History

Medical Advisory Board Review:

v2.2022 03/17/2022: Approved

v1.2022 09/20/2021: Approved

v2.2021 03/12/2021: Approved

v1.2021 11/13/2020: Approved

v2.2020 05/08/2020: Reviewed

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v1.2019 11/07/2018: Reviewed

v1.2018 03/31/2018: Reviewed

Clinical Steering Committee Review:

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Revisions:

Version	Date	Editor	Description
v2.2022 *GEN05-0922.2*	02/02/2022	Samantha Freeze, MS, CGC	Semi-annual review. Significant revisions were made to criteria (Appropriate Use Criteria, Genetic Testing of Affected Individuals, Genetic Testing in the Evaluation of Unexplained Cardiac Arrest, Post Mortem Genetic Testing). CPT codes, professional society guidelines, background and references were updated.
v1.2022 *GEN05-0322.1*	8/16/2021	Samantha Freeze, MS, CGC	Semi-annual review. No criteria changes. Professional society guidelines were updated.
v2.2021 *GEN05-0921.1*	02/15/2021	Samantha Freeze, MS, CGC	Semi-annual review. No criteria changes. CPT codes, professional society guidelines, background and references were updated.
v1.2021	9/11/2020	Samantha Freeze, MS, CGC	Semi-annual review. Genetic counseling requirements were updated. CPT codes, background, professional society guidelines, and references were updated.
v2.2020	03/13/2020	Samantha Freeze, MS, CGC	Semi-annual review. Criteria was clarified for Non-Covered Tests to include genetic testing for isolated LVNC. Background and references updated.
v1.2020	09/11/2019	Samantha Freeze, MS, CGC	Semi-annual update. No criteria changes. Background and references updated.
v2.2019	4/03/2019	Samantha Freeze, MS, CGC	Semi-annual review. No criteria changes. Updated references.

v1.2019	10/03/2018	Samantha Freeze, MS, GCG	Semi-annual review. PMID added. Updated professional society guidelines. Reformatted CPT code list. Administrative change to genetic counseling requirement - moved from client policy to guidelines. Renumbered to 2019.
v1.2018	03/31/2018	Heather Dorsey, MS, CGC	Semi-annual review. Disclaimer sentence added to Scope. Reformatted placement of Long QT familial variant coverage, no change to criteria. Clarified Dilated Cardiomyopathy criteria. Updated professional society guidelines. No additional criteria changes. Renumbered to 2018.
v3.2017	10/27/2017	Kate Charyk, MS, CGC	Quarterly review. No criteria changes.
v3.2017	09/15/2017	Megan Czarniecki, MS, CGC	Revised general criteria language. Formatted references to NLM style. Moved methodological considerations to appropriate use criteria and background. Updated associated CPT codes. Renumbered to v3.2017 and submitted to CSC for approval.
v2.2017	06/19/2017	Kate Charyk, MS, CGC	Quarterly review. No criteria changes. Updated references.
v2.2017	04/21/2017	Kate Charyk, MS, CGC	Quarterly review. No criteria changes. Updated references.
v2.2017	03/29/2017	Kate Charyk, MS, CGC	Added criteria for post-mortem genetic testing. Updated references.
v1.2017	01/23/2017	Kate Charyk, MS, CGC	Quarterly review. No criteria changes. Updated references. Renumbered to 2017 version.
v1.2016	09/27/2016	Gwen Fraley, MS, CGC	Added general criteria. Updated references.

v1.2015	06/18/2015	Tricia See, MS, CGC	Original version

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