

Dean Health Plan Coverage Policy

Policy Name: Genetic Testing - Specialty Testing: Cardiovascular

Effective Date: July 01, 2025

Important Information – Please Read Before Using This Policy

These services may or may not be covered by Dean Health Plan. Coverage is subject to requirements in applicable federal or state laws. Please refer to the member's plan document for other specific coverage information. If there is a difference between this general information and the member's plan document, the member's plan document will be used to determine coverage. With respect to Medicare, Medicaid, and other government programs, this policy will apply unless these programs require different coverage.

Members may contact Dean Health Plan Customer Service at the phone number listed on their member identification card to discuss their benefits more specifically. Providers with questions about this medical policy see Provider Communications for additional information.

<https://deancare.com/Providers/Provider-communications>

Dean Health Plan medical policies are not medical advice. Members should consult with appropriate health care providers to obtain needed medical advice, care and treatment.

OVERVIEW

This policy addresses the use of tests for the diagnosis and management of inherited and sporadic cardiovascular conditions, including structural or electrical defects, disorders of the blood vessels, cholesterol disorders, and lipid profiling. Genetic evaluation for other types of EDS are addressed within this policy.

Due to the complexity of genetic testing for hereditary cardiomyopathies and arrhythmias and the potential for misinterpretation of results, the decision to test and the interpretation of test results should be performed by, or in consultation with, an expert in the area of cardiac genetics. Pre-test and post-test genetic counseling that facilitates informed decision-making, addresses the possibility of secondary or incidental findings, and a plan for returning results before testing occurs is strongly advised.

For additional information see the [Rationale](#) sections.

The tests, CPT codes, and ICD codes referenced in this policy are not comprehensive, and their inclusion does not represent a guarantee of coverage or non-coverage.

Dean Health Plan Coverage Policy

POLICY REFERENCE TABLE

<u>COVERAGE CRITERIA SECTIONS</u>	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	<u>REF</u>
<u>Comprehensive Cardiomyopathy and/or Arrhythmia Multigene Panels</u>			
<u>Comprehensive Cardiomyopathy Panels</u>	Cardiomyopathy Panel (GeneDx)	81439, I42.0, I42.1, I42.2, I42.5, I42.8, I42.9, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	1, 5
	Cardiomyopathy Comprehensive Panels (Invitae)		
	CMNext (Ambry Genetics)		
<u>Comprehensive Arrhythmia Panels</u>	Arrhythmia Panel (GeneDx)	81413, 81414, 0237U, I45.81, I49.8, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	11
	RhythmNext (Ambry Genetics)		
	Arrhythmia Comprehensive Panel (Invitae)		
	Genomic Unity Cardiac Ion Channelopathies Analysis - 0237U (Variantyx Inc)		
<u>Comprehensive Arrhythmia and Cardiomyopathy (Sudden Cardiac or Unexplained Death) Panels</u>	Arrhythmia and Cardiomyopathy Comprehensive Panel (Invitae)	81413, 81414, 81439, I42.0, I42.1, I42.2, I42.5, I45.81, I49.8, I42.9, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	5
	CardioNext (Ambry Genetics)		
	Cardiomyopathy and Arrhythmia Panel, Sequencing and		

Dean Health Plan Coverage Policy

COVERAGE CRITERIA SECTIONS	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
	Deletion/Duplication (ARUP Laboratories)		
Hypertrophic Cardiomyopathy (HCM)			
Hypertrophic Cardiomyopathy Panels	Hypertrophic Cardiomyopathy Panel (Invitae)	81439, S3865, I42.1, I42.2, I42.9, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	2, 7
	HCMNext (Ambry Genetics)		
	Hypertrophic Cardiomyopathy (HCM) Panel (GeneDx)		
Dilated Cardiomyopathy (DCM)			
Dilated Cardiomyopathy Panels	Dilated Cardiomyopathy Panel (PreventionGenetics, part of Exact Sciences)	81439, I42.0, I42.9, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	1, 10, 11
	DCMNext (Ambry Genetics)		
Arrhythmogenic Cardiomyopathy			
Arrhythmogenic Cardiomyopathy Panels	Arrhythmogenic Right Ventricular Cardiomyopathy Panel (GeneDx)	81439, I42.8, I42.9, Z82.41, Z82.49, Z84.81, Z84.89	15
	Arrhythmogenic Cardiomyopathy Panel (Invitae)		
Restrictive Cardiomyopathy (RCM)			

Dean Health Plan Coverage Policy

<u>COVERAGE CRITERIA SECTIONS</u>	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	<u>REF</u>
Restrictive Cardiomyopathy Panels	Restrictive Cardiomyopathy (RCM) Panel (Cincinnati Children's Hospital Medical Center - Molecular Genetics and Cytogenetics Laboratories)	81439, I42.5, I42.8, I42.9, Z82.41, Z82.49	4
<u>Long QT Syndrome (LQTS)</u>			
Long QT Syndrome Panels	Long QT Syndrome Panel (Invitae)	81403, 81406, 81407, 81413, 81414, 81479, I45.81, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	3, 9, 11
	LQTS Panel (GeneDx)		
<u>Short QT Syndrome (SQTS)</u>			
Short QT Syndrome Panels	Short QT Syndrome Panel (Invitae)	81403, 81406, 81413, 81414, 81479, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	11, 12
	Short QT Syndrome Panel (PreventionGenetics, part of Exact Sciences)		
<u>Brugada Syndrome (BrS)</u>			
Brugada Syndrome Panels or SCN5A Variant Analysis	Brugada Panel (GeneDx)	81404, 81406, 81407, 81413, 81414, 81479, S3861, I49.8, Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	11, 13
	Brugada Syndrome Panel (Invitae)		
	Brugada Panel (GeneDx)		
<u>Catecholaminergic Polymorphic Ventricular Tachycardia (CPVT)</u>			
Catecholaminergic Polymorphic Ventricular Tachycardia Panels	Catecholaminergic Polymorphic Tachycardia Panel (Invitae)	81403, 81405, 81408, 81413, 81414, 81479,	14

Dean Health Plan Coverage Policy

COVERAGE CRITERIA SECTIONS	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
	CPVTNext (Ambry Genetics)	Z13.71, Z82.41, Z82.49, Z84.81, Z84.89	
Familial Hypercholesterolemia (FH)			
Familial Hypercholesterolemia (FH) Panels	Familial Hypercholesterolemia (FH) Panel (GeneDx)	81401, 81405, 81406, 81407, 81479, E78, E78.01	8, 16
	Invitae Familial Hypercholesterolemia Panel (Invitae)		
Congenital Heart Malformations			
Congenital Heart Malformation Panels	Nonsyndromic Congenital Heart Disease Panel (PreventionGenetics, part of Exact Sciences)	81405, 81406, 81407, 81408, 81479, Q20, Q21, Q22, Q23, Q24	6
	Congenital Heart Disease Panel (Invitae)		
Familial Thoracic Aortic Aneurysm and Dissection (TAAD)			
Familial Thoracic Aortic Aneurysm and Dissection (TAAD) Multigene Panel	Thoracic Aortic Aneurysm Panel (Cincinnati Children's Hospital Medical Center-Molecular Genetics and Cytogenetics Laboratories)	81405, 81406, 81408, 81410, 81411, 81479, I71.00-I71.9, Q87.5	17, 18, 19
	TAAD Panel Next Generation Sequencing (DDC Clinic Laboratory)		

Dean Health Plan Coverage Policy

COVERAGE CRITERIA SECTIONS	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
	TAADNext (Ambry Genetics)		
	Marfan syndrome, Loeys-Dietz syndrome, Familial thoracic aortic aneurysms & dissections, and Related disorders NGS Panel - Comprehensive (CTGT)		
	Marfan Syndrome and Thoracic Aortic Aneurysm and Dissection NGS Panel (Sequencing & Deletion/Duplication) (Fulgent Genetics)		
	Marfan/TAAD Panel (GeneDx)		
	Aortopathy Comprehensive Panel (Invitae)		
Hereditary Hemorrhagic Telangiectasia (HHT)			
Hereditary Hemorrhagic Telangiectasia Multigene Panel	HHTNext (Ambry Genetics)	81405, 81406, 81479, R04.0, Q27.30- Q27.39	20, 21
	Hereditary Hemorrhagic Telangiectasia (HHT) Panel (Blueprint Genetics)		

RELATED POLICIES

This policy document provides coverage criteria for testing related to cardiac disorders. Please refer to:

Dean Health Plan Coverage Policy

- **Specialty Testing: Multisystem Genetic Conditions** for coverage criteria related to diagnostic tests for genetic disorders that affect multiple organ systems (e.g. whole exome and genome sequencing, chromosomal microarray, and multigene panels for broad phenotypes).
- **Reproductive Testing: Prenatal Diagnosis** for coverage criteria related to fetal diagnostic testing for genetic disorders during pregnancy and following a pregnancy loss.
- **Reproductive Testing: Fertility** for coverage criteria related to preimplantation diagnosis.
- **General Approach to Laboratory Testing** for coverage criteria related to cardiovascular conditions, including known familial variant testing, that is not specifically discussed in this or another non-general policy.

[back to top](#)

COVERAGE CRITERIA

COMPREHENSIVE CARDIOMYOPATHY AND/OR ARRHYTHMIA MULTIGENE PANELS

Comprehensive Cardiomyopathy Panels

- I. Comprehensive cardiomyopathy panels are considered **medically necessary** when:
 - A. The member has a diagnosis of cardiomyopathy, **OR**
 - B. The member has a [first-degree relative](#) with [sudden cardiac death \(SCD\)](#) or [sudden unexplained death \(SUD\)](#), **AND**
 1. This relative's autopsy revealed unspecified cardiomyopathy (e.g., cardiomegaly or cardiomyopathy), **OR**
 2. This relative's autopsy revealed an anatomically normal heart, **AND**
 - a) The autopsy did not reveal a cause of death.
- II. Comprehensive cardiomyopathy panels are considered **investigational** for all other indications.

NOTE: Multigene panels that are targeted to the cardiomyopathy phenotype observed are recommended by professional guidelines

[view rationale](#)

[back to top](#)

Comprehensive Arrhythmia Panels

- I. Comprehensive arrhythmia panels are considered **medically necessary** when:
 - A. The member meets one of the following:

Dean Health Plan Coverage Policy

1. The member has a [first-degree relative](#) with [sudden cardiac death \(SCD\)](#) or [sudden unexplained death \(SUD\)](#) before age 50 years, **OR**
 2. The member has a [first-degree relative](#) with [sudden cardiac death \(SCD\)](#) at age 50 years or older, **AND**
 - a) The deceased individual had family history of premature [SCD](#), **OR**
 - b) The deceased individual's death is suspicious for genetic heart disease, **OR**
- B. The member has unexplained [sudden cardiac arrest](#), **AND**
1. Clinical tests were non-diagnostic for reversible, ischemic, or structural causes (e.g., ECG, cardiac stress tests, echocardiogram, intravenous pharmacologic provocation testing).
- II. Comprehensive arrhythmia panels are considered **investigational** for all other indications.

[view rationale](#)

[back to top](#)

Comprehensive Arrhythmia and Cardiomyopathy (Sudden Cardiac or Unexplained Death) Panels

- I. Comprehensive panels including genes for both cardiomyopathies and arrhythmias are considered **medically necessary** when:
 - A. The member meets clinical criteria for [Comprehensive Cardiomyopathy Panels](#), **AND**
 - B. The member meets clinical criteria for [Comprehensive Arrhythmia Panels](#).
- II. Comprehensive panels including genes for both cardiomyopathies and arrhythmias are considered **investigational** for all other indications.

[view rationale](#)

[back to top](#)

HYPERTROPHIC CARDIOMYOPATHY (HCM)

Hypertrophic Cardiomyopathy Panels

- I. Genetic testing for hypertrophic cardiomyopathy via a multigene panel is considered **medically necessary** when:
 - A. The member has unexplained left ventricular hypertrophy (LVH), as defined by myocardial wall thickness of 15mm or greater (in adults), or a z-score of 2 or greater (in children) based on echocardiogram or cardiac MRI.

Dean Health Plan Coverage Policy

- II. Genetic testing for hypertrophic cardiomyopathy via a multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

[view rationale](#)

[back to top](#)

DILATED CARDIOMYOPATHY (DCM)

Dilated Cardiomyopathy Panels

- I. Genetic testing for dilated cardiomyopathy (DCM) via a multigene panel is considered **medically necessary** when:
 - A. The member has findings characteristic of DCM including all of the following:
 - 1. Left ventricular enlargement or biventricular dilatation based on echocardiogram or cardiac MRI, **AND**
 - 2. Systolic dysfunction (e.g., ejection fraction less than 50%) based on echocardiogram, cardiac MRI, or left ventricular angiogram, **AND**
 - 3. Non-genetic causes of DCM have been ruled out, such as prior myocardial infarction from coronary artery disease, valvular and congenital heart disease, toxins (most commonly, anthracyclines or other chemotherapeutic agents; various drugs with idiosyncratic reactions), thyroid disease, inflammatory or infectious conditions, severe long-standing hypertension, and radiation.
- II. Genetic testing for dilated cardiomyopathy (DCM) via a multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

[view rationale](#)

[back to top](#)

ARRHYTHMOGENIC CARDIOMYOPATHY

Arrhythmogenic Cardiomyopathy Panels

- I. Genetic testing for arrhythmogenic cardiomyopathy via a multigene panel is considered **medically necessary** when:
 - A. The member has any one of the following:
 - 1. On echo:

Dean Health Plan Coverage Policy

- a) Regional right ventricular (RV) akinesia or dyskinesia, **OR**
 - (1) Aneurysm, **AND**
- b) At least one of the following (end diastole):
 - (1) PLAX RVOT ≥ 32 mm (PLAX/BSA ≥ 19 mm/m²), **OR**
 - (2) PSAX RVOT ≥ 36 mm (PSAX/BSA ≥ 21 mm/m²), **OR**
 - (3) Fractional area change $\leq 33\%$, **OR**
- 2. On MRI:
 - a) Regional RV akinesia or dyskinesia, **OR**
 - (1) Dyssynchronous RV contraction, **AND**
 - b) At least one of the following:
 - (1) Rao RVEDV/BSA ≥ 110 mL/m² (male), ≥ 100 mL/m² (female), **OR**
 - (2) RVEF $\leq 40\%$, **OR**
- 3. On RV Angiography:
 - a) Regional RV akinesia, dyskinesia, or aneurysm, **OR**
- 4. Endomyocardial biopsy showing fibrous replacement of the RV free wall myocardium in more than 1 sample, with or without fatty replacement, **AND**:
 - a) Residual myocytes $< 60\%$ by morphometric analysis (or $< 50\%$ if estimated), **OR**
- 5. On ECG:
 - a) Inverted T waves in right precordial leads (V1, V2, and V3) or beyond in individuals > 14 years of age (in the absence of complete RBBB QRS ≥ 120 ms), **OR**
 - b) Epsilon wave (reproducible low-amplitude signals between end of QRS complex to onset of the T wave) in the right precordial leads (V1 to V3), **OR**
 - c) Nonsustained or sustained VT of LBBB with superior axis (negative or indeterminate QRS in leads II, III, and aVF and positive in lead aVL), **OR**
- 6. On Family History:
 - a) ARVC confirmed in a [first-degree relative](#) who meets current Task Force Criteria, **OR**

Dean Health Plan Coverage Policy

- b) ARVC confirmed pathologically at autopsy or surgery in a [first-degree relative](#), **OR**
- c) Identification of a pathogenic mutation categorized as associated or probably associated with ARVC in the member under evaluation, **OR**

B. The member has any two of the following:

1. On echo, either:

- a) Regional RV akinesia or dyskinesia, **OR**
 - (1) Aneurysm, **AND**
- b) At least one of the following (end diastole):
 - (1) PLAX RVOT ≥ 29 mm to < 32 mm (PLAX/BSA ≥ 16 to < 19 mm/m²), **OR**
 - (2) PSAX RVOT ≥ 32 to < 36 mm (PSAX/BSA ≥ 18 to < 21 mm/m²), **OR**
 - (3) Fractional area change > 33 to $\leq 40\%$, **OR**

2. On MRI, either:

- a) Regional RV akinesia or dyskinesia, **OR**
 - (1) Dyssynchronous RV contraction, **AND**
- b) At least one of the following:
 - (1) Rao RVEDV/BSA ≥ 100 to < 110 mL/m² (male), ≥ 90 to 100 mL/m² (female), **OR**
 - (2) RVEF > 40 to $\leq 45\%$, **OR**

3. Endomyocardial biopsy showing fibrous replacement of the RV free wall myocardium in more than 1 sample, with or without fatty replacement, **AND**

- a) Residual myocytes 60% to 75% by morphometric analysis (or 50% to 65% if estimated), **OR**

4. On ECG:

- a) Inverted T waves in leads V1 and V2 in individuals > 14 years of age (in the absence of complete RBBB), or in V4, V5, or V6, **OR**
- b) Inverted T waves in leads V1, V2, V3, and V4 in individuals > 14 years of age in the presence of complete RBBB, **OR**
- c) Late potentials by SAECG in ≥ 1 of 3 parameters in the absence of QRS duration of ≥ 110 ms on the standard ECG:
 - (1) Filtered QRS duration (fQRS) ≥ 114 ms, **OR**

Dean Health Plan Coverage Policy

- (2) Duration of terminal QRS <40 μ V (low-amplitude signal duration) \geq 38 ms, **OR**
 - (3) Root-mean-square voltage of terminal 40 ms \leq 20 μ V, **OR**
 - d) Terminal activation duration of QRS \geq 55 ms measured from the nadir of the S wave to the end of the QRS, including R' in V1, V2, or V3 in the absence of complete RBBB, **OR**
 - e) Nonsustained or sustained VT or RV outflow configuration, LBBB morphology with inferior axis (positive QRS in II, III and aVF and negative in lead aVL) or of unknown axis, **OR**
 - f) >500 ventricular extrasystoles per 24 hours (Holter), **OR**
5. On Family History:
- a) History of ARVC in a [first-degree relative](#) in whom it is not possible or practical to determine whether the family member meets current Task Force Criteria, **OR**
 - b) Premature sudden death (<35 years of age) due to suspected ARVC in a [first-degree relative](#), **OR**
 - c) ARVC confirmed pathologically or by current Task Force Criteria in [second-degree relative](#).
- II. Genetic testing for arrhythmogenic cardiomyopathy via a multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

[view rationale](#)

[back to top](#)

RESTRICTIVE CARDIOMYOPATHY (RCM)

Restrictive Cardiomyopathy Panels

- I. Genetic testing for restrictive cardiomyopathy (RCM) via a multigene panel is considered **investigational** for all indications.

[view rationale](#)

[back to top](#)

LONG QT SYNDROME (LQTS)

Long QT Syndrome Panels

- I. Genetic testing for long QT syndrome (LQTS) via multigene panel is considered **medically necessary** when:

Dean Health Plan Coverage Policy

A. The member is asymptomatic, **AND**

1. The member has a confirmed prolonged QTc (greater than 460ms prepuberty, greater than 480 ms for adults) on resting ECG and/or provocative stress testing with exercise or during intravenous pharmacologic provocation testing (eg, with epinephrine), **OR**
2. The member has a [close relative](#) with a clinical diagnosis of LQTS, whose genetic status is unknown,¹ **OR**

B. The member is symptomatic (e.g., a history of syncope, cardiac arrest, and/or aborted sudden death), **AND**

1. The member meets either of the following:
 - a) A cardiologist has established a strong clinical suspicion for LQTS based on examination of the member's clinical history, family history, and expressed electrographic phenotype, **OR**
 - b) The member has a Schwartz score of 3.0 or more, **AND**
2. Non-genetic causes of a prolonged QTc interval have been ruled out, such as QT-prolonging drugs, hypokalemia, structural heart disease, or certain neurologic conditions including subarachnoid bleed.

II. Genetic testing for long QT syndrome (LQTS) via multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

¹If a pathogenic or likely pathogenic variant has been identified in an explanatory gene in the affected family member, refer to the *General Criteria for Known Familial Variant Analysis for a Genetic Condition* within the *General Approach to Laboratory Testing*.

[view rationale](#)

[back to top](#)

SHORT QT SYNDROME (SQTS)

Short QT Syndrome Panels

I. Genetic testing for short QT syndrome (SQTS) via multigene panel is considered **medically necessary** when:

- A. The member has a QTc of 330ms or less, **OR**
- B. The member has a SQTS diagnostic score of 4 or greater utilizing the criteria below, **OR**
- C. The member is asymptomatic, **AND**
 1. The member has a [first-degree relative](#) with a clinical diagnosis of SQTS, whose genetic status is unknown.¹

Dean Health Plan Coverage Policy

- II. Genetic testing for short QT syndrome (SQTS) via multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

¹If a pathogenic or likely pathogenic variant has been identified in an explanatory gene in the affected family member, refer to the *General Criteria for Known Familial Variant Analysis for a Genetic Condition* within the *General Approach to Laboratory Testing*.

Criteria	Points
Electrocardiogram ^a	
QTc less than 370 ms	1
QTc less than 350 ms	2
QTc less than 330 ms	3
J point-T peak interval ^b less than 120 ms	1
Clinical history ^{c*}	
History of sudden cardiac arrest	2
Documented polymorphic VT or VF	2
Unexplained syncope	1
Atrial fibrillation	1
Family history ^{d*}	
First- or second-degree relative with high-probability SQTS	2
First- or second-degree relative with autopsy-negative SCD	1

Dean Health Plan Coverage Policy

Sudden infant death syndrome	1
Genotype*	
Genotype positive	2
Mutation of undetermined significance in a culprit gene	1

SQTS score: High-probability SQTS: greater than or equal to 4 points, intermediate-probability SQTS: 3 points, low-probability SQTS: less than or equal to 2 points.

^a Electrocardiogram: must be recorded in the absence of modifiers known to shorten the QT.

^b Jpoint-Tpeak interval must be measured in the precordial lead with the greatest amplitude T-wave.

^c Clinical history: events must occur in the absence of an identifiable etiology, including structural heart disease. Points can only be received for 1 of cardiac arrest, documented polymorphic VT, or unexplained syncope.

^d Family history: points can only be received once in this section.

*A minimum of 1 point must be obtained in the electrocardiographic section in order to obtain additional points.

[view rationale](#)

[back to top](#)

BRUGADA SYNDROME (BRS)

Brugada Syndrome Panels or SCN5A Variant Analysis

- I. Genetic testing for Brugada syndrome (BrS) via *SCN5A* variant analysis is considered **medically necessary** when:
 - A. The member meets one of the following:
 1. Type 1 ECG (elevation of the J wave greater than or equal to 2 mm with a negative T wave and ST segment that is coved type and gradually descending) in more than one right precordial lead with or without administration of a sodium channel blocker (e.g., flecainide, pilsicainide, ajmaline, or procainamide), **OR**
 2. Type 2 ECG (elevation of the J wave greater than or equal to 2 mm with a positive or biphasic T wave; ST segment with saddle-back configuration and elevated greater than or equal to 1 mm) in more than one right precordial lead under baseline conditions with conversion to type 1 ECG following challenge with a sodium channel blocker, **OR**
 3. Type 3 ECG (elevation of the J wave greater than or equal to 2 mm with a positive T wave; ST segment with saddle-back configuration and elevated less than 1 mm) in more than one lead under baseline conditions with conversion to type 1 ECG following challenge with a sodium channel blocker, **AND**

Dean Health Plan Coverage Policy

B. Conditions causing a Brugada syndrome [phenocopy](#) (e.g., as myocardial ischaemia, electrolyte disturbances, and drug intoxications) have been ruled out, **AND**

C. Any of the following:

1. Recurrent syncope, **OR**
2. Ventricular fibrillation, **OR**
3. Self-terminating polymorphic ventricular tachycardia, **OR**
4. Cardiac arrest, **OR**
5. A family history of [sudden cardiac death \(SCD\)](#).

II. Genetic testing for Brugada syndrome (BrS) via *SCN5A* variant analysis is considered **investigational** for all other indications.

III. Genetic testing for Brugada syndrome (BrS) via genes other than *SCN5A*, including multigene panel analysis is considered **investigational**.

[view rationale](#)

[back to top](#)

CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA (CPVT)

Catecholaminergic Polymorphic Ventricular Tachycardia Panels

I. Genetic testing for catecholaminergic polymorphic ventricular tachycardia (CPVT) via multigene panel is considered **medically necessary** when:

A. The member has no known structural cardiac abnormalities, **AND**

B. The member has any of the following:

1. Syncope occurring during physical activity or acute emotion, **OR**
2. History of exercise- or emotion-related palpitations and dizziness, **OR**
3. Sudden unexpected cardiac death triggered by acute emotional stress or exercise, **OR**
4. Family history of juvenile [sudden cardiac death \(SCD\)](#) triggered by exercise or acute emotion, **OR**
5. Exercise-induced bidirectional or polymorphic ventricular arrhythmias, **OR**
6. Ventricular fibrillation occurring in the setting of acute stress.

II. Genetic testing for catecholaminergic polymorphic ventricular tachycardia (CPVT) via multigene panel is considered **investigational** for all other indications.

NOTE: If a panel is performed, the appropriate panel code should be used

[view rationale](#)

[back to top](#)

Dean Health Plan Coverage Policy

FAMILIAL HYPERCHOLESTEROLEMIA (FH)

Familial Hypercholesterolemia (FH) Panels

- I. Genetic testing for familial hypercholesterolemia (FH) via multigene panel to establish or confirm a diagnosis of familial hypercholesterolemia (FH) is considered **medically necessary** when:
 - A. The member has at least two or more elevated LDL-C measurements, including assessment after intensive lifestyle modification, **AND**
 - B. There is no apparent secondary cause of hypercholesterolemia (e.g., hypothyroidism, diabetes, renal disease, nephrotic syndrome, liver disease, medications), **AND**
 1. The member is a child with LDL-C levels greater than or equal to 190 mg/dl, **OR**
 2. The member is a child with LDL-C levels greater than or equal to 160 mg/dl with one of the following:
 - a) At least one [first-degree relative](#) with elevated LDL-C, **OR**
 - b) At least one [first-degree relative](#) with [premature coronary artery disease \(CAD\)](#), **OR**
 - c) Limited family history (e.g., adoption), **OR**
 - d) A family history of both hypercholesterolemia and [premature coronary artery disease \(CAD\)](#), **OR**
 3. The member is an adult with LDL-C levels greater than or equal to 250 mg/dl, **OR**
 4. The member is an adult with LDL-C levels greater than or equal to 190 mg/dl with one of the following:
 - a) At least one [first-degree relative](#) with elevated LDL-C, **OR**
 - b) At least one [first-degree relative](#) with [premature coronary artery disease \(CAD\)](#), **OR**
 - c) Limited family history (e.g. adoption), **OR**
 5. The member is an adult with LDL-C levels greater than or equal to 160 mg/dl with one of the following:
 - a) A family history of both hypercholesterolemia and [premature coronary artery disease \(CAD\)](#), **OR**
 - b) A personal history of [premature coronary artery disease \(CAD\)](#), **OR**
 - C. The member is an adult with [premature coronary artery disease \(CAD\)](#), **AND**
 1. A family history of both hypercholesterolemia and [premature coronary artery disease \(CAD\)](#).

Dean Health Plan Coverage Policy

- II. Genetic testing for familial hypercholesterolemia (FH) via multigene panel to establish or confirm a diagnosis of familial hypercholesterolemia (FH) is considered **investigational** for all other indications.

[view rationale](#)

[back to top](#)

CONGENITAL HEART MALFORMATIONS

Congenital Heart Malformation Panels

- I. Genetic testing for congenital heart malformations via multigene panel analysis may be considered **medically necessary** when:
 - A. The member has a complex congenital heart malformation (e.g., hypoplastic left heart, transposition of the great vessels, tetralogy of Fallot, etc), **AND**
 - B. The member's clinical features do not fit a known genetic disorder for which targeted testing could be performed (e.g., 22q11.2 deletion syndrome, Down syndrome/Trisomy 21, Williams syndrome, etc.), **AND**
 - C. Prenatal teratogen exposure has been considered, and ruled out when possible.
- II. Genetic testing for congenital heart malformations via multigene panel analysis is considered **investigational** for all other indications, including "simple" congenital heart defects (e.g. ventricular septal defects, atrial septal defects, patent ductus arteriosus).

[view rationale](#)

[back to top](#)

FAMILIAL THORACIC AORTIC ANEURYSM AND DISSECTION (TAAD)

Familial Thoracic Aortic Aneurysm and Dissection (TAAD) Multigene Panel

- I. Familial thoracic aortic aneurysm and dissection (TAAD) multigene panel analysis to establish a genetic diagnosis for TAAD is considered **medically necessary** when:
 - A. The member has a history of any of the following:
 - 1. Aortic root enlargement, **OR**
 - 2. Thoracic aneurysm, **OR**
 - 3. [Type A aortic dissection](#) or [type B aortic dissection](#), **AND**
 - B. The member does not otherwise meet diagnostic criteria for another connective tissue disorder, **AND**
 - C. The member has a family history of dilation or dissection of the aortic root, consistent with autosomal dominant inheritance.
- II. Thoracic aortic aneurysm and dissection (TAAD) multigene panel analysis to establish a genetic diagnosis for TAAD is considered **investigational** for all other indications.

Dean Health Plan Coverage Policy

NOTE: If a panel is performed, the appropriate panel code should be used

[view rationale](#)

[back to top](#)

HEREDITARY HEMORRHAGIC TELANGIECTASIA (HHT)

Hereditary Hemorrhagic Telangiectasia Multigene Panel

- I. Hereditary hemorrhagic telangiectasia (HHT) multigene panel analysis to establish or confirm a diagnosis of HHT is considered **medically necessary** when:
 - A. The member has any of the following clinical features of HHT:
 1. Spontaneous and recurrent nosebleeds (epistaxis), **OR**
 2. Mucocutaneous telangiectases at characteristic sites, including lips, oral cavity, fingers, and nose, **OR**
 3. Visceral arteriovenous malformation (AVM) (either pulmonary, cerebral, spinal, gastrointestinal or pancreatic), **AND**
 - B. The panel includes, at a minimum, the following genes: *ACVRL1*, *ENG*.
- II. Hereditary hemorrhagic telangiectasia (HHT) multigene panel analysis to establish or confirm a diagnosis of HHT is considered **investigational** for all other indications.

[view rationale](#)

[back to top](#)

PRIOR AUTHORIZATION

Prior authorization is not required. However, services with specific coverage criteria may be reviewed retrospectively to determine if criteria are being met. Retrospective denial may result if criteria are not met.

RATIONALE

Comprehensive Cardiomyopathy Panels

Heart Failure Society of America and American College of Medical Genetics and Genomics (ACMG)

The Heart Failure Society of America published joint guidelines with the American College of Medical Genetics and Genomics (Hershberger et al, 2018) and made the following recommendations:

- Guideline 4: Genetic testing is recommended for patients with cardiomyopathy (Level of evidence A)
 - 4a: Genetic testing is recommended for the most clearly affected family member.
 - 4b: Cascade genetic testing of at-risk family members is recommended for pathogenic and likely pathogenic variants.
 - 4c: In addition to routine newborn screening tests, specialized evaluation of infants with cardiomyopathy is recommended, and genetic testing should be considered (p. 289).

Per the guideline, multigene panel genetic testing is recommended over a serial single-gene testing approach owing to the genetically and heterogeneous nature of cardiomyopathy (p. 290).

Dean Health Plan Coverage Policy

Asia Pacific Heart Rhythm Society (APHRS) and Heart Rhythm Society (HRS)

The Asia Pacific Heart Rhythm Society (APHRS) and Heart Rhythm Society (HRS) published an expert consensus statement (Stiles et al, 2020) on the investigation of decedents with sudden unexplained death and patients with sudden cardiac arrest, and of their families that includes the following “take-home messages” related to genetic testing:

- For survivors of sudden cardiac arrest (SCA), victims of sudden unexplained death (SUD), and their relatives, a multidisciplinary team is central to thorough investigation, so as to maximize the opportunity to make a diagnosis. Where there has been an SCD or resuscitated SCA and a genetic cause is suspected, genetic testing and counseling is essential for families, to ensure that risks, benefits, results, and the clinical significance of genetic testing can be discussed (p. e3).
- A comprehensive autopsy is an essential part of the investigation of SUD and should include collection and storage of tissue suitable for genetic analysis. When the autopsy suggests a possible genetic cause, or no cause and the heart is normal, referral to a multidisciplinary team for further investigation is indicated (p. e3).
- For victims of SCD or survivors of cardiac arrest where the phenotype is known, genetic testing of the proband focused on likely candidate genes, along with clinical evaluation of family members, aids in identifying family members with, or at risk of developing, the same condition (p. e3).
- For the investigation of SCA survivors, essential inquiry includes detailed personal and family history, witness accounts, physical examination, multiple electrocardiograms (ECGs), and cardiac imaging. Ambulatory monitoring and/or provocative testing (exercise, pharmacological, and invasive electrophysiological) may provide additional useful information. A sample suitable for future DNA testing should be taken early in the patient’s course and stored (p. e4).
- Genetic investigation of SCA survivors is best undertaken at a center with multidisciplinary care infrastructure and should focus on likely candidate genes known to be causally related to the suspected phenotype. In some cases, genetic evaluation without a suspected phenotype may be undertaken with appropriate genetic counseling, although genetic evaluation of patients with a known nongenetic cause of cardiac arrest is discouraged (p. e4).

[back to top](#)

Comprehensive Arrhythmia Panels

European Heart Rhythm Association, Heart Rhythm Society, Asia Pacific Heart Rhythm Society, Latin American Heart Rhythm Society

The EHRA/HRS/APHRS/LAHR 2022 expert consensus statement on the state of genetic testing for cardiac diseases provided guidance on the investigation of decedents with sudden unexplained death and patients / families with sudden cardiac arrest.

“In relatives of UCA [unexplained cardiac arrest] survivors or SCD [sudden cardiac death] decedents, clinical evaluation of first degree family members should be performed, and targeted to the index case’s phenotype if present” (p. 1350).

These guidelines also provide a flowchart for workup for a sudden cardiac death or non-fatal cardiac arrest, recommending that for individuals who died from a SUD or UCA in which no autopsy was

Dean Health Plan Coverage Policy

performed, and were less than age 50 years, and/or had a family history of premature SCD and/or genetic heart disease, and/or circumstances of death were suspicious for genetic heart disease, clinical evaluation of first degree family members is indicated (p. 1351).

[back to top](#)

Comprehensive Arrhythmia and Cardiomyopathy (Sudden Cardiac or Unexplained Death) Panels

Asia Pacific Heart Rhythm Society (APHRS) and Heart Rhythm Society (HRS)

The Asia Pacific Heart Rhythm Society (APHRS) and Heart Rhythm Society (HRS) published an expert consensus statement (Stiles et al, 2020) on the investigation of decedents with sudden unexplained death and patients with sudden cardiac arrest, and of their families, which states that hypothesis-free genetic testing is not indicated in cases of SCD where the phenotype remains unknown. Genetic testing using any range from large unfocused gene panels to whole-exome or whole-genome sequencing in the absence of a clinical phenotype or diagnosis may be considered in the context of a scientific effort but is not recommended for routine patient care and counseling (p. e26).

Concert Note

While large unfocused gene panels are generally discouraged for this indication, because there is a path to coverage for both Comprehensive Arrhythmia Panels and Comprehensive Cardiomyopathy Panels (both phenotypically-focused tests), it is the philosophy of Concert that, if a member meets criteria for both individual panels, that member should also meet criteria for the combined test.

[back to top](#)

Hypertrophic Cardiomyopathy Panels

American College of Cardiology and American Heart Association (ACC/AHA)

The American College of Cardiology/American Heart Association Joint Committee on Clinical Practice Guidelines published an updated guideline for the diagnosis and treatment of patients with hypertrophic cardiomyopathy (2020), which stated the following with regard to genetic testing for HCM:

“Counseling patients with HCM regarding the potential for genetic transmission of HCM is one of the corner-stones of care. Screening first-degree family members of patients with HCM, using either genetic testing or an imaging/electrocardiographic surveillance protocol, can begin at any age and can be influenced by specifics of the patient/family history and family preference. As screening recommendations for family members hinge on the pathogenicity of any detected variants, the reported pathogenicity should be reconfirmed every 2 to 3 years” (p. e161).

The ACC/AHA says HCM is “characterized predominantly by LVH in the absence of another cardiac, systemic, or metabolic disease capable... A clinical diagnosis of HCM in adult patients can therefore be established by imaging, with 2D echocardiography or cardiovascular magnetic resonance (CMR) showing a maximal end-diastolic wall thickness of greater than or equal to 15 mm anywhere in the left ventricle, in the absence of another cause of hypertrophy in adults. More limited hypertrophy (13–14 mm) can be diagnostic when present in family members of a patient with HCM or in conjunction with a positive genetic test. For children, the diagnostic criteria are confounded by needing to adjust for

Dean Health Plan Coverage Policy

body size and growth. Traditionally, a body surface area adjusted z-score of 2 or more standard deviations above the mean has been used” (p. e167).

“Postmortem testing for HCM-associated variants using blood or tissue collected at autopsy has been reported, particularly in instances where the family variant is unknown and no other affected family members are still living....identification of a likely pathogenic or pathogenic variant not only confirms the diagnosis of HCM but allows cascade genetic testing of other at-risk relatives as outlined previously” (p. e184).

American College of Cardiology Foundation and American Heart Association

The American College of Cardiology Foundation (ACCF) and the American Heart Association (AHA) (2011) issued joint guidelines on the diagnosis and treatment of hypertrophic cardiomyopathy. They state that hypertrophic cardiomyopathy is clinically recognized by a maximal left ventricular wall thickness of 15mm or greater in adults, and the equivalent relative to body surface area in children. They also recommended that screening (with or without genetic testing) be performed in first-degree relatives of individuals with hypertrophic cardiomyopathy (p. e792).

[back to top](#)

Dilated Cardiomyopathy Panels

European Heart Rhythm Association, Heart Rhythm Society, Asia Pacific Heart Rhythm Society, Latin American Heart Rhythm Society

In their 2022 expert consensus statement, the European Heart Rhythm Association, Heart Rhythm Society, Asia Pacific Heart Rhythm Society, and Latin American Heart Rhythm Society defines dilated cardiomyopathy as left ventricle or biventricular dilatation and systolic dysfunction in the absence of abnormal loading conditions or coronary artery disease (p. 1342). The expert consensus states the following:

“Genetic testing is...useful in all DCM [dilated cardiomyopathy] patients, is recommended in DCM patients with the highest yield of pathogenic variant screening and should be considered even in the absence of familial context or associated clinical features” (p. 1343).

Heart Failure Society of America

Hershberger, et al published guidelines in 2018 on cardiomyopathy genetic evaluation. They state the following:

“That familial dilated cardiomyopathy (DCM) has a genetic basis is also well accepted. (The term DCM is used herein instead of the more technical attribution, “idiopathic dilated cardiomyopathy”, where the other common and easily clinically detected causes of systolic dysfunction such as coronary artery disease, primary valvular or congenital heart disease, or previous exposure to cancer chemotherapy or other injurious drugs, have been excluded)” (p. 282).

GeneReviews: Dilated Cardiomyopathy Overview

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The recommended diagnostic screening for dilated cardiomyopathy is as follows:

Dean Health Plan Coverage Policy

DCM is established when a patient has both left ventricular enlargement and systolic dysfunction. “An ejection fraction of less than 50% is considered systolic dysfunction. The left ventricular ejection fraction is the most commonly used clinical measure of systolic function, and is usually estimated from a two-dimensional echocardiogram or from cardiac MRI. ... Ejection fractions can also be estimated from a left ventricular angiogram.”

[back to top](#)

Arrhythmogenic Cardiomyopathy Panels

Towbin et al 2019

Modification of the Task Force Criteria for the diagnosis of arrhythmogenic right ventricular cardiomyopathy (ARVC) were published in 2010 and outlined clinical criteria for individuals with possible ARVC, which the Task Force defined as individuals with one major criteria or two minor criteria from different categories. The major and minor criteria are as follows:

Major Criteria

- I. Echo:
 - A. Regional RV akinesia dyskinesia, or aneurysm and 1 of the following (end diastole):
 - 1. PLAX RVOT ≥ 32 mm (PLAX/BSA ≥ 19 mm/m²)
 - 2. PSAX RVOT ≥ 36 mm (PSAX/BSA ≥ 21 mm/m²)
 - 3. Fractional area change $\leq 33\%$
- II. MRI
 - A. Regional RV akinesia or dyskinesia, or dyssynchronous RV contraction and 1 of the following:
 - 1. Rao RVEDV/BSA ≥ 110 mL/m² (male), ≥ 100 mL/m² (female)
 - 2. RVEF $\leq 40\%$
- III. RV Angiography
 - A. Regional RV akinesia, dyskinesia, or aneurysm
- IV. Endomyocardial biopsy showing fibrous replacement of the RV free wall myocardium in more than 1 sample, with or without fatty replacement and with:
 - A. Residual myocytes $< 60\%$ by morphometric analysis (or $< 50\%$ if estimated)
- V. ECG
 - A. Inverted T waves in right precordial leads (V1, V2, and V3) or beyond in individuals > 14 years of age (in the absence of complete RBBB QRS ≥ 120 ms)
 - B. Epsilon wave (reproducible low-amplitude signals between end of QRS complex to onset of the T wave) in the right precordial leads (V1 to V3)
 - C. Nonsustained or sustained VT of LBBB with superior axis (negative or indeterminate QRS in leads II, III, and aVF and positive in lead aVL)
- VI. Family History
 - A. ARVC confirmed in a first-degree relative who meets current Task Force Criteria
 - B. ARVC confirmed pathologically at autopsy or surgery in a first-degree relative
 - C. Identification of a pathogenic mutation categorized as associated or probably associated with ARVC in the patient under evaluation

Minor Criteria

- I. Echo
 - A. Regional RV akinesia, dyskinesia, or aneurysm and 1 of the following (end diastole):

Dean Health Plan Coverage Policy

1. PLAX RVOT ≥ 29 mm to < 32 mm (PLAX/BSA ≥ 16 to < 19 mm/m²)
 2. PSAX RVOT ≥ 32 to < 36 mm (PSAX/BSA ≥ 18 to < 21 mm/m²)
 3. Fractional area change > 33 to $\leq 40\%$
- II. MRI
- A. Regional RV akinesia or dyskinesia, OR
 - B. Dyssynchronous RV contraction and 1 of the following:
 1. Rao RVEDV/BSA ≥ 100 to < 110 mL/m² (male), ≥ 90 to 100 mL/m² (female)
 2. RVEF > 40 to $\leq 45\%$
- III. Endomyocardial biopsy showing fibrous replacement of the RV free wall myocardium in more than 1 sample, with or without fatty replacement and with:
- A. Residual myocytes 60% to 75% by morphometric analysis (or 50% to 65% if estimated)
- IV. ECG
- A. Inverted T waves in leads V1 and V2 in individuals > 14 years of age (in the absence of complete RBBB), or in V4, V5, or V6.
 - B. Inverted T waves in leads V1, V2, V3, and V4 in individuals > 14 years of age in the presence of complete RBBB
 - C. Late potentials by SAECG in ≥ 1 of 3 parameters in the absence of QRS duration of ≥ 110 ms on the standard ECG:
 1. Filtered QRS duration (fQRS) ≥ 114 ms
 2. Duration of terminal QRS < 40 μ V (low-amplitude signal duration) ≥ 38 ms
 3. Root-mean-square voltage of terminal 40 ms ≤ 20 μ V
 - D. Terminal activation duration of QRS ≥ 55 ms measured from the nadir of the S wave to the end of the QRS, including R' in V1, V2, or V3 in the absence of complete RBBB
 - E. Nonsustained or sustained VT or RV outflow configuration, LBBB morphology with inferior axis (positive QRS in II, III and aVF and negative in lead aVL) or of unknown axis
 - F. > 500 ventricular extrasystoles per 24 hours (Holter)
- V. Family History
- A. History of ARVC in a first-degree relative in whom it is not possible or practical to determine whether the family member meets current Task Force Criteria
 - B. Premature sudden death (< 35 years of age) due to suspected ARVC in a first-degree relative
 - C. ARVC confirmed pathologically or by current Task Force Criteria in second-degree relative (p. 311)

[back to top](#)

Restrictive Cardiomyopathy Panels

American College of Medical Genetics and Genomics (ACMG)

The American College of Medical Genetics and Genomics (ACMG) (2018) published clinical practice recommendations for the genetic evaluation of cardiomyopathy. The following recommendations were made for RCM:

In regard to selecting genes to test in association with the cardiomyopathy, "Consider HCM or DCM panel."

Dean Health Plan Coverage Policy

“Genetic causes of RCM continue to be identified, but because RCM is a relatively rare form of cardiomyopathy, numbers remain limited. A recent study identified a pathogenic variant in 60% of subjects, primarily occurring in genes known to cause HCM. Family members were frequently identified with HCM or HCM with restrictive physiology... Cardiac amyloidosis resulting from pathogenic variants in TTR needs to be differentiated from other forms of RCM due to the age demographic in which this occurs, the slowly progressive nature of this disease, and therefore different management strategies. The TTR allele p.Val142Ile (commonly referred to as Val122Ile based on nomenclature for the circulating protein after N-terminal peptide cleavage) has been found in 10% of African Americans older than age 65 with severe congestive heart failure. Substantial recent progress with amyloidosis, both in imaging strategies, including cardiac magnetic resonance and pyrophosphate scanning, and therapeutic interventions in ongoing clinical trials, provide new incentives for genetic diagnosis” (p. 904).

[back to top](#)

Long QT Syndrome Panels

European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS)

This expert consensus statement on the state of genetic testing for cardiac diseases published in 2022 by Wilde et al. states the following:

“Molecular genetic testing for definitive disease associated genes (currently *KCNQ1*, *KCNH2*, *SCN5A*, *CALM1*, *CALM2*, and *CALM3*) should be offered to all index patients with a high probability diagnosis of LQTS, based on examination of the patient’s clinical history, family history, and ECG characteristics obtained at baseline, during ECG Holter recording and exercise stress test (Schwartz Score 3.5)” (p. e.15).

“In patients with an intermediate probability of LQTS (e.g. prolonged QTc with a Schwartz score 1.5–3.0), testing of genes with limited, disputed and refuted evidence should not be performed, while testing of the established genes may be considered, mostly to help rule out the diagnosis after extensive phenotypic investigation” (p. e17).

Heart Rhythm Society (HRS) and European Heart Rhythm Association (EHRA)

The HRS and the EHRA (Ackerman, et al 2011) published joint recommendations and made the following recommendations for LQTS genetic testing in asymptomatic individuals:

- “Comprehensive or LQT1-3 (*KCNQ1*, *KCNH2*, and *SCN5A*) targeted LQTS genetic testing is recommended for any patient in whom a cardiologist has established a strong clinical index of suspicion for LQTS based on examination of the patient’s clinical history, family history, and expressed electrocardiographic (resting 12-lead ECGs and/or provocative stress testing with exercise or catecholamine infusion) phenotype. (Class I)
- Comprehensive or LQT1-3 (*KCNQ1*, *KCNH2*, *SCN5A*) targeted LQTS genetic testing is recommended for any asymptomatic patient with QT prolongation in the absence of other clinical conditions that might prolong the QT interval (such as electrolyte abnormalities, hypertrophy, bundle branch block, etc, ie, otherwise idiopathic) on serial 12-lead ECGs defined as QTc greater than 480 ms (prepuberty) or greater than 500 ms (adults). (Class I)
- Comprehensive or LQT1-3 (*KCNQ1*, *KCNH2*, *SCN5A*) targeted LQTS genetic testing may be considered for any asymptomatic patient with otherwise idiopathic QTc values greater than

Dean Health Plan Coverage Policy

460 ms (prepuberty) or greater than 480 ms (adults) on serial 12-lead ECGs. (Class IIB)” (p. 1311).

Schwartz, Crotti; 2011

Schwartz and Crotti published a scoring system in which to diagnose LQTS. They suggest using the Schwartz score for “selection of those patients who should undergo molecular screening (everyone with a score greater than or equal to 3.0) and in the use of ‘cascade screening’ for the identification of all affected family members including the silent mutation carriers” (p. 5).

SCORE:

- Less than or equal to 1 point: low probability of LQTS
- 1.5 to 3 points: intermediate probability of LQTS
- 3.5 points or more: high probability (p. 23)

[back to top](#)

Short QT Syndrome Panels

Heart Rhythm Society, European Heart Rhythm Society, Asia Pacific Heart Rhythm Society

Priori et al HRS/EHRA/APHRS published an expert consensus statement in 2013 with the following Class 1 clinical diagnostic criteria (which are later referenced in Wilde AAM, Semsarian C, Márquez MF, et al. European Heart Rhythm Association/Heart Rhythm Society/Asia Pacific Heart Rhythm Society/Latin American Heart Rhythm Society expert consensus statement on the state of genetic testing for cardiac diseases. *Journal of Arrhythmia*. 2022;38(4):491-553) for short QT syndrome (SQTS):

“This group has reached a consensus that a cutoff value less than or equal to 330ms should be used for the diagnosis” (p. 1943).

European Heart Rhythm Association, Heart Rhythm Society, Asia Pacific Heart Rhythm Society, Latin American Heart Rhythm Society

In 2022, Wilde et al published the following guidelines regarding SQTS:

“In any patient satisfying the diagnostic criteria for SQTS (such as Class 1 clinical diagnosis [see Priori et al HRS/EHRA/APHRS 2013 expert consensus statement] or SQTS diagnostic score greater [than or equal to] 4), molecular genetic testing is recommended for the definitive disease associated genes (currently *KCNH2*, *KCNQ1*). Testing of *KCNJ2* and *SLC4A3* may be performed in all index patients in whom a cardiologist has established with a high probability a diagnosis of SQTS, based on examination of the patient’s clinical history, family history, and ECG characteristics obtained at baseline or during ECG Holter recording and exercise stress test (SQTS diagnostic score greater than or equal to 4)” (p. 515).

“Cascade testing for at-risk family members is recommended when a disease-causing mutation is identified” (p. 516).

Dean Health Plan Coverage Policy

Supplementary Table 9. Diagnostic score cards for short QT syndrome (4)

Criteria	Points
Electrocardiogram ^a	
QTc less than 370 ms	1
QTc less than 350 ms	2
QTc less than 330 ms	3
J point-T peak interval ^b less than 120 ms	1
Clinical history ^{c*}	
History of sudden cardiac arrest	2
Documented polymorphic VT or VF	2
Unexplained syncope	1
Atrial fibrillation	1
Family history ^{d*}	
First- or second-degree relative with high-probability SQTS	2
First- or second-degree relative with autopsy-negative SCD	1
Sudden infant death syndrome	1
Genotype [*]	
Genotype positive	2

Dean Health Plan Coverage Policy

Mutation of undetermined significance in a culprit gene	1
---	---

SQTS score: High-probability SQTS: greater than or equal to 4 points, intermediate-probability SQTS: 3 points, low-probability SQTS: less than or equal to 2 points.

^a Electrocardiogram: must be recorded in the absence of modifiers known to shorten the QT.

^b Jpoint-Tpeak interval must be measured in the precordial lead with the greatest amplitude T-wave.

^c Clinical history: events must occur in the absence of an identifiable etiology, including structural heart disease. Points can only be received for 1 of cardiac arrest, documented polymorphic VT, or unexplained syncope.

^d Family history: points can only be received once in this section.

*A minimum of 1 point must be obtained in the electrocardiographic section in order to obtain additional points.

[back to top](#)

Brugada Syndrome Panels or SCN5A Variant Analysis

GeneReviews: Brugada Syndrome

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

The recommended diagnostic screening for Brugada syndrome is as follows:

“Brugada syndrome [BrS] should be suspected in individuals with any of the following findings:

- Recurrent syncope
- Ventricular fibrillation
- Self-terminating polymorphic ventricular tachycardia
- Cardiac arrest
- Family history of sudden cardiac death

AND one of the following EKG patterns:

Type 1 EKG (elevation of the J wave greater than or equal to 2 mm with a negative T wave and ST segment that is coved type and gradually descending) in more than one right precordial lead (V1-V3)*... with or without administration of a sodium channel blocker (e.g., flecainide, pilsicainide, ajmaline, or procainamide)

Type 2 EKG (elevation of the J wave greater than or equal to 2 mm with a positive or biphasic T wave; ST segment with saddleback configuration and elevated greater than or equal to 1 mm) in more than one right precordial lead under baseline conditions with conversion to type 1 EKG following challenge with a sodium channel blocker

Type 3 EKG (elevation of the J wave greater than or equal to 2 mm with a positive T wave; ST segment with saddleback configuration and elevated less than 1 mm) in more than one lead under baseline conditions with conversion to type 1 EKG following challenge with a sodium channel blocker.”

European Heart Rhythm Association, Heart Rhythm Society, Asia Pacific Heart Rhythm Society, Latin American Heart Rhythm Society (2022)

Dean Health Plan Coverage Policy

“Brugada syndrome phenocopies such as myocardial ischaemia, electrolyte disturbances and drug intoxications should be excluded before a diagnosis of BrS can be made” (p. 510-511).

“Other genes [besides *SCN5A*] have been implicated in BrS. However, the gene-disease validity of most of those genes (other than *SCN5A*) has been disputed following rigorous assessment of available data using the ClinGen framework. Although a disputed ClinGen status does not challenge a role of the gene product in BrS pathophysiology, it strongly argues against reporting those genes in the diagnostic setting” (p. 511).

*No other factor(s) should account for the EKG abnormality.

[back to top](#)

Catecholaminergic Polymorphic Ventricular Tachycardia Panels

GeneReviews: Catecholaminergic Polymorphic Ventricular Tachycardia

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

The recommended diagnostic screening for catecholaminergic polymorphic ventricular tachycardia is as follows:

“Catecholaminergic polymorphic ventricular tachycardia (CPVT) should be suspected in individuals who have one or more of the following:

- Syncope occurring during physical activity or acute emotion; mean onset is age seven to 12 years. Less frequently, first manifestations may occur later in life; individuals with a first event up to age 40 years have been reported.
- History of exercise- or emotion-related palpitations and dizziness in some individuals
- Sudden unexpected cardiac death triggered by acute emotional stress or exercise
- Family history of juvenile sudden cardiac death triggered by exercise or acute emotion
- Exercise-induced bidirectional or polymorphic ventricular arrhythmias...
- Ventricular fibrillation occurring in the setting of acute stress

The diagnosis of CPVT is established in the presence of a structurally normal heart, normal resting EKG, and exercise- or emotion-induced bidirectional or polymorphic ventricular tachycardia...”

[back to top](#)

Familial Hypercholesterolemia (FH) Panels

Journal of the American College of Cardiology (2018)

“Genetic testing for FH should be offered to individuals of any age in whom a strong clinical index of suspicion for FH exists based on examination of the patient’s clinical and/or family histories. This index of suspicion includes the following:

1. Children with persistent* LDL-C levels ≥ 160 mg/dl or adults with persistent* LDL-C levels ≥ 190 mg/dl without an apparent secondary cause of hypercholesterolemia[†] and with at least 1 first-degree relative similarly affected or with premature CAD[‡] or where family history is not available (e.g., adoption)

Dean Health Plan Coverage Policy

2. Children with persistent* LDL-C levels ≥ 190 mg/dl or adults with persistent* LDL-C levels ≥ 250 mg/dl without an apparent secondary cause of hypercholesterolemia,† even in the absence of a positive family history.

Evidence Grade: Class of Recommendation IIa, Strength of Evidence B-NR.

Genetic testing for FH may be considered in the following clinical scenarios:

1. Children with persistent* LDL-C levels ≥ 160 mg/dl (without an apparent secondary cause of hypercholesterolemia†) with an LDL-C level ≥ 190 mg/dl in at least 1 parent or a family history of hypercholesterolemia and premature CAD‡
2. Adults with no pre-treatment LDL-C levels available but with a personal history of premature CAD‡ and family history of both hypercholesterolemia and premature CAD‡
3. Adults with persistent* LDL-C levels ≥ 160 mg/dl (without an apparent secondary cause of hypercholesterolemia†) in the setting of a family history of hypercholesterolemia and either a personal history or a family history of premature CAD‡

Evidence Grade: Class of Recommendation IIb, Strength of Evidence C-EO"

If LDL-C values are unavailable, total cholesterol values ≥ 320 , 260, and 230 mg/dl (corresponding to LDL-C levels ≥ 250 , 190, and 160 mg/dl, respectively) could be used.

*Two or more measurements, including assessment after intensive lifestyle modification.

† Hypothyroidism, diabetes, renal disease, nephrotic syndrome, liver disease, medications.

‡ Premature coronary artery disease (CAD) = male subjects ≤ 55 years of age, female subjects ≤ 65 years of age; adapted from the American Heart Association phenotype definition of HeFH" (p. 674).

"Genetic testing for patients with suspected FH should, at a minimum, include analysis of LDLR, APOB, and PCSK9. This analysis should include for LDLR and PCSK9 sequencing of all exons and exon/intron boundaries, as well as LDLR deletion/duplication analysis, and for APOB the exons encoding the LDLR ligand-binding region... Larger, more inclusive, lipid disorder NGS panels are also available that provide evaluation of not only the main FH genes but also the genes causing conditions with phenotypic overlap previously described. These expanded panels should be considered to improve the diagnosis of patients with these "phenocopy" conditions that may require specific therapies, and they should include the following genes: *LDLR*, *APOB*, *PCSK9*, *LDLRAP1*, *LIPA*, *ABCG5*, *ABCG8*, and *APOE*" (p. 674).

Musunuru et al, (2020)

"An international expert panel convened by the FH Foundation wrote a scientific statement on clinical genetic testing for FH. This statement generally recommends genetic testing of FH genes (*LDLR*, *APOB*, *PCSK9*, and potentially other genes if warranted by the patient phenotype...) for individuals with hypercholesterolemia for which an inherited variant is a likely cause. The statement highlights individuals with some combination of persistent elevated low-density lipoprotein cholesterol levels, personal history of premature coronary artery disease, family history of hypercholesterolemia, and family history of premature coronary artery disease who should be offered or may be considered for genetic testing... In addition, cascade genetic testing should be offered to all at-risk family members of an individual found to have a pathogenic variant in a FH gene. Genetic testing for FH is expected to result in a higher rate of diagnosis among patients with FH, more effective cascade testing, the initiation of therapies at earlier ages, and more accurate risk stratification" (p. 381).

[back to top](#)

Dean Health Plan Coverage Policy

Congenital Heart Malformation Panels

American Heart Association

The American Heart Association published a statement entitled “Genetic Basis for Congenital Heart Disease: Revisited” in September 2018 (correction published in November 2018) which states the following:

“Uncovering a genetic pathogenesis for congenital HD is increasingly clinically relevant, in part because of the aforementioned improved survival. For the clinician caring for a child or adult with congenital HD, important reasons for determining the genetic cause can include (1) assessing recurrence risks for the offspring of the congenital HD survivor, additional offspring of the parents, or other close relatives; (2) evaluating for associated extracardiac involvement; (3) assessing risk for neurodevelopmental delays for newborns and infants; and (4) providing more accurate prognosis for the congenital HD and outcomes for congenital HD–related interventions” (p. 3).

[back to top](#)

Familial Thoracic Aortic Aneurysm and Dissection (TAAD) Multigene Panel

American College of Medical Genetics and Genomics (ACMG)

American College of Medical Genetics and Genomics (2012) issued guidelines on the evaluation of adolescents or adults with some features of Marfan syndrome (MFS) (including TAAD), which recommendations included the following (p. 174-175):

Genetic testing for TAAD can aid in the diagnosis in addition to physical exam, family history, dilated eye exam, echocardiography and vasculature imaging. Diagnostic criteria for TAAD include autosomal dominant history of dilatation or dissection of the aortic root, ascending aorta or descending aorta in the absence of major criteria for the diagnosis of Marfan syndrome or other connective tissue disease.

American Heart Association/American College of Cardiology

The AHA and ACC published a joint guideline (2022) in which genetic testing is recommended for patients with aortic root/ascending aortic aneurysms or aortic dissection and risk factors for hereditary thoracic aortic disease (strong recommendation, moderate quality of evidence). These risk factors include:

- Thoracic aortic disease (TAD) and syndromic features of Marfan, Loeys-Dietz or vascular Ehlers-Danlos syndrome
- TAD presentation under 60 years of age
- Family history of either TAD or peripheral/intracranial aneurysms in first or second degree relative
- History of unexplained sudden death at a relatively young age in first or second degree relative (p. e361).
- A multigene panel comprising all genes suspected to cause HTAD [heritable thoracic aortic disease] is the most cost-effective and clinically useful approach to testing (p. e362).

GeneReviews: Heritable Thoracic Aortic Disease Overview

Dean Health Plan Coverage Policy

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

Per the Heritable Thoracic Aortic Disease GeneReviews article, “A multigene panel that includes genes associated with HTAD [heritable thoracic aortic disease] is recommended.” Per Table 1 of this article, these genes include: *ACTA2, COL3A, FBN1, MYH11, MYLK, SMAD3, TGFB2, TGFB1, TGFB2, LOX, PRKG1, EFEMP2, FOXE3, MFAP5, SMAD2, BGN, CBS, COL4A5, ELN, FBN2, FLNA, HCN4, NOTCH1, MAT2A, PKD1, PKD2, SKI, SLC2A10, SMAD4, TGFB3.*

[back to top](#)

Hereditary Hemorrhagic Telangiectasia Multigene Panel

Second International Guidelines for the Diagnosis and Management of Hereditary Hemorrhagic Telangiectasia

The goal of the Second International HHT Guidelines process was to develop evidence-based consensus guidelines for the management and prevention of HHT-related symptoms and complications. The expert panel generated and approved new recommendations. With regard to diagnosis, the following was recommended:

The expert panel recommends that clinicians refer patients for diagnostic genetic testing for HHT (page 992):

- to identify the causative mutation in a family with clinically confirmed HHT;
- to establish a diagnosis in relatives of a person with a known causative mutation, including:
 - individuals who are asymptomatic or minimally symptomatic and
 - individuals who desire prenatal testing; and
- to assist in establishing a diagnosis of HHT in individuals who do not meet clinical diagnostic criteria.

The expert panel recommends that for individuals who test negative for *ENG* and *ACVRL1* coding sequence mutations, *SMAD4* testing should be considered to identify the causative mutation.

GeneReviews: Hereditary Hemorrhagic Telangiectasia

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

Diagnostic testing for HHT is recommended when the following clinical findings are seen:

- Spontaneous and recurrent nosebleeds (epistaxis).
 - With night-time nosebleeds heightening the concern for HHT.
- Multiple telangiectases at characteristic sites.
 - Lips, oral cavity, fingers, and nose
- Visceral arteriovenous malformation (AVM).
 - Typically pulmonary, cerebral, hepatic, spinal, gastrointestinal, or pancreatic. AVMs outside these locations are uncommon and not suggestive of HHT.
- Family history. A first-degree relative in whom HHT has been diagnosed according to these Curaçao criteria.

Dean Health Plan Coverage Policy

- The clinical diagnosis of HHT can be established in a proband using the Curaçao criteria, which requires three or more of the above suggestive findings, or the molecular diagnosis can be established in a proband with suggestive findings and a heterozygous pathogenic variant in one of the highly associated genes.

GeneReviews also states that concurrent gene testing can be considered using an HHT multigene panel that includes *ACVRL1*, *ENG*, *SMAD4*, and other genes of interest.

[back to top](#)

DEFINITIONS

1. **Close relatives** include first, second, and third degree blood relatives:
 - a. **First-degree relatives** are parents, siblings, and children
 - b. **Second-degree relatives** are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half siblings
 - c. **Third-degree relatives** are great grandparents, great aunts, great uncles, great grandchildren, and first cousins
2. **Phenocopy** is a trait or disease that resembles the trait expressed by a certain genotype, but in an individual that is not a carrier of that genotype
3. **Premature coronary artery disease (CAD)** is defined as male subjects at or under 55 years of age, female subjects at or under 65 years of age; adapted from the American Heart Association phenotype definition of HeFH (Sturm, et al).
4. **Sudden cardiac arrest** is defined as “the sudden cessation of cardiac activity so that the victim becomes unresponsive, with no normal breathing and no signs of circulation. If corrective measures are not taken rapidly, this condition progresses to sudden death. Cardiac arrest should be used to signify an event as described above, that is reversed, usually by CPR and/or defibrillation or cardioversion, or cardiac pacing” (Buxton, et al).
5. **Sudden cardiac death (SCD)** is death due to a cardiovascular cause that occurs within one hour of the onset of symptoms
6. **Sudden unexplained death (SUD)** (also known as Sudden unexplained death syndrome or SUDS) refers to a sudden cardiac death that occurs in an apparently healthy and often young individual within an hour of the onset of symptoms and for no apparent reason
7. **Type A aortic dissection** occurs at the ascending part of the aorta, just as it branches off of the heart
8. **Type B aortic dissection** occurs at the descending part of the aorta, and may extend into the abdomen

[back to top](#)

Dean Health Plan Coverage Policy

REFERENCES

1. Hershberger RE, Givertz MM, Ho CY, et al. Genetic Evaluation of Cardiomyopathy-A Heart Failure Society of America Practice Guideline. *J Card Fail*. 2018;24(5):281-302. doi:10.1016/j.cardfail.2018.03.004
2. Gersh BJ, Maron BJ, Bonow RO, et al. 2011 ACCF/AHA guideline for the diagnosis and treatment of hypertrophic cardiomyopathy: a report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines. *Circulation*. 2011;124(24):e783-e831. doi:10.1161/CIR.0b013e318223e2bd
3. Ackerman MJ, Priori SG, Willems S, et al. HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies this document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA). *Heart Rhythm*. 2011;8(8):1308-1339. doi:10.1016/j.hrthm.2011.05.020
4. Hershberger RE, Givertz MM, Ho CY, et al. Genetic evaluation of cardiomyopathy: a clinical practice resource of the American College of Medical Genetics and Genomics (ACMG) [originally accepted 2018, published correction appears in *Genet Med*. 2019 Oct;21(10):2406-2409]. *Genet Med*. 2018;20(9):899-909. doi:10.1038/s41436-018-0039-z
5. Stiles MK, Wilde AAM, Abrams DJ, et al. 2020 APHRS/HRS Expert Consensus Statement on the Investigation of Decedents with Sudden Unexplained Death and Patients with Sudden Cardiac Arrest, and of Their Families [published online ahead of print, 2020 Oct 13]. *Heart Rhythm*. 2020;S1547-5271(20)30953-X. doi:10.1016/j.hrthm.2020.10.010
6. Pierpont ME, Brueckner M, Chung WK, et al. Genetic Basis for Congenital Heart Disease: Revisited: A Scientific Statement From the American Heart Association [published correction appears in *Circulation*. 2018 Nov 20;138(21):e713]. *Circulation*. 2018;138(21):e653-e711. doi:10.1161/CIR.0000000000000606
7. Ommen SR, Mital S, Burke MA, et al. 2020 AHA/ACC Guideline for the Diagnosis and Treatment of Patients With Hypertrophic Cardiomyopathy: A Report of the American College of Cardiology/American Heart Association Joint Committee on Clinical Practice Guidelines. *J Am Coll Cardiol*. 2020;76(25):e159-e240. doi:10.1016/j.jacc.2020.08.045
8. Musunuru K, Hershberger RE, Day SM, Klindinst NJ, Landstrom AP, Parikh VN, Prakash S, Semsarian C, Sturm AC; American Heart Association Council on Genomic and Precision Medicine; Council on Arteriosclerosis, Thrombosis and Vascular Biology; Council on Cardiovascular and Stroke Nursing; and Council on Clinical Cardiology. Genetic Testing for Inherited Cardiovascular Diseases: A Scientific Statement From the American Heart Association. *Circ Genom Precis Med*. 2020 Aug;13(4):e000067. doi: 10.1161/HCG.000000000000067. Epub 2020 Jul 23. PMID: 32698598.
9. Schwartz PJ, Crotti L. QTc behavior during exercise and genetic testing for the long-QT syndrome. *Circulation*. 2011 Nov 15;124(20):2181-4. doi: 10.1161/CIRCULATIONAHA.111.062182. PMID: 22083145
10. Hershberger, R and Jordan, E. Dilated Cardiomyopathy Overview. 2007 Jul 27 [Updated 2022 Apr 7]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2024. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1309/>
11. Wilde AAM, Semsarian C, Márquez MF, et al. European Heart Rhythm Association/Heart Rhythm Society/Asia Pacific Heart Rhythm Society/Latin American Heart Rhythm Society expert consensus statement on the state of genetic testing for cardiac diseases. [published correction appears in *Europace*. 2022 Aug 30]. *Europace*. 2022;24(8):1307-1367. doi:10.1093/europace/euac030

Dean Health Plan Coverage Policy

12. Priori SG, Wilde AA, Horie M, et al. HRS/EHRA/APHRS expert consensus statement on the diagnosis and management of patients with inherited primary arrhythmia syndromes. *Heart Rhythm*. 2013;10(12):1932-1963.
13. Brugada R, Campuzano O, Sarquella-Brugada G, et al. Brugada Syndrome. 2005 Mar 31 [Updated 2022 Aug 25]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2024. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1517/>
14. Napolitano C, Mazzanti A, Bloise R, and Priori S. et al. Catecholaminergic Polymorphic Ventricular Tachycardia. 2004 Oct 14 [Updated 2022 Jun 23]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2024. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1289/>
15. 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;16(11):e301-e372.
16. Sturm, A, Knowles, J, Gidding, S. et al. Clinical Genetic Testing for Familial Hypercholesterolemia: JACC Scientific Expert Panel. *J Am Coll Cardiol*. 2018 Aug, 72 (6) 662–680. <https://doi.org/10.1016/j.jacc.2018.05.044>
17. Pyeritz RE; American College of Medical Genetics and Genomics. Evaluation of the adolescent or adult with some features of Marfan syndrome. *Genet Med*. 2012;14(1):171-177. doi:10.1038/gim.2011.48
18. Milewicz DM, Checchi AC. Heritable Thoracic Aortic Disease Overview. 2003 Feb 13 [Updated 2023 May 4]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2024. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1120/>
19. Isselbacher EM, Preventza O, Hamilton Black J 3rd, et al. 2022 ACC/AHA Guideline for the Diagnosis and Management of Aortic Disease: A Report of the American Heart Association/American College of Cardiology Joint Committee on Clinical Practice Guidelines. *Circulation*. 2022;146(24):e334-e482.
20. McDonald J, Pyeritz RE. Hereditary Hemorrhagic Telangiectasia. 2000 Jun 26 [Updated 2021 Nov 24]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2024. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK1351/>
21. Faughnan ME, Mager JJ, Hetts SW, et al. Second International Guidelines for the Diagnosis and Management of Hereditary Hemorrhagic Telangiectasia [published online ahead of print, 2020 Sep 8]. *Ann Intern Med*. 2020;10.7326/M20-1443. doi:10.7326/M20-1443

[back to top](#)

Note: The Health Plan uses the genetic testing clinical criteria developed by Concert Genetics, an industry-leader in genetic testing technology assessment and policy development.

Dean Health Plan Coverage Policy

	Committee/Source	Date(s)
Document Created:	Medical Policy Committee/Health Services Division	November 16, 2022
Revised:	Medical Policy Committee/Health Services Division	February 15, 2023
	Medical Policy Committee/Health Services Division	March 15, 2023
	Medical Policy Committee/Health Services Division	August 16, 2023
	Medical Policy Committee/Health Services Division	March 20, 2024
Reviewed:	Medical Policy Committee/Health Services Division	February 15, 2023
	Medical Policy Committee/Health Services Division	March 15, 2023
	Medical Policy Committee/Health Services Division	August 16, 2023
	Medical Policy Committee/Health Services Division	March 20, 2024

Original Effective Date: 03/01/2023

Re-Review Date(s): 12/19/2024- Concert Genetics Effective Date: January 01, 2025 (V.1.2025)

06/18/2025 Concert Genetics Effective Date: July 01, 2025 (V.2.2025)

Administrative Update:

© 2023-2025 Dean Health Plan.