Helix Hypertrophic Cardiomyopathy Panel

Item	Description
Test Name	Helix Hypertrophic Cardiomyopathy Panel
Test Type	Cardio
Catalog Number	HCMM1
Procedure Code	81860-9 (LOINC)
Test Description	This panel evaluates 48 genes associated with hereditary forms of hypertrophic cardiomyopathy.
Genes Tested	*ACAD9, ACADVL, ACTC1, ACTN2, AGL, ALPK3, BRAF, CPT2, CSRP3, ELAC2, FHL1, FLNC, GAA, GLA, HRAS, JPH2, KRAS, LAMP2, LZTR1, MAP2K1, MAP2K2, MRAS, MTO1, MYBPC3, MYH7, MYL2, MYL3, NEXN, NRAS, PLN, PPA2, PRKAG2, PTPN11, RAF1, RIT1, SHOC2, SLC22A5, SOS1, SOS2, TCAP, TMEM70, TNNC1, TNNI3, TNNT2, TPM1, TRIM63, TTR, and VCL*
Genetics Information	This test utilizes next-generation sequencing to detect single nucleotide variants, insertions and deletions up to 20 bp, and copy number variants in genes associated with hereditary forms of hypertrophic cardiomyopathy.
Indications For Testing	A personal or family history suggestive of a hereditary form of hypertrophic cardiomyopathy.
Clinical Descriptions	Cardiomyopathies are a broad spectrum of structural and functional disorders of the heart musculature. There are many different causes of cardiomyopathies, which range from environmental exposures to inherited genetic risk factors. In cases where an external cause is not identified, and/or a family history is suspicious for hereditary risk, diagnostic genetic testing may be indicated. Hypertrophic Cardiomyopathy (HCM) is a condition in which the heart muscle becomes abnormally thick. This leads to a decrease in the heart's ability to pump blood effectively. This can cause fatigue, shortness of breath, swelling of the legs, heart rhythm abnormalities and, in severe cases, heart failure or sudden cardiac arrest. It is important to note that in some cases HCM may be a feature of a syndromic condition with other extracardiac findings. Hereditary forms of HCM may follow autosomal dominant, autosomal recessive, X-linked, or mitochondrial inheritance patterns. This panel does not assess mitochondrial causes of HCM. Note that some of these genes may also be associated with other unrelated conditions; this means that when undergoing this test, there is a possibility of incidentally detecting carrier status for, or predisposition to, one of these unrelated conditions.
Conditions	Hypertrophic cardiomyopathy (HCM)
Interpretation	All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

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Reclassification Of Variants	Helix does not systematically review their variant database looking for classification changes. Helix will review the classification of previously reported variants upon request of the ordering physician/provider. Ordering physicians/providers may contact Helix Customer Support or their Dedicated Advisor and request a review of the variant classification to be performed. At the discretion of the laboratory director, the frequency of reclassification requests may be limited to once per year, no earlier than 12 months after initial variant interpretation has been performed.
Variant Evaluation	Variant classification is performed using the guidelines set forth by the American College of Medical Genetics and Genomics and the Association for Molecular Pathology, with modifications as suggested by domain specific Expert Panels of the Clinical genome Resource (ClinGen) when available. Variant pathogenicity is categorized as benign, likely benign, variant of uncertain significance (VUS), likely pathogenic, or pathogenic.
Turnaround Time	7 to 24 days
Available In NY State	No
Test Classification	This test was developed, and its performance characteristics determined, by Helix, Inc. in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.
Performing Laboratory Information	CLIA Laboratory Number: 05D2117342 Laboratory Hours of Operation: Monday-Saturday (7AM-10:30PM PST) Address: 10170 Sorrento Valley Road, Suite 100, San Diego, CA 92121 Helix Customer Service: (844) 211-2070 Email: support@helix.com
Regulatory Information	CLIA Complexity: High Test Classification: Non-Waived/ Laboratory Developed Test
CLIA Category	Chemistry / Routine Chemistry

Methods & Limitations for Helix Hypertrophic Cardiomyopathy Panel

Extracted DNA is enriched for targeted regions and then sequenced using the Helix Exome+ (R) assay on an Illumina DNA sequencing system. Data is then aligned to a modified version of GRCh38 and all genes are analyzed using the MANE transcript and MANE Plus Clinical transcript, when available. Small variant calling is completed using a customized version of Sentieon's DNAseq software, augmented by a proprietary small variant caller for difficult variants. Copy number variants (CNVs) are then called using a proprietary bioinformatics pipeline based on depth analysis with a comparison to similarly sequenced samples. Interpretation is based upon guidelines published by the American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP) or their modification by ClinGen Variant Curation Expert Panels when available. Interpretation is limited to the transcripts indicated on the report, +/- 10 bp into intronic regions, except as noted below. Helix variant classifications include pathogenic, likely pathogenic, variant of uncertain significance (VUS), likely benign, and benign. Variants classified as pathogenic, likely pathogenic, or VUS are included in the report. All reported variants (except for VUSs with limited evidence of pathogenicity) are confirmed through secondary manual inspection of DNA sequence data or orthogonal testing. Benign and likely benign variants are not reported but are available upon request. Risk estimations and management guidelines included in this report are based on analysis of primary literature and recommendations of applicable professional societies, and should be regarded as approximations.

Based on validation studies, this assay delivers > 99% sensitivity and specificity for single nucleotide variants and insertions and deletions (indels) up to 20 bp. Larger indels and complex variants are also reported but sensitivity may be reduced. Based on validation studies, this assay delivers > 99% sensitivity to multi-exon CNVs and > 90% sensitivity to single-exon CNVs. This test may not detect variants in challenging regions (such as short tandem repeats, homopolymer runs, and segment duplications), sub-exonic CNVs, chromosomal aneuploidy, or variants in the presence of mosaicism. Phasing will be attempted and reported, when possible. Structural rearrangements such as inversions, translocations, and gene conversions are not tested in this assay unless explicitly indicated. Additionally, deep intronic, promoter, and enhancer regions may not be covered. It is important to note that this assay cannot detect all variants known to increase disease risk, and that a negative result does not guarantee that the tested individual does not carry a rare, undetectable variant in genes analyzed. Any potential incidental findings outside of these genes and conditions will not be identified, nor reported. The results of a genetic test may be influenced by various factors, including bone marrow transplantation, blood transfusions, or in rare cases, hematolymphoid neoplasms.

Gene Specific Notes:
AGL: Evaluation of chr1: 99916398 (c.4260-12A>G) will be performed. *ALPK3*: Sensitivity in exon 1 may be reduced. *BRAF*: Sensitivity in exon 1 may be reduced. *GAA*: Evaluation of chr17:80104542 (c.-32-13T>G), chr17:80104552 (c.-32-3C>A), chr17:80104554 (c.-32-1G>C), and chr17:80108467 (c.1076-22T>G) will be performed. *GLA*: Evaluation of chrX: 101399747 (c.640-801G>A) will be performed. *MAP2K2*: Sensitivity in exon 1 may be reduced. *MYBPC3*: Evaluation of chr11:47332275-47332299 (c.3628-41_2628-17del25), chr11:47347065 (c.906-36G>A), chr11:47346372 (c.927-2A>G), chr11:47343281 (c.1224-19G>A), chr11:47343314 (c.1224-52G>A), chr11:47343158 (c.1227-13G>A), and chr11:47340403 (c.1927+600C>T) will be performed. *PRKAG2*: Sensitivity in exon 5 may be reduced. *SLC22A5*: Evaluation of chr5:132369824 (c.-149G>A), chr5:132378362 (c.394-16T>A), and chr5:132386973 (c.825-52G>A) will be performed. SOS2: Sensitivity in exon 1 may be reduced.

Disclaimer:
This test was developed and validated by Helix, Inc. This test has not been cleared or approved by the United States Food and Drug Administration (FDA). The Helix laboratory is accredited by the College of American Pathologists (CAP) and certified under the Clinical Laboratory Improvement Amendments (CLIA #: 05D2117342) to perform high-complexity clinical tests. This test is used for clinical purposes. It should not be regarded as investigational or for research.

Targeted Genes & Methodology for Helix Hypertrophic Cardiomyopathy Panel

The following applies to the Helix Hypertrophic Cardiomyopathy Panel. Testing is performed to evaluate for the presence of variants in coding regions and extending to +/- 10 base pairs of adjacent intronic sequence on either side of the coding exons of the genes analyzed. In addition, the analysis will cover select non-coding variants, as listed below. Next-generation sequencing is performed to test for the presence of small variants and copy number variants in the genes analyzed. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

This list is current from March 2024 to the present. This document is intended to highlight additional evaluations for variants of high clinical interest as well as technical limitations. For questions regarding genes, reference transcripts, or specific regions covered, contact Helix Customer Service at (844) 211-2070.

Genomic Build: GRCh38
Catalog Number: HCMM1

Gene	Transcript	Additional Evaluations	Technical Limitations
ACAD9	NM_014049.5	–	–
ACADVL	NM_000018.4	–	–
ACTC1	NM_005159.5	–	–
ACTN2	NM_001103.4	–	–
AGL	NM_000642.3	Chr1: 99916398 (c.4260-12A>G)	–
ALPK3	NM_020778.5	–	Sensitivity to ALPK3 exon1 may be reduced
BRAF	NM_004333.6; NM_001374258.1	–	Sensitivity to BRAF exon1 may be reduced
CPT2	NM_000098.3	–	–
CSRP3	NM_003476.5	–	–
ELAC2	NM_018127.7	–	–
FHL1	NM_001159699.2; NM_001159702.3	–	–
FLNC	NM_001458.5	–	–
GAA	NM_000152.5	Chr17:80104542 (c.-32-13T>G) Chr17:80104552 (c.-32-3C>A) Chr17:80104554 (c.-32-1G>C) Chr17:80108467 (c.1076-22T>G)	–
GLA	NM_000169.3	ChrX: 101399747 (c.640-801G>A)	–
HRAS	NM_005343.4; NM_176795.5	–	–
JPH2	NM_020433.5	–	–
KRAS	NM_004985.5; NM_033360.4	–	–

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Gene	Transcript	Additional Evaluations	Technical Limitations
LAMP2	NM_002294.3	–	–
LZTR1	NM_006767.4	–	–
MAP2K1	NM_002755.4	–	–
MAP2K2	NM_030662.4	–	Sensitivity to MAP2K2 exon 1 may be reduced
MRAS	NM_001085049.3	–	–
MTO1	NM_012123.4	–	–
MYBPC3	NM_000256.3	Chr11:47332275-47332299 (c.3628-41_2628-17del25) Chr11:47347065 (c.906-36G>A) Chr11:47346372 (c.927-2A>G) Chr11:47343281 (c.1224-19G>A) Chr11:47343314 (c.1224-52G>A) Chr11:47343158 (c.1227-13G>A) Chr11:47340403 (c.1927+600C>T)	–
MYH7	NM_000257.4	–	–
MYL2	NM_000432.4	–	–
MYL3	NM_000258.3	–	–
NEXN	NM_144573.4	–	–
NRAS	NM_002524.5	–	–
PLN	NM_002667.5	–	–
PPA2	NM_176869.3	–	–
PRKAG2	NM_016203.4	–	Sensitivity to PRKAG2 exon 5 may be reduced
PTPN11	NM_002834.5	–	–
RAF1	NM_002880.4	–	–
RIT1	NM_006912.6	–	–
SHOC2	NM_007373.4	–	–
SLC22A5	NM_003060.4	Chr5:132369824 (c.-149G>A) Chr5:132378362 (c.394-16T>A) Chr5:132386973 (c.825-52G>A)	–
SOS1	NM_005633.4	–	–
SOS2	NM_006939.4	–	Sensitivity to SOS2 exon 1 may be reduced
TCAP	NM_003673.4	–	–
TMEM70	NM_017866.6	–	–

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Gene	Transcript	Additional Evaluations	Technical Limitations
TNNC1	NM_003280.3	–	–
TNNI3	NM_000363.5	–	–
TNNT2	NM_001276345.2	–	–
TPM1	NM_001018005.2	–	–
TRIM63	NM_032588.4	–	–
TTR	NM_000371.4	–	–
VCL	NM_014000.3	–	–