Helix Familial Hypercholesterolemia (FH) Panel

Item	Description
Test Name	Helix Familial Hypercholesterolemia (FH) Panel
Test Type	Cardio
Catalog Number	FHCL1
Procedure Code	73748-6 (LOINC)
Test Description	This panel evaluates 4 genes that have an established, primary association with familial hypercholesterolemia.
Genes Tested	*APOB, LDLR, LDLRAP1, PCSK9*
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 Familial Hypercholesterolemia.
Indications For Testing	Providing a genetic evaluation for individuals with a A personal and/or family history suggestive of familial hypercholesterolemia. Establishing a diagnosis of familial hypercholesterolemia.
Clinical Descriptions	Dyslipidemias are a broad spectrum of disorders that affect blood (serum) levels of cholesterol and/or triglycerides. There are many different causes of dyslipidemias, which may range from environmental exposures to inherited genetic risk factors. In cases where an external cause is not identified, or a family history is suspicious of a hereditary dyslipidemia, diagnostic genetic testing may be ordered. A common dyslipidemia with known hereditary causes is familial hypercholesterolemia (FH). FH is characterized by elevated serum low-density lipoprotein cholesterol (LDL-C) which form plaques in the aorta and coronary arteries. Hereditary forms of FH may follow autosomal dominant or autosomal recessive inheritance patterns.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	Familial hypercholesterolemia In addition, one or more of the genes on this panel are associated with other conditions for which a predisposition to, or carrier status of, may incidentally be identified: Autosomal dominant familial hypobetalipoproteinemia (APOB)
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 Familial Hypercholesterolemia (FH) 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:
LDLR: Evaluation of Chr19: 11117009 (c.1845+11C>G), Chr19: 11089400 (c.-149C>A), Chr19: 11089414 (c.-135C>G), Chr19: 11089413 (c.-136C>T), and Chr19: 11110640 (c.941-12G>A) will be performed. *LDLRAP1*: Evaluation of Chr1: 25564565 (c748-608G>A) will be performed.

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 Familial Hypercholesterolemia (FH) Panel

The following applies to the Helix Familial Hypercholesterolemia (FH) 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 September 2023 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: FHCL1

Gene	Transcript	Additional Evaluations	Technical Limitations
APOB	NM_000384.3	–	–
LDLR	NM_000527.5	Chr19: 11117009 (c.1845+11C>G) Chr19: 11089400 (c.-149C>A) Chr19: 11089414 (c.-135C>G) Chr19: 11089413 (c.-136C>T) Chr19: 11110640 (c.941-12G>A)	–
LDLRAP1	NM_015627.3	Chr1: 25564565 (c748-608G>A)	–
PCSK9	NM_174936.4	–	–