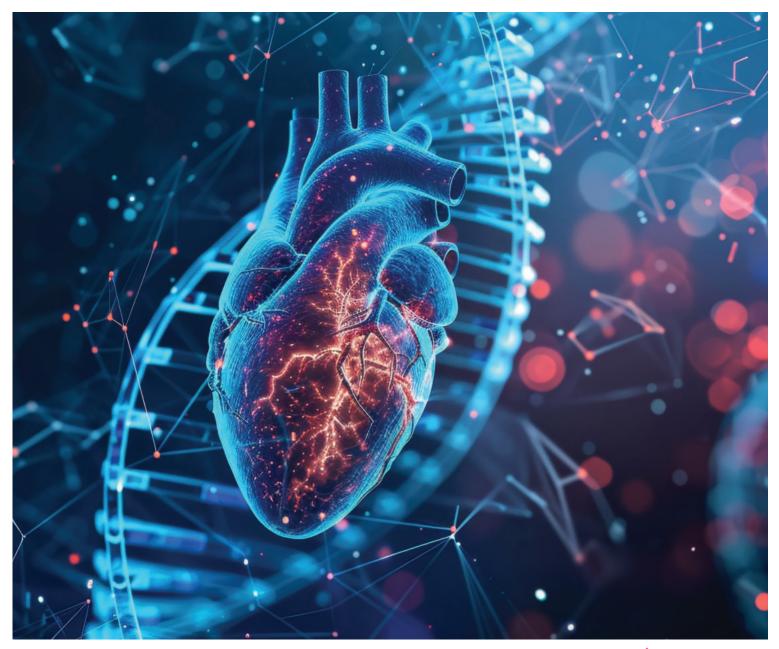


Microcen CARDIOGENETIC TESTING



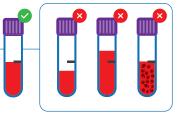


MicroceN Cardiogenetic Testing

Test code	Test Parameters	Method
GG1	MicroGen Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC) gene Panel	NGS
GG2	MicroGen Aorta gene Panel	NGS
GG3	MicroGen Arrhythmia gene Panel	NGS
GG4	MicroGen Atrial Fibrillation gene Panel	NGS
GG5	MicroGen Brugada Syndrome gene Panel	NGS
GG6	MicroGen Cardiac channelopathy gene panel	NGS
GG7	MicroGen Cardiomyopathy gene panel	NGS
GG8	MicroGen Cardiomyopathy predisposition - MYBPC3 (25bp deletion)	PCR
GG9	MicroGen Catecholaminergic Polymorphic Ventricular Tachycardia (CPVT) Panel	NGS
GG10	MicroGen Comprehensive Cardiology gene Panel	NGS
GG11	MicroGen Congenital Structural Heart Disease gene Panel	NGS
GG12	MicroGen Connective tissue disorder gene panel	NGS
GG13	MicroGen Coronary artery disease (CAD) Polygenic Risk Test	Microarray
GG14	MicroGen Cutis-laxa gene panel	NGS
GG15	MicroGen CYP2C19 Clopidogrel resistance (All CPIC alleles)	NGS
GG16	MicroGen Dilated Cardiomyopathy (DCM) gene Panel	NGS
GG17	MicroGen Ehler Danlos syndrome gene panel	NGS
GG18	MicroGen Ehlers-Danlos syndrome type VI (PLOD1) deletion/duplication analysis	MLPA
GG19	MicroGen Fibrodysplasia ossificans progressive (ACVR1) gene sequencing	NGS
GG20	MicroGen GDF1 and PKD1L1 gene sequencing	NGS
GG21	MicroGen Hereditary Hemorrhagic Telangiectasia (HHT) gene Panel	NGS
GG22	MicroGen Hereditary Transthyretin-mediated amyloidosis (hATTR amyloidosis) TTR gene analysis	NGS
GG23	MicroGen Heterotaxy and Situs Inversus gene Panel	NGS
GG24	MicroGen Hypercholesterolemia gene panel	NGS
GG25	MicroGen Hyperlipidemia gene Panel	NGS
GG26	MicroGen Hypertrophic Cardiomyopathy (HCM) gene Panel	NGS
GG27	MicroGen Left Ventricular Non-Compaction Cardiomyopathy (LVNC) gene Panel	NGS
GG28	MicroGen Liddle Syndrome gene Panel	NGS
GG29	MicroGen Long QT Syndrome (LQTS) gene Panel	NGS
GG30	MicroGen Marfan syndrome (FBN1) gene analysis	NGS
GG31	MicroGen Marfan Syndrome gene Panel	NGS
GG32	MicroGen Noonan and RASopathies gene panel	NGS
GG33	MicroGen Pulmonary Artery Hypertension (PAH) gene Panel	NGS
GG34	MicroGen Short QT Syndrome (SQTS) gene Panel	NGS
GG35	MicroGen SHOX deletion/duplication analysis	MLPA
GG36	MicroPlex Clopidogrel dosage CYP2C19*2 & CYP2C19*3	RTPCR
GG37	MicroPlex Statin induced myopathy predisposition SLCO1B1 p.(Val174Ala)	RTPCR
GG38	MicroPlex Tangier Disease (ABCA1) gene sequencing	NGS
GG39	MicroPlex Warfarin dosage-VKORC1 (c1639 G>A), CYP2C9*2,CYP2C9*3	RTPCR

Sample

EDTA Blood - 4 ml.



Method	TAT
NGS test	28 days
Rt. PCR	10 days
MLPA test	21 days

Required Family History.

Relevant clinical Information and symptoms.

Microgen CARDIOGENETIC TESTING

THE



CARDIOGENETIC TESTING

About the Test

Approximately 1 in 60 people have a hereditary cardiovascular condition. Heart disorders are often inherited and can affect individuals of any age, posing life-threatening risks. These conditions exhibit genetic heterogeneity, meaning that a single pathogenic variant in one gene can lead to various cardiac conditions (clinical heterogeneity), while mutations in different genes may result in similar cardiac phenotypes (genetic heterogeneity). Inheritance patterns can vary, with conditions transmitted in autosomal dominant, autosomal recessive, or X-linked manners, and some cardiomyopathies may follow a mitochondrial inheritance pattern. The significant genotypic and phenotypic diversity among heart disorders complicates diagnosis. For example, Marfan syndrome and Loeys-Dietz syndrome can present similarly, making clinical differentiation challenging. Given this complexity, genetic testing is an effective approach for accurately diagnosing these cardiac disorders.

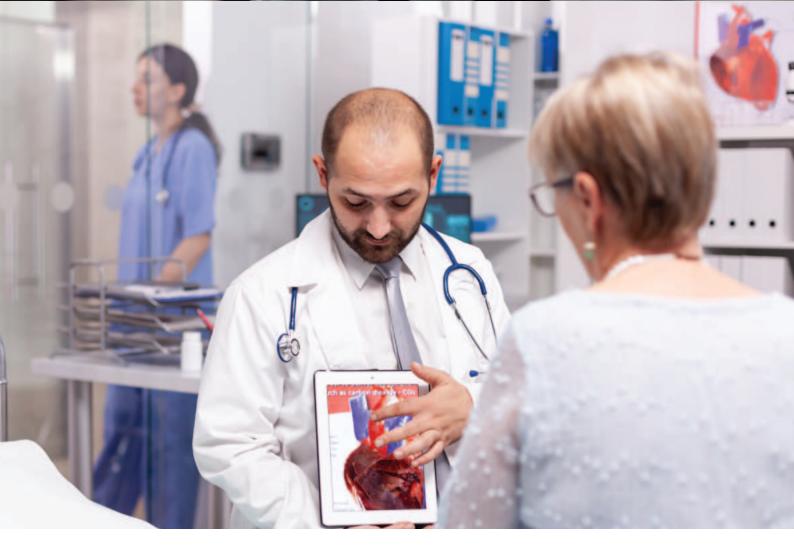
Enhancing Personalized Care

Genetic testing is rapidly becoming a mainstream practice in cardiology, endorsed by leading guidelines from the American Heart Association (AHA), Heart Rhythm Society-European Heart Rhythm Association (HRS-EH-RA), European Society of Cardiology (ESC), and Canadian Cardiovascular Society (CCS) (PMID: 32698598, 22075469, 20823110, 21810866, and 21459272). This approach not only enhances diagnosis and treatment but is also proven to be cost-effective compared to regular clinical screening (PMID: 22128210 and 21139095).

Understanding Inherited Cardiovascular Disorders

Inherited cardiovascular disorders are diverse and can affect the heart in various ways.

- Structural disorders, such as cardiomyopathies, alter the heart's structure and function.
- Nonstructural disorders, such as arrhythmias, affect the heart's electrical system.
- Isolated Conditions: Like familial thoracic aortic disease, which typically presents independently.
- Syndromic conditions, such as Marfan syndrome, are associated with other systemic features.



Importance of Genetic Diagnosis

- **Channelopathies:** Identifying genetic mutations helps guide lifestyle choices and medication selection. It is also crucial for deciding on the implantation of an implantable cardioverter-defibrillator (ICD), ensuring optimal patient care.
- Aortic Diseases: Knowing the specific genetic defect can determine the appropriate timing for surgical interventions, potentially saving lives and improving outcomes.
- Hypertrophic Cardiomyopathy (HCM): Genetic testing can differentiate classical sarcomere diseases from phenocopies such as Fabry disease and glycogen storage disease. This differentiation is essential for tailoring treatment strategies and follow-up care.



Family Member Risk Stratification

As many hereditary cardiovascular diseases are inherited in an autosomal dominant manner and carry a heightened risk for sudden cardiac death, genetic testing is vital for assessing family risk. Identifying at-risk family members allows for:

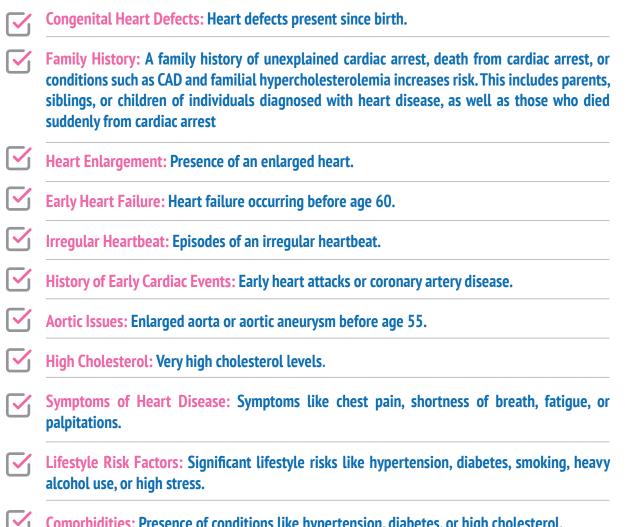
Preventive Measures: initiating early treatment or lifestyle modifications to mitigate risks.

Routine Follow-Ups: Justifying ongoing monitoring by healthcare professionals to ensure timely interventions.

Family planning and future generations: Genetic testing not only informs current health decisions but also plays a critical role in family planning. Understanding genetic risks can help families make informed choices about their future.

Lifestyle Recommendations: Genetic insights significantly influence lifestyle choices. For individuals with channelopathy and cardiomyopathy mutations, avoiding competitive sports and adhering to specific health guidelines can lead to better outcomes.

When to Consider Cardiogenetic Testing



Comorbidities: Presence of conditions like hypertension, diabetes, or high cholesterol.

Genetic testing is a cornerstone of personalized medicine for hereditary cardiovascular diseases. By providing essential insights into diagnosis, treatment, and family risk, it empowers patients and families to take proactive steps toward a healthier future.

Precision Diagnostics with MicroGen NGS Panels

Micro Health Laboratories (MHL) utilizes next-generation sequencing (NGS), a cutting-edge molecular genetics method, to analyze patient DNA for genetic variants. MicroGen NGS panels offer simultaneous analysis of a large number of genes, significantly increasing the chances of identifying the genetic cause of diseases with complex or non-specific symptoms. These panels reduce both the time and cost from symptom presentation to diagnosis and enhance diagnostic yield. Additionally, the results can provide information about recurrence risk (the likelihood of having another child with a similar condition) and may also benefit other family members.

MHL offers over 500+ NGS panels covering all medical specialties.

These panels are recommended for patients who meet any or multiple of the following criteria:

- Clinical features
- Family history of a particular disorder
- Multiple genes linked to the condition Well-defined disease-associated genes

(Reference: Genet Med 2015 Jun;17(6): 444-51.doi: 10.1038/gim.2014.122. Epub 2014 Sep 18

Comprehensive Analysis

Genetic variants, or changes in the DNA sequence, can be harmful and may cause serious medical conditions, particularly hereditary diseases originating in germ cells and present in all body cells.

Identifying these disease-causing variants is essential for accurate diagnosis, prognosis, and determining the most effective treatments for patients.

NGS enables the thorough analysis of thousands of clinically relevant target genes, providing results quickly enough to support timely clinical decisions. NGS can detect various types of DNA variants, including point mutations (nucleotide substitutions) and small insertions or deletions.

MHL uses targeted sequencing to identify both known variants linked to specific genetic disorders and novel variants in disease-associated genes.

Microcen Carrier Sequencing

For cases where the genetic cause is unknown, MHL offers the MicroGen Carrier Sequencing. This test covers all protein-coding regions, including the intron-exon boundary regions of approximately 23,000 genes, as well as mitochondrially encoded genes. The sequencing provides uniform coverage across the exome with a mean depth of over 80-100x, ensuring that more than 98% of targeted base pairs are covered at ≥10x. The MicroGen Carrier Seq enables the detailed detection and analysis of both single nucleotide variants (SNVs) and copy number variants (CNVs), with a sensitivity range of 75-99% for CNVs, depending on the length and zygosity of the deletion or duplication.

Adherence to **Best-Practice Guidelines**

The identified variants are reported following international best-practice guidelines, including those from the American College of Medical Genetics (ACMG) and Clinical Molecular Science Standards (CMSS).

Comprehensive Reporting

Each report includes a detailed description of the methods used, references to publications that support the medical and scientific findings, and recommendations for follow-up analyses for specific diseases. We provide thorough reporting of pathogenic variants, likely pathogenic variants, and variants of uncertain significance (VUS), ensuring that all clinically relevant information is communicated.

MHL provide high-quality sequencing and best-in-class data analysis - interpreted and communicated in comprehensive medical reports. Our multidisciplinary team of experts, including consultant geneticists, genetic counselors, genome analysts, and bioinformaticians, is involved in the interpretation and validation of genetic variants, ensuring the highest standards of accuracy and reliability. Our experienced professionals meticulously interpret genomic data, providing clear and actionable results. This integrated approach ensures that every analysis is conducted with precision, offering clear insights and recommendations for patient care.

Medical Genetic Counselling

MHL offer expert medical genetic counseling as an integral part of the genetic testing journey. Genetic counseling is a communicative process designed to support patients and their families both before and after genetic testing. This service is educational, impartial, and nondirective. Before any genetic test is conducted, genetic counselors gather a detailed family history, explain the testing methods to be used, and discuss the risks, benefits, limitations, and implications of a potential genetic diagnosis

After receiving genetic test results, genetic counseling assists both the specialist physician and the patient in interpreting the findings. Patients are informed about the potential consequences of the results, including the likelihood of developing the genetic disorder, the risk of passing it on to future children, and strategies to prevent, reduce, or manage these risks. Our goal in providing counseling is to equip patients with a deeper understanding of their results, enabling them to make more informed decisions regarding their health and future.

Reference: Nat Rev Genet. 2018 Dec;19(12):735-736. doi: 10.1038/s41576-018-0057-3. Ann Lab Med. 2018 Jul;38(4):291-295. doi: 10.3343/alm.2018.38.4.291.

For more information on **MicroGen NGS panels** and their benefits, **Please contact us**

Limitations

Genetic testing plays a crucial role in the diagnostic process, but it doesn't always provide a clear answer. In some cases, a genetic variant may exist but not be identified due to limitations in current medical knowledge or testing technology. Accurate interpretation of test results may also depend on understanding the true biological relationships within a family. Failing to disclose these relationships accurately may lead to incorrect interpretations, misdiagnoses, or inconclusive test outcomes.

Contextual Interpretation: It's important to consider that test results are interpreted in the context of clinical findings, family history, and other laboratory data. Genetic testing only reports variations in genes potentially related to the proband's medical condition. Rare polymorphisms can result in false negative or positive results, and misinterpretation may occur if the provided information is inaccurate or incomplete.

Detection Limitations: Certain events, such as CNVs (detection range 75-99%), translocations, repeat expansions, and chromosomal rearrangements, may not be reliably detected by MicroGen Panel testing. Additionally, variants in untranslated regions, promoters, and intronic regions are not assessed using this method. Deep intronic variants are not assessed by this method.

Accuracy Considerations: While genetic testing is highly accurate, rare instances of inaccurate results may occur due to various factors. These factors may include mislabeled samples, incorrect clinical or medical information, rare technical errors, or unusual circumstances such as bone marrow transplantation, blood transfusion, or mosaicism (where a genetic change is present in only a small percentage of cells, making it undetectable by the test).

Variant Annotation Discrepancies: The population allele frequencies and in silico predictions for the GRCh38 version of the human genome are obtained by lifting over the coordinates from the hg19 genome build. Since existing population allele frequencies (e.g., 1000 Genomes, ExAC, gnomAD-Exome) are available only for the hg19 genome version, some discrepancies in variant annotation may occur due to complex changes in certain regions of the genome.

