

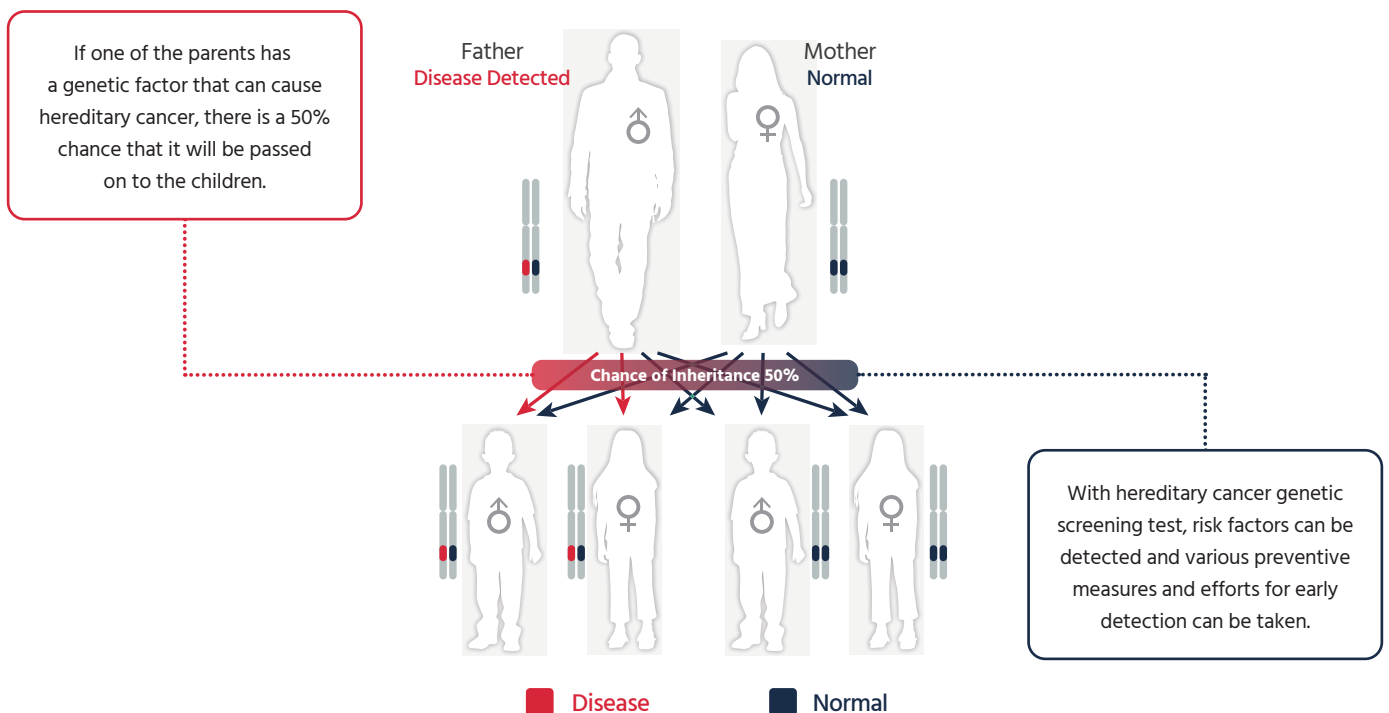
What is Genome Screen?

Cancer Genome Screen	34 genes	Screens 24 types of cancers including breast, colorectal cancer etc.
Stroke Genome Screen	34 genes	Screens 23 types of diseases and predict the risk associated with diseases
Hyperlipidemia Genome Screen	31 genes	Screens 12 types of diseases and predict the risk associated with diseases
Sudden Cardiac Arrest Genome Screen	40 genes	Screens 15 types of diseases including hereditary arrhythmia

Genome Screen is a premium test that analyzes the **entire region of the representative** genes related to the onset of diseases using **NGS** method and provides customized medical guidelines according to the results.

This test reports pathogenic variant and likely pathogenic variant which is highly likely to be associated with a disease.

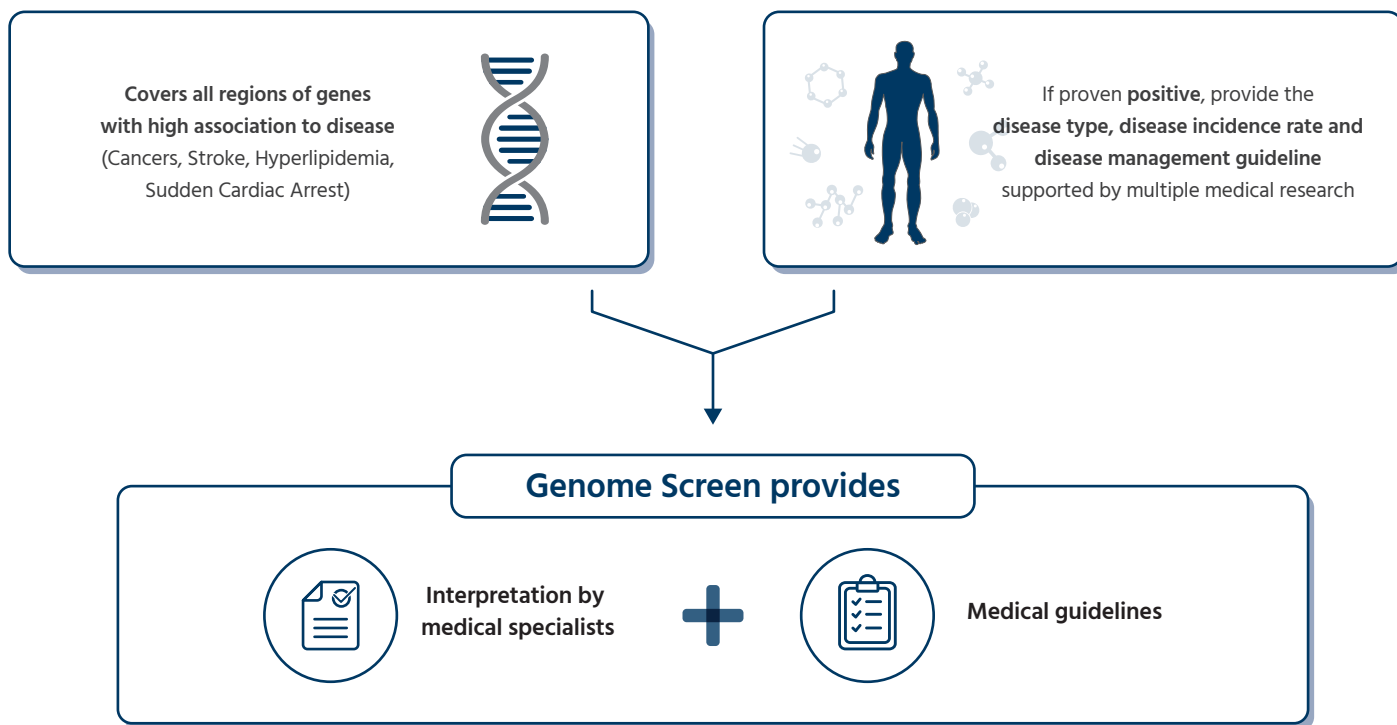
Risk of Hereditary Diseases



Genetic variants that influence diseases can be inherited by your children.

By identifying genetic variations closely associated with disease onset, you can take **preventive measures to protect your family from diseases.**

Test of Whole exome of the genes closely related to disease



Service features

Test & Code	Cancer Genome Screen (ON090), Stroke Genome Screen (ON087), Hyperlipidemia Genome Screen (ON088), Sudden Cardiac Arrest Genome Screen (ON089)		
Specimen	EDTA WB 3 ml	TAT	14 days * Cancer : 12 days
Method	NGS (Next Generation Sequencing)	Sample Storage	Room temperature (Refrigerated is recommended.)
Test description	This test analyzes the whole region on the genes that are highly correlated to the disease such as Cancer, Stroke, Hyperlipidemia, and Sudden Cardiac Arrest.		
Caution & Limitation	<ul style="list-style-type: none"> Genetic variant is divided into pathogenic variant (PV), likely pathogenic variant (LPV), variant of unknown significance (VUS), likely benign variant (LBV), and benign variant (BV), according to 2015 ACMG/AMP. This test reports pathogenic variant (PV) and likely pathogenic variant (LPV) which is highly associated with the disease. The genes included in the test include the entire exon, but in some areas sequencing may not be sufficiently covered. In addition, if a highly homologous sequence exists, the sequencing of the base may not be accurate, and variations in large deletions or duplications or non-protein-coding sequence areas may be difficult to detect. Even if a pathogenic variant is found in disease-related genes, it does not guarantee a 100% occurrence of the disease. The timing and clinical manifestation of disease onset can vary among individuals. Even if no pathogenic variant associated with the disease is found, there is still a possibility of disease occurrence due to non-genetic factors such as environmental influences and lifestyle habits. 		