Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen				
	Institution		Sample ID	
	Name		Medical record No.	
	Age / Sex		Accepted	
	Sample type		Reported	

The test result of

Test Description

This is a brief description of hyperlipidemia genome screening.

This test, being the latest gene analysis technique, analyzes genes that can cause hyperlipidemia and the results of existing research papers to provide personalized information to help people manage their health. Even if any pathogenic variant (PV) associated with hereditary hyperlipidemia is found, individuals may have no symptoms(reduced penetrance). However, such individual may have higher risk of hyperlipidemia compared to the general population, measures to reduce the hyperlipidemia risk and regular thorough examinations for early detection are recommended.

Summary of Test Results

Pathogenic Variant (PV) in ABCG5 gene related to Sitosterolemia was detected.

Gene	DNA Change	Predicted AA change	Zygosity	Class
ABCG5	c.751C>T	p.(Gln251Ter)	Het	PV
ABCG5	c.315C>G	p.(Arg105=)	Het	PV

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Interpretation

A pathogenic variant (PV) and a variant of uncertain significance (VUS) in the ABCG5 gene were detected.

The ABCG5 c.751C>T (p.Gln251Ter) variant has been reported in patients with sitosterolemia (PMID: 28521186, 32166861) and has been classified as a deleterious mutation in HGMD (Accession No: CM178558).

The ABCG5 c.315C>G p.(Arg105=) variant has not been reported in the population database (gnomAD) as well as mutation databases (ClinVar and HGMD). Although this is a synonymous variant that does not change amino acid residue, it is uncertain whether it has an aberrant splicing effect or not.

The ABCG5 gene encodes sterolin-1, which makes up half of a protein called sterolin. Sterolin is involved in eliminating plant sterols, which are fatty components of plant-based foods that cannot be used by human cells.

PVs in ABCG5 are known to cause sitosterolemia, which is a condition in which fatty substances (lipids) from plant sterols (or phytosterols) such as vegetable oils, nuts, and other plant-based foods accumulate in the blood and tissues. Clinical features of sitosterolemia include elevated blood cholesterol level, xanthomas, joint stiffness, etc.

Clinical correlation and family testing are recommended.

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Relevant Disease Information

Disease	Test guidebook
Sitosterolemia	**03.Prevention and Treatment page7~9**

Sitosterolemia is a disease caused by excessive absorption and accumulation of plant sterols ingested as food. Vegetable sterols, which are rich in olive oil, vegetable oils and nuts, are poorly absorbed and are excreted back even when consumed in large quantity, and are known to be good food for hyperlipidemia by suppressing the absorption of cholesterol. However, in patients with sitosterolemia, all of the plant sterols contained in these foods are absorbed and accumulate in the blood vessels and then can cause vascular sclerosis. Some patients may have hyperlipidemia, but in some cases, cholesterol levels are almost normal, however xanthoma may appear on the skin and sudden symptoms of cardiovascular disease as angina pectoris can occur. Overseas, patients who have sudden death by myocardial infarction at a young age may be diagnosed with sitosterolemia after death.

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The test result of

The result details and related diseases

* Hypercholesterolemia

Dyslipidemia with elevated cholesterol levels in the blood caused by abnormal cholesterol metabolism.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Familial Hypercholesterolemia	APOB	☐	☑
	APOA2	☐	☑
	LDLR	☐	☑
	LDLRAP1	☐	☑
	PCSK9	☐	☑
	STAP1	☐	☑
Cerebrotendinous xanthomatosis	CYP27A1	☐	☑
Sitosterolemia	ABCG5	☑	☐
	ABCG8	☐	☑
Hyperalphalipoproteinemia	APOC3	☐	☑
	CETP	☐	☑
	SCARB1	☐	☑

* Medication fitness

Related to the metabolism of drugs to treat hyperlipidemia.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Statin response	SLCO1B1	☐	☑

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The test result of

The result details and related diseases

* Lipoprotein deficiency

Dyslipidemia caused by deficiency of lipoprotein due to abnormality in the formation of lipoprotein, which transports cholesterol and lipids for energy metabolism.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Hypobetalipoproteinemia	MTTP	☐	☑
	APOB	☐	☑
	SAR1B	☐	☑
	ANGPTL3	☐	☑
Hypoalphalipoproteinemia	ABCA1	☐	☑
	APOA1	☐	☑
	LCAT	☐	☑

* Combined dyslipidemia

Dyslipidemia which increases cholesterol and triglyceride levels in blood due to abnormality in the process of forming lipoprotein.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Dysbetalipoproteinemia	APOE	☐	☑
Combined hyperlipidemia	LPL	☐	☑
	LIPA	☐	☑
	LIPC	☐	☑

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The test result of

The result details and related diseases

* Hypertriglyceridemia

Dyslipidemia which increases triglyceride levels in the blood due to abnormality in the triglyceride metabolism.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Familial lipoprotein lipase deficiency	APOC2	☐	☑
	APOA5	☐	☑
	GPIHBP1	☐	☑
	LMF1	☐	☑
	LPL	☐	☑
Hypertriglyceridemia	CREB3L3	☐	☑
	CYP7A1	☐	☑
	GPD1	☐	☑
	GPIHBP1	☐	☑
Alstrom syndrome	ALMS1	☐	☑

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What is Hyperlipidemia Genome Screen?

Hyperlipidemia or dyslipidemia is out of normal range of lipid levels in the blood that increases the risk of complications such as coronary artery disease and cerebrovascular disease. Major risk factors for hyperlipidemia or dyslipidemia are known as obesity, diabetes, drinking and smoking, and genetic factors are also involved here. Hyperlipidemia or dyslipidemia due to genetic factors as familial hypercholesterolemia and familial hypertriglyceridemia may cause symptoms of xanthoma, xanthelasma, hepatomegaly and nephromegaly. Hyperlipidemia or dyslipidemia is associated with various circulatory system as well as cardiovascular diseases as atherosclerosis, and therefore requires a more comprehensive assessment than a basic evaluation. Hyperlipidemia Genome Screen is a test that can be expected to prevent, diagnose early, and improve the treatment effects regarding hereditary hyperlipidemia or dyslipidemia by examining 31 genes known to increase the risk of developing hereditary hyperlipidemia or dyslipidemia with NGS test.

Hereditary hyperlipidemia have these characteristics.

- Even if pathogenic variant (PV) is found in genes related to hereditary hyperlipidemia or dyslipidemia, disease does not occur 100% (Reduced Penetrance). The time of onset and clinical patterns of diseases vary widely from person to person.
- Hereditary hyperlipidemia or hereditary dyslipidemia included in this test may be associated various clinical manifestations and diseases as well as hyperlipidemia or dyslipidemia.
- Hereditary hyperlipidemia or hereditary dyslipidemia included in this test may be associated with hyperlipidemia or dyslipidemia as well as various other clinical manifestations and diseases.
- Even if genetic testing related to hereditary hyperlipidemia or dyslipidemia does not identify any disease-related PV, there is still a possibility of hyperlipidemia or dyslipidemia occurrence due to non-hereditary causes such as environmental effects and lifestyle.

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Disease-associated Genes

Hyperlipidemia genome screen tests following diseases and genes.

Diseases		Gene
Hypercholesterolemia	Familial Hypercholesterolemia	APOB
		APOA2
		LDLR
		LDLRAP1
		PCSK9
		STAP1
	Cerebrotendinous xanthomatosis	CYP27A1
	Sitosterolemia	ABCG5
		ABCG8
	Hyperalphalipoproteinemia	APOC3
		CETP
		SCARB1
Medication fitness	Statin response	SLCO1B1
Lipoprotein deficiency	Hypobetalipoproteinemia -Abetalipoproteinemia(ABL) -Chylomicron retention disease(CMRD)	MTTP
		APOB
		SAR1B
		ANGPTL3
	Hypoalphalipoproteinemia (Familial HDL deficiency)	ABCA1
		APOA1
		LCAT
Combined dyslipidemia	Dysbetalipoproteinemia -Hyperlipoproteinemia type 3	APOE
	Combined hyperlipidemia	LPL
		LIPA
		LIPC
Hypertriglyceridemia	Familial lipoprotein lipase deficiency	APOC2
		APOA5
		GPIHBP1
		LMF1
		LPL
	Hypertriglyceridemia	CREB3L3
		CYP7A1
		GPD1
		GPIHBP1
	Alstrom syndrome	ALMS1

Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen	Institution		Sample ID	
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Test Information and Limitations

- Genetic variation is divided into five categories, 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.
- The disease relevance of sequence variation according to 2015 ACMG/AMP guidelines is analyzed by a specialist in the department of laboratory medicine, combining various evidences such as allele frequency in population databases, frequency, function analysis and computer prediction, and papers and mutation databases. However, the interpretation of the variation could be changed as additional evidence builds up after the results are reported.
- In this test, it is a rule to report mainly pathogenic variant and likely pathogenic variant, which have high or very high disease relevance, and not to report variant of unknown significance, likely benign variant , and benign variant.
- 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.

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Test Information

Specimen	Peripheral Blood Leukocytes
Method	Next-Generation Sequencing; NGS

Next-Generations Sequencing Test

This technique breaks down the genome into many pieces, reads each piece at the same time, and combines the data obtained with bioinformatic techniques to quickly decode vast amounts of genome information.

Reference Transcript					
ABCA1	NM_005502.3	APOE	NM_000041.3	LIPA	NM_000235.3
ABCG5	NM_022436.2	CETP	NM_000078.2	LIPC	NM_000236.2
ABCG8	NM_022437.2	CREB3L3	NM_032607.2	LMF1	NM_022773.3
ALMS1	NM_015120.4	CYP27A1	NM_000784.3	LPL	NM_000237.2
ANGPTL3	NM_014495.3	CYP7A1	NM_000780.4	MTTP	NM_000253.3
APOA1	NM_000039.2	GPD1	NM_005276.3	PCSK9	NM_174936.3
APOA2	NM_001643.1	GPIHBP1	NM_178172.5	SAR1B	NM_001033503.2
APOA5	NM_052968.4	LCAT	NM_000229.1	SCARB1	NM_005505.4
APOB	NM_000384.2	LDLR	NM_000527.4	SLCO1B1	NM_006446.4
APOC2	NM_000483.4	LDLRAP1	NM_015627.2	STAP1	NM_012108.3
APOC3	NM_000040.2				

Reference

1.Genetic causes of monogenic heterozygous familial hypercholesterolemia: a HuGE prevalence review.
2.Identification of people with heterozygous familial hypercholesterolemia. Current opinion in lipidology. 2012
3.Clinical Chemistry and Laboratory Medicine. 2008 Starr B, et al
4.Maio A., Dowd F. J. Hypertriglyceridemia.The Comprehensive Pharmacology. 2010
5.The Korean Society of Lipid and Atherosclerosis, Treatment Guidelines of Dyslipidemia(4 edtion), 2018

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Clinical significance of each tested gene

Even in people with positive result in the test, the onset and symptoms of the disease vary and it doesn't mean that necessarily the disease necessarily occur. In addition, even in people with negative result, the disease can be caused by other genes that have not been tested or other factors.

Genes with high clinical significance

LDLR	

Genes with clinical significance partially proven

ABCA1	*MedlinePlus*
	Pathogenic variants in the ABCA1 gene can cause a condition called familial HDL deficiency. People with this condition have reduced levels of HDL in their blood and may experience early-onset cardiovascular disease, often before age 50. While one copy of the altered ABCA1 gene causes familial HDL deficiency, two copies of the altered gene cause a more severe related disorder called Tangier disease.
ABCG5	*MedlinePlus*
	At least 24 ABCG5 pathogenic variants have been identified in people with sitosterolemia, which is a condition caused by accumulation of plant sterols. The pathogenic variants result in a defective sterolin transporter and impair the elimination of plant sterols and, to a lesser degree, cholesterol from the body. These fatty substances build up in the arteries, skin, and other tissues, resulting in clogged blood vessels that can impair blood flow (atherosclerosis), fatty skin growths (xanthomas), and the additional signs and symptoms of sitosterolemia.
ABCG8	*MedlinePlus*
	At least 28 ABCG8 pathogenic variants have been identified in people with sitosterolemia, which is a condition caused by accumulation of plant sterols. The pathogenic variants result in a defective sterolin transporter and impair the elimination of plant sterols and, to a lesser degree, cholesterol from the body. These fatty substances build up in the arteries, skin, and other tissues, resulting in clogged blood vessels that can impair blood flow (atherosclerosis), fatty skin growths (xanthomas), and the additional signs and symptoms of sitosterolemia.
ALMS1	*MedlinePlus*
	More than 80 pathogenic variants in the ALMS1 gene have been identified in people with Alström syndrome. A lack of normally functioning ALMS1 protein in the brain could lead to overeating. A loss of this protein in the pancreas may cause insulin resistance, a condition in which the body cannot use insulin properly. The combined effects of overeating and insulin resistance impair the body's ability to handle excess sugar, leading to diabetes and obesity (two common features of Alström syndrome).
ANGPTL3	*New England Journal of Medicine. 2010;363(23):2220–7*
	ANGPTL3 is a determinant factor of HDL level and positively correlates with plasma HDL cholesterol. In humans with genetic loss-of-function variants in one copy of ANGPTL3, the serum LDL-C levels are reduced. In those with loss-of-function variants in both copies of ANGPTL3, low LDL-C, low HDL-C, and low triglycerides are seen ("familial combined hypolipidemia").
APOA1	*MedlinePlus*
	Pathogenic variants in the APOA1 gene cause familial HDL deficiency, an inherited condition characterized by low levels of HDL in the blood and an elevated risk for early-onset cardiovascular disease, which often occurs before age 50. These pathogenic variants lead to an altered apoA-I protein. Some versions of the altered protein are less able to promote the removal of cholesterol and phospholipids from cells, which decreases the amount of these substances available to form HDL. Other versions of the altered protein are less able to stimulate cholesterol esterification, which means cholesterol cannot be integrated into HDL particles. Both types of mutation result in low HDL levels. A shortage (deficiency) of HDL is believed to increase the risk of cardiovascular disease.
APOA2	*GeneCards*
	APOA2 gene encodes apolipoprotein (apo-) A-II, which is the second most abundant protein of the high density lipoprotein particles. The protein is found in plasma as a monomer, homodimer, or heterodimer with apolipoprotein D. Defects in this gene may result in apolipoprotein A-II deficiency or hypercholesterolemia.

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APOA5	*GeneCards*
	APOA5 gene encodes an apolipoprotein that plays an important role in regulating the plasma triglyceride levels, a major risk factor for coronary artery disease. It is a component of high density lipoprotein and is highly similar to a rat protein that is upregulated in response to liver injury. Pathogenic variants in this gene have been associated with hypertriglyceridemia and hyperlipoproteinemia type 5.
APOB	*MedlinePlus*
	More than 100 pathogenic variants in the APOB gene are known to cause familial hypercholesterolemia. This condition is characterized by very high levels of cholesterol in the blood and an increased risk of developing heart disease. Each pathogenic variant that causes this condition changes a single protein building block (amino acid) in a critical region of apolipoprotein B-100. (Apolipoprotein B-48 is normal.)
APOC2	*GeneCards*
	APOC2 gene encodes a lipid-binding protein belonging to the apolipoprotein gene family. The protein is secreted in plasma where it is a component of very low density lipoprotein. This protein activates the enzyme lipoprotein lipase, which hydrolyzes triglycerides and thus provides free fatty acids for cells. Pathogenic variants in this gene cause hyperlipoproteinemia type IB, characterized by hypertriglyceridemia, xanthomas, and increased risk of pancreatitis and early atherosclerosis.
APOC3	*GeneCards*
	APOC3 gene encodes a protein component of triglyceride (TG)-rich lipoproteins (TRLs) including very low density lipoproteins (VLDL), high density lipoproteins (HDL) and chylomicrons. The encoded protein plays a role in role in the metabolism of these TRLs through multiple modes. This protein has been shown to promote the secretion of VLDL1, inhibit lipoprotein lipase enzyme activity, and delay catabolism of TRL remnants. Pathogenic variants in this gene are associated with low plasma triglyceride levels and reduced risk of ischemic cardiovascular disease, and hyperalphalipoproteinemia, which is characterized by elevated levels of high density lipoprotein (HDL) and HDL cholesterol in human patients.
CETP	*GeneCards*
	The protein encoded by the CETP gene is found in plasma, where it is involved in the transfer of cholesteryl ester from high density lipoprotein (HDL) to other lipoproteins. Defects in this gene are a cause of hyperalphalipoproteinemia 1 (HALP1).
CREB3L3	*NCBI Gene*
	The transcription factor cyclic AMP-responsive element–binding protein H (CREB-H, encoded by CRE-binding protein 3–like 3 [CREB3L3]) has been genetically associated with hypertriglyceridemia in humans,7 and to date, 4 kindred with dominant hypertriglyceridemia associated with CREB3L3 heterozygous pathogenic variants (245fs and W46X) have been described.
CYP27A1	*MedlinePlus*
	At least 90 pathogenic variants that cause cerebrotendinous xanthomatosis have been identified in the CYP27A1 gene. Cerebrotendinous xanthomatosis is a disorder characterized by abnormal storage of fats (lipids) in many areas of the body. Most CYP27A1 pathogenic variants change one protein building block (amino acid) in the sterol 27-hydroxylase enzyme. Changes in amino acids typically disrupt the normal function of the protein and impair its ability to help form chenodeoxycholic acid. Other pathogenic variants cause no functional enzyme to be made. As a result, other molecules are formed by an alternative pathway. A molecule called cholestanol, which is similar to cholesterol, is produced and accumulates in blood and tissues. Cholesterol also accumulates in tissues, but levels in blood are typically normal. The accumulation of cholesterol and cholestanol throughout the body's tissues causes the signs and symptoms of cerebrotendinous xanthomatosis.
CYP7A1	*J Clin Invest 2002;110(1):29-31*
	CYP7A1 deficiency would reduce the conversion of cholesterol to bile acids, resulting in elevated liver cholesterol levels, downregulated LDL receptors, and hypercholesterolemia. The increased hepatic cholesterol levels would render these patients resistant to the hypocholesterolemic effect of statins and that CYP7A1 deficiency would cause premature gallstone disease, a result of reduced bile acid secretion rates.

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GPD1	*GeneCards*
	The PD1 gene encodes a member of the NAD-dependent glycerol-3-phosphate dehydrogenase family. The encoded protein plays a critical role in carbohydrate and lipid metabolism by catalyzing the reversible conversion of dihydroxyacetone phosphate (DHAP) and reduced nicotine adenine dinucleotide (NADH) to glycerol-3-phosphate (G3P) and NAD+. The encoded cytosolic protein and mitochondrial glycerol-3-phosphate dehydrogenase also form a glycerol phosphate shuttle that facilitates the transfer of reducing equivalents from the cytosol to mitochondria. Mutations in this gene are a cause of transient infantile hypertriglyceridemia.
GPIHBP1	GeneCards
	The GPIHBP1 gene encodes a capillary endothelial cell protein that facilitates the lipolytic processing of triglyceride-rich lipoproteins. The encoded protein is a glycosylphosphatidylinositol-anchored protein that is a member of the lymphocyte antigen 6 (Ly6) family. This protein plays a major role in transporting lipoprotein lipase (LPL) from the subendothelial spaces to the capillary lumen. Pathogenic variants in this gene are the cause of hyperlipoproteinemia, type 1D.
LCAT	MedlinePlus
	People with one LCAT pathogenic variant in each cell may have an increased risk of atherosclerosis, which is an accumulation of cholesterol-rich fatty deposits and scar-like tissue in the lining of the arteries that can impede blood flow and lead to heart attacks, strokes, and other health problems. A single LCAT pathogenic variant likely reduces alpha-LCAT activity and binding of cholesterol to HDL, leading to less efficient transport of cholesterol from the blood and resulting in the development of atherosclerosis.
LDLRAP1	*MedlinePlus*
	More than 20 pathogenic variants in the LDLRAP1 gene have been shown to cause a form of familial hypercholesterolemia called autosomal recessive hypercholesterolemia. These mutations lead to the production of an abnormally small, nonfunctional version of the LDLRAP1 protein or prevent cells from making any of this protein. Without the LDLRAP1 protein, low-density lipoprotein receptors are unable to remove LDLs from the bloodstream effectively. Although the receptors can still bind normally to LDLs, these molecules are not properly transported into cells (particularly liver cells). As a result, many extra LDLs remain in the blood.
LIPA	*MedlinePlus*
	Approximately 60 pathogenic variants in the LIPA gene have been found to cause lysosomal acid lipase deficiency. This inherited condition is characterized by the accumulation of harmful amounts of lipids in cells and tissues throughout the body. Pathogenic variants in the LIPA gene lead to a shortage (deficiency) of functional lysosomal acid lipase. The severity of the condition depends on how much working enzyme is available. In individuals with a complete loss of enzyme activity, the condition begins in infancy and is often fatal. In individuals with some remaining enzyme activity, the amount of enzyme activity generally determines the severity of the condition.
LIPC	*MedlinePlus*
	At least 10 pathogenic variants in the LIPC gene have been found to cause hepatic lipase deficiency. This condition leads to abnormal levels of various fats (lipids) in the bloodstream, although it is unclear whether these changes impact the risk of developing heart disease. The LIPC pathogenic variants that cause this condition change single protein building blocks (amino acids) in the hepatic lipase enzyme. These mutations prevent the enzyme's release from the liver or decrease its activity in the bloodstream.
LMF1	*MedlinePlus*
	LMF1 is an important candidate gene for severe hypertriglyceridemia. A patient carrying a homozygous nonsense pathogenic variant in LMF1 gene (p.Y439X) responsible for combined lipase deficiency with severe hypertriglyceridemia and concomitant-associated disorders as recurrent episodes of pancreatitis, tuberous xanthomas, and lipodystrophy.
LPL	*MedlinePlus*
	More than 220 pathogenic variants in the LPL gene have been found to cause familial lipoprotein lipase deficiency. This condition disrupts the normal breakdown of triglycerides in the body, resulting in an increase of these fats. The most common pathogenic variant in people of European ancestry replaces the protein building block (amino acid) glycine with the amino acid glutamic acid at position 188 in the enzyme (written as Gly188Glu or G188E). Pathogenic variants that cause familial lipoprotein lipase deficiency reduce or eliminate lipoprotein lipase activity, which prevents the enzyme from effectively breaking down triglycerides in the bloodstream.

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MTTP	*MedlinePlus*
	Most MTTP pathogenic variants lead to the production of microsomal triglyceride transfer protein with reduced or absent function, preventing the formation of beta-lipoproteins. One particular pathogenic variant is common in affected individuals of Ashkenazi (eastern and central European) Jewish descent; this pathogenic variant replaces the protein building block (amino acid) glycine with a premature stop signal at position 865 (written as Gly865Ter or G865X) in the instructions used to make the microsomal triglyceride transfer protein. All MTTP pathogenic variants that cause abetalipoproteinemia impair beta-lipoprotein formation and result in a severe shortage of chylomicrons, LDLs, and VLDLs.
PCSK9	*MedlinePlus*
	More than 50 PCSK9 pathogenic variants have been identified that cause familial hypercholesterolemia. Most of these pathogenic variants change single protein building blocks (amino acids) in the PCSK9 protein. Pathogenic variants responsible for familial hypercholesterolemia are usually "gain-of-function" variants because they appear to enhance the activity of the PCSK9 protein.
SAR1B	MedlinePlus
	More than 20 pathogenic variants in the SAR1B gene have been found to cause chylomicron retention disease. This is an inherited disorder that impairs the normal absorption of fats, cholesterol, and fat-soluble vitamins from food. Most of the pathogenic variants change one protein building block (amino acid) in the SAR1B protein. Other pathogenic variants lead to the production of an abnormally small version of the protein that cannot function properly.
SCARB1	GeneCards
	SCARB1 is a HDL receptor and selectively uptakes HDL-cholesterol esters (CE), but not HDL apolipoprotein. Pathogenic variants in the SCARB1 gene are known to be associated with a reduction in HDL-CE liver uptake, a reduction in macrophage cholesterol efflux capacity, and an increase in HDL-C levels.
STAP1	GeneCards
	The protein encoded by STAP1 gene contains a proline-rich region, a pleckstrin homology (PH) domain, and a region in the carboxy terminal half with similarity to the Src Homology 2 (SH2) domain. This protein is thought to participate in a positive feedback loop by upregulating the activity of tyrosine-protein kinase Tec. Variants of this gene have been associated with autosomal-dominant hypercholesterolemia (ADH), which is characterized by elevated low-density lipoprotein cholesterol levels and in increased risk of coronary vascular disease.

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The test result of

Test Description

A brief description of the hyperlipidemia risk screen.

This test uses the genetic analysis techniques to check for genetic factors that may increase the risk of hyperlipidemia. Previous research findings are analyzed to provide individually tailored information that may help with health management. However, the test is not relevant to the diagnosis of illnesses, and therefore a patient must be consulted in order to obtain a diagnosis and make treatment decisions.

Summary of Test Results

Disease information	Hyperlipidemia (dyslipidemia)			Adverse effects of medications
Overall result	Caution			Standard
Item	LDL cholesterol	Neutral fat		Adverse effects upon statin drug administration
Level of risk	Standard	About 2.7 times increase	About 4.4 times increase	Standard
Gene tested	APOE	APOE	APOA5	COQ2

* The genotypes associated with increased risk of hyperlipidemia was detected. The medication or the prevention for hyperlipidemia is recommended.
* The genotype associated with increased risk of hyperlipidemia was not detected.

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The test result of

Test Results

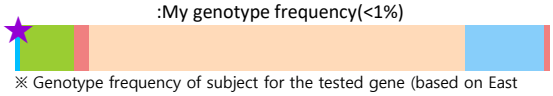
Hyperlipidemia (dyslipidemia) — A description of the genetic risk factors of hyperlipidemia. — **Caution**

Genetic risk factor for LDL cholesterol

0 out of 1 risk

Gene	My genotype	
	Standard	High-risk
APOE ★	e2e2	

APOE e2e2/e2e3/e2e4/e3e3/e3e4/e4e4
:My genotype frequency(<1%)



※ Genotype frequency of subject for the tested gene (based on East Asian population)

Test gene information - APOE

The APOE gene helps neutral fats and other lipoproteins in plasma to be absorbed by cells. If serum lipoproteins cannot be absorbed due to a high-risk APOE genotype, serum LDL cholesterol or neutral fat levels become elevated.

Test gene information - APOA5

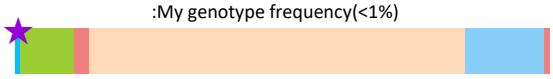
The APOA5 gene helps neutral fats and other lipoproteins in plasma to be absorbed by cells. If serum lipoproteins cannot be absorbed due to a high-risk APOA5 genotype, serum neutral fat levels become elevated.

Genetic risk factors for neutral fat

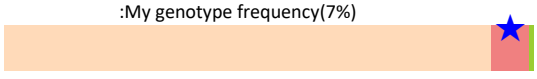
2 out of 3 risk

Gene	My genotype	
	Standard	High-risk
APOE ★		e2e2
APOA5 ★		GT
APOA5 ★	CC	

APOE e2e2/e2e3/e2e4/e3e3/e3e4/e4e4
:My genotype frequency(<1%)



APOA5 c.553 GG/GT/TT
:My genotype frequency(7%)



APOA5 c.56 CC/CG/GG
:My genotype frequency(100.0%)

※ Genotype frequency of subject for the tested gene (based on East Asian population)

Interpretation of results

- The genotype of APOE is e2e2. The individual with e2e2 genotype has about 2.7 times higher risk of increased Triglyceride. The genotype associated with increased risk of hyperlipidemia was not detected.
- e2e2 genotype of APOE is associate with poor response to a low fat diet.
- The genotype of APOA5 c.553 position is GT. The individual with GT genotype has about 4.4 times higher risk of hyperlipidemia. The risk of hyperlipidemia increases compared to standard genotype.
- The genotype of APOA5 c.56 position is CC. The genotype associated with increased risk of hyperlipidemia was not detected.

Recommendations

- The occurrence of hyperlipidemia may be influenced by environmental factors as well as genetic factors other than the APOE genotype. Therefore, the individual with high-risk genotype for hyperlipidemia may not necessarily develop hyperlipidemia.
- The individual with high-risk genotype for hyperlipidemia may have difficulty to reduce blood lipid level by diets or exercise. If you're diagnosed with hyperlipidemia, medical consultation for treatment is recommended.
- If the individual has the genotype associated with poor response to a low fat diet, it can be difficult to control blood lipid level through diet. if you are diagnosed with hyperlipidemia, it is advisable to consult a medical doctors regarding to the proper treatment option.

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Lab Director(medical doctor) : Chang-Seok Ki M.D(547) CSki
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Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen				
	Institution		Sample ID	
	Name		Medical record No.	
	Age / Sex		Accepted	
	Sample type		Reported	

The test result of

Test Results

Hyperlipidemia medications	Genetic risk factors for adverse effects of statins for the treatment of hyperlipidemia	Standard

Genetic risk factors for adverse effects of medications

0 out of 1 risk

Gene	My genotype	
	Standard	High-risk
COQ2 ★	GG	

COQ2 c.779-1022 GG/GC/CC
:My genotype frequency(72.1%)

※ Genotype frequency of subject for the tested gene (based on East Asian population)

Test gene information - COQ2

Statins, lipid lowering medication are known to cause such adverse effects as myopathy by interfering with the synthesis of coenzyme Q10. The COQ2 gene is involved in the synthesis of coenzyme Q10, and a high-risk COQ2 genotype may increase the risk of the adverse effects of statins.

Interpretation of results

- The genotype of COQ2 is GG. The genotype associated with increased risk of statin-induced side effects was not detected.

Recommendations

- Statin-induced myopathy can be developed even if the individual has the genotype with standard risk since genetic factors other than COQ2 genotype and environmental factors are involved in development of statin-induced myopathy.
- If you've ever experienced muscle symptoms upon statin administration, it is advisable to consult medical professional regarding decreasing dosage or changing to a different medication, etc.

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Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen				
	Institution		Sample ID	
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The test result of

Diseases with increased risk secondary to hyperlipidemia

Increase in the risk of associated diseases when hyperlipidemia is present

The chart below shows the kinds of diseases with increased risk sceondary to hyperlipidemia and their magnitudes of risk.

Disease / Secondary diseases	Hyperlipidemia
Hyperlipidemia risk screen results for 양성(여)123	Caution
☐ Ischemic stroke	About 2.1 times
☐ Coronary artery disease	About 1.5 times
☐ Atherosclerotic cardiovascular disease	About 1.4 times
☐ Cancer	About 1.4 times

Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen				
	Institution		Sample ID	
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Hyperlipidemia Terminology

* LDL cholesterol: LDL cholesterol is classified as “bad.” It burrows into vascular walls to cause various inflammatory responses, and then clumps together to form atherosclerotic plaque on the vascular walls or make the vascular walls thicker in general.
* HDL cholesterol: HDL cholesterol is classified as “good.” It removes bad cholesterol that have accumulated on vascular walls. However, if HDL cholesterol levels decrease or mostly consist of HDL cholesterol that cannot function properly, it does not have a beneficial effect on blood vessels.
* Neutral fat: Neutral fat is synthesized in the body. It exists in various places throughout our bodies and can be used by the body as an energy source when calorie intake is inadequate. However, increased levels of neutral fat may pose a threat to cardiovascular health.

Hyperlipidemia Prevention

A description of simple ways to prevent hyperlipidemia.

Diet guideline

Serum lipids are influenced by such factors as excess intake of saturated fatty acids and cholesterol, imbalance between caloric intake and expenditure, excessive intake of sugar, inadequate intake of dietary fiber, and excessive intake of alcohol. Serum cholesterol and saturated fatty acid concentration should be reduced, and sugars should be limited to not more than 60% of total calories.

Good

Bad

Exercise guideline

Type of exercise	Walking	Running	Stretching	Cycling	Swimming
Intensity	Similar to aerobic exercise				
Frequency	5 days a week, 30 to 60 minutes per session				

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Hyperlipidemia GENOME screen Report

Hyperlipidemia Genome Screen				
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	Name		Medical record No.	
	Age / Sex		Accepted	
	Sample type		Reported	

Clinical significance of each tested gene

Even in people with positive result in the test, the onset and symptoms of the disease vary and it doesn't mean that necessarily the disease necessarily occur. In addition, even in people with negative result, the disease can be caused by other genes that have not been tested or other factors.

▶ Genes with low clinical significance
*** The following genes are lacking objective validity for action related to health.**

APOE SLCO1B1

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