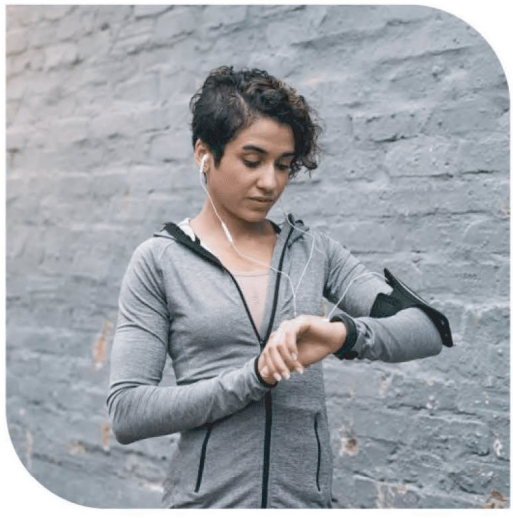








HEALTH
ASSESSMENT TEST

Unlock your true potential

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HaystackAnalytics

Genomics Simplified

Patient Information

Name	Sample Report	**Reporting date**	31-07-2023
Sample ID	20XXXXXXX28	**Sample receiving date**	07-07-2023
Sample type	Blood	**User ID**	HAT12345

Dear Xxxxx,

Congratulations on taking the first step towards a healthier future by opting for the innovative health assessment test offered by Godrej Memorial Hospital in collaboration with HaystackAnalytics.

This report has three major sections.

In the first section, the report provides insights into actionable genetic medical conditions.

The second section highlights the health risks organwise for several conditions where genetic factors play an important role.

The third section gives a wealth of information regarding sensitivities, intolerances, and genetic predispositions to nutritional deficiencies enabling personalised recommendations for optimal health, as well as genetic traits to bridge the gaps in fitness and prevent any serious injuries.

This comprehensive genetic report consolidates up-to-date research based on scientific evidence to help you proactively make decisions to optimise your health, physical as well as mental well-being.

We also help you understand the report through a medical consultation and genetic counselling.

Wishing You A Healthier You,

HaystackAnalytics

Medical Conditions

This section highlights the phenotypes (or disorders) for which genetic variants have been screened. A total of **78 genes** associated with **41 clinical conditions** have been analyzed. Of these, the clinical conditions for which genetic variants were detected in your DNA are highlighted in red.

Cancer	Heart diseases	Pancreas	Rare diseases
			
28 GENES FOR 19 CONDITIONS	34 GENES FOR 9 CONDITIONS	1 GENE FOR 1 CONDITION	17 GENES FOR 12 CONDITIONS

Following are the list of conditions which were screened for in your DNA. For each condition the gene/s screened for is/are mentioned under the condition name.

Cancer (0/19)

Familial adenomatous polyposis *APC*	Lynch syndrome *MSH2* *MSH6* *MLH1* *PMS2*	Multiple endocrine neoplasia, type 2A *RET*
Hereditary breast and ovarian cancer (HBOC) *BRCA1* *BRCA2*	MUTYH-associated polyposis *MUTYH*	Von hippel-lindau syndrome *VHL*
Hereditary breast cancer *PALB2*	Multiple endocrine neoplasia, type 1 *MEN1*	Tuberous sclerosis complex *TSC1* *TSC2*
Neurofibromatosis, type 2 *NF2*	PTEN hamartoma tumor syndrome *PTEN*	WT1-related wilms tumor *WT1*
Hereditary paraganglioma-pheochromocytoma syndrome *SDHB* *SDHC* *SDHAF2* *SDHD*	Juvenile polyposis syndrome *BMPR1A* *SMAD4*	Peutz-jeghers syndrome *STK11*
Li-fraumeni syndrome *TP53*	Retinoblastoma *RB1*	
Familial medullary thyroid carcinoma *RET*	Multiple endocrine neoplasia, type 2B *RET*	

Medical Conditions

Heart diseases (0/9)

Arrhythmogenic right ventricular Cardiomyopathy (ARVC) *PKP2* *DSP* *DSC2* *TMEM43* *DSG2*	Dilated cardiomyopathy *FLNC* *LMNA* *DES* *TTN* *BAG3* *RBM20* *TNNT2* *TNNC1*	Familial hypertrophic cardiomyopathy *MYH7* *MYBPC3* *TNNI3* *TPM1* *MYL3* *ACTC1* *PRKAG2* *MYL2* *TNNT2* *MAX* *TMEM127*
Catecholaminergic polymorphic ventricular tachycardia *RYR2* *CASQ2* *TRDN*	Familial hypercholesterolemia *LDLR* *APOB* *PCSK9*	Familial thoracic aortic aneurysm *MYH11* *ACTA2*
Long QT syndrome 1,2,3 *KCNQ1* *KCNH2* *SCN5A* *TRDN*	Myofibrillar myopathy *BAG3* *DES* *FLNC*	Ehlers-danlos syndrome, vascular type *COL3A1*

Pancreas (0/1)

Maturity-onset of diabetes of the young (MODY) *HNF1A*		

Rare diseases (1/12)

Biotinidase deficiency *BTD*	Ornithine Transcarbamylase Deficiency *OTC*	Malignant hyperthermia *RYR1* *CACNA1S*
Fabry's disease *GLA*	RPE65-related retinopathy *RPE65*	Hereditary transthyretin related amyloidosis *TTR*
Hereditary hemochromatosis *HFE*	Pompe disease *GAA*	Wilson disease *ATP7B*
Marfan's syndrome *FBN1*	**Loeys dietz syndrome** *SMAD3* *TGFBR1* *TGFBR2*	Hereditary hemorrhagic telangiectasia *ACVRL1* *ENG* *SMAD4*

Medical Conditions
(American College Of Medical Genetics, ACMG)

This section lists the disorders for which genetic variants have been screened. A total of 78 genes associated with 41 clinical conditions have been analysed as per the ACMG guidelines v3.1 for incidental findings.

RARE DISEASE

DISEASE	GENE	MUTATION	ZYGOSITY	INHERITENCE	CLASSIFICATION
Loeys dietz syndrome	SMAD3	NM_005902.4:C.1222G>C(P.Asp408His)	Heterozygous	Autosomal dominant	Pathogenic

Loeys-Dietz syndrome is a connective tissue disorder predisposing individuals to aortic and arterial aneurysms. Presenting with a wide spectrum of multisystem involvement, medical management for some individuals is complex.

VARIANT INTERPRETATION

A likely pathogenic heterozygous variant NM_005902.4 (SMAD3):C.364G>A (p.VAL122MET) in SMAD3 gene was identified in this individual. This variant shows an autosomal dominant inheritance and may be associated with Loeys-Dietz Syndrome type 3 (MIM 613795).

RECOMMENDATION

Mutation in these 4 genes, TGFBR1, TGFBR2, SMAD3, or TGFB2, in combination with arterial aneurysm or dissection or a family history of documented Loeys-Dietz Syndrome (LDS), may be sufficient to establish the diagnosis of LDS. Clinical correlation and genetic counseling is recommended.

REFERENCES

MacCarrick G, Black JH 3rd, Bowdin S, El-Hamamsy I, Frischmeyer-Guerrerio PA, Guerrerio AL, Sponseller PD, Loeys B, Dietz HC 3rd. Loeys-Dietz Syndrome: A primer for diagnosis and management. Genet Med. 2014 Aug;16(8):576-87. doi: 10.1038/gim.2014.11. PMID: 24577266

Health Snapshot

We have screened you for **4000+ genes** and **65+ blood parameters** of your key organs. This helps us ascertain your current health condition and genetic health risks.

ORGAN	GENOMIC RISK	PATHOLOGICAL RISK	ASSESSMENT/ADVICE
 **HEART** 11 Conditions	🔴	🔴	• **High Genomic Risk & High Pathological Risk** • Higher likelihood of developing heart ailments. Genetic counselling and clinical consultation recommended.
 **KIDNEY & INTESTINE** 5 Conditions	🔴	🔴	• **High Genomic Risk & High Pathological Risk** • Higher likelihood of developing kidney & intestine ailments. Genetic counselling and clinical consultation recommended.
 **THYROID** 5 Conditions	🔴	🔴	• **High Genomic Risk & High Pathological Risk** • Higher likelihood of developing thyroid ailments. Genetic counselling and clinical consultation recommended.
 **BRAIN** 4 Conditions	🔴	⚫	• **High Genomic Risk** • Genetic counselling recommended for risk mitigation strategies.
 **LIVER & GALLBLADDER** 2 Conditions	🔴	⚫	• **High Genomic Risk** • Genetic counselling recommended for risk mitigation strategies.

Risk Levels: 🔴 High Risk ⚫ No Elevated Risk

Risk Types: Genomic / Pathological

Health Snapshot

ORGAN	GENOMIC RISK	PATHOLOGICAL RISK	ASSESSMENT/ADVICE
 PANCREAS 1 Condition			• **High Genomic Risk** • Genetic counselling recommended for risk mitigation strategies.

Risk Levels: High Risk No Elevated Risk

Risk Types: Genomic / Pathological

Heart Health

You have been screened for 300+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Venous Thromboembolism
Coronary Heart Disease
Hypertriglyceridemia
Hypercholesterolimia
Sudden Cardiac Arrest
Hypertension
HDL Cholesterol
Atrial Fibrillation

No Elevated Risk

Hyperhomocysteinemia
Myocardial Infarction
Total Cholesterol

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Venous Thromboembolism	*SLC44A2*	chr19:10631494A>G	30634167
	PROCR	chr20:35176751A>G	31420334
	FAM228A	chr2:24190429A>G	23509962

VARIANT INTERPRETATION

The *SLC44A2 gene* Is involved in choline transport, and this may affect lipid metabolism and other cardiovascular-related processes. Studies suggest that this could contribute to the risk of venous thromboembolism (VTE).

The *PROCR gene* encodes the endothelial protein C receptor, involved in the protein c anticoagulant pathway. Genetic variations in *PROCR* could potentially influence this pathway, impacting clotting regulation and possibly contributing to the risk of venous thromboembolism.

Studies suggest that genetic variants in the *FAM228A gene* may increase the risk of *VTE* by interfering with the regulation of blood clotting.

RECOMMENDATION

To minimize the risk of venous thromboembolism, it's important to engage in regular physical activity and sustain a healthy weight through a well-balanced diet and exercise routine. For personalized prevention strategies, seek advice from a healthcare professional and follow their recommendations closely.

TRAIT	GENE	VARIANT	PUBMED ID
Coronary Heart Disease	*CDKN2B*	chr9:22096056A>G	22751097
	HNF1A	chr12:120997784G>T	19198612

VARIANT INTERPRETATION

The cluster of the CDKN2B-AS1 gene produces an active RNA molecule which is responsible for repressing the expression of other genes. Variations in the genetic makeup of CDKN2B-AS1 have been associated with a higher susceptibility to developing coronary heart disease, particularly atherosclerotic coronary artery disease.

Heart Health

VARIANT INTERPRETATION

The *HNF1A Gene* is a transcription factor that plays a role in the regulation of lipid metabolism, glucose metabolism, and other important biological processes. Studies suggest that variants in this gene can affect multiple signaling cascades, which can lead to increased levels of triglycerides, LDL cholesterol, and insulin resistance. This condition may increase the risk of hypertriglyceridemia, type 2 diabetes, and coronary artery disease.

RECOMMENDATION

To reduce your risk of coronary artery disease, it is important to prioritize a balanced lifestyle encompassing a healthy diet and regular exercise. Abstain from smoking, manage stress through relaxation techniques, and maintain regular check-ups with your healthcare provider to monitor blood pressure, cholesterol levels, and overall cardiovascular health.

TRAIT	GENE	VARIANT	PUBMED ID
Hypertriglyceridemia	***GCKR***	chr2:27508073T>C	29507422
	PNPLA3	chr22:43928847C>G	26690388
	ZPR1	chr11:116778201G>C	26690388
	PDXDC1	chr16:15036083C>T	24097068
	ZNF101	chr19:19678719A>G	19060911
	GPAM	chr10:112180571T>C	32302712
	SNX13	chr7:17880990C>T	20139978

VARIANT INTERPRETATION

The *GCKR gene* produces glucokinase regulatory protein (GKRP), which plays a vital role in regulating glucose storage and disposal. Studies suggest that people with genetic variations in this gene may be more susceptible to hypertriglyceridemia, type 2 diabetes, and metabolic disorders.

The *PNPLA3 gene* is expressed in the liver, where it plays a role in breaking down fats. Genetic variations in the PNPLA3 gene can impair the liver's ability to break down fats, leading to increased levels of fat in the blood. This can increase the risk of fatty liver and type 2 diabetes.

The ZPR1 gene plays a significant role in lipid and triglyceride metabolism. Research suggests that genetic variations in the zpr1 gene are linked to hypertriglyceridemia and heart-related issues.

Research indicates an association between the PDXDC1 gene and metabolic syndrome as well as inflammation. furthermore, specific variants within this gene have been reported to contribute to the development of hypertriglyceridemia.

The ZNF101 gene encodes a protein that is involved in the regulation of lipid metabolism. Studies suggest that variations in this gene can lead to changes in the way lipids are metabolized, which can affect triglyceride levels. High levels of triglycerides in the blood can increase the risk of hypertriglyceridemia and heart-related problems.

Recent reports suggest that genetic variants in the GPAM gene may interact with long non-coding RNAs to modulate triglyceride metabolism, which could increase the risk of developing hypertriglyceridemia.

The SNX13 protein, which localizes to the endoplasmic reticulum (ER), plays a role in the export of cholesterol from lysosomes. Studies suggest that genetic variations in this gene could increase lipid accumulation in the ER, which could increase the risk for neurological disorders.

RECOMMENDATION

Engaging in regular physical activity, maintaining a healthy weight, and limiting alcohol intake can help manage triglyceride levels. Consulting a healthcare professional for personalized guidance and considering medications if needed can aid in effectively managing the condition and reducing associated health risks.

Heart Health

TRAIT	GENE	VARIANT	PUBMED ID
Hypercholesterolemia	*HMGCR*	chr5:75352778A>T	18193044
	HNF1A	chr12:120978847A>C	24097068
	LDLR	chr19:11131631G>C	28334899
	VTN	chr17:28367840G>A	30275531
	ZNF101	chr19:19678719A>G	19060911
	ZPR1	chr11:116778201G>C	28334899

VARIANT INTERPRETATION

The *HMGCR* gene is involved in cholesterol metabolism. Studies suggest that certain variants in this gene may lead to the dysregulation of cholesterol biosynthesis, which may increase the risk of hypercholesterolemia.

The *HNF1A* gene is a transcription factor that plays a role in the regulation of lipid metabolism, glucose metabolism, and other important biological processes. Studies suggest that variants in this gene can affect multiple signaling cascades, which can lead to increased levels of triglycerides, LDL cholesterol, and insulin resistance. This condition may increase the risk of hypertriglyceridemia, type 2 diabetes, and coronary artery disease.

LDLR encodes the low-density lipoprotein receptor (LDLR), which helps the body remove LDL cholesterol ("Bad" Cholesterol) from the blood. Recent studies suggest that certain variations in this gene may affect its normal function, which may increase the risk of hypercholesterolemia and heart-related disorders.

The *VTN* gene encodes the vitronectin protein, which has been found to be associated with higher levels of lipoprotein(A), a type of cholesterol that is associated with an increased risk of heart disease. Recent reports suggest that the vtn gene may also be associated with higher levels of apolipoprotein B, which could increase the risk for hypertension, reduced high-density lipoprotein (HDL) cholesterol, and increased low-density lipoprotein (LDL) cholesterol.

The *ZNF101* gene encodes a protein that is involved in the regulation of lipid metabolism. Studies suggest that variations in this gene can lead to changes in the way lipids are metabolized, which can affect triglyceride levels. High levels of triglycerides in the blood can increase the risk of hypertriglyceridemia and heart-related problems.

The *ZPR1* gene plays a significant role in lipid and triglyceride metabolism. Research suggests that genetic variations in the *ZPR1* gene are linked to hypertriglyceridemia and heart-related issues.

RECOMMENDATION

Regular physical activity and maintaining a healthy weight can help improve cholesterol levels. Consult a healthcare professional for personalized guidance, considering medications if necessary, to effectively manage and reduce the risk associated with high cholesterol.

TRAIT	GENE	VARIANT	PUBMED ID
Sudden Cardiac Arrest	*CASQ2*	chr1:115700759G>A	31053292

VARIANT INTERPRETATION

The *CASQ2* gene has been associated with a cardiac condition known as catecholaminergic polymorphic ventricular tachycardia (CPVT). CPVT is a rare inherited disorder characterized by abnormal heart rhythms (Ventricular Tachycardia) that can lead to sudden cardiac death.

Heart Health

RECOMMENDATION

Giving priority to a healthy lifestyle through balanced nutrition, regular exercise, and stress management supports overall heart health. Make sure to schedule regular medical check-ups to monitor your heart's well-being and to address any potential concerns.

TRAIT	GENE	VARIANT	PUBMED ID
Hypertension	*CD164L2*	chr1:27382530C>T	33230300
	NCOR2	chr12:124341916C>T	36899621
	PLCE1	chr10:94136183A>G	21909115
	PTPRD	chr9:9059545G>A	30237584
	TBX2	chr17:61406405C>T	27618447
	VTN	chr17:28367840G>A	33230300

VARIANT INTERPRETATION

The *CD164L2* gene is involved in the regulation of the immune system and blood pressure. Studies have found that genetic variants in the *CD164L2* gene are associated with an increased risk of developing high blood pressure, and may also increase the risk of developing heart disease and stroke.

NCOR2 is a transcription factor that regulates multiple signaling pathways. studies suggest that certain variants in the *NCOR2* gene may be associated with the development of idiopathic pulmonary arterial hypertension and other blood pressure-related problems.

The *PLCE1* gene is involved in multiple signal transduction pathways. research indicates that specific genetic variants in this gene, leading to diminished expression levels, may elevate the risk of glomerular injury and hypertension.

The *PTPRD* gene plays a role in the regulation of various cellular and metabolic processes. Studies suggest that genetic variants in the *PTPRD* gene are associated with the development of type 2 diabetes and blood pressure related problems.

TBX2 is a transcription factor that plays a role in multiple signaling cascades. Studies suggest that genetic variants in the tbx2 gene may be associated with an increased risk of developing hypertension and cardiovascular disease.

The *VTN* gene encodes the vitronectin protein, which has been found to be associated with higher levels of lipoprotein(A), a type of cholesterol that is associated with an increased risk of heart disease. Recent reports suggest that the vtn gene may also be associated with higher levels of apolipoprotein B, which could increase the risk for hypertension, reduced high-density lipoprotein (hdl) cholesterol, and increased low-density lipoprotein (LDL) cholesterol.

RECOMMENDATION

To manage hypertension, maintain regular physical activity, a healthy weight, and consider reducing alcohol and quitting smoking. Regularly monitor blood pressure, adhere to prescribed medications, practice stress-reduction methods, and seek guidance from healthcare experts through personalized consultations and checkups.

TRAIT	GENE	VARIANT	PUBMED ID
HDL Cholesterol	*ANGPTL8*	chr19:11239812C>T	33462484
	BHMT	chr5:79126136G>A	33462484
	DOCK6	chr19:11236817T>C	24097068
	GALNT2	chr1:230159169C>T	28334899
	LPA	chr6:160585140T>G	33462484
	MLXIPL	chr7:73605971T>C	33462484
	NR1D1	chr17:40096975T>C	26556724
	RRBP1	chr20:17615510C>A	33462484
	TNFSF12, TNFSF13	chr17:7559652A>G	33462484
	ZPR1	chr11:116778201G>C	30926973

VARIANT INTERPRETATION

The *ANGPTL8* gene plays a role in lipid metabolism and maintaining triglyceride balance. Genetic variations within the *ANGPTL8* gene may result in elevated *ANGPTL8* protein levels, which can hinder triglyceride breakdown. Consequently, elevated blood triglyceride levels can occur, heightening the risk of elevated cholesterol levels.

BHMT is an enzyme that catalyzes the conversion of homocysteine to methionine and maintains its plasma concentration. Studies suggest that certain variants in this gene may affect the activity of this enzyme, which could increase the risk of elevated homocysteine and cholesterol levels in the blood.

DOCK6 is a gene encoding a protein engaged in cholesterol transportation within the body. Genetic variations in the *DOCK6* gene correlate with an escalated risk of elevated cholesterol levels, heightening the susceptibility to heart disease and stroke.

GALNT2 is involved in the production of high-density lipoproteins (HDL), also known as good cholesterol. genetic variations in the *GALNT2* gene can lead to a loss of function of the GALNAC-T2 protein, which can lower HDL levels and increase the risk of heart disease.

Lipoprotein(A), or LPA, is a type of Lipoprotein that is made up of cholesterol and a protein called apolipoprotein(A). Elevated Levels Of LPA can promote the formation of plaque in the arteries, which can narrow the arteries and restrict blood flow. This can increase the risk of heart disease, stroke, and other cardiovascular diseases. studies suggest that LPA may pose an even greater cardiovascular risk in people with familial hypercholesterolemia (FH).

Research indicates that certain variations in the *MLXIPL* gene are connected to elevated serum triglyceride levels, potentially heightening the risk of hypertriglyceridemia. nonetheless, additional factors like diet, pre-existing medical conditions, and lifestyle also contribute to the risk of developing this condition.

The *NR1D1* gene plays a role in cholesterol metabolism in liver tissue. Research suggests that certain variants in this gene may lead to decreased expression of *NR1D1*, which could cause elevated cholesterol levels in our bloodstream.

The *RRBP1* gene regulates blood pressure and potassium homeostasis, and may be involved in lipid metabolism. Studies suggest that certain variants in this gene may be associated with higher levels of LDL cholesterol in the blood, which could increase the risk of cardiovascular disease.

The *TNFSF12-TNFSF13* genes are involved in the regulation of cholesterol metabolism in adipose tissue. Studies suggest that specific variations in this genetic complex may impair cholesterol metabolism, which could increase the risk for obesity and type 2 diabetes.

The *ZPR1* gene plays a significant role in lipid and triglyceride metabolism. Research suggests that genetic variations in the *ZPR1* gene are linked to hypertriglyceridemia and heart-related issues.

Heart Health

RECOMMENDATION

Engage in regular physical activity to boost HDL levels, while avoiding smoking and excess alcohol. Consult a healthcare professional for personalized guidance and, if necessary, explore medication options to effectively manage your cholesterol and lower your risk of heart disease.

TRAIT	GENE	VARIANT	PUBMED ID
Atrial Fibrillation	*MYH6*	chr14:23392602A>G	34515533
	ZNF292	chr6:87258847A>G	37270590

VARIANT INTERPRETATION

The *MYH6* gene encodes the alpha-myosin heavy chain protein, a major component of the contractile apparatus of heart muscle cells. Recent reports suggest that genetic variations in the MYH6 gene are associated with an increased risk of atrial fibrillation and sick sinus syndrome.

ZNF292 is a transcription factor that is involved in multiple signaling cascades. Reports suggest that genetic variations in this gene are associated with an increased risk of atrial fibrillation and heart failure susceptibility.

RECOMMENDATION

To manage atrial fibrillation, adhere to prescribed medications, maintain a heart-healthy diet, participate in moderate exercise, address underlying conditions, employ stress reduction techniques, restrict caffeine and alcohol, quit smoking, and attend routine medical checkups for heart rhythm monitoring and treatment adjustments as required.

Kidney and Intestine Health

You have been screened for 30+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Chronic Kidney Disease
Gout
Celiac Disease
Ulcerative Colitis

No Elevated Risk

Kidney Stones

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Chronic Kidney Disease	***PYROXD2***	chr10:98388419A<G	31959995
	CYP4A11	chr1:46932824A<G	31959995
	ACOX1	chr17:75973754C<T	31959995
	ACOX1	chr1:201983470G<A	28038565

VARIANT INTERPRETATION

The *PYROXD2* gene plays a significant role in regulating mitochondrial function and diverse metabolic pathways. Variations in its genetic makeup might impact its function, potentially contributing to various health conditions like chronic kidney disease, premature aging, and imbalances in urine metabolites.

The *CYP4A11* gene encodes cytochrome P450 proteins that are involved in drug metabolism and the synthesis of cholesterol, steroids, and other lipids. Studies suggest that certain variants of this gene may increase the expression levels of lipoxygenase and cytochrome P450 products, which could lead to an elevated production of reactive oxygen species (ROS). This condition could increase the risk for chronic kidney disease and coronary artery disease.

Studies suggest that genetic variants in the *FAM228A gene* may increase the risk of vte by interfering with the regulation of blood clotting.

The *ACOX1 gene* is involved in the oxidation of fatty acids, which is a major source of energy for the kidney. Research reports suggest that variations in this gene may reduce its expression levels, which could increase the risk of fatty acids accumulating in the kidneys and may contribute to chronic kidney disease.

the *RNPEP* gene encodes an enzyme that is involved in the breakdown of proteins. Studies suggest that certain variants in the *RNPEP* gene may be associated with an imbalance in urine metabolite levels, which could increase the risk for the development of chronic kidney disease.

RECOMMENDATION

To minimize the risk of venous thromboembolism, it's important to engage in regular physical activity and sustain a healthy weight through a well-balanced diet and exercise routine. For personalized prevention strategies, seek advice from a healthcare professional and follow their recommendations closely.

Kidney and Intestine Health

TRAIT	GENE	VARIANT	PUBMED ID
Gout	*ABCG2*	chr4:88131171G<T	29453348

VARIANT INTERPRETATION

The *ABCG2* gene is responsible for transporting uric acid out of the body. Studies show that specific variants of this gene can affect its normal functioning, leading to increased levels of uremic toxins, such as urea, in the body. This condition can progressively contribute to chronic kidney disease and gout.

RECOMMENDATION

To manage gout, it is important to drink plenty of fluids, avoid alcohol and sugary drinks, and eat a healthy diet that is low in purines. You should also maintain a healthy weight and exercise regularly. If you have gout, it is important to see a doctor to get the right treatment.

TRAIT	GENE	VARIANT	PUBMED ID
Celiac Disease	*SH2B3*	chr12:111446804T<C	22057235

VARIANT INTERPRETATION

The *SH2B3* gene, involved in the regulation of immune responses, has been found to have specific variants in patients with celiac disease. There are also reports suggesting that these variants may play a role in the development of diabetes.

RECOMMENDATION

To manage celiac disease it is important to follow a strict gluten-free diet. This means avoiding all foods that contain gluten, such as wheat, barley, and rye. if you are not sure about what foods are gluten-free, talk to your doctor or a registered dietitian.

TRAIT	GENE	VARIANT	PUBMED ID
Ulcerative Colitis	*CARD9*	chr9:136371953G>A	30572963
	IL17REL	chr22:49997051A>G	21297633
	TNFSF15	chr9:114790969T>C	30199539
	PTGIR	chr19:46620526A>G	23128233
	MST1	chr3:49684099G>A	26192919

VARIANT INTERPRETATION

The *CARD9* gene encodes a protein that regulates the immune system. Research suggests that specific variants in this gene are associated with an increased risk of developing crohn's disease and ulcerative colitis.

IL17REL encodes the IL-17 receptor accessory protein, which helps to activate the immune system. Studies suggest that certain genetic variations in this gene are associated with familial and sporadic inflammatory bowel disease, which may result in the development of ulcerative colitis.

Kidney and Intestine Health

VARIANT INTERPRETATION

The TNFSF15 Gene Encodes A Protein That Regulates Inflammation. Research Suggests That Genetic Variants In This Gene May Be Associated With Ulcerative Colitis. However, Environmental Factors Such As Diet, Stress, Medication, And Lack Of Physical Activity May Also Increase The Risk Of Intestinal Inflammation.

PTGIR is a receptor for prostaglandins, which play a role in regulating inflammation. Studies suggest that certain genetic variants in this gene are associated with high levels of the inflammatory protein calprotectin, which increases the risk of ulcerative colitis.

The *MST1* gene is involved in the regulation of inflammation. Studies have indicated that genetic variants in this gene are associated with the development of crohn's disease and ulcerative colitis.

RECOMMENDATION

Ulcerative colitis is an inflammatory bowel disease (IBD). Working closely with a healthcare professional is essential for managing ulcerative colitis. This includes taking prescribed medications and following treatment plans carefully, avoiding trigger foods, and maintaining a balanced lifestyle with regular exercise, stress management, and adequate sleep.

Thyroid Health

You have been screened for 4+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Graves Disease
Hashimoto Thyroiditis

No Elevated Risk

Autoimmune Thyroid Disease
Hypothyroidism

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Graves Disease	*CD40*	chr20:46118343T>C	34867801
	CTLA4	chr2:203867991A>G	19438904

VARIANT INTERPRETATION

The *CD40* gene regulates the immune system and is also associated with graves disease. Recent reports suggest that variants in the *CD40* gene can activate inflammatory cytokines. These cytokines can stimulate thyroid cells, causing them to overproduce thyroid hormone, leading to a condition known as hyperthyroidism.

The *CTLA4* gene product, a protein that helps suppress the immune system, preventing it from attacking healthy cells. Recent reports suggest that certain variants in the *CTLA4* gene may have lower expression levels, which could increase the risk of developing autoimmune thyroid disease like graves disease.

RECOMMENDATION

To manage hyperthyroidism, consult a healthcare professional for accurate diagnosis and treatment. Follow their medical recommendations, take prescribed medications, manage stress, maintain a balanced diet, and prioritize regular checkups to ensure effective management of thyroid hormone levels and overall well-being.

TRAIT	GENE	VARIANT	PUBMED ID
Hashimoto Thyroiditis	*CTLA4*	chr2:203867991A>G	21503616

VARIANT INTERPRETATION

The *CTLA4* gene product, a protein that helps suppress the immune system, preventing it from attacking healthy cells. Recent reports suggest that certain variants in the *CTLA4* gene may have lower expression levels, which could increase the risk of developing autoimmune thyroid disease, like hashimoto thyroiditis.

Thyroid Health

RECOMMENDATION

To manage hyperthyroidism, consult a healthcare professional for accurate diagnosis and treatment. Follow their medical recommendations, take prescribed medications, manage stress, maintain a balanced diet, and prioritize regular checkups to ensure effective management of thyroid hormone levels and overall well-being.

Pancreas Health

You have been screened for 75+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Type 2 Diabetes

No Elevated Risk

None Found

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Type 2 Diabetes	*ABCC8*	chr11:17396930C>A	33462484
	CDKAL1	chr6:20661019G>C	33462484
	FGFR4	chr5:177089630G>A	33462484
	GCKR	chr2:27508073T>C	36437455
	GIPR	chr19:45678134G>C	35999016
	IGF2BP2	chr3:185793899G>T	34594039
	KCNQ1	chr11:2835964A>C	33462484
	NUP160	chr11:47835701T>C	36432414
	PLXND1	chr3:129574413T>C	32410861
	PNPLA3	chr22:43928850C>T	29083408
	PTPRD	chr9:8879118C>T	34624089
	SENP2	chr3:185613377C>A	28334899
	SH2B3	chr12:111446804T>C	28334899
	SLC2A2	chr3:171007094T>C	28334899
	SPHKAP	chr2:228108944A>G	28334899
	UBE2Z	chr17:48922889C>T	28334899

VARIANT INTERPRETATION

The ABCC8 gene plays a role in insulin secretion from beta cells in the pancreas. Research indicates that genetic variations in this gene could potentially elevate the risk of type 2 diabetes.

The CDKAL1 gene encodes a protein that is involved in the regulation of insulin secretion and sensitivity. Studies suggest that certain variants in this gene can alter its functioning, which can increase the risk of type 2 diabetes. It is important to note that other factors, such as eating habits, sedentary lifestyle, and pre-existing medical conditions, can also play a role in the development of diabetes.

The FGFR4 gene plays a role in cell growth, proliferation, and differentiation. Studies suggest that certain variants in this gene may lead to its overexpression, which could increase the risk of developing type 2 diabetes and heart-related problems.

The GCKR gene produces glucokinase regulatory protein (GKRP), which plays a vital role in regulating glucose storage and disposal. Studies suggest that people with genetic variations in this gene may be more susceptible to hypertriglyceridemia, type 2 diabetes, and metabolic disorders.

The GIPR gene is involved in maintaining glucose homeostasis. Research reports suggest that genetic variants in this gene may be associated with the development of type 2 diabetes and obesity

Pancreas Health

VARIANT INTERPRETATION

IGF2BP2 plays an important role in regulating insulin signaling, glucose metabolism, and cell growth. Studies have associated genetic variations in the IGF2BP2 gene with an increased risk of type 2 diabetes and obesity. However, environmental factors such as eating disorders, overweight, and physical inactivity can also contribute to these conditions.

The KCNQ1 gene encodes a potassium channel that regulates insulin secretion from the pancreas. Studies suggest that certain variants in this gene are associated with an increased risk of type 2 diabetes. However, it is important to note that lifestyle factors such as diet, exercise, and weight management also play an important role in the development of type 2 diabetes.

NUP160 is a nucleoporin protein that is involved in the movement of cytoplasmic cargo between the nucleus and the cytoplasm of the cell. Studies suggest that certain variants in this gene may lead to its overexpression, which could increase the risk for high blood sugar levels and nephrotic syndromes.

The PLXND1 gene is involved in the regulation of body fat distribution. Studies suggest that genetic variation in this gene is linked to the regulation of the type V collagen microenvironment in visceral adipose tissue, a type of fat tissue that is associated with metabolic disorders such as type 2 diabetes.

The PNPLA3 gene is expressed in the liver, where it plays a role in breaking down fats. Genetic variations in the PNPLA3 gene can impair the liver's ability to break down fats, leading to increased levels of fat in the blood. This can increase the risk of fatty liver and type 2 diabetes

The PTPRD gene plays a role in the regulation of various cellular and metabolic processes. Studies suggest that genetic variants in the PTPRD gene are associated with the development of type 2 diabetes and blood pressure related problems.

SENP2 regulates mitochondrial function and insulin secretion in pancreatic beta cells. Studies suggest that certain variants in this gene may impair insulin signaling and glycogen synthesis, which could increase the risk of developing type 2 diabetes.

The SH2B3 gene, involved in the regulation of immune responses, has been found to have specific variants in patients with celiac disease. There are also reports suggesting that these variants may play a role in the development of diabetes.

The SLC2A2 gene is expressed in the liver, kidney, and intestine, helping to move glucose from the bloodstream into these tissues. Studies suggest that certain variations in this gene may increase the risk of developing type 2 diabetes.

The SPHKAP gene plays an important role in regulating glucose-stimulated insulin secretion. Studies suggest that certain variants in this gene may be associated with abnormal blood glucose levels, which could increase the risk of type 2 diabetes and kidney problems.

The GLP1R gene is involved in the control of blood sugar levels by enhancing insulin secretion. Research reports indicate that variants in this gene may be involved in the development of type 2 diabetes.

RECOMMENDATION

Regular physical activity is crucial for blood sugar control. Monitor your blood sugar levels consistently, take prescribed medications as directed by your healthcare provider, and maintain a healthy weight. Regular medical check-ups and communication with your healthcare team are essential for effective management of the condition.

Brain Health

You have been screened for 10+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Alzheimer's Disease
Parkinson's Disease
Schizophrenia
Stroke

No Elevated Risk

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Alzheimer's Disease	*SORL1*	chr11:121577381T>G	26611835

VARIANT INTERPRETATION

Genetic studies have suggested that certain variants of the SORL1 gene may be associated with an increased risk of late-onset Alzheimer's disease. Variants that lead to reduced function of SORL1 may result in altered amyloid precursor protein (APP) processing and metabolism, contributing to the accumulation of amyloid-beta in the brain.

RECOMMENDATION

Maintaining a healthy lifestyle is crucial for Alzheimer's disease. This includes regular physical activity, a balanced diet, mental stimulation, quality sleep, stress management, and social engagement. Regular check-ups and open communication with healthcare professionals can help with early detection and management.

TRAIT	GENE	VARIANT	PUBMED ID
Parkinson's Disease	*ATP13A2*	chr1:16992516G>A	33335927

VARIANT INTERPRETATION

The ATP13A2 gene encodes a protein called lysosomal type 5 ATPase (ATPase), which is responsible for transporting metal ions across membranes. Studies suggest that certain variants of the ATP13A2 gene can cause disturbances in metal ion transport and lysosomal function, which can ultimately contribute to neurodegeneration, such as early-onset Parkinson's disease, spasticity, and cognitive decline.

RECOMMENDATION

It is a complex neurological disorder that can manifest in a variety of symptoms, which may vary from person to person. Diagnosis is based on a clinical assessment by a qualified professional, which includes a thorough review of medical history, a comprehensive physical examination, and careful observation of symptoms. Seeking professional medical evaluation is essential to ensure an accurate diagnosis and to determine the most appropriate clinical approach.

Brain Health

TRAIT	GENE	VARIANT	PUBMED ID
Schizophrenia	*DRD3*	chr3:114171968C>T	9674978

VARIANT INTERPRETATION

The DRD3 gene encodes the dopamine receptor D3, a type of G protein-coupled receptor that binds dopamine. Abnormalities in the dopamine system have been implicated in schizophrenia, making the DRD3 receptor a suitable target for schizophrenia research and treatment.

RECOMMENDATION

It is a complex condition that necessitates assessment by a certified mental health specialist. Seeking assistance from qualified professionals for a comprehensive evaluation and suitable treatment is essential.

TRAIT	GENE	VARIANT	PUBMED ID
Stroke	*ADH1B*	chr4:99318162T>C	34051793

VARIANT INTERPRETATION

Genetic variants in the ADH1B gene have been associated with both increased and decreased stroke risk. These associations may be influenced by alcohol consumption and its effects on stroke risk factors.

RECOMMENDATION

Stroke constitutes a medical emergency; should stroke symptoms manifest, prompt medical attention is crucial. To avert stroke, embrace a health-conscious lifestyle?Çöparticipate in regular exercise, maintain a healthy weight, quit smoking, manage blood pressure and cholesterol levels, and effectively handle diabetes if relevant. These actions substantially curtail stroke risk and enhance overall wellness.

Liver & Gallbladder Health

You have been screened for 4+ genes, of which at risk variants were detected in your DNA.

DNA TEST RESULT

High risk

Gallstones
Non-Alcoholic Fatty Liver Disease

No Elevated Risk

None Found

High Risk Traits

TRAIT	GENE	VARIANT	PUBMED ID
Gallstones	*GCKR*	chr2:27508073T>C	27094239
	LRBA	chr4:150277928G>A	34594039

VARIANT INTERPRETATION

The GCKR gene produces glucokinase regulatory protein (GKRP), which plays a vital role in regulating glucose storage and disposal. Studies suggest that people with genetic variations in this gene may be more susceptible to hypertriglyceridemia, type 2 diabetes, and metabolic disorders.

The LRBA gene encodes a protein that helps the body clear cholesterol. Certain variants in the LRBA gene can impair cholesterol clearance, which may increase the risk of gallstone formation.

RECOMMENDATION

When dealing with gallstones, it is important to maintain a healthy lifestyle. This includes staying hydrated, managing your weight, and engaging in regular physical activity. These lifestyle changes can help prevent gallstones and promote overall digestive health. If you experience severe pain or nausea, consult a healthcare professional promptly.

TRAIT	GENE	VARIANT	PUBMED ID
Non-Alcoholic Fatty Liver Disease	*PNPLA3*	chr22:43928847C>G	22719876

VARIANT INTERPRETATION

The PNPLA3 gene is expressed in the liver, where it plays a role in breaking down fats. Genetic variations in the PNPLA3 gene can impair the liver's ability to break down fats, leading to increased levels of fat in the blood. This can increase the risk of fatty liver and type 2 diabetes

RECOMMENDATION

Regular physical activity can aid in weight management and improve liver health. Avoid excessive alcohol consumption and aim to maintain a healthy weight through a combination of diet and exercise. If you have underlying health conditions, consult a healthcare professional for personalized guidance on managing NAFLD and preventing its progression.

Nutrition Health Snapshot

We have screened you for **250+** genes and **290+** variants in your DNA. This helps us ascertain your genetic health risks.



Genetic Response to Macronutrients



Micronutrient Deficiency



Micronutrient Toxicity



Food Sensitivity and Intolerance



Addiction



Weight Management

Genetic Response to Macronutrients

You have been screened for **50+ genes** for the 'Genetic Response to Macronutrients' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Response to fibre intake	Favourable
Response to protein intake	Favourable
Response to monounsaturated fat intake	Unfavourable
Response to saturated fat intake	Unfavourable
Response to carbohydrate intake	Normal
Response to omega 3 intake	Normal
Response to omega 6 intake	Normal

INFERENCE INTERPRETATION

- Favourable outcome means that nutrients have a positive impact in preventing health risks.
- Unfavourable outcome means that nutrients have a negative impact in preventing health risks.
- Normal outcome means that nutrients have a typical impact in preventing health risks.

DNA TEST RESULT: IN DETAIL

Response to fibre intake

GENE	VARIANT	INFORMATION	PUBMED ID
CYP7A1	8:58500365G>G	The *CYP7A1* gene is involved in cholesterol metabolism. Variation in this gene is linked to changes in blood cholesterol levels in response to dietary interventions.	26936139

INTERPRETATION:

As per your genetics, fibre consumption is beneficial for you to lower the risk of hypercholesterolemia.

ADVICE:

It is recommended for you to consume soluble fibre (beta glucan) from barley and monitor blood cholesterol levels. Consult a dietitian for fibre requirements for your health.

Response to protein intake

GENE	VARIANT	INFORMATION	PUBMED ID
UCP2	11:73983709C>C	The *UCP2* gene is involved in energy metabolism and body weight regulation. Variation in this gene is associated with differences in BMI and increased risk of obesity.	31751449
MTHFR	1:11796321G>A	The *MTHFR* gene is involved in folate metabolism. Variation in this gene may affect folate metabolism contributing to weight gain and obesity.	31751449

INTERPRETATION:

As per your genetics, moderately high protein diet is beneficial for you to lower high BMI.

ADVICE:

It is recommended for you to consume an energy restricted diet with moderately high protein and monitor BMI. Consult a dietitian for protein requirements for your health.

Genetic Response to Macronutrients

Response to monounsaturated fat intake

GENE	VARIANT	INFORMATION	PUBMED ID
NOS3	7:150999023T>T	The *NOS3* gene is involved in production of protein nitric oxide synthase that acts as a vasodilator and increases blood flow improving blood pressure. Variation in this gene can contribute to high blood pressure.	26994605
CETP	16:56982180G>G	The *CETP* gene is involved in lipid metabolism and helps regulate cholesterol levels. Variation in this gene may affect the activity of *CETP* enzyme, causing low levels of good cholesterol. The type and amount of dietary fats consumed can also impact the functioning of the *CETP* gene.	29942448
CLOCK	4:55435202A>G	The *CLOCK* gene is involved in regulating circadian rhythm that controls various bodily processes including metabolism. Variation in this gene can disrupt circadian rhythm and contribute to development of metabolic syndrome.	34068889

INTERPRETATION:

As per your genetics, high and very low monounsaturated fat consumption is detrimental for you and might increase the risk of low HDL cholesterol, high blood pressure, and metabolic syndrome.

ADVICE:

It is recommended for you to consume optimum monounsaturated fat foods and monitor blood pressure, lipid profile, blood sugar profile, BMI. Maintain a healthy weight. Consult a dietitian for monounsaturated fat requirements for your health.

Response to saturated fat intake

GENE	VARIANT	INFORMATION	PUBMED ID
ABCA1	9:104858586C>C	The *ABCA1* gene plays a role in the body's ability to transport cholesterol and other fats including triglycerides to other tissues via bloodstream. Variation in this gene can impair normal functioning of *ABCA1* protein and have an impact on lipid metabolism resulting in high triglyceride levels.	23021345
APOA5	11:116791691G>G	The *APOA5* gene is a key regulator of plasma triglyceride levels. Variation in this gene can impair normal functioning of *APOA5* protein and have an impact on lipid metabolism resulting in dyslipidemia and obesity.	26365669
TCF7L2	10:112998590C>T	The *TCF7L2* gene plays an important role in the body's ability to process insulin, a hormone that regulates blood sugar levels. Variation in this gene can impair insulin function, decrease insulin sensitivity, and contribute to development of metabolic syndrome.	21543200

Genetic Response to Macronutrients

GENE	VARIANT	INFORMATION	PUBMED ID
CLOCK	4:55435202A>G	The *CLOCK* gene is involved in regulating circadian rhythm that controls various bodily processes including metabolism. Variation in this gene can disrupt circadian rhythm and contribute to development of metabolic syndrome.	19846548
APOE	19:44905579T>T	The *APOE* gene plays a role in triglyceride-rich lipoprotein metabolism and regulation of cholesterol. Variation in this gene is linked to dyslipidemia.	23021345
FTO	16:53786615T>A	The *FTO* gene is involved in regulation of appetite and energy balance. Variation in this gene is linked to increased appetite that contributes to development of obesity.	22457394
LEPR	1:65592830A>G	The *LEPR* gene is involved in production of protein that regulates body weight. Variation in this gene can impact the functioning of the leptin receptor leading to disturbances in appetite control and energy balance and can contribute to dyslipidemia and obesity.	26365669

INTERPRETATION:

As per your genetics, high saturated fat consumption is detrimental for you and might increase the risk of dyslipidemia, obesity, and other metabolic abnormalities.

ADVICE:

It is recommended for you to limit saturated fat foods and monitor lipid profile, blood sugar profile, BMI. Consult a dietitian for saturated fat requirements for your health.

Micronutrient Deficiency

You have been screened for **100+ Genes** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

VITAMINS

TRAIT	INFERENCE
Vitamin B12	Higher likelihood of deficiency
Vitamin D	Lower likelihood of deficiency
Vitamin A	Lower likelihood of deficiency
Vitamin E	Lower likelihood of deficiency
Vitamin K	Lower likelihood of deficiency
Vitamin B6	Lower likelihood of deficiency
Vitamin B9	Lower likelihood of deficiency

INFERENCE INTERPRETATION

- Reduced predisposition to vitamin deficiency.
- Increased predisposition to vitamin deficiency.

DNA TEST RESULT: IN DETAIL

Vitamin B12

GENE	VARIANT	INFORMATION	PUBMED ID
FUT2	chr19:48703160A>C	The *FUT2* Gene Provides Instruction For Making Protein That Is Involved In Determining Blood Type And Influencing The Gut Microbiota. Variation In This Gene Can Impact The Absorption Of Vitamin B12 In The Intestine, Potentially Increasing The Risk Of Vitamin B12 Deficiency.	25147783

INTERPRETATION:

As per your genetics, you have a higher likelihood of vitamin B12 deficiency.

ADVICE:

It is recommended for you to monitor serum vitamin B12 levels and consume vitamin B12 containing foods. Consult an expert for vitamin B12 requirements for your health.

Micronutrient Deficiency

You have been screened for **100+ Genes** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

MINERALS

TRAIT	INFERENCE
Calcium	Lower likelihood of deficiency
Iron	Lower likelihood of deficiency
Phosphate	Lower likelihood of deficiency
Selenium	Lower likelihood of deficiency
Magnesium	Lower likelihood of deficiency
Potassium	Lower likelihood of deficiency
Zinc	Lower likelihood of deficiency

INFERENCE INTERPRETATION

Reduced predisposition to mineral deficiency.

Increased predisposition to mineral deficiency.

Micronutrient Deficiency

You have been screened for **100+ Genes** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

OTHER MICRONUTRIENTS

TRAIT	INFERENCE
Choline	Lower likelihood of deficiency
Antioxidant	Lower likelihood of deficiency

INFERENCE INTERPRETATION

- Reduced predisposition to micronutrient deficiency.
- Increased predisposition to micronutrient deficiency.

Micronutrient Toxicity

You have been screened for **1 Gene** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Iron Overload	**Lower likelihood of toxicity**

INFERENCE INTERPRETATION

Reduced predisposition to iron toxicity.

Increased predisposition to Iron toxicity.

Food Sensitivity and Intolerance

You have been screened for 100+ genes for the 'food sensitivity and intolerance' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Gluten	Higher likelihood of addiction
Alcohol Flush Reaction	Lower likelihood of addiction
Caffeine intake and Hypertension Risk	Lower likelihood of addiction
Lactose Intolerance	Lower likelihood of addiction
Salt Intake and Hypertension Risk	Lower likelihood of addiction

INFERENCE INTERPRETATION

Reduced predisposition to food sensitivity and intolerance.

Increased predisposition to food sensitivity and intolerance.

DNA TEST RESULT: IN DETAIL

Gluten Intolerance

GENE	VARIANT	INFORMATION	PUBMED ID
NCF2	chr1:183563445G>T	The *NCF2* gene is involved in production of a protein that is essential in formation of *NADPH* oxidase enzyme complex. NADPH OXIDASE ENZYME COMPLEX IS VITAL FOR THE IMMUNE SYSTEM. Variation in this gene has been associated with celiac disease, a condition caused by an abnormal immune reaction to gluten.	31591516

INTERPRETATION:

As per your genetics, you have a higher likelihood of gluten intolerance and celiac disease.

ADVICE:

It is recommended for you to strictly limit or avoid gluten containing food and food products. Consult an expert for diagnosis and personalized diet recommendation for your health.

Addiction

You have been screened for **35+ Genes** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Alcohol Dependence	Higher likelihood of addiction
Nicotine Dependence	Lower likelihood of addiction

INFERENCE INTERPRETATION

Reduced predisposition to addiction.

Increased predisposition to addiction.

Addiction

DNA TEST RESULT: IN DETAIL

Alcohol Dependence

GENE	VARIANT	INFORMATION	PUBMED ID
ADH1B	chr4:99318162T>C	The ADH1B gene is involved in alcohol metabolism. Variation in this gene can affect the efficiency of ethanol breakdown, contributing to an individual's susceptibility to alcohol dependence.	24166409

INTERPRETATION:

As per your genetics, you have a higher likelihood of alcohol addiction.

ADVICE:

It is recommended for you to avoid heavy alcohol consumption.

Weight Management

You have been screened for **100+ Genes** For The 'Micronutrient Deficiency' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Obesity	Lower Likelihood Of Obesity
Weight Regain Tendency	Lower likelihood of weight regain

INFERENCE INTERPRETATION

Reduced predisposition to weight regain and obesity.

Increased predisposition to weight regain and obesity.

Fitness Health Snapshot

We have screened you for **75+** genes and **85+** variants in your DNA. This helps us ascertain your genetic health risks.



Exercise Potential



Response to Exercise



Exercise Fatigue and Recovery



Response to Supplementation



Health and Injury Risk



Exercise Behaviour

Exercise Potential

You have been screened for **60+ genes** for the 'Exercise Potential' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Power	Favourable
Endurance	Favourable
Resistance Training	Normal
VO2 Maximum Potential	Normal
Sprint Performance	Normal

INFERENCE INTERPRETATION

- Favourable outcome means that you have a higher ability to excel in performing these exercises or sport.
- Unfavourable outcome means that you have a lower ability to excel in performing these exercises or sport.
- Normal outcome means that you have a typical ability to excel in performing these exercises or sport.

Exercise Potential

DNA TEST RESULT: IN DETAIL

Power

GENE	VARIANT	INFORMATION	PUBMED ID
NOS3	chr7:150992991C>T	The *NOS3* gene provides instruction for making enzyme nitric oxide synthase 3 that is responsible for producing nitric oxide. Nitric oxide plays a role in vasodilation and blood flow regulation. Variation in this gene may influence cardiovascular function and oxygen delivery during power sport, potentially impacting performance and recovery.	24744483

INTERPRETATION:

As per your genetics, power sport is favourable for you.

ADVICE:

You can opt for weightlifting, powerlifting, calisthenics, or other power based activities. It is recommended to perform activity under supervision of an expert.

Endurance

GENE	VARIANT	INFORMATION	PUBMED ID
NOS3	chr7:150999023T>G	The *NOS3* gene provides instruction for making enzyme nitric oxide synthase 3 that is responsible for producing nitric oxide. Nitric oxide plays a role in vasodilation and blood flow regulation. Variation in this gene may influence cardiovascular function, potentially impacting endurance sports performance.	24744483

INTERPRETATION:

As per your genetics, endurance sport is unfavourable for you. Prominent especially in men.

Response to Exercise

You have been screened for **40+ genes** for the 'Response to Exercise' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Weight Loss Response To Exercise	Normal
Exercise Induced Fat Loss	Normal
Blood Pressure Response to Exercise	Normal
Insulin Sensitivity Response to Exercise	Normal
Hdl Cholesterol Levels with Exercise	Normal
Triglyceride Levels with Exercise	Normal
Heart Rate Recovery Post-Exercise	Normal
Heart Rate Response to Exercise	Normal

INFERENCE INTERPRETATION

- Favourable outcome means that exercise has a positive impact in preventing health risks.
- Unfavourable outcome means that exercise has a negative or no impact in preventing health risks.
- Normal outcome means that exercise has a typical impact in preventing health risks.

Exercise Fatigue and Recovery

You have been screened for **20+ genes** for the 'Exercise Fatigue and Recovery' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Lactate Accumulation During Training	**Good Lactate Threshold**
Muscle Soreness	**Lower Likelihood of Muscle Soreness**
Exercise Recovery	**Good Exercise Recovery Rate**

INFERENCE INTERPRETATION

- Good genetic ability to have a good lactate threshold and exercise recovery rate.
- Lower likelihood means decreased risk of muscle soreness and fatigue.
- Poor genetic ability to have a good lactate threshold and exercise recovery rate.
- Higher likelihood means increased risk of muscle soreness and fatigue.

Response to Supplementation

You have been screened for 3 genes for the 'Response to Supplementation' Category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Caffeine Supplementation and Exercise Performance	Favourable

INFERENCE INTERPRETATION

- Favourable outcome means that supplementing caffeine is beneficial in enhancing exercise performance.
- Unfavourable outcome means that supplementing caffeine has detrimental or has no impact in enhancing exercise performance.
- Normal outcome means that supplementing caffeine has a typical impact in enhancing exercise performance.

Response to Supplementation

DNA TEST RESULT: IN DETAIL

Caffeine Supplementation and Exercise Performance

GENE	VARIANT	INFORMATION	PUBMED ID
CYP1A2	chr15:74749576C>A	The *CYP1A2* gene affects how an individual's body processes caffeine. People with a certain gene variant may benefit more from caffeine before exercise, as it can enhance their performance by providing energy and reducing perceived effort. others may not experience the same benefits.	32823594

INTERPRETATION:

As per your genetics, caffeine supplementation is favourable to improve countermovement jump, and 9m ball throwing sport.

ADVICE:

It is recommended for you to consume 3 mg caffeine per kg body mass 60 minutes pre-exercise for a favourable outcome. Consult an expert for caffeine dosage for your health.

Health and Injury Risk

You have been screened for **40+ genes** for the 'Health and Injury Risk' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Bone Mineral Density	Good Bone Health
Exercise Induced Muscle Damage	Higher Likelihood Of Cramping
Flexibility	Good Flexibility
Exercise Induced Muscle Damage	Lower Likelihood Of Muscle Damage
Lower Back Pain	Lower Likelihood Of Lower Back Pain
Concussion	Lower Likelihood Of Injury
Achilles Tendinopathy	Lower Likelihood Of Injury
Tennis Elbow Injury	Lower Likelihood Of Injury

INFERENCE INTERPRETATION

- Good genetic ability to have good flexibility, bone health and resting metabolic rate.
- Poor genetic ability to have good flexibility, bone health and resting metabolic rate.
- Higher likelihood means increased risk of injury.
- Lower likelihood means decreased risk of injury.

Health and Injury Risk

TRAIT	INFERENCE
Rotator Cuff Injury	Lower Likelihood Of Injury
Resting Metabolic Rate	Good Resting Metabolic Rate
Anterior Cruciate Ligament Injury	Lower Likelihood Of Injury

INFERENCE INTERPRETATION

- Good genetic ability to have good flexibility, bone health and resting metabolic rate.
- Poor genetic ability to have good flexibility, bone health and resting metabolic rate.
- Higher likelihood means increased risk of injury.
- Lower likelihood means decreased risk of injury.

DNA TEST RESULT: IN DETAIL

Exercise Associated Muscle Cramping

GENE	VARIANT	INFORMATION	PUBMED ID
COL5A1	chr9:134842570C>T	The *COL5A1* gene provides instruction for making a protein that contributes to the structure of connective tissues like tendons and ligaments. Variation in this gene may affect collagen integrity, potentially increasing the susceptibility to muscle cramping.	22894972

INTERPRETATION:

As per your genetics, you have a higher likelihood of exercise related muscle cramping.

ADVICE:

It Is Recommended For You To Do Stretching Exercise After Training And At Bedtime, Warm Up Before Training To Prevent Exercise Associated Muscle Cramps.

Bone Mineral Density

GENE	VARIANT	INFORMATION	PUBMED ID
CCDC170	chr6:151615542G>A	The CCDC170 Gene Is Involved In Bone Mineral Density Regulation. Variation In This Gene Might Influence BMD Levels, Potentially Impacting Bone Health And Osteoporosis Risk.	21760950

INTERPRETATION:

As per your genetics, you have a higher likelihood of good bone health

Exercise Aversion

You have been screened for **1 gene** for the ‘ Exercise Aversion' category.

DNA TEST RESULT: SUMMARY

TRAIT	INFERENCE
Exercise Aversion	Higher Likelihood Of Desire Towards Exercise.

INFERENCE INTERPRETATION

Higher likelihood means that an individual has a positive attitude towards exercise.

Lower likelihood means that an individual does not have any motivation towards exercise.

Pathological Risk

BLOOD TEST RESULT	VALUE		RANGE
Heart Health			
Triglycerides	105	mg/dl	<150
APOA1:APOB Ratio	2.05	Ratio	1.01-5.00
Creatine Phosphokinase (CPK)	63	U/L	<170
Total Cholesterol	217	mg/dl	<200
Apolipoprotein-B (APOB)	89	mg/dl	66-133
LDL Cholesterol	136	mg/dl	<100
HSCRP (High Sensitivity C-Reactive Protein)	0.05	mg/l	1-3
Apolipoprotein-A1 (APOA1)	183	mg/dl	104-202
HDL Cholesterol	60	mg/dl	40-60
VLDL Cholesterol	21	mg/dl	0-30
LDL:HDL Ratio	2.26	mg/dl	<3.5
Total Cholesterol:HDL Ratio	3.61	mg/dl	3.4-7.1
Kidney & Intestine Health			
Total Protein	6.9	G/Dl	6.6-8.7
BUN - Blood Urea Nitrogen	10.28	mg/dl	8-25
Serum Creatinine	0.64	mg/dl	0.57-1.11
Serum Uric Acid	4	mg/dl	2.4-5.7
Serum Urea	22	U/L	16.6-48.5
Liver & Gallbladder Health			
Bilirubin Total	0.2	U/L	<1.2
Bilirubin Indirect	0.1	mg/dl	0.2-0.7
Bilirubin Direct	0.1	mg/dl	<0.3
SGOT (AST)	29	U/L	5-34
SGPT (ALT)	21	U/L	0-33
Gamma Glutamyl Transferase (GGT)	14	U/L	<40
Alkaline Phosphatase	62	U/L	35-105
Albumin	4	G/Dl	3.5-5.2
Globulin	2.9	G/Dl	2.5-3.5
Albumin/Globulin Ratio	1.38	Ratio	1.10-2.50

Pathological Risk

BLOOD TEST RESULT	VALUE		RANGE
Pancreas Health			
Average Glucose	111.15	%	<114
Glycosylated Haemoglobin (HbA1C)	5.5	%	4.5-6.3
Fasting Glucose	86	mg/dl	65-110
Post Prandial Glucose	99	mg/dl	70-140
Thyroid Health			
Thyroid Stimulating Hormone	2.2	uiu/ml	0.4-4.2
Triiodothyronine (T3)	1.6	ng/ml	0.58-1.59
Thyroxine (T4)	8.05	µg/dl	4.87-11.72
Nutrition Health			
Vitamin D	91	Nmol/L	75-250
Vitamin B12	796	Pg/Ml	211-946
Folate (Folic Acid)	16	Ng/Ml	7 - 15
Iron	127	Ug/DL	37-145
Transferrin Saturation	35.27	%	18-35
Calcium	8.9	Mg/Dl	8.8-10.2
Potassium	4.8	Mmol/L	3.5-5.2
Sodium	140	Mmol/L	136-146
Phosphorus	3.1	Mg/Dl	2.5-4.5
Chloride	110	Mmol/L	98-107
Other Pathological Parameters			
Haemoglobin	12.6	G/Dl	12-15
RBC Count (Red Blood Cell)	4.15	Millions/ Cu.Mm	3.8- 4.8
Hematocrit	38.8	%	36-46
MCV	93.5	FL	83-101
MCH	30.4	Pg	27-32
MCHC	32.5	G/Dl	31.5-34.5
RDW	13.1	%	11.6-14.1

Pathological Risk

BLOOD TEST RESULT	VALUE		RANGE
Other Pathological Parameters			
Total Leukocyte Count	**4370**	/cumm	4000-10000
Neutrophils	**54.4**	%	40-80
Eosinophils	**3.4**	%	1-6
Lymphocytes	**36.2**	%	20-40
Monocytes	**5.1**	%	2-10
Basophils	**0.9**	%	0-2
Platelet Count	**2.44**	lakh/cumm	1.5-4
MPV	**10**	FL	7-11
Absolute Neutrophils Count	**23.77**	/L	15-80
Absolute Lymphocytes Count	**15.82**	/L	10-30
Absolute Eosinophil Count	**1.49**	/L	0-4
Absolute Monocytes Count	**2.23**	/L	2-10
Total Iron Binding Capacity	**360**	ug/dl	250-450
Homocysteine, Quantitative	**3.48**	µmol/l	4-16
ESR	**21**	mm/hr	0-20

Monitoring (Tests & Investigations)

Test	Frequency
LIPID PROFILE THYROID PROFILE RENAL PROFILE ESR - ERYTHROCYTE SEDEMENTATION RATE IRON STUDIES FOLATE (FOLIC ACID) CHLORIDE	EVERY 6 MONTHS
GLUCOSE FASTING, GLYCATED HAEMOGLOBIN, AVERAGE GLUCOSE, INSULIN LEVELS, HOMA-IR (ESTIMATES INSULIN RESISTANCE) VITAMIN B12 VITAMIN D3 (25-HYDROXY CHOLECALCIFEROL) PHOSPHORUS CALCIUM ANTHROPOMETRIC MEASUREMENTS	EVERY 12 MONTHS

Disclaimer

This test was designed and performed by HaystackAnalytics using standard technical and operational protocols.

The interpretation of the test results is based on currently available information and might be updated subject to future data availability and research.

Godrej Memorial Hospital & HaystackAnalytics test a limited number of highly relevant markers for each trait/condition and not all genotypes that have reportedly been associated with specific traits. A low risk for a condition/trait does not rule out a higher risk for the condition/trait caused due to another genotype/SNP that was not tested at Godrej Memorial Hospital & HaystackAnalytics. The genotypes selected are globally reported and not specifically relevant to any ethnic groups. Reporting for these genotypes has been done as per the information that was available on current research today.

NGS is a highly sensitive technique; common reasons for paradoxical results are contamination during specimen collection, selection of inappropriate specimens, DNA quality and inherent PCR inhibitors in the specimen, rare technical errors and rare genetic variants.

Approximately 10% of exons may not be covered at sufficient levels to reliably call heterozygous variants.

Large deletions, duplications, copy number variations (CNV) /chromosomal rearrangements, mtDNA mutations, epigenetic factors, mosaicism, uniparental disomy (UPD), repetitive/ high GC rich regions, mononucleotide repeats (n >8) and mutations in genes with pseudogenes/highly homologous sequences cannot be assessed using this method.

The test report does not assess variants in deep intronic regions, regulatory domains and uncharacterized alternative exons, unless indicated otherwise.

The sequences obtained are aligned to the human reference genome (GrCh38/hg38) which has limitations and is continually being updated.

It is presumed that the specimen belongs to a patient named or identified. Godrej Memorial Hospital & HaystackAnalytics shall not be liable for any specimen errors or damage during transit before the specimen arrives.

A negative finding does not rule out a genetic diagnosis.

Clinical consultation and/or genetic counseling helps to explain test results to the patients and to discuss reproductive options is recommended. Results can be used for both diagnostic and scientific research purposes.

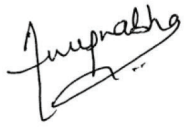
Godrej Memorial Hospital & HaystackAnalytics provides genetic assessment services only for investigational purposes and the information thus given should be interpreted and used exclusively only by qualified medical practitioners, certified physicians, dieticians, nutritionists, sports therapists and others in similar professions. The company does not provide any medical advice and this report does not constitute a medical diagnostic Report.

Incidental findings will be reported as per the American College of Medical Genetics guidelines and have to be correlated with clinical and family history by qualified medical practitioners and subject matter experts.

The following representatives have reviewed this document.



Dr Aparna Bhanushali, PhD
Head of Growth & Scientific Support

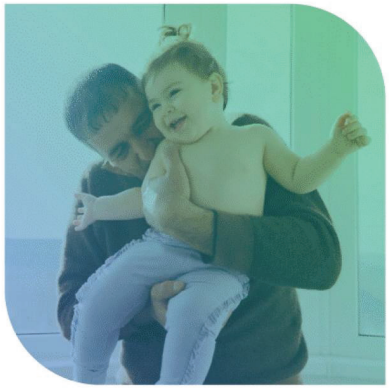


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