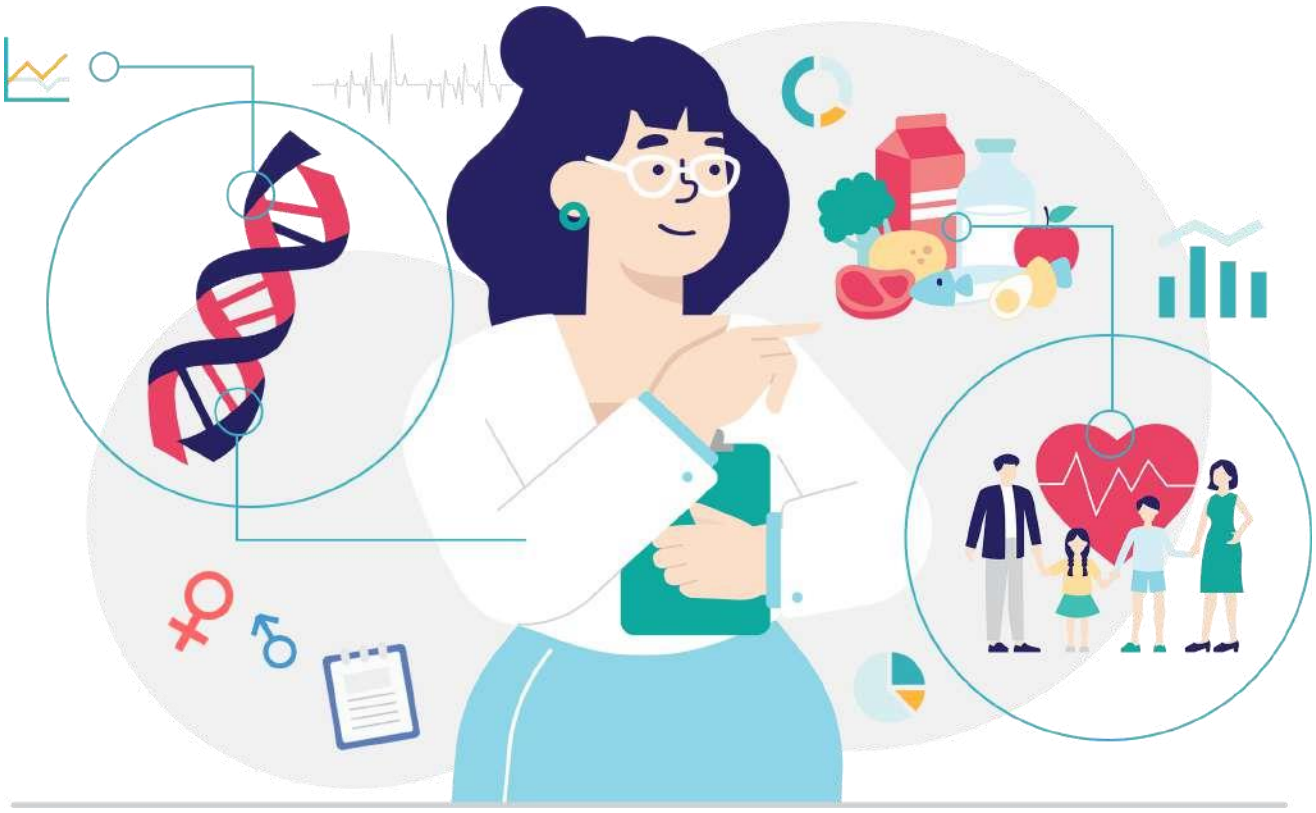
# Personal Genomics Report

| | |
|---|---|
| **Customer ID:** | **36220513024104** |
| **Date of Birth (DD/MM/YYYY):** | **01/01/1970** |
| **Gender:** | **/** |
| **Reported Date (DD/MM/YYYY):** | **22/08/2024** |



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# Let us introduce you to the world of DNA

DNA, namely deoxyribonucleic acid, is a complex molecule that is present deep inside cells through all over your body. DNA contains all of the information necessary to build and define you. DNA is written in code to form genes, making you one-of-a-kind on this planet.

The DNA molecule consists of two strands that wind around one another to form a shape known as a double helix. Each strand has a sugar-phosphate backbone loaded with four bases: Adenine (A), Cytosine (C), Guanine (G) and Thymine (T). The two strands spiral about one another by base-pairing: an A with a T, and a C with a G. DNA strands are so long that they must be packed, in the form of chromosome, in order to fit in the nucleus of every cell.

# Explore your DNA, know yourself better.

*"Genes are like the story, and DNA is the language that the story is written in."*

Our service can help you understand your "*stories*" better by exploring through your DNA. You can make a better living with food your body may prefer, or even know what exercise options are safer and effective for you.

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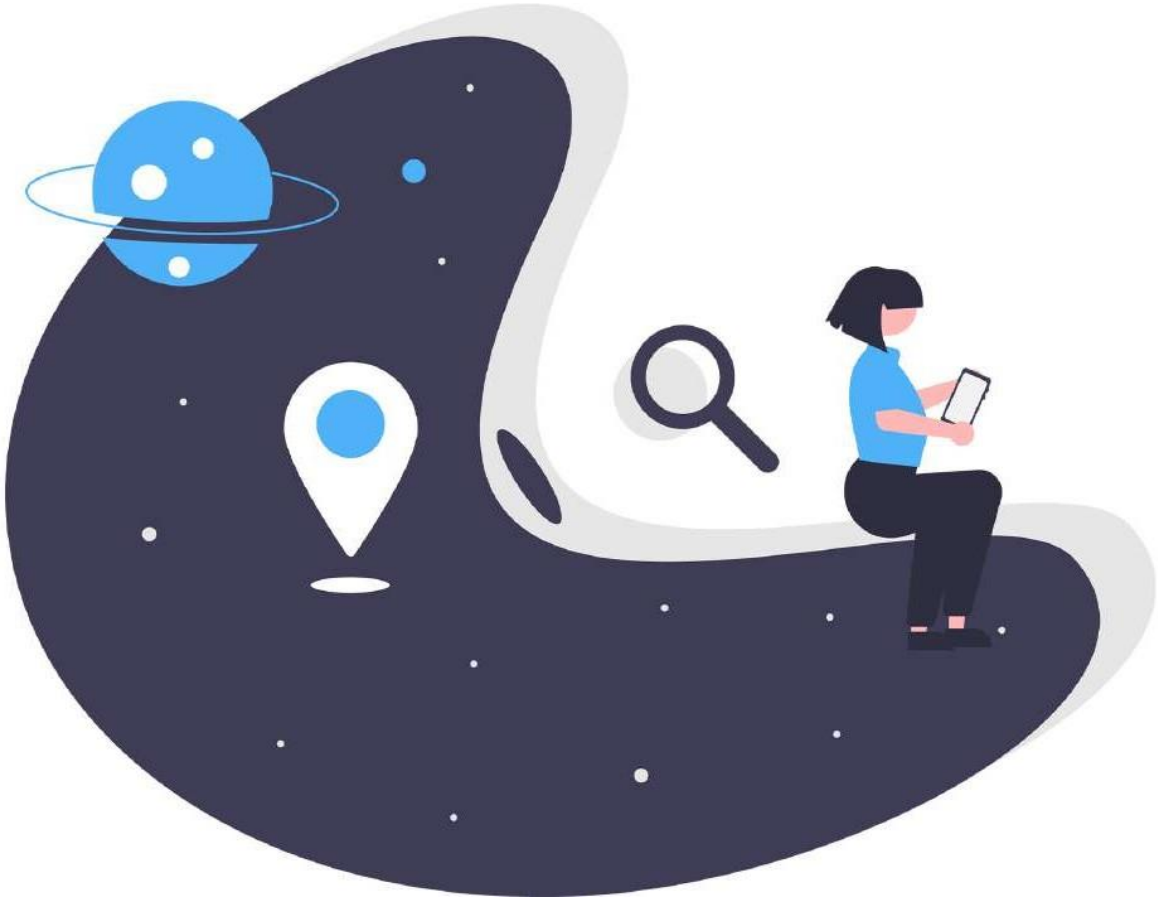
# Ancestry Analysis

Discovering the secret of your origin through genetic testing allows you to not only find out about your ancestral composition and trace it back to your ancestor's historical migration routes, but also reveal the genetic traces of extinct human races concealed in your body.



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# Ancestry Analysis

4 Reports

## My Ancestry

| | |
|---|---|
| Ancestry Composition | 95.83% Southern Han Chinese |
| Paternal Haplogroup | Unknown |
| Maternal Haplogroup | F1e3 |
| Neandrethal Ancestry | 3.381% |

# Content

# Ancestry Analysis

Everybody's own unique ancestral history is encrypted in their DNA. The following DNAset report helps to decode your story by analyzing hundreds of thousands of your autosomal polymorphisms.

## My Ancestry Composition

| | |
|---|---|
| Chinese | 96.95% |
| • Southern Han Chinese | 95.83% |
| • Tibetan | 0.82% |
| • Tungusic | 0.28% |
| • Other | 0.02% |
| Northeast Asian | 3.01% |
| • Korean | 3.01% |
| Others | 0.03% |

## My Ancestry Timeline

Genomic information allows us to know our ethnic makeup and to better understand ourselves from the ancestral level. However, apart from the specific ethnic components in our DNA, we may also want to know when these genes were passed on to us. DNAset estimates the approximate time each ancestral component was mixed into your genome to help interpret how the ancestral footprints have shaped you.

In general, homologous recombination during human reproduction makes the above calculations very difficult. Thus, we introduce two presuppositions:

1. Each ancestral component is derived from a single ancestor with pure ancestral makeup.

2. On average, each generation passes ~50% of their genetic materials to the next generation.

| | | |
|---|---|---|
| 1 – 2 Generation | 1970 – 1945 | Southern Han Chinese |
| 6 – 7 Generation | 1845 – 1820 | Korean |
| 7 – 8 Generation | 1820 – 1795 | Tibetan |

## The Basics of Ancestry Analysis

Genetic characteristics are passed on to successive generations via DNA replication. Human gametes are produced by a process called meiosis, during which homologous recombination occurs. This leads to the random exchange of genetic materials between two strands of DNA inherited from each parent. This complex process not only enables parental DNA to be passed on to offspring, but also generates mutations to ensure genetic diversity in a population. Single nucleotide polymorphisms (SNPs) are the most common among the mutations. These SNPs have a strong ethnic specificity and can be used to reflect the genetic characteristics of a population.

## Method of Ancestry Analysis

DNAset's supervised machine learning algorithm is based on the Admixture ancestor analysis tool developed by the University of California, Los Angeles (UCLA). The algorithm compares your autosomal DNA information with 42 reference populations in the DNAset database, and quantifies the similarities between your genome and the 42 reference DNA.

# Paternal Y-DNA haplogroup

Molecular anthropologists have established a haplogroup tree of human populations based on particular variants of the Y chromosome, which is passed on from fathers to son. DNAset helps to trace your paternal origin, evolution and migration history according to your Y-DNA haplogroup inference.

**My Paternal Haplogroup**

**Unknown**

## Why Is It Unknown?

The paternal lineage is based on analysis of the Y chromosome, which only exists in males and is strictly passed from father to son. As females do not have the Y chromosome, female users would not have a paternal haplogroup result.

You can link the paternal haplogroup results from your father, brother or other direct male relatives in your family if they have their DNA tested.

Note for female users: The Y chromosome of your son is inherited from his own father, not your father.

## The Basics of Paternal Lineage Analysis

The Y Chromosome (Chr) is the sex-determining chromosome in humans - only males have the Y Chr and it's passed from father to son. The Y Chr generally does not undergo homologous recombination and is inherited almost identically between father and son. But due to copying errors during DNA replication, roughly 2 mutations in the Y Chr is produced per generation. Such Y-chromosomal mutations accumulate in the evolutionary history of human populations for tens of thousands of years, and are used by molecular anthropologists to infer paternal lineages.

Studies have shown that modern humans originate from Africa. According to recent estimates, the common ancestor of all males - the Y-chromosomal Adam - appeared in Africa about

236,000 years ago (or 275,000 years), while the most recent common ancestry of Eurasia males has been traced back to about 69,000 years ago.

Based on the Y Chr data of different populations, molecular anthropologists have established a tree-like Y- DNA haplogroup map. Each branch of the tree corresponds to a haplogroup where Y chromosomes contain similar mutations. DNAset can accurately predict your Y-DNA haplogroup through the comparison between your DNA test results and the reference Y-DNA haplogroup tree. This allows us to trace the origin, evolution and migration history of your paternal lineage

## Method of Paternal Lineage Analysis

Referring to the Y-DNA haplogroup tree published by ISOGG, DNAset developed a method which can predict Y-DNA haplogroup, quickly and accurately. Specifically, by comparing the Y Chromosome test result to each haplogroup on the tree, probability scores are evaluated, and the highest scored haplogroup will be assigned as the best matching Y-DNA haplogroup for the user. After continuous optimization of the scoring system, DNAset now offers highly accurate Y-DNA haplogroup results and details of all detected variants on the ISOGG reference tree, which can be accessed conveniently.

## Maternal MT-DNA haplogroup

Molecular anthropologists have established a human mitochondrial DNA (MT-DNA) haplogroup tree based on particular variants of the MT-DNA, which is generally only passed from mother to offspring. DNAset helps to trace your maternal origin, evolution and migration history according to your MT-DNA haplogroup inference.

**My Maternal Haplogroup**

# F1e3

### Brief Introduction to My Haplogroup

About My Haplogroup

Haplogroup F, sister group of Haplogroup B, P, U, subclade of Haplogroup R

Time of Origin

43,400 Years Ago

Mainly Distributed Areas

East Asia, Southest Asia and America

Representative Populations

Ladhulsi, Shors and Han

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Migratory Track


Principles of Maternal Lineage Analysis

MT-DNA is a kind of unique circular DNA outside the nucleus. Unlike the inheritance of the Y Chr of paternal lineage, the MT-DNA is generally only from the egg provided by the mother. The MT-DNA does not undergo homologous recombination and is inherited almost identically between the offspring and his/her mother. The MT-DNA is a circular DNA resembling prokaryotic genes that mutates more frequently than the Y Chr during replication. Such mitochondrial mutations accumulate in the evolutionary history of the human populations for tens of thousands of years, and are used by molecular anthropologists to infer maternal lineages.

Studies have shown that modern humans originate from Africa. According to the maternal lineage estimations, the most recent common ancestor - the mitochondrial Eve - appeared in Africa about 200,000 years ago.

Based on MT data of different populations, molecular anthropologists have established a tree-like MT-DNA haplogroup map. Each branch of the tree represents a MT haplogroup with similar mutations. DNAset can accurately predict your MT-DNA haplogroup through comparison between your DNA test results and the reference MT-DNA haplogroup tree, so as to trace the origin, evolution and migration history of your maternal lineage.

## Method of Maternal Lineage Analysis

DNAset refers to the MT haplotype typing method published by the Chinese Academy of Sciences to predict users' MT-DNA haplogroup. Specifically, by comparing the user's MT-DNA result to each haplogroup on the MT-DNA haplogroup tree published by phylotree, probability scores are evaluated, and the highest scored haplogroup will be assigned as the best matching MT-DNA haplogroup for the user.

DNAset now offers highly accurate MT-DNA haplogroup results and details of all detected variants on the phylotree reference tree, which can be accessed conveniently.

## Neanderthal Variants Percentage

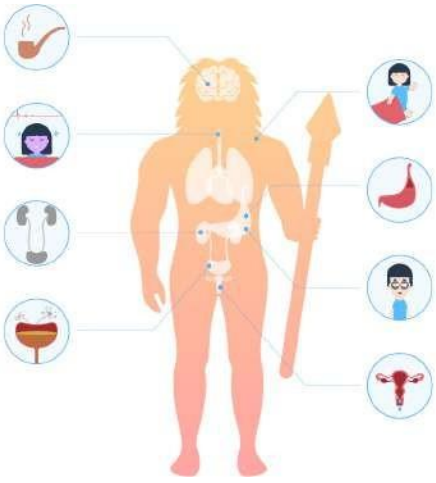
The Neanderthals are a group of extinct ancient humans, but they have passed on genetic information through gene flow with ancestors of modern humans. DNAset attempts to explore the secrets of human origin by analyzing the percentage of Neanderthal variants in your genome.

**My percentage of Neanderthal variants is**

**3.381 %**

**72.34% of DNAset users are similar to me**

## Health risks possibly related to Neanderthal variants



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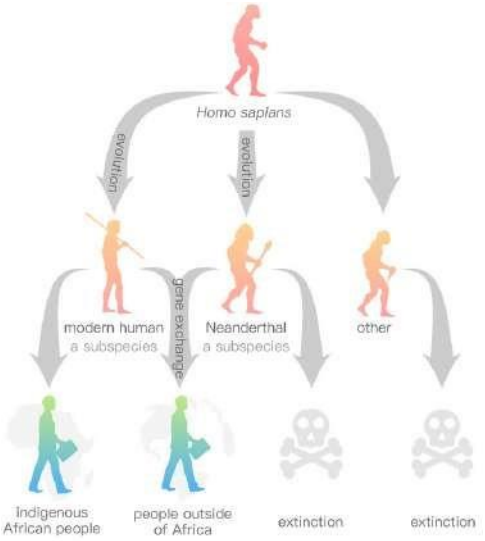
| | |
|---|---|
| **Tobacco Use Disorder**<br>It is a neuropsychiatric disease, which is also known as tobacco dependence. When smokers become addicted to nicotine, their physical manifestations are increased tolerance and withdrawal symptoms, and their behavior is manifested as loss of control. | Positive |
| **Protein-Calorie Malnutrition**<br>It is a nutritional deficiency disease caused by insufficient food supply or diseases. Wasting and kwashiorkor syndrome are the main clinical manifestations. Weight loss is due to the long-term lack of calories, protein and other nutrients in the diet, or there is malfunction in patient's digestion, absorption and utilization of food. | Negative |
| **Functional Disorders of Bladder**<br>It is urinary dysfunctions caused by damage to the central or peripheral nerves that control urination. It is a relatively common disease and is sometimes misdiagnosed as urinary tract infection in clinical practice. | Negative |
| **Symptoms Involving Urinary System**<br>Diseases can occur in various organs of the urinary system (kidneys, ureters, bladder, urethra) and affect the entire system. It can be caused by pathological changes in other systems of the body, and can also affect other systems or even the whole body. | Negative |
| **Stress Urinary Incontinence in Female**<br>It refers to the involuntary leakage of urine from the external urethra when the abdominal pressure increases due to sneezing or coughing in women. The major symptom is involuntary urination when abdominal pressure increases, such as during coughing, sneezing, and laughing. Body signs include increased abdominal pressure, observable involuntary outflow of urine from the urethra. | Negative |
| **Obstructive Sleep Apnea**<br>It is characterized by recurrent episodes of complete or partial obstruction of the upper airway leading to reduced or absent breathing during sleep. The airflow through the mouth and nose may stop for 10 seconds or more, and is accompanied by decreased blood oxygen saturation during each episode. There can be 30 or more episodes during a 7-hour sleep in an adult at night. | Negative |
| **Sleep Related Movement Disorders**<br>It is characterized by excessive limb movement when a person is about to fall asleep. Physical activity of the limbs usually will not affect sleep, but if this occurs too frequently, it may lead to periodic limb twitch disorder, which in turn leads to insomnia. | Negative |
| **Gastroparesis**<br>It is also known as paralysis or weakness of the stomach, which is a group of clinical symptoms characterized by delayed gastric emptying. Main symptoms include early satiety, epigastric postprandial fullness, nausea, episodic retching, vomiting, weight loss, etc. | Negative |

# Who Were the Neanderthals?




Based on current anthropological research, both modern humans and the Neanderthals are subspecies of Homo sapiens.

Studies show that the Neanderthals and modern humans outside of Africa share 1%~4% of their total genomes. Scientists believe that about 100,000 to 50,000 years ago, one branch of the modern humans came out of Africa and mixed with the Neanderthals in the Middle East. The mixed descendants are scattered throughout Europe, Asia, the Americas, and Oceania. But the modern Africans don't have any Neanderthal genes, because their ancestors stayed in Africa.

Method of Neanderthal Variants Analysis

DNAset uses AdmixTools, the ancestry analysis toolkit developed by Harvard University, to calculate your Neanderthal genetic composition by comparing your genome sequences with the Neanderthal sequences.

# Genes Tested



Nicotine Dependence：SLC6A11

rs901033, where the non-neanderthal allele is C and the Neanderthal allele is T. Studies found that individuals with the T allele had an increased risk of nicotine dependence.

Protein-Caloric Malnutrition：SLC35F3

rs12049593, where the non-neanderthal allele is C, and the Neanderthal allele is T. Studies have found that individuals with the T allele have an increased risk of protein-caloric malnutrition.

Bladder Dysfunction：DAB1

rs17115796, where the non-neanderthal allele is T, and the Neanderthal allele is C. Studies have found that individuals with the C allele have an increased risk of bladder dysfunction



Urinary Symptoms：STIM1

rs11030043, where the non-neanderthal allele is A, and the Neanderthal allele is G. Studies have found that individuals with the G allele have an increased risk of urinary symptoms.

Obstructive Sleep Apnea：PIK3C2G

rs7133666, where the non-neanderthal allele is C, and the Neanderthal allele is A. Studies found that individuals with the A allele have an increased risk of obstructive sleep apnea.

Sleep Limb Hyperactivity Disorder：PKP4

rs3771635, where the non-neanderthal allele is T and the Neanderthal allele is C. Studies found that individuals with the C allele have a reduced risk of developing sleep hyperactivity disorder.

Gastroparesis：SOX5

rs4963700, where the non-neanderthal allele is T and the Neanderthal allele is C. Studies found that individuals with the C allele have an increased risk of gastroparesis.

Details of Variants

| Report | Gene loci | My Gene | Description |
|---|---|---|---|
| Tobacco Use Disorder | RS901033 | CT | Higher risk of nicotine dependence |
| Protein-Calorie Malnutrition | RS12049593 | CC | No rise in the risk of protein-calorie deficiency malnutrition |
| Functional Disorders of Bladder | RS17115796 | TT | No rise in the risk of bladder dysfunction |
| Symptoms Involving Urinary System | RS11030043 | AA | No rising in the risk of urinary symptoms |
| Stress Urinary Incontinence in Female | RS17766531 | TT | No rising in the risk of stress urinary incontinence in female |