Comprehensive Genomic Report

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DoB: —	Subject ID: 30793
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Phenome Longevity

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Dear patient,

Congratulations on reaching a pivotal moment in your personal health journey. The comprehensive insights in your unique report are designed to empower both you and your healthcare provider, paving the way for informed decisions about your well-being.

Your genome analysis is grounded in the latest advancements in medical genomics. It's an exciting field that continues to grow—expect ongoing enhancements to your insights as science advances. We're committed to updating you with new findings that can further illuminate your health picture.

For additional information and support resources, please visit our website. It's filled with useful content that can help you deepen your understanding of your health.

Should you have any inquiries or wish to discuss your results in detail, don't hesitate to reach out. Our team of expert genetic counselors is at your service. You can schedule an appointment via email at info@phenomelongevity.com or visit our contact page at www.phenomelongevity.com for local contact information.

We are honored to have played a part in unlocking the secrets of your genome. As your explorations into your genetics continue, remember that Phenome Longevity is here to guide you every step of the way. Your feedback is invaluable to us—it helps enhance our services, ensuring that your journey with us is nothing short of exceptional.

Warm regards,

Phenome Longevity Team

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Information Overview

What is a Gene?

Genes are fundamental units of heredity, composed of DNA sequences that act as blueprints for building proteins—molecules that play critical roles in cellular function, structure, and regulation. Humans have approximately 20,000 genes, each responsible for guiding biological processes such as metabolism, immune response, and neurological development. Genes determine traits like eye color, hair texture, and even aspects of personality. Additionally, genes influence how we process nutrients, respond to environmental factors, and metabolize medications. Inheritance patterns shape genetic diversity, with each individual carrying two copies of most genes—one from each parent. Small changes in gene sequences, known as mutations or variants, can have significant effects, sometimes leading to inherited diseases, while other times contributing to beneficial adaptations such as resistance to certain infections. As scientific advancements continue, understanding our genetic blueprint helps us uncover the underlying mechanisms of health, disease, and evolution.

Understanding Inheritance Patterns

Genetic inheritance follows distinct patterns that determine how traits and conditions are passed down through generations. Dominant inheritance occurs when a single altered copy of a gene is sufficient to express a trait or condition, as seen in disorders like Huntington's disease. In contrast, recessive inheritance requires two altered copies, one from each parent, for the trait to manifest, as is the case with cystic fibrosis or sickle cell anemia. Some traits follow sex-linked inheritance, where genes located on the X or Y chromosomes influence characteristics and disease susceptibility—such as hemophilia, which predominantly affects males due to the presence of only one X chromosome. Additionally, mitochondrial inheritance follows a maternal pattern, as mitochondria, the energy-producing structures in cells, contain their own DNA and are passed exclusively from mothers to offspring. Polygenic inheritance involves multiple genes working together to determine complex traits like intelligence, height, and disease susceptibility. Understanding inheritance patterns helps identify genetic risks, improve diagnostic accuracy, and guide reproductive decision-making.

How We Interpret Your Results

Genetic analysis involves sequencing DNA to identify variations and comparing findings with global scientific databases, clinical studies, and bioinformatics models. Using cutting-edge sequencing technologies like next-generation sequencing (NGS), we can detect genetic variants and assess their potential significance. Variants are classified into categories such as pathogenic (disease-causing), likely pathogenic, benign (harmless), and variants of uncertain significance (VUS). Our interpretation process considers multiple factors, including variant frequency in populations, inheritance patterns, and functional studies assessing gene expression and protein interactions. Additionally, pharmacogenetics—the study of how genes affect drug response—enables personalized treatment plans, ensuring that medications are prescribed based on an individual's genetic profile. This approach enhances precision medicine by tailoring healthcare strategies to prevent diseases, improve early diagnosis, and optimize therapeutic interventions. By continuously integrating the latest medical knowledge, we empower individuals to make informed health decisions based on their unique genetic landscape.

How Do Variants Occur?

Genetic variants are alterations in the DNA sequence that contribute to biological diversity and individuality. These variants can be inherited from parents or arise spontaneously due to environmental factors, cellular replication errors, or exposure to radiation and chemicals. While most genetic changes have no impact or even offer advantages—such as increased disease resistance—others may alter protein function, potentially leading to disorders or increased susceptibility to conditions like heart disease, cancer, or neurodegenerative disorders. There are several types of genetic variants, including single nucleotide polymorphisms (SNPs), insertions, deletions, and copy number variations (CNVs). Some variants influence physical characteristics, such as height and skin tone, while others affect internal processes, such as how the body metabolizes caffeine or responds to stress. Understanding genetic variations allows researchers and medical professionals to predict disease risk, develop targeted therapies, and personalize treatments based on an individual's unique genetic makeup.

Understanding Your Report

How Your Data is Organized

There is a lot of information here. Take a look, and feel free to contact us at info@phenomelongevity.com if you have questions about your report. The first several summary pages of your report include all results that may have a medical impact on you and possibly other family members. Results are organized by their level of clinical relevance.

Immediate Attention Needed

These genetic findings require immediate medical attention. We have identified pathogenic or likely pathogenic variants in genes associated with serious health conditions that may significantly impact your well-being. For autosomal dominant conditions, having just one copy of these variants can be clinically significant, while for recessive conditions, the presence of two copies increases the likelihood of disease manifestation. These variants are well-documented in medical literature, including the American College of Medical Genetics and Genomics (ACMG) guidelines, which provide expert-reviewed classifications of genetic variants based on their clinical significance. The identified genetic changes may necessitate proactive medical management, further diagnostic testing, or consultations with healthcare professionals to assess potential implications and preventive measures.

What This Means For You:

- Consult with healthcare providers promptly
- May need specialist referrals
- Could require immediate preventive measures
- Important for family planning discussions
- May impact treatment decisions

Next Steps:

- Schedule an appointment with your healthcare provider
- Share this report with your medical team
- Consider genetic counseling for detailed guidance
- Discuss screening and prevention strategies
- Evaluate family testing options

Monitor Closely

These genetic findings, while important, may have a less immediate impact on your health. They include variants of uncertain significance in clinically important genes, or pathogenic variants with reduced penetrance. This means that while these genetic changes are significant, their exact impact on your health may vary.

What This Means For You:

- Regular medical monitoring recommended
- May influence preventive care decisions
- Could affect long-term health planning
- Relevant for family health history
- May need periodic reassessment

Next Steps:

- Discuss these findings during your next medical visit
- Develop a monitoring plan with your healthcare provider
- Stay informed about new research
- Consider lifestyle modifications if recommended
- Keep records for future medical reference

For Your Information

These genetic findings provide valuable information about your health but typically have lower immediate clinical impact. They may include variants associated with more common conditions or those with reduced penetrance. While not requiring urgent attention, this information can be valuable for your overall health management.

What This Means For You:

- Useful for general health awareness
- May influence lifestyle choices
- Could be relevant for future health decisions
- Part of your complete genetic profile
- May become more significant with new research

Next Steps:

- Keep this information for future reference
- Consider discussing during routine check-ups
- Be aware of related symptoms or conditions
- Update your family health history
- Stay informed about advances in genetic research

Summary

Summary

Health Results

This section summarizes genetic variants that may impact your health, categorized by importance. Very important variants require immediate medical attention, while important variants may need monitoring and potential lifestyle changes. Each finding includes recommendations for next steps and actions to manage health risks.

No Significant Disease Risk Variants Detected

Summary

Carrier Results

This section summarizes genetic variants that indicate carrier status for various conditions. Being a carrier typically does not affect your health but may be relevant for family planning decisions, understanding potential risks for future children, and informing relatives who may be planning families. Each finding includes recommendations for next steps and potential implications for family planning.

Monitor Closely

Close monitoring and medical evaluation are advised. These findings suggest a moderate increase in disease risk, often due to variants with conflicting interpretations of pathogenicity or novel variants with uncertain clinical significance. While the direct impact on health may be less severe, a proactive approach is recommended, including routine medical check-ups, family history assessment, and targeted health screenings. Guidelines from organizations such as the American College of Medical Genetics (ACMG) emphasize the importance of discussing these results with a healthcare provider to determine if further genetic testing or additional clinical follow-up is needed.

Endocrine and Metabolic Disorders

Endocrine and metabolic disorders are characterized by disruptions in the body's hormonal systems and metabolic processes. These disorders can lead to serious health conditions such as diabetes, thyroid diseases, obesity, metabolic syndrome, and adrenal insufficiency. Hormonal imbalances can negatively affect energy production, growth and development, immune function, and overall body regulation. Genetic factors, environmental influences, dietary habits, and lifestyle choices play a crucial role in the development of these conditions. Early diagnosis and appropriate treatment can help manage symptoms and reduce the risk of complications.

Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency

Gene(s) & Variant(s)

- CYP21A2
- NM_000500.9:c.293-13C>G
- Uncertain Significance
- Heterozygous
- Autosomal recessive

What It Means

You have a variant linked to Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency, flagged by ACMG. Actions can be taken to lower its impact. See the Detailed Disease Section for more.

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Summary

Pharmacogenetics Analysis

Your genetic profile plays a crucial role in how your body processes and responds to medications. Pharmacogenetics is the study of how genetic differences influence individual responses to medications.

Immediate Attention Needed

(Major Gene-Drug Interaction)

These medications are classified under PharmGKB Level 1A, meaning they have the highest level of clinical evidence. Level 1A includes drug-gene interactions with specific dosing recommendations in FDA-approved labels or clinical guidelines. These interactions can significantly alter drug response, requiring immediate adjustments based on CPIC or FDA guidelines.

Fluorouracil

Gene	Genotype	Used for
DPYD	CT	Neoplasms

Both variants of rs1801159 are assigned normal function by CPIC. Patients with the CT genotype and cancer who are treated with fluorouracil, a fluoropyrimidine-based chemotherapy, may not have altered risk of drug toxicity as compared to patients with the CC or TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence risk of drug toxicity.

rs1801159 — Toxicity

Capecitabine

Gene	Genotype	Used for
DPYD	CT	Neoplasms

Both variants of rs1801159 are assigned normal function by CPIC. Patients with the CT genotype and cancer who are treated with capecitabine, a fluoropyrimidine-based chemotherapy, may not have altered risk of drug toxicity as compared to patients with the CC or TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence risk of drug toxicity.

rs1801159 — Toxicity

Warfarin

Gene	Genotype	Used for
CYP4F2	CT	

Patients with the rs2108622 CT genotype may have increased warfarin dosage requirements as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also affect warfarin dosage requirements.

rs2108622 — Dosage

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C

Patients with the rs12979860 CT genotype and hepatitis C infection may have decreased response (typically assayed as sustained virological response, SVR) when administered peg interferon alpha 2a or 2b in combination with ribavirin as compared to patients with the CC genotype, but an increased response as compared to patients with the TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence response to peginterferon alpha and ribavirin.

rs12979860 — Efficacy

Boceprevir, Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C, Chronic

Patients with the rs12979860 CT genotype and hepatitis C infection may have decreased response to triple therapy (boceprevir, peginterferon alfa-2a/2b and ribavirin) as compared to patients with the CC genotype. Other genetic and clinical factors may also influence response to boceprevir-peginterferon based therapy.

rs12979860 — Efficacy

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin, Telaprevir

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C, Chronic

Patients with the rs12979860 CT genotype and hepatitis C infection may have lower response rates (SVR) to triple therapy (telaprevir, peginterferon alfa-2a/b and ribavirin) as compared to patients with the CC genotype. However, conflicting evidence has been reported. The impact of IL28B genotype may be dampened in patients with prior PegIFN/RBV treatment failure. Other genetic and clinical factors may also influence response to HCV triple therapy.

rs12979860 **Efficacy**

Monitor Closely

(Significant Gene-Drug Interaction)

These interactions fall under PharmGKB Levels 1B, indicating limited or emerging evidence. Level 1B includes single-study reports or conflicting findings. While these findings are not currently actionable, they may become relevant as further research develops. Consider discussing with a healthcare provider for additional insights.

Warfarin

Gene	Genotype	Used for
VKORC1	CT	

Patients with the rs7294 CT genotype may require a higher dose of warfarin as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also affect warfarin dose requirements.

rs7294 **Dosage**

Gene	Genotype	Used for
VKORC1	GG	

Patients with the rs2359612 GG genotype may require an increased dose of warfarin as compared to patients with the AG or AA genotype. Other genetic and clinical factors may also influence dose of warfarin.

rs2359612 **Dosage**

Interferons, Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3	GT	Hepatitis C, Chronic

Patients with the rs8099917 GT genotype and chronic hepatitis C infection may have decreased response (lower SVR) to peginterferon alfa and ribavirin therapy as compared to patients with the TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence response to peginterferon alfa and ribavirin therapy. Please note that this SNP has been found to be in high LD with rs12979860 which is also associated with response to pegIFN-alpha/ribavirin.

rs8099917 **Efficacy**

Disease Risk Detailed

Disease Risk Detailed

Health Results

This section summarizes genetic variants that may impact your health, categorized by importance. Very important variants require immediate medical attention, while important variants may need monitoring and potential lifestyle changes. Each finding includes recommendations for next steps and actions to manage health risks.

No Significant Disease Risk Variants Detected

For Your Information

Miscellaneous Diseases

The miscellaneous category encapsulates a diverse array of conditions with genetic underpinnings not easily classified under the conventional disease groups. This includes rare genetic disorders, malignancies, and conditions with complex genetic etiologies. Genetic testing in this area can uncover unique genetic profiles, guiding bespoke interventions, research opportunities, and support for affected individuals and their families. Tailored healthcare approaches can significantly improve outcomes for these often overlooked conditions.

Peroxisome biogenesis disorder 4B

(Total reads: 37, Reference allele: 16, Alternative allele: 21)

Gene(s) & Variant(s)

Gene: PEX6
Variant: NM_000287.4:c.1802G>A
Zygosity: Heterozygous
Inheritance: Autosomal recessive, Autosomal dominant
Pathogenicity: Uncertain Significance
rsID: rs34324426

What It Means

This is a noteworthy genetic finding in your sequencing results, it is within one of the disease-causing genes in our database (except the ACMG SF v3.1 list). This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in Your variant is a heterozygous variant, which means the variant is existed on only one copy of the paired chromosomes (you've inherited the different alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Peroxisome Biogenesis Disorder 4B (PBD-4B) is a rare autosomal recessive disorder affecting the biogenesis of peroxisomes, with an estimated prevalence of 1-2 in a million individuals worldwide. This condition is caused by mutations in the PEX16 gene and is characterized by the accumulation of very long-chain fatty acids, pipecolic acid, and bile acid intermediates. PBD-4B exhibits a wide range of clinical manifestations, including neurological impairment, sensorineural hearing loss, retinopathy, and hepatomegaly. The severity and age of onset of PBD-4B vary significantly among affected individuals, with some individuals exhibiting symptoms in infancy and others not developing symptoms until later in childhood or even adulthood. Both genders can be affected, and the disorder has been reported in individuals of diverse ethnic backgrounds. The rarity and variability of PBD-4B contribute to its complexity, making it a challenging condition to diagnose and manage.

Lifestyle and Prevention

Managing Peroxisome Biogenesis Disorder 4B requires a comprehensive lifestyle approach focused on prevention and symptom management. Regular medical assessments are crucial to monitor the progression of the disorder, and strict adherence to prescribed medications is essential. A key aspect of managing this condition involves implementing lifestyle modifications that can significantly improve the individual's quality of life. This includes adopting a balanced diet, rich in essential nutrients and low in processed foods, to support overall health. Regular physical activity, as recommended by a healthcare provider, can help improve mobility and muscle function. It is also important to ensure adequate rest and avoid overexertion, as fatigue and weakness are common symptoms of the disorder. Furthermore, stress management techniques, such as meditation and mindfulness, can help reduce anxiety and improve overall well-being. Genetic counseling may also be beneficial in providing a better understanding of the disorder and developing personalized prevention strategies for individuals and their families.

Risk Factors

Peroxisome biogenesis disorder 4B (PBD-ZSD) is a rare, inherited metabolic disorder that affects the function of peroxisomes in the body. While the condition is primarily caused by genetic mutations, various risk factors can exacerbate its severity and influence the age of onset and the range of symptoms experienced by affected individuals. One such factor is environmental exposure to toxins, such as pesticides and pollutants, which can further impair peroxisome function and lead to worsened health outcomes. Additionally, certain medications, particularly those that are metabolized by peroxisomes, may pose increased risks for individuals with PBD-ZSD. Pre-existing medical conditions, such as liver disease or neurological disorders, can also interact with PBD-ZSD and contribute to a more complicated clinical picture. Furthermore, nutritional factors, such as deficiencies in certain vitamins and minerals, can exacerbate the symptoms of PBD-ZSD. Lastly, age-related factors, such as the natural decline in peroxisome function over time, can also play a role in the progression of PBD-ZSD. These diverse risk factors highlight the complex interplay influencing susceptibility to PBD-ZSD and emphasize the importance of a multidisciplinary approach to managing the condition.

Miscellaneous Diseases

Peroxisome biogenesis disorder 2B

(Total reads: 17, Reference allele: 0, Alternative allele: 17)

Gene(s) & Variant(s)

Gene: PEX5
Variant: NM_001351132.2:c.147+77_147+121del
Zygosity: Homozygous
Inheritance: Autosomal recessive
Pathogenicity: Not Found in ClinVar

What It Means

This is a noteworthy genetic finding in your sequencing results, it is within one of the disease-causing genes in our database (except the ACMG SF v3.1 list). This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in an autosomal recessive manner. An autosomal recessive disorder means two copies of an abnormal gene must be present in order for the disease or trait to develop. Your variant is a homozygous variant, which means the variant is existed on both copies of the paired chromosomes (you've inherited the same alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Peroxisome biogenesis disorder 2B (PBD-2B), also known as classical Refsum disease, is a rare autosomal recessive disorder affecting the metabolism of lipids and fat-soluble vitamins. It is caused by mutations in the PHARC1 gene, leading to defects in peroxisome biogenesis and function. The prevalence of PBD-2B is estimated to be 1-9 per million individuals worldwide, with a higher incidence in certain populations due to consanguinity. The disorder exhibits considerable variability in clinical presentation, even among siblings with the same genetic mutations. Symptoms typically appear in infancy or early childhood, but milder cases may not become apparent until later in life. Both genders can be affected, and the disorder transcends ethnic boundaries. Key features of PBD-2B include retinitis pigmentosa, peripheral neuropathy, cerebellar ataxia, and elevated levels of very-long-chain fatty acids in plasma and tissues. Early diagnosis and intervention are crucial for managing the disease and improving the quality of life for affected individuals.

Lifestyle and Prevention

Managing Peroxisome Biogenesis Disorder 2B requires a comprehensive lifestyle approach for optimal prevention and symptom management. Regular medical check-ups and adherence to prescribed medications are crucial. A key aspect of managing this disorder involves a customized diet plan, low in long-chain fatty acids and high in nutrients, to support overall health. Regular exercise, tailored to the individual's abilities, can help improve motor skills and quality of life. Additionally, avoiding certain substances, such as alcohol and tobacco, is essential for overall well-being. Genetic counseling is also recommended for individuals and their families to understand the genetic implications and develop personalized prevention strategies. Adequate rest and stress management techniques, such as meditation and mindfulness, can help improve symptoms and daily functioning. With a comprehensive lifestyle approach, individuals with Peroxisome Biogenesis Disorder 2B can lead fulfilling lives and mitigate the progression of the disorder.

Risk Factors

Peroxisome biogenesis disorder 2B (PBD-2B) is a rare inherited condition associated with an increased risk of developing various health complications. The disorder affects the normal functioning of peroxisomes, which play a crucial role in several metabolic processes within cells. While the specific risk factors for PBD-2B are not well-established due to its rarity, certain factors may contribute to the exacerbation and progression of the disease. Genetic predisposition is a significant factor, as PBD-2B is caused by mutations in the PEX2 gene, inherited in an autosomal recessive manner. Exposure to environmental toxins, such as pesticides and industrial chemicals, may further impair peroxisome function and contribute to the development of PBD-2B symptoms. Additionally, nutritional factors, like insufficient intake of essential fatty acids, can exacerbate the disorder. Moreover, the presence of other medical conditions, such as neurological disorders or metabolic diseases, may interact with PBD-2B, leading to more severe complications. While these factors do not directly cause PBD-2B, they can influence the disease's progression and the individual's overall health. Further research is needed to better understand the risk factors and develop effective prevention and treatment strategies for PBD-2B.

Miscellaneous Diseases

Rhizomelic chondrodysplasia punctata type 5

(Total reads: 17, Reference allele: 0, Alternative allele: 17)

Gene(s) & Variant(s)

Gene: PEX5
Variant: NM_001351132.2:c.147+77_147+121del
Zygosity: Homozygous
Inheritance: Autosomal recessive
Pathogenicity: Not Found in ClinVar

What It Means

This is a noteworthy genetic finding in your sequencing results, it is within one of the disease-causing genes in our database (except the ACMG SF v3.1 list). This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in an autosomal recessive manner. An autosomal recessive disorder means two copies of an abnormal gene must be present in order for the disease or trait to develop. Your variant is a homozygous variant, which means the variant is existed on both copies of the paired chromosomes (you've inherited the same alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Rhizomelic chondrodysplasia punctata type 5 (RCDP5) is a rare inherited disorder of peroxisome biogenesis, with an estimated prevalence of about 1 in 1,000,000 individuals globally. This condition is caused by mutations in the PEX7 gene and is characterized by congenital cataracts, hypotonia, seizures, and developmental delay. RCDP5 exhibits autosomal recessive inheritance, and its symptoms can vary widely in severity even among siblings who inherit the same genetic mutations. The disorder affects both genders equally and is found in individuals of all ethnic backgrounds. RCDP5 is often diagnosed in infancy or early childhood, and its progression can lead to significant physical and intellectual disabilities. Due to the rarity of RCDP5, research and clinical management are ongoing to improve the understanding, treatment, and prognosis of this debilitating condition.

Lifestyle and Prevention

Managing Rhizomelic Chondrodysplasia Punctata Type 5 requires a holistic lifestyle approach for effective prevention and symptom management. Regular developmental assessments, physical therapy, and adherence to prescribed medications are crucial components of care. Lifestyle modifications, such as maintaining a balanced diet, promoting physical activity appropriate for the individual's abilities, and ensuring adequate calcium and vitamin D intake, can significantly contribute to long-term well-being. Early intervention and genetic counseling play a vital role in developing personalized prevention strategies for individuals with this rare condition and their families. It is essential to work closely with healthcare professionals to monitor symptoms and optimize quality of life for those affected by Rhizomelic Chondrodysplasia Punctata Type 5.

Risk Factors

Rhizomelic chondrodysplasia punctata type 5 (RCDP5) is a rare genetic disorder caused by mutations in the PIGV gene. While many risk factors for RCDP5 are not yet fully understood, several contributing elements have been identified. Exposure to environmental toxins, such as heavy metals and organic pollutants, during critical periods of fetal development may increase the risk of developing RCDP5. Additionally, maternal factors, such as advanced maternal age, poor nutrition, and inadequate prenatal care, can also contribute to the risk. Genetic predisposition, particularly in individuals with a family history of the condition, plays a significant role in RCDP5 development. Furthermore, certain lifestyle factors, such as poor diet, lack of exercise, and exposure to secondhand smoke, may exacerbate the severity of symptoms in individuals with RCDP5. While these risk factors do not guarantee the development of RCDP5, they can significantly increase the likelihood. Further research is needed to better understand the complex interplay of risk factors associated with RCDP5.

Organ Health

Genetic factors significantly influence the health of various organs, including the liver, kidneys, and lungs. Genetic predispositions can affect the risk of organ-specific diseases such as polycystic kidney disease, liver cirrhosis, and cystic fibrosis. Genetic testing enables targeted actions to preserve organ health, including lifestyle adjustments, regular monitoring, and preventive treatments, aiming to prevent or delay the onset of disease and maintain organ function.

Tubulointerstitial kidney disease, autosomal dominant, 2

(Total reads: 22, Reference allele: 7, Alternative allele: 15)

Gene(s) & Variant(s)

Gene: MUC1
Variant: NM_001371720.2:c.1419-1C>G
Zygosity: Heterozygous
Inheritance: Autosomal dominant
Pathogenicity: Not Found in ClinVar
rsID: rs1553199150

What It Means

This is a noteworthy genetic finding in your sequencing results, it is within one of the disease-causing genes in our database (except the ACMG SF v3.1 list). This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in an autosomal dominant manner. Dominant means that a single copy of the mutated gene (from one parent) is enough to cause the disorder. Your variant is a heterozygous variant, which means the variant is existed on only one copy of the paired chromosomes (you've inherited the different alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Tubulointerstitial kidney disease, autosomal dominant, type 2 (ADTKD-Type 2) is a rare inherited renal disorder with a prevalence estimated to be around 1-9 in 1,000,000 individuals worldwide. This condition is characterized by the progressive degeneration and fibrosis of the kidney's tubules and interstitium, leading to a decline in renal function over time. ADTKD-Type 2 exhibits autosomal dominant inheritance, meaning that affected individuals have a 50% chance of passing the disorder on to their offspring. The age of onset and severity of ADTKD-Type 2 can vary significantly, even among family members, contributing to its complexity. Both men and women are susceptible to this disorder, and it affects individuals across diverse ethnic backgrounds. The disease often manifests in adulthood, typically between the third and fifth decades of life, and is characterized by chronic kidney disease, proteinuria, and, in some cases, kidney failure.

Lifestyle and Prevention

Managing autosomal dominant tubulointerstitial kidney disease requires a proactive lifestyle approach for effective prevention and symptom management. Regular nephrology check-ups, monitoring of kidney function, and adherence to prescribed medications are crucial. Lifestyle modifications, such as maintaining a healthy fluid intake, following a balanced diet, and avoiding nephrotoxic substances, contribute significantly to long-term well-being. In addition, addressing and controlling any underlying conditions, like hypertension or diabetes, is essential for preventing disease progression. Genetic counseling plays a vital role in providing personalized prevention strategies for individuals and their families, helping them understand the genetic components and potential implications of the disease.

Risk Factors

Tubulointerstitial kidney disease, autosomal dominant, 2 is a genetic disorder that primarily affects the kidneys' functional units, the tubules and interstitium. Several risk factors contribute to the progression and severity of this condition. A key risk factor is a family history of the disease, as it is inherited in an autosomal dominant pattern. Additionally, exposure to certain medications, such as lithium, analgesics, and chemotherapy drugs, can increase the risk of developing tubulointerstitial kidney disease. Long-term dehydration and recurrent kidney infections may also contribute to the disease's onset and progression. Environmental factors, such as lead exposure, can exacerbate kidney damage and accelerate disease progression. Moreover, certain comorbidities, like hypertension and diabetes, can further strain the kidneys and increase the risk of tubulointerstitial kidney disease. Lastly, advanced age and male gender have been identified as risk factors, with the disease more prevalent in older males. Understanding these risk factors is crucial for early detection, intervention, and management of tubulointerstitial kidney disease, autosomal dominant, 2.

Hereditary Disease

Microcephaly, facial dysmorphism, renal agenesis, and ambiguous genitalia syndrome

(Total reads: 37, Reference allele: 0, Alternative allele: 37)

Gene(s) & Variant(s)

Gene: CTU2
Variant: NM_001012759.3:c.1097+6_1097+11del
Zygosity: Homozygous
Inheritance: Autosomal recessive
Pathogenicity: Not Found in ClinVar

What It Means

This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in an autosomal recessive manner. An autosomal recessive disorder means two copies of an abnormal gene must be present in order for the disease or trait to develop. Your variant is a homozygous variant, which means the variant is existed on both copies of the paired chromosomes (you've inherited the same alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Microcephaly, facial dysmorphism, renal agenesis, and ambiguous genitalia syndrome is a rare genetic disorder with a complex inheritance pattern, affecting multiple organ systems. The prevalence of this condition is estimated to be very low, but its true incidence is difficult to determine due to underdiagnosis and varying clinical presentations. This syndrome can affect individuals of any gender and ethnic background, with symptoms often present at birth or becoming apparent in early childhood. The severity of the disorder varies widely, even among family members, indicating variable expressivity and incomplete penetrance. Microcephaly, or abnormally small head size, is a hallmark feature, along with distinctive facial dysmorphisms. Renal agenesis, or the absence of one or both kidneys, and ambiguous genitalia are also common in this syndrome. The underlying genetic causes are heterogeneous, and the diagnosis is often made based on clinical examination, imaging studies, and genetic testing.

Lifestyle and Prevention

Managing a syndrome that includes microcephaly, facial dysmorphism, renal agenesis, and ambiguous genitalia requires a comprehensive and personalized approach to effectively prevent associated complications. Regular developmental assessments, monitoring of overall health, and adherence to prescribed medications are crucial. Lifestyle adjustments, such as implementing a healthy and balanced diet, regular exercise, and avoiding harmful habits, play a significant role in promoting long-term well-being for individuals with this syndrome. Genetic counseling is also essential for developing tailored prevention strategies and providing necessary support for the individual and their family. Early intervention therapies, such as physical, occupational, and speech therapy, can greatly improve outcomes and quality of life. By staying proactive and engaged in a comprehensive management plan, individuals with this syndrome can lead fulfilling and rewarding lives.

Risk Factors

Microcephaly, facial dysmorphism, renal agenesis, and ambiguous genitalia syndrome is a complex genetic condition with various contributing factors. Genetic mutations, often de novo, play a significant role in the expression of this syndrome. However, environmental factors and maternal health also contribute to the risk and severity of the syndrome. Maternal exposure to certain infectious agents, such as cytomegalovirus or rubella, during pregnancy can increase the risk of microcephaly and other anomalies. Poor maternal nutrition, particularly insufficient intake of essential nutrients like folic acid, may also play a role in the development of this syndrome. Advanced maternal age has been linked to a higher likelihood of chromosomal abnormalities, which can contribute to the occurrence of the syndrome. Furthermore, exposure to teratogens, including alcohol, drugs, and certain medications, can increase the risk of facial dysmorphism, renal agenesis, and ambiguous genitalia. Lastly, consanguinity between parents can also increase the risk of this syndrome due to the potential for recessive gene expression. Early identification and intervention can significantly improve outcomes for affected individuals, highlighting the importance of prenatal screening and monitoring for mothers and fetuses at risk.

Carrier Status Detailed

Carrier Results

This section summarizes genetic variants that indicate carrier status for various conditions. Being a carrier typically does not affect your health but may be relevant for family planning decisions, understanding potential risks for future children, and informing relatives who may be planning families. Each finding includes recommendations for next steps and potential implications for family planning.

Monitor Closely

Category	Disease	Variant
Endocrine and Metabolic Disorders	Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency	NM_000500.9:c.293-13C>G

Monitor Closely

Endocrine and Metabolic Disorders

Endocrine and metabolic disorders are characterized by disruptions in the body's hormonal systems and metabolic processes. These disorders can lead to serious health conditions such as diabetes, thyroid diseases, obesity, metabolic syndrome, and adrenal insufficiency. Hormonal imbalances can negatively affect energy production, growth and development, immune function, and overall body regulation. Genetic factors, environmental influences, dietary habits, and lifestyle choices play a crucial role in the development of these conditions. Early diagnosis and appropriate treatment can help manage symptoms and reduce the risk of complications.

Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency

(Total reads: 150, Reference allele: 6, Alternative allele: ?)

Gene(s) & Variant(s)

Gene: CYP21A2
Variant: NM_000500.9:c.293-13C>G
Zygosity: Heterozygous
Inheritance: Autosomal recessive
Pathogenicity: Uncertain Significance
rsID: rs6467

What It Means

This is a important genetic finding on your sequencing results, because this variant falls into one of the 78 most promising disease-causing genes suggested by American College of Medical Genetics and Genomics Secondary findings (SF), version3.1.(PMID: 35802134). This variant is presented in ClinVar, as identified as pathogenic/likely pathogenic; or that it could affect protein function. This disease is inherited in an autosomal recessive manner. An autosomal recessive disorder means two copies of an abnormal gene must be present in order for the disease or trait to develop. Your variant is a heterozygous variant, which means the variant is existed on only one copy of the paired chromosomes (you've inherited the different alleles of a gene from each of your parents).

Recommendations

- Share this information with at-risk relatives. They may benefit from genetic testing.
- Consider genetic counseling.
- Discuss results with your physician at your next annual physical, as they may impact your health.
- Additional testing or confirmatory genetic testing may be recommended by your physician before taking any medical action.
- Lifestyle modifications may be helpful.

Disease Epidemiology

Classic congenital adrenal hyperplasia (CAH) due to 21-hydroxylase deficiency is a rare inherited autosomal recessive disorder affecting the adrenal glands. It has a global incidence of approximately 1 in 10,000 to 1 in 18,000 newborns. This condition is characterized by a deficiency in the 21-hydroxylase enzyme, leading to impaired cortisol and aldosterone production, and overproduction of androgens. The severity of CAH can vary, with the classic form presenting in infancy or early childhood, and the non-classic form presenting in late childhood or even adulthood. Both males and females can be affected, and it is more prevalent in certain ethnic groups, such as Ashkenazi Jews, Hispanics, and certain Arab populations. The disorder exhibits complete penetrance but variable expressivity, contributing to its complexity. Early diagnosis and treatment are crucial to prevent serious complications, such as adrenal crisis and abnormal sexual development.

Lifestyle and Prevention

Managing classic congenital adrenal hyperplasia (CAH) due to 21-hydroxylase deficiency requires a holistic lifestyle approach for optimal prevention and control. Regular medical check-ups, including monitoring hormone levels and electrolyte balance, are crucial for early detection and management of potential complications. Adherence to prescribed medications, such as hormone replacement therapy, is essential for maintaining hormonal balance and preventing associated health issues. Lifestyle adjustments, including a balanced diet, regular exercise, and stress management, significantly contribute to long-term well-being for individuals with CAH. Furthermore, genetic counseling plays a vital role in providing comprehensive information, supporting informed decision-making, and facilitating family planning for affected individuals and their families. By combining medical management, lifestyle modifications, and genetic counseling, individuals with CAH can effectively manage their condition and enhance their overall quality of life.

Risk Factors

Classical Congenital Adrenal Hyperplasia (CAH) due to 21-hydroxylase deficiency is a genetic disorder that affects the adrenal glands, leading to a decrease in the production of certain hormones and an overproduction of others. Several risk factors contribute to the development and progression of CAH due to 21-hydroxylase deficiency. Genetic predisposition plays a significant role, with the disorder being inherited in an autosomal recessive pattern. Individuals who have a family history of CAH due to 21-hydroxylase deficiency are at a higher risk of developing the disorder. Additionally, environmental factors, such as maternal exposure to certain medications during pregnancy, can increase the risk of CAH due to 21-hydroxylase deficiency. Certain medications, such as those containing progestin, can cross the placenta and interfere with fetal hormone production, leading to the development of CAH due to 21-hydroxylase deficiency. Furthermore, consanguinity between parents can increase the risk of CAH due to 21-hydroxylase deficiency, as it increases the chances of inheriting the defective gene from both parents. These risk factors highlight the complex interplay of genetic and environmental factors that contribute to the development of CAH due to 21-hydroxylase deficiency.

Detailed Results

Pharmacogenetics Analysis

Your genetic profile plays a crucial role in how your body processes and responds to medications. Pharmacogenetics is the study of how genetic differences influence individual responses to medications.

Immediate Attention Needed

(Major Gene-Drug Interaction)

These medications are classified under PharmGKB Level 1A, meaning they have the highest level of clinical evidence. Level 1A includes drug-gene interactions with specific dosing recommendations in FDA-approved labels or clinical guidelines. These interactions can significantly alter drug response, requiring immediate adjustments based on CPIC or FDA guidelines.

Fluorouracil

Gene	Genotype	Used for
DPYD	CT	Neoplasms

Both variants of rs1801159 are assigned normal function by CPIC. Patients with the CT genotype and cancer who are treated with fluorouracil, a fluoropyrimidine-based chemotherapy, may not have altered risk of drug toxicity as compared to patients with the CC or TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence risk of drug toxicity.

rs1801159 — Toxicity

Capecitabine

Gene	Genotype	Used for
DPYD	CT	Neoplasms

Both variants of rs1801159 are assigned normal function by CPIC. Patients with the CT genotype and cancer who are treated with capecitabine, a fluoropyrimidine-based chemotherapy, may not have altered risk of drug toxicity as compared to patients with the CC or TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence risk of drug toxicity.

rs1801159 — Toxicity

Warfarin

Gene	Genotype	Used for
CYP4F2	CT	

Patients with the rs2108622 CT genotype may have increased warfarin dosage requirements as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also affect warfarin dosage requirements.

rs2108622 — Dosage

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C

Patients with the rs12979860 CT genotype and hepatitis C infection may have decreased response (typically assayed as sustained virological response, SVR) when administered peg interferon alpha 2a or 2b in combination with ribavirin as compared to patients with the CC genotype, but an increased response as compared to patients with the TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence response to peginterferon alpha and ribavirin.

rs12979860 — Efficacy

Boceprevir, Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C, Chronic

Patients with the rs12979860 CT genotype and hepatitis C infection may have decreased response to triple therapy (boceprevir, peginterferon alfa-2a/2b and ribavirin) as compared to patients with the CC genotype. Other genetic and clinical factors may also influence response to boceprevir-peginterferon based therapy.

rs12979860 — Efficacy

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin, Telaprevir

Gene	Genotype	Used for
IFNL3;IFNL4	CT	Hepatitis C, Chronic

Patients with the rs12979860 CT genotype and hepatitis C infection may have lower response rates (SVR) to triple therapy (telaprevir, peginterferon alfa-2a/b and ribavirin) as compared to patients with the CC genotype. However, conflicting evidence has been reported. The impact of IL28B genotype may be dampened in patients with prior PegIFN/RBV treatment failure. Other genetic and clinical factors may also influence response to HCV triple therapy.

rs12979860 **Efficacy**

Monitor Closely

(Significant Gene-Drug Interaction)

These interactions fall under PharmGKB Levels 1B, indicating limited or emerging evidence. Level 1B includes single-study reports or conflicting findings. While these findings are not currently actionable, they may become relevant as further research develops. Consider discussing with a healthcare provider for additional insights.

Warfarin

Gene	Genotype	Used for
VKORC1	CT	

Patients with the rs7294 CT genotype may require a higher dose of warfarin as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also affect warfarin dose requirements.

rs7294 **Dosage**

Gene	Genotype	Used for
VKORC1	GG	

Patients with the rs2359612 GG genotype may require an increased dose of warfarin as compared to patients with the AG or AA genotype. Other genetic and clinical factors may also influence dose of warfarin.

rs2359612 **Dosage**

Interferons, Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3	GT	Hepatitis C, Chronic

Patients with the rs8099917 GT genotype and chronic hepatitis C infection may have decreased response (lower SVR) to peginterferon alfa and ribavirin therapy as compared to patients with the TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence response to peginterferon alfa and ribavirin therapy. Please note that this SNP has been found to be in high LD with rs12979860 which is also associated with response to pegIFN-alpha/ribavirin.

rs8099917 **Efficacy**

For Your Information

(Minor Gene-Drug Interaction)

These interactions fall under PharmGKB Levels 2A and 2B, indicating limited or emerging evidence. Level 2A includes single-study reports or conflicting findings, while Level 2B represents preliminary in vitro or computational data with uncertain clinical significance. While these findings are not currently actionable, they may become relevant as further research develops. Consider discussing with a healthcare provider for additional insights.

Methotrexate

Gene	Genotype	Used for
MTHFR	AG	Arthritis, Juvenile Rheumatoid;Arthritis, Psoriatic;Arthritis, Rheumatoid;Drug Toxicity

Patients with the rs1801133 AG genotype and Arthritis who are treated with methotrexate may have an increased risk of toxicity as compared to patients with the GG genotype, or may have a decreased risk of adverse events as compared to patients with the AA genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence methotrexate toxicity. This drug-variant pair has been assigned a "no recommendation" by DPWG, as it was determined to be not clinically actionable.

rs1801133 **Toxicity**

Gene	Genotype	Used for
MTHFR	AG	Drug Toxicity;hematotoxicity;Leukopenia;Lymphoma;mucositis;Neoplasms;Neutropenia;Osteosarcoma;Precursor Cell Lymphoblastic Leukemia-Lymphoma;primary central nervous system lymphoma;Thrombocytopenia;Toxic liver disease

Patients with the rs1801133 AG genotype and cancer who are treated with methotrexate may be at increased risk of toxicity as compared to patients with the GG genotype, and may be at decreased risk of toxicity compared to patients with the AA genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence risk of toxicity following methotrexate treatment. This drug-variant pair has been assigned a "no recommendation" by DPWG, as it was determined to be not clinically actionable.

rs1801133 **Toxicity**

Gene	Genotype	Used for
ATIC	CC	Arthritis, Rheumatoid

Patients with the rs4673993 CC genotype and Rheumatoid Arthritis may have increased response when treated with methotrexate as compared to patients with the TT genotype. Other genetic and clinical factors may also influence methotrexate response.

rs4673993 **Efficacy**

Gene	Genotype	Used for
SLC19A1	CC	Arthritis, Rheumatoid

Patients with the rs1051266 CC genotype and rheumatoid arthritis may have decreased response when treated with methotrexate as compared to patients with the TT genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence methotrexate response.

rs1051266 **Efficacy**

Hormonal contraceptives for systemic use

Gene	Genotype	Used for
F5	CT	Thrombosis

Patients with the rs6025 CT genotype (heterozygote for Factor V Leiden) may have an increased risk of experiencing thrombosis when receiving oral contraceptives as compared to patients with the CC genotype (normal Factor V). However, conflicting evidence has been reported. Both Factor V Leiden and oral contraceptives have been found to independently increase the risk for thrombosis, but together they may have a cumulative effect on thrombosis risk. Other genetic and clinical factors may also influence risk of thrombosis.

rs6025 **Toxicity**

Sorafenib

Gene	Genotype	Used for
EPAS1	CG	Drug Toxicity

Patients with the rs7557402 CG genotype may have a decreased risk of dermatologic toxicity when treated with sorafenib as compared to patients with the GG genotype. Other genetic and clinical factors may also influence risk of dermatologic toxicity when treated with sorafenib.

rs7557402 **Toxicity**

Irinotecan

Gene	Genotype	Used for
UGT1A1	AG	Neutropenia

Patients with the rs10929302 AG genotype may have decreased risk of neutropenia when treated with irinotecan as compared to patients with the AA genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence irinotecan-related toxicity.

rs10929302 **Toxicity**

Nicotine

Gene	Genotype	Used for
CHRNA5	AG	Tobacco Use Disorder

Patients with rs16969968 AG genotype may have an increased risk for nicotine dependence when exposed to nicotine as compared to patients with the GG genotype, but a decreased risk as compared to patients with the AA genotype. However, conflicting evidence has been reported. Some findings are based on haplotype studies with either rs680244 or rs680244, rs569207 rs578776, and rs1051730. Other genetic and clinical factors may influence risk of nicotine dependency.

rs16969968 — **Toxicity**

Carbamazepine

Gene	Genotype	Used for
SCN1A	CT	Epilepsy

Patients with the rs3812718 CT genotype who are treated with carbamazepine may require a higher dose as compared to patients with the CC genotype but a lower dose as compared to patients with the TT genotype. Other genetic and clinical factors may also influence dose of carbamazepine.

rs3812718 — **Dosage**

Acenocoumarol

Gene	Genotype	Used for
CYP4F2	CT	Atrial Fibrillation

Patients with the rs2108622 CT genotype who are treated with acenocoumarol may require a lower dose as compared to patients with the TT genotype or may require a higher dose as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence required acenocoumarol dose.

rs2108622 — **Dosage**

Etanercept

Gene	Genotype	Used for
TNF	AG	Arthritis, Psoriatic;Arthritis, Rheumatoid;Crohn Disease;Inflammation;Psoriasis;Spondylitis, Ankylosing

Patients with the rs1800629 AG genotype may have increased response to etanercept as compared to patients with the AA genotype. Other genetic and clinical factors may also influence response to etanercept.

rs1800629 — **Efficacy**

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin

Gene	Genotype	Used for
IFNL3	AG	Hepatitis C;HIV Infections

Patients with the rs11881222 AG genotype and hepatitis C or HIV may have a poorer response to treatment with peginterferon-alpha and ribavirin as compared to patients with the AA genotype. Other genetic and clinical factors may also influence response to peginterferon-alpha and ribavirin treatment.

rs11881222 — **Efficacy**

Peginterferon alfa-2a, Peginterferon alfa-2b, Ribavirin, Telaprevir

Gene	Genotype	Used for
IFNL3	GT	Hepatitis C, Chronic

Patients with the rs8099917 GT genotype may have lower response rates (SVR) to triple therapy (telaprevir, peginterferon alfa-2a/b and ribavirin) in people with Hepatitis C genotype 1 as compared to patients with the TT genotype. Other genetic and clinical factors may also influence response to HCV triple therapy.

rs8099917 — **Efficacy**

Platinum compounds

Gene	Genotype	Used for
XRCC1	**CT**	**Neoplasms**

Patients with cancer and the rs25487 CT genotype may have decreased response when treated with platinum-based therapies as compared to patients with the CC genotype. However, conflicting evidence has been reported. Other genetic and clinical factors may also influence response to platinum-based regimens.

rs25487 **Efficacy**

Genetic Susceptibilities that Influence Your Lifestyle

Your genetic profile contains valuable insights about how your genes influence various aspects of your life, from cognitive abilities to physical traits. Each category below represents a collection of genetic markers that may affect your predispositions and characteristics. Understanding these genetic influences can help you make more informed decisions about your lifestyle, diet, and wellness strategies.

Neurogenic and Cognitive Functions

Genetic factors play a crucial role in shaping brain development, synaptic plasticity, and neurotransmitter regulation, directly impacting cognitive functions like memory retention, learning abilities, and mental agility. Variants in genes related to neurogenesis can influence susceptibility to neurological disorders, cognitive resilience, and adaptability to learning environments, affecting both short-term memory and long-term cognitive health.

Cardiovascular

Cardiovascular health is significantly influenced by genetic variants that regulate blood pressure, cholesterol metabolism, and arterial integrity. These genetic factors can determine an individual's predisposition to conditions such as hypertension, atherosclerosis, and myocardial infarction. Moreover, genetic insights can guide personalized lifestyle changes to enhance heart health and reduce cardiovascular risks.

Immune System

The immune system's effectiveness is modulated by genetic variants that control cytokine production, pathogen recognition, and immune cell activation. These genetic differences can impact an individual's susceptibility to autoimmune diseases, infection resilience, and allergic reactions. Understanding these genetic factors can provide insights into personalized approaches to bolstering immune defense mechanisms.

Athleticism

Athletic performance is deeply intertwined with genetic factors that influence muscle fiber composition, aerobic capacity, and recovery rates. Genes affecting mitochondrial efficiency, oxygen utilization, and muscle hypertrophy can predict an individual's potential in endurance versus power-based sports. Genetic profiling can thus guide training regimens tailored to maximize athletic output.

Metabolism

Metabolic rate and nutrient processing are governed by genetic variants that influence insulin sensitivity, fat oxidation, and energy expenditure. These genetic factors can determine tendencies toward weight gain, energy levels, and responses to different dietary macronutrients. Personalized dietary strategies based on genetic information can optimize metabolic health and weight management.

Behavior

Behavioral tendencies, such as impulsivity, risk tolerance, and social interaction styles, are shaped by genetic factors affecting neurotransmitter pathways and receptor sensitivities. These genetic influences can affect decision-making patterns, stress responses, and even susceptibility to behavioral conditions. Understanding these factors allows for tailored behavioral interventions and stress management techniques.

Nutrition and Diet

Genetic variations can influence how nutrients are metabolized, impacting dietary preferences, nutrient deficiencies, and even food sensitivities. For instance, polymorphisms in genes related to lactose tolerance, gluten sensitivity, or omega-3 metabolism can determine the optimal diet for an individual. Nutrigenomics enables personalized nutrition plans for improved health outcomes.

Sensory Perception

The way we perceive sensory inputs such as taste, smell, and sound is influenced by genetic variants that affect receptor function and neural processing. These variations can alter taste preferences, odor sensitivities, and even auditory perception. Understanding these genetic traits can explain individual differences in sensory experiences and preferences.

Substance Reaction

Reactions to substances like caffeine, alcohol, and various medications are influenced by genetic variants affecting metabolic pathways. Enzyme activity levels, influenced by genetic polymorphisms, can determine the speed at which substances are metabolized, influencing tolerance levels and adverse reactions. Pharmacogenomics uses this knowledge to optimize drug efficacy and minimize side effects.

Wellness

Overall wellness is affected by genetic predispositions towards certain health conditions, stress resilience, and lifestyle adaptability. Genes influencing circadian rhythms, inflammation pathways, and detoxification processes can impact daily energy levels, mood stability, and overall health. Genetic insights provide a roadmap for lifestyle modifications that enhance well-being and longevity.

Hormones

Hormonal balance, crucial for physiological and psychological health, is regulated by genetic variants that influence hormone synthesis, receptor sensitivity, and feedback mechanisms. These genetic factors can determine susceptibility to conditions like thyroid disorders, metabolic syndrome, and reproductive health issues. Understanding these influences aids in personalized hormone management strategies.

Longevity

Longevity is shaped by genetic variants that regulate cellular repair mechanisms, oxidative stress response, and metabolic efficiency. Telomere length, mitochondrial function, and DNA repair capacity are key factors influenced by these genes, contributing to the aging process and lifespan. Genetic profiling for longevity markers provides insights into personalized anti-aging interventions.

Physical Appearance

Genetic factors significantly determine physical characteristics such as skin pigmentation, hair texture, and facial features. Variants in genes affecting melanin production, hair follicle shape, and facial bone structure contribute to the diversity in human appearance. Understanding these genetic influences can also provide insights into conditions like alopecia and skin disorders.

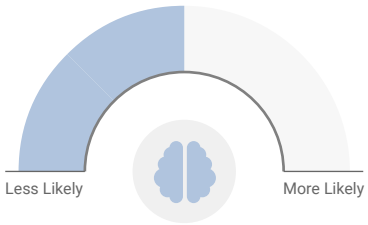
Personality

Personality traits, such as extroversion, conscientiousness, and emotional stability, have genetic underpinnings linked to neurotransmitter activity and brain structure. Genetic variations in serotonin and dopamine pathways can influence mood regulation, stress resilience, and social behavior. These insights help in understanding individual differences in personality and psychological well-being.

Neurogenic and Cognitive Functions

Genetic factors play a crucial role in shaping brain development, synaptic plasticity, and neurotransmitter regulation, directly impacting cognitive functions like memory retention, learning abilities, and mental agility. Variants in genes related to neurogenesis can influence susceptibility to neurological disorders, cognitive resilience, and adaptability to learning environments, affecting both short-term memory and long-term cognitive health.

Alzheimer's disease risk



Having the C/C genotype in FN1 provides no conclusive evidence about your risk for Alzheimer's.

• **Gene:** FN1 • **rsID:** rs140926439 • **Your Genotype:** C/C • **Zygosity:** Homozygous

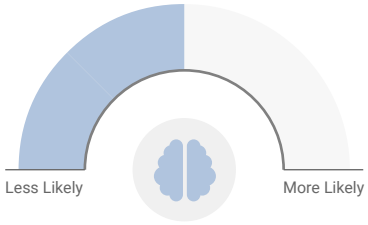
Description

In most cases, Alzheimer? does not have a single genetic cause. Instead, it can be influenced by multiple genes in combination with lifestyle and environmental factors. Consequently, a person may carry more than one genetic variant or group of variants that can either increase or reduce the risk of Alzheimer?.The apolipoprotein E (ApoE) gene makes a protein which, when combined with fat, becomes a lipoprotein. The lipoprotein ApoE is a very low-density lipoprotein, responsible in part for removing cholesterol from the bloodstream. Variations in ApoE affect cholesterol metabolism, which in turn alter your chances of having heart disease and in particular a heart attack or a stroke. Variations in ApoE are also associated with altered odds of having Alzheimer's disease and other diseases.There are three relatively common allelic variants of ApoE, as defined by two SNPs, rs429358 and rs7412 known as ApoE-_2, ApoE-_3, and ApoE-_4. The proteins produced by these genes are called ApoE2, ApoE3, and ApoE4. When rs429358 has the allele C and rs7412 has the allele T, the resulting isoform is _1.When rs429358 has the allele T and rs7412 has the allele T, the resulting isoform is _2.When rs429358 has the allele T and rs7412 has the allele C, the resulting isoform is _3.When rs429358 has the allele C and rs7412 has the allele C, the resulting isoform is _4.The most common variant overall is the "standard" ApoE-_3, and therefore more people inherited one ApoE-_3 from each parent than any other of the possible pairs of variants. Note that each of these types can actually have additional changes too, so there are different subtypes as well.APOE _2 may provide some protection against the disease. If Alzheimer? occurs in a person with this allele, it usually develops later in life than it would in someone with the APOE _4 gene. Roughly 5% to 10% of people have this allele.APOE _3, the most common allele, is believed to have a neutral effect on the disease ?neither decreasing nor increasing risk of Alzheimer?.APOE _4 increases risk for Alzheimer? and is associated with an earlier age of disease onset in certain populations. About 15% to 25% of people have this allele, and 2% to 5% carry two copies.

Extra Information

The variant rs140926439 located in FN1 was associated with strongly reduced risk of AD in APOE_4/4 carriers (OR_=_0.29; 95% CI [0.11, 0.78], P_=_0.014(PMID:38598053)An independent analysis in a large cohort of 7185 APOE_4 homozygous carriers found that rs140926439 variant in FN1 was protective of AD (OR_=_0.29; 95% CI [0.11, 0.78], P_=_0.014) and delayed age at onset of disease by 3.37 years (95% CI [0.42, 6.32], P_=_0.025). This is a relatively new finding in recent years.

Alzheimer's disease risk



The ε3/ε3 genotype is the most common, found in about 60% of the population. This genotype is considered neutral, meaning it does not significantly increase or decrease the risk of developing Alzheimer's disease.

• **Gene:** APOE • **rsID:** rs429358+rs7412 • **Your Genotype:** e3/e3 • **Zygosity:** Homozygous

Description

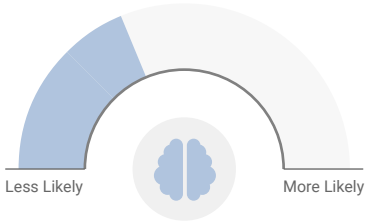
In most cases, Alzheimer? does not have a single genetic cause. Instead, it can be influenced by multiple genes in combination with lifestyle and environmental factors. Consequently, a person may carry more than one genetic variant or group of variants that can either increase or reduce the risk of Alzheimer?.The apolipoprotein E (ApoE) gene makes a protein which, when combined with fat, becomes a lipoprotein. The lipoprotein ApoE is a very low-density lipoprotein, responsible in part for removing cholesterol from the bloodstream. Variations in ApoE affect cholesterol metabolism, which in turn alter your chances of having heart disease and in particular a heart attack or a stroke. Variations in ApoE are also associated with altered odds of having Alzheimer's disease and other diseases.There are three relatively common allelic variants of ApoE, as defined by two SNPs, rs429358 and rs7412 known as ApoE-_2, ApoE-_3, and ApoE-_4. The proteins produced by these genes are called ApoE2, ApoE3, and ApoE4. When rs429358 has the allele C and rs7412 has the allele T, the resulting isoform is _1.When rs429358 has the allele T and rs7412 has the allele T, the resulting isoform is _2.When rs429358 has the allele T and rs7412 has the allele C, the resulting isoform is _3.When rs429358 has the allele C and rs7412 has the allele C, the resulting isoform is _4.The most common variant overall is the "standard" ApoE-_3, and therefore more people inherited one ApoE-_3 from each parent than any other of the possible pairs of variants. Note that each of these types can actually have additional changes too, so there are different subtypes as well.APOE _2 may provide some protection against the disease. If Alzheimer? occurs in a person with this allele, it usually develops later in life than it would in someone with the APOE _4 gene. Roughly 5% to 10% of people have this allele.APOE _3, the most common allele, is believed to have a neutral effect on the disease ?neither decreasing nor increasing risk of Alzheimer?.APOE _4 increases risk for Alzheimer? and is associated with an earlier age of disease onset in certain populations. About 15% to 25% of people have this allele, and 2% to 5% carry two copies.

Extra Information

This SNP, located in the fourth exon of the ApoE gene, affects the amino acid at position 130 of the resulting protein. The more common rs429358 allele is (T). If the allele is (C) and the same chromosome also harbors the rs7412(C) allele, the combination is known as an APOE-_4 allele. The APOE-_4 allele has a strong influence on the risk of Alzheimer's disease.CC genotype represents one of 2 snps relevant to classifying APOE genotype;CT genotype represents >3x increased risk for Alzheimer's; 1.4x increased risk for heart disease while TT represents common risk.

The rs7412(T) allele, also known as Arg176Cys, generally indicates the presence of an Apo_2 allele.APOE _2 may provide some protection against the disease.

Parkinson's disease risk



The G/G genotype suggests a more typical risk for Parkinson's compared to the other variants.

• **Gene:** LRRK2 • **rsID:** rs34637584 • **Your Genotype:** G/G • **Zygosity:** Homozygous

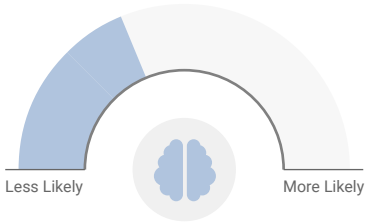
Description

Parkinson's disease is a neurodegenerative disorder that affects movement and can lead to tremors, stiffness, and difficulty with balance and coordination. While the exact cause of Parkinson's is not fully understood, research has identified several genetic variants that can increase the risk of developing the disease.

Extra Information

First discovered in 2004, rs34637584 is a SNP indicating a position within the LRRK2 that encodes a variant protein. This SNP is commonly referred to as the G2019S variant (or, mutation) based on the potential change from glycine (encoded by rs34637584(G) allele) to serine (encoded by the rs34637584(A) allele) at position 2019 of the LRRK2 protein.[PMID 15680456][PMID 15680455]One copy of a rs34637584(A) allele is sufficient to greatly increase one's risk for Parkinson's disease(refer to GA and AA genotype). It is considered a disease causing mutation because it is rarely found in healthy, elderly people without Parkinson's disease, and it has been found in both familial and sporadic types of the disease. While there are many different SNPs that can influence one's risk for Parkinson's disease, rs34637584 is an especially common cause of the disease in Berber Arabs and Ashkenazi Jews. Overall, the risk of Parkinson's disease for a person who inherits a rs34637584(A) allele is 28% at age 59, 51% at 69, and 74% at 79, according to the International LRRK2 Consortium.[PMID 18539534]The GG genotype represents a normal risk of developing Parkinson's diseases.

Parkinson's disease risk



For Parkinson's disease risk, having the T/T genotype is generally seen as typical, with no increased risk.

• **Gene:** GBA • **rsID:** rs76763715 • **Your Genotype:** T/T • **Zygosity:** Homozygous

Description

Parkinson's disease is a neurodegenerative disorder that affects movement and can lead to tremors, stiffness, and difficulty with balance and coordination. While the exact cause of Parkinson's is not fully understood, research has identified several genetic variants that can increase the risk of developing the disease.

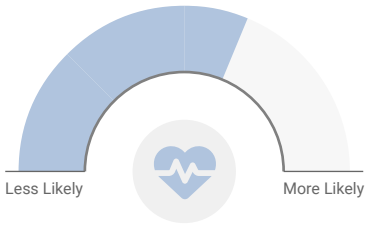
Extra Information

The N370S mutation in the GBA gene is linked to Gaucher disease Type 1, but it also increases the risk of developing Parkinson's disease. This connection highlights the broader impact of GBA gene mutations beyond Gaucher disease, particularly in relation to neurodegenerative diseases. The relationship is believed to be due to the role of glucocerebrosidase in cellular pathways that, when disrupted, contribute to the development of Parkinson's disease.C;C): High risk (6) for Gaucher's disease, type 1.(C;T): Carrier (3) of Gaucher disease allele; potential increased risk for Parkinson's.For the N370S variant (rs76763715) in the GBA gene: (C;C) High risk (6) for Gaucher's disease type 1;(C;T) Carrier (3) of Gaucher disease allele potential increased risk for Parkinson's (T;T) Common (0) variant with no associated risk.

Cardiovascular

Cardiovascular health is significantly influenced by genetic variants that regulate blood pressure, cholesterol metabolism, and arterial integrity. These genetic factors can determine an individual's predisposition to conditions such as hypertension, atherosclerosis, and myocardial infarction. Moreover, genetic insights can guide personalized lifestyle changes to enhance heart health and reduce cardiovascular risks.

Baseline Cholesterol



The TT genotype might mean you're more inclined to have higher baseline cholesterol, so monitoring these levels could be beneficial.

• **Gene:** PPARD • **rsID:** rs2016520 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

Description

Cholesterol, a lipid (fat) molecule, is present in the cell membranes and plays a crucial role in synthesizing certain molecules like hormones and maintaining cell membrane structure. Adequate cholesterol levels are necessary for these physiological functions. Apart from obtaining cholesterol from dietary sources, our bodies can also synthesize it. Two main types of cholesterol, high-density lipoprotein (HDL) and low-density lipoprotein (LDL), exist. Both environmental factors and genetic influences contribute to our baseline cholesterol levels.

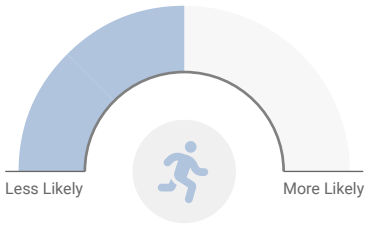
Extra Information

The rs2016520 CT/TT genotype has been linked to elevated cholesterol levels, as reported in a study (PMID: 18288282), compared to CC genotypes.The C or minor allele has been associated with higher production of PPAR delta gene products and lower risk of obesity(PMID: 22968028).

Athleticism

Athletic performance is deeply intertwined with genetic factors that influence muscle fiber composition, aerobic capacity, and recovery rates. Genes affecting mitochondrial efficiency, oxygen utilization, and muscle hypertrophy can predict an individual's potential in endurance versus power-based sports. Genetic profiling can thus guide training regimens tailored to maximize athletic output.

Achilles Tendinopathy



With the C/T genotype, your risk for Achilles Tendinopathy doesn't stand out according to current data.

• **Gene:** MMP3 • **rsID:** rs679620 • **Your Genotype:** T/T>T/C • **Zygosity:** Heterozygous

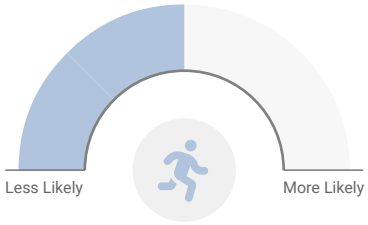
Description

Achilles tendinopathy is characterized by the degeneration of collagen in the tendons connecting calf muscles to heel bones, leading to pain, swelling, and stiffness during and after activities like walking. More strenuous pursuits, such as running and jumping, can exacerbate these symptoms. The condition is often attributed to persistent overuse of the tendon without adequate rest, making it particularly prevalent among athletes, including runners.

Extra Information

The rs679620 AG genotype is associated with the typical likelihood of Achilles tendinopathy, as indicated by various studies (PMID(s): 19042922, 27222816, 28358823), while individuals with the GG genotype face a heightened risk for Achilles tendinopathy. In cases of Achilles tendon rupture (RUP), the MMP3 rs679620 GG genotype is notably more prevalent (44.0%) compared to controls (19.1%), where the AG genotype is more common (54.2%) (PMID: 19042922). Another study, albeit relatively small (~100 patients), found associations between Achilles tendinopathy risk and single nucleotide polymorphisms (SNPs) in the MMP3 gene. For rs679620, they found individuals with the (G;G) genotype exhibited an odds ratio of 2.5 (CI: 1.2 - 4.90, p = 0.010). Moreover, there's evidence of an interaction between rs679620(G) and COL5A1 rs12722(T) alleles, contributing to an increased risk for Achilles tendinopathy with a p-value of 0.006.

Endurance



For your Endurance trait with the SPEG gene (rs7564856), the A/A genotype doesn't indicate strong effects on your endurance.

• **Gene:** SPEG • **rsID:** rs7564856 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

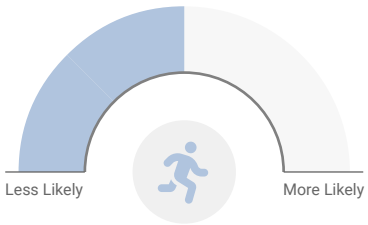
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs7564856 allele G is related allele, see the Studies with Positive Results (if available)[230] and see the Studies with Negative or Controversial Results (if available).

Endurance



In the context of endurance, the A/T genotype for the VEGFR2 gene doesn't seem to affect your performance notably.

• **Gene:** VEGFR2 • **rsID:** rs1870377 • **Your Genotype:** T/T>T/A • **Zygosity:** Heterozygous

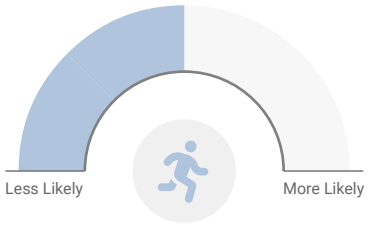
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1870377 allele A is related allele, see the Studies with Positive Results (if available)[236,237] and see the Studies with Negative or Controversial Results (if available).

Endurance



For your endurance trait, the G/G genotype in the VEGFA gene doesn't show a significant impact on your capabilities.

• **Gene:** VEGFA • **rsID:** rs2010963 • **Your Genotype:** C/C>G/G • **Zygosity:** Homozygous

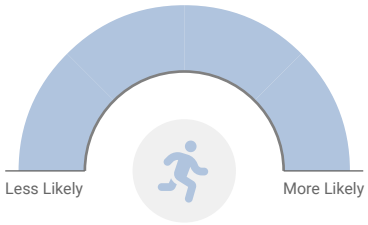
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs2010963 allele C is related allele, see the Studies with Positive Results (if available)[144,234,235] and see the Studies with Negative or Controversial Results (if available).

Endurance



Having the C/C genotype may optimize your endurance capacity thanks to the C allele in the AQP1 gene.

• **Gene:** AQP1 • **rsID:** rs1049305 • **Your Genotype:** G/G>C/C • **Zygosity:** Homozygous

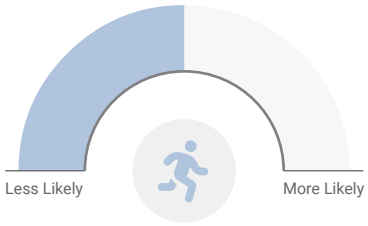
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1049305 allele C is related allele, see the Studies with Positive Results (if available)[178,179,180] and see the Studies with Negative or Controversial Results (if available).

Endurance



Holding the C/T genotype in your COL5A1 gene doesn't have a notable effect on endurance.

• **Gene:** COL5A1 • **rsID:** rs12722 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

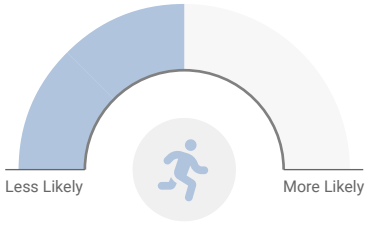
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs12722 allele T is related allele, see the Studies with Positive Results (if available)[194,195] and see the Studies with Negative or Controversial Results (if available).

Endurance



There is no significant endurance effect tied to the C/G genotype in SIRT1.

• **Gene:** SIRT1 • **rsID:** rs41299232 • **Your Genotype:** C/C>C/G • **Zygosity:** Heterozygous

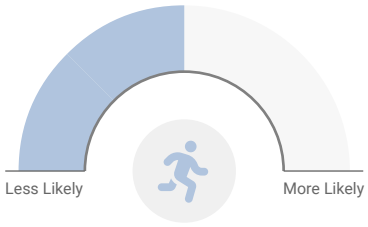
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs41299232 allele G is related allele, see the Studies with Positive Results (if available)[45] and see the Studies with Negative or Controversial Results (if available).

Endurance



C/T genotype for MYBPC3 is not linked with significant changes in Endurance.

• **Gene:** MYBPC3 • **rsID:** rs1052373 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

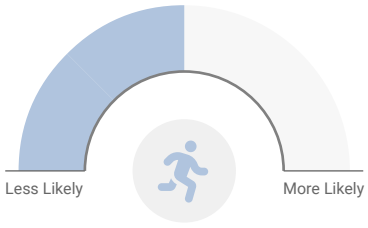
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1052373 allele G is related allele, see the Studies with Positive Results (if available)[42] and see the Studies with Negative or Controversial Results (if available).

Endurance



Having the A/G genotype in the GSTP1 gene might offer a moderate improvement in endurance, though evidence is not definitive.

• **Gene:** GSTP1 • **rsID:** rs1695 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

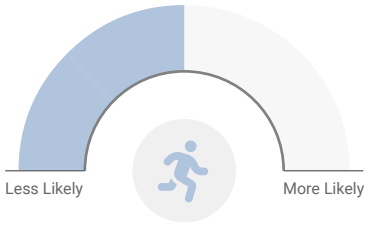
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1695 allele G is related allele, see the Studies with Positive Results (if available)[202,203] and see the Studies with Negative or Controversial Results (if available).

Endurance



Having an A/G genotype shows no specific link to endurance performance regarding the UCP2 gene.

• **Gene:** UCP2 • **rsID:** rs660339 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

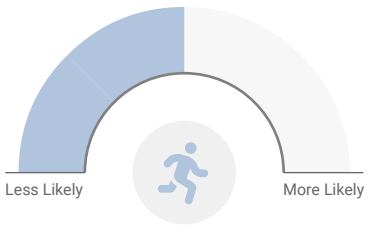
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs660339 allele T is related allele, see the Studies with Positive Results (if available)[130,144,232]Ê and see the Studies with Negative or Controversial Results (if available).

Endurance



No notable effects are seen with the T/T genotype concerning your Endurance trait in relation to the TSHR gene.

• **Gene:** TSHR • **rsID:** rs7144481 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

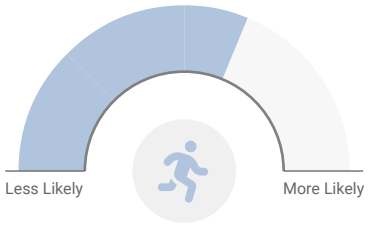
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs7144481 allele C is related allele, see the Studies with Positive Results (if available)[39] and see the Studies with Negative or Controversial Results (if available).

Endurance



For your Endurance trait with the GABPB1 gene (rs12594956), having the A/A genotype could enhance your endurance capabilities.

• **Gene:** GABPB1 • **rsID:** rs12594956 • **Your Genotype:** C/C>A/A • **Zygosity:** Homozygous

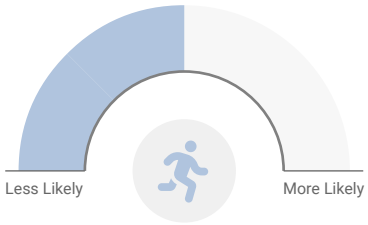
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs12594956 allele A is related allele, see the Studies with Positive Results (if available)[199,200] and see the Studies with Negative or Controversial Results (if available).

Endurance



With A/G in RBFOX1, no clear evidence points to an effect on your endurance.

• **Gene:** RBFOX1 • **rsID:** rs7191721 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

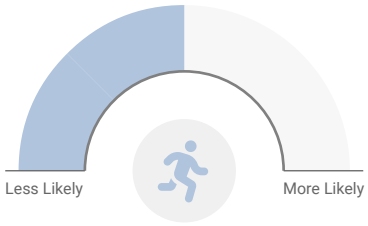
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs7191721 allele G is related allele, see the Studies with Positive Results (if available)[39] and see the Studies with Negative or Controversial Results (if available).

Endurance



Having an A/T genotype in your FTO gene doesn't suggest a strong impact on endurance.

• **Gene:** FTO • **rsID:** rs9939609 • **Your Genotype:** T/T>T/A • **Zygosity:** Heterozygous

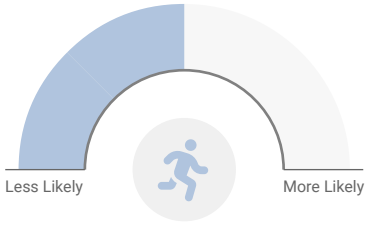
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs9939609 allele T is related allele, see the Studies with Positive Results (if available)[196,197] and see the Studies with Negative or Controversial Results (if available)[198].

Endurance



No substantial endurance-related effects noted with the A/G genotype in TRPM2.

• **Gene:** TRPM2 • **rsID:** rs1785440 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

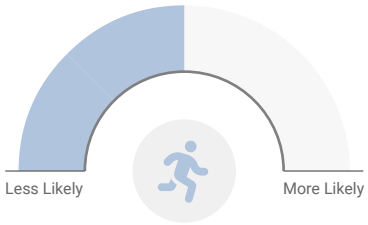
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1785440 allele G is related allele, see the Studies with Positive Results (if available)[45] and see the Studies with Negative or Controversial Results (if available).

Endurance



For your Endurance trait with the ADRB2 gene (rs1042713), having the G/G genotype doesn't show notable effects.

• **Gene:** ADRB2 • **rsID:** rs1042713 • **Your Genotype:** G/G • **Zygosity:** Homozygous

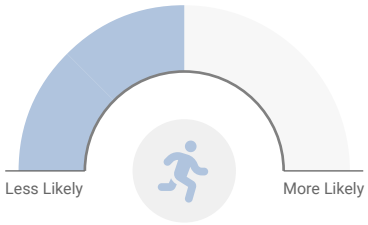
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1042713 allele A is related allele, see the Studies with Positive Results (if available)[160,171,172] and see the Studies with Negative or Controversial Results (if available)[173,174].

Endurance



For your Endurance trait with the ADRB3 gene (rs4994), having the A/A genotype doesn't reveal any notable effects on endurance.

• **Gene:** ADRB3 • **rsID:** rs4994 • **Your Genotype:** A/A • **Zygosity:** Homozygous

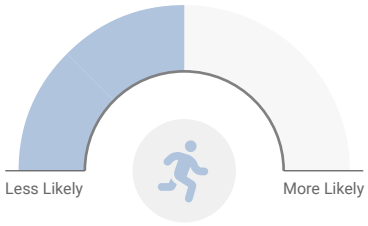
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs4994 allele G is related allele, see the Studies with Positive Results (if available)[170,173] and see the Studies with Negative or Controversial Results (if available).

Endurance



For T/T at CKM, we don't find any major impact on endurance traits.

• **Gene:** CKM • **rsID:** rs8111989 • **Your Genotype:** T/T • **Zygosity:** Homozygous

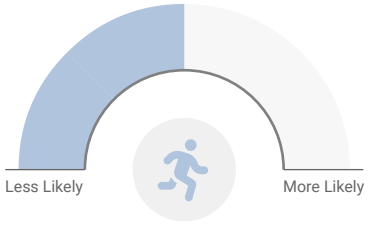
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs8111989 allele A is related allele, see the Studies with Positive Results (if available)[190,191,192] and see the Studies with Negative or Controversial Results (if available)[133,193].

Endurance



For your Endurance trait with the GABPB1 gene (rs7181866), having the A/A genotype doesn't show a strong impact, so your endurance might be determined more by other factors.

• **Gene:** GABPB1 • **rsID:** rs7181866 • **Your Genotype:** A/A • **Zygosity:** Homozygous

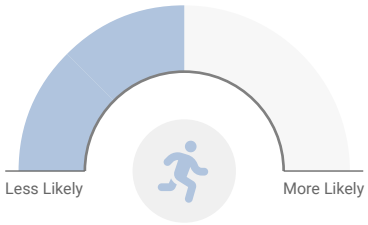
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs7181866 allele G is related allele, see the Studies with Positive Results (if available)[199,201] and see the Studies with Negative or Controversial Results (if available)[200].

Endurance



You have the C/C genotype in the HFE gene, which hasn't shown a strong link to Endurance.

• **Gene:** HFE • **rsID:** rs1799945 • **Your Genotype:** C/C • **Zygosity:** Homozygous

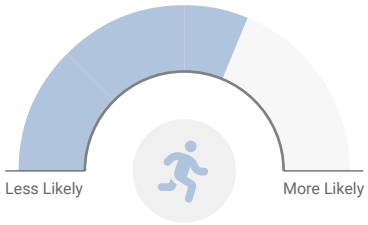
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1799945 allele G is related allele, see the Studies with Positive Results (if available) [153,204,205,206,207] and see the Studies with Negative or Controversial Results (if available).

Endurance



Having the G/G genotype could be beneficial for your endurance, potentially aiding your performance.

• **Gene:** NFATC4 • **rsID:** rs2229309 • **Your Genotype:** G/G • **Zygosity:** Homozygous

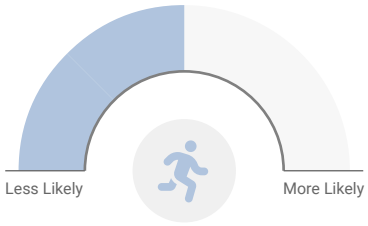
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs2229309 allele G is related allele, see the Studies with Positive Results (if available)[144] and see the Studies with Negative or Controversial Results (if available).

Endurance



G/G doesn't appear to be linked with endurance outcomes for the NFIA-AS2 gene.

• **Gene:** NFIA-AS2 • **rsID:** rs1572312 • **Your Genotype:** G/G • **Zygosity:** Homozygous

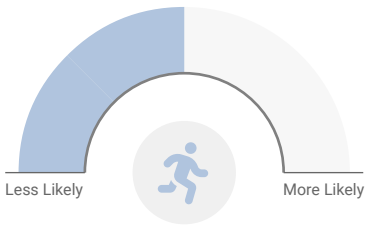
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1572312 allele C is related allele, see the Studies with Positive Results (if available)[39,46] and see the Studies with Negative or Controversial Results (if available).

Endurance



C/C doesn't seem to strongly affect endurance, according to the NOS3 gene data.

• **Gene:** NOS3 • **rsID:** rs2070744 • **Your Genotype:** C/C • **Zygosity:** Homozygous

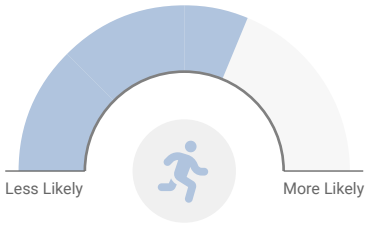
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs2070744 allele T is related allele, see the Studies with Positive Results (if available)[153,217,218] and see the Studies with Negative or Controversial Results (if available)[219].

Endurance



Having G/G in PPARA might really help you excel in endurance sports with an advantageous endurance capacity.

• **Gene:** PPARA • **rsID:** rs4253778 • **Your Genotype:** G/G • **Zygosity:** Homozygous

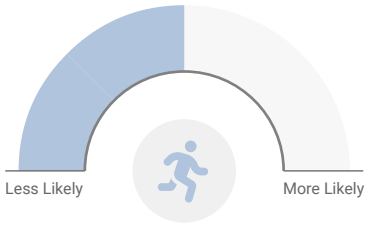
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs4253778 allele G is related allele, see the Studies with Positive Results (if available)[20,220,221,222] and see the Studies with Negative or Controversial Results (if available).

Endurance



The C/C genotype in PPARGC1A suggests standard endurance potential without strong genetic influence.

• **Gene:** PPARGC1A • **rsID:** rs8192678 • **Your Genotype:** C/C • **Zygosity:** Homozygous

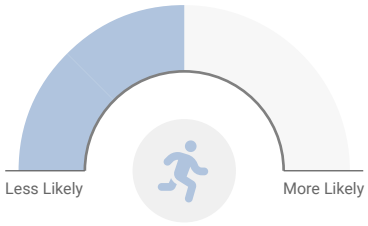
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs8192678 allele G is related allele, see the Studies with Positive Results (if available)[18,20,170,223] and see the Studies with Negative or Controversial Results (if available)[216,224,225].

Endurance



The G/G genotype in PPARGC1B lacks robust data linking it to endurance differences.

• **Gene:** PPARGC1B • **rsID:** rs7732671 • **Your Genotype:** G/G • **Zygosity:** Homozygous

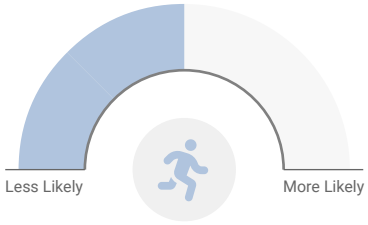
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs7732671 allele C is related allele, see the Studies with Positive Results (if available)[144,226]Ê and see the Studies with Negative or Controversial Results (if available).

Endurance



There aren't any known effects on endurance from the C/C genotype in PRDM1.

• **Gene:** PRDM1 • **rsID:** rs10499043 • **Your Genotype:** C/C • **Zygosity:** Homozygous

Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

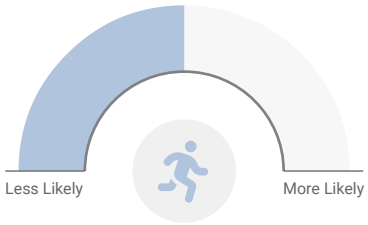
The rs10499043 allele T is related allele, see the Studies with Positive Results (if available)[228,229] and see the Studies with Negative or Controversial Results (if available).

Phenome Longevity

Name:
DoB: –
Gender: female

Report ID: WB
Subject ID: 30793
Date: 2026-10-30

Endurance



No strong relation found between the G/G genotype and endurance in the TFAM gene.

• **Gene:** TFAM • **rsID:** rs1937 • **Your Genotype:** G/G • **Zygosity:** Homozygous

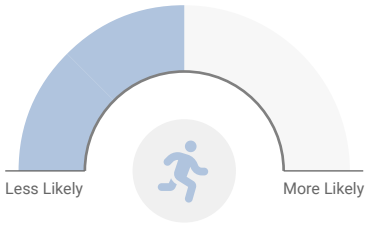
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1937 allele C is related allele, see the Studies with Positive Results (if available)[144,231]Ê and see the Studies with Negative or Controversial Results (if available)[216].

Endurance



Your G/G genotype does not indicate distinct effects on endurance in context with the UCP3 gene.

• **Gene:** UCP3 • **rsID:** rs1800849 • **Your Genotype:** G/G • **Zygosity:** Homozygous

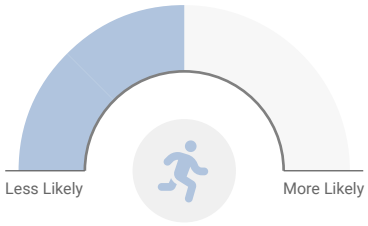
Description

An individualÕs endurance capacity is determined by many factors, including their muscle fibre typology, haemoglobin mass, mitochondrial biogenesis, maximal cardiac output, and maximal rate of oxygen consumption (VO2max), among others [118,119,120,121,122,123,124]. Indeed, there is evidence that these intermediate phenotypes have a substantial genetic influence, with literature indicating that genetic factors account for up to 70% of the variability in endurance-related traits [125]. Usually, genetic markers associated with endurance athlete status are determined by comparing allelic frequencies between endurance athletes (e.g., biathletes, road cyclists etc.) and controls.

Extra Information

The rs1800849 allele T is related allele, see the Studies with Positive Results (if available)[130,144] and see the Studies with Negative or Controversial Results (if available)[233].

Exercise Response



For your Exercise Response with the PPARD gene (rs2267668), having the A/A genotype might provide you with average exercise benefits.

• **Gene:** PPARD • **rsID:** rs2267668 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

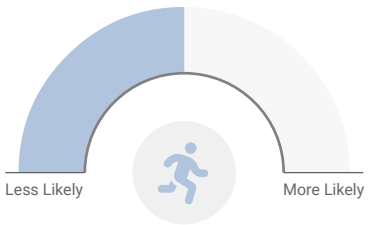
Description

The body's response to exercise involves coordination among various systems, including musculoskeletal, cardiovascular, respiratory, endocrine, immune, and others. Genetic variants have the potential to influence this exercise response. For instance, certain variants may be associated with a lower VO2 max, a higher body fat percentage, or a more pronounced decrease in blood pressure following exercise.

Extra Information

The rs2267668 AA genotype has been associated with average exercise benefits in studies (PMID(s): 17327385, 18252792). The minor allele 'G' is independently linked to a less increase in individual anaerobic threshold (P = 0.002),and also decreased aerobic physical fitness. This allele (G) is also significantly associated with dynamic balance performance (P = 0.015, Pcorrected < 0.05). Moreover, young carriers of the 'G' allele exhibit low skeletal muscle mitochondrial function (P = 0.02). Furthermore, the GA genotype/polymorphism of rs2267668 is connected to polycystic ovary syndrome (PCOS) (OR = 1.24, P = 0.008).

Ligament Injury Susceptibility



No notable effects of the C/C genotype on ligament injury risk have been observed.

• **Gene:** COL1A1 • **rsID:** rs1800012 • **Your Genotype:** C/C • **Zygosity:** Homozygous

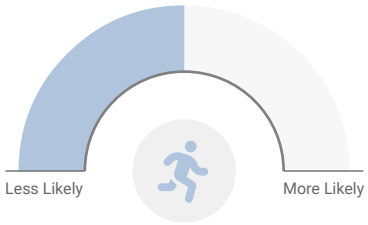
Description

A ligament is a band of tissue that connects bone to bone. Ligament injuries, often involving the knee, are common. The knee has several ligaments, each serving a specific function. The Medial Collateral Ligament (MCL) runs along the inside of the knee, preventing it from bending inward, while the Lateral Collateral Ligament (LCL) runs along the outside, preventing excessive outward bending. The Anterior Cruciate Ligament (ACL), located in the middle, helps prevent the shin bone from sliding forward. The Posterior Cruciate Ligament (PCL) complements the ACL by preventing the shin bone from sliding backward under the thigh bone. Injuries to these ligaments can range from stretching to partial or complete tears, leading to symptoms such as pain, swelling, and a sensation of the knee ""giving out"" when pressure is applied.

Extra Information

Research involving individuals of European ancestry suggests that the rs1800012 GG genotype is associated with an average likelihood of tendon and/or ligament injuries, and rs1800012 GT/TT polymorphism may be associated with the reduced risk of sports-related tendon or ligament injuries(PMID: 28206959).rs1800012 represents a common (allele frequency ~20%) polymorphism consisting of a G-to-T substitution at the first base of a consensus site for the transcription factor Sp1 in the first intron of the COL1A1 gene. COL1A1 rs1800012 polymorphism (G-to-T) may be associated with the reduced risk of sports-related tendon or ligament injuries, especially in ACL injuries, and that rare TT may played as a protective role.The rs1800012(T) allele has been extensively studied, with most observations supporting at least some association with decreased bone mineral density, and increased risk for osteoporosis, fractures, and intervertebral disc disease.

Lumbar Disc Disease Susceptibility



Your A/G genotype does not appear to influence lumbar disc issues significantly.

• **Gene:** CILP • **rsID:** rs2073711 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

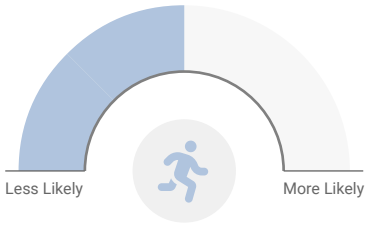
Description

Lumbar disc disease is a term commonly used to encompass various causes of back pain or sciatica. While muscle strain or ligament sprain can contribute to low back pain (LBP), the intervertebral disc is often implicated more frequently as a source of discomfort. However, it's essential to note that no single lumbar disc injury has been definitively identified as the sole cause of pain associated with lumbar disc disease.

Extra Information

In summary, the rs2073711 CC genotype has been associated with a typical risk of intervertebral disc degeneration (IVD), while CT and TT are representing lower risk of Lumbar Disk Disease.The rs2073711 SNP (1184T_C) is located in exon 8 of the cartilage intermediate layer protein gene (CILP). However, CILP gene is primarily known to be expressed abundantly in intervertebral discs, and was reported to have increased expression when degeneration occurs [PMID 15864306]. For the rs2073711 SNP, the ancestral allele is T and the disease associated risk allele is C. A study of Asian patients with lumbar disc disease (LDD) implicates each copy of a (C) allele of SNP rs2073711 (as oriented with respect to dbSNP) as increasing risk about 1.6 fold. [PMID 15864306].

Muscle Strength



If you have the G/G genotype, expect typical muscle strength, with studies highlighting its role, especially in women.

• **Gene:** CNTF • **rsID:** rs1800169 • **Your Genotype:** G/G • **Zygosity:** Homozygous

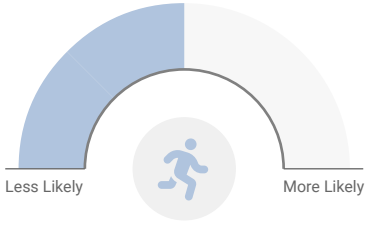
Description

Muscle strength is defined as the maximum amount of force that a group of muscles (such as biceps, triceps, quadriceps, etc.) can apply to an object simultaneously. The growth and development of muscles are influenced by specific genetic variants, leading to variations in muscle strength among individuals. Additionally, environmental factors, including physical activity and the type of exercise training, play a significant role in determining muscle strength.

Extra Information

The rs1800169 GG genotype has been associated with typical muscle strength and grip strength in women, as reported in studies (PMID(s): 16696750, 17539378, 19628720).CNTF 1357 G _ A (rs1800169), which is GA or AA genotype is associated with muscle strength/power phenotypes in women. The associations in men still need furture investigation.

Muscle Volume



We don't have strong data linking the G/T genotype to changes in Muscle Volume here.

• **Gene:** IL15RA • **rsID:** rs2228059 • **Your Genotype:** T/T>T/G • **Zygosity:** Heterozygous

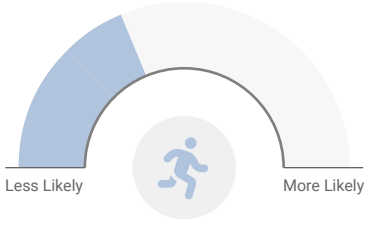
Description

Muscle volume refers to the overall size of one's muscles, particularly skeletal muscles responsible for movement. These muscles are composed of bundles of muscle fibers within individual muscle cells. The augmentation of muscle volume is typically attributed to the enlargement of muscle cell size rather than an increase in the number of cells. Environmental factors, such as exercise, can impact muscle volume, and genetic factors play a role in determining both one's inherent muscle volume and how effectively muscles respond to training.

Extra Information

The rs2228059 CC genotype has been associated with typical muscle volume and typical baseline cortical bone volume in males, according to a study (PMID: 18514540).The A-allele (CA,AA genotype) in rs2228059 was also reported associated with larger muscle volume but lower muscle quality in men (Pistilli et al., 2008).

Muscular Endurance



G/G in the ADRB2 gene typically aligns with average endurance capacities. Explore diverse activities to find your strength zone!

• **Gene:** ADRB2 • **rsID:** rs1042713 • **Your Genotype:** G/G • **Zygosity:** Homozygous

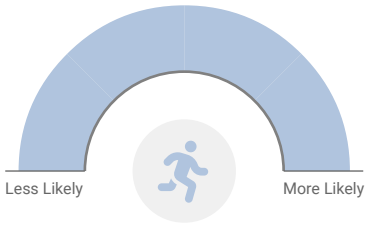
Description

Muscular endurance refers to the ability of muscles to exert strength over an extended period at a submaximal (less than the maximum) capacity. Sports that demand endurance often involve activities such as cycling, swimming, long-distance running, triathlons, and cross-country skiing.

Extra Information

The rs1042713 AG genotype may be associated with increased performance in endurance sports, while GG is a major allele with normal performance according to studies (PMID(s): 17998016, 20044476). rs1042713, also known as Arg16, G16R, and 16Arg>Gly, is a SNP in the adrenergic, beta-2-, surface receptor ADRB2 gene. The rs1042713(G) allele encodes the G/glycine form that is the more common one in most populations, while rs1042713(A) encodes the R/arginine residue at this position of the ADRB2 protein.[PMID 20044476]. The presence of the rs1042713 A allele (Arginine) has been associated with increased power and speed, which are essential components of muscular endurance.

Muscular Endurance



Your G/G genotype in the PPARA gene is an excellent match for endurance athletes, potentially enhancing your long-distance capabilities.

• **Gene:** PPARA • **rsID:** rs4253778 • **Your Genotype:** G/G • **Zygosity:** Homozygous

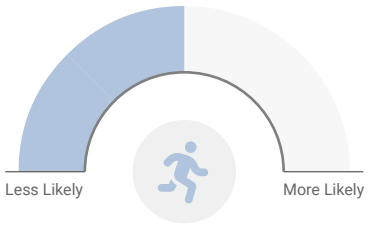
Description

Muscular endurance refers to the ability of muscles to exert strength over an extended period at a submaximal (less than the maximum) capacity. Sports that demand endurance often involve activities such as cycling, swimming, long-distance running, triathlons, and cross-country skiing.

Extra Information

The rs4253778 GG genotype and G allele has been associated with increased performance in endurance sports, as reported in a study (PMID: 26985127)*, compared to CC genotype.Note:Further studies recruiting athletes that represented different sports disciplines have revealed that it was more likely to find C allele carriers in a group of power-oriented athletes who were involved in short and very intense anaerobic effort (Ahmetov et al., 2006), while GG homozygotes were more prevalent among endurance-type athletes performing predominantly prolonged aerobic exertion (Eynon et al., 2010; Maciejewska et al., 2011). Gineviciene et al. (2010) confirmed the results of previous studies in Lithuanian male athletes showing that those with allele PPARA rs4253778 C had significantly higher muscle mass and better results in explosive strength of lower extremities than GG homozygotes (Ginevi_ien_ et al., 2010). Those results were in part explained by the analysis of muscle fiber composition of young men. It was shown that GG homozygotes had a higher percentage of slow-twitch fibers compared to CC homozygotes and the C allele was associated with the propensity to skeletal muscle hypertrophy (Ahmetov et al., 2006).

Power



There's no significant relationship between the A/G genotype and power performance noted.

• **Gene:** AMPD1 • **rsID:** rs17602729 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

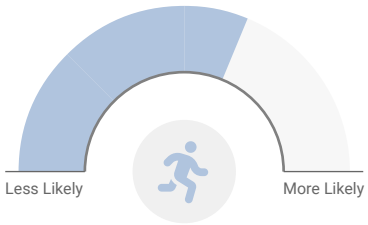
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs17602729 allele CÊ is related allele, see the Studies with Positive Results (if available)[184,269,270] and see the Studies with Negative or Controversial Results (if available).

Power



Possessing the A/G genotype in your ADAM15 gene might give you some advantages in power activities.

• **Gene:** ADAM15 • **rsID:** rs11264302 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

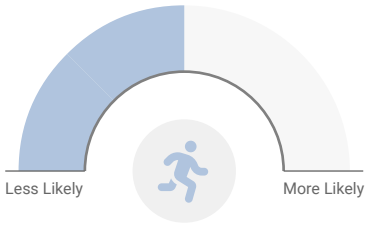
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs11264302 allele G is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



C/C doesn't seem to provide any clear advantage in power attributes based on current data.

• **Gene:** ADRB2 • **rsID:** rs1042714 • **Your Genotype:** G/G>C/C • **Zygosity:** Homozygous

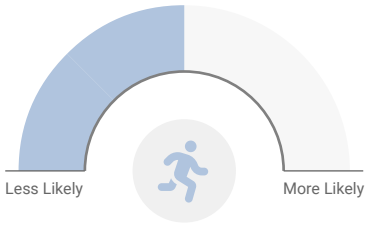
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs1042714 allele GÊ is related allele, see the Studies with Positive Results (if available)[41,174] and see the Studies with Negative or Controversial Results (if available).

Power



Having C/T could modestly support your power attributes, but it's not highly conclusive.

• **Gene:** E2F3 • **rsID:** rs4134943 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

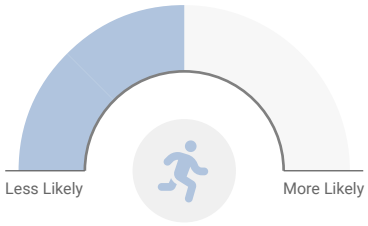
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs4134943 allele T is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



With the A/C genotype, you have a slightly increased association with power performance related to the C allele.

• **Gene:** CDKN1A • **rsID:** rs236448 • **Your Genotype:** A/A>A/C • **Zygosity:** Heterozygous

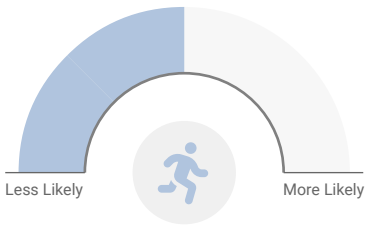
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs236448 allele C is related allele, see the Studies with Positive Results (if available)[43] and see the Studies with Negative or Controversial Results (if available).

Power



Having a C/T genotype doesn't strongly correlate with changes in your Power trait.

• **Gene:** CPNE5 • **rsID:** rs3213537 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

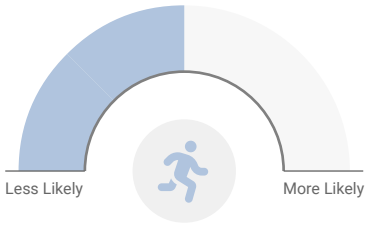
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs3213537 allele G is related allele, see the Studies with Positive Results (if available)[41,48] and see the Studies with Negative or Controversial Results (if available).

Power



For your A/G genotype, we don't have strong evidence of an effect on power performance.

• **Gene:** AUTS2 • **rsID:** rs10452738 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

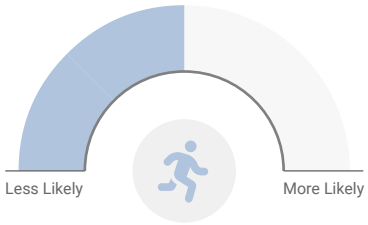
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs10452738 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



If you have an A/G genotype, we don't observe strong implications for your Power trait.

• **Gene:** CRTAC1 • **rsID:** rs2439823 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

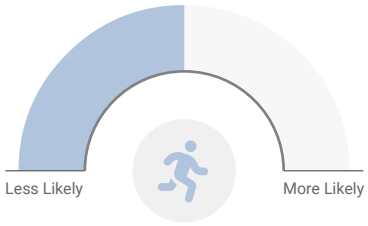
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs2439823 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



For your Power trait with the IGF2 gene (rs680), the C/C genotype doesn't seem to impact your power capabilities significantly.

• **Gene:** IGF2 • **rsID:** rs680 • **Your Genotype:** T/T>C/C • **Zygosity:** Homozygous

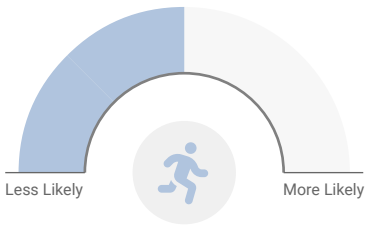
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs680 allele GÊ is related allele, see the Studies with Positive Results (if available)[41,281,282] and see the Studies with Negative or Controversial Results (if available).

Power



There's no strong evidence linking A/G in ACVR1B (rs2854464) to changes in power ability.

• **Gene:** ACVR1B • **rsID:** rs2854464 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

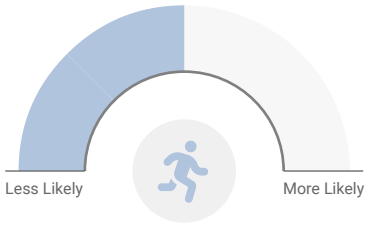
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs2854464 allele A is related allele, see the Studies with Positive Results (if available)[255,256] and see the Studies with Negative or Controversial Results (if available)[256,257].

Power



There's no strong data linking the C/T genotype with power differences.

• **Gene:** AKAP6 • **rsID:** rs12883788 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

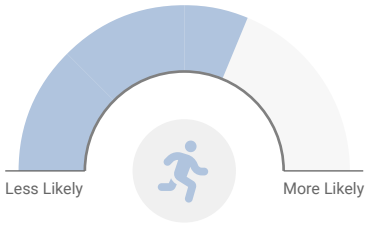
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs12883788 allele C is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



With the A/A genotype in your Power trait's CRTC1 gene, you might notice enhancements in explosive strength or speed.

• **Gene:** CRTC1 • **rsID:** rs11881338 • **Your Genotype:** T/T>A/A • **Zygosity:** Homozygous

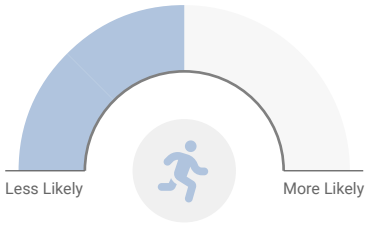
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs11881338 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



Having the A/C genotype of ZNF568 could give you a moderate boost in power-related traits, balancing both athletic potentials.

• **Gene:** ZNF568 • **rsID:** rs1667369 • **Your Genotype:** A/A>A/C • **Zygosity:** Heterozygous

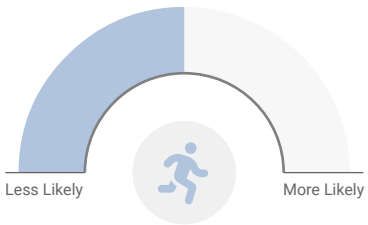
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs1667369 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



An A/G genotype might give you a slight edge in power performance, linked to HSD17B14.

• **Gene:** HSD17B14 • **rsID:** rs7247312 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

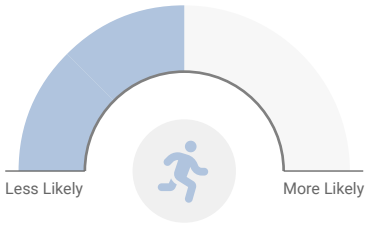
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs7247312 allele G is related allele, see the Studies with Positive Results (if available)[41] and see the Studies with Negative or Controversial Results (if available).

Power



Currently, there's no strong evidence linking the A/A genotype with power traits related to the GDF5 gene.

• **Gene:** GDF5 • **rsID:** rs143384 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

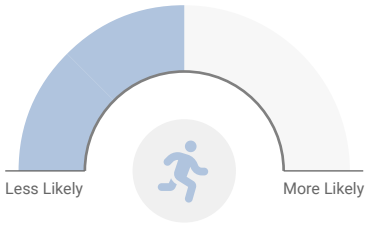
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs143384 allele G is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



The C/C genotype suggests a baseline potential for power traits, similar to non-carriers.

• **Gene:** AGTR2 • **rsID:** rs11091046 • **Your Genotype:** A/A>C/C • **Zygosity:** Homozygous

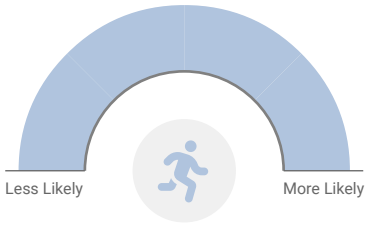
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs11091046 allele A is related allele, see the Studies with Positive Results (if available)[176,177] and see the Studies with Negative or Controversial Results (if available)[55].

Power



With the G/G genotype in your ADRB2 gene, you might excel in power-demanding activities.

• **Gene:** ADRB2 • **rsID:** rs1042713 • **Your Genotype:** G/G • **Zygosity:** Homozygous

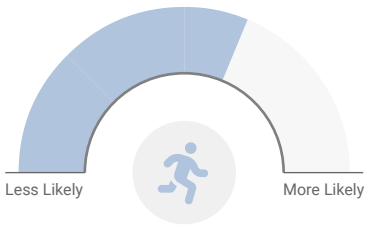
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs1042713 allele GÊ is related allele, see the Studies with Positive Results (if available)[41,174] and see the Studies with Negative or Controversial Results (if available).

Power



Your C/C genotype in AGRN may help enhance your power performance, as C is a favorable allele.

• **Gene:** AGRN • **rsID:** rs4074992 • **Your Genotype:** C/C • **Zygosity:** Homozygous

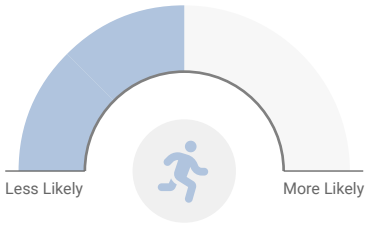
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs4074992 allele C is related allele, see the Studies with Positive Results (if available)[45] and see the Studies with Negative or Controversial Results (if available).

Power



There's not enough evidence to suggest that the C/C genotype impacts power abilities.

• **Gene:** BDNF • **rsID:** rs10501089 • **Your Genotype:** C/C • **Zygosity:** Homozygous

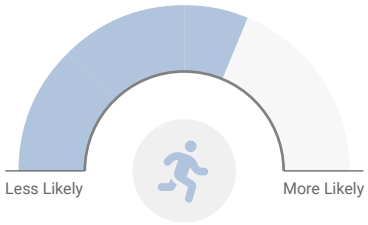
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs10501089 allele A is related allele, see the Studies with Positive Results (if available)[271] and see the Studies with Negative or Controversial Results (if available).

Power



Having a T/T genotype might align you more with traits that favor power performance, such as muscle strength.

• **Gene:** CCT3 • **rsID:** rs11548200 • **Your Genotype:** T/T • **Zygosity:** Homozygous

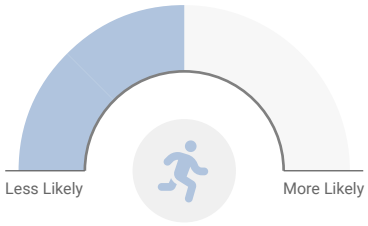
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs11548200 allele T is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



Having the T/T genotype doesn't show relevant effects on power performance.

• **Gene:** CKM • **rsID:** rs8111989 • **Your Genotype:** T/T • **Zygosity:** Homozygous

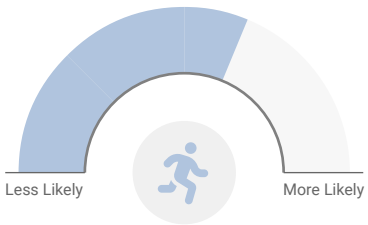
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs8111989 allele G is related allele, see the Studies with Positive Results (if available)[65,272,273] and see the Studies with Negative or Controversial Results (if available)[274].

Power



For those with the C/C genotype, you might have a better predisposition for power activities, perhaps benefiting from improved muscle strength.

• **Gene:** FHL2 • **rsID:** rs55680124 • **Your Genotype:** C/C • **Zygosity:** Homozygous

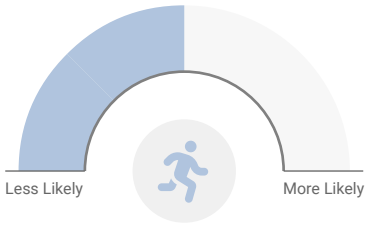
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs55680124 allele C is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



For your Power trait with the IGSF3 gene (rs699785), the G/G genotype isn't strongly associated with power performance changes.

• **Gene:** IGSF3 • **rsID:** rs699785 • **Your Genotype:** G/G • **Zygosity:** Homozygous

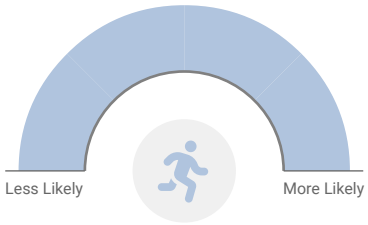
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs699785 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



For your power trait with the ILRUN gene (rs205262), having the A/A genotype could boost your sprinting or weightlifting prowess.

• **Gene:** ILRUN • **rsID:** rs205262 • **Your Genotype:** A/A • **Zygosity:** Homozygous

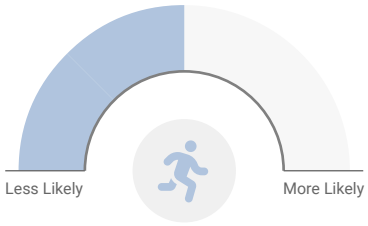
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs205262 allele A is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



The C/C genotype doesn't appear to relate significantly to your power trait.

• **Gene:** NOS3 • **rsID:** rs2070744 • **Your Genotype:** C/C • **Zygosity:** Homozygous

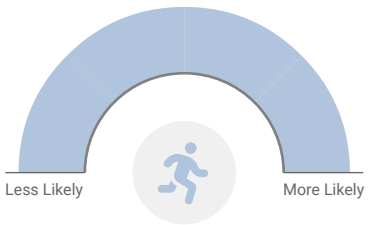
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs2070744 allele T is related allele, see the Studies with Positive Results (if available)[219,279,287] and see the Studies with Negative or Controversial Results (if available).

Power



Great news! The G/G genotype in the NRXN3 gene could potentially boost your power-oriented skills.

• **Gene:** NRXN3 • **rsID:** rs8011870 • **Your Genotype:** G/G • **Zygosity:** Homozygous

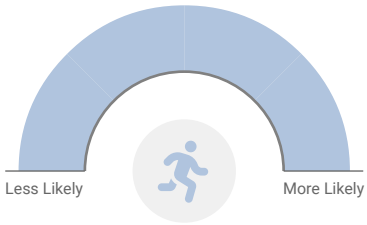
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs8011870 allele G is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



Fantastic! With a C/C genotype, you could potentially outperform in power-demanding events.

• **Gene:** NUP210 • **rsID:** rs2280084 • **Your Genotype:** C/C • **Zygosity:** Homozygous

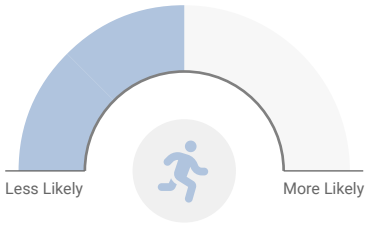
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs2280084 allele C is related allele, see the Studies with Positive Results (if available)[45] and see the Studies with Negative or Controversial Results (if available).

Power



• **Gene:** PIEZO1 • **rsID:** rs572934641 • **Your Genotype:** TCCTCCTCCTCCTCCTCCTCCT/TCCTCCTCCTCCTCCTCCTCCT • **Zygosity:** Homozygous

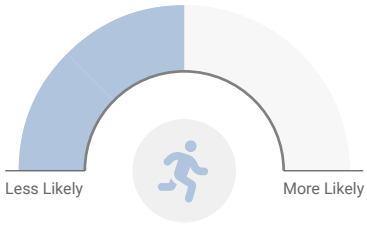
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs572934641 allele D is related allele, see the Studies with Positive Results (if available)[288] and see the Studies with Negative or Controversial Results (if available).

Power



For G/G in PPARA, no meaningful impact on power is evident.

• **Gene:** PPARA • **rsID:** rs4253778 • **Your Genotype:** G/G • **Zygosity:** Homozygous

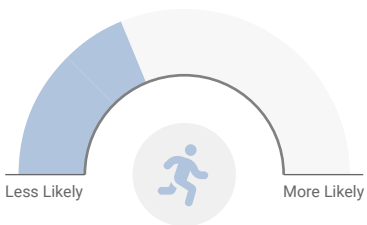
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs4253778 allele C is related allele, see the Studies with Positive Results (if available)[159,220,289] and see the Studies with Negative or Controversial Results (if available).

Power



C/C might not greatly influence your power characteristics based on current data.

• **Gene:** PPARG • **rsID:** rs1801282 • **Your Genotype:** C/C • **Zygosity:** Homozygous

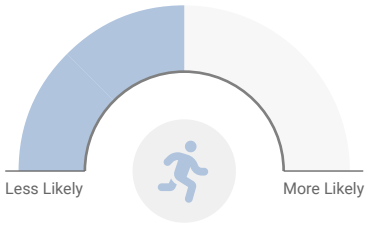
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs1801282 allele G is related allele, see the Studies with Positive Results (if available)[279,290,291] and see the Studies with Negative or Controversial Results (if available)[292].

Power



The C/C genotype doesn't show notable effects on your power performance.

• **Gene:** PPARG • **rsID:** rs2920503 • **Your Genotype:** C/C • **Zygosity:** Homozygous

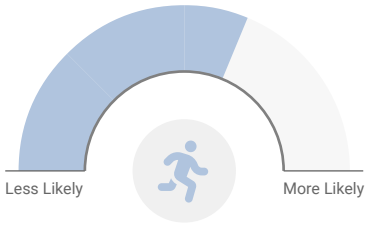
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs2920503 allele T is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



You could experience enhanced power performance with the C/C genotype in SLC39A8.

• **Gene:** SLC39A8 • **rsID:** rs13107325 • **Your Genotype:** C/C • **Zygosity:** Homozygous

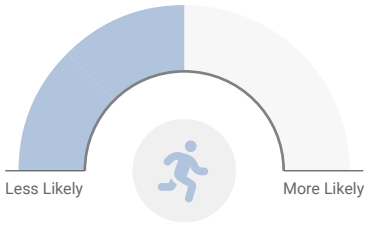
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs13107325 allele C is related allele, see the Studies with Positive Results (if available)[49] and see the Studies with Negative or Controversial Results (if available).

Power



For the Power trait in the SOD2 gene (rs4880), having an A/A genotype reveals no particular effects.

• **Gene:** SOD2 • **rsID:** rs4880 • **Your Genotype:** A/A • **Zygosity:** Homozygous

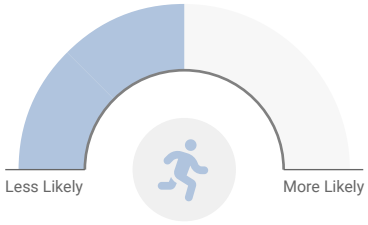
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs4880 allele C is related allele, see the Studies with Positive Results (if available)[293] and see the Studies with Negative or Controversial Results (if available).

Power



With the C/C genotype in the TRHR gene variant rs7832552, we don't see notable power performance effects.

• **Gene:** TRHR • **rsID:** rs7832552 • **Your Genotype:** C/C • **Zygosity:** Homozygous

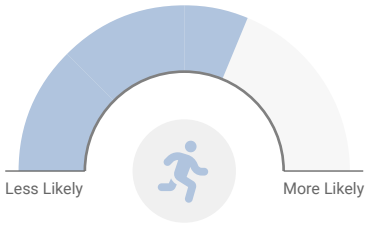
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs7832552 allele T is related allele, see the Studies with Positive Results (if available)[65,294,295] and see the Studies with Negative or Controversial Results (if available).

Power



With the UBR5 gene rs10505025, having an A/A genotype may be associated with enhanced power performance, like being able to jump higher.

• **Gene:** UBR5 • **rsID:** rs10505025 • **Your Genotype:** A/A • **Zygosity:** Homozygous

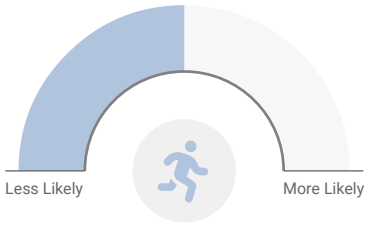
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs10505025 allele A is related allele, see the Studies with Positive Results (if available)[296] and see the Studies with Negative or Controversial Results (if available).

Power



Your T/T genotype in UBR5 rs4734621 shows no clear evidence of influence on power performance.

• **Gene:** UBR5 • **rsID:** rs4734621 • **Your Genotype:** T/T • **Zygosity:** Homozygous

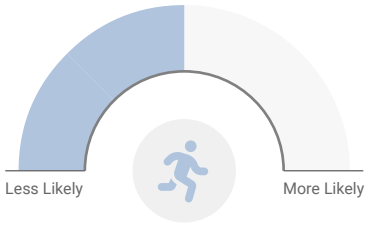
Description

Several characteristics are positively associated with power performance, including circulating levels of testosterone, percentage and cross-sectional area of fast-twitch muscle fibres, muscle mass and strength, body and calcaneus height, muscle fascicle length, and reaction time, among others [3,238,239,240,241,242,243,244]. The heritability of power-related phenotypes has been reported in the literature to range from approximately 49 to 86% in a range of phenotypes, including jumping ability [245,246]. Typically, genetic markers associated with power athlete status are determined by comparing allelic frequencies between power athletes (e.g., 100 m runners, shot putters, arm wrestlers, etc.) and untrained subjects.

Extra Information

The rs4734621 allele A is related allele, see the Studies with Positive Results (if available)[296] and see the Studies with Negative or Controversial Results (if available).

Strength



G/T in MTHFR generally doesn't correlate with significant strength changes.

• **Gene:** MTHFR • **rsID:** rs1801131 • **Your Genotype:** T/T>T/G • **Zygosity:** Heterozygous

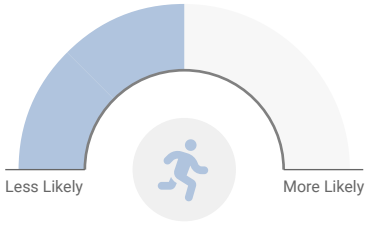
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1801131 allele C is related allele, see the Studies with Positive Results (if available)[51,286,298] and see the Studies with Negative or Controversial Results (if available).

Strength



The G/G genotype in your AGT gene isn't known to influence strength performance notably.

• **Gene:** AGT • **rsID:** rs699 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

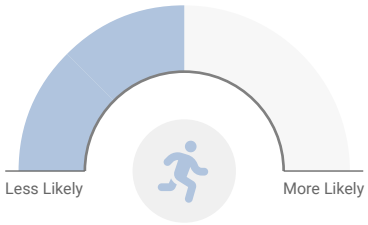
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs699 allele C is related allele, see the Studies with Positive Results (if available)[310,311] and see the Studies with Negative or Controversial Results (if available)[51].

Strength



For your Strength trait with the LRPPRC gene (rs10186876), having the G/G genotype doesn't show notable effects.

• **Gene:** LRPPRC • **rsID:** rs10186876 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

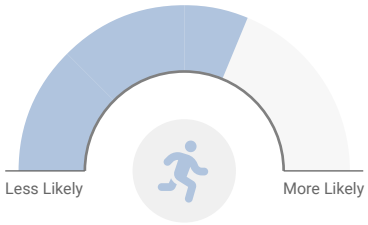
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs10186876 allele A is related allele, see the Studies with Positive Results (if available)[34,51,298] and see the Studies with Negative or Controversial Results (if available).

Strength



With T/T for R3HDM1, you might enjoy enhanced strength-related traits!

• **Gene:** R3HDM1 • **rsID:** rs6759321 • **Your Genotype:** G/G>T/T • **Zygosity:** Homozygous

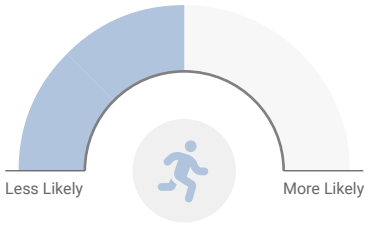
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs6759321 allele T is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



With the A/G genotype in the GBE1 gene (rs9877408), there's no strong impact connected to strength performance.

• **Gene:** GBE1 • **rsID:** rs9877408 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

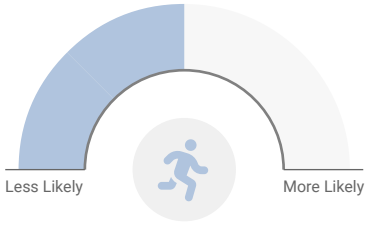
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs9877408 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Having an A/G genotype in the GALNTL6 gene (rs558129) shows no marked impact on enhancing your strength.

• **Gene:** GALNTL6 • **rsID:** rs558129 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

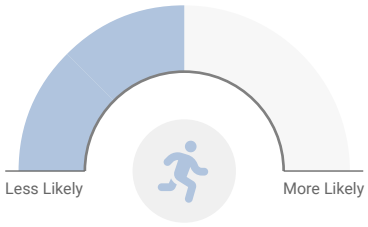
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs558129 allele T is related allele, see the Studies with Positive Results (if available)[47] and see the Studies with Negative or Controversial Results (if available).

Strength



A C/C genotype for MMS22L doesn't appear to have notable effects on your strength.

• **Gene:** MMS22L • **rsID:** rs9320823 • **Your Genotype:** T/T>C/C • **Zygosity:** Homozygous

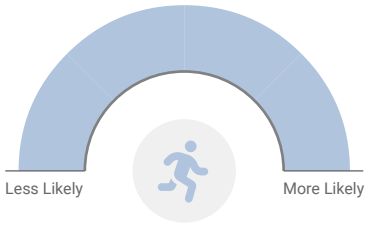
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs9320823 allele T is related allele, see the Studies with Positive Results (if available)[35,51,298] and see the Studies with Negative or Controversial Results (if available).

Strength



Having the G/G genotype could give you a boost in strength-focused activities due to the G allele's association.

• **Gene:** IL6 • **rsID:** rs1800795 • **Your Genotype:** C/C>G/G • **Zygosity:** Homozygous

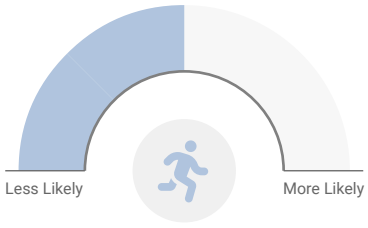
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1800795 allele G is related allele, see the Studies with Positive Results (if available)[51,283] and see the Studies with Negative or Controversial Results (if available).

Strength



For CNTFR, having A/G seems to lack strong evidence of strength impact.

• **Gene:** CNTFR • **rsID:** rs41274853 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

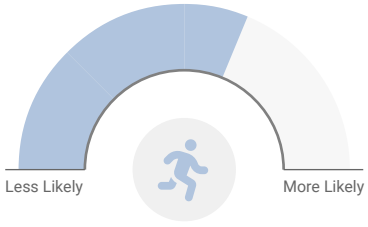
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs41274853 allele T is related allele, see the Studies with Positive Results (if available)[275,316] and see the Studies with Negative or Controversial Results (if available)[51].

Strength



Your A/G genotype with CRTAC1 suggests possible benefits for strength.

• **Gene:** CRTAC1 • **rsID:** rs563296 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

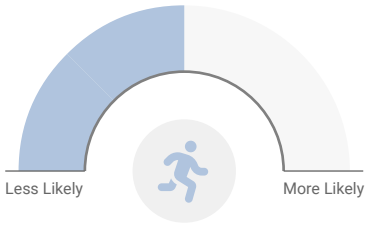
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs563296 allele G is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



For your Strength trait with the GBF1 gene (rs2273555), carrying the A/A genotype might moderately enhance your strength performance.

• **Gene:** GBF1 • **rsID:** rs2273555 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

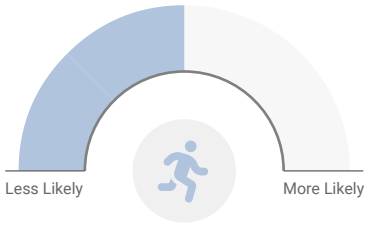
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs2273555 allele A is related allele, see the Studies with Positive Results (if available)[34,317] and see the Studies with Negative or Controversial Results (if available).

Strength



The C/T genotype in ACTN3 hasn't shown a meaningful impact on your strength trait.

• **Gene:** ACTN3 • **rsID:** rs1815739 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

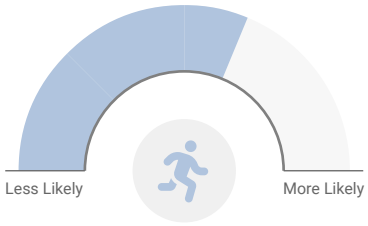
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1815739 allele C is related allele, see the Studies with Positive Results (if available) [302,306,307,308] and see the Studies with Negative or Controversial Results (if available) [51,305,309,310].

Strength



For your Strength trait related to PLEKHB1, having the G/G genotype could support better performance.

• **Gene:** PLEKHB1 • **rsID:** rs7128512 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

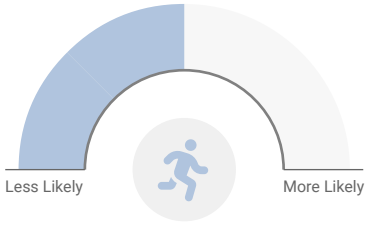
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs7128512 allele G is related allele, see the Studies with Positive Results (if available)[51,312] and see the Studies with Negative or Controversial Results (if available).

Strength



The A/G genotype under IGF1 for strength doesn't have a strong correlation with particular traits.

• **Gene:** IGF1 • **rsID:** rs35767 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

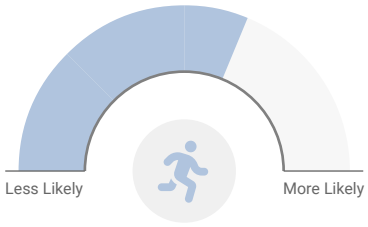
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs35767 allele T is related allele, see the Studies with Positive Results (if available)[51,280,319] and see the Studies with Negative or Controversial Results (if available).

Strength



The C/T genotype for HIF1A (rs11549465) might give you a moderate edge in strength performance.

• **Gene:** HIF1A • **rsID:** rs11549465 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

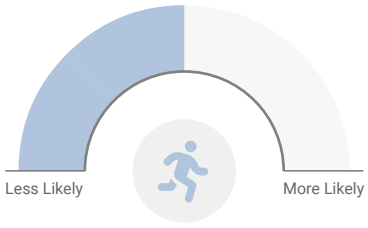
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs11549465 allele T is related allele, see the Studies with Positive Results (if available)[278,295,318] and see the Studies with Negative or Controversial Results (if available)[51].

Strength



For your Strength trait, currently, we don't see a notable effect of the A/G genotype with your ABHD17C gene.

• **Gene:** ABHD17C • **rsID:** rs7165759 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

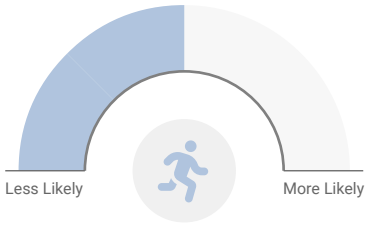
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs7165759 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Possessing the A/G genotype in the DHODH gene (rs12599952) doesn't show any strong links to strength performance.

• **Gene:** DHODH • **rsID:** rs12599952 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

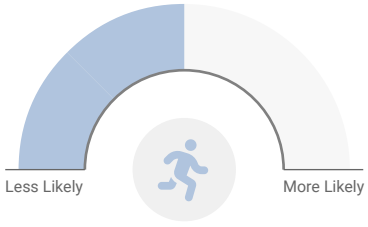
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs12599952 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



For your Strength trait, currently, we don't see a notable effect of the C/G genotype with your ACE gene.

• **Gene:** ACE • **rsID:** rs4341 • **Your Genotype:** G/G>G/C • **Zygosity:** Heterozygous

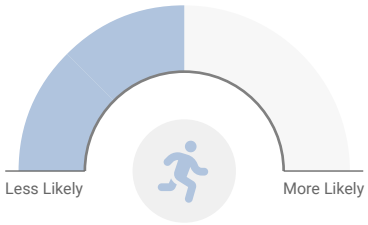
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs4341 allele G is related allele, see the Studies with Positive Results (if available) [299,300,301,302,303,304] and see the Studies with Negative or Controversial Results (if available)[305].

Strength



For your Strength trait, currently, we don't see a notable effect of the A/G genotype with your ACE gene.

• **Gene:** ACE • **rsID:** rs4343 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

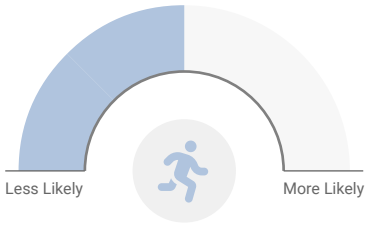
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs4343 allele G is related allele, see the Studies with Positive Results (if available)[299,300,301,302,303,304] and see the Studies with Negative or Controversial Results (if available)[305].

Strength



Having an A/T genotype doesn't significantly affect your strength levels according to current data.

• **Gene:** ACTG1 • **rsID:** rs6565586 • **Your Genotype:** T/T>T/A • **Zygosity:** Heterozygous

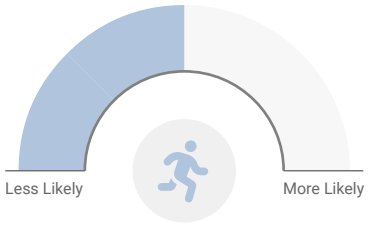
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs6565586 allele A is related allele, see the Studies with Positive Results (if available)[34,51] and see the Studies with Negative or Controversial Results (if available).

Strength



The T/T genotype in RMC1 (rs303760) hasn't shown relevant strength-related changes.

• **Gene:** RMC1 • **rsID:** rs303760 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

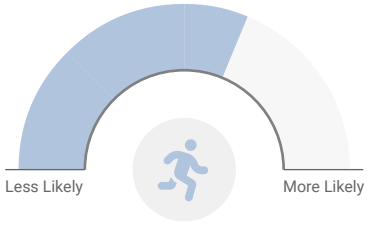
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs303760 allele C is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



For the Strength trait with ADCY3 (rs10203386), having T/T might slightly favor power-related activities.

• **Gene:** ADCY3 • **rsID:** rs10203386 • **Your Genotype:** T/T • **Zygosity:** Homozygous

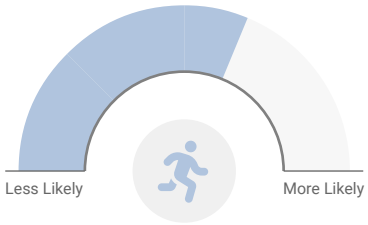
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs10203386 allele T is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Having the C/C genotype in the ADPGK gene could help enhance your performance in strength-oriented activities.

• **Gene:** ADPGK • **rsID:** rs4776614 • **Your Genotype:** C/C • **Zygosity:** Homozygous

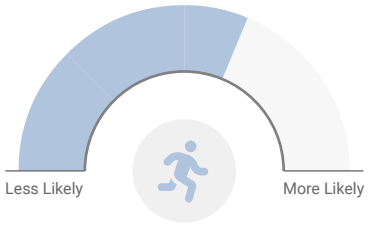
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs4776614 allele C is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Possessing the G/G genotype in the ALDH2 gene may correlate with improved strength performance!

• **Gene:** ALDH2 • **rsID:** rs671 • **Your Genotype:** G/G • **Zygosity:** Homozygous

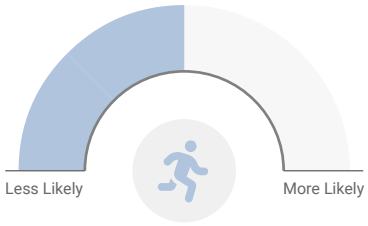
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs671 allele G is related allele, see the Studies with Positive Results (if available)[66,67,68] and see the Studies with Negative or Controversial Results (if available).

Strength



We haven't found any noteworthy effects related to strength for the G/G genotype here.

• **Gene:** ANGPT2 • **rsID:** rs890022 • **Your Genotype:** G/G • **Zygosity:** Homozygous

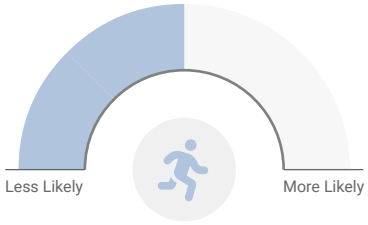
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs890022 allele A is related allele, see the Studies with Positive Results (if available)[51,312] and see the Studies with Negative or Controversial Results (if available).

Strength



We haven't identified significant effects for strength with the T/T genotype in ARPP21.

• **Gene:** ARPP21 • **rsID:** rs1513475 • **Your Genotype:** T/T • **Zygosity:** Homozygous

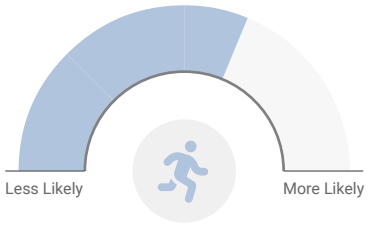
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1513475 allele C is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



The C/C genotype in BCDIN3D might give you an advantage in strength activities.

• **Gene:** BCDIN3D • **rsID:** rs12367809 • **Your Genotype:** C/C • **Zygosity:** Homozygous

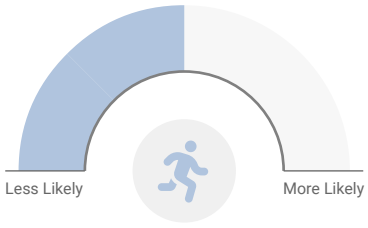
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs12367809 allele C is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



The T/T genotype in CKM does not reveal a significant connection with strength.

• **Gene:** CKM • **rsID:** rs8111989 • **Your Genotype:** T/T • **Zygosity:** Homozygous

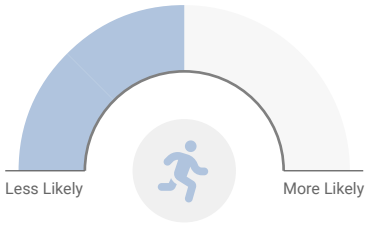
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs8111989 allele G is related allele, see the Studies with Positive Results (if available)[54,315] and see the Studies with Negative or Controversial Results (if available)[51,274].

Strength



• **Gene:** GLIS3 • **rsID:** rs34706136 • **Your Genotype:** -/- • **Zygosity:** Homozygous

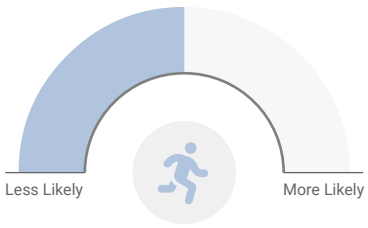
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs34706136 allele TG is related allele, see the Studies with Positive Results (if available)[50] and see the Studies with Negative or Controversial Results (if available).

Strength



As a G/G carrier, we don't find a strong relationship with strength for your ITPR1 variant.

• **Gene:** ITPR1 • **rsID:** rs901850 • **Your Genotype:** G/G • **Zygosity:** Homozygous

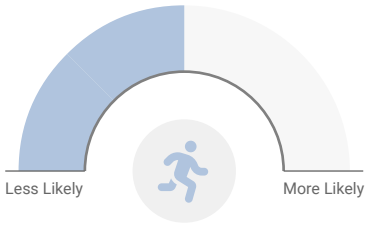
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs901850 allele T is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



With your G/G genotype for the KIF1B gene (rs11121542), you might perform well in activities involving strength.

• **Gene:** KIF1B • **rsID:** rs11121542 • **Your Genotype:** G/G • **Zygosity:** Homozygous

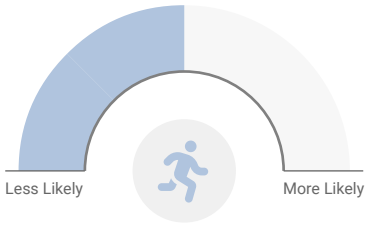
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs11121542 allele G is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



For your Strength trait with the MLN gene (rs12055409), having the A/A genotype doesn't show notable effects.

• **Gene:** MLN • **rsID:** rs12055409 • **Your Genotype:** A/A • **Zygosity:** Homozygous

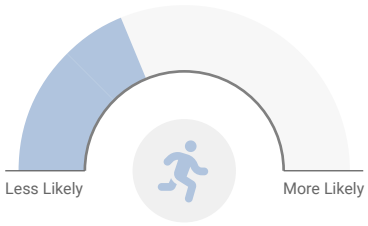
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs12055409 allele G is related allele, see the Studies with Positive Results (if available)[35,317] and see the Studies with Negative or Controversial Results (if available).

Strength



With the A/A genotype in NPIPB6, you might enjoy enhanced strength benefits.

• **Gene:** NPIPB6 • **rsID:** rs2726036 • **Your Genotype:** A/A • **Zygosity:** Homozygous

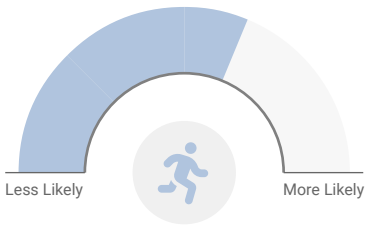
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs2726036 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



For your Strength trait with the PHACTR1 gene (rs6905419), having the C/C genotype might support better performance in strength sports.

• **Gene:** PHACTR1 • **rsID:** rs6905419 • **Your Genotype:** C/C • **Zygosity:** Homozygous

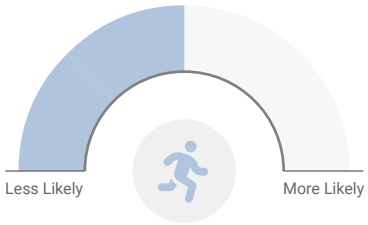
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs6905419 allele C is related allele, see the Studies with Positive Results (if available)[35,51,298] and see the Studies with Negative or Controversial Results (if available).

Strength



The G/G genotype for Strength with PPARA doesn't indicate a significant impact on your capabilities.

• **Gene:** PPARA • **rsID:** rs4253778 • **Your Genotype:** G/G • **Zygosity:** Homozygous

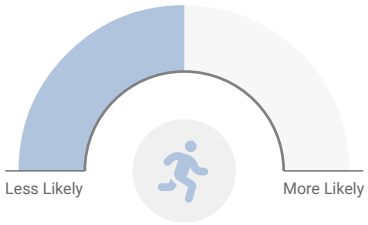
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs4253778 allele C is related allele, see the Studies with Positive Results (if available)[220,320,321] and see the Studies with Negative or Controversial Results (if available)[51].

Strength



Having C/C under the PPARG gene doesn't show a strong impact on your strength capabilities.

• **Gene:** PPARG • **rsID:** rs1801282 • **Your Genotype:** C/C • **Zygosity:** Homozygous

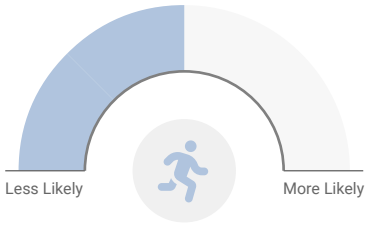
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1801282 allele G is related allele, see the Studies with Positive Results (if available)[51,290,291] and see the Studies with Negative or Controversial Results (if available).

Strength



Having C/C for PPARGC1A isn't strongly linked to strength improvements.

• **Gene:** PPARGC1A • **rsID:** rs8192678 • **Your Genotype:** C/C • **Zygosity:** Homozygous

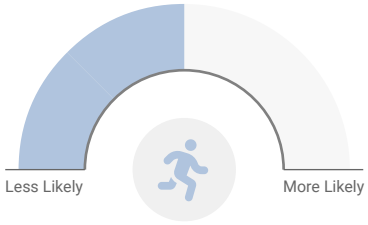
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs8192678 allele A is related allele, see the Studies with Positive Results (if available)[51,305,308] and see the Studies with Negative or Controversial Results (if available).

Strength



The C/C genotype in RASGRF1 (rs1521624) doesn't show significant effects on your strength traits.

• **Gene:** RASGRF1 • **rsID:** rs1521624 • **Your Genotype:** C/C • **Zygosity:** Homozygous

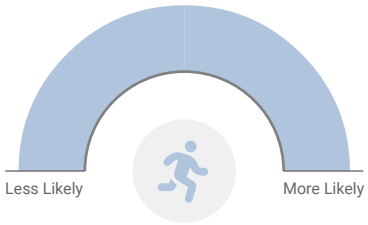
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs1521624 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Having the A/A genotype in SLC39A8 (rs13135092) might enhance your strength, possibly aiding performance in strength sports.

• **Gene:** SLC39A8 • **rsID:** rs13135092 • **Your Genotype:** A/A • **Zygosity:** Homozygous

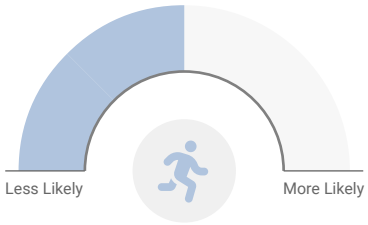
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs13135092 allele A is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Having the G/G genotype in the TFAP2D gene doesn't appear to influence strength significantly.

• **Gene:** TFAP2D • **rsID:** rs56068671 • **Your Genotype:** G/G • **Zygosity:** Homozygous

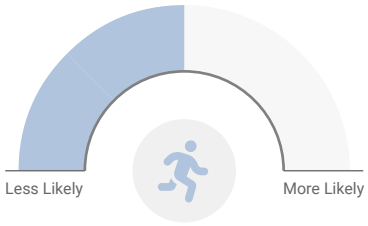
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs56068671 allele T is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



Possessing a T/T genotype hasn't shown notable correlations with strength in the context of ZKSCAN5.

• **Gene:** ZKSCAN5 • **rsID:** rs3843540 • **Your Genotype:** T/T • **Zygosity:** Homozygous

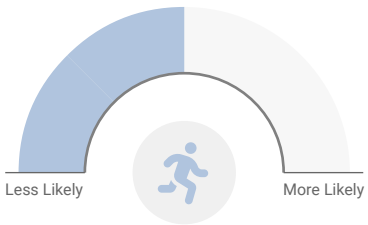
Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

Extra Information

The rs3843540 allele C is related allele, see the Studies with Positive Results (if available)[35,51] and see the Studies with Negative or Controversial Results (if available).

Strength



A C/C genotype doesn't display a significant relationship with strength changes for the ZNF608 gene.

• **Gene:** ZNF608 • **rsID:** rs4626333 • **Your Genotype:** C/C • **Zygosity:** Homozygous

Description

Performance in strength-based sports is based on multiple factors. However, the factors considered to contribute substantially to strength phenotypes include skeletal muscle hypertrophy (muscle fibre size), hyperplasia, the predominance of fast-twitch muscle fibres, a greater muscle fascicle pennation angle, improved neurological adaptation, high glycolytic capacity, and increased circulatory testosterone [297]. Importantly, evidence exists that strength athletes exhibit vastly different transcriptomic, biochemical, anthropometric, physiological, and biomechanical characteristics compared to endurance athletes and/or controlsÊ

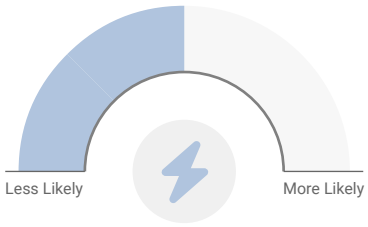
Extra Information

The rs4626333 allele G is related allele, see the Studies with Positive Results (if available)[312,317] and see the Studies with Negative or Controversial Results (if available).

Metabolism

Metabolic rate and nutrient processing are governed by genetic variants that influence insulin sensitivity, fat oxidation, and energy expenditure. These genetic factors can determine tendencies toward weight gain, energy levels, and responses to different dietary macronutrients. Personalized dietary strategies based on genetic information can optimize metabolic health and weight management.

Metabolic Syndrome



With the TT/AA genotype in the APOA5 gene, your likelihood of metabolic syndrome is average.

• **Gene:** APOA5 • **rsID:** rs662799 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

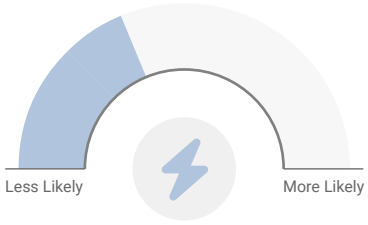
Description

Metabolic syndrome is a term used to describe a cluster of risk factors that elevate the likelihood of developing heart disease and other health issues, including diabetes and stroke. The term ""metabolic"" refers to the biochemical processes integral to the body's normal functioning. Risk factors encompass traits, conditions, or habits that increase the probability of disease development. In this context, ""heart disease"" primarily refers to coronary heart disease (CHD), wherein plaque, a waxy substance, accumulates inside the coronary arteries, leading to their hardening and narrowing. This process reduces blood flow to the heart muscle, potentially causing chest pain, heart attacks, cardiac damage, or even death. For more information, you can visit the National Heart, Lung, and Blood Institute; National Institutes of Health; U.S. Department of Health and Human Services website: https://www.nhlbi.nih.gov/health-topics/metabolic-syndrome.

Extra Information

rs662799 (G-A, or C-T) is a SNP in the APOA5 gene.The rarer rs662799(G or C) allele has been associated in multiple other reports to be associated with higher triglyceride levels. The rs662799 AA/TT genotype has been associated with an average likelihood of metabolic syndrome, according to a study (PMID: 23468858). In summary for other studies, The G allele is considered the minor allele and has several associations: each G allele is linked to higher triglyceride levels; the AG genotype is associated with a 1.4 times higher risk of early heart attacks and less weight gain on high-fat diets; while the GG genotype is associated with a 2 times higher risk of early heart attacks and also less weight gain on high-fat diets.

Obesity



Your G/G genotype puts you at an average likelihood for obesity, but balancing diet can help.

• **Gene:** ADIPOQ • **rsID:** rs17300539 • **Your Genotype:** G/G • **Zygosity:** Homozygous

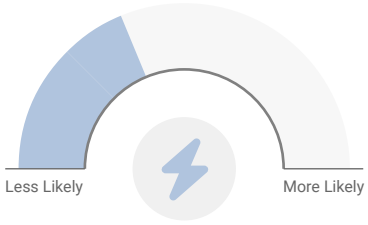
Description

Overweight and obesity have become prevalent conditions in the United States, characterized by an increase in the size and number of fat cells in the body. Medical professionals utilize measurements such as body mass index (BMI) and waist circumference to screen and diagnose these conditions. Obesity, a serious medical issue, can lead to complications like metabolic syndrome, high blood pressure, atherosclerosis, heart disease, diabetes, high blood cholesterol, cancers, and sleep disorders. Treatment approaches vary based on the cause, severity, and presence of complications, including lifestyle changes such as heart-healthy eating and increased physical activity, FDA-approved weight-loss medicines, and, in some cases, surgical interventions. (Source: National Heart, Lung, and Blood Institute; National Institutes of Health; U.S. Department of Health and Human Services.)

Extra Information

The rs17300539 GG genotype is associated with an average likelihood of obesity susceptibility, as indicated by studies (PMID: 25223469).The rs17300539(A) allele confered protection from weight regain, particularly at 32-60 weeks after the low-calorie dietary intervention, when improvement in GG subjects had disappeared [PMID 18949681].A: Increased adiponectin levels. G: Lower production of adiponectin.

Obesity



The G/G genotype seems to be associated with a normal likelihood of obesity for you.

• **Gene:** Intergenic • **rsID:** rs7138803 • **Your Genotype:** G/G • **Zygosity:** Homozygous

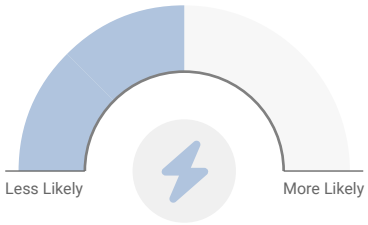
Description

Overweight and obesity have become prevalent conditions in the United States, characterized by an increase in the size and number of fat cells in the body. Medical professionals utilize measurements such as body mass index (BMI) and waist circumference to screen and diagnose these conditions. Obesity, a serious medical issue, can lead to complications like metabolic syndrome, high blood pressure, atherosclerosis, heart disease, diabetes, high blood cholesterol, cancers, and sleep disorders. Treatment approaches vary based on the cause, severity, and presence of complications, including lifestyle changes such as heart-healthy eating and increased physical activity, FDA-approved weight-loss medicines, and, in some cases, surgical interventions. (Source: National Heart, Lung, and Blood Institute; National Institutes of Health; U.S. Department of Health and Human Services.)

Extra Information

The rs7138803 AG genotype has been linked to an increased likelihood of obesity, as reported in studies (PMID(s): 21912638, 21527513). The risk allele A is asoosciated with body mass index[PMID 20935630].The GG genotype seems have anormal likelihood of obesity.

Obesity



Having the G/G genotype indicates an average likelihood for obesity according to current studies.

• **Gene:** Intergenic • **rsID:** rs12970134 • **Your Genotype:** G/G • **Zygosity:** Homozygous

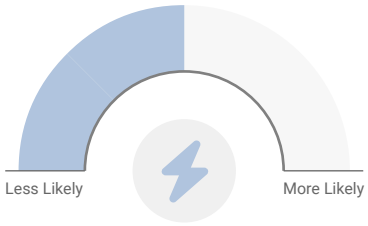
Description

Overweight and obesity have become prevalent conditions in the United States, characterized by an increase in the size and number of fat cells in the body. Medical professionals utilize measurements such as body mass index (BMI) and waist circumference to screen and diagnose these conditions. Obesity, a serious medical issue, can lead to complications like metabolic syndrome, high blood pressure, atherosclerosis, heart disease, diabetes, high blood cholesterol, cancers, and sleep disorders. Treatment approaches vary based on the cause, severity, and presence of complications, including lifestyle changes such as heart-healthy eating and increased physical activity, FDA-approved weight-loss medicines, and, in some cases, surgical interventions. (Source: National Heart, Lung, and Blood Institute; National Institutes of Health; U.S. Department of Health and Human Services.)

Extra Information

The rs12970134 GG genotype is associated with an average likelihood of obesity and GA/AA is associated with higher risk of obesity, as indicated by studies (PMID(s): 18454146, 23049848). The risk allele A is asoociated with high BMI in obese women(PMID: 31429705). A study of 14,000 Indian Asian or Caucasian adults indicates that rs12970134(A) alleles are associated with obesity. The average increase in waist circumference is 0.9cm BMI units per risk allele. [PMID 18454146]

Resting Metabolic Rate



The G/G genotype suggests a typical resting metabolic rate and reduced weight gain potential with certain antipsychotic medications.

• **Gene:** LEPR • **rsID:** rs8179183 • **Your Genotype:** G/G • **Zygosity:** Homozygous

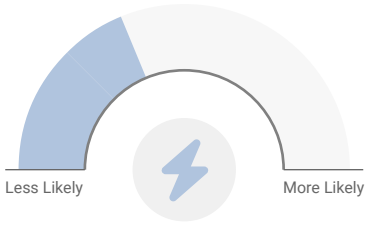
Description

Resting (basal) metabolic rate is a measure that quantifies the energy expended in performing and sustaining basic autonomic functions, including pupillary response, respiration, and heartbeat. These essential functions are typically carried out involuntarily and contribute to the body's overall energy expenditure.

Extra Information

The rs8179183 CG/GG genotype is linked to the usual resting metabolic rate (PMID: 16231024).rs8179183 is a SNP in the leptin receptor LEPR gene.In a study of 101 mostly Caucasian patients prescribed the atypical antipsychotic risperidone, carriers of a rs8179183(G) allele were less likely to gain significant weight compared to rs8179183 CC genotype carriers, as assessed by physiogenomic analysis of corresponding weight profiles. Two other SNPs, rs6837793 and rs705381, were also significantly associated with weight profiles in these patients.[PMID 17199131]

Weight Gain



With a C/C genotype, you are likely at an average risk for weight gain.

• **Gene:** PPARG • **rsID:** rs1801282 • **Your Genotype:** C/C • **Zygosity:** Homozygous

Description

The ease with which one gains or loses weight is influenced by many factors, such as physical activity and diet. Other biological factors also influence the rate at which one gains or loses weight, including age, sex, and specific genetic variants.

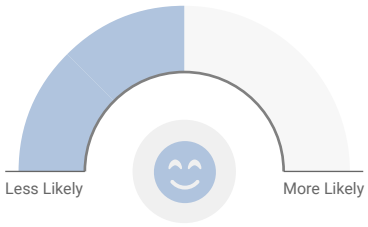
Extra Information

The rs1801282 CC genotype is associated with an average risk of weight gain (PMID(s): 23666678, 26361038).In comparison, the minor G allele is associated with reduced weight gain. rs1801282, also known as Pro12Ala, is a common SNP in the peroxisome proliferator-activated receptor PPARG gene. The more common (C) allele (in dbSNP orientation) encodes the 'Pro' amino acid at this SNP position. rs1801282 G allele has been also reported to be associated with:lower PPAR gamma activity,more benefits to exercise(having one G allele makes you more responsive to the beneficial health effects of exercise),increased obesity rates,lower heart disease,lower risk for diabetes,poor response to a high-fat diet,protective against colorectal cancer,protective against psoriatic arthritis.higher risk for rheumatoid arthritishigher risk for sarcoidosis.

Behavior

Behavioral tendencies, such as impulsivity, risk tolerance, and social interaction styles, are shaped by genetic factors affecting neurotransmitter pathways and receptor sensitivities. These genetic influences can affect decision-making patterns, stress responses, and even susceptibility to behavioral conditions. Understanding these factors allows for tailored behavioral interventions and stress management techniques.

Hunger Response Control



With the G/T genotype, you might experience average dietary disinhibition and have a usual hunger response.

• **Gene:** NMB • **rsID:** rs1051168 • **Your Genotype:** G/G>G/T • **Zygosity:** Heterozygous

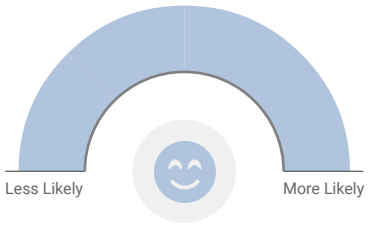
Description

Hunger is characterized by a sense of physical discomfort and potentially mental anxiety when food is not present, coupled with a desire to eat. The body's capacity to regulate the sensation of hunger, known as hunger response control, is influenced by factors such as diet and lifestyle. Additionally, specific genetic variants can also contribute to shaping this aspect of hunger regulation.

Extra Information

The rs1051168, a missense mutation (G to T, p.P73T) that located in the neuromedin-_ gene is associated with higher levels of disinhibition, susceptibility to hunger, and body weight gain over time(PMID:21527296). Also it has been earlier associated with obesity and abnormal eating behaviour in adults(PMID:20010906). TG/GG(AC/CC) genotype has been linked to an average likelihood of dietary disinhibition and hunger susceptibility, according to studies (PMID(s): 18271693, 15585758, Arguello 2018).and TT/AA polymorphism has been associated with eating behaviors and increased risk of obesity.

Snacking Behavior



Those with the G/G genotype might engage in 'extreme snacking behavior,' increasing their snack intake significantly.

• **Gene:** LEPR • **rsID:** rs2025804 • **Your Genotype:** G/G • **Zygosity:** Homozygous

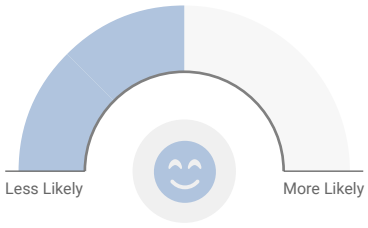
Description

Snacking is generally defined as the behavior of eating a small portion of food in between regular meals.

Extra Information

The rs2025804 AG genotype is linked to the usual snacking eating pattern and an average BMI (PMID(s): 17192493, 17903300, 22810975).Scientists established that people with two copies of the G allele (GG genotype) at position rs2025804 are twice as likely to show 'extreme snacking behaviour' (which is defined as consuming more than 15% of their energy intake as snacks in between meals).Common Genetic Variations in CCK, Leptin, and Leptin Receptor Genes Are Associated With Specific Human Eating Patterns.

Sugar Intake



No notable sugar intake patterns are associated with the A/G genotype.

• **Gene:** SLC2A2 • **rsID:** rs5400 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

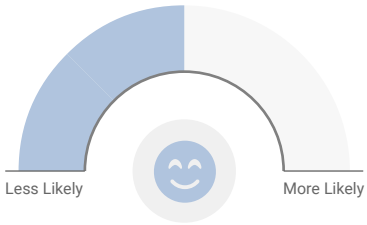
Description

Genetic factors play a role in the variation of daily sugar intake levels among individuals, influenced by environmental factors such as the availability of sugars and dietary choices. Recent studies have identified genetic associations with differences in sugar consumption patterns.

Extra Information

The rs5400 CC(GG) genotype is linked to average sugar intake and typical susceptibility to developing dental cavities, according to studies (PMID(s): 18349384, 26112465).The CT(GA) and TT(AA) genotype is associated with significantly higher sugar consumption.

Sweet Tooth



G/G genotype doesn't show notable impact on your preference for sweet foods.

• **Gene:** FUT1 • **rsID:** rs838133 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

Description

Some individuals greatly enjoy the taste of sweets, such as candy, frosting, cookies, and ice cream. Others express preferences for various non-sweet flavors. Certain genetic variants are associated with sweet taste preference.

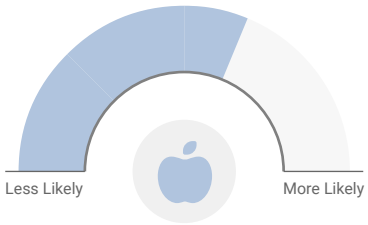
Extra Information

The rs838133 TT genotype is associated with a higher likelihood of preferring sweet food (PMID(s): 23372041, 28467924)*.A 2017 study of ~6,500 individuals with detailed eating records concluded that the rs838133(T) allele (in SNPedia and dbSNP orientation) increased the odds ratio (OR) of being in the top 33% of people for total intake of all types of sweet-tasting foods, with an OR of 1.18 per T-allele (CI: 1.06?.32, p = 0.003). When sweet intake was divided into ?andy?and ?ake,?individuals carrying the T-allele had higher candy intake (OR 1.19, CI: 1.07?.32, p = 0.0007), whereas intake of cake was the same regardless of rs838133 genotype.In comparison, CC genotype is associated with lower odds of preferring candy or sweet snacks, and CT represents sweeth tooth tendency and slightly higher odds of preferring candy.

Nutrition and Diet

Genetic variations can influence how nutrients are metabolized, impacting dietary preferences, nutrient deficiencies, and even food sensitivities. For instance, polymorphisms in genes related to lactose tolerance, gluten sensitivity, or omega-3 metabolism can determine the optimal diet for an individual. Nutrigenomics enables personalized nutrition plans for improved health outcomes.

Polyunsaturated Fats



As a C/T carrier, you might notice lower levels of certain polyunsaturated fatty acids and modest influences on fat distribution.

• **Gene:** FADS1 • **rsID:** rs174547 • **Your Genotype:** T/T>T/C • **Zygosity:** Heterozygous

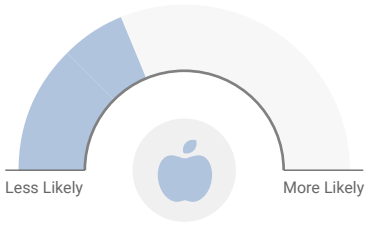
Description

This type of fat, known as polyunsaturated fatty acids (PUFAs), remains in a liquid state at room temperature. Two main categories of PUFAs are omega-6 and omega-3. Omega-6 fatty acids are present in liquid vegetable oils like corn oil, safflower oil, and soybean oil. On the other hand, omega-3 fatty acids are derived from plant sources such as canola oil, flaxseed, soybean oil, and walnuts, as well as from seafood, including fatty fish (e.g., salmon, tuna, trout) and shellfish (e.g., crab, mussels, oysters). Specific omega-3 fatty acids like EPA and DHA are abundant in seafood, while another type, ALA (alpha-linolenic acid), is found in various foods, including some vegetable oils like canola and soy. Omega-3s are also available in dietary supplements, with fish oil supplements containing EPA and DHA, and flaxseed oil supplements containing ALA. While there is moderate evidence supporting the health benefits of consuming seafood, the health advantages of omega-3 dietary supplements remain unclear (Source: National Center for Complementary and Integrative Health; National Institutes of Health; U.S. Department of Health and Human Services). For additional information, you can visit https://ods.od.nih.gov/factsheets/Omega3FattyAcids-HealthProfessional/.

Extra Information

The genomic variant c.1248+52 A to G , or T to C, also known as rs174547. Studies involving individuals of European descent indicate that those with the rs174547 homozygous mutated GG/CC genotype exhibit lower levels of polyunsaturated fatty acid(PMID: 24823311) and also for CT genotype as the risk allele carrier.The "C" allele was associated with lower LDL (low density lipoprotein) concentration (P = 0.03) [PMID: 22451038].This rs174547 C minor allele was associated with a higher proportion of linoleic acid, lower arachidonic acid and docosahexaenoic acid, as well as lower delta-6-desaturase and delta-5-desaturase activity. Female C allele carriers had lower android fat percentages and lower levels of low-density lipoprotein-cholesterol, while male C allele carriers had lower gynoid fat percentages and higher triglyceride after adjusting for age, income, BMI, behavioral risk factors, and regional fat percentages(PMID: 28359317).

Vitamin B12



The G/G genotype suggests lower levels of vitamin B12, which might affect your energy levels.

• **Gene:** FUT2 • **rsID:** rs602662 • **Your Genotype:** G/G • **Zygosity:** Homozygous

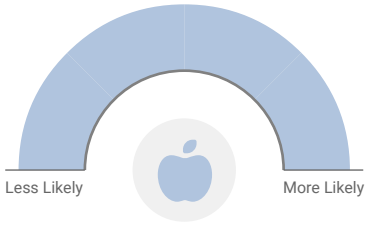
Description

Vitamin B12 (cobalamin) is a compound crucial for various metabolic processes in the body. It naturally occurs in animal products like meat, organs, and dairy. Additionally, lower levels of vitamin B12 are present in fortified plant-based foods and grains, as well as in vitamin supplements. Inadequate levels of vitamin B12 can lead to conditions such as anemia, fatigue, constipation, and peripheral neuropathy, affecting nerve sensation in the hands and feet. Specific genetic variants have been identified to influence the circulating levels of vitamin B12 in the bloodstream.

Extra Information

The rs602662 AG genotype is linked to reduced vitamin B12 levels (PMID(s): 18776911, 27995393)*.In comparison, AA represents Higher vitamin B12 levels, GG represents Lower vitamin B12 levels.

Vitamin B6



With the C/C genotype, you might have lower levels of vitamin B6, which could influence your health.

• **Gene:** NBPF3 • **rsID:** rs4654748 • **Your Genotype:** C/C • **Zygosity:** Homozygous

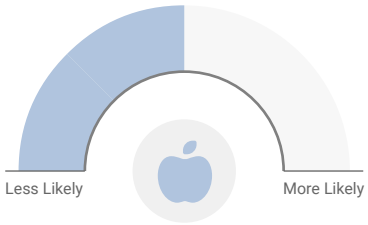
Description

Vitamin B6 is composed of six compounds that play crucial roles in various metabolic processes in the body, including the production of neurotransmitters used for nerve communication and other vital biological functions. It is naturally present in meats, animal organs (such as beef liver), starchy vegetables, and non-citrus fruits. Additionally, vitamin B6 can be found in lower amounts in fortified plant-based foods, grains, and vitamin supplements. Inadequate levels of vitamin B6 may lead to anemia, skin issues, and a weakened immune system. Specific gene variants have been identified as influencers of the circulating levels of vitamin B6 in the bloodstream.

Extra Information

The rs4654748 CT and CC genotype is linked to reduced serum levels of vitamin B6 (PMID: 19303062), especially CC geotype on a biger extent.TT genptype is more likely to have normal levels of serum Vitamin B6.

Vitamin C



With C/C, Vitamin C levels aren't clearly impacted in any direction, so keep munching on those veggies!

• **Gene:** SLC23A1 • **rsID:** rs33972313 • **Your Genotype:** C/C • **Zygosity:** Homozygous

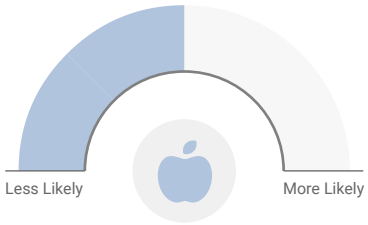
Description

Vitamin C (L-ascorbic acid) is a compound utilized in various biological processes, including the synthesis of collagen (a skin component), immune system function, and acting as an antioxidant. Antioxidants like vitamin C help eliminate free radicals and reactive oxygen species that could harm cells. Natural sources of vitamin C include citrus fruits, vegetables, and fortified foods, and it is also available in vitamin supplements. Severe vitamin C deficiency may lead to scurvy, characterized by symptoms such as fatigue, anemia, skin issues, and immune system deficiencies. Specific genetic variations have been identified as influencing the levels of circulating vitamin C in the bloodstream.

Extra Information

The rs33972313 GG genotype is associated with typical or higher serum levels of vitamin C (PMID(s): 20519558, 23737080,25948669).The GA and AA genptype is more likely to have lower plasma vitamin C levels.

Vitamin D



For G/T, there's no significant Vitamin D impact, so keep soaking up the sun as usual.

• **Gene:** GC • **rsID:** rs2282679 • **Your Genotype:** T/T>T/G • **Zygosity:** Heterozygous

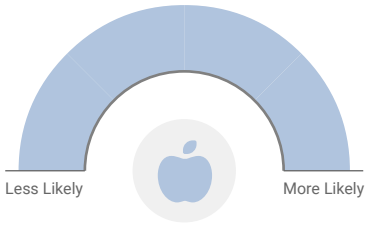
Description

Vitamin D plays multiple roles in the body and is technically classified as a hormone rather than a vitamin. It facilitates the absorption of calcium, a crucial component for bone formation. Inadequate levels of vitamin D can contribute to bone disorders like osteoporosis or rickets. Additionally, vitamin D is involved in the proper functioning of the nervous, muscular, and immune systems.

Extra Information

The rs2282679 AA genotype is linked to typical vitamin D levels (PMID(s): 20541252, 23924835, 23191998, 25174667).rs2282679, located in the group-specific component (vitamin D binding protein) GC gene on chromosome 4p12, has been linked by several studies to vitamin D serum concentrations.In both studies, the allele associated with lower vitamin D, and thus the potential for vitamin D insufficiency, is rs2282679(C). Carriers of two such alleles have lower vitamin D than carriers of one allele, who in turn on average have lower vitamin D levels than rs2282679(AA) individuals.In comparision, CC genotype represents lower vitamin D levels.

Vitamin E



You have the C/C genotype, which aligns with typical vitamin E levels. Keep on indulging in those nutritious seeds and nuts!

• **Gene:** Intergenic • **rsID:** rs12272004 • **Your Genotype:** C/C • **Zygosity:** Homozygous

Description

Vitamin E is an antioxidant that contributes to immune system function and metabolic processes. It can be obtained from various sources, including vegetable oils, nuts, seeds, leafy greens like spinach, and fortified foods or drinks. In most cases, people receive sufficient vitamin E from their diet, and supplements are usually unnecessary. However, individuals with specific conditions like cystic fibrosis, liver diseases, or Crohn's disease might require additional vitamin E.

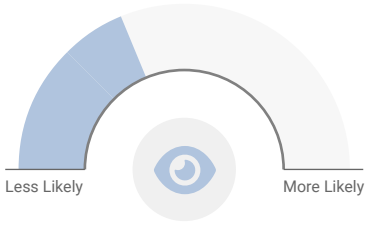
Extra Information

The rs12272004 CC genotype is associated with typical vitamin E levels (PMID(s): 19185284, 21729881).The A allele of rs12272004 was associated with 0.07 SD higher _-tocopherol (a type of vitamin E), with a p value of 7.8 _ 10_10.

Sensory Perception

The way we perceive sensory inputs such as taste, smell, and sound is influenced by genetic variants that affect receptor function and neural processing. These variations can alter taste preferences, odor sensitivities, and even auditory perception. Understanding these genetic traits can explain individual differences in sensory experiences and preferences.

Asparagus Odor Detection



As someone with the G/G genotype, you might struggle to detect the unmistakable asparagus scent in urine.

• **Gene:** Near OR2M7 • **rsID:** rs4481887 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

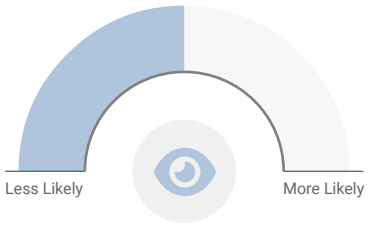
Description

Asparagus contains a unique compound called asparagusic acid, believed to be responsible for the distinctive scent in urine after its consumption, along with its sulfur-containing metabolites. However, not everyone can perceive this odor. Research indicates variations among individuals in the production of these odorous compounds and their ability to detect the scent. Anosmia, the loss of the sense of smell, is often referred to as 'asparagus anosmia' when describing the inability to detect these compounds in urine. Genetic changes have been identified as factors linked to the ability to perceive the scent of asparagus urine.

Extra Information

Studies involving people of European ancestry suggest that individuals with the rs4481887 AG genotype are more adept at detecting the scent of asparagus in urine, reducing the chances of experiencing asparagus anosmia (PMID(s): 20585627, 20876394, 27965198). Those with the AA genotype are the most likely to detect the scent of asparagus metabolites in urine, while those with the GG genotype are the least likely to perceive it.

Cilantro (Coriander) Preference



We don't see notable effects on cilantro taste perception for the G/G genotype.

• **Gene:** Intergenic • **rsID:** rs2741762 • **Your Genotype:** G/G • **Zygosity:** Homozygous

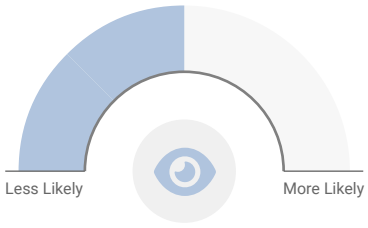
Description

Coriandrum sativum is the plant responsible for producing both cilantro and coriander. Cilantro is typically harvested during the initial growth cycle before flowering, while coriander is harvested after the plant has blossomed and developed seeds. While some people enjoy the taste of cilantro, incorporating it into dishes like rice, burritos, and guacamole, others strongly dislike its flavor and aroma, often describing it as ""soapy."" Research has identified specific genetic variants associated with cilantro preference.

Extra Information

A allele (AA/AG) associated with lower chance of thinking cilantro tastes like soap(p=2.1x10_14,OR=1.1)per A allele.GG Genotype associated with normal or higher preference towatds cilantro.

Cilantro (Coriander) Preference



With a T/T genotype, you might have a moderate likelihood of finding cilantro's taste disagreeable.

• **Gene:** Intergenic • **rsID:** rs3930459 • **Your Genotype:** T/T • **Zygosity:** Homozygous

Description

Coriandrum sativum is the plant responsible for producing both cilantro and coriander. Cilantro is typically harvested during the initial growth cycle before flowering, while coriander is harvested after the plant has blossomed and developed seeds. While some people enjoy the taste of cilantro, incorporating it into dishes like rice, burritos, and guacamole, others strongly dislike its flavor and aroma, often describing it as ""soapy."" Research has identified specific genetic variants associated with cilantro preference.

Extra Information

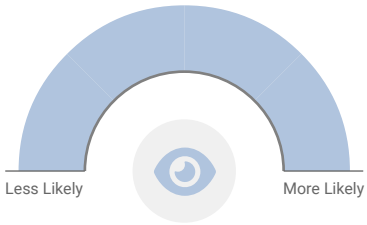
The rs3930459 TT genotype has been associated with an average likelihood of disliking the taste of cilantro, as indicated in the study by Fayzullina in 2015.C allele (CC genotype) associated with slightly higher odds of disliking cilantro (p=4.2x10_13,OR=1.1).

Phenome Longevity

Name:
DoB: –
Gender: female

Report ID: WB
Subject ID: 30793
Date: 2026-10-30

Misophonia



With your A/G genotype, you might have a heightened sensitivity to chewing sounds (misophonia).

• **Gene:** Intergenic • **rsID:** rs2937573 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

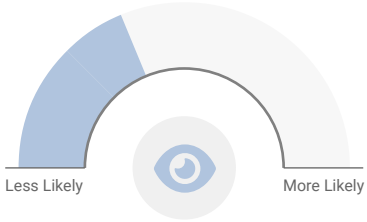
Description

Misophonia is a term used to describe a sensitivity to certain sounds, combining the Greek words 'misein' (to hate) and 'phonos' (voice or sound). Individuals with this condition may struggle to tolerate specific sounds like keyboard typing, pen clicking, or breathing. Notably, misophonia related to the sound of chewing has been found to be associated with a specific genetic variant.

Extra Information

The rs2937573 AG genotype has been associated with an increased likelihood of being sensitive to the sound of chewing, known as misophonia, according to a study (Fayzullina 2015).Other genotypes seems showing typical likelihood of the sound.

Nearsightedness(myopia)



Having T/T might offer a protective effect against developing high-grade myopia.

• **Gene:** Intergenic • **rsID:** rs10034228 • **Your Genotype:** T/T • **Zygosity:** Homozygous

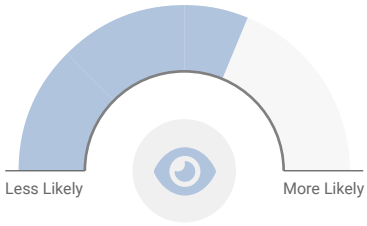
Description

Nearsightedness, also known as myopia or short-sightedness, is a condition characterized by a mismatch between the focusing power of the eye and the length of the eye. In nearsightedness, light rays are focused in front of the retina rather than directly on it. Individuals with nearsightedness may experience difficulty seeing objects that are far away, while maintaining the ability to focus on close objects.

Extra Information

The rs10034228 TT genotype has been found to be associated with a typical risk of high-grade myopia in the Chinese population, as reported in studies (PMID(s): 21505071, 22150588).Specifically, the T allele at this locus was found to have a protective effect against high myopia. Individuals carrying the C/C genotype at rs10034228 were found to have a higher risk of high myopia compared to those with the T allele.

Nearsightedness(myopia)



Possessing G/G may suggest a lower risk for nearsightedness versus A/A.

• **Gene:** Intergenic • **rsID:** rs560766 • **Your Genotype:** G/G • **Zygosity:** Homozygous

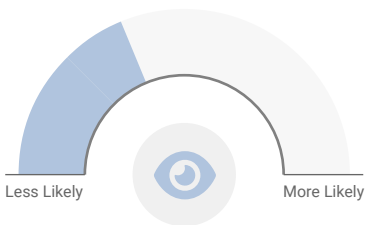
Description

Nearsightedness, also known as myopia or short-sightedness, is a condition characterized by a mismatch between the focusing power of the eye and the length of the eye. In nearsightedness, light rays are focused in front of the retina rather than directly on it. Individuals with nearsightedness may experience difficulty seeing objects that are far away, while maintaining the ability to focus on close objects.

Extra Information

The rs560766 AA genotype has been associated with increased odds of being nearsighted, according to studies (PMID(s): 20835239, 23131718, 22665138)*,compared to AG or GG genotype.

Odor detection



T/T could make detecting some odors a bit tougher, like the smell of isovaleric acid.

• **Gene:** Intergenic • **rsID:** rs1953558 • **Your Genotype:** T/T • **Zygosity:** Homozygous

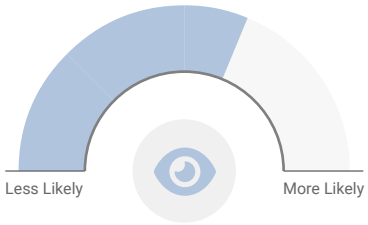
Description

The ability to smell is attributed to olfactory receptors located in the nasal cavity. These receptors interact with airborne molecules, and the olfactory nerves connected to them transmit signals to the brain, which interprets the scent. While each individual has a unique perception of scents, genetic factors play a role in determining the ability to detect specific molecules.

Extra Information

The rs1953558 single nucleotide polymorphism (SNP) is located within the human OR11H7 gene, which encodes for an olfactory receptor. This receptor is involved in the sense of smell and can influence an individual's sensitivity to specific odors. Specifically, the rs1953558 SNP has been associated with the perception of isovaleric acid, a chemical compound commonly associated with the smell of sweat, particularly the odor of feet.According to the search results provided, individuals with the TT genotype at the rs1953558 locus exhibit a slightly reduced sensitivity to the smell of isovaleric acid. This means that these individuals may require a higher concentration of isovaleric acid to detect the odor compared to those with other genotypes. In contrast, individuals with the TC or CC genotypes may have a heightened sensitivity to this odorant.The variation in olfactory sensitivity linked to the rs1953558 SNP is part of a broader pattern of genetic diversity in human olfaction. It is estimated that there is about a 30% difference in olfactory receptors among individuals, which can explain why some people can detect certain smells while others cannot. (PMID: 17973576)*.

Pain Sensitivity



With the A/A genotype for the COMT gene (rs6269), you likely experience typical pain sensitivity, often regarded as standard for most individuals.

• **Gene:** COMT • **rsID:** rs6269 • **Your Genotype:** A/A • **Zygosity:** Homozygous

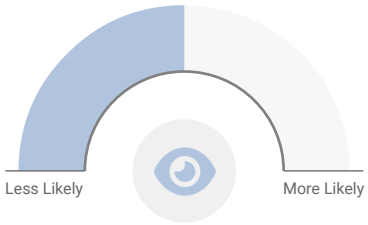
Description

Sensitivity to pain varies among individuals, and genetic differences contribute to this variation.

Extra Information

The rs6269 AA genotype is associated with typical pain sensitivity (PMID(s): 19094200, 24533707)*.The SNP rs6269 accounted for 6% of the variation in pain sensitivity as determined by analysis of variance (ANOVA, P <0.01).In the context of pain sensitivity, individuals with the GG genotype at the rs6269 locus (homozygous for the Val allele) may exhibit increased pain sensitivity compared to those with the AG or AA genotypes. This is because the higher COMT activity associated with the GG genotype may result in reduced levels of pain-modulating neurotransmitters, such as dopamine, in brain regions involved in pain processing.

Photic Sneeze Reflex



Carrying a C/T genotype doesn't present notable effects on your likelihood of photic sneezing.

• **Gene:** Intergenic • **rsID:** rs10427255 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

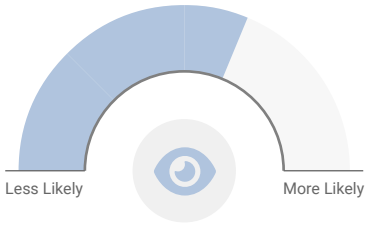
Description

Genetic variants influence the occurrence of the photic sneeze reflex, a phenomenon where an individual is compelled to sneeze upon sudden exposure to bright light, such as looking at a fluorescent light bulb or exiting a dark building or tunnel into bright sunlight.

Extra Information

The rs10427255 TT genotype is associated with typical odds of having the photic sneeze reflex (PMID: 20585627). This association has not yet been replicated.For photic sneeze reflex, we find a novel association with rs10427255 (score 10.9 and an OR of 1.32). We also find a suggestive association with rs11856995 (score 7.13 and OR of 0.78). 10.1371/journal.pgen.1000993.The C allele appears to be associated with higher odds of photic sneezing.

Sweetness Detection



Possessing the C/C genotype for the TAS1R3 gene, you might have typical sensitivity to sucrose.

• **Gene:** TAS1R3 • **rsID:** rs35744813 • **Your Genotype:** T/T>C/C • **Zygosity:** Homozygous

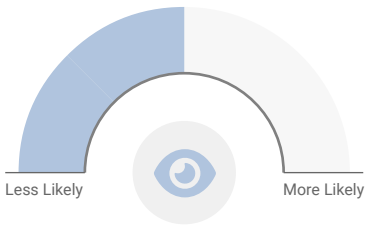
Description

Sugar is a carbohydrate molecule known for its sweet taste and can exist in various forms, including fructose, sucrose, galactose, and glucose. Sucrose, commonly known as table sugar, is a compound of fructose and glucose naturally present in sources like sugar cane. Variations in individuals' ability to perceive differences in sucrose levels have been associated with specific gene variants.

Extra Information

The rs35744813 CC genotype is linked to the typical sensitivity to sucrose , TT and CT genptype strongly correlate with human taste sensitivity to sucrose (decreased Sucrose Sensitivity) and explain 16% of population variability in perception (PMID: 19559618). T alleles of rs35744813 occur at lowest frequencies in European populations.

Taste Preference and Perception: bitter taste



With a G/G genotype, you might find yourself less sensitive to bitter tastes compared to C/C.

• **Gene:** TAS2R38 • **rsID:** rs713598 • **Your Genotype:** C/C>G/G • **Zygosity:** Homozygous

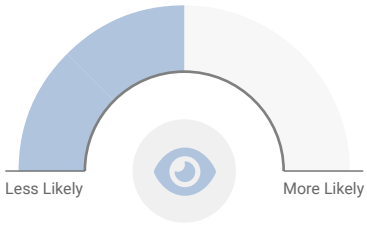
Description

The perception of ""bitterness"" is inherent in our taste buds. Compounds like the phenylthiocarbamide (PTC) molecule and its counterparts are recognized for their bitter taste and can be present in various foods, including coffee, broccoli, and Brussels sprouts. The sensitivity of our taste bud receptors to these compounds is influenced by a combination of environmental and genetic factors.

Extra Information

rs713598 is one of three SNPs that form the main haplotypes behind the ability to perceive as bitter the taste of the compound phenylthiocarbamide (PTC) and similar molecules in foods (like cabbage and raw broccoli) or drinks (like coffee and dark beers).Due to it's minus orientation and nearly 50/50 split of allele frequency it is easily confused.In the orientation shown in dbSNP and used in SNPedia, rs713598(G) is the ""non-tasting"" allele,rs713598(C) is the ""tasting"" allele.In the GRCh37 orientation currently (2017) reported by 23andMe, rs713598(C) is the ""non-tasting"" allele rs713598(G) is the ""tasting"" allele. Tasting is dominant, so heterozygotes are able to taste bitterness.If you are a ""taster"", you're also likely to carry at least one rs10246939(C) and one rs1726866(C) allele since, along with rs713598(G), these three SNPs form the most common tasting haplotype. If you lack these alleles, you're quite likely (~80%) to be a non-taster of bitterness, meaning that foods that may taste bitter to others taste far less bitter to you.[PMID 12595690]

Taste Preference and Perception: bitter taste



There's no clear genetic influence from the G/G genotype on bitterness detection.

• **Gene:** TAS2R38 • **rsID:** rs1726866 • **Your Genotype:** G/G • **Zygosity:** Homozygous

Description

The perception of ""bitterness"" is inherent in our taste buds. Compounds like the phenylthiocarbamide (PTC) molecule and its counterparts are recognized for their bitter taste and can be present in various foods, including coffee, broccoli, and Brussels sprouts. The sensitivity of our taste bud receptors to these compounds is influenced by a combination of environmental and genetic factors.

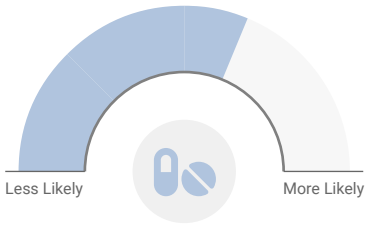
Extra Information

The rs1726866 CC genotype has been linked to an elevated ability to detect bitter taste, as reported in studies (PMID(s): 12595690, 27711175)*.The TT genotype represents a possibility of unabling to taste bitter.

Substance Reaction

Reactions to substances like caffeine, alcohol, and various medications are influenced by genetic variants affecting metabolic pathways. Enzyme activity levels, influenced by genetic polymorphisms, can determine the speed at which substances are metabolized, influencing tolerance levels and adverse reactions. Pharmacogenomics uses this knowledge to optimize drug efficacy and minimize side effects.

Nicotine Response



Having a G/A genotype may cause you to smoke more and be at higher risk for lung cancer if you're a smoker.

• **Gene:** CHRNA3 • **rsID:** rs1051730 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

Description

Nicotine is a naturally occurring compound found in the tobacco plant, Nicotiana tabacum, and is present in tobacco products like cigarettes, dip, and chew. Its high addictiveness is attributed to its interaction with receptors in the brain, leading to the release of neurotransmitters, including dopamine, associated with pleasurable feelings. The response to nicotine exposure is influenced by specific genetic factors, which can impact susceptibility to addiction.

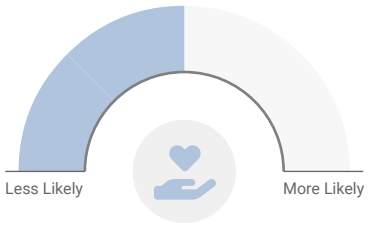
Extra Information

The rs1051730 GA genotype has been associated with an increased quantity of cigarettes smoked per day among smokers, as reported in studies (PMID(s): 18385739, 19247474, 19132693, 20418890, 27127891)*.TT genotype is associated with increased risk of lung cancer; reduced response to alcohol, therefore possibly increased risk of alcohol abusers1051730, also known as D398N, is a SNP in the nicotinic acetylcholine receptor alpha 3 subunit CHRNA3 gene.In two recent (2008) studies, together comprising over 6,000 lung cancer patients of European ancestry, the rs1051730(T) allele was very significantly associated with increased risk. Having one copy (i.e. being a rs1051730(CT) genotype) increased risk for lung cancer about 1.3x, and having two copies (rs1051730(T;T) individuals) represented 1.8x increased risk. Up to 14% of lung cancer incidence may be attributable to this allele.[PMID 18385738, PMID 18385676]An independent study published at the same time concluded that (T) allele carriers for SNP rs1051730 are not at higher risk of becoming smokers compared to (C) carriers. However, if they do smoke, (T) carriers are quite likely to smoke more cigarettes than (C) carriers, and as an apparent consequence, they are at higher risk for lung cancer as reported in this and other studies. This study therefore links rs1051730 directly to nicotine dependence, and indirectly to lung cancer. [PMID 18385739] 23andMe blog (TT) makes it harder to quit smoking.According to DeCODE, the CC genotype at rs1051730 is associated with 0.88x risk of peripheral arterial disease (PAD).

Wellness

Overall wellness is affected by genetic predispositions towards certain health conditions, stress resilience, and lifestyle adaptability. Genes influencing circadian rhythms, inflammation pathways, and detoxification processes can impact daily energy levels, mood stability, and overall health. Genetic insights provide a roadmap for lifestyle modifications that enhance well-being and longevity.

Alcohol Flush



With the G/G genotype, you likely have a typical reaction to alcohol without the flush.

• **Gene:** ALDH2 • **rsID:** rs671 • **Your Genotype:** G/G • **Zygosity:** Homozygous

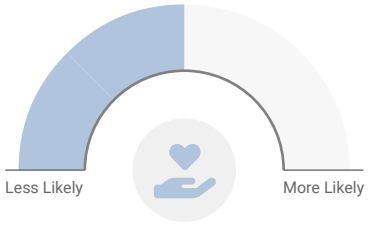
Description

Alcohol sensitivity, also recognized as alcohol flush reaction or alcohol intolerance, is associated with the body's capacity to metabolize alcohol. This response commonly manifests as facial flushing (reddening of the face), heart palpitations (rapid, irregular, or fluttering heartbeat), lightheadedness, and nausea. These symptoms arise mainly from the accumulation of acetaldehyde, a byproduct formed when the enzyme aldehyde dehydrogenase fails to convert ethanol (alcohol) into acetate at an adequate pace. There are identifiable genetic variations that play a role in influencing alcohol sensitivity.

Extra Information

AA: Commonly referred to as ""Asian Flushers,"" individuals with this genotype have an increased risk of esophageal cancer, particularly those of East Asian ancestry. Disulfiram, a medication used to treat alcoholism, is usually not effective for individuals with this genotype.AG: Individuals with this genotype also experience the Asian Flush phenomenon and may have worse hangovers. They share an increased risk of esophageal cancer, especially among those of East Asian ancestry. Disulfiram is also likely ineffective for treating alcoholism in individuals with this genotype.GG: Individuals with this genotype do not typically experience the alcohol flush reaction. They have normal hangovers and are at average risk for alcoholism and esophageal cancer. Disulfiram is considered effective for treating alcoholism in individuals with this genotype.

Caffeine Metabolism



For your Caffeine Metabolism trait with the Near AHR gene (rs4410790), having the C/T genotype suggests moderate caffeine consumption.

• **Gene:** Near AHR • **rsID:** rs4410790 • **Your Genotype:** T/T>T/C • **Zygosity:** Heterozygous

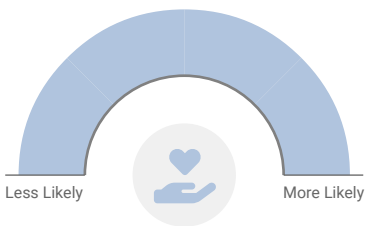
Description

Caffeine, a bitter substance, naturally occurs in over 60 plants, including coffee beans, tea leaves, kola nuts (used to flavor colas), and cacao pods (utilized in chocolate production). Synthetic caffeine is also artificially created and added to certain medicines, foods, and beverages. Examples include pain relievers, cold medicines, over-the-counter alertness medications, energy drinks, as well as energy-boosting gums and snacks.The primary sources of caffeine consumption are beverages, with varying caffeine content in different drinks. Generally, the caffeine amounts are as follows: 8-ounce cup of coffee = 95-200 mg, 12-ounce can of cola = 35-45 mg, 8-ounce energy drink = 70-100 mg, 8-ounce cup of tea = 14-60 mg. Caffeine affects the body's metabolism in various ways; it stimulates the central nervous system, providing a feeling of wakefulness and energy boost. Caffeine acts as a diuretic, promoting the elimination of excess salt and water through increased urination. It also enhances stomach acid release, potentially causing upset stomach or heartburn. Moreover, caffeine may impact calcium absorption and elevate blood pressure.Upon consumption, caffeine reaches its peak level in the bloodstream within one hour, with effects lasting for four to six hours. For more detailed information, you can visit https://medlineplus.gov/caffeine.html#summary.

Extra Information

The C allele is linked to lower levels of caffeine intake. Individuals with the TT genotype tend to consume about one-third more coffee per day compared to those with the CT or CC genotypes. A genome-wide meta-analysis has pinpointed regions on chromosomes 7p21 (AHR) and 15q24 (CYP1A2) as key determinants of habitual caffeine consumption. The AHR protein enhances the production of enzymes CYP1A1 and CYP1A2, responsible for metabolizing caffeine. This finding is supported by research indicating associations between genetic variations in the AHR and CYP1A1-CYP1A2 gene regions and habitual caffeine consumption.

Caffeine Metabolism



With the A/A genotype, you likely metabolize caffeine quickly, so that extra coffee might not cause jitters!

• **Gene:** CYP1A2 • **rsID:** rs762551 • **Your Genotype:** C/C>A/A • **Zygosity:** Homozygous

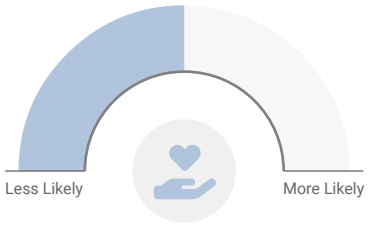
Description

Caffeine, a bitter substance, naturally occurs in over 60 plants, including coffee beans, tea leaves, kola nuts (used to flavor colas), and cacao pods (utilized in chocolate production). Synthetic caffeine is also artificially created and added to certain medicines, foods, and beverages. Examples include pain relievers, cold medicines, over-the-counter alertness medications, energy drinks, as well as energy-boosting gums and snacks.The primary sources of caffeine consumption are beverages, with varying caffeine content in different drinks. Generally, the caffeine amounts are as follows: 8-ounce cup of coffee = 95-200 mg, 12-ounce can of cola = 35-45 mg, 8-ounce energy drink = 70-100 mg, 8-ounce cup of tea = 14-60 mg. Caffeine affects the body's metabolism in various ways; it stimulates the central nervous system, providing a feeling of wakefulness and energy boost. Caffeine acts as a diuretic, promoting the elimination of excess salt and water through increased urination. It also enhances stomach acid release, potentially causing upset stomach or heartburn. Moreover, caffeine may impact calcium absorption and elevate blood pressure.Upon consumption, caffeine reaches its peak level in the bloodstream within one hour, with effects lasting for four to six hours. For more detailed information, you can visit https://medlineplus.gov/caffeine.html#summary.

Extra Information

A meta-analysis conducted by Denden et al. showed that the rs762551 AA genotype is associated with higher coffee intake and faster caffeine clearance than CC and CA genotype. CA genotype is associated with a slightly faster rate of caffeine metabolism than CC genptype (PMID(s): 29282363, 20390257,27173183).

Caffeine Metabolism



For your Caffeine Metabolism trait with the Near CYP1A2 gene (rs2472297), having the C/C genotype is linked to average coffee consumption.

• **Gene:** Near CYP1A2 • **rsID:** rs2472297 • **Your Genotype:** C/C • **Zygosity:** Homozygous

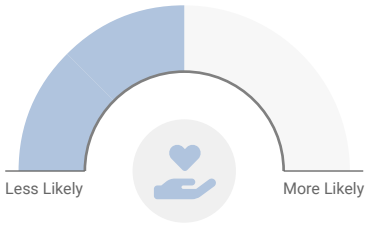
Description

Caffeine, a bitter substance, naturally occurs in over 60 plants, including coffee beans, tea leaves, kola nuts (used to flavor colas), and cacao pods (utilized in chocolate production). Synthetic caffeine is also artificially created and added to certain medicines, foods, and beverages. Examples include pain relievers, cold medicines, over-the-counter alertness medications, energy drinks, as well as energy-boosting gums and snacks.The primary sources of caffeine consumption are beverages, with varying caffeine content in different drinks. Generally, the caffeine amounts are as follows: 8-ounce cup of coffee = 95-200 mg, 12-ounce can of cola = 35-45 mg, 8-ounce energy drink = 70-100 mg, 8-ounce cup of tea = 14-60 mg. Caffeine affects the body's metabolism in various ways; it stimulates the central nervous system, providing a feeling of wakefulness and energy boost. Caffeine acts as a diuretic, promoting the elimination of excess salt and water through increased urination. It also enhances stomach acid release, potentially causing upset stomach or heartburn. Moreover, caffeine may impact calcium absorption and elevate blood pressure.Upon consumption, caffeine reaches its peak level in the bloodstream within one hour, with effects lasting for four to six hours. For more detailed information, you can visit https://medlineplus.gov/caffeine.html#summary.

Extra Information

The rs2472297 CC genotype has been associated with average daily coffee consumption, as indicated by studies (PMID(s): 21357676, 21876539, 25288136).A meta-analysis of four GWAS studies of coffee consumption among a total of ~8,000 coffee drinkers of European ancestry found that the?s2472297(T) was strongly associated with increased consumption (p = 5.4 x 10e-14). The estimated effect was an increase of 0.2 cups a day per allele for both this SNP and one other (rs6968865).[PMID 21357676]. CYP1A2 contains instructions for an enzyme that breaks down caffeine.CT-Associated with (slightly) increased coffee consumption.TT-Associated with (slightly) increased coffee consumption.

Deep Sleep



For your Deep Sleep trait with the ADA gene (rs73598374), having a C/C genotype doesn't show notable effects.

• **Gene:** ADA • **rsID:** rs73598374 • **Your Genotype:** C/C • **Zygosity:** Homozygous

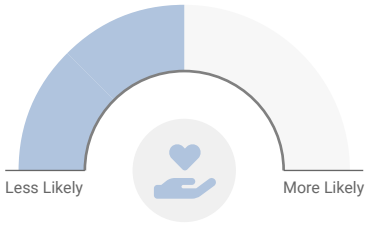
Description

Deep sleep, also called slow-wave sleep,?ccurs in the third stage of?on-rapid eye movement?NREM) sleep. During deep sleep, electrical activity in the brain appears in long, slow waves called delta waves. These waves have a frequency of 0.5 to 2 Hertz.Research studies have identified a variation in the ADA gene, revealing its influence on deep sleep. The ADA gene, responsible for producing the adenosine deaminase enzyme, plays a crucial role in breaking down adenosine? molecule central to the regulation of various physiological processes. Alterations in the ADA gene correlate with a diminished conversion of adenosine, potentially resulting in an accumulation of adenosine and heightened fatigue. This insight underscores the significance of genetic factors in shaping the intricacies of deep sleep and its impact on overall physiological well-being.

Extra Information

The rs73598374 polymorphism with T allele leading to decreased adenosine deaminase (ADA) activity due to an amino acid substitution, has been extensively studied regarding its impact on sleep patterns and cognitive functions in humans. ADA enzyme is vital in the metabolic pathway of adenosine, a key regulator of sleep and arousal. A study (PMID: 21734253) highlights that this functional ADA polymorphism, particularly the T allele (TT genotype) of rs73598374, results in reduced ADA activity due to an amino acid substitution, and is associated with deeper sleep and decreased vigilant attention. Consequently, individuals carrying the T allele may experience more profound sleep phases and might find it challenging to sustain alertness during specific tasks.

Lactose Intolerance



For lactose intolerance, with the MCM6 gene (rs4988235), your G/G genotype doesn't show notable effects.

• **Gene:** MCM6 • **rsID:** rs4988235 • **Your Genotype:** G/G • **Zygosity:** Homozygous

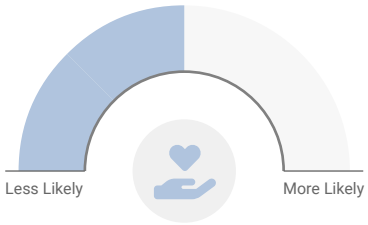
Description

Lactose intolerance refers to an impaired ability to digest lactose, a sugar present in milk and other dairy products. In infancy, lactose is typically broken down by an enzyme called lactase, produced by cells in the lining of the small intestine. However, the production of this enzyme ceases during or after weaning, and most adult mammals, including humans, become unable to efficiently digest lactose. Primary lactase deficiency, also known as lactase nonpersistence, is the most prevalent type of lactase deficiency.

Extra Information

The rs4988235 CC genotype is associated with lactose intolerance in adults.Individuals with the CC genotype at the rs4988235 SNP are typically unable to continue producing lactase into adulthood, leading to lactose intolerance. This intolerance manifests as gastrointestinal symptoms such as bloating, diarrhea, and abdominal pain following the consumption of dairy products due to the undigested lactose fermenting in the gut.On the other hand, individuals with the CT or TT genotypes are more likely to continue producing lactase throughout their lives, allowing them to digest milk and other dairy products without adverse effects. The TT genotype is associated with a higher likelihood of being able to digest milk in adulthood compared to the CT genotype.

Saturated Fat and Weight



There's no strong evidence showing a notable effect on your weight regarding saturated fat intake with the A/A genotype near APOA2.

• **Gene:** Near APOA2 • **rsID:** rs5082 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

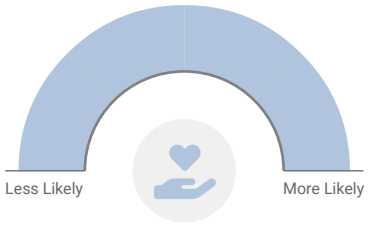
Description

Saturated fat is a type of?ietary fat. It is one of the unhealthy fats, along with?rans fat. These fats are most often solid at room temperature. Foods like butter, palm and coconut oils, cheese, and red meat have high amounts of saturated fat.Weight gain. Many high-fat foods such as pizza, baked goods, and fried foods have a lot of saturated fat. Eating too much fat can add extra calories to your diet and cause you to gain weight. All fats contain 9 calories per gram of fat. This is more than twice the amount found in carbohydrates and protein.

Extra Information

rs5082 is a SNP in the apolipoprotein APOA2 gene, and may influence obesity and heart disease risk.Individuals homozygous for the -265T>C polymorphism in rs5082, i.e. individuals with the rs5082(CC) genotype of the Apolipoprotein A-II gene (APOA2) promoter, are associated with increased Body Mass Index and food intake in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study of ~1000 individuals. The odds ratio for obesity in (CC) individuals compared to rs5082(T) allele carriers was 1.70 (CI: 1.02-2.80, p=0.039). Total energy, total fat, and total protein intake were all significantly higher in (CC) individuals.[PMID 17446329].CC genotype is associated with saturated fat contributes to obesity, but 0.57 % lower risk for coronary artery disease.

Sleep Movement



Your A/A genotype in the BTBD9 gene increases your likelihood of experiencing restless legs syndrome.

• **Gene:** BTBD9 • **rsID:** rs3923809 • **Your Genotype:** A/A • **Zygosity:** Homozygous

Description

Abnormal movements and behaviors during sleep are part of a larger group of nocturnal events that may occur during sleep, wake, or the transitions into or out of sleep. These events are most common early in life, affecting approximately 15 to 20 percent of children and 4 percent of adults?"This SNP, located in an intron of the BTBD9 gene, has a variant that is seen somewhat more frequently in individuals with restless legs syndrome. The risk allele is rs3923809(A). Carriers of two such alleles, i.e. those with rs3923809(AA) genotypes, are estimated to be 1.9 fold more likely to have restless legs syndrome than rs3923809(G;G) individuals. The authors of this study suggest that perhaps half of the cases of restless legs syndrome may involve the rs3923809 risk genotypes. [PMID 17634447]Consistent with this finding, another report about rs3923809 links the (G) minor allele to a lower frequency of restless legs syndrome with an overall odds ratio of 0.57 (CI: 0.48-0.68). [PMID 17637780].AA genotype represents 1.9x risk for developing restless legs syndrome; AG genotype represents slightly increased risk of developing restless legs syndrome;GG genotype represents normal risk of developing restless legs syndrome."

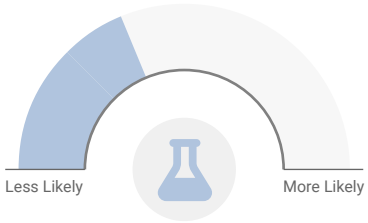
Extra Information

This SNP, located in an intron of the BTBD9 gene, has a variant that is seen somewhat more frequently in individuals with restless legs syndrome. The risk allele is rs3923809(A). Carriers of two such alleles, i.e. those with rs3923809(AA) genotypes, are estimated to be 1.9 fold more likely to have restless legs syndrome than rs3923809(G;G) individuals. The authors of this study suggest that perhaps half of the cases of restless legs syndrome may involve the rs3923809 risk genotypes. [PMID 17634447]Consistent with this finding, another report about rs3923809 links the (G) minor allele to a lower frequency of restless legs syndrome with an overall odds ratio of 0.57 (CI: 0.48-0.68). [PMID 17637780].AA genotype represents 1.9x risk for developing restless legs syndrome; AG genotype represents slightly increased risk of developing restless legs syndrome;GG genotype represents normal risk of developing restless legs syndrome.

Hormones

Hormonal balance, crucial for physiological and psychological health, is regulated by genetic variants that influence hormone synthesis, receptor sensitivity, and feedback mechanisms. These genetic factors can determine susceptibility to conditions like thyroid disorders, metabolic syndrome, and reproductive health issues. Understanding these influences aids in personalized hormone management strategies.

Menopause Age



For G/G, the typical age of menopause onset is expected, possibly slightly sooner than average.

• **Gene:** MCM8 • **rsID:** rs16991615 • **Your Genotype:** G/G • **Zygosity:** Homozygous

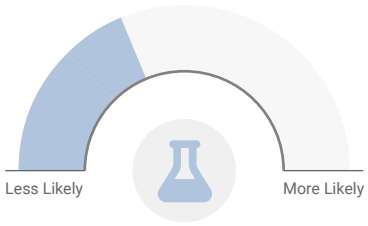
Description

Menopause refers to the cessation of a woman's menstrual cycle, indicating the end of her reproductive capability. This natural biological process also signifies the conclusion of her ability to conceive children. Menopause involves significant hormonal changes, leading to symptoms like hot flashes and mood alterations. The onset of menopause is typically recognized when there has been a 12-month span without menstruation. In the United States, the average age of menopause is around 51 years, though individual variations exist. Factors influencing the timing of menopause include natural hormonal variations, medical conditions or treatments affecting hormone production, and surgical interventions like the removal of the ovaries, a key source of female sex hormones. Additionally, genetic variations play a role in determining the age at which menopause occurs.

Extra Information

The rs16991615 GG genotype has been associated with the typical age of menopause onset, according to studies (PMID(s): 20952801, 23508249, 23592221, 19448621).The AA genotype is associated with menopause increased by avg of 22 months and AG genotype is slight increase (11 months) in avg age at menopause.rs16991615 is a nonsynonymous SNP on chromosome 20.A case control study of ~2,000 women found that each rs16991615(A) allele was associated with an average increase in age at menopause of 11 months. This also meant that each rs16991615(G) allele yielded an odds ratio of 1.85 (CI: 1.51?.2, p = 1.45 x 10e-9) of early menopause, defined as occurring before the age of 46.[PMID 20952801].Overall, women homozygous for the ""early"" alleles at all 4 SNPs found in this study were ~4 times more likely to undergo menopause early compared to women who had a total of 3 or less risk alleles.

Testosterone Levels



The G/G genotype might mean standard Testosterone Levels, without strong effects on SHBG.

• **Gene:** SHBG • **rsID:** rs1799941 • **Your Genotype:** G/G • **Zygosity:** Homozygous

Description

Testosterone, an androgenic hormone associated with male development, is primarily produced in the testicles and ovaries. Additionally, it can be converted from other androgens produced by the adrenal glands. In men, testosterone levels are correlated with aspects such as sexual interest (libido), fertility, mood, and erectile function. These levels naturally decline with age, and genetic factors can contribute to individual variations in testosterone levels.

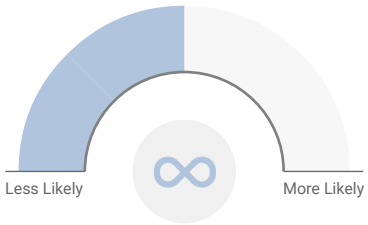
Extra Information

The rs1799941 is significantly associated with sex-hormone binding globulin (SHBG) levels as well as sex hormone regulation. AG genotype is linked to elevated levels of serum testosterone and Sex Hormone-Binding Globulin (PMID(s): 24327369, 29264510). "A" allele was associated with increasing testosterone levels in men (P= 8.11 _ 10_6)(PMID: 19574343).Subjects with the "A" allele (GA+AA) had a trend for lower free estradiol index (FEI) compared to the GG genotype (p=0.04)(PMID: 19679209). Each copy of the "A" allele is associated with a 0.20 SDs increase in sex hormone binding globulin (SHBG) levels(PMID: 19933169). Carriers of the minor allele "A" had higher circulating SHBG, independently of sex, age, and total body fat (P = 0.025)(PMID: 20841609).

Longevity

Longevity is shaped by genetic variants that regulate cellular repair mechanisms, oxidative stress response, and metabolic efficiency. Telomere length, mitochondrial function, and DNA repair capacity are key factors influenced by these genes, contributing to the aging process and lifespan. Genetic profiling for longevity markers provides insights into personalized anti-aging interventions.

Longevity



For longevity in FOXO3, the T/T genotype lacks strong evidence indicating notable effects.

• **Gene:** FOXO3 • **rsID:** rs2764264 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

Description

Longevity is a complex trait influenced by numerous factors, exhibiting significant variability between individuals. The aging process can manifest differently, with some individuals showing signs of aging, such as extensive skin wrinkles, completely gray hair, loss of muscle tone, and reduced mobility, in their 60s. In contrast, others may maintain a more youthful appearance well into their 90s or even close to 100 years of age. This diversity in aging patterns is attributed to the interplay of genetic and environmental factors, both of which contribute significantly to the observed variability in the aging process.

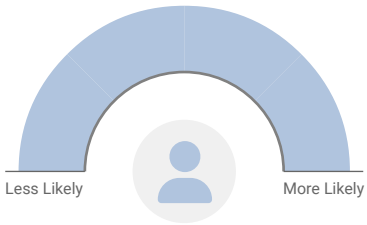
Extra Information

The rs2764264 CT genotype has been associated with a longer lifespan in men, as indicated by studies (PMID(s): 18765803, 19196970, 24350933). Also, CC genotype is associated with greater odds of longevity [PMID 20849522].Replication of an association of variation in the FOXO3A gene with human longevity using both case-control and longitudinal data.[PMID 19415983] Association of the FOXO3A locus with extreme longevity in a southern Italian centenarian study.[PMID 18765803] FOXO3A genotype is strongly associated with human longevity.[PMID 19196970] Association of FOXO3A variation with human longevity confirmed in German centenarians.[PMID 24350933] Association Between Genetic Variations In The Insulin/Insulin-Like Growth Factor (Igf-1) Signaling Pathway And Longevity: A Systematic Review And Meta-Analysis[PMID 31009445] Longevity-Associated Forkhead Box O3 (FOXO3) Single Nucleotide Polymorphisms are Associated with Type 2 Diabetes Mellitus in Chinese Elderly Women.

Physical Appearance

Genetic factors significantly determine physical characteristics such as skin pigmentation, hair texture, and facial features. Variants in genes affecting melanin production, hair follicle shape, and facial bone structure contribute to the diversity in human appearance. Understanding these genetic influences can also provide insights into conditions like alopecia and skin disorders.

Earwax Type



For your Earwax Type trait with the ABCC11 gene (rs17822931), having the C/C genotype likely means you have wet earwax, which is common in European and African populations.

• **Gene:** ABCC11 • **rsID:** rs17822931 • **Your Genotype:** C/C • **Zygosity:** Homozygous

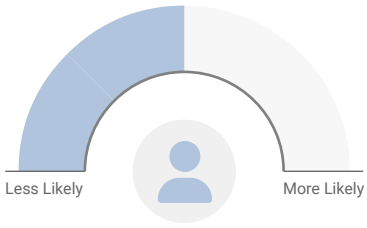
Description

Earwax, scientifically termed cerumen, is a universal waxy substance produced by glands in the ear canals, serving as a protective barrier for the ear's sensitive skin and defense against germs. Determined by the ABCC11 gene variant, individuals of European and African descent typically have wet earwax, while those of East Asian descent often exhibit dry, crumbly earwax. This genetic diversity highlights the subtle yet fascinating ways in which our genes shape seemingly ordinary aspects of our physiology, emphasizing the essential role earwax plays in maintaining ear health across different populations.

Extra Information

rs17822931, also known as c.538G>A (C>T) or G180R, is a SNP in the ATP-binding cassette, sub-family C (CFTR/MRP), member 11 ABCC11 gene. The ABCC11 protein helps transport small molecules across apical membranes such as those in apocrine secretory cells.[PMID 16444273] This SNP determines wet vs dry earwax as well as sweat production, and it is also associated with lipid secretion. The C allele is associated increased wetness of earwax. The T allele is associated with increased dryness of earwax. It is commonly presenting TT genotype for East Asians and CC for Europeans and Africans.

Eye Color



Your G/G genotype hasn't shown significant influence on eye color in studies.

• **Gene:** TYR • **rsID:** rs1393350 • **Your Genotype:** G/G • **Zygosity:** Homozygous

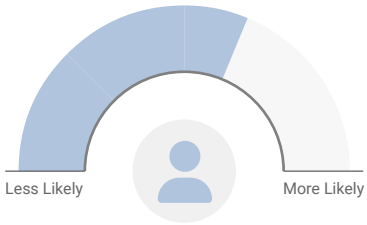
Description

Eye colors are determined by the variable pigmentation of the iris and the scattering of light by the iris. Individuals with a higher concentration of the dark pigment melanin tend to have darker eye colors, while those with a lower concentration generally have lighter-colored eyes. Light eye colors, such as blue, green, and hazel, are not produced by pigments but are mainly the result of the variable scattering of light by the iris.

Extra Information

Research conducted on individuals of European ancestry indicates that the rs1393350 AA genotype is linked to an increased likelihood of having blue eyes (PMID(s): 17952075, 23100201, 23986280, 20585627) while other genotypes are less likely to have blue eyes.

Eye Color



For your Eye Color trait with the HERC2 gene (rs12913832), the A/A genotype is often linked with brown eyes.

• **Gene:** HERC2 • **rsID:** rs12913832 • **Your Genotype:** A/A • **Zygosity:** Homozygous

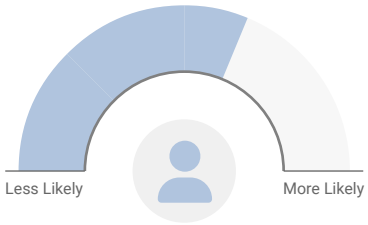
Description

Eye colors are determined by the variable pigmentation of the iris and the scattering of light by the iris. Individuals with a higher concentration of the dark pigment melanin tend to have darker eye colors, while those with a lower concentration generally have lighter-colored eyes. Light eye colors, such as blue, green, and hazel, are not produced by pigments but are mainly the result of the variable scattering of light by the iris.

Extra Information

Studies conducted on individuals of European ancestry indicate that the rs12913832 CT genotype is associated with an increased likelihood of having brown eye color (PMID(s): 18252222, 18172690)*.rs12913832?s a SNP near the?CA2/HERC2?ene that may be functionally linked to blue or brown?ye color, due to a lowering of promoter activity of the?CA2?ene. The genotypes rs12913832:AA and rs12913832:GA are most often observed in individuals with brown eye colours, whereas rs12913832:GG is most often observed in individuals with blue eye colours.

Finger Length Ratio



For your Finger Length Ratio trait with the SMOC1 gene (rs2332175), having the A/A genotype is linked with a typical 2D:4D ratio.

• **Gene:** SMOC1 • **rsID:** rs2332175 • **Your Genotype:** G/G>A/A • **Zygosity:** Homozygous

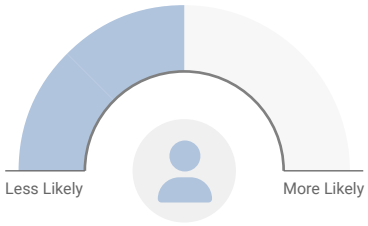
Description

Finger length is commonly measured from the point where the finger joins the hand to the tip of the finger. The finger length ratio, often denoted as 2D:4D, represents the ratio of the lengths of the index and ring fingers. This ratio is calculated by dividing the length of the index finger on one hand by the length of the ring finger on the same hand. Evidence suggests that the 2D:4D ratio may correlate with certain human characteristics, such as increased reproductive success or a reduced risk of video game addiction. These correlations vary between males and females, with the differences thought to result from in utero exposure to hormones.In general, 2D:4D is higher in females (M = 0.979 SD = 0.030) than in males (M = 0.964, SD = 0.031); this difference was highly significant [t(977) = _7.3, P = 6.48 _ 10_13].More men than women have shorter index fingers than ring fingers, resulting in a lower 2D:4D ratio. Therefore, a lower 2D:4D ratio is indicative of a more masculine hormonal profile or environment during fetal development. These differences are influenced by a combination of genetic and environmental factors.

Extra Information

The rs2332175 AA genotype is reported to be associated with the typical difference in length between the 2nd and 4th fingers, as indicated by a study (PMID: 23263445). Each additional copy of the G allele was associated with a 0.0074 decrease in 2D:4D(P value 3.44 _ 10_8).

Freckling



With the C/C genotype, you have an average likelihood of freckling.

• **Gene:** MC1R • **rsID:** rs1805007 • **Your Genotype:** C/C • **Zygosity:** Homozygous

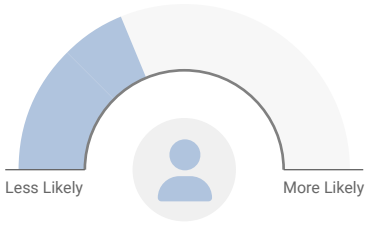
Description

Freckles are clusters of concentrated melaninized cells that are particularly noticeable on fair skin. The primary environmental trigger for the formation of freckles is exposure to sunlight. When exposed to UV-B radiation, melanocytes, the cells responsible for producing melanin, increase their melanin production. This heightened melanin production causes freckles to darken, making them more visible. In cases where there are densely distributed concentrations of melanin, freckles may multiply and extend over a broader area of the skin.

Extra Information

Research conducted on individuals of European ancestry suggests that the rs1805007 CC genotype is associated with an average likelihood of freckling (PMID(s): 20876667, 17952075). CT genotype represents carrier of a red hair associated variant; higher risk of melanoma.TT genotype represents increased response to anesthetics, 13-20x higher likelihood of red hair, higher likelihood of freckling presense in childhood and increased risk of melanoma.

Hair Color



A T/T genotype might mean an average chance of having blonde hair.

• **Gene:** Intergenic • **rsID:** rs12821256 • **Your Genotype:** T/T • **Zygosity:** Homozygous

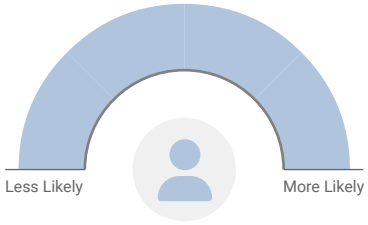
Description

Hair color is primarily determined by the relative levels of two pigments in the hair: eumelanin, comprising brown and black variants, and pheomelanin, contributing a red hue. Higher eumelanin levels result in dark hair, while lower levels of both pigments lead to nearly white to yellowish hair. With varying eumelanin proportions, hair color spans from very pale blond to brown shades. Hair low in eumelanin can exhibit colors from light blond to reddish ""strawberry"" blond or red, depending on varying pheomelanin amounts.

Extra Information

Research on individuals of European ancestry indicates that the rs12821256 TT genotype is associated with an average likelihood of having blond hair (PMID(s): 24880339, 17952075, 26184321),CC genotype is 4x more likely to have blond hair and CT genptype is 2x more likely to have blond hair.

Hair curl



For your Hair curl trait with the WNT10A gene (rs7349332), having the C/C genotype might mean you're more likely to enjoy straighter hair.

• **Gene:** WNT10A • **rsID:** rs7349332 • **Your Genotype:** C/C • **Zygosity:** Homozygous

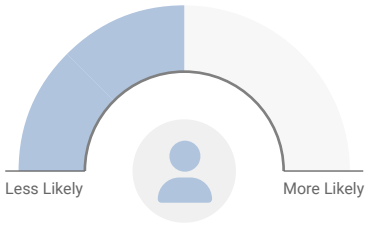
Description

The curliness of an individual's hair is determined by the shape of the hair shaft. A hair shaft that is very round allows for fewer bonds between molecules, resulting in straight hair. Conversely, a flatter hair shaft promotes more bonds between adjacent molecules, leading to a bent shape and expressing as hair curl.

Extra Information

The rs7349332 CT and TT genotype has been associated with an increased likelihood of having curly hair, according to studies (PMID(s): 26414620, 28370528, 20585627)*.CC genotype is associated with straighter hair.

Hair curl



For the Hair curl trait with the TCHHL1 gene (rs17646946), we don't have strong data linking the G/G genotype to specific hair textures.

• **Gene:** TCHHL1 • **rsID:** rs17646946 • **Your Genotype:** G/G • **Zygosity:** Homozygous

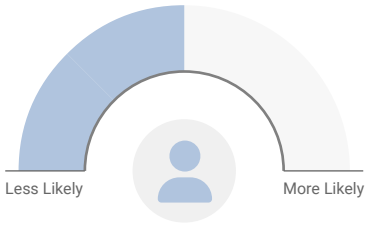
Description

The curliness of an individual's hair is determined by the shape of the hair shaft. A hair shaft that is very round allows for fewer bonds between molecules, resulting in straight hair. Conversely, a flatter hair shaft promotes more bonds between adjacent molecules, leading to a bent shape and expressing as hair curl.

Extra Information

Research conducted on individuals of European ancestry suggests that the rs17646946 CC genotype is associated with an average likelihood of having straight hair (PMID(s): 29220522, 20585627, 19896111, 26414620) .The minor allele is associated with straighter hair, with each A conferring a reduction in curliness of about 0.29 points on a scale from 0 to 5(PMID: 20585627).

Hair thickness



For Hair thickness with your EDAR gene (rs3827760), we don't have strong data correlating the A/A genotype with hair thickness.

• **Gene:** EDAR • **rsID:** rs3827760 • **Your Genotype:** A/A • **Zygosity:** Homozygous

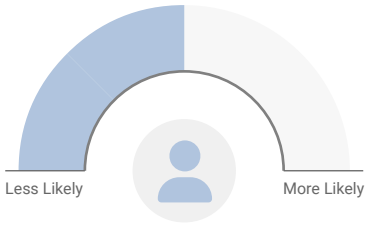
Description

Hair thickness, or volume, is contingent on the size of the hair follicle. A larger circumference of the hair follicle typically results in thicker hair.

Extra Information

In Asian individuals, the rs3827760 TT genotype has been associated with typical hair thickness, as suggested by studies (PMID(s): 18065779, 18704500, 18561327, 23793515, 27487801).CC genotype: Associated with straighter, thicker hair and an increased likelihood of having shovel-shaped incisors.CT genotype: Linked to an increased chance of having straighter, thicker hair, as well as shovel-shaped incisors.The rs3827760(C) allele is far more prevalent in East Asians and Native Americans than in any other population, and it is used as such in ancestry tests [PMID 22749789]. There are at least four physical characteristics that have been linked to this allele, and pretty much all in a copy-dependent manner as well (inheriting both alleles leads to a stronger expression than inheriting one):Hair follicle thickness [PMID 18065779]Hair straightness (i.e. lack of curliness).

Height



With the C/T genotype in the HMGA2 gene, you might stand a little taller, about 0.4 cm more than average.

• **Gene:** HMGA2 • **rsID:** rs1042725 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

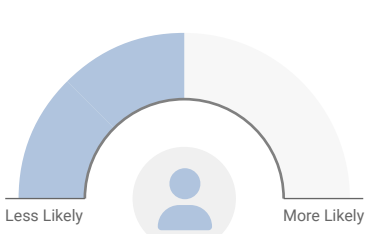
Description

Height is the measurement of the length from the floor to the top of an individual's head when standing upright. This measurement is expressed in inches, feet, centimeters, or meters and tends to remain relatively stable throughout adulthood until later stages of life. Both genetic and environmental factors, including nutrition and exercise, play roles in influencing an individual's height. Specific genetic variations have been identified in association with the final height achieved by an individual.

Extra Information

The rs1042725 TT genotype has been associated with average height, based on studies (PMID(s): 19139030, 17767157, 19930247, 21921580, 26536448) while CC genotype indicates- ~0.8cm taller height; CT genotype indicates ~0.4cm taller height. SNP rs1042725 is associated with height (P = 4E-8) in a study involving over 20,000 individuals. The gene harboring this SNP, HMGA2, is a strong biological candidate for having an influence on height, since rare, severe mutations in this gene are known to alter body size in mice and humans.rs1042725 is estimated to explain approx 0.3% of population variation in height in both adults and children (approx 0.4 cm increased adult height per C allele).[PMID 19139030] rs1042725 is associated with increased height (0.36 cm 95% IC[0.12-0.61] per C allele, P=0.004). in men rs1042725 may explain 3% of height variability.

Iris Patterns



For your Iris Patterns trait with the TRAF3IP1 gene, having the A/C genotype doesn't show notable effects.

• **Gene:** TRAF3IP1 • **rsID:** rs3739070 • **Your Genotype:** A/A>A/C • **Zygosity:** Heterozygous

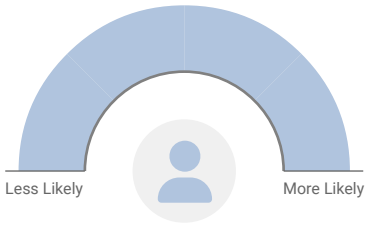
Description

The human iris, aside from its color, exhibits distinctive features such as Fuchs?crypts, nevi, Wolfflin nodules, and contraction furrows (circular grooves running in a circular pattern around the iris). These unique characteristics are currently employed as biomarkers for various purposes. The tissue patterns present in the human iris are utilized for automatic personal identification, providing a reliable basis for distinguishing individuals. Additionally, these tissue markers in the iris can be associated with various eye diseases, offering insights and diagnostic potential in the field of ophthalmology.

Extra Information

Research involving individuals of European ancestry suggests that the rs3739070 AA genotype is associated with the presence of extended contraction furrows, as indicated in studies (PMID(s): 21835309, 26909168)*compared to other genotypes.

Male Pattern Baldness



With the C/C genotype, the SLC14A2 gene might increase your likelihood of experiencing male pattern baldness.

• **Gene:** SLC14A2 • **rsID:** rs8085664 • **Your Genotype:** C/C • **Zygosity:** Homozygous

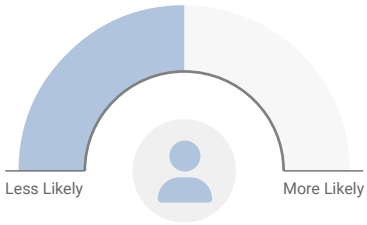
Description

Male Pattern Baldness is characterized by hair loss that occurs when the hair follicle starts to shrink and continues to do so over time. This loss is attributed to an interaction between specific genetic factors and the male hormone dihydrotestosterone (DHT). The hair loss follows a well-defined pattern, typically starting above both temples. As the hair follicle continues to shrink, the affected hair becomes shorter and finer, ultimately leading to a lack of new hair growth in the affected areas.

Extra Information

Research on individuals of European ancestry suggests that the rs8085664 CC genotype is associated with higher risk of baldness, while other genotypes may be associated with an average likelihood of male baldness, as reported in studies (PMID(s): 22693459, 28196072)*.

Male Pattern Baldness



Currently, C/C doesn't show a strong effect on your likelihood of male pattern baldness.

• **Gene:** C1orf127 • **rsID:** rs2003046 • **Your Genotype:** C/C • **Zygosity:** Homozygous

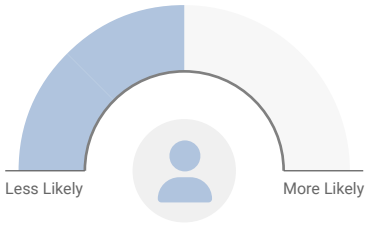
Description

Male Pattern Baldness is characterized by hair loss that occurs when the hair follicle starts to shrink and continues to do so over time. This loss is attributed to an interaction between specific genetic factors and the male hormone dihydrotestosterone (DHT). The hair loss follows a well-defined pattern, typically starting above both temples. As the hair follicle continues to shrink, the affected hair becomes shorter and finer, ultimately leading to a lack of new hair growth in the affected areas.

Extra Information

Research involving individuals of European ancestry indicates that the rs2003046 GG genotype (homozygous mutation) is associated with a higher likelihood of male baldness, as reported in studies (PMID(s): 22693459, 28196072) while other genotypes are associated with lower risk of baldness.

Pigmentation



For T/T, we don't have notable evidence connecting this genotype with changes in pigmentation.

• **Gene:** HERC2 • **rsID:** rs1667394 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

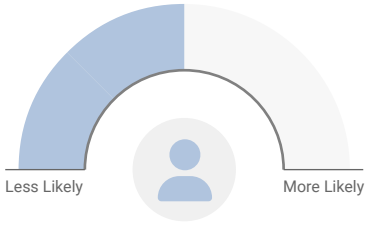
Description

Pigmentation refers to the coloring of skin, eyes, hair, and nails, with melanocytes responsible for producing melanin?he primary pigment influencing coloration. Higher melanin levels are linked to darker hues, while lower levels are associated with lighter tones. Melanin also contributes to the formation of freckles, characterized by brown spots resulting from sun exposure. The synthesis of melanin involves a complex pathway influenced by various environmental factors, including UV rays, alongside genetic factors.

Extra Information

The rs1667394 A allele increases susceptibility to Blue rather than brown eyes 29.43 times [PMID 17952075] and increases susceptibility to Blue rather than green eyes 6.74 times [PMID 17952075]. GG genotype is associated with darker skin, eye and hair color. AA genotype is associated with blond hair and blue eyes.

Pigmentation



For Pigmentation, your A/A genotype doesn't show a notable effect on the trait.

• **Gene:** OCA2 • **rsID:** rs4778138 • **Your Genotype:** A/A • **Zygosity:** Homozygous

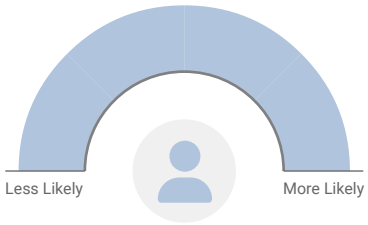
Description

Pigmentation refers to the coloring of skin, eyes, hair, and nails, with melanocytes responsible for producing melanin?he primary pigment influencing coloration. Higher melanin levels are linked to darker hues, while lower levels are associated with lighter tones. Melanin also contributes to the formation of freckles, characterized by brown spots resulting from sun exposure. The synthesis of melanin involves a complex pathway influenced by various environmental factors, including UV rays, alongside genetic factors.

Extra Information

The rs4778138 TT genotype is linked to blue eye color, heightened freckling, and a greater number of moles in comparison to individuals with brown eyes (PMID: 17236130). Other genptypes are assoicated with brwon eyes and darker skin.

Pigmentation



For your pigmentation with the LOC105370627 gene (rs12896399), having the G/G genotype often means a likelihood of blue eyes and blond hair.

• **Gene:** LOC105370627 • **rsID:** rs12896399 • **Your Genotype:** G/G • **Zygosity:** Homozygous

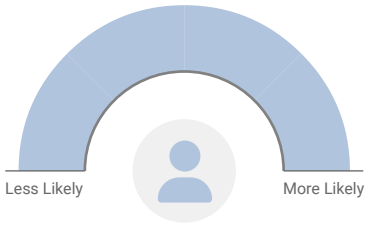
Description

Pigmentation refers to the coloring of skin, eyes, hair, and nails, with melanocytes responsible for producing melanin?he primary pigment influencing coloration. Higher melanin levels are linked to darker hues, while lower levels are associated with lighter tones. Melanin also contributes to the formation of freckles, characterized by brown spots resulting from sun exposure. The synthesis of melanin involves a complex pathway influenced by various environmental factors, including UV rays, alongside genetic factors.

Extra Information

Studies in Europeans show that the rs12896399 GG genotype is associated with a typical likelihood of having blue eyes and blond hair and TT genotype is associated with lighter hair color and more likelyhood of blue eyes (PMID: 17952075).

Red hair color



For your Red hair color trait with the MC1R gene (rs1805007), having the C/C genotype significantly increases your chance of having red hair and potentially higher melanoma risk.

• **Gene:** MC1R • **rsID:** rs1805007 • **Your Genotype:** C/C • **Zygosity:** Homozygous

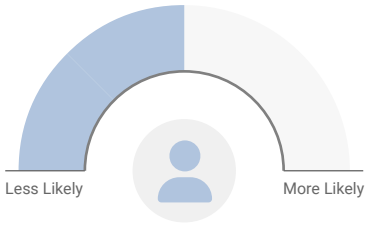
Description

Red hair, often referred to as orange or ginger hair, is a distinctive human hair color present in 1?% of the global population, with a higher prevalence (2?%) among individuals of Northern or Northwestern European descent and less common occurrence in other populations. The unique hue is primarily attributed to a recessive allele on chromosome 16, leading to a modified version of the MC1R protein. This genetic trait is most prevalent in individuals homozygous for this recessive allele, highlighting the fascinating interplay between genetics and hair color expression in human populations.

Extra Information

rs1805007 CC genotype, known as Arg151Cys or R151C, one of several SNPs in the MC1R gene associated with red hair color (redheads), and in redheaded females.CT genotype represents carrier of a red hair associated variant; higher risk of melanoma.TT genotype represents increased response to anesthetics, 13-20x higher likelihood of red hair, higher likelihood of freckling presense in childhood and increased risk of melanoma.

Red hair color



This genotype is not typically associated with red hair.

• **Gene:** MC1R • **rsID:** rs1805008 • **Your Genotype:** C/C • **Zygosity:** Homozygous

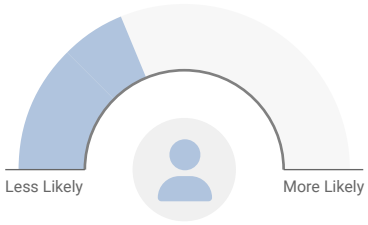
Description

Red hair, often referred to as orange or ginger hair, is a distinctive human hair color present in 1?% of the global population, with a higher prevalence (2?%) among individuals of Northern or Northwestern European descent and less common occurrence in other populations. The unique hue is primarily attributed to a recessive allele on chromosome 16, leading to a modified version of the MC1R protein. This genetic trait is most prevalent in individuals homozygous for this recessive allele, highlighting the fascinating interplay between genetics and hair color expression in human populations.

Extra Information

rs1805008, known as Arg160Trp or R160W, is one of several SNPs in the MC1R gene associated with red hair color (redheads), in this case in an Irish population [PMID 9665397] although this has also been reported in Icelandic and Dutch populations [PMID 18488028].The TT genotype is associated with ~7-10x higher likelihood of red hair and higher risk of melanoma, compared to CC genotype. CT genotype represents carrier for red hair gene.

Red hair color



The G/G genotype is common and may not increase your chances of having red hair.

• **Gene:** MC1R • **rsID:** rs1805009 • **Your Genotype:** G/G • **Zygosity:** Homozygous

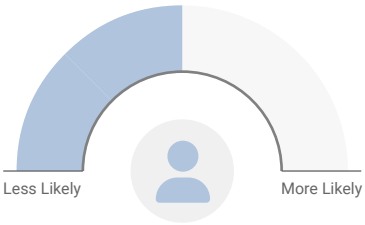
Description

Red hair, often referred to as orange or ginger hair, is a distinctive human hair color present in 1?% of the global population, with a higher prevalence (2?%) among individuals of Northern or Northwestern European descent and less common occurrence in other populations. The unique hue is primarily attributed to a recessive allele on chromosome 16, leading to a modified version of the MC1R protein. This genetic trait is most prevalent in individuals homozygous for this recessive allele, highlighting the fascinating interplay between genetics and hair color expression in human populations.

Extra Information

rs1805009, known as Asp294His or D294H and located in the MC1R gene, is a variant associated with red hair (redheads) and low tanning in one study. [PMID 305318250A-icon.png],[PMID 7581459] Reported as i3002507 by 23andMe in January 2015.CC-red hair possible, higher risk of melanoma. CG genotype represents red hair carrier, higher risk of melanoma and GG represents common risk.

Skin pigmentation



If you have the C/G genotype in rs16891982, you might see mixed pigmentation traits, common in diverse ancestries.

• **Gene:** SLC45A2 • **rsID:** rs16891982 • **Your Genotype:** C/C>C/G • **Zygosity:** Heterozygous

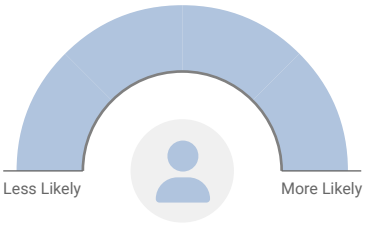
Description

Skin pigmentation, which refers to how much melanin the body generates, determines the color of the skin. The two main types of melanin, eumelanin, and pheomelanin, are produced by melanocytes in the epidermal layer of the skin.Constitutive skin pigmentation is a polygenic trait and, in recent years, the number of genes and the allelic variants that affect human skin pigmentation that have been identified has significantly increased.

Extra Information

This SNP is associated with skin, hair, and eye colour, and risk of melanoma. Individuals with the G;G genotype are generally of European descent and have fair skin.CC:generally non-European, but if European, 7x more likely to have black hair, average skin pigmentation.CG:if European, 7x more likely to have black hair;lower risk of melanoma. GG:Generally European; Lighter skin pigmentation; Possibly an increased risk of melanoma. Brown eye color is predicted for the C/C gneotype plus A/A or G/A at rs12913832, green eye color is predcited by C/Cc genotype plus G/G at rs12913832 [R].The "C" allele was strongly associated with melanoma and pigmentation traits (OR 0.51; P_=_0.001) [R].

Skin pigmentation



Having the A/A genotype for skin pigmentation in the SLC24A5 gene (rs1426654) suggests a likelihood of light skin, typical of West Eurasian ancestry.

• **Gene:** SLC24A5 • **rsID:** rs1426654 • **Your Genotype:** A/A • **Zygosity:** Homozygous

Description

Skin pigmentation, which refers to how much melanin the body generates, determines the color of the skin. The two main types of melanin, eumelanin, and pheomelanin, are produced by melanocytes in the epidermal layer of the skin.Constitutive skin pigmentation is a polygenic trait and, in recent years, the number of genes and the allelic variants that affect human skin pigmentation that have been identified has significantly increased.

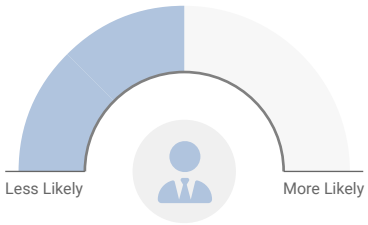
Extra Information

This SNP influences skin pigmentation. The rs1426654 A allele, indicates light-skinned West Eurasian ancestry. [PMID 16847698, PMID 16357253]It appears as if this SNP is a relatively new one in human evolution; one estimate [PMID 17182896] is that the rs1426654(A) allele, in other words, light skin pigmentation, spread through the European population around 6,000 - 12,000 years ago. Prior to that, ""European ancestors"" were most likely relatively brown-skinned. Another study ([PMID 24048645]) has concluded that almost individuals carrying the A111T variant can trace ancestry back to a single person who most likely lived at least 10,000 years ago.This SNP is one of three from the SLC24A5 gene that can be analyzed to categorize the ancestry of a person as either West Eurasian (Middle Eastern, Caucasian, European, etc.), African, or East Eurasian, based on a 2009 study.[PMID 19440451]

Personality

Personality traits, such as extroversion, conscientiousness, and emotional stability, have genetic underpinnings linked to neurotransmitter activity and brain structure. Genetic variations in serotonin and dopamine pathways can influence mood regulation, stress resilience, and social behavior. These insights help in understanding individual differences in personality and psychological well-being.

Agreeableness



Your G/T combination doesn't seem to lead to differences in agreeableness.

• **Gene:** Intergenic • **rsID:** rs7833945 • **Your Genotype:** T/T>T/G • **Zygosity:** Heterozygous

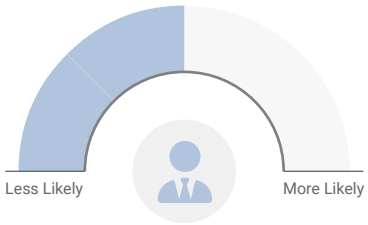
Description

Agreeableness is personality trait that describes a person's ability to put others needs before their own. Those who are more agreeable are more likely to be empathetic and find pleasure in helping others and working with people who need more help

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small decrease in agreeableness with an effect size of -0.03161.

Agreeableness



Carrying the A/G genotype doesn't have a noticeable effect on your level of agreeableness, so just be yourself.

• **Gene:** TCF4 • **rsID:** rs7240986 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

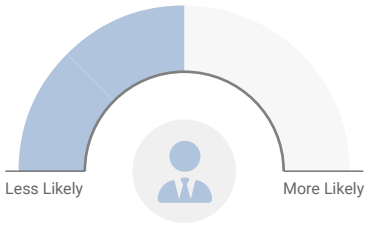
Description

Agreeableness is personality trait that describes a person's ability to put others needs before their own. Those who are more agreeable are more likely to be empathetic and find pleasure in helping others and working with people who need more help

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant is associated with a small decrease in agreeableness with an effect size of -0.0307.

Agreeableness



The C/C genotype at this location doesn't seem to significantly impact your agreeableness levels.

• **Gene:** FOXP2 • **rsID:** rs17137124 • **Your Genotype:** C/C • **Zygosity:** Homozygous

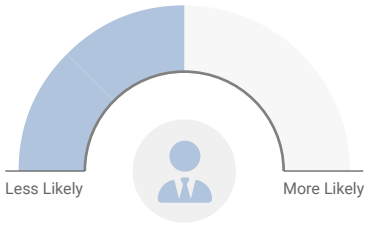
Description

Agreeableness is personality trait that describes a person's ability to put others needs before their own. Those who are more agreeable are more likely to be empathetic and find pleasure in helping others and working with people who need more help

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases agreeableness with an effect size of -0.03273.

Conscientiousness



Your A/A genotype doesn't indicate any specific effect on conscientiousness, leaving room for your unique character to thrive.

• **Gene:** Intergenic • **rsID:** rs78446248 • **Your Genotype:** A/A • **Zygosity:** Homozygous

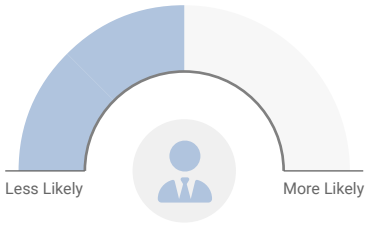
Description

Conscientiousness is a core personality trait that involves being diligent, responsible, and careful. When someone is conscientious, they are able to exercise self-discipline and self-control in order to pursue and ultimately achieve their goals.People with high conscientiousness are also organized, determined, and able to postpone immediate gratification?ll of which contribute to a more successful life.

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant is associated with a moderate decrease in conscientiousness with an effect size of -0.08581.

Conscientiousness



Possessing the A/A genotype does not show notable influences on conscientiousness, leaving your discipline up to you.

• **Gene:** FOXP2 • **rsID:** rs936145 • **Your Genotype:** A/A • **Zygosity:** Homozygous

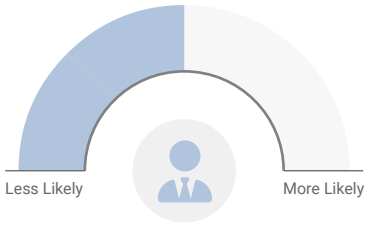
Description

Conscientiousness is a core personality trait that involves being diligent, responsible, and careful. When someone is conscientious, they are able to exercise self-discipline and self-control in order to pursue and ultimately achieve their goals.People with high conscientiousness are also organized, determined, and able to postpone immediate gratification?ll of which contribute to a more successful life.

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a small decrease in conscientiousness with an effect size of -0.0331.

Extraversion



G/G genotype isn't linked to any strong differences in your extraversion trait.

• **Gene:** Intergenic • **rsID:** rs11209774 • **Your Genotype:** T/T>G/G • **Zygosity:** Homozygous

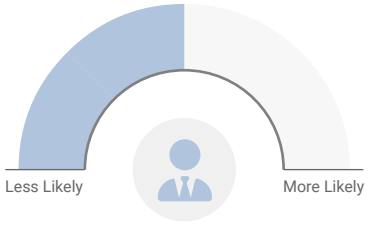
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small decrease in extraversion with an effect size of -0.03406.

Extraversion



The G/G genotype doesn't appear to affect Extraversion.

• **Gene:** Intergenic • **rsID:** rs5831479 • **Your Genotype:** GA/GA>G/G • **Zygosity:** Homozygous

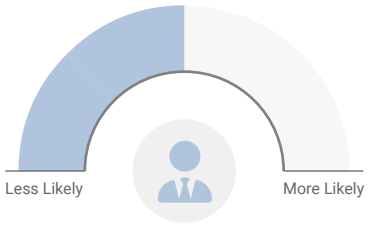
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele GAis identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases extraversion with an effect size of -0.03516.

Extraversion



Having a G/G genotype doesn't lead to a significant shift in extraversion.

• **Gene:** Intergenic • **rsID:** rs7606514 • **Your Genotype:** A/A>G/G • **Zygosity:** Homozygous

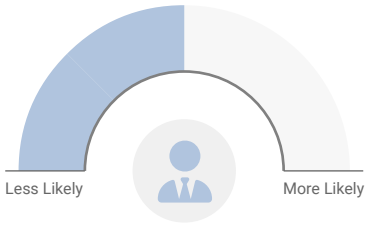
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight decrease in extraversion with an effect size of -0.04297.

Extraversion



With the C/T genotype, we don't see significant changes in your extraversion trait.

• **Gene:** Intergenic • **rsID:** rs1444978 • **Your Genotype:** T/T>T/C • **Zygosity:** Heterozygous

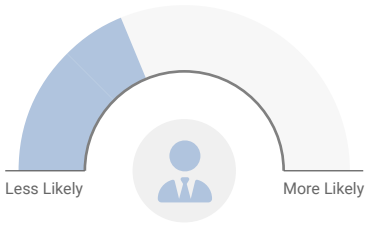
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight increase in extraversion with an effect size of 0.036666.

Extraversion



Your G/T genotype could subtly reduce your levels of extraversion.

• **Gene:** Intergenic • **rsID:** rs7739331 • **Your Genotype:** G/G>G/T • **Zygosity:** Heterozygous

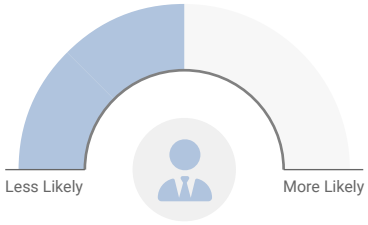
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant is associated with a small decrease in extraversion with an effect size of -0.03211.

Extraversion



For your Extraversion trait with this genetic variant, the A/T genotype does not exhibit a notable impact.

• **Gene:** Intergenic • **rsID:** rs17688916 • **Your Genotype:** T/T>T/A • **Zygosity:** Heterozygous

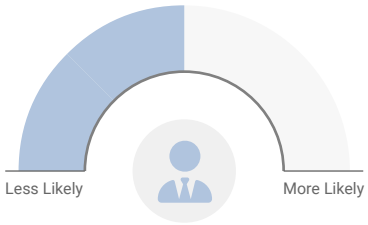
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small decrease in extraversion, with an effect size of _0.04406.

Extraversion



For your Extraversion trait with this genetic variant, the A/C genotype does not exhibit a notable impact.

• **Gene:** Intergenic • **rsID:** rs12971383 • **Your Genotype:** A/A>A/C • **Zygosity:** Heterozygous

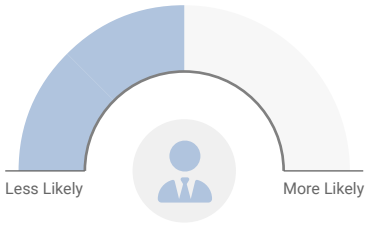
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight increase in extraversion with an effect size of 0.054198.

Extraversion



The T/T genotype shows no evident impact on your extraversion.

• **Gene:** Intergenic • **rsID:** rs35424804 • **Your Genotype:** T/T • **Zygosity:** Homozygous

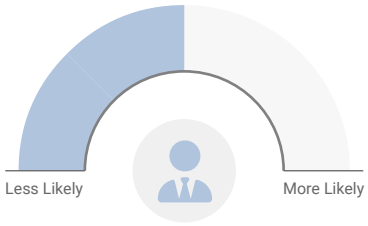
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant is associated with a slight increase in extraversion with an effect size of 0.037166

Extraversion



For your Extraversion trait with this genetic variant, the T/T genotype does not exhibit a notable impact.

• **Gene:** WSCD2 • **rsID:** rs3764002 • **Your Genotype:** T/T • **Zygosity:** Homozygous

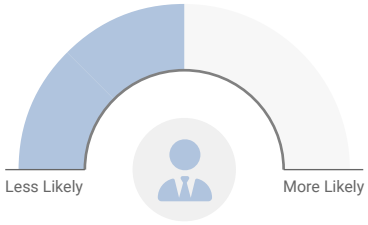
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases extraversion with an effect size of -0.03928.

Extraversion



The C/C genotype doesn't show notable effects on your Extraversion trait.

• **Gene:** FAM172A • **rsID:** rs1011501 • **Your Genotype:** C/C • **Zygosity:** Homozygous

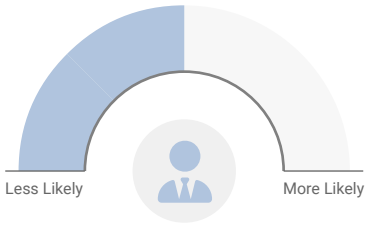
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small decrease in extraversion with an effect size of -0.03858.

Extraversion



• **Gene:** Intergenic • **rsID:** rs35918640 • **Your Genotype:** AT/AT • **Zygosity:** Homozygous

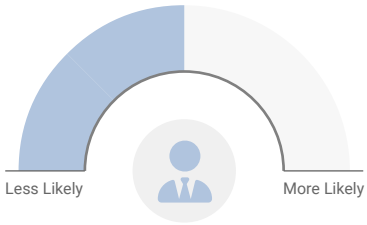
Description

Extroversion is personality trait typically characterized by outgoingness, high energy, and/or talkativeness. In general, the term refers to a state of being where someone ?echarges,?or draws energy, from being with other people; the opposite?rawing energy from being alone?s known as introversion

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight increase in extraversion with an effect size of 0.034989.

Neuroticism



There's no notable impact from the C/C genotype on neuroticism for this gene variant.

• **Gene:** Intergenic • **rsID:** rs2139053 • **Your Genotype:** T/T>C/C • **Zygosity:** Homozygous

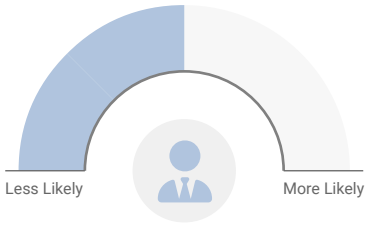
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small increase in neuroticism, with an effect size of 0.042452.

Neuroticism



Having the C/C genotype for this gene could modestly decrease your neuroticism, promoting a bit more emotional stability.

• **Gene:** MAD1L1 • **rsID:** rs6948912 • **Your Genotype:** T/T>C/C • **Zygosity:** Homozygous

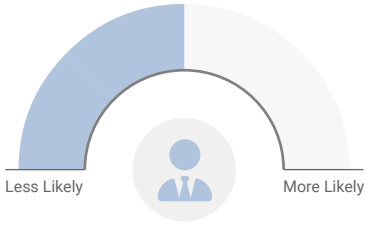
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases neuroticism with an effect size of -0.04524.

Neuroticism



For the A/G genotype, there's no notable change in neuroticism.

• **Gene:** Intergenic • **rsID:** rs7825636 • **Your Genotype:** A/A>A/G • **Zygosity:** Heterozygous

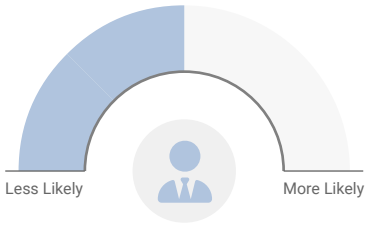
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Results in a slight increase in neuroticism with an effect size of 0.04446.

Neuroticism



Currently, the C/T genotype doesn't show a notable effect on neuroticism.

• **Gene:** Intergenic • **rsID:** rs615632 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

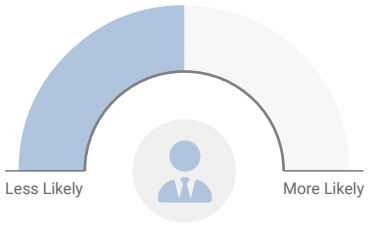
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly increases neuroticism with an effect size of 0.040914.

Neuroticism



The A/T genotype might slightly increase your neuroticism, but not by much.

• **Gene:** XKR6 • **rsID:** rs2001433 • **Your Genotype:** T/T>T/A • **Zygosity:** Heterozygous

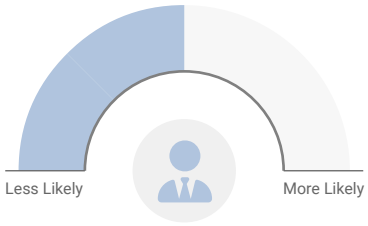
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly increases neuroticism with an effect size of 0.046409.

Neuroticism



Having C/C for the TSNARE1 gene suggests no significant effect on your neuroticism trait.

• **Gene:** TSNARE1 • **rsID:** rs4129585 • **Your Genotype:** A/A>C/C • **Zygosity:** Homozygous

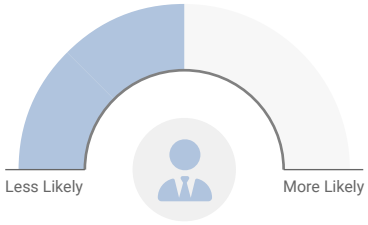
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant is associated with a small decrease in neuroticism scores, with an effect size of -0.05241.

Neuroticism



The T/T genotype doesn't appear to influence your level of neuroticism.

• **Gene:** CDH8 • **rsID:** rs6498809 • **Your Genotype:** C/C>T/T • **Zygosity:** Homozygous

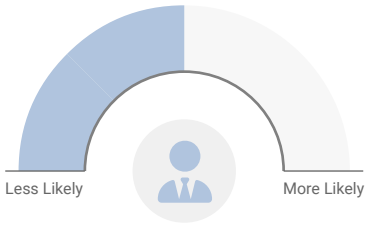
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small increase in neuroticism, with an effect size of 0.03672.

Neuroticism



With an A/G combo in NSF (rs116956554), there's no strong evidence of impact on neuroticism.

• **Gene:** NSF • **rsID:** rs116956554 • **Your Genotype:** G/G>G/A • **Zygosity:** Heterozygous

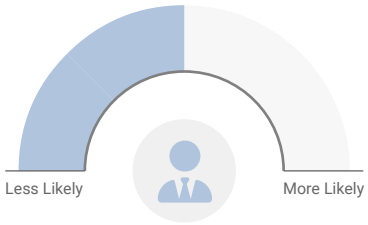
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight increase in neuroticism with an positive effect size of 0.057427.

Neuroticism



G/G at this intergenic spot does not present a notable effect on neuroticism.

• **Gene:** Intergenic • **rsID:** rs574307253 • **Your Genotype:** G/G • **Zygosity:** Homozygous

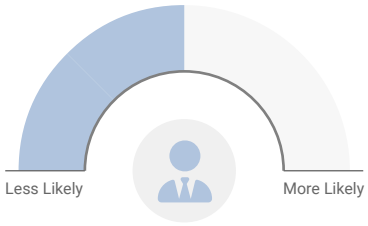
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small increase in neuroticism, with an effect size of 0.059817.

Neuroticism



Having C/C means no noticeable change in emotional stability.

• **Gene:** BMAL1 • **rsID:** rs7396943 • **Your Genotype:** C/C • **Zygosity:** Homozygous

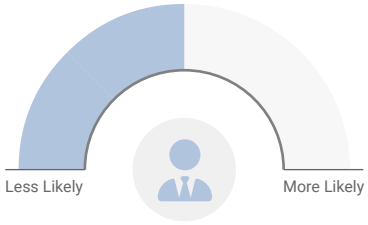
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small increase in neuroticism, with an effect size of 0.046283.

Neuroticism



For the T/T genotype, there's no indication of significant influence on neuroticism.

• **Gene:** TSNARE1 • **rsID:** rs117713019 • **Your Genotype:** T/T • **Zygosity:** Homozygous

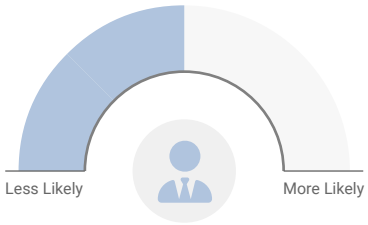
Description

Neuroticism is trait that reflects a person's level of emotional stability. It is often defined as a negative personality trait involving negative emotions, poor self-regulation (an inability to manage urges), trouble dealing with stress, a strong reaction to perceived threats, and the tendency to complain

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a moderate increase in neuroticism with an effect size of 0.08952.

Openness



Currently, there's no clear evidence that the C/T genotype impacts your openness trait significantly.

• **Gene:** Intergenic • **rsID:** rs6996198 • **Your Genotype:** C/C>C/T • **Zygosity:** Heterozygous

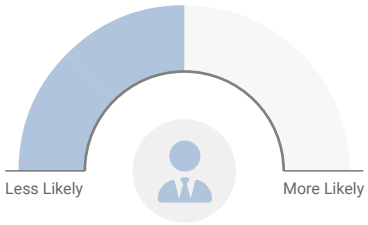
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small decrease in openness with an effect size of -0.04602.

Openness



With an A/C genotype for openness and variant rs11996715, the data doesn't suggest strong correlations currently.

• **Gene:** Intergenic • **rsID:** rs11996715 • **Your Genotype:** C/C>C/A • **Zygosity:** Heterozygous

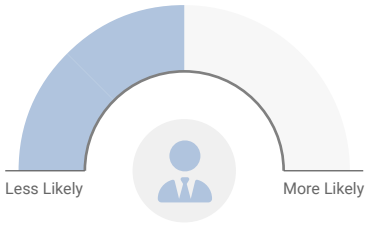
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with allele C is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Associated with a small increase in openness with an effect size of 0.030703.

Openness



• **Gene:** Intergenic • **rsID:** rs61689447 • **Your Genotype:** GTT/GTT>GTT/G • **Zygosity:** Heterozygous

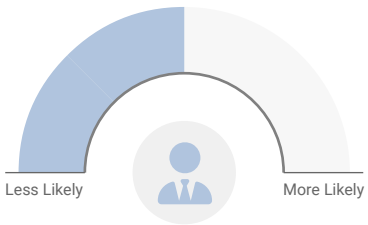
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with deletions of one or more T allele is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases openness with an effect size of -0.03312.

Openness



No significant effect on your openness from having the C/C genotype.

• **Gene:** C11orf80 • **rsID:** rs7570 • **Your Genotype:** C/C • **Zygosity:** Homozygous

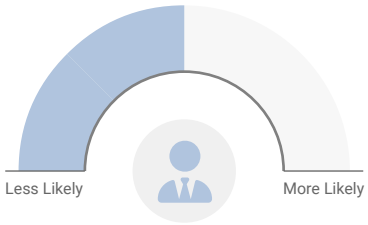
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with allele G is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly decreases openness with an effect size of -0.04711.

Openness



Having the G/G genotype doesn't notably affect your openness.

• **Gene:** Intergenic • **rsID:** rs117890891 • **Your Genotype:** G/G • **Zygosity:** Homozygous

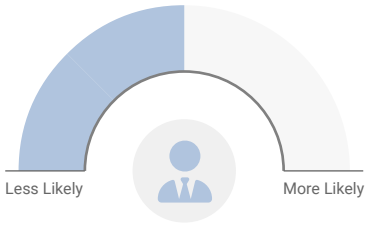
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with allele T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a significant increase in openness with an effect size of 0.145052.

Openness



Having the C/C genotype doesn't noticeably change your openness.

• **Gene:** Intergenic • **rsID:** rs919013 • **Your Genotype:** C/C • **Zygosity:** Homozygous

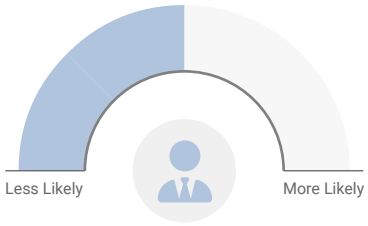
Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with T is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).This variant slightly increases openness with an effect size of 0.033444.

Openness



The T/T genotype seems to maintain your openness level unchanged in this context.

• **Gene:** CLIP4 • **rsID:** rs6725323 • **Your Genotype:** T/T • **Zygosity:** Homozygous

Description

Openness to experience, or simply openness, is a basic?ersonality?rait denoting receptivity to new ideas and new experiences. It is one of the five core personality dimensions that drive behavior?nown as the?ive-factor model?f personality, or the Big 5. People with high levels of openness are more likely to seek out a variety of experiences, be comfortable with the unfamiliar, and pay?ttention?o their inner feelings more than those who are less open to novelty. They tend to exhibit high levels of curiosity and often enjoy being surprised. People with low levels of openness prefer familiar routines, people, and ideas; they can be perceived as closed-minded"

Extra Information

This variant with allele A is identified from the paper "A genome-wide investigation into the underlying genetic architecture of personality traits and overlap with psychopathology"(PMID: 39134740).Shows a slight decrease in openness with an effect size of -0.03361.

Genetic Terms Glossary

Understanding Your Genetic Report

This glossary provides definitions for common genetic terms used throughout your report. Understanding these terms will help you better comprehend your genetic findings.

Benign Variant

A genetic change that is not known to cause disease or increase health risks.

Carrier Status

When a person has one copy of a genetic variant associated with a recessive condition but typically does not have the condition themselves.

Chromosome

A structured package of DNA found in the nucleus of cells. Humans typically have 23 pairs of chromosomes.

DNA (Deoxyribonucleic Acid)

The molecule that carries genetic instructions for the development and functioning of all known living organisms.

Dominant Inheritance

A pattern where a genetic trait or disorder can be passed on to offspring even if only one parent has the variant.

Exome

The part of the genome that contains protein-coding sequences. Most known disease-causing variants are found in the exome.

Gene

A segment of DNA that contains the instructions for making a specific protein or determines a particular characteristic.

Genotype

The genetic makeup of an organism, which determines traits in combination with environmental factors.

Pathogenic Variant

A genetic change that is known to increase the risk of disease or cause a specific condition.

Penetrance

The proportion of people with a particular genetic variant who exhibit the associated trait or condition.

Pharmacogenetics

The study of how genetic differences influence individual responses to medications.

Phenotype

The observable physical or biochemical characteristics of an organism, as determined by both genetic makeup and environmental influences.

Recessive Inheritance

A pattern where a genetic trait or disorder only appears when a person has two copies of the variant, one from each parent.

Genetic Variant

A change in the DNA sequence compared to a reference genome. Variants can be benign, pathogenic, or of uncertain significance.

VUS (Variant of Uncertain Significance)

A genetic change where there is not enough evidence to classify it as either pathogenic or benign.

Technical Notes and Methodology

Variant Annotation and Classification

Variants are extensively annotated using Ensembl's Variant Effect Predictor (VEP), incorporating SIFT, PolyPhen-2, and other in silico prediction tools. Our custom annotation pipeline integrates data from multiple sources including gnomAD for population frequencies, ClinVar for clinical significance, and COSMIC for somatic mutations.

Variant classification follows ACMG/AMP guidelines, incorporating evidence from multiple databases and literature sources. We utilize a sophisticated scoring system that weighs different types of evidence, including:
• Population databases (gnomAD, 1000 Genomes)
• Disease databases (ClinVar, OMIM, HGMD)
• Functional studies from published literature
• Computational predictions
• Segregation data when available

Bioinformatics Pipeline

Raw sequencing data undergoes rigorous quality control using FastQC, followed by adapter trimming and quality filtering. Reads are aligned to the GRCh38/hg38 reference genome using BWA-MEM2, chosen for its superior performance with long reads and improved accuracy in repetitive regions. Post-alignment processing includes duplicate marking, base quality score recalibration, and local realignment around indels.

Variant calling is performed using an ensemble approach combining GATK HaplotypeCaller, DeepVariant, and Strelka2, leveraging the strengths of each caller. This multi-caller strategy, combined with sophisticated filtering and machine learning-based recalibration, achieves high sensitivity while maintaining a low false discovery rate. Structural variants are detected using a combination of Manta, DELLY, and CNVnator, providing comprehensive coverage of different variant types.

Reference Databases

Our analysis incorporates data from numerous authoritative sources:

• Population Databases:
- gnomAD (>140,000 individuals)
- 1000 Genomes Project (2,504 individuals)
- UK Biobank (500,000 participants)

• Clinical Databases:
- ClinVar (NIH-curated clinical variants)
- OMIM (Online Mendelian Inheritance in Man)
- HGMD (Human Gene Mutation Database)

Technical Limitations and Considerations

While our sequencing and analysis pipeline represents current best practices, it's important to acknowledge certain limitations:

• Some genomic regions may have suboptimal coverage due to technical limitations
• Complex structural variants may be more challenging to detect accurately
• Novel variants may have limited available evidence for classification
• Some regions of the genome remain difficult to sequence or interpret
• Certain types of mutations (e.g., some repeat expansions) may not be reliably detected

We continuously update our methodologies as new technologies and knowledge become available, always striving to provide the most accurate and comprehensive genetic analysis possible.

DNA Sequencing Technology

Our whole genome sequencing is performed using Illumina's NovaSeq™ 6000 Sequencing System, representing the pinnacle of next-generation sequencing technology. This platform utilizes sequencing by synthesis (SBS) technology, capable of generating up to 6 terabases of data per run with exceptional accuracy. We maintain an average coverage depth of 30x across the genome, ensuring high-quality variant calling and minimal false positives. The system's advanced patterned flow cell technology and two-channel chemistry significantly reduce noise and cross-talk between bases, resulting in superior base calling accuracy.

Our DNA extraction and library preparation protocols follow industry-leading standards, incorporating quality controls at each step. We use the Illumina DNA PCR-Free Prep kit to minimize PCR-induced artifacts and biases, ensuring a more uniform coverage across the genome, including traditionally difficult-to-sequence regions rich in GC content.

Phenome Longevity

Name:
DoB: –
Gender: female

Report ID: WB
Subject ID: 30793
Date: 2026-10-30

Gene List

American College of Medical Genetics and Genomics (Secondary Finding List v3.1) (ACMG Genes)

ACTA2, ACTC1, ACVRL1, APC, APOB, ATP7B, BMPR1A, BRCA1, BRCA2, BTD, CACNA1S, CASQ2, COL3A1, DSC2, DSG2, DSP, DSP, ENG, FBN1, FLNC, GAA, GLA, HFE, HNF1A, KCNH2, KCNQ1, LDLR, LMNA, MAX, MEN1, MLH1, MSH2, MSH6, MUTYH, MYBPC3, MYH11, MYH7, MYH7, MYL2, MYL3, NF2, OTC, PALB2, PCSK9, PKP2, PMS2, PRKAG2, PTEN, RB1, RET, RET, RET, RPE65, RYR1, RYR2, SCN5A, SCN5A, SCN5A, SDHAF2, SDHB, SDHC, SDHD, SMAD3, SMAD4, SMAD4, STK11, TGFBR1, TGFBR2, TMEM127, TMEM43, TNNI3, TNNT2, TNNT2, TP53, TPM1, TRDN, TSC1, TSC2, TTN, VHL, WT1, BAG3, DES, RBM20, TNNC1, TTR

Cardiovascular Diseases (219 Genes)

ACTA2, ACTC1, APOB, BAG3, CASQ2, COL3A1, DES, DSC2, DSG2, DSP, FBN1, FLNC, GLA, KCNH2, KCNQ1, LDLR, LMNA, MYBPC3, MYH11, MYH7, MYL2, MYL3, PCSK9, PKP2, PRKAG2, RBM20, RYR2, SCN5A, SMAD3, TGFBR1, TGFBR2, TMEM43, TNNC1, TNNI3, TNNT2, TPM1, TRDN, TTN, ABCC6, ABCC9, ACTN2, ACVRL1, ADD1, AGT, AGTR1, AKAP9, ALG10B, ATP13A3, ATP1A2, ATP1B1, BMPR2, CACNA1A, CACNA1C, CACNB2, CAV1, CAV3, CFC1, CRYAB, CSRP3, CYP3A5, DPP6, ECE1, EDNRA, EIF2AK4, ENG, ENPP1, ESR1, EYA4, FKTN, FOXF1, GATA4, GDF1, GDF2, GJA5, GNAI2, GNAQ, GNB3, GPD1L, HCN4, HTRA1, JPH2, KCNA5, KCNE1, KCNE2, KCNE3, KCNJ2, KCNJ5, KCNK18, KCNK3, LAMA4, LDB3, LOX, MFAP5, MYH6, MYLK2, MYOZ2, NEXN, NOS3, NOTCH1, NPPA, PLN, PRKG1, PSEN2, PTGIS, RGS5, ROBO4, SCN1A, SCN1B, SCN3B, SCN4B, SDHA, SGCD, SMAD4, SMAD6, SMAD9, SNTA1, TAFAZZIN, TBX20, TCAP, TGFB2, TLL1, TNF, VCL, ACE, ADRB1, ALPK3, ANGPT1, ANKRD1, APOA2, BAG5, CALM3, CDH2, CFAP45, CFAP52, CIROP, COL4A1, COL5A1, COLGALT1, DZIP1, EPHB4, EPHX2, FHOD3, GATA5, GHR, HAAO, HS3ST6, KIF20A, KNG1, KYNU, LMOD2, MNS1, MYLK, MYOF, NADSYN1, NOTCH3, PLG, PPCS, PPP1CB, PPP1R17, PRDM6, PSEN1, RNF213, RPL3L, SMAD2, TBX1, THSD1, THSD4, TMPO, ACVR2B, ADA2, CALM1, CALM2, CCDC174, CFAP53, CITED2, COL1A2, COL4A2, CORIN, CRELD1, CTNNA3, DCHS1, F12, FLNA, GATAD1, GJA1, GLMN, JAG1, KCND3, LRP6, MED13L, MEF2A, MGAT2, MMP21, MYL4, MYPN, NKX2-5, NKX2-6, NODAL, NR2F2, NT5E, NUP155, PKD1L1, PRPH2, PUF60, RAF1, RBM10, SCN2B, SCN9A, SERPING1, SHOC2, STOX1, TAB2, TECRL, TEK, TFAP2B, TGFB3, TKT, TNNI3K, ZFPM2

Endocrine and Metabolic Disorders (691 Genes)

BTD, GAA, OTC, ABCA1, ABCC8, ACADM, ACADVL, ACAT1, AGL, AGPAT2, AGXT, ALDH18A1, ALDOA, ALG1, ALG11, ALG12, ALG2, ALG3, ALG6, ALG8, ALG9, ANOS1, APOA1, APOA2, APOA5, APOC2, APOE, ARG1, ASL, ASS1, ATAD1, ATP13A2, AUH, B4GALT1, BCKDHA, BCKDHB, BMP2, BSCL2, BTK, C19orf12, CACNA1S, CHD7, CIDEC, CLCN2, CLN3, CLN5, CLN6, CLN8, CLPB, COG1, COG4, COG5, COG6, COG7, COG8, CP, CPS1, CPT1A, CPT2, CTNS, CTSD, CTSF, CYP11B1, CYP17A1, CYP21A2, DBT, DCAF17, DDB2, DLL3, DNAJC19, DNAJC5, DOLK, DPAGT1, DPM1, DPM3, DUOX2, ELN, ENO3, EPHX2, ERCC2, ERCC3, ERCC4, ERCC5, ERCC6, ERCC8, ETFA, ETFB, ETFDH, FA2H, FAH, FBLN5, FCSK, FGF8, FGFR1, FTH1, FTL, FUT8, G6PC1, GALE, GALK1, GALT, GAMT, GATM, GBE1, GCDH, GCH1, GCK, GH1, GHR, GLB1, GLRA1, GLRB, GLUD1, GNAS, GNAS-AS1, GNE, GPHN, GPIHBP1, GRHPR, GRN, GYG1, HADH, HADHA, HADHB, HAMP, HES7, HFE, HJV, HLCS, HMGCL, HOGA1, HPRT1, HSD3B2, HTRA2, HYMAI, IDUA, INS, INSR, IVD, IYD, KCNJ11, KCNJ5, KRT5, LARS1, LCAT, LDHA, LDLR, LDLRAP1, LEP, LEPR, LFNG, LIPE, LMBRD1, LMNA, LPL, LRMDA, MAN2C1, MARS1, MC1R, MCCC1, MCCC2, MCEE, MESP2, MFSD8, MGAT2, MMAA, MMAB, MMACHC, MMADHC, MMUT, MOCOS, MOCS1, MOCS2, MOGS, MPDU1, MPI, MTR, MTRR, NAGS, NEU1, NGLY1, NPC1, NPC2, NUDT15, OPA3, Oca.02, PAH, PANK2, PAX8, PCCA, PCCB, PCSK1, PDE10A, PDE8B, PDX1, PFKM, PGAM2, PGM1, PHKA1, PHKA2, PHKB, PHKG2, PLA2G6, PLIN1, PLPBP, PMM2, POFUT1, POGLUT1, POLH, POMC, PPARG, PPP1R17, PPT1, PRDX1, PROK2, PROKR2, PSAP, PYGM, QDPR, RFT1, SCN4A, SDHA, SDHAF2, SDHB, SDHC, SDHD, SERAC1, SLC10A1, SLC16A1, SLC17A5, SLC22A12, SLC22A5, SLC25A13, SLC25A20, SLC2A1, SLC2A9, SLC35A1, SLC35C1, SLC37A4, SLC40A1, SLC45A2, SLC5A2, SLC6A5, SLC6A8, SMPD1, SRD5A3, SRY, STAR, STX16, TAFAZZIN, TFR2, TIMM50, TJP2, TPO, TPP1, TSHB, TSHR, TYR, TYRP1, VDR, WDR45, XDH, XPA, XPC, ZFP57, ABCB4, ABCD4, ACOX1, ADCY10, ADRB2, ADRB3, AGRP, ALG13, ALKBH8, ALPL, AMPD3, ANGPTL3, APOB, APPL1, AQP7, ARSK, ATP1A1, ATP6AP2, AXL, BCAT2, BCHE, BNC1, C12orf4, C14orf39, C18orf32, CAMK2A, CAPN10, CARTPT, CCDC141, CCR5, CES1, CLDN16, CLPX, COA7, CRAT, CREB3L3, CTH, CTSA, CYP2C8, DBH, DCT, DDOST, DIO1, DPM2, DPYS, DUSP6, EDEM3, EGR2, EIF3F, ENPP1, ERCC1, ESR2, F9, FEZF1, FGF17, FSHR, FTCD, GALM, GALNT2, GATA1, GBA1, GCM2, GCSH, GDF9, GGT1, GHRL, GLS, GNRH1, GPAA1, GPNMB, GRIA1, HAL, HCFC1, HNF4A, HSF2BP, IL2RA, IMPDH2, IRS4, KCNMB1, KDM5B, KRT18, LCT, LDHD, LHCGR, LINGO1, LRP5, MAFA, MAGT1, MAX, MCM6, METTL5, MPZ, MRPS22, MSH2, MSH4, MSH5, MSH6, MTHFS, NAA20, NAXD, NDNF, NHLH2, NKX2-5, NR0B2, NUP107, ODC1, PANK4, PAX4, PCK2, PCSK9, PEX7, PIDD1, PIGB, PIGC, PIGH, PIGK, PIGP, PIGQ, PIGS, PMP22, PMS2, PRKACA, PRX, PTH, REPS1, RINT1, RSRC1, RUSC2, SDC3, SEMA3E, SERPINA7, SLC28A1, SLC36A2, SLC6A19, SLC6A20, SLCO1B1, SLCO1B3, SMAD6, SNCA, SNCB, SOHLH1, SPIDR, SPRY4, SQOR, SRA1, SSR4, STT3A, SUGCT, SUMO4, TAF13, TBC1D4, TBL1X, TCF12, TDO2, THAP11, TMEM165, TMLHE, TPH2, TPMT, TREH, TRH, TRHR, TRMT1, TRPV6, TUSC3, TXNRD2, UCP3, USF1, UVSSA, WDR11, XRCC2, ZBTB11, ZNF143, ZSWIM7, A2M, AARS1, AASS, ABAT, ABCB11, ABCD3, ABHD5, ACADSB, ACOX2, ACP2, ACY1, ADSL, AFP, AKT2, ALAD, ALAS2, ALB, ALDH4A1, ALDH6A1, AMACR, AMH, AMHR2, ANKH, AP2S1, AP5Z1, APC2, APOC3, APRT, ARSL, ASAH1, ATL1, ATL3, ATP6V0A2, ATP6V1A, ATP6V1E1, ATP8B1, BCO1, BLK, BLVRA, BMP15, BPGM, BPNT2, CACNA1A, CACNA1H, CAD, CAT, CAV1, CC2D1A, CCDC115, CD320, CEL, CEP19, CERS1, CETP, CHST3, CNNM2, COASY, COG2, CRADD, CRBN, CTLA4, CYP11B2, CYP19A1, CYP24A1, CYP2R1, CYP7B1, DCDC2, DCPS, DCXR, DHCR24, DHTKD1, DIAPH2, DMGDH, DNAJC12, DNMT1, DPYD, DUOXA2, EBP, ECM1, EDC3, EEF1A2, EGF, ELOVL5, ELP2, EXOSC3, EXOSC8, EXT2, FBXO31, FECH, FGF12, FIGLA, FMN2, FMR1, FOLR1, FOXL2, FSHB, FXYD2, GABRB1, GCLC, GK, GLI3, GLUL, GLYCTK, GM2A, GNA11, GNMT, GNRHR, GOT1, GPD1, GPX4, GRID2, GRIK2, GRIN2D, GRM1, GYS1, H6PD, HCN1, HFM1, HIBCH, HMGCS2, HMOX1, HNMT, HSD11B1, HYAL1, IDH2, IL31RA, IMPA1, ITPA, KCNA2, KCNB1, KCNJ6, KHK, KISS1, KISS1R, KLF11, KYNU, L2HGDH, LBR, LDHB, LHB, LINS1, LIPC, LMAN2L, LTC4S, MAN1B1, MAOA, MBOAT7, MCM8, MCM9, MED23, METTL23, MKRN3, MLH1, MSMO1, NADK2, NBAS, NDST1, NECAP1, NEUROD1, NOBOX, NR3C1, NSUN2, NUS1, OPLAH, PAPSS2, PCK1, PCNA, PDE11A, PEPD, PEX1, PEX6, PGAP1, PGK1, PIGN, PIGT, PNLIP, PNPLA2, POF1B, PPM1K, PPOX, PRKAR1A, PRKCSH, PRLR, PRODH, PRPS1, PRSS12, PSMC3IP, PYCR1, RAD50, RBCK1, RIPPLY2, RSPO1, SAR1B, SARDH, SC5D, SCP2, SEC63, SECISBP2, SERPINA6, SHPK, SLC16A12, SLC1A1, SLC1A3, SLC1A4, SLC24A5, SLC25A19, SLC26A2, SLC30A10, SLC34A1, SLC35A3, SLC39A14, SLC4A4, SLC52A1, SLC6A17, SLC6A9, SPINK1, SPTLC1, SPTLC2, SQSTM1, SRD5A2, ST3GAL3, ST3GAL5, STAG3, STT3B, SUMF1, SYCE1, TAC3, TALDO1, TBXAS1, TDP1, TECR, TG, THRB, TMEM199, TNIK, TPK1, TRAPPC9, TRPM6, TSPYL1, TTR, UBA5, UGT1A1, UPB1, UROC1, VAC14, VPS33A, VRK1, WASHC4, WNT4, WWOX, ZC3H14, ZMPSTE24

Hematologic Disorder (176 Genes)

ABCD4, ANK1, C3, CD46, CDAN1, CDIN1, CFB, CFH, CFHR1, CFHR3, CFHR4, CFI, CYB5A, CYB5R3, CYBA, CYBB, ELANE, EPB41, EPB42, F10, F5, F8, F9, G6PC3, GATA1, GFI1, HAMP, HAX1, HBA1, HBA2, HBB, HBB-LCR, HJV, JAGN1, KIF23, KLF1, KLKB1, LMAN1, LMBRD1, MCFD2, MMACHC, MMADHC, NCF1, NCF2, NCF4, PIK3CD, PIK3R1, PRDX1, PROC, PROS1, RPL11, RPL15, RPL18, RPL26, RPL27, RPL35, RPL35A, RPL5, RPS10, RPS15A, RPS17, RPS19, RPS24, RPS26, RPS27, RPS28, RPS29, RPS7, SEC23B, SERPINC1, SLC11A2, SLC4A1, SPTA1, SPTB, STEAP3, THBD, TMPRSS6, TSR2, VPS45, WAS, ATP11C, ATRX, BCAM, CALR, CASK, CLPB, CYBC1, EPHB2, EPX, F7, FGA, FGB, FGG, FLI1, FYB1, GP1BA, GP1BB, GP9, GSR, HABP2, HBG1, HBG2, HOXA11, HSCB, IKZF5, IL6R, IL6ST, ITGA2B, ITGB3, MECOM, PLA2G4A, PLAT, RACGAP1, RHCE, RHD, SH2B3, SH3KBP1, SLC39A7, SMARCD2, SPI1, TBXA2R, TCF3, TERT, TNFRSF13B, TUBA8, VWF, ZNF341, ABCB6, AICDA, AK1, ANO6, CD36, CD40, CD59, CDC42, CEBPE, CYCS, DHFR, F12, FCGR2C, FTL, GFI1B, GGCX, GP6, GPI, HRG, HSPA9, IFNG, IKBKG, JAK2, KCNN4, KNG1, MPL, MPO, NBEAL2, NT5C3A, P2RY12, PIEZO1, PIGM, PLAU, PRKACG, RAC2, RASGRP2, RHAG, RPIA, SERPIND1, SERPINE1, SERPINF2, SLFN14, STIM1, THPO, TPI1, TUBB1, UMPS, UNG, VKORC1

Phenome Longevity

Name:
DoB: –
Gender: female

Report ID: WB
Subject ID: 30793
Date: 2026-10-30

Immune Disorders (204 Genes)

ADA, CTLA4, FGA, FGB, FGG, FLG, GSS, HLA-DQA1, HLA-DQB1, IL2RG, MYO9B, NLRC4, NLRP12, NLRP3, NPC1, NPC2, PLCG2, PRF1, SH2D1A, STX11, STXBP2, UNC13D, XIAP, ABCB1, ANGPT2, ARHGEF1, BACH2, C1QA, C1QB, C1QC, CALCRL, CARD10, CARD11, CARD8, CARMIL2, CCL11, CCL2, CCL3, CCL3L1, CCL5, CCR5, CD209, CD3G, CD4, CD70, CELSR1, CTNNBL1, CX3CR1, CXCL12, CXCR1, DEF6, EPHB4, F10, FCHO1, FNIP1, GINS1, GPX1, HLA-C, IFIH1, IFITM3, IFNAR1, IFNG, IFNGR1, IFNGR2, IFNL3, IKBKB, IKBKG, IKZF3, IL10, IL21R, IL23R, IL37, IL4R, INAVA, IRF3, IRF9, IVNS1ABP, KIR3DL1, KNSTRN, LAT, LCP2, LIG1, LTA, MBL2, MCM10, MPEG1, MRTFA, MS4A2, NCKAP1L, PIK3CD, PIK3CG, PLA2G7, POLR3F, POMP, PRNP, PSMB10, PSMB4, PSMB9, PSMG2, PTPRC, RAC2, RASGRP1, RC3H1, REL, RELB, RIPK1, SASH3, SLC11A1, SLC29A3, SPPL2A, SYK, TAP1, TAPBP, TBX21, TET2, TICAM1, TIE1, TLR1, TLR2, TLR3, TLR7, TLR8, TOM1, TPP2, TRAF3, UNC93B1, ZNFX1, ATG16L1, ATP2C1, ATP6AP1, B2M, BCL10, BCL11B, C1S, C4A, C4B, CARD14, CARD9, CD247, CD27, CD8A, CIITA, CORO1A, DNASE1L3, DOCK2, EPG5, FADD, FBN1, FCGR3A, FCN3, FLT4, GATA2, GJC2, IFNAR2, IGKC, IL12B, IL12RB1, IL17F, IL17RA, IL17RC, IL2RA, IL6, IRF5, IRF7, IRF8, IRGM, ISG15, ITK, LBR, LCK, MAGT1, MALT1, MASP2, MCM4, MSN, MYD88, NOD2, ORAI1, OTULIN, PIEZO1, PSMB8, PSTPIP1, RAG1, RFX5, RFXAP, RORC, RPSA, SERPING1, STAT1, STAT2, STIM1, STK4, TAP2, TFRC, TNFRSF1A, TNFRSF4, TRAC, TRAF3IP2, TYK2, UNC119, VEGFC, WIPF1, ZAP70

Neurological Disorders (1145 Genes)

AARS1, ABCA4, ABCA7, ACTG1, ADCY1, ADH1C, AIFM1, AIPL1, ALS2, AMPD2, ANG, ANO5, APOE, APP, ARHGEF9, ARMS2, ARX, ASPM, ATAD1, ATP13A2, ATP1A3, ATP2B2, ATXN2, ATXN7, ATXN8OS, BSCL2, C3, CACNA1A, CACNA1F, CACNA1H, CACNB4, CAPN3, CAV3, CC2D2A, CCDC50, CCDC88C, CCM2, CDC14A, CDH23, CDK5RAP2, CDK6, CENPE, CENPJ, CEP135, CEP152, CEP290, CFH, CFHR1, CFHR3, CHMP1A, CHRNA2, CHRNA4, CHRNB2, CIB2, CISD2, CLCF1, CLCN2, CLDN14, CLP1, CLPP, CNTNAP1, COCH, COL11A2, COL6A1, COL6A2, COL6A3, CRB1, CRLF1, CRX, CST3, CSTB, CTC1, DAG1, DCAF8, DCDC2, DCTN1, DCX, DES, DIABLO, DIAPH1, DISC1, DNAJB2, DNAJB6, DRD3, DYNC1H1, DYNC2H1, DYSF, EFHC1, EGR2, ELOVL4, ELP4, EPM2A, ERCC6, ESPN, ESRRB, EXOSC3, EXOSC8, EXOSC9, EYA4, F12, FBLN5, FBXO7, FGD4, FGFR1, FIG4, FKRP, FKTN, FOXI1, FUS, FXN, GAB1, GABRA1, GABRB3, GAN, GARS1, GBA1, GDAP1, GH1, GIGYF2, GIPC1, GIPC3, GJB1, GJB2, GJB3, GJB6, GLI2, GLRA1, GLRB, GLUD2, GMPPB, GNB4, GPHN, GPSM2, GRHL2, GRIN2A, GRK1, GRM6, GRXCR1, GSDME, GUCY2D, HFE, HGF, HK1, HLA-DQB1, HMCN1, HNRNPDL, HSPB1, HSPB8, HTRA1, HTRA2, IFT80, IGHMBP2, ILDR1, IMPDH1, IMPG1, IMPG2, INF2, ITGA7, JPH1, KARS1, KCNA1, KCNJ10, KCNJ13, KCNQ2, KCNQ3, KCNQ4, KCNT1, KCTD17, KIF1A, KIF1B, KIF21A, KLHL7, KNL1, KRIT1, LAMA2, LAMB1, LARGE1, LCA5, LGI1, LHFPL5, LITAF, LMNA, LMX1A, LOXHD1, LRAT, LRP12, LRRK2, LRTOMT, MAPT, MARS1, MARVELD2, MCPH1, MECP2, MFN2, MFSD2A, MICAL1, MIR96, MME, MPDZ, MPO, MPZ, MSRB3, MT-CO1, MT-RNR1, MT-TS1, MT-TT, MTMR2, MYH14, MYH6, MYH7, MYH9, MYLK2, MYO15A, MYO3A, MYO6, MYO7A, MYOT, NAXD, NAXE, NDRG1, NEFH, NEFL, NHLRC1, NLGN3, NLGN4X, NMNAT1, NOS3, NOTCH2NLC, NR4A2, NRG1, NRXN1, NUP62, NYX, OTOA, OTOF, P2RX2, PAFAH1B1, PARK7, PAX6, PCDH15, PCLO, PDCD10, PDXK, PHC1, PHOX2A, PIK3CA, PINK1, PJVK, PLA2G6, PLAU, PLEC, PLK4, PMP22, PNKD, POLR3A, POLR3B, POMGNT1, POMT1, POMT2, POU3F4, POU4F3, PRICKLE1, PRKN, PRNP, PRODH, PROM1, PRPH, PRPH2, PRPS1, PRRT2, PRRX1, PRX, PSEN1, PSEN2, PTCH1, PTPRQ, RAB7A, RARS2, RAX2, RBM12, RD3, RDH12, RDX, REEP1, RELN, REST, RETREG1, 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CAMK2B, CAMK2G, CCDC88A, CCL2, CCNF, CDC40, CDC42BPB, CDH2, CDK19, CEACAM16, CELF2, CEP85L, CFAP43, CFB, CHD5, CHI3L1, CHP1, CHRNA7, CIC, CILK1, CLCN3, CLDN11, CLDN9, CLEC3B, CLRN2, CLTC, CNP, CNPY3, COASY, COL11A1, COMP, COMT, COPB2, CPLX1, CPSF3, CSF1R, CSNK2B, CTNNA2, CUL3, CUX2, CYB561, CYFIP2, CYLD, DAB1, DALRD3, DAOA, DCTN2, DEGS1, DHDDS, DHPS, DHX30, DHX37, DLG4, DLL1, DMD, DMXL2, DNM1L, DNMT3B, DOCK3, DPYSL5, DRD4, DRD5, DRP2, DTYMK, DYNC1I2, EIF2AK2, ELMOD3, EMC10, EPRS1, EPS8L2, ESRP1, EXOC2, EXOC7, EXOC8, EXOSC1, F2, F5, FAT2, FBP2, FBXO28, FDFT1, FGF13, FKBP5, FOXH1, FRG1, GABBR2, GABRA2, GABRA5, GABRB2, GABRD, GABRG2, GAD1, GBF1, GDAP2, GEMIN2, GEMIN4, GEMIN5, GNAI1, GNAO1, GNAQ, GNB2, GPRASP2, GRAP, GREB1L, GRIA1, GRIA2, GRIA4, GRIK2, GRIN1, GRM1, GRM7, HCN1, HCN4, HDAC4, HEPACAM, HID1, HPDL, HTR2A, IL6, INPP5K, INTS1, INTS8, JAG1, JAG2, JAM2, KAT5, KCNC2, KCND3, KCNMA1, KCNN2, KCNQ5, KCNT2, KDM4B, KDM6B, KIF14, KLF13, KMT2B, KMT5B, KRAS, LIPT2, LMAN2L, LMNB1, LMNB2, 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LAMC3, LDB3, LRIT3, MAPKAPK3, MATR3, MBD5, MCM2, MDH2, MED17, MED25, MEF2C, MET, MFSD8, MICU1, MID2, MOG, MR1, MRE11, MYF6, MYT1L, NACC1, NAGLU, NALCN, NDE1, NGF, NIPA1, NOL3, NOP56, NOTCH3, NPRL2, NPRL3, OPN1SW, OSBPL2, OTOG, PABPN1, PDE6B, PDE6C, PDE6H, PDK3, PDYN, PER2, PER3, PFN1, PIK3R2, PIK3R5, PITPNM3, PLA2G5, PLEKHG5, PMPCA, POC1B, POLR1C, POMK, PPP2R2B, PRDM12, PRDM8, PRKCG, PRKRA, PURA, PYCR2, RAB28, RAB39B, RAD51, RARS1, RBP4, RCBTB1, REEP2, RERE, RHO, RIMS1, RLBP1, RLIM, RNASET2, RNF168, RP1L1, RPGR, RPS6KA3, RTN2, RTN4IP1, RUBCN, RXYLT1, SCARB2, SCN10A, SCN11A, SCN1B, SEMA4A, SERPINI1, SLC20A2, SLC24A1, SLC33A1, SLC6A2, SLC9A1, SLITRK1, SMPX, SNX14, SPAST, SPEG, SPG21, SPTBN2, SRPX2, STAC3, STRADA, STX1B, SYNE1, SYNE4, SYNGAP1, SYNJ1, SYP, SYT14, SZT2, TAF1, TANGO2, TBC1D7, TBCD, TBCK, TBK1, TBL1XR1, TDP2, TEAD1, TELO2, TENM4, TGFBI, TGM6, THAP1, TIMP3, TM4SF20, TMEM240, TMTC3, TNC, TOR1A, TOR1AIP1, TPP1, TRIM2, TRIP4, TRPA1, TRPC3, TSPAN7, TSPEAR, TTBK2, TTLL5, TUBA4A, TUBA8, TUBB, TUBB2A, TUBB2B, TUBB4A, TUBG1, TYROBP, UBA1, UBA5, UNC80, USP27X, USP9X, VANGL2, VMA21, VPS13C, VWA3B, WASHC5, WWOX, XK, XPR1, XYLT2, YME1L1, ZBTB18, ZC4H2, ZDHHC15, ZFYVE27, ZNF711

Hereditary Cancers (148 Genes)

AIP, AKT1, ALK, ANKRD26, APC, ATM, ATR, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CASR, CDC73, CDH1, CDK4, CDKN1B, CDKN1C, CDKN2A, CEBPA, CEP57, CHEK2, CTC1, CTNNA1, CTRC, CYLD, DDB2, DDX41, DICER1, DIS3L2, DKC1, EGFR, EGLN1, ELANE, ENG, EPCAM, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, EXT1, EXT2, EZH2, FAN1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FH, FLCN, GALNT12, GATA2, GPC3, HOXB13, HRAS, IKZF1, KIF1B, KIT, LZTR1, MAX, MBD4, MEN1, MET, MITF, MLH1, MLH3, MRE11, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NF2, NHP2, NOP10, NTHL1, PALB2, PALLD, PAX5, PDGFRA, PHOX2B, PIK3CA, PMS2, POLD1, POLE, POLH, POT1, PRKAR1A, PRSS1, PTCH1, PTCH2, PTEN, RAD50, RAD51C, RAD51D, RB1, RECQL4, REST, RET, RHBDF2, RNF43, RUNX1, SAMD9L, SBDS, SDHA, SDHAF2, SDHB, SDHC, SDHD, SLC45A2, SLX4, SMAD4, SMARCA4, SMARCB1, SMARCE1, SPINK1, SRP72, STK11, SUFU, TERC, TERT, TGFBR1, TINF2, TMEM127, TP53, TRIP13, TSC1, TSC2, TYR, VHL, WRAP53, WRN, WT1, XPA, XPC, XRCC2

Organ Health

(934 Genes)

AAGAB, ABCA12, ABCA3, ABCC6, ACE, ACP5, ACTA1, ACTG1, ACTG2, ADAMTSL4, ADCY1, AGT, AGTR1, ALDH18A1, ALOX12B, ALOXE3, AMPD1, AQP2, ARHGAP31, ARX, ASB10, ATP2B2, ATP5F1E, ATP6V0A2, ATPAF2, AVPR2, BAG3, BCOR, BCS1L, BIN1, BMP4, BMPR1B, BTD, CAV3, CCDC50, CDC14A, CDH23, CEP290, CERS3, CFAP410, CFHR5, CFL2, CFTR, CHRDL1, CIB2, CISD2, CLCN1, CLCN5, CLCN7, CLDN14, CLMP, CLPP, CLRN1, COCH, COL11A1, COL11A2, COL2A1, COL4A3, COL4A4, COL4A5, COL8A2, COL9A1, COL9A2, COL9A3, COMP, CPAMD8, CRTAP, CRYAB, CSF2RA, CTSC, CUL3, CYP1B1, CYP4F22, DCDC2, DCX, DES, DGUOK, DIABLO, DIAPH1, DLAT, DLD, DLL3, DMP1, DNM2, DOCK6, DZIP1L, ECE1, ECEL1, EDN3, EDNRA, EDNRB, EFEMP2, ELP4, ENPP1, EOGT, ESPN, ESRRB, EXT2, EYA1, EYA4, FBLN5, FBN1, FBXL4, FGF23, FGFR1, FGFR2, FGFR3, FKBP10, FLNA, FLNB, FLNC, FN1, FOXC1, FOXE3, FOXI1, GAA, GAB1, GANAB, GDF3, GDF5, GDF6, GDNF, GIPC3, GJB2, GJB3, GJB6, GLIS2, GPSM2, GPX4, GRHL2, GRXCR1, GSDME, GUCY2C, GYG1, HARS1, HGF, HMOX1, HOXD13, IFITM5, IHH, ILDR1, INVS, IQCB1, IRF6, 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SDHA, SERPINB6, SERPINF1, SERPINH1, SFTPA2, SFTPB, SFTPC, SIX1, SIX5, SIX6, SLC17A8, SLC26A2, SLC26A4, SLC26A5, SLC34A1, SLC4A11, SLC9A3R1, SNAI2, SOS1, SOST, SOX10, SOX17, SOX2, SP7, SQSTM1, STRC, SUCLA2, SUCLG1, SUMO1, SURF1, TBX6, TCHH, TCOF1, TECTA, TERT, TGM1, TGM3, TIMM8A, TMC1, TMEM67, TMEM70, TMIE, TMPRSS3, TNNI2, TNNT1, TNNT3, TNXB, TP63, TPM2, TPM3, TPRN, TRAF3IP1, TRIM44, TRIOBP, TRIP11, TRPV4, TUBA1A, TWNK, USH1C, USH1G, VSX2, WDR19, WDR36, WFS1, WHRN, WNK1, WNK4, WT1, XYLT1, XYLT2, ZEB1, ZFPM2, ABCG8, ACTL9, ACTN2, AGBL1, AIFM1, AK7, ALPK1, AMTN, AR, ARMC2, ARR3, ASCC1, ASIP, ASPN, ASPRV1, ASTL, B2M, BPY2, BRDT, BTG4, C14orf39, C2CD6, C9, CALCR, CANT1, CASP14, CATIP, CATSPER2, CCDC134, CCDC62, CD55, CDY1, CDY2A, CEP112, CFAP251, CFAP43, CFAP44, CFAP47, CFAP58, CFAP65, CFAP69, CFAP70, CFAP91, CFI, CIBAR1, CILP, CLDN10, COG4, COL1A1, COL1A2, CPSF1, CREB3L1, CRYBA4, CTHRC1, CTRC, CTSB, CYP3A4, DACH1, DAZ1, DAZ2, DAZ3, DDRGK1, DDX3Y, DGKE, DLX5, DNAH1, DNAH10, DNAH17, DNAH2, DNAH8, DNAJB11, DNHD1, DNMBP, DSTYK, DZIP1, EPS8L3, ERBB3, ERCC1, ERCC6, EXOC6B, EXTL3, FANCM, FARSA, FARSB, FBXO43, FCGR2A, FGA, FHL1, FLG2, FREM2, FSIP2, FXR1, FZD2, FZD6, GATD3, GCNA, GFRA1, GGN, GJA1, GJB4, GLI1, GP1BA, GPR68, GREB1L, HACD1, HERC2, HES7, HESX1, HLA-A, HLA-B, HRURF, HSFY1, IFT172, IFT74, IKBKG, INSL3, IQCE, IRF4, ITGA6, ITGB4, KDELR2, KDM5D, KIAA0825, KITLG, KRT1, KRT10, KRT83, LBR, LFNG, LGR4, LMX1B, LOXL1, LOXL3, LRRK1, LSS, LTBP1, LTBP3, M1AP, MAMLD1, MAP2K1, MAP3K20, MATN3, MBTPS1, MBTPS2, MC1R, MEFV, MEIOB, MESD, MESP2, MET, METTL13, MIR140, MMP13, MOV10L1, MSH4, MSH5, MSMO1, MSR1, MT-CO1, MT-CO3, MT-CYB, MT-ND2, MT-ND4L, MT-RNR1, MT-TS1, MYH11, MYL1, MYL11, MYL2, MYMK, MYOD1, NEPRO, NHS, NRIP1, NRTN, OTX2, Oca.02, PANK4, PANX1, PAPPA2, PATL2, PAX2, PAX7, PDHA2, PDLIM4, PERCC1, PERP, PIK3CA, PLEC, PLEKHM1, PLVAP, PMFBP1, PMVK, PNLDC1, POLE, PORCN, POU3F4, PPP2R3C, PRDX3, PRICKLE3, PRKG2, PRPS1, PRSS2, PRY, PRY2, QRICH2, RAX, RBMY1A1, REC114, RELT, RNF212, 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CRYGS, CSF2RB, CSTA, DCN, DDR2, DLL4, DLX3, DLX4, DNMT3A, DPY19L2, DSC3, DSG1, DSG4, DSPP, DST, DYM, EDA, EIF4A3, ELN, ENAM, EPCAM, EPHA2, ESCO2, EXPH5, FAM111A, FAM111B, FAM20A, FAM83H, FAN1, FBLN1, FDPS, FERMT1, FGF10, FGF16, FGF20, FLCN, FLG, FREM1, FTL, FYCO1, GCNT2, GGCX, GJA3, GJA8, GLB1, GLI3, GORAB, GPC6, GREM2, GSC, HPGD, HR, HSF4, HTR1A, IGSF3, INF2, INPPL1, IRAK4, ITGA3, ITGA8, ITGB6, KANK2, KERA, KIF22, KIF7, KLHL10, KLHL24, KLK4, KLLN, KRT16, KRT17, KRT2, KRT25, KRT6B, KRT6C, KRT71, KRT74, KRT81, KRT86, KRT9, KY, LEMD2, LIM2, LIPH, LMBR1, LMNA, LORICRIN, LPAR6, LRP1, LRP6, LRPAP1, LYZ, MAF, MAP3K7, MAPKBP1, MAPRE2, MARS1, MFRP, MIP, MMP19, MMP20, MMP9, MSTN, MSX2, MUC1, MVD, MYO1E, MYO5B, MYPN, NANOS1, NANS, NBAS, NCSTN, NEK9, NKX3-2, NLRP1, NOG, NOTCH1, NPR2, ODAPH, ORAI1, P3H2, P4HA2, PAX9, PCYT1A, PDE10A, PDGFRB, PIKFYVE, PITX1, PLCD1, PLCZ1, POLR1A, POMP, POP1, PRIMPOL, PRKAR1A, PRSS1, PRSS56, PSEN1, PSENEN, PTH1R, PTHLH, PTPN11, PUS3, PYROXD1, RAB33B, RBP4, RIN2, RPL21, RSPO4, RSPRY1, SALL2, SALL4, SCO2, SEC23B, SEC61A1, SEPTIN12, SERPINB7, SERPINB8, SF3B4, SHH, SIPA1L3, SLC17A9, SLC26A8, SLC39A5, SLC4A1, SLC9A3, SLURP1, SMOC2, SNRPE, SNX10, SPARC, SPATA16, SPATA5, SPINK1, SPINT2, ST14, STIM1, SUN5, SYCE1, SYCP3, TACSTD2, TAF4B, TAPT1, TBX15, TBX18, TBX22, TBXAS1, TDRD7, TENM3, TERC, TEX11, TGDS, TGFBI, TMEM38B, TMEM98, TMPRSS15, TRPC6, TRPV3, TSHZ1, TTC21B, TUBB, TUBB8, TWIST1, UBB, UBIAD1, UMOD, USP9Y, VIM, VSX1, WDR72, WNT10B, WNT3, WNT4, XPNPEP3, ZIC1, ZMYND15, ZNF141, ZNF423, ZNF644, ZNF687, ZNF750, ZP1, ZSWIM6

Syndromic Diseases

(723 Genes)

ACTB, ACTG1, ACTG2, ACTN4, ADAMTS10, ADAMTS2, ADGRG1, AHI1, AKT1, APOC2, ARFGEF2, ARL13B, ARL6, B3GALT6, B4GALT7, B9D1, B9D2, BBS10, BBS12, BBS2, BBS5, BBS7, BBS9, BCOR, BSND, C1R, C1S, CC2D2A, CCDC103, CCDC28B, CCDC39, CCDC40, CCDC65, CCDC8, CCNO, CDH23, CENPF, CEP290, CFAP298, CFAP300, CHAT, CHRNA1, CHRNE, CISD2, CLCNKA, CLCNKB, CLRN1, COLQ, COX7B, CST6, CUL7, DNAAF1, DNAAF11, DNAAF2, DNAAF3, DNAAF4, DNAAF6, DNAH1, DNAH11, DNAH5, DNAI1, DNAI2, DNAJB13, DNAL1, DOK7, DRC1, DYNC2H1, EDA, EDAR, EDARADD, EDN3, EDNRB, EFL1, ELF4, EPS8L3, ERF, EYA1, FBN1, FGD1, FGF9, FGFR1, FGFR2, FGFR3, FKBP14, FLNA, GAS8, GDF5, GDF6, GFPT1, GNS, GPC3, GPC4, GPIHBP1, GRHL3, H19-ICR, HARS1, HCCS, HGSNAT, HMGA2, HRURF, HYDIN, IFNG, IFT122, IFT43, IGF2, INF2, INPP5E, IRF6, KCNJ1, KIF7, KRT16, KRT17, KRT6A, KRT6B, L1CAM, LAGE3, LMNA, LPL, LTBP2, MAGED2, MITF, MKS1, MMP14, MMP2, MSX2, MVK, MYO7A, NAA10, NAGLU, NDUFB11, NEK1, NIPBL, NME8, NOG, NPHP1, NPHP3, NPHS1, NPHS2, OBSL1, ODAD1, ODAD2, ODAD3, ODAD4, OFD1, OSGEP, PCDH15, PGAP2, PGAP3, PI4KA, PIGO, PIGV, PIGW, PIGY, PLAG1, PLK4, PLOD1, POLR1C, POLR1D, POR, PRDM5, RIPK4, ROR2, RPGRIP1L, RSPH1, RSPH3, RSPH4A, RSPH9, SCN4A, SF3B2, SGSH, SIX1, SLC12A1, SLC39A13, SMC1A, SMC3, SNAI2, SOX10, SPAG1, TBX5, TCF12, TCOF1, TCTN1, TCTN2, TMEM216, TMEM67, TNFAIP3, TP53RK, TPRKB, TRIM32, TRPC6, TSC1, TSC2, TTC8, TUBGCP4, TUBGCP6, TWIST1, UGT1A1, USH1C, USH1G, WDPCP, WDR19, WDR35, WDR73, WFS1, WT1, ZMYND10, ZNF469, AARS1, ABCA5, AEBP1, AFF3, AHSG, APC, ARF1, ARL3, ARMC9, ARSG, AVIL, BBS4, BCL11B, BICRA, BLTP1, BMP2, BMPR1B, BRD4, C1GALT1C1, CAPN15, CDH1, CDH11, CDKL5, CELA2A, CEP120, CEP41, CEP55, CHUK, CLCN4, CLIC2, CNKSR2, COL1A1, COL1A2, COL4A3, COL4A4, CPLANE1, CPLX1, CTBP1, CTNND1, CWC27, DACT1, DNAAF5, DNAH9, DNAJC21, DNASE2, DPF2, DVL1, DYNC2LI1, EIF2S3, ESCO2, EXOSC2, FAM149B1, FAM50A, FANCB, FAR1, FBXO11, FGFRL1, FLCN, FOXI1, FOXJ1, FRA16E, FREM2, GAS2L2, GATM, GLE1, GLRA2, GNAS, GON7, GTPBP2, GZF1, H1-4, HDAC8, HDC, HEPHL1, HS6ST2, HTT, HUWE1, 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APOE, AR, ARHGDIA, ARID1A, ARL6IP1, ARMC5, ARX, ASCL1, ASNS, ASXL1, ATP13A2, ATP6AP2, ATP6V1B2, ATP8A2, ATR, ATRX, AUTS2, AXIN1, B4GALNT1, BBIP1, BGN, BMP4, BRPF1, BSCL2, C19orf12, C2CD3, CA8, CAPN1, CASK, CAST, CCDC88A, CCT5, CD96, CDC45, CDC6, CDH3, CDT1, CENPJ, CEP104, CEP63, CFAP418, CHRM3, CHRNG, CIB2, CNTNAP2, COG5, COL10A1, COL11A1, COL2A1, COL4A5, CTCF, CTNNB1, CTSC, CUL4B, CYP26B1, CYP26C1, DCTN1, DDHD2, DDX59, DEAF1, DGKE, DHODH, DIAPH1, DIS3L2, DLX3, DNA2, DPH1, DSG1, DSP, DSTYK, DVL3, DYM, DYNC2I1, DYNC2I2, DYNLT2B, DYRK1A, DYRK1B, EDNRA, EFNB1, EHHADH, ELOVL4, EML1, EMP2, ENTPD1, ERCC6, ERLIN2, ERMARD, EVC, EVC2, FAM111A, FGF10, FIG4, FKBP10, FMR1, FOXE1, FOXP1, FREM1, GABRB3, GATA3, GATAD2B, GBA2, GDNF, GJA1, GJB2, GJB6, GJC2, GMNN, GMPPA, GPT2, GRHL2, GRIA3, GRIN2B, GTF2E2, GUF1, H19, HACE1, HDAC6, HMGB3, HMX1, HNRNPH2, HOXA1, HOXA13, HOXB1, HOXC13, HPGD, HSD11B2, HSPA9, IARS1, IBA57, IFIH1, IFT140, IFT27, IFT52, IFT80, IGBP1, IGF1, IGF1R, IGFALS, IL11RA, INSR, KAT6B, KATNIP, KCTD1, KDF1, KDM5C, KIAA0586, KIDINS220, KIF14, KIF1C, KIFBP, KLC2, KREMEN1, KRT14, KRT74, KRT85, LAMA3, LAMB2, LARP7, LAS1L, LEMD3, LMF1, LONP1, LZTFL1, MAB21L2, MAF, MAG, MBTPS2, MECP2, MED12, MEGF8, MIR17HG, MIR184, MIR204, MPLKIP, MPZ, MSX1, MYH8, MYH9, NECTIN1, NECTIN4, NEDD4L, NEXMIF, NFIX, NIN, NLRC4, NONO, NPR2, NR2F1, NSDHL, NSMCE2, NT5C2, NUP205, NUP93, OPHN1, ORC4, ORC6, OTX2, P4HB, PACS1, PAX2, PAX3, PCDH19, PDE3A, PDE6D, PHF8, PITX2, PKP1, PLCB1, PLCG2, PLOD2, PMP22, PNPLA6, POC1A, POGZ, PPP2R1A, PPP2R5D, PRPS1, PSAP, PTDSS1, PTPRO, QARS1, RARB, RBBP8, RBMX, RDH11, RHBDF2, RIGI, RNF113A, RNF135, ROGDI, RTTN, RUNX2, SALL4, SAMD9, SATB2, SCN9A, SCNN1G, SEC24D, SETBP1, SETD2, SGO1, SH3PXD2B, SHROOM4, SIN3A, SIX5, SLC2A2, SLC34A1, SLC4A11, SLC6A3, SLITRK1, SLITRK6, SMARCA2, SMARCA4, SMARCAD1, SMARCB1, SMARCE1, SMCHD1, SNAP29, SNRPB, SOX11, SOX2, SOX3, SPART, SPECC1L, SPG11, SPTAN1, ST3GAL3, STAMBP, SYN1, TAF1, TBX22, TBX3, TCF4, TECPR2, TFG, TGFB1, THOC2, TMCO1, TP63, TRAIP, TRIO, TRPS1, TWIST2, TYR, UBE2A, UBE3A, UBE3B, UPF3B, USP18, USP9X, VAX1, VPS37A, WDR81, WHRN, WNT10A, WNT5A, WNT7A, ZBTB20, ZDHHC9, ZFYVE26, ZIC3, ZMYND11

Other Diseases (925 Genes)

ABCC9, ACE, ACTC1, ACTN2, AIP, ALX4, ANKRD1, ARHGAP26, ARMC5, ASPA, ATP1A2, ATRX, AVP, BAG3, BCL10, BLM, BMP2, BRAF, BRCA2, CACNA1A, CASP10, CAV3, CBL, CBX2, CDH1, CDH11, CEP250, CEP78, CFTR, CHRNA4, CLCN1, CLIC2, CNGA3, CNGB3, COL6A2, COL6A3, CR2, CREBBP, CRYAB, CSRP3, CTNNB1, CYP2A6, DCHS1, DES, DGUOK, DHH, DSC2, DSG2, DSP, EDN1, EDNRA, ELP1, EP300, EPO, ERBB2, ERBB3, ESR1, EWSR1, EYA4, FANCC, FAT4, FCGR2A, FKTN, GABBR2, GATA1, GBA1, GCH1, GIMAP5, GLB1, GNAI3, GNAS, GNAT2, GPC3, GPC4, H19, H19-ICR, H3-3A, H3-3B, H4C11, H4C3, HCN4, HEXA, HFE, HRAS, HSPG2, IDH1, IER3IP1, IFNL3, IGF2, IL1RN, IL6, IL6ST, IRF5, JPH2, JUP, KCNK18, KCNN4, KIF15, KRAS, KRT74, LAMA4, LBX1, LDB3, LIFR, LMNA, LPAR6, LZTR1, MAP2K1, MAP3K1, MCOLN1, MLH3, MSH3, MSH6, MSX2, MYBPC3, MYH6, MYH7, MYL2, MYL3, MYLK2, MYO1H, MYOZ2, NEXN, NF1, NR0B1, NR5A1, NRAS, PDCD1, PHOX2B, PI4KA, PIEZO1, PIGA, PIGN, PIGQ, PIGT, PKP2, PLCB4, PLN, PON1, POU6F2, PRF1, PRKAG2, PRKAR1A, PRLR, PSEN1, PSEN2, PTCH2, PTPN11, PTRH2, RAB39B, RAD54B, RAD54L, RAF1, RBM20, RIT1, RMRP, RYR2, SCN1A, SCN5A, SCUBE3, SDHA, SGCD, SHOC2, SLC6A3, SMPD1, SOD2, SOS1, SPECC1L, SPR, SPRED1, SRY, STAT3, STAT4, SUFU, TAFAZZIN, TCAP, TGFB1, TGFB3, TH, TLR5, TMEM43, TMPO, TNF, TNNC1, TNNI3, TNNT2, TP53, TPM1, TTC7A, TTN, USP8, VCL, VEGFA, WT1, YARS1, YIPF5, A2ML1, AARS1, ABCA2, ABCC11, ABCC8, ABCG2, ABL1, ACBD5, ACKR1, ACKR3, ACTL6B, ACTN3, ADCY3, ADCY5, ADRB1, ADRB2, AGO2, AGTPBP1, AGXT2, AKT1, AKT2, ALOX5, ANGPTL4, ANKRD17, ANXA5, AP1B1, AP1G1, AP1S3, APC, APOA1, APOL1, ARL2, ASPN, ASXL1, ATAD3A, ATN1, ATP5MC3, AURKA, AXIN1, AXIN2, B4GALNT2, BAP1, BAX, BCAS3, BCORL1, BCR, BHLHE41, BICC1, BNC2, BTNL2, BUB1, BUB1B, C5, CACNA1S, CACNA2D2, CALR, CARS1, CASP8, CATSPER2, CBFB, CCDC32, CCDC47, CCL11, CCL2, CCND1, CCNK, CD209, CD244, CD36, CDH2, CDK10, CDK8, CEBPA, CENPT, CFAP410, CFHR3, CHD1, CHD3, CHD8, CHEK2, CHI3L1, CHIC2, CHRNA3, CHRNA5, CHST11, CIB1, CIITA, CISH, CLCN6, CLDN2, CLEC1A, CLEC7A, CNOT1, CNOT2, CNOT3, CNTNAP2, COL18A1, COL2A1, COL4A1, COL4A2, COL4A3, COL4A4, COL6A1, COLEC10, COPB1, COPB2, COQ2, CPE, CR1, CRY1, CSF1R, CSGALNACT1, CTBP1, CTLA4, CTU2, CUBN, CUX1, CX3CR1, CXCR2, DAAM2, DBR1, DCC, DDB1, DDR2, DDX6, DHX16, DICER1, DLC1, DNAAF4, DNASE1, DNMT3A, DONSON, DSG3, EDAR, EDN3, EDNRB, EED, EGLN1, EIF2AK1, EIF2AK2, EIF4E, EIF5A, ELN, ELOVL1, EN1, ENPP1, ERCC6, ERGIC1, ESPN, ETV6, EXOSC5, F13A1, F2, F5, F7, FAAH, FASLG, FBXL3, FBXW11, FCGR2B, FFAR4, FGFR2, FGFR3, FITM2, FLCN, FLT3, FLT4, FOXD3, FOXE3, FRZB, FSHR, FTO, FUT2, FUT3, G6PD, GARS1, GATA2, GCGR, GCK, GCKR, GCLC, GCLM, GDF11, GDNF, GGPS1, GJA5, GJA8, GLCCI1, GLS, GNB1, GPD2, GPR101, GSTZ1, GSX2, GYPA, GYPB, GYPC, H4C5, H4C9, HBB, HCN2, HDAC4, HLA-B, HLA-C, HLA-DQA1, HLA-DQB1, HLA-DRB1, HLA-G, HMGA1, HNF1A, HNF1B, HNF4A, HNMT, HS2ST1, HTR2A, HYOU1, ICAM1, IFNAR2, IFNG, IFNGR1, IGF2BP2, IGF2R, IL10, IL10RB, IL13, IL18BP, IL1B, IL23R, IL6R, IL7, IPO8, IQSEC1, IRAK3, IREB2, IRF1, IRGM, IRS1, IRS2, ITGB3, ITPA, ITPR3, JAG1, JAK1, JAK2, KARS1, KAT8, KCNA4, KCNJ11, KCNJ16, KCNJ18, KCNK4, KCNMA1, KCNN3, KDM3B, KIDINS220, KIF3B, KIF5A, KIT, KLF6, KLHDC8B, KMT2C, KMT2E, KRT75, LACC1, LEMD2, LGALS2, LGI4, LGR4, LIG4, LIMA1, LIPC, LMBRD2, LMNB2, LPA, LPP, LRP5, LRP8, LRRC32, LTA, MAB21L1, MADD, MAP3K8, MAPK8IP1, MAPKAPK5, MARK3, MAST1, MATN3, MC1R, MC3R, MC4R, MCC, MCM3AP, MDM2, MECP2, MED12, MED12L, MEIS2, MET, MIAT, MIEF2, MLLT10, MLXIPL, MMP3, MN1, MORC2, MPIG6B, MPL, MRAP2, MRPS25, MTHFD1, MTNR1B, MTX2, MUC7, MUTYH, MYF5, MYMX, MYO9B, MYOCD, MYRF, NCAPG2, NCR3, NDUFB10, NEB, NEK1, NEMF, NEUROD1, NFE2L2, NFIA, NFIB, NFKBIL1, NHLRC2, NLGN1, NLGN3, NLGN4X, NLRP1, NLRP3, NOS2, NPC1L1, NPM1, NPR3, NPSR1, NR2F2, NR4A2, NRROS, NSD2, NUDT2, NUMA1, NUP188, NUP214, NUTM2B-AS1, OAS1, OGG1, OLR1, OPA1, OPN1MW, OPTN, OR2J3, OTUD5, P4HTM, PAICS, PAK1, PAX4, PBRM1, PBX1, PCDH12, PCGF2, PCSK1, PDE2A, PDE6C, PDE6H, PDGFRA, PDGFRL, PDX1, PHF21A, PICALM, PIGF, PIGG, PIGU, PIK3CA, PKDCC, PLA2G2A, PLA2G7, PLCB3, PLD1, POLR3GL, POU3F3, POU4F1, PPARG, 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TRIM8, TRPV4, TRRAP, TTC26, TUBB6, TUBGCP2, TULP3, UBA2, UBR7, UCHL1, UCP2, UGT1A1, UGT2B17, UNC45A, VHL, WBP11, WDR37, WDR4, WFS1, WIPI2, WLS, WWC1, XPNPEP2, YIF1B, ZBTB7A, ZFAT, ZFHX2, ZIC1, ZMYM2, ZNF365, ZNF407, ZNF462, ZNF699, ZPR1, A4GALT, ACACA, ACAT2, ADCY6, ADGRG6, ADGRV1, ADIPOQ, ARCN1, ARNT2, ASXL2, ASXL3, ATP6V1B2, BCL11A, BHLHA9, C12orf57, CAPN5, CAV1, CD207, CD2AP, CD4, CDCA7, CDK13, CHD4, CHUK, CNNM4, CNTNAP1, COLEC11, CPN1, CRB2, CYP2B6, DDX11, DIP2B, EBF3, ECE1, EGFR, EHMT1, EIF4G1, ELANE, EMG1, ERF, EYA1, FBN1, FGF23, FGF5, FIBP, FLVCR2, FN1, FREM1, FUT1, FUT6, GALNT3, GDF5, GFI1, GHR, GIGYF2, GLDN, GLE1, GNB5, GPR88, HAGH, HELLS, HERC1, HOXA2, HOXD10, HP, HPSE2, HTRA2, HYLS1, INPP5E, INSR, IRF6, IRX5, ITCH, JAM3, KCNK9, KDM1A, KIF7, KL, KLF1, KLK1, KMT2A, KPTN, L1CAM, LHCGR, LRIG2, MASP1, MED25, MIR2861, MITF, MKKS, MYBPC1, NALCN, NAT8L, NEK8, NEK9, NFIX, NHS, NKX2-1, NOD2, NPHP3, NPR2, NRXN1, NSMCE3, NTRK2, OCLN, PADI6, PANK2, PAX1, PAX3, PDGFRB, PGR, PHYKPL, 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