HKG *epi* THERAPEUTICS Ltd.
Harnessing the epigenome

Harnessing the Epigenome

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Your MetaGen Mutations Panel Report

Your Barcode:

Date:

Testing Laboratory:
HKG epiTherapeutics Limited

Your Results

Gene	SNP	Reference	Alternate	Your Genotype
AHCY	rs121918607	C	T	
AHCY	rs121918608	T	C	
COMT	rs4680	G	A	
MTHFR	rs1801133	G	A	
MTHFR	rs1801131	T	G	
MTR	rs1805087	A	G	
MTRR	rs1801394	A	G	
MTRR	rs1532268	C	T	

SNP (Single Nucleotide Polymorphism):

Refers to a common variation in a single nucleotide that occurs at a specific position in the genome, distinguishing one genome from another.

Reference Allele:

This is the common allele (version of a gene) found in the general population.

Alternate Allele:

This represents a different version of the gene that varies from the common type.

Your Genotype:

Indicates your specific alleles for each gene. '+/+' denotes both alleles are altered, '+/-' indicates one altered allele, and '-/-' means no mutations are found in either allele. This column reflects your unique genetic makeup as revealed by the tested SNPs.

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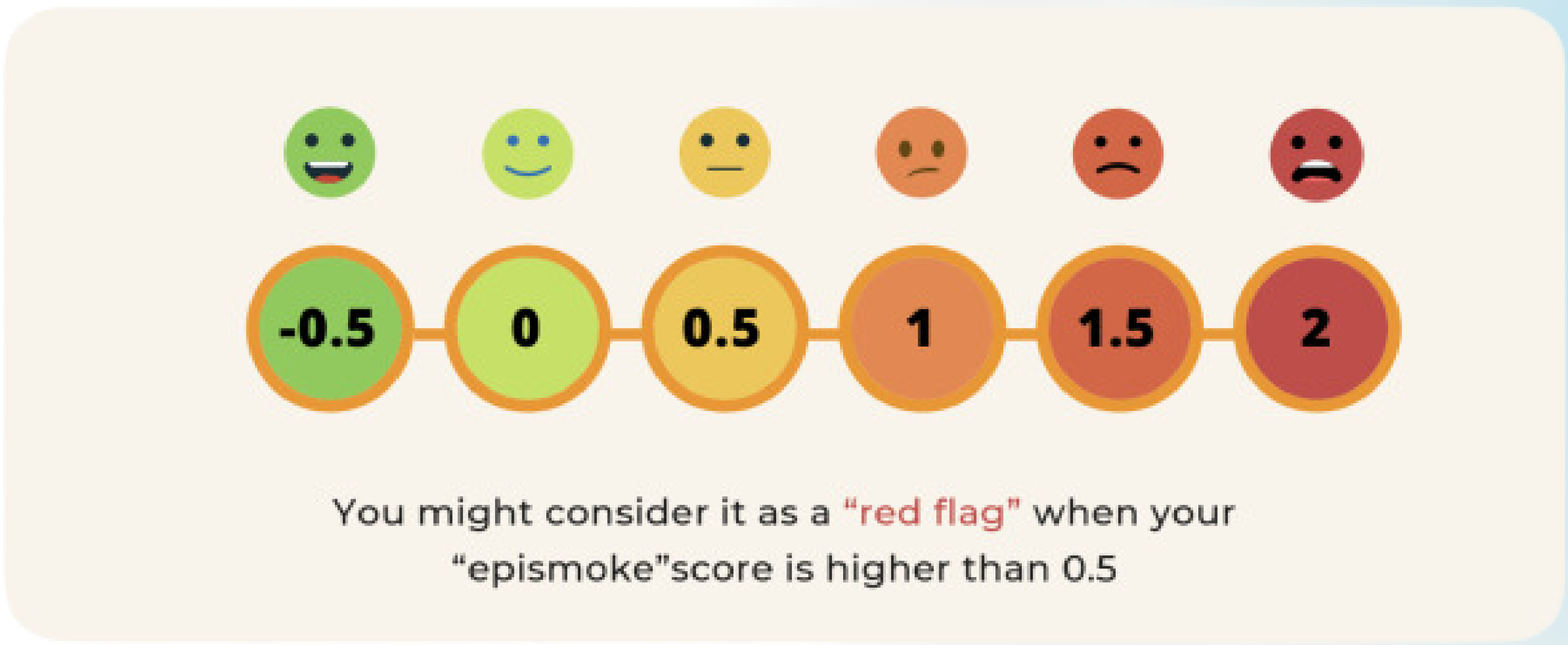
Your Results

epiAge Result	*Technical Accuracy %

*Technical accuracy refers to the reliability of test results, determined by the consistency of multiple independent tests of the same sample. A high technical accuracy percentage, close to 100%, indicates reliable results. It's calculated by dividing the standard deviation by the epiAge, considering varying significance across different age groups.

epiSmoke Score



Bioinformatics Analysis: Performed using Metagen V1.0

METAGEN

1 Introduction

Understanding DNA Methylation, SNPs, and Your Health

Welcome to the fascinating world of DNA methylation and Single Nucleotide Polymorphisms (SNPs), crucial components of our body's genetic regulation. Imagine DNA as a sophisticated computer in each cell, with DNA methylation acting like versatile software. This process adds chemical marks to our DNA, influencing whether a gene is active or silenced, ensuring the correct functioning of our body.

DNA methylation is vital as it enables the same gene to have different roles in various cells. In essence, it is like a binary code, programming our DNA to ensure our body functions correctly. Each cell type has a unique combination of active and silent genes, orchestrated by DNA methylation. This orchestration is crucial for our health and well-being, allowing cells to perform their specific functions while maintaining the overall harmony of our body's systems.

Beyond its role in cellular function, DNA methylation is tightly associated with our biological age, which is suggested by several studies to be a more accurate measure of health than chronological age. Certain alterations in DNA methylation patterns can lead to disease development, as research has shown that these changes can transform healthy tissues into diseased ones, impacting conditions like cancer. Furthermore, environmental factors, including diet and maternal care, can influence DNA methylation, highlighting its dynamic nature and the interplay between genetics and lifestyle.

Our report delves into what is known in the literature about the intricate relationship between DNA methylation, genetic mutations, and health, providing insights that are crucial for understanding your personal health journey. By exploring these genetic and epigenetic interactions, we offer a comprehensive view of how your unique genetic makeup and lifestyle choices impact your overall health and aging process.

In tandem with the intricate processes of DNA methylation, Single Nucleotide Polymorphisms, or SNPs (pronounced 'snips'), represent another crucial aspect of our genetic landscape. SNPs are the most common type of genetic variation among people, occurring at specific positions within the DNA sequence. These small yet significant variations contribute to the unique traits that make each individual distinct, such as variations in eye color. But their impact extends beyond physical attributes. SNPs can significantly influence our health, including our susceptibility to certain diseases and how we respond to various medications.

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2 Introduction

Understanding Your Unique Genetic Makeup: The Role of SNPs

What are SNPs?

Think of your DNA as a long string of letters, each representing a building block of your genetic code. Sometimes, these letters can differ slightly between individuals. These tiny differences are what we refer to as Single Nucleotide Polymorphisms.

A Common Type of Genetic Variation

SNPs are the most frequent type of genetic variation in the human genome. To visualize this, imagine you and a friend have nearly identical recipes for a cake, but in one recipe, a single ingredient is slightly different. This minor difference can change the cake's flavor, just as SNPs create small variations in our genetic 'recipes.'

Why are SNPs Important?

- **Unique Traits:** SNPs are a key factor in determining our individual traits, such as eye color or hair texture.
- **Health Connections:** Certain SNPs can influence how our bodies react to medications or increase our risk of developing specific health conditions.
- **Ancestral Insights:** These genetic variations are also tools for scientists to trace human history and understand population migrations.

SNPs in Our Health Report

- **Focus on Health-Related Genes:** In this report, we specifically analyze SNPs in genes crucial for your body's methylation processes—chemical reactions vital for many bodily functions.
- **Personal Health Insights:** By examining these SNPs, we offer insights into your health risks, potential for certain conditions, and how your body might react to changes in diet or lifestyle.
- **A Personalized Guide to Your Health:** Understanding your SNPs is akin to having a personalized guide to your body. This knowledge, combined with what we learn from studying your DNA methylation, empowers you with detailed information for managing your health and wellness more effectively.

Together, the study of DNA methylation and SNPs provides a comprehensive picture of how our genetic and epigenetic makeup interacts with our environment, lifestyle, and health. This report aims to bring these insights to you in a clear and actionable way, helping to guide your personal health decisions.

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3 Introduction

The MetaGen Mutations Panel: A Comprehensive Genetic Analysis

Following our exploration of DNA methylation and SNPs, we now introduce the MetaGen Mutations Panel. This report presents a comprehensive analysis of your genetic methylation test results, focusing on key mutations in the AHCY, COMT, MTHFR, MTR, and MTRR genes. Paired with this detailed genetic analysis is the innovative epiAge assessment, which offers a dynamic evaluation of your biological age, an important aspect of understanding overall health and wellness.

Insights into Genetic Variations and Biological Age

- **Genetic Variations:** We delve into specific genetic variations that play crucial roles in methylation processes, vital for cellular functions and overall health.
- **epiAge Assessment: epiAge** goes beyond traditional measures, providing a more nuanced view of aging by examining changes in DNA methylation patterns that are associated with aging.

Understanding Gene Functions and Implications

- **Mutation Analysis:** The report reviews the implications of mutations in these genes, drawing from the latest scientific literature.
- **Gene Functions:** We discuss the primary functions of each gene, shedding light on how they contribute to your body's methylation processes and overall health.

Recommendations and Consultations

- **Dietary Modifications:** Based on the literature, we provide a summary of what the current literature recommendations for dietary modifications that might be beneficial considering your genetic profile.
- **Consulting Healthcare Professionals:** While we offer insights and suggestions based on published literature, for personalized medical advice, it is essential to consult your physician or dietician. This report is intended to provide some background, not replace, professional medical consultation.

An Integrated Approach for Holistic Understanding

Our integrated approach in the MetaGen Mutations Panel report aims to provide some information on your genetic predispositions and what is currently known about their possible influence on your health and aging process. By combining genetic analysis with epigenetic assessment, we offer a view of factors that might be contributing to your well-being.

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4 Introduction

HKG epiTherapeutics
Pioneering Advances in Genetic Testing

HKG epiTherapeutics: Accredited Excellence

HKG epiTherapeutics, established in 2016, is renowned for its cutting-edge approach to healthcare, particularly in epigenetic research and testing. Our laboratory, situated within the prestigious HKG Science Park, has earned accreditations from the United States' College of American Pathologists (CAP) and the Clinical Laboratory Improvement Amendments (CLIA), signifying our commitment to the highest standards in laboratory testing and research integrity.

Professor Moshe Szyf: Visionary Founder

The founding of HKG epiTherapeutics was inspired and led by Professor Moshe Szyf, a luminary in the field of epigenetics from McGill University's Department of Pharmacology and Therapeutics. Professor Szyf's pioneering work includes:

- Being an inventor of the first broad patents in the field of epigenetics and the first patents linking DNA methylation and cancer.
- Founding the field of behavioral and psychiatry epigenetics.
- Publishing over 320 papers, significantly contributing to the advancement of epigenetics.
- Serving as a Fellow of the Royal Society of Canada and the Canadian Academy of Health Sciences.

Professor Szyf's illustrious career extends beyond research and innovation. He has authored more than 320 peer-reviewed articles, solidifying his role as a key figure in epigenetics. He founded and served as the inaugural chief editor of a leading journal in the field, is an associate editor for Clinical Epigenetics, and holds a position on the Editorial Board of Environmental Epigenetics. His contributions have been instrumental in shaping the understanding and application of epigenetic science in medicine.

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5 Introduction

HKG epiTherapeutics: Bringing Innovation to the world

HKG epiTherapeutics specialize in providing advanced genetic and epigenetic testing, ensuring that our customers benefit from the latest developments in epigenetics and genetic research.

Our Collective Mission and Expansion

HKG epiTherapeutics are dedicated to harnessing the power of epigenetics combined with state-of-the-art sequencing technologies. We are committed to early disease detection and prevention, with our expertise spanning across various aspects of personalized medicine. Our expansion plans aim to replicate the success of our Hong Kong laboratory in North America and beyond.

Conclusion

Customers of HKG epiTherapeutics can rest assured that they are receiving services backed by pioneering research, accredited facilities, and a team of experts led by one of the foremost authorities in epigenetics, Professor Moshe Szyf. Our mission is to bring innovative health solutions to the forefront of medical science, improving healthcare outcomes worldwide.

Mutation Analysis, Gene Functions, and Recommendations

HKG epiTherapeutics Limited

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1

rs121918607 and rs121918608

AHCY Gene Mutations

AHCY, SAM, and SAH in the Methylation Cycle:

AHCY (Adenosylhomocysteinase) is an enzyme that plays a crucial role in breaking down S-adenosylhomocysteine (SAH), a by-product of methylation processes, back into homocysteine. This functions is a key part of methionine metabolism (Baric et al., 2004), helping to maintain the balance of SAM and SAH in the body (Cooper et al., 2006; Motzek et al., 2016). Such balance is essential for the proper functioning of various biochemical processes, including DNA repair, neurotransmitter synthesis, and detoxification (Vizan, Di Croce, & Aranda, 2021).

Mutation Details and Health Implications:

rs121918607 (TRP112TER) Mutation:

Type: SNP where cytosine (C) is replaced by thymine (T).

Frequency: This genetic variation is rare, occurring in about 0.2% of the global population.

Clinical Significance:

This mutation is associated with Hypermethioninemia (Baric et al., 2004), a condition characterized by high methionine levels in the blood, leading to various health issues (Mudd, 2011).

rs121918608 TYR143CYS Mutation:

Type: This is a SNP where thymine (T) is replaced by cytosine (C).

Frequency: The variation is very rare, observed more frequently in European populations but remains uncommon overall.

Clinical Significance:

The mutation is considered pathogenic or likely pathogenic, being associated with conditions such as Hypermethioninemia—a metabolic disorder marked by elevated methionine levels, leading to potential neurological issues—and rhabdomyolysis, a serious condition caused by the breakdown of muscle tissue that can lead to kidney damage. This mutation results in reduced enzyme activity, significantly affecting methionine metabolism.

We suggest that you consult your health provider as to the health style changes that might be required.

rs121918607 and rs121918608

AHCY Gene Mutations

Take Action:

This guidance is what the literature is suggesting for individuals with either of the AHCY gene mutations rs121918607 or rs121918608.

Enhance B Vitamin Intake: Emphasize the importance of B vitamins (B6, B12, and folate) due to their crucial role in the methylation process. This process is vital in managing the impacts of these mutations on methionine metabolism.

B Vitamin Dosage Guidelines:
For Vitamin B12, refer to the NIH guidelines here.
For Vitamin B6, consult the NIH guidelines here.
For Folate, guidelines can be found here.

Beneficial Foods:

Incorporate foods high in B vitamins into your diet, such as leafy greens, eggs, and whole grains. These foods can naturally support your body's methylation processes.

Interpretation:

This dietary enhancement with B vitamins is advised for individuals with the specified AHCY gene mutations. B vitamins are key in supporting methylation processes (Selhub, Bagley, Miller, & Rosenberg, 2000), essential for mitigating disruptions in methionine metabolism associated with these mutations.

Remember, this advice is based on current literature and is tailored to those with these specific genetic mutations. The effectiveness and need for such dietary changes may vary for individuals without these mutations.

Important Note:

Consult with healthcare professionals or a genetic counselor for personalized advice, especially before making significant changes to your diet or starting new supplements. This is crucial in the context of managing health with genetic mutations.

2

Rs4680 (Val158Met)

COMT Gene Mutation

COMT Gene Role

Function: The COMT (Catechol-O-Methyltransferase) gene plays a critical role in the metabolism of catecholamines, including neurotransmitters like dopamine, epinephrine, and norepinephrine (Tunbridge, Bannerman, Sharp, & Harrison, 2004). This metabolic process is essential for maintaining balanced neurotransmitter levels in the brain, impacting various aspects of neurological and mental health.

Mutation Details and Health Implications:

Type: This is a SNP where guanine (G) is replaced by adenine (A).

Frequency: This genetic variation is relatively common, occurring in approximately 36.921% of the global population. The frequency varies by population:

- European: Approximately 50.9%
- African: Approximately 30.4%
- Asian: Approximately 26.5%
- Latin American: Approximately 41.6%

Metabolic Impact:

This variant can lead to differences in dopamine metabolism, which may affect neurological and psychiatric health (Sundermann et al., 2015).

Take Action:

Dietary Recommendations: The literature recommends a diet enriched with omega-3 fatty acids and antioxidants to support neurological health, as highlighted in Artemis P. Simopoulos's study (Simopoulos, 2011). These nutrients are vital for brain function and may help in balancing neurotransmitter activity.

- Sources of Omega-3s: To support brain function, the literature advises to include sources of Omega-3s such as fish, nuts, and seeds in your diet, as they are suggested by the literature to be beneficial for neurological health. For more detailed information on Omega-3 fatty acids and their sources, you can refer to the NIH's resource.
- Sources of Antioxidants: Incorporate berries and dark chocolate for their reported beneficial effects on brain health (Shukitt-Hale, Lau, & Joseph, 2008; Tokede, Gaziano, & Djousse, 2011).

Important Note:

It's important to discuss any health concerns or symptoms, particularly those related to neurological conditions or medication responses, with a healthcare provider.

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3

rs1801133 (C677T) and rs1801131 (A1298C)

MTHFR

MTHFR Gene Role:

The MTHFR gene, short for Methylenetetrahydrofolate Reductase, plays a pivotal role in your body's handling of folate or vitamin B9. This gene is involved in converting folate into a form your body can effectively use, impacting vital functions like DNA creation and cell repair. Understanding how this gene operates can offer insights into your overall health, particularly in how your body utilizes this essential vitamin.

Folate, a critical B-vitamin, is naturally present in a variety of foods. It's vital for DNA synthesis and cell division. According to the literature different life stages have varying recommended amounts of folate, measured in micrograms (mcg) of dietary folate equivalents (DFEs). For instance, adults typically need 400 mcg DFE, while pregnant women require 600 mcg DFE. This literature recommended intake can be met through a balanced diet including foods like liver, green vegetables, nuts, and beans, as well as fortified bread and cereals.

Additionally, folate is available in supplements, commonly as folic acid or methylfolate (5-MTHF). The latter might be more suitable for individuals with certain gene variants like MTHFR C677T, as their bodies can utilize this form more efficiently. However, those who could become pregnant are advised to consume folic acid, not 5-MTHF, even with an MTHFR C677T gene variant, due to its effectiveness in preventing neural tube defects in babies.

For more comprehensive information about folate, its recommended intake, sources, and supplements, you can refer to the U.S. Department of Health & Human Services, National Institutes of Health, Office of Dietary Supplements.

Mutation Details and Health Implications:

Impact on Folate Metabolism: Mutations in the MTHFR gene can lead to reduced efficiency in folate metabolism (Ozarda, Sucu, Hizli, & Aslan, 2009), which might affect various health aspects, particularly those related to cellular growth and repair.

rs1801133 (C677T) and rs1801131 (A1298C)

MTHFR

rs1801133 (C677T) Mutation:

Type: This is a SNP where guanine (G) is replaced by either adenine (A) or cytosine (C).
Frequency: The frequency of the rs1801133 SNP for the G>A variation is common, with global frequencies around 30-35%. However, the frequency of the G>C variation is not well-established and is likely to be significantly lower, indicating it is a much rarer occurrence in the general population.

Clinical Significance:

Associated with methotrexate response and potentially impacts drug metabolism.
Population Frequency: Varied frequency across populations, generally higher in Europeans and lower in African and Asian groups.

Take Action:

For individuals with the MTHFR C677T mutation, the NIH Office of Dietary Supplements recommends:

- **Folate-rich Foods:** Include leafy greens like spinach, fruits like oranges, legumes such as peanuts and beans, and liver in your diet. These foods are naturally high in folate.
- **Fortified Foods:** Consume foods fortified with folic acid, such as enriched bread, cereals, flour, and pasta, to help meet your daily folate needs.
- **Supplement Consideration:** Methylfolate (5-MTHF) supplements might be more effective for those with the mutation, but women of childbearing age should focus on folic acid intake.
- **Professional Consultation:** Always seek advice from healthcare professionals, especially for dietary changes or supplementation related to the MTHFR mutation.

For more information, refer to the NIH Office of Dietary Supplements.

rs1801133 (C677T) and rs1801131 (A1298C)

MTHFR

rs1801131 (A1298C) Mutation:

Type: This is a SNP where thymine (T) is replaced by guanine (G).
Frequency: Relatively common, with minor allele frequencies around 25-29% globally.

Clinical Significance:

It has conflicting interpretations; linked to Homocystinuria (Price, Wilcock, & Weekman, 2018), Neural tube defects (folate-sensitive) (Zhang et al., 2019), and more. While some studies have shown an association between the A1298C polymorphism and NTDs (Abbas, Sifi, Benembarek, & Abadi, 2021; Aranda-Sánchez et al., 2021; Fu, Wang, & Kong, 2017; Isotalo, Wells, & Donnelly, 2000; Put et al., 1998; Yaliwal & Desai, 2012), others have not found a significant link (Das, 2014).

A1298C maybe associated with increased homocysteine level (Kumar et al., 2005). The C677T variant in the *MTHFR* gene is known to affect the enzyme's function, often leading to higher levels of homocysteine and reduced folate levels. However, the implications of the A1298C variant are less clear-cut. This variant tends to have a milder impact on the enzyme's activity. Typically, individuals with the A1298C variant maintain normal levels of homocysteine and plasma folate (Yamada, Chen, Rozen, & Matthews, 2001).

Take Action:

Conflicting results and controversies regarding A1298C mutation significance indicate the need for further research to elucidate its precise role and implications for dietary recommendations (Botto & Yang, 2000; Ghaznavi, Zahra, Shahram, & Soltanpour, 2015; Jiang, Liu, Townsend, & Wang, 2023; Kim et al., 2015; B. J. Wang et al., 2015; Zhu & Li, 2016)

Important Note:

For a comprehensive understanding of how these mutations might affect individual health, it's important to consult healthcare professionals. They can provide tailored advice and recommendations based on one's genetic makeup.

4

rs1805087 (A2756G)

MTR

MTR Gene Role:

Function: The MTR (Methionine Synthase) gene plays a pivotal role in the conversion of homocysteine to methionine, a critical step in the methylation cycle (Ding, Zhou, Jiang, & Lu, 2013). Methionine synthesis is essential for DNA synthesis and the overall functioning of cellular processes (Maddocks, Labuschagne, Adams, & Vousden, 2016).

Mutation Details and Health Implications:

Type: This is a SNP where adenine (A) is replaced by guanine (G).

Frequency: About 21.8% of people worldwide have a specific variation of a gene.

Population-Specific Frequencies:

· European: ~18.8%
· African: ~26.5%
· Asian: ~11.9%
· Latin American: ~19.8%

Clinical Significance according to the literature:

- Homocysteine and Methionine Levels: Individuals with the MTR A2756G mutation may have altered homocysteine and methionine levels, is believed to be risk factor for various health conditions, including cardiovascular diseases (Biselli et al., 2009; Leclerc et al., 1996; Paradkar, Padate, Vora, & Ashavaid, 2019).
- Vitamin B12 Metabolism: The MTR gene's function is also closely linked with vitamin B12 metabolism. Mutations in this gene, including A2756G, can potentially affect the efficiency of vitamin B12 use in the body(Raghubeer & Matsha, 2021).
- Variable Expression: The effects of the MTR A2756G mutation can vary widely among individuals. Diet, lifestyle, and other genetic factors can influence how this mutation manifests in each person (Wen-Xing Li, Dai, Zheng, Liu, & Huang, 2015).
- Folate Usage: Although the exact impact of the A2756G mutation on how the body uses folate isn't fully clear, it's involved in processes that are linked with folate. This means it might have some indirect effects on folate in the body, especially in how it relates to homocysteine, a substance that folate helps process (W. X. Li et al., 2017).

While there are various interpretations, the predominant view suggests a benign nature of this mutation (Y. Wang, 2013).

rs1805087 (A2756G)

MTR

Take Action:

B Vitamin Intake: Given the role of the MTR gene in homocysteine and methionine metabolism, and its connection to vitamin B12, maintaining adequate levels of B vitamins, particularly vitamin B12, may be beneficial. This aligns with general recommendations from the NIH Vitamin B12 Health Professional Fact Sheet, which emphasizes the importance of vitamin B12 for health, including its role in methionine synthesis and homocysteine metabolism.

Dietary Sources: Include foods rich in B12 such as meat, poultry, fish, eggs, and dairy products, along with fortified grains and cereals, in your diet.

Monitoring and Consultation: Regular monitoring of homocysteine and methionine levels, along with consultation with healthcare professionals, is advisable for personalized management based on individual health needs and genetic profiles.

For more detailed information, refer to the NIH Vitamin B12 Health Professional Fact Sheet.

Important Note:

It's essential to discuss these insights with healthcare professionals for personalized recommendations, ensuring that your health decisions are well-informed and tailored to your genetic profile.

5

rs1801394 (A66G) and rs1532268 (C524T)

MTRR

MTRR Gene Role:

The MTRR gene, known as Methionine Synthase Reductase, is integral to the metabolic pathway of homocysteine and methionine. It's pivotal in producing S-adenosyl methionine, the primary methyl donor in cellular processes (Greenop et al., 2015), and plays a key role in the folate and vitamin B12-dependent conversion of homocysteine to methionine (Shi et al., 2019). MTRR also has significant functions in embryonic stem cell development and folate metabolism. Crucially, it maintains the active form of vitamin B12, which is essential for DNA synthesis and methylation, underscoring its importance in cellular health and genetic stability.

Mutation Details and Health Implications:

MTRR rs1801394 (A66G)

Type: This SNP involves the change of adenine (A) to guanine (G)
Frequency: Approximately 36.4% of people globally have this genetic variant.
Population-Specific Frequencies:

European: Approximately 54.4%
African: Around 28.7%
Asian: About 26.9%

Clinical Significance:

The MTRR A66G polymorphism has been the subject of extensive research due to its potential impact on DNA methylation. This polymorphism in the MTRR gene is believed to influence the efficiency of methionine synthase reductase, an enzyme vital for maintaining adequate levels of methionine and S-adenosylmethionine (SAM), a key methyl donor in DNA methylation processes (X. Y. Li et al., 2015). Variations in the MTRR gene could potentially influence DNA methylation patterns, thereby affecting gene expression and susceptibility to various health conditions (Crescenti et al., 2013).
However, it is important to note that while these studies provide valuable insights into the potential implications of the MTRR A66G polymorphism on DNA methylation and health outcomes, more research is needed to fully understand its broader health effects (X. Y. Li et al., 2015).

rs1801394 (A66G) and rs1532268 (C524T)

MTRR

MTRR rs1532268 (C524T)

Type: This SNP involving the change of cytosine (C) to thymine (T).
Frequency: Relatively common, approximately 27% of people globally have this genetic variant.

Clinical Significance:

Classification: Most often classified as Benign.

Take Action:

Dietary Recommendations: A diet rich in vitamin B12 and folate is advisable by the literature. These nutrients are essential for proper methylation processes and DNA synthesis.

Food Sources: Include foods like meat, dairy, fortified grains, leafy greens, and legumes to ensure sufficient intake of these vitamins.

Important Note:

Your dietary choices and any supplements should be in line with your unique genetic profile, and it's important to discuss these with healthcare professionals for personalized guidance.

6 epiAge

Understanding and Tracking DNA Methylation Changes:

The epiAge test, integral to our MetaGen Mutations Panel, is designed to assess your biological age through DNA methylation analysis, complementing the genetic mutation analysis. This innovative approach transcends traditional chronological age assessment by illuminating the intricate interplay between your genetic and lifestyle factors on aging.

Tracking Methylation and Lifestyle Interventions:

After identifying specific gene mutations (MTHFR, MTRR, MTR, AHCY, and COMT) and implementing dietary recommendations, the epiAge test becomes an invaluable tool for tracking changes in your DNA methylation patterns. This is crucial for observing how lifestyle changes, influenced by genetic predispositions might impact your biological aging.

Regular Testing for Dynamic Health Insights:

To capture the dynamic nature of epigenetic changes, regular epiAge testing might be used (every 1-3 months). This frequent monitoring might help assess the effectiveness of dietary and lifestyle interventions tailored to your unique genetic profile, providing feedback on DNA methylation changes.

Personalized Health Insights:

By combining genetic mutation analysis with epiAge's epigenetic profiling, you might gain insight into how your unique genetic makeup interacts with your lifestyle choices, affecting DNA methylation age.

Actionable Steps:

The epiAge report offers a snapshot of your current biological age according to this specific DNA methylation clock but also serves as a tool for tracking the trajectory of changes in DNA methylation of this clock as you implement the recommended changes based on your genetic profile.

Conclusion of epiAge Report:

This holistic approach, blending genetic and epigenetic analysis, underscores the dynamic and multifaceted nature of health and wellness. The epiAge report is a crucial metric in understanding and managing your health, complementing the genetic insights provided in this report. For individualized interpretation and advice, consulting healthcare professionals is highly recommended.

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7 epiSmoke

Smoking causes lung and other cancers, respiratory and cardiovascular diseases, increases the risk of stroke and is a risk factor contributing to impotence. It is therefore important to monitor and prevent exposure to tobacco smoking.

Cigarette smoke or exposure to smoke alters the way genes are marked by epigenetic tags. We can therefore detect exposure to smoking by measuring changes in these epigenetic tags.

After extensive data mining, using proprietary methodology, we have discovered those smoke-related CG methylation region that accurately measures the level of the exposure to smoke.

We prepare DNA from your saliva and then measure the level of DNA methylation in your genome using next-generation sequencing and bisulfite mapping. Your states of DNA methylation are inserted into a mathematical equation/algorithm that calculates the “epigenetic change” as a function of the level of DNA methylation.

You could consider an “epiSmoke” score of 0.5 or higher as a “red flag” which might suggest that you act to change your smoking habits, reduce your exposure to second-hand smoke, or consult your physician.

WHAT DO THE RESULTS OF THE epiSmoke TEST MEAN?

According to Centers for Disease Control and Prevention, “Smoking causes cancer, heart disease, stroke, lung diseases, diabetes, and chronic obstructive pulmonary disease (COPD), which includes emphysema and chronic bronchitis. Smoking also increases risk for tuberculosis, certain eye diseases, and problems of the immune system, including rheumatoid arthritis.” Importantly, exposure to smoke contributes to approximately 41,000 deaths among non-smoking adults and 400 deaths in infants each year. Second-hand smoke causes stroke, lung cancer and coronary heart disease in adults. Children who are exposed to second-hand smoke are at increased risk for sudden infant death syndrome, acute respiratory infections, middle ear disease, more severe asthma, respiratory symptoms, and slowed lung growth.

For personalized interpretation and advice based on both your genetic profile, epiAge and epiSmoke results, consulting with healthcare professionals is highly recommended.

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Conclusion

MetaGen Mutations Panel offers a comprehensive and holistic view of your health. While genetic mutations provide a static glimpse into your predispositions, **epiAge** reveals how your lifestyle choices actively influence your biological aging process. **epiSmoke** assesses your exposure to tobacco smoke and its epigenetic impacts. This comprehensive assessment not only provides insights into your genetic and epigenetic makeup but also underscores the importance of environmental factors, such as tobacco smoke exposure, in shaping your overall health and well-being.

For personalized interpretation and advice, consult with healthcare professionals.

Disclaimer

Intended Use: This report is for informational purposes for a better understanding of how specific genetic variations might impact your health and should not be considered medical advice.

Consult Healthcare Professionals: Always seek professional advice for health-related decisions. It's important to discuss these findings with a healthcare provider for a comprehensive assessment and tailored recommendations. This report is not a substitute for medical consultation.

Regulatory Status: The tests and analyses here are not FDA or Health Canada approved and are meant for personal health insights only.

Limitations: Genetic data should be interpreted as part of a broader health assessment, including lifestyle and environmental factors.

Recommendations: The suggestions in this report are for discussion with your healthcare provider and are not definitive medical directives.

Data Source Acknowledgment: The information in this report is derived from the dbSNP NCBI database and clinical genetic studies, ensuring a scientifically sound foundation for the provided insights and reflecting current scientific understanding in genetics.

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