7 Reasons You Can’t Afford *Not* to Sequence Your Genome

For most of human history, your genome was invisible.

It shaped your risk of heart disease, cancer, dementia, diabetes, drug response, and even how your body responds to food, exercise, and medications — but you could not see it, measure it, or use it to guide prevention.

That has changed.

More than two decades ago, decoding the first human genome required years of work and billions of dollars through the combined efforts of Dr. J. Craig Venter, Celera Genomics, and the government-led Human Genome Project. The Human Genome Project was originally projected to cost roughly \$3 billion, and the first draft human genome changed the course of modern biology and medicine. [1,2]

Today, at Human Longevity, Inc., a clinical-grade whole genome sequence is available for \$599 — with AI-powered interpretation designed to help you and your physician understand what your genome means for your lifetime health. [3,4]

This may be one of the most important medical opportunities of our time.

Here are seven reasons why you can’t afford not to sequence your genome.

1. Whole genome sequencing used to be impossible for most people. Now it is accessible for \$599, creating a lifelong health asset that costs only a few dollars per year over a lifetime.

Just a few years ago, whole genome sequencing was expensive, complex, and largely limited to research institutions, rare disease cases, or advanced academic medical centers.

Today, HLI offers clinical-grade whole genome sequencing for \$599. [3,4]

This is not a consumer ancestry test. It is not a small gene panel. It is a clinical-grade analysis of your complete genome — all 6.4 billion base pairs — interpreted through advanced AI algorithms built to help identify disease risks, drug-response risks, and prevention opportunities. [3]

Your genome does not change. Sequencing it once creates a lifelong health asset.

But the science changes every day. That is why interpretation matters as much as sequencing itself.

2. The biggest killers of our time are deeply connected to your genome.

The leading threats to human healthspan are cardiovascular disease, cancer, dementia, and diabetes. Together, these chronic diseases drive a large share of mortality and disability worldwide — and they represent some of the greatest opportunities for earlier prevention.

These diseases often develop silently for years or decades before symptoms appear. By the time symptoms show up, the disease may already be advanced.

Genomics changes the timing.

Your genome can reveal inherited risk long before disease becomes visible. In cardiovascular disease, for example, a 2026 Journal of the American College of Cardiology study using UK Biobank data showed that combining a coronary artery disease polygenic risk score with LDL cholesterol, Lp(a), and hsCRP improved prediction of future coronary artery disease risk. [5]

This is the future of prevention: not waiting for a heart attack, stroke, tumor, or dementia diagnosis, but identifying risk early enough to act.

If you know you carry high inherited risk for coronary artery disease, prostate cancer, breast cancer, colon cancer, Alzheimer's disease, or diabetes, you and your physician can build a more personalized prevention plan years earlier.

3. Your genome can help determine which drugs are right for you.

Medicine is still too often based on trial and error.

One person benefits greatly from a drug. Another person gets side effects with little benefit. A third person needs a different dose.

Your genome is one reason why.

Pharmacogenomics — the study of how genes affect drug response — can help physicians understand why patients respond differently to medications.

For example, with GLP-1 drugs used for diabetes and weight loss, a 2026 Nature study of 27,885 people found that genetic variation in GLP1R was associated with differences in weight-loss response, while variants in GLP1R and GIPR were associated with medication-related nausea or vomiting. [6]

This does not mean most people should avoid GLP-1 drugs. It means the future of obesity and diabetes treatment will become more precise.

Recent evidence shows that GLP-1 drugs do not work the same way in everyone. In a 2026 Nature study, genetic variation in GLP1R was associated with differences in weight-loss response, while variants in GLP1R and GIPR were associated with nausea or vomiting. Importantly, the paper does not show that most people should avoid GLP-1 therapy. Instead, it supports a more precise future: some patients may be strong responders, some may lose very little weight, and some may be more likely to experience side effects. Pharmacogenomics can help physicians move beyond trial and error when selecting obesity and diabetes therapies.

For statins, pharmacogenomic guidelines from the Clinical Pharmacogenetics Implementation Consortium identify variants in genes such as SLCO1B1, ABCG2, and CYP2C9 that can influence statin-associated muscle symptoms and help guide statin selection or dosing in appropriate clinical settings. [7]

For blood thinners, antidepressants, pain medications, diabetes medications, and many other drugs, genetics can influence safety and effectiveness.

When I used the HLI AI App to ask, “Which statin should I discuss with my physician to lower my LDL?” the app suggested that low-dose rosuvastatin (Crestor) could be a reasonable option to discuss, given my genetic profile and prior side effects with other statins. My doctor agreed. With low-dose Crestor plus 10 mg ezetimibe (Zetia), my LDL has fallen from about 140 mg/dL a few years ago to about 30 mg/dL, with fewer side effects. This is exactly the point: genetic interpretation can turn trial-and-error prescribing into a more personalized conversation with your physician.

The goal is not to replace your doctor.

The goal is to give your doctor better information.

4. Many people carry hidden disease-risk variants — and most do not know it.

You may feel healthy. Your blood tests may look normal. Your family history may appear reassuring.

But your genome may still carry silent risks.

Large population studies show that pathogenic or likely pathogenic variants in medically important genes are found in a meaningful fraction of apparently healthy people. In the All of Us Research Program, a Nature-family Communications Biology study found pathogenic or likely pathogenic variants in actionable genes across ancestry groups, including genes related to hereditary breast and ovarian cancer and familial hypercholesterolemia. [8]

This is why clinical interpretation matters. Not every variant causes disease, and not every genetic risk is destiny. But some variants are actionable — and knowing about them can change screening, prevention, medication choice, and family counseling.

Angelina Jolie brought global attention to this issue when she publicly discussed carrying a BRCA1 mutation, which increased her risk of breast and ovarian cancer and led her to consider preventive medical options. [9]

The same principle applies far beyond BRCA1 and BRCA2.

There are inherited variants linked to colon cancer, prostate cancer, pancreatic cancer, heart disease, cardiomyopathy, arrhythmia, high cholesterol, and many other conditions.

For about the cost of a single imaging test or a few routine specialist visits, whole genome sequencing can give you information that may matter for the rest of your life.

You should not ignore silent risks simply because they are silent.

5. Your genome is not just about you. It is about your family.

When you sequence your genome, you are not only learning about yourself.

You may be learning something important for your children, siblings, parents, and extended family.

At HLI, we recently saw a powerful example.

In 2025, Johns Hopkins researchers reported a recurrent frameshift mutation called F722fs in the MMS22L gene, associated with higher prostate cancer risk among Ashkenazi Jewish men. The paper reported that MMS22L may be a major prostate cancer susceptibility gene, with carrier rate and effect size similar to BRCA2 in the studied population. [10]

After the paper appeared, HLI searched its genomic database and identified seven families carrying this mutation.

Three of the HLI clients identified were women.

They will never develop prostate cancer. But their sons, brothers, fathers, and other male relatives may carry the same mutation — and may face a higher risk of aggressive prostate cancer.

That is the power of family genomics.

One person’s genome can become a warning system for an entire family.

It can lead to earlier screening, more appropriate surveillance, and in some cases more aggressive treatment when disease is found.

6. Static genetic reports are not enough. You need a dynamic AI-powered genomic interpreter.

Sequencing your genome is only the beginning.

The bigger question is: who will keep interpreting it as science advances?

Every week, new papers are published. New disease genes are discovered. New drug-response variants are reported. New polygenic risk models are developed. New clinical guidelines emerge.

A printed genetic report can become outdated.

A dynamic AI-powered genomic platform can continue to learn.

In the MMS22L prostate cancer example, the time from publication to identifying relevant HLI families was less than a day. Without a dynamic platform, those families might not have known about that risk for years — or ever.

This is why HLI has spent more than a decade building a platform that combines genomics, longitudinal health data, advanced diagnostics, and AI interpretation.

The future is not just sequencing.

The future is continuous interpretation.

7. The process is simple — and the opportunity is historic.

Sequencing your genome no longer requires a hospital visit or complicated procedure.

At HLI, the process is simple:

You sign up. https://www.humanlongevity.com/genomics

GENOMICS FOR ALL

Clinical-Grade Whole Genome Sequencing

SCAN TO LEARN MORE

A saliva collection kit is sent to your home.
Collection takes only a few minutes, and you return the kit by mail.
You download the HLI app, where your genomic report becomes available in a few weeks.
Your genome becomes part of a lifelong AI-powered prevention platform.

That is it.

Homo sapiens have lived on Earth for roughly 300,000 years. For almost all of that time, we had no way to read the code that helps shape our health and disease risk.

In 2001, humanity decoded the first human genome at enormous cost and effort.

Today, you can sequence your own clinical-grade genome for $599. [3,4]

That is not just a price drop.

It is a medical revolution.

Your genome may reveal heart attack risk before a heart attack. Cancer risk before cancer. Drug-response risk before side effects. Family risk before tragedy.

The question is no longer whether genome sequencing will become part of modern medicine.

The question is whether you will use it early enough to change your future.

At Human Longevity, our mission is simple:

Know early. Live longer.

Your genome is the foundation.
AI is the interpreter.
Prevention is the goal. This matters because many cancers, including breast and prostate cancer, are far more treatable when found early. Stage I disease can often be treated with curative intent, while Stage IV disease is much more difficult and often deadly.

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