Every individual is unique. Even identical twins do not share a completely identical genetic structure. Twins are born with more than 100 differences arising from mitochondrial DNA inherited from their mother, epigenetic influences, or de novo variants that develop uniquely in one of the babies. Throughout life, these differences continue to increase. In other words, there is no one exactly like us, and our genetic code is the most fundamental map that defines who we are.

This map should serve as a guiding reference in the diagnosis and treatment of diseases; however, until now, it has remained largely unread and silent. One of the main reasons for this has been limited accessibility, while another important factor has been the lack of awareness about the importance of genetics. Many panels developed and marketed as “Genetic Check-up” tests typically analyze 200–300 known variants in selected genes and provide interpretations based on these limited findings. Panels offering recommendations such as “What should we avoid eating?” or “How much exercise should we do?” may positively influence individuals’ lifestyles. We scientifically support lifestyle recommendations that improve quality of life, whether directly related to the test findings or not. If a test result encourages you to be more physically active or to adopt healthier nutrition, it will benefit your life regardless of the specific test performed. However, such limited data only sketch a small portion of your life map.

If each of us is truly unique, then both our susceptibility to diseases and our responses to medications will differ from those of others. Yet, nearly everyone diagnosed with the same condition often receives the same medication at the same dosage. Personalized and preventive medicine is now possible. Genetic knowledge has advanced to a level where we can better understand what to pay attention to during life in order to live longer, maintain quality of life, and age well—while also identifying which conditions we have long accepted as “normal aging” but that actually limit our independence and well-being.

These comprehensive data cannot be generated by every device or laboratory. More importantly, producing and interpreting such data requires time and expertise. Therefore, generating and securely storing this information while you are still healthy ensures that, in urgent situations—such as accidents or new diagnoses—your complete genetic data can be accessed immediately without loss of time.

Lifemap has been designed to make this previously unread and silent map visible. Its goal is to transform complex and extensive genetic information into clear, meaningful, and actionable insights. Rather than offering a simple genetic test, Lifemap establishes a comprehensive structure that includes personalized risk analysis, genetic counseling, and periodic reanalysis services. These panels go beyond the traditional “check-up” concept and can be positioned as a biological awareness platform.

With the guidance of your genetic information, Lifemap serves as a compass—helping you direct your life consciously, transform data into awareness, replace fear with knowledge, replace coincidence with planning, anticipate risks, and design a healthier future. Guided by science and technology, it brings the most advanced approaches of personalized medicine within reach for everyone.

lifemap basic

This panel includes the protein-coding (exonic) regions of all genes present in humans. From the collected sample, Whole Exome Sequencing (WES) is performed. During standard exome sequencing, additional kits that include the mitochondrial genome are also incorporated, enabling the generation of data that allows evaluation of mitochondrial DNA as well. In this way, the data obtained from the Lifemap panels enables analysis of both the exonic regions of the approximately 20,000 genes in nuclear DNA and disease-associated variants found in mitochondrial DNA.

Variants are evaluated across genes related to all organ systems, including cardiogenic risk genes, cancer predisposition genes, metabolic disease risk genes, and neurodegenerative disease risk genes. While this panel can support early detection for many multifactorial diseases, it also provides highly valuable data on carrier status for genetic disorders.

What does it provide?

- Early identification of silent genetic risks
- Identifying the underlying causes of certain common findings that we may have normalized despite their impact on quality of life, and developing solutions
- Screening for individuals with a family history of disease
- Identifying carrier statuses present in the family and, if necessary, selecting embryos that do not carry these variants through IVF
- Evaluating certain drug metabolism genes to support medication selection and dose adjustment

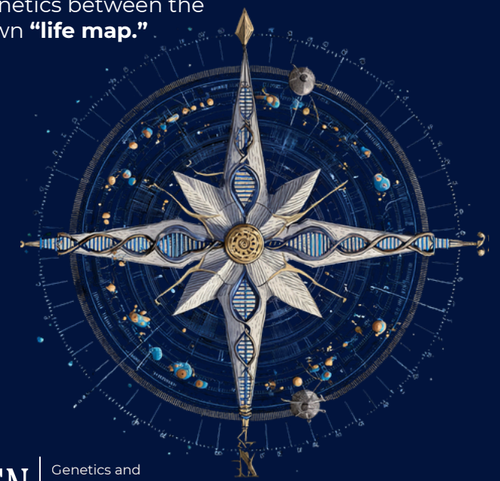
The generated whole exome data remains valid for a lifetime. However, new studies related to genetic diseases are published every day, and information that was unknown yesterday may explain the cause of a person’s condition today. For this reason, storing the generated data and performing re-analysis using advanced artificial intelligence technologies will allow your genetic map to be reinterpreted in light of new knowledge and shared with you accordingly.

Note: The generated data will be stored at our center to enable re-analysis. Our center holds an ISO 27001 Information Security Management System certification. Your data will also be provided to you on a portable storage device. If you do not wish your data to be stored, it will be deleted from our system with your consent.

Health for **Human,**
Science for **Health**

lifemap
Risk Assessment Panels

For each individual, personalized and preventive medicine is hidden within our genetics between the lines of our own **“life map.”**



İNTERGEN | Genetics and Rare Diseases Diagnosis Center

Phone: 444 6 436
Website: www.intergen.com.tr
e-mail: info@intergen.com.tr

lifemap extended

In this panel, Whole Genome Sequencing (WGS) data will be generated. The human genome is approximately 3.2 billion base pairs (3.2 GB) in length. Whole Genome Sequencing analyzes nearly the entire human DNA—approximately 98–99% of it. In addition to the protein-coding regions of all genes, it includes non-coding (intronic) regions, regulatory regions (promoters and enhancers), non-coding RNAs, microRNAs, and repetitive sequences.

Importantly, many of the most clinically relevant variants that influence our lives are located in non-coding regions, including pharmacogenetic variants involved in drug metabolism (such as CYP2D6, CYP2C9, CYP2C19, SLCO1B1, VKORC1). This test also enables the creation of comprehensive risk profiles for cardiovascular diseases, cardiometabolic conditions (e.g., APOE, LDLR, PCSK9, HFE), diabetes, obesity, autoimmune disorders, and neuropsychiatric diseases, providing far more extensive information compared to exome sequencing alone. Disease-associated variants located in both nuclear DNA and mitochondrial DNA can be detected through Whole Genome Sequencing data.

What Does This Panel Provide?

- Evaluation of all diseases and risk factors detectable by exome sequencing, and beyond
- Treatment optimization for individuals with chronic diseases
- Significantly stronger performance than exome sequencing in avoiding drug side effects and enabling personalized treatment
- Genetic guidance for lifestyle modifications

The generated Whole Genome data remains valid for a lifetime. However, new discoveries related to genetic diseases are published daily, and information unknown yesterday may explain the cause of a condition today. Therefore, storing the generated data and performing re-analysis using advanced artificial intelligence technologies allows your genetic map to be reinterpreted in light of new scientific findings and shared with you accordingly.

Note: The generated data will be stored at our center to enable re-analysis. Our center holds an ISO 27001 Information Security Management System certification. Your data will also be provided to you on a portable storage device. If you do not wish your data to be stored, it will be deleted from our system with your consent.

lifemap pro

In this panel, Long-Read Whole Genome Sequencing (Long-Read WGS) data will be generated. This technology has been the focus of genetic engineers and bioinformaticians for the past two decades.

Traditional genetic tests (such as exome sequencing or short-read genome sequencing) analyze DNA by fragmenting it into small pieces and then reassembling those pieces computationally. In the initial step, DNA is broken into short fragments. These fragments are sequenced individually using specialized instruments, and bioinformatics tools reconstruct the data by aligning each fragment to its correct position in the reference genome. The results are then compared with a standard reference genome to identify disease-associated variants. This method allows us to access the majority of genetic information reliably. Exome sequencing in particular has provided diagnostic opportunities to millions of individuals worldwide.

However, these methods may not fully detect large structural variations, repetitive regions, or complex genomic rearrangements. For this reason, Long-Read Whole Genome Sequencing has begun to be used, especially in patients who remain undiagnosed with conventional approaches.

Another important advantage of this technology is its ability to detect certain epigenetic disorders and methylation abnormalities. With recent advances, this highly anticipated technology has reached a level where it can now be effectively used in cases of undiagnosed diseases. In addition to all the data obtained through short-read whole genome sequencing, long-read WGS can identify chromosomal rearrangements (such as translocations, inversions, and deletions), repeat expansion disorders, enable accurate HLA interpretation, perform haplotype analysis (distinguishing genes inherited separately from the mother and the father), and detect methylation abnormalities. As accessibility increases in the coming years, it is highly likely that this technology will replace many existing sequencing methods.

With this approach, it becomes possible to:

- Detect complex variants that cannot be identified by standard WGS or WES
- Capture genomic rearrangements and translocations
- Clarify rare or uncertain genetic findings
- Establish diagnoses in previously undiagnosed conditions
- Evaluate methylation abnormalities

The generated Whole Genome data remains valid for a lifetime. However, new discoveries related to genetic diseases are published daily, and information unknown yesterday may explain the cause of a condition today. Therefore, storing the generated data and performing re-analysis using advanced artificial intelligence technologies allows your genetic map to be reinterpreted in light of new scientific knowledge and shared with you accordingly.

Note: The generated data will be stored at our center to enable re-analysis. Our center holds an ISO 27001 Information Security Management System certification. Your data will also be provided to you on a portable storage device. If you do not wish your data to be stored, it will be deleted from our system upon your request and consent.

lifemap immun pro+

In this expanded panel, Long-Read Whole Genome Sequencing (Long-Read WGS) data will be generated. This dataset captures large-scale DNA changes, repetitive regions, complex variants, chromosomal rearrangements (such as translocations, inversions, and deletions), repeat expansion disorders, accurate interpretation of HLA regions, all situations requiring haplotype analysis (i.e., distinguishing the genes inherited separately from the mother and the father), and methylation abnormalities. It represents the most comprehensive analysis currently achievable at the genomic level, and no technology is expected to provide substantially more information than this approach at the genome scale for a long period of time.

Nevertheless, even whole genome data may be insufficient to establish a diagnosis in some rare cases. When analyzing genome data, the primary goal is to predict what the detected genetic changes mean clinically. While these methods are highly successful for many disorders, interpreting certain multifactorial diseases can sometimes be extremely challenging. In some cases, a result from a single-gene disorder may involve a previously unreported change, or a variant may be detected in an uncharacterized region of a gene—situations in which even the most advanced interpretation tools may be insufficient. Some immune system–related conditions also fall into this category.

For many patients with immune system–related disorders in whom a diagnosis cannot be established—or in whom two pathogenic variants are expected but only one is identified—RNA-based studies can help clarify the underlying mechanism. Performing Long-Read WGS + RNA Sequencing (RNA-Seq) increases diagnostic success in such patients. Together, these two tests provide both genomic evaluation and information on gene expression levels, reflecting how actively genes are functioning. This enables assessment of immune-related genes, cytokine response pathways, interferon signaling, HLA genes, regulation of adaptive immunity, and broader immune response profiles.

This expanded panel is especially valuable for:

- Individuals with immune deficiency or autoimmune disorders
- People with atypical responses to infections, vaccines, or immunotherapy
- Individuals with abnormally low or high inflammatory responses, or those diagnosed with immune dysfunction
- Improving treatment pathway selection and clarifying mechanisms underlying inadequate treatment response

Genomic data remain valid for a lifetime. However, new studies related to genetic diseases are published every day, and information unknown yesterday may explain the cause of a condition today. Therefore, storing the generated data and performing re-analysis using advanced artificial intelligence technologies will enable your genetic map to be reinterpreted in light of new findings and communicated to you accordingly.

In contrast, RNA data reflect the time point at which the sample is collected—they indicate how actively a gene is expressed in that specific tissue at that moment. If new clinical suspicions arise in the future, a new sample must be collected and the RNA test should be repeated.