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| **PERSONAL INFORMATION**  **BARCODE** | **NAME SURNAME** |  | **GENDER** | **□ FEMALE □ MALE** | |
| **BIRTH DATE** |  | **SAMPLE INFORMATION** | | |
|  | **ADDRESS** |  | **□ Peripheral Blood (3 ml, EDTA tube)**  **□ Peripheral Blood (PAXgene)**  **□ Saliva**  **□ Feces  □ Urine**  **□ Other (please specify)** | | |
| **PHONE (MOBILE)** |  |
| **PHYSICIAN**  **STAMP/SIGNATURE** | **NAME SURNAME** |  |
| **INSTITUTION** |  |
|  | **PHONE** |  | **DATE** | |  |
| **EMAIL** |  | **TIME** | |  |
| **TEST SELECTION** | | | | | |
| **□** Whole Genome Sequencing  **□** Blood Transcriptome Sequencing  **□** Gut Microbiome Shotgun Sequencing  **□** Oral Microbiome Shotgun Sequencing  **□** Plasma Metabolome Analysis  **□** Plasma Proteome Analysis  **□** Plasma Lipidome Analysis  **□** Urine Lipidome Analysis  **□** Urine Metabolome Analysis | | | | | |

1. **What is the SZALongevity Program?**

The SZALongevity program aim at elucidating the molecular component of the difference between health and disease in individuals by performing single or integrated analyses of omics data. Those who provide biological samples will be able to access detailed information about their omics reports via a mobile system. Additionally, they will be contributing significantly to entire scientific community in multiple areas such as preventive medicine by providing sample for a groundbreaking research.

1. **How your biological samples will be used?**

All biological samples obtained within the scope of the SZALongevity will be used to generate single or multiple omics of whole genome sequences, blood transcriptome sequences, oral microbiome sequences, gut microbiome sequences, plasma metabolome profile, plasma lipidome profile, plasma proteome profile, urine metabolome profile, and urine lipidome profile data. Any remaining samples will be stored at -80°C until the data analysis is completed and for the duration of the samples' shelf life.

1. **How will your omics data be used and how will the security of your personal data be ensured?**

Personal biological data obtained in SZALongevity program will be processed through analysis algorithms developed within the scope of the project to produce single omics or integrated omics reports. Your data will not be transferred to the third parties or the organizations without your knowledge and consent. Your data will be stored in a secure digital environment at SZALongevity Inc. facility. The biological data will be used in scientific articles after only being anonymized.

1. **Who is the owner of the data generated in the SZALongevity Program?**

Within the scope of SZALongevity program, the provider of the biological samples is the owner of the data. At any time, the individual providing the sample can request that their data not be used or can withdraw from the project. SZALongevity Inc. has the right to use these data within the framework of rules defined by the current personal data protection law and other relevant national regulations.

1. **OMICS REPORTS:**

**5.1 WHOLE GENOME SEQUENCING REPORT:**

Within the scope of the SZALongevity program, the sequence of the entire genome is determined, and variations are identified by matching your results with the reference human genome. Identifying variations related to diseases is possible through detailed bioinformatic data analysis, alongside clinical and molecular biological evaluations. The analysis of variants in your genome can yield three possible outcomes:

**Positive:** A positive result indicates that pathogenic variant(s) that could lead to clinical symptoms, the identification of which is based on current scientific data.

**Negative:** A negative result indicates that no pathogenic variant(s) that could lead to your clinical symptoms are detected, after a thorough analysis of your data on the bases of current scientific level in the field. A negative result does not mean that you do not have a pathogenic variant potentially is the reason of your phenotype.

**Uncertain:** Indicates that the variants of uncertain significance (VUS) are detected. There is not yet sufficient scientific and medical information to determine the pathogenicity of them with certainty. Further testing of family members and re-analysis with the updated literature could help to clarify the impact of these types of variants. It is the responsibility of the attending clinician to request additional tests (e.g., parents and other family members) or reanalysis, for which a separate consent form is required. Requests for re-analysis or additional tests fall under the responsibility of the primary care physician. Re-evaluation of the data may incur additional financial obligations.

# 5.2 GUT and ORAL METAGENOMIC SEQUENCE REPORTS

The individual shotgun metagenomic sequencing of your gut and oral samples aims to unravel the composition of your intestinal and oral microbiome. This test analyzes the sequencing of the genomes of all microorganisms in your gut and mouth to determine the community structure, diversity, and functional potential of them. Gut and oral metagenomic sequence reports composed from the following three major sections:

**General overview of the microbiome structure:** The diversity of microorganism species in your microbiome is assessed. While high diversity is generally associated with a healthy gut microbiome, low diversity may be associated with certain health issues.

**Dominant microorganisms:** The dominant microorganism species in your microbiome and their ratios are identified. This can provide important information about overall metabolism and the activity level of the immune system.

**Associations of the microbiome with specific disease types:** The amounts of potentially associated and protective microorganisms can be determined. An imbalance in microbial equilibrium can lead to health problems.

**5.3 BLOOD TRANSCRIPTOME SEQUENCE REPORT:**

The blood transcriptome sequencing aims to understand how your body gives a systemic response to different conditions and circumstances. This test consists the sequences of total RNA molecules in your blood samples and determination of the number of RNA molecules produced by each gene. This data can provide important clues for the diagnosis and treatment of diseases. The blood transcriptome sequence report analysis results are grouped under these titles:

**Increased Gene Expression:** The test may indicate that the expression levels of some genes are increased significantly in comparison to the reference. This increase can indicate the presence of certain diseases or conditions and can be helpful for the diagnosis and the treatment of the diseases associated with the gene.

**Decreased Gene Expression:** The test may indicate that the expression levels of some genes are decreased relative to the average of the reference database. This could denote certain metabolic disorders, infections, or other diseases and may help for the more accurate clinical assessment.

**Normal Gene Expression:** The test may determine that gene expression is the same with the average level of control population. This can indicate the absence of a specific pathological condition associated with these genes.

**Uncertain Results:** In some cases, gene expression levels can yield uncertain results. This could be due to a lack of sufficient scientific and medical knowledge or because test results can be interpreted in multiple conflicting ways. In such cases, additional tests or testing of family members may be necessary.

**5.4 PLASMA AND URINE METABOLOMIC/LIPIDOMIC SEQUENCE REPORT:**

The plasma and urine metabolomic/lipidomic analysis aims to analyze an individual's plasma metabolic and lipid profiles. These tests are used to detect and quantitatively measure level of small molecules, namely metabolites and lipids, in plasma and urine. The plasma and urine metabolomic/lipidomic profile report are evaluated under the following subtitles:

**Metabolite Profiles:** The determination of dominant metabolites in plasma and urine and their concentrations.

**Lipid Profile: The** identification of lipids in plasma and urine and their relative abundances.

**Metabolic Pathways:** The identification of the main metabolic pathways, the detected metabolites and lipids are part which.

**Potential Anomalies:** Deviations in metabolite or lipid concentrations can indicate potential health risks or disorders.

**Uncertain Results:** Some metabolite or lipid concentrations obtained during the analysis could be uncertain. This could be due to a lack of sufficient scientific or medical information.

**5.5 PLASMA PROTEOME PROFILE REPORT:**

The plasma proteomic analysis aims to create a comprehensive profile of the proteins in an individual's plasma. Proteomics aims to gain knowledge about the structures, functions, and interactions of proteins. This test is used to determine the proteins and their concentrations in plasma. The plasma proteome profile report is evaluated under the following headings:

**Protein Profile:** The determination of the dominant proteins in plasma and their concentrations.

**Functional Groups:** The classification of the detected proteins into categories according to their functional groups.

**Biological Pathways:** The identification of the main biological pathways that the detected proteins contribute to.

**Potential Anomalies:** Deviations in protein concentrations could indicate potential health risks or disorders.

**Uncertain Results:** Some protein concentrations obtained during the analysis could be uncertain. This could be due to a lack of sufficient scientific or medical information.

1. **LIMITATIONS**

# Despite the use of the most current technology and methods in data production and analysis in SZALongevity program, there are certain limitations of the generated data and the analysis reports:

# 1. Technical Limitations: Techniques such as Whole Genome Sequencing cannot cover all regions of the genome uniformly. This means that some variants may not be accurately identified (False Negative: Missing an existing variant, False Positive: Finding a variant that does not actually exist). Although rare, this situation may require the variant to be confirmed with other methods. The approach used in Whole Genome Sequencing (based on short reads) makes it impossible to detect some variants (e.g., base deletions longer than the read length). Since the interpretation of results is based on current genetic data, it is possible that the results could change with new scientific developments in the future.

# 2. Dynamic Changes: Metabolomic, lipidomic, proteomic, and transcriptomic analyses reflect only the biological state at the time of testing. These profiles can change over time due to many factors such as diet, medication, lifestyle, and health status.

# 3. Limited Scope: Analytical methods may not cover all the metabolites, lipids, proteins, or RNA molecules being examined. This means that the results obtained only contain the components that are within the detection limits of the analyses.

# 4. Challenges in Information and Interpretation: Accurate interpretation of test results requires detailed and correct clinical phenotypic additional information. Incomplete or missing or false information can lead to misinterpretations.

# 5. Need for Additional Testing: Test results sometimes require additional analyses or tests. This is particularly important when results are inconsistent with clinical findings. It is the responsibility of the primary physician to request re-analysis or re-testing in case of inconsistency with the clinic, and this is of significant importance.

# 6. Possibility of Errors: Errors that may occur during laboratory processes, although it is very unlikely, can lead to incorrect results. This could be due to human errors such as mislabeling or clerical mistakes.

# 7. CONSENT

Your consent is required for the omics analyses to be legally conducted by SZALongevity Inc. Written consent must be obtained from you, or if you are under 18, from your parents/guardians or legally authorized relative, and the signed consent form is legal requirement for your samples to be analyzed in SZALongevity program. **This form becomes valid only after it is signed, and the signee the form affirms their approval of the contents of this document.**

**Experimental Procedures (one or more):**

1. Whole Genome Sequencing

2. Blood Transcriptome Sequencing

3. Gut Microbiome Shotgun Sequencing

4. Oral Microbiome Shotgun Sequencing

5. Plasma Metabolome Analysis

6. Plasma Proteome Analysis

7. Plasma Lipidome Analysis

8. Urine Lipidome Analysis

9. Urine Metabolome Analysis

**Research Material:** For this purpose, one or more type of samples (blood, urine, feces, and/or saliva) will be requested from you. Providing samples is harmless and painless for your health. Providing a blood sample is generally without known health risks except for rare mild bruising, slight pain, and very rarely infection or possible nerve-vascular damage due to the traumatizing effect of the needle. Re-sampling may be required in exceptional cases where the samples are insufficient or there are issues with quality.

**Completion Time:** The times indicated on our website or by the physician or staff from whom you received information are the average times for test results under normal conditions; however, the process may be extended in unusual circumstances such as patient-specific variations or the need for further examination.

If you have any questions or concerns about the study and the tests, please contact SZALongevity at info@szalongevity.com or by phone at +902165702000.

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| **Storage Consent** | **Usage Consent** |
| The remaining biological samples will be stored for the duration of test are concluded and then destroyed.  The obtained DNA/RNA samples and the generated data can be stored for a period of five years.  Analyses can be repeated or expanded on the samples and data without the need for new sampling.  **□ I agree.**   * **I do not agree, destroy my samples once the legal obligations are fulfilled.** | Omics data is a very valuable resource for researchers who study genetic diseases and related fields and help them to improve their diagnoses and better treat diseases. Therefore, we request the use of omics data for scientific purposes after anonymizing it (i.e., remove any personal identifiers). You may request the deletion of the anonymized or non-anonymized test data at any time after giving your consent.  After anonymization, the rights to the data and material will belong to SZALongevity Inc.  I consent for my test results to be stored and used in a database for scientific purposes; to improve and facilitate the treatment of diseases, and to provide statistical information.  **□ I agree.**  **□ I do not agree, keep it stored only for additional studies that I have consented to.** |

**Patient or Guardian Consent**

I have been informed about the SZALongevity program, received a document containing a written explanation, read it, and understood it. I have been fully informed about how my biological data will be used within the scope of the project. I understand that there may be a need to re-process and/or analyze the samples and that additional samples may be requested. I was given enough time to ask questions and make an informed decision after the terms in the consent form were explained to me. I know that I have the right to request additional information at any time.

I declare that I am aware that the responsibility for providing samples to the SZALongevity program is mine, and that I have provided my biological samples willingly and without any threat or material or moral pressure, and I permit the use of my samples and personal biological data for the purposes stated in this form within the scope of the project.

**I am aware that I can withdraw this permission at any time without having to provide any reason and that I have the right to be informed about the analysis results.**

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| **PATIENT/GUARDIAN (Name-Surname/Signature/Date)** | **WITNESS**  **(Name-Surname/Signature/Date)** | **PHYSICIAN**  **(Name-Surname/Signature/Date)** |
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