CARILION CLINIC

# IRB Submission Guideline for Human Sample Testing for genomics and proteomics (DNA, mRNA and Protein Analysis)

## 1. Purpose and Research Objectives

- Clearly articulate the purpose of using human samples for DNA, mRNA and protein analysis.
- Describe how these analyses will support the study's objectives (e.g., identifying biomarkers (diagnostics/therapeutic targets), understanding disease mechanisms or new drugs development.
- Specify if your aim is to correlate molecular findings with clinical outcomes or other data points and their importance in human health.

## 2. Source and Type of Biological Material

- **Source**: Detail the sample type (e.g., whole blood, tissue biopsies, cerebrospinal fluid and other body fluids) and the patient population (e.g., individuals with Disease X).
- **Collection Details**: Specify who will collect the samples (e.g., trained personnel, phlebotomists, physicians and surgeons), describe the collection setting (e.g., hospital, clinic) and method(s).
- **Sample Handling and Storage**: Indicate how samples will be stabilized and stored to maintain integrity of the cellular and biological components. For example:
    - RNA stability reagents (e.g., PaxGene tubes) should be used to prevent DNA and RNA degradation.
- **Frequency and Volume of Collection**: Define the number of collections, timing, and sample volume to minimize patient burden; avoid excessive sampling.

## 3. Procedures for DNA and RNA Analysis

- **DNA and Total RNA Extraction methods**: Describe the process, including:
    - The extraction methods (e.g., column-based, TRIzol) and any measures taken to ensure DNA and RNA quality by 1% agarose gel electrophoresis or Agilent Bioanalyzer, and Nanodrop quantification.
- **DNA and RNA Quality Control**: Indicate how RNA quality will be assessed using Agilent Bioanalyzer (e.g., using an RNA integrity number, RIN)
- **DNA Genome analysis**: Whole genome sequencing by Illumina sequencing platform with CD Genomics.
- **RNA Quantification and Analysis**:
    - **mRNA Sequencing (RNA-Seq)**: Specify if whole transcriptome or targeted sequencing will be used, along with the sequencing depth.
    - **Quantitative PCR (qPCR)**: Mention any specific target genes and controls for validation.
    - **Data Analysis**: Outline the analysis pipeline, such as alignment, quantification, and differential expression analysis. Specify software and statistical methods (e.g., DESeq2, edgeR).
- **Expected Outcomes**: Describe the intended outcome of genome analysis for single nucleotide polymorphism (SNPs) and mRNA expression analysis, such as identifying differentially expressed genes or validating biomarkers for clinical features.

## 4. Procedures for Protein Analysis

- **Protein Source and extraction (if needed)**:
    - Source tissue: Sera, and if tissue, what buffer systems are used, and what protease inhibitors are used?
- **Protein Quantification and Analysis Techniques**:
    - **Western Blotting**: Specify the proteins or markers targeted
    - **Enzyme-Linked Immunosorbent Assay (ELISA)**: Describe the assays for specific proteins, such as cytokines or neuroinflammatory markers, and the expected detection range.

- **Mass Spectrometry (if applicable)**: If using proteomics, detail sample preparation, any fractionation, and the data analysis pipeline.

- **Validation and Replication**: Discuss plans for validating findings through multiple assays or replicates, especially for novel biomarkers or exploratory markers.

## 5. Expected Benefits to Participants or Society

- Clarify the scientific and clinical value of the research, such as advancing understanding of disease mechanisms or identifying biomarkers that could inform future therapies.

## 6. Future Use and Storage of Samples

- If samples are to be retained for future research (so requested in the study consent form), provide details on long-term storage and future use plans.
- Specify any restrictions on future uses as agreed upon in the informed consent form.
- Specify how the samples will be retained securely.

## 7. Specimen Identification

- The manner or type of specimen identification should be stipulated in the proposal/IRB Application.
- If specimens are to be shared outside of a Carilion Clinic facility and/or with non-Carilion Clinic Co-Principle Investigator/non-employee, all such specimens must be de-identified prior to sharing, with no PHI information associated with the specimen which might allow the source study enrollee to be identified.
- If the consent form does not stipulate/request permission to retain a specimen for future research, there must be a statement as to any left-over specimen being discarded after analysis is completed.