

## Translational Research Institute for Space Health (TRISH)



### Request For Information (RFI): Optimizing the Scientific Impact of the EXPAND Commercial Spaceflight Biosample Collection

**Release Date: August 3, 2026**  
**Response Date: September 8, 2026**

## Description

The [Translational Research Institute for Space Health \(TRISH\)](#) developed a program enabling space health research through partnerships with commercial space providers and their customers. Initiated with the Inspiration4 mission in 2021, TRISH launched the Enhancing eXploration Platforms and ANalog Definition (EXPAND), the first-of-its-kind research program to study human health and performance in private spaceflight participants. TRISH's EXPAND Program collects mission data from commercial spaceflight participants across all phases of flight into a centralized database. An important component of the EXPAND program is a repository of biospecimens collected pre- and post-flight. These samples were collected and biobanked under the GENESTAR protocol ([Krishnavajhala et al., 2025](#)), and they are one of the only sources of biological material available from a pool of non-governmental astronaut population. The collection is limited, and any sample used to generate data is consumed in the process and cannot be recovered. For that reason, TRISH wants to understand what data the research community would find most valuable to generate from these samples before committing material to any particular assay.

Through this Request for Information (RFI), TRISH seeks inputs from the research community regarding the molecular data that would be of greatest scientific value if generated from EXPAND biospecimens.

The molecular basis of many known spaceflight health risks remains incompletely understood. Conditions such as immune dysregulation and latent viral reactivation, oxidative stress and DNA damage, microbiome or metabolic alterations, venous thromboembolism, and Spaceflight-Associated Neuro-ocular Syndrome (SANS) all represent areas in which biobanked samples could enable targeted hypothesis testing. Because each biospecimen aliquot can be used only once, the selection and sequence of assays is critical. If many groups seek similar data types, TRISH can prioritize generating those data once and distributing the results broadly, rather than spending scarce material redundantly. If a smaller number of groups want specialized data, TRISH can design more focused funded efforts to support those specific needs. Input from the research community is therefore essential to inform this prioritization and planning process.

## Available Biospecimens

The EXPAND biorepository holds the biospecimen types listed in Table 1, together with the omics assays each type can support. Biospecimens and their biobanked derivatives, including nucleic acids that were extracted at the time of collection, may be available for new data generation where sample quality and remaining volume allow.

**Table 1. Available EXPAND biospecimens and supported omics assays**

| Biospecimen                                          | Primary Derivatives             | Omics Data That Can Be Generated                                                          |
|------------------------------------------------------|---------------------------------|-------------------------------------------------------------------------------------------|
| Whole blood (K2 EDTA)                                | Genomic DNA                     | Whole Genome Sequencing (WGS);<br>Whole Exome Sequencing (WES)                            |
| Whole blood (PAXgene RNA)                            | Total RNA                       | Bulk RNA sequencing (RNA-Seq)                                                             |
| Plasma (EDTA and Streck cfDNA BCT)                   | Plasma aliquots                 | Proteomics (e.g., Olink Explore HT);<br>metabolomics                                      |
| PBMC (CPT)                                           | Cryopreserved mononuclear cells | Single-cell RNA sequencing (scRNA-seq)                                                    |
| Plasma-derived cell-free DNA (blood collection tube) | cfDNA                           | Cell-free DNA sequencing                                                                  |
| Body swabs (10 body sites)                           | Microbial nucleic acids         | Microbiome sequencing (16S rRNA;<br>metagenomic WGS and RNA-Seq where<br>biomass permits) |
| Saliva                                               | Microbial nucleic acids         | Microbiome sequencing (16S rRNA)                                                          |
| Stool                                                | Microbial nucleic acids         | Microbiome sequencing (16S rRNA)                                                          |
| Urine (cell pellet and supernatant)                  | Microbial nucleic acids         | Microbiome sequencing (16S rRNA)                                                          |

## Collection Timepoints and Missions

Biospecimens were collected before and after flight on the schedule defined in the GENESTAR protocol ([Krishnavajhala et al.](#), 2025). Pre-flight collections were taken at approximately 90, 30, and 3 days prior to launch (L-90, L-30, and L-3), and post-flight collections at return day and approximately 14 and 30 days after return (R+0, R+14, and R+30). No in-flight biospecimens were collected. Currently, samples are available from the Axiom-2, Axiom-3, Axiom-4, Fram2, and Polaris Dawn missions, which include both orbital missions that docked with the International Space Station (ISS) and free-flyer orbital missions. Not every biospecimen type was collected at every timepoint or on every mission, and the number of subjects varies by mission. Respondents do not need to specify exact timepoints, but it helps to know whether a given analysis would require one or more pre-flight baseline samples, post-flight samples, or both.

## Existing EXPAND Data Available for Integration

Alongside the biospecimens, EXPAND holds physiological, behavioral, and environmental data collected on the same missions through the EXPAND Essential Measures. Data of this kind can often be combined with newly generated molecular data to provide additional insights, which is particularly useful given the small size of these cohorts. The measures currently available are summarized in Table 2. Data points are generally available for ten to twenty subjects across the

pre-flight, in-flight, and post-flight timepoints shown. Respondents are encouraged to note whether the data they want generated would be analyzed together with any of these existing measures.

**Table 2. Existing EXPAND data available for integration**

| Essential Measures                                                                                                                 | Pre-flight                     | In-flight | Post-flight           |
|------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|-----------|-----------------------|
| Cognition, Alertness and Mood Survey                                                                                               | L-90±60, L-45, L-30, L-15, L-3 | In-flight | R+0, R+2, R+7, R+30   |
| Wearable Sensor and Actigraphy Data (accelerometer, heart rate, heart rate variability, blood oxygen saturation, respiration rate) | L-3 to L-0                     | In-flight | R+0 to R+3            |
| Questionnaires (NASA Essential Measures Sleep Quality and Team)                                                                    | L-90±30                        | FD+4±1    | R+0, R+4±1            |
| SANS Surveillance (optical coherence tomography imaging)                                                                           | L-60±30                        |           | R+0±1                 |
| Sensorimotor Function and Space Motion Sickness (VAN and TAN tests, sit-to-stand, posture and sway, tandem walk)                   | Pre-flight                     | In-flight | R+0±1                 |
| SpaceOmics (WGS, RNA, scRNA, Metagenomics, Proteomics)                                                                             | L-90±60, L-30±30, L-3±2        |           | R+0±1, R+14±7, R+30±7 |
| Radiation Measurement Data (dose per minute and Linear Energy Transfer (LET) spectra)                                              |                                | In-flight |                       |
| Environmental Data (CO <sub>2</sub> , noise levels)                                                                                |                                | In-flight |                       |

*Table Key: L = Launch (days before or after launch); FD = Flight Day; R = Return (days before or after return to Earth).*

*Note: Data and biospecimen availability may vary across flights based on mission specifics.*

## Information Requested

TRISH invites respondents to describe data they would want generated and the scientific rationale behind it. A useful response should address the following elements:

- The molecular data or assay to be generated from EXPAND biospecimens, including the biospecimen types it would require. Please indicate whether the assay is routinely performed in core facilities or whether it is a bespoke assay requiring a specialized site or platform.
- The spaceflight health risk or potential research question the data would help address, including relevant risk(s) and gap(s) identified in the [NASA Human Research Roadmap](#)

and the [NASA Human Research Program \(HRP\) Research Approach Plans](#) to which the data map.

- A brief description of the planned analytical and interpretive approach, including whether and how the proposed data would be integrated with existing EXPAND data.
- Whether the question depends on pre-flight samples, post-flight samples, or both, and any sensitivity to the number of pre/post flight samples, subjects or missions involved.
- Any preliminary data or prior work that informs the request.
- The type of performer that is best suited to conduct the initial analysis of the molecular data/assay and explain why. TRISH is seeking this information to inform future planning regarding how initial analyses may be conducted.

## **How Responses Will Be Used**

This is an RFI only. Responses will not be reviewed competitively, nor will they necessarily result in funding or award.

TRISH will use the information received to assess community interest, to identify assays with broad applicability, and to inform strategies for generating and distributing data from a limited biospecimen set in a manner that supports the widest range of scientifically sound research questions.

TRISH will review all responses internally to understand the range and depth of community interest in different assays and questions. Where multiple investigators express interest in similar type of data, TRISH may choose to generate those data centrally or select one laboratory to generate that data and make it available for more broad subsequent research use. Where a smaller number of well-supported requests point to specialized data, TRISH may consider more targeted approaches to data generation.

Responding to this RFI is not a prerequisite for any future opportunity, and choosing not to respond will not disadvantage anyone in a later activity. Responses to this RFI are solely for informational purposes, TRISH is under no obligation to use any information submitted in response to this RFI and does not intend to make an award or otherwise pay for any information submitted in response to this RFI. This RFI does not constitute a solicitation or a commitment by TRISH to issue a Request for Proposals (RFP) or any other funding opportunity, and TRISH reserves the right to determine whether and how to proceed with any future procurement or funding activity.

## **Response Instructions**

Responses may be submitted by U.S. and non-U.S. individuals and entities. This RFI is issued solely for information and planning purposes and does not constitute a commitment to issue, or confer eligibility for, any future procurement, funding opportunity, or award. Any future solicitation,

if issued, will be governed by its own terms and eligibility requirements, which may include restrictions on non-U.S. participation.

TRISH encourages respondents to use the response template provided below. Responses are expected to be approximately 1–2 pages in length, which may be included where helpful to support the scientific rationale.

To register on TRISH GRID:

- Go to <https://spacehealth.bcm.edu/> and follow these [instructions](#).
- Fill in the requested information and click the “Create Account” button at the bottom of the page.
- Verify your email via the “Send verification link” button at the top right. Email verification is required to submit an application. You will receive an email from [noreply@smapply.io](mailto:noreply@smapply.io) to “Confirm Your Email Address.” The website will state that your email address has been verified.
- Click the “Continue” button.

To submit an application:

- After you have registered and verified your email, login to your GRID account.
- Click “Programs” in the top navigation bar.
- Select “Request For Information (RFI): Optimizing the Scientific Impact of the EXPAND Commercial Spaceflight Biosample Collection” and click “Apply.”
- Complete the tasks listed under “Your tasks.” When all sections are marked as complete, you will be able to review and submit your response.

Requests for assistance in accessing and/or using this website may be sent to [TRISH's Cosmic Concierge](#) by selecting “Open Solicitation” from the drop-down menu. We understand that this is not an open solicitation, but an RFI falls into this category for the purpose of this portal

RFI Response Template:

TRISH encourages respondents to use the response template provided below.

**1. Requested Molecular Data or Assay**

*[Describe the molecular data or assay that would be of scientific interest if generated from EXPAND biospecimens, including any relevant biospecimen types]*

**2. Scientific Rationale**

*[Describe the scientific question(s), spaceflight health risk(s)/ gap(s) that the data would help address]*

**3. Data Analysis and Use**

*[Briefly describe how the data could be analyzed, interpreted, and/or integrated with existing datasets]*

**4. Sample Requirements**

*[Indicate whether the scientific use case would require pre-flight samples, post-flight samples, or both, and note any considerations related to sample numbers, participants, or missions]*

## **5. Supporting Information (Optional)**

*[Provide any preliminary data, prior work, or references that support the input provided]*

## **6. Recommendations for Initial Data Analysis (Optional)**

*[If appropriate, please identify the organization(s), facility(ies), research group(s), or other entity(ies) that you believe are best positioned to perform the initial analysis of biosamples. Please provide the rationale for your recommendation.]*