Rapid Biomonitoring after an Environmental Disaster

Pilot Study Results: Moss Landing Battery Storage Facility Fire

A collaboration between Homeworld Collective and ImYoo

Executive Summary

The January 2025 fire at the Moss Landing lithium-ion battery storage facility was one of the largest in the world. For weeks following the fire, residents reported persistent symptoms including respiratory issues, skin irritation, and neurological complaints. Traditional clinical tests failed to capture objective biomarkers of exposure or immune dysfunction despite the potential high exposure levels documented by citizen scientists and local researchers.

This pilot study demonstrates that **single-cell transcriptomic analysis could detect meaningful immune signatures in affected populations**. Our findings reveal consistent patterns of immune activation that would not be detected by clinical blood panels, validating the biological basis of community-reported health effects and demonstrating the feasibility of rapid biomonitoring after acute chemical events.

The Problem: A Critical Gap in Public Health Response

The long term health effects of sudden chemical exposure events are poorly captured by public health departments. According to NOAA's Incident Archive, there were more than 70 chemical incidents in 2023 alone, yet the health consequences remain largely undocumented because the biological transients fade before traditional clinical studies can be deployed. There is a lag time before action is taken.

Many toxicants are eliminated from the body within days, though health effects linger. Later studies can only infer causation or defer to future research. This data gap has historically made it nearly impossible to establish causal links between industrial events and downstream health outcomes, leaving affected communities without scientific support for medical care or legal recourse.

Our Approach: Technology-Enabled Rapid Deployment

This pilot leveraged existing infrastructure for remote molecular monitoring: FDA-approved self-collection blood kits (TAP II device), cold-chain shipping logistics, and automated single-cell RNA sequencing workflows. Six participants who reported experiencing inflammatory-related health events, provided samples processed through 10x Genomics 3' single-cell gene expression analysis, with results compared against ImYoo's baseline atlas of individuals across a wide spectrum of age and health.

This approach captures data at the resolution of individual immune cells, analyzing thousands of genes across thousands of cells per participant and revealing patterns that aggregate measures cannot detect. Critically, this workflow can be deployed within days of an incident, capturing biological signals that would otherwise be lost.

Key Findings

Disclosure: *These results are preliminary research findings shared to advance scientific understanding*

and inform future study design. They do not constitute medical diagnosis, and individual results should not be interpreted as confirmation of exposure-related illness.

1. T Cell Population Shifts Indicate Persistent Immune Activation

Participants showed significantly elevated CD4 Memory T cells, CD8 Cytotoxic T cells, and a subtype of Gamma-Delta T Cells ($p < 0.05$, age-adjusted, FDR corrected). There is also a notable decrease of CD4 and CD8 Naive T Cells. This pattern—naive cells being converted to memory/effector cells—is potentially characteristic of ongoing immune challenge and suggests persistent antigen exposure or chronic inflammation.

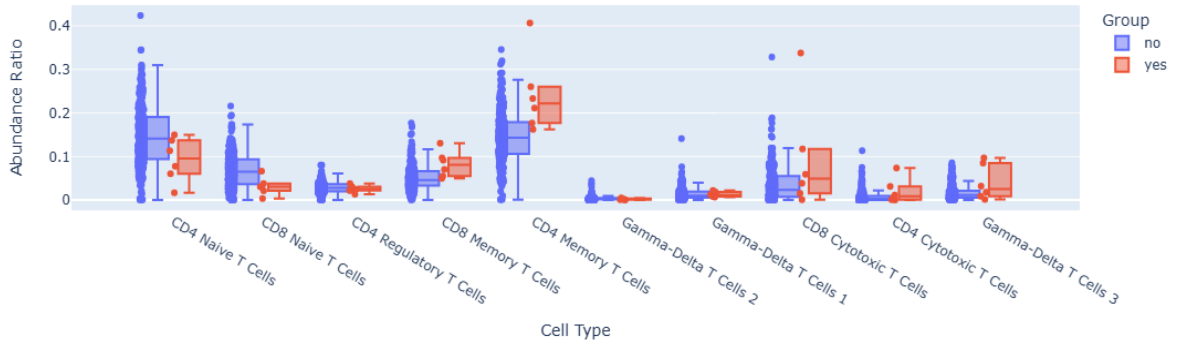

Figure 1: T cell subtype abundance in Moss Landing participants (red) vs. broad immune atlas (blue). Note elevated Memory T cells and reduced Naive T cells in the exposed cohort.

2. Inflammatory Gene Signatures Across Multiple Cell Types

We identified elevated expression of key inflammatory genes that replicated across our larger baseline atlas:

TNFSF14: Elevated in gamma-delta T cells, suggesting increased signaling between innate and adaptive immune compartments.

GIMAP4: Upregulated across T cells and monocytes—a gene implicated in immune cell survival under chronic challenge.

TNFSF12: Elevated in monocytes, dendritic cells, and T cells—involved in inflammation, apoptosis, and tissue remodeling, indicating systemic immune activation.

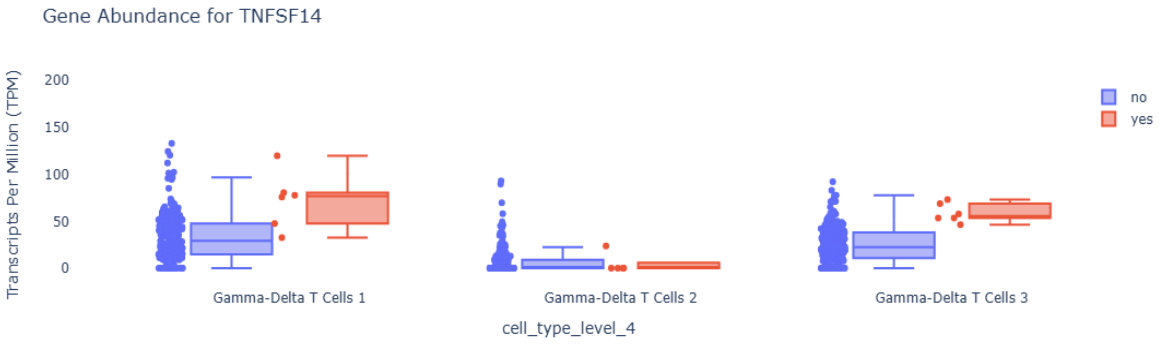

Figure 2: TNFSF12 gene expression across cell types. Moss Landing participants (red) show elevated inflammatory signaling compared to healthy baseline (blue), particularly in monocytes and dendritic cells.

Impact and Implications

This pilot study showcases how intricate immune response data can be quickly captured through collaborating with communities that are impacted by environmental exposure events. Combining at-home collection with research-grade analysis can reveal biomarkers that inform future treatment and rapid response. This scalable approach has implications that extend beyond Moss Landing:

For affected communities: Objective biological data validates health concerns that traditional tests miss, supporting both clinical management and legal documentation.

For researchers: Datasets from acute exposures enable identification of early pathological signals and mechanistic research into exposure-disease relationships.

For public health infrastructure: A deployable biomonitoring system creates capacity for rapid response to chemical incidents, industrial accidents, and climate-related disasters.

For policy and accountability: Robust exposure-outcome data provides the evidentiary foundation for public health interventions, regulatory action, and liability assignment.

Potential Next Steps

We are pursuing several directions to building upon these findings:

Biomarker Discovery: Evaluate circulating molecular markers in blood plasma that are indicative of heavy metal exposure (manganese, cobalt, nickel) or downstream health effects.

Further T-cell analysis: Investigate whether specific T-cells express similar genes across affected individuals by conducting more detailed “repertoire sequencing” of unique clones

Cohort expansion: Enroll more participants and match asymptomatic controls to exposed subjects for to detect meaningful differences in expression with robust statistical power

Longitudinal monitoring: Repeat sampling over 12-24 months to capture the trajectory of immune changes, correlating molecular signatures with symptom resolution or persistence.

Opportunity

This pilot demonstrates both the scientific validity and practical feasibility of rapid biomonitoring post-disaster events. Infrastructure, coordination, and funding are needed to deploy this systematically across affected populations. Investment in scaling this approach would create a fundamentally new capability for public health response, filling the data void with opportunities for new clinical treatments and better population-level protection. For those interested in contributing to this joint effort and continuing this study, please reach out to us.

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