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# Cellworks Study Supports Liquid Biopsy for Predicting Chemo-Immunotherapy Benefit in Advanced NSCLC

*New findings show potential for liquid biopsy to expand access to personalized treatment prediction in advanced NSCLC*

Cellworks
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SAN DIEGO, CA, UNITED STATES, April 22, 2026 /EINPresswire.com/ -- Cellworks Group Inc., the leader in Personalized Therapy Solutions across the Drug Development and Clinical Care Lifecycle, today announced results from a new clinical study demonstrating that liquid biopsy genomic profiling may provide a practical alternative to solid tissue profiling for predicting benefit from chemo-immunotherapy in advanced non-small cell lung cancer (NSCLC). The findings showed that the Cellworks predictive scores derived from liquid biopsy samples were strongly aligned with scores generated from matched solid tissue samples, supporting the potential future use of blood-based genomic profiling to inform personalized treatment decisions when tissue is unavailable, limited, or difficult to obtain.

Results from the study were presented at the AACR 2026 Annual Meeting in San Diego, California, as poster #2449, titled “Comparison of Liquid Versus Solid Tissue Genomic Profiling for the Prediction of Chemo-Immunotherapy Benefit in Advanced NSCLC.”

"Comprehensive genomic profiling is increasingly being performed using liquid biopsy, particularly when tissue is limited or inaccessible,” said Charu Aggarwal, MD, MPH, FASCO, Leslye M. Heisler Professor of Lung Cancer Excellence in the Perelman School of Medicine at the University of Pennsylvania, and lead author of the study. “These findings suggest that liquid biopsy may also support treatment benefit prediction—not just mutation detection—opening the door to broader use of personalized treatment strategies in advanced NSCLC.”

“Treatment decisions in advanced NSCLC often need to be made quickly, and tissue is not always available in sufficient quantity or quality for comprehensive analysis,” said Tejas Patil, MD, Assistant Professor of Medicine-Medical Oncology, at the University of Colorado School of Medicine and co-principal investigator of the study. “This study demonstrates that liquid biopsy can provide a clinically practical path to generating personalized treatment predictions using the same mechanistic AI framework validated in tissue-based profiling.”

Cellworks previously demonstrated that its ΔTRI algorithm, generated using genomic profiling from solid tissue, could distinguish advanced NSCLC patients likely to benefit from immune checkpoint inhibitor plus chemotherapy (ICI+C) from those unlikely to benefit from the addition of chemotherapy. In this new study, Cellworks evaluated whether the same validated framework could generate similar treatment benefit predictions using matched liquid biopsy genomic data.

## Key Findings

- Strong Agreement Between Liquid and Solid Profiling: ΔTRI scores generated from liquid biopsy samples were significantly correlated with scores generated from solid tissue genomic profiling ($R^2 = 0.61$, $p < 0.001$), demonstrating strong overall agreement between the two approaches.
- High Similarity in Genomic Alteration Profiles: Mutational profiles were highly similar between liquid and solid platforms, with a median Jaccard index of 0.84, indicating substantial overlap in detected genomic aberrations.
- Minimal Median Difference in Predicted Benefit: The median difference in ΔTRI score was 2.39, corresponding to roughly a 2% difference in predicted chemo-immunotherapy benefit, suggesting that liquid biopsy can often produce clinically comparable treatment predictions.
- Discordant Cases Were Primarily Driven by Novel Liquid-Detected Mutations: In patients with genomic differences between liquid and solid samples, discordance was driven 81% of the time by novel mutations identified in liquid biopsy, highlighting the potential biological relevance of tumor evolution and ctDNA shedding.

## Study Design

To conduct the analysis, researchers applied the previously validated ΔTRI algorithm and its predefined clinical threshold to 20 non-squamous advanced NSCLC patients with matched genomic data derived from solid and liquid samples. The ΔTRI algorithm uses output from Cellworks' mechanistic model of a patient's tumor genomics to predict potential benefit from ICI+C therapy. Researchers compared liquid- and solid-derived ΔTRI scores and assessed differences in relation to genomic and clinical factors.

## The Cellworks Platform

The Cellworks Platform applies mechanistic AI to perform computational biosimulation of protein-protein interactions, enabling in silico modeling of tumor behavior using genomic data from next-generation sequencing (NGS). This approach allows clinicians to evaluate how personalized treatment strategies interact with a patient's unique tumor network. At the core of the platform is the Cellworks Computational Biology Model (CBM), a mechanistic network encompassing more than 6,000 human genes, 30,000 molecular species, and 600,000 molecular interactions. The CBM and its drug models biosimulate how specific compounds or combinations affect disease pathways, producing a therapy response prediction that can guide treatment selection. The CBM has been validated across multiple clinical datasets, with findings featured in more than 125 peer-reviewed presentations and publications in collaboration with global partners.

About Cellworks Group

Cellworks Group, Inc. is dedicated to improving patient outcomes by harnessing the power of computational science to deliver Personalized Therapy Solutions across the Drug Development and Clinical Care Lifecycle. The Cellworks Platform predicts patient-specific therapy response for oncology and other complex diseases using a mechanistic Computational Biology Model (CBM), AI and biosimulation technology. Cellworks is backed by Artiman Ventures, Bering Capital, Sequoia Capital, UnitedHealth Group and Agilent Ventures. Headquartered in South San Francisco, the company also operates a CLIA-certified computational lab in Franklin, Tennessee. Learn more at www.cellworks.life.

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