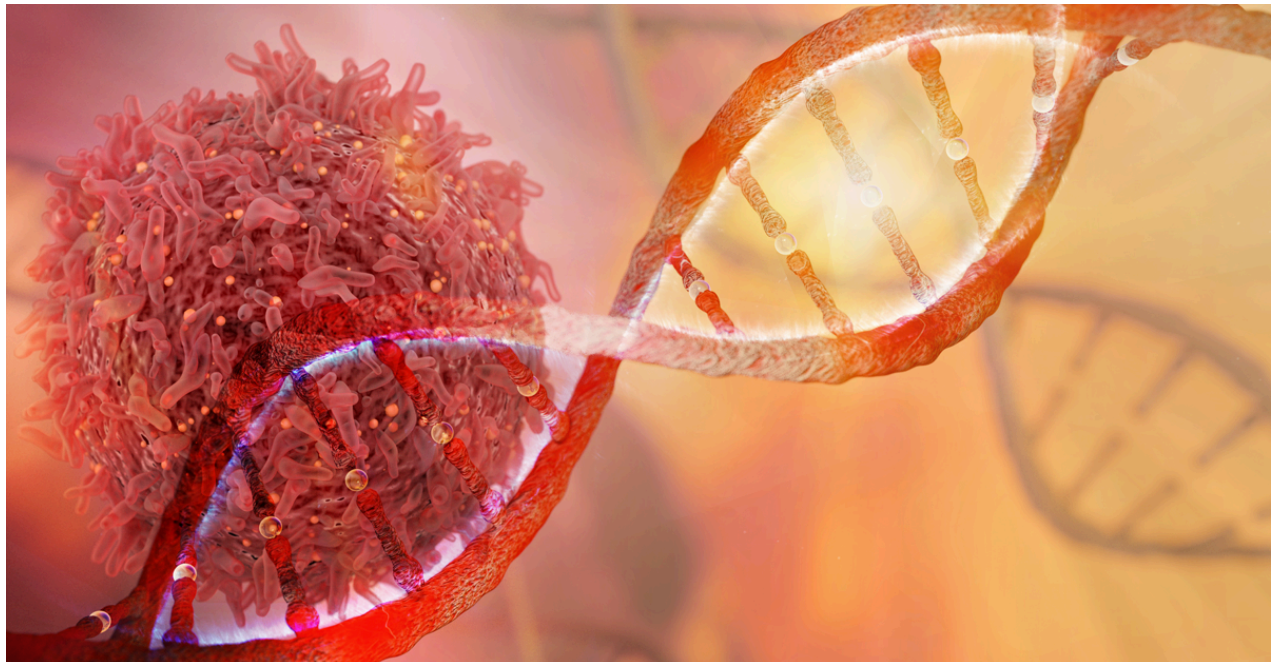


# AI Model Links Tumor Mutations to Treatment Response

Model uses tumor DNA to predict immunotherapy and chemotherapy outcomes across multiple cancers



This illustration shows a cancer cell and a DNA strand. In a new study, UC San Diego researchers introduce an AI tool that could help translate a tumor's genetics into actionable predictions how that tumor will respond to treatment. Courtesy of iStock/CIPhotos

May 26, 2026

### Key Takeaways

- Cancer tumors often contain many mutations, but doctors still have limited tools for interpreting them to select treatments
- A new AI tool discovered by UC San Diego improved prediction of how multiple cancers may respond to treatment
- Approach could help make tumor DNA testing more clinically actionable

**R**esearchers at University of California San Diego have developed a new artificial intelligence (AI) model that can translate a tumor's complex genetic profile into predictions about how that cancer may respond to treatment. The model, called MutationProjector, was trained on genomic data from more than 30,000 tumors across 10 solid cancer types and offers a new framework for connecting cancer mutations to the biological pathways that drive treatment response. The model is

Story by:

[Miles Martin - milesmartin@ucsd.edu](mailto:milesmartin@ucsd.edu)



Topics covered:

[Cancer](#), [Cancer Therapy](#), [AI](#), [Treatment Resistance](#)

Share This:



described in a new study, published in *Cancer Discovery*, a journal of the American Association for Cancer Research, in which researchers validated the approach by testing it across multiple independent patient cohorts.

“Genetic sequencing is already routine in cancer care, but we still struggle to fully interpret the many mutations found in a patient’s tumor,” said Trey Ideker, PhD, professor of medicine at UC San Diego School of Medicine and director of the Big Data Institute at the University of Oxford. Ideker also holds a second appointment at UC San Diego Jacobs School of Engineering and is a member of UC San Diego Moores Cancer Center.

“Our goal with MutationProjector was to build a general-purpose model that can learn from tens of thousands of tumor genomes and turn those mutation patterns into more precise predictions about treatment response.”

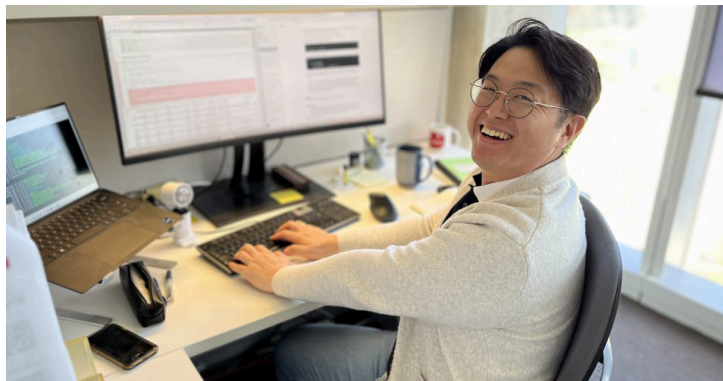
Following a cancer diagnosis, one of the next steps is often genetic testing, which helps doctors classify the tumor and decide which treatments to pursue. Genetic testing is relatively low cost, fast and has a strong track record in cases where validated genetic biomarkers are available. However, those cases remain limited, because this type of treatment stratification is currently based on only a small number of known biomarkers. Today, only about 8% of cases are successfully matched to an FDA-approved therapy on the basis of genetics.

Unlike existing approaches that rely on a small number of biomarkers, MutationProjector analyzes the broader combination of genetic alterations present in a tumor. The model then uses this information to generate a compact representation of the tumor’s biological state, helping researchers interpret which molecular pathways may be disrupted and, by extension, which treatments may be most effective.

Across several independent cohorts of cancer patients, including those with bladder cancer, lung cancer and melanoma, MutationProjector matched or exceeded existing methods for predicting response to common immunotherapy and chemotherapy treatments. The model also identified both known and unexpected biomarkers associated with treatment outcomes, which could help improve current approaches to genetic testing and patient stratification.



*Trey Ideker is a professor of medicine at UC San Diego School of Medicine and director of the Big Data Institute at the University of Oxford. Photo by Erik Jepsen/UC San Diego*



*First study author JungHo Kong, shown here, is a postdoctoral researcher at UC San Diego School of Medicine.*

“Many cancer mutations are individually rare, which makes them difficult to study one at a time,” said JungHo Kong, PhD, first author of the study and a postdoctoral researcher in the Department of Medicine at UC San Diego School of Medicine. “By pretraining on a large collection of tumors and integrating molecular network knowledge, MutationProjector can detect patterns that would be easy to miss with conventional biomarker approaches. That gives us a way to move from long lists of mutations toward a more functional understanding of the tumor.”

The researchers emphasize that the model was designed not only to make predictions, but also to provide insight into why those predictions are made, which could help when refining biomarkers and treatment strategies. This interpretability is especially important in precision oncology, where clinicians need to understand how tumor genotypes relate to treatment decisions. The team also hopes to expand the model to additional cancer types and data sources, including international cancer genome datasets and other forms of clinical information, such as imaging, transcriptomics, and electronic health records.

“Our results suggest that tumor genome foundation models may help extend the clinical value of sequencing beyond a handful of well-known genes,” Ideker said. “This could support a more comprehensive and biologically grounded approach to precision oncology.”

Read the [full study](#).

Additional coauthors on the study include: Ingoo Lee, Dean Boecher, Akshat Singhal, Marcus R. Kelly, Dexter Pratt, Tannavee Kumar, Timothy J. Sears, David Laub, Sarah Wright, Patrick Wall, Hannah Carter and Zhen Wang at UC San Diego, and Jimin Moon, Chang Ho Ahn and Chan-Young Ock at Lunit Incorporated.

This work was supported in part by grants from the National Institutes of Health (T32CA121938, U54CA274502, R01ES014811, P41 GM103504) and the Advanced Research Projects Agency for Health (ARPA-H) contract number 140D042590013.

Disclosures: Ideker is a co-founder, member of the advisory board, and has an equity interest in Data4Cure and Serinus Biosciences. He is also a consultant for and has an equity interest in Ideaya Biosciences and Eikon Therapeutics.

*“Our results suggest that tumor genome foundation models may help extend the clinical value of sequencing beyond a handful of well-known genes. This could support a more comprehensive and biologically grounded approach to precision oncology.”*

– Trey Ideker

Learn more about research and education at UC San Diego in: [Artificial Intelligence](#)

YOU MAY ALSO LIKE



**TECHNOLOGY & ENGINEERING**  
Optical Device Uses Humidity to Unlock Hidden Information, Offers New Option for Data Storage



**HEALTH & BEHAVIOR**  
Naturally Occurring Molecule May Help Outsmart Melanoma



**HEALTH & BEHAVIOR**  
UC San Diego Awarded \$4.85M to Grow NEMAR into HPC Hub for Neuro-AI



**How Can We Better Connect with Each Other?**