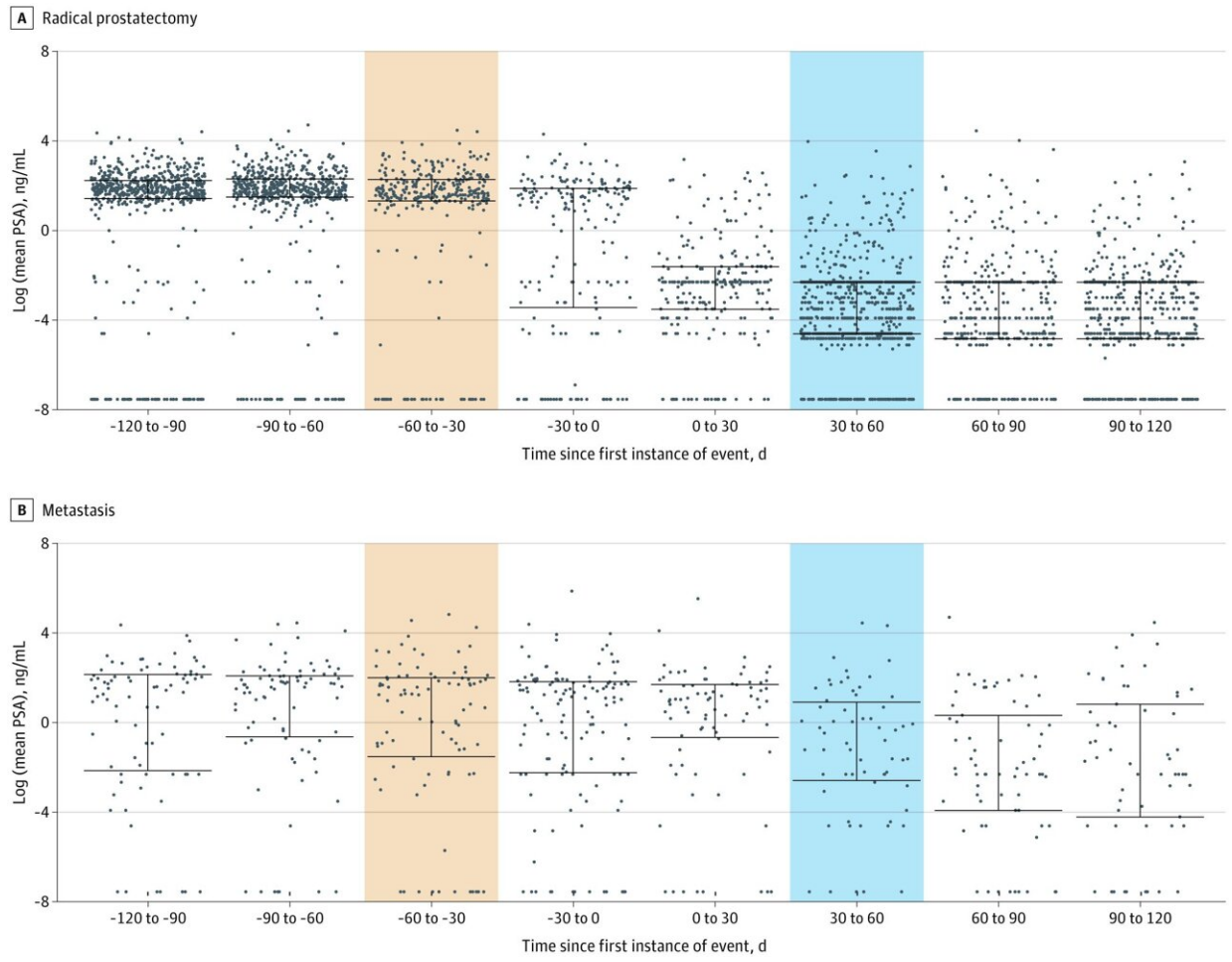
Combining genomic analyses and outcome data is promising strategy for prostate cancer treatment

June 26 2024, by Cheri Lewis



Distribution of prostate-specific antigen (psa) values in relation to index clinical event (radical prostatectomy and metastasis) assessed using claims, pharmacy records, and electronic health record data. Median PSA values were assessed in

the 30- to 60-day periods before (orange shading) and after (blue shading) event. Each point represents the log of the mean PSA value of a patient in the time window. Credit: *JAMA Network Open* (2024). DOI: 10.1001/jamanetworkopen.2024.17274

Combining genomic analyses with information about clinical outcomes is a highly promising strategy to understanding prostate cancer and its treatment. Researchers say it could change how the disease is predicted and make treatment timelier and more personalized.

Yale Urology Associate Professors Michael S. Leapman, MD, MHS, and Preston C. Sprenkle, MD, led the research efforts published June 14 in *JAMA Network Open*.

In a large collaborative study, touted as the most extensive clinical-transcriptomic linkage ever accomplished, more than 92,000 patients were reviewed. Each had undergone genomic classifier testing between 2016 and 2022 with the Decipher Classifier, a commercially available tool used to estimate prostate cancer risk.

They were then linked with administrative information, including insurance claims, pharmacy records, and electronic health record [EHR] data.

"Alignment of this data [both clinical and genomic]," says Leapman, "is especially important as it provides a platform for understanding how observed cancer genomic signatures relate to short- and long-term patient outcomes.

"This information, and future expansions of this work could help refine the ways in which key clinical decisions are made—such as which

prostate cancers should be treated, and with what approach."

The study leverages transcriptomic profiling using the Decipher Classifier. Leapman says it contains "over 1.4 million features including 46,000 coding and non-coding genes."

According to the paper, the study's authors "validate[d] and refine[d] algorithms that identif[ied] key prostate cancer events," such as dates of diagnosis, rising PSA levels, and metastasis.

"One of the exciting opportunities with large scale research like this," says Sprenkle, "is the potential to evaluate the impact of testing and interventions on men with lower risk prostate cancer to better understand who can avoid intervention. This is something typically difficult to assess in small single-institution studies or even clinical trials."

More information: Michael S. Leapman et al, Development of a Longitudinal Prostate Cancer Transcriptomic and Clinical Data Linkage, *JAMA Network Open* (2024). DOI: 10.1001/jamanetworkopen.2024.17274

Provided by Yale University