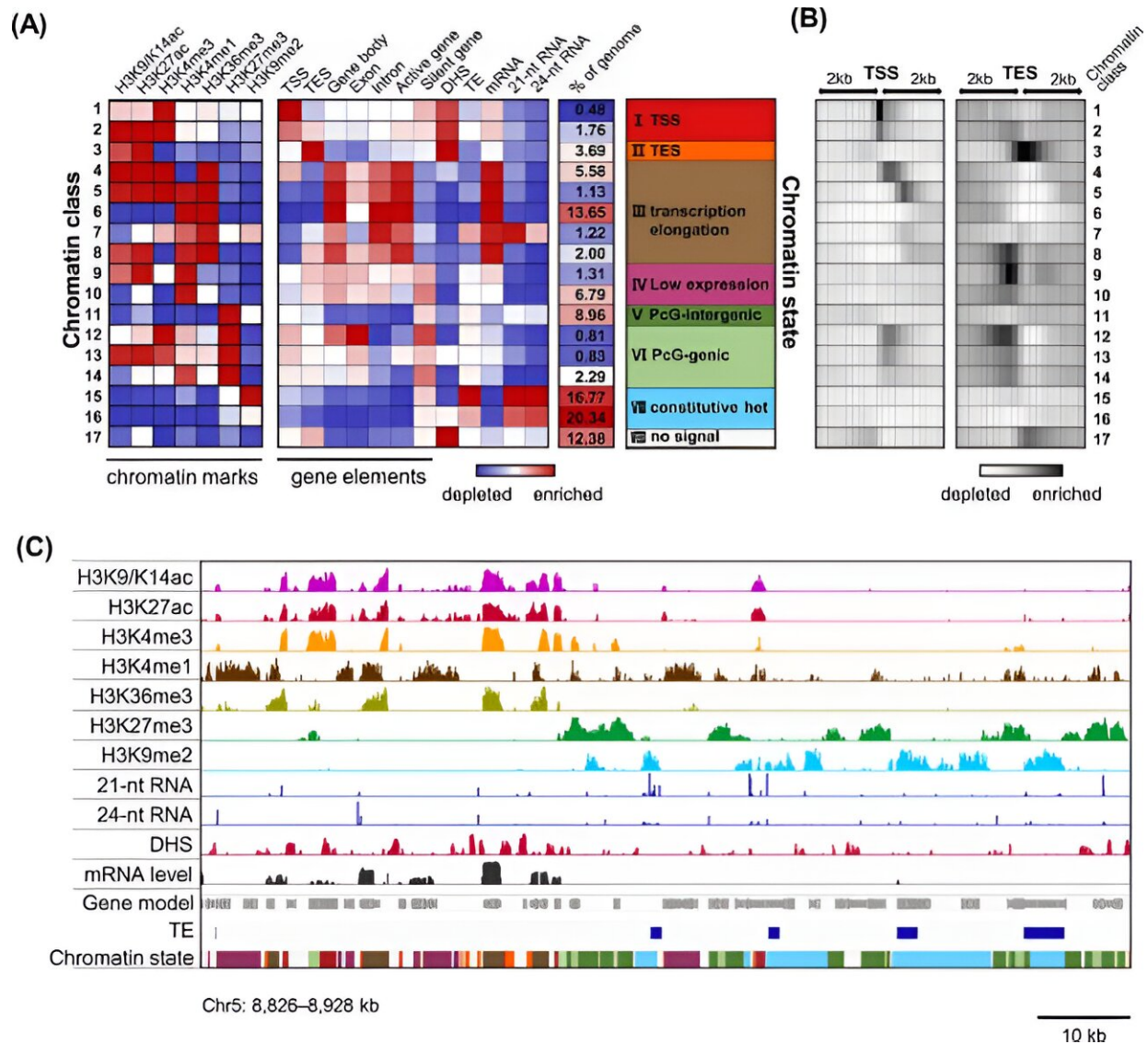


Strawberry ripening revealed: Key histone modifications uncovered

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Eight chromatin states based on the distribution of histone modifications are closely associated with transcriptional status in the woodland strawberry. Credit:

Fruit ripening is a tightly coordinated process driven by both hormonal and environmental factors, yet the epigenetic mechanisms controlling this process remain unclear.

Histone modifications, known for altering [chromatin structure](#) and [gene expression](#), are key regulators of plant development. However, their role in the ripening of non-climacteric fruits like strawberries has not been fully explored.

Addressing these gaps, a study investigates how histone modifications influence fruit ripening at the chromatin level. Researchers from Nanjing Agricultural University and the University of Connecticut [published](#) their findings in *Horticulture Research* on June 7, 2024.

The study offers a comprehensive chromatin-centric annotation of the strawberry genome, revealing how dynamic histone modifications drive gene expression changes during fruit ripening. The identification of eight distinct chromatin states linked to transcriptional activity provides deeper insights into epigenetic regulation in fruit development.

Using [chromatin immunoprecipitation](#) sequencing (ChIP-seq), the team mapped seven histone modifications in immature and mature strawberry fruits, uncovering a complex interaction of active and repressive chromatin states that regulate ripening-related genes.

Key findings include the discovery of active genic states enriched with acetylation marks like H3K9/K14ac and H3K27ac, which are associated with genes involved in anthocyanin accumulation, fruit softening, and aroma production. Repressive states marked by H3K27me3 correspond

to silenced genes during ripening.

These findings highlight the pivotal role of histone acetylation in creating an open chromatin environment that facilitates gene expression, driving the ripening process.

"This study provides a new perspective on how [histone modifications](#) control fruit ripening at the chromatin level," said Professor Yi Li, a corresponding author from the University of Connecticut. "By mapping these dynamic chromatin changes, we can better understand the transcriptional mechanisms that guide key developmental transitions in fruits, informing breeding strategies for enhanced crop quality."

The study's findings have significant implications for agriculture and fruit quality enhancement. Understanding chromatin state dynamics during ripening could pave the way for targeted genetic modifications, enabling the development of strawberry varieties with optimized ripening profiles, superior taste, and longer shelf life.

Additionally, the research sets a foundation for exploring epigenetic regulation in other non-climacteric fruits, broadening the potential impact on crop improvement efforts.

More information: Qinwei Pan et al, Dynamic histone modification signatures coordinate developmental programs in strawberry fruit ripening, *Horticulture Research* (2024). [DOI: 10.1093/hr/uhae158](https://doi.org/10.1093/hr/uhae158)

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