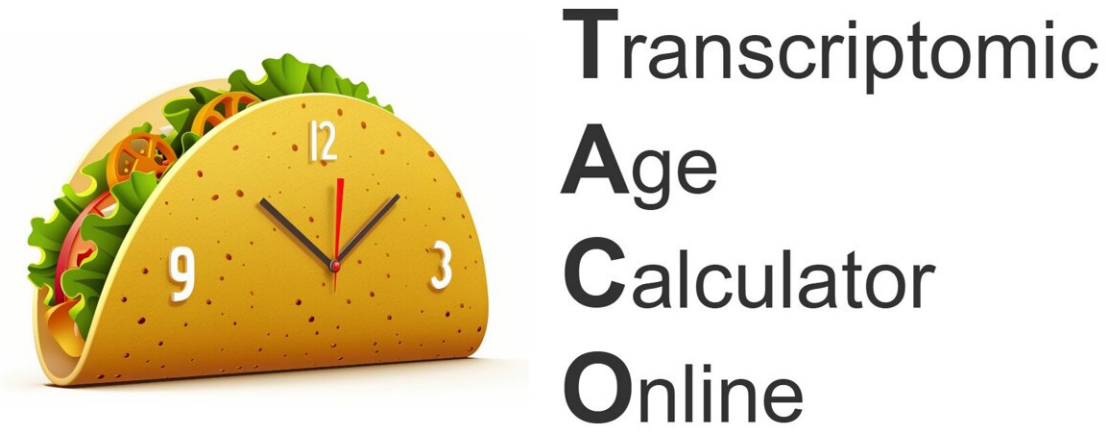
Universal aging clock predicts death risk across multiple mammalian species

May 31 2026, by Sanjukta Mondal



Credit: Adrian Molière

What's common between rats, humans, dogs and dolphins? We are all mammals, and one day will be the last day of our lives. A multinational team of researchers have now given us a powerful molecular clock that, with the help of biological markers, can predict age as well as the risk of death in mammals.

They discovered that certain genes serve as universal markers of aging, and that these genes behave almost identically across mammals as they get older, regardless of species. By analyzing gene expression of these

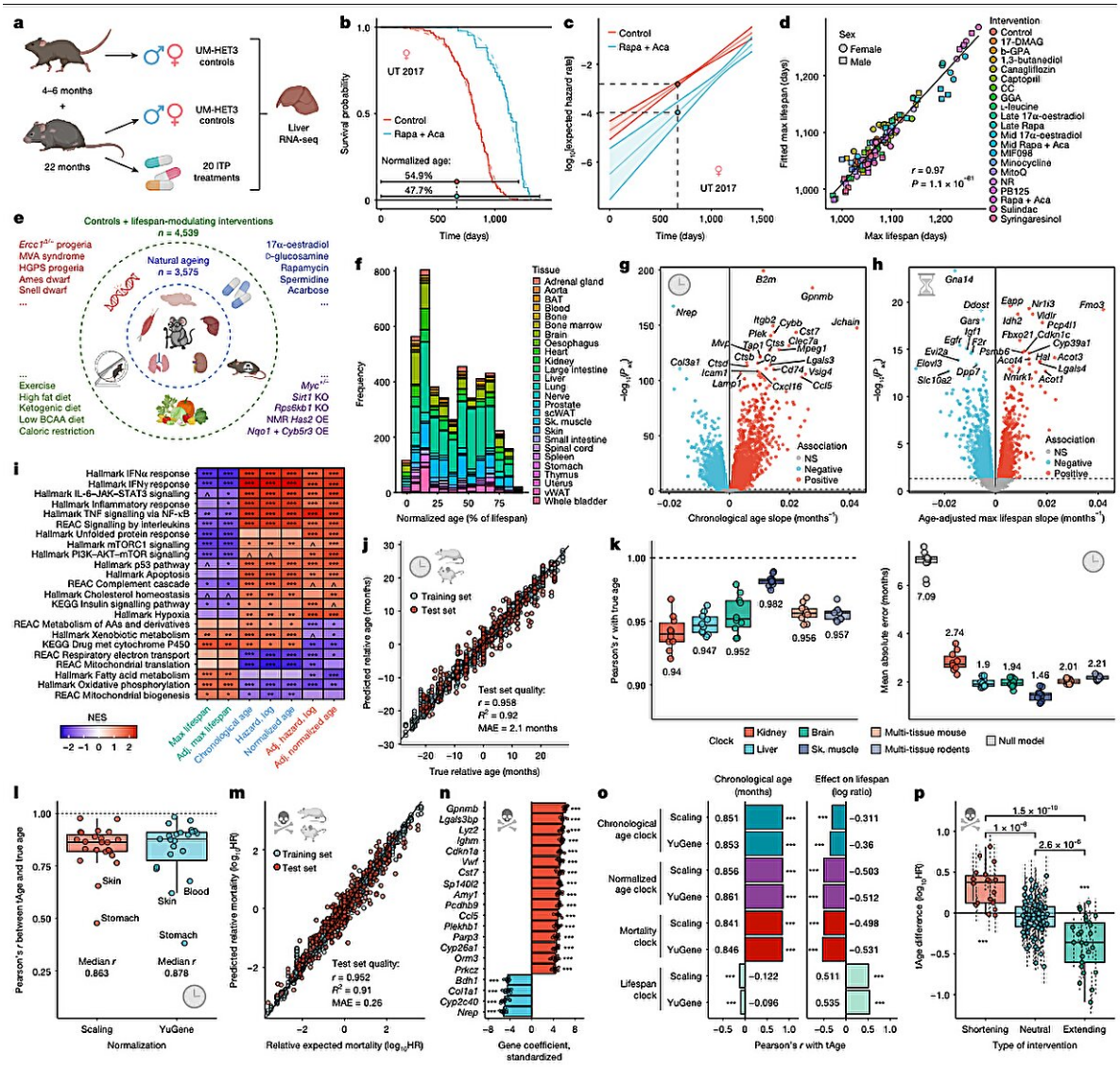
markers across more than 11,000 samples from mice, rats, macaques, and humans, researchers developed a universal aging clock.

What can it do? It can predict how close an individual is to death, detect chronic diseases, and measure signs of rejuvenation or healthy aging, making it a promising tool for identifying longevity treatments.

The findings are published in *Nature*.

Clocking biology

Aging involves the gradual accumulation of a wide variety of molecular and cellular damage over time in the body, which can cause a decline in the function of biological processes, including those involved in growth and repair. Studies have shown that these changes can be influenced by genetic conditions, diet, medications, and diseases such as Hutchinson-Gilford progeria syndrome, which is known to cause rapid aging.



Scientists build universal gene-expression clocks for mammals. Credit: *Nature* (2026). DOI: 10.1038/s41586-026-10542-3

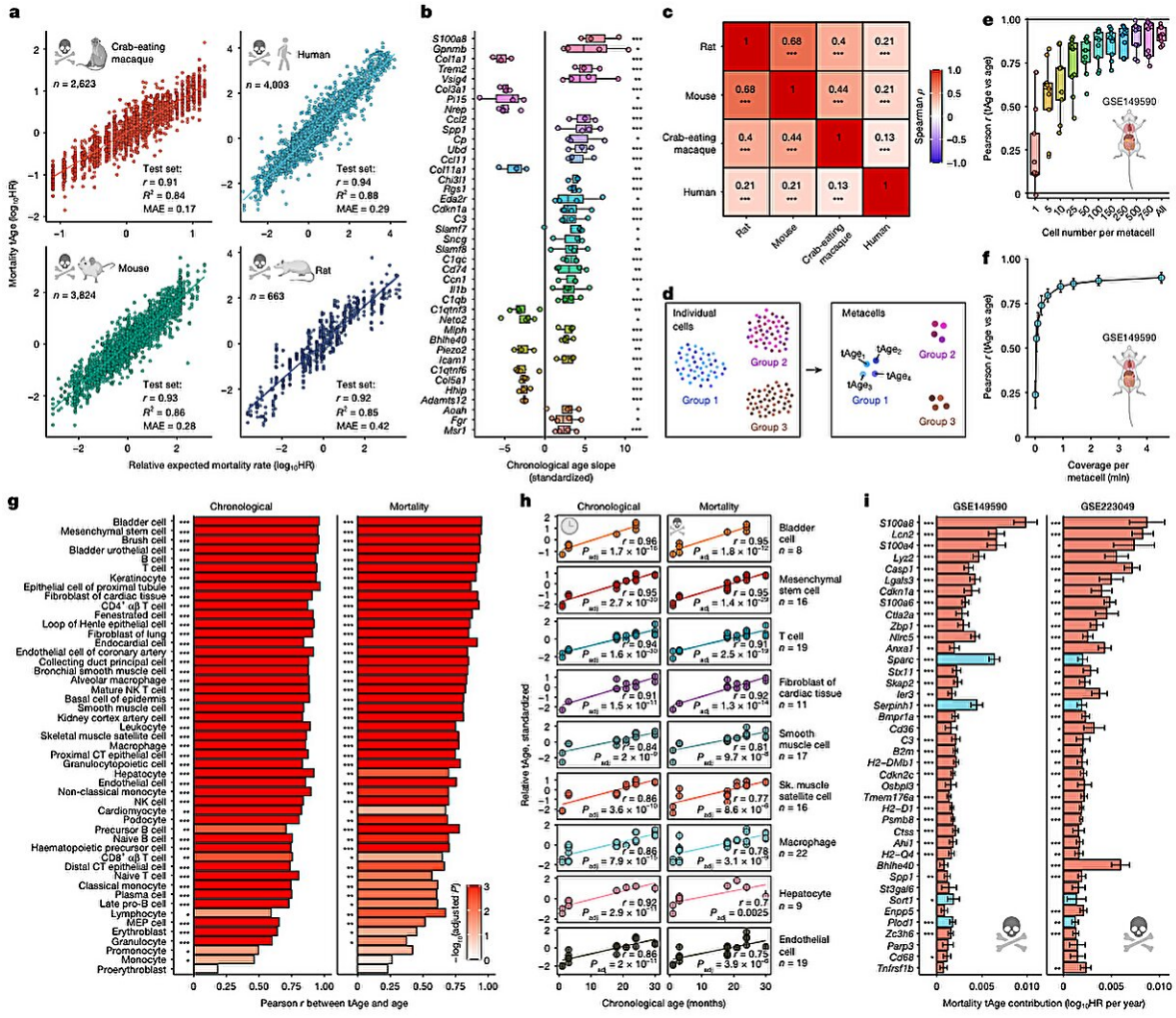
Scientists have been trying to estimate these changes using different biological clocks. Epigenetic clocks, for instance, measure chemical changes to DNA such as methylation to predict chronological age, which is the time passed since birth.

Whereas, transcriptomic clocks look at gene expression patterns in biological samples like blood or tissues to estimate biological age, which reflects how old cells and tissues are. Then there are hazard or expected mortality clocks, which predict instantaneous mortality risk and molecular age, reflecting the accumulation of actual biological damage rather than chronological age.

However, a clock that can provide a unified, cross-species view of gene expression changes linked to aging and mortality has been lacking.

Gene-activity powered universal biological clock

In this study, the researchers collected a large amount of gene expression data from more than 11,000 samples across 25 different tissues, including liver, brain, and muscle. Their data wasn't limited to humans to ensure their findings were universal across mammals, so they chose three other animals.



Transcriptomic biomarkers of aging and mortality are conserved across mammalian species and cell types. Credit: *Nature* (2026). DOI: 10.1038/s41586-026-10542-3

They identified certain genes, such as GPNMB, CDKN1A, and LGALS3, as universal molecular hallmarks of aging and of increasing risk of death, and they changed in almost identical ways during aging across species.

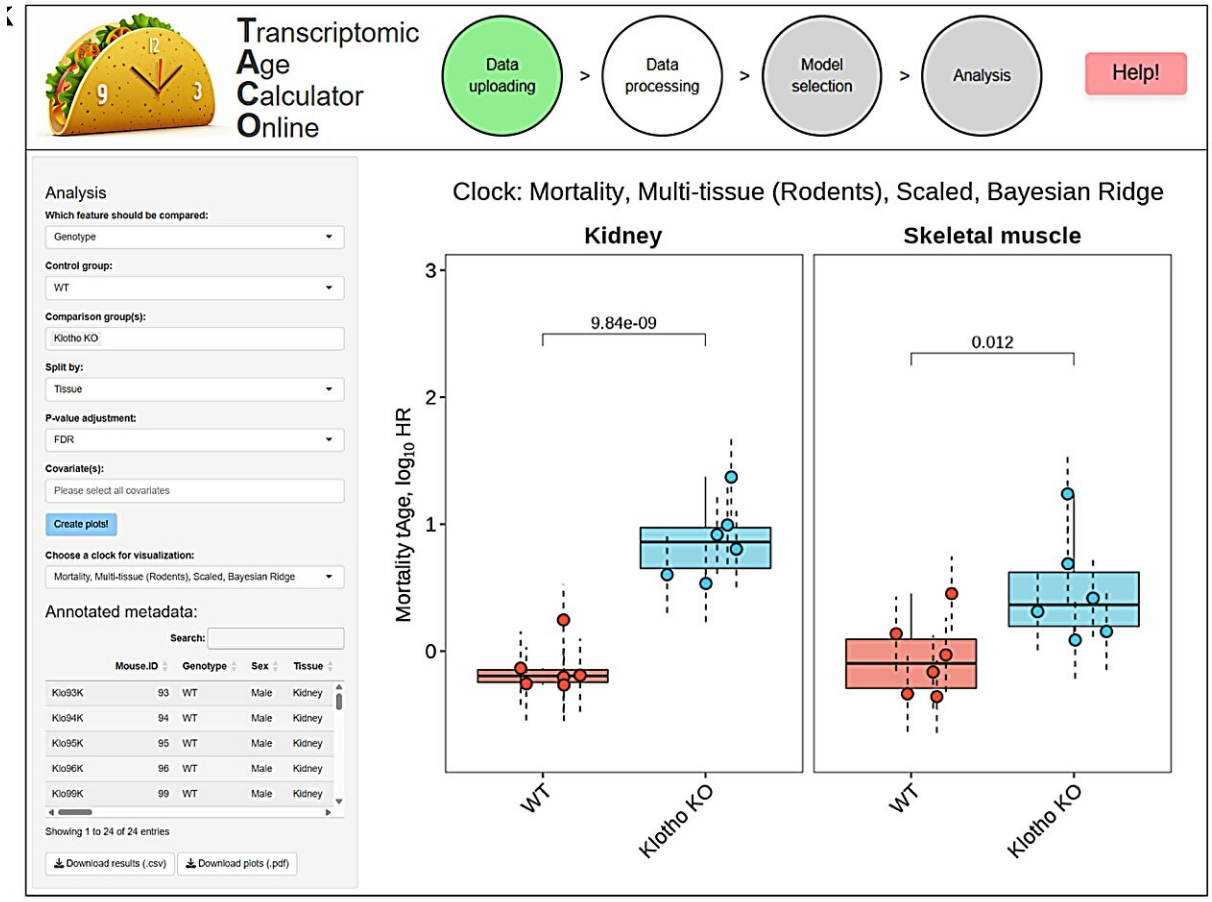
Using this data, the researchers built clocks that could measure three

things: how long a mammal had been alive, its current risk of death based on the amount of biological damage accumulated, and its age, expressed as a percentage of its total expected lifespan.

The study found that aging isn't just one single process. It is organized into different modules, which are groups of genes that handle specific tasks, such as inflammation, energy production, or DNA repair.

By building separate clocks for each cellular module, they discovered that different conditions age different parts of the cell in distinct ways. Chronic diseases, for example, mainly accelerated inflammation-related aging, while caloric restriction primarily affected modules tied to energy use and metabolism.

Based on the insights obtained, the team also created a web application called TACO (Transcriptomic Age Calculator Online), which will allow researchers to calculate the biological age of their own samples.



Transcriptomic Age Calculator Online (TACO; https://app.gladyshevlab.org/TACO/) web app to facilitate application of these biomarkers.

This study reveals the shared signatures and an organized system that controls how mortality develops. Understanding these patterns could help scientists detect and monitor diseases that speed up aging and develop new strategies that enable us to live longer, healthier lives.

More information: Alexander Tyshkovskiy et al, Universal transcriptomic hallmarks of mammalian ageing and mortality, *Nature*

(2026). DOI: 10.1038/s41586-026-10542-3

João Pedro de Magalhães, Gene-expression patterns can be used to estimate mortality risk and chronological age, *Nature* (2026). DOI: 10.1038/d41586-026-01326-w