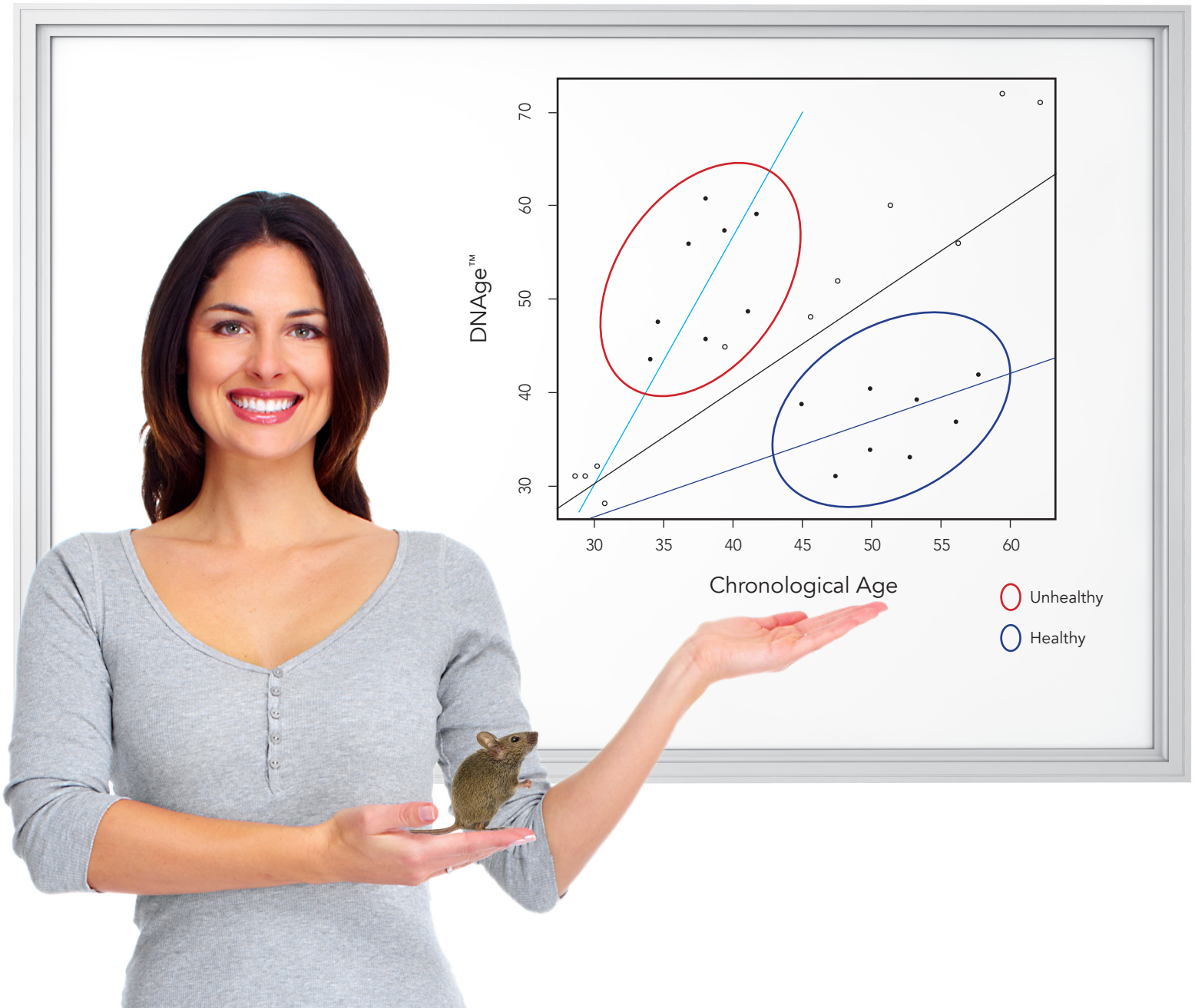


Quantify Aging Precisely

Understanding Health Through Epigenetics



Exclusive License of the Epigenetic Aging Clock from
Dr. Steve Horvath, professor at UCLA

DNAge™ Epigenetic Aging Clock

Highlights:

- Precisely quantify biological age at molecular levels for both human and mouse
- Low cost and high-throughput
- Fast sample processing ability empowered by SWARM™ automation system

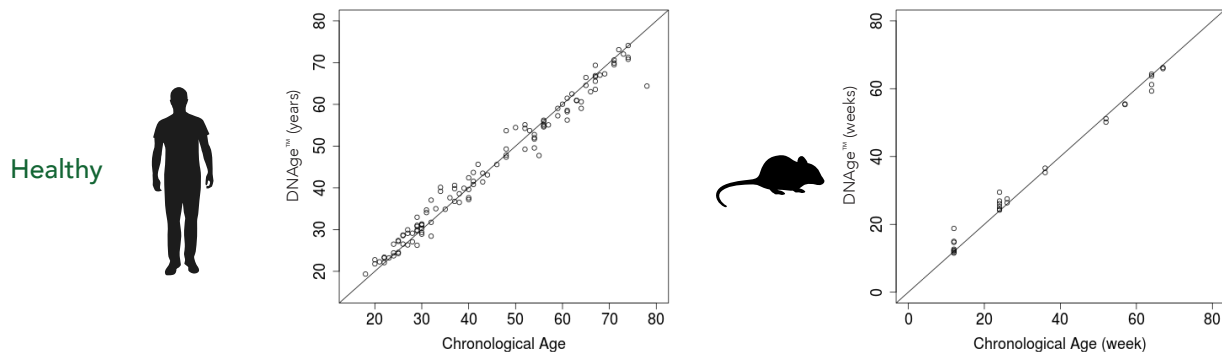
What is the Epigenetic Aging Clock?

Epigenetic modifications refer to heritable changes, which play crucial biology roles independently of genetic changes. DNA methylation, one of the most studied epigenetic modification, is now recognized as a reliable indicator of biological age and reflects diseases status¹⁻⁵. Dr. Steven Horvath's epigenetic aging clock, the golden standard of aging clocks, was built from 8000 samples and his works have been cited more than 600 times. The DNAge™ Epigenetic Aging Clock service is based on Steven Horvath's aging clock and utilizes SWARM™ (Simplified Whole-panel Amplification Reaction Method) technology to analyze DNA methylation patterns of >500 loci and provide epigenetic age predictions in a high throughput manner.

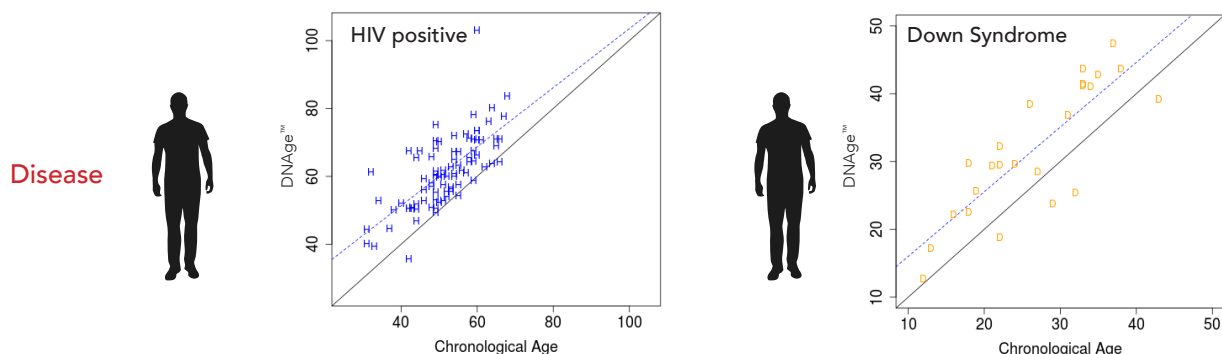
How SWARM™ technology works to predict epigenetic age:



DNAge™ is highly correlated with chronological age:



DNAge™ is altered by certain diseases:

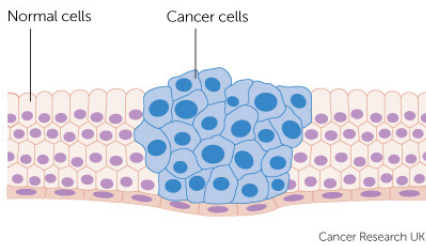


Dotted line: the regression line of DNAm ages. Solid line: a hypothetical line of perfect match between DNAm age and chronological age.

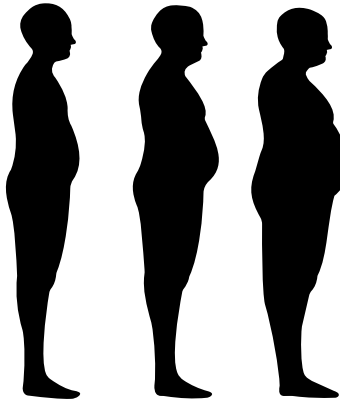
Determining how cancer, obesity, immune diseases, diet, lifestyle and supplements/drugs affect your biological age:

The reversible, dynamic nature of DNA methylation modifications (in contrast to genetic changes) make the DNAge™ clock an ideal tool to directly study aging-related diseases and monitor lifestyle interventions.

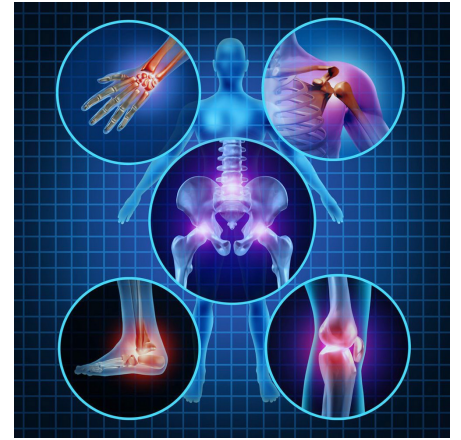
Cancer



Obesity



Immune Disease



Diet



Lifestyle



Supplement/Drug



Please contact us @ www.zymoresearch.com/dnage

Simply send us your samples, and we will provide you with an accurate epigenetic age estimate and detailed data report.

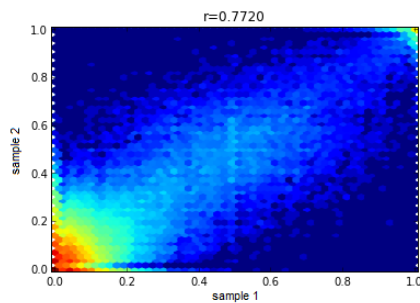
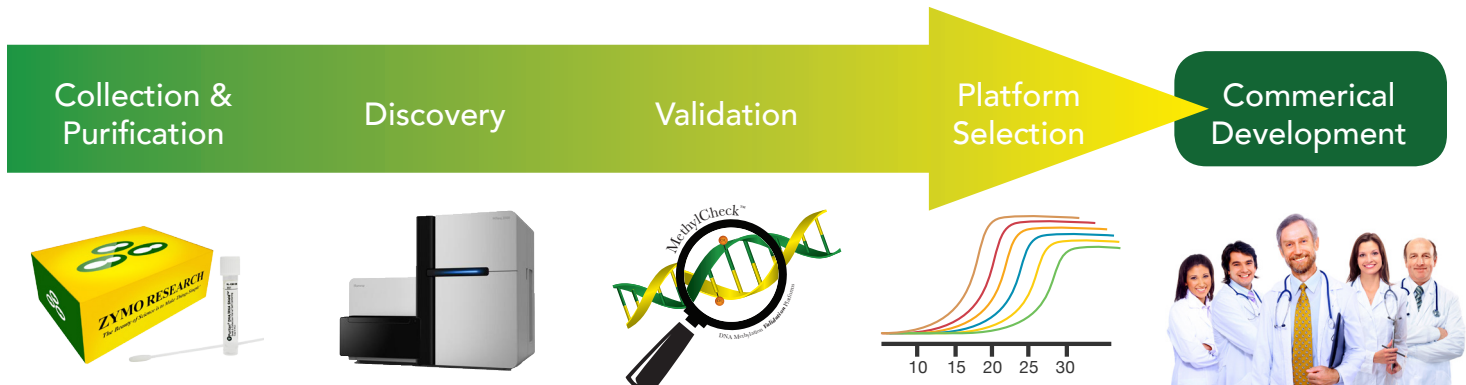
References:

1. Horvath S. DNA methylation age of human tissues and cell types. *Genome Biology*. 2013;14(10): R115. doi:10.1186/gb-2013-14-10-r115.
2. Jones MJ, Goodman SJ, Kober MS. DNA methylation and healthy human aging. *Aging Cell*. 2015;14(6):924-932. doi:10.1111/acel.12349.
3. Horvath S, Langfelder P, Kwak S, et al. Huntington's disease accelerates epigenetic aging of human brain and disrupts DNA methylation levels. *Aging (Albany NY)*. 2016;8(7):1485-1504. doi:10.18632/aging.101005.
4. Horvath S, Garagnani P, Bacalini MG, et al. Accelerated epigenetic aging in Down syndrome. *Aging Cell*. 2015;14(3):491-495. doi:10.1111/acel.12325.
5. Horvath S, Levine AJ. HIV-1 Infection Accelerates Age According to the Epigenetic Clock. *The Journal of Infectious Diseases*. 2015;212(10):1563-1573. doi:10.1093/infdis/jiv277.

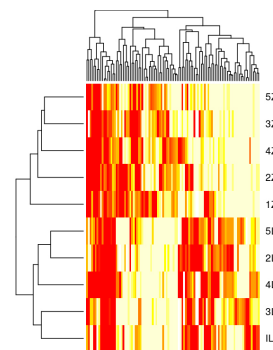
Epigenetic Biomarker Discovery Program

Zymo Research offers a new Epigenetic Biomarker Discovery Program for the development of epigenetic lab diagnostic tests. Whether you are interested in developing epigenetic tests for cancer, developmental disorders, autoimmune diseases, obesity and other anomalies, Zymo Research provides a solution for sample collection through to commercial development. The experts at Zymo Research can help you at any step in the development pipeline by offering a portfolio of products and services for sample collection and purification, biomarker discovery, biomarker validation, platform selection and commercial development.

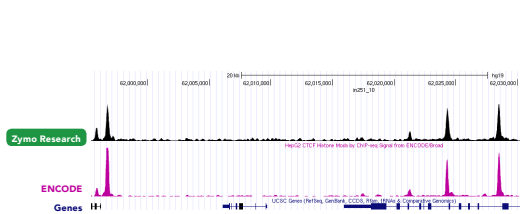
From Collection to Conclusion!



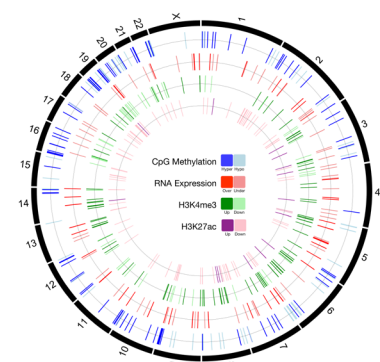
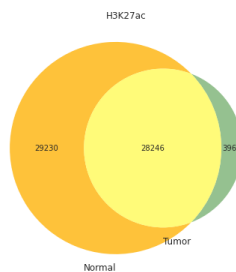
Correlation Plot Heatmap



Clustering Analysis Diagrams



Comparative ChIP-Seq Enrichment Analysis



Integrated Epigenetic & Gene Expression Analysis