

SUPPLEMENTARY DATA

Lower Epigenetic Age Acceleration in Older Adults with Preserved Global Cognitive Performance

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Supplementary Table 1. Comparison of epigenetic clock measures between Healthy Cognitive Aged and controls using the epigenetic age gap approach.

Clock	Healthy Cognitive Aged (Mean $\pm$ SD)	Controls (Mean $\pm$ SD)	t (Welch)	p value	Cohen's d
Horvath age acceleration (years)	-13.50 ± 5.73	1.65 ± 4.73	-12.89	< 0.001	-2.88
GrimAge acceleration (years)	-1.06 ± 3.27	4.82 ± 5.23	-6.02	< 0.001	-1.35
PhenoAge acceleration (years)	-15.63 ± 8.79	-3.12 ± 5.62	-7.58	< 0.001	-1.70
DNAmTL (kb)	6.39 ± 0.27	5.39 ± 0.21	18.56	< 0.001	4.15

Values are presented as mean $\pm$ standard deviation. Epigenetic age gap was defined as epigenetic age minus chronological age, with negative values indicating a younger epigenetic age relative to chronological age. DNAm-derived telomere length (DNAmTL) is expressed in kilobases, with higher values indicating longer telomeres. Between-group comparisons were conducted using Welch's t-test. P-values are two-sided and unadjusted. Effect sizes are reported as Cohen's d.

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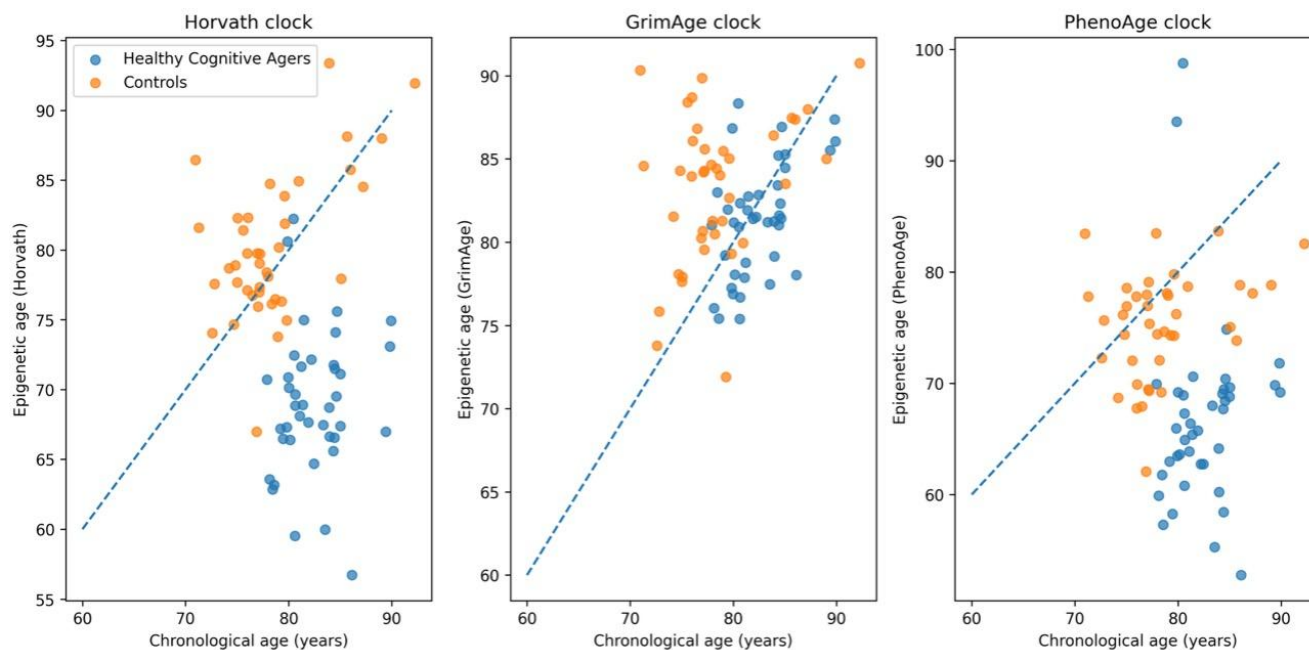
Supplementary Table 2. Sensitivity analysis restricted to participants aged ≥ 80 years.

Clock	Healthy Cognitive Agers (n=40) Mean $\pm$ SD	Controls ≥ 80 years (n=8) Mean $\pm$ SD	t (Welch)	p- value	Cohen's d
Horvath residual-based EAA	-2.34 ± 5.73	11.71 ± 4.91	-7.18	<0.001	-2.50
PhenoAge residual-based EAA	-1.56 ± 8.52	7.79 ± 3.53	-5.09	<0.001	-1.18
GrimAge residual-based EAA	-0.33 ± 3.02	1.64 ± 2.03	-2.29	0.038	-0.67
DNAmTL, kb	6.39 ± 0.27	5.41 ± 0.18	13.27	<0.001	3.76

Values are presented as mean $\pm$ standard deviation. Residual-based epigenetic age acceleration (EAA) was calculated as the residual from linear regression models of epigenetic age on chronological age, with negative values indicating lower-than-expected epigenetic age and positive values indicating higher-than-expected epigenetic age relative to chronological age. DNAm-derived telomere length (DNAmTL) is expressed in kilobases, with higher values indicating longer telomeres. Between-group comparisons were performed using Welch's t-test. P-values are two-sided and unadjusted. Effect sizes are reported as Cohen's d. Negative Cohen's d values indicate lower residual-based EAA in Healthy Cognitive Agers compared with age-restricted controls, whereas positive Cohen's d values for DNAmTL indicate longer telomeres in Healthy Cognitive Agers.

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Supplementary Figure 1



Supplementary Figure 1. Chronological age versus epigenetic age in Healthy Cognitive Agers and controls. Scatterplots show the relationship between chronological age and epigenetic age estimated using the Horvath, GrimAge, and PhenoAge clocks. The dashed line represents the line of identity. Healthy Cognitive Agers (n=40) consistently exhibit lower epigenetic age relative to chronological age across all clocks compared with controls (n=40). Between-group comparisons were performed using Welch's t-test. P-values are two-sided and unadjusted.