Supplemental Material

Table S1. Differences of general characteristics between hypertensive and non-hypertensive participants (N=280).

Characteristics	Hypertension (n=147)	Non-hypertension (n=133)	P value
Sex, Female, n (%)	89 (60.5)	71 (53.4)	0.276
Chronological age (years, mean ±SD)	81.3±16.2	75.5±16.1	0.003
DNAm age (years, mean ± SD)	79.9±12.4	74.2±9.96	<0.001
ΔAge† (years, mean ± SD)	-2.54±0.61	-3.83±0.56	<0.001
Aging rate*(mean ± SD)	0.965±0.10	0.931±0.09	0.001
BMI (kg/m^2, mean ±SD)	22.3 ±4.15	21.5±3.06	0.057
Socioeconomic status, n (%)			
Lower	56 (38.1)	54 (40.6)	0.690
Middle	49 (33.3)	38 (28.6)	
Higher	42 (28.6)	41 (30.8)	
Cigarette smoking, n (%)	19 (12.9)	17 (12.8)	0.990
Alcohol drinking, n (%)	42 (28.6)	25 (18.8)	0.080
Sleep duration (hours, mean ± SD)	9.76±1.68	9.46±1.54	0.121
Physical activity, n (%)	70 (47.6)	60 (45.1)	0.764
Diabetes, n (%)	13 (8.8)	10 (7.5)	0.853
Hyperlipidemia, n (%)	62 (42.2)	39 (29.3)	0.035

Abbreviations: BMI, body mass index; SD, standard deviance; DNAm age, DNA methylation age. †ΔAge was calculated as residual from regressing DNAm on chronological age. *Aging rate was calculated as the methylation age divided by chronological age. Data are presented as n (%) for categorical variables, and mean ± SD for continuous variables.

Table S2. Univariate analysis of related factors with epigenetic age acceleration (N=280).

Factors	β (95% CI) of ΔAge	P value	β (95% CI) of aging rate	P value
Sex (Female vs. Male)	2.08 (0.65, 3.51)	<0.001	0.016 (0.005, 0.027)	<0.001
BMI (kg/m^2)	0.492(0.161, 0.823)	0.004	0.007(0.002, 0.011)	0.003
Socioeconomic status				
Middle vs. Lower	-3.95(-6.84, -1.06)	0.008	-0.052(-0.088, -0.016)	0.005
Upper vs. Lower	-6.00 (-8.92, -3.07)	<0.001	-0.078(-0.115, -0.042)	<0.001
Cigarette smoking (yes vs. no)	4.57(0.916, 8.23)	0.015	0.071(0.023, 0.12)	0.004
Alcohol drinking (yes vs. no)	1.36(-1.54, 4.26)	0.358	0.024(-0.015, 0.062)	0.234
Sleep (hours)	-2.80 (-3.49, -2.11)	<0.001	-0.039(-0.048, -0.03)	<0.001
Physical activity (yes vs. no)	-2.36 (-4.56, -0.164)	0.010	0.046(0.016, 0.076)	<0.001
Diabetes (yes vs. no)	2.99 (-1.51, 7.48)	0.194	0.038(-0.022, 0.098)	0.213
Hyperlipidemia (yes vs. no)	1.01(-1.56, 3.59）	0.442	0.009(-0.024, 0.041)	0.603

Abbreviations: BMI, body mass index. ΔAge was calculated as residual from regressing DNAm on chronological age. Aging rate was calculated as the methylation age divided by chronological age.

Table S3. Sensitivity analysis for associations of blood pressure with epigenetic age acceleration in participants without taking antihypertensive medications (n=241)

Variables	Estimated changes of ΔAge (years) per 10 mmHg increase in blood pressure		Estimated changes of ageing rate per 10 mmHg increase in blood pressure	
	β (95%CI)	*P*	β (95%CI)	*P*
SBP	0.613 (0.019, 1.21)	0.045	0.009(0.001, 0.017)	0.033
DBP	-0.17(-1.14, 0.80)	0.731	-0.002(-0.015, 0.011)	0.769
PP	0.973 (0.27, 1.68)	0.008	0.012(0.003, 0.022)	0.012
MAP	0.37(-0.542, 1.28)	0.428	0.005(-0.007, 0.017)	0.440

Abbreviations: SBP, systolic blood pressure; DBP, diastolic blood pressure; PP, pulse pressure; MAP, mean arterial pressure; β, regression coefficients; CI, confidence interval. ΔAge was calculated as residual from regressing DNAm age on chronological age. Ageing rate was calculated as DNAm age divided by chronological age. The β was estimated with adjustment for sex, BMI, socioeconomic status, cigarette smoking, alcohol drinking, physical activity, sleep duration, hyperlipidemia, and diabetes

Table S4. Sensitivity analysis for associations between blood pressure and epigenetic age acceleration based on Hannum's clock (n=280)

Variables	Estimated changes in ΔAge (years) by tertiles of blood pressure parameters			Per 10 mmHg increase in blood pressure	*P* value for trend
	T1 β (95%CI)	T2 β (95%CI)	T3 β (95%CI)		
SBP	≤129 mmHg	129 to 147 mmHg	>147 mmHg		
ΔAge	0(referent)	1.298(-1.179, 3.775)	4.021(1.598, 6.445)	0.682(0.281, 1.083)	0.001
Ageing rate	0(referent)	0.014(-0.02, 0.049)	0.052(0.018, 0.085)	0.009(0.003, 0.014)	0.003
DBP	≤74 mmHg	74 to 83 mmHg	>83 mmHg		
ΔAge	0(referent)	-0.172(-2.711, 2.367)	0.001(-2.546, 2.548)	-0.029(-0.799, 0.741)	0.993
Ageing rate	0(referent)	-0.001(-0.036, 0.034)	0.001(-0.034, 0.035)	-0.001(-0.01, 0.011)	0.966
PP	≤53 mmHg	53 to 66 mmHg	>66 mmHg		
ΔAge	0(referent)	1.283(-1.138, 3.705)	4.864(2.472, 7.256)	1.221(0.696, 1.745)	<0.001
Ageing rate	0(referent)	0.011(-0.022, 0.045)	0.061(0.028, 0.094)	0.016(0.008, 0.023)	<0.001
MAP	≤93 mmHg	93 to 105 mmHg	>105 mmHg		
ΔAge	0(referent)	0.335(-2.215, 2.886)	2.464(-0.082, 5.009)	0.561(-0.086, 1.207)	0.054

Ageing rate	0(referent)	0.006(-0.03, 0.041)	0.031(-0.004, 0.066)	0.008(-0.001, 0.016)	0.075

Abbreviations: SBP, systolic blood pressure; DBP, diastolic blood pressure; PP, pulse pressure; MAP, mean arterial pressure; β, regression coefficients; CI, confidence interval. ΔAge was calculated as residual from regressing DNAm age on chronological age. Ageing rate was calculated as DNAm age divided by chronological age. All models were adjusted for sex, BMI, socioeconomic status, cigarette smoking, alcohol drinking, physical activity, sleep duration, hyperlipidemia, and diabetes.

Table S5. The associations of hypertension with epigenetic age acceleration (N=280).

Models	β (95% CI) of ΔAge	β (95% CI) of aging rate
Crude model for hypertension		
No	0 (referent)	0 (referent)
Yes	3.96 (1.53, 6.40)	0.051(0.02-0.082)
P value	0.002	0.001
Adjusted model for hypertension		
No	0 (referent)	0 (referent)
Yes	3.10 (1.07-5.13)	0.04(0.015-0.065)
P value	0.003	0.002

Abbreviations: ΔAge was calculated as residual from regressing DNAm on chronological age. Aging rate was calculated as the methylation age divided by chronological age. Adjusted models were adjusted for sex, BMI, socioeconomic status, cigarette smoking, alcohol drinking, physical activity, sleep duration, hyperlipidemia, and diabetes.

Table S6. Summary of EWAS-derived differentially methylated region analysis in relation to hypertension (N=280).

DMR location (hg 19)	No. (CpGs)	Mean effect*	P	Nearest gene
chr1:203320223-203320732	10	0.255	0.004	FMOD
chr1:55267046-55267293	8	-0.205	0.019	TTC22
chr2:37423361-37424104	11	-0.187	0.009	CEBPZOS
chr4:57547347-57548290	9	0.222	0.009	HOPX
chr5:68628240-68628856	8	-0.211	0.016	CCDC125
chr5:135416029-135416613	9	-0.18	0.023	MIR886
chr6:32551749-32552453	10	-0.24	0.005	HLA-DRB1
chr6:31650735-31651070	11	0.161	0.014	-
chr7:27183133-27183990	16	0.186	0.002	HOXA5
chr10:81967195-81967666	7	0.255	0.007	LINC00857
chr12:75784855-75785295	9	-0.19	0.018	GLIPR1L2

*Mean effect was estimated from limma models of Beta-values. P values were false discovery rate (FDR) values.

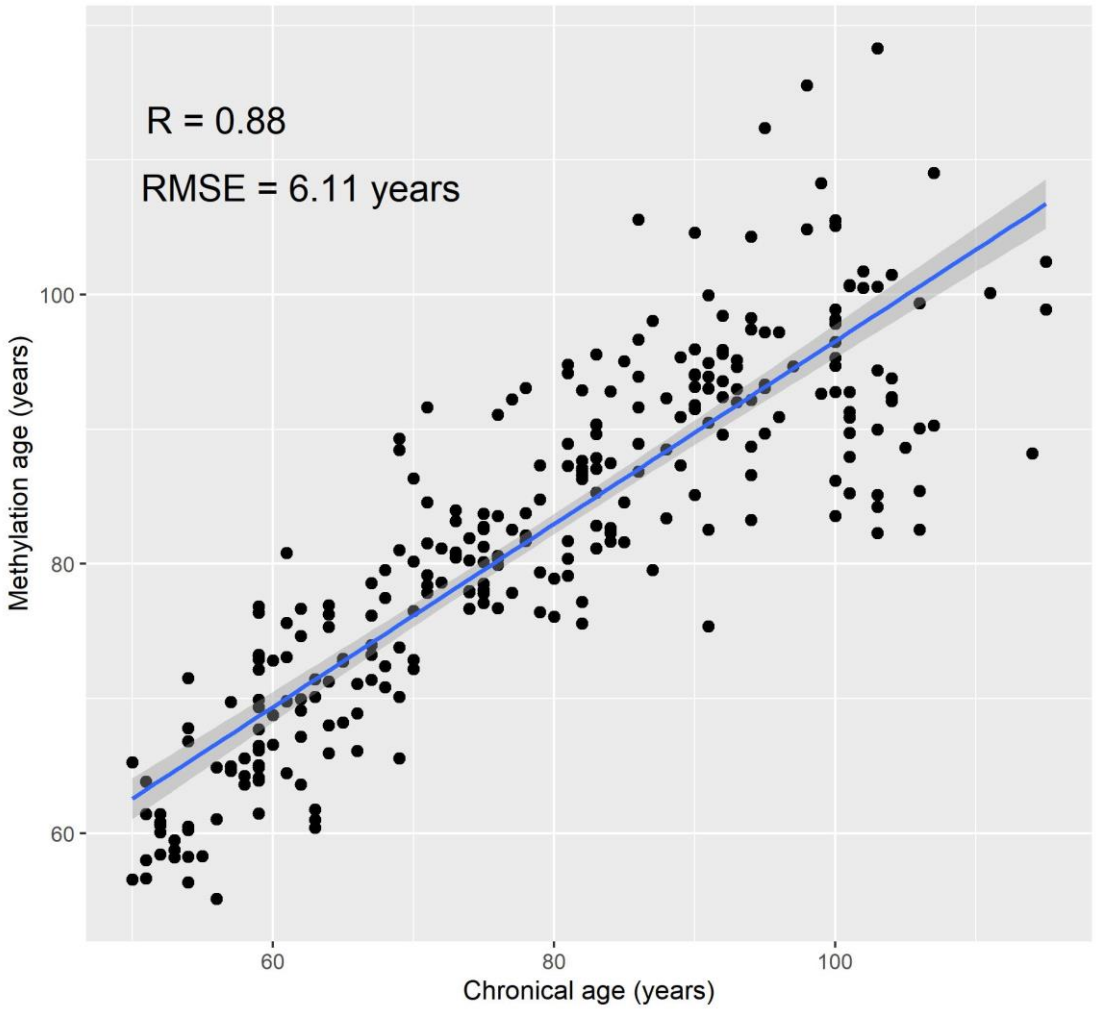

Figure S1. Scatter plot for the correlation between chronological age and Horvath's DNAm age in the elder study population (N=280). R denotes the Pearson's correlation coefficients. RMSE denotes the root-mean-square error.

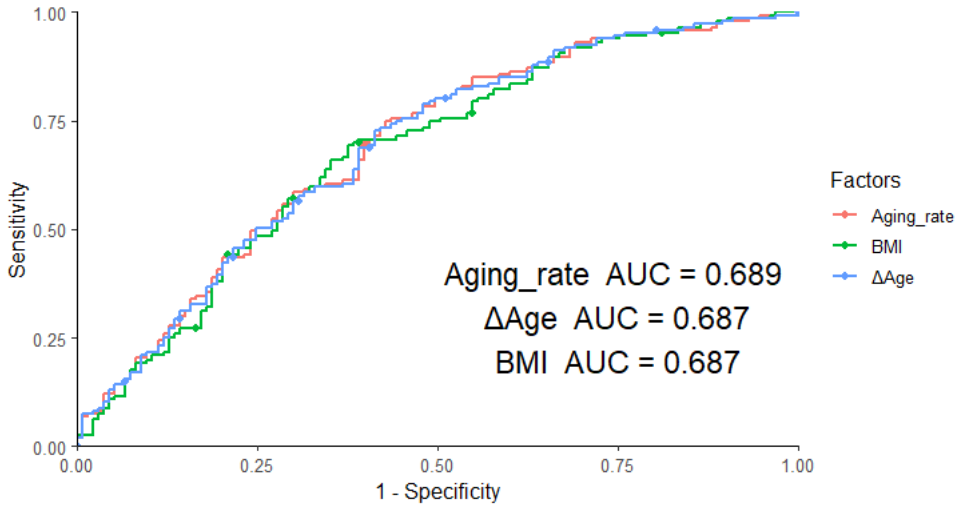

Figure S2. Receiver operating characteristic (ROC) curve analysis for epigenetic age acceleration (ΔAge and aging rate) and BMI to distinguish subjects with hypertension (N=280).