

Supplementary

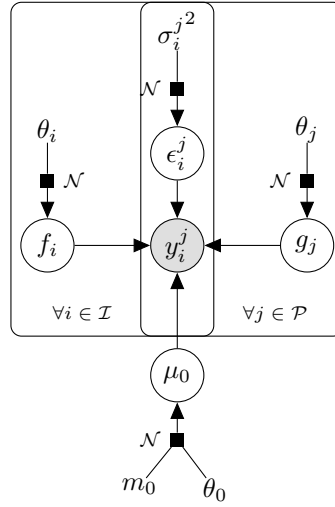


Fig. S1 Graphical model of dependencies between variables in the multi-mean Gaussian processes model.

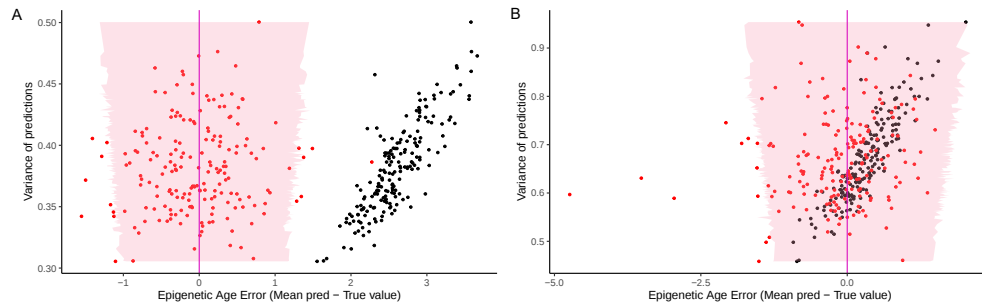


Fig. S2 Illustration of the bias between true age and epigenetic age when estimated from the PedBE clock (**A**) compared with the Horvath skin&blood clock (**B**). The predicted mean ages are used as a reference and displayed as a purple line; the pink region corresponds to the associated 95% credible intervals; each red dot corresponds to the error with the epigenetic age computed using *true observed methylation values*. Each black dot corresponds to the error with *the true age* at the time of data collection.

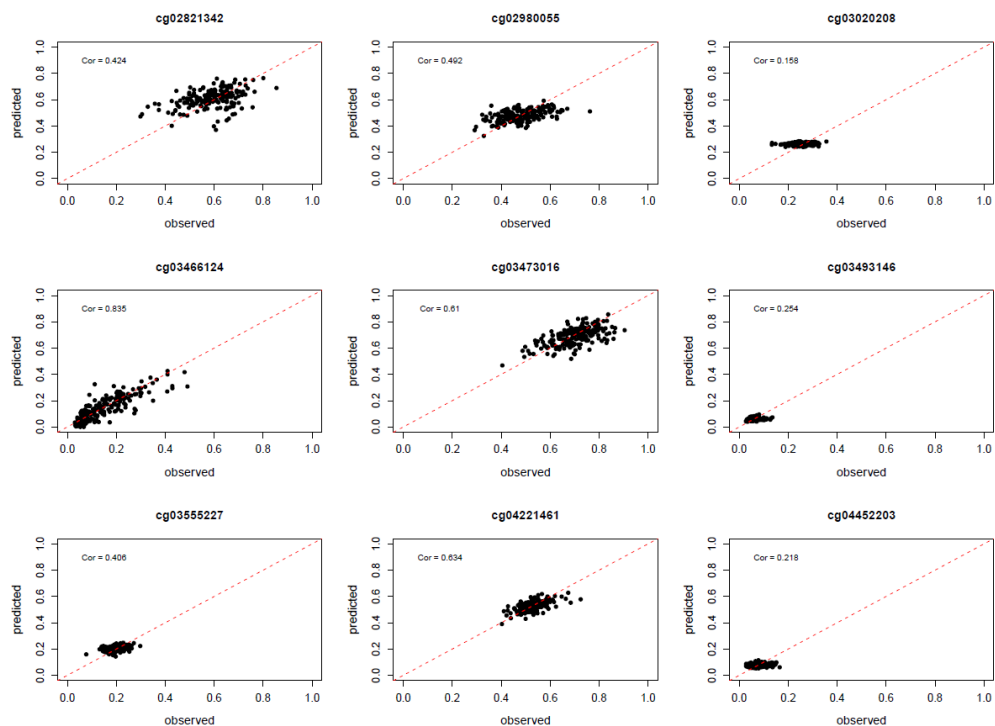


Fig. S3 Example of predicted methylation values against observed methylation values for the CpGs in PedBE clock plotted for 6 illustrative CpGs.

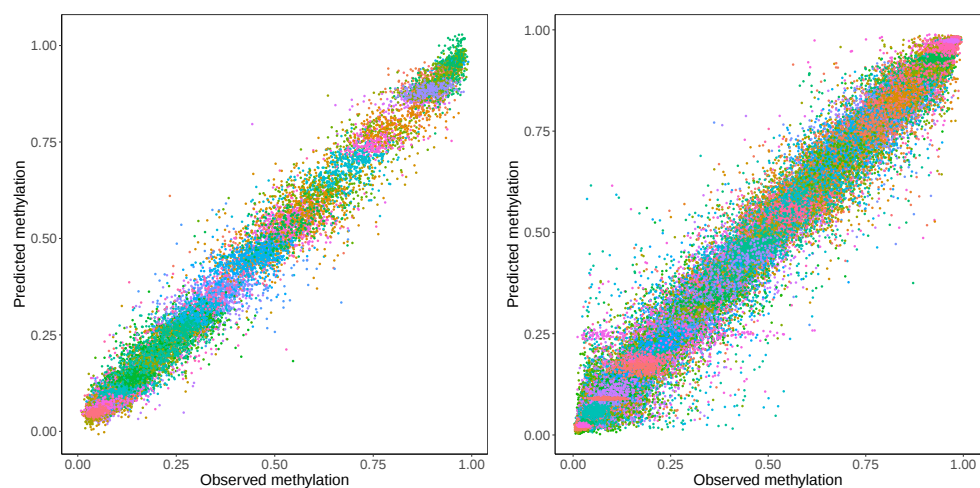


Fig. S4 Mean predicted values (y-axis) plotted against observed methylation values (x-axis) for each CpG-individual couple of the testing set (188 individuals) involved in the PedBE clock (91 CpGs, **left**) and the Horvath skin&blood clock (368 CpGs, **right**). Each colour corresponds to a specific CpG.

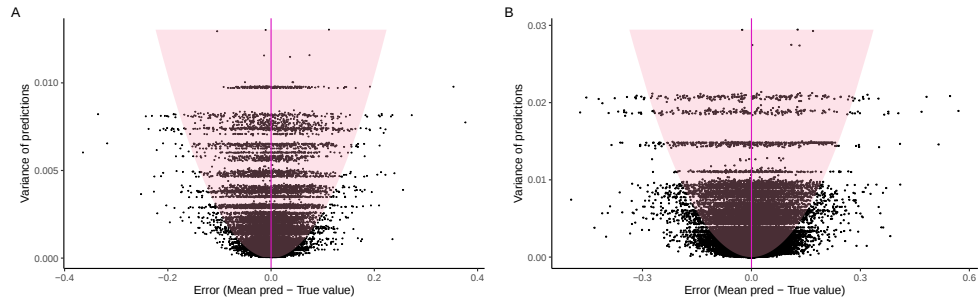


Fig. S5 Distribution of prediction errors (differences between predicted and observed methylation value) sorted by predictive variance for both PedBE clock (**A**) and skin&blood (**B**). For each individual-CpG couple of the testing set (188 individuals), each error value is displayed as a black dot, and the pink region represents the 95% credible interval associated with the predicted mean (purple vertical line).

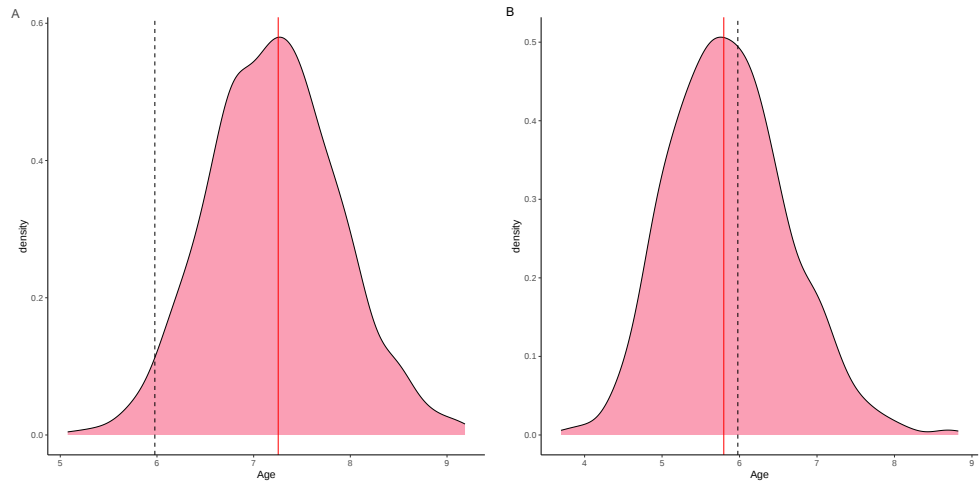


Fig. S6 Posterior distribution of the epigenetic age (pink area) estimated from PedBE (**A**) and Horvath skin and blood (**B**) clocks, using *CpG predictions* at 6 years for the same illustrative individual. The true age is displayed as a dashed black line, while the red vertical line represents the epigenetic age estimated from the *true CpG values* at 6 years.

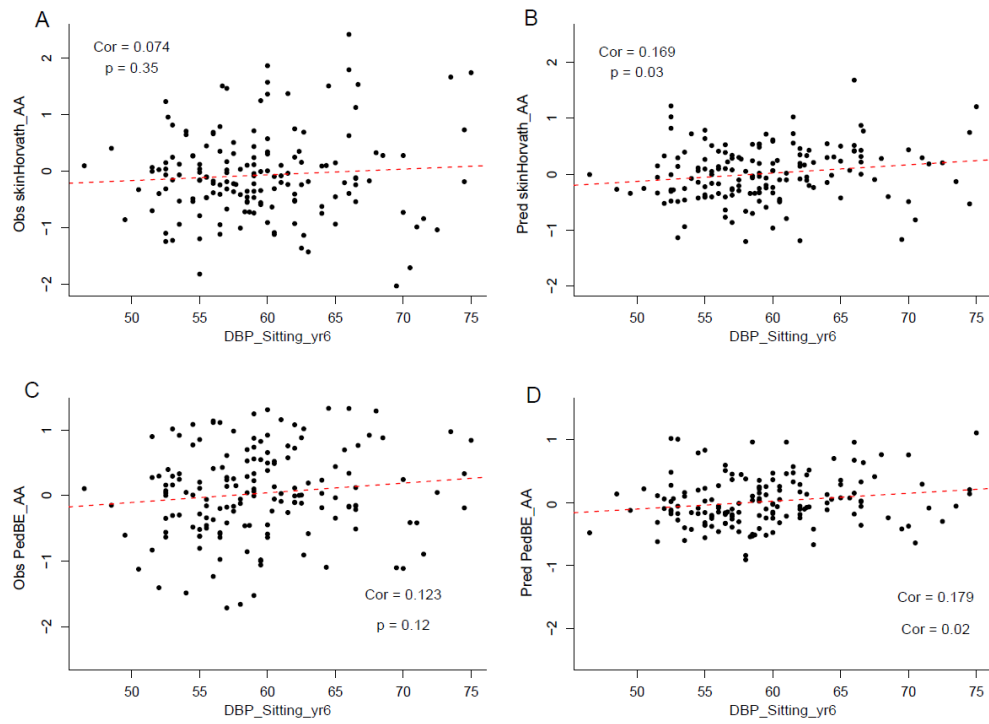


Fig. S7 Scatter plot of age acceleration against diastolic blood pressure measured at 6 years old

Table S1 Demographic Information of training and testing samples.

Variables		Training: Timepoints				Testing: Timepoints			
		3 months	9 months	48 months	72 months	3 months	9 months	48 months	72 months
Ethnicity	Chinese	61 (55.5%)				114 (60.6%)			
	Malay	30 (27.3%)				41 (21.8%)			
	Indian	19 (17.3%)				33 (17.6%)			
Sex	Male	53 (48.2%)				93 (49.5%)			
Gestational age (weeks)		38.8 (1.1)				38.7 (1.3)			
Birthweight (kg)		3.1 (0.4)				3.1 (0.5)			
Age at collection (years)		0.26 (0.02)	0.76 (0.02)	4.05 (0.09)	6.05 (0.10)	0.25 (0.02)	0.76 (0.03)	4.08 (0.09)	6.06 (0.09)
Weight (kg)		6.1 (0.8)	8.6 (1.0)	16.3 (3.4)	20.8 (4.9)	6.1 (0.8)	8.5 (1.1)	16.5 (3.0)	20.9 (4.3)
Length/Height (cm)		60.9 (2.4)	71.5 (2.9)	101.7 (4.8)	114.8 (5.5)	60.9 (2.5)	71.3 (2.9)	102.3 (4.3)	115.4 (5.0)
Head circumference (cm)		39.9 (1.2)	44.5 (1.4)	49.8 (1.4)	50.9 (1.5)	39.9 (1.4)	44.3 (1.4)	49.8 (1.5)	51.0 (1.5)
Systolic blood pressure		-	-	-	102.0 (9.0)	-	-	-	100.2 (7.8)
Diastolic blood pressure		-	-	-	60.2 (5.8)	-	-	-	59.4 (5.6)

Table S2 Average (sd) values of RMSE and CIC_{95} for predicted epigenetic age compared with observed epigenetic age and chronological age at 6 years for 188 testing individuals, using Horvath skin&blood and PedBE clocks.

Epigenetic Clock	Epigenetic Age		True Age	
	RMSE	CIC_{95}	RMSE	CIC_{95}
Skin&Blood	0.70 (2.03)	95.20 (21.41)	0.328 (0.54)	99.50 (7.29)
PedBE	0.36 (0.59)	93.6 (24.5)	4.09 (1.65)	4.79 (21.4)