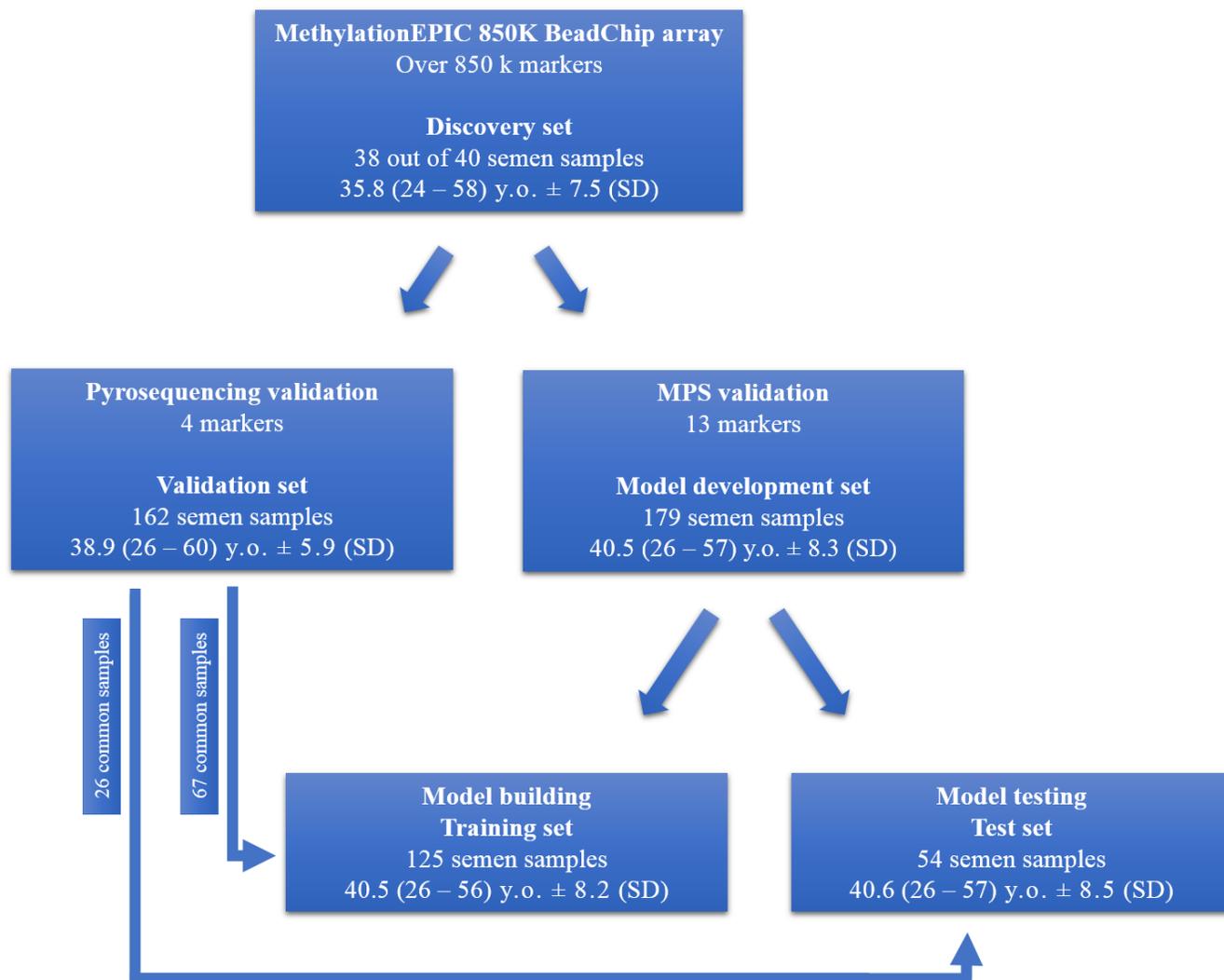
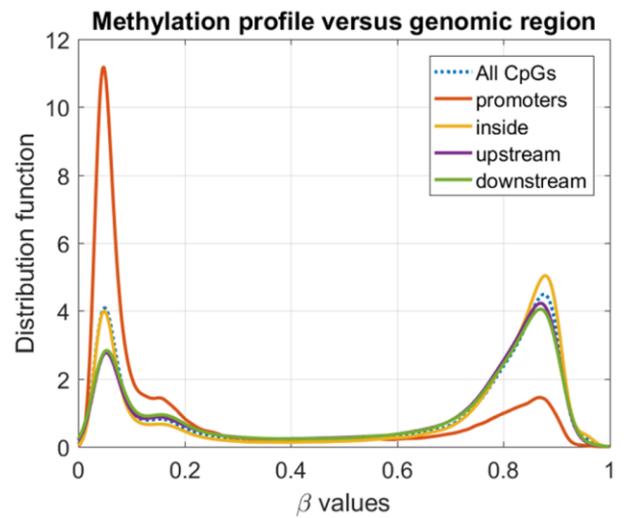
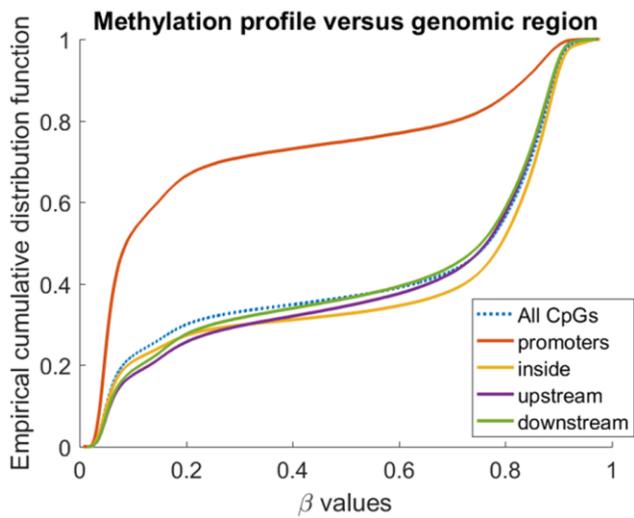


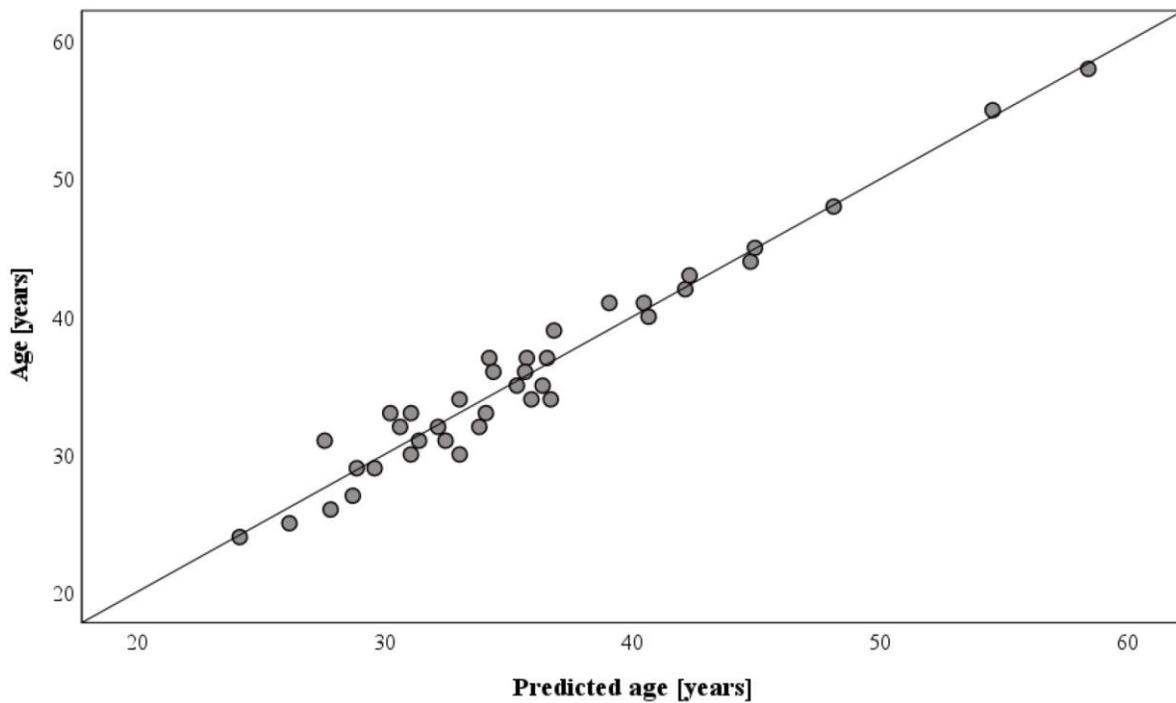
## SUPPLEMENTARY FIGURES



Supplementary Figure 1. Marker selection workflow and model development.



Supplementary Figure 2. Methylation profile in various genome regions.



Supplementary Figure 3. Parameters of the initial predictive model based on 10 CpG markers. F-stat = 47.7;  $P$ -value =  $3.56 \times 10^{-14}$ ;  $R^2_{\text{adjusted}} = 0.94$ ; Absolute error for age prediction: Range: [0.06, 3.42]. Mean value: 1.20; Standard deviation: 0.93; RMSE = 1.5.