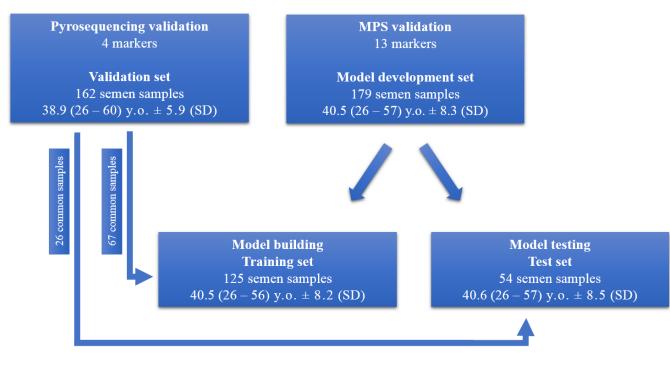
SUPPLEMENTARY FIGURES

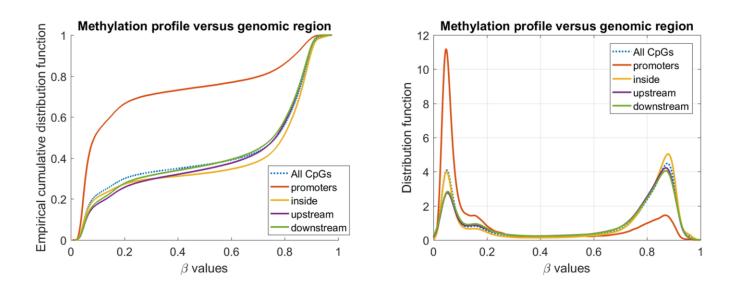
MethylationEPIC 850K BeadChip array Over 850 k markers

> **Discovery set** 38 out of 40 semen samples 35.8 (24 – 58) y.o. ± 7.5 (SD)

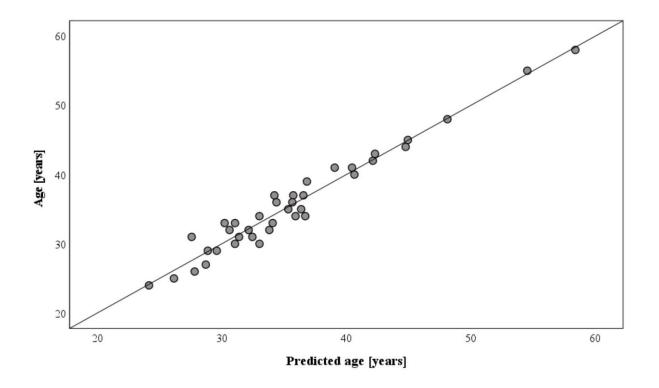




Supplementary Figure 1. Marker selection workflow and model development.



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 = 3.56×10^{-14} ; R²_{adjusted}= 0.94; Absolute error for age prediction: Range: [0.06. 3.42]. Mean value: 1.20; Standard deviation: 0.93; RMSE = 1.5.