

## SUPPLEMENTARY TABLE

**Supplementary Table 1. Description of the four epigenetic clocks used.**

Epigenetic clock	Mathematical approach	Formula
Bekaert [1]	Multiple Quadratic Regression (MQR)	$26.444119 - 0.201902 \times ASPA \text{ (CpG}_1) - 0.239205 \times EDARADD \text{ (CpG}_1) + 0.0063745 \times ELOVL2 \text{ (CpG}_6)^2 + 0.6352654 \times PDE4C \text{ (CpG}_1)$
Thong [2]	Multiple Linear Regression (MLR)	$-20.372 + 0.830 \times ELOVL2 \text{ (CpG}_5) + 1.723 \times KLF14 \text{ (CpG}_2) + 0.715 \times TRIM59 \text{ (CpG}_5)$
Garali [3]	Multiple Quadratic Regression (MQR)	$13.4944951 - 0.8224263 \times ELOVL2 \text{ (CpG}_6) - 0.0001978 \times ELOVL2 \text{ (CpG}_4)^2 + 0.0143482 \times ELOVL2 \text{ (CpG}_6)^2 + 0.004438 \times ELOVL2 \text{ (CpG}_7)$
Garali [3]	Gradient Boosting Regressor (GBR)	DNA methylation of <i>ELOVL2</i> (CpG <sub>6</sub> and CpG <sub>7</sub> ) was used as an input testing set in the provided GBR R code using a training set of 1028 samples [3]

## REFERENCES

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