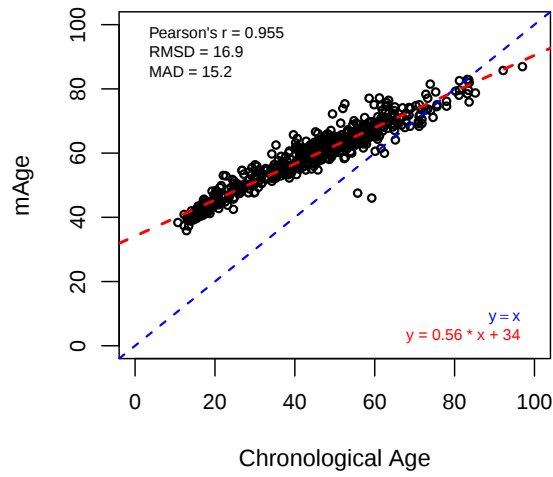
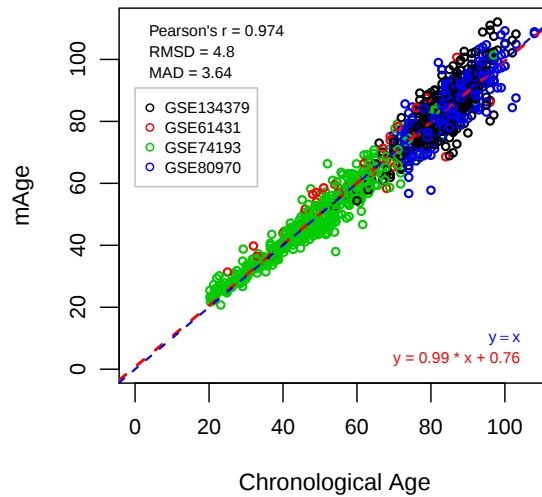


Supplementary figures



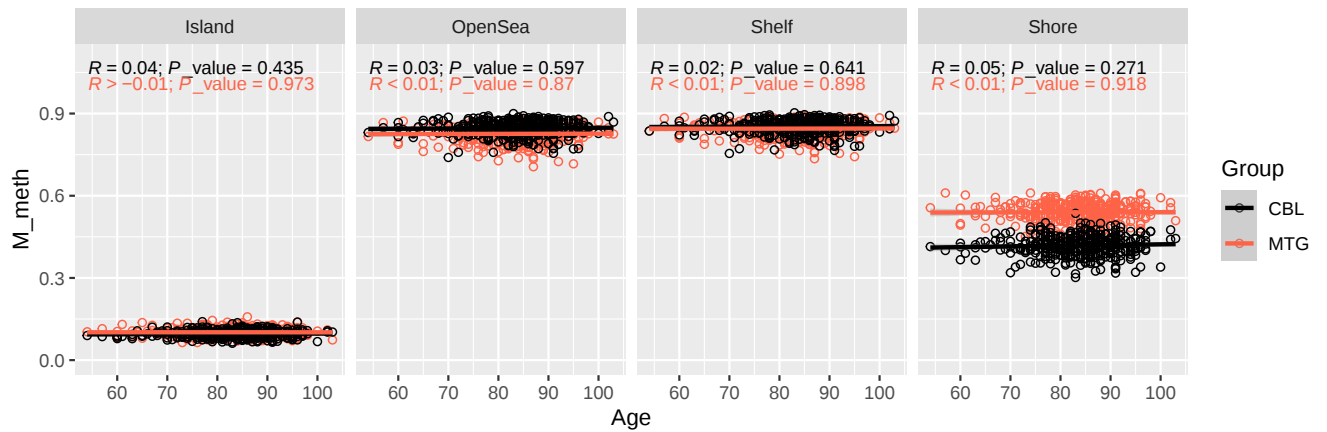
Supplementary Figure 1: Young cortex tissues are overestimated by $\text{CerebellumClock}_{\text{specific}}$. The cortex samples are from GSE74193.



Supplementary Figure 2: The leave-one(fold)-out cross validation evaluate the age prediction performance of $\text{CortexClock}_{\text{common}}$. Colors represent samples from different datasets.



Supplementary Figure 3: The fluctuation of the mean methylation level is not correlated with chronological age either in the CBL or in the MTG.



Supplementary Figure 4: The fluctuation of the mean methylation level is not correlated with chronological age in any of the four genomic regions, i.e. island, open sea, shelf and shore. Red denotes CBL sample and cyan denotes MTG sample.