



**S3 Fig. Age-associated DNAm changes in AML.**

(A)  $\beta$ -values were compared in DNAm profiles of normal blood and AML. CpGs with age-associated hypo- and hypermethylation (green and purple, respectively) are indicated as defined in Fig 1A ( $\rho > 0.5$  or  $\rho < -0.5$ ). CpGs with age-associated hypermethylation reveal higher DNAm levels in AML. (B) Correlation of epigenetic age predictions using either the 99 CpG model or Horvath-predictor on AML profiles. (C) Heatmap analysis of DNAm changes in age-associated CpGs in AML in relation to either chronological age (equivalent to Fig 1D) or epigenetic age-predictions using Horvath-predictor. (D) Correlation coefficients of these  $\beta$ -values revealed that CpGs with age-associated hypermethylation were significantly more associated with predicted age (Horvath-predictor) than with chronological age. In contrast, hypomethylated CpGs revealed only moderate correlation with chronological age and did not correlate with epigenetic age-predictions (Wilcoxon rank-sum test). Please note that results are very similar using either the 99 CpG model or Horvath-predictor, albeit the two epigenetic aging signatures are independent.