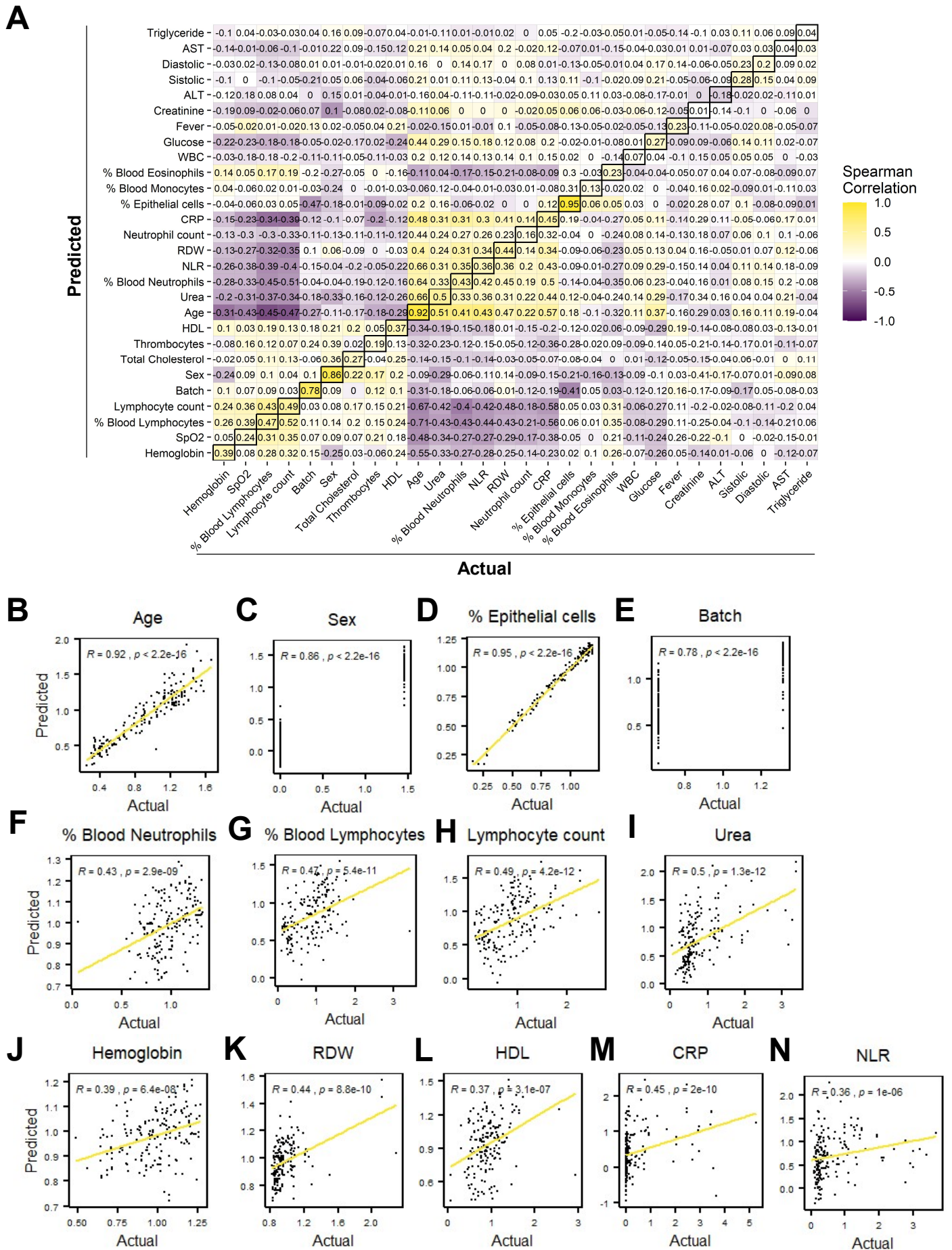


Supplementary Figure 1.

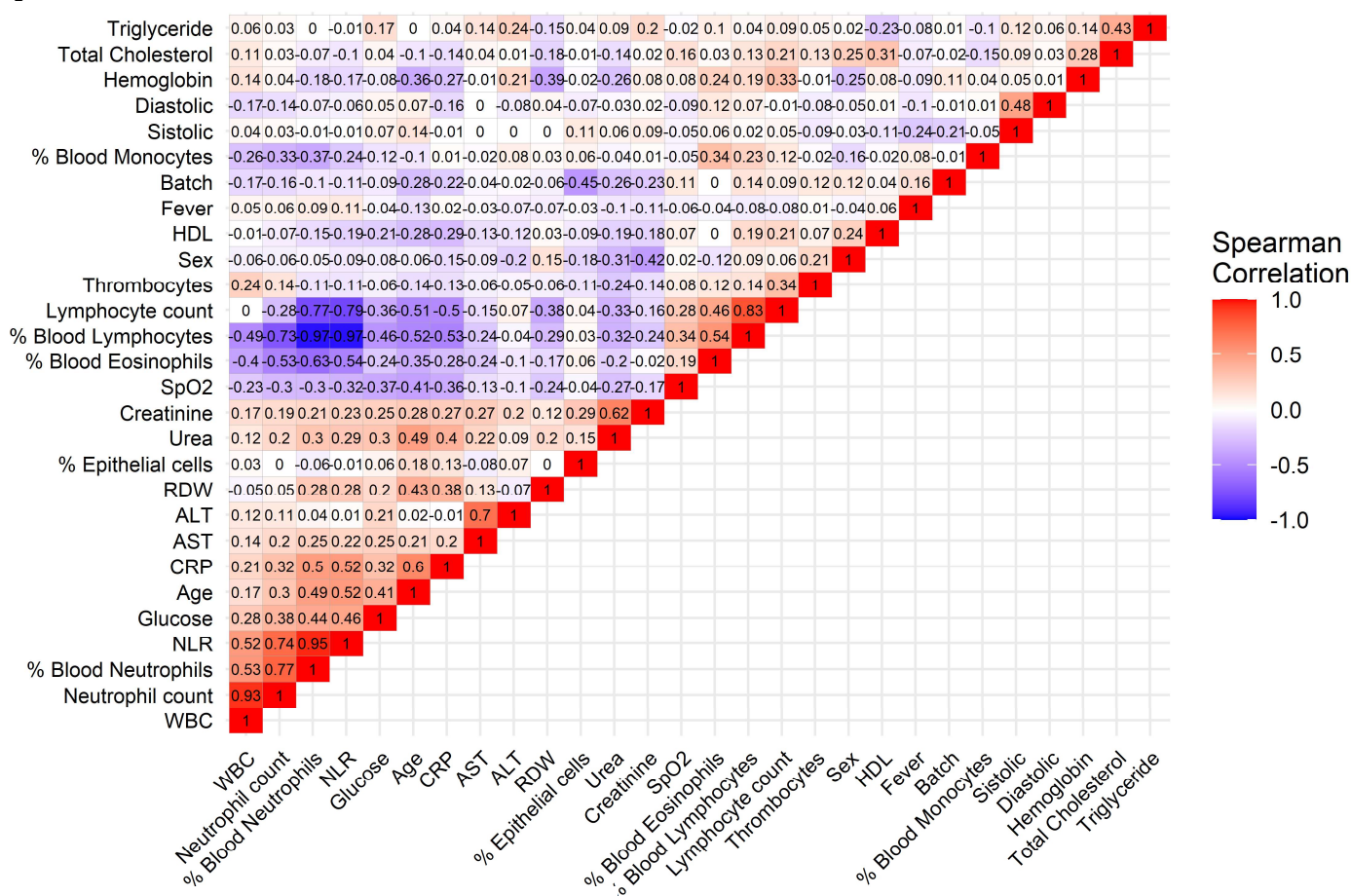
(A) Age distribution. (B) Sex distribution. (C) Overview of methylation data processing. (D) Coverage distribution.



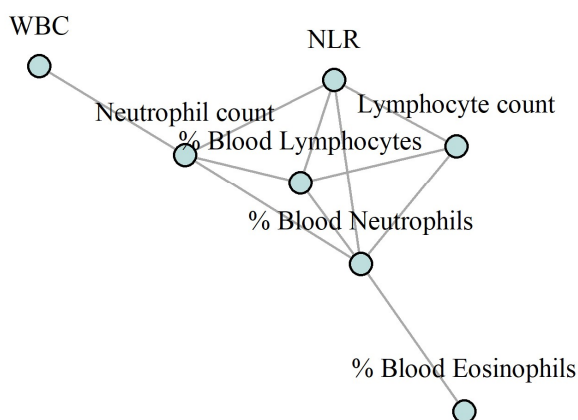
Supplementary Figure 2.

(A) Heatmap showing the Spearman correlation between the actual values and the predicted values of the variables available for this study. (B-N) Scatterplots showing the Spearman correlation and the p-value between the actual values and the predicted values for each individual factor. RDW, red cell distribution width; HDL, high-density lipoprotein; CRP, C-reactive protein; NLR, neutrophil to lymphocyte ratio.

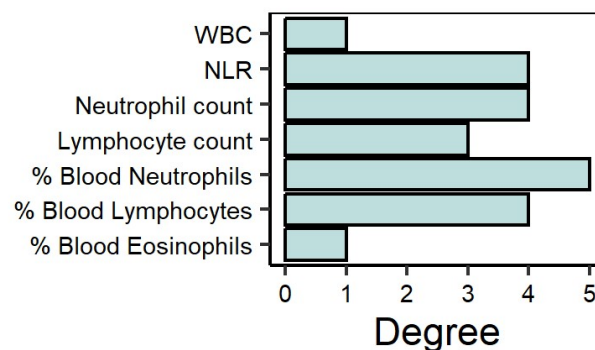
A



B

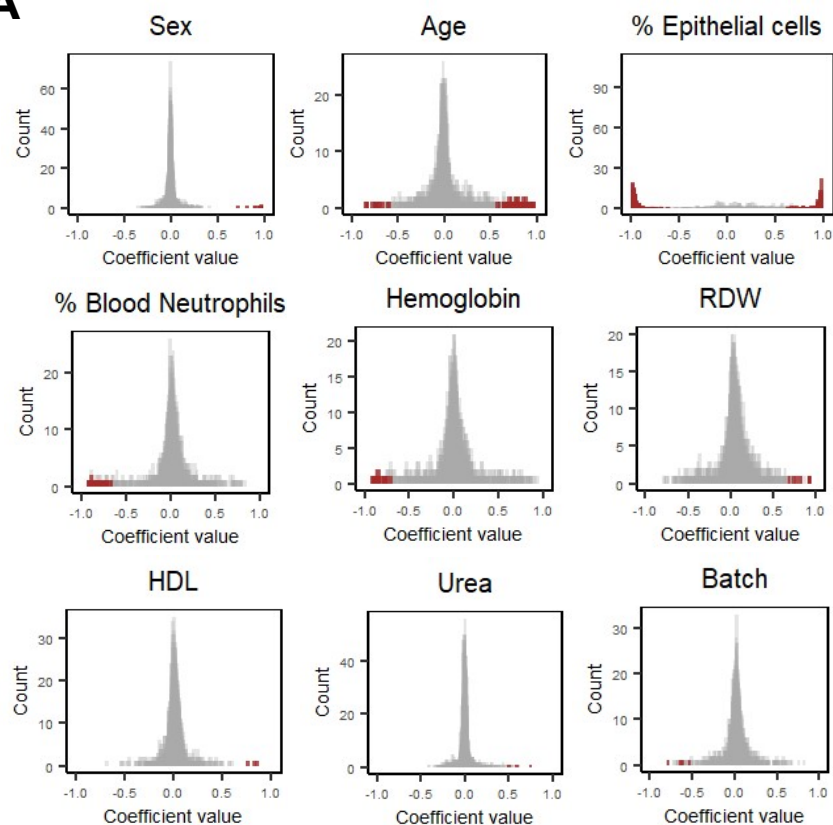


C



Supplementary Figure 3.

(A) Heatmap showing the Spearman correlation among the demographic and health-related variables. (B) Graph network among WBC, NLR, neutrophil count, percentage of blood neutrophils, lymphocyte count, percentage of blood lymphocytes, and percentage of blood eosinophils. (C) Degree of each factor referred to the graph network in (B).

A**B**

Factor	Sites
Sex	N=16
Age (C > 0)	N=87
Age (C < 0)	N=13
Epithelial cells (C < 0)	N=1196
Epithelial cells (C > 0)	N=1000
Neutrophils	N=47
Hemoglobin	N=27
RDW	N=8
Urea	N=3
HDL	N=3
Batch	N=4

Supplementary Figure 4.

(A) Distribution of coefficient values for the nine methylation-associated factors. Factor-specific site coefficients are shown in red. (B) For each factor, the number of associated sites is shown.