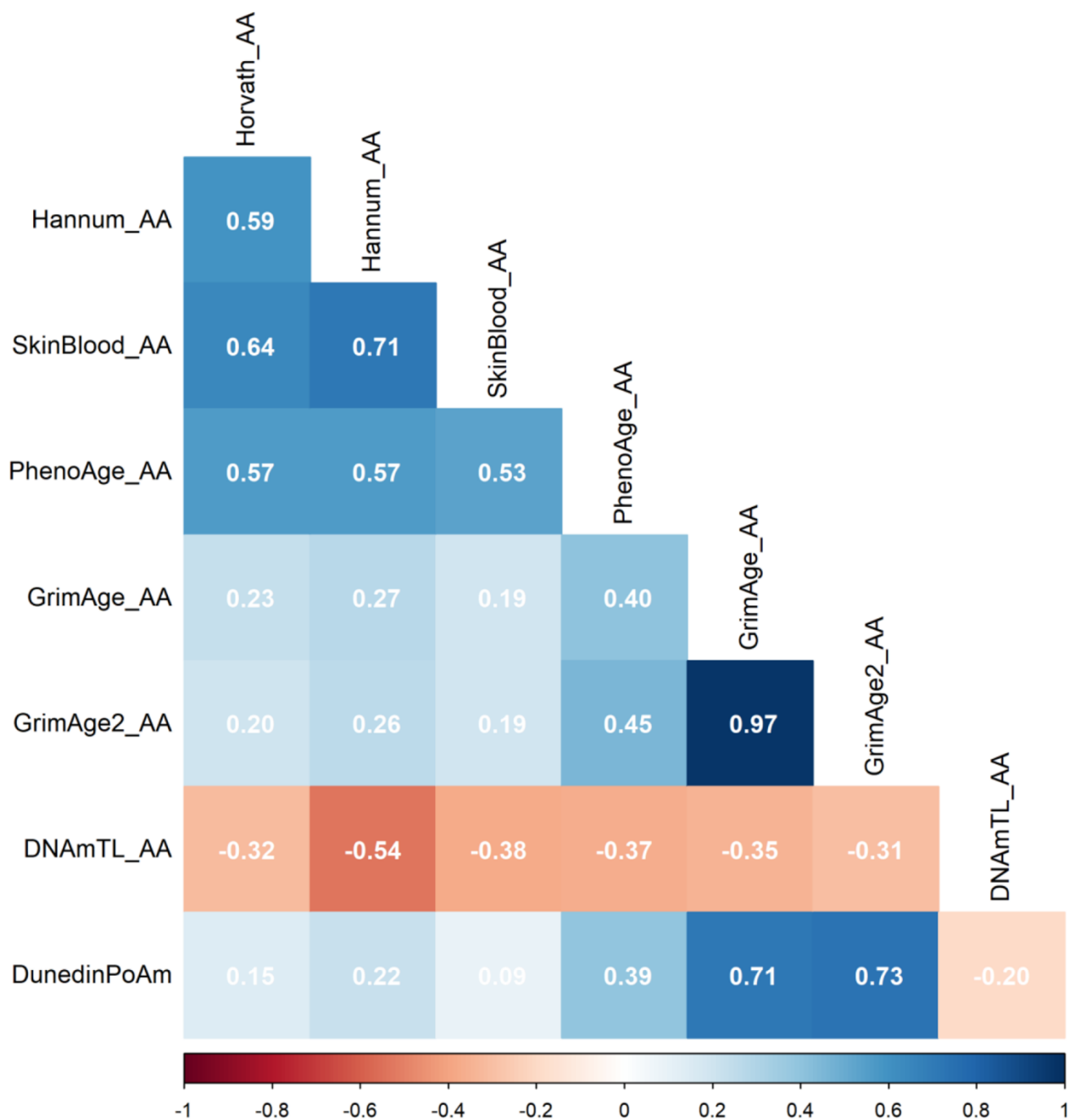
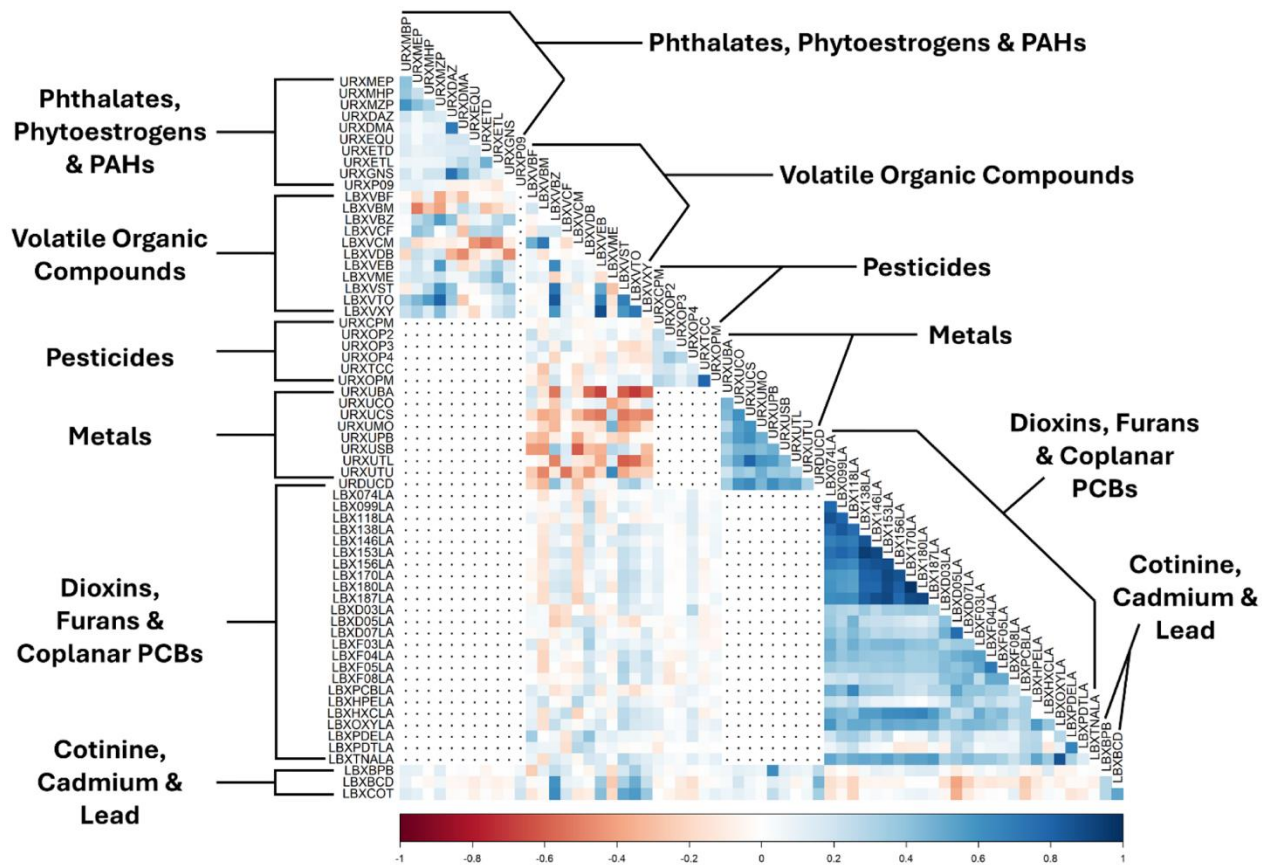


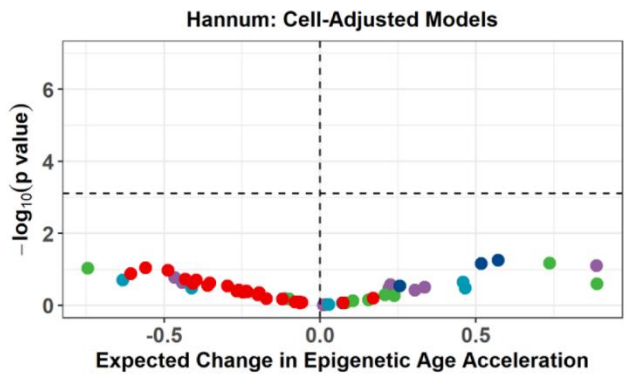
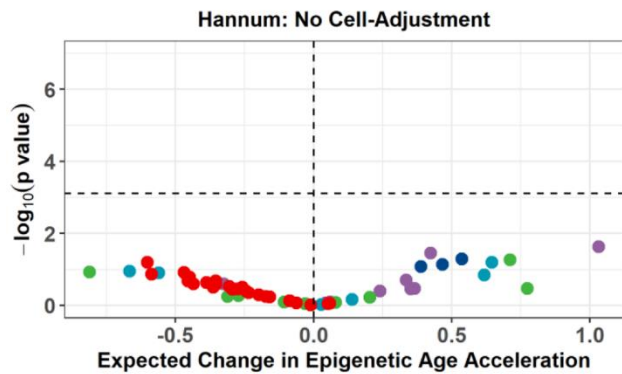
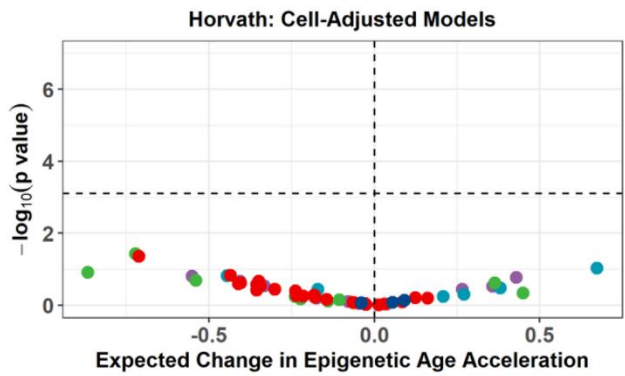
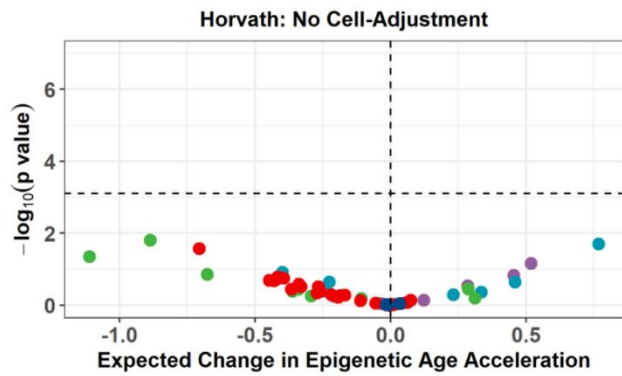
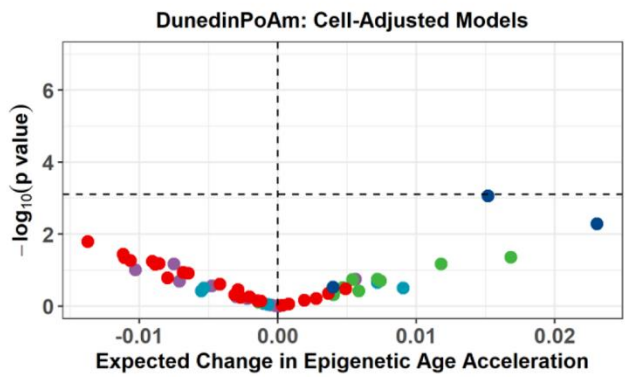
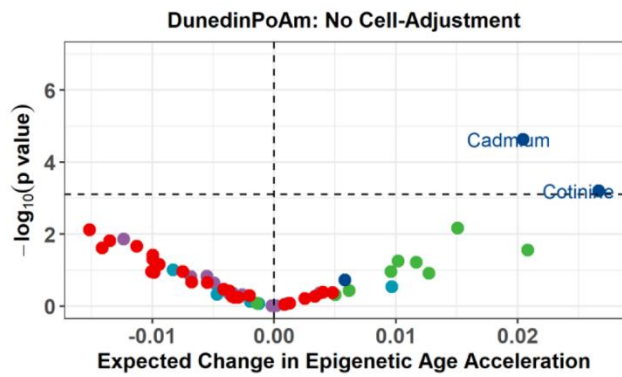
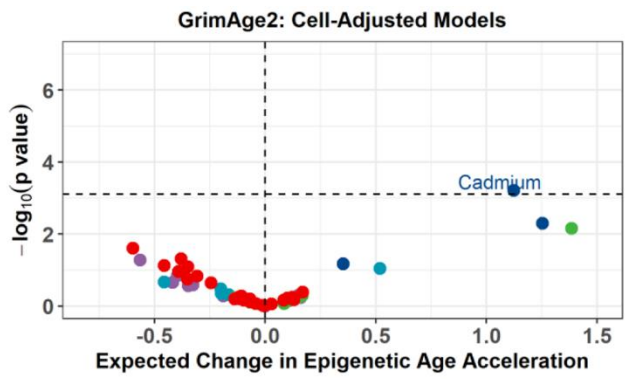
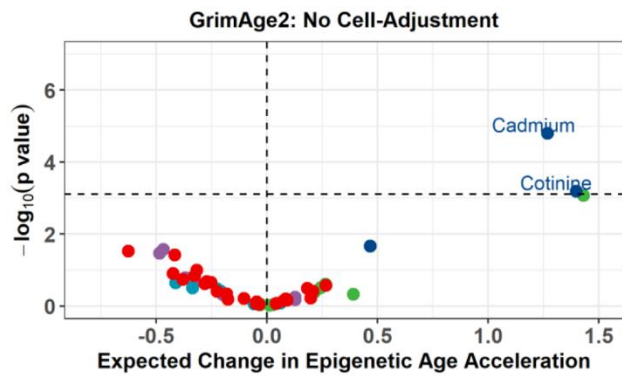
SUPPLEMENTARY FIGURES

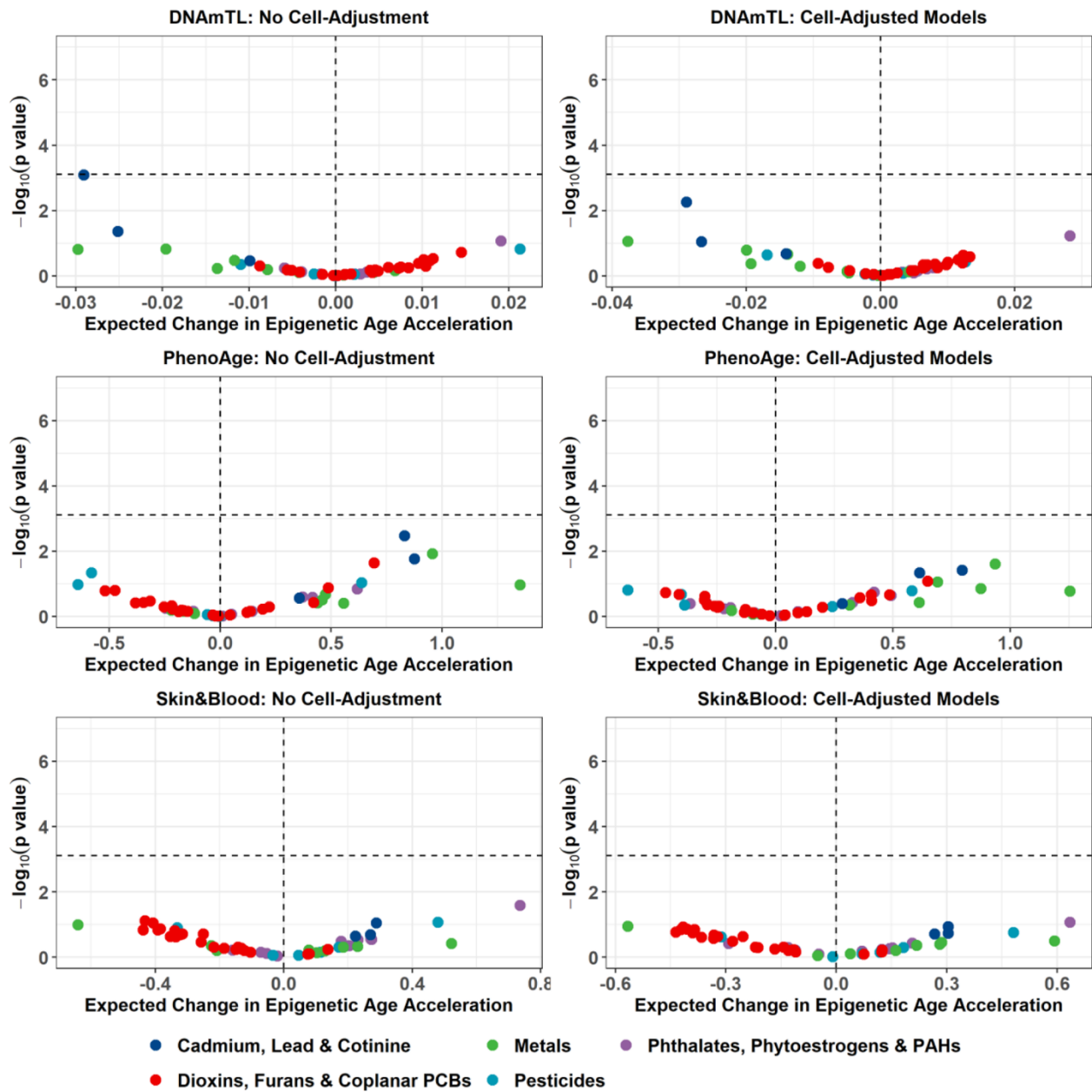


Supplementary Figure 1. Pearson correlation coefficients between epigenetic age acceleration measures from each epigenetic clock for the study sample (N = 2,346).

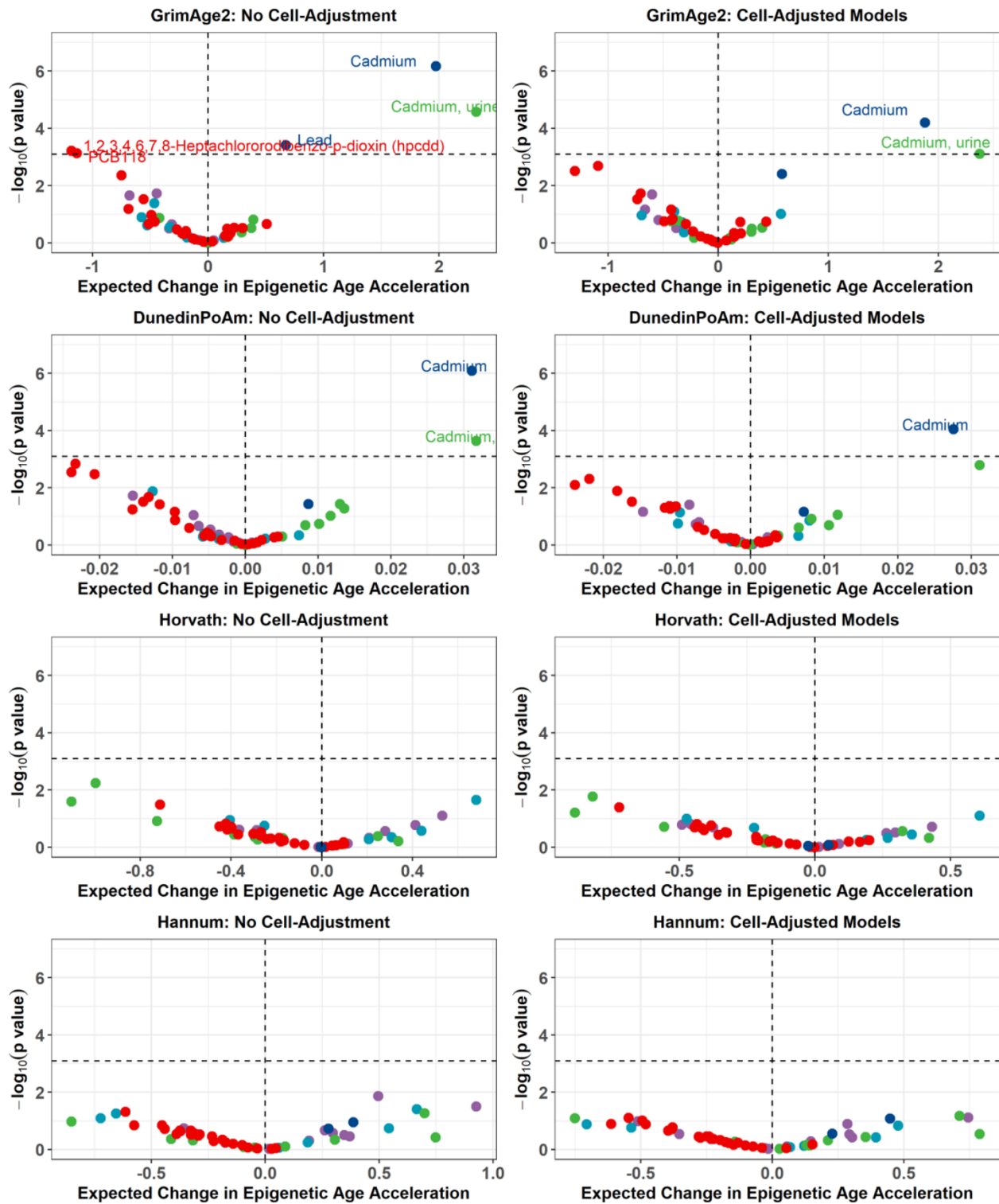


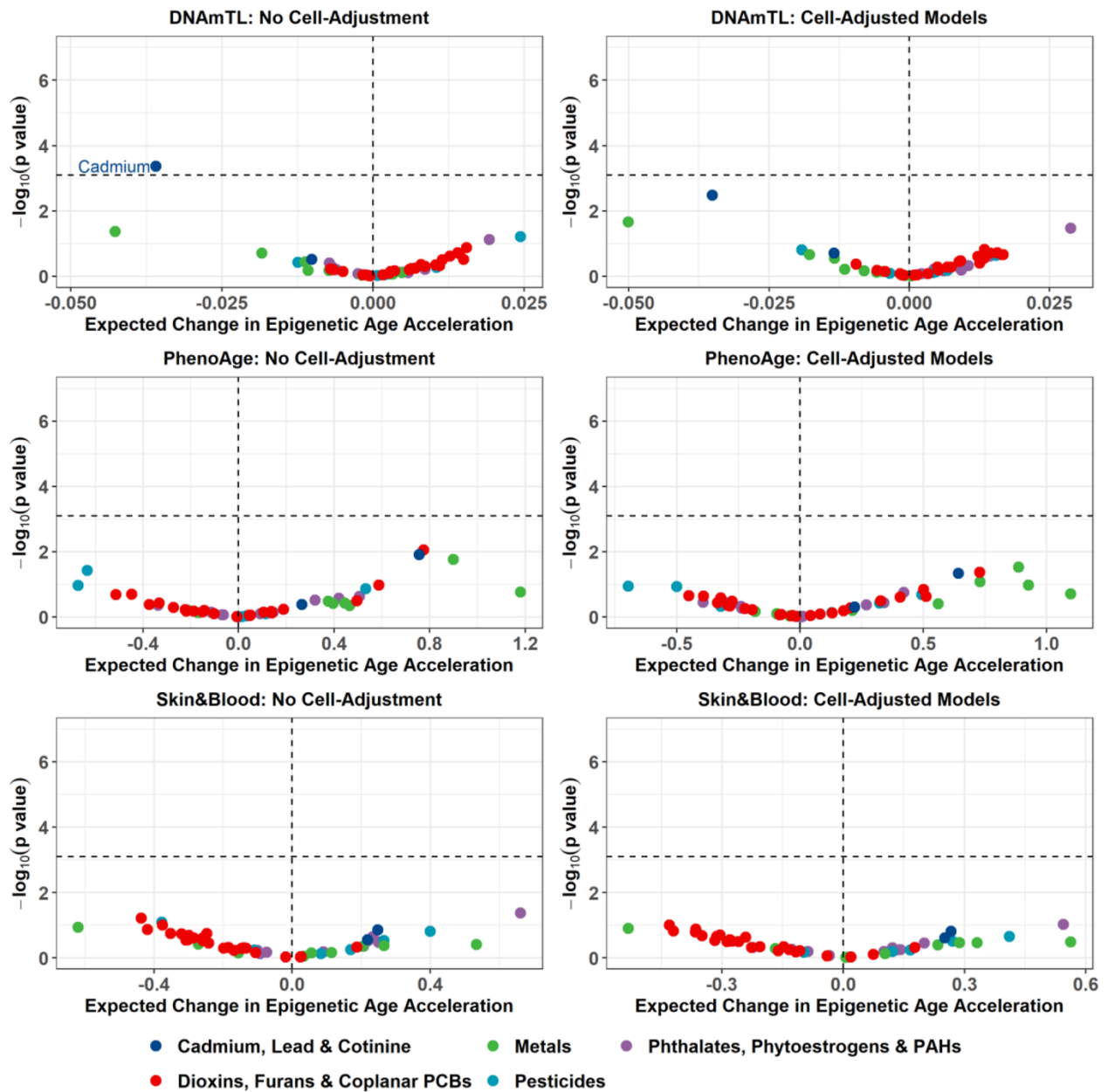
Supplementary Figure 2. Pearson correlation coefficients between each log₂-transformed environmental exposure. Black points represent exposure comparisons with 0 overlapping study subjects.



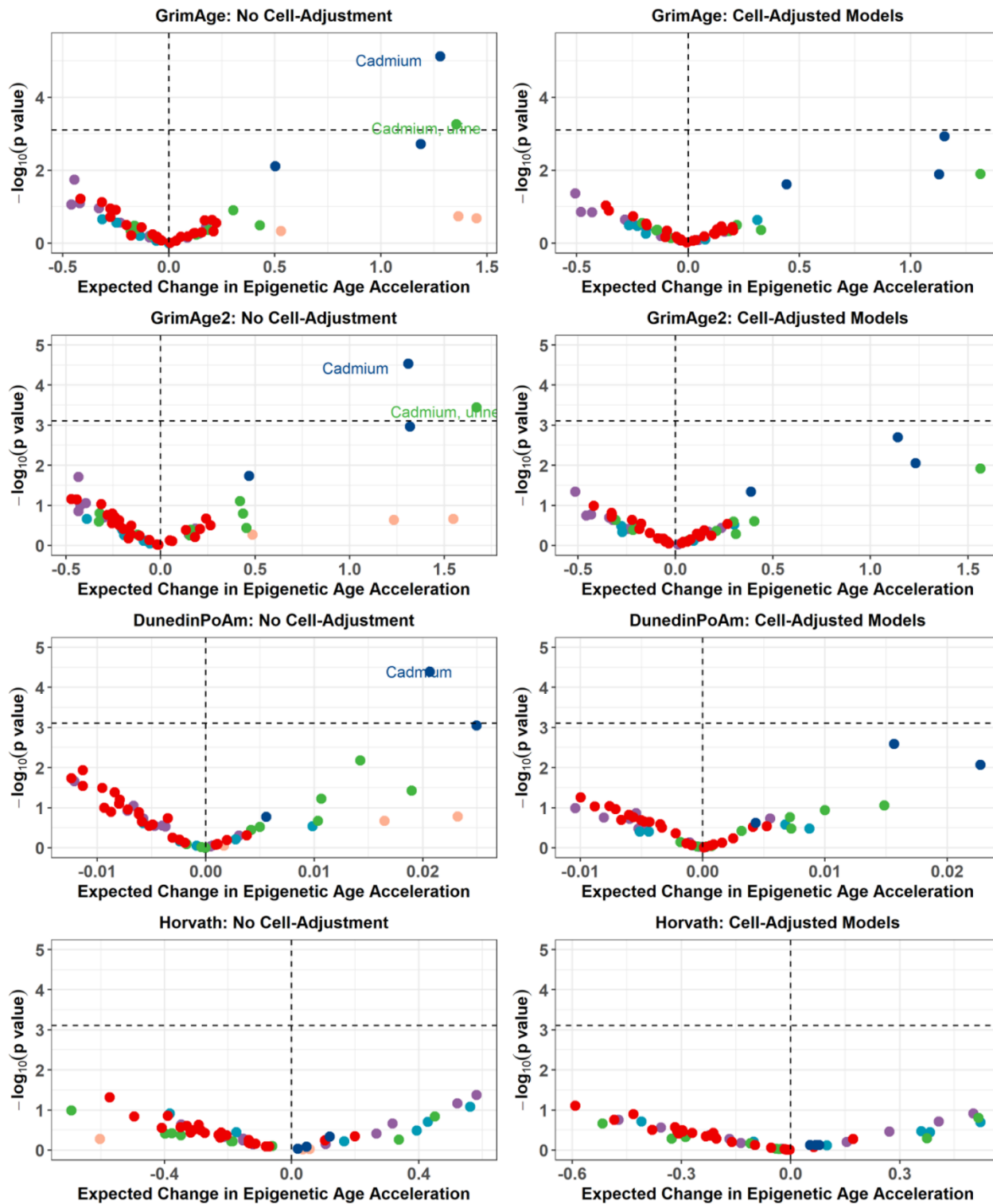


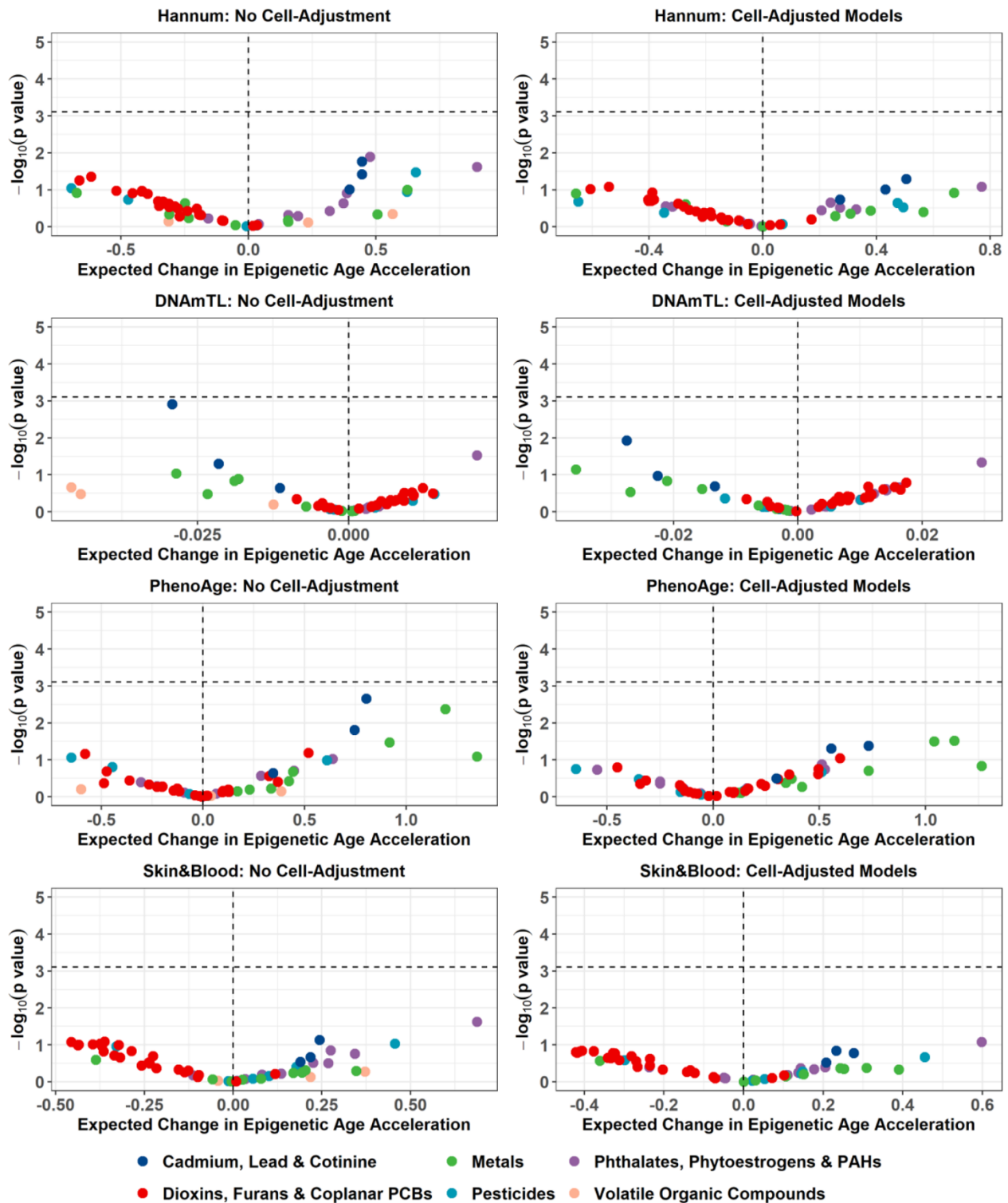
Supplementary Figure 3. Volcano plots displaying the expected change in epigenetic acceleration for a 1 SD increase in \log_2 -transformed exposure on the X-axis, and $-\log_{10}$ p-values on the Y-axis from the primary models. Color corresponds to the broad category of exposure. Volcano plots for GrimAge are presented in the main text.





Supplementary Figure 4. Volcano plots displaying the expected change in epigenetic acceleration for a 1 SD increase in \log_2 -transformed exposure on the X-axis, and $-\log_{10}$ p-values on the Y-axis from the sensitivity models adjusting for cotinine exposure. Color corresponds to the broad category of exposure. Volcano plots for GrimAge are presented in the main text.





Supplementary Figure 5. Volcano plots displaying the expected change in epigenetic acceleration for a 1 SD increase in log₂-transformed exposure on the X-axis, and -log₁₀ p-values on the Y-axis from the sensitivity models considering imputation of missing covariates. Color corresponds to the broad category of exposure.