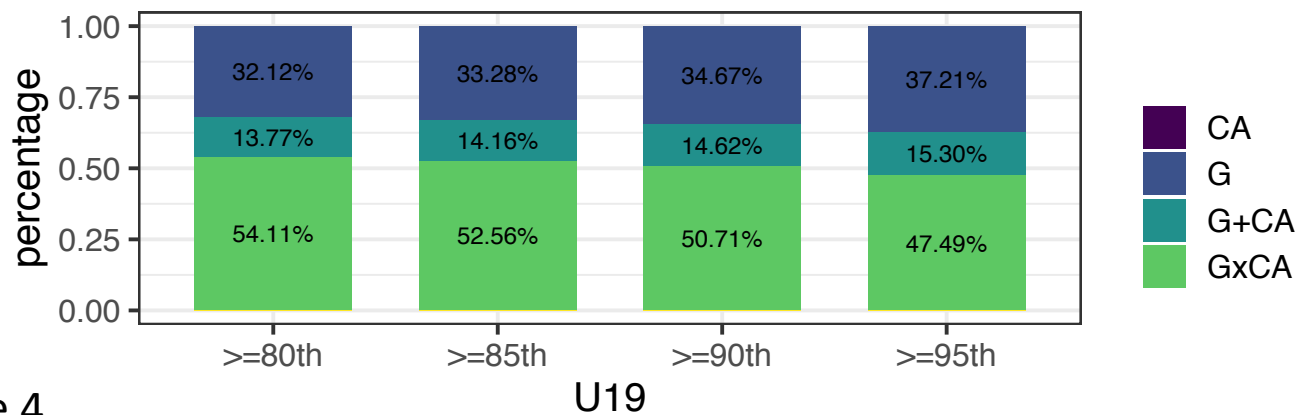
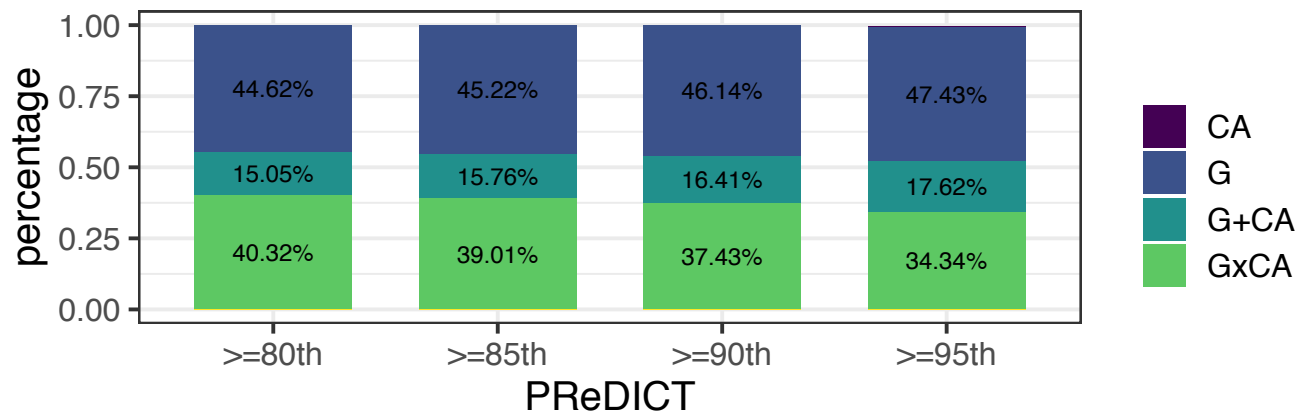
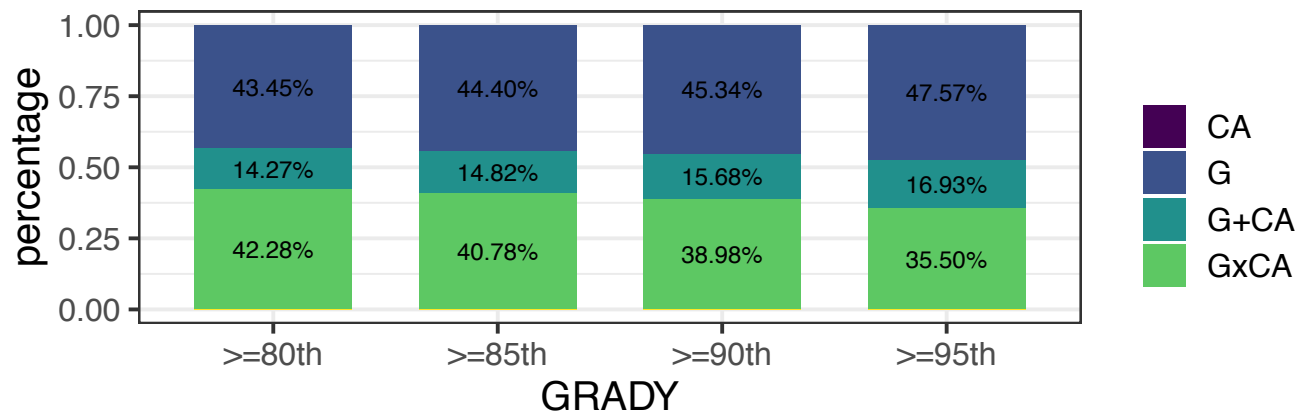




Suppl. Figure 4

**Suppl. Figure 4:** Distribution of the best models explaining variation in DNAm across the three adult cohorts, after correction for additional cohort-specific covariates. Percentage of overlapping VMPs (n=45,672) best explained by G, CA, G+CA or G×CA in each cohort using the highest adjusted  $R^2$ . Plots are stratified by MAD-score cutoff ( $\geq 80^{\text{th}}$  percentile: n=45,672 sites;  $\geq 85^{\text{th}}$  percentile: n=31,988 sites;  $\geq 90^{\text{th}}$  percentile: n=20,196 sites;  $\geq 95^{\text{th}}$  percentile: n=9,681 sites).