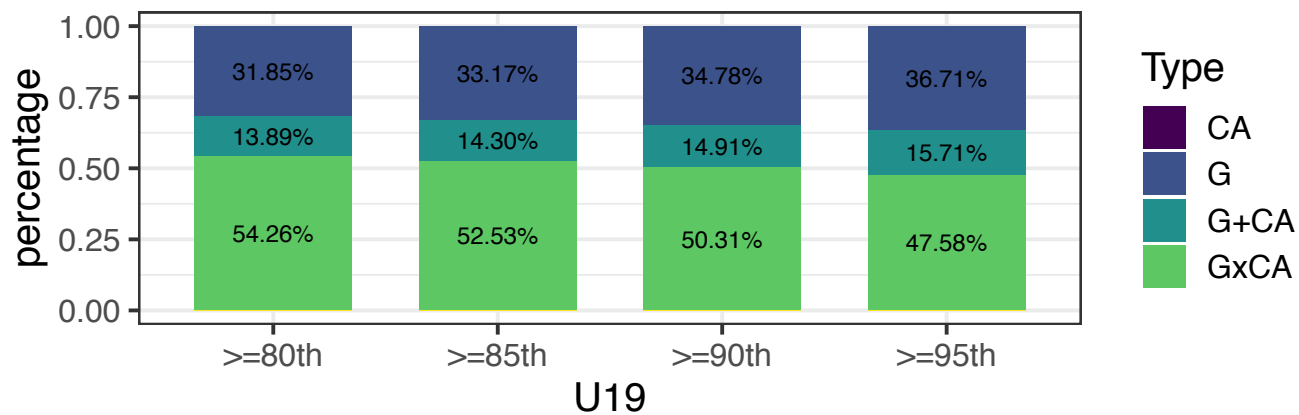
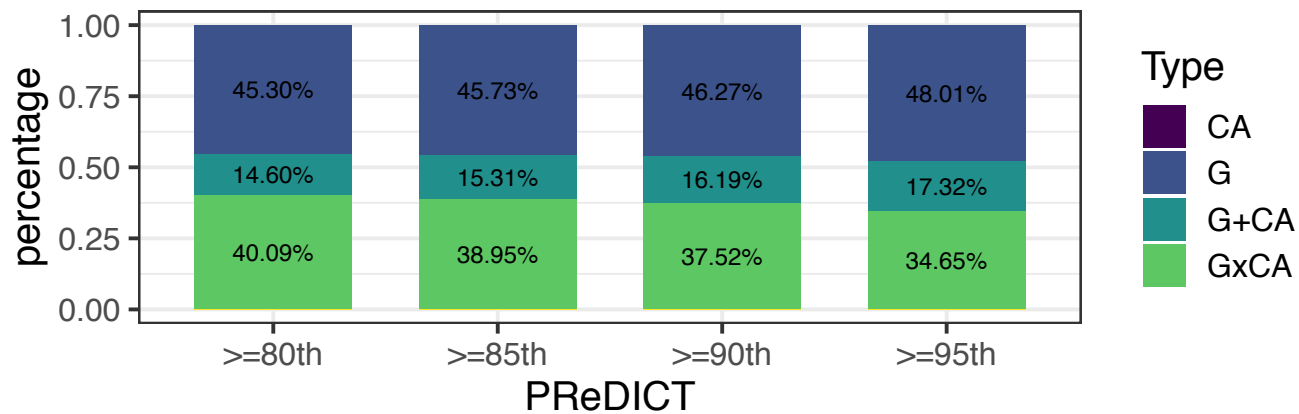
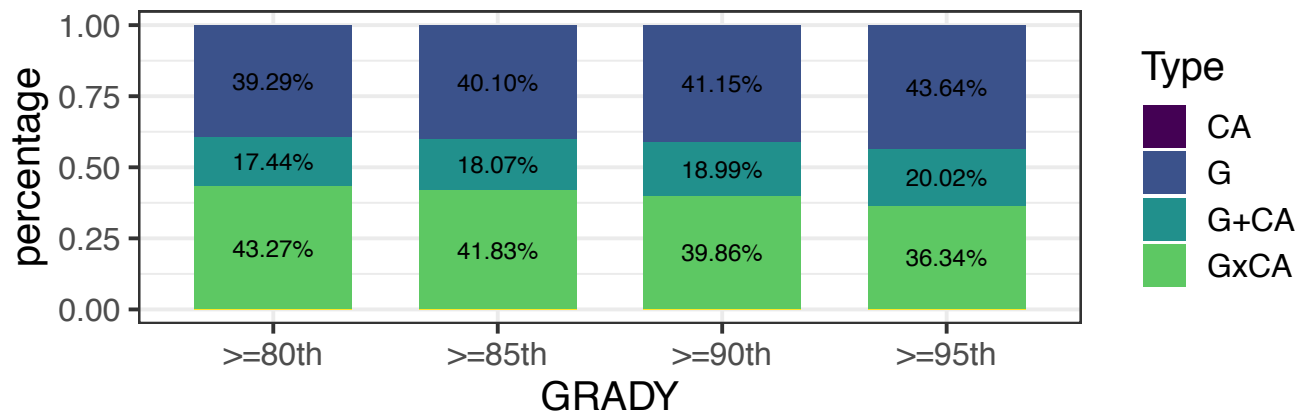




Suppl. Figure 2: Distribution of the best models explaining variation in DNAm across the three adult cohorts. Percentage of overlapping VMPs (n=45,962) best explained by G, CA, G+CA or G×CA in each cohort using the highest adjusted R^2 . Plots are stratified by MAD-score cutoff ($\geq 80^{\text{th}}$ percentile: n=45,962 sites; $\geq 85^{\text{th}}$ percentile: n=31,177 sites; $\geq 90^{\text{th}}$ percentile: n=20,360 sites; $\geq 95^{\text{th}}$ percentile: n=9,738 sites). The distribution of best models remained rather stable when varying the MAD-score threshold between the 80^{th} and the 95^{th} percentile with a small but significant increase of best model G with increasing methylation variability.