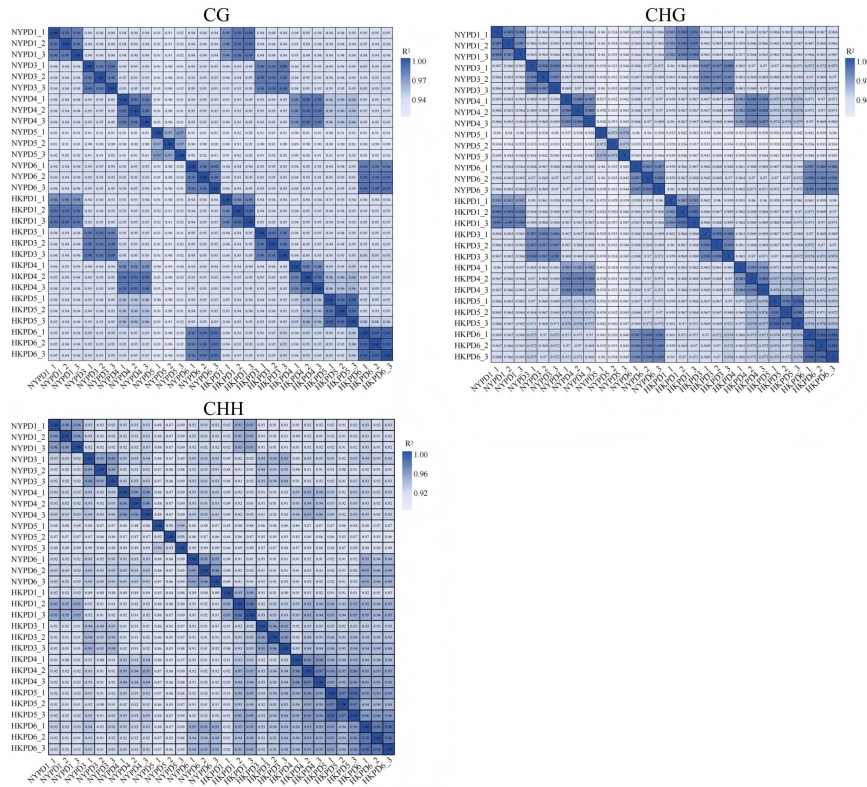




**Fig. S1** Correlation heatmap of methylation profiles in CG, CHG, and CHH sequence contexts across samples. For each sequence context, methylation levels were calculated within 2 kb bins across the genome, and Pearson correlation analysis was then performed between samples based on these values.