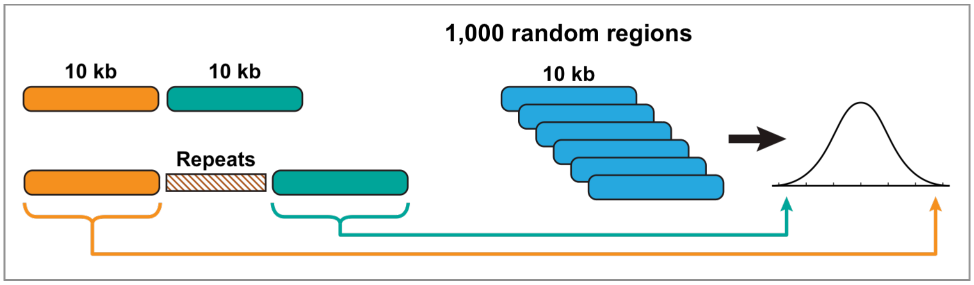
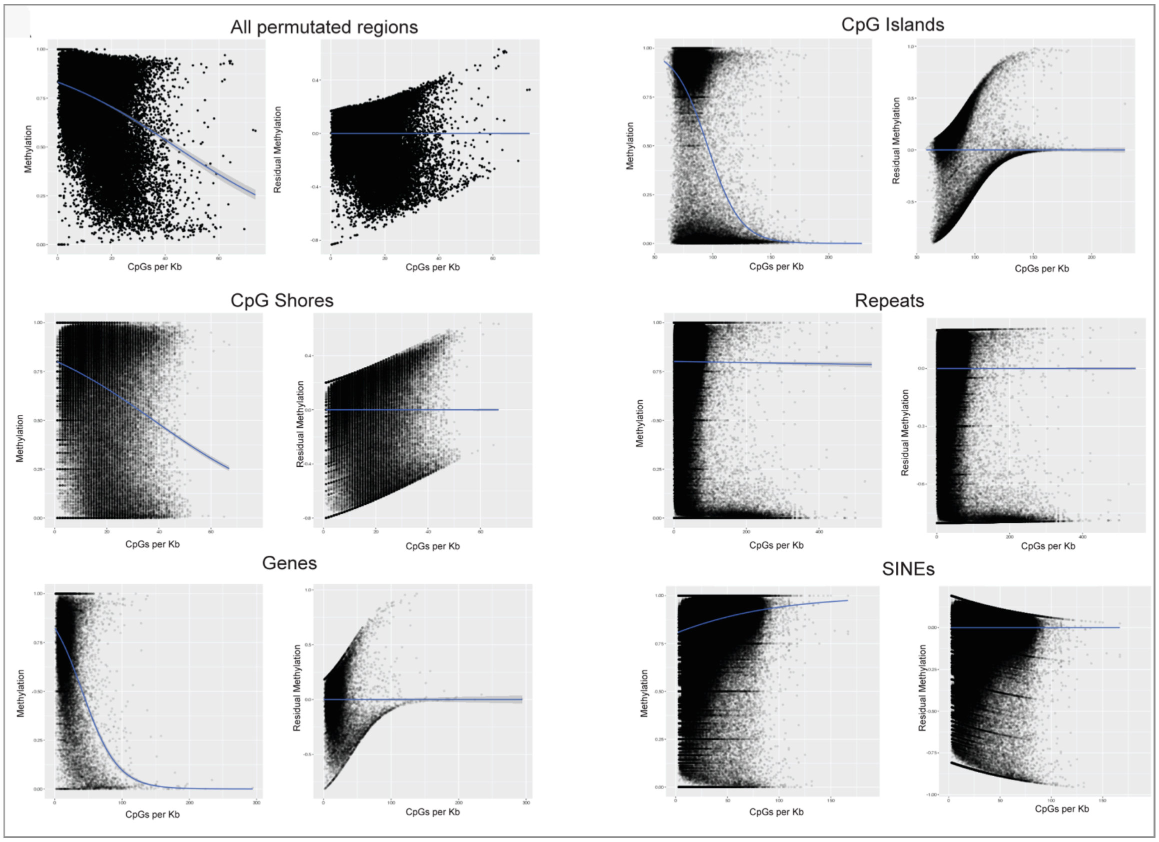


Supplemental Figure S3 - Permutation tests schematic. For both the BOS regions and for each of the simulated regions, the percentage of the region covered by each type of feature, the number of CpGs/Kb and the average methylation in regions and features is recorded. Two-sided p-values are obtained by counting the proportion of random region sets showing values as extreme as those seen in the set of BOS regions.



Supplemental Figure S4 - Plots showing logistic regressions correcting for the correlation between CpG density and methylation in gibbon. Panels on the left for the permutated regions and genomic features show uncorrected methylation values and logistic curve fit. The number of CpGs per kilobase of sequence is given on the x-axis and the methylation rate is on the y-axis. Each point represents one permutation region or one feature within a permutation region. The residual methylation after correcting for CpG density is shown in the right panels. Plots for other species and features are similar (data not shown).