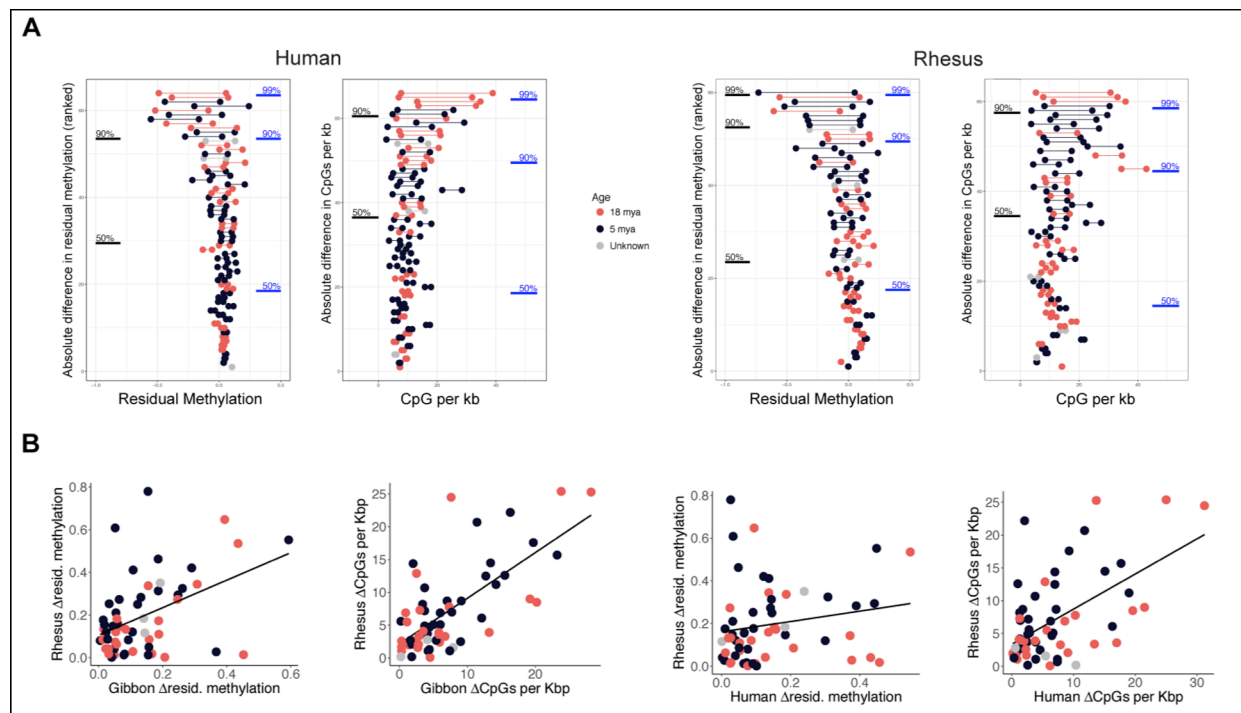


**Supplemental Figure S12** - Schematic of the permutation analysis to analyze the absolute difference (D) for CpG density and residual CpG methylation (Meth) between the two sides of the rearrangements performed for gibbon and orthologous regions in human and rhesus. 10kb regions were used for CpG density and methylation whereas H3K4me3 peak density was measured over 500kb regions. Two-sided p-values from the permutation analyses for each species are reported.



**Supplemental Figure S13** – A) Barbell plots (ranked) for human and rhesus show the difference in residual methylation and CpG density between the two sides of the BOS. Each point represents one side of a BOS and a line segment, representing the magnitude of the difference, joins sides of the same BOS. BOS are ordered vertically by the rank of the magnitude of the difference. Black lines on the side indicate the rank associated with percentiles of distal permutation regions while blue lines indicate ranks for percentiles for adjacent permutation regions. Color-coding by age of the rearrangement highlights the random distribution of old and more recent BOS. B) Scatter plots showing the relationship between the change in residual methylation across breakpoints and the change in CpG density across breakpoints between species. Lines show least-squares linear fit and colors show approximate BOS age.