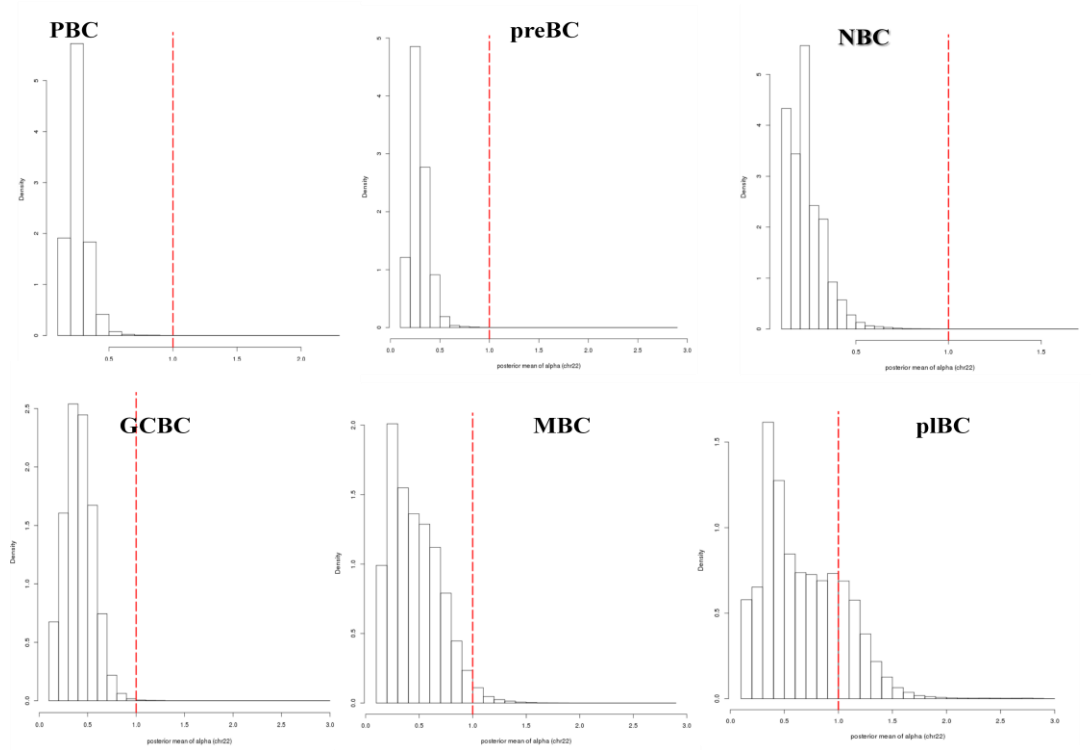
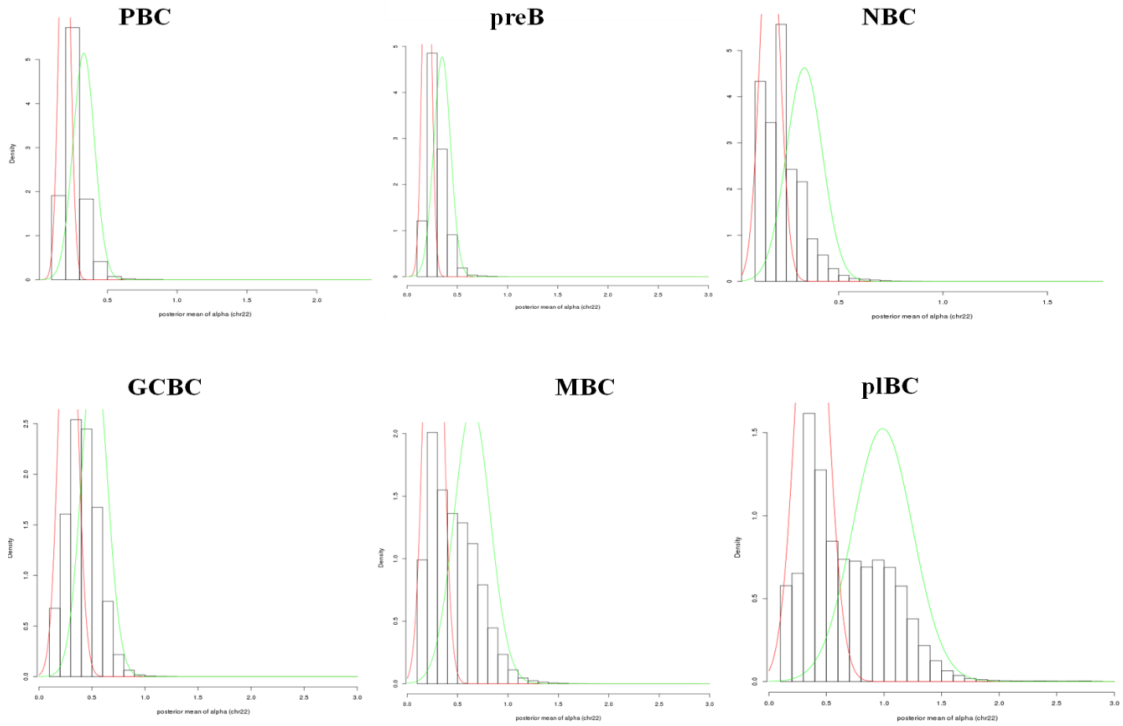
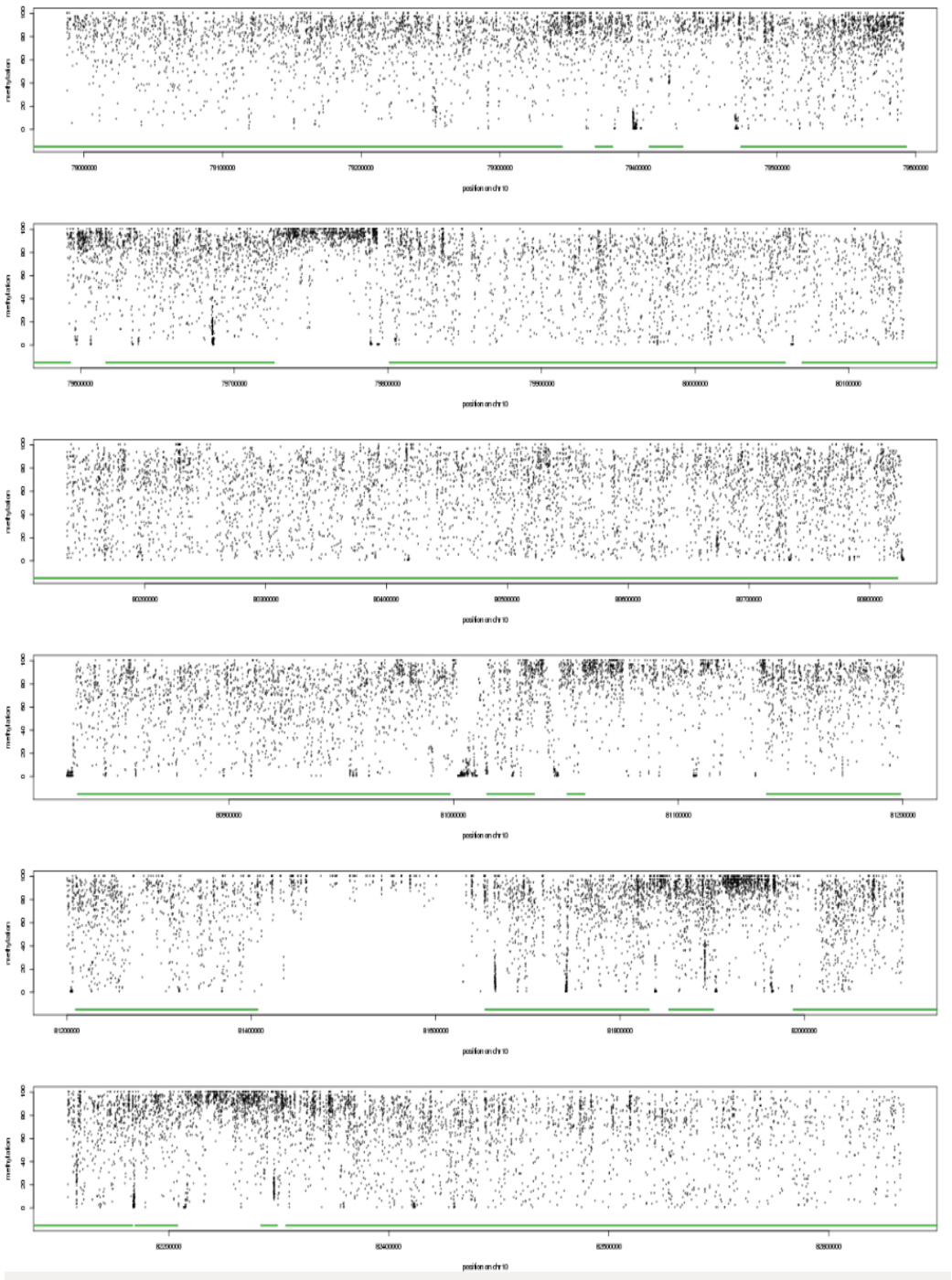


Supplementary Figure 1A. α distribution in the samples of the B cell differentiation dataset.. Long-tailed or almost bimodal distribution of the posterior means of α is present in plBC genome. α-distributions with long-tailed shape or a bimodal one with a considerable fraction of α-values greater than 1 are indicative of PMDs. PBC (Progenitor B cell), preBC(pre B cell), GCBC (Germinal Center B cell), MBC (Memory B cell) and plBC (plasma B cell).

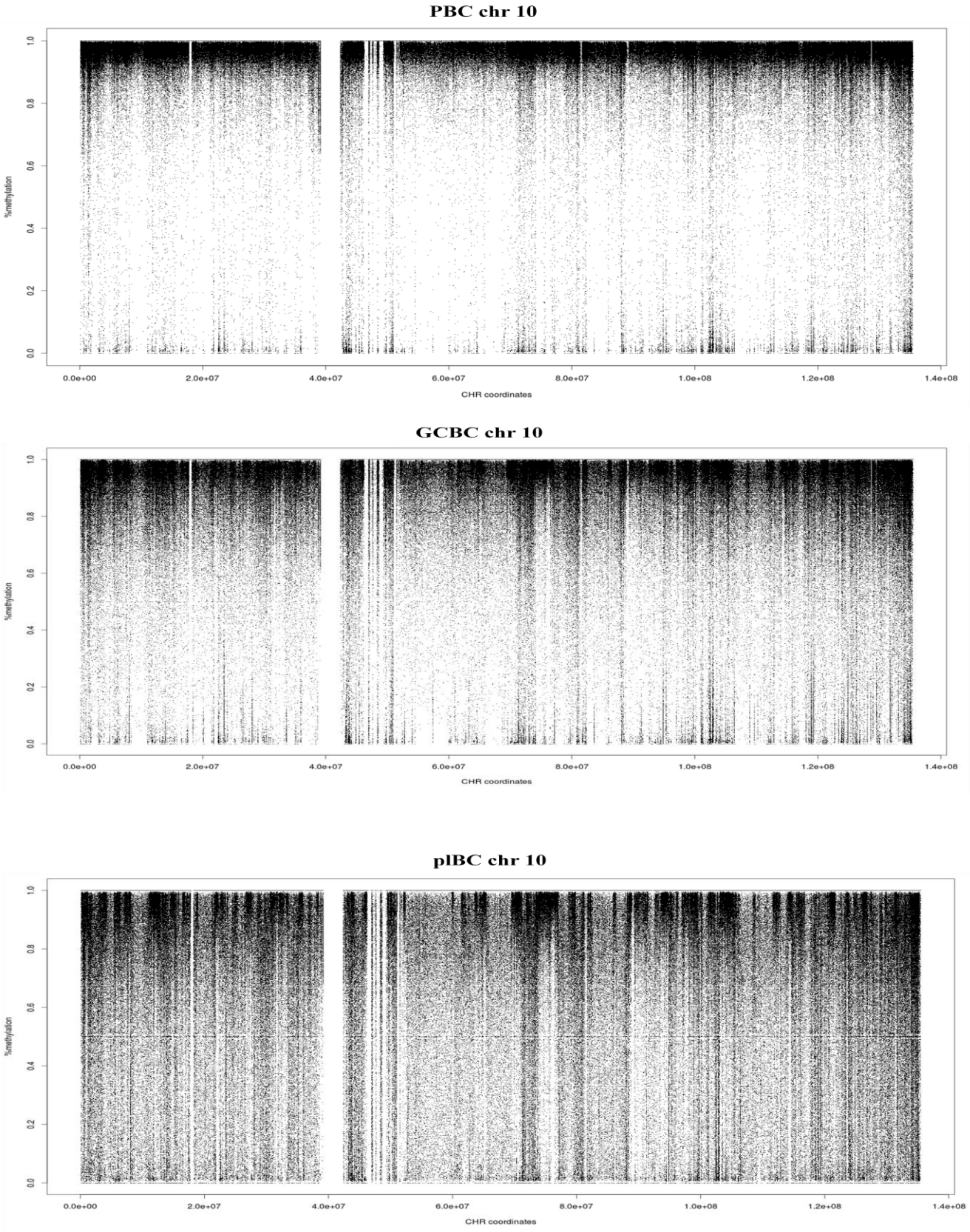


Supplementary Figure 1B. Gaussian emissions fitted with two states HMM trained on α distribution previously obtained. It can be shown that the only sample that is

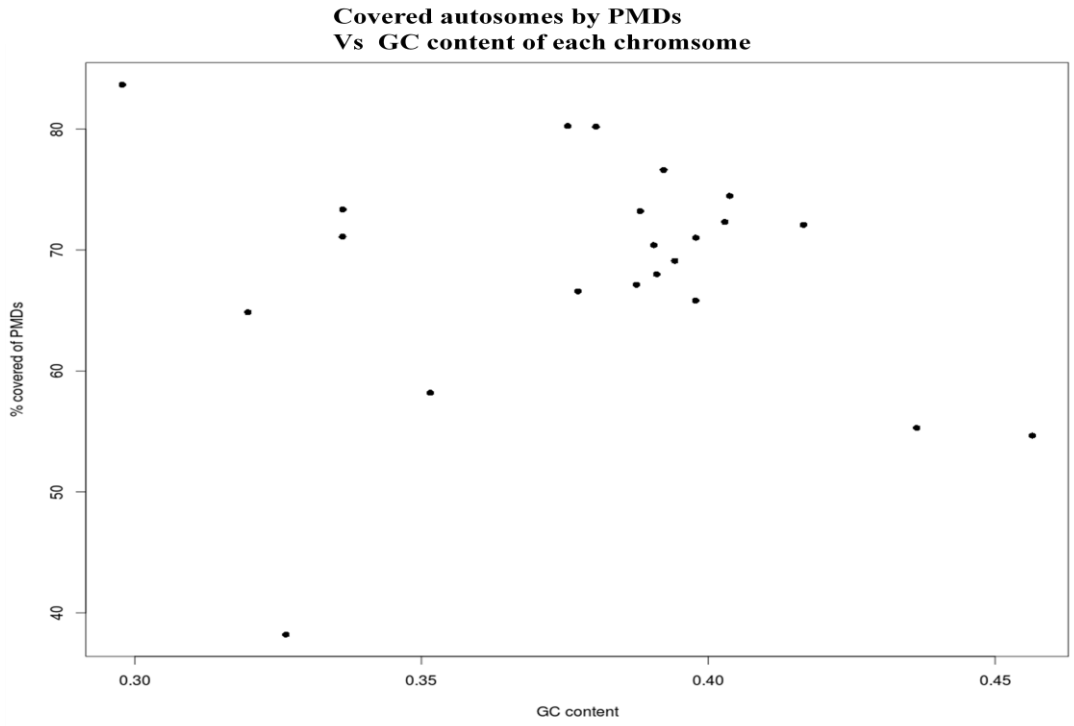
well fitted with the HMM is plBC. Gaussian emissions should correspond to the two peaks of the bimodal distribution, or to the main peak and the tail in the case where the α distribution would be long-tailed.



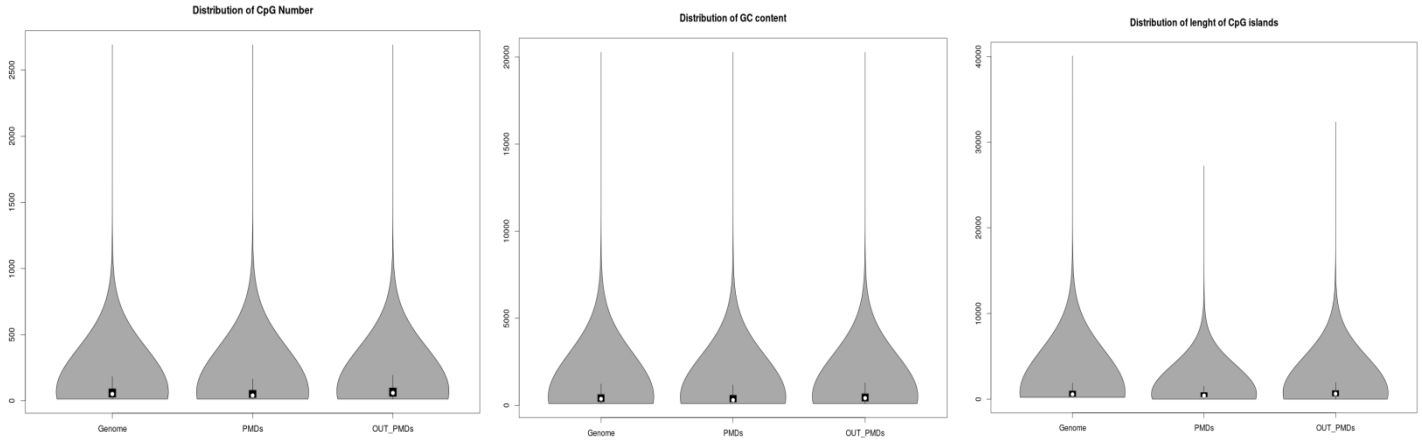
Supplementary Figure 1C. PMDs segmentation of a randomly selected region in the plasma B cell genome. Raw methylaiton values are plotted aginst chromosome coordinates. Green lines mark PMDs.



Supplementary Figure 2. PMDs appear during differentiation and are visible at chromosome level. Chromosome 10, which have 72 % covered by PMDs **(Supplementary Table 1)** and thus represent a mean coverage of all chromomes.



Supplementary Figure 3. Relationship between PMD coverage and average GC% per chormosome. There is no correlation of % of PMDs in each autosome and its total GC content. Pearson's correlation of -0.096, Adjusted R^2 = -0.04



Supplementary Figure 4. Distributions of CpG number, GC content and length of CGI genome-wide, inside and outside of PMDs. There are no differences in the number of CpGs, GC content and CGi length of CGi present in each group.