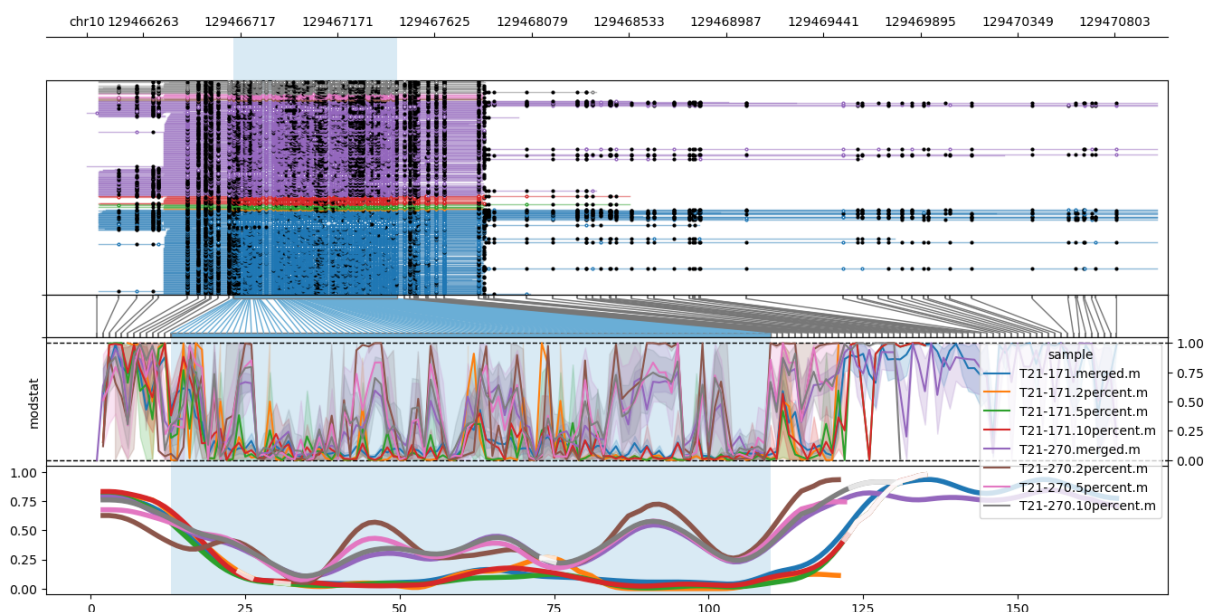
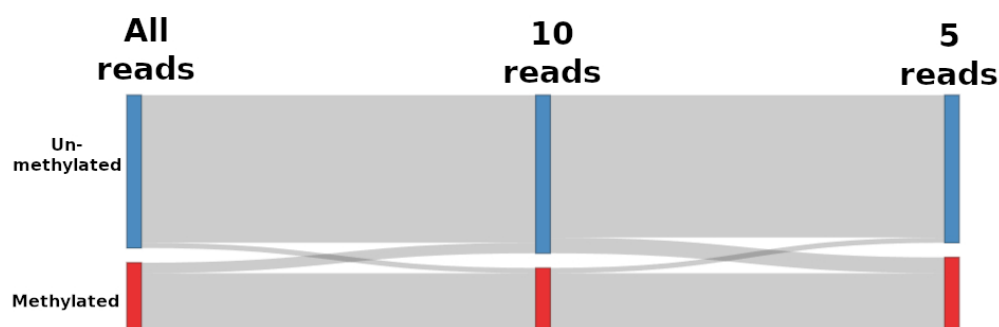


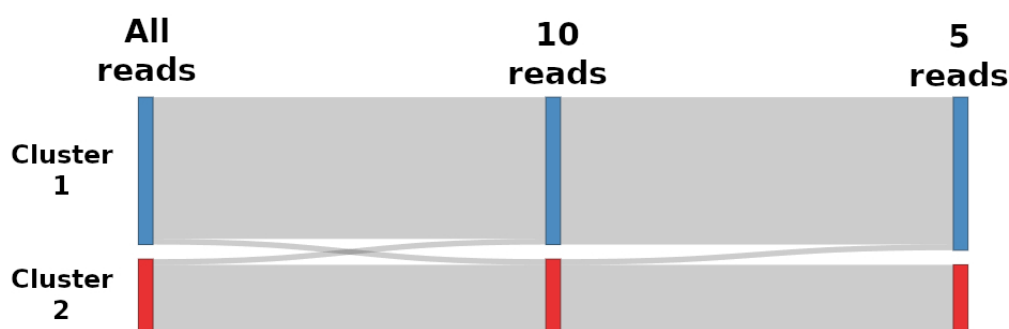
Supplementary figure 1



(a)



(b)



(c)

Supplementary figure 1. Two samples with read depth ~ 100 covering the MGMT CpG-island were randomly downsampled to ten, five, and two reads. Although fluctuations in per site methylation are apparent, the overall smoothed methylation profiles are relatively stable down to five reads (a). Random downsampling of 42 samples with read depth over 20 to ten or five reads and subsequent classification as methylated or unmethylated according to average methylation on the four CpG sites included in the MGMT-Pyro kit resulted in 38 of 42 samples (90%) retaining their classification through all read depths (b). Similarly, 37 of 39 samples (95%) were assigned to the same cluster through all read depths when knn-regression ($k=2$) according to hierarchical clustering of all samples was applied (c).