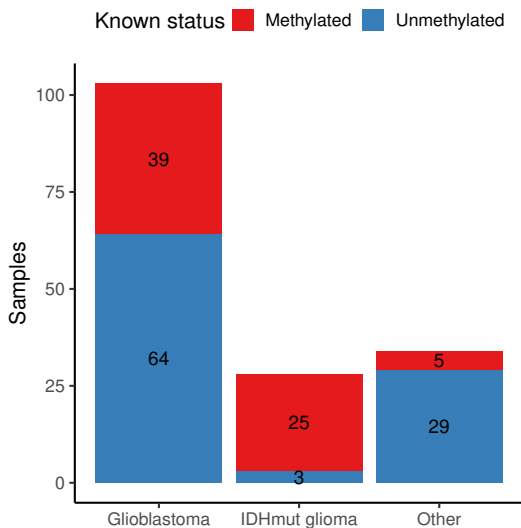
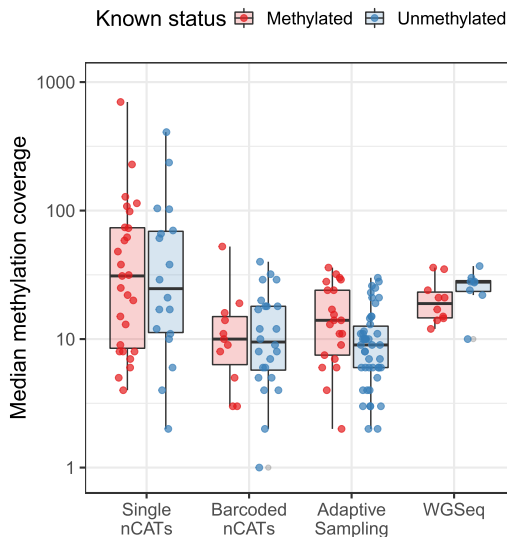


(a)



(b)



(c)

Figure 1: (a) Schematic overview of the 98 CpG sites of the *MGMT* CpG-island with relevant functional areas including the transcription start site (TSS), minimal promoter and enhancer as defined by Harris *et al.* [9, 10] as well as the differentially methylated regions (DMR) one and two as described by Malley *et al.* [20]. The two CpG sites used by the *MGMT*-STP27 classifier [2] and the four CpG sites included in the Qiagen® *MGMT* pyrosequencing kit are shown below. (b) Distribution of diagnosis and known methylation status of the sample cohort. (c) Median methylation coverage of the 98 CpG sites in the *MGMT* promoter region of methylated and unmethylated samples by method of acquisition (Adaptive sampling, multiplexed nCats, single sample nCats and whole genome sequencing).