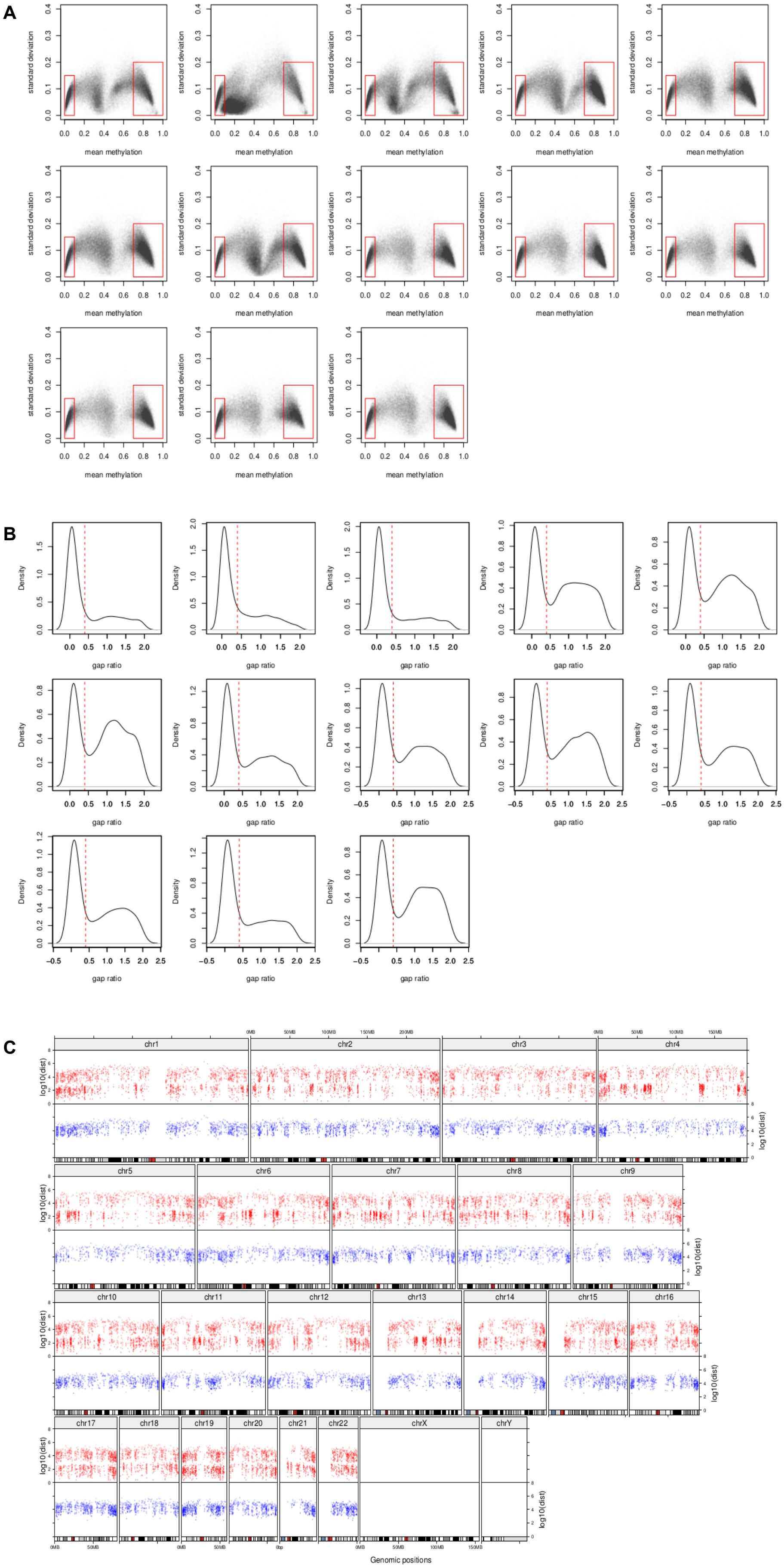

Methods Figure 1. A. Distribution of both the mean (x-axes) and the standard deviation (y-axes) of methylation in the segments. **B.** Distribution of gap ratios for all samples. From left to right and top to bottom samples are NP1 to NP6 and PDAC1 to PDAC7. Dotted lines indicates selected cutoff. A,B. From left to right and top to bottom samples are NP1 to NP6 and PDAC1 to PDAC7. **C,** Representative rainfall plot after cluster merging (red track: before merging, blue track: after merging).