

## **Description of Additional Supplementary Files**

File Name: Supplementary Data 1

Description: Conversion efficiency of EMSeq datasets as measured on exogenous spike-ins.

File Name: Supplementary Data 2

Description: Nanopore and EMSeq datasets generated in this study and their quality metrics.

File Name: Supplementary Data 3

Description: Sequence contexts expected to carry methylation in various bacterial species used in this study.

File Name: Supplementary Data 4

Description: Representation of 9-mers and 11-mers covered by the datasets used for evaluation of 5mC.

File Name: Supplementary Data 5

Description: Overall abundance of various marks in the species and datasets used in the study.

File Name: Supplementary Data 6

Description: Versions of models used for calling methylation using various tools.

File Name: Supplementary Data 7

Description: Read level performance metrics and associated details across the tools and datasets.

File Name: Supplementary Data 8

Description: Effect of changing probability thresholds on various F1 metrics, and corresponding data loss.

File Name: Supplementary Data 9

Description: Site level evaluation metrics for 5mC calls across the datasets.

File Name: Supplementary Data 10

Description: Computational performance metrics of various tools utilized in this study.

File Name: Supplementary Data 11

Description: Reference genome versions used in the study.

File Name: Supplementary Data 12

Description: Cytosines profiled across genomic regions.

