

Description of Additional Supplementary Information

Supplementary Data S1. Description of all strains used in this study.

Supplementary Data S2. Sequencing statistics of total RNA from *E.coli* untreated and antibiotic-treated samples sequenced using DRS.

Supplementary Data S3. Sequencing statistics of total RNA from *E. coli*, *S. cerevisiae* and *M.musculus* datasets used to benchmark the RNA modification detection algorithms.

Supplementary Data S4. Sequencing statistics from Nano3Pseq datasets used in this work.

Supplementary Data S5. Description of all replicable sites identified by NanoConsensus in both antibiotic exposures (kasugamycin and streptomycin) and time points (1h and 16h).

Supplementary Data S6. List of differentially expressed genes upon streptomycin or kasugamycin at 1h exposure.

Supplementary Data S7. Running time for every algorithm used in this study.