

Description of Additional Supplementary Information

Supplemental Data 1: Description of profiles evaluated for differential expression.

Supplemental Data 2: The results of the two pipelines (featureCounts+SARTools, pipelinetranscriptome-de): gene expression quantification (with featureCounts and salmon, respectively), and differential expression analyses (with SARTools/DESeq2 and edgeR, respectively). Only the genes for which at least one assessed profile yields a significant comparison with at least one pipeline are included.

Supplemental Data 3: Median z-scores related to the expression of genes in each assessed pathway.

Supplemental Data 4: The results from Transcription Factor Enrichment Analysis on the differential expressed genes identified in Supplemental Data 2.

Supplemental Data 5: Per-site methylation probabilities obtained with m6anet, and the results of the differential methylation analysis with methylKit in each assessed profile; only the sites where at least one profile yields a significant comparison ($q\text{-value} < 0.01$) are included.

Supplemental Data 6: Transcript-level coverage, precision, and sensitivity scores for each analyzed direct-RNA sequencing sample.

Supplemental Data 7: MultiQC report providing statistics on Nanopore sample run quality.

Supplementary Data 8: Transcripts uniquely associated with each time point.