

## **Description of Additional Supplementary Files**

**Supplementary Data 1** – Sample metadata, hardware and software specifics, CNN architecture and performance (benchmark).

**Supplementary Data 2** – Summarized data used for orthogonal validation of Ninetails/Nanopore vs FLAMseq/PacBio based on datasets from publicly available repositories (Legnini et al. 2019 and Tavakoli et al. 2023). Source data for Figure 2.

**Supplementary Data 3** – Summarized data used for comparison of non-adenosine incorporation frequency by various enzymes based on an in vitro synthesized molecules analyzed with Ninetails pipeline. Source data for Figure 3.

**Supplementary Data 4** – Summarized data from moderna mRNA-1273-derived reads obtained as a result of crude mRNA-1273 and bone-marrow derived murine macrophages subjected to mRNA-1273 in various time points analyzed with Ninetails pipeline. Reads were classified based on pentamer (UCUAG) presence/absence with DTW algorithm described by Krawczyk et al. 2023. Source data for Figure 4.

**Supplementary Data 5** – Summarized data from reads corresponding to murine endogenous transcripts bone-marrow derived murine macrophages subjected to mRNA-1273 in various time points analyzed with Ninetails pipeline. Source data for Figure 5.

**Supplementary Data 6** – Summarized data from reads corresponding to murine endogenous transcripts from various cell types (bone-marrow derived murine macrophages, dendritic cells, B cells, T cells) analyzed with Ninetails pipeline. Source data for Figure 6.