Supplementary Information

List of Figures

1 Supplementary Figures

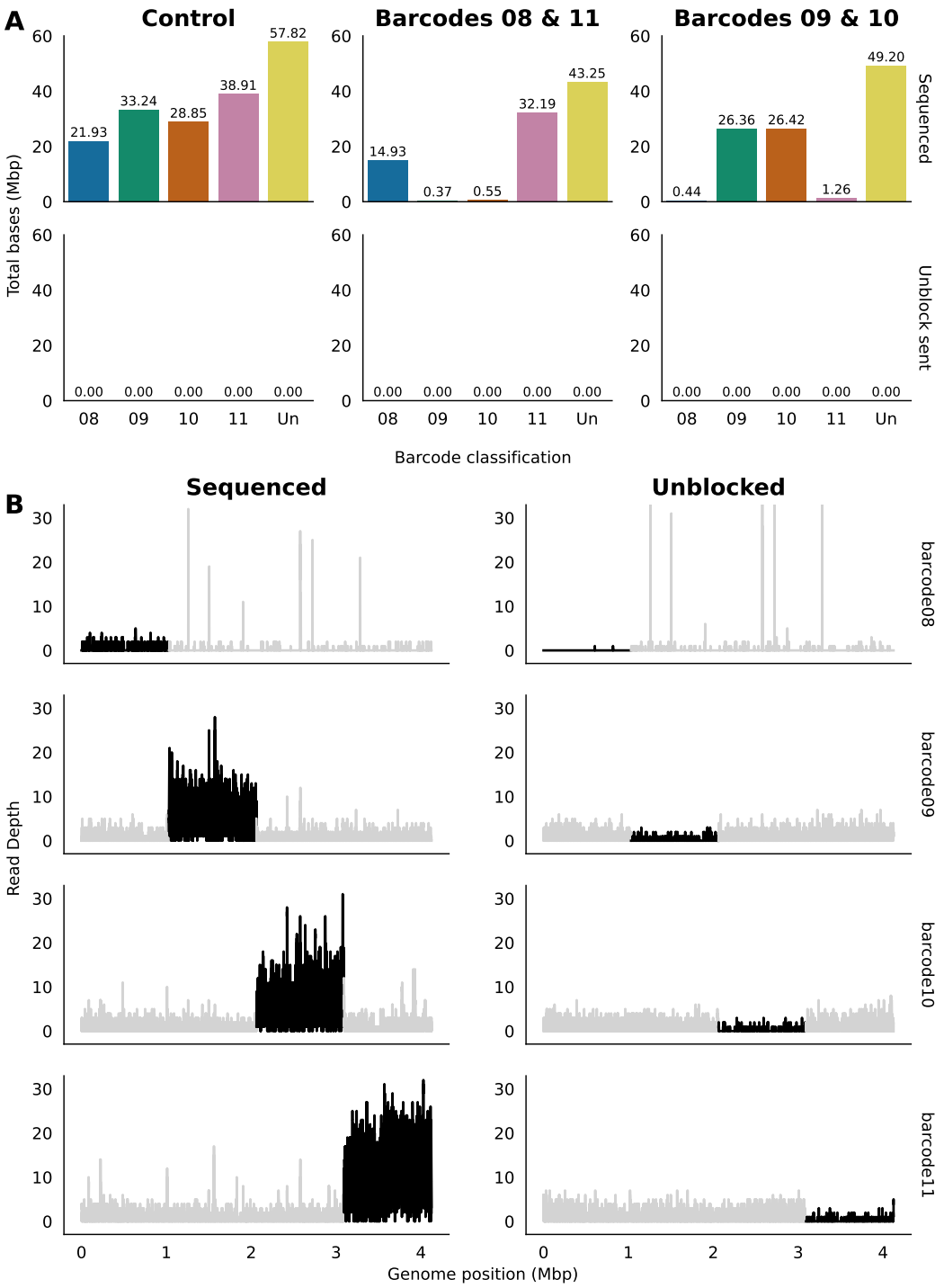

Figure S1: Naive barcoding selective sequencing. A) Demonstration of "switching off" individual barcodes from a sequencing library. Selected barcodes identified in the panel titles. Top row shows sequenced reads, lower panel shows the rejected or unblocked reads. As barcoding both ends is used to specify barcode, all rejected reads become unclassified (Un) by default. B) Switching the mode of operation for readfish from simple barcode rejection to differential targets. Sample shown is *Clostridioides difficile*. Targeted regions are shown in black. Unfortunately barcode08 was under-represented in this sample, leading to low sequenced read count.

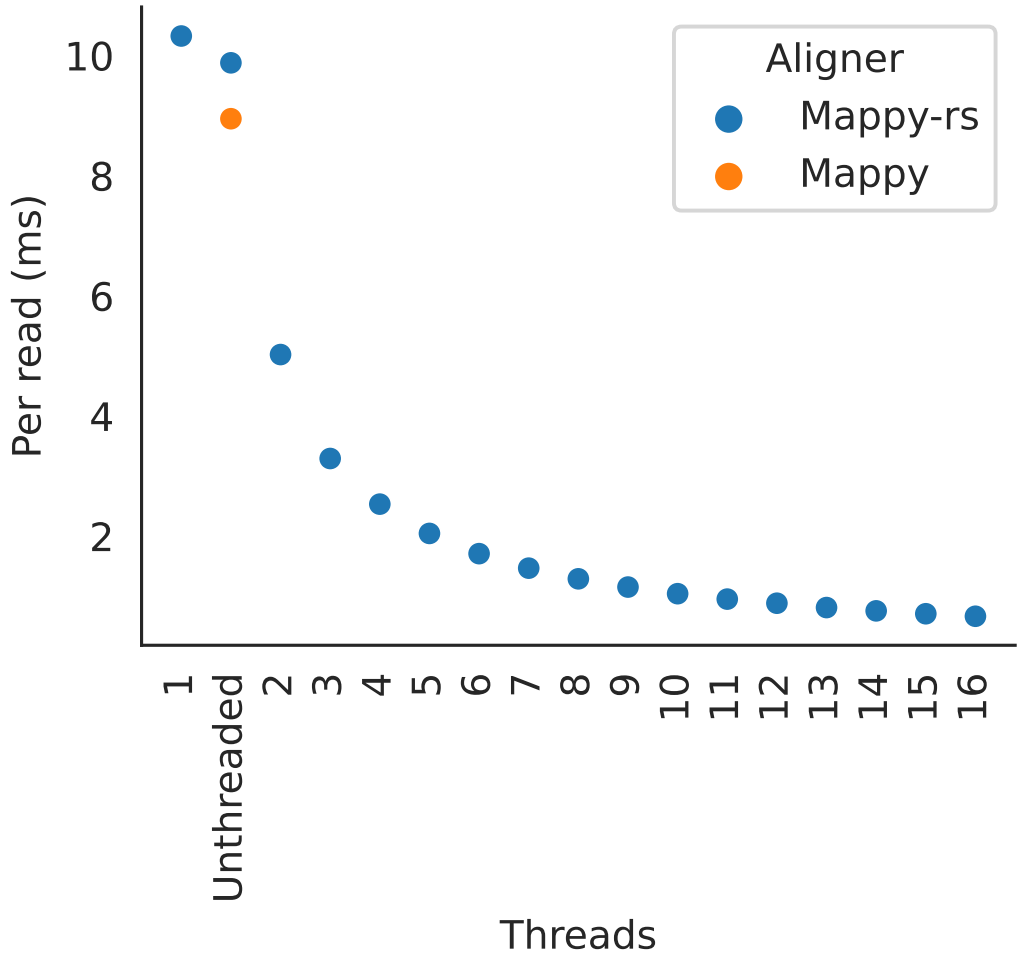

Figure S2: Mapping speed, in reads per second for an increasing number of threads with mappy-rs. Unthreaded indicates that non threadpool based mapping was used. Original mappy aligner is shown in Orange.

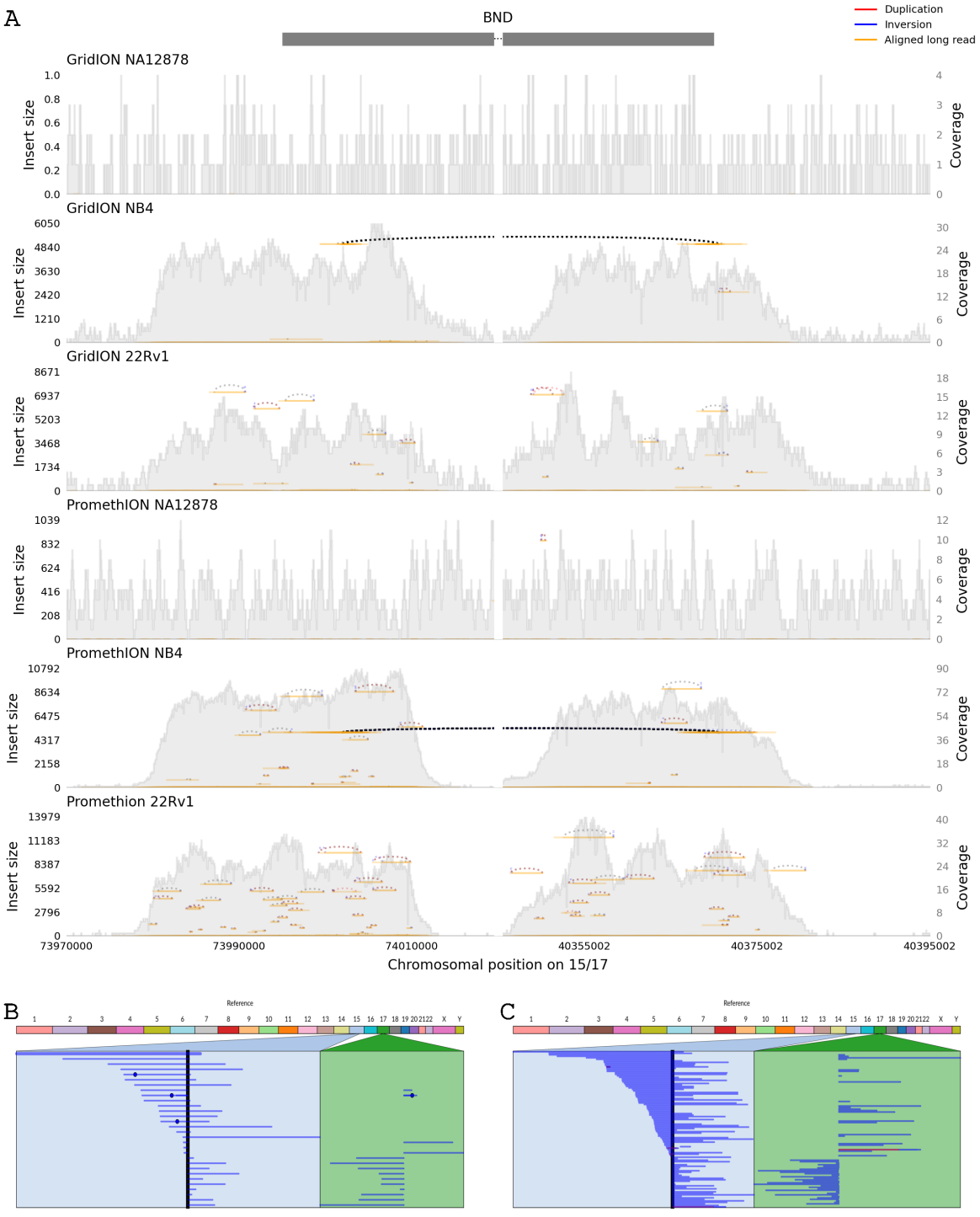

Figure S3: Visualising Structural Variation. A) Using samplot23, we visualise reads linking *PML* (chromosome 15) and the known fusion with *RARA* (Chromosome 17). Only the NB4 sample carries this fusion (indicated by the dashed lines). B), C) Using Ribbon we can visualise individual reads from B) the GridION NB4 sample and C) the PromethION NB4 sample. SVs were identified using CuteSV.

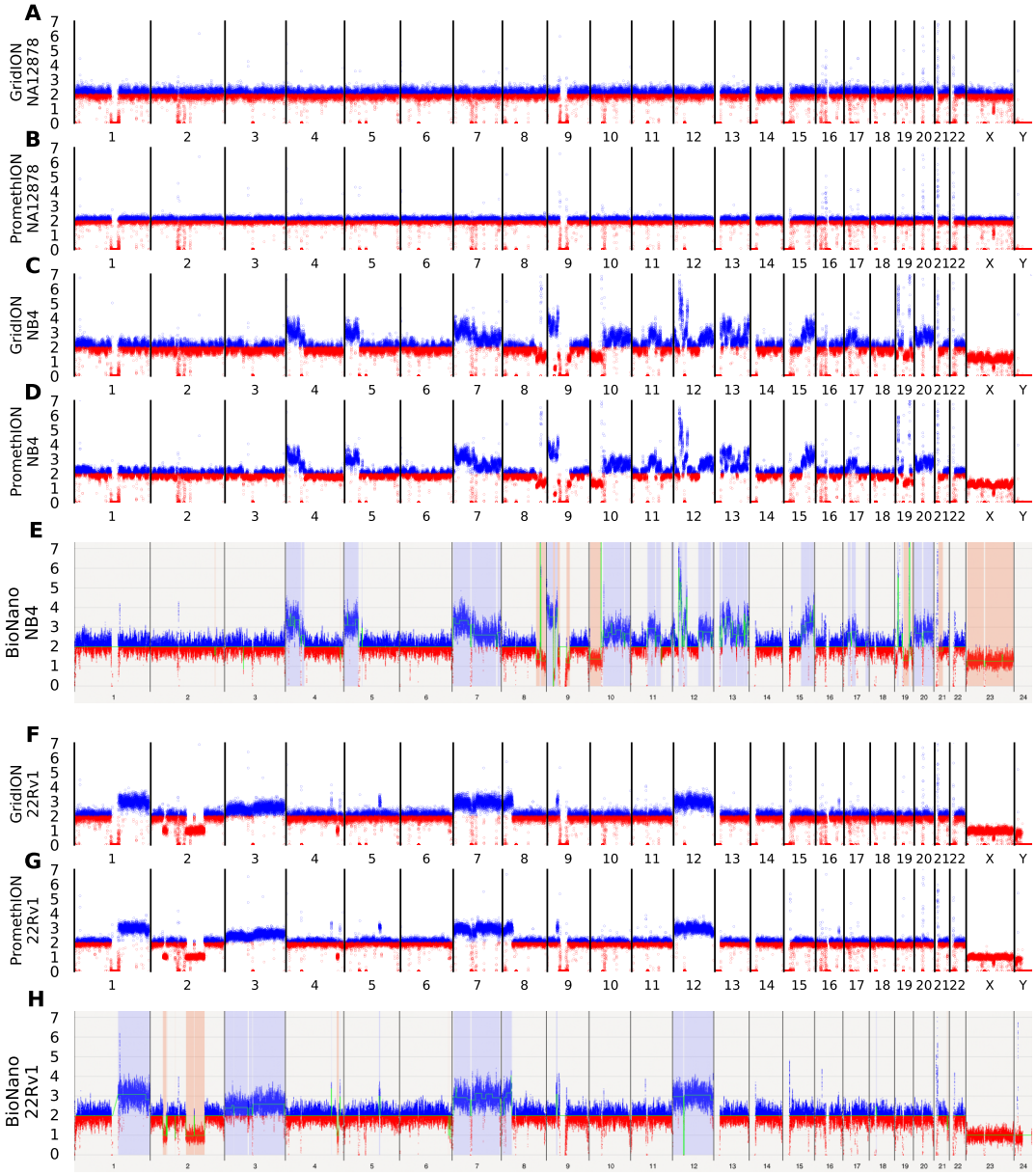

Figure S4: Matched Nanopore and Bionano CNV visualisation. Nanopore sequence data from GridION and PromethION compared with Bionano optical reads, all mapped against hg38. Blue points show where binned data indicates greater than expected copy number, red points where binned data indicates lower than expected copy number. A, B) Copy number of the NA12878 cell line as calculated from Nanopore adaptive sampling on GridION and PromethION. C, D) NB4 copy number using nanopore adaptive sampling data on GridION and PromethION compared with E) showing Bionano optical mapping data for this cell line. F, G) 22rv1 copy number derived from Nanopore adaptive sampling data on GridION and PromethION compared with H) the same cell line visualised using Bionano optical mapping.

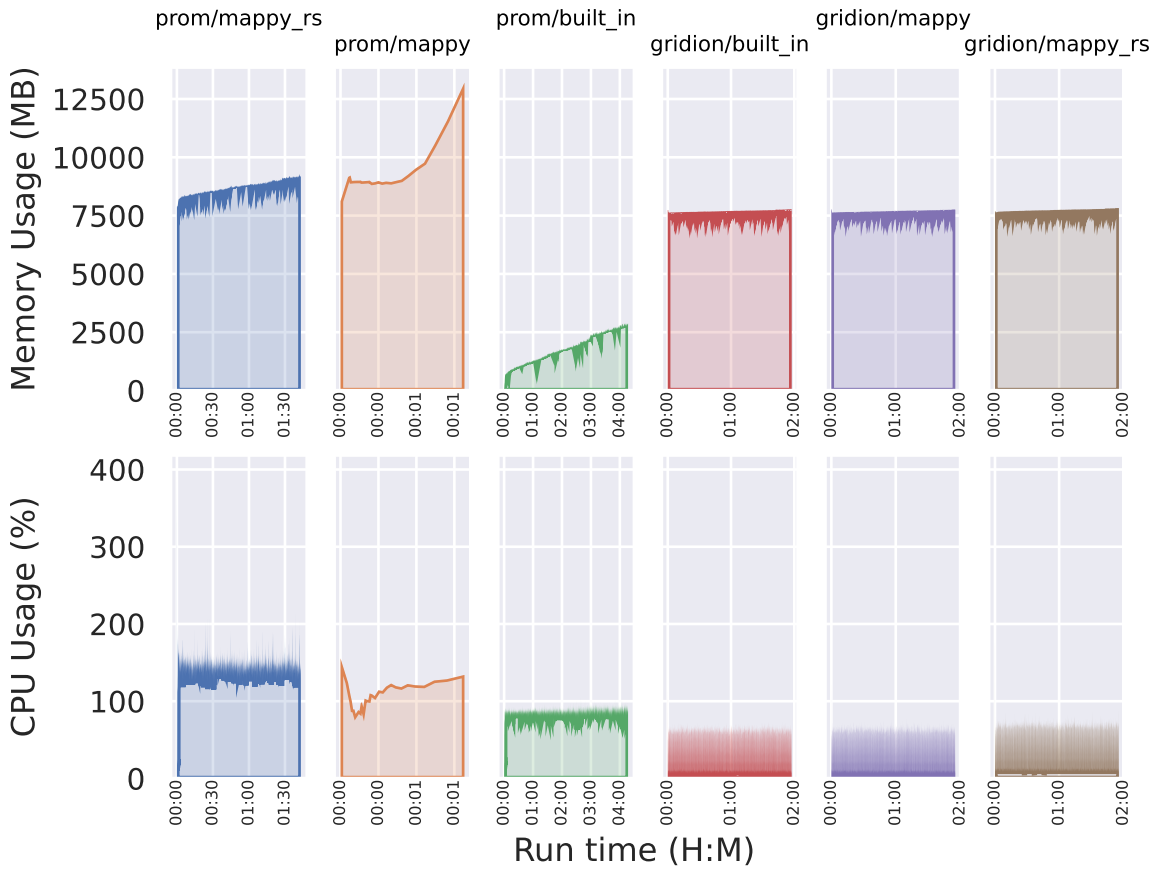

Figure S5: CPU and Memory usage for mappy-rs testing runs, not including the compute required for sequencing. The sequencer and aligner used for the readfish experiment is shown along the top of the panel. Top row displays memory usage after every iteration of signal is processed. Note prom/built_in uses less memory, as the memory used for the reference index for alignment is stored under the basecaller process. prom/mappy has sharp increase due to the build up of signal as the aligner is unable to process basecalled chunks in a timely manner. The lower row displays the average CPU usage over a whole iteration. Note, for gridion runs, several batches are empty, meaning they use next to no CPU, given a spiky appearance.