

Supporting Information for: High-Fidelity Capture, Threading and Infinite-Depth Sequencing of Single DNA Molecules with a Double-Nanopore System

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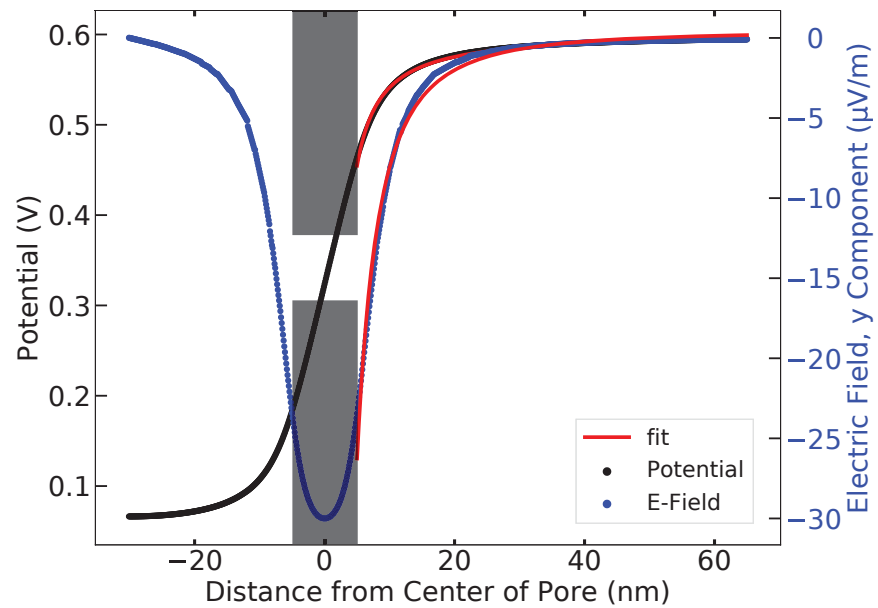


Figure S1: Electric potential and electric field along the axis of the first pore. We see that they each fit the expected functional forms $1/r$ and $1/r^2$, respectively.

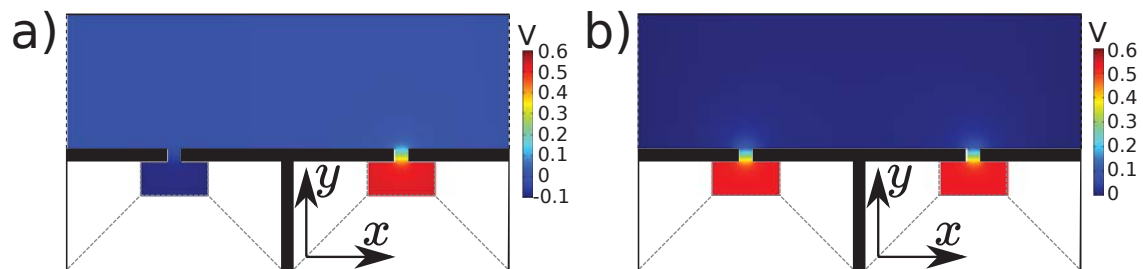


Figure S2: The electrostatic potential in the x - y cross section passing through the two nanopores right before (a), $V_1 = -100$ mV; $V_2 = 600$ mV, and right after (b), $V_1 = V_2 = 600$ mV, the second nanopore capture.

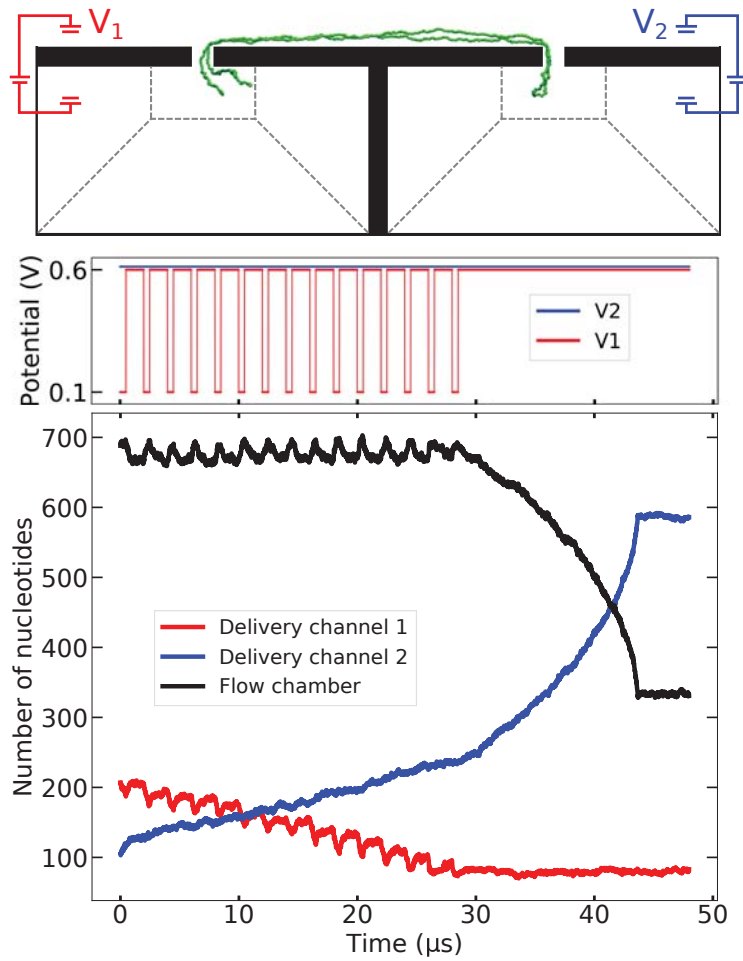


Figure S3: DNA captured with both ends in the same pore. To obtain this conformation, we switched the electrostatic potentials to $V_1 = V_2 = 0.6\text{V}$ sooner than the $4 \mu\text{s}$ we usually waited. For this conformation, one of its ends can be brought out of the first pore and into the second by periodically pulsing the first pore's potential in the manner shown.

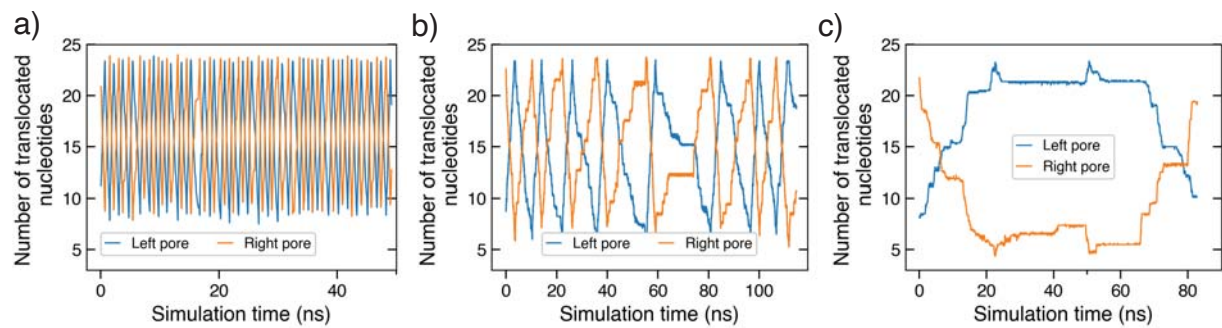


Figure S4: Number of DNA nucleotides translocated through each nanopore during all-atom MD simulations of the ssDNA flossing carried out under 20 V (panel a), 10 V (panel b) and 5 V (panel b) magnitude of the transmembrane bias. Figure 6a shows the simulation system. Data in panel b are the same as in Fig. 6b.

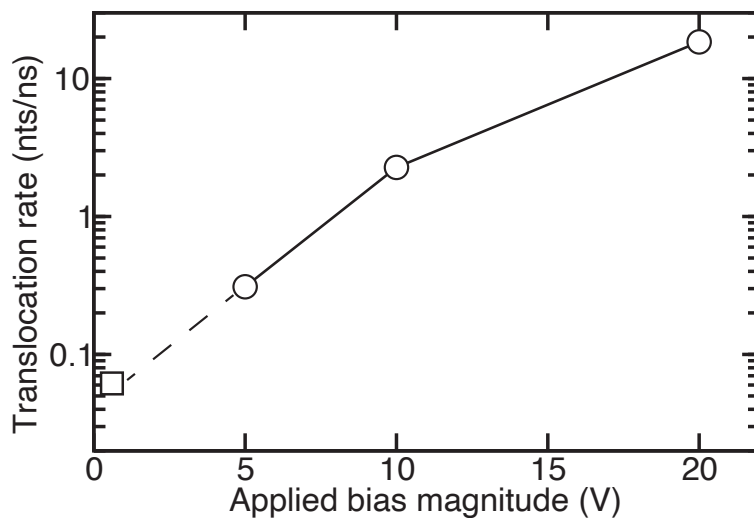


Figure S5: The average rate of nucleotide transport observed in the all-atom MD simulations of ssDNA flossing through a double hBN nanopore system, SI Fig. S4, *versus* the magnitude of the voltage bias (open circles). The square symbol indicates the average translocation rate, ~ 0.05 nts/s, observed in the previous all-atom simulations of ssDNA transport through a single, two-layer graphene nanopore at 500 mV bias.⁵³ Lines are guides to the eye.

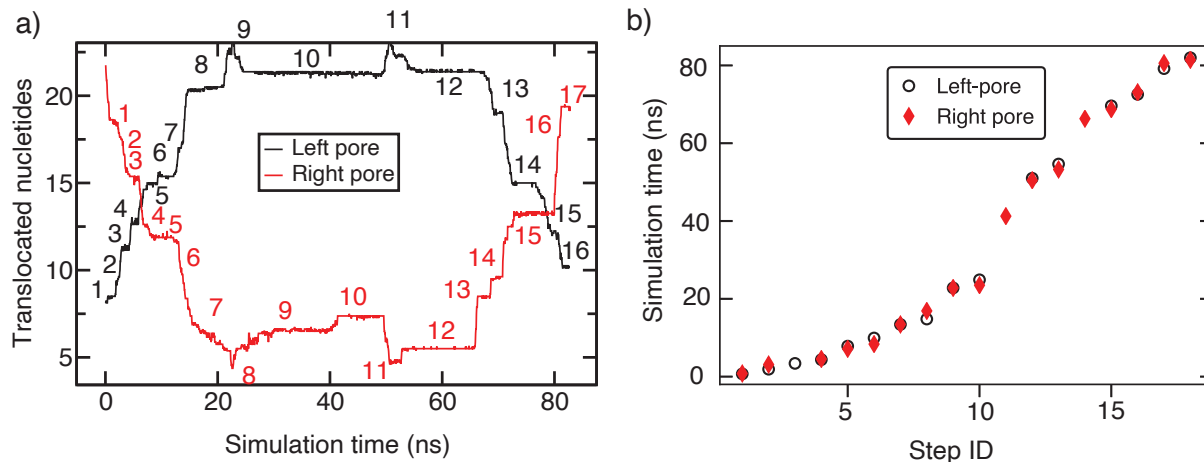
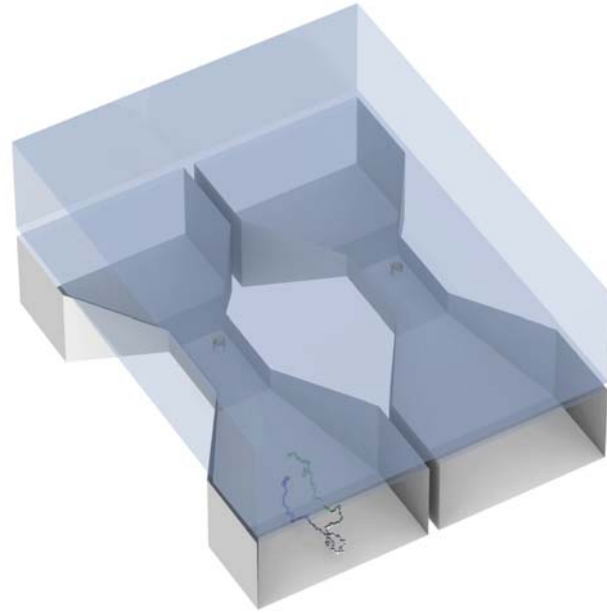
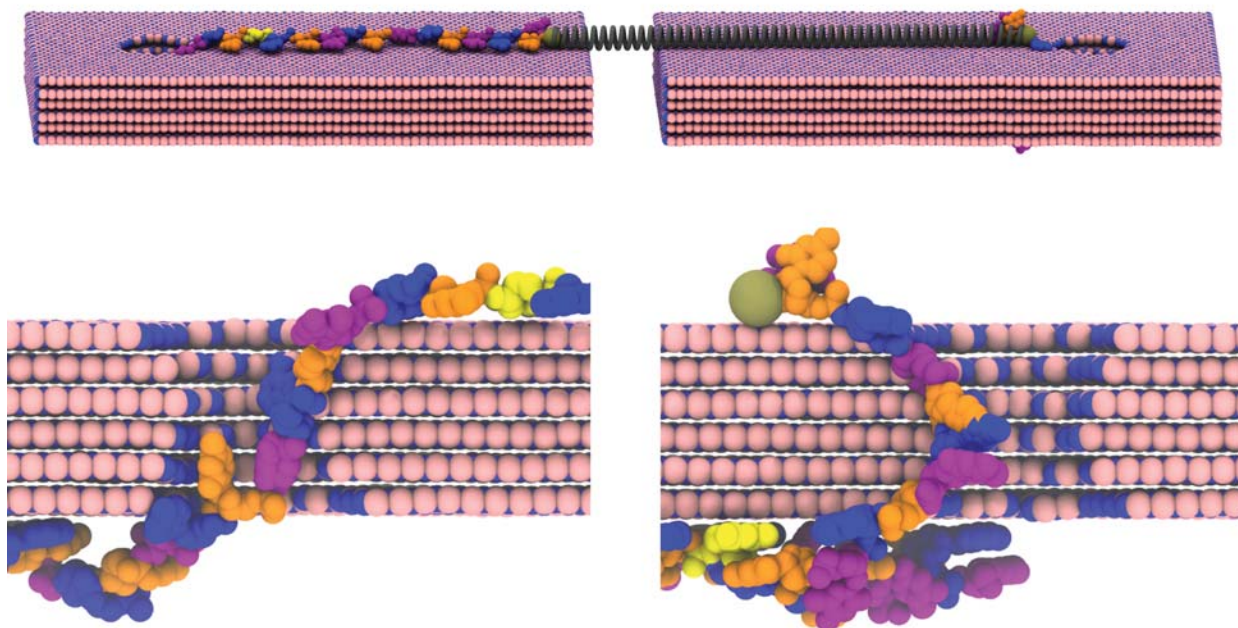


Figure S6: Correlated stepwise displacement of an ssDNA strand through the nanopores of the double-nanopore hBN system. (a) Number of DNA nucleotides translocated through each nanopore during all-atom MD simulations carried out at a 5 V bias (same as in SI Fig. S4c). The numbers shown in black and red count the number of stepwise displacements undertaken by the ssDNA strand through each nanopore. The steps were assigned through visual inspection; steps of less than one nucleotide or lasting less than 1 ns were not considered in the analysis. (b) The simulation time at which each stepwise displacement took place in each of the two nanopores.



Movie 1: Animation illustrating the capture, threading and sequencing of single-stranded DNA molecule in a nanofluidic double nanopore system.



Movie 2: Animation illustrating an all-atom MD simulation of repeat flossing of ssDNA through a double nanopore system. The bottom left and right movies show a cut-away, zoomed in view of individual nanopores of the double nanopore system shown at the top. The animation illustrates the simulation trajectory featured in Figure 6 of the main text.