Supporting Information

A Pressure-Voltage Trap for DNA near a Solid-State Nanopore

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S1. Transient deep blockages

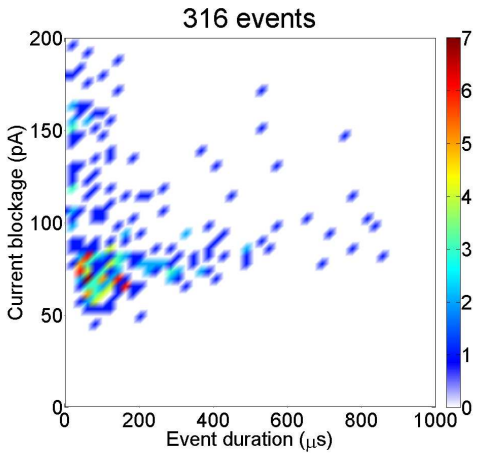
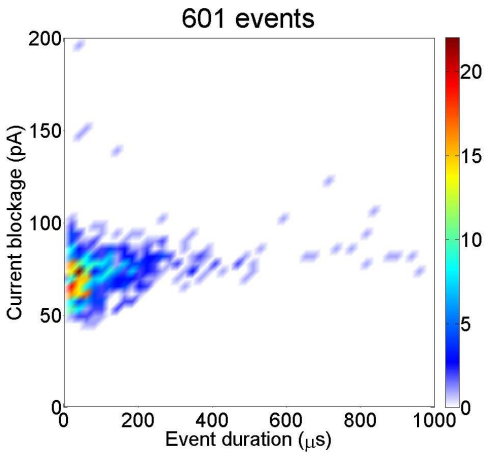
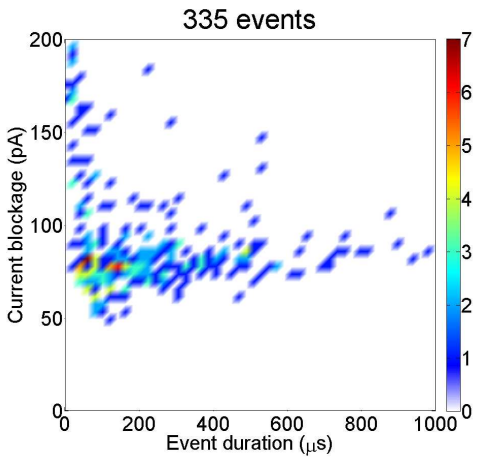
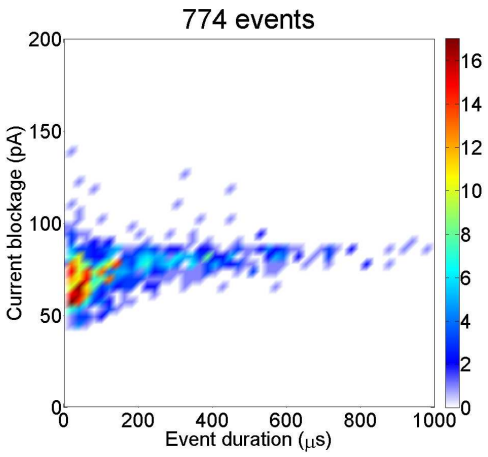
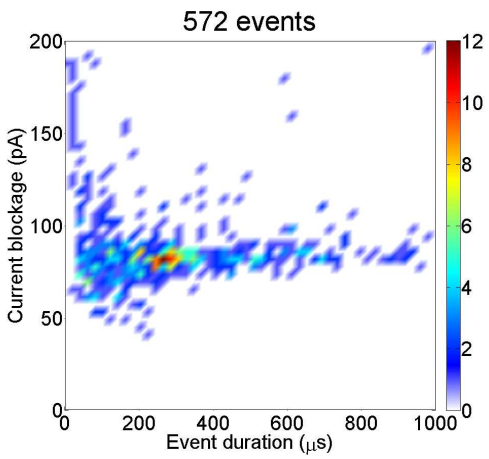
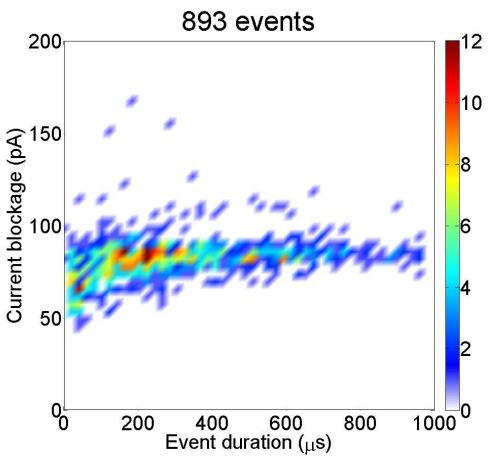
In Figure 1f-g, inspection of individual long translocation attempts reveals that the current blockage occasionally increases for a short period of time from the level expected for a single strand. These "transient deep blockages" are typically observed in traditional translocation experiments at the beginning of an event, where they signal that the molecule was captured in the middle instead of at an end, and very occasionally at the end, indicating that the trailing end of the molecule was captured into the nanopore before the rest of the molecule completed the translocation process. When translocation is slowed by well-balanced forces, we observe an

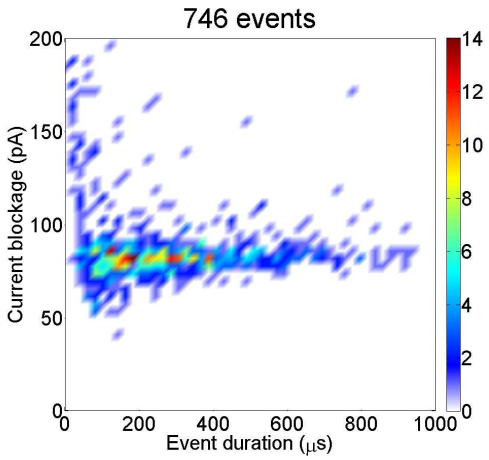
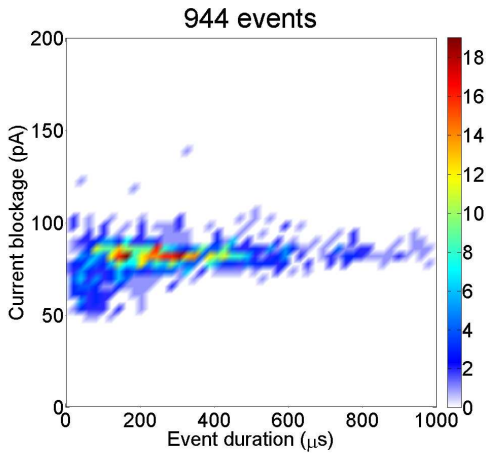
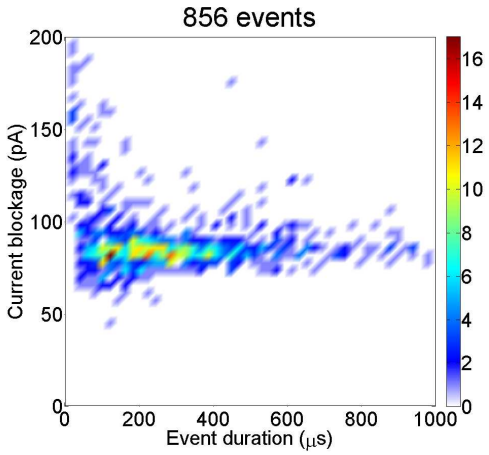
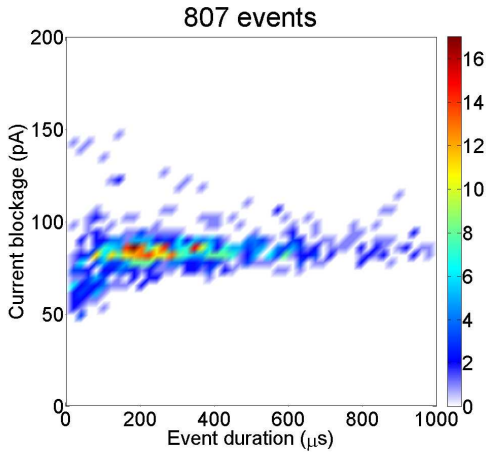
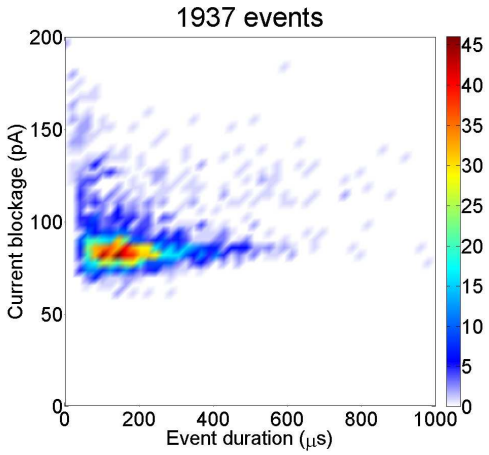
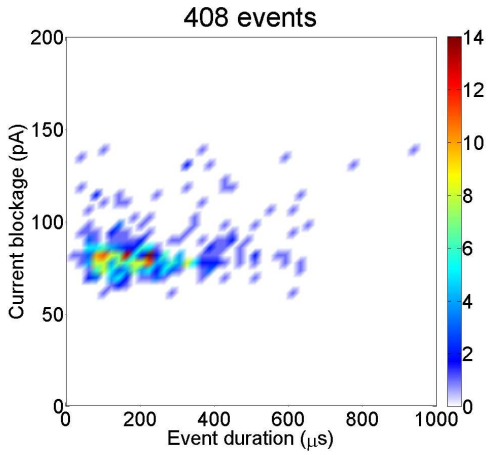
increase in the number of transient deep blockages in the middle of translocation attempts (see Figure 1 of the main text).

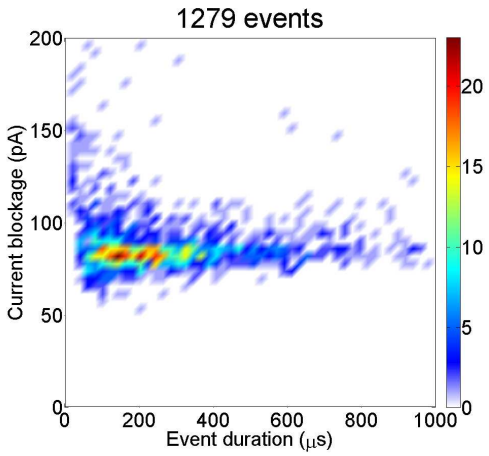
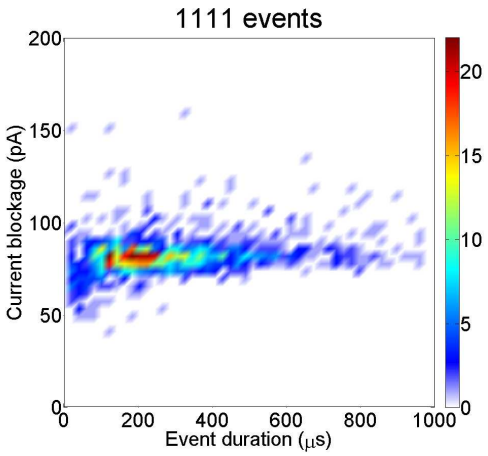
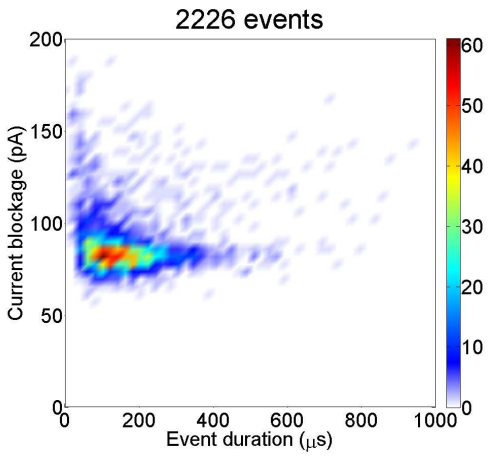
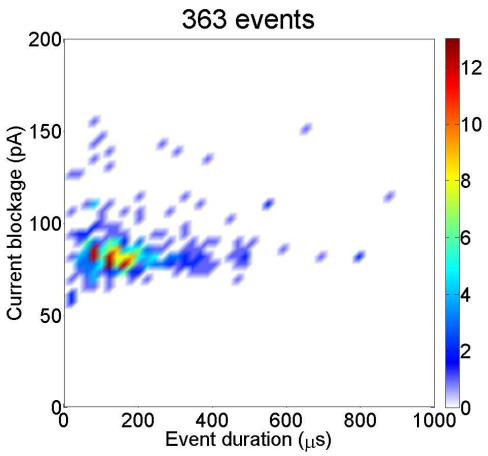
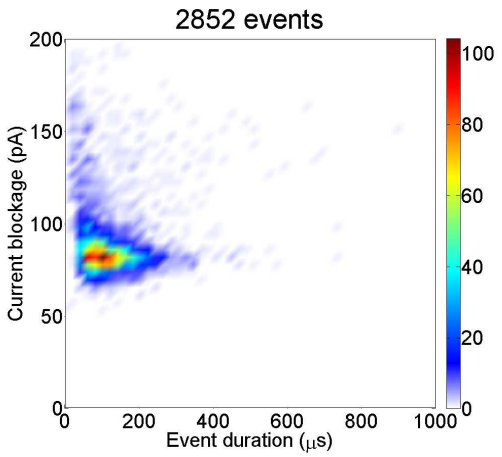
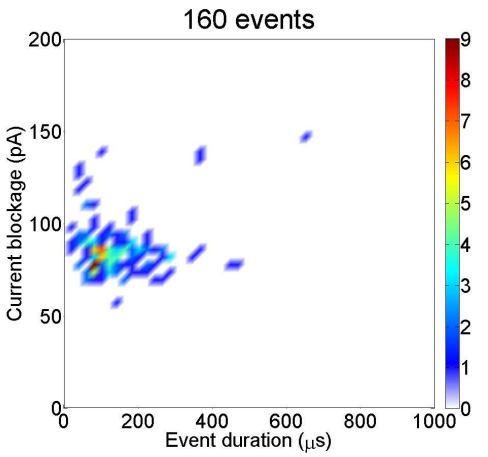
We seek an explanation for transient deep blockages that is consistent with the data in the main text and Supporting Information. In Figure 1b of the main text, we have shown that the pressure force is dominant in the access region close to the nanopore, even when the forces on the molecule in the pore are balanced. Figure 1b of Ref. 6 also shows that in this balanced case the voltage-derived forces are dominant at the periphery of the pore. We therefore propose that in the case of slow translocation and relatively long molecules, the part of the molecule in the pore is moving sufficiently slowly that the trailing end has time to be driven into the pore by the pressure-driven flow, increasing the current blockage. We attribute the transience of the signal to the rapid ejection of this end by the voltage-derived forces at the periphery of the pore. When the forces are carefully balanced, there is not enough space for both the main strand and the trailing end in the region of the pore where the pressure force dominates (see Figure 1b of Ref. 15).

S2. Additional data for reduced-force 615 bp dsDNA experiments

Figure S1 documents the single- and multiple-attempt translocation events at each pressure using a two-dimensional current blockage-event duration histogram. For multiple-attempt events, the event duration and current blockage are determined only from the last attempt. The total number of events for each histogram is indicated. The distributions for the two types of events are indistinguishable (see also the inset to Figure 2b).

	Single-attempt events	Multiple-attempt events
1.64 atm		
1.70 atm		
1.76 atm		

	Single-attempt events	Multiple-attempt events
1.82 atm		
1.87 atm		
1.96 atm		

	Single-attempt events	Multiple-attempt events
2.06 atm		
2.12 atm		
2.17 atm		

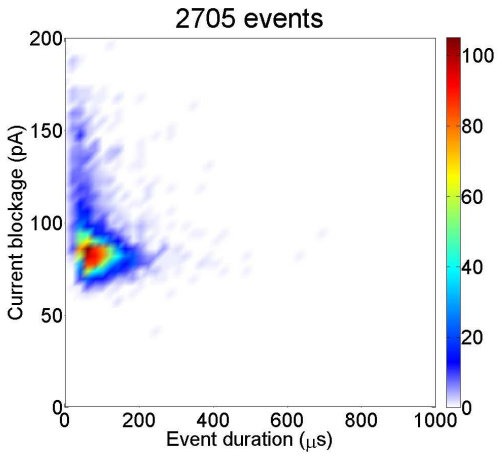
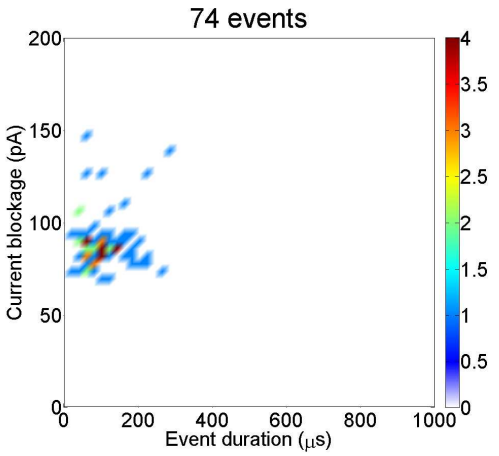
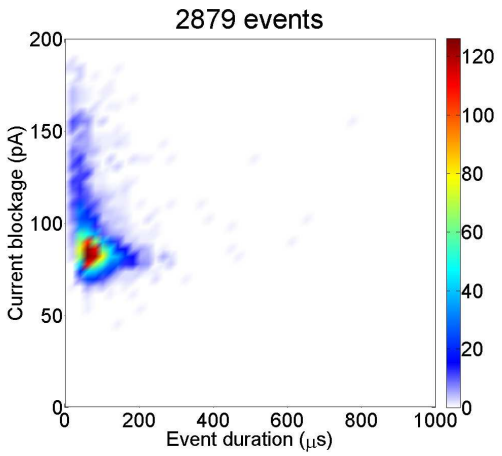
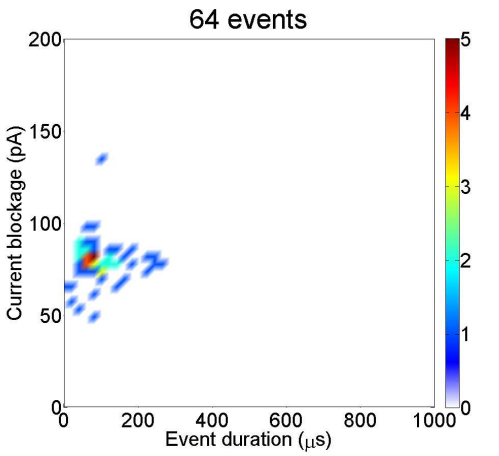
	Single-attempt events	Multiple-attempt events
2.25 atm		
2.44 atm		

Figure S1. Density histograms of single-attempt and multiple-attempt events for 615 bp dsDNA at different pressures and –100 mV counter voltage.

S3. Translocation attempts in voltage-only experiments

In conventional translocation experiments involving only a voltage bias, very short events have routinely been detected and are distinguished from ordinary translocation events. Figure S2a,b shows data from a voltage-biased pore of diameter ~10 nm using V = +100 mV and 3.27 kbp dsDNA. The short events, marked in red, are clearly visible. These events have naturally been interpreted as translocation attempts or failed translocations.

The threshold detection algorithm can be applied to these data as well. The time interval histogram is shown in Figure 2c. As expected from extrapolation of the results of this study to the high-force regime, there is no high-frequency (short-time) peak in the time interval histogram. This demonstrates that there is no correlation between these short events and the next event. Thus these short events are not translocation "attempts" as described in this paper.

Could these events be molecules that fail to translocate and are then lost to diffusion? We assume that the dynamics of the 3.27 kbp dsDNA and 615 bp dsDNA are not significantly different, allowing us to estimate the expected loss rate for the 3.27 kbp dsDNA at V = 100 mV from the 615 bp dsDNA data. For the 615 bp dsDNA, a 22% loss rate occurs with ΔP = 1.82 atm and V = -100 mV, and the loss rate drops to < 1% at ΔP = 2.44 atm and V = -100 mV (see Figure 4a). This suppression of the loss rate is accompanied by an increase in the translocation speed of the 615 bp dsDNA by only a factor of 2 (Figure S3b). For 3.27 kbp dsDNA at ΔP = 0.865 atm and V = -100 mV, the loss rate is also about 20%. At ΔP = 0 atm and V = +100 mV, however, the translocation speed of 3.27 kbp dsDNA is a factor of 20 larger, so by analogy to the 615 bp dsDNA (where the suppression of the loss rate from 20% to <1% occurs with an increase in the translocation speed by a factor of 2) we expect the loss rate to be much less than 1%. The

observed fraction of spikes, however, is 11% for the 3.27 kbp dsDNA under V = +100 mV only, which is much too large to attribute all of them to molecules lost to diffusion.

We conclude that most of these short events are not collisions at all. They are likely due to some other phenomenon, such as the translocation of short DNA fragments, translocation of small impurities, or electronic noise.

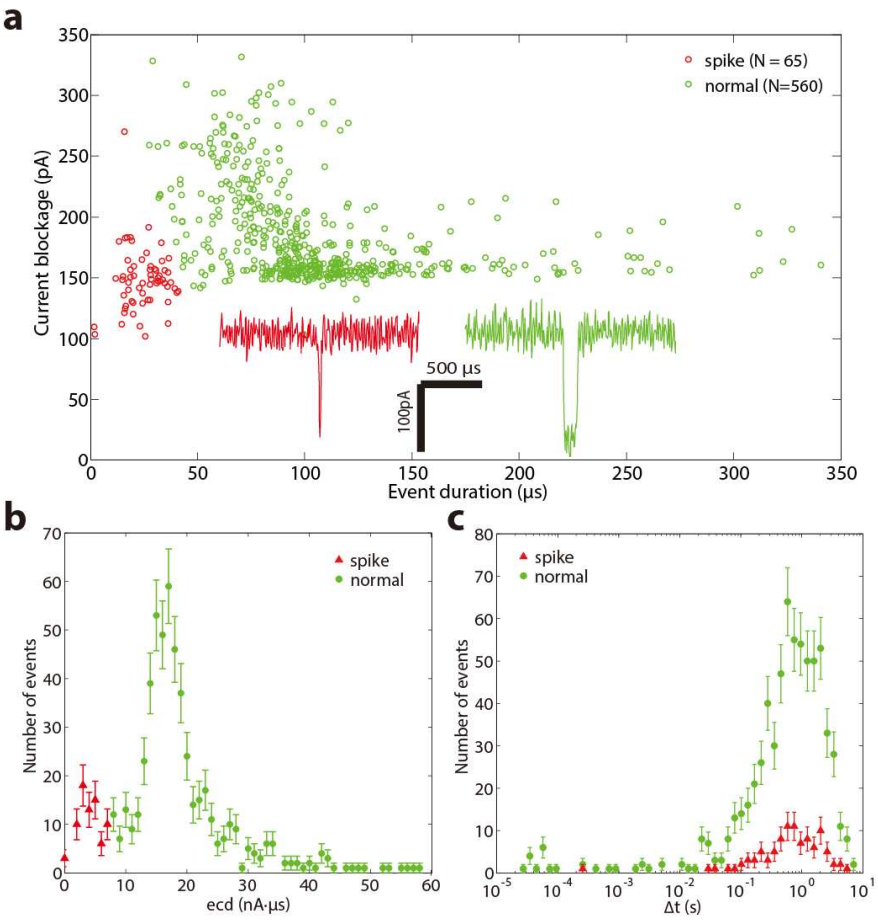


Figure S2. (a) Two dimensional current blockage/event duration histogram of ordinary translocation events (green) and very short events (red) in a conventional voltage-biased nanopore. (Inset) Typical events of each type. (b) Event charge deficit (ecd) histogram. (c) Time interval histogram showing the absence of a peak at short times. Also note that the time intervals

between the spikes and the next events are indistinguishable from the time intervals between normal events, showing that there is no correlation between spikes and normal events.

S4. Detailed results of finite element calculation

In Figure 4, we show the predictions of our optimized drift-diffusion model. The inset to Figure S3a shows the geometry of the calculation at $x = 0$, where the head of molecule is in the center of the nanopore. The main Figure S3a shows the force fields calculated using the optimized parameters for several pressures. Note that a true P-V trap, in which the force field crosses zero with a positive slope, exists only for some of the pressures, such as 1.76 atm and 1.70 atm, corresponding to those pressures at which the failure rate is about 50% and the dwell time is maximum. Multiple attempts at translocation are observed for the entire pressure range, however, because diffusive motion is significant relative to the force-induced motion for all the pressures studied here.

The curves in Figure S3a also help explain the experimental observation that the capture rate does not drop to zero at the same pressure as the average translocation speed, as shown in Figure S3b. This is consistent with the presence of a small attractive region near $x = 0$ and suggests that the attractive viscous forces are stronger than the repulsive electrical forces outside the nanopore. Note that the method for calculating the average translocation speed (which is meaningful only for successful translocations) is the same as the method used to calculate the average trapping time, as described in the text.

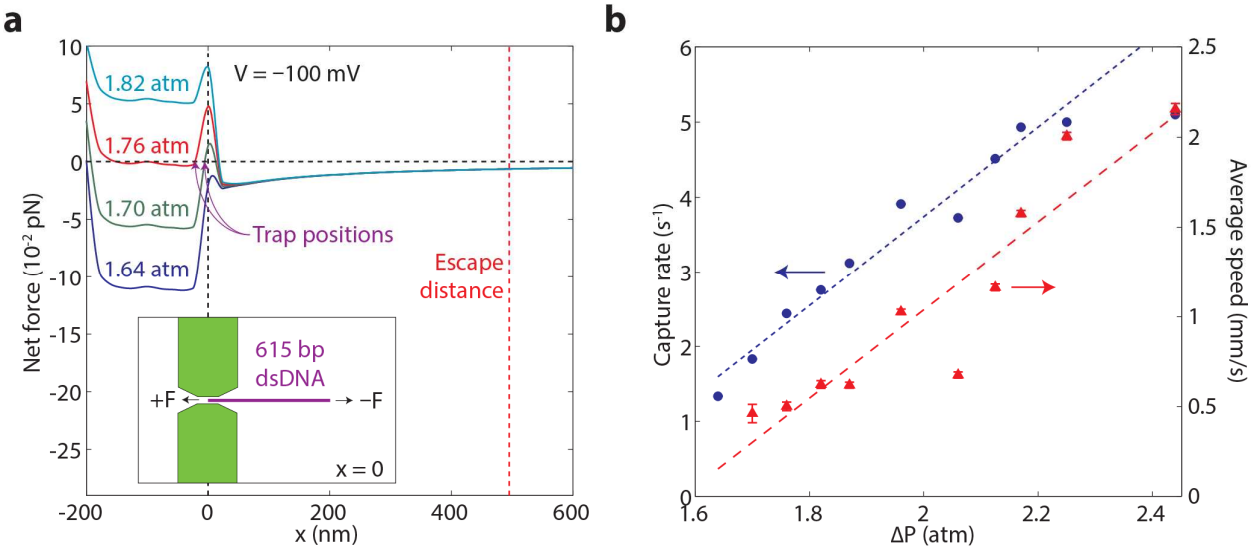


Figure S3. (a) Sample force fields used to calculate the curves in Figure 4a-b. Inset: geometry of the calculation at $x = 0$. (b) Comparison of the capture rate (left axis) and average translocation speed (right axis) at different pressures. Lines are regression fits to the data below $\Delta P = 2.3$ atm.