Supplemental Information

Gel mesh as "brake" to slow down DNA translocation Through solid-state nanopores

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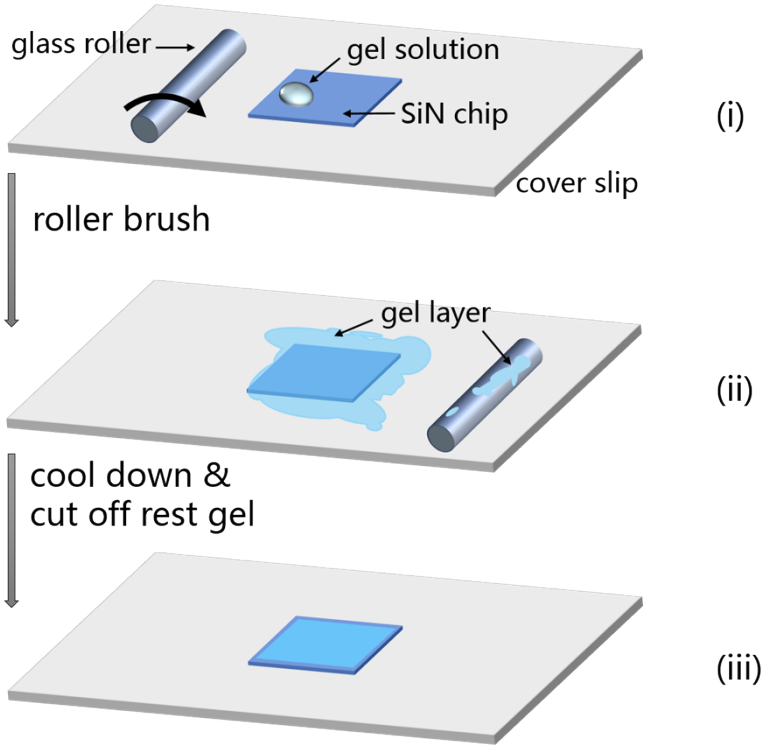

Figure S1. Schematic diagram of various steps for loading agarose gel layer by rolling method.

Agarose powder is bought from Sigma Aldrich (CAS: 9012-36-6). The powder is added in DI water in proportion of 1 to 100, then the turbid liquid is heated to ebullition and last for 3 minutes so that agarose powder completely dissolves and the solution gets uniformly mixed. Transfer the solution in water bath of 50°C to maintain

the agarose gel in liquid state. Simultaneously, the 3 mm*3 mm chip with a nanopore is pre-rinsed by standard protocol and then plasma cleaned for 30 seconds to acquire hydrophilic surface property. And the chip is placed on a piece of coverslip as a holder, Cis side (flat SiN membrane surface) up. Afterwards, a droplet of warm agarose gel solution (1 μL in volume) is injected on the Cis side of the chip by an accurate pipette (0.5~2.5 μL in range), followed by a glass roller brush (2 mm in diameter) rolling across (i), thus spreading the gel solution evenly on the SiN surface (ii). Rest of the gel layer that beyond the chip edge during the rolling process is cut off by blade after the solution cools down and solidifies, leaving the chip square covered by gel layer only (iii).

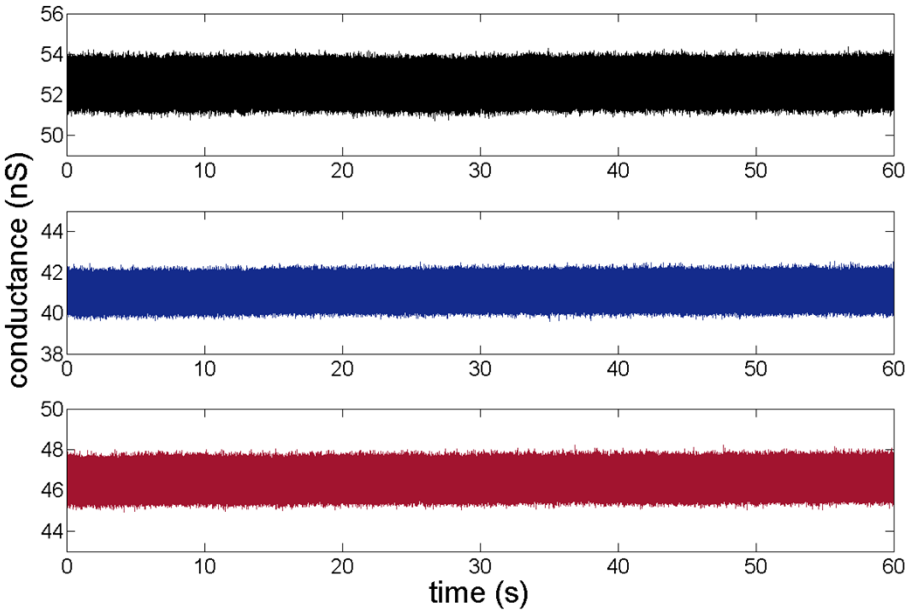

Figure S2. Typical raw current trace after gel loading of 3 nanopore samples. Time scale is adjusted to 0~60s for clarity of comparison.

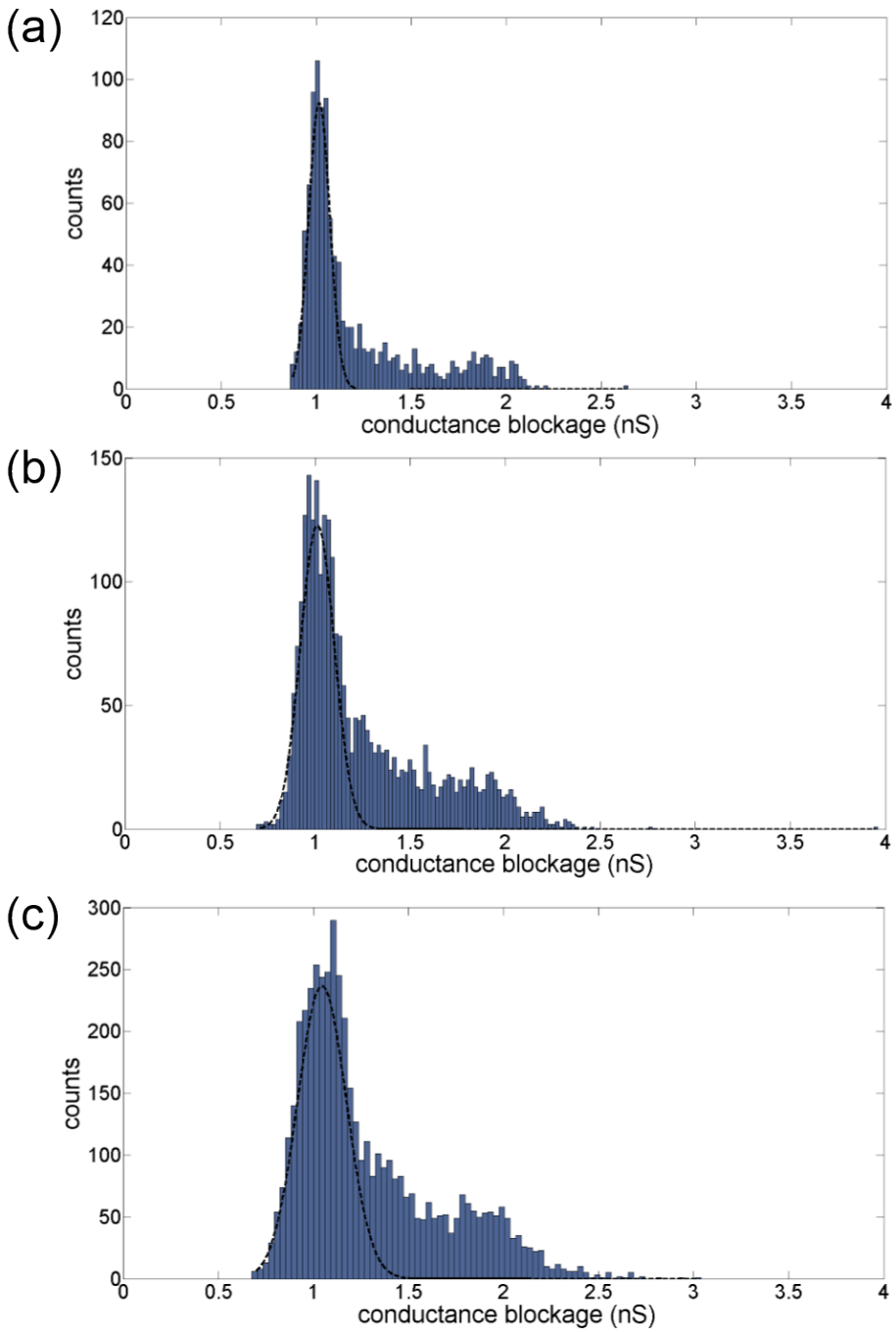

Figure S3. Conductance blockage double-Gaussian fit of 5 kbp dsDNA translocation through gel meshed pore (100, 200 and 300 mV respectively). Only single level component of the double-Gaussian fit is launched in plot to simplify analysis.

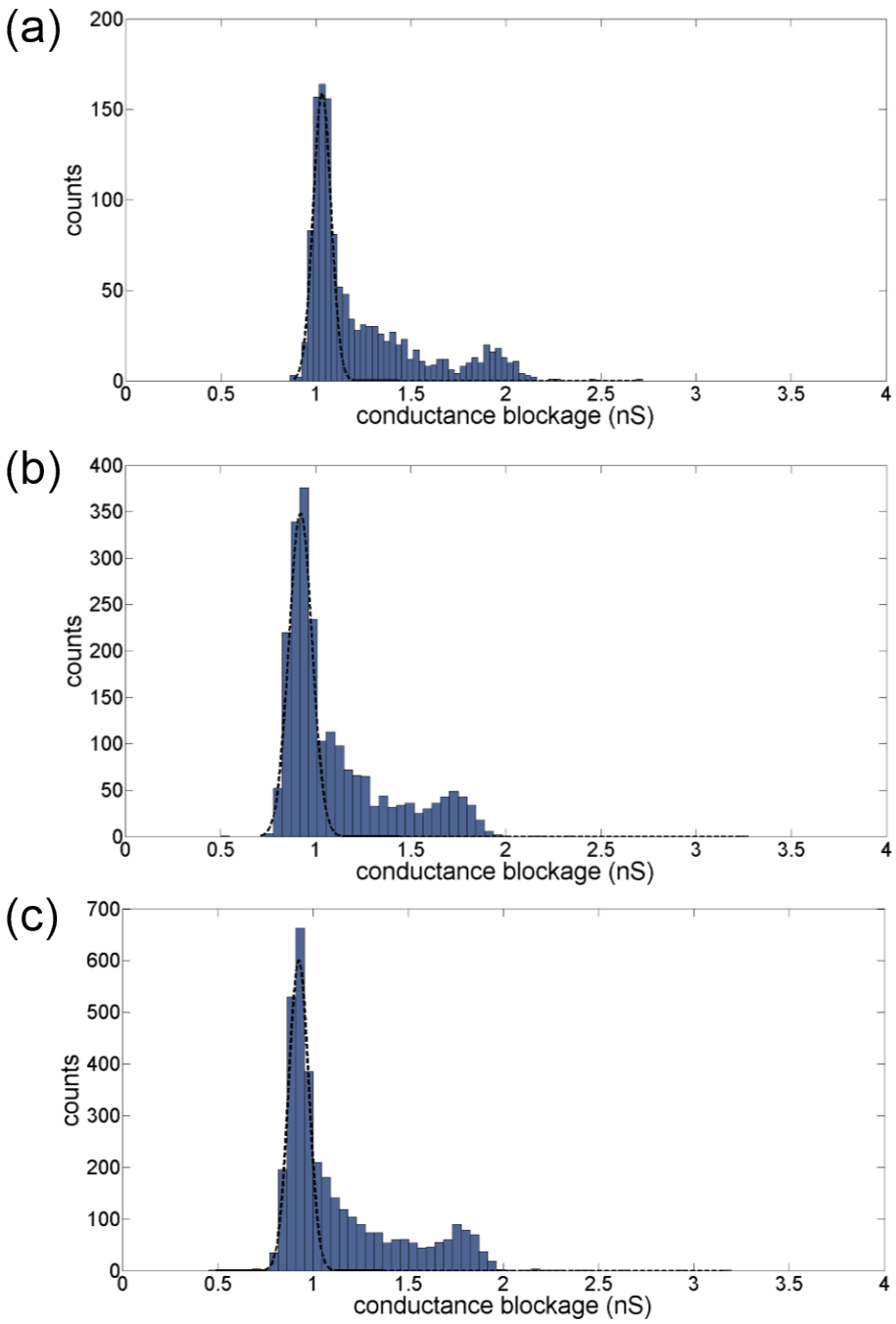

Figure S4. Conductance blockage double-Gaussian fit of 10 kbp dsDNA translocation through gel meshed pore (100, 200 and 300 mV respectively).

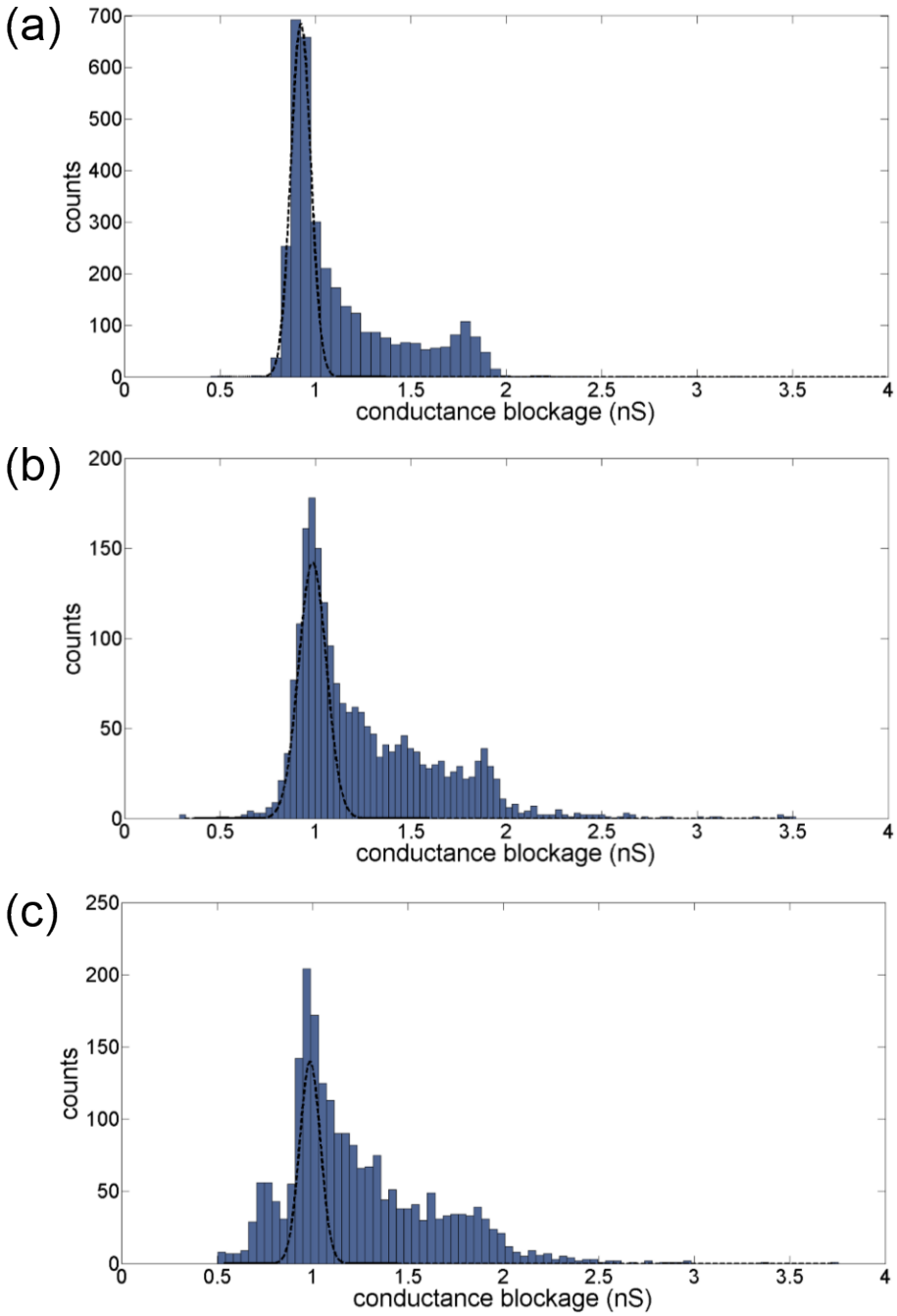

Figure S5. Conductance blockage double-Gaussian fit of 48.5 kbp dsDNA translocation through gel meshed pore (200 and 300 mV respectively for a & b) and through bare nanopore under 300 mV (c).

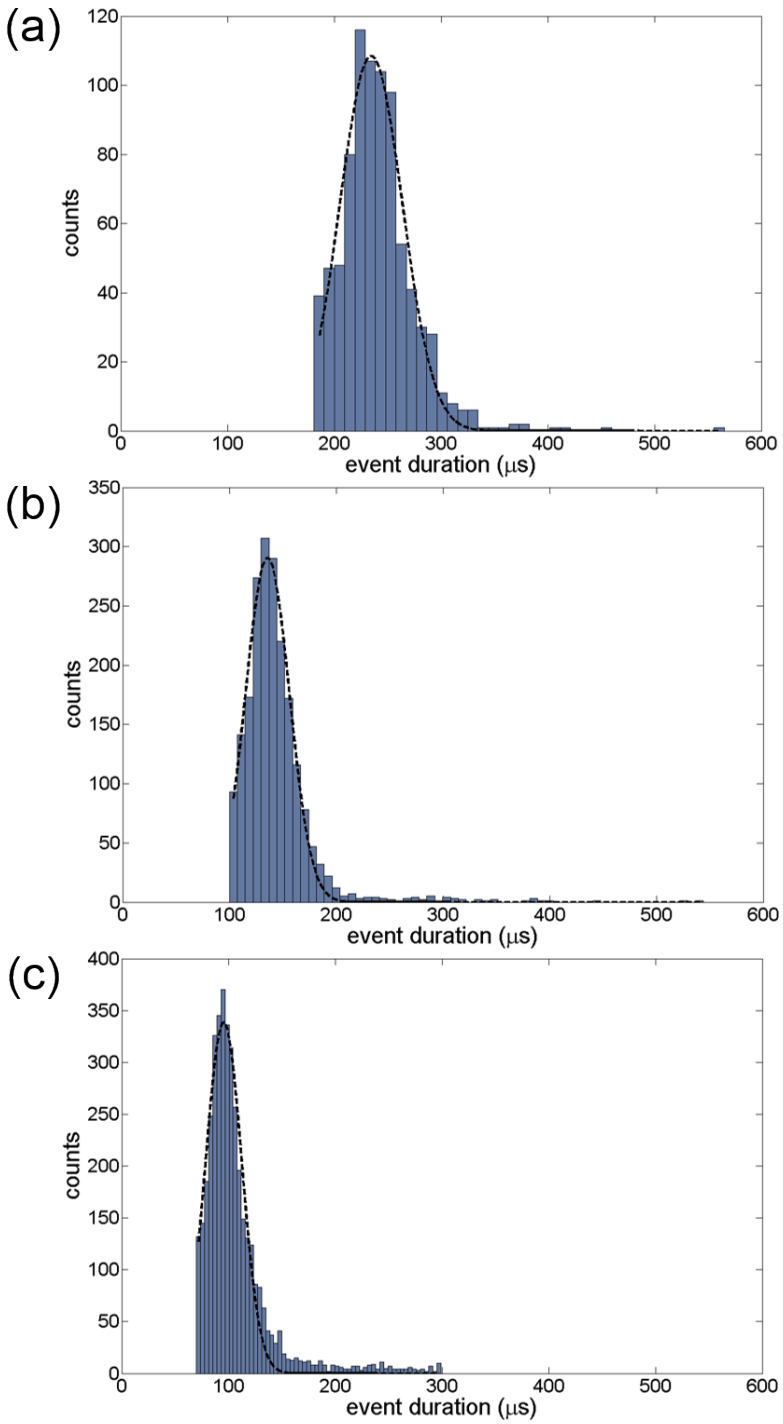

Figure S6. Event duration Gaussian fit of 5 kbp dsDNA translocation through gel meshed pore (100, 200 and 300 mV respectively). Only unfolded DNA events are launched in plot for clarity.

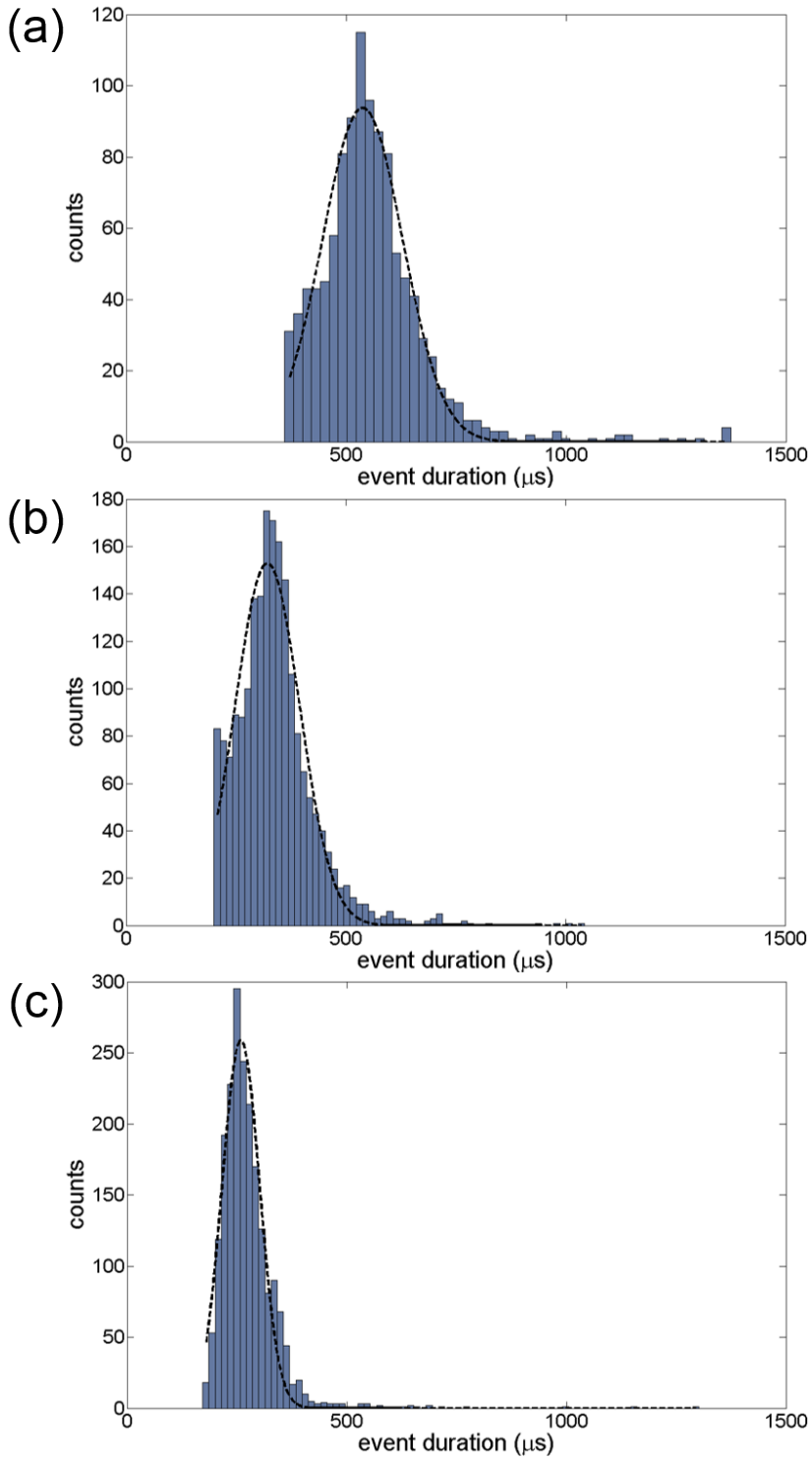

Figure S7. Event duration Gaussian fit of 10 kbp unfolded dsDNA translocation through gel meshed pore (100, 200 and 300 mV, respectively).

Table S-1

DNA length	voltage (mV)	whether gel meshed	number of events	t_d of single level (μs)	R-square	relative t (t_{gel}/t_{bare})
5 kbp	100	1	1097	240±20	0.9598	1.47±0.42
	200	1	2654	140±20	0.9908	1.63±0.49
	300	1	4897	100±20	0.9763	1.83±0.63
10 kbp	100	1	1273	550±50	0.9755	1.73±0.48
	200	1	2215	330±60	0.9808	2.13±0.82
	300	1	3557	240±50	0.9922	2.08±0.83
48.5 kbp	100	1	/	/	/	/
	200	1	1748	3070±920	0.9877	3.04±1.32
	300	1	2122	2230±740	0.9728	3.65±2.07
5 kbp	100	0	2661	160±50	0.9668	/
	200	0	1649	80±20	0.9816	/
	300	0	1782	50±20	0.9834	/
10 kbp	100	0	1342	320±80	0.9747	/
	200	0	1078	150±50	0.9692	/
	300	0	875	120±403	0.9803	/
48.5 kbp	100	0	2451	2140±980	0.9628	/
	200	0	1876	1010±320	0.9751	/
	300	0	2183	610±280	0.9642	/

Detailed data processing and integration of all events distribution for the data sets used in the main text.

Simulation section

Each initial conformation of DNA molecule is generated by a 3D random walk. The process can be divided into two parts. First, we set the step length of the random walk as 99 nm which is approximate to the persistence length of a dsDNA molecule in free solvent and then random walk for 165 steps to generate a freely-jointed chain representing the 48.5 kb lambda DNA.

As for the case of a bare pore, the random walk start from the entrance of the nanopore channel on the cis side and the nanopore chip surface acts as a reflecting boundary which can avoid the random walk from crossing into the nanopore chip. 10000 freely-jointed chains have been generated to analyze the distribution of center of mass distance.

With the existance of the gel mesh on cis side of the nanopore chip, the lambda DNA's dynamic in the gel mesh can be described by a reptation theory which indicates that the DNA will move along a tube-like path while electrophoresisly passing through the gel mesh towards the nanopore channel entrance. We separated the process into two part, in gel and off gel. First, as for the DNA segment that trapped in gel, it will be driven by the electric field towards the nanopore entrance and thus leaving a straight tube that also direct towards the nanopore entrance. As mentioned in the main text, a capture radius is used to describe the range in which DNA can be captured by electical field. Since the lambda DNA cannot diffuse into the gel mesh, only those DNA molecules within the capture radius and also off the gel mesh (capture region in Figure S8a) can be captured. Secondly, after the path in the gel has been determined, the rest part of the lambda can be generated by random walk. The gel mesh surface is set to be a reflecting boundary to prevent the rest part of DNA from crossing into the gel mesh (Figure S8b).

Previous research has shown that there is a proportional correlation between the average translocation duration and the polymer's center of mass distance. With the existance of the gel mesh, the calculation for center of mass (CM) distance is a little different. For the segment of the polymer which is in the gel mesh, its CM distance is the average distance from the

entrance of the nanopore channel. For the rest segment which is in the free solution, since it has to pass through the tube before translocation, its CM distance is the average distance from the entrance of the tube path plus the length of the tube path. And the total CM distance is calculated as a weighted average of these tow parts.

According to the experiments, no translocation events have been recorded under 100 mV, and numerous events occured under 200 mV, the thickness of the gel mesh can be estimated between the capture radius of 100 mV and 200 mV, say 2 μm~2.8 μm. We set the thickness of the gel mesh as 2 μm and the capture radius under 100 mV as 2 μm in simulation. For different capture radius (different applied voltage), 10000 initial conformations of DNA molecules have been generated respectively.

The simulation result shows that the relative t is 3.9 under 200 mV and 4.3 under 300 mV (Table 2), which is close to the experimental data. The tendency that the relative t increases as the applied voltage increases also accord with the experiments.

The simulation also predicts reduction in FWHM/t_{mean} with the existance of gel mesh which is observed in the experiment. After loading the gel, the FWHM changed slightly but the t_{mean} increased greatly due to the far CM distance and thus lead to a reduction in FWHM/t_{mean}. Note that the simulation predicts a much larger reduction in FWHM/t_{mean} than experimental data. We believe this is mainly due to the assumption in our simulation that the DNA electrophoresis path is a straight tube towards the nanopore entrance. Actually, in weak electrical field, the direction of the tube may fluctuate and thus may not parallel with the electrical field and thus will lead to a crooked tube path which will increase the value of FWHM/t_{mean}.

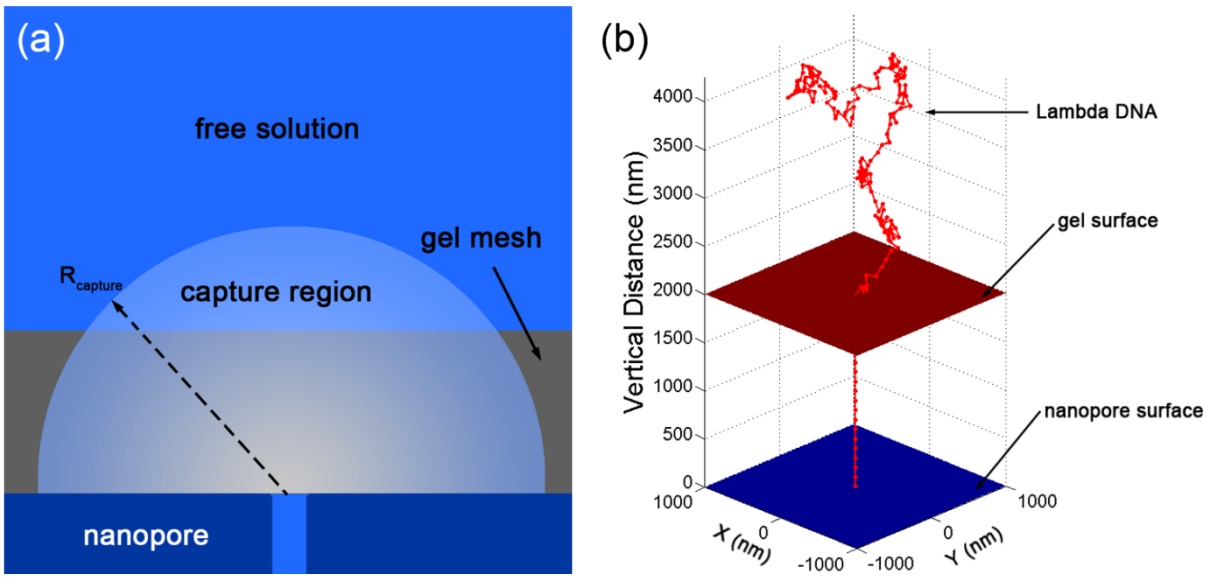

Figure S8. (a) the hemisphere with a radius of $R_{capture}$ reprensent the region in which the DNA can be captured by the electrical field. However, due to the existance of the gel mesh, the Lambda DNA cannot diffuse into the gel mesh. Thus, only those DNA molecules in the "capture region" can be driven into the gel. (b) Schematic diagram displaying the initial conformation of a Lambda DNA captured and driven through the gel mesh. The DNA electrophoresis path inner the gel mesh is set to be a straight tube towards the nanopore entrance, and rest conformation of the polymer off the gel is generated by random walking in simulation.