

# Supplementary Material for “Discriminating protein tags on a dsDNA construct using a Dual Nanopore Device”

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## I. BROWNIAN DYNAMICS (BD) SIMULATION DETAILS

We have coarse grained a  $16.6\mu\text{m}$  long  $\lambda$ -phage dsDNA (please see the supplementary material-II) into 1024 beads with each bead having a diameter of  $\sigma$ . This translates to  $\sigma \simeq 47 \text{ bp} \simeq 16\text{nm}$  per bead. The polymer model was originally introduced for a fully flexible chain by Grest and Kremer [S1]. A short-ranged Lennard-Jones (LJ) potential

$$U_{\text{LJ}}(r_{ij}) = 4\epsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right] + \epsilon, \text{ for } r_{ij} \leq 2^{1/6}\sigma;$$

$$= 0, \text{ for } r_{ij} > 2^{1/6}\sigma. \quad (\text{S1})$$

is used to model the excluded volume interaction of strength  $\epsilon$  between the any two beads  $i$  and  $j$  separated by a distance  $r_{ij}$ . The connectivity between two neighboring beads is constructed using the finitely extensible nonlinear elastic (FENE) spring potential

$$U_{\text{FENE}}(r_{ij}) = -\frac{1}{2}k_F R_0^2 \ln(1 - r_{ij}^2/R_0^2). \quad (\text{S2})$$

Here,  $j = i \pm 1$ , so that  $r_{ij} = |\vec{r}_i - \vec{r}_j|$  is the distance between two consecutive monomer beads,  $k_F$  is the spring constant, and  $R_0$  is the maximum allowed separation between two connected monomers. An angle dependent three body interaction term is introduced between successive bonds which accounts for the chain stiffness  $\kappa$

$$U_{\text{bend}}(\theta_i) = \kappa(1 - \cos \theta_i) \quad (\text{S3})$$

and  $\theta_i$  is the angle between the bond vectors  $\vec{b}_{i-1} = \vec{r}_i - \vec{r}_{i-1}$  and  $\vec{b}_i = \vec{r}_{i+1} - \vec{r}_i$ , respectively. For a homopolymer chain the persistence length  $\ell_p$  in three dimensions (3D) is given by [S2]

$$\ell_p/\sigma = \kappa/k_B T. \quad (\text{S4})$$

The double nanopore device is constructed by drilling two nanopores into a single thick slab and the nanopores are separated by a distance of  $32\sigma$  which translates to 550 nm pore-to-pore separation in the experiment. The left nanopore of diameter  $7\sigma$  and the right nanopore of diameter  $6\sigma$  are constructed by removing out particles from the  $6\sigma$  thick top slab consists of immobile LJ particles. Two reservoirs having a depth and width of  $96\sigma$  are attached below the left and right pores respectively (shown in the Fig.1 in the main article). We use the Brownian dynamics simulation following the equations of motion for the  $i^{\text{th}}$  monomer

$$m_i \ddot{\vec{r}}_i = -\nabla(U_{\text{LJ}} + U_{\text{FENE}} + U_{\text{bend}} + U_{\text{wall}}) - \Gamma_i \vec{v}_i + \vec{\eta}_i. \quad (\text{S5})$$

Here  $\vec{\eta}_i(t)$  is the Gaussian white noise with zero mean at temperature  $T$ , and satisfies the fluctuation-dissipation relation in  $d$  physical dimensions (here  $d = 3$ ):

$$\langle \vec{\eta}_i(t) \cdot \vec{\eta}_j(t') \rangle = 2dk_B T \Gamma_i \delta_{ij} \delta(t - t'). \quad (\text{S6})$$

We express length and energy in units of  $\sigma$  and  $\epsilon$ , respectively. The parameters for the FENE potential in Eq. (S2),  $k_F$  and  $R_0$ , are set to  $k_F = 30\epsilon/\sigma$  and  $R_0 = 1.5\sigma$ , respectively. The friction coefficient and the temperature are set to  $\Gamma_i = 0.7\sqrt{m_i\epsilon/\sigma^2}$  and  $k_B T/\epsilon = 1.0$ . The numerical integration of Equation (S5) is implemented using the algorithm introduced by Gunsteren and Berendsen [S3]. Our previous experiences with BD simulation suggests that for a time step  $\Delta t = 0.01$  these parameters values produce stable trajectories over a very long period of time and do not lead to unphysical crossing of a bond by a monomer [S4, S5]. The average bond length stabilizes to  $\langle b_l \rangle = 0.971 \pm 0.001\sigma$  with negligible fluctuation regardless of the chain size and rigidity [S4]. Hence, we relate the polymer's contour length  $L$  and the number of monomers  $N$  as  $L = (N - 1)\langle b_l \rangle$ .

## II. SIMULATION MOVIE

The simulation movie (generated using the VMD software [S6]) will help to understand further how the capture and flossing of a dsDNA works in a double nanopore system.

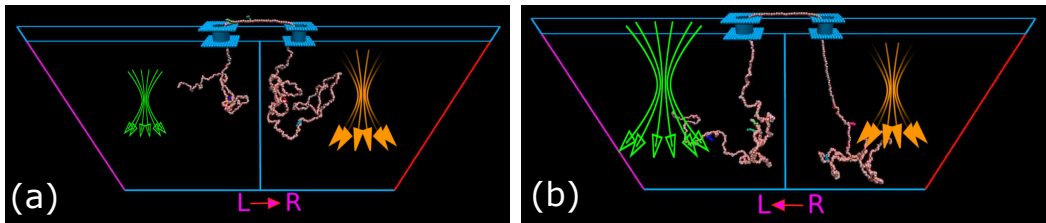


FIG. S1. (a) A single movie frame (screen-shot) depicting the  $L \rightarrow R$  scan the dsDNA through the double nanopore setup in presence of the extended electric fields. (b) The frame shows the dsDNA during the  $R \rightarrow L$  scan. In both cases, the left/right nanopore forces are shown in green/orange arrows (not to scale). The dsDNA backbone monomers are depicted using the pink beads and the seven sidechain tags are shown in their respective colors.

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