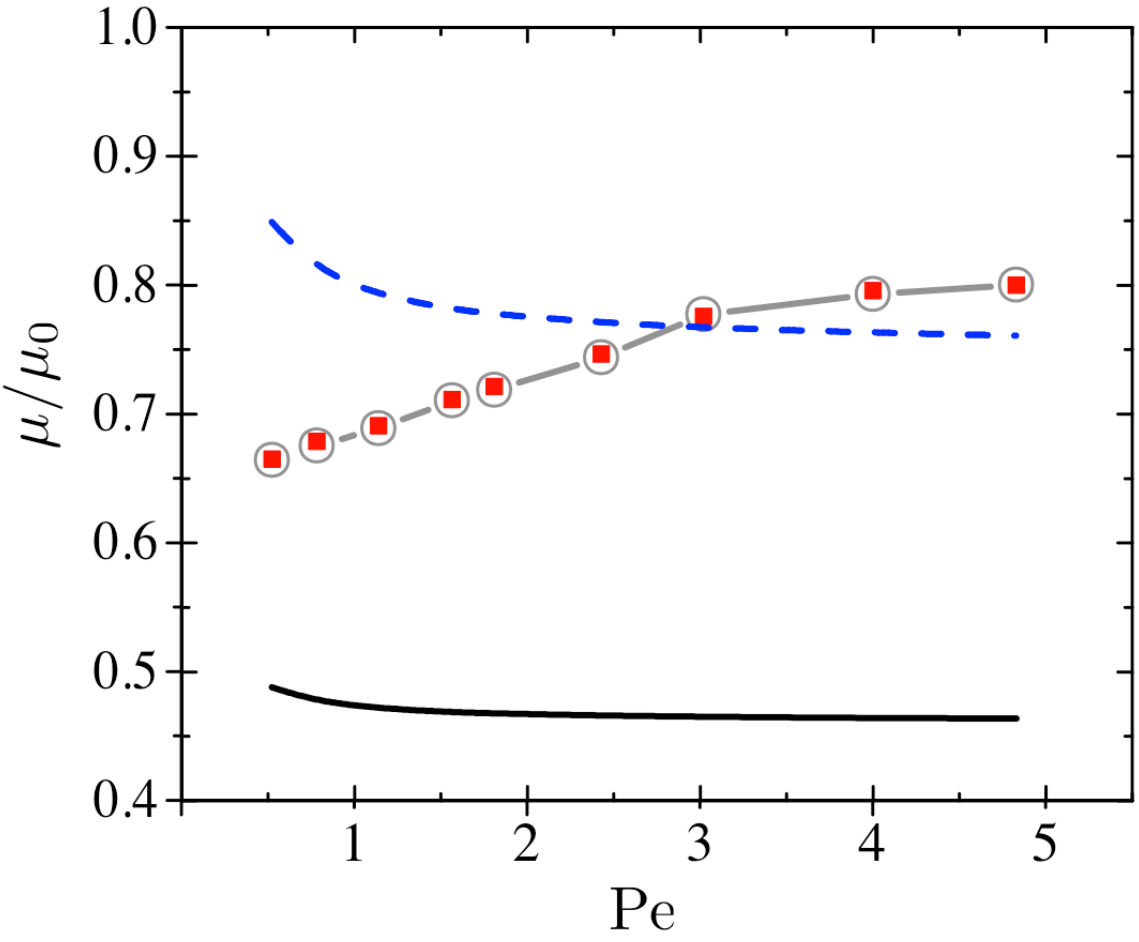

Figure A1: Dimensionless electrophoretic mobility of λ DNA in an array of 1 μm posts with 3 μm center to center spacing predicted from the worm-like chain extension model [8] (blue dashed line), and from the stem-flower extension model (black solid line) [6, 7]. The red squares show the mobility measured from Brownian dynamics simulations in the same geometry [19]. Gray circles show the dimensionless mobility calculated from the model presented in this paper.

In Part I [17] we motivated the evaluation of current CTRW models with a comparison of the model predictions to the mobility measured from BD simulations. Figure A1 shows the mobility calculated from the new CTRW presented in Part II.

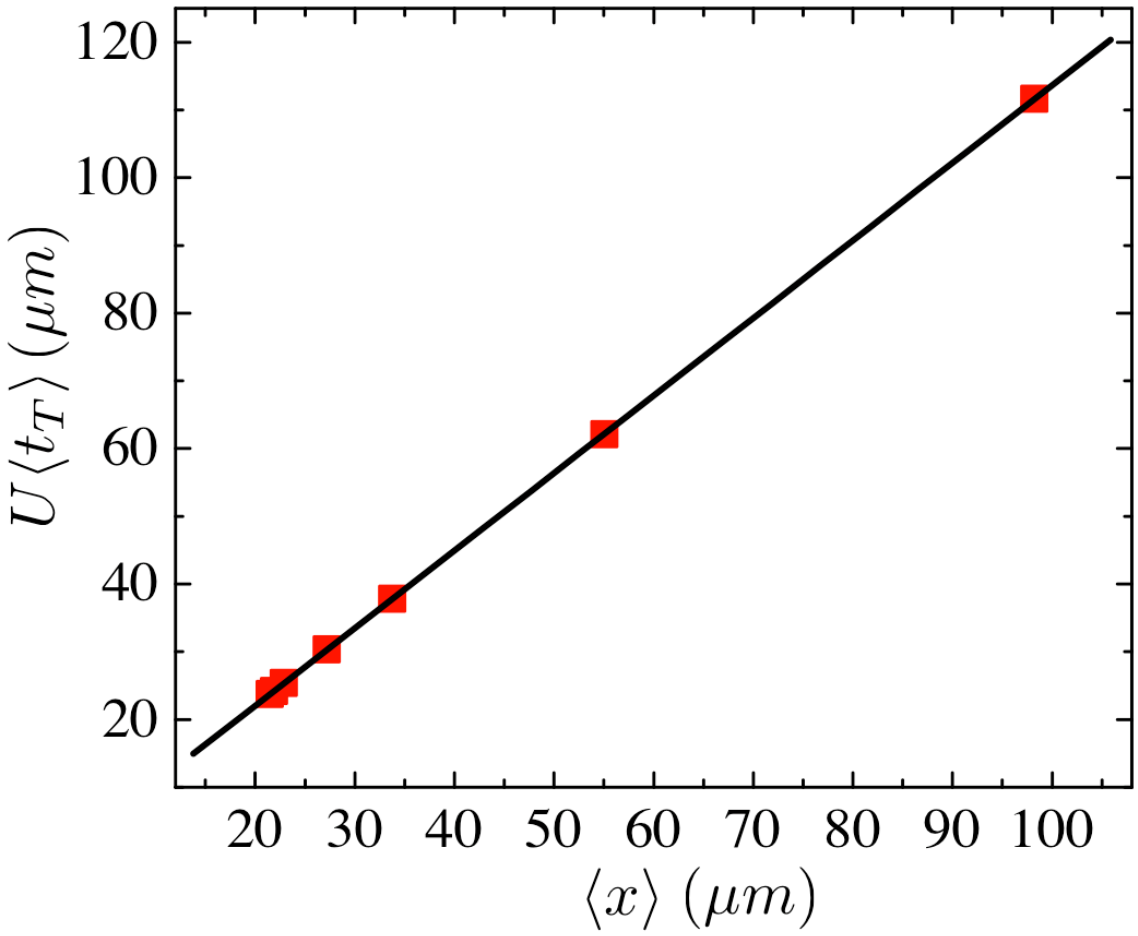

Figure A2: Plot of the translation time against the distance between collisions for the constant Péclet number case. The black line is a linear fit to the data, showing a linear relationship ($R^2 = 0.999$).

The translation time, $\langle t_T \rangle$, is related to the distance traveled during translation, $\langle x \rangle$, by the relation $\langle x \rangle = [f\,(\mathrm{Pe})]\, U\langle t_T \rangle$. Here, $f\,(\mathrm{Pe})$ accounts for the difference between the mean velocity and the instantaneous velocity of the molecule. In contrast to previous CTRW models, we are able to measure the value of f instead of guessing its value. From Fig. A2 we find $f\,(\mathrm{Pe} = 1.14) = 0.89$ ($R^2 = 0.999$).

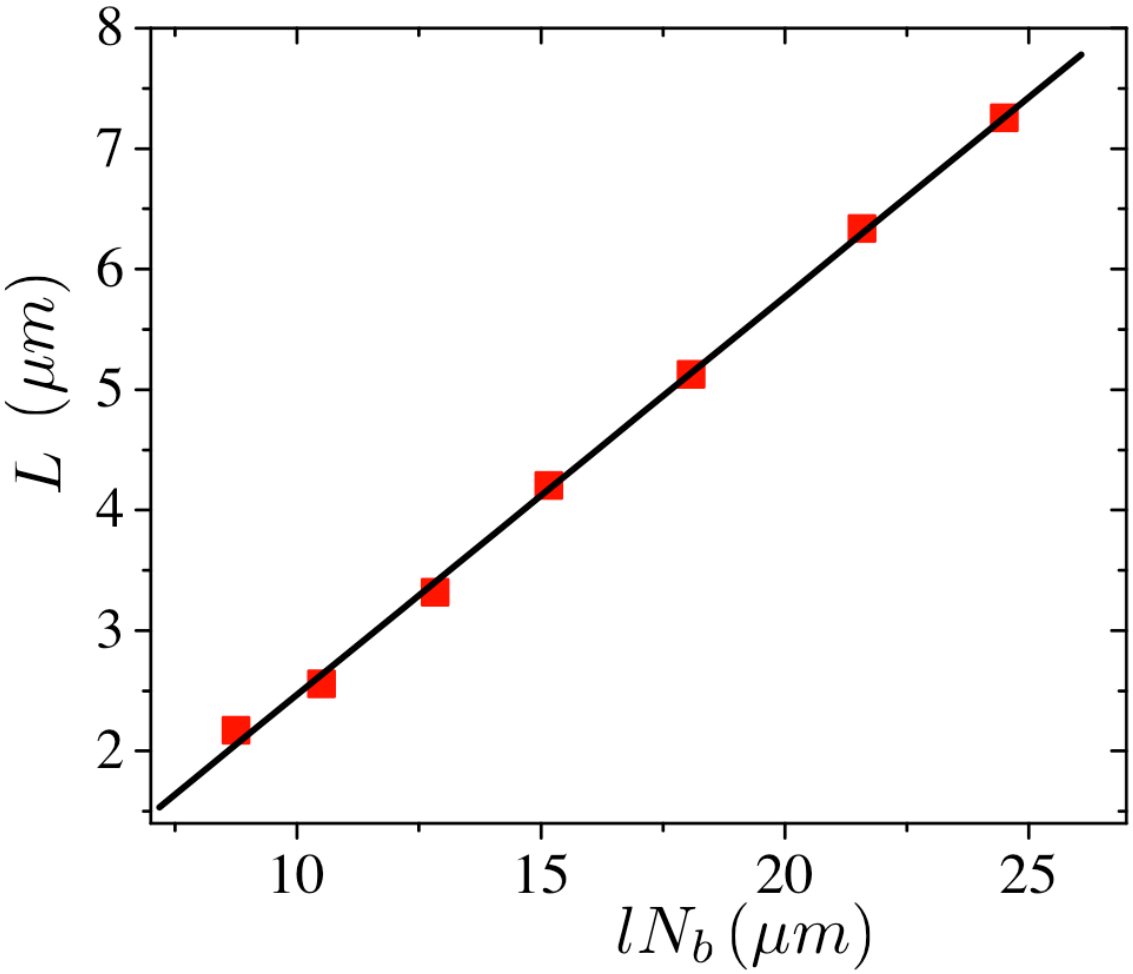

Figure A3: Maximum extension during collision versus the scaled size of the molecule at a constant Péclet number of 1.14. The black line is a linear fit to the data, showing a linear relationship ($R^2 = 0.999$).

Based on the rope-over-pulley model of DNA unhooking, we expect the hold-up time to scale with the maximum extension of the molecule, L. Under a constant force, or equivalently a constant Pe, the extension of the molecule depends on the DNA size. In Fig. A3 we show the linear relationship between the maximum extension during a collision and the DNA size, $L = 0.33\ lN_b$ ($R^2 = 0.999$).

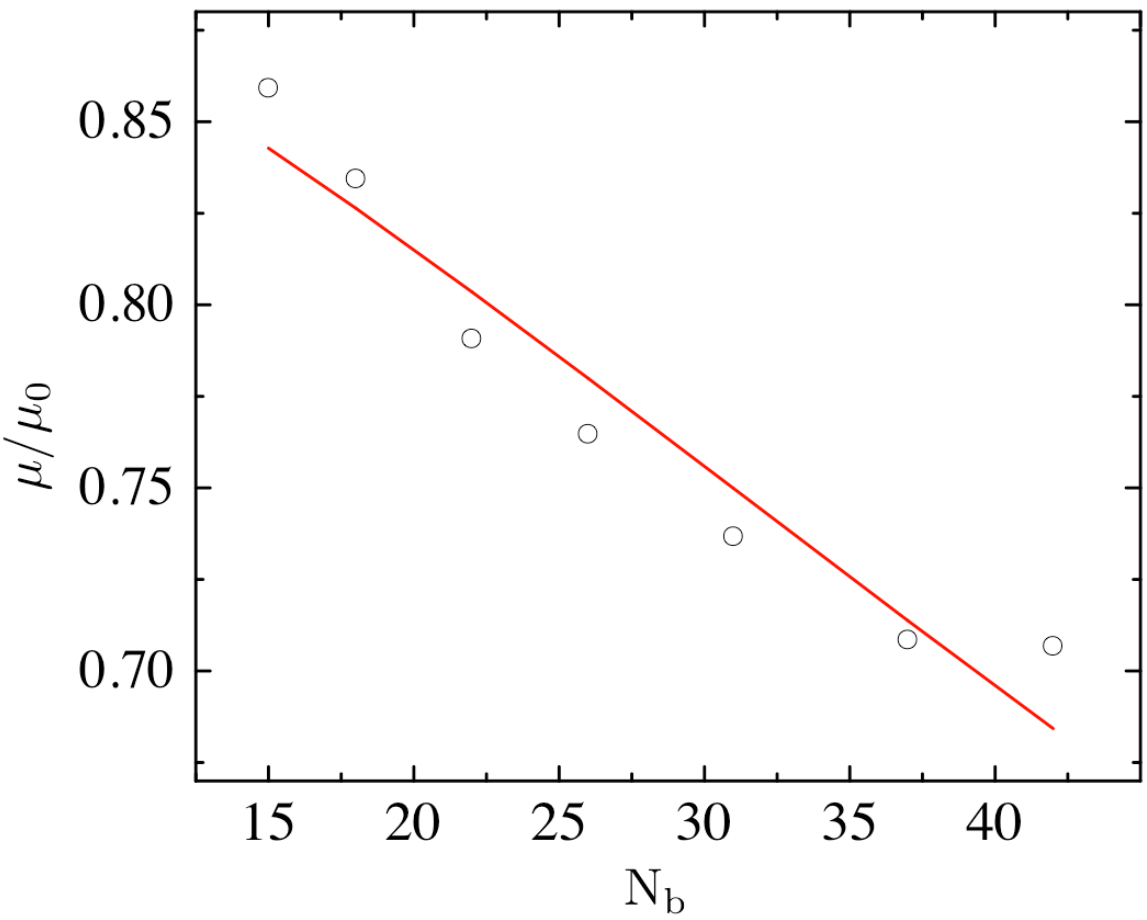

Figure A4: Dimensionless mobility versus the size of the molecule. The downward trend shows that separation based on size is possible provided that the dispersion in the system is low enough. The red line is Eq. (8), $R^2 = 0.961$.

Since the hold-up time scales with extension and the extension depends linearly on chain size, we assume that the hold-up time dominates the second term of Eq. (7) and that $U\langle t_H \rangle / \langle x \rangle$ depends linearly on N_b . We then find an equation for the mobility as a function of DNA size given in the paper as Eq. (8). Figure A4 shows Eq. (8) plotted against the simulation data.

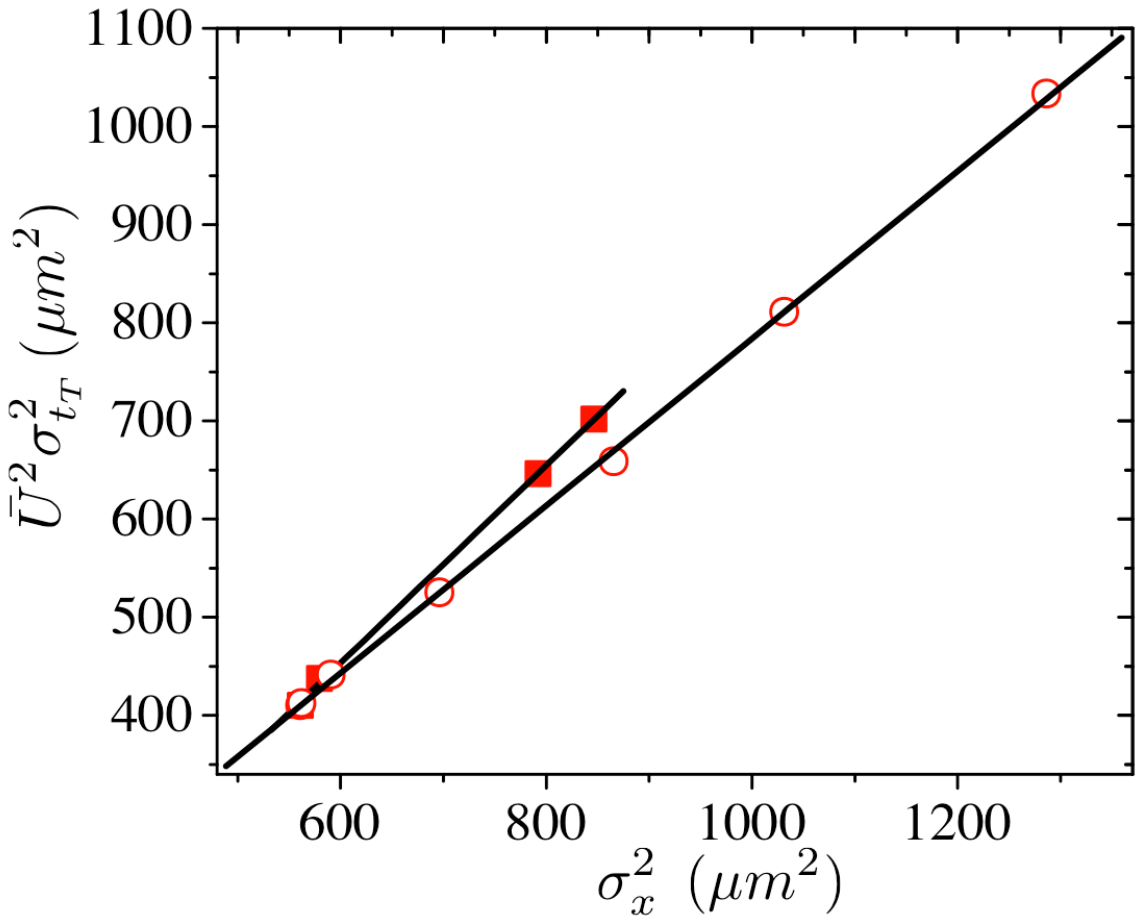

Figure A5: Variance of the translation time versus the variance in the distance between collisions at a constant DNA size of N_b = 26. Closed squares correspond to Pe < Pe*, and open circles correspond to Pe > Pe*. Black lines show linear fits to the data in each Pe regime (both fits have R^2 = 0.999).

There is a linear relationship between the variance in the travel time, $\sigma_{t_T}^2$, and the variance in the distance between collisions, $\sigma_{t_T}^2$, as the Péclet number is varied as shown in Fig. A5. Because of this relationship, $\sigma_{x-\bar{U}t_T}^2$ is nearly independent of Pe. Thus, for a constant DNA size, the plate height due to fluctuations in the distance between collisions depends primarily on $1/\langle x \rangle$.

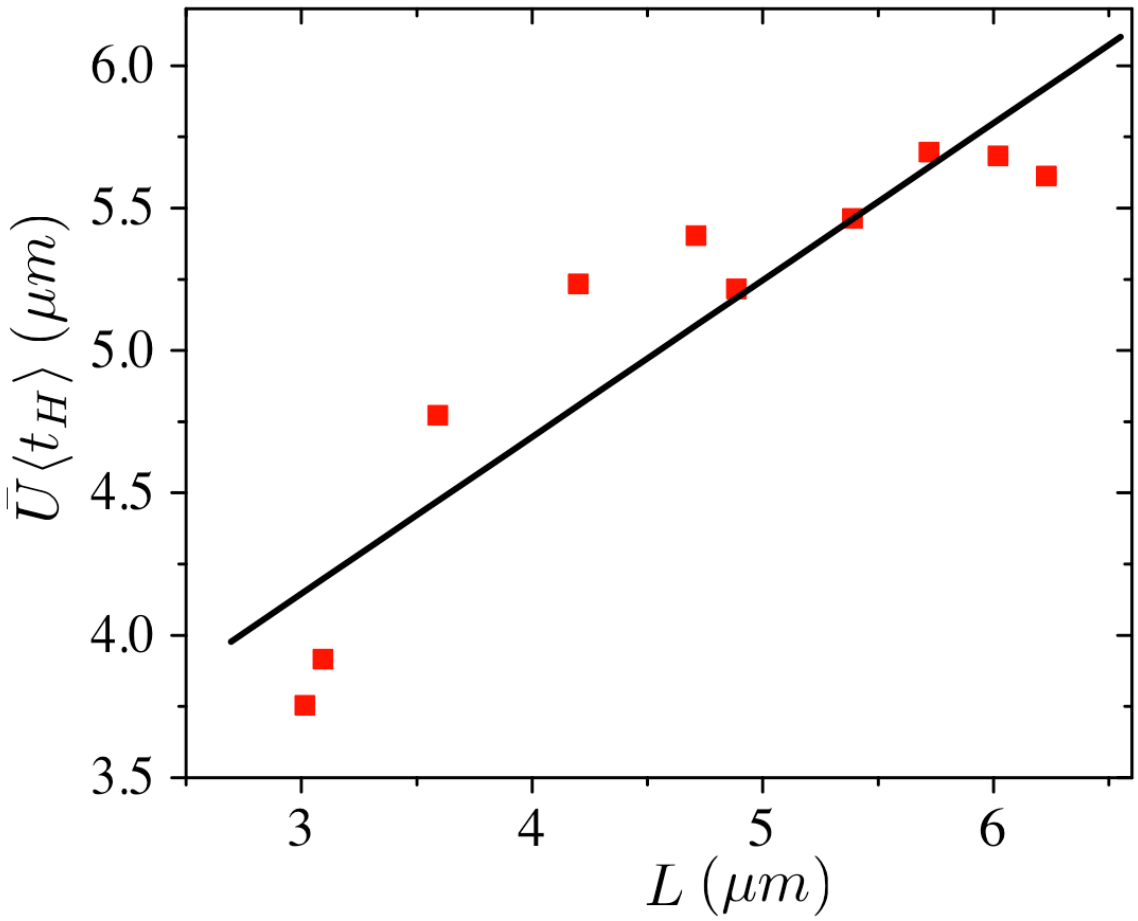

Figure A6: Hold-up time of the molecule versus the maximum extension of the molecule during a collision for a constant size of DNA, $N_b = 26$. The black line is a linear fit to the data ($R^2 = 0.839$).

The plate height due to the colliding state is dependent on the hold-up time of the collision. Based on rope-over-pulley unhooking dynamics, we expect that the hold-up time is proportional to the chain extension during the collision. From Fig. A6, we find $U\langle t_H \rangle = 0.55L + 0.83a$ ($R^2 = 0.839$).

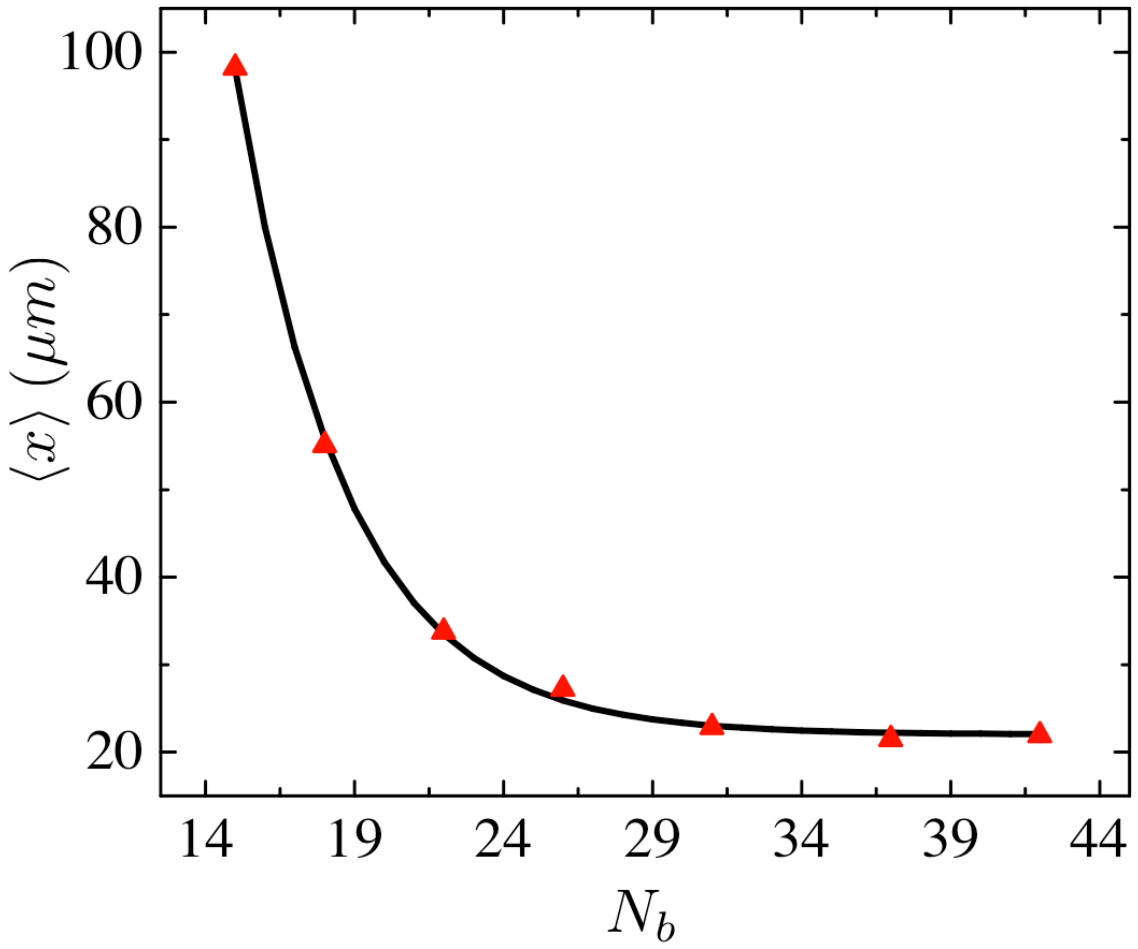

Figure A7: Mean distance between collisions as a function of the DNA size for the constant Pe case. Red triangles show the simulation data while the black curve is Eq. (16).

We plot the phenomenological fit in Fig. A7 from Eq. (16). The equation is used to find a relation between the plate height due to fluctuations in the hold-up time, H_2 , and DNA size, N_b.