Electronic Supplementary Material (ESI) for Lab on a Chip

Supporting Information for

DNA electrophoresis in a nanofence array

*Sung-Gyu Park, Daniel W. Olson, and Kevin D. Dorfman**

Department of Chemical Engineering and Materials Science, University of Minnesota – Twin Cities, Minneapolis, MN 55455 USA
E-mail: dorfman@umn.edu

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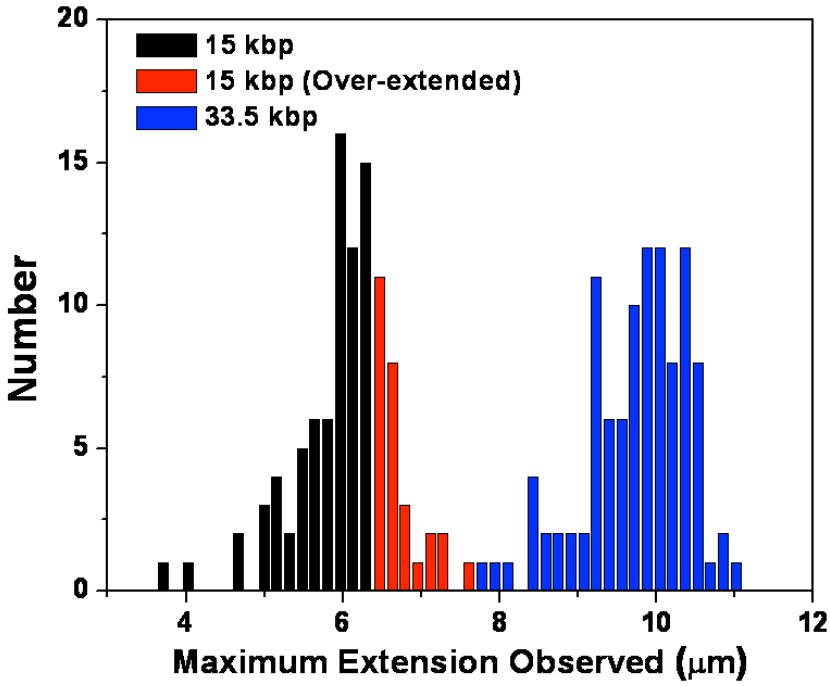

Fig. S1 Frequency distributions for the maximum extension of the hooked DNA at 10 V/cm for the mixture of 15 kbp and 33.5 kbp DNA. The data in black were definitively identified as 15 kbp fragments and the data in blue were definitively identified as 33.5 kbp fragments. The data in red were tentatively identified as 15 kbp fragments but their extension exceeds the maximum extension of a 15 kbp fragment. The measurements of these short distances are hindered by blooming of the image and streaking of the DNA, so we cannot be certain whether these DNA are strongly extended 15 kbp or weakly extended 33.5 kbp DNA.

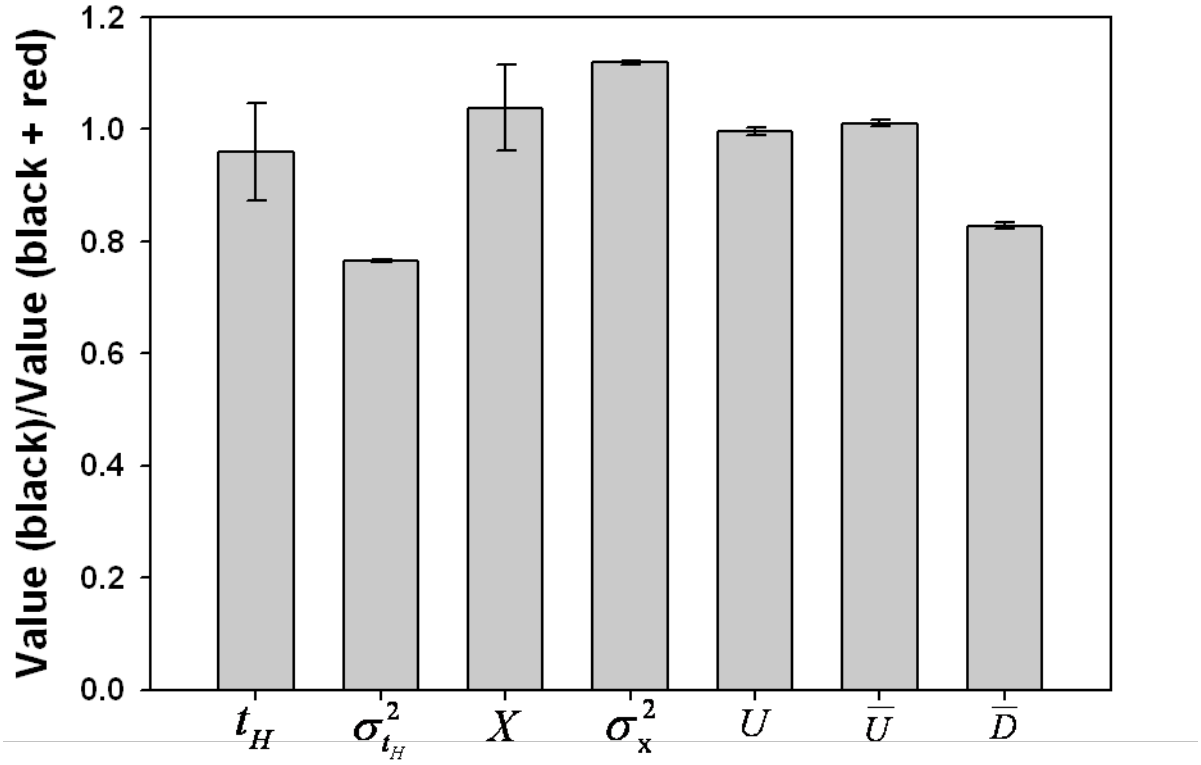

Fig. S2 In the data analysis, we only include those DNA that can be definitively identified as 15 kbp DNA (the black data in Fig S1). The histogram shows how the various CTRW parameters appearing in Table 1 are affected by excluding over-extended 15 kbp molecules from the distribution. The results are presented as the ratio of the data appearing in the main text (black in Fig. S1) relative to all potential 15 kbp DNA (black + red in Fig. S1). The error bars are the sampling error. The key difference is a reduction in the variance of the holdup time distribution and a corresponding reduction in the predicted dispersion coefficient.

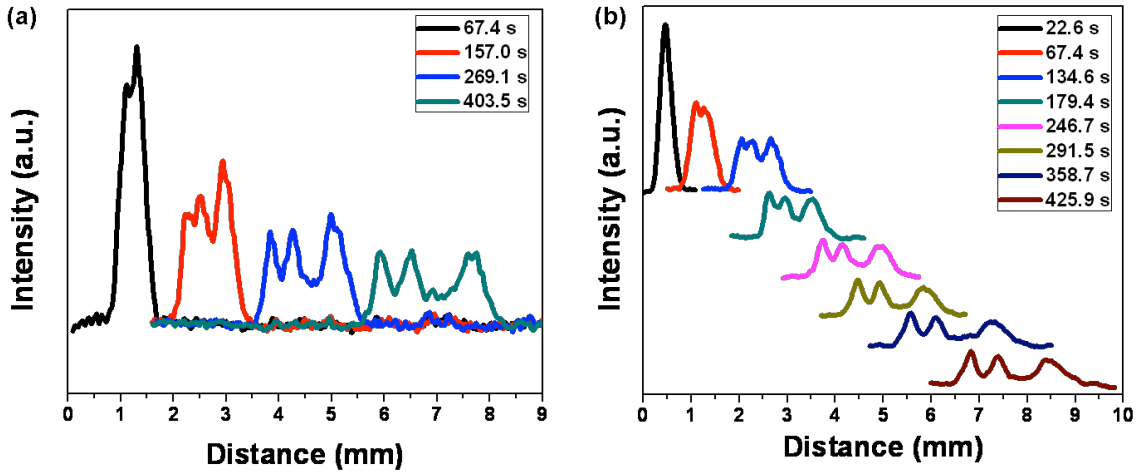

Fig. S3 Evolution of the bands for two different sets of DNA electrophoresis at 10 V/cm. Each experiment used the same scanning interval but only selected data are included here for clarity.

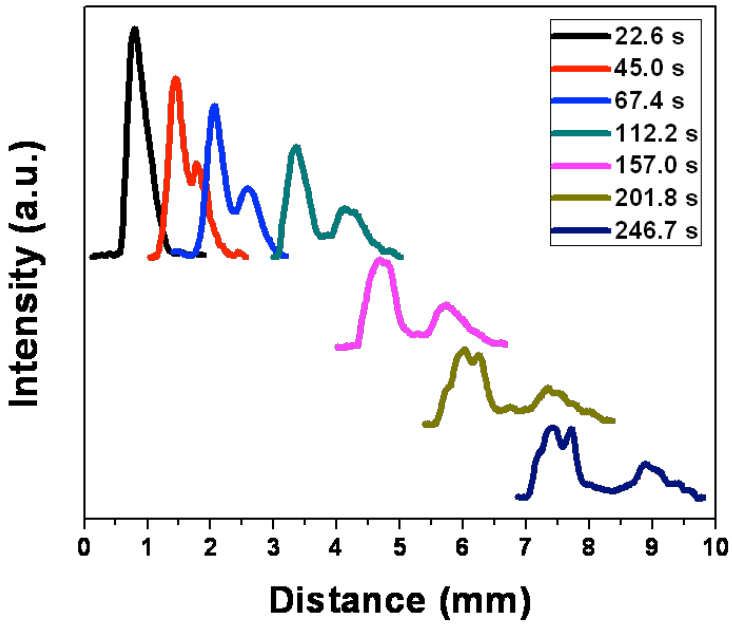

Fig. S4 Evolution of the bands during DNA electrophoresis at 20 V/cm. Three distinct peaks start to be resolved after 201.8 s.

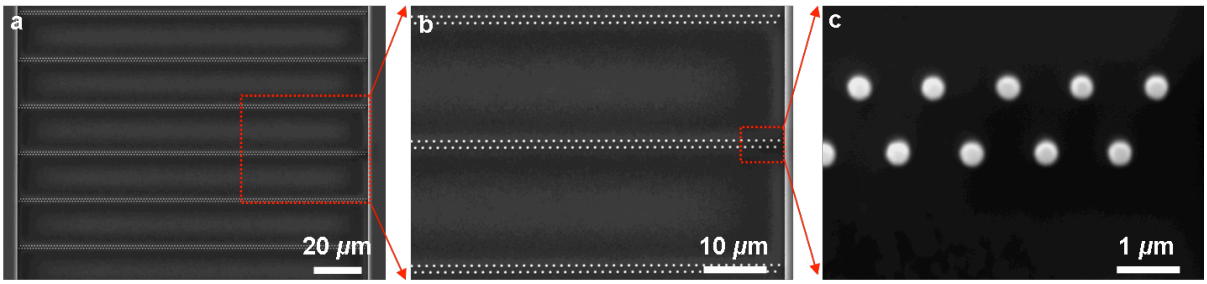

Fig. S5 SEM images of the silicon nanofence array after the silicon etching process (Fig. 2d). The diameter of silicon posts was 360 nm, which was 140 nm smaller than the patterns from the stepper mask due to undercutting during the dry etching process.

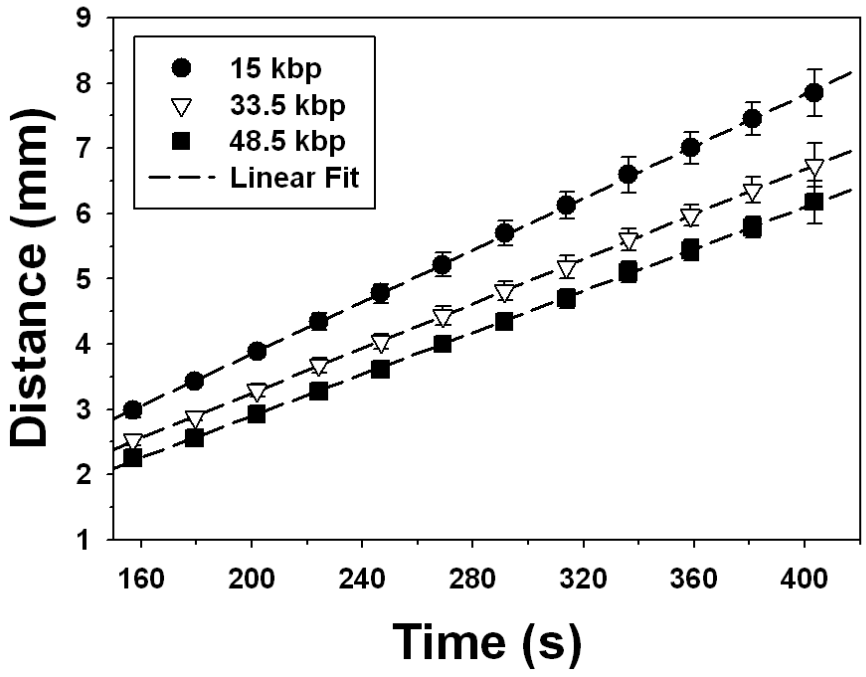

Fig. S6 Migration distance as a function of time. Error bars represent the standard deviations for three different data sets. The linear equations fit the data with negligible standard errors on the order of 10^{-5}. The equations for fitting the data are $X(t) = 0.0199\ t - 0.126$ for the 15 kbp DNA ($R^2 = 0.999$), $X(t) = 0.0172\ t - 0.182$ for the 33.5 kbp DNA ($R^2 = 0.999$), and $X(t) = 0.0160\ t - 0.300$ for the 48.5 kbp DNA ($R^2 = 0.999$).

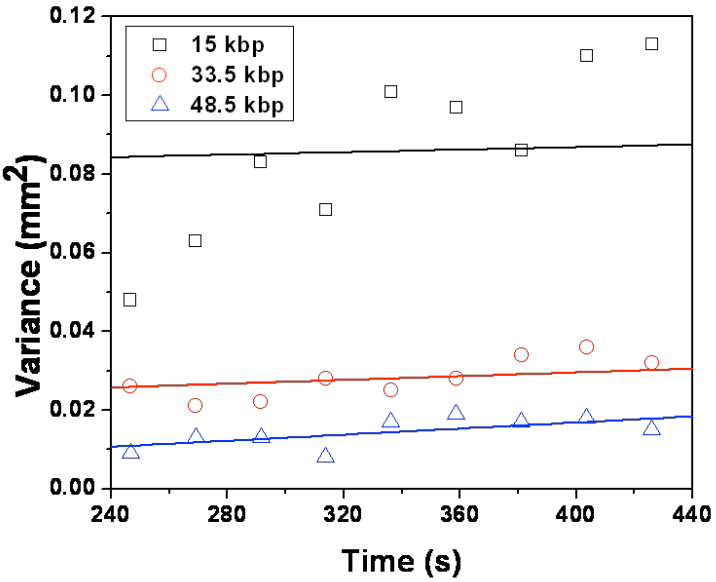

Fig. S7 Variance of the peaks during the separation as a function of time and the comparison with the prediction of the single-molecule data for (a) 15 kbp, (b) 33.5 kbp and (c) 48.5 kbp (trial #2, Fig. S3a). The intercept for the single-molecule data is the best fit of a line with slope of twice the dispersion coefficient in Table 1 to the separation data.

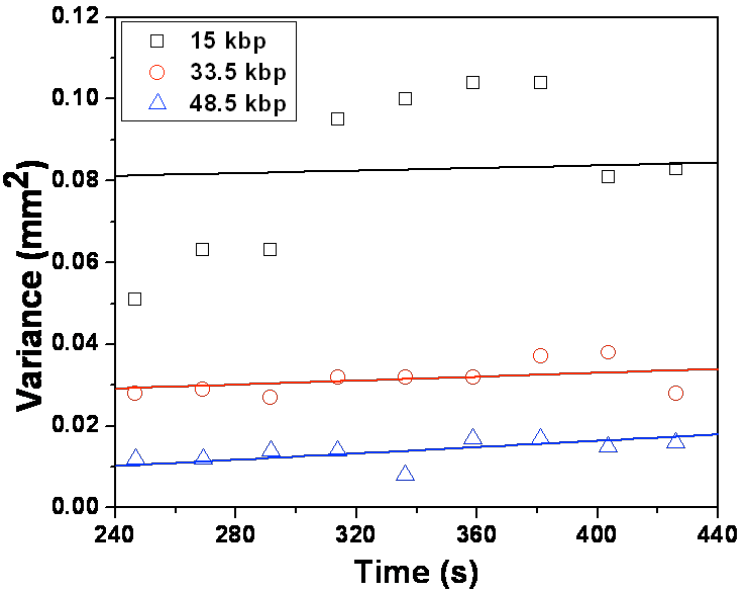

Fig. S8 Variance of the peaks during the separation as a function of time and the comparison with the prediction of the single-molecule data for (a) 15 kbp, (b) 33.5 kbp and (c) 48.5 kbp (trial #3, Fig. S3b). The intercept for the single-molecule data is the best fit of a line with slope of twice the dispersion coefficient in Table 1 to the separation data.