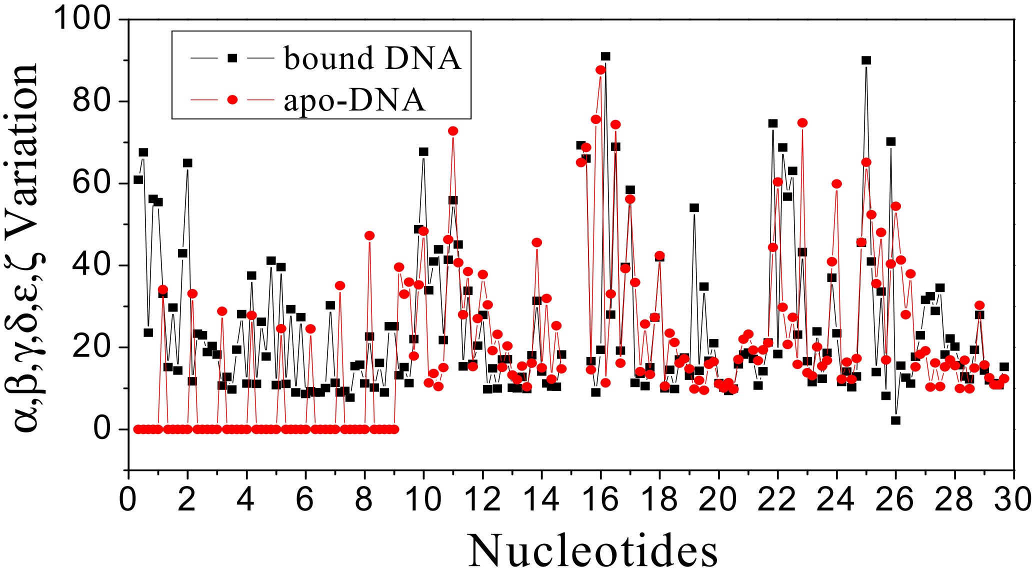


Figure 1S. α, β, γ, δ, ε, and ζ fluctuation for bound and apo-DNA.

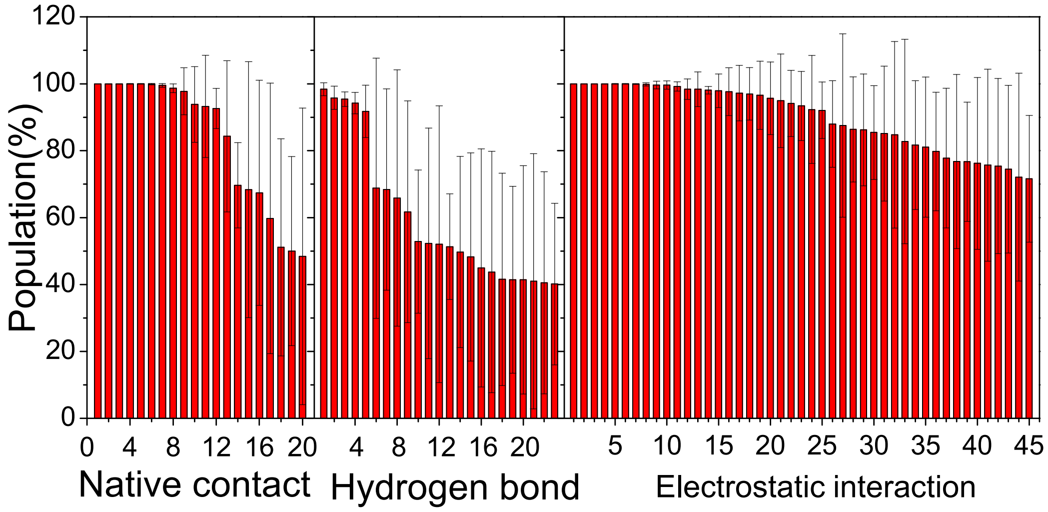


Figure 2S. Interaction between DNA and LEF. Native Contact: 1 for Asn8/G9, 2 for Ser30/A25, 3 for Ser30/G26, 4 for Phe10/T8, 5 for Ala31/T6, 6 for Ala31/C5, 7 for Asn34/T7, 8 for Asn8/T8, 9 for Met11/A24, 10 for Tyr76/T21, 11 for Met11/A23, 12 for Asn34/T6, 13 for Glu29/G27, 14 for Phe10/T7, 15 for Glu29/G26, 16 for Tyr76/G12, 17 for Met14/A24, 18 for Ala31/G26, 19 for Arg82/C4, 20 for Lys5/C22. Hydrogen Bond: 1 for Asn8/T8, 2 for Asn8(ND2)/G9(N3), 3 for Trp41/T8, 4 for Trp41/G9, 5 for Asn34/T6, 6 for Ser30(N)/G26(O4'), 7 for Gly77/T21, 8 for Tyr76/T20, 9 for Gly77/ C22, 10 for Asn34(ND2)/T7(O2), 11 for Arg18/G26, 12 for Lys78/C22, 13 for Gln35/T6, 14 for Arg82/C4, 15 for Lys15/A25, 16 for Lys79/A23, 17 for Tyr76/G12, 18 for Lys81/ T21, 19 for His42/ T8, 20 for Ser30/ A25, 21 for Lys5/ A23, 22 for Arg60/A11, 23 for Lys28/ G27. Electrostatic interactions: 1 for Lys5/A23, 2 for Lys28/G27, 3 for Arg60/A11, 4 for His42/T8, 5 for Lys4/A24, 6 for Lys15/A25, 7 for Arg18/A25, 8 for Arg73/G12, 9 for Lys81/T21, 10 for Arg18/G26, 11 for Arg73/C13, 12 for Arg84/T21, 13 for Arg82/C4, 14 for Arg39/T8, 15 for Arg60/A10, 16 for Lys79/C22, 17 for Lys5/A24, 18 for His42/G9, 19 for Lys78/C22, 20 for Lys81/C22, 21 for Lys80/C3, 22 for Arg82/C5, 23 for Lys79/A23, 24 for Lys80/C4, 25 for Arg39/T7, 26 for Arg57/A10, 27 for Arg84/T20, 28 for Arg60/G12, 29 for Lys79/C3, 30 for Lys28/G28, 31 for Lys15/A24, 32 for Lys5/C22, 33 for Lys4/A23, 34 for Lys83/C5, 35 for Lys28/G26, 36 for Lys81/T20, 37 for Arg82/T6, 38 for Lys83/C4, 39 for Lys79/T21, 40 for Arg57/A11, 41 for Arg82/C22, 42 for Lys4/A25, 43 for Lys78/A23, 44 for Arg82/C3, 45 for Arg84/C22

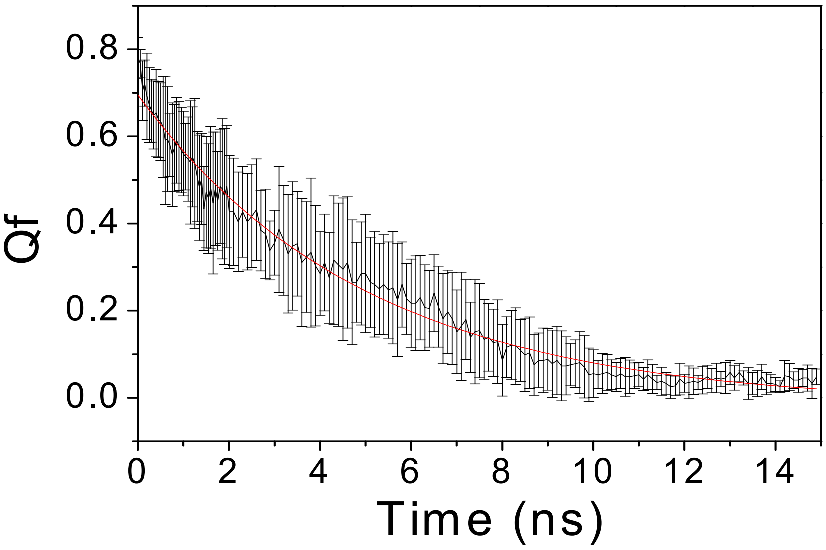


Figure 3S. Kinetics fitting for apo-DNA. The curve is fitted by exponential function.

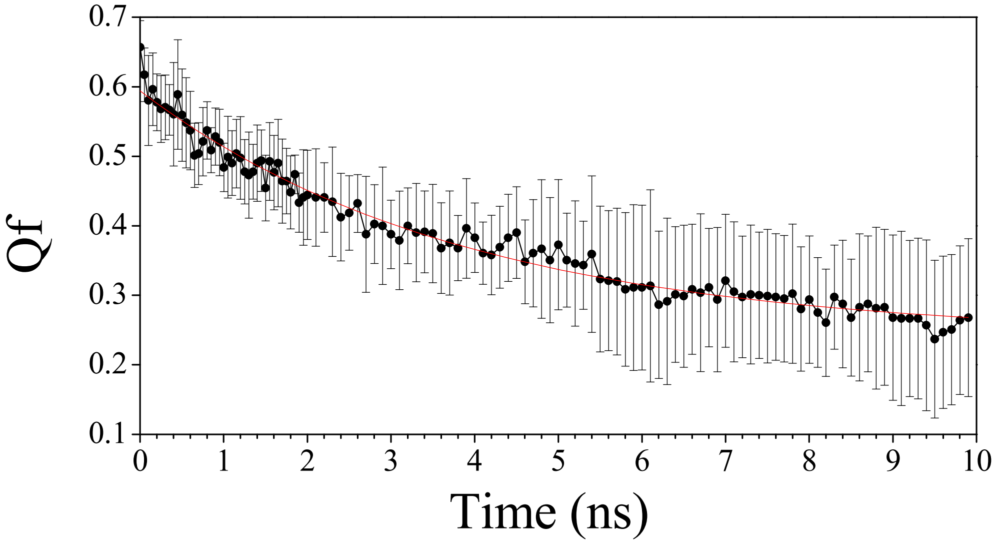


Figure 4S. Kinetics fitting for apo-LEF. The curve is fitted by exponential function.

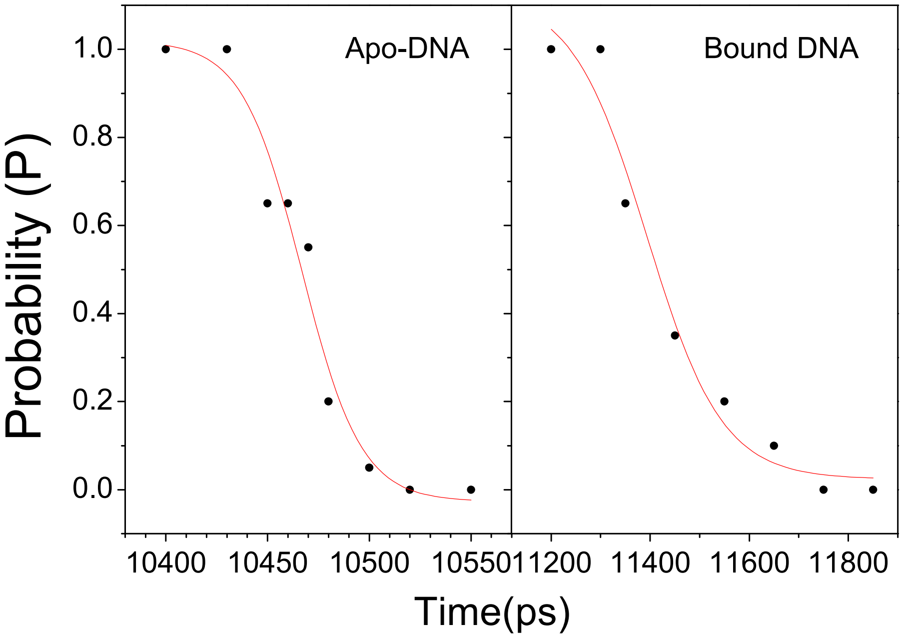


Figure 5S. A representative transition probability P calculated at 498K for the F⇔U transition for snapshot in the transition region for one of trajectories for bound and apo-DNA, respectively. The red line is the fit to $P = 1/\{1+ \exp[(\tau-\tau_{TS})/\tau_{trans}]\}$

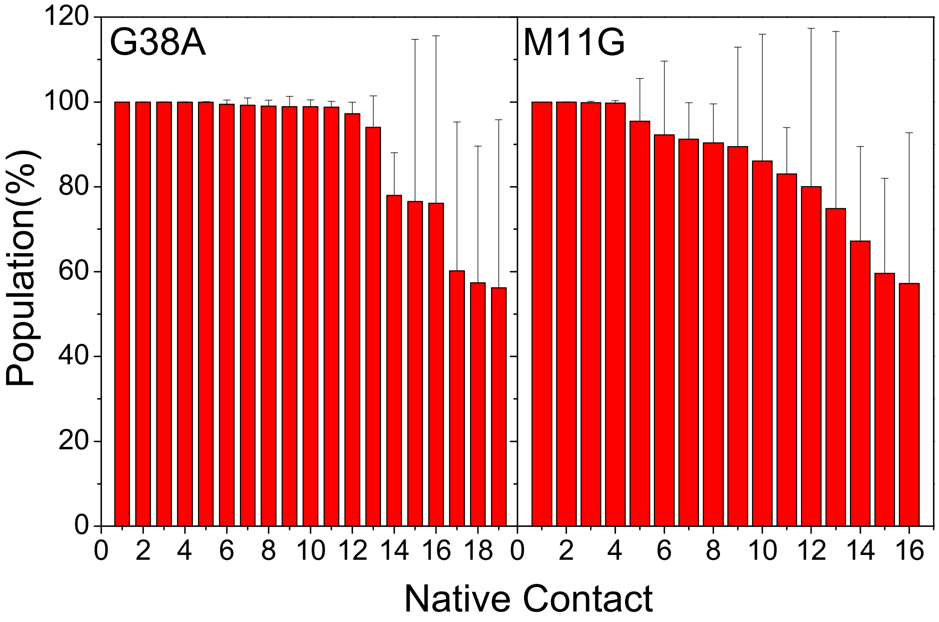


Figure 6S. Native contact between DNA and mutant LEF. G37A: 1 for Asn8/G9, 2 for Tyr76/T21, 3 for Phe10/T8, 4 for Met11/ A24, 5 for Ser30/G26, 6 for Ala31/ T6, 7 for Ser30/A25, 8 for Ala31/ C5, 9 for Asn34/T7, 10 for Met11/A23, 11 for Tyr76/G12, 12 for Asn8/T8, 13 for Asn34/T6, 14 for Ala38/ T7, 15 for Glu29/G27, 16 for Glu29/G26, 17 for Ala31/G26, 18 for Met14/A24, 19 for Lys5/C22. M10G: 1 for Ser30/G26, 2 for Ser30/A25, 3 for Tyr76/T21, 4 for Ala31/T6, 5 for Asn34/T7, 6 for Asn8/G9, 7 for Glu29/G27, 8 for Tyr76/G12, 9 for Phe10/T8, 10 for Ala31/C5, 11 for Glu29/G26, 12 for Asn34/T6, 13 for Asn8/T8, 14 for Met14/A24, 15 for Ala31/G26, 16 for Phe10/T7.

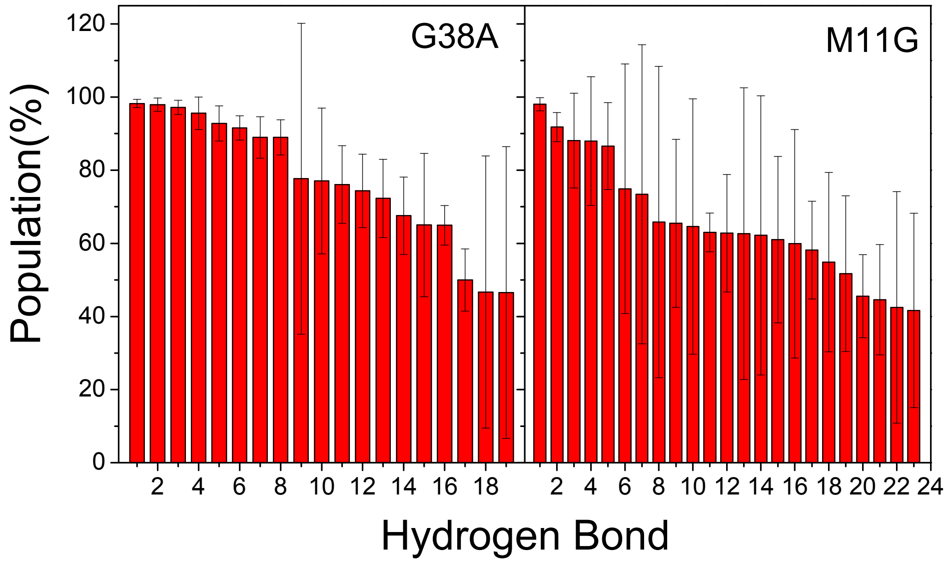


Figure 7S. Hydrogen bond between DNA and mutant LEF. G38A: 1 for Asn8(ND2)/G9(N3), 2 for Gly77/T21, 3 for Asn8/T8, 4 for Tyr76/T20, 5 for Lys78/C22, 6 for Gly77/ C22, 7 for Trp41/T8, 8 for Trp41/G9, 9 for Ser30(N)/G26(O4'), 10 for Asn34(ND2)/T7(O2), 11 for Lys79/C22, 12 for Tyr76(OH)/G12(N2), 13 for Lys79/A23, 14 for Gln35/T6, 15 for Asn34/T6, 16 for Tyr76/ T21, 17 for Gln35/T7, 18 for Glu29/G26, 19 for Arg60/A11. M11G: 1 for Gly77/T21, 2 for Gly77/ C22, 3 for Tyr76/T20, 4 for Ser30(N)/G26(O4'), 5 for Lys78/C22, 6 for Asn8(ND2)/G9(N3), 7 for Asn8/T8, 8 for Trp41/T8, 9 for Ser30(OG)/A25(N3), 10 for Asn34(ND2)/T7(O2), 11 for Tyr76/T21, 12 for Lys79/C22, 13 for Trp41/G9, 14 for Asn34/T6, 15 for Lys79/A23, 16 for Ala72/G12, 17 for Arg60/A11, 18 for Arg18(NH1)/G26(O1P), 19 for Tyr76(OH)/G12(N2), 20 for Lys81/ T21, 21 for Glu29/G26, 22 for Lys5/A23, 23 for Gln35/T6

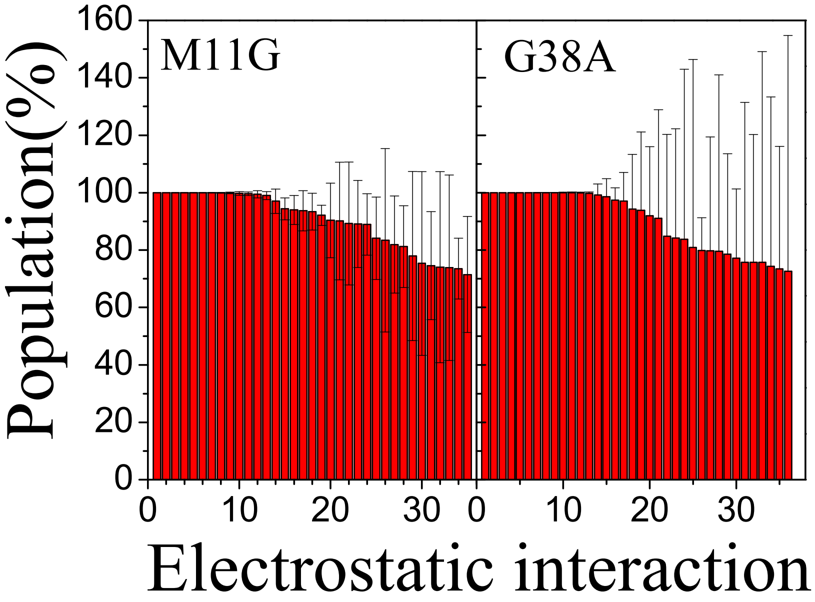


Figure 8S. Electrostatic interactions between DNA and LEF-1 for M11G and G38A mutants. M11G: 1 for Lys79/C22, 2 for Arg18/G26, 3 for Lys78/C22, 4 for Arg60/A11, 5 for Arg18/A25, 6 for Lys28/G27, 7 for Lys5/A23, 8 for Lys81/T21, 9 for Lys79/A23, 10 for Arg82/C4, 11 for Lys15/A25, 12 for Arg73/C13, 13 for Lys80/C3, 14 for Arg73/G12, 15 for Arg82/C5, 16 for Lys81/T20, 17 for Lys15/A24, 18 for Lys79/T21, 19 for Lys81/C22, 20 for Arg82/C3, 21 for Arg60/A10, 22 for Lys5/A24, 23 for Lys4/A24, 24 for Lys79/C3, 25 for Arg39/T8, 26 for Lys5/G12, 27 for Lys80/C4, 28 for Lys78/A23, 29 for Lys5/C22, 30 for Arg57/A10, 31 for Arg60/G12, 32 for Lys5/A11, 33 for Lys4/A23, 34 for Lys83/C4, 35 for Arg18/G27. G38A: 1 for Lys78/C22, 2 for Lys78/C22, 3 for Lys5/A23, 4 for Lys79/A23, 5 for Arg18/A25, 6 for Arg60/A11, 7 for Lys15/A25, 8 for Arg73/C13, 9 for Arg73/G12, 10 for Lys80/C3, 11 for Arg18/G26, 12 for Arg60/A10, 13 for Lys4/A24, 14 for Lys81/T21, 15 for Lys28/G27, 16 for Lys5/A24, 17 for Arg82/C4, 18 for Lys15/A24, 19 for Lys81/C22, 20 for Arg82/C5, 21 for Lys5/C22, 22 for Lys83/C4, 23 for Lys80/C4, 24 for Lys83/C5, 25 for Lys81/T20, 26 for Arg46/G9, 27 for Arg60/G12, 28 for Lys4/A23, 29 for Lys80/A2, 30 for Arg39/T8, 31 for Lys79/T21, 32 for Lys78/A23, 33 for Lys5/G12, 34 for Arg57/A10, 35 for Lys79/C3, 36 for Arg84/T20.

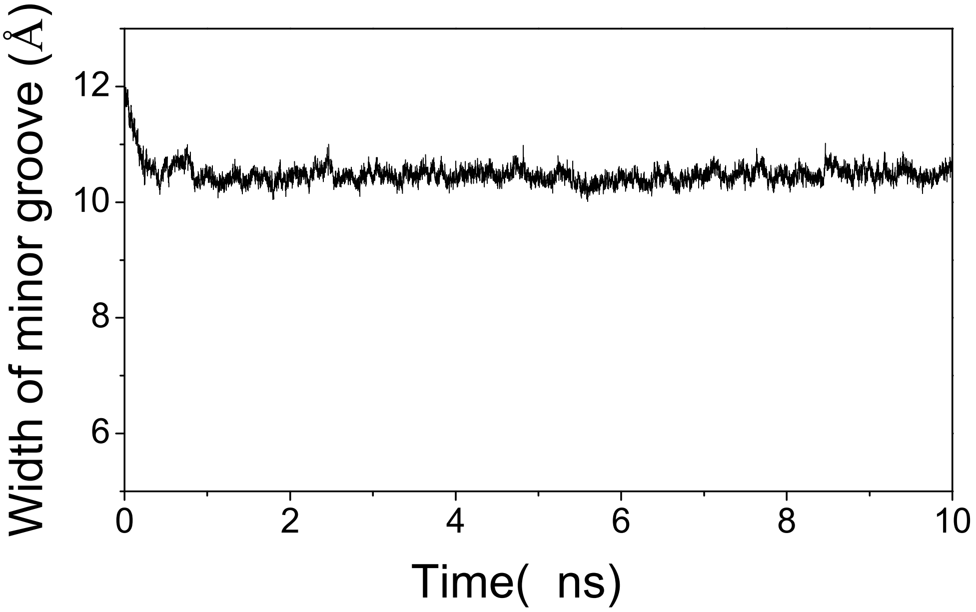


Figure 9S. The width of minor groove for apo-DNA *vs* simulation time.

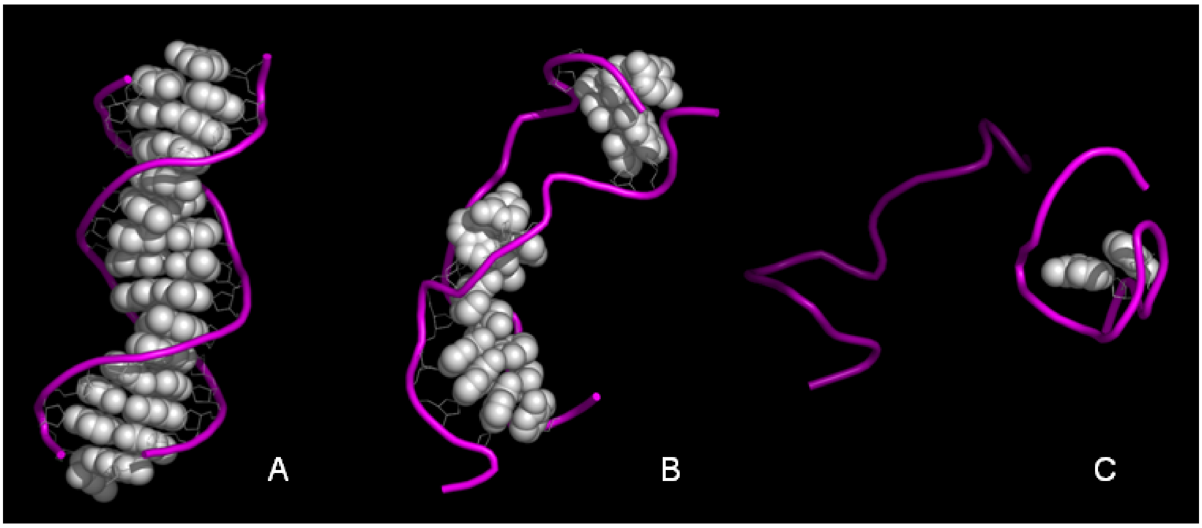
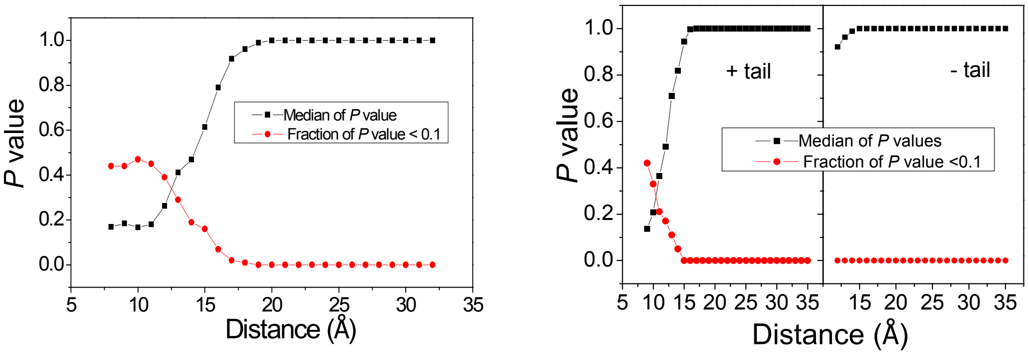


Figure 10S. Unfolding pathway of apo-DNA. A: <0ns (F), B :4.98ns (τ_{Qf}), C: > 15ns (U).



A: DNA B: LEF

Figure 11S. Statistical significance of induced fit motions in DNA or LEF binding. The KS *P* value analysis of statistical significance of local conformational deviations from those of the molecule as a whole as a function of distance from the binding site. The black curve depicts the median of *P* values from 100 pairs of structures, and the red curve captures the fraction of structures with $P < 0.1$ in each distance range, for DNA (A) and for LEF (B): without the C-tail (right) or with the C-tail (left) included.