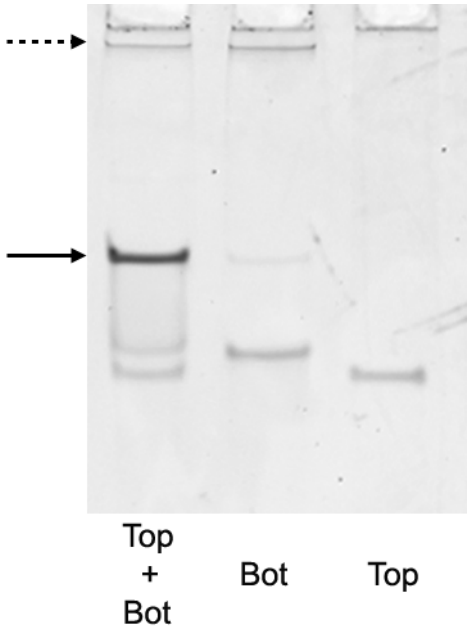
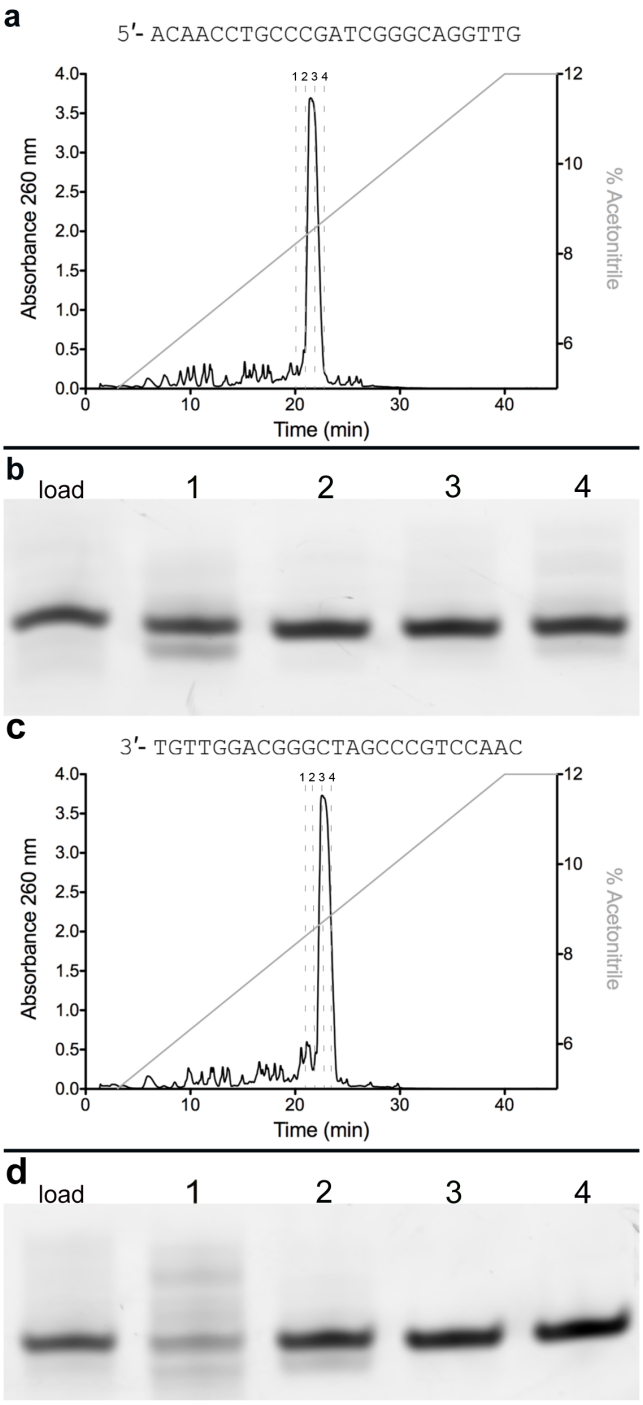
Supplementary Figures

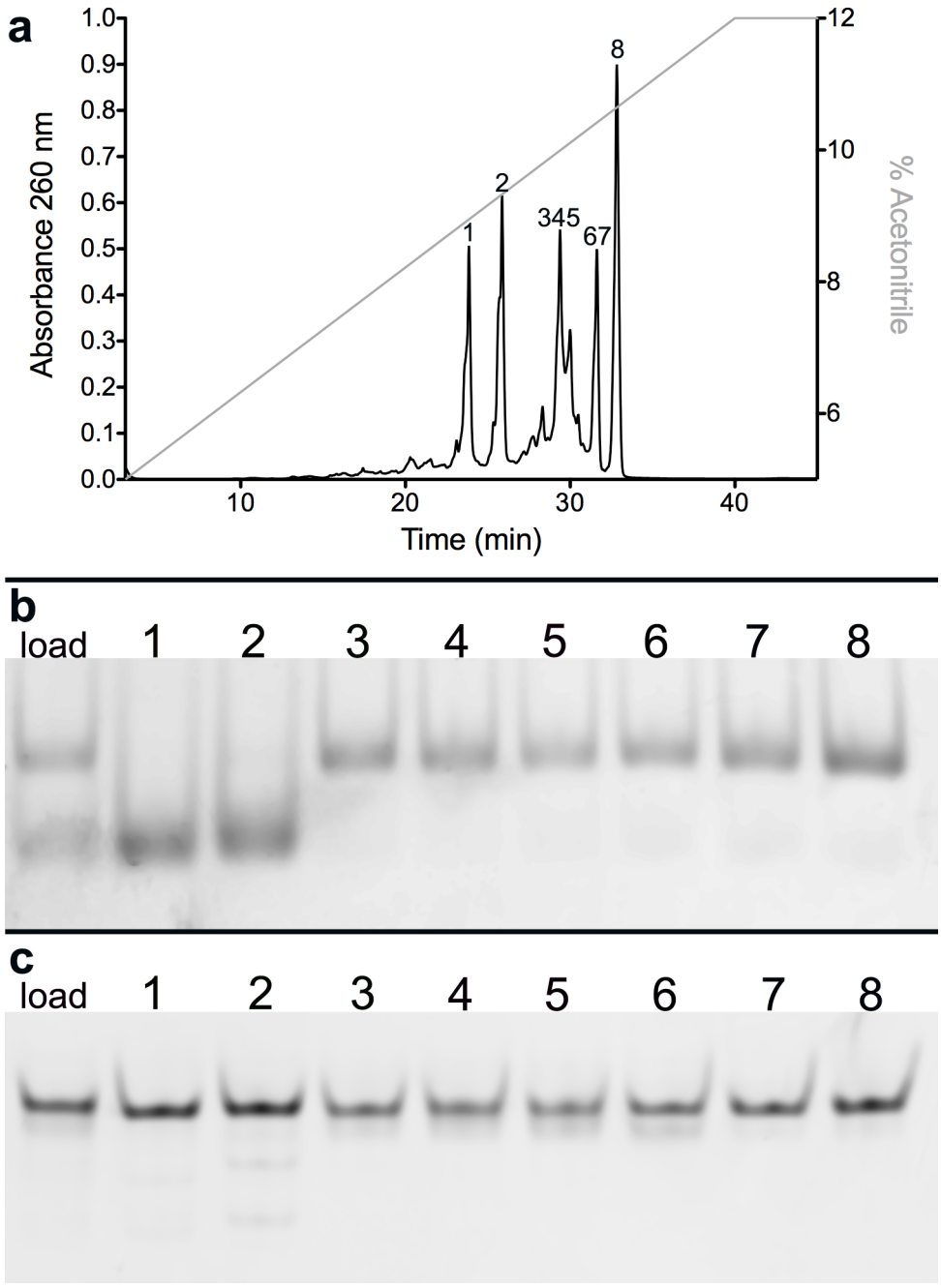
Supplementary Figure 1



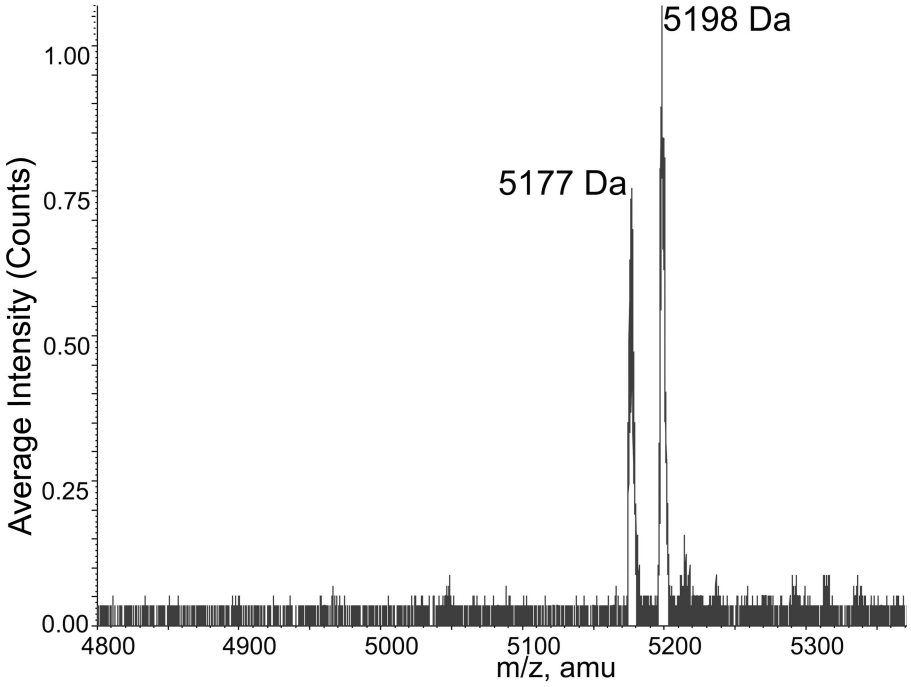
Supplementary Figure 2



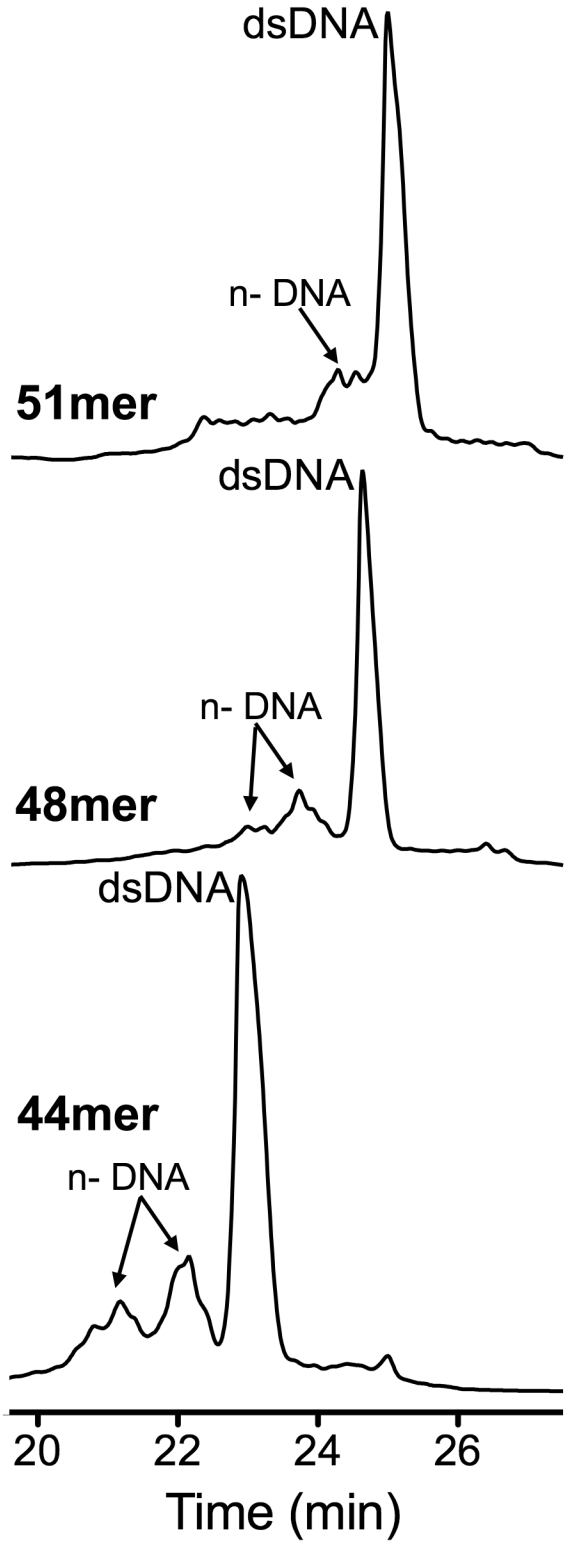
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



Supplementary Figure Legends

Supplementary Figure 1

16 % acrylamide 7 M urea denaturing gel of single stranded DNA after SepPak purification. DNA was not heated before loading. The left lane contains 12.5 ng of both the top and bottom (bot) strands of LSP 28mer. The center right lane contains 25 ng of the bottom LSP 28mer strand while the right lane was loaded with 25 ng of the top LSP 28mer strand, respectively. The black arrow indicates the location of double stranded DNA while the dotted black arrow indicates the formation of high molecular weight cruciform DNA.

Supplementary Figure 2

A) Chromatogram of the forward strand oligomer: the 25mer forward strand eluted as a single peak that was collected in four fractions. **B)** 16% polyacrylamide 7 M urea gel of the single-stranded material that eluted from the column of the forward strand oligomer purification. Each lane corresponds to a fraction (1-4). Lane 1 yielded DNA that contained pre-attenuated failure products from the synthesis of the oligomer. Lanes 2, 3, and 4 yield pure product, and pre-attenuated failure products are not evident. **C)** Chromatogram of the reverse strand oligomer: the 25mer reverse strand eluted as a single peak that was collected in four fractions. **D)** 16% polyacrylamide 7 M urea gel of the single-stranded material that eluted from the column of the reverse strand oligomer purification. Each lane corresponds to a fraction (1-4). Lane 1, yielded DNA that contained pre-attenuated failure products from the synthesis of the oligomer. Lanes 3, and 4 yield pure product, and pre-attenuated failure products are not evident. All chromatograms in this figure used 0.25 mg of DNA, and were collected at 60°C. DNA absorbance was monitored at 260 nm (black trace, left Y-axis) as DNA was eluted from

the column using an acetonitrile gradient (gray trace, right Y-axis) for both chromatograms.

Supplementary Figure 3

(**A**) DNA elution profile of 0.25 mg of 5′-forward and 5′-reverse DNA after single-stranded purification and anealing. DNA absorbance was monitored at 260 nm (black trace, left Y-axis) as DNA was eluted from the column using an acetonitrile gradient (gray trace, right Y-axis) (**B**) 8% native polyacrylamide gel demonstrating the later three peaks (fractions 3-8) are double stranded DNA. (**C**) 16 % acrylamide, 7 M urea denaturing gel showing fractions collected from the DNA peaks in the elution profile of panel **A.**

Supplementary Figure 4. Mass spectrometry analysis if progesterone receptor DNA

Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) spectrum of 17 base pair DNA corresponding to the progesterone receptor (PR) binding site collected in the negative ion mode. The calculated average mass-to-charge ratios of the forward and reverse PR strands are 5199 Da and 5177 Da, respectively.

Supplementary Figure 5. Purification DNA up to 51 base pairs in length

DNA duplexes with lengths of 51 base pairs (top), 48 base pairs (middle), and 44 base pairs (bottom), were purified using an acetonitrile gradient of 5-20% over the course of 40 minutes. Arrows indicate the peaks corresponding to n– products. 0.5 mg of DNA was loaded on the X-Bridge column for each chromatogram. DNA absorbance was

monitored at 260 nm (black trace, left Y-axis) as DNA was eluted from the column using an acetonitrile gradient (gray trace, right Y-axis).