

Supplemental Information

Probing the Effect of Bulky Lesion-Induced Replication Fork Conformational Heterogeneity Using 4-Aminobiphenyl-Modified DNA

Ang Cai, Ke Bian, Fangyi Chen, Qi Tang, Rachel Carley, Deyu Li,* and Bongsup Cho*

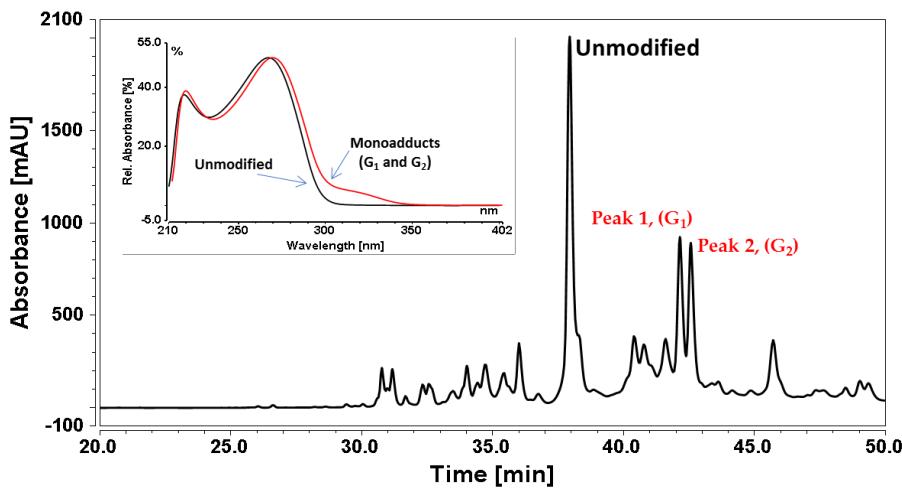
A.C. and K.B. contributed equally to this work.

*Co-correspondence: bcho@uri.edu, Tel: +1 401-874-5024; deyuli@uri.edu, Tel: +1 401-874-9361

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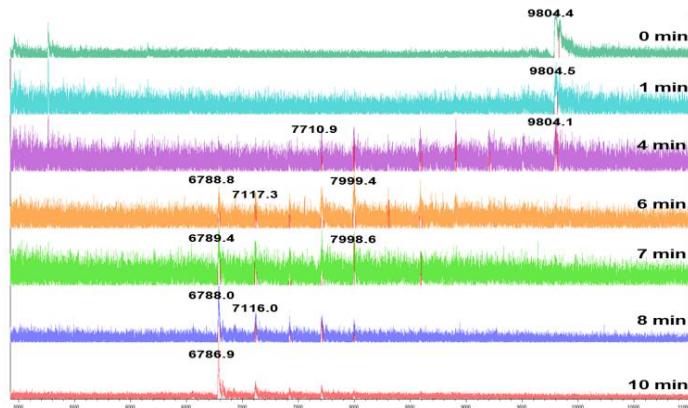
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(a)



(b)

mass	sequence
9803.1	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCATTC (31mer)
9513.9	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCATT
9209.7	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCAT
8905.5	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCA
8592.3	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTC
8303.1	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCTT
7998.9	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCC
7709.7	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TC
7420.6	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ T
7116.4	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂
6787.3	Bio-CCTCTCCCTCACCTCTTCTG₁ (21mer)
6271.1	Bio-CCTCTCCCTCACCTCTTCT



(c)

mass	sequence
9803.1	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCATTC (31mer)
9513.9	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCATT
9209.7	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ TCCTCAT
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7420.6	Bio-CCTCTCCCTCACCTCTTCTG ₁ G ₂ T
7116.4	Bio-CCTCTCCCTCACCTCTTCTG₁G₂ (22mer)
6600.1	Bio-CCTCTCCCTCACCTCTTCTG ₁
6271.1	Bio-CCTCTCCCTCACCTCTTCT

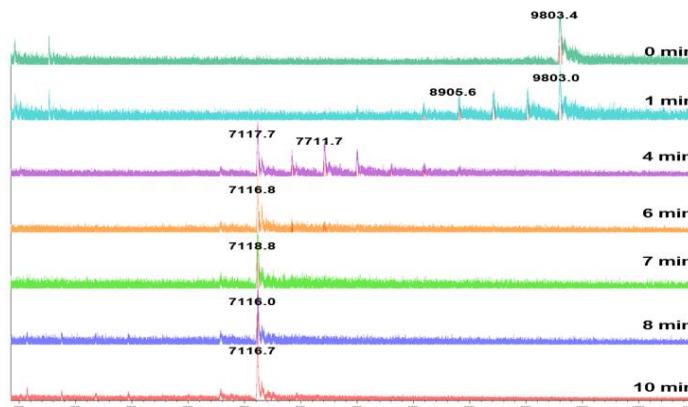


Figure S1. HPLC profile of FABP-modified bio-31mer TGGT template and MALDI-TOF characterization of peak 1 and peak 2. (a) HPLC chromatogram of a reaction mixture of biotinylated-31-mer sequence (5'-Bio-CCTCTCCCTCACCTCTTCTG₁G₂TCCTCATTC-3') with an activated FABP (*N*-Acetoxy-*N*-(trifluoroacetyl)-4'-fluoro-4-aminobiphenyl) and photodiode array UV spectra of unmodified and mono-adducts. (b) and (c): MALDI-TOF mass spectra of FABP modified biotinylated-31mer-TGGT. (b) 3'-Exonuclease digestions of **peak 1** at 0, 1, 4, 6, 7, 8 and 10min. (c) 3'-Exonuclease digestions of **peak 2** at 0, 1, 4, 6, 7, 8 and 10min. Insets show the theoretical MW of the corresponding fragments that should form after 3'-exonuclease digestion.

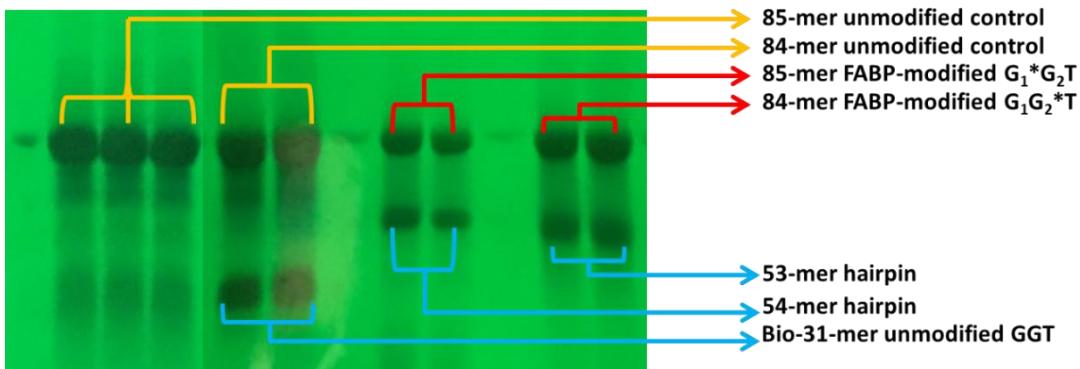
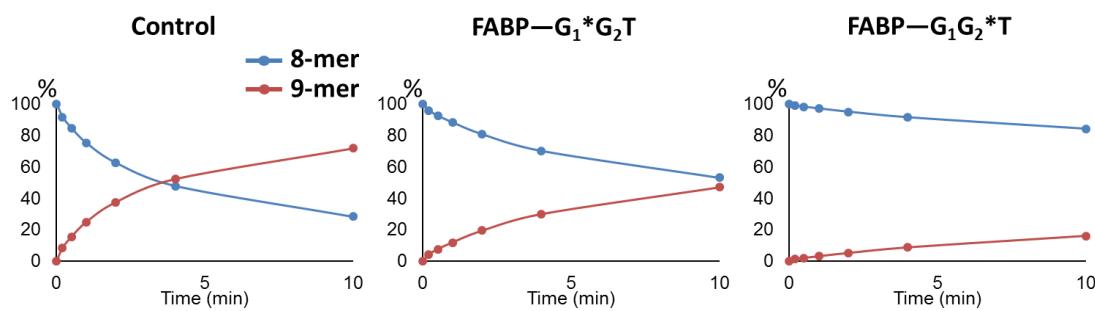


Figure S2. Denaturing gel (15%) profiles of 84-mer and 85-mer ligated oligonucleotides, 31-mer, 53-mer and 54-mer non-ligated oligonucleotides.

(a)



(b)

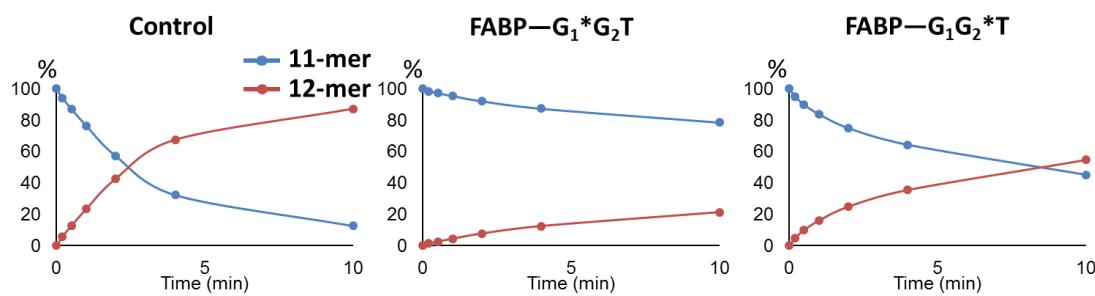


Figure S3. dATP Insertion efficiency of (a) 8-mer to 9-mer and (b) 11-mer to 12-mer in control, TG₁*G₂T-FABP and TG₁G₂*T-FABP, respectively, at 10 min (see Figure 3 for sequences).

Table S1. Binding net stabilization energy of unmodified and FABP-adducts with Kf-exo⁻ in binary system (1:1 binding).

Sequence	<i>k_d</i> (1/s)	*Net stabilization Energy (kcal/mol)
85-mer control	0.84 (0.004)	0.00
85-mer TG₁[FABP]G₂T	0.17 (0.002)	0.95
84-mer control	0.03 (0.002)	0.00
84-mer TG₁G₂[FABP]T	0.009 (0.0001)	0.71

*Net stabilization energy (kcal/mol)= -RTln(*k_d*)_{modified} - [-RTln(*k_d*)_{unmodified}]