## **Supplemental Information**

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

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(b)

mass	sequence	9804.4 0 min
111855	sequence	9804.5 1 min
9803.1	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCTCATTC (31mer)	
9513.9	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCTCATT	7710.9 9804.1
9209.7	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCTCAT	n na hEarthaile an a thaile ann anns anns anns a' a' a
8905.5	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCTCA	6788.8 7999.4
8592.3	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCTC	d have been a second and the second
8303.1	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCCT	6789.4 7998.6
7998.9	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TCC	Mailline that is a strategic design of the indicated by a filling of the difference of which is discovery a strategic of <b>Z min</b>
7709.7	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> TC	Consection on a state contract sector of a consection of the sector of the
7420.6	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub> T	7116.0 8 min
7116.4	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> G <sub>2</sub>	A Ballouth Midd Resident as the send and be descended in the sendence of the s
6787.3	Bio-CCTCTTCCCTCACCTCTTCTG <sub>1</sub> (21mer)	6786.9
6271.1	Bio-CCTCTTCCCTCACCTCTTCT	10 min
		500 500 500 600 500 500 100 100 100 100 100 100 100 1

(c)





**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-CCTCTTCCCTCACCTCTTCTG<sub>1</sub>G<sub>2</sub>TCCTCATTC-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.



**Figure S3.** dATP Insertion efficiency of (a) 8-mer to 9-mer and (b) 11-mer to 12-mer in control, TG<sub>1</sub>\*G<sub>2</sub>T-FABP and TG<sub>1</sub>G<sub>2</sub>\*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<sup>-</sup> in binary system (1:1 binding).

Sequence	ka (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(kd)modified - [-RTln(kd)unmodified]