

## **Supporting Information**

### **Effect of thiazole orange double-labeled thymidine on DNA duplex formation**

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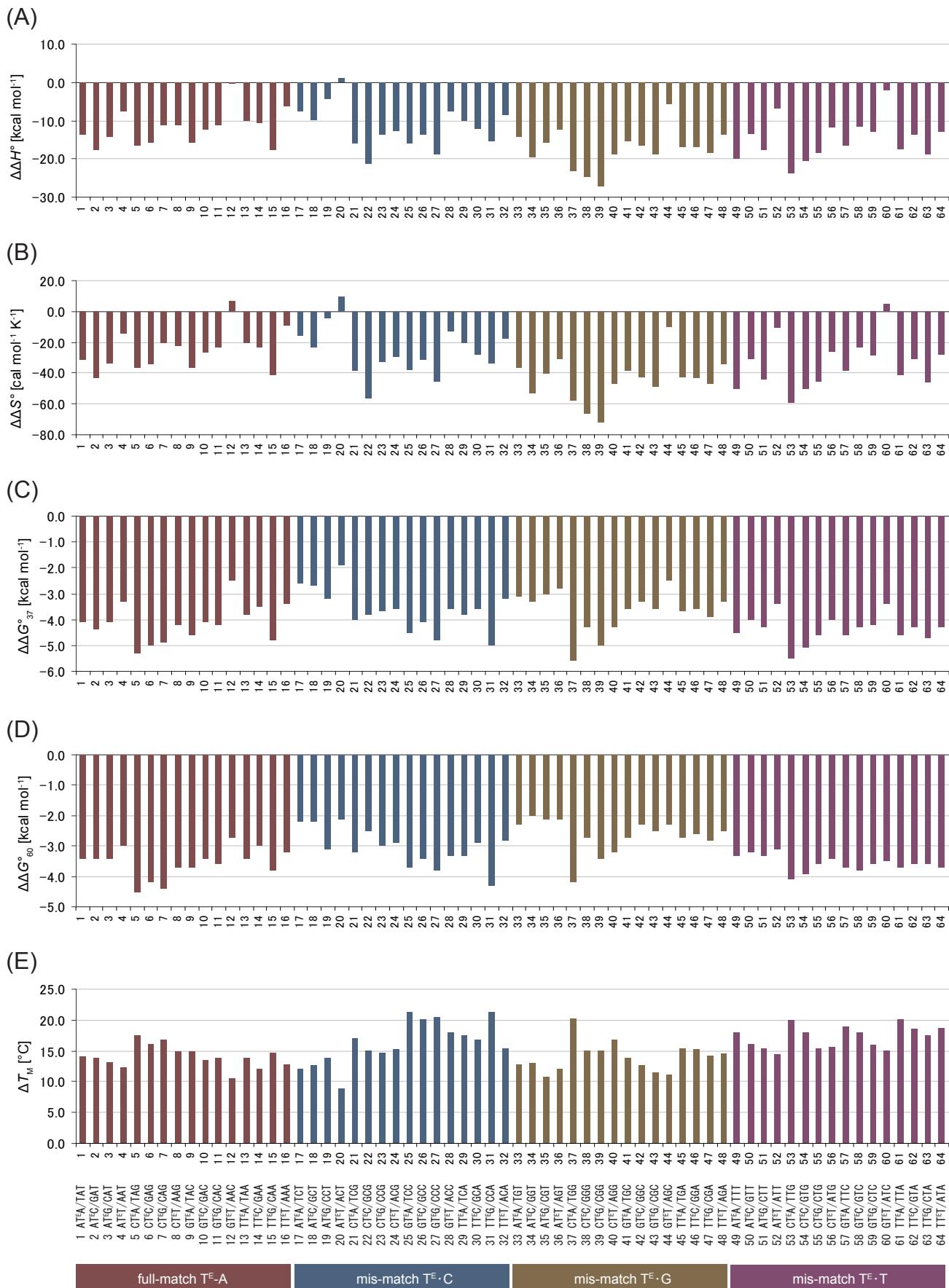


Figure S1.

Incremental thermodynamic effect of T<sup>E</sup> obtained from fluorescence measurements. (A)  $\Delta\Delta H^\circ$ . (B)  $\Delta\Delta S^\circ$ . (C)  $\Delta\Delta G^\circ_{37}$ . (D)  $\Delta\Delta G^\circ_{60}$ . (E)  $\Delta T_M$ . Trinucleotide sequences around T<sup>E</sup> are indicated in the figure.

Table S3. Average thermodynamic parameters derived from fluorescence measurements.

group	$\Delta H^\circ$ [kcal mol <sup>-1</sup> ]	$\Delta S^\circ$ [cal mol <sup>-1</sup> K <sup>-1</sup> ]	$\Delta G^\circ_{37}$ [kcal mol <sup>-1</sup> ]	$\Delta G^\circ_{60}$ [kcal mol <sup>-1</sup> ]	T <sub>M</sub> [°C]	$\Delta\Delta H^\circ$ [kcal mol <sup>-1</sup> ]	$\Delta\Delta S^\circ$ [cal mol <sup>-1</sup> K <sup>-1</sup> ]	$\Delta\Delta G^\circ_{37}$ [kcal mol <sup>-1</sup> ]	$\Delta\Delta G^\circ_{60}$ [kcal mol <sup>-1</sup> ]	$\Delta T_M$ [°C]
full-match										
T <sup>E</sup> -A	-91.9 ± 4.9	-246 ± 12.8	-15.7 ± 1.3	-10.0 ± 1.1	59.8 ± 4.1	-12.0 ± 4.6	-25.5 ± 12.9	-4.1 ± 0.7	-3.5 ± 0.5	14.1 ± 1.8
mis-match										
T <sup>E</sup> -C	-74.1 ± 6.1	-202 ± 16.9	-11.5 ± 1.1	-6.9 ± 0.9	46.1 ± 4.5	-11.7 ± 5.6	-26.0 ± 16.1	-3.6 ± 0.8	-3.0 ± 0.6	16.3 ± 3.5
T <sup>E</sup> -G	-84.3 ± 6.8	-230 ± 17.8	-12.9 ± 1.5	-7.6 ± 1.2	50.5 ± 4.8	-17.4 ± 5.1	-44.3 ± 14.3	-3.7 ± 0.8	-2.7 ± 0.6	14.0 ± 2.4
T <sup>E</sup> -T	-83.9 ± 6.8	-229 ± 18.4	-12.8 ± 1.2	-7.6 ± 0.9	50.2 ± 3.9	-15.0 ± 5.5	-34.2 ± 16.1	-4.4 ± 0.6	-3.6 ± 0.3	17.2 ± 1.8
all										
T <sup>E</sup> -N	-83.6 ± 8.8	-227 ± 22.8	-13.2 ± 2.0	-8.0 ± 1.6	51.7 ± 6.6	-14.0 ± 5.6	-32.5 ± 16.5	-4.0 ± 0.8	-3.2 ± 0.6	15.4 ± 2.8

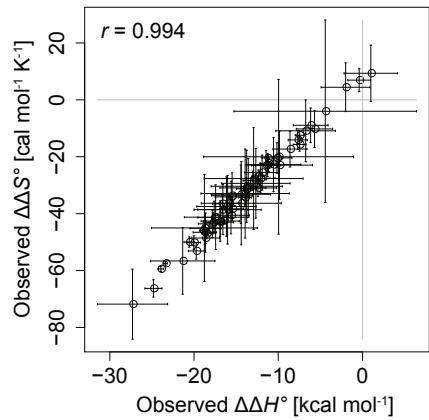


Figure S2.  
Relationship of  $\Delta\Delta H^\circ$  versus  $\Delta\Delta S^\circ$  obtained from fluorescence measurements.

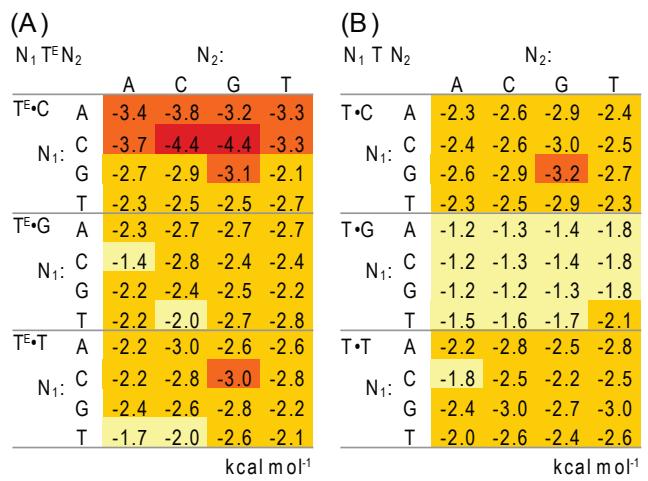


Figure S3.  
Effect of mismatches on  $\Delta G^\circ_{60}$ . Differences in the free energies at 60 °C ( $\Delta_{\text{full/mis}} \Delta G^\circ_{60}$ ) between full-match T<sup>E</sup>-A and mismatches T<sup>E</sup>-C, T<sup>E</sup>-G, T<sup>E</sup>-T were calculated and visualized in heat maps based on fluorescence measurements. (A) ECHO/DNA duplexes. (B) DNA/DNA duplexes. Red indicates larger changes whereas yellow indicates smaller effects on  $\Delta_{\text{full/mis}} \Delta G^\circ_{60}$ .

Table S4. Nearest neighbor parameters derived from fluorescence measurements.

nearest neighbor (5' to 3' / 5' to 3')	$\Delta\Delta H^\circ$ [kcal mol <sup>-1</sup> ]	$\Delta\Delta S^\circ$ [cal mol <sup>-1</sup> K <sup>-1</sup> ]	$\Delta\Delta G^\circ_{37}$ [kcal mol <sup>-1</sup> ]	$\Delta\Delta G^\circ_{60}$ [kcal mol <sup>-1</sup> ]
<b>full-match</b>				
AT <sup>E</sup> /AT	-6.9 ± 0.8	-16.1 ± 1.3	-1.9 ± 0.2	-1.5 ± 0.1
CT <sup>E</sup> /AG	-6.9 ± 0.6	-13.4 ± 1.0	-2.7 ± 0.2	-2.4 ± 0.1
GT <sup>E</sup> /AC	-3.9 ± 0.7	-7.0 ± 1.2	-1.8 ± 0.2	-1.6 ± 0.1
TT <sup>E</sup> /AA	-5.7 ± 0.9	-12.5 ± 1.6	-1.8 ± 0.3	-1.6 ± 0.1
T <sup>E</sup> A/TA	-8.9 ± 0.7	-20.7 ± 1.3	-2.4 ± 0.2	-1.9 ± 0.1
T <sup>E</sup> C/GA	-8.9 ± 0.7	-21.3 ± 1.3	-2.3 ± 0.2	-1.8 ± 0.1
T <sup>E</sup> G/CA	-4.5 ± 0.6	-7.5 ± 1.0	-2.2 ± 0.2	-2.0 ± 0.1
T <sup>E</sup> T/AA	-1.2 ± 0.7	0.5 ± 1.2	-1.3 ± 0.2	-1.3 ± 0.1
<b>mis-match T<sup>E</sup>•C</b>				
AT <sup>E</sup> /CT	0.0 ± 1.0	2.5 ± 1.8	-0.8 ± 0.2	-0.8 ± 0.2
CT <sup>E</sup> /CG	-10.7 ± 1.3	-27.7 ± 2.3	-2.1 ± 0.3	-1.4 ± 0.2
GT <sup>E</sup> /CC	-6.7 ± 0.8	-13.8 ± 1.3	-2.5 ± 0.3	-2.1 ± 0.2
TT <sup>E</sup> /CA	-6.4 ± 1.0	-13.6 ± 1.8	-2.1 ± 0.2	-1.6 ± 0.2
T <sup>E</sup> A/TC	-7.5 ± 1.0	-18.1 ± 1.8	-1.8 ± 0.2	-1.6 ± 0.2
T <sup>E</sup> G/CC	-8.4 ± 1.3	-18.2 ± 2.4	-2.8 ± 0.3	-1.6 ± 0.2
T <sup>E</sup> C/GC	-7.1 ± 0.8	-17.4 ± 1.4	-1.7 ± 0.3	-1.3 ± 0.2
T <sup>E</sup> T/AC	-0.8 ± 0.8	1.1 ± 1.4	-1.1 ± 0.2	-1.4 ± 0.2
<b>mis-match T<sup>E</sup>•G</b>				
AT <sup>E</sup> /GT	-7.9 ± 0.7	-20.9 ± 1.3	-1.4 ± 0.2	-0.9 ± 0.1
CT <sup>E</sup> /GG	-14.0 ± 0.6	-35.6 ± 1.1	-3.0 ± 0.2	-1.8 ± 0.1
GT <sup>E</sup> /GC	-5.6 ± 0.5	-13.0 ± 0.9	-1.6 ± 0.1	-1.3 ± 0.1
TT <sup>E</sup> /GA	-8.2 ± 0.7	-20.4 ± 1.2	-1.8 ± 0.1	-1.5 ± 0.1
T <sup>E</sup> A/TG	-9.4 ± 0.6	-21.9 ± 1.1	-2.5 ± 0.2	-2.1 ± 0.1
T <sup>E</sup> C/GG	-10.9 ± 0.5	-29.4 ± 0.9	-1.7 ± 0.1	-1.0 ± 0.1
T <sup>E</sup> G/GC	-10.5 ± 0.7	-27.3 ± 1.3	-2.1 ± 0.2	-1.2 ± 0.1
T <sup>E</sup> T/AG	-4.9 ± 0.7	-11.2 ± 1.2	-1.4 ± 0.1	-1.1 ± 0.1
<b>mis-match T<sup>E</sup>•T</b>				
AT <sup>E</sup> /TT	-7.5 ± 0.8	-18.5 ± 1.3	-1.8 ± 0.2	-1.4 ± 0.1
CT <sup>E</sup> /TG	-11.5 ± 0.6	-28.2 ± 1.0	-2.7 ± 0.2	-2.0 ± 0.1
GT <sup>E</sup> /TC	-3.0 ± 0.9	-3.6 ± 1.5	-1.9 ± 0.3	-1.8 ± 0.2
TT <sup>E</sup> /TA	-9.1 ± 0.8	-21.7 ± 1.3	-2.3 ± 0.3	-1.9 ± 0.2
T <sup>E</sup> A/TT	-12.4 ± 0.6	-31.3 ± 1.1	-2.7 ± 0.2	-2.0 ± 0.1
T <sup>E</sup> C/GT	-8.8 ± 0.7	-21.1 ± 1.3	-2.3 ± 0.2	-1.9 ± 0.1
T <sup>E</sup> G/CT	-9.8 ± 0.7	-24.1 ± 1.2	-2.3 ± 0.2	-1.7 ± 0.2
T <sup>E</sup> T/AT	-0.1 ± 1.1	4.4 ± 1.9	-1.5 ± 0.3	-1.6 ± 0.2