



### Correction: Base recognition by L-nucleotides in heterochiral DNA

Shuji Ogawa, Shun-ichi Wada and Hidehito Urata\*

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Correction for 'Base recognition by L-nucleotides in heterochiral DNA' by Shuji Ogawa *et al.*, *RSC Adv.*, 2012, 2, 2274–2275.

The authors regret that some of the data in the original article were presented incorrectly. Some of the oligonucleotide sequences in the Graphical Abstract, Fig. 2 and Table 1 were originally presented in reverse sequence. The corrected versions of the Graphical Abstract, Fig. 2 and Table 1 are presented below.

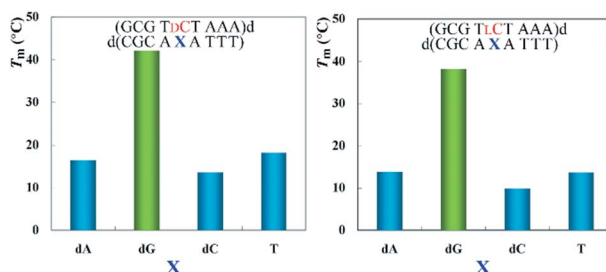


Table 1 UV-melting points of homo- and heterochiral duplexes<sup>a</sup>

Duplex	Template strand	Complementary strand	$T_m$ (°C)	$\Delta T_m^b$ (°C)
<b>Homochiral strand</b>				
1	d(AAATCTGCG)	d(CGCAGATTT)	42.1	—
<b>Heterochiral strand</b>				
2	d(AAATCTGCG)	d(CGCAGATTT)	33.6	−8.5
3	d(AAATCTL <sup>b</sup> GCG)	d(CGCAGATTT)	32.6	−9.5
4	d(AAAT <sup>b</sup> CTGCG)	d(CGCAGATTT)	38.2	−3.9
5	d(AAA <sup>b</sup> LCTGCG)	d(CGCAGATTT)	33.9	−8.2

<sup>a</sup> Samples contained 6  $\mu$ M duplex in 10 mM MgCl<sub>2</sub>, 100 mM NaCl, and 70 mM MOPS (pH 7.1). <sup>b</sup> Melting temperature difference from the homochiral duplex.



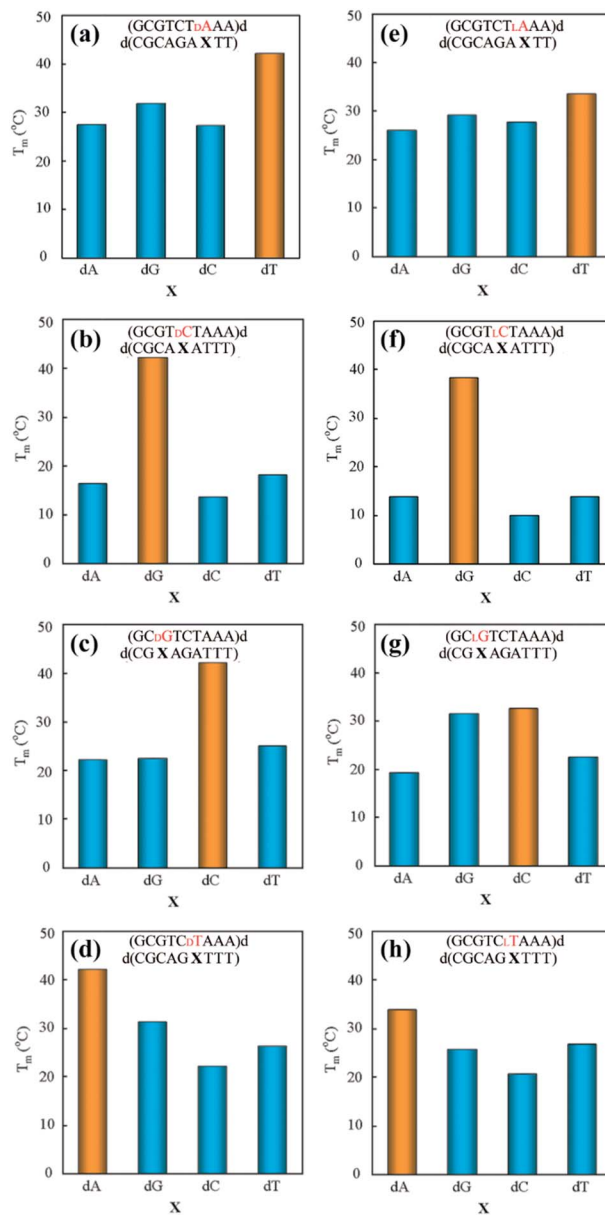


Fig. 2 Effects of base pair mismatch of D- (a–d) and L-nucleotide (e–h) on duplex stability. Samples contained 6 mM duplex in 10 mM  $MgCl_2$ , 100 mM NaCl, and 70 mM MOPS (pH 7.1). Yellow bars denote  $T_m$  values of fully matched duplexes, and blue bars denote  $T_m$  values of mismatched duplexes.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

