Table 1ES1 Results of Scatchard analysis of MB and QNA binding to polynucleotides in CP buffer at different salt concentration, PH 7.0 at 20°C[a]

Polynucleotide	Drug	$[Na^+]$ mM	n	$K(xM^{-1})$
Poly(dG-dC). poly(dG-dC)	MB	10	3.76	$1.89x10^6$
		20	3.96	$8.38x10^5$
		50	4.32	$3.25x10^5$
		100	4.80	$1.58x10^5$
	QNA	10	2.24	$6.82x10^6$
		20	2.36	$3.19x10^6$
		50	2.44	$1.03x10^6$
		100	2.74	$4.41x10^5$
Poly(dG). poly(dC)	MB	10	3.52	$1.12x10^6$
		20	3.69	$6.06x10^5$
		50	3.96	$2.29x10^5$
		100	4.28	$1.05x10^5$
	QNA	10	2.39	$2.45x10^6$
		20	2.48	$9.97x10^5$
		50	2.61	$4.25x10^5$
		100	2.84	$1.74x10^5$
Poly(dA-dT).poly(dA-dT)	MB	10	3.36	$4.40x10^5$
		20	3.72	$2.60x10^5$
		50	3.90	$9.28x10^4$
		100	4.18	$4.20x10^4$
	QNA	10	2.35	$5.25x10^6$
		20	2.53	$3.02x10^6$
		50	2.61	$8.86x10^5$
		100	2.71	$4.23x10^5$
Poly(dA).poly(dT)	MB	10	3.36	$1.03x10^5$
		20	3.56	$5.47x10^4$
		50	4.37	$1.76x10^4$
		100	4.80	$.89x10^4$
	QNA	10	3.63	$9.55x10^5$
		20	4.03	$4.50x10^5$
		50	4.70	$1.46x10^5$
		100	5.24	$5.79x10^4$

[a]Data presented from the average of four determinations in each.

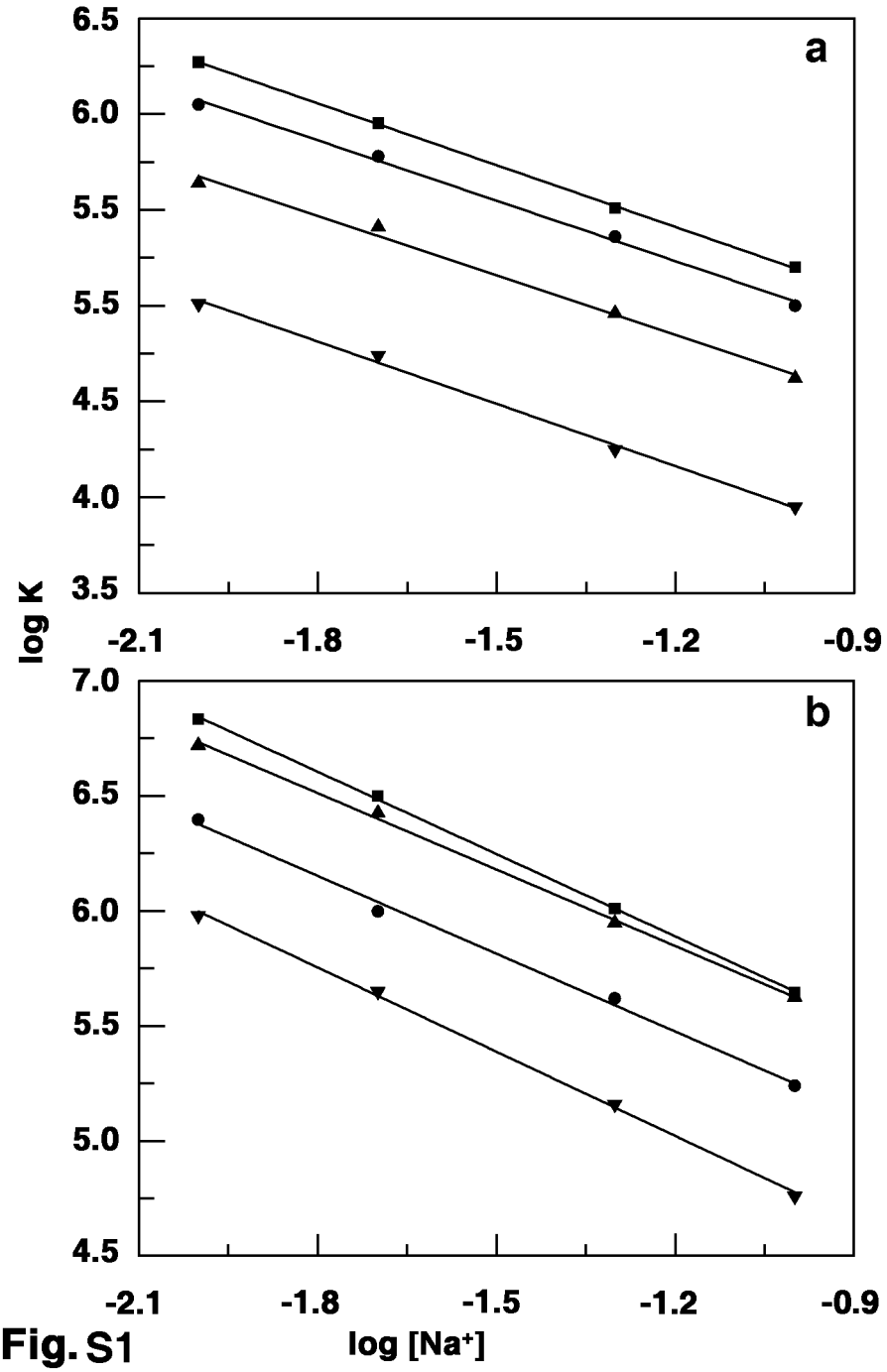

Fig. S1

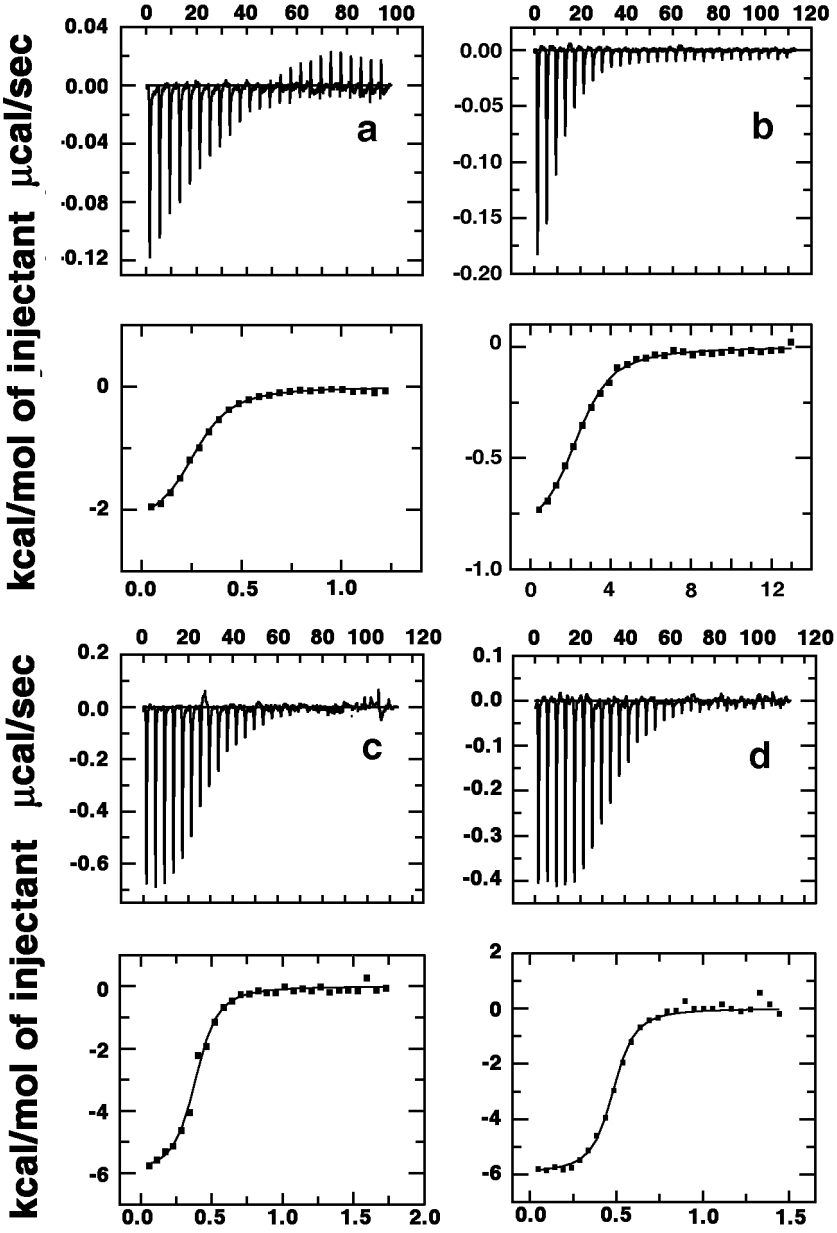

Fig. S2

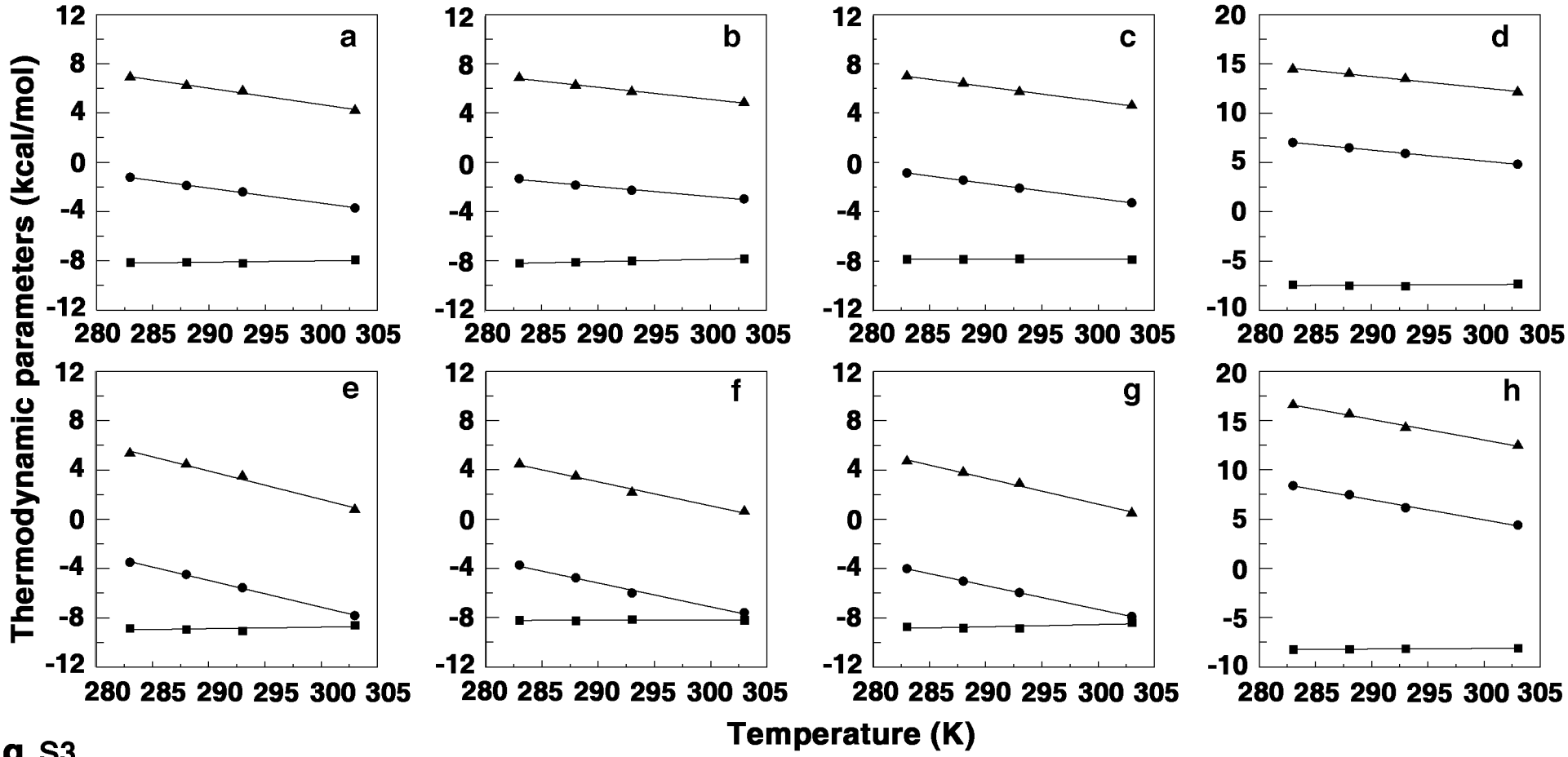

Fig. S3

FIGURE LEGENDS OF ESI

Fig. S1 of ESI. Log-log plot of the variation of the intrinsic binding *K* as a function of ionic strength [Na^+] for the complexation of (Panel a) MB-Poly(dG-dC).poly(dG-dC) (■), MB-Poly(dG).poly(dC) (●),MB-Poly(dA-dT). poly(dA-dT) (▲), and MB-Poly(dA).poly(dT) (▼) and (panel b) QNA-Poly(dG-dC).poly(dG-dC) (■), QNA-Poly(dG).poly(dC) (●),QNA-Poly(dA-dT). poly(dA-dT) (▲) and QNA-Poly(dA).poly(dT) (▼), The solid lines represent the best fit to the experimental points.

Fig. S2 of ESI. The top panels (a), (b), represent the raw ITC data for the sequential injection of aliquots of the MB (panel a) 10 μL each form a stock of 200μM for poly(dG).poly(dC).) was injected into the isothermal sample chamber containing 30 μM poly(dG).poly(dC). but in case of poly(dA-dT).poly(dA-dT),(panel b) the reverse titration was performed by injecting poly(dA-dT).poly(dA-dT), 10 μL each from a stock of 600 μM into MB solution (10 μM) in the calorimeter cell. The top panels (c), (d), represent the raw ITC data for the sequential injection of aliquots of the QNA, 10 μL each form a stock of 400 μM for poly(dG-dC).poly(dG-dC), poly(dG).poly(dC). and 200 μM for poly(dA-dT).poly(dA-dT), were injected into the isothermal sample chamber containing 30μM poly(dG-dC).poly(dG-dC) and 50μM poly(dA-dT).poly(dA-dT), solution. The bottom panels show the integrated heat data after correction of heat of dilution against the mole ratio of Drug/DNA of MB and QNA respectively. The data (closed squares) were fitted to a one-site model and the solid lines represent the best-fit data.

Fig. S3 of ESI. Temperature dependence of the thermodynamic binding parameters, $T\Delta S$ (▲-▲) ΔH (● -●), and ΔG (■ - ■) for binding of MB (panel a, b, c, d) poly(dG-dC).poly(dG-dC), poly(dG).poly(dC).), poly(dA-dT).poly(dA-dT), poly(dA).poly(dT) and QNA (panel e, f, g, h)

to poly(dG-dC).poly(dG-dC), poly(dG).poly(dC).), poly(dA-dT).poly(dA-dT), poly(dA).poly(dT) respectively.