Supplementary material.

Figure legends.

Figure S1. SPR spectroscopy analysis of interaction of KpnI MTase with non-specific DNA. The sensorgrams depicting the interaction of KpnI MTase with the non specific DNA immobilized on a streptavidin chip are shown. The indicated concentrations of MTase was injected for 300 sec at a flow rate of 10µl/min followed by 300 sec dissociation phase. The K_D values for specific DNA were determined by the same procedure is already reported (10,15).

Figure. S2. DNase I footprinting analysis of KpnI REase. (A). The 38 mer double stranded oligonucleotide containing KpnI site in which the top strand has been labeled was incubated with 30, 150, 300 and 700 nM of KpnI REase (lanes 1-4 respectively) and treated with DNase I. The resulting cleavage products were analyzed as described in experimental procedure. Lane G, refers to the corresponding guanine specific sequencing ladder and F indicates the DNase I cleavage reactions in the absence of the REase. The cleavage product by KpnI REase and the DNase I protected region are indicated. (B). DNase I footprinting with DNA substrate in which the bottom strand was labeled.

Figure. S3. DNase I footprinting analysis of KpnI MTase. The 38 mer duplex oligonucleotide containing KpnI site (with either top or bottom strand labeled) was incubated with 100, 400 and 800 nM of KpnI MTase (lanes 1-3) and treated with DNase I. Lane G, refers to the corresponding guanine specific sequencing ladder and F indicates the DNase I cleavage reactions in the absence of the MTase.

Figure S4. Methylation protection footprinting analysis of KpnI MTase. The labeled duplex oligonucleotides (either top and bottom strand labeled) were incubated with 100, 200, 400, 600 and 1000 nM of KpnI MTase (lanes 1-5) and the enzyme-DNA complex was treated with 1% DMS. The samples were analyzed on 15% denaturing PAGE. Lanes, G and F refer to guanine specific sequencing ladder and the DMS reaction carried in the absence of enzyme respectively.

Fig. S1

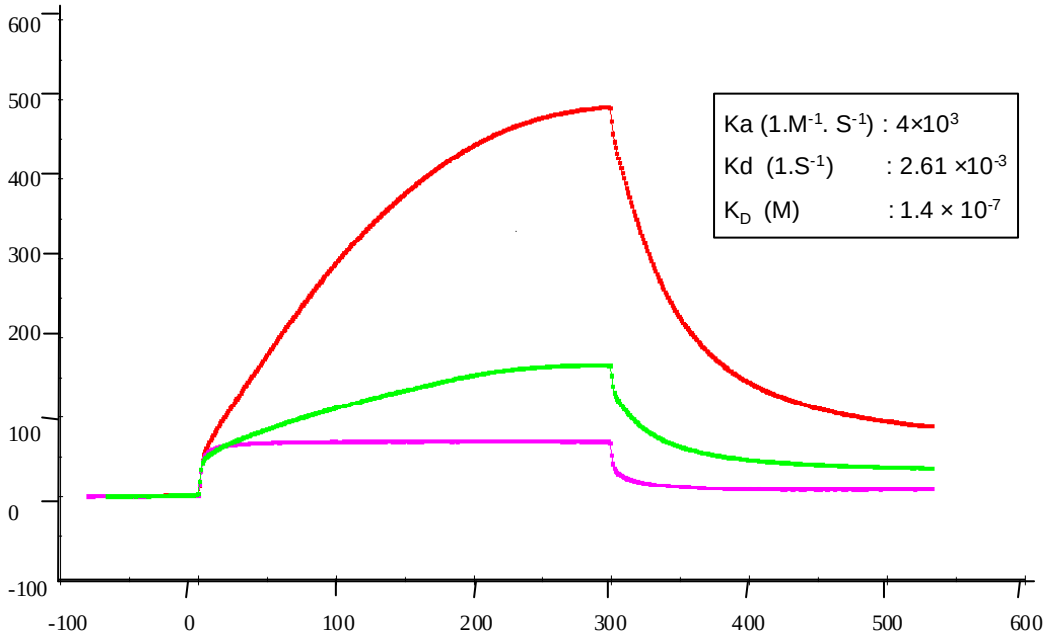

600
500
400
300
200
100
0
-100
-100
0
100
200
300
400
500
600
Ka (1.M-1. S-1) : 4×103
Kd (1.S-1) : 2.61 ×10-3
KD (M) : 1.4 × 10-7

Fig. S2

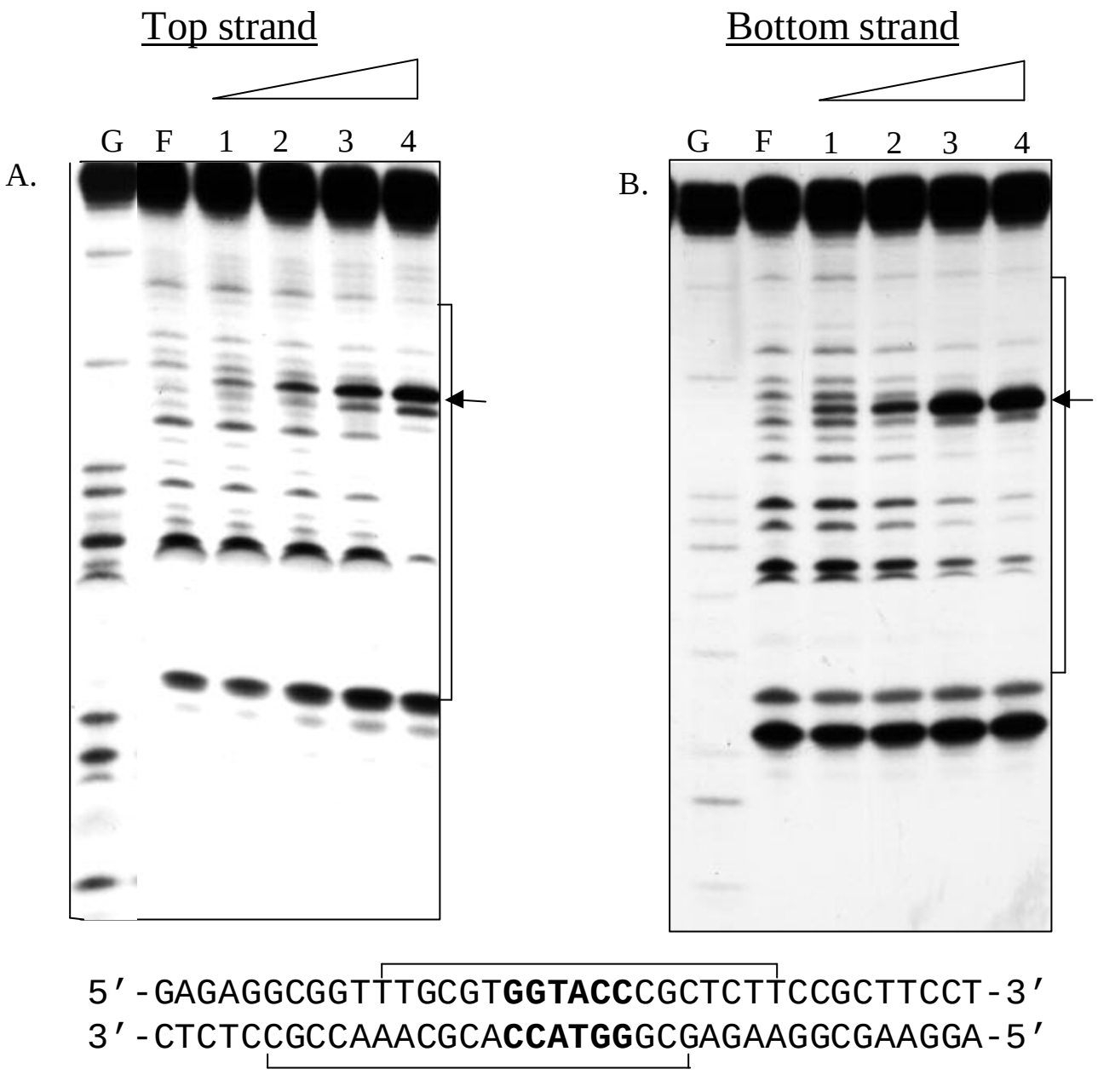
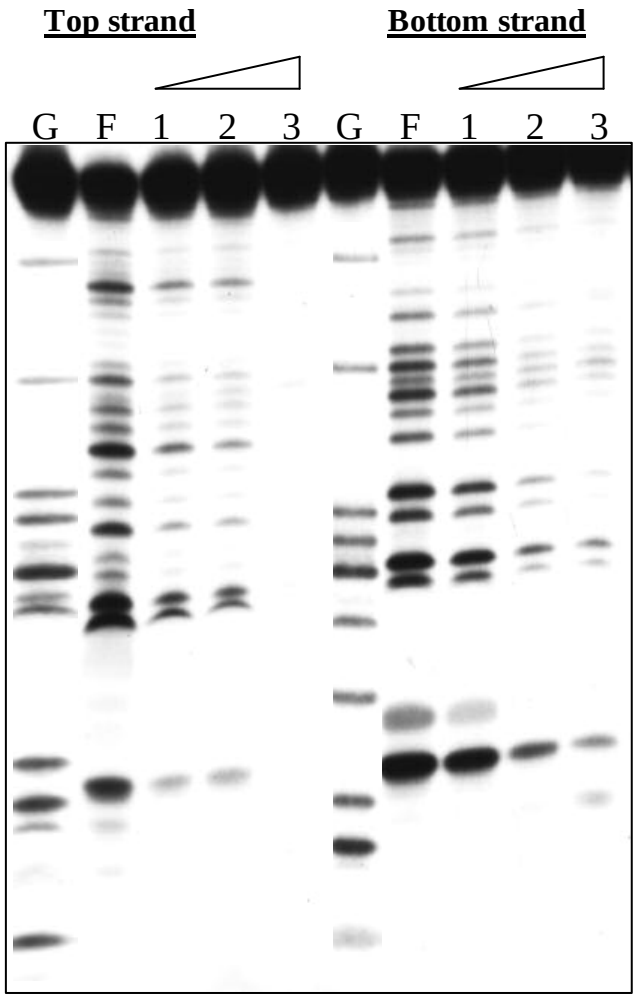

Top strand
Bottom strand
A.
B.
G F 1 2 3 4
G F 1 2 3 4
5′-GAGAGGCGGTTTGCGTGGTACCCGCTCTTCCGCTTCCT-3′
3′-CTCTCCGCCAAACGCACCATGGGCGAGAAGGCGAAGGA-5′

Fig. S3



5′-GAGAGGCGGTTTGCGT**GGTACC**CGCTCTTCCGCTTCCT-3′
3′-CTCTCCGCCAAACGCA**CCATGG**GCGAGAAGGCGAAGGA-5′

Fig. S4