

SUPPLEMENTARY TABLE I

*Stimulation of hMSH2-hMSH6 ATPase activity by
G/T mismatch DNA substrates*

Each value represents the mean derived from three independent experiments

DNA Substrate*	k_{cat} min^{-1}	K_{m} μM	$k_{\text{cat}}/K_{\text{m}}$ $M^{-1}\text{min}^{-1} (x10^{-4})$
CGA	21.6	30.4	71.1
TGA	22.2	35.4	63.4
CGG	20.0	39.6	50.5
TGG	22.8	36.6	62.3
CGC	20.6	35.4	58.3
TGC	21.6	34.0	63.5
CGT	21.0	32.2	65.2
TGT	21.4	32.3	66.3
AGA	20.3	32.2	63.0
GGA	19.2	32.7	58.7
AGG	21.4	36.6	58.5
GGG	19.0	28.8	67.9
AGC	15.1	24.5	61.6
GGC	11.7	19.6	59.7
AGT	16.4	26.7	61.4
GGT	14.9	23.9	62.3
2x 3' Pur	21.7 (+/-1.2)	35.5 (+/-3.8)	61.8 (+/-8.5)
1x 3' Pur	20.6 (+/-1.0)	33.0 (+/-2.6)	62.7 (+/-3.8)
2x 3' Pyr	14.5 (+/-2.0)	23.7 (+/-3.0)	61.3 (+/-1.1)

*Only the G strand of the G/T mismatch is shown. Duplexes where both the mismatched G and T are followed by a 3' purine are color coded **red**. Duplexes where only one of the mismatched G or T is followed by a 3' purine are color coded **green**. Duplexes where both the mismatched G and T are followed by a 3' pyrimidine are color coded **blue**. At least three independent experiments were performed with each oligonucleotide and the average and standard of deviation calculated (SD not shown for individual assays). Combined average and standard of deviation (in parenthesis) for the three grouped sequence context are shown at the bottom.