SUPPLEMENTARY TABLE II
Stimulation of hMSH2-hMSH6 ATPase activity by
C/A mismatch DNA substrates
Each value represents the mean derived from three independent experiments

DNA Substrate*	k_{cat}	K_m	k_{cat}/K_m
	min^{-1}	μM	$M^{-1}min^{-1}$ $(x10^{-4})$
CCA	15.8	32.6	48.5
TCA	14.4	31.9	45.1
CCG	15.7	30.0	52.3
TCG	15.5	32.2	48.1
CCC	14.6	27.5	53.1
TCC	15.3	37.4	40.9
CCT	16.0	28.1	56.9
TCT	14.3	34.4	41.6
ACA	14.4	25.4	56.7
GCA	16.5	32.0	51.6
ACG	15.2	30.0	38.8
GCG	14.8	29.0	51.0
ACC	14.0	27.3	51.3
GCC	13.4	28.3	47.3
ACT	11.8	29.9	39.5
GCT	13.2	28.7	46.0
2x 3′Pur	15.4 (+/-0.6)	31.7 (+/-1.2)	48.5 (+/-3.0)
1x 3′Pur	15.1 (+/-0.8)	30.5 (+/-3.9)	48.8 (+/-7.3)
2x 3′Pyr	13.1 (+/-0.9)	28.6 (+/-1.1)	46.0 (+/-4.9)

*Only the C strand of the C/A mismatch is shown. Duplexes where both the mismatched C and A are followed by a 3′ purine are color coded **red**. Duplexes where only one of the mismatched C or A is followed by a 3′ purine are color coded **green**. Duplexes where both the mismatched C and A 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.