

### SUPPLEMENTARY TABLE IV

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

Each value represents the mean derived from three independent experiments

DNA Substrate*	$k_{\text{cat}}$ $\text{min}^{-1}$	$K_{\text{m}}$ $\mu\text{M}$	$k_{\text{cat}}/K_{\text{m}}$ $M^{-1}\text{min}^{-1} (x10^{-4})$
<b>CGA</b>	<b>16.3</b>	<b>41.3</b>	<b>39.5</b>
<b>TGA</b>	<b>16.3</b>	<b>43.3</b>	<b>37.6</b>
<b>CGG</b>	<b>16.8</b>	<b>38.0</b>	<b>44.2</b>
<b>TGG</b>	<b>21.6</b>	<b>62.2</b>	<b>34.7</b>
<b>CGC</b>	<b>17.0</b>	<b>43.4</b>	<b>39.2</b>
<b>TGC</b>	<b>17.8</b>	<b>58.0</b>	<b>30.7</b>
<b>CGT</b>	<b>17.9</b>	<b>51.5</b>	<b>34.8</b>
<b>TGT</b>	<b>18.1</b>	<b>69.0</b>	<b>26.2</b>
<b>AGA</b>	<b>12.4</b>	<b>79.3</b>	<b>15.6</b>
<b>GGA</b>	<b>10.0</b>	<b>55.5</b>	<b>18.0</b>
<b>AGG</b>	<b>11.9</b>	<b>53.5</b>	<b>22.2</b>
<b>GGG</b>	<b>12.6</b>	<b>59.8</b>	<b>21.1</b>
<b>AGC</b>	<b>12.7</b>	<b>65.2</b>	<b>19.5</b>
<b>GGC</b>	<b>11.1</b>	<b>34.4</b>	<b>32.3</b>
<b>AGT</b>	<b>11.8</b>	<b>28.9</b>	<b>40.8</b>
<b>GGT</b>	<b>10.6</b>	<b>29.6</b>	<b>35.8</b>
<b>2x 3' Pur</b>	<b>17.8 (+/-2.6)</b>	<b>46.2 (+/-10.9)</b>	<b>39.0 (+/- 4.0)</b>
<b>1x 3' Pur</b>	<b>14.7 (+/-3.3)</b>	<b>58.8 (+/-11.1)</b>	<b>26.0 (+/- 8.3)</b>
<b>2x 3' Pyr</b>	<b>11.6 (+/-0.9)</b>	<b>39.5 (+/-17.3)</b>	<b>32.1 (+/- 9.1)</b>

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