```
Results of restriction analysis:  My working sequence (330 bp)
Enzyme set: my_working_set    Cut frequency: 1 - 2
Sequence covered from bp 0 to 329
Minimum length of open reading frames: 200

                                                          DpnI
   0   CCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTA

  60   GGTGAGCCGTTACCCCACCTACTAGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGC

 120   CCTAAGGTCCCCCTCTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAG

 180   TTATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCAGCG

 240   AAGCAGCAAGCTGCTTCCTGTTACCGTTCGACTTGCATGTGTTAGGCCTGCCGCCAGCGT

                             DpnI
 300   TCAATCTGAGCCATGATCAAACTCTTCAAT
```

Figure S2. *Dpn*I restriction enzyme cut sites (red boxes with arrows) located within the previously sequenced amplicons generated from no-template control reactions. The image was obtained from WatCut, an online restriction analysis tool (http://watcut.uwaterloo.ca/template.php).