

Figure S7

A

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.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
   5      15      25      35      45      55
TGTCTATAAG CTCATCACTT GGCACATTTT GAGGCAATTC ACATTTGCCG CATTTACATT

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
  65      75      85      95     105     115
TAAATTCGCT TTCTTTAAAA TAAGGGTTAT TTTTCATTTT CTTCTTCTCC TTCTGGTTTT

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 125     135     145     155     165     175
GAAAAAATTT CTATATTAAA TTTAAGCCTA TAAGCAAATA AAGAACTGCT TATAAAACCA

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 185     195     205     215     225     235
CTTTCGATAC TGCTTAAAAG CTTTTAGCTT GTATCAAATT CAAAAAGTTT TAGTCTTAAT

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 245     255     265     275     285     295
TCATCTATTT TTTTAATCAA AGAATCTTTA TCTTTATTAA AAGTATGAGA ACTAAAAATC

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 305     315     325     335     345     355
AATGAAAAAT TCACACTATC TTTATGATGA TTAATACTTG TTAGGCTTTC AAGCATTAGA

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 365     375     385     395     405     415
TAAAGTCCGC CTTGTTTGAC ATCTTCGTAA TTTGCTATGC CTATCGCATT AAAATGCTTT

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 425     435     445     455     465     475
AATAAATCTT TGCTAACACT ATCTAAAGTC AAAACCTGTC CTTTCTTTGC ATAATTTTAA

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 485     495     505     515     525     535
GTCTTAAAGA GCTTAAATTT CCTTCTTTAT CAATCAAAGG TGCATTTTCA ATTCGTTTTA

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 545     555     565     575     585     595
AAGCATTATC TAGAAGGATT TTATCTTCAT CATCTAAGAC GATTTTAAGA TAAATTTTTA



.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 605     615     625     635     645     655
TGCGAATGTA TGCAAAATCC TCCCAAATAA AATCAGCAAT ATCTTTATTT TTGCAAATAT

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 665     675     685     695     705     715
CATCTGCATC TTTTGCTGCT TTAGCTACTA CTTCTCTTGT AATTTTCATCG ATATTTGCTA

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
 725     735     745     755     765     775
AGTTTTGTTG TGCTCTTTTC ATCAGTGCTA ACTCTTTTAA AGTAAGAGCT AGCATTTTAG

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B

 **CJE0241 [Campylobacter jejuni RM1221] Expect = 5e-15**
 **Unknown Sequence**