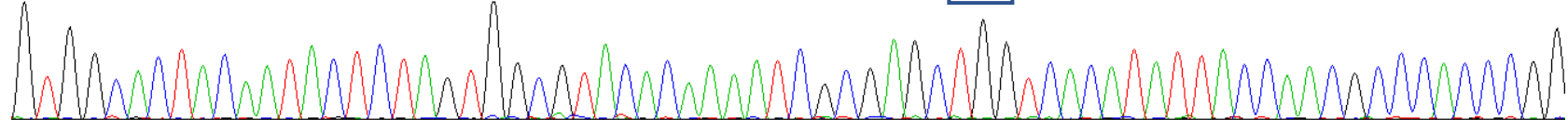


WT GTGGCACTACAATACTCTAGTGGCGTACACAAAATCGCG-----AGCTGGTCACATATTACCAACGCCCACCCGG
 (+1 nt) 10⁻¹ GTGGCACTACAATACTCTAGTGGCGTACACAAAATCGCGT-----AGCTGGTCACATATTACCAACGCCCACCCGG
 (+33 nt) 10⁻² GTGGCACTACAATACTCTAGTGGCGTACACAAAATCGCGCAATCTCTTATACACATCTGTGATCGTCGTGCTAGCTGGTCACATATTACCAACGCCCACCCGG

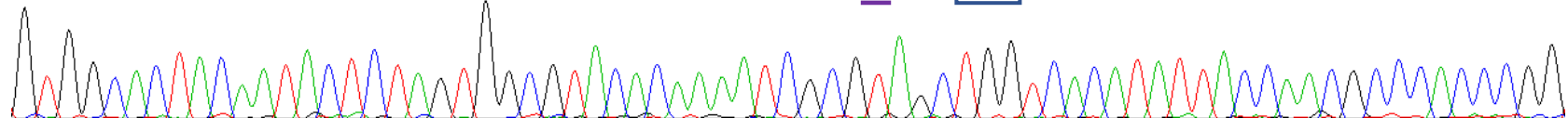
G T G G C A C T A C A A T A C T C T A G T G G C G G T A C A C A A A A T C G C G A G C T G G T C A C A T A T T A C C A A C G C C C A C C C G G

WT



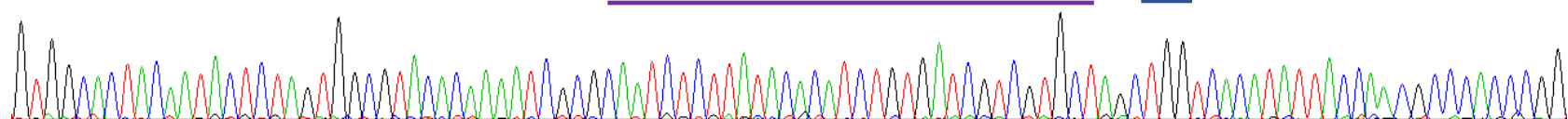
G T G G C A C T A C A A T A C T C T A G T G G C G G T A C A C A A A A T C G C G A G C T G G T C A C A T A T T A C C A A C G C C C A C C C G G

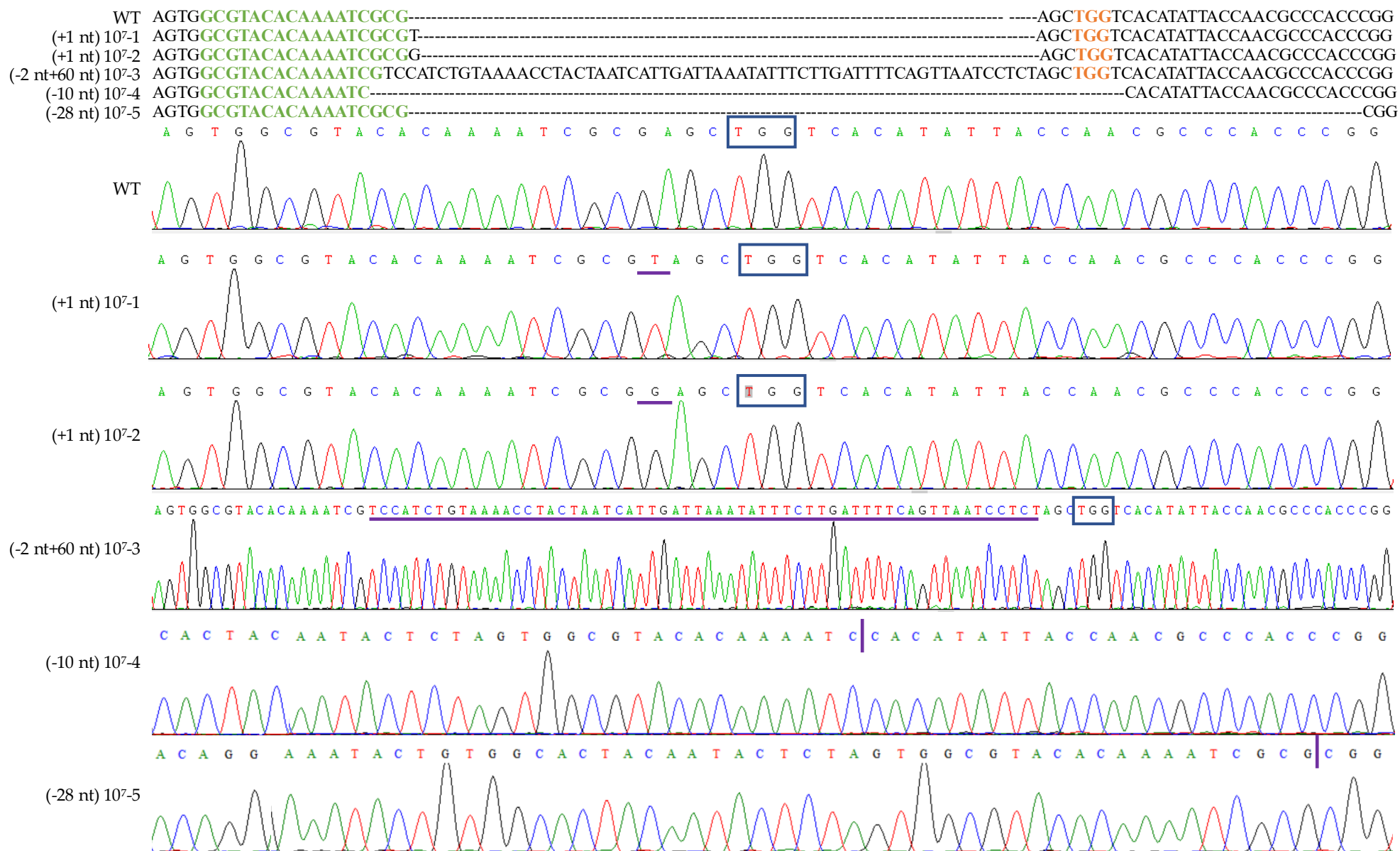
(+1 nt) 10⁻¹

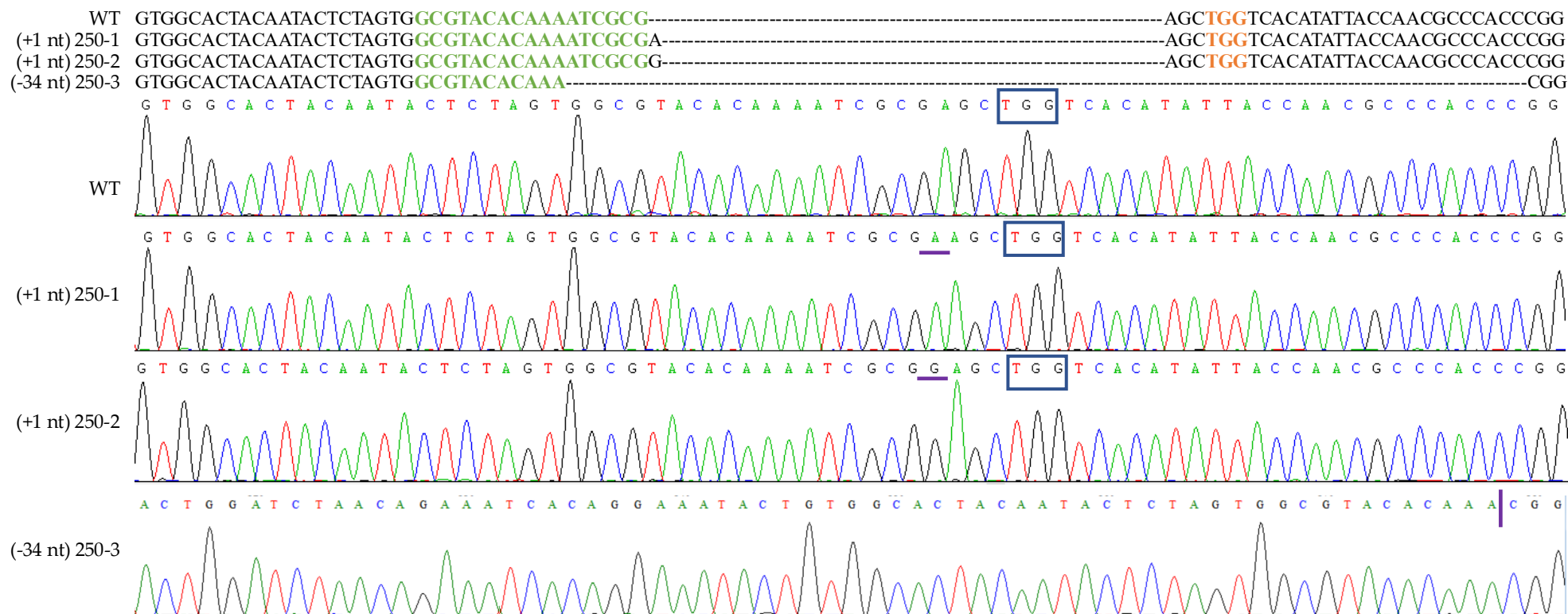


G T G G C A C T A C A A T A C T C T A G T G G C G G T A C A C A A A A T C G C G A A T C T C T T A T A C A C A T C T G T G A T C G T C G T G C T A G C T G G T C A C A T A T T A C C A A C G C C C A C C C G G

(+33 nt) 10⁻²







WT GTGGCACTACAATACTCTAGTGGCGGTACACAAAATCGCG-----AGCTGGTCACATATTACCAACGCCACCCGG
 (+1 nt) 300-1 GTGGCACTACAATACTCTAGTGGCGGTACACAAAATCGCGT-----AGCTGGTCACATATTACCAACGCCACCCGG
 (-78 nt) 300-2 AGC-----AGCTGGTCACATATTACCAACGCCACCCGG
 (-65 nt) 300-3 G-----CCGG
 (+115 nt) 300-4 GTGGCACTACAATACTCTAGTGGCGGTACACAAAATCGCGGTGAAGATTATCCTTCCCGTCCATTTCATCATGTGCGCGCGTCAAAATCGCGTCTCCCGCTCACCATCGTCTTACCAGCCCGTCGCTGCCAGAAAGCGCTCGTCAATGCTAGCTGGTCACATATTACCA

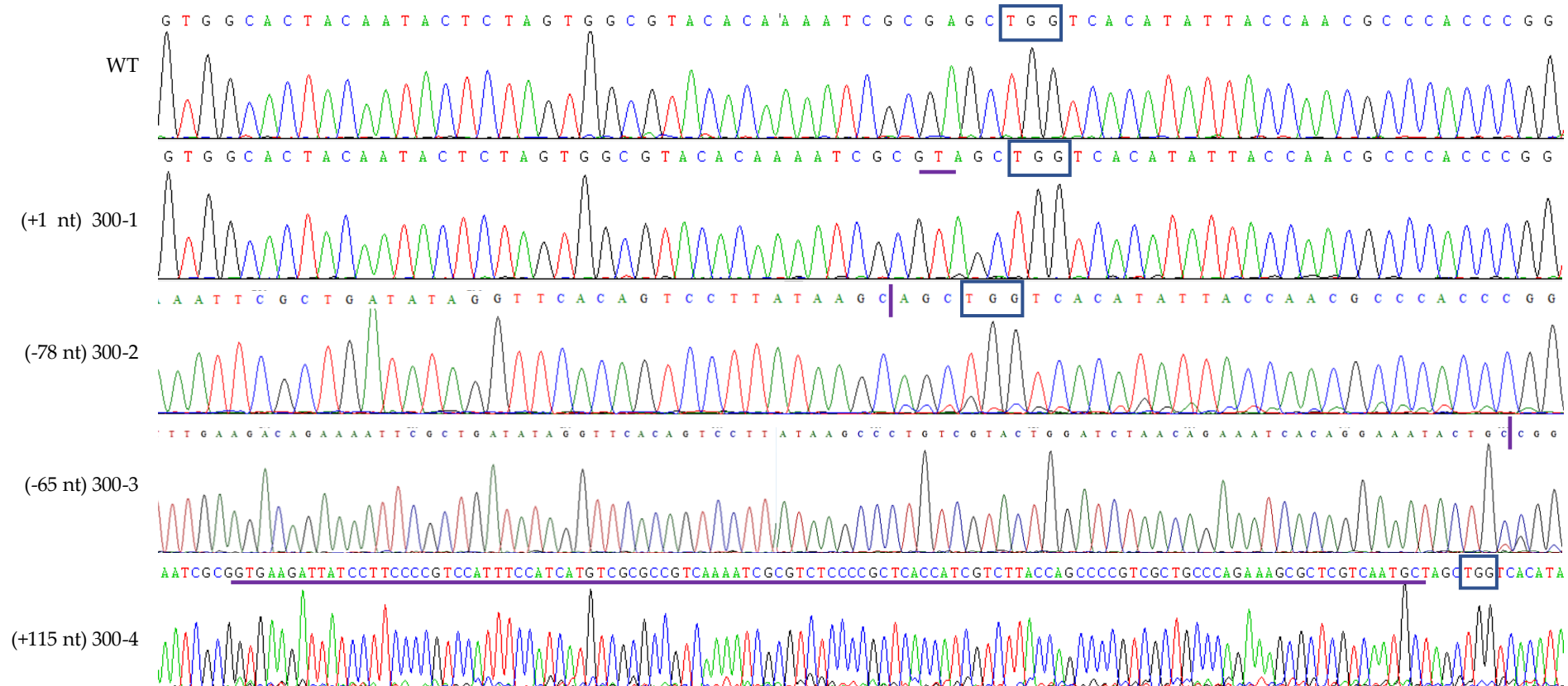




Figure S1. Chromatogram and alignment of pyrG sequences and corresponding mutants.