| Oligo’s ID   | Sequence (5’ > 3’)                                                                 | Description                                                                 |
|-------------|-----------------------------------------------------------------------------------|-------------------------------------------------------------------------------|
| PyrG-F1     | CGATCCCCGAGAAAAGAAAAAAGGG                                                         | To amplify pyrG ORF + 1570 bp upstream sequence                               |
| PyrG-R2     | GTTTTCCGTCTATCCTTTAGAAAG                                                         | To amplify pyrG ORF + 2247 bp extra downstream sequence                       |
| oKE-21      | CCACTCACCATATGACGAAATATATTTTTGTAACCCTGGGG                                       | pyrG + pSF14 overhangs (11 nucleotides)                                      |
| oKE-22      | CAGCCGGATCTTTACTTCTTGATTTGCGACGTTCGACAG                                           | pyrG + pSF14 overhangs (10 nucleotides)                                       |
| oKE-23      | CAATCAGAAGTAAGATCCGGCTGCTAA CAAGGCC                                              | pSF14 Fw + pyrG 11 nucleotides overhangs including the stop codon             |
| oKE-24      | TATATTTTCGTCATATGATGGGCGCCTGCTGATGAGG                                          | pSF14 Rv +14x His + pyrG 13 nucleotides overhangs, including the start codon |
| oKE-29-Pyr- | CGAATCAGTCCCATCCTTGAGCGATCTG                                          Site directed mutagenesis-Mutant 1 |
| Mut1F       |                                                                                   |                                                                               |
| oKE-30-Pyr- | GCTCTTACATTTTATGACGATCTGCAAGAAN                                              Site directed mutagenesis-Mutant 1 |
| Mut1R       |                                                                                   |                                                                               |
| oKE-31-Pyr- | CCATCTTGAAGCAGATCTGCAAGAAN                                              Site directed mutagenesis-Mutant 11 |
| Mut11F      |                                                                                   |                                                                               |
| oKE-32-Pyr- | CCGATTCGCTTTACATTGGGCTGCAAGATCTGCAAGAAN                                           Site directed mutagenesis-Mutant 11 |
| Mut11R      |                                                                                   |                                                                               |
| oKE-35-Pyr- | GCCCTGATGGGACGCGCTTGTGAGG                                                      Site directed mutagenesis-Mutant 5 |
| Mut5F       |                                                                                   |                                                                               |
| oKE-36-Pyr- | GTTCTCAGGAGGCTTGTGCTGAG                                                        Site directed mutagenesis-Mutant 5 |
| Mut5R       |                                                                                   |                                                                               |
| oKE-37-PyrG- | GACGAAATATATATTTTTGTAACCCTGGGG                                                   To check mutation sites in PyrG |
| F           |                                                                                   |                                                                               |
| okE38-PyrG- | CTTACTTCTGATTTTGCAGCTTGACAG                                                      To check mutation sites in PyrG |
| R           |                                                                                   |                                                                               |
| oKE39-pSF14 | CCGTCAGTCTGTGAGACATGAC                                                          To check the sequence of pyrG |
| -F          |                                                                                   |                                                                               |