**S1 Table.**  **Primers used for complete genomic sequencing of isolate 44624.**

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| **Primer** | **Sequence** | **Genome orientation** |
| 001F\_Hind | 5’-TCGATGTCGACTAATACGACTCACTATAGGTTAAAACAGCTCTGGGG-3’ | Forward |
| S2 F2 | 5’-CTCCGGCCCCTGAATGCGGCTA-3’ | Forward |
| S2 R1 | 5’-ATTGTCACCATAAGCAGCC-3’ | Reverse |
| S2 F3 | 5’-AGCCTATGGCGGGTCCACCATCAA-3’ | Forward |
| S2 R2 | 5’- TGGTGATCGTTGAATTGCCCAG-3’ | Reverse |
| S2 F4 | 5’-ACAGTGCACGTACAGTGCAATGCTTTCAAG-3’ | Forward |
| S2 R3 | 5’-TTTTTCGCCTGGATTCGCATTCTCGTACTT-3’ | Reverse |
| S2F5 | 5’-TGAACACTCCAGGGAGTAACCA-3’ | Forward |
| S2 R4 | 5’-GGTATCGCACACGGAGACTGGT-3’ | Reverse |
| S2 F6 | 5’-GATAGTTTCACAGAAGGTGGCT-3’ | Forward |
| Y7 | 5′-GGGTTTGTGTCAGCCTGTAATGA-3 | Forward |
| S2 R5 | 5’-CATTGCAAGCTGACACAAA-3’ | Reverse |
| S2 F7 | 5’- CTGTTCAACTGAGACACGCAAACTGGAATTT-3’ | Forward |
| S2 R6 | 5’-GGACGTCTGCCACGTATAGTCATTCCATTT-3’ | Reverse |
| S2 F8 | 5’-GGCTACAAAATTTGCAATTACCAC-3’ | Forward |
| Q8 (S2 R7) | 5′-AAGAGGTCTCTRTTCCACAT-3′ | Reverse |
| S2 F9 | 5’-TCATCACTTGTGATCATTACTA-3’ | Forward |
| S2 R8 | 5’-GCAAGCACTGTGGTAGTGTCCT-3’ | Reverse |
| S2 F10 | 5’-ATTGCTAGAGCAATAGCCGAGA-3’ | Forward |
| S2 R9 | 5’-GGAGGCAGTGAGTATGTGGAGC-3’ | Reverse |
| S2 F11 | 5’-TGATCAGATCACTACAATGATTGTTAATGA-3’ | Forward |
| S2 F12 | 5’-AGATCAGGCAGGAACTAATCTT-3’ | Forward |
| S2 R11 | 5’-GCCTGATATCTCTGAACTTCTC-3’ | Reverse |
| S2 F13 | 5’-CTCAGGACAGACTTTGAAGAAGCAATAT-3’ | Forward |
| S2 R12 | 5’-ATGTCTCTCTTTTTCTTTCCCATTGCTAC-3’ | Reverse |
| S2 F14 | 5’-CCCACCACCTGTACAAAAACAA-3’ | Forward |
| S2 R13 | 5’-TAATCATTGAGTTAAAAATTGA-3’ | Reverse |
| S2 7439R\_Sal | 5’-TCGATAAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCCGAATT-3’ | Reverse |

The primers are cited in order of position in the S2 genome.