|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Isolate name** | **Primer name** | **Sequence (5’-3’)** | **PCR fragment size (nt)** | **SPAdes coverage** |
| P1-c2 | P1-C2F | GTTATCACTTCGACCCGCCGGCAC | 2427 | 107.43 |
| P1-C2R | CTCGTACTCACACTGCCAGTCCTCCTT |
| P1-C2R2 | CCTCCTTAGTGGGAGGACGA |  |  |
| P1-C2F2 | CCAAGGCCAGCACTGAGG |  |  |
| P1-c4 | P1-C4F | CAGAGCCTAACCCCGAGCAGCCATG | 2430 | 7.62 |
| P1-C4R | GGGGTAGTAAGGCCTGTCTGTGTGGTT |  |  |
| P1-C4F2 | CACATTAGAAGACTGGCTGTACAC |  |  |
| P1-c16 | P1-C16F | GCGGTTGCGATTCTACTATTTGCCACTT | 2143 | 249.61 |
| P1-C16R | CAGCTTCTGTTTGTTCTTCCCATGGATA |  |  |
| P1-c23 | P1-C23F | CCTGACCATCCAGACAGACAACTT | 2059 | 156.52 |
| P1-C23R | TTCTGTTTGTAGTTCAAAGCCTGGT |
| P3-c4 | P3-C4F | CCTACTGCTTCACATCTTTTCTCACGGAG | 2200 | 6.21 |
| P3-C4R | AGAGGTTCAGGTACAAGCCAGTCATAGT |
| P3-C4F2 | GACTACCAACGTGGAACAGCAC |  |  |
| P3-c5 | P3-C5F | TGGTGGAGAAGAAGAAACAAACCATGGTACT | 1993 | 34.38 |
| P3-C5R | GGCTCTACTCTAAAATTCCCGTTTGTAGT |
| P3-C5F2 | CCATTGCAACTGGCTCTGCAG |  |  |
| P3-c6 | P3-C6F | AGTCCAGACAACAATAACCCGAGAC | 2350 | 125.10 |
| P3-C6R | TGCATATTCTGTTTCCCAGTCTCCT |
| P3-C6F2 | CCAGCTTTTGGCAGTCAAATATAGCAA |  |  |
| P3-c8 | P3-C8F | TTGTGAATGTGAAAAACCACTTCAA | 2214 | 351.31 |
| P3-C8R | AAAACAAATCATCTGCCCTTTCTTG |
| P3-C8F2 | GCAGCTCCAGGACTACTAAAACCAGG |  |  |
| P5-c2 | P5-C2F | ACCCACACCGCTACTTTTATCTTTGAACA | 2189 | 1.96 |
| P5-C2R | CCTCAAATTCTCTAGCAGTCATACGTCT |
| P5-C2R2 | GGACAAATACCAACCACAAACCTAC |  |  |
| P7-c3 | P7-C3F | CAACCATCCTTTTGCTCATTTGCTTGCT | 2269 | 105.41 |
| P7-C3R | AGGCTAAAGTTGACATAGGGTTCAGGGG |
| P7-C3F2 | TCTGCAGCTGACTTTAGACACCCAACA |  |  |
| P7-c14 | P7-C14F | CTACCAACCATTAGCACATACAGCAAC | 2211 | 3.22 |
| P7-C14R | CTTGTTCATATTCTTCAGGAGTCATTCTCC |
| P7-C14F2 | GCACAACAATATGGATATGGCACAG |  |  |
| P7-c18 | P7-C18F | TAATCACCAGAGACTACCAACAATGCCA | 2079 | 91.86 |
| P7-C18R | CCTTGGTGGTCTGTGAAATGCTG |
| P7-C18F2 | CTACTGGTTGGTTTCAACCAGAC |  |  |
| P7-c20 | P7-C20F | AAGTAGGTGAGCAAAGGGTAAGTTACA | 2081 | 5.50 |
| P7-C20R | TGGTCACAGCGATCGAGAATTAACTG |
| P7-c21 | P7-C21F | GCTGCAACGACACCACTCTACATA | 2119 | 157.93 |
| P7-C21R | CAGGGGTAAATCGTCTAGGTGGTC |
| P7-c22 | P7-C22F | CTGCTTGCCAATATCTTTCCTGTG | 2121 | 482.31 |
| P7-C22R | TCACGTTCTGTGTCTTCTTCAAAGC |
| P7-C22F2 | AACAGCCTGCACATTTAGATACCCT |  |  |
| P7-c24 | P7-C24F | ATTTTTCCACTTGGCCATTCTGAT | 2086 | 150.74 |
| P7-C24R | TTCTGTGTCTTGTTCAAATCCTGGT |
| P7-C24F2 | CTGATTCATACAGAAAACCAAGCTC |  |  |
| P8-c17 | P8-C17F | GCAACTATTAACTGCCACGATCTCTGCT | 2109 | 156.85 |
| P8-C17R | TCAGCCTCCCAACTCTTTCCCCTTATAG |
| P8-C17R2 | CCAGTTTGTGGATACCAGTGCAG |  |  |
| P8-c22 | P8-C22F | TCCCATCTTAGATTTACAACTGAGGAA | 2166 | 142.89 |
| P8-C22R | TGTCTGGGATAGTGGTCCCATATTT |
| P8-C22F2 | GGAAACAGCAATGCACAAAGTTTAACC |  |  |
| P8-c23 | P8-C23F | AACTACTGGCAATATCCAACAAGCA | 1796 | 53.68 |
| P8-C23R | TAACTCTCTCTCATGGGGTGCAAAG |
| P8-c25 | P8-C25F | CACTGCAAATCACCTTTAAACCACA | 2109 | 132.74 |
| P8-C25R | CATGGTTTCATGCGTCTGTTTTTAG |
| P8-C25F2 | CAGAAAGCAGCACAATAACATTACATACCC |  |  |
| P9-c4 | P9-C4F | TCCCGCTCCTGATTCCCAAAACAATCC | 2442 | 16.43 |
| P9-C4R | AGGGGTAGTATGGAGTGTCTGACAGGT |
| P9-C4F2 | AGACTTCTATTACCCCATAATCGG |  |  |
| P9-c5 | P9-C5F | TTTTCCTCCTGGCCATCAAGACAG | 2140 | 9.27 |
| P9-C5R | GGGGTGTCCTCTTTAAACAATCTAGGGG |
| P10-c9 | P10-C9F | GGATTCCAAAAACCCGAAACAGATA | 2122 | 15.59 |
| P10-C9R | TTGTTGTTCCCAGGGTGTTAGTCTT |
| P10-C9F2 | GATACAATACACACACATGCAGACTC |  |  |
| P10-C9R2 | GTTCATATCTTCGTATGGGTCAAAG |  |  |
| P12-c3 | P12-C3F | TGCTTGCCAGTATCTTTCCTGTGGGTCA | 2149 | 6.16 |
| P12-C3R | CAGGTCTGAGAAATGCAAAAGCAAGTTCA |
| P12-C3F2 | TGCCCAGAAGCAACTTACACATAC |  |  |