Table S1Primersequences and results of sequences alignment of the amplicons

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| Primer pairs | Length (bp) | Location | Similarity% |
| F:5'GTTATAGACATGAAAGCGTA3' | 450 | 21,006-21,455 | 100 |
| R:5'AGGTTAAATGAGGGAAAC3' |
| F:5'TGGGCTCTTCTTTATATT3' | 452 | 33,790-34,241 | 99.34 |
| R:5'ATCTCACTTCGGATTCTC3' |
| F:5'TACATCTAATCCATACAG3' | 307 | 48,387-48,693 | 100 |
| R:5'GGGTCAAACTTTCTTATA3' |
| F:5'AGACCCGCAATACAAGGA3' | 368 | 58,521-58,888 | 100 |
| R:5'GCAACAGATACAACTGGAAAA3' |
| F:5'ATAGAAATGGGGCGTGGC3' | 470 | 79,373-79,842 | 100 |
| R:5'AACCAAACCGCTGGAATA3' |
| F:5'TTATTGGATTTGCTGTGA3' | 469 | 79,891-80,359 | 100 |
| R:5'TTTCCATTCATTCCTTTC3' |
| F:5'CGTTTACCTAGCCAACAT3' | 1083 | 85,210-86,292 | 99.54 |
| R:5'TAACCATAGAATACGACCCT3' |
| F:5'CCTTTCCCGGGAGTCGAT3' | 676 | 86,653-87,328 | 100 |
| R:5'TCGGGAGTCCAAGAGTTT3' |
| F:5'TGAATCCCGTGAAACCAT3' | 401 | 90,174-90,574 | 100 |
| R:5'AACGTCTGCGATAGAATA3' |
| F:5'CTCGAAAGATATGAAAGACC3' | 576 | 98,586-99,161 | 100 |
| R:5'GAGGAACCCTAGATGCTG3' |
| F:5'ACACGGCCCAGACTCCTA3' | 442 | 101,782-102,223 | 100 |
| R:5'CTAATCCCATTCGCTCCC3' |
| F:5'TTTGGTTTGACACTGCTT3' | 1090 | 103,006-104,095 | 99.72 |
| R:5'TTGAAATAACTCCGATGAG3' |
| F:5'GGTAGGATGGGTAGTTGGT3' | 1479 | 104,564-106,042 | 99.73 |
| R:5'ATTAAGACTCGCTTTCGC3' |
| F:5'CGAGAATGTCGGCTTGAG3' | 792 | 106,654-107,445 | 100 |
| R:5'CAGGTAGTCCGCATCTTC3' |
| F:5'GCGAGACGAGCCGTTTAT3' | 361 | 108,303-108,666 | 100 |
| R:5'GCCTCTGCCCTTCCATCA3' |
| F:5'GGAACAATCACAAACACT3' | 457 | 110,514-110,970 | 99.34 |
| R:5'TCCCTTTCTTCCGTTTCT3' |
| F:5'GGCTTTACGAGTTTCTTTG3' | 371 | 128,018-128,388 | 99.19 |
| R:5'TTTGAGTGGGCTCTATCG3' |
| F:5'CTGTCTCGGCTGTGCTAC3' | 762 | 131,858-132,619 | 100 |
| R:5'CACTGTTCCCTGGGATTGG3' |
| F:5'CACCAACTTCCTTGACCTT3' | 477 | 132,834-135,410 | 99.58 |
| R:5'TGGACAACAGGCGAATA3' |
| F:5'AGCCCCGTTCATCTTCG3' | 1365 | 133,541-134,905 | 100 |
| R:5'TTTACCCTGTGGCGGATGT3' |
| F:5'AGCCGCACCTTCCAGTA3' | 994 | 137,131-138,014 | 100 |
| R:5'CAGAGGATGCAAGCGTTAT3' |
| F:5'CAGGCTACCATGAGACAA3' | 359 | 141,100-141,458 | 100 |
| R:5'CGAATACGGCTTTCCACA3' |
| F:5'TTCCACGACTCTACCACTCA3' | 370 | 145,980-146,349 | 100 |
| R:5'TTCCCAAACAGATCCTCC3' |
| F:5'TCTCGTACATTGGAACCC3' | 913 | 147,388-148,300 | 100 |
| R:5'ATAGTGATCATTTATCAAA3' |
| F:5'CTGCTAAACAGGGTGTATT3' | 685 | 148,166-148,850 | 100 |
| R:5'TTTGTTTCCCGAGCCTATA3' |
| F:5'AAATGGTTTCACGGGATTC3' | 352 | 149,901-150,252 | 100 |
| R:5'CTTTGTGAGTTTCGGGAA3' |
| F:5'CGAACCATATCACATCCC3' | 729 | 151,234-151,962 | 100 |
| R:5'CCGCCAAGACCTCTTCGT3' |
| F:5'TCCAGTTCCTCCACCACCG3' | 366 | 152,381-152,746 | 100 |
| R:5'GAACCCTGTGAATTGCGTG3' |
| F:5'TCCTCCTAAATTTAAATTG3' | 680 | 152,938-153,617 | 100 |
| R:5'GGCTCCATTGCGTGTGCT3' |
| F:5'CAGTTTGGGAAGAGGTTT3' | 343 | 154,584-154,926 | 100 |
| R:5'GGATGGTCTACAGGGTTC3' |