**Mitochondrial genomics of human pathogenic parasite *Leishmania* Viannia *panamensis***

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**Supplementary File 1, Table 1.** Sequence of primers designed and used to close internal gaps and the ends of the maxicircle kDNA of *L. panamensis*.

|  |  |
| --- | --- |
| **ID** | **Sequence** |
| CLOSE\_MAXI\_F | AACAAATCCCCAACAATCACAAATA |
| CLOSE\_MAXI\_R | GGCTACAACTAATCCCATCCA |
|  |  |
| MAXI\_2\_F | TTTTTATGTATGGATACACGTTTTG |
| MAXI\_2\_R | CCTTTTCTTTCCTCTCCGCTT |
|  |  |
| MAXI\_5\_F | TGACATTTTGTGGATTGCGTA |
| MAXI\_5\_R | CATAATCAAACACCAATCACTGGC |
|  |  |
| MAXI\_3\_F | TTTTTATGTATGGATACACGTTTTG |
| MAXI\_3\_R | CCTTTTCTTTCCTCTCCGCTT |
|  |  |
| MAXI\_8\_F | TGAGATTTTGATTTAGGTTTTGTGA |
| MAXI\_8\_R | CCAGTAAATTTATCAGGTACTGCTTTT |
|  |  |
| MAXI\_11\_F | TGTGCCAGTGATTGGTGTTT |
| MAXI\_11\_R | AACCAGTAAATTTATCAGGTACTGCTT |
|  |  |
| MAXI\_13\_F | TGATAAAATTTTACCTGAATGG |
| MAXI\_13\_R | CACCAACTAAAGGGGTACTA |
|  |  |
| CLOSE\_GAP1\_F | AGGAATTTTATTTGGTTTTT |
| CLOSE\_GAP1\_R | TTTTAATTTCTAGTAGATTTGGA |
|  |  |
| CLOSE\_GAP2\_F | TTTGATTGAcATTTTATTGTAATGG |
| CLOSE\_GAP2\_R | TTCTCAACCACAGTATGCTGTTAAA |

**Supplementary File 1, Table 2.** A. List of the 21 minicircles of an infective strain of *L. panamensis* assembled in the present work. B. Comparison of the minicircles of *L. panamensis* assembled in 1999 by Sanger sequencing and the minicircles assembled in 2017 by 454 reported in the present work.

