**S1 Table. Primers used to amplify fragments of the genome of SARS-CoV-2 in the present study.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Primer** | **Sequence 5'-3'** | **Tm** | **Position according to the reference strain\*** |
| hCoV-19\_54F | TGCAAAGAATAGAGCTCGCACC | 61,3 | 15086 | 15108 |
| hCoV-19\_54R | CGCCACACATGACCATTTCACT | 61,7 | 15451 | 15429 |
| hCoV-19\_55F | TGCTCGCAAACATACAACGTGT | 61,6 | 15353 | 15375 |
| hCoV-19\_55R | AGCCACTAGACCTTGAGATGCA | 61,2 | 15771 | 15749 |
| hCoV-19\_56F | TTTGTGAATGAGTTTTACGCATATTTGC | 60,4 | 15660 | 15688 |
| hCoV-19\_56R | AGCTAAAGACACGAACCGTTCA | 60,2 | 16029 | 16007 |
| hCoV-19\_88F | ACCACAAATCATTACTACAGACAACACA | 61,3 | 24894 | 24922 |
| hCoV-19\_88R | GCAGCAGGATCCACAAGAACAA | 61,4 | 25324 | 25302 |
| hCoV-19\_89F | CTAGGTTTTATAGCTGGCTTGATTGC | 60,5 | 25213 | 25239 |
| hCoV-19\_89R | TGGAGAGTGCTAGTTGCCATCT | 61,2 | 25615 | 25593 |
| hCoV-19\_90F | TTCGGATGGCTTATTGTTGGCG | 61,8 | 25518 | 25540 |
| hCoV-19\_90R | GACTTGTTGTGCCATCACCTGA | 61,1 | 25924 | 25902 |

**\*** hCoV-19/Wuhan/WIV04/2019 (WIV04) (EPI\_ISL\_402124)