**Virologica Sinica**

**Supplementary Data**

**The mutational dynamics of the SARS-CoV-2 virus in serial passages in vitro**

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**Supplementary Table S1** List of all samples in whole genome sequencing and their quality characteristics.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **P** | **Sample** | **State** | **Mapped reads** | **Target reads** | **Mean depth** | **Uniformity** |
| **P0** | B5155 | Moderate quality | 569,729 | 99.9 | 4,271 | 79.5 |
| **P0** | B4926 | Moderate quality | 641,314 | 99.9 | 6,521 | 77.1 |
| **P0** | B5845 | Moderate quality | 995,654 | 99.9 | 22,418 | 97.2 |
| **P0** | A607 | High quality | 3,399,149 | 99.9 | 27,321 | 93.6 |
| **P0** | A818 | High quality | 4,119,785 | 99.9 | 8,932 | 90.1 |
| **P0** | A893 | High quality | 1,383,720 | 99.9 | 4,8 | 84.5 |
| **P0** | A6301 | Moderate quality | 774,583 | 99.9 | 4,916 | 79.8 |
| **P0** | A7326 | Moderate quality | 810,496 | 99.9 | 23,126 | 85.2 |
| **P0** | A6137 | High quality | 2,204,823 | 99.9 | 15,444 | 98.8 |
| **P0** | A4707 | High quality | 1,806,579 | 99.9 | 12,652 | 97.9 |
| **P3** | B5155 | Low quality | 250,929 | 99.5 | 338.2 | 97.9 |
| **P3** | B4926 | Moderate quality | 352,129 | 89.9 | 1,83 | 83.9 |
| **P3** | B5845 | Low quality | 285,513 | 97.3 | 556.7 | 97.3 |
| **P3** | A607 | High quality | 3,690,518 | 99.9 | 25,063 | 96.1 |
| **P3** | A818 | High quality | 9,172,810 | 99.9 | 62,594 | 96.1 |
| **P3** | A893 | High quality | 13,923,787 | 99.9 | 94,941 | 96.8 |
| **P3** | A6301 | High quality | 5,131,355 | 99.9 | 34,602 | 95.3 |
| **P3** | A7326 | High quality | 5,238,0,58 | 99.9 | 35,51 | 86.6 |
| **P3** | A6137 | High quality | 2,208,600 | 99.9 | 14,96 | 97.0 |
| **P3** | A4707 | Insufficient quality | < 200,000 |  |  |  |
| **P4** | B5155 | No replication |  |  |  |  |
| **P4** | B4926 | No replication |  |  |  |  |
| **P4** | B5845 | Low quality | 153,059 | 98.9 | 344.2 | 99.2 |
| **P4** | A607 | High quality | 3,225,087 | 99.9 | 22,466 | 99,4 |
| **P4** | A818 | High quality | 1,174,37 | 99.9 | 507.5 | 99.5 |
| **P4** | A893 | Moderate quality | 759,481 | 99.9 | 5,051 | 99.1 |
| **P4** | A6301 | Moderate quality | 648,135 | 99.9 | 2,252 | 99.0 |
| **P4** | A7326 | Insufficient quality | < 200,000 |  |  |  |
| **P4** | A6137 | High quality | 1,407,702 | 99.9 | 9,198 | 96.4 |
| **P4** | A4707 | High quality | 2,614,105 | 99.9 | 19,052 | 99.3 |
| **P5** | B5155 | No replication |  |  |  |  |
| **P5** | B4926 | No replication |  |  |  |  |
| **P5** | B5845 | No replication |  |  |  |  |
| **P5** | A607 | High quality | 3,505,365 | 99.6 | 24,345 | 99,6 |
| **P5** | A818 | High quality | 2,045,696 | 99.9 | 13,942 | 98.5 |
| **P5** | A893 | Insufficient quality | < 200,000 |  |  |  |
| **P5** | A6301 | High quality | 1,287,563 | 99.9 | 8,683 | 96,9 |
| **P5** | A7326 | High quality | 3,851,880 | 99.9 | 26,123 | 96.5 |
| **P5** | A6137 | Insufficient quality | < 200,000 |  |  |  |
| **P5** | A4707 | High quality | 5,515,904 | 99.9 | 16,881 | 99.3 |
| **P6** | B5155 | No replication |  |  |  |  |
| **P6** | B4926 | No replication |  |  |  |  |
| **P6** | B5845 | No replication |  |  |  |  |
| **P6** | A607 | Insufficient quality | < 200,000 |  |  |  |
| **P6** | A818 | High quality | 8,271,578 | 99.9 | 55,905 | 98.5 |
| **P6** | A893 | High quality | 1,188,697 | 99.9 | 8,018 | 97.6 |
| **P6** | A6301 | High quality | 3,124,939 | 99.9 | 20,825 | 98.1 |
| **P6** | A7326 | High quality | 2,094,962 | 99.9 | 14,12 | 97.9 |
| **P6** | A6137 | High quality | 4,152,052 | 99.9 | 27,67 | 99.0 |
| **P6** | A4707 | High quality | 6,324,621 | 99.9 | 42,796 | 98.1 |
| **P7** | B5155 | No replication |  |  |  |  |
| **P7** | B4926 | No replication |  |  |  |  |
| **P7** | B5845 | No replication |  |  |  |  |
| **P7** | A607 | High quality | 1,761,366 | 99.9 | 11,927 | 99,3 |
| **P7** | A818 | High quality | 1,325,485 | 99.9 | 12,568 | 99.9 |
| **P7** | A893 | Moderate quality | 746,583 | 99.9 | 5,006 | 99.5 |
| **P7** | A6301 | Insufficient quality | < 200,000 |  |  |  |
| **P7** | A7326 | Insufficient quality | < 200,000 |  |  |  |
| **P7** | A6137 | Insufficient quality | < 200,000 |  |  |  |
| **P7** | A4707 | High quality | 1,811,122 | 99.9 | 12,633 | 99.3 |
| **P10** | B5155 | No replication |  |  |  |  |
| **P10** | B4926 | No replication |  |  |  |  |
| **P10** | B5845 | No replication |  |  |  |  |
| **P10** | A607 | Low quality | 222,449 | 98.6 | 82.1 | 97.0 |
| **P10** | A818 | Moderate quality | 444,505 | 96.1 | 172 | 97.8 |
| **P10** | A893 | Low quality | 223,054 | 99.9 | 1,488 | 97.0 |
| **P10** | A6301 | Low quality | 246,227 | 99.9 | 1,624 | 97.3 |
| **P10** | A7326 | Low quality | 266,465 | 99.9 | 420.4 | 96.0 |
| **P10** | A6137 | High quality | 1,787,960 | 99.9 | 11,914 | 96.7 |
| **P10** | A4707 | High quality | 1,441,737 | 99.9 | 10,036 | 98.6 |

P, passage; State, quality state of the diverse sequences, divided into high quality (mapped reads > 300,000), moderate quality (mapped reads between 300,000 and 1,000,000), low quality (mapped reads between 300,000 and 200,000), insufficient quality (< 200,000 mapped reads, sequences have not been used for analysis) and no replication (no viral load in the sample, so sequencing possible). Quality control parameters generated were the number of mapped reads, mean depth and uniformity. The mean depth reflects how often a given nucleotide has been read in the sequencing run and is aimed to be at least 50 ×. Uniformity was aimed to be higher than 95% to strengthen the reliability of the diverse nucleotide sequence.