

Electronic Supplementary Material

Isolation, characterization, and phylogenetic analysis of three new severe fever with thrombocytopenia syndrome bunyavirus strains derived from Hubei Province, China

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Table S1. Primers used to sequence the complete genome of SFTSV isolates

| Primers | Sequences (5'-3') | Locations of primers |
|------------------|---------------------------|----------------------|
| S segment | | |
| S1F | ACACAAAGACCCCTTCATTTRG | 1–23 |
| S1R | ACACAAAGAACCCCCAAAAAAGGA | 1722–1744 |
| M segment | | |
| M1F | ACACARAGACGCCAACATGA | 1–22 |
| M1R | TCTCCCAGTTGTGAYGCATTCCCTC | 1767–1791 |
| M2F | GGCAACCAWGATGATGTTAGGAT | 1597–1619 |
| M2R | ACACAAAGACCGGCCAACACT | 3358–3378 |
| L segment | | |
| L1F | ACACARAGACGCCAGATGRAC | 1–22 |
| L1R | GAGACCACTGRACCACATTRCTG | 1549–1571 |
| L2F | GTGTCAATCTTGGAAAARGCAT | 1463–1487 |
| L2R | GAGCTTGAGACGAAATARGAC | 3313–3314 |
| L3F | GGTTGAAGTCAGCCCGYAGTCT | 2913–2934 |
| L3R | ATTCTRACTACTGGCTTATGGTGG | 4800–4824 |
| L4F | TTAGGGAGAGAACATTGTCAGGAG | 4485–4509 |
| L4R | ACACAAAGACCGCCCAGATCTTA | 6346–6368 |