

## Electronic Supplementary Material

# A new strain of Crimean-Congo hemorrhagic fever virus isolated from Xinjiang, China

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Table S1. Primers used to sequence the complete genome of the CCHFV isolate

Primers	Sequences (5'-3')	Locations of primers
S segment		
S1F*	TCTCAAAGAAACACGTGCCGC	1–21
S1R*	GACAAATCCCTGCACCA	653–670
S2F*	CCCAGTGAGCCGTGAACAT	628–646
S2R*	CAGGGTGCATGTAGATCCTG	1168–1187
S3F*	CTTTATGAGCTCTTTGCTGATG	1130–1151
S3R*	TCTCAAAGATATCGTTGCCGC	1652–1672
M segment		
M1F*	TCTCAAAGAAATACTTGCGGCAC	1–22
M1R*	ATGRTGTGYAYYYTGTGGTGT	504–524
M2F*	GTGCATGCAAGCCCATCACC	504–523
M2R*	CRTTGATCARCTGMARYCCTG	1201–1221
M3 F	TACTATGCCAAAGGGTCTC	1151–1170
M3 R	ATTTGACTGGGATGCTATCT	1901–1920
M4F*	TWYAAGCTDTGCGAGAACAGTGC	1833–1855
M4R*	CTNACAACCCARGGDATTCTTTC	2481–2503
M5F*	CGGARGGARAARGTRGAAGAAACY	2439–2462
M5R*	GTWGGTTTGAAGGTTGAYTGRACAT	3307–3331
M6F-2†*	CGTGGGGAGCAATCAATGTTC	3316–3336
M6R-2†*	GTGTGCAGCTCTGTAGCTTGC	4030–4050

To be continued

Primers	Sequences (5'–3')	Locations of primers
M7F*	GAAGGTTTTTTTTGAYYTRATGCATG	3951–3975
M7R*	GCTCTGTGGWTGSTCAAGYTT	4719–4739
M8F*	AGCTGCASYRAAGAWGAYACACAA	4680–4703
M8R*	TCTCAAAGATATAGTGGCGGCAC	5345–5367
L segment		
L1 F	TCTCAAAGATATCAATCCCC	1–20
L1 R	GAGTGCTAATGCAAGGTCTT	652–671
L2F*	CTCTCAGAATACTGCCACAG	538–557
L2R*	GTTGATAACATGACGCCAAGTG	1123–1144
L3F*	CCCTGGAACAGGAATAGAAAAG	1052–1072
L3R*	ATTGCCCTGCCTGAGGTAC	1666–1684
L4–F1	ACTTCTCGGCTTATCACATT	1500–1519
L4–R1	ATTCAACGGAGTCTCAGGTA	2287–2306
L5 F	CAAACCAAGTCTGACCATGT	2048–2067
L5 R	TCTGTCCTTATTTTCCCGTC	2571–2590
L6F*	GACTATGGAGAGAGGGGAATAG	2463–2484
L6R*	TGACTTGATGTCTTCACTTAACC	3130–3152
L7 F	CTACCCGTTAGTTTGAACA	2934–2953
L7 R	CTATCTTGGGACACCTCTTG	3311–3330
L8 F	GATTGAGCTGCTTGCTTATA	3218–3237
L8 R	GACCTTGGCACAGAACACTT	3723–3742
L9 F	CAACCTATGCAAAAGGAGTA	3661–3680
L9 R	TATGATGAGCCAAGGACAGC	4287–4306
L10 <sup>+</sup> F	AGTAAAGGTAAGGCATTGTG	4154–4173
L10 <sup>+</sup> R	GTTTATTCTGTTGTTGGGAG	4616–4635
L11 <sup>+</sup> F	ACCTAGTTTATGGCTTCCTT	4573–4592
L11 <sup>+</sup> R	ACTGGCAGATGTCTGTTATT	5309–5328
L10F*	TGCCCAAATGTGAGAAAAGC	5076–5095
L10R*	GAGYYTCTTCTTYAAGCTTCC	5889–5909
L11F*	CAATCTCTTCHTCAGTYAAAGG	5869–5890
L11R*	CTATCTTTGTYTGATGTAGYAGC	6614–6636
L12F*	GAYYTRCACAARACCACTGACG	6588–6609
L12R*	CTGACCCATATGGTTGTARCTGTT	7473–7496
L13 F	TAGACAGTTGGGAAGGAAAT	7396–7415
L13 R	TAAAGGCAGTGTTGGTGATA	7955–7974
L14 F	CTTATCACCAACACTGCCTTTA	7953–7974
L14 R	AAACTCCCAACCTTTCCAAC	8699–8718
L15 F	CATTTGGAGGAGAAGGAACT	8587–8606
L15 R	AAGGCTCTTTGACAGTGGTAT	9106–9126
L16 <sup>+</sup> F	GATGGTCCACCAAGCACAGC	8980–8999
L16 <sup>+</sup> R	TGCCCTTTAGCATGTAGAAA	9656–9675

To be continued

Primers	Sequences (5'–3')	Locations of primers
L17 F	TACAACAAGCAAAGCCAACC	9628–9647
L17 R	GTATGTGAACTTCCCAGACC	10129–10148
L16F*	CTGTRAAACGAGATTCTGAACGC	10000–10022
L16R*	ACCTCCTGATTTGAGGTACTTGTG	10794–10817
L18 <sup>+</sup> F	AGACTACATAACCACGAGAATC	10564–10584
L18 <sup>+</sup> R	CTCTGGAAATAGAAGGCACA	11277–11296
L19 F	GTTAATGAACTTAATCAGCCAGTG	11183–11206
L19 R	ACCCGTCAACATCAGAATCAAATC	11718–11741
L18F*	CAAAGCCTGARAGAGTGGTYATRG	11473–11496
L18R*	TCTCAAAGAAATCGTTCCCCCCAC	12133–12156

Note: \*Primers were used in reference to a previous study of CCHFV genome announcement (Zhou et al., 2013b).