

26155	4b	G	•	•	•	•	•	•	•	A	•	A	•	A	A
26168	4b	C	•	•	•	•	•	•	•	•	•	T	•	•	•
26186	4b	C	•	•	•	•	•	•	•	•	•	•	•	•	C/G ^g
26339-27064	4b,5	No Δ^f	•	•	726nt Δ^{f1}	•	•	•	•	•	726nt Δ^{f1}	•	•	•	•
27383	5	C	•	•	C/T ^g	•	•	•	•	•	•	•	•	•	•
27863	M	T	C	•	•	•	C	C	•	C	•	C	C	C	C
28229	M	C	•	•	G	•	•	•	•	•	•	•	•	•	•

Supplementary Table 1. Genetic differences in Jordan Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak genomes compared with four contemporaneous undeleted genomes from Riyadh, Saudi Arabia.

^a Specimen type: nasopharyngeal swab (NPS); bronchoalveolar lavage (BAL); sputum; tracheal aspirate (Aspirate).

^b Real-time reverse transcription-polymerase chain reaction (rRT-PCR) cycle threshold (Ct) value.

^c Genome nucleotide position numbering based on MERS-CoV strain Hu/EMC/2012, GenBank accession no. JX869059.2.

^d Open reading frame.

^e Reference consensus sequence of Hu/Riyadh-KSA-16121/2015 (KU851860), Hu/Riyadh-KSA-16120/2015 (KU851861), Hu/Riyadh-KSA-16117/2015 (KU851862), Hu/Riyadh-KSA-16098/2015 (KU851864).

^f Deletion (Δ); superscript numbers indicate genome assignment.

^g Mixed base at indicated position.