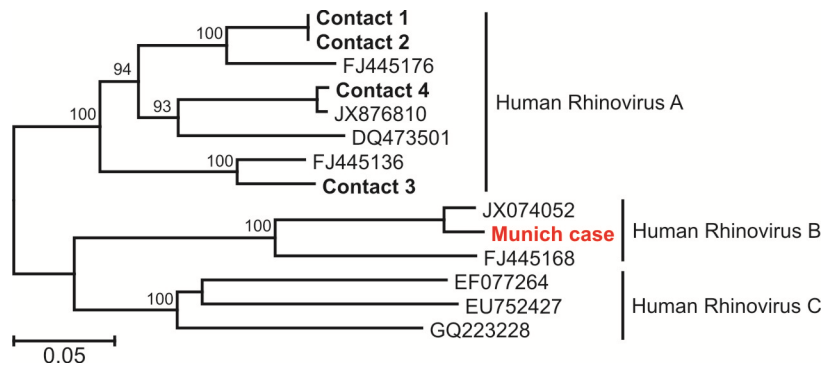


Supplementary webappendix

This webappendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Drosten C, Seilmaier M, Corman VM, et al. Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection. *Lancet Infect Dis* 2013; published online June 17. [http://dx.doi.org/10.1016/S1473-3099\(13\)70154-3](http://dx.doi.org/10.1016/S1473-3099(13)70154-3).



Supplementary Figure 1.

Phylogeny of partial VP4/VP1 sequences of rhinoviruses detected in the cluster, along with reference sequences. The tree was inferred using the Neighbor-Joining algorithm in MEGA. The scale bar represents corrected percent nucleotide distance. The sequence found in the MERS-CoV patient is printed in red, those determined in four symptomatic contact patients are shown in boldface (Contact 1 - 4). The dataset comprised 410 nucleotide positions (nt 619 –1028 in the human rhinovirus 7 reference genome, FJ445176). Values at deep nodes represent support in 1,000 bootstrap replicates.