THE LANCET Infectious Diseases

Supplementary webappendix
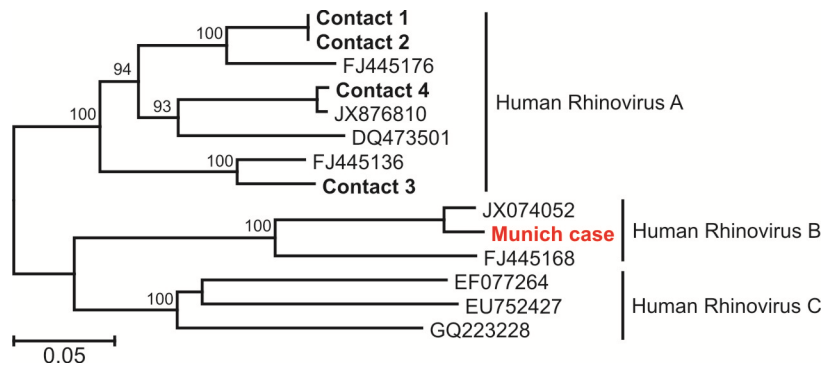
Supplementary Figure 1.
Phylogeny of partial VP4/VP1 sequences of rhinoviruses detected in the cluster, along with reference sequences. The tree was inferred using the Neighbor-Joining algorithm in MEGA. The scale bar represents corrected percent nucleotide distance. The sequence found in the MERS-CoV 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.