



Figure S1 Phylogenetic tree of *S* gene of MERS CoV built with Neighbor Joining method using MEGA6.0 and tested with 1,000 bootstrap replicates. 50 strains with high similarity isolated from Saudi Arabia and United Arab Emirates in 2013–2014 were compressed in the phylogenetic tree of *S* gene.

Table S1 The differences between three MERS CoVs

	Site (No.nt)											
	5632	5982	6142	8851	18931	21494	21720	22899	23159	24239	25824	25965
KT036372	T	G	T	G	A	C	A	G	C	T	A	C
KT006149	C	C	T	T	A	G	A	G	C	T	A	C
KT029139	C	G	G	G	G	C	C	C	T	C	T	T

The number of sites is based on the sequence of KT036372.