

## Legend of the Supplementary Figures

### Supplementary Figure 1:

Geographic distribution of rubella virus genotypes based on collection countries and likely-source countries between 2010 and 2014. The top panels show the distribution for the period 2010-2014 period. The panels below show the distribution year per year. The number of sequences analyzed by country as well as the genotype is color coded according to the legends shown at the bottom of the figure. Pie charts show the genotype distribution for each country.

### Supplementary Figure 2

Phylogenetic tree of rubella viruses of 1J genotype: a neighbor joining tree was generated with Mega 6 using the maximum composite likelihood nucleotide substitution model (Kumar *et al.*, 2004; Saitou & Nei, 1987; Tamura *et al.*, 2011). The phylogenetic inference was tested with the bootstrap method with 1000 replications. Bootstraps values greater than 70% are shown. Sequences of viruses collected after 2010 are identified with a black circle. The tree was rooted with RVi/Pennsylvania.USA/64VACC\_JF727653.2.

### Supplementary Figure 3:

Analysis workflow of genotype 1G. The analysis process leading up to the designation of primary, secondary and tertiary lineages within the 1G genotype is described. Reasons for splitting a genetic group are boxed and resulting groups are circled. All the relevant information is summarized in Table 2. \* The tertiary lineages 1G-L2b1, 2 and 3 collected Uganda were previously described by Namuwulya *et al.* (Namuwulya *et al.*, 2014)

### Supplementary Figure 4

Phylogenetic tree of rubella viruses of 1E genotype, as indicated in Supplementary Figure 2.

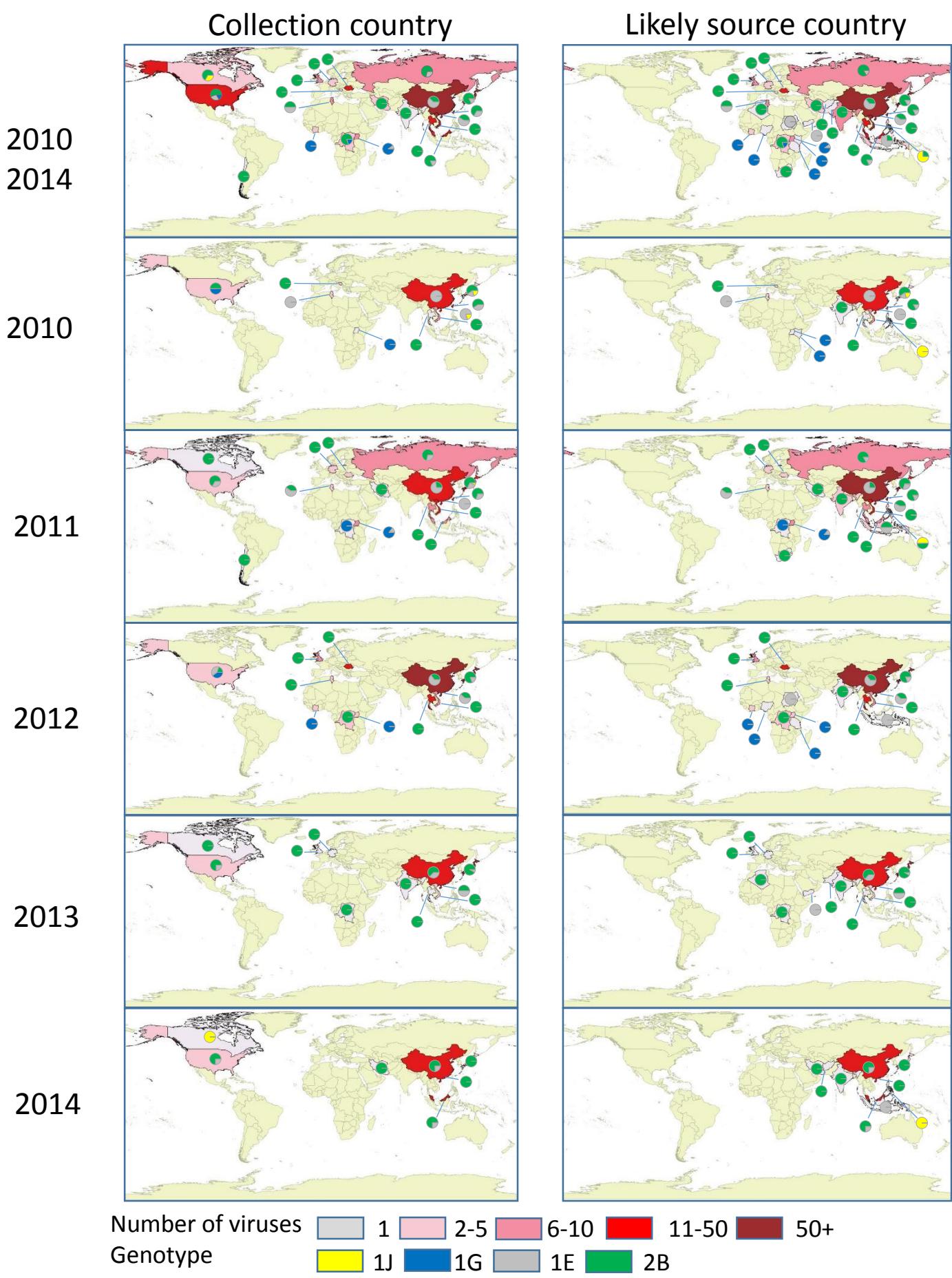
### Supplementary Figure 5

Phylogenetic tree of rubella viruses of 2B genotype: as indicated in Supplementary Figure 2.

Supplementary Table 1: List of known imported cases

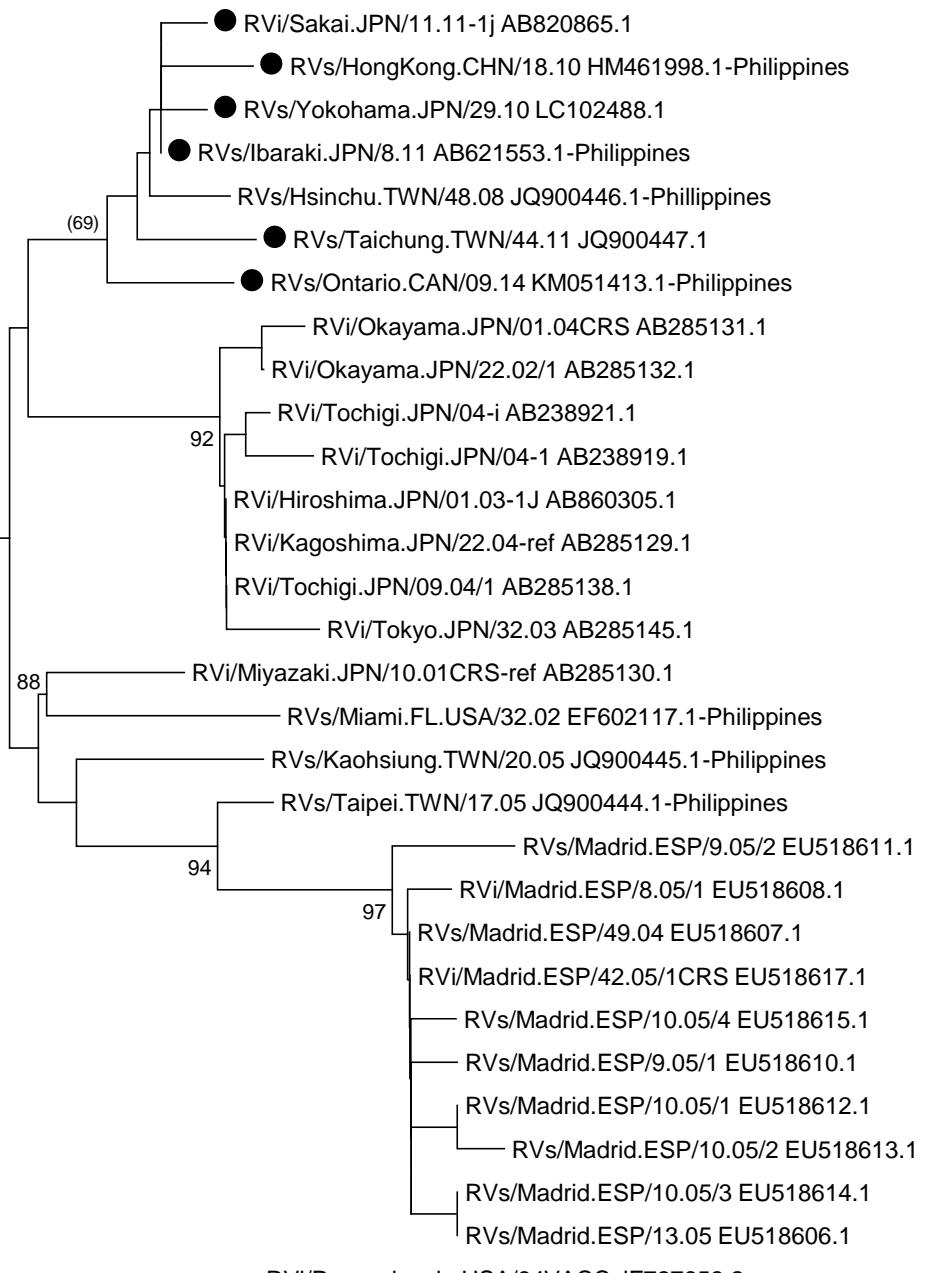
Collection Country	Source Country	Year	Genotype	CRS *
Taiwan	China	2010	1E	
Taiwan	China	2010	1E	
Taiwan	China	2010	1E	
Taiwan	China	2010	1E	
Taiwan	China	2010	1E	
United States	India	2010	2B	
United States	Kenya	2010	1G	
Hong Kong	Philippines	2010	1J	
Russia	China	2011	1E	
Taiwan	China	2011	1E	
Taiwan	China	2011	1E	
Taiwan	China	2011	1E	
Taiwan	China	2011	1E	
Chile	India	2011	2B	
United States	India	2011	2B	
United States	Indonesia	2011	1E	
Hong Kong	Indonesia	2011	2B	
Japan	Philippines	2011	1J	
Canada	Philippines	2011	2B	
United States	South Africa	2011	2B	
Taiwan	Vietnam	2011	1E	
United States	India	2012	2B	
United States	Indonesia	2012	1E	
United States	Nigeria	2012	1G	yes
United Kingdom	Romania	2012	2B	
United States	Sudan	2012	1E	yes
United States	Tanzania, United Republic of	2012	1G	yes
United States	Algeria	2013	2B	
Canada	Japan	2013	2B	
United States	Japan	2013	2B	
United States	Pakistan	2013	2B	
United States	Yemen	2013	1E	yes
United States	Afghanistan	2014	2B	
United States	China	2014	2B	
United States	India	2014	2B	
United States	Indonesia	2014	1E	
Canada	Philippines	2014	1J	

\*: sequence obtained from a case of congenital rubella syndrome (CRS)



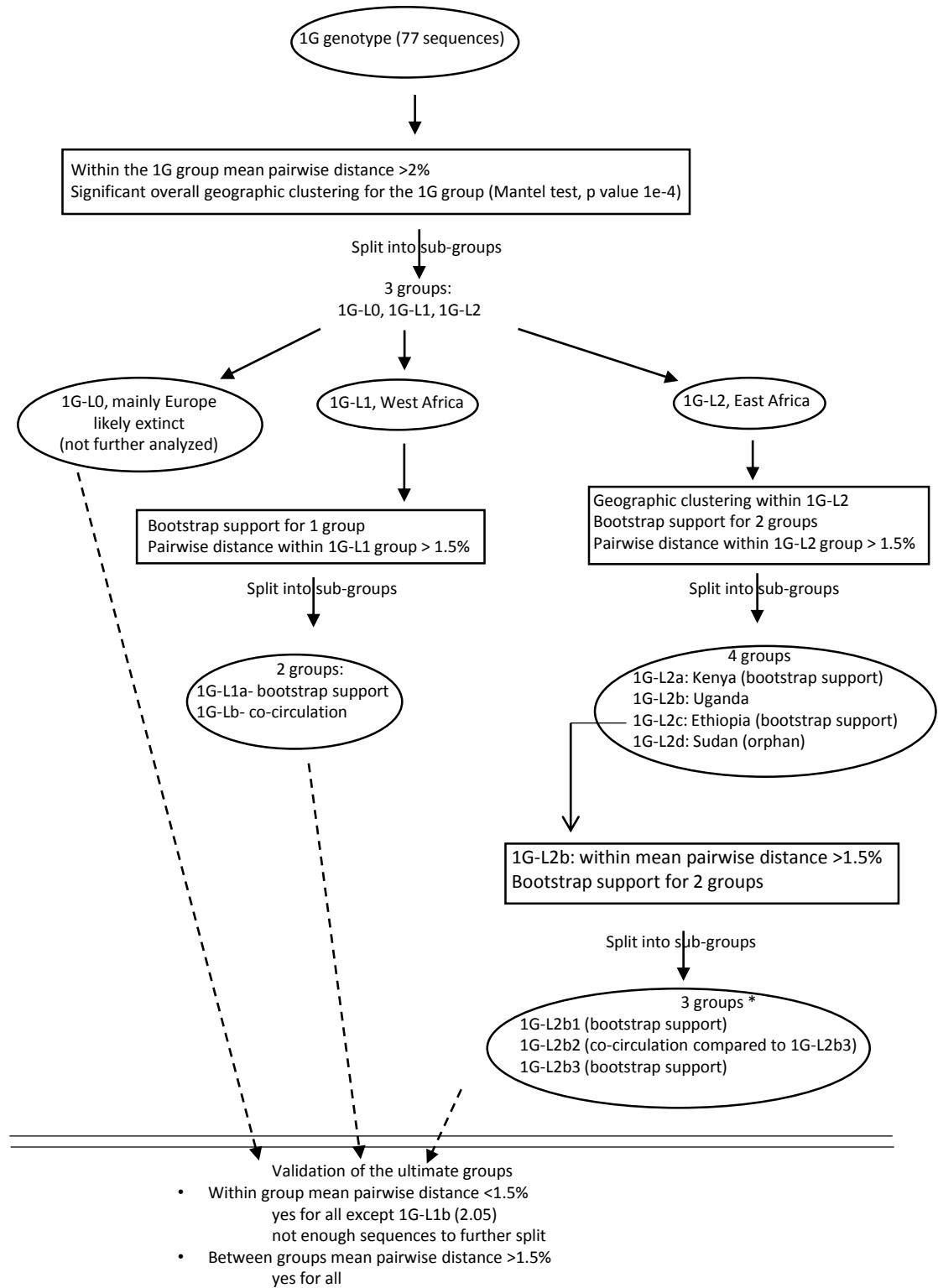
Supplementary Figure 1

1J



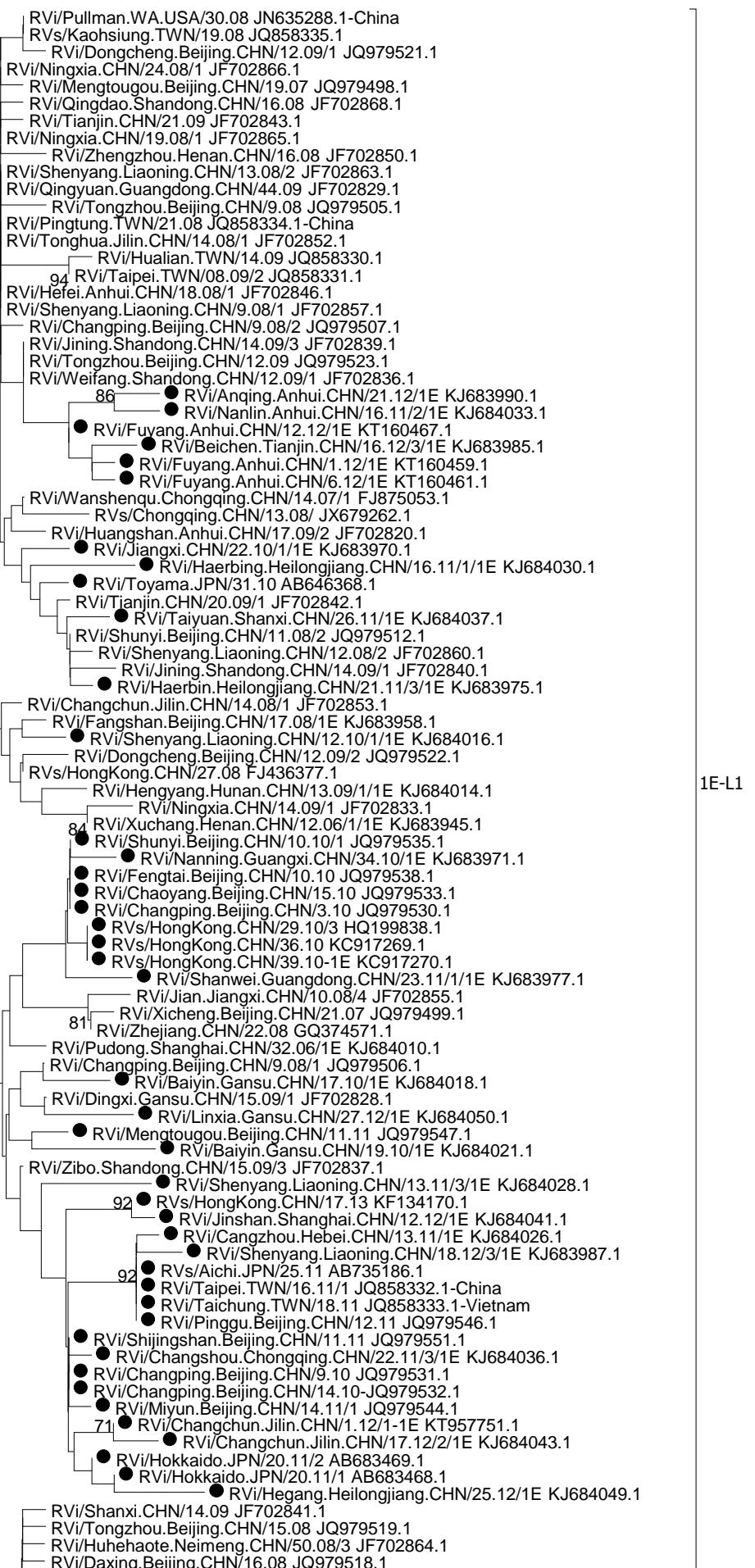
0.005

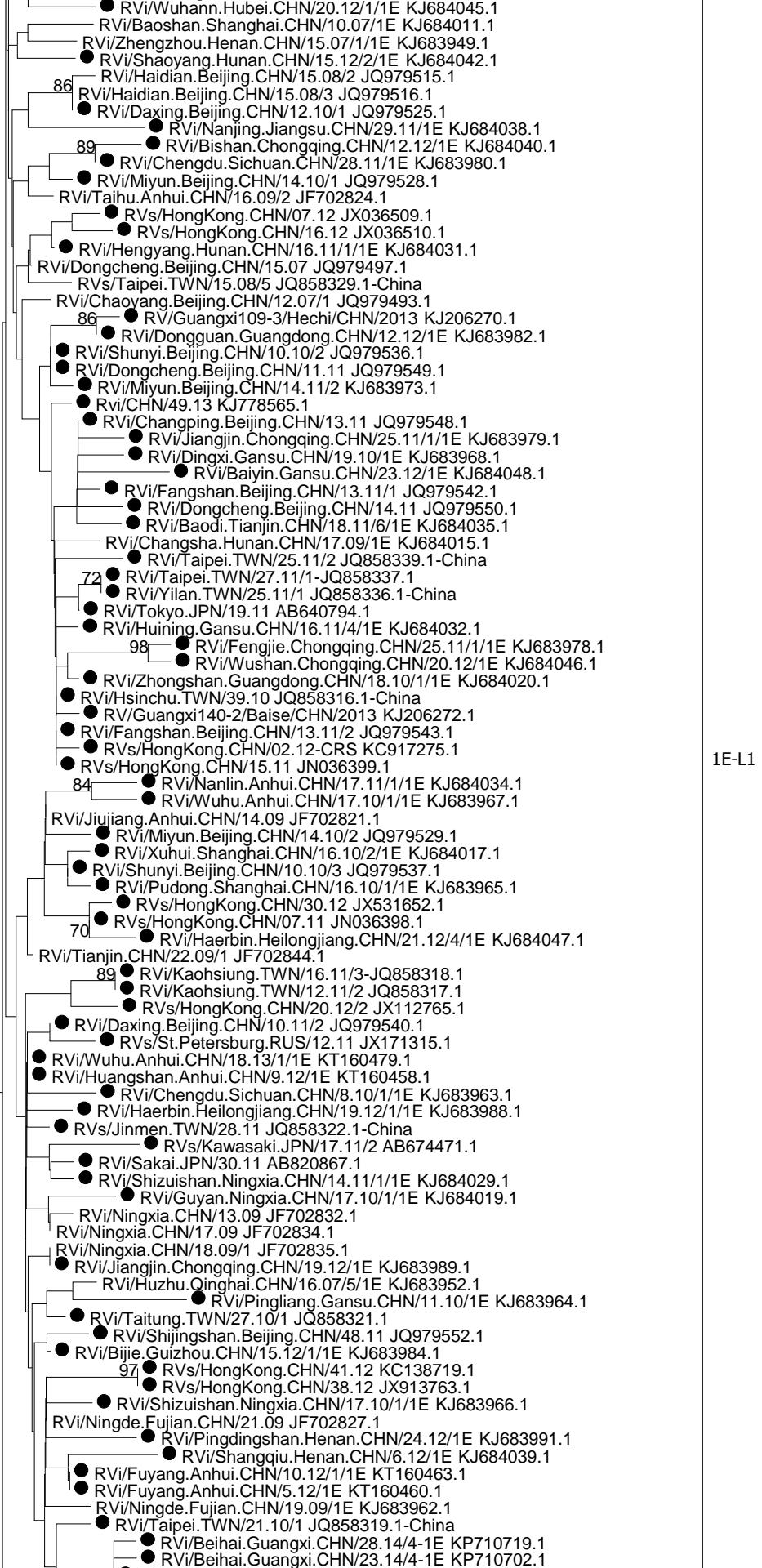
Supplementary Figure 2

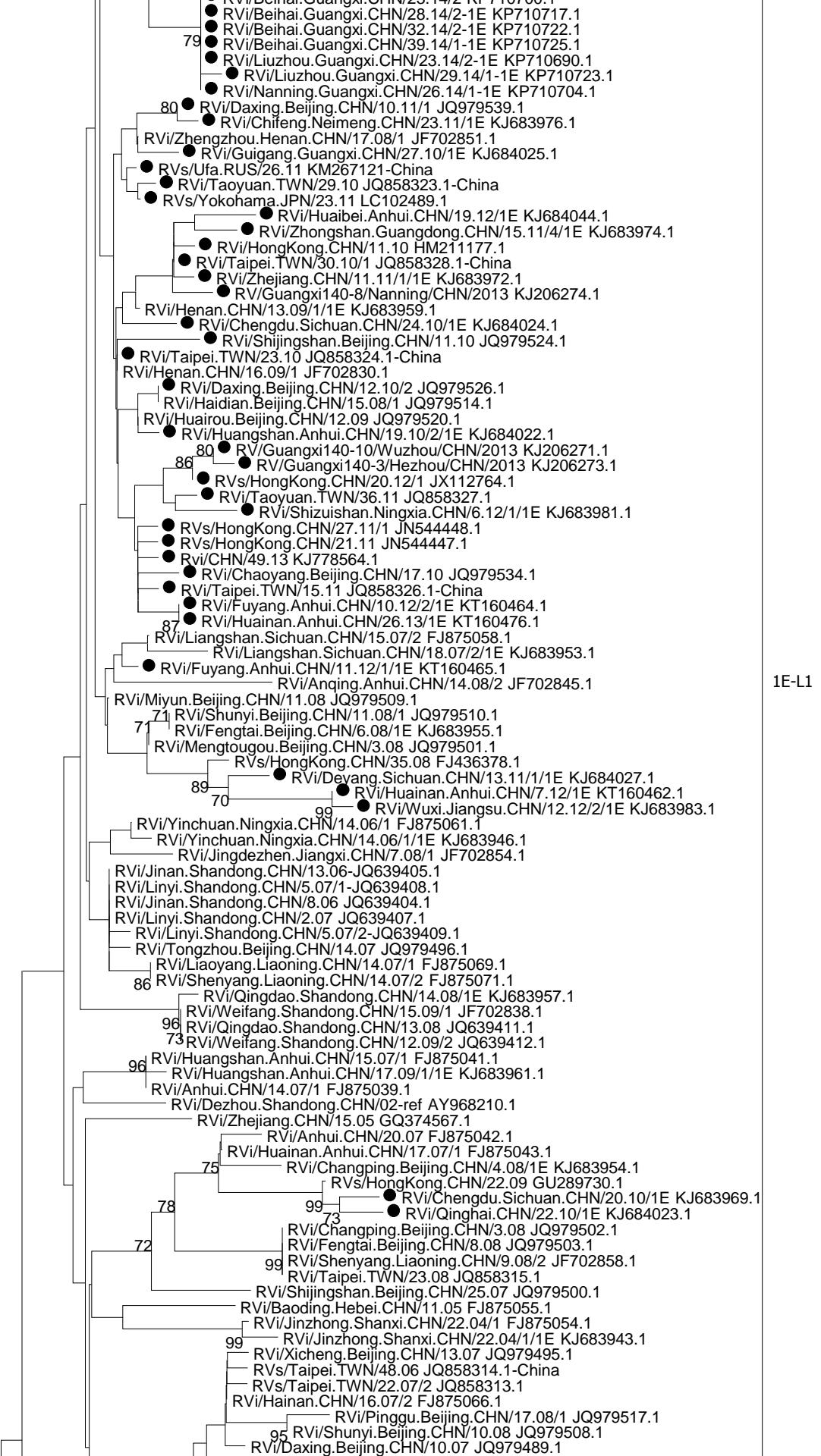


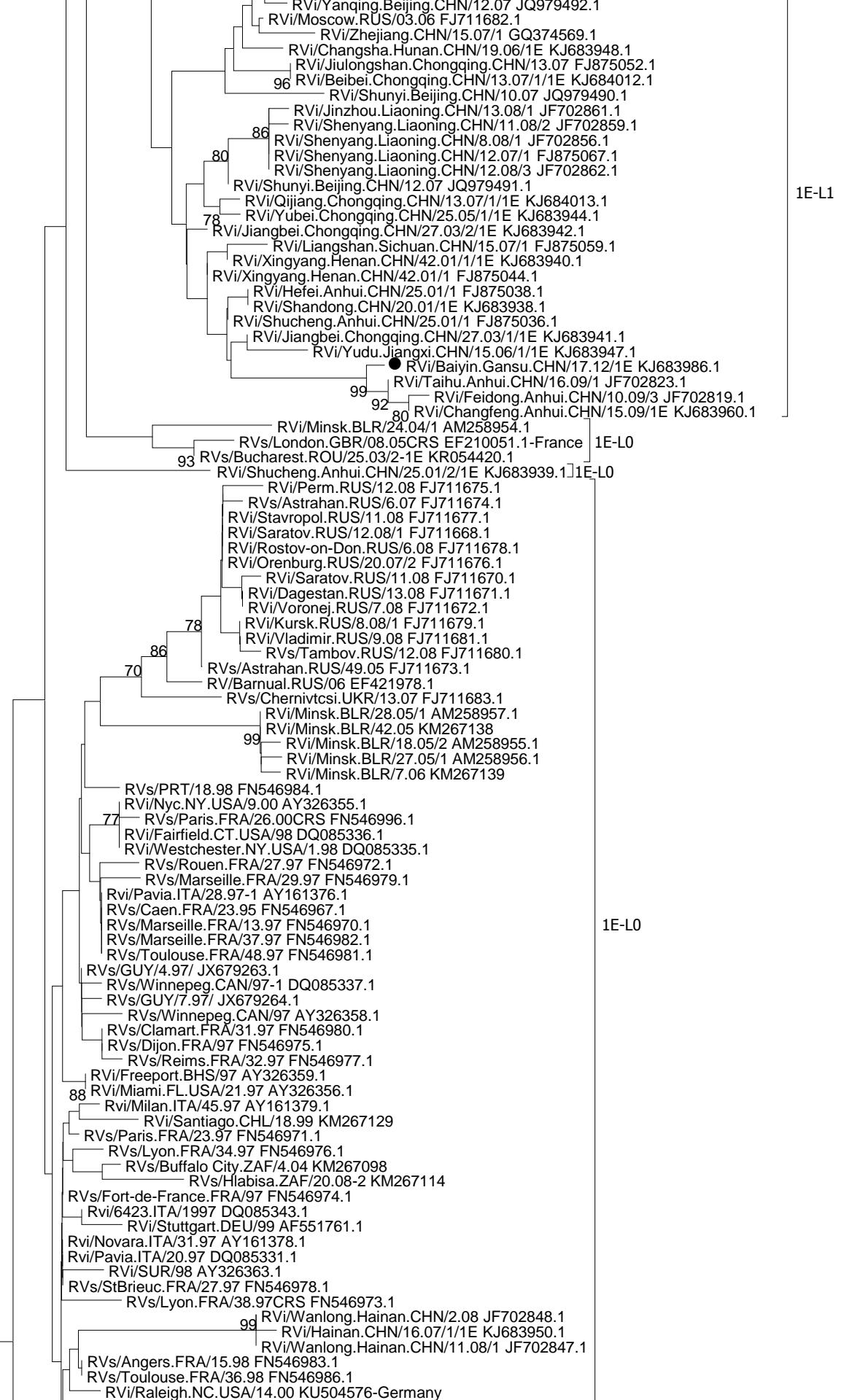
Supplementary Figure 3

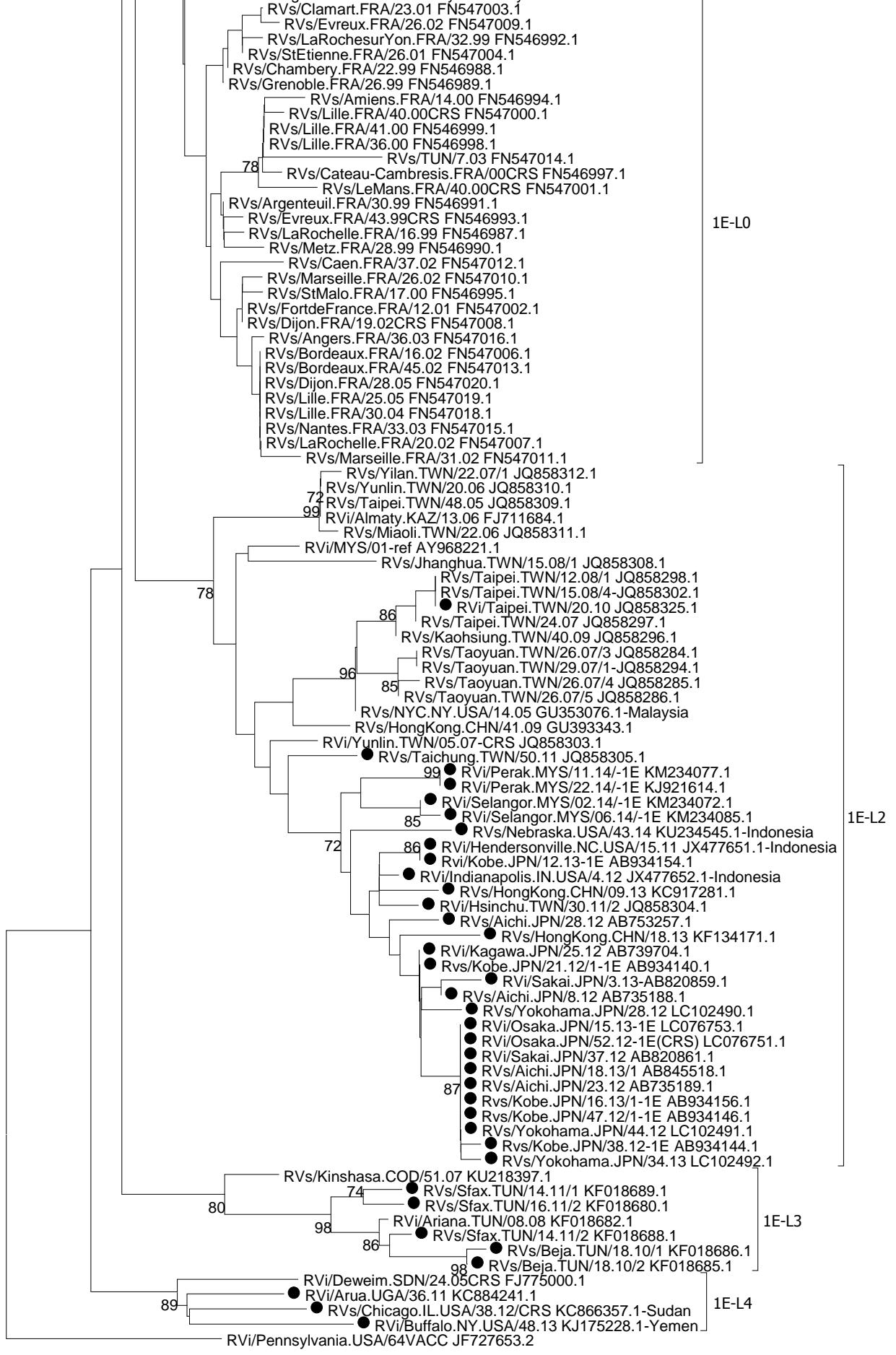
# Supplementary Figure 4





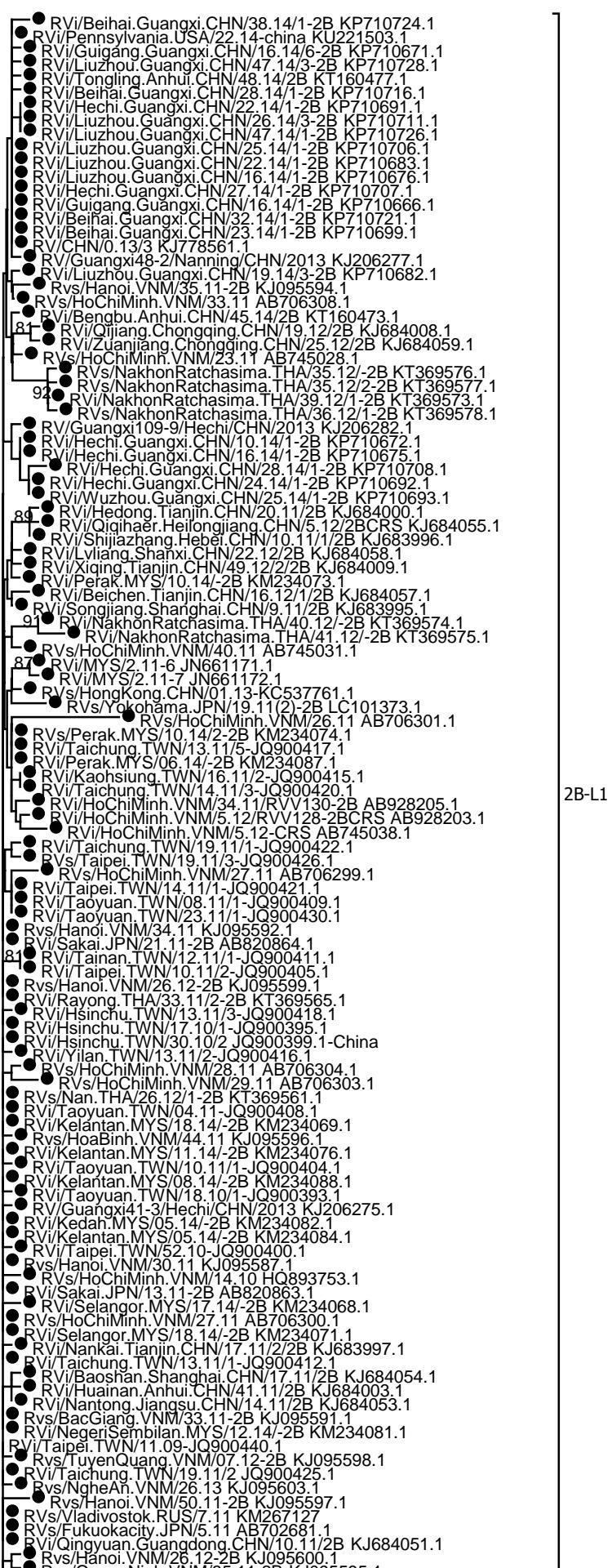


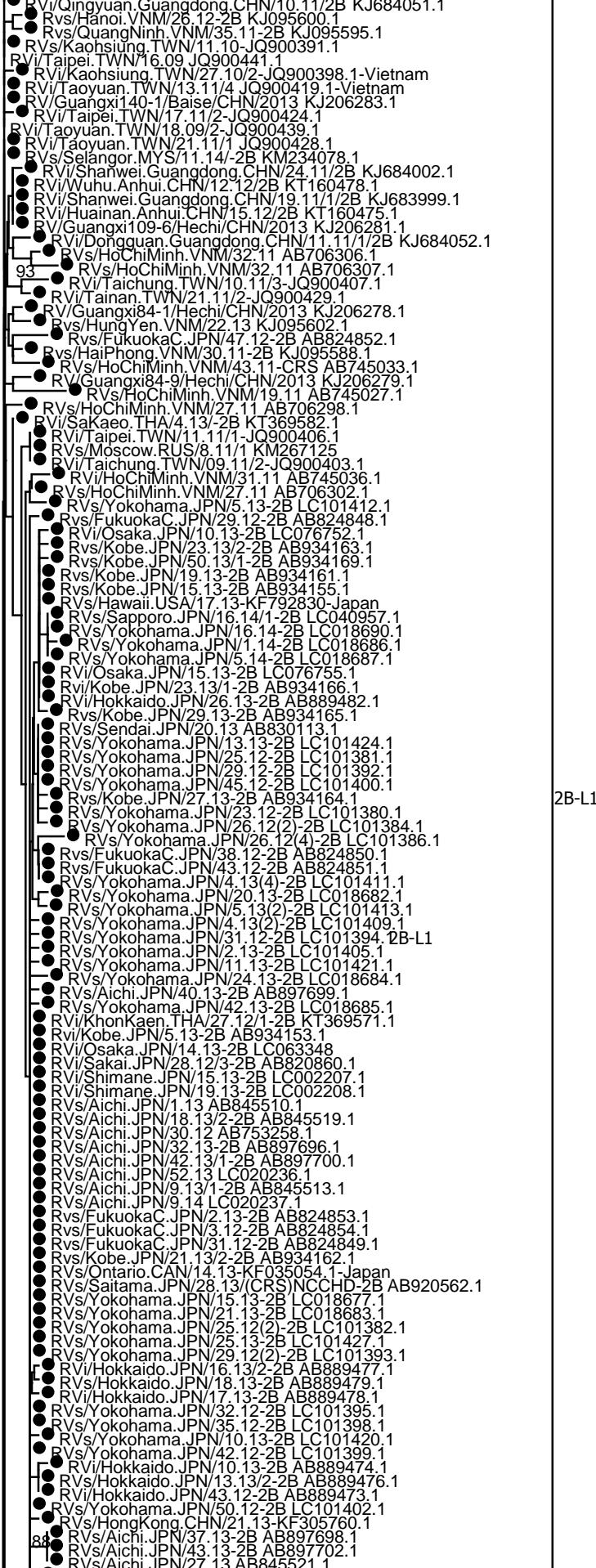


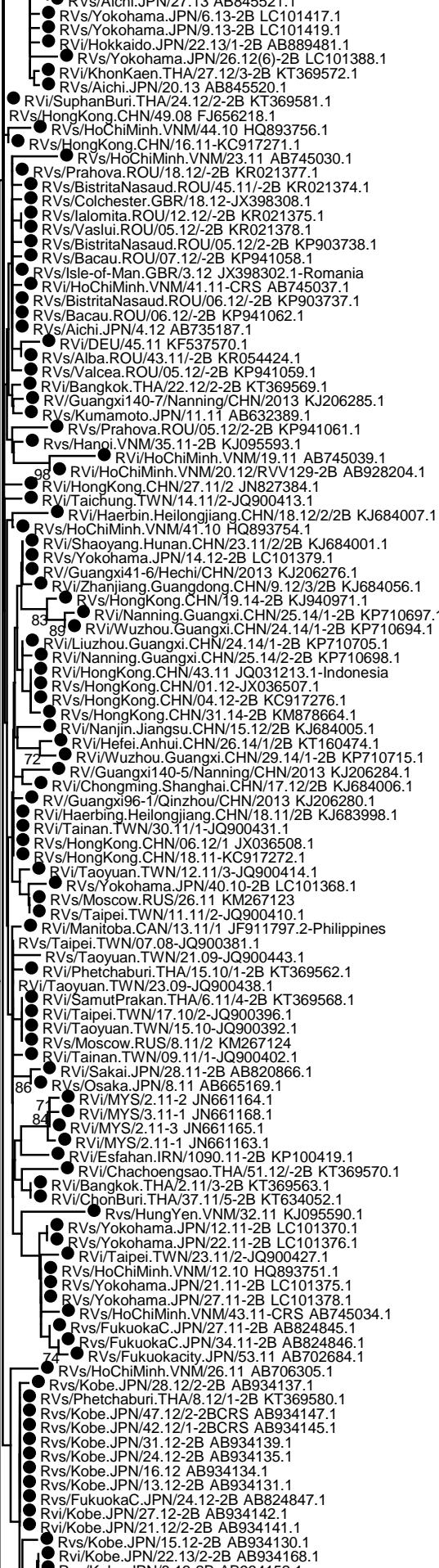


0.005

# Supplementary Figure 5







2B-L1

