



Supplementary figure 1. Genetic diversity of RSV sampled in different regions of the world (based on 1491 sequences available in the GenBank database). Genetic distance was calculated from the matrix containing squared root of the pairwise distances using `dist.alignment` function from “`seqinr`” package [47]. Black line in the box represents the median value, the length of the box represents the interquartile range (IQR), i.e. the difference between the lower (Q1) and the upper (Q3) quartile