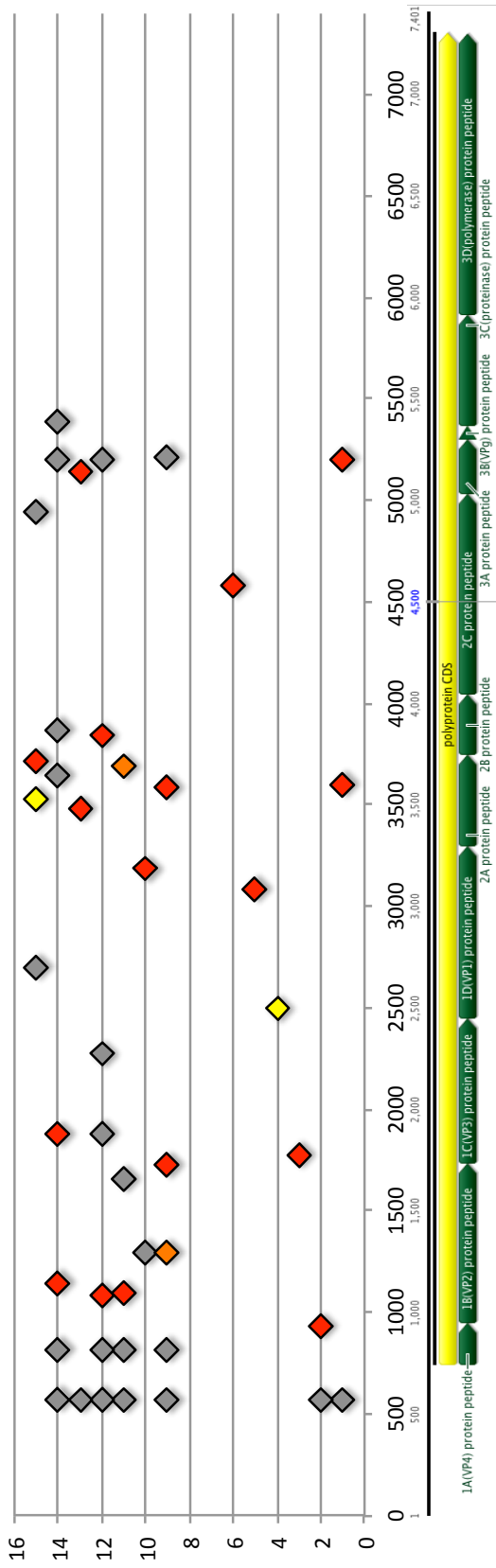


## SUPPLEMENTARY FIGURE S1

### Results from the GARD recombination analysis

On the y-axis the numbers for the individual GARD analyses, which can be seen in Supplementary Table 2. Along the x-axis, genome positions and layout of an SVDV genome (H/3 76 D00435, Japan 1976). All recombination signals for all analyses are shown. Grey indicates no significant support from the Kishino-Hasegawa test in GARD. Yellow, orange, and red, indicate support at  $p = 0.1$ ,  $p = 0.05$  and  $p = 0.01$  respectively (see Supplementary Table 2).

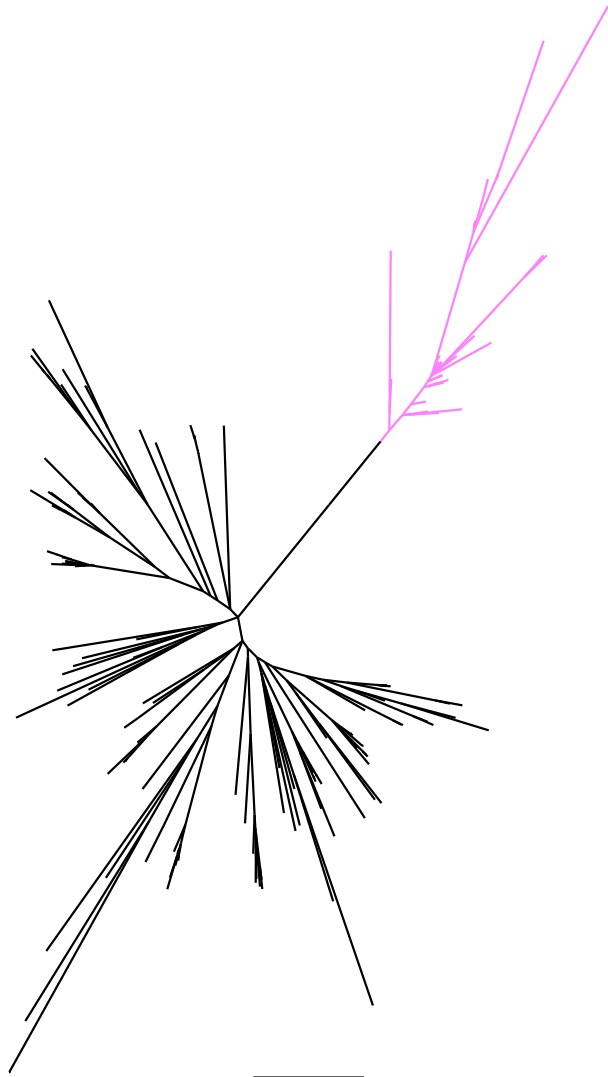


## SUPPLEMENTARY FIGURE S2

### Trees from the maximum likelihood phylogenetic analysis

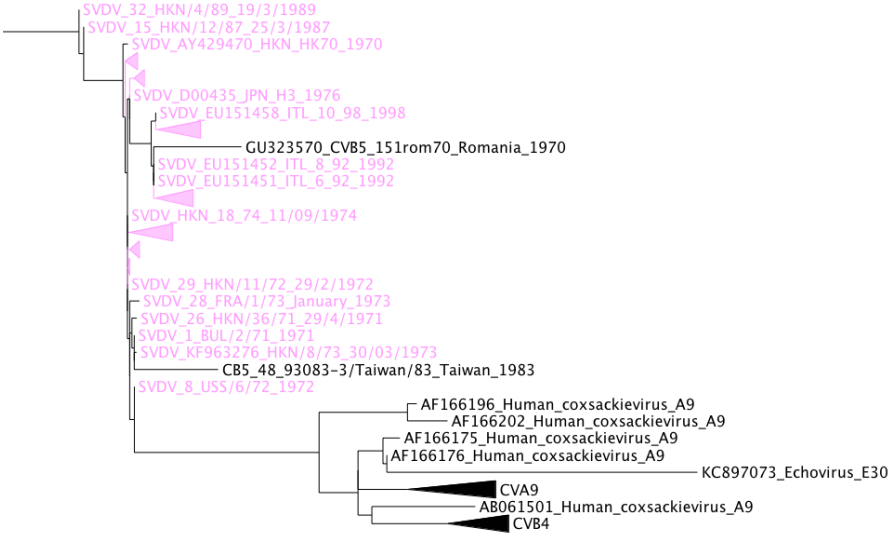
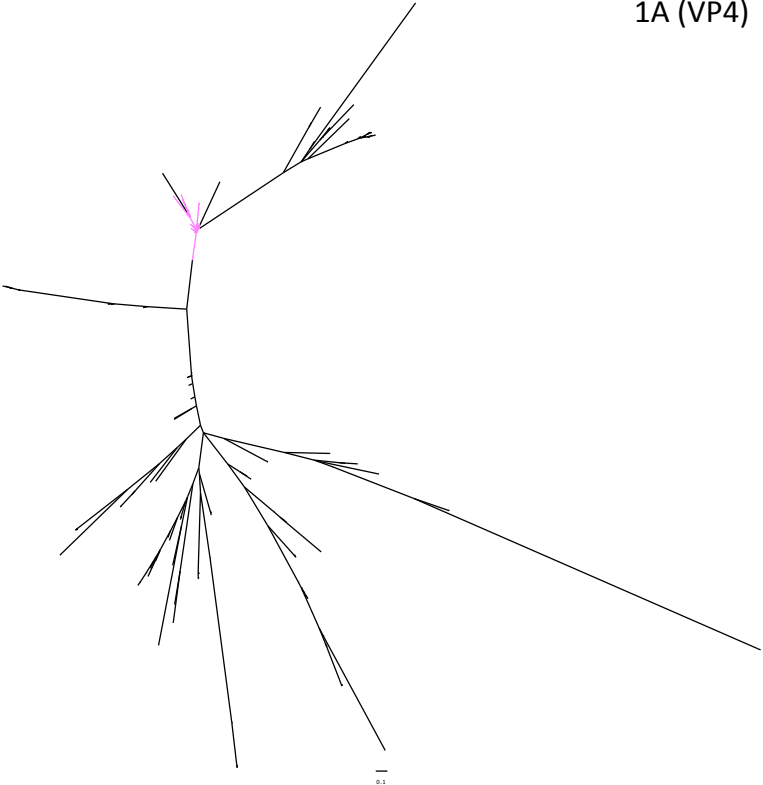
Results from the phylogenetic analyses of 8 of the 9 chosen genomic sections (see Fig. 1 for 3D section) ordered according to their genomic positions. All show an unrooted tree with no taxa designations, except that branches leading to an SVDV isolate are coloured pink. The branch leading to the root of the SVDV cluster is shown in black, like the remainder of the tree. When in some analyses part of the branch leading to the SVDV cluster is pink, this is because there is an SVDV sequence (i.e. ITL/1/66) at the root of the cluster at the beginning of the colour change. The unrooted trees give an immediate overview of the relation between SVDV and all other sequences in the analysis, including relative (and if conferring with the 0.1 substitution per site bar, also absolute) distance to the nearest neighbours. A single analysis, that of 1A (VP4) does not show SVDV as monophyletic – it is clear, from the unrooted tree that this analysis suffers from some very long branches. Even though the analysis only contains 180 taxa in total (see Supplementary Table 5), it is clear that more sequences could have been left out. Furthermore, the only closely related sequences match with what is found for the other 3 capsid protein coding sections. All sections, except 5' UTR, are also illustrated with taxa designations and support values (aBayes) for the closest related sequences to the SVDV cluster. These are cut-outs of mid-point rooted versions of the trees. The 5'UTR is not illustrated in this manner, since the structure and taxa of the tree renders such a transformation uninformative (see main text).

5'UTR

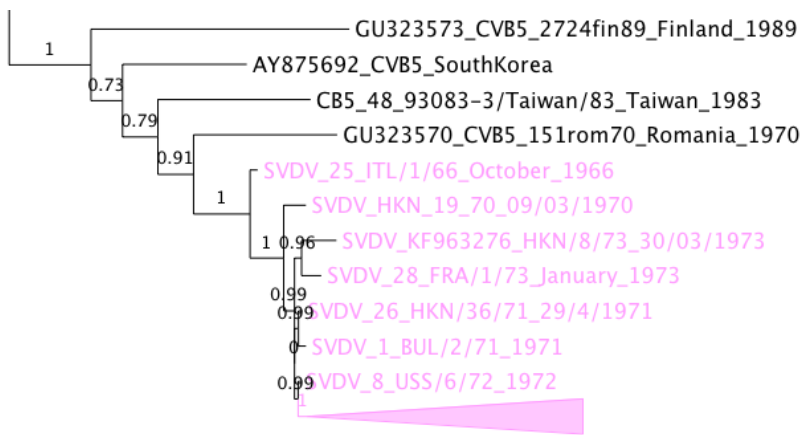
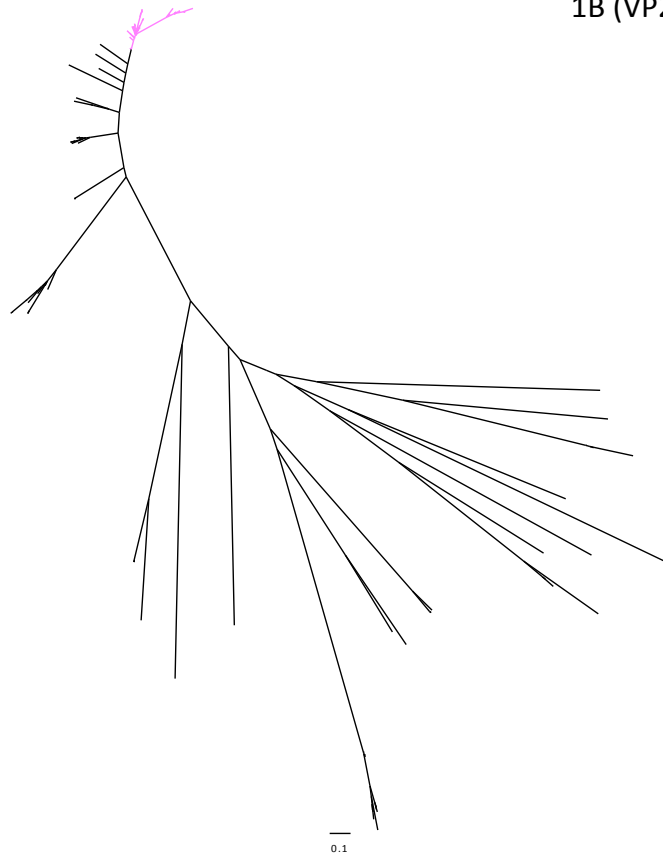


0.1

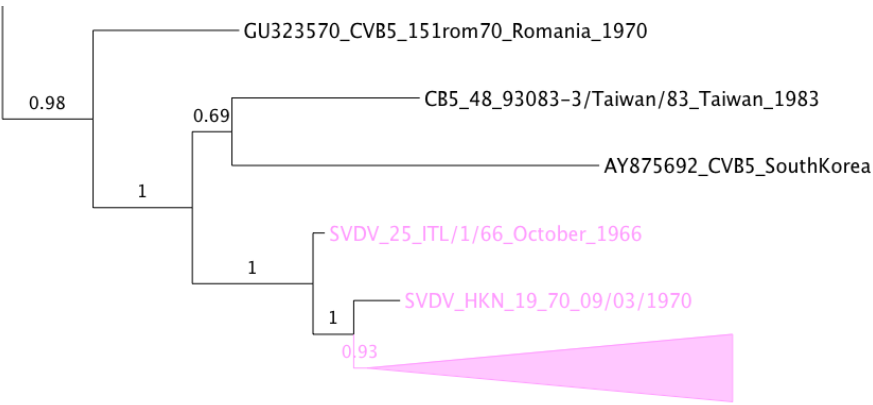
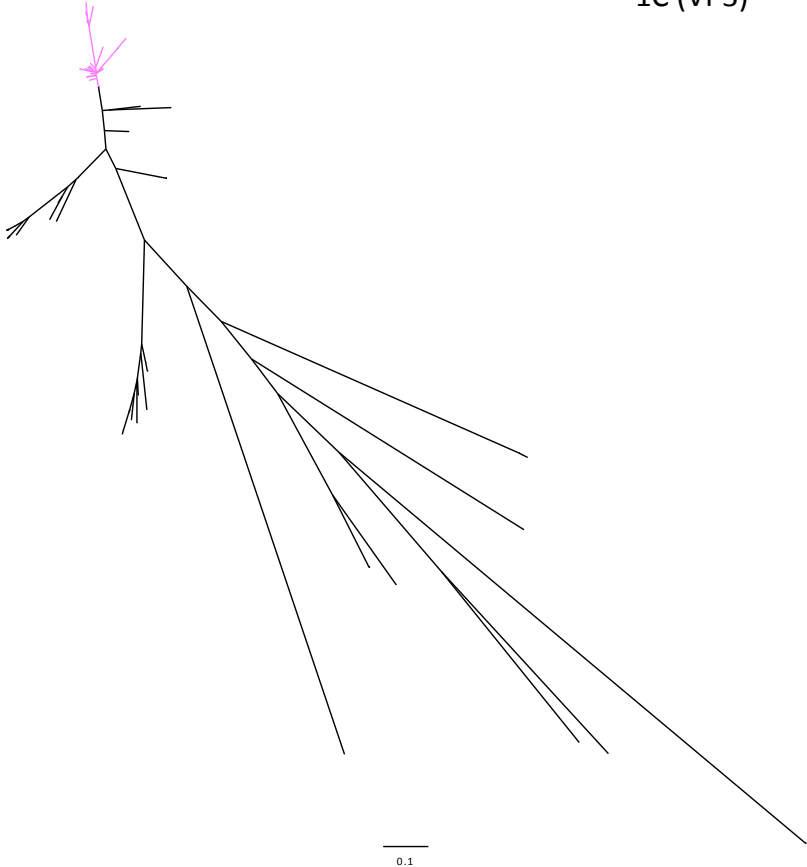
1A (VP4)



1B (VP2)



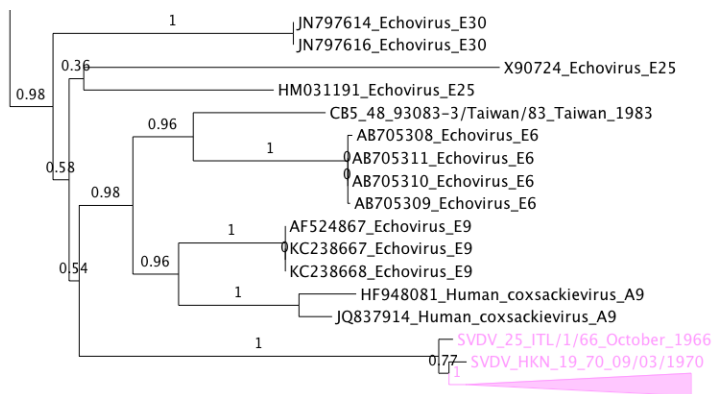
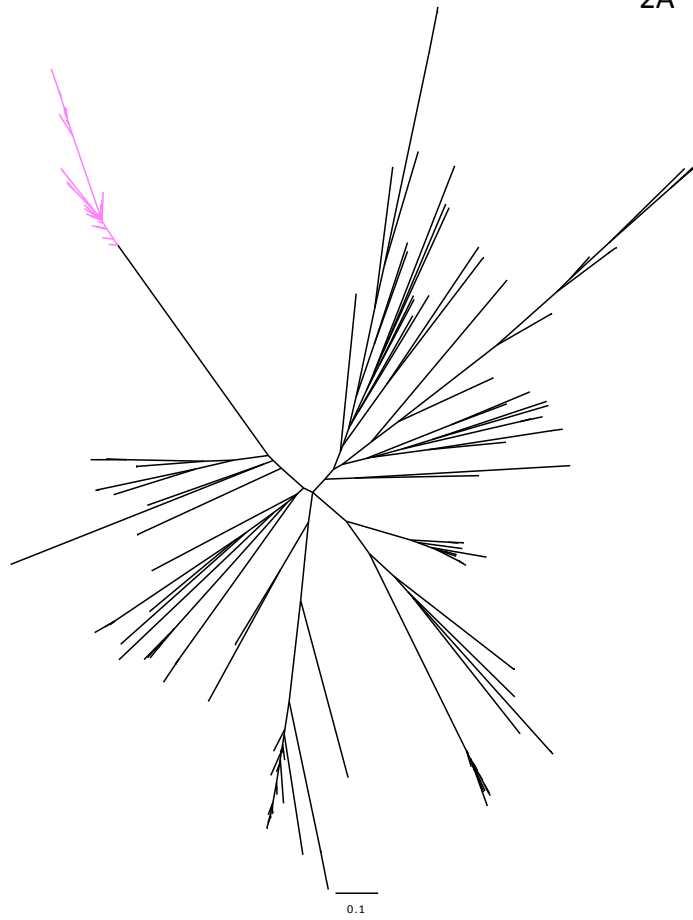
1C (VP3)



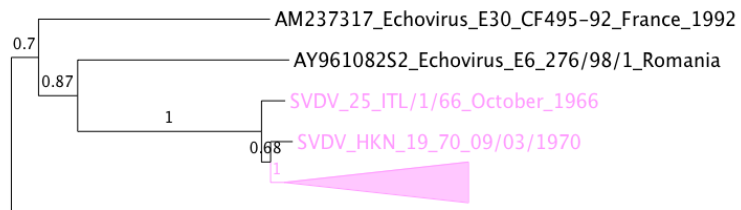
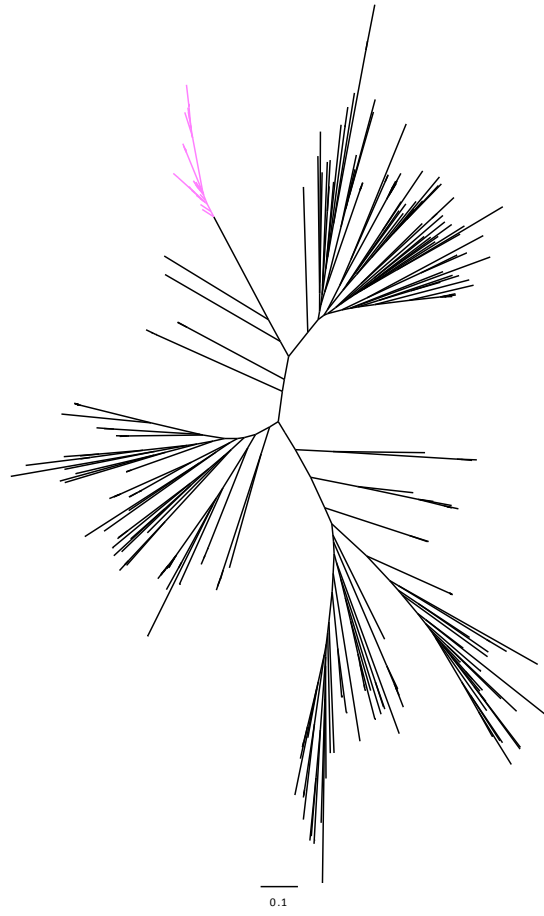


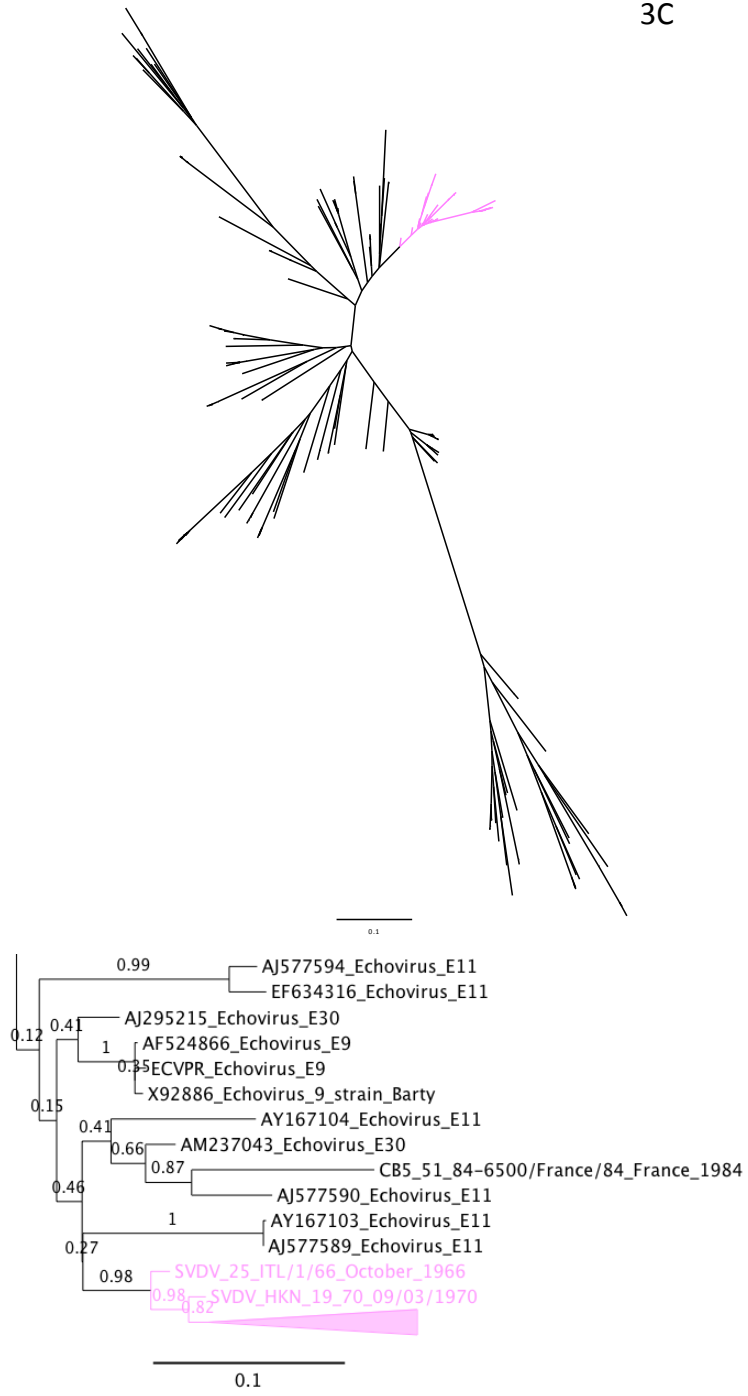


2A



2C



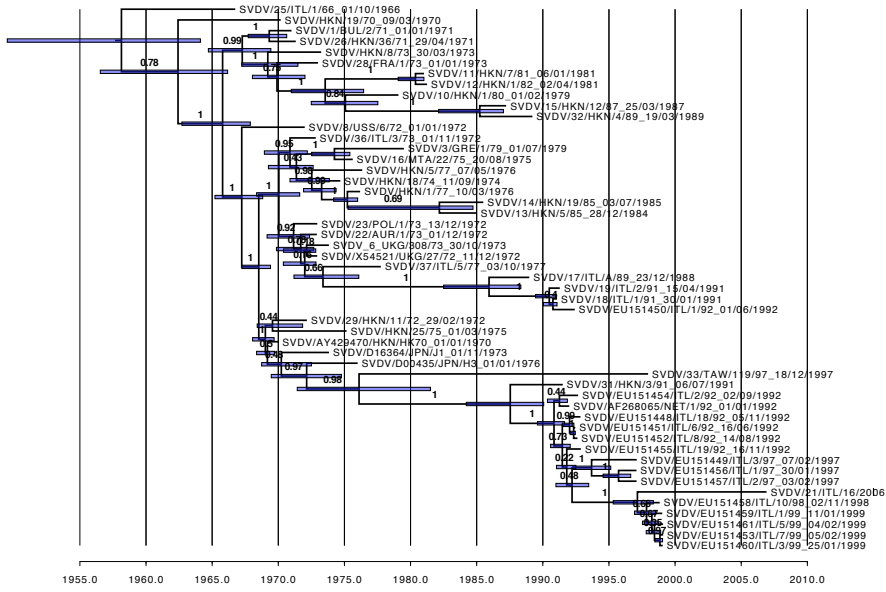


## SUPPLEMENTARY FIGURE S3

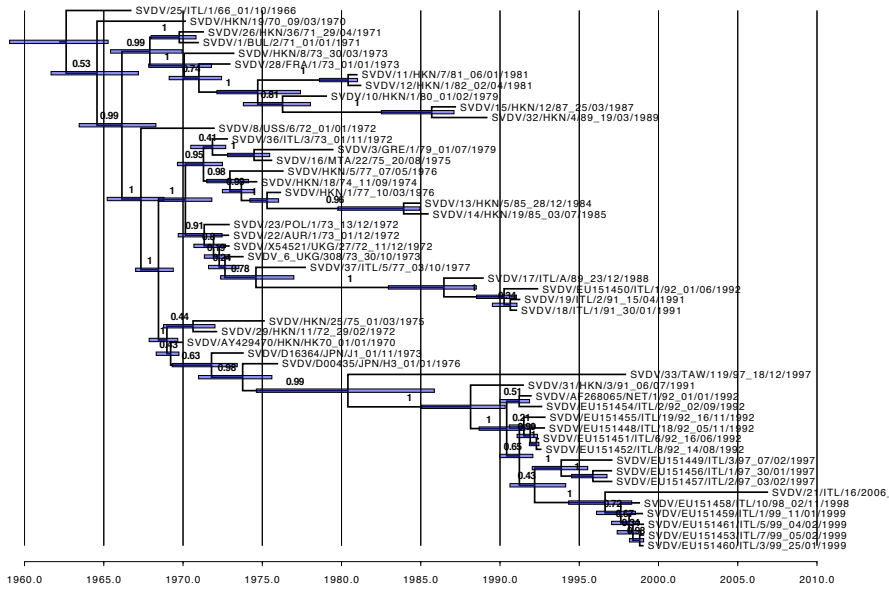
### Dating estimate trees from the BEAST analyses

Results annotated onto the maximum clade credibility tree for each of the four analyses marked in bold in Table 1. Blue bars indicate 95% HPD intervals for the age of the given node, and numbers indicate posterior support for the clusters (see also Methodology).





3C-3D (Protease-Polymerase), full region, Coalescent Bayesian Skyline



3C-3D (Protease-Polymerase), full region, Epidemic Birth-Death Model

## SUPPLEMENTARY FIGURE S4

### Marginal density plots for the tree model root height parameter

Marginal density plots for the tree model roots height (age of most recent common ancestor) for the 4 best scoring analysis (shown in bold in Table 1) in the BEAST dating estimates. On top, results from the Bayesian coalescent skyline prior based analyses for each of the two analysed segments, the capsid section in grey and the protease-polymerase section in blue. Below, results from the Epidemiological birth-death prior. The results correspond to the root of the trees shown in Supplementary Fig. S3. See also Methodology and Table 1 for further details.

