

1   **Supplementary Figure Legends.**

2   FIG. S1. Phylogenetic tree showing relationship between the nucleotide coding  
3   regions for Seg-1 (VP1) for all serotypes (45 taxa). The optimal tree with the sum of  
4   branch length = 3892.44291306 is shown and there was a total of 3883 positions in  
5   the final dataset. Australian sequences; ● prototype o non-prototype.

6

7   FIG. S2. Phylogenetic tree showing relationship between the nucleotide coding  
8   regions for Seg-2 (VP2) for all serotypes (191 taxa). The optimal tree with the sum of  
9   branch length = 4453.04850168 is shown and there was a total of 606 positions in the  
10   final dataset. Australian sequences; ● prototype o non-prototype.

11

12   FIG. S3. Phylogenetic tree showing relationship between the nucleotide coding  
13   regions for Seg-3 (VP3) for all serotypes (79 taxa). The optimal tree with the sum of  
14   branch length = 891.98144531 is shown and there was a total of 2698 positions in the  
15   final dataset. Australian sequences; ● prototype o non-prototype.

16

17   FIG. S4. Phylogenetic tree showing relationship between the nucleotide coding  
18   regions for Seg-4 (VP4) for all serotypes (52 taxa). The optimal tree with the sum of  
19   branch length = 2170.19720459 is shown and there was a total of 1930 positions in  
20   the final dataset. Australian sequences; ● prototype o non-prototype.

21

22   FIG. S5. Phylogenetic tree showing relationship between the nucleotide coding  
23   regions for Seg-5 (NS1) for all serotypes (78 taxa). The optimal tree with the sum of  
24   branch length = 1998.10635376 is shown and there was a total of 1655 positions in  
25   the final dataset. Australian sequences; ● prototype o non-prototype.

26

27 FIG. S6. Phylogenetic tree showing relationship between the nucleotide coding  
28 regions for Seg-6 (VP5) for all serotypes (150 taxa). The optimal tree with the sum of  
29 branch length = 6928.09214830 is shown and there was a total of 1557 positions in  
30 the final dataset. Australian sequences; ● prototype o non-prototype.

31

32 FIG. S7. Phylogenetic tree showing relationship between the nucleotide coding  
33 regions for Seg-7 (VP7) for all serotypes (117 taxa). The optimal tree with the sum of  
34 branch length = 2272.16035652 is shown and there was a total of 881 positions in the  
35 final dataset. Australian sequences; ● prototype o non-prototype.

36

37 FIG. S8. Phylogenetic tree showing relationship between the nucleotide coding  
38 regions for Seg-8 (NS2) for all serotypes (77 taxa). The optimal tree with the sum of  
39 branch length = 1516.43063641 is shown and there was a total of 1054 positions in  
40 the final dataset. Australian sequences; ● prototype o non-prototype.

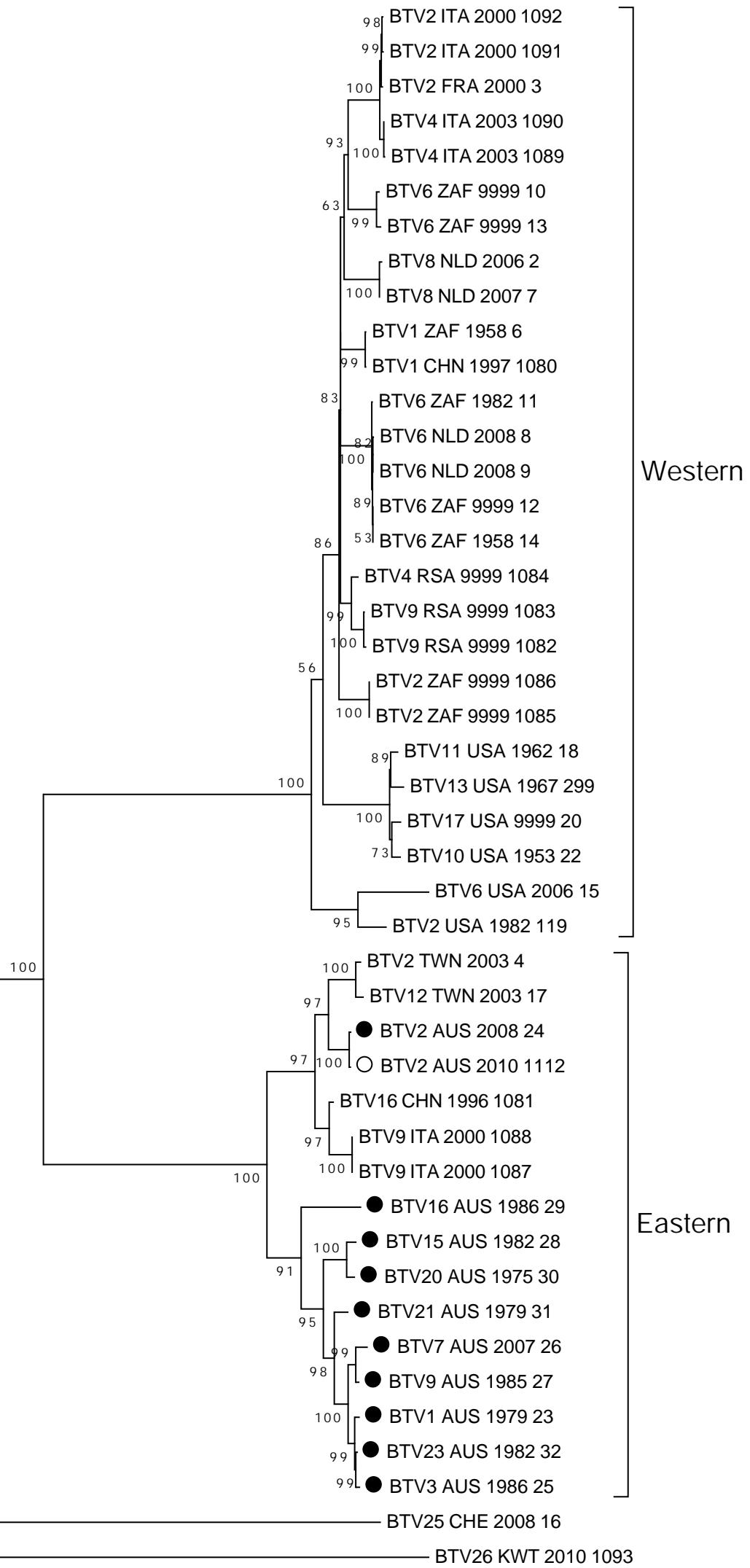
41

42 FIG. S9. Phylogenetic tree showing relationship between the nucleotide coding  
43 regions for Seg-9 (VP6) for all serotypes (57 taxa). The optimal tree with the sum of  
44 branch length = 1338.26550293 is shown and there was a total of 981 positions in the  
45 final dataset. Australian sequences; ● prototype o non-prototype.

46

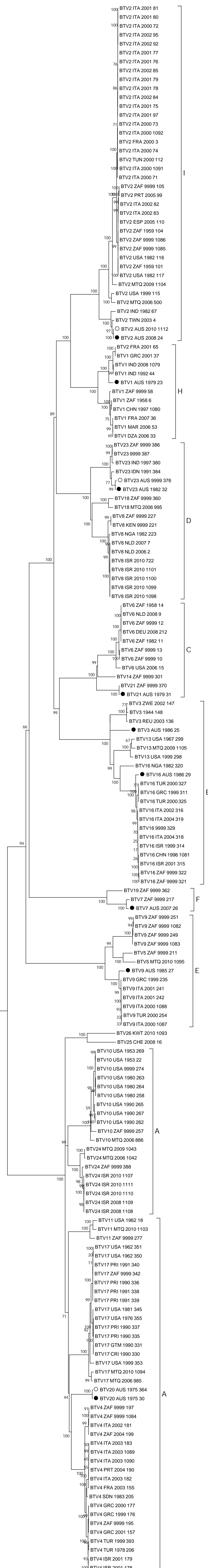
47 FIG. S10. Phylogenetic tree showing relationship between the nucleotide coding  
48 regions for Seg-10 (NS3) for all serotypes (176 taxa). The optimal tree with the sum  
49 of branch length = 1295.08600247 is shown and there was a total of 684 positions in  
50 the final dataset. Australian sequences; ● prototype o non-prototype.

Fig. S1



0.1

Fig. 32



**Fig. S3**

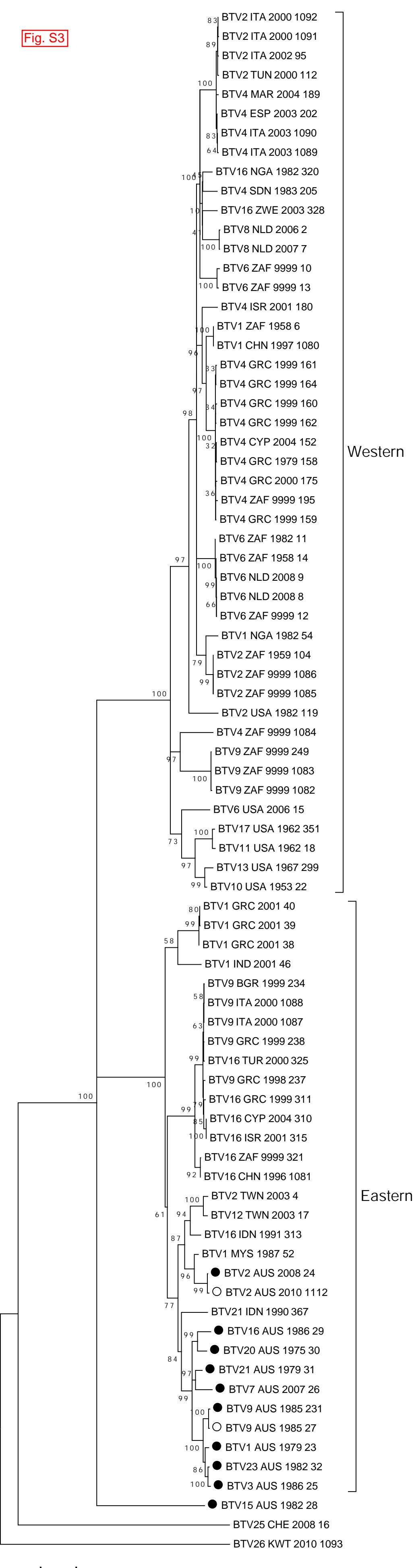


Fig. S4

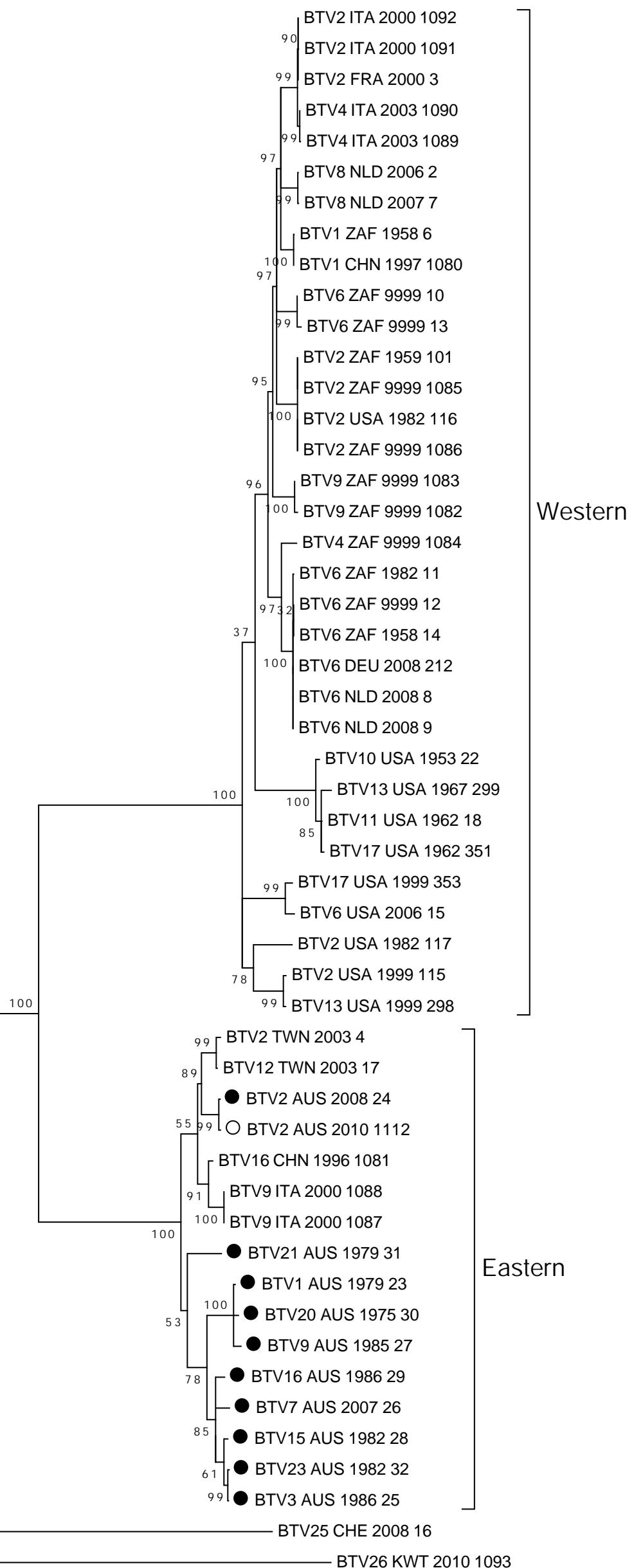
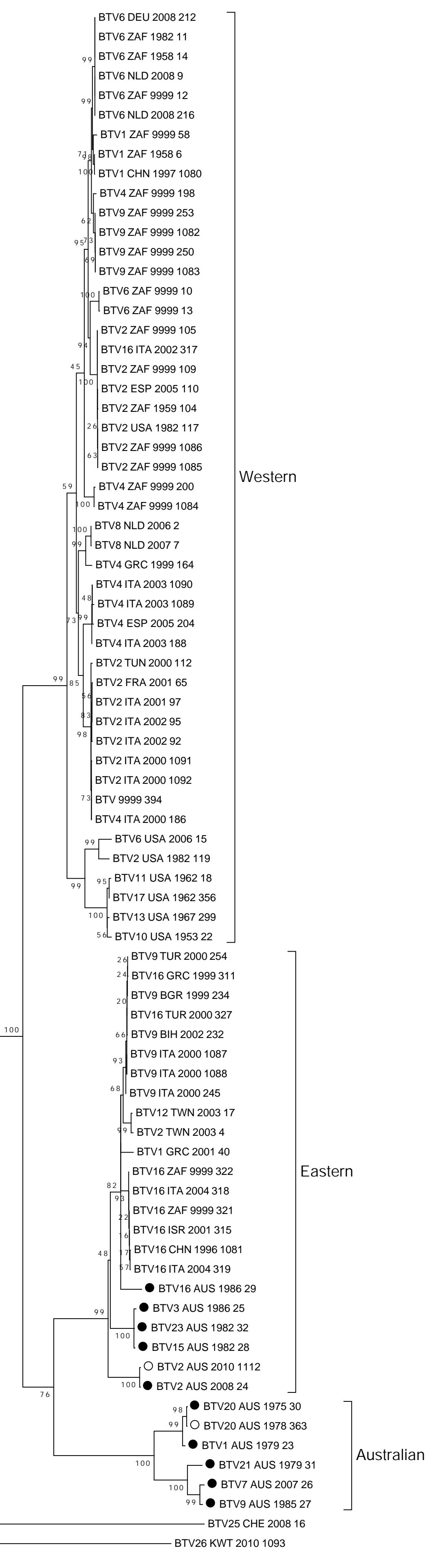


Fig. S5



0.1

Fig. 3.

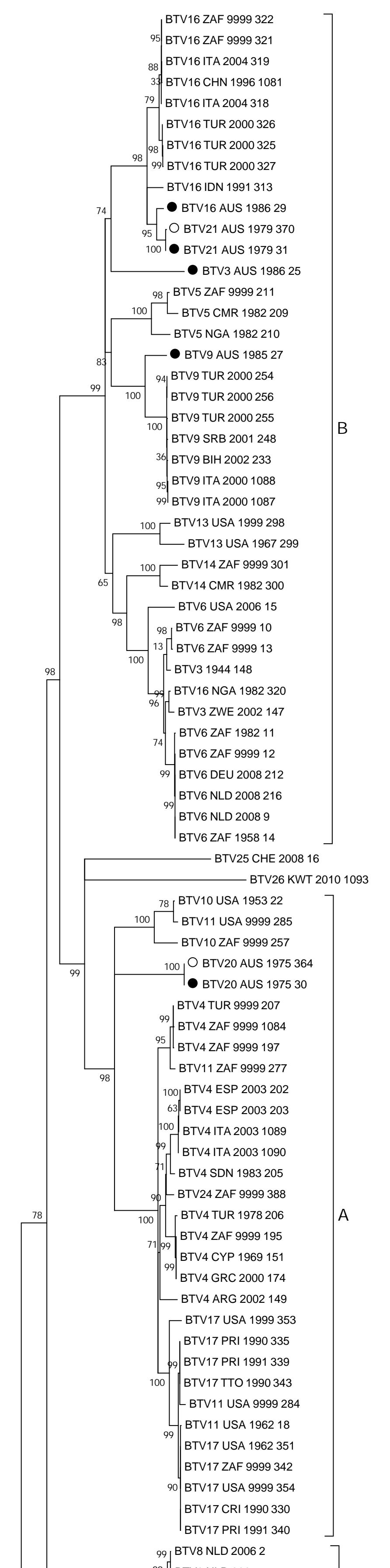


Fig. S7

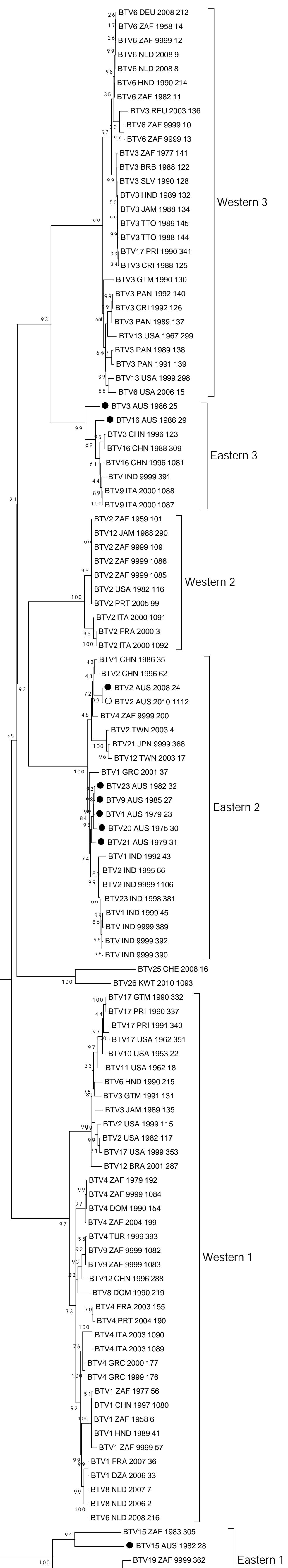


Fig. S8

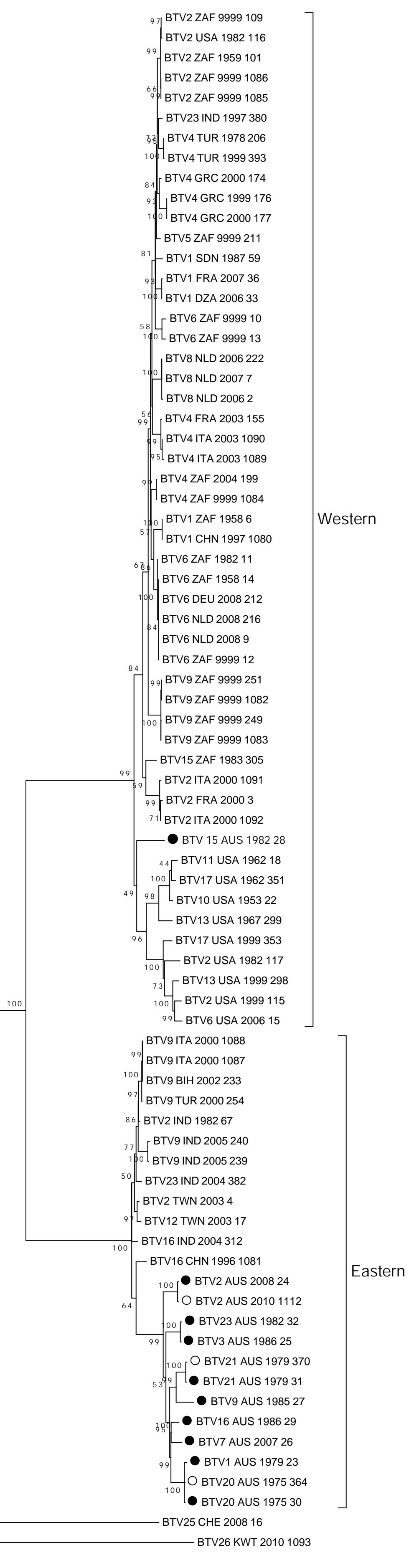


Fig. S9

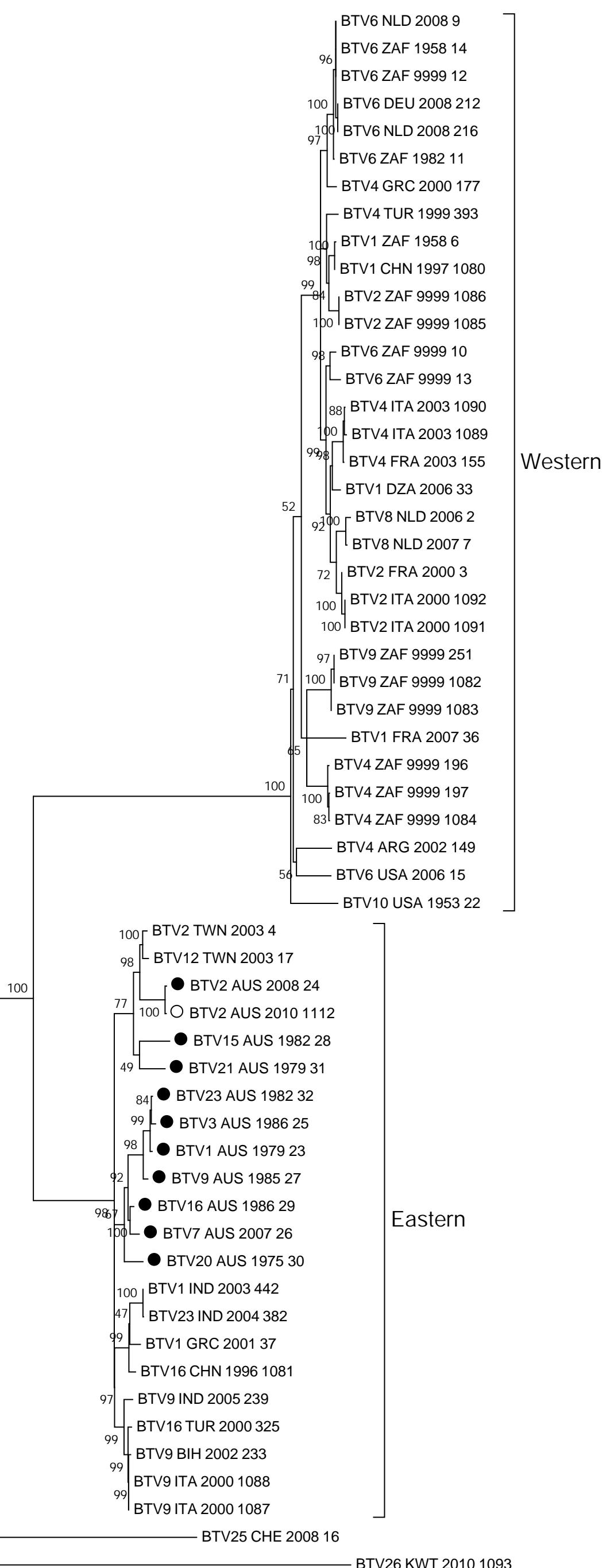


Fig. S10

