

1 **Supplemental material**

2 **Fig. S1.** Maximum likelihood phylogenetic tree of Dasyurid herpesvirus 3 in the context of
3 representatives of the *Herpesviridae* family based on the amino acid sequences of
4 glycoprotein M. The tree is mid-point rooted and scaled to the number of amino acid
5 substitutions per site. Bootstrap values (>80%) are shown at the key nodes. The newly
6 discovered Dasyurid herpesvirus 3 is shown in red.

7 **Fig. S2.** Maximum likelihood phylogenetic tree of Dasyurid herpesvirus 3 in the context of
8 representatives of the *Herpesviridae* family based on the amino acid sequences of major
9 capsid. The tree is mid-point rooted and scaled to the number of amino acid substitutions
10 per site. Bootstrap values (>80%) are shown at the key nodes. The newly discovered
11 DaHV-3 is shown in red.

12 **Fig. S3.** Maximum likelihood phylogenetic tree of Tasmanian devil-associated
13 papillomavirus 1 and 2 in the context of representatives of the *Papillomaviridae* family
14 based on the amino acid sequences of E1 protein. The tree is mid-point rooted and scaled
15 to the number of amino acid substitutions per site. Bootstrap values (>80%) are shown at
16 the key nodes. The 2 newly discovered papillomaviruses is shown in red.

17 **Fig. S4.** Maximum likelihood phylogenetic tree of Tasmanian devil-associated polyomavirus
18 1 in the context of representatives of the *Polyomaviridae* family based on the amino acid
19 sequences of VP1. The tree is mid-point rooted and scaled to the number of amino acid
20 substitutions per site. Bootstrap values (>80%) are shown at the key nodes. The newly
21 discovered polyomavirus is shown in red.

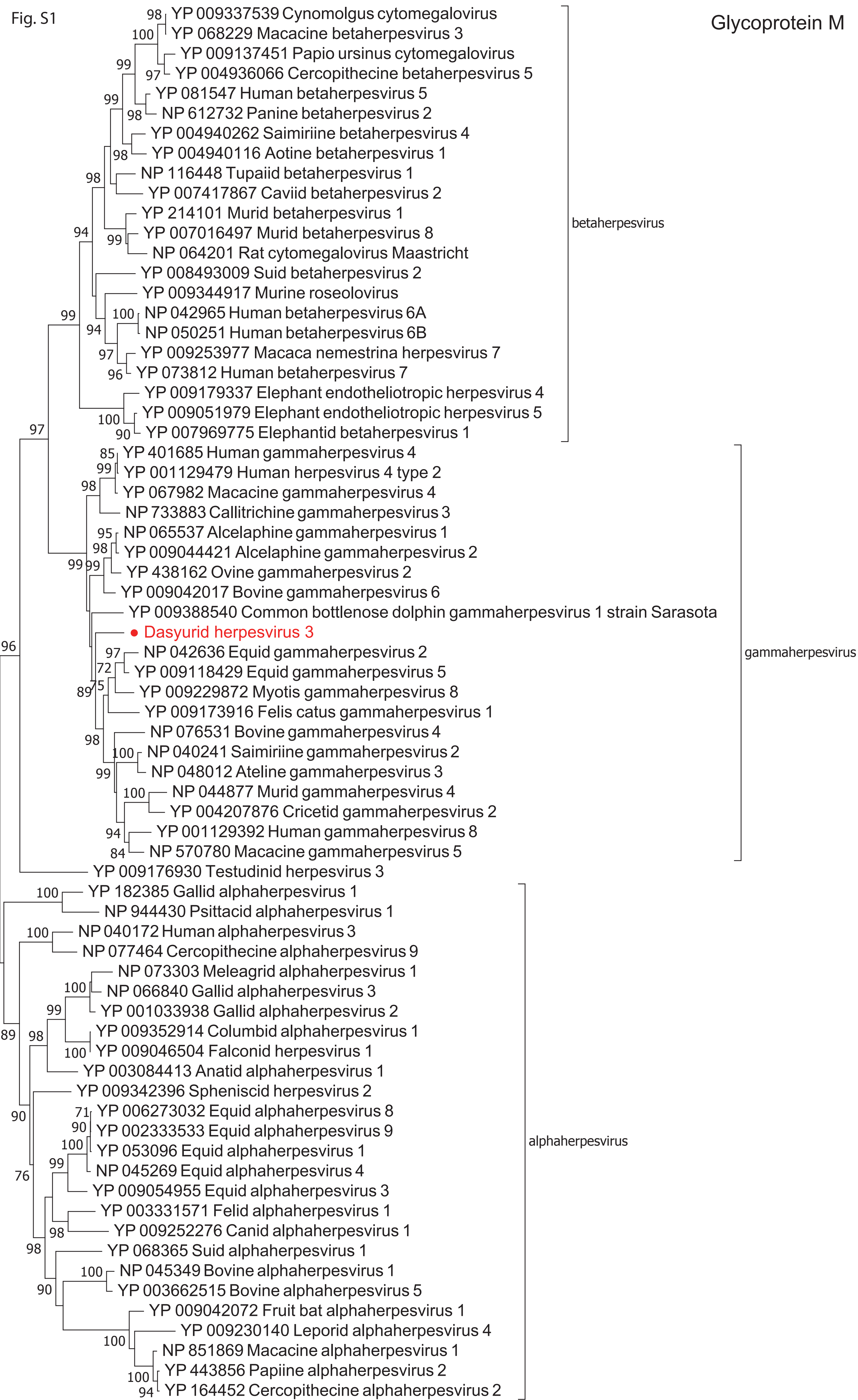
22 **Fig. S5.** Maximum likelihood phylogenetic tree of Tasmanian devil-associated polyomavirus
23 1 and Tasmanian devil-associated polyoma-like virus 2 in the context of representatives of
24 the *Polyomaviridae* family based on the amino acid sequences of the large T antigen. The
25 tree is mid-point rooted and scaled to the number of amino acid substitutions per site.
26 Bootstrap values (>80%) are shown at the key nodes. The 2 newly discovered viruses are
27 shown in red.

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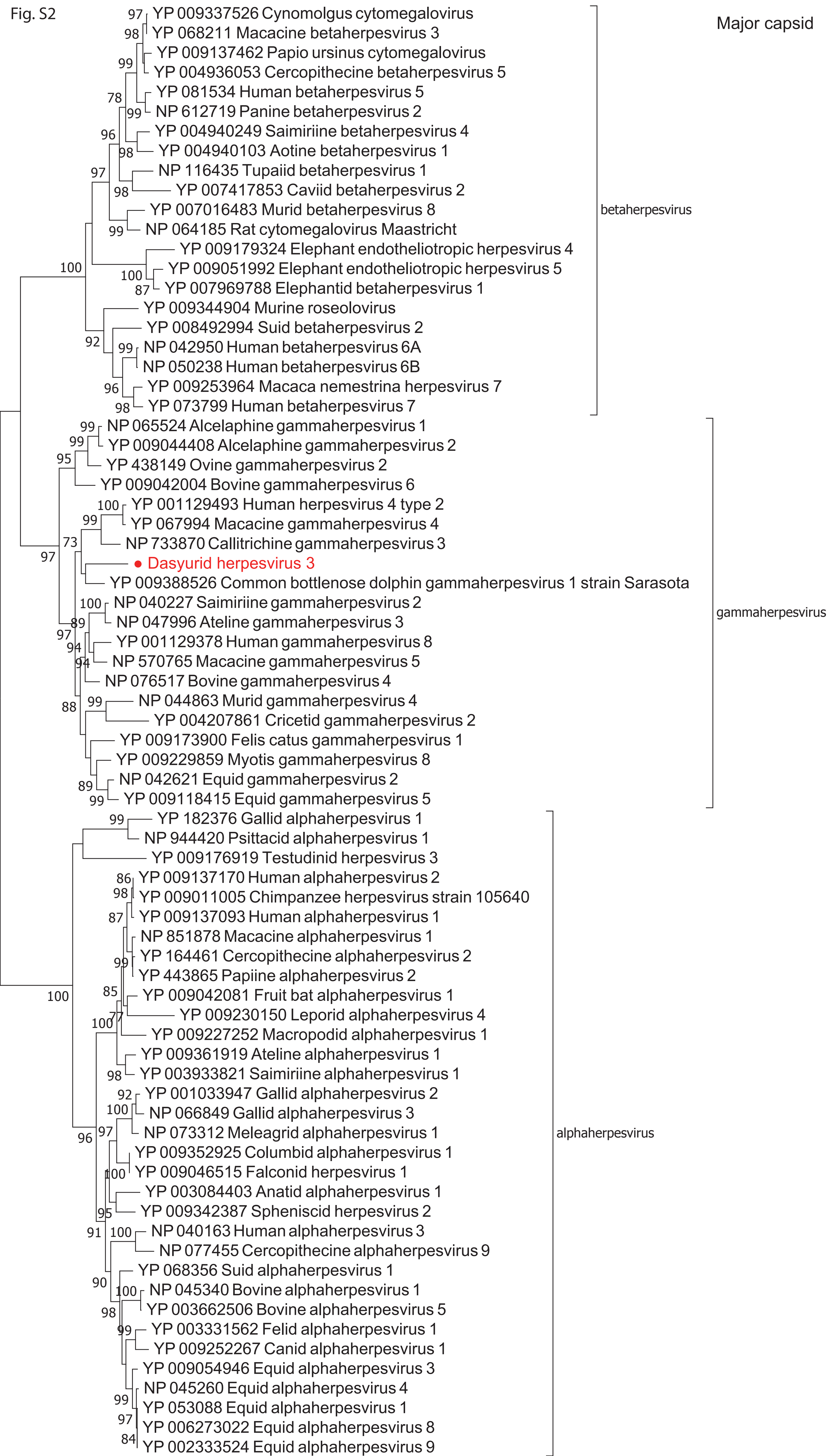
Fig. S1

Glycoprotein M



0.5

Fig. S2



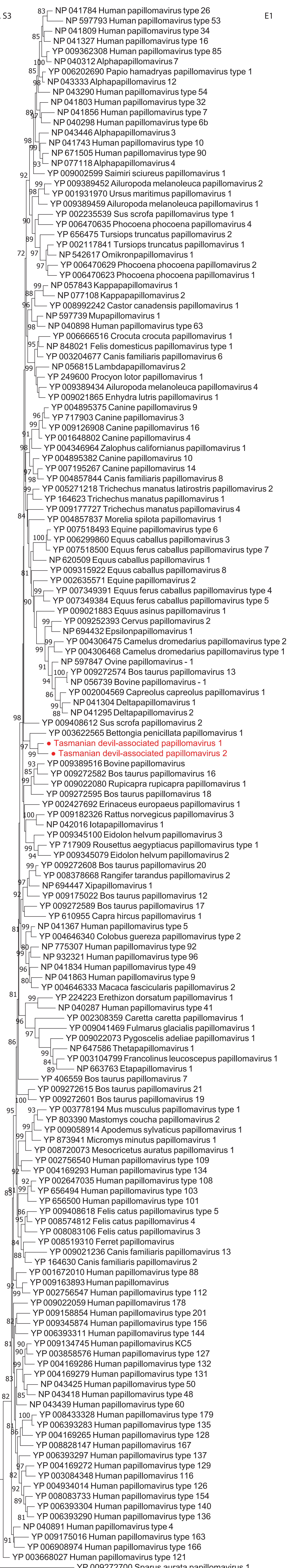
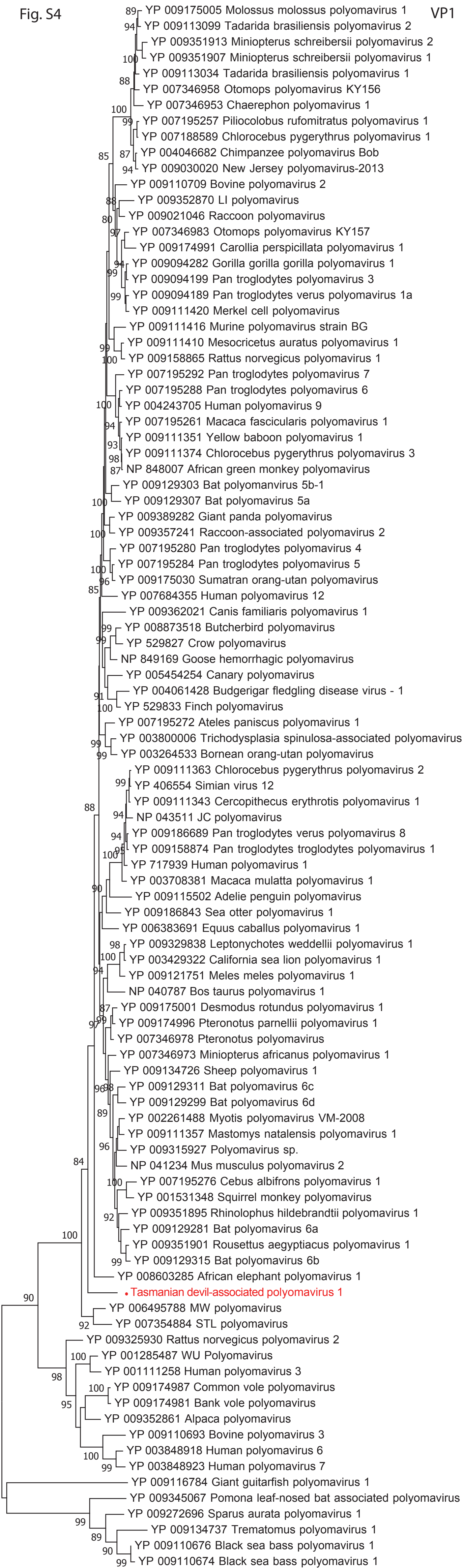


Fig. S4

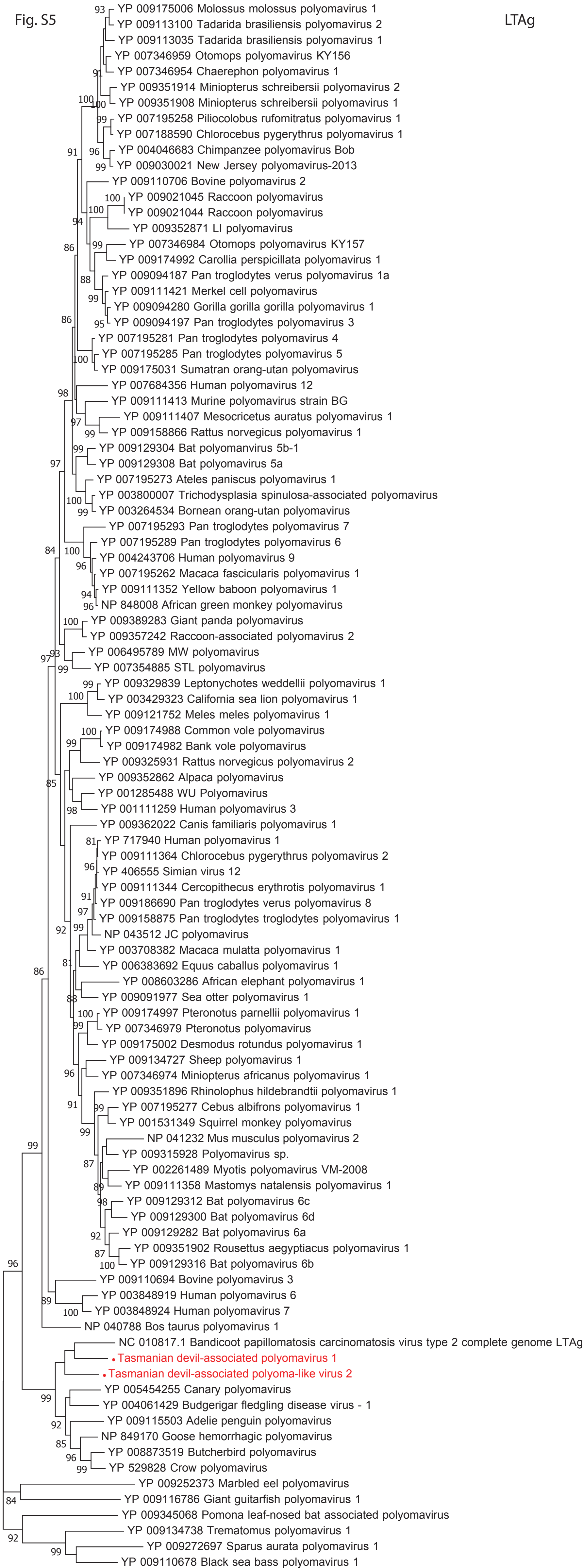
VP1



0.5

Fig. S5

LTA_g



0.5