

Additional file 4

A comprehensive atlas of nuclear sequences of mitochondrial origin (NUMTs) inserted into the pig genome

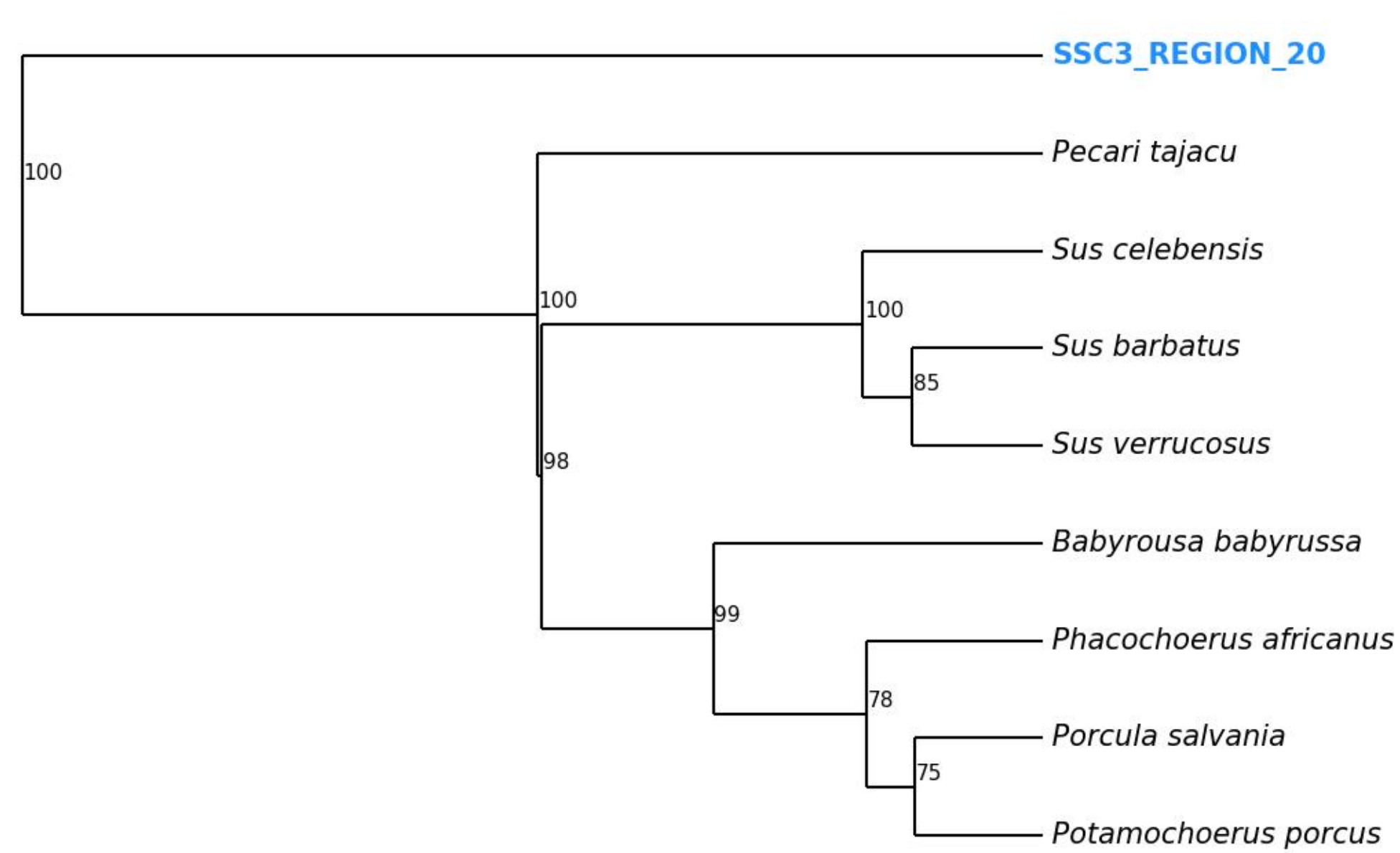
Matteo Bolner, Samuele Bovo, Mohamad Ballan, Giuseppina Schiavo, Valeria Taurisano, Anisa Ribani, Francesca Bertolini and Luca Fontanesi

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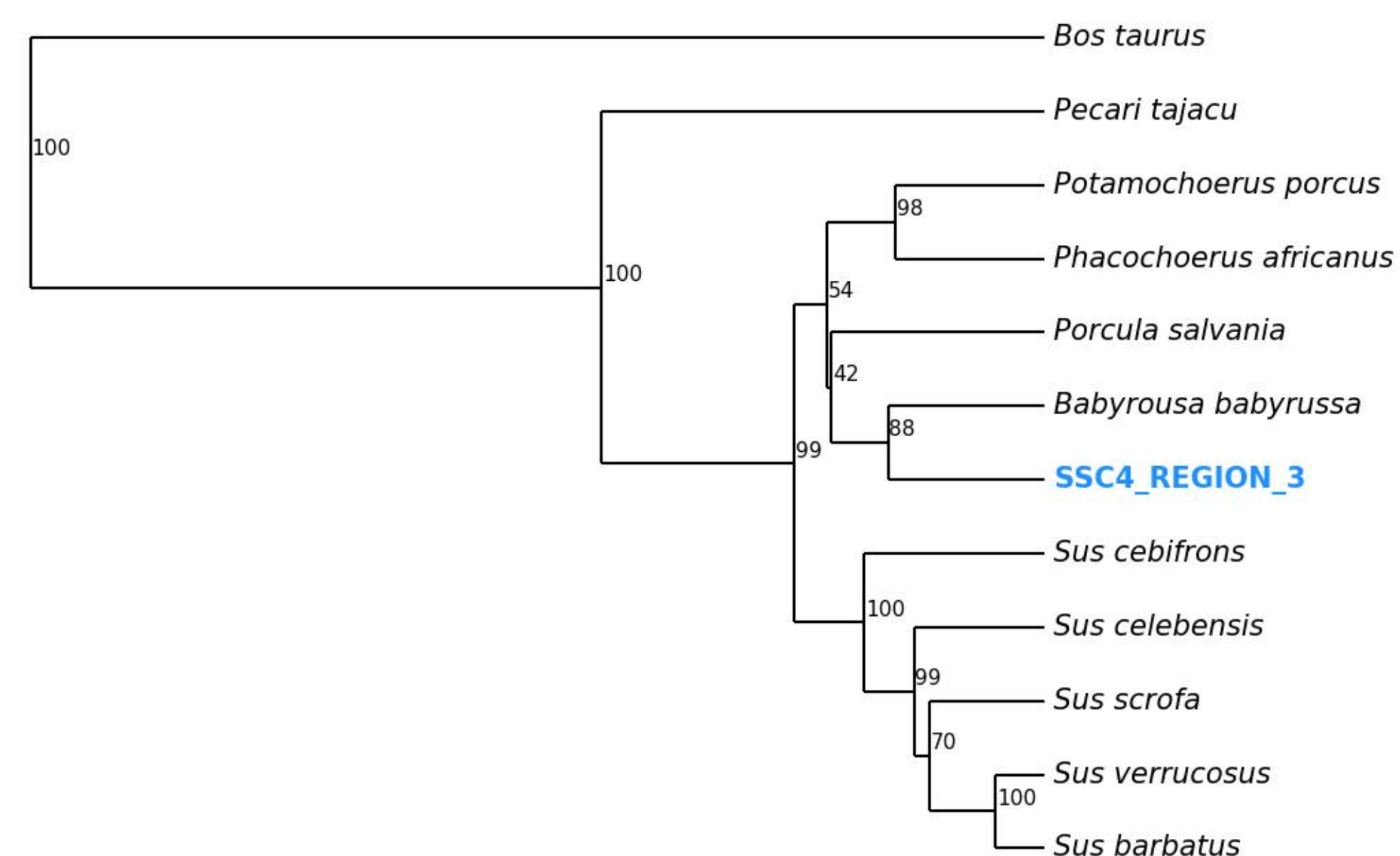
Additional file 4: Figure S7. Phylogenetic trees obtained for all NUMT regions (n. 178) for which a NUMT sequence was longer than 150 bp.

Each tree was computed from the longest NUMT sequence in the region. The title of the tree reports the name of the NUMT region. The X axis of each tree represents the branch length. Polymorphic NUMT regions are colored red, and fixed NUMT regions are colored blue. The NUMT nuclear sequence is compared with the corresponding sequences in the mitochondrial DNA of several species (the other branches). The posterior probability computed by BEAST is reported along each node in the tree, and ranges from 0 to 100.

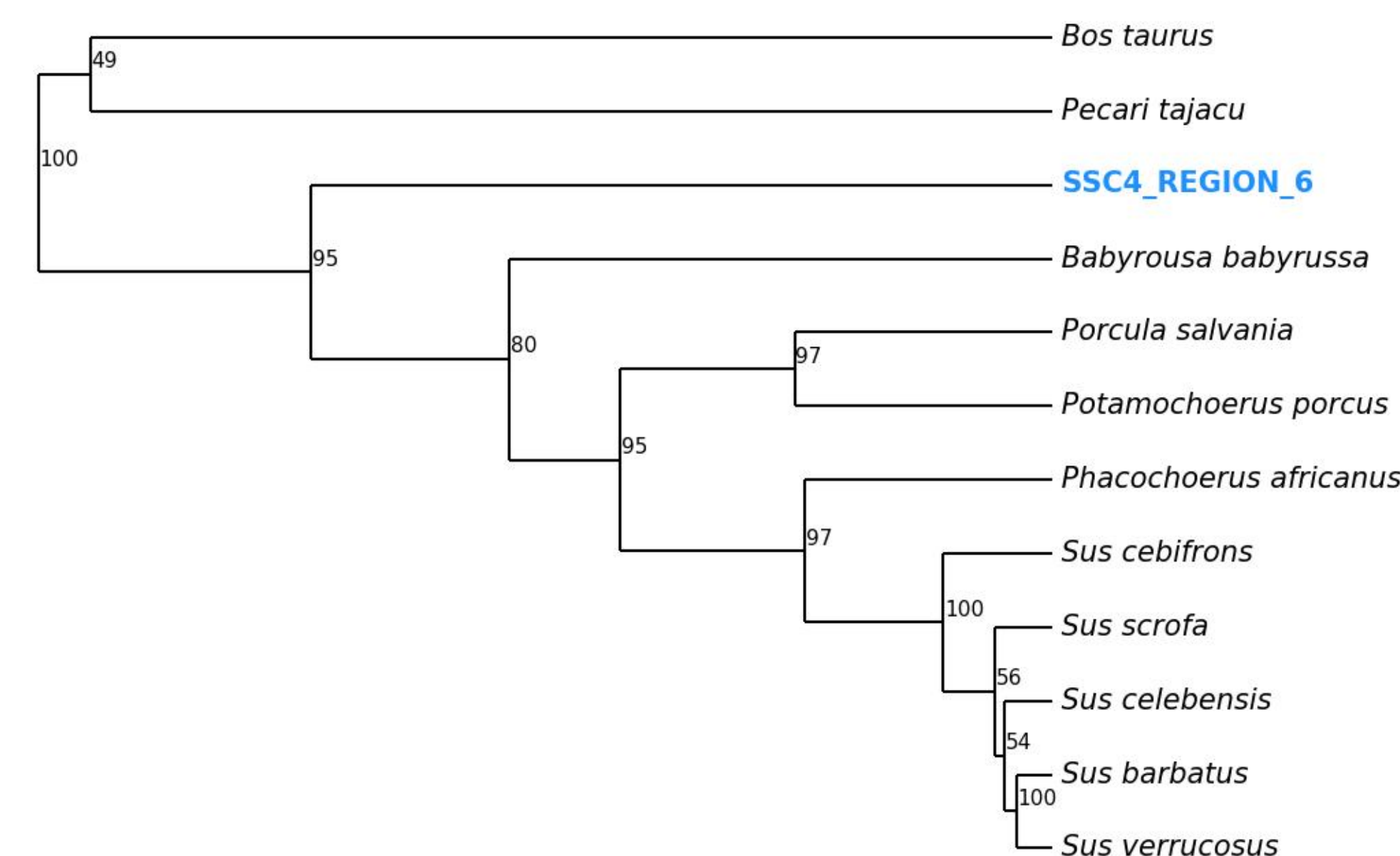
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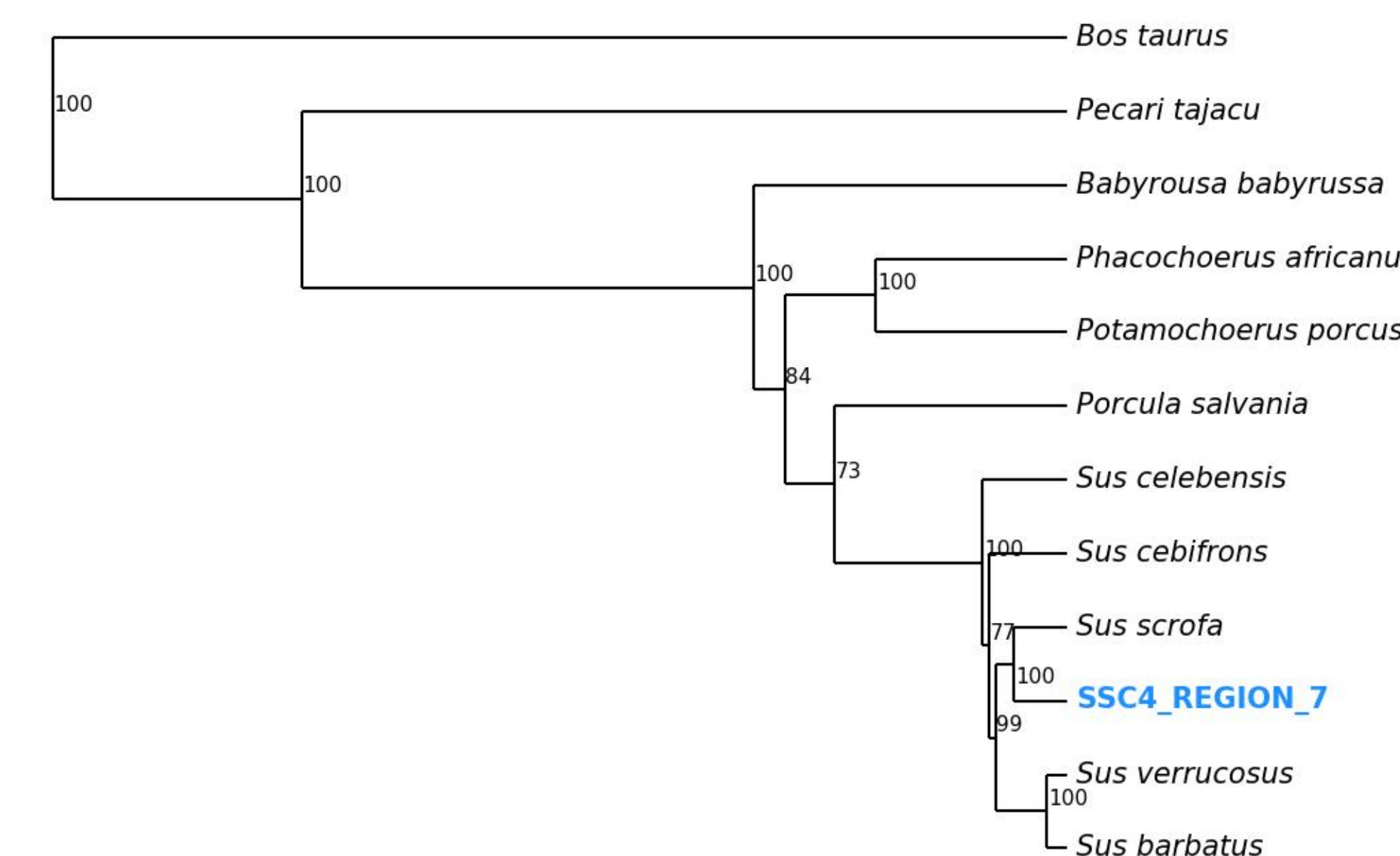
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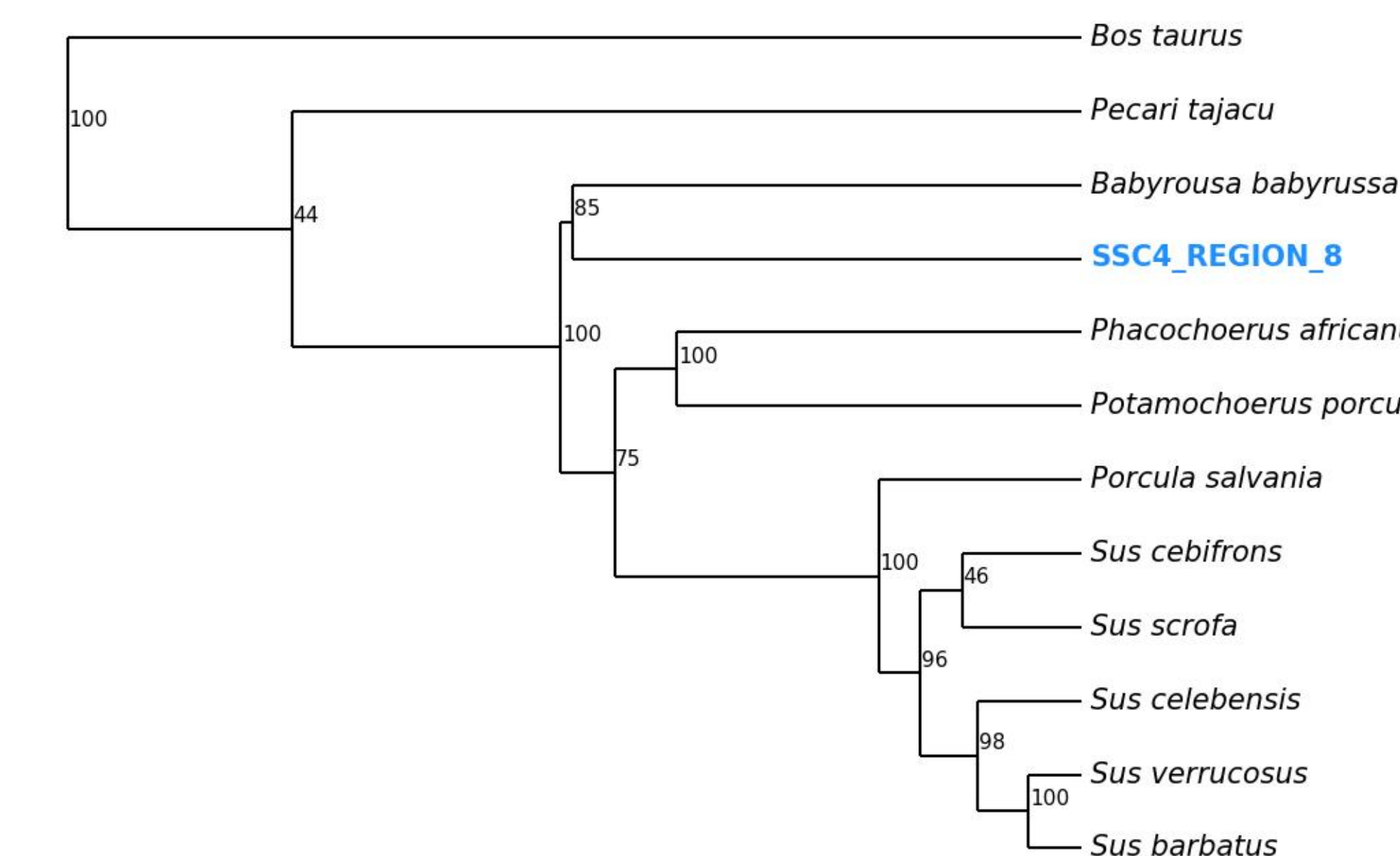
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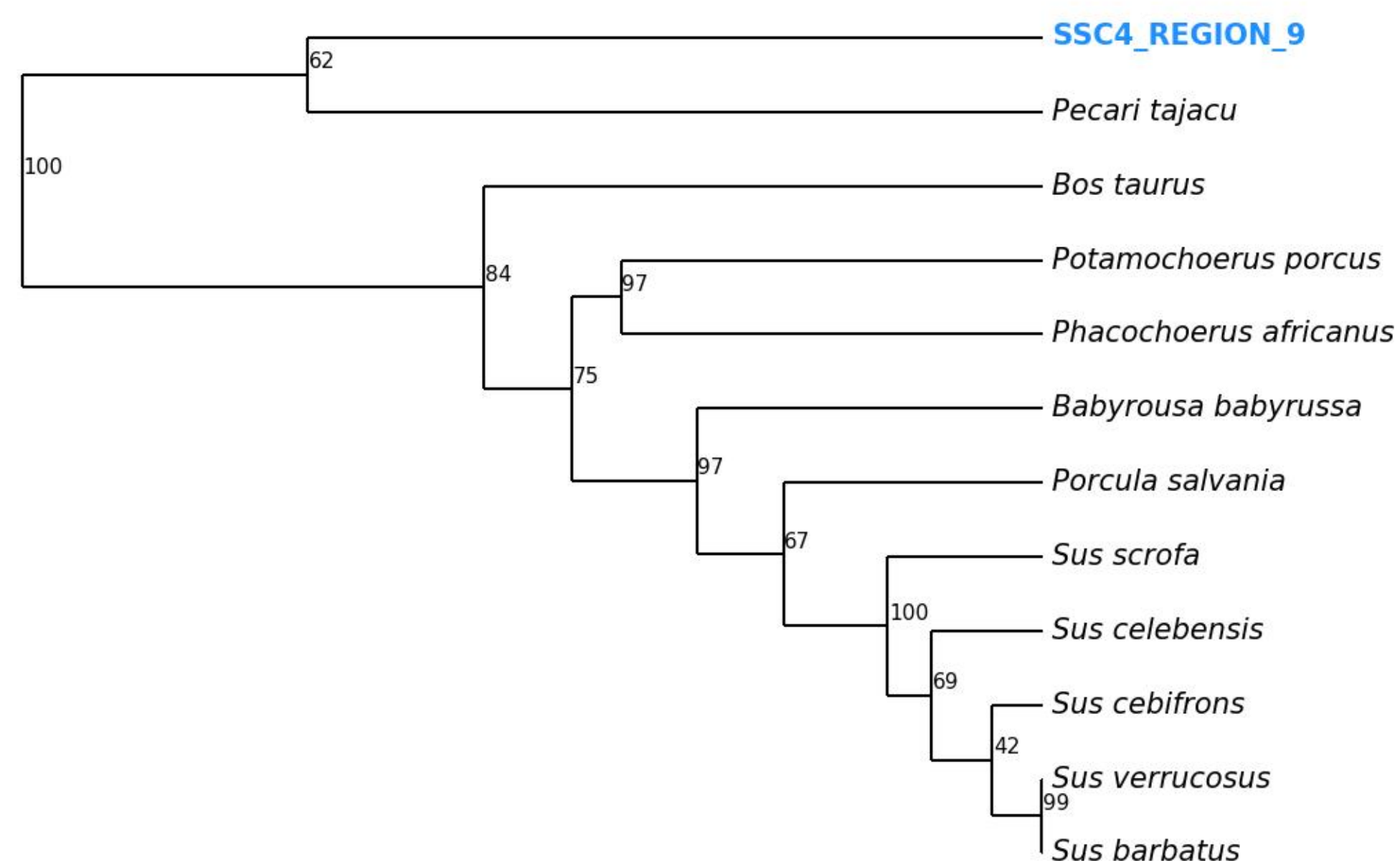
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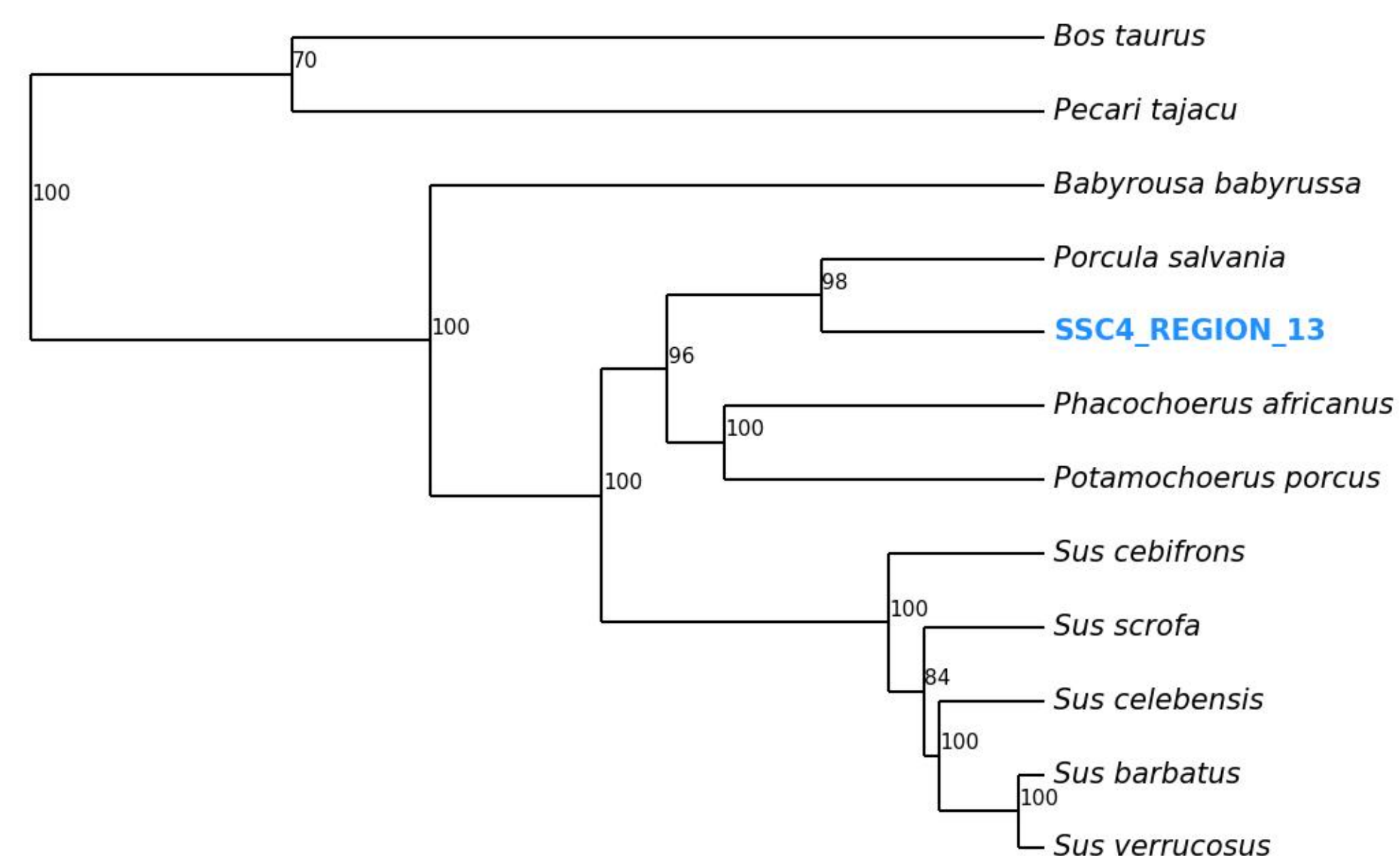
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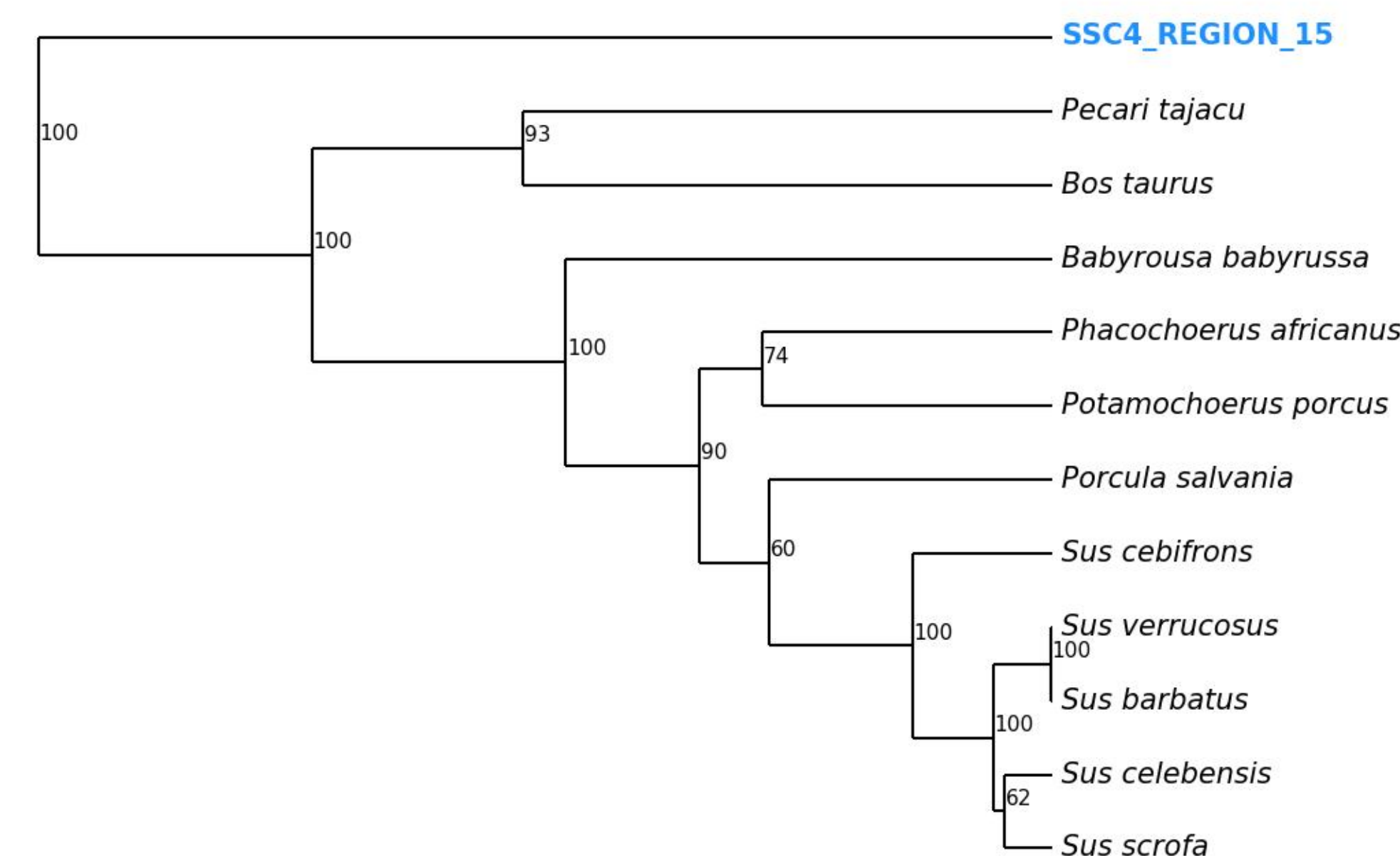
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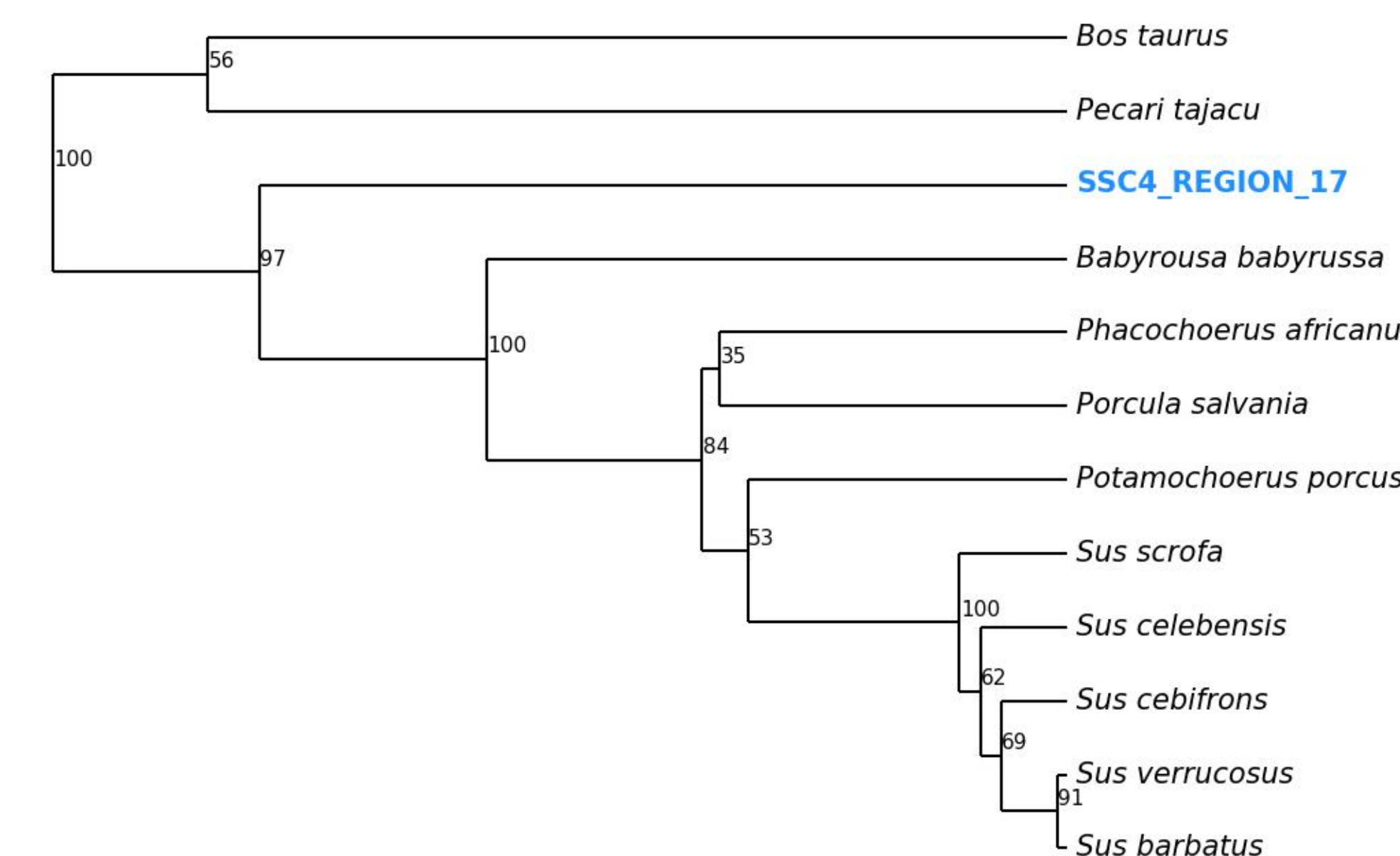
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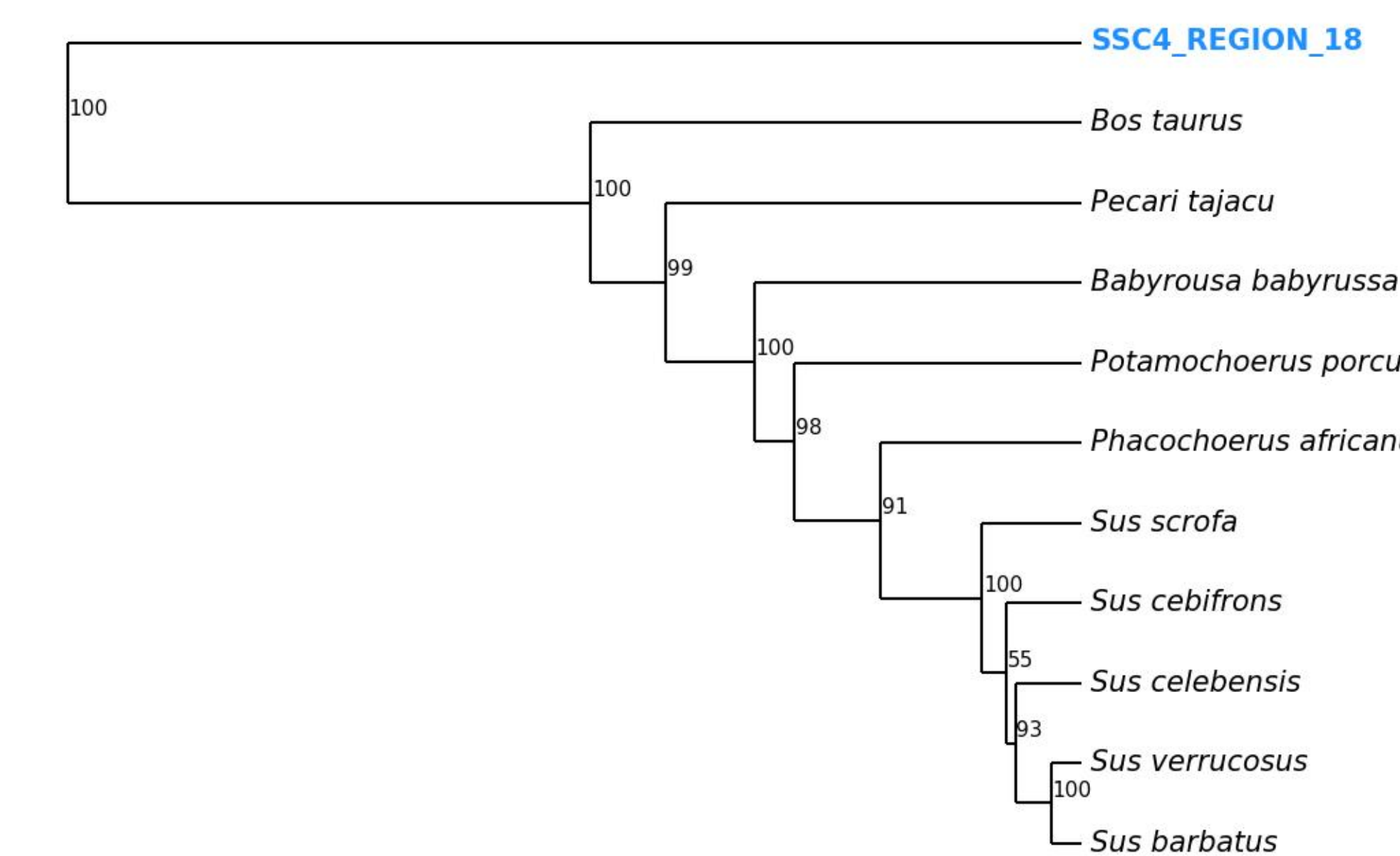
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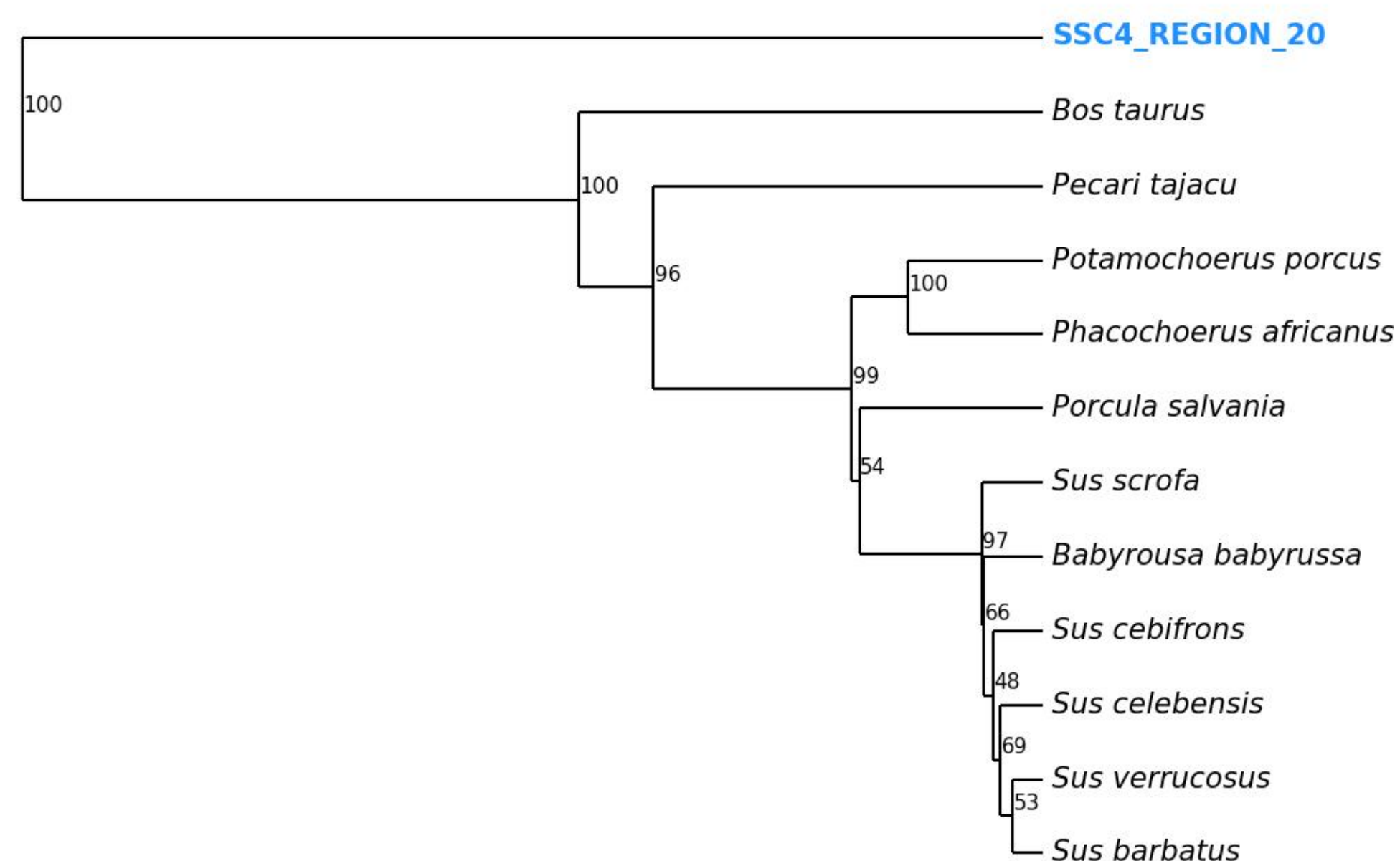
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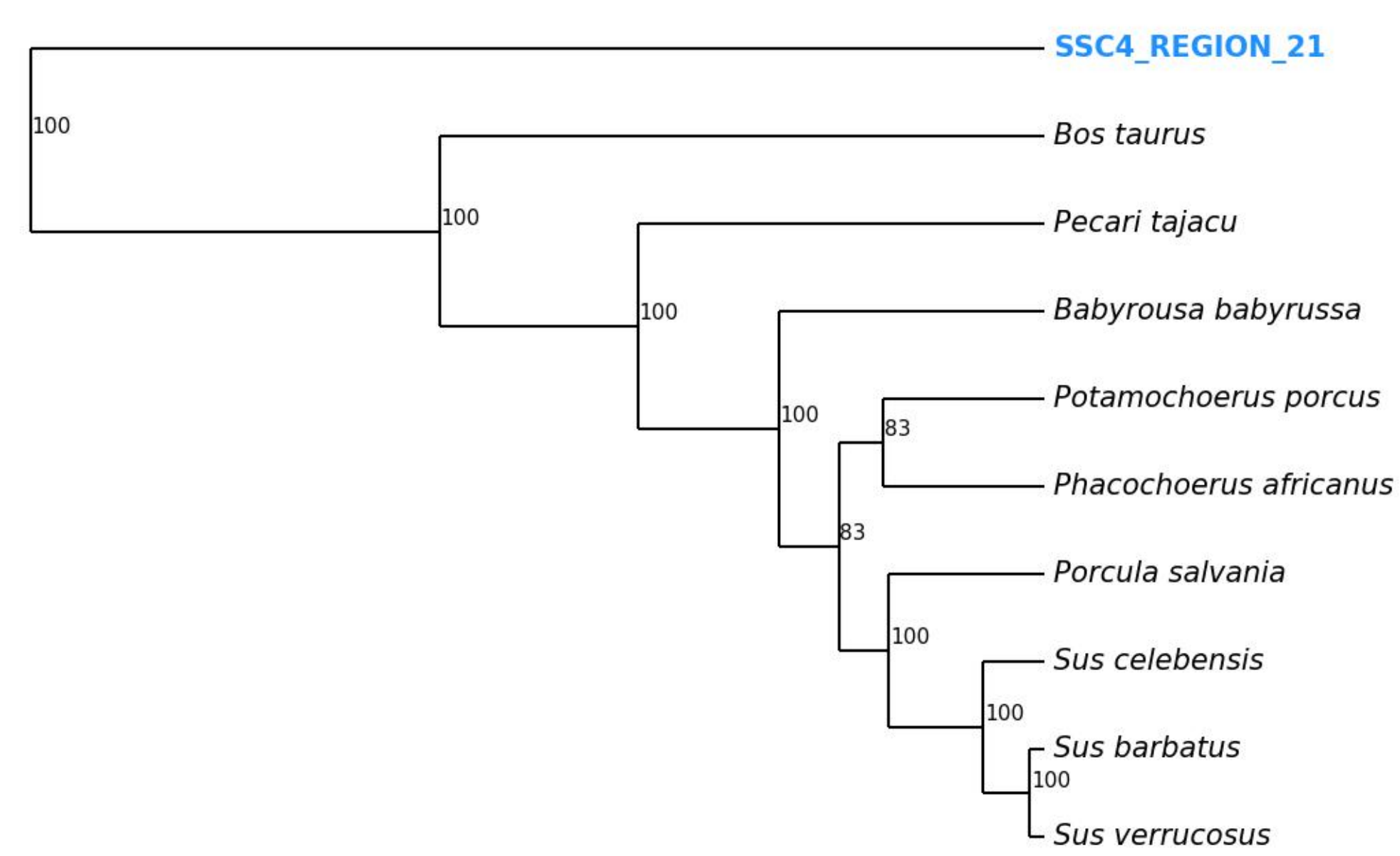
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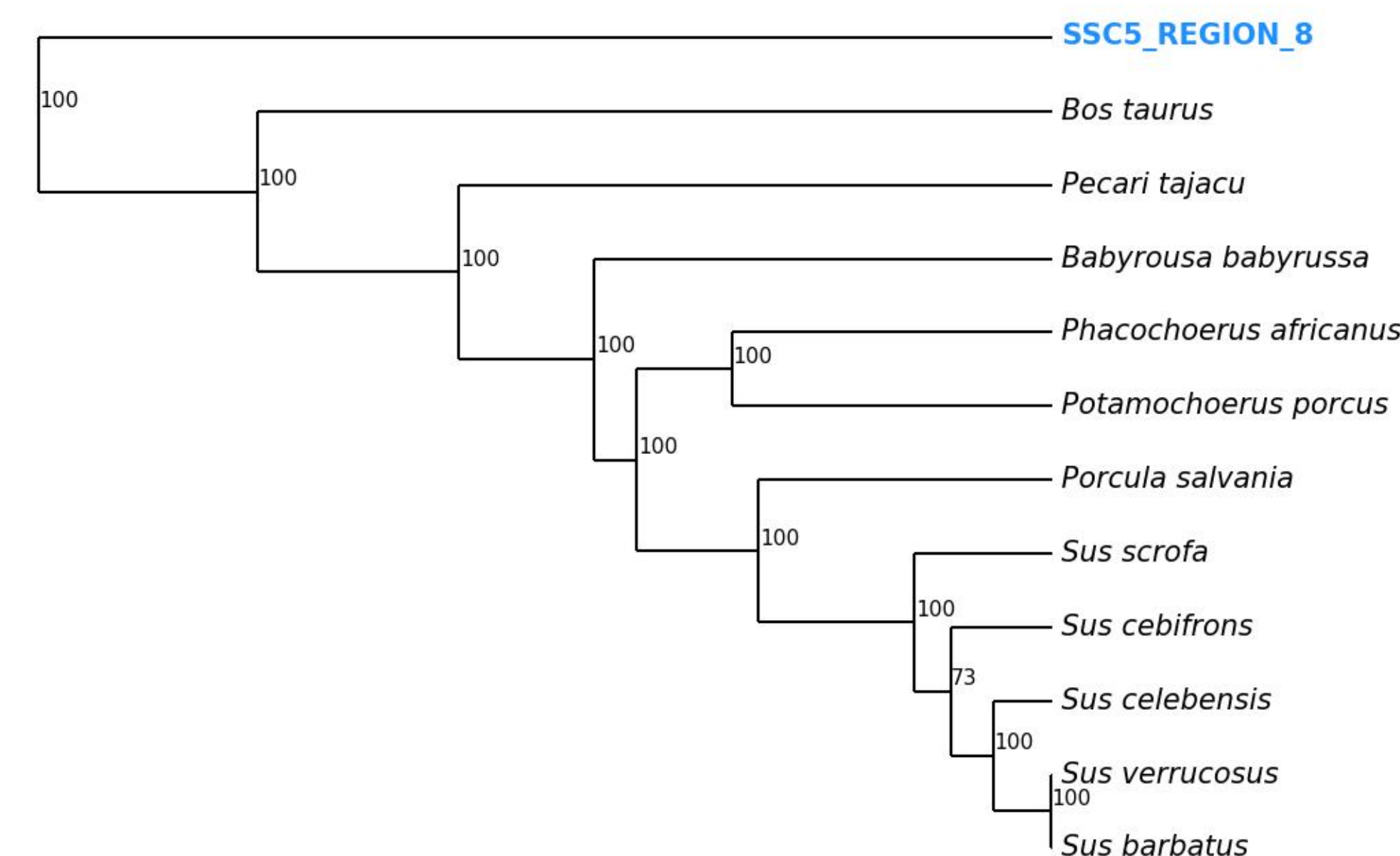
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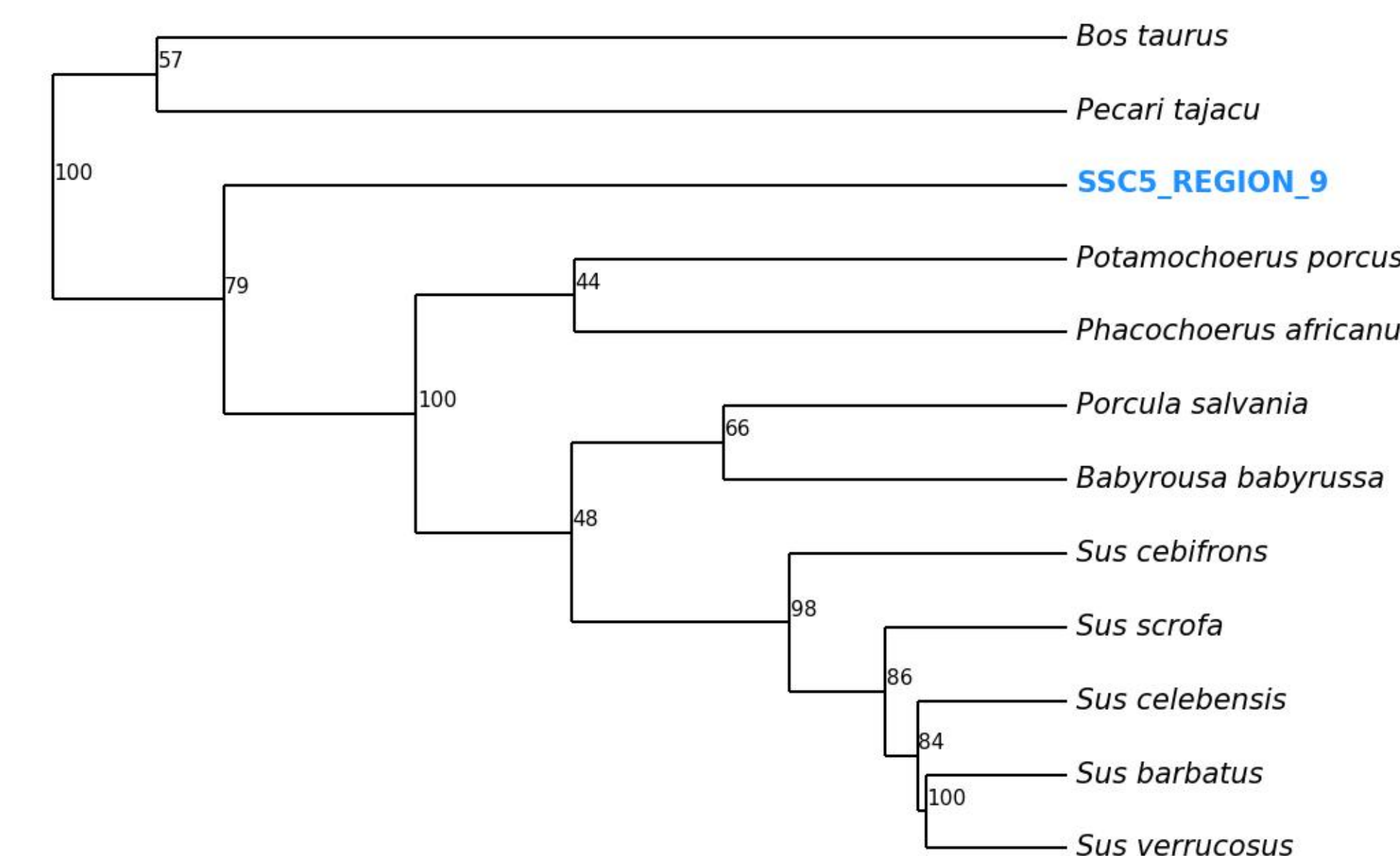
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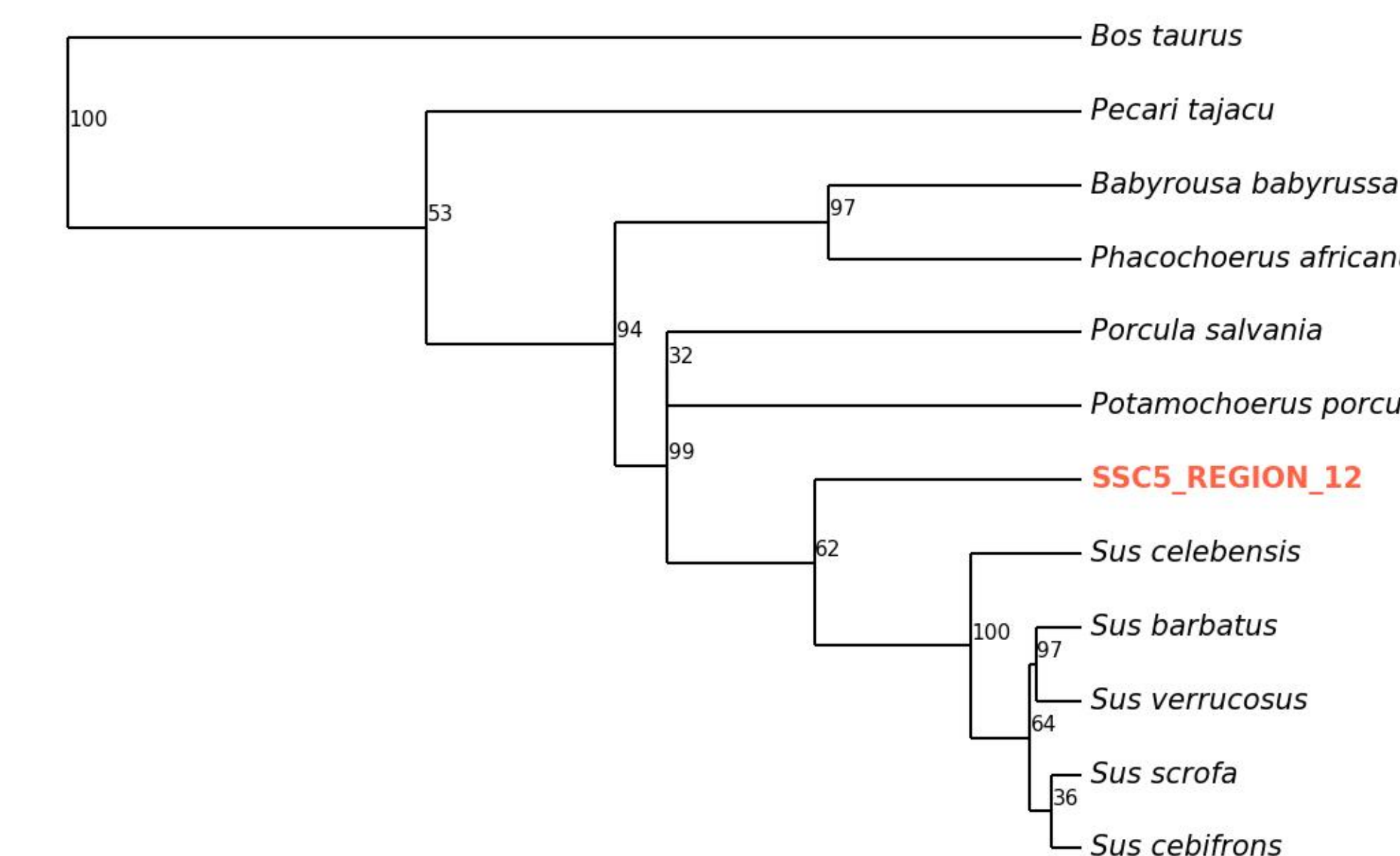
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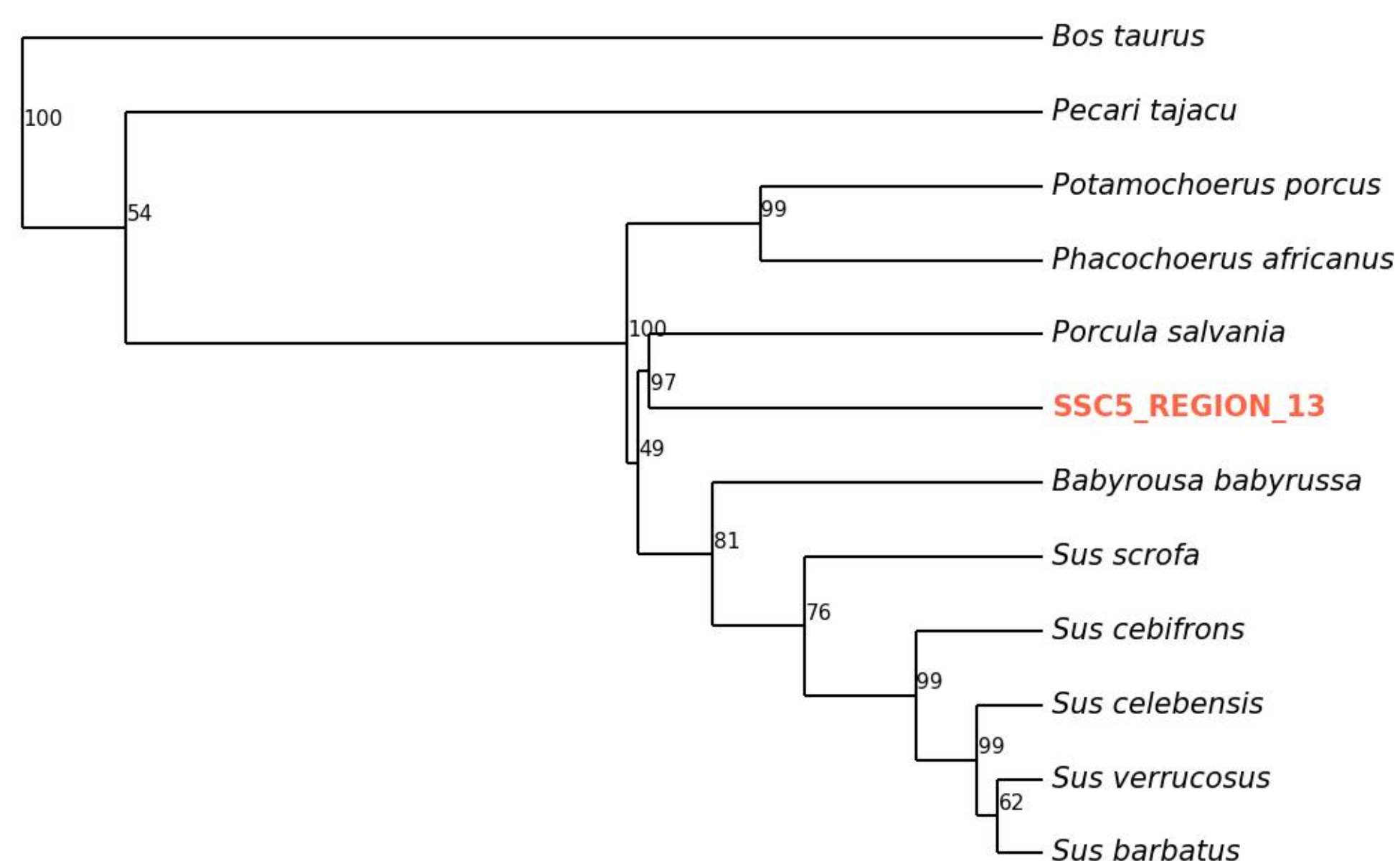
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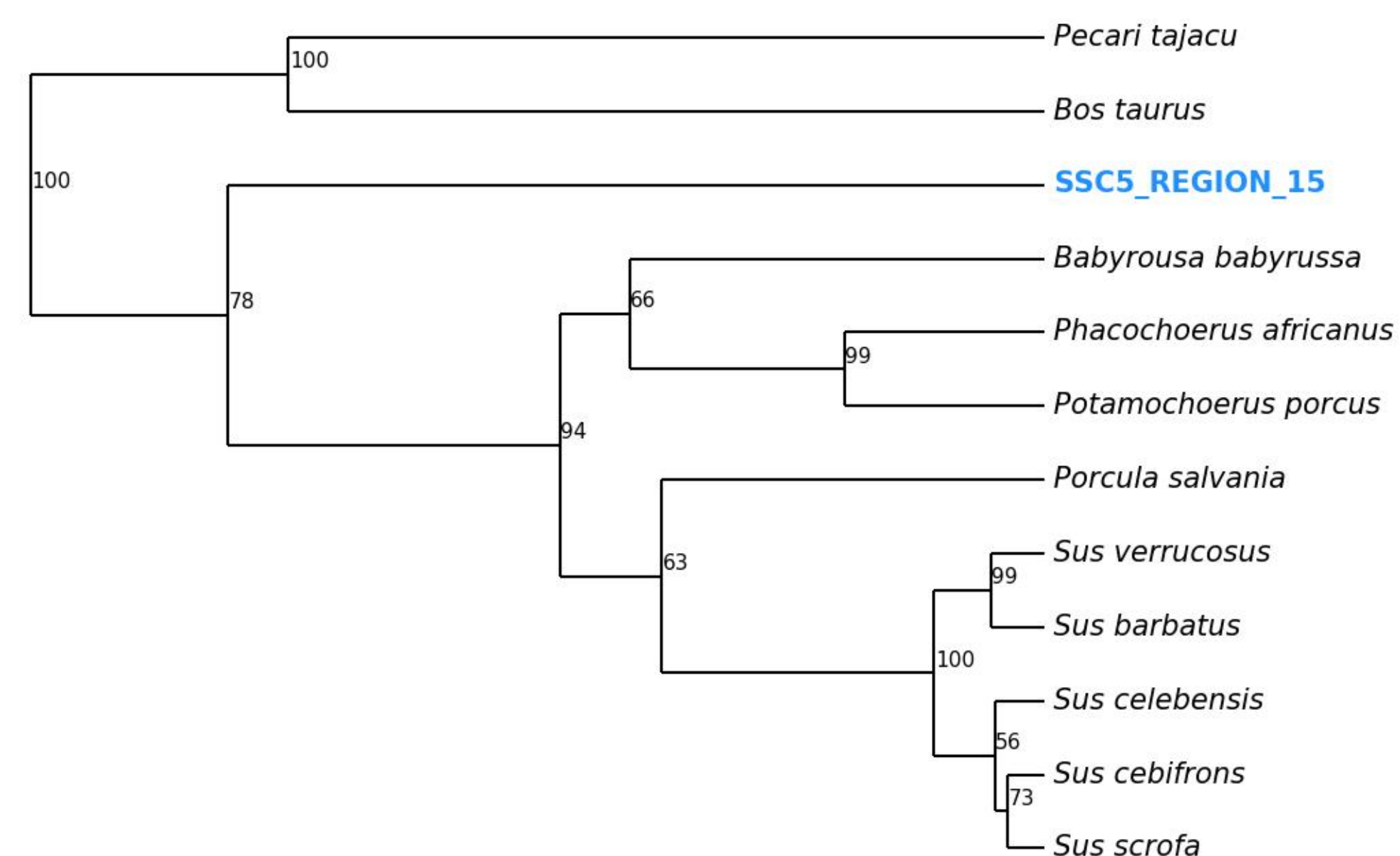
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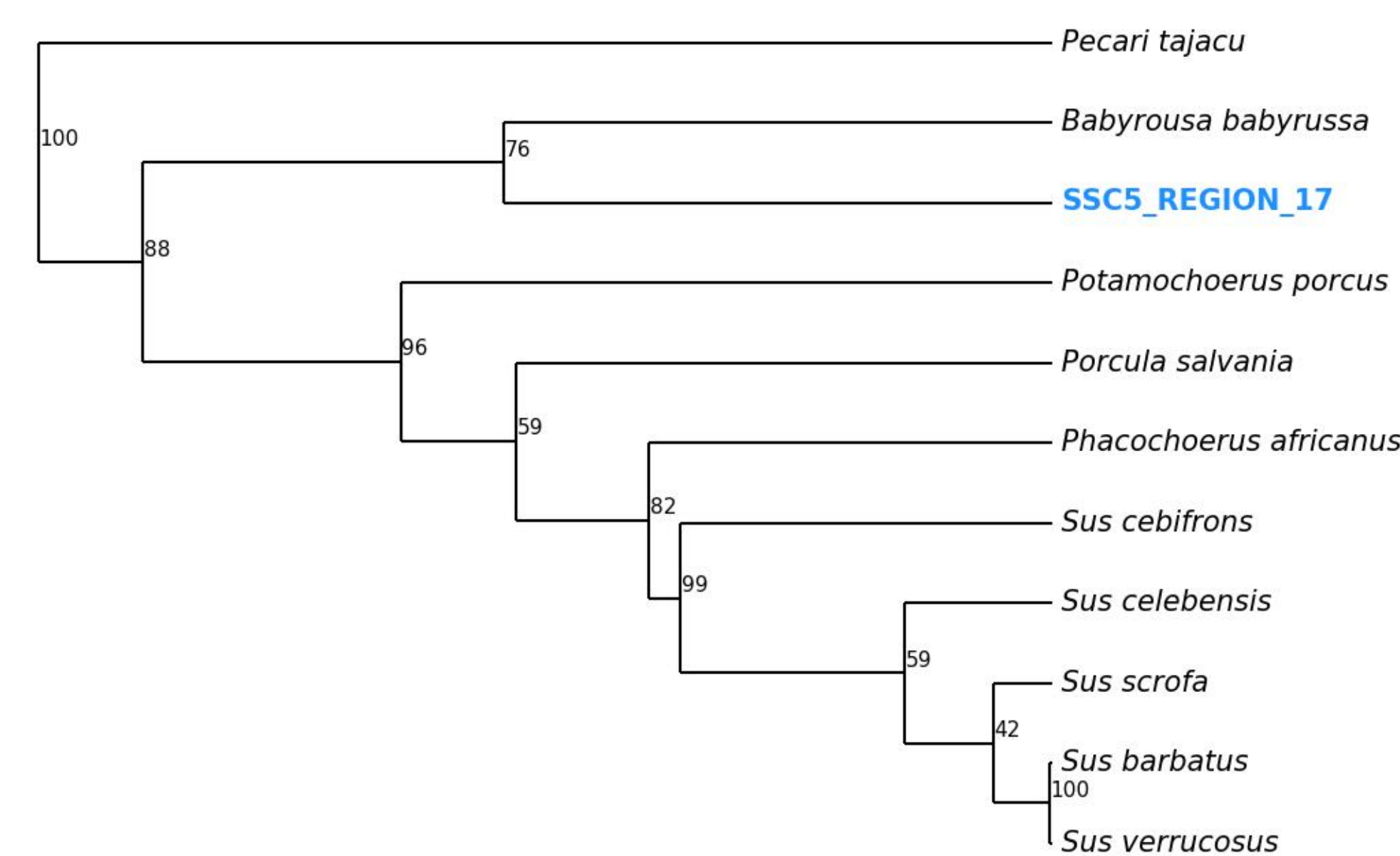
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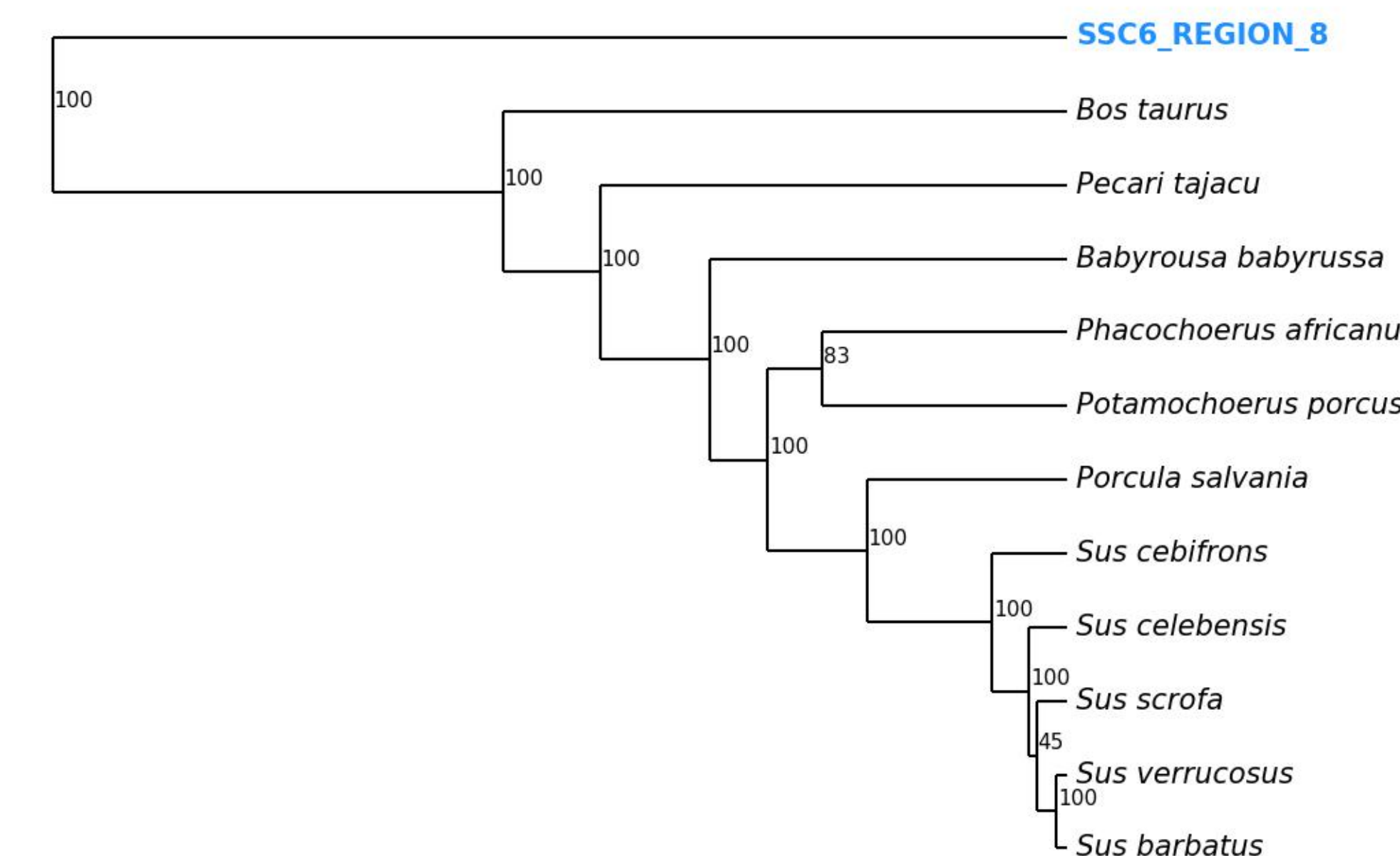
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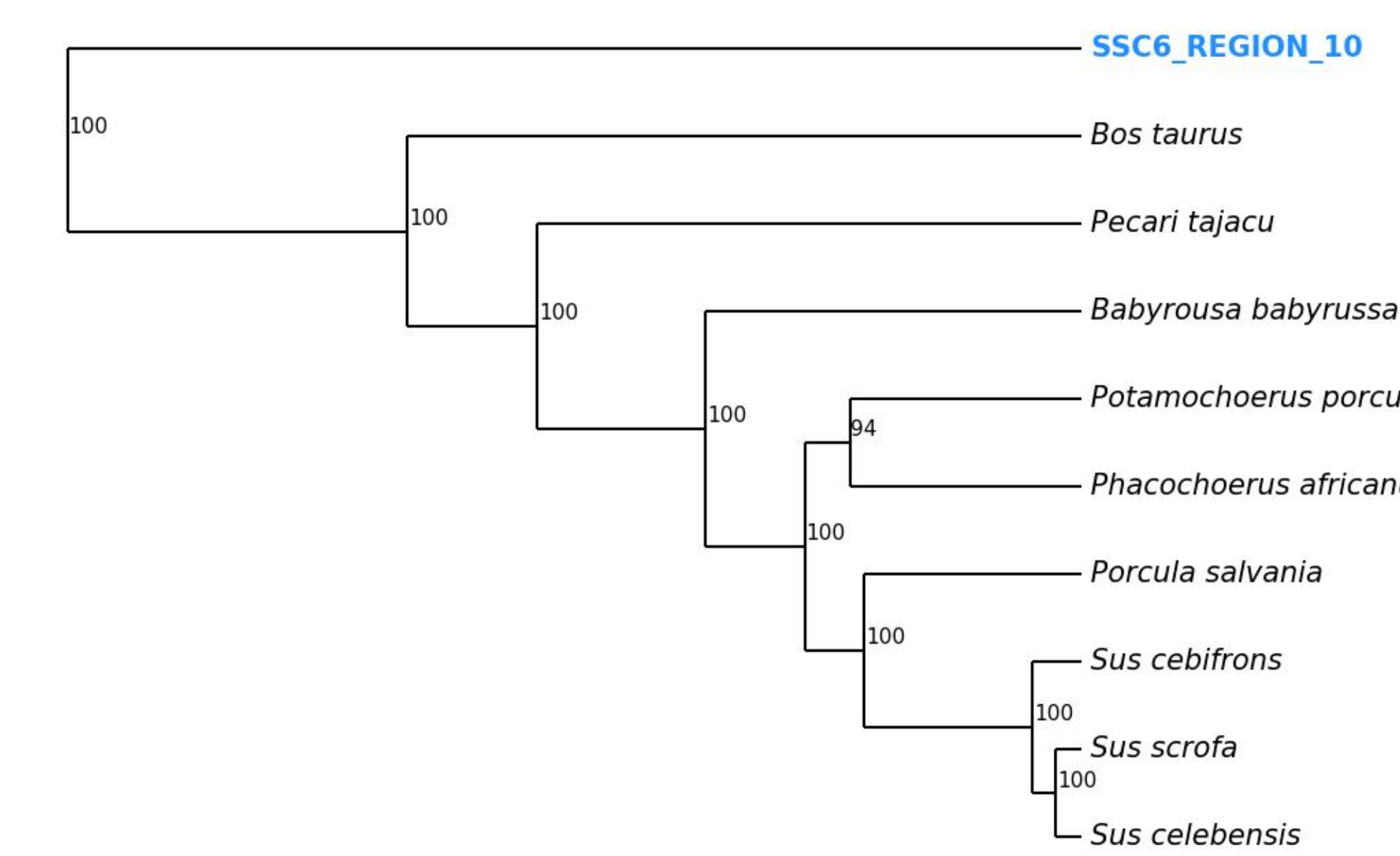
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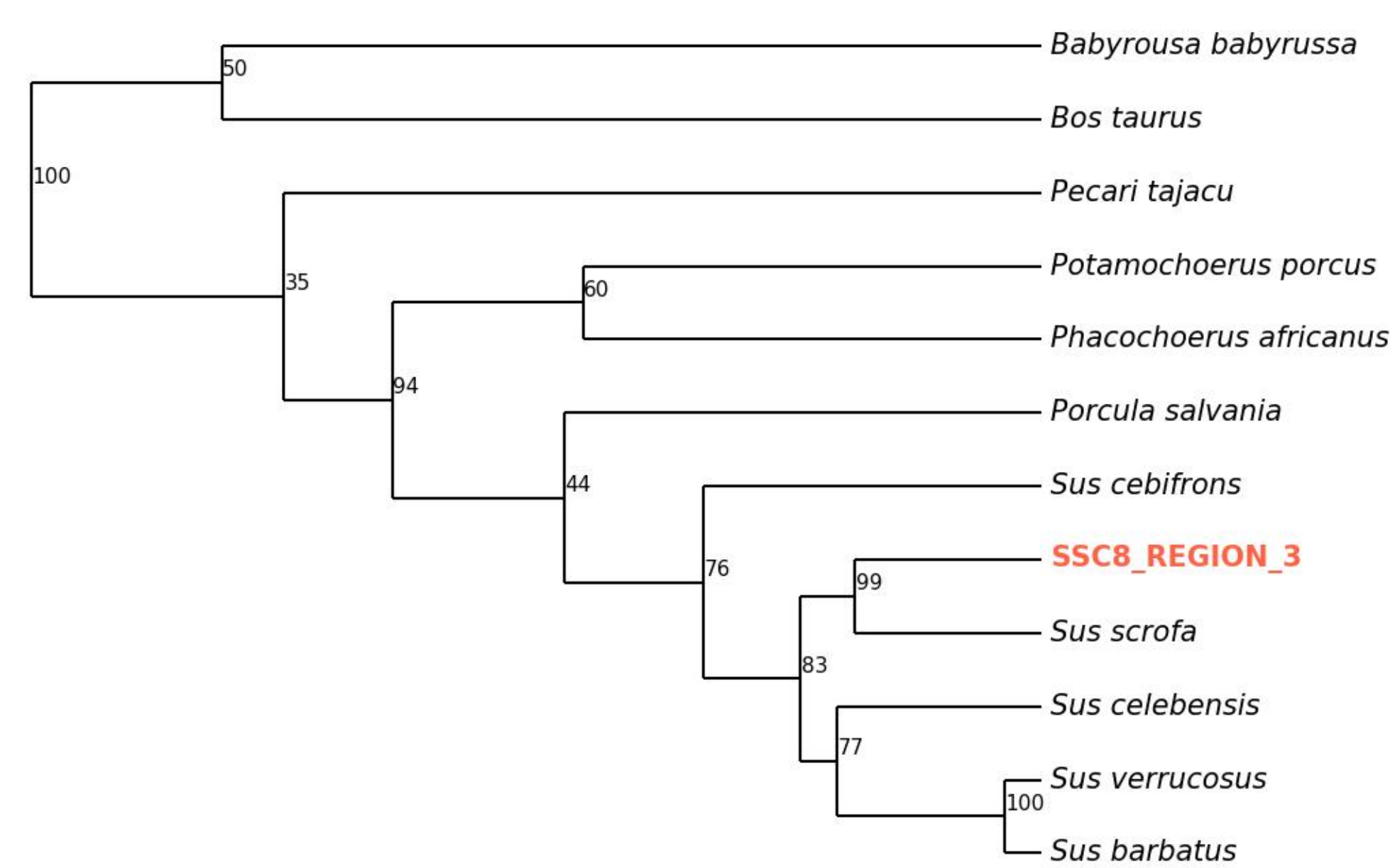
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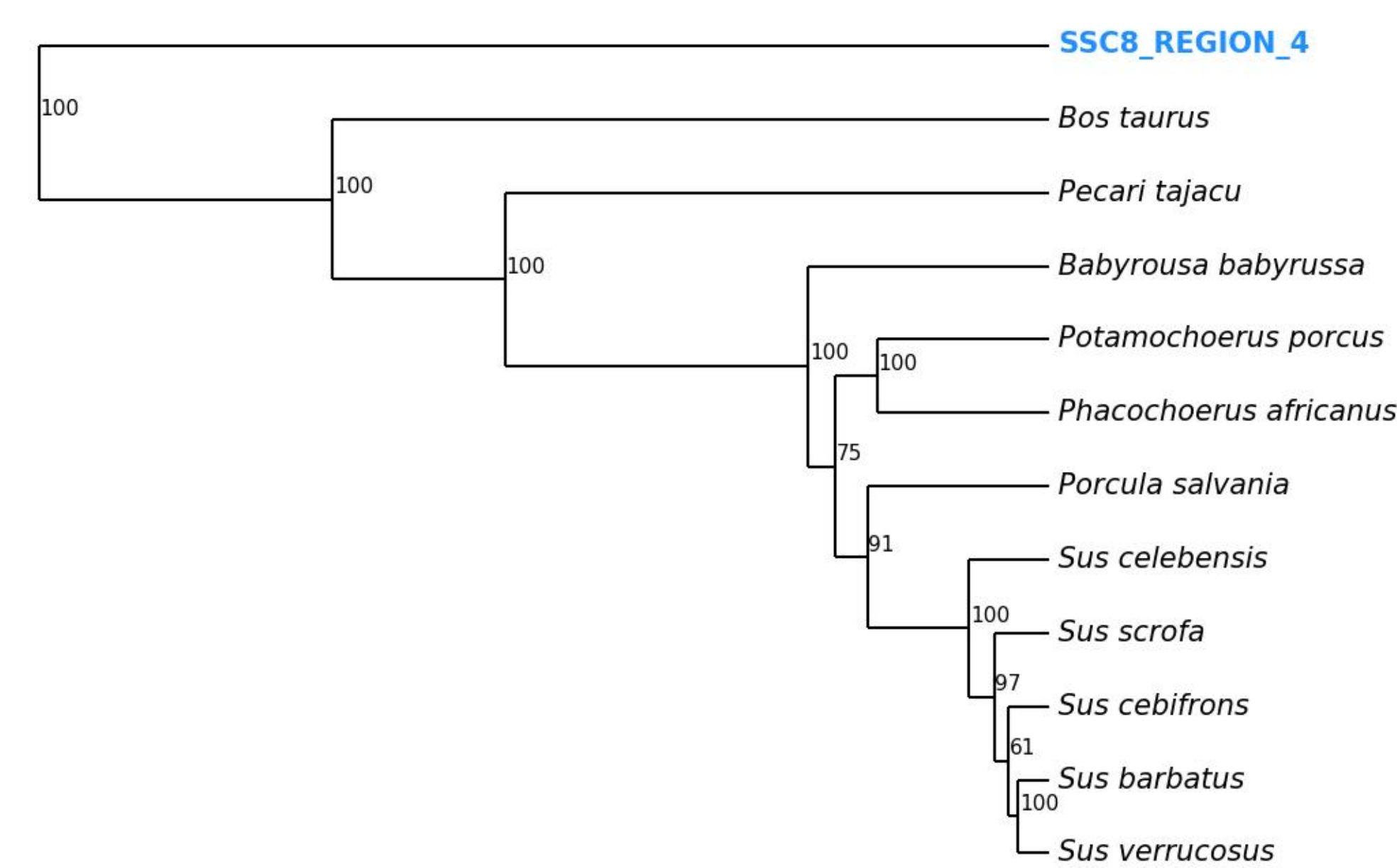
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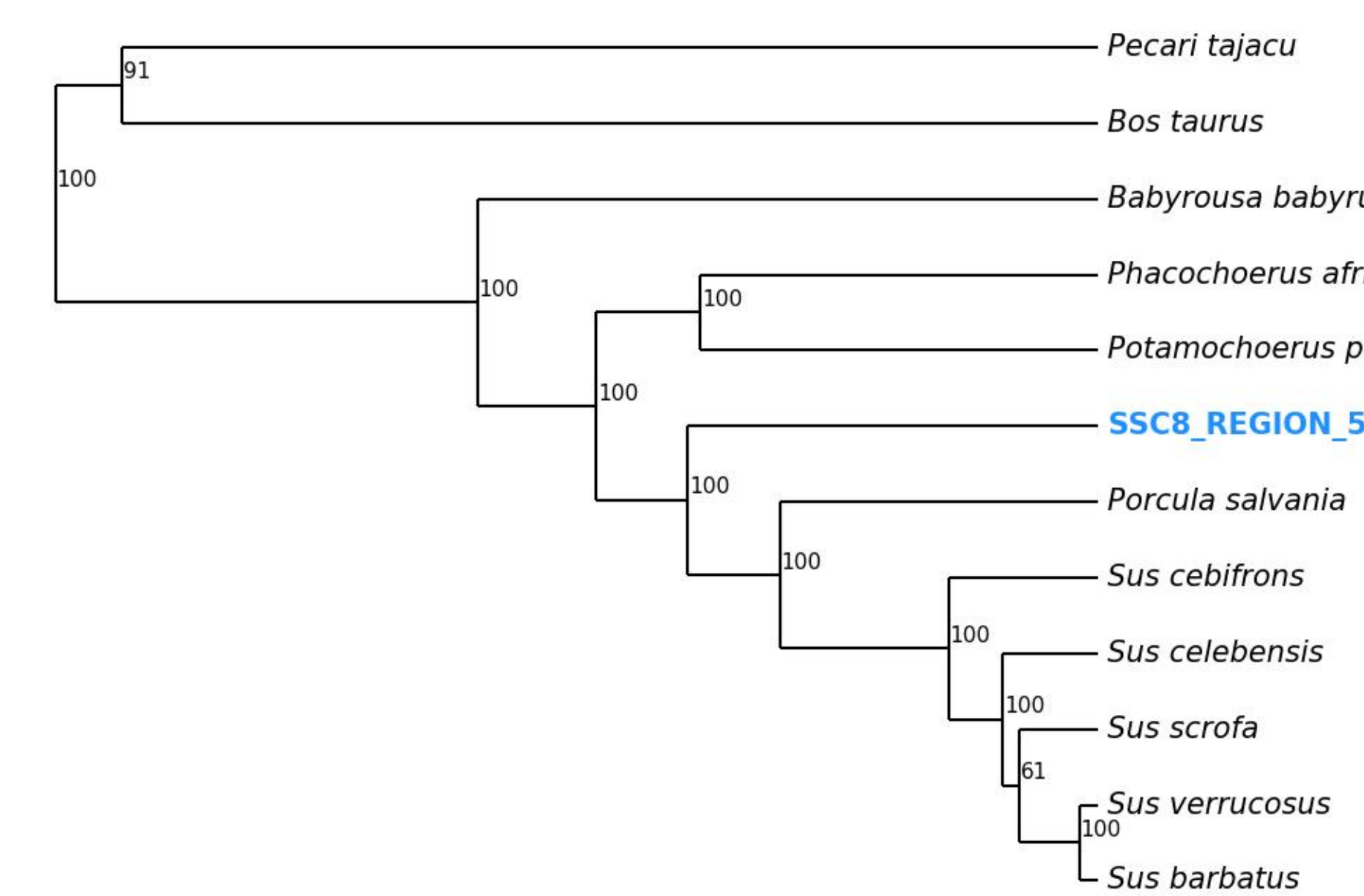
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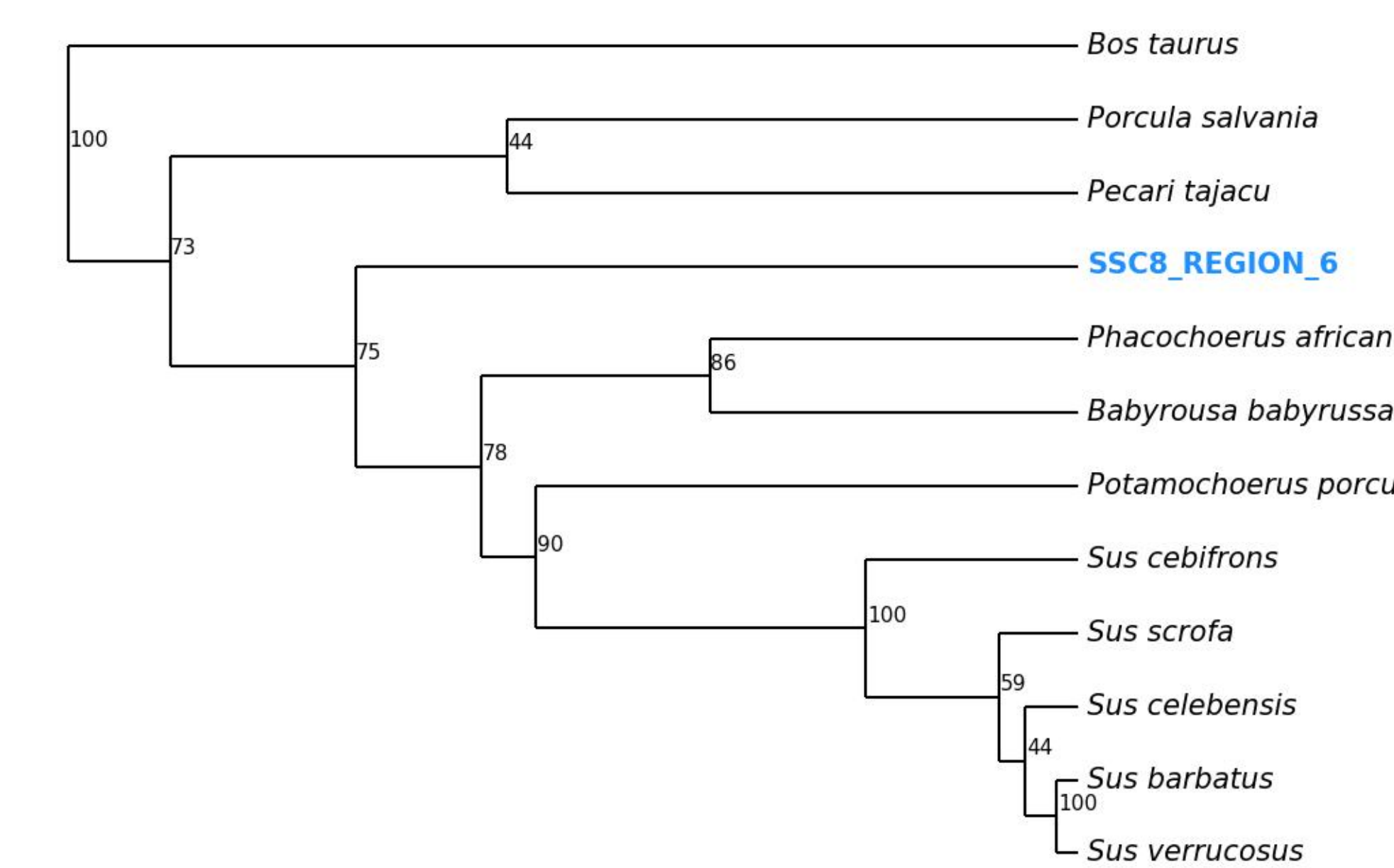
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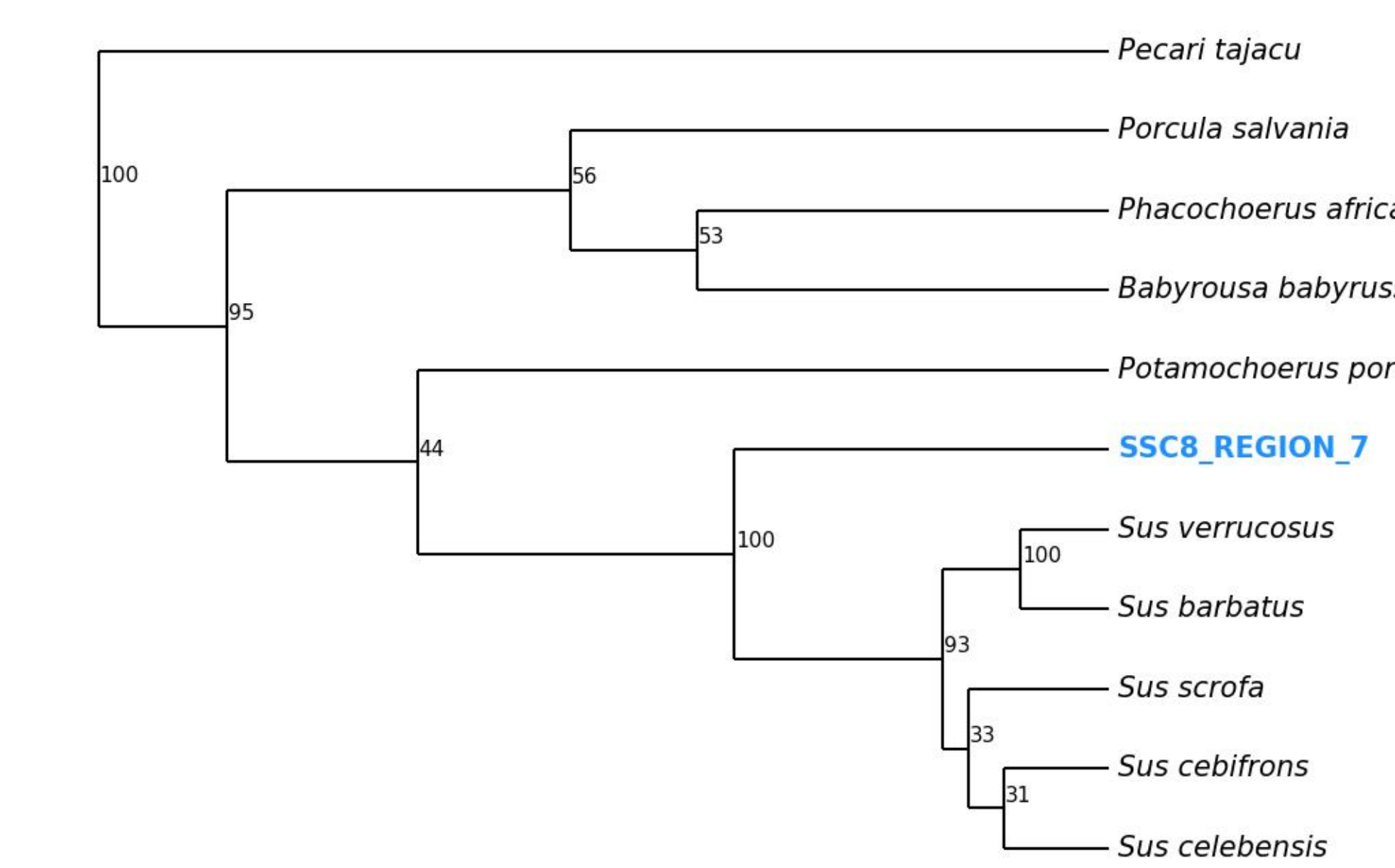
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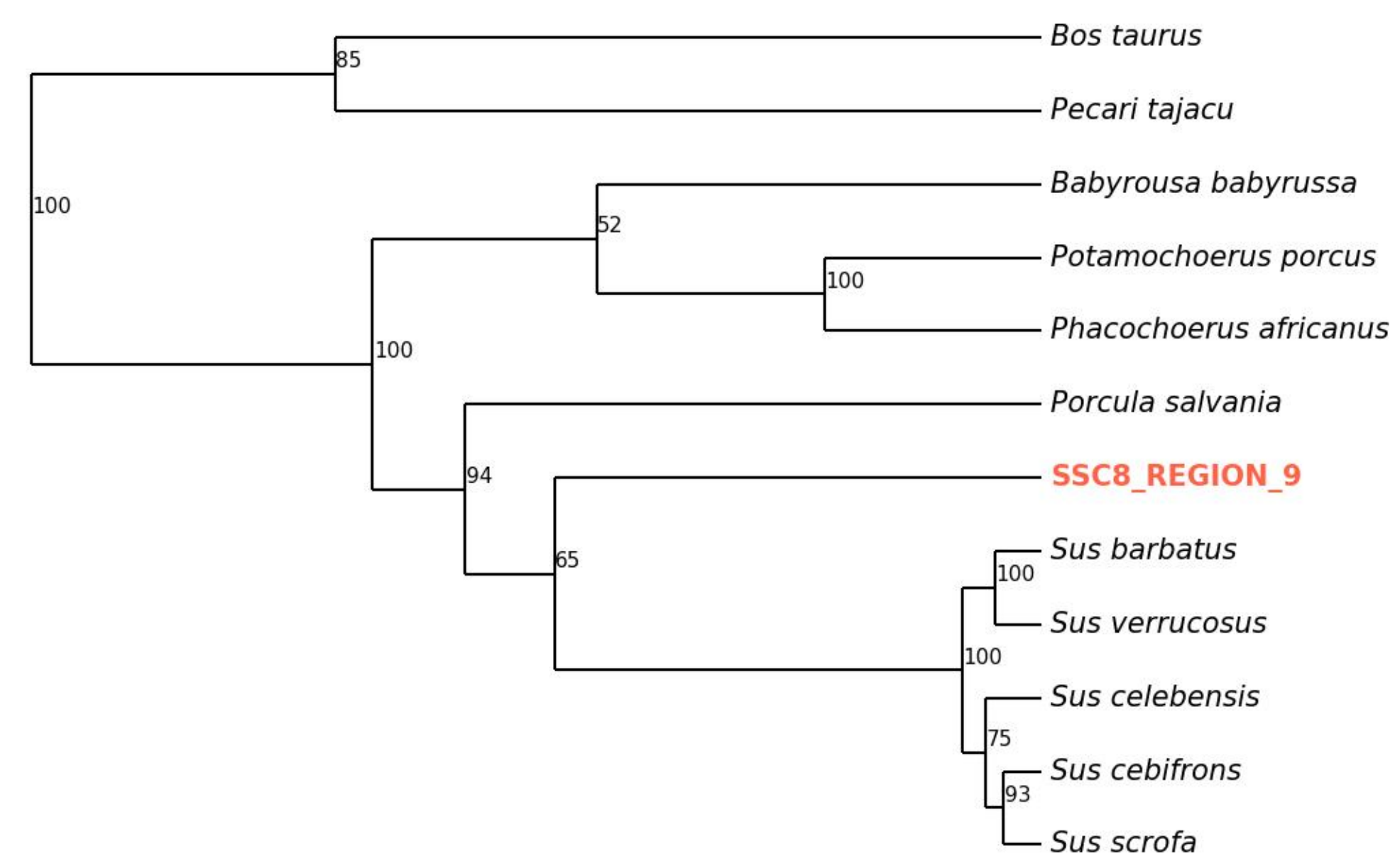
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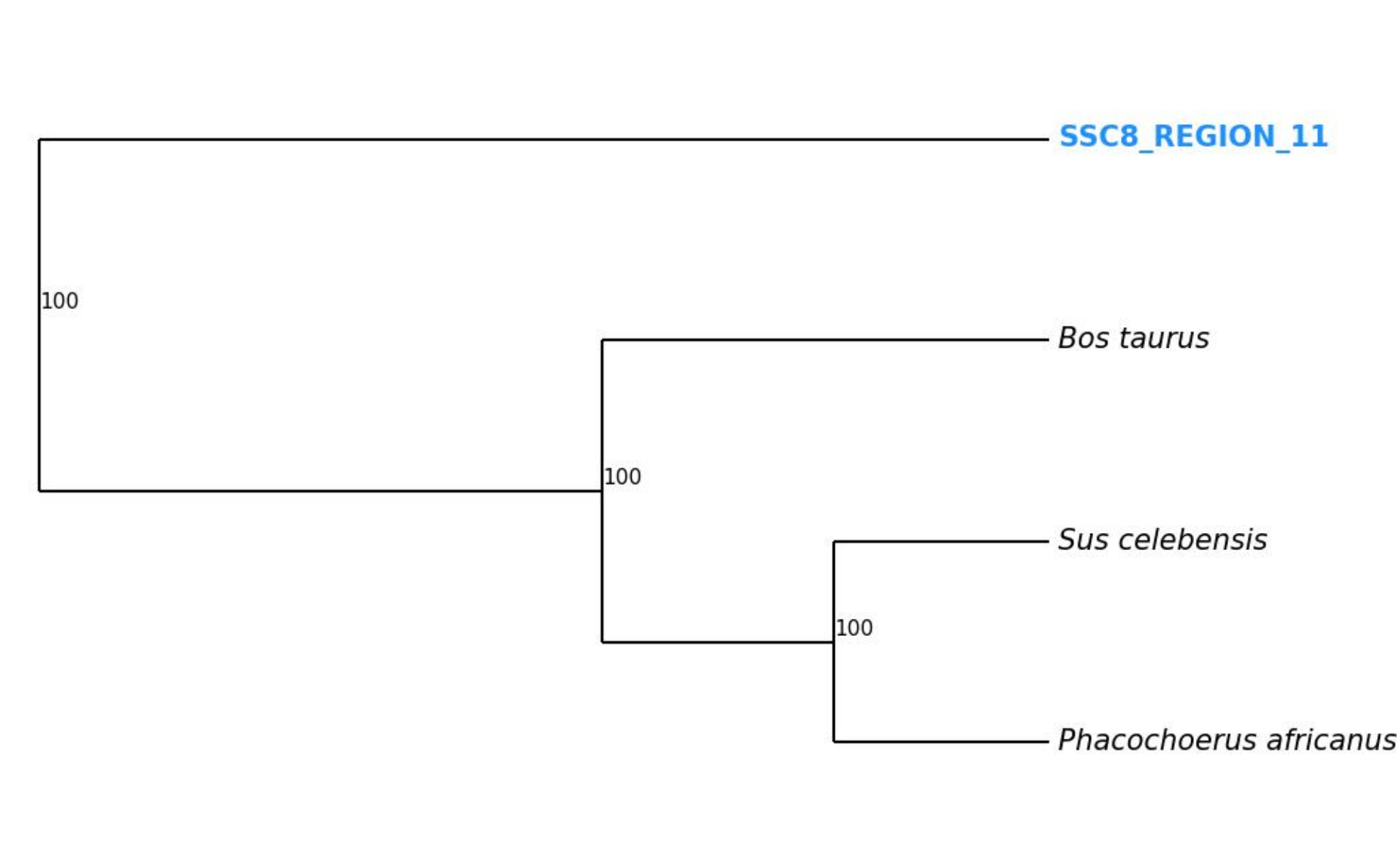
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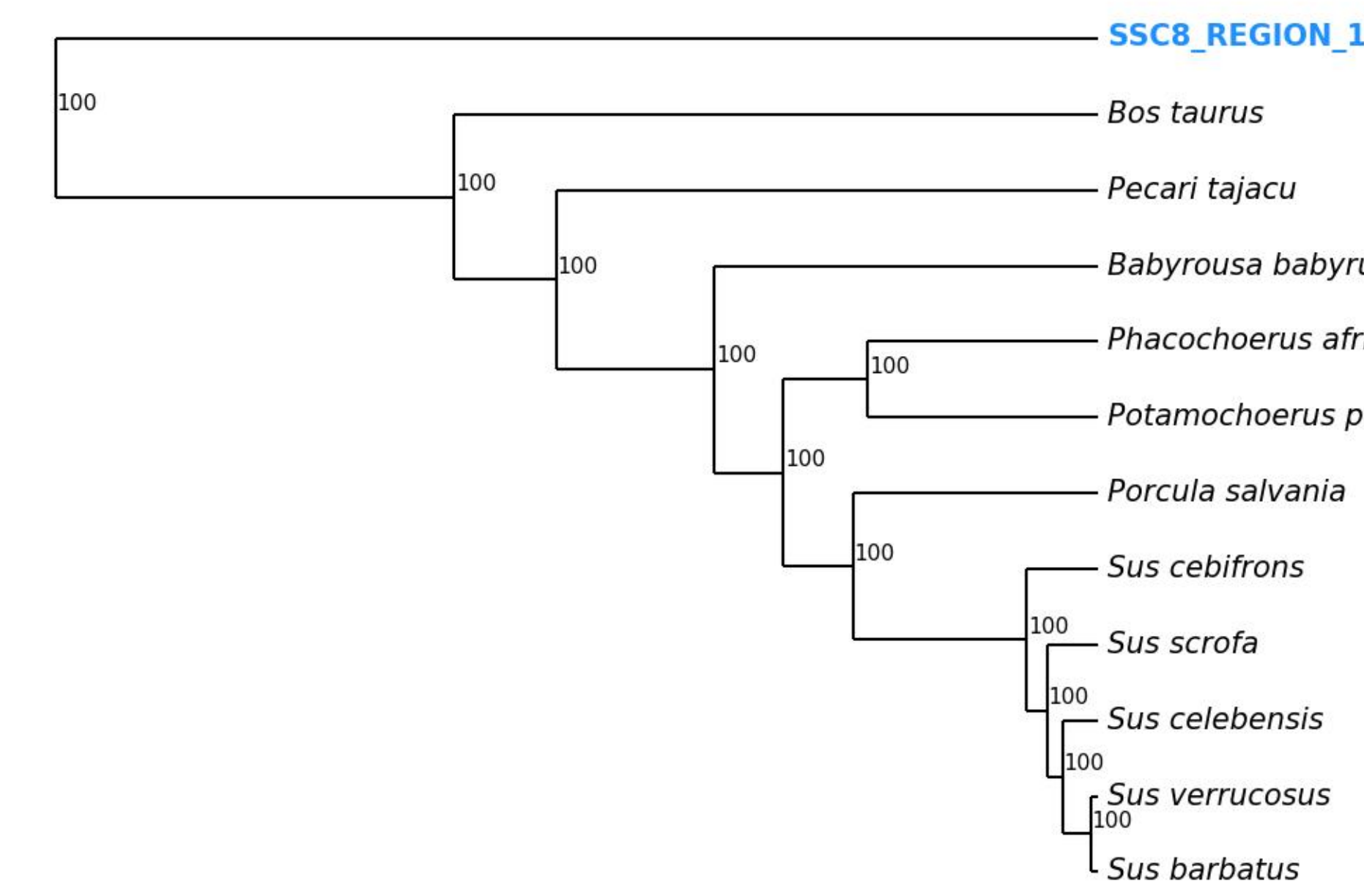
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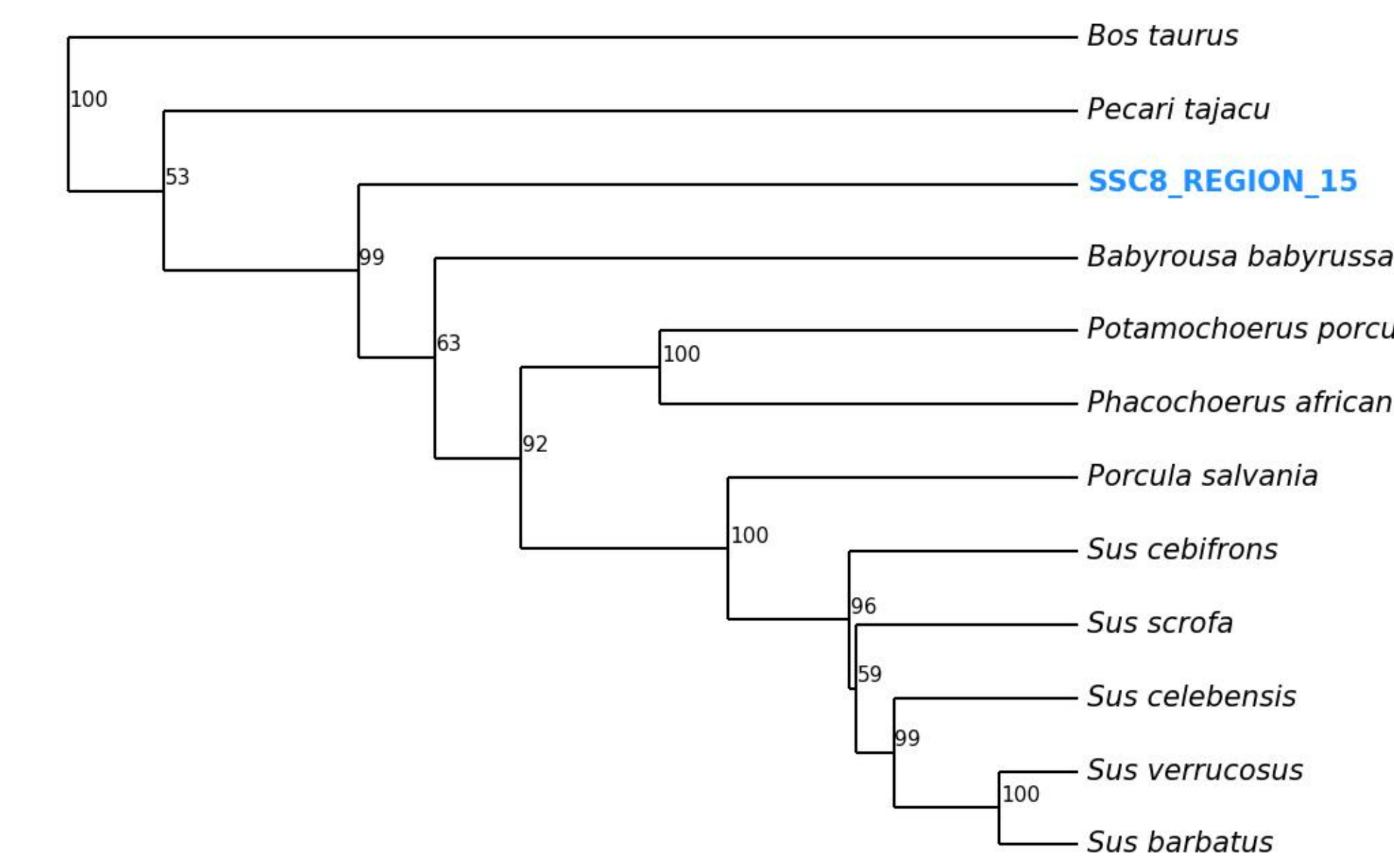
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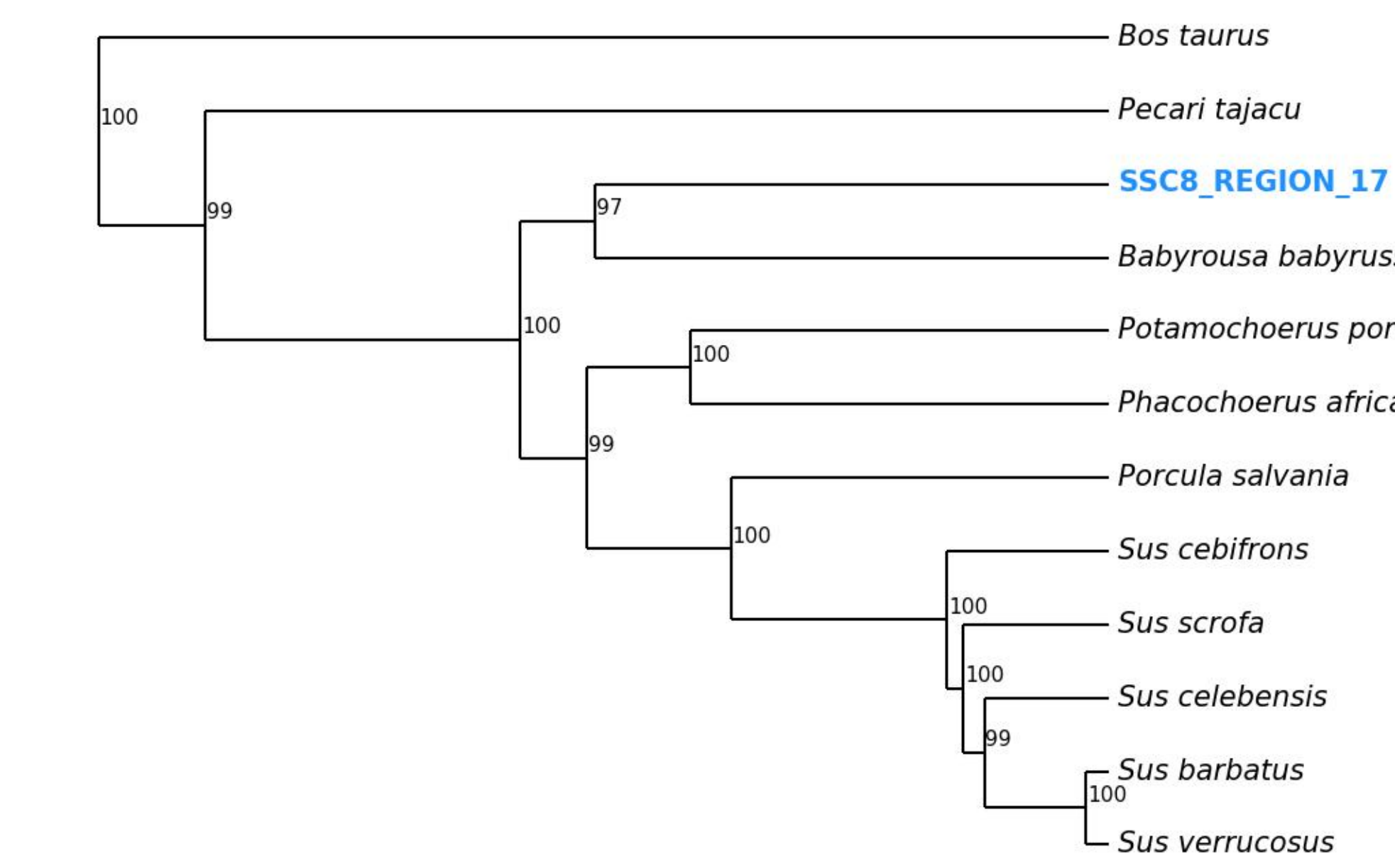
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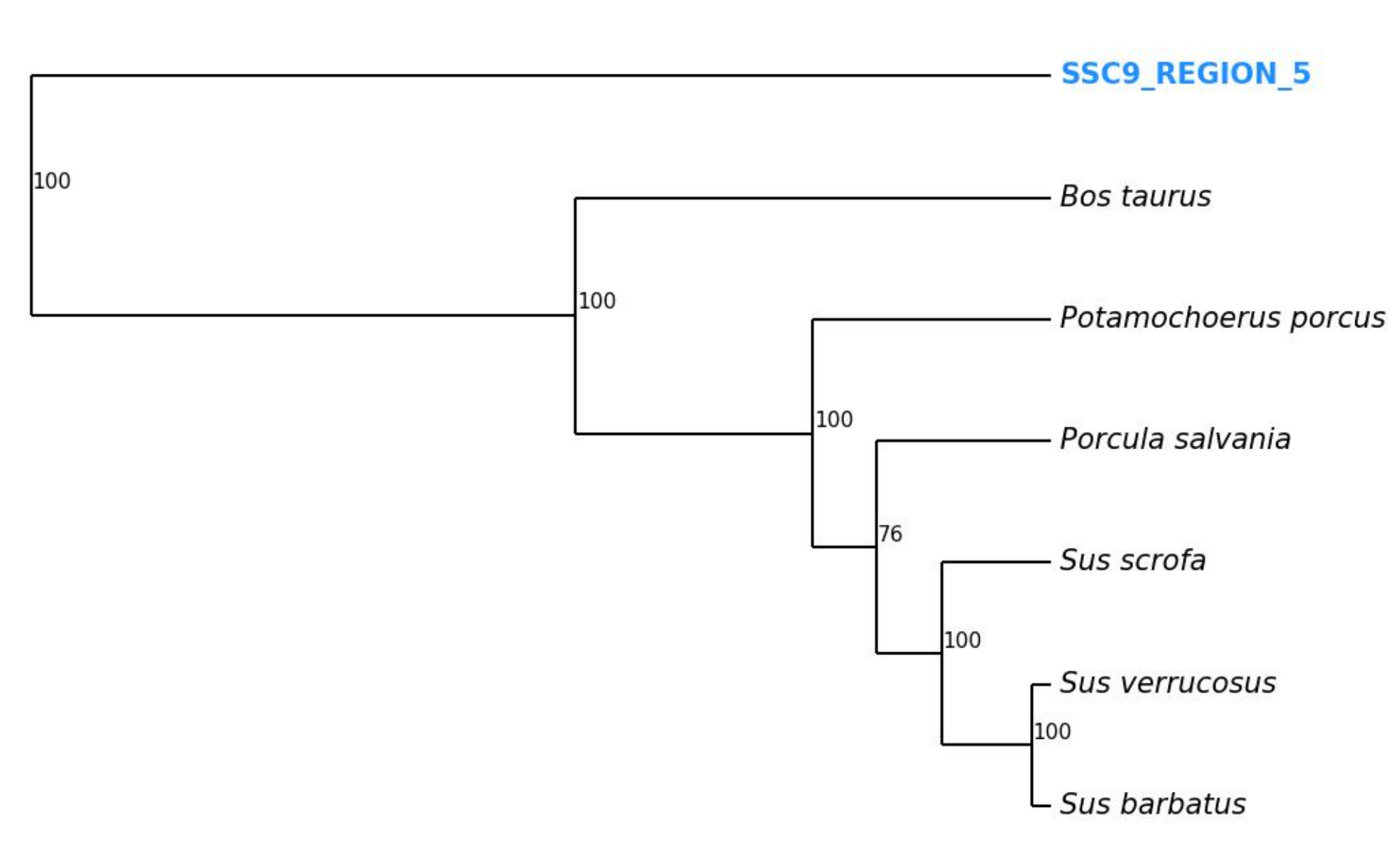
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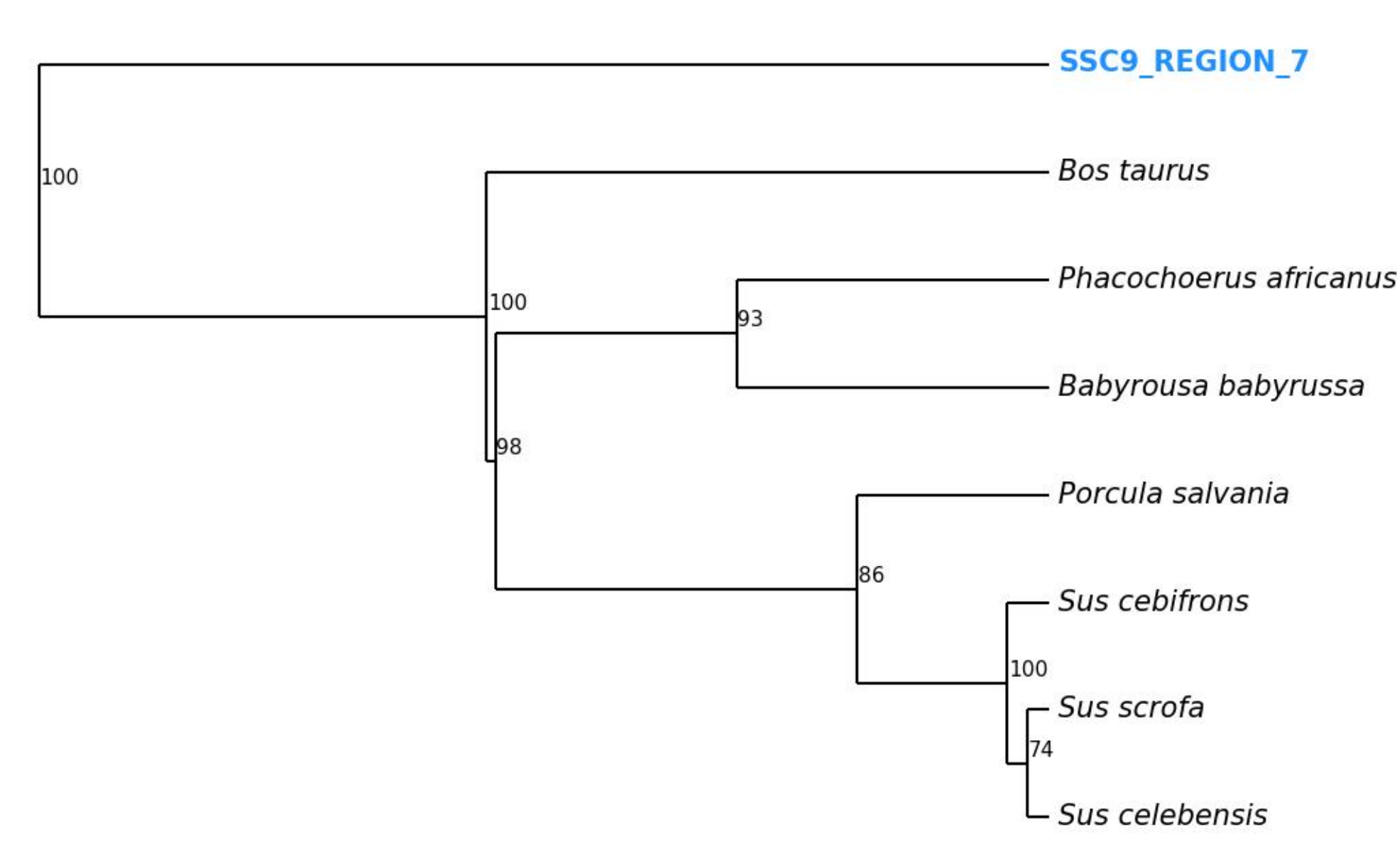
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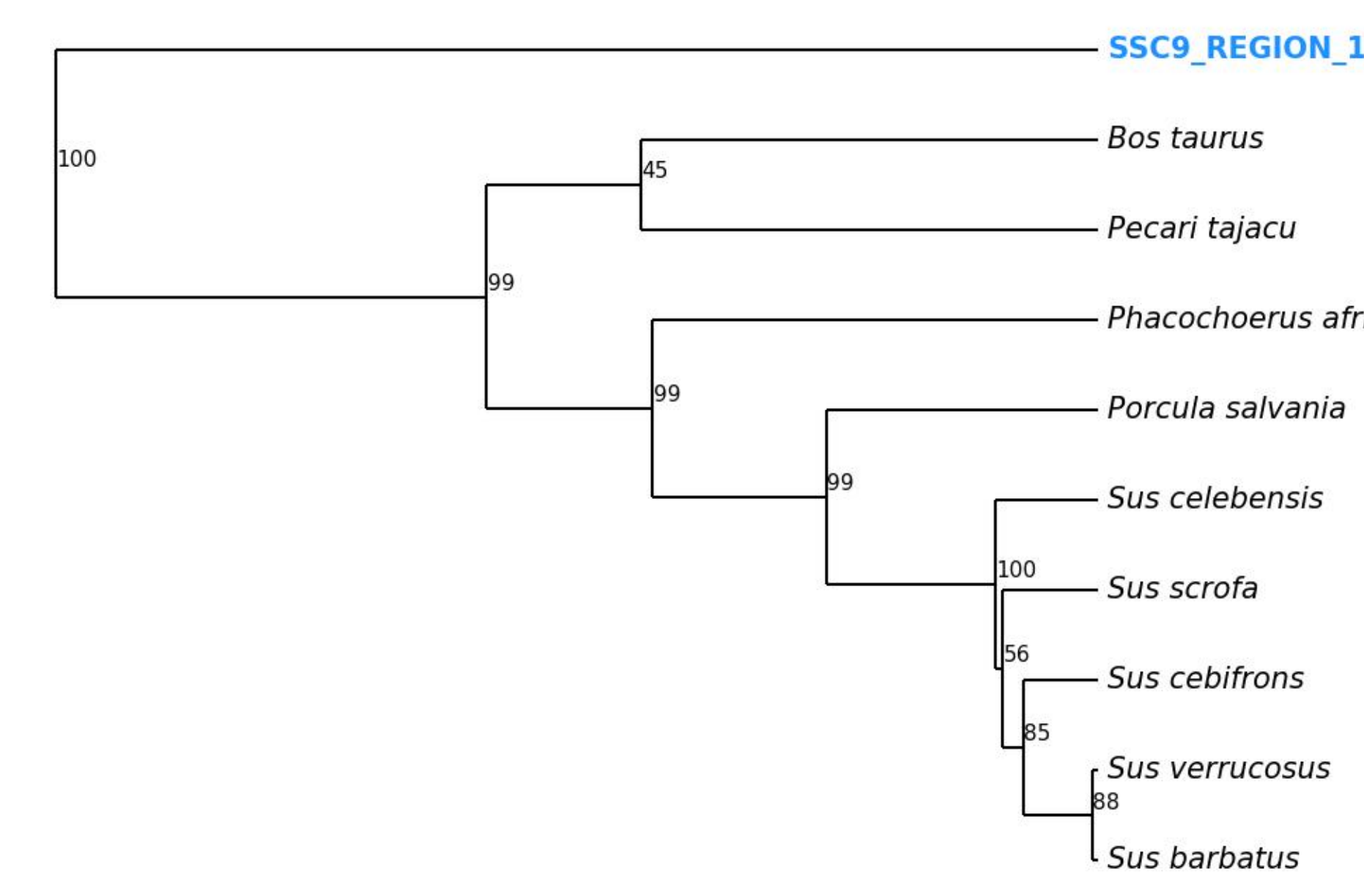
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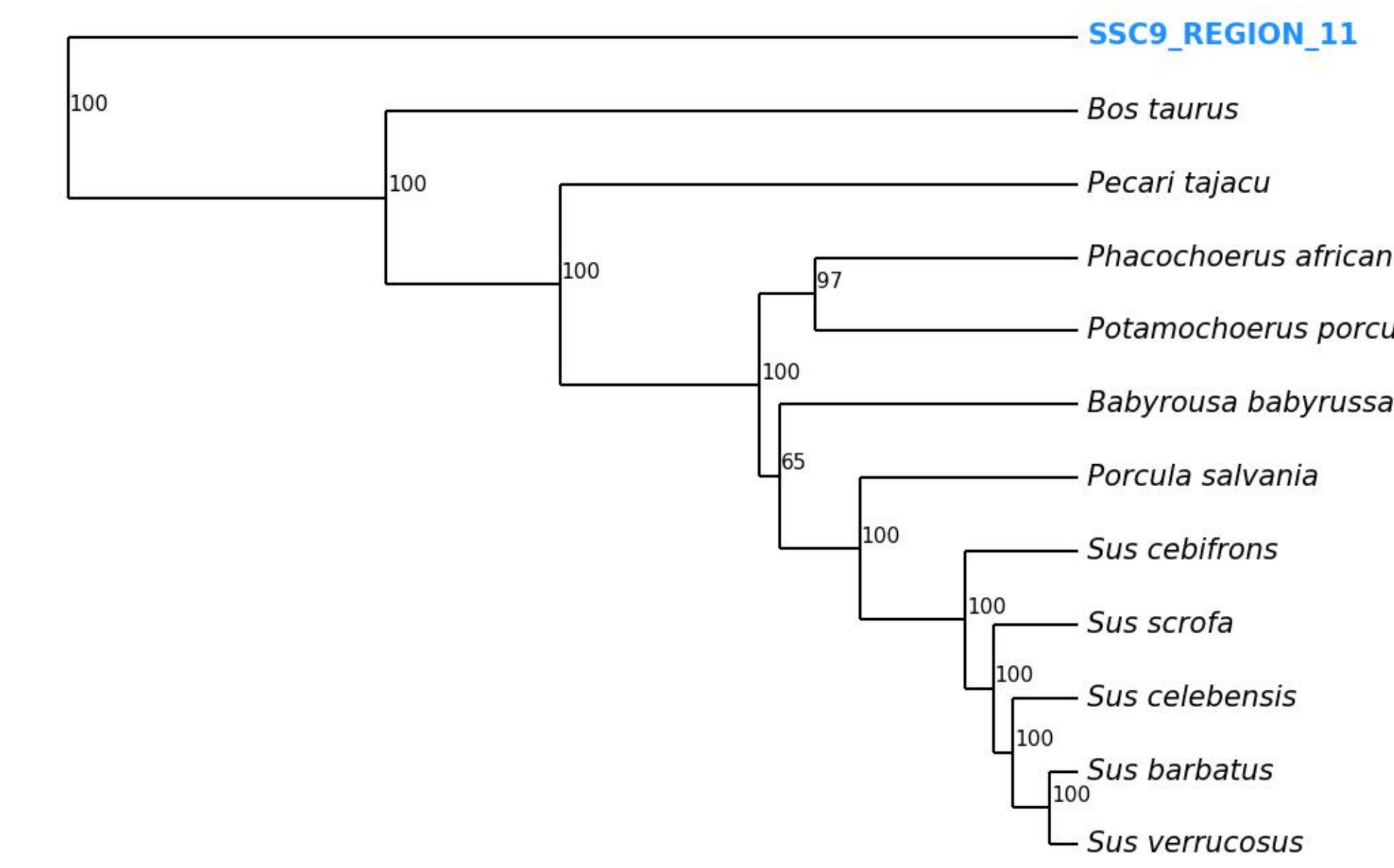
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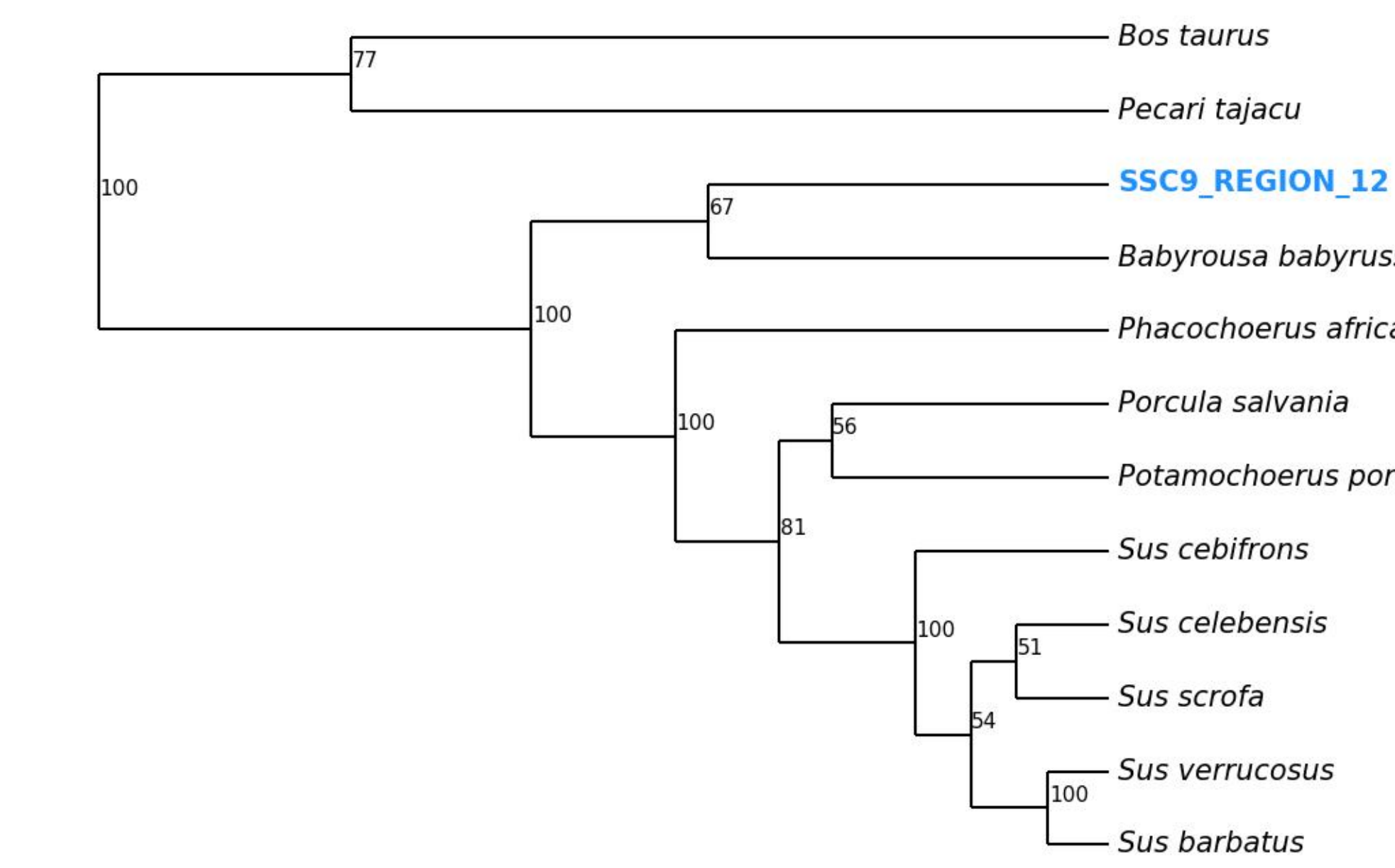
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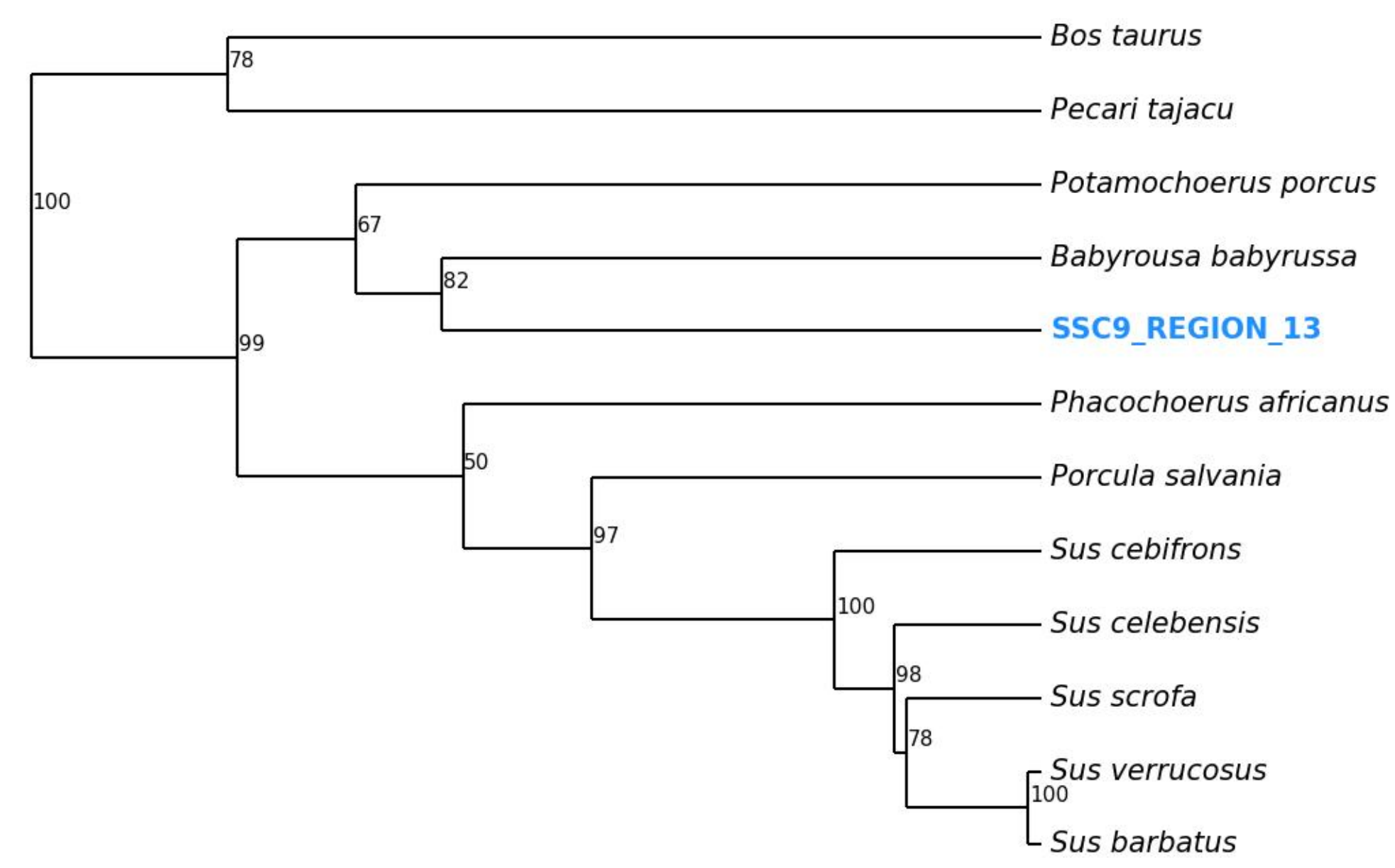
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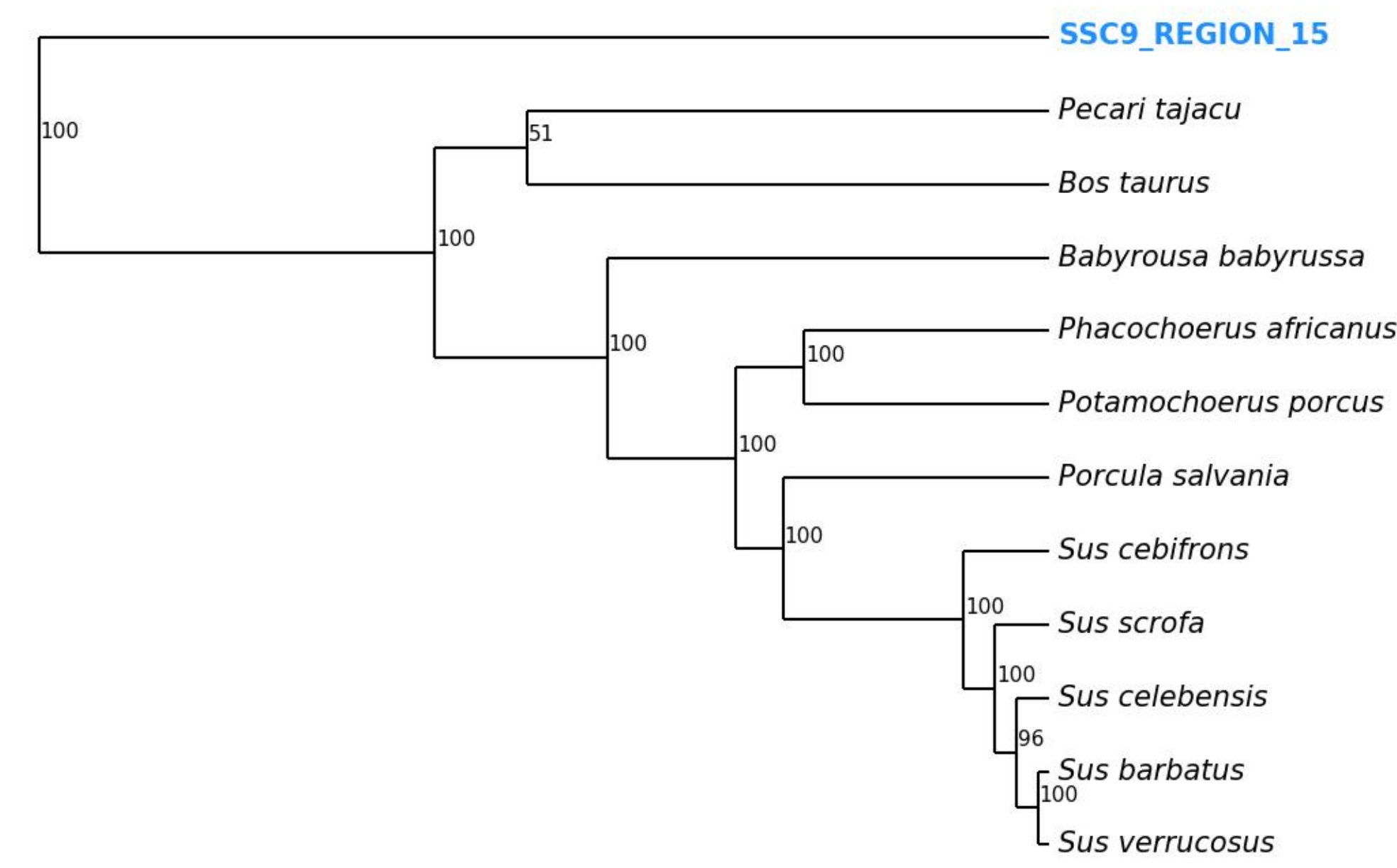
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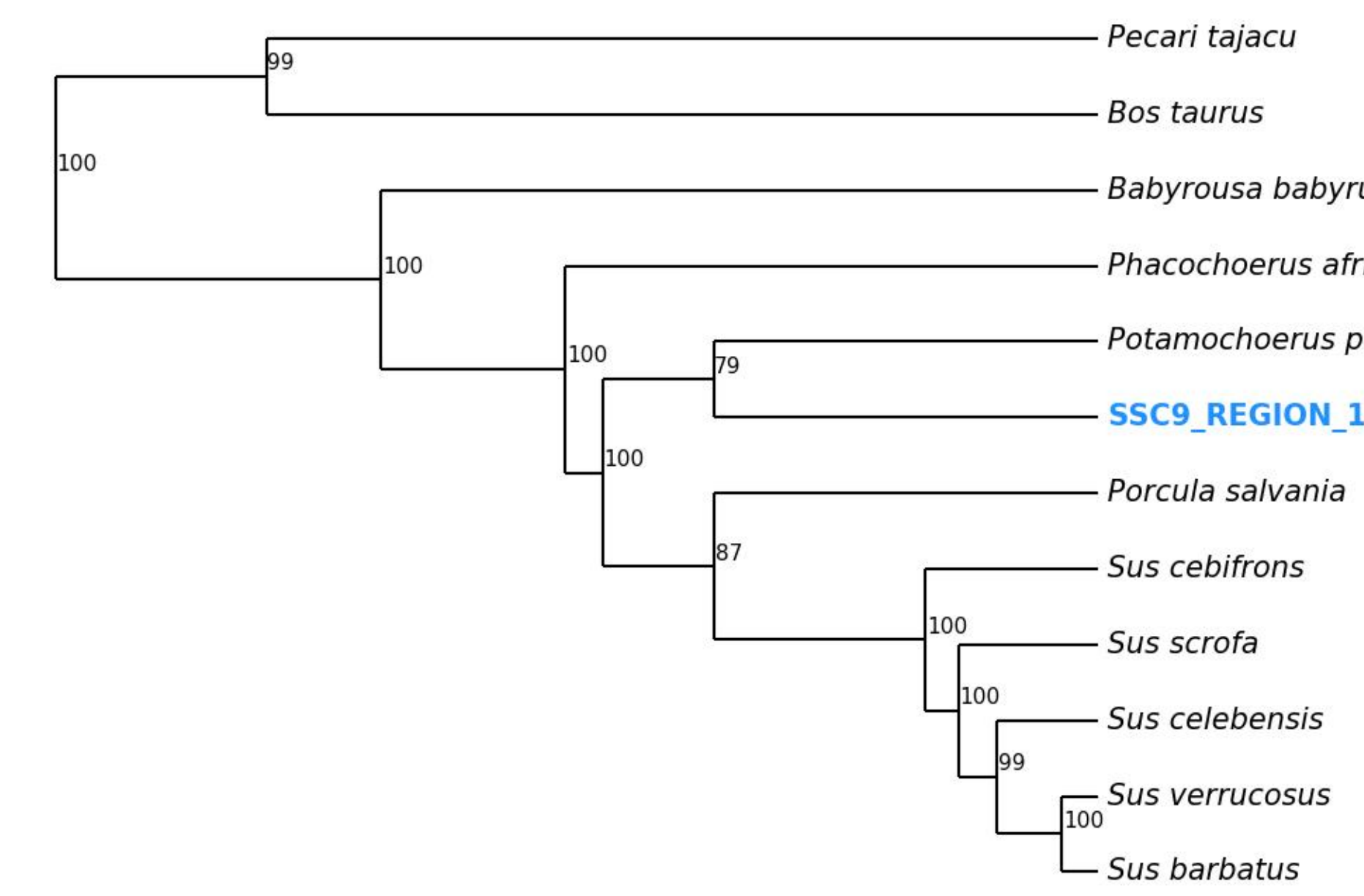
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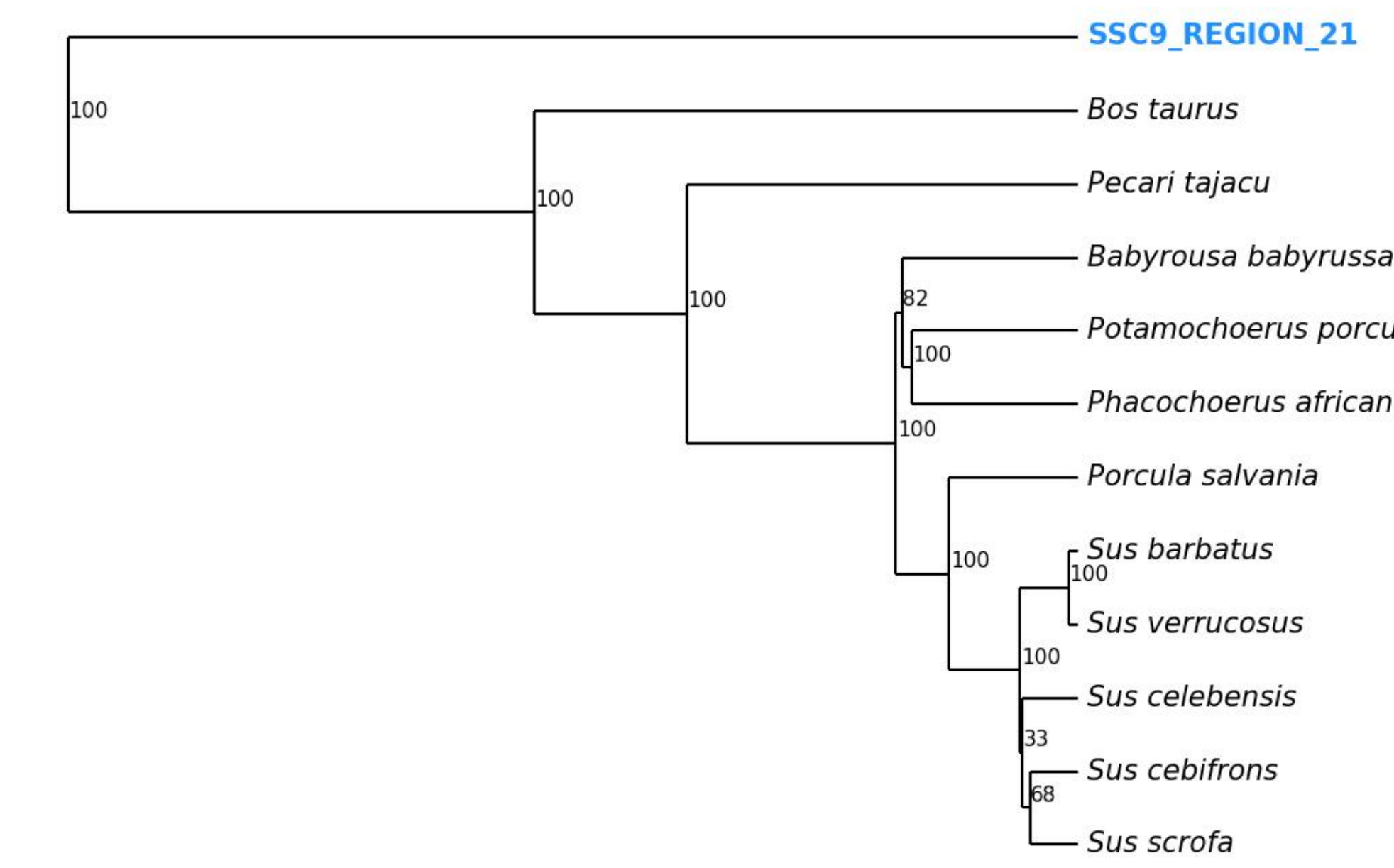
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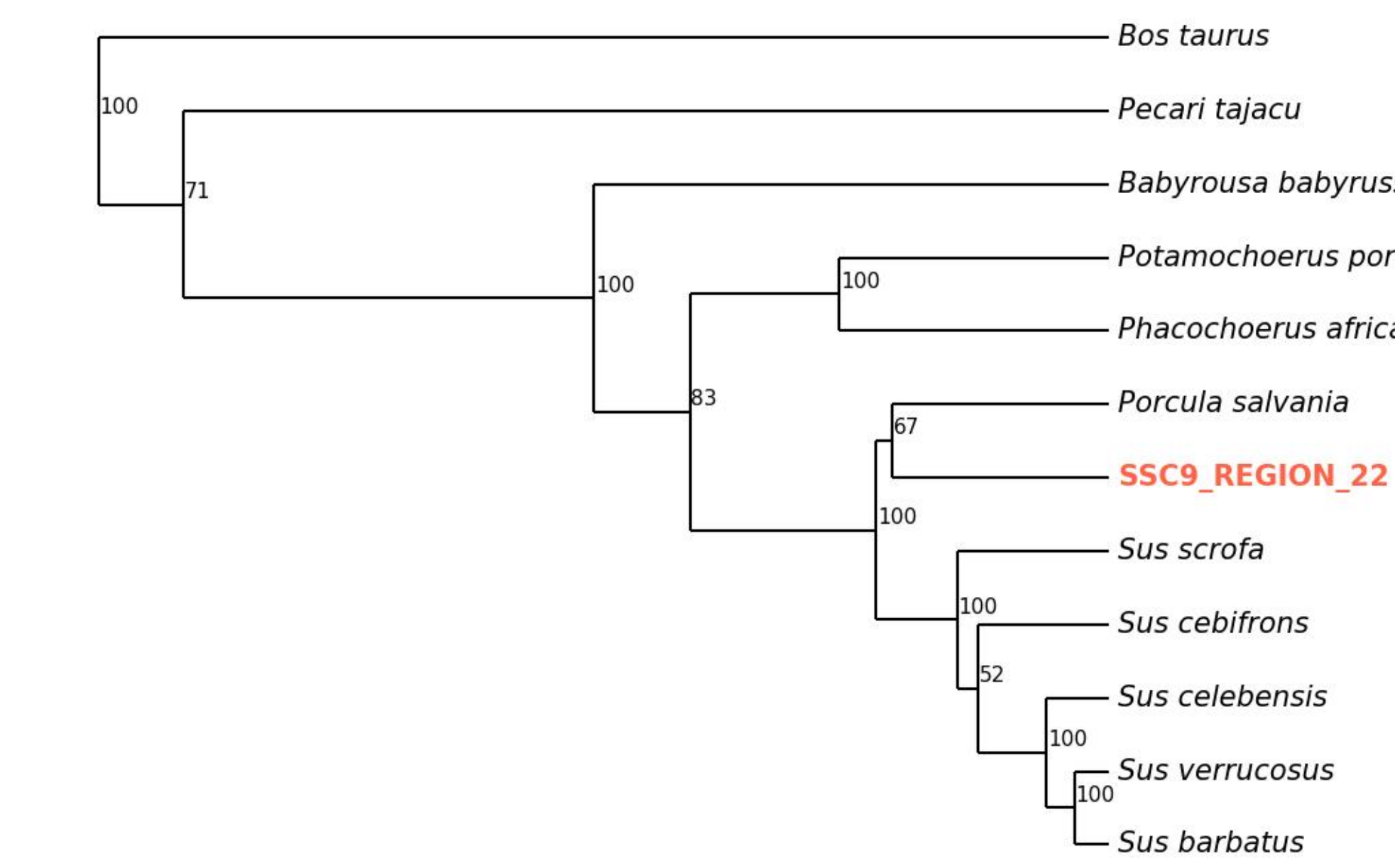
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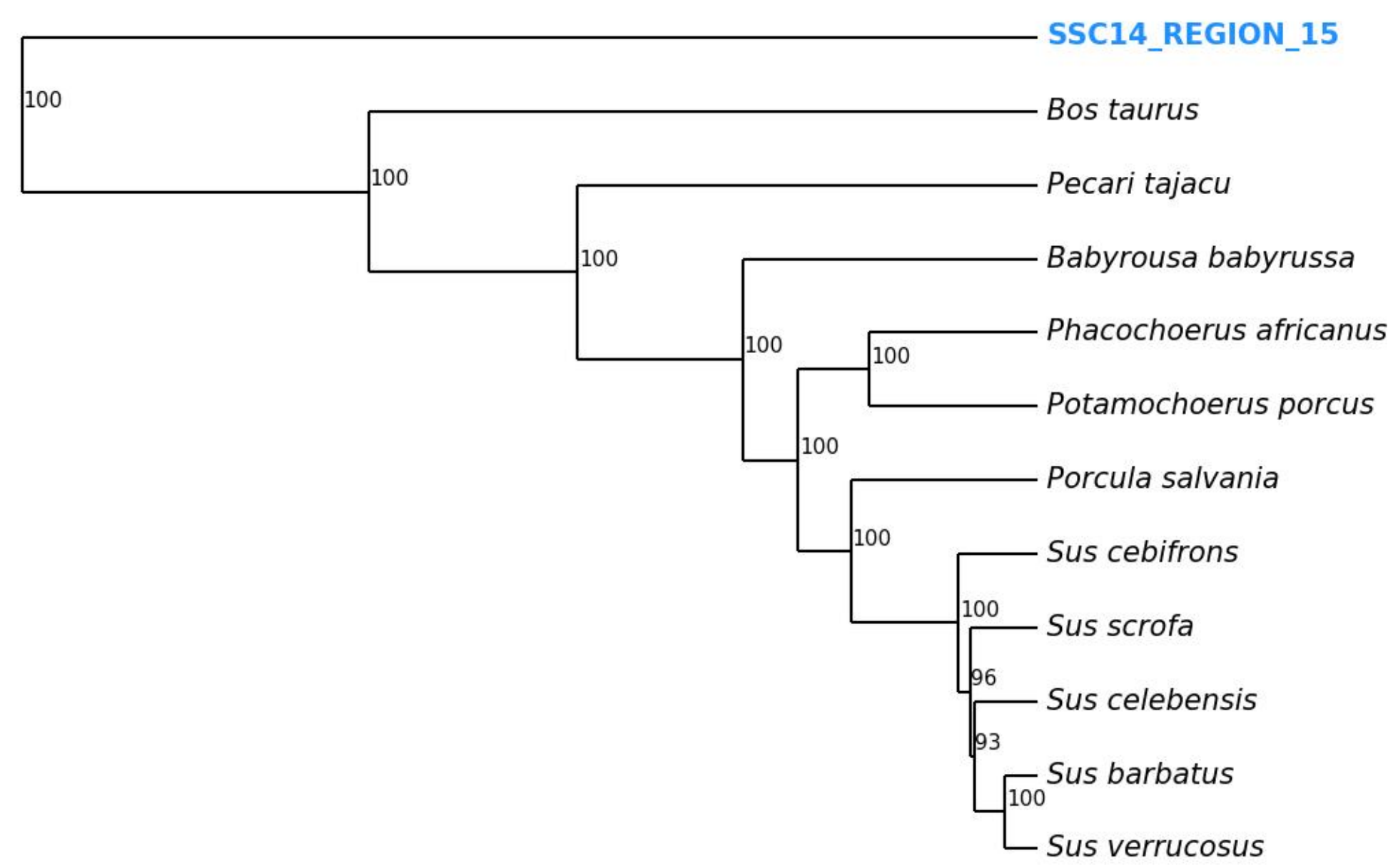
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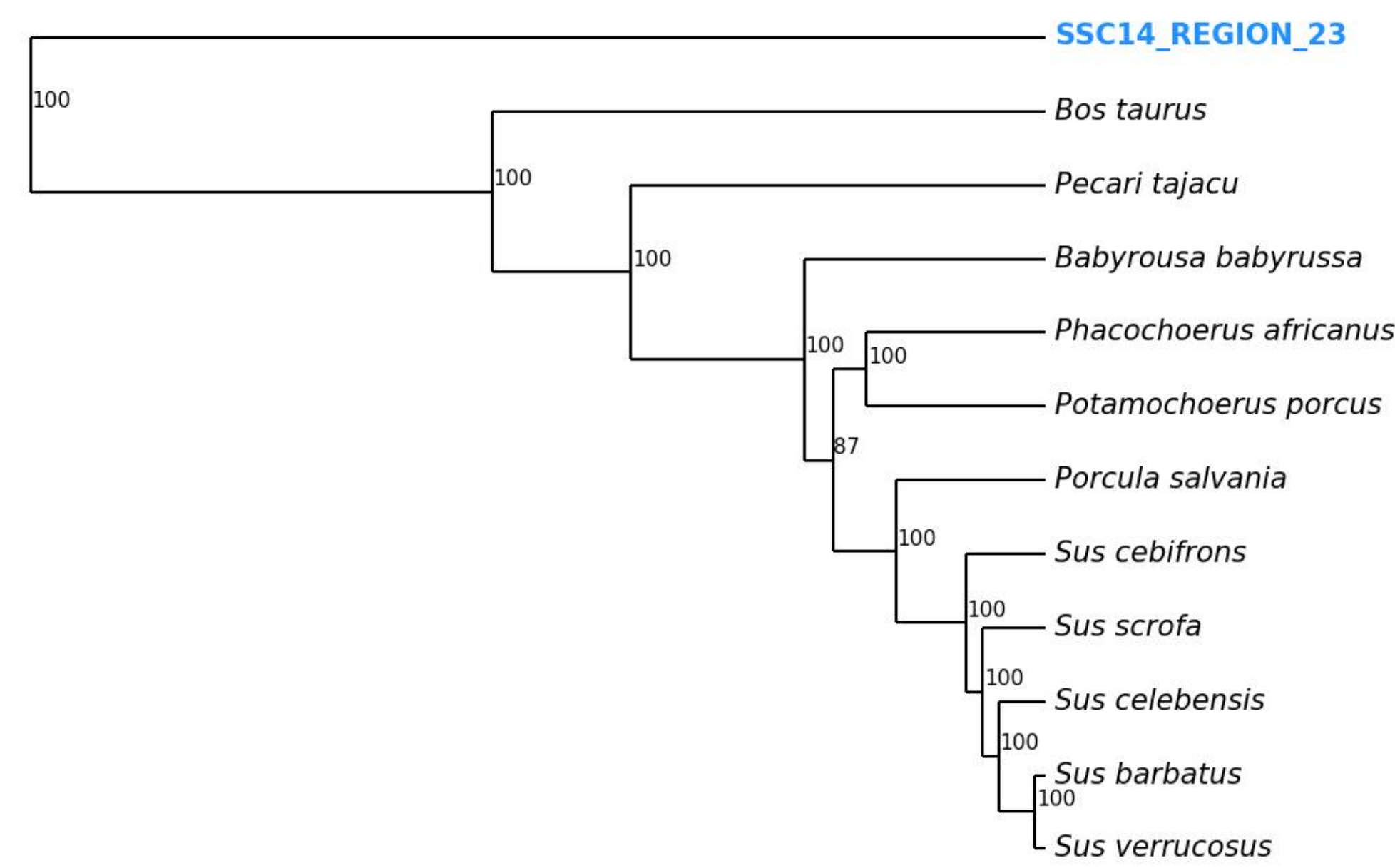
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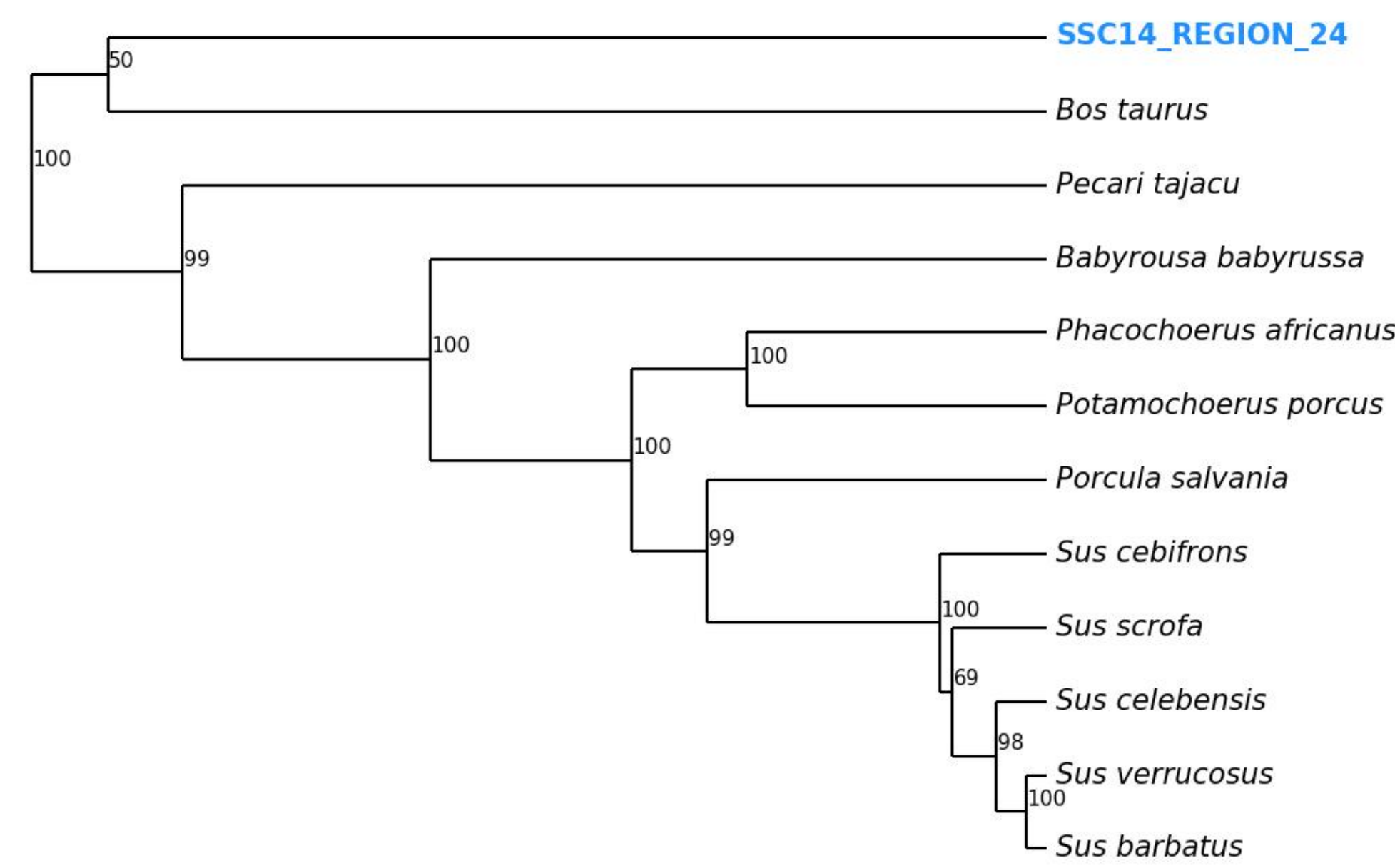
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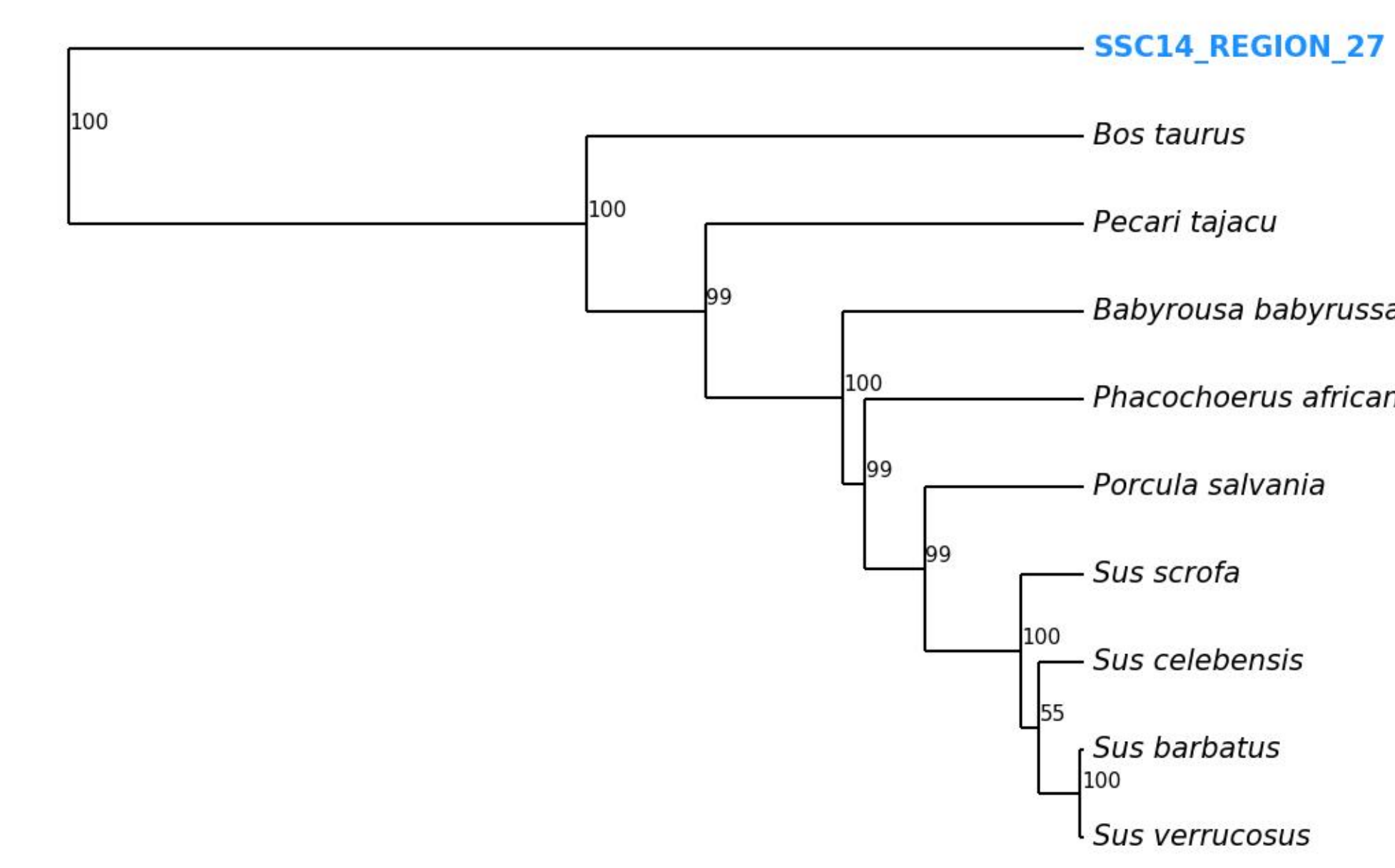
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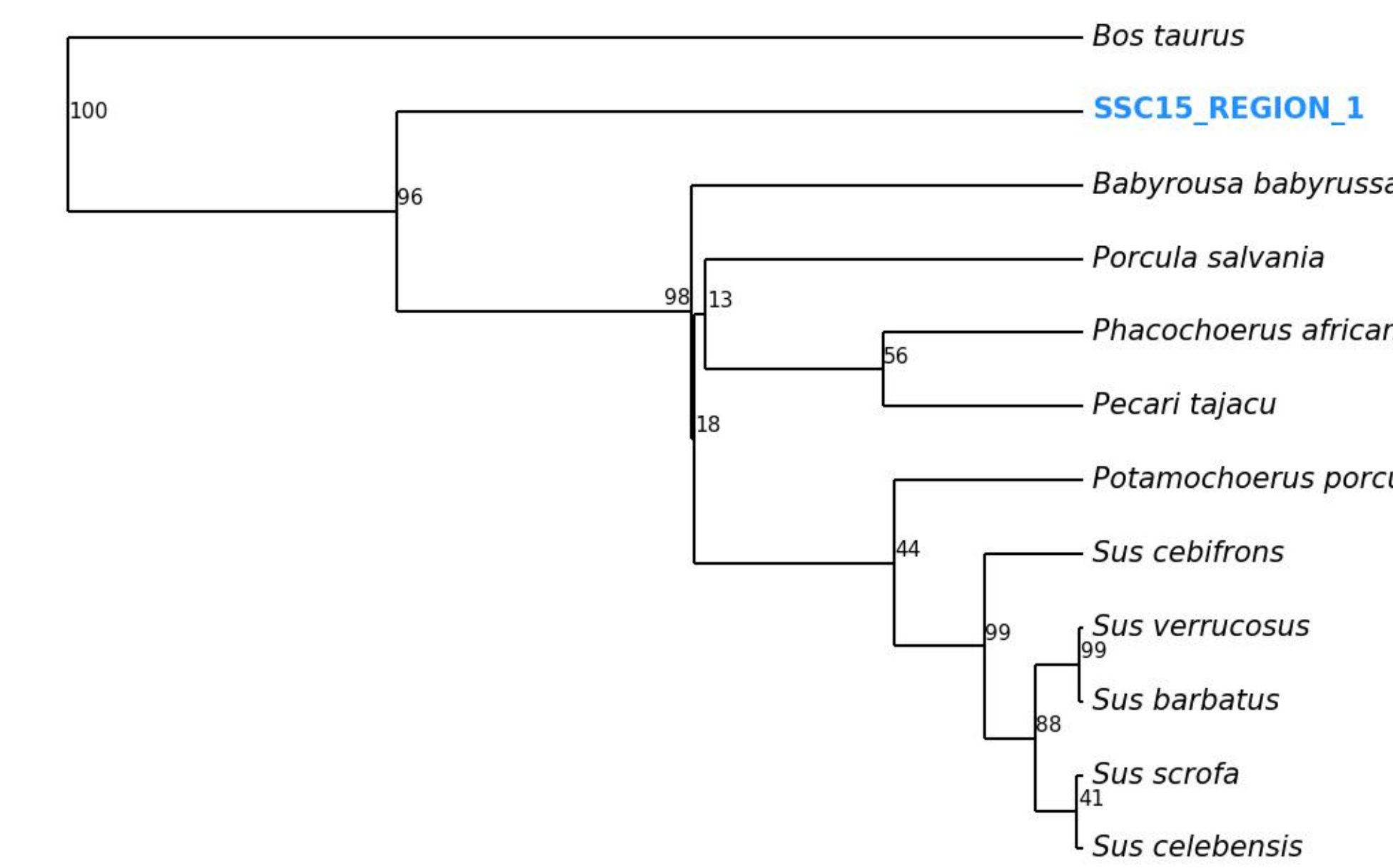
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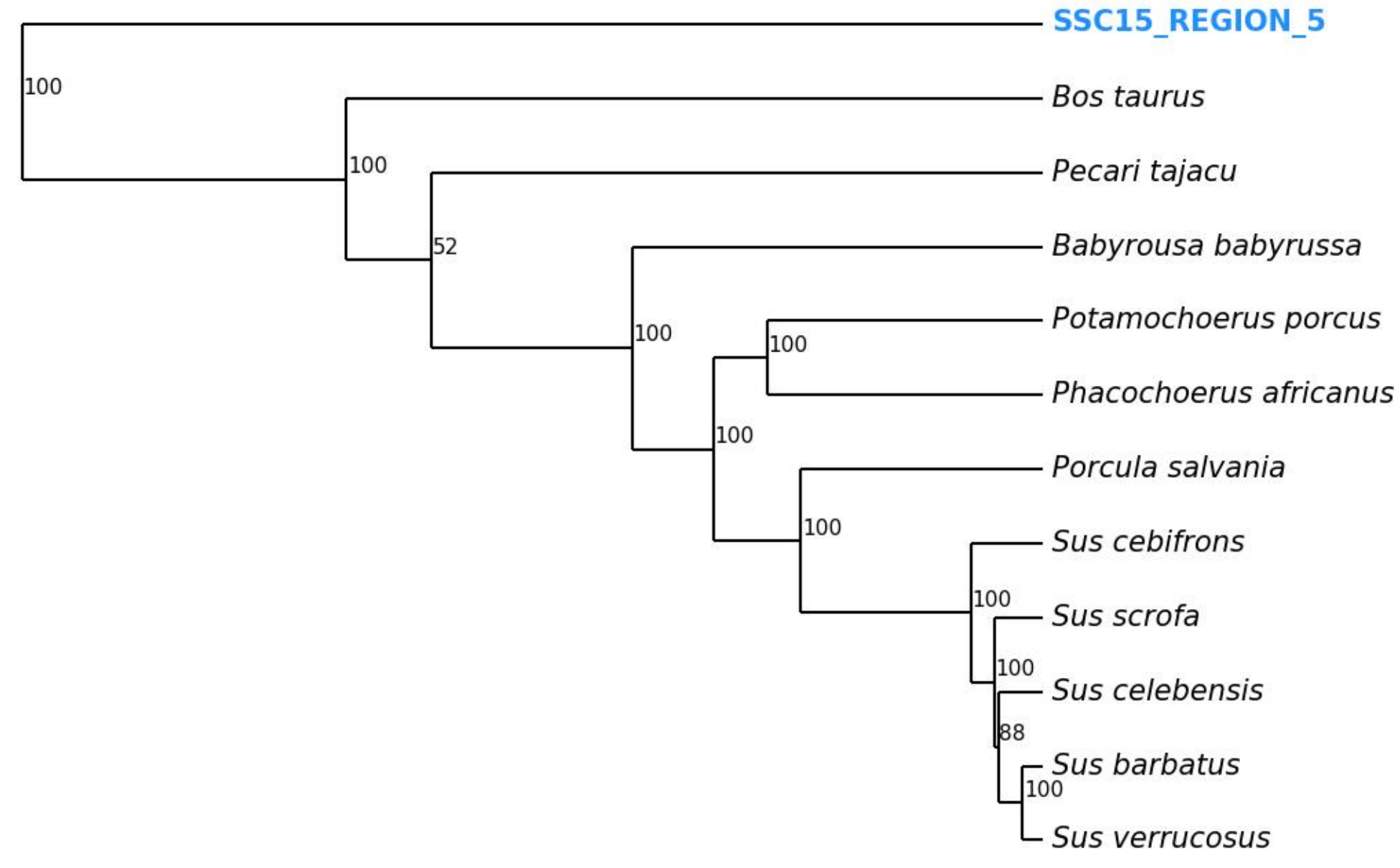
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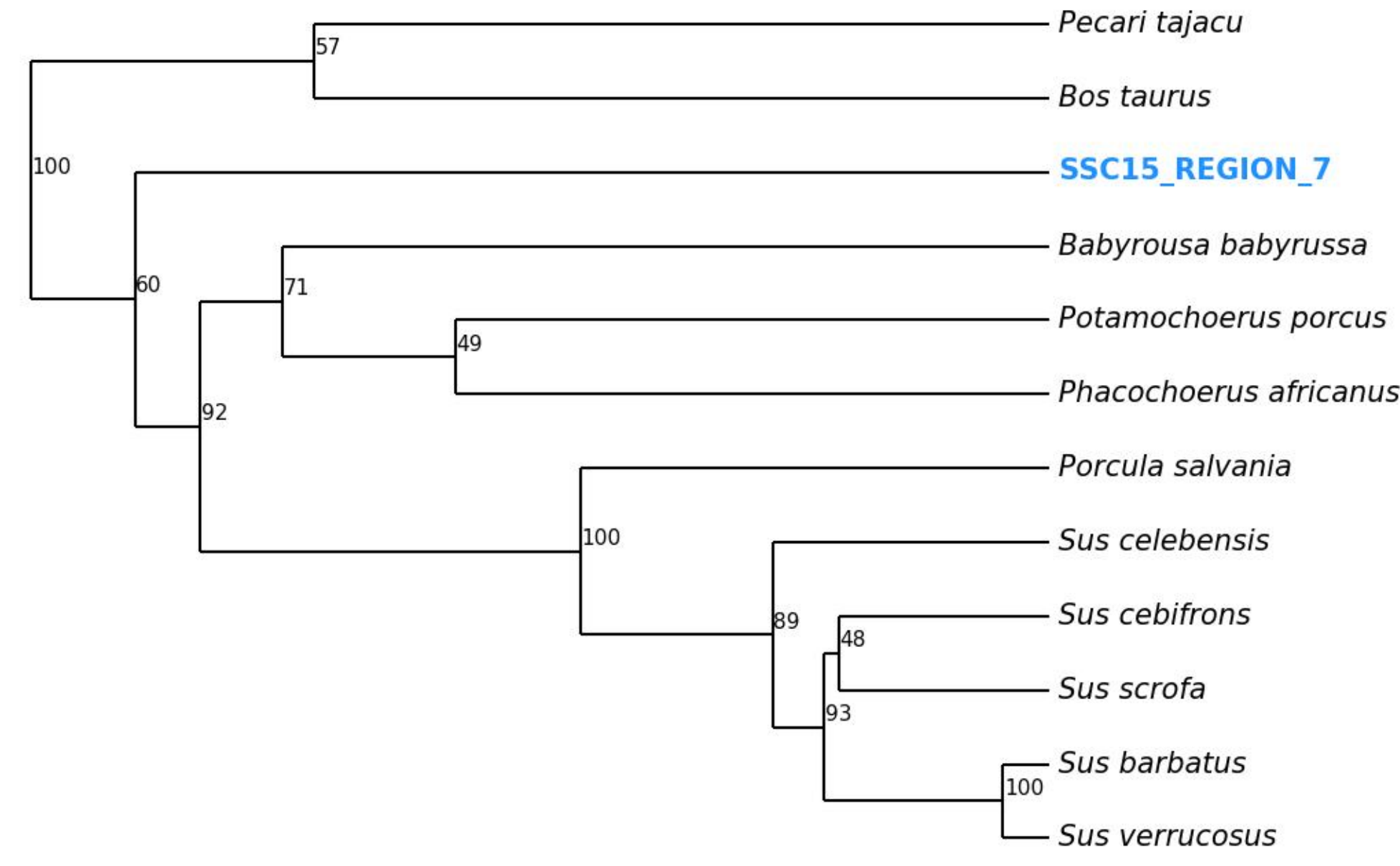
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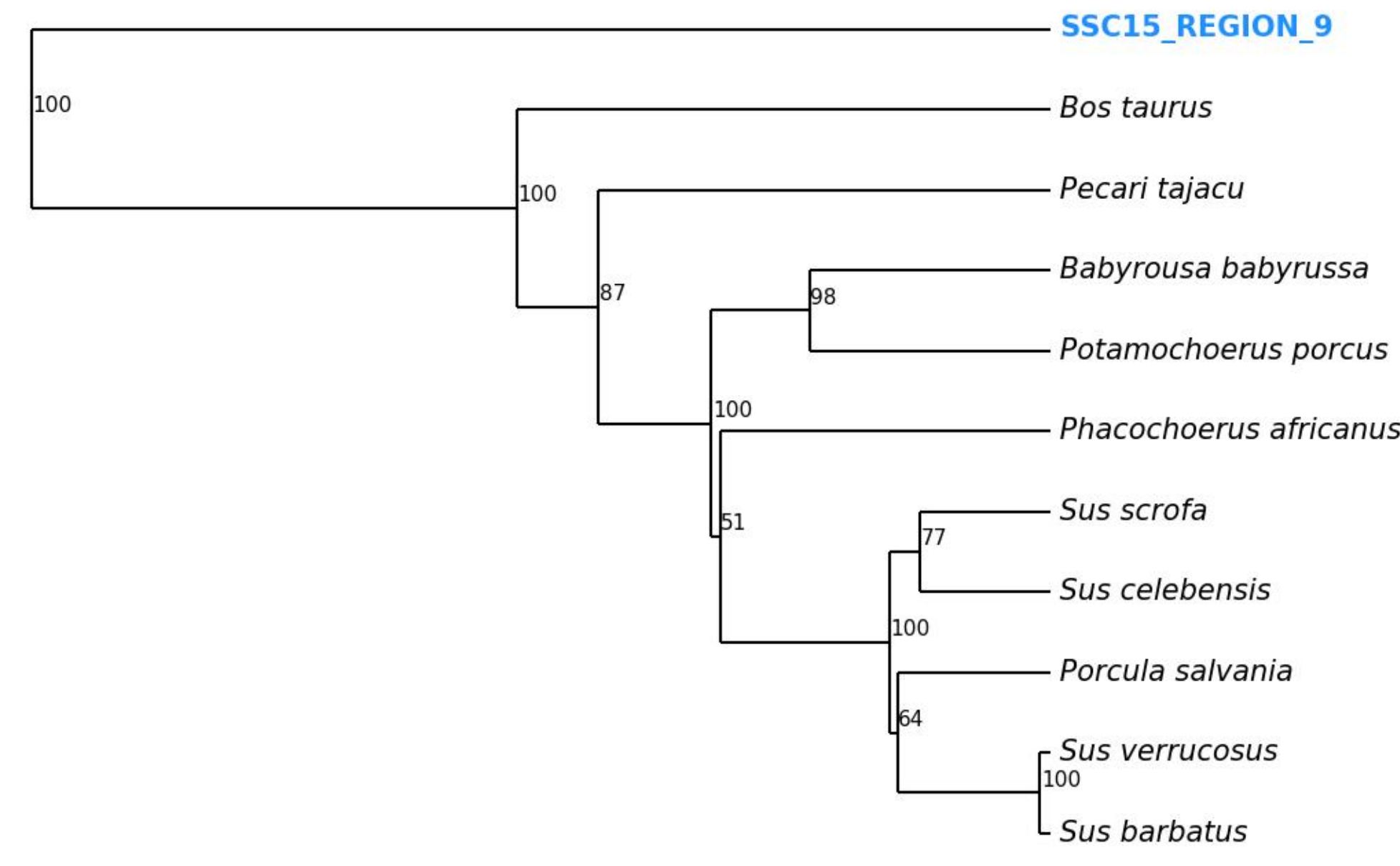
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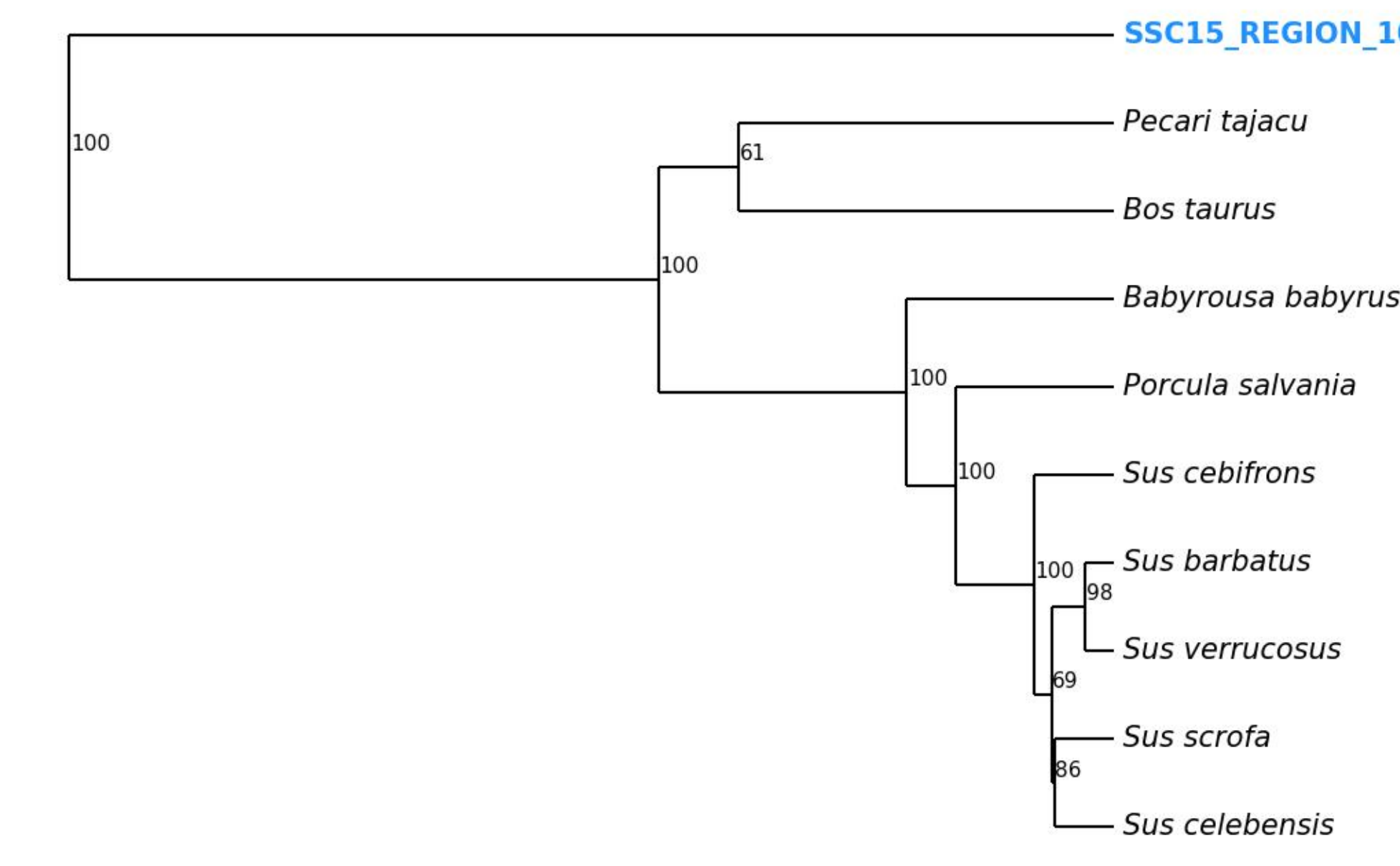
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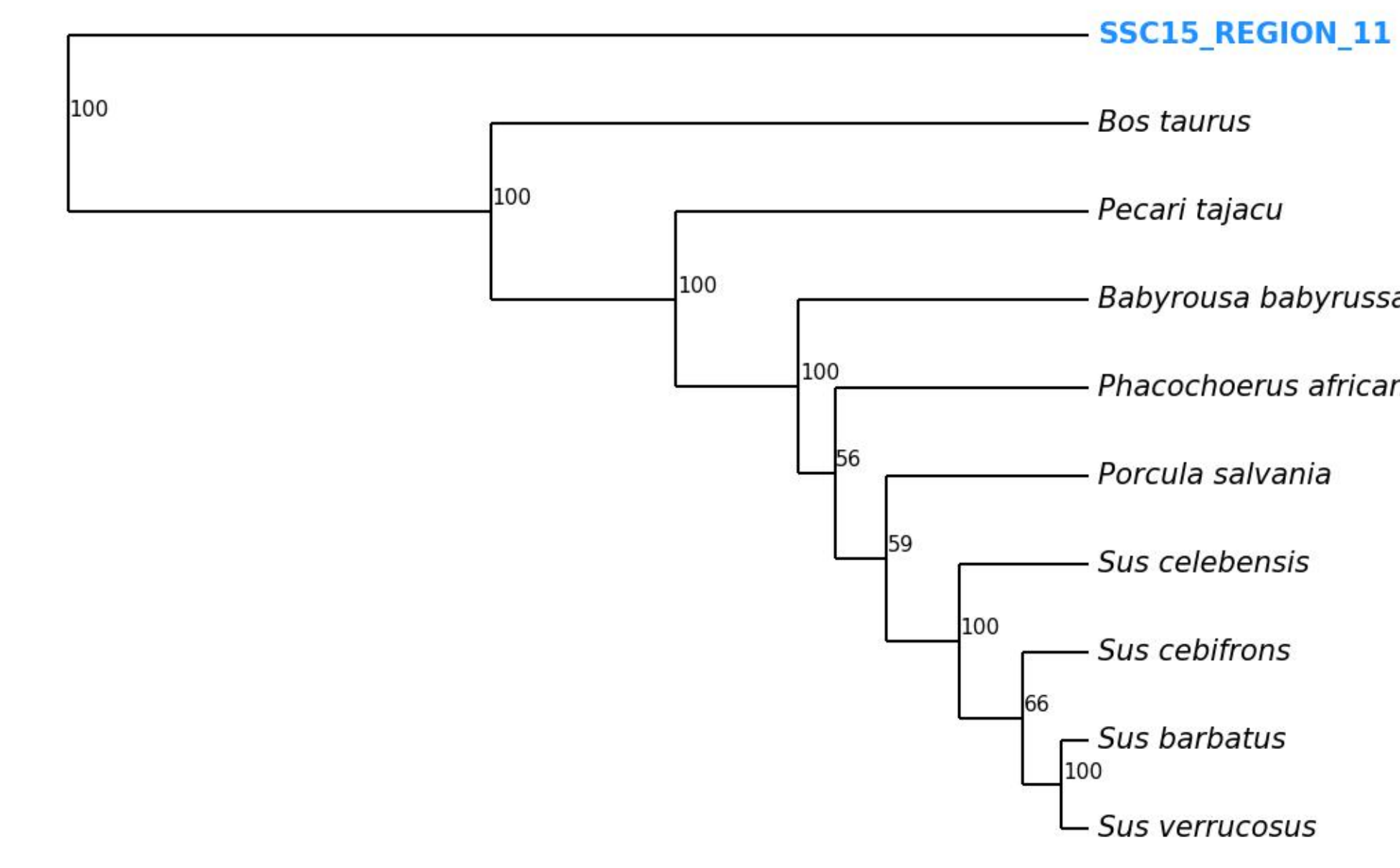
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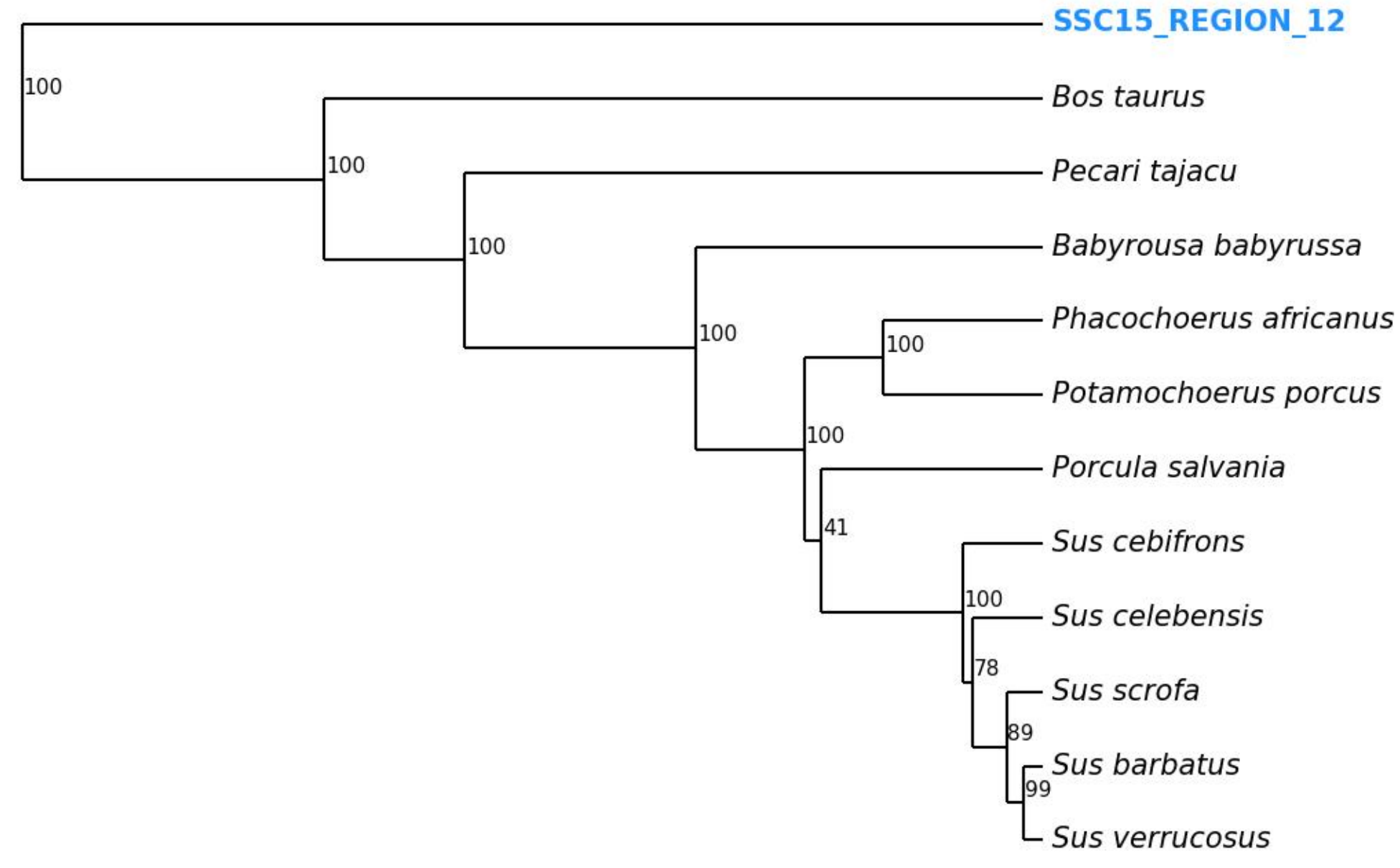
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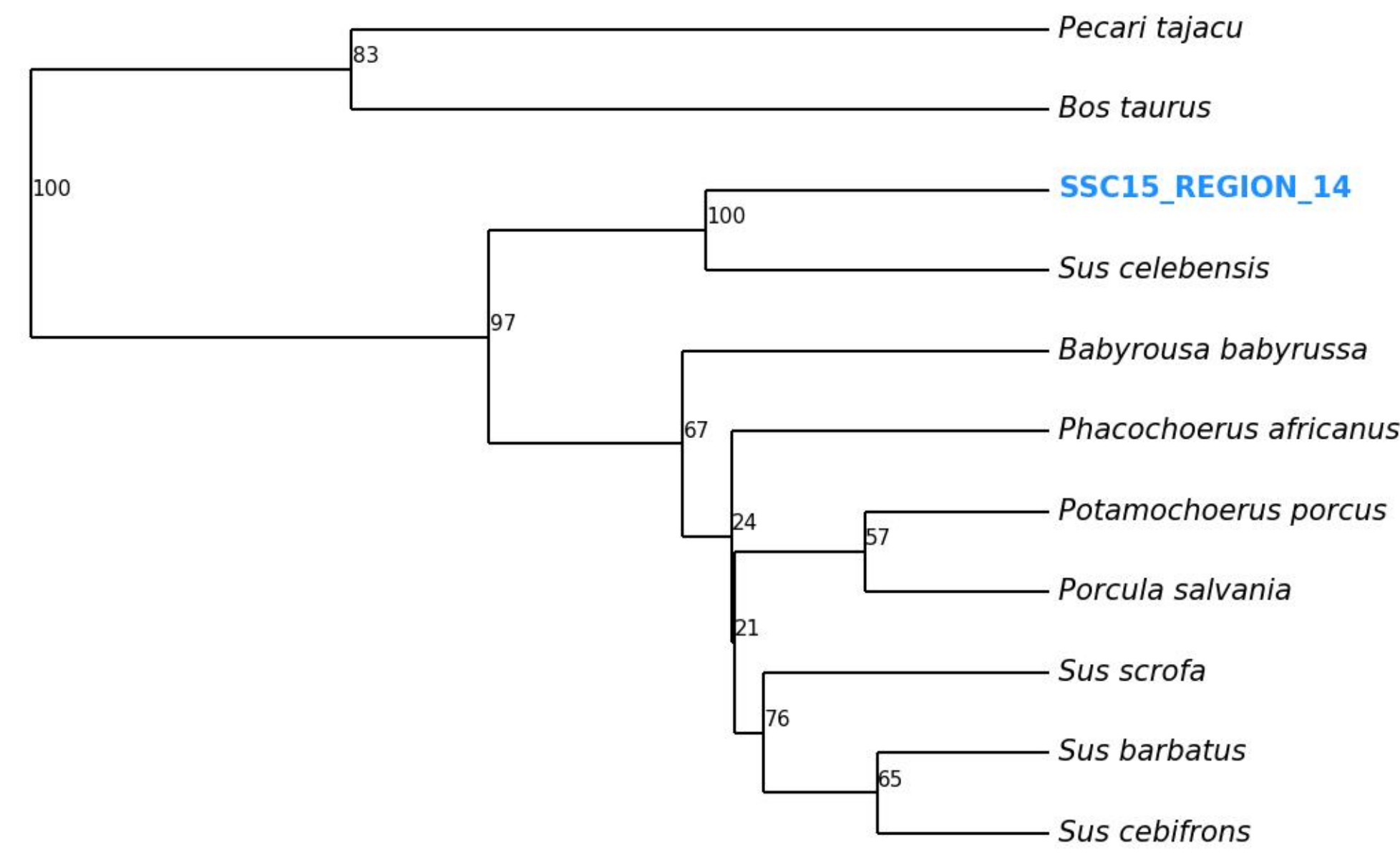
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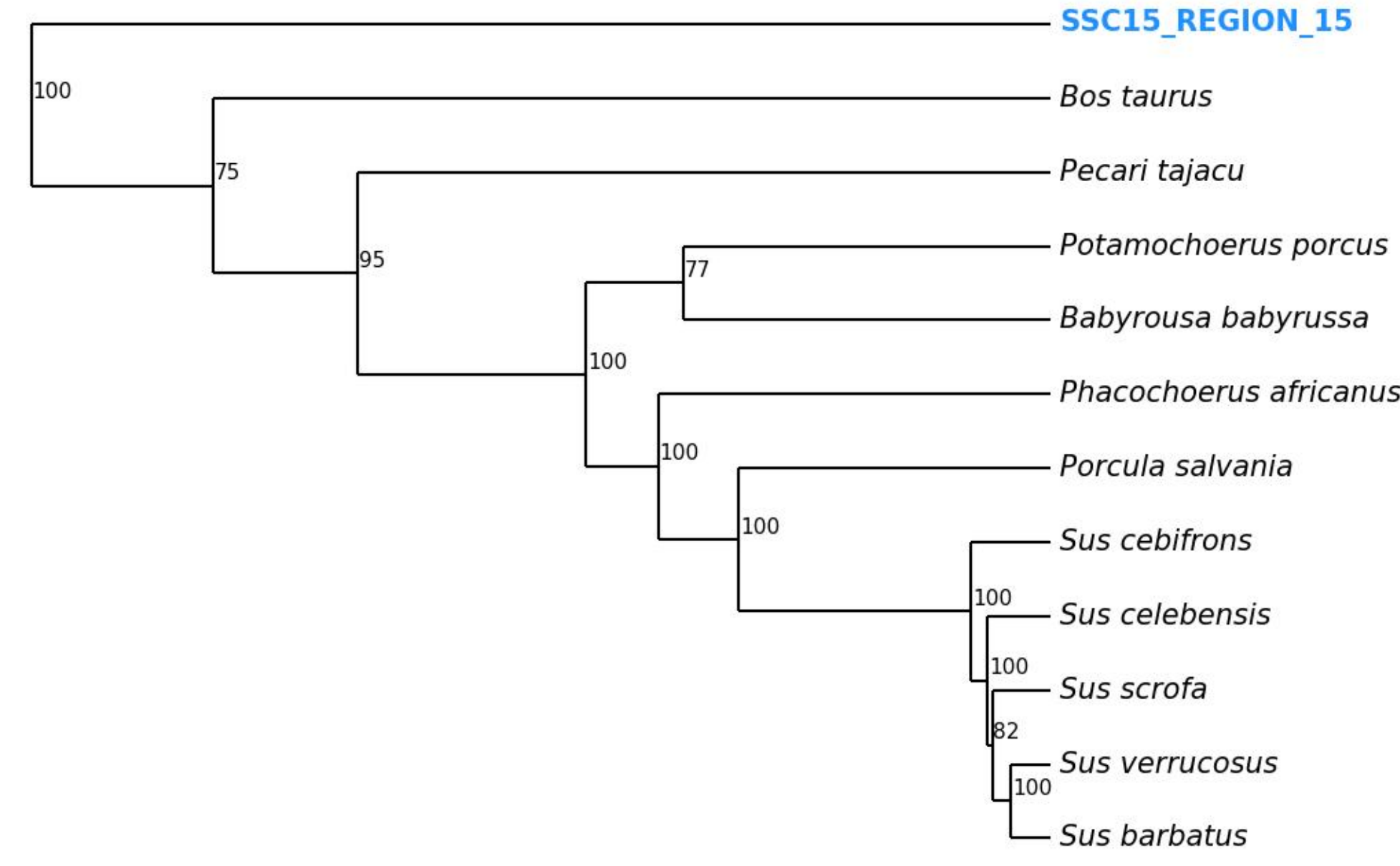
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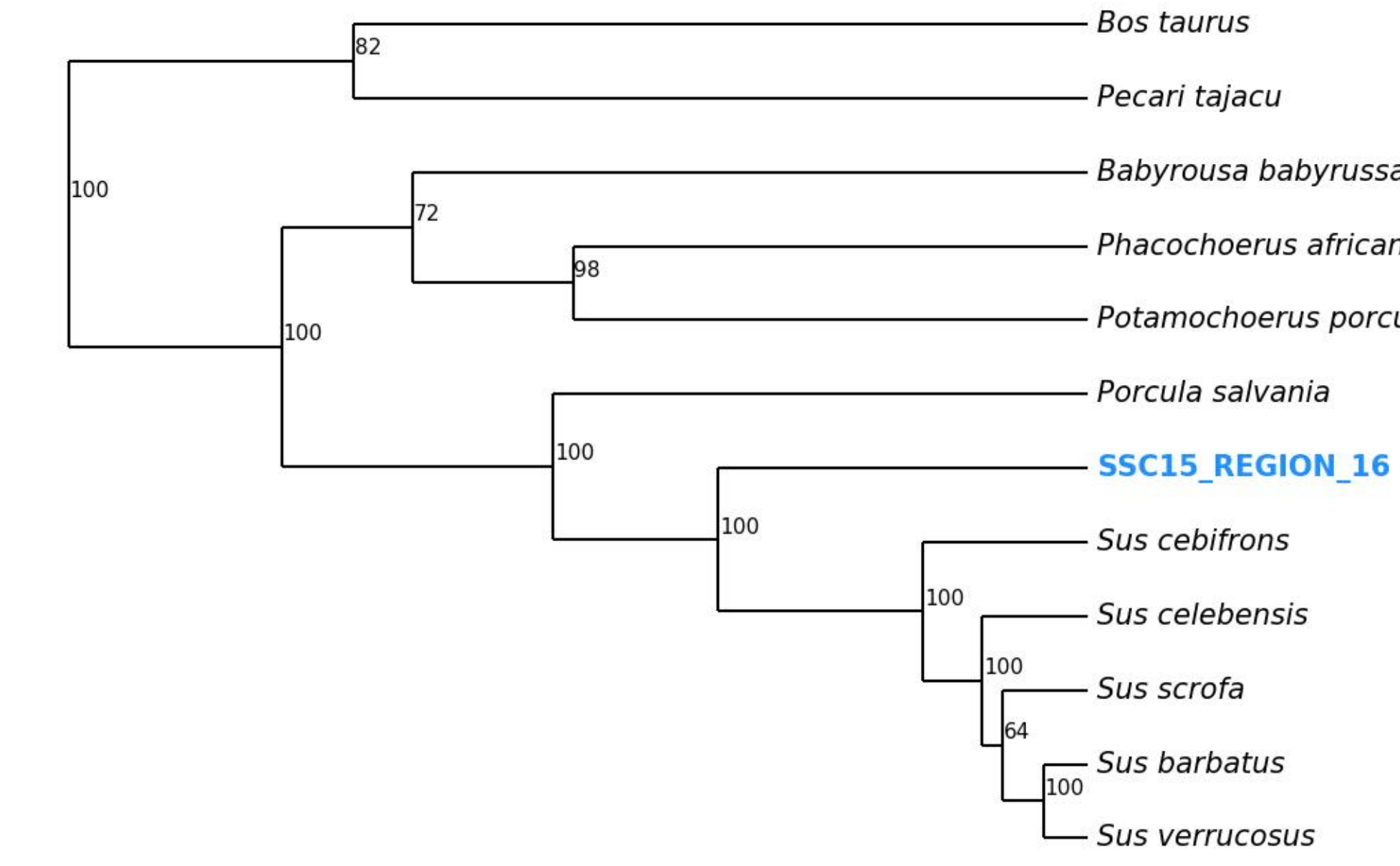
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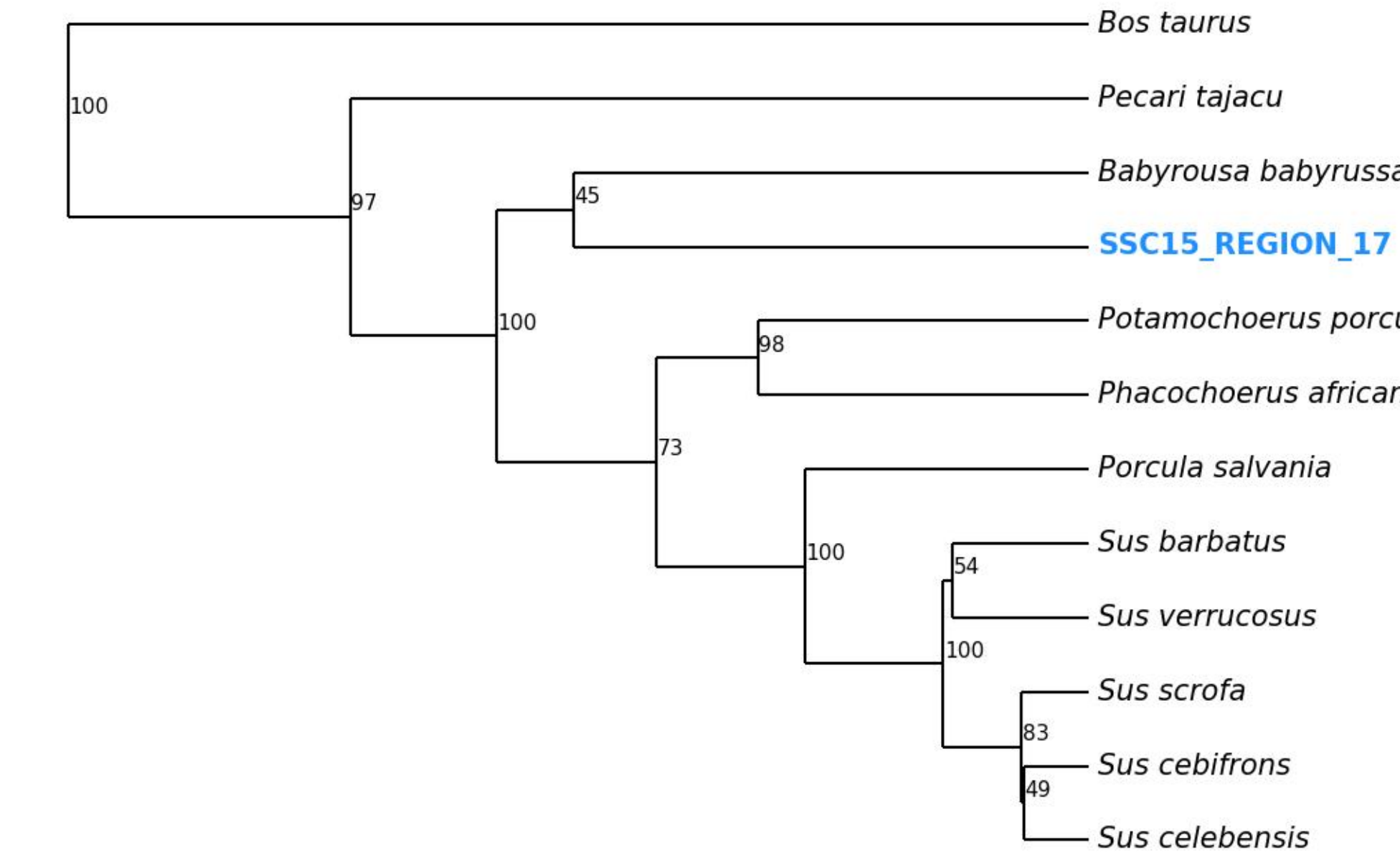
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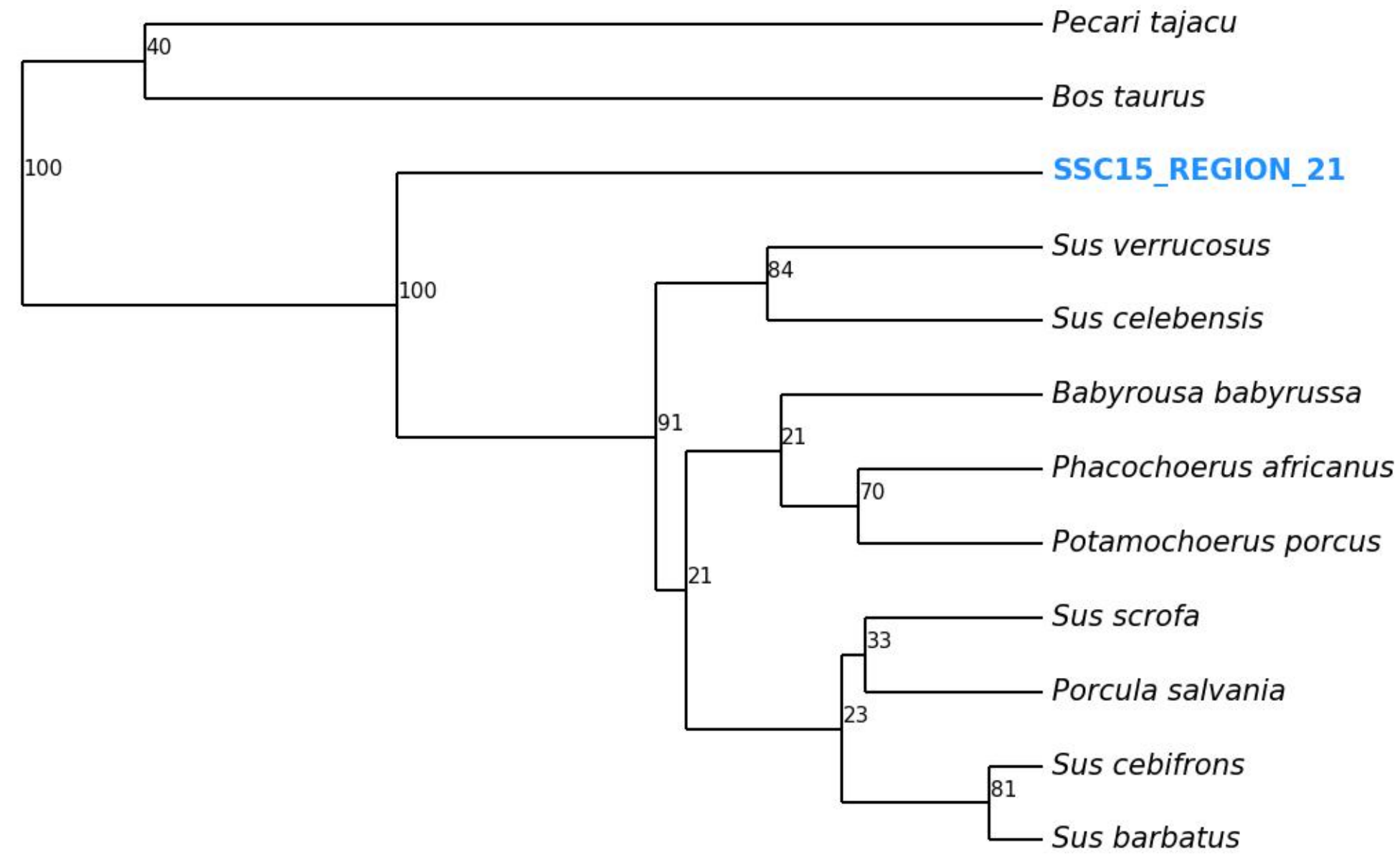
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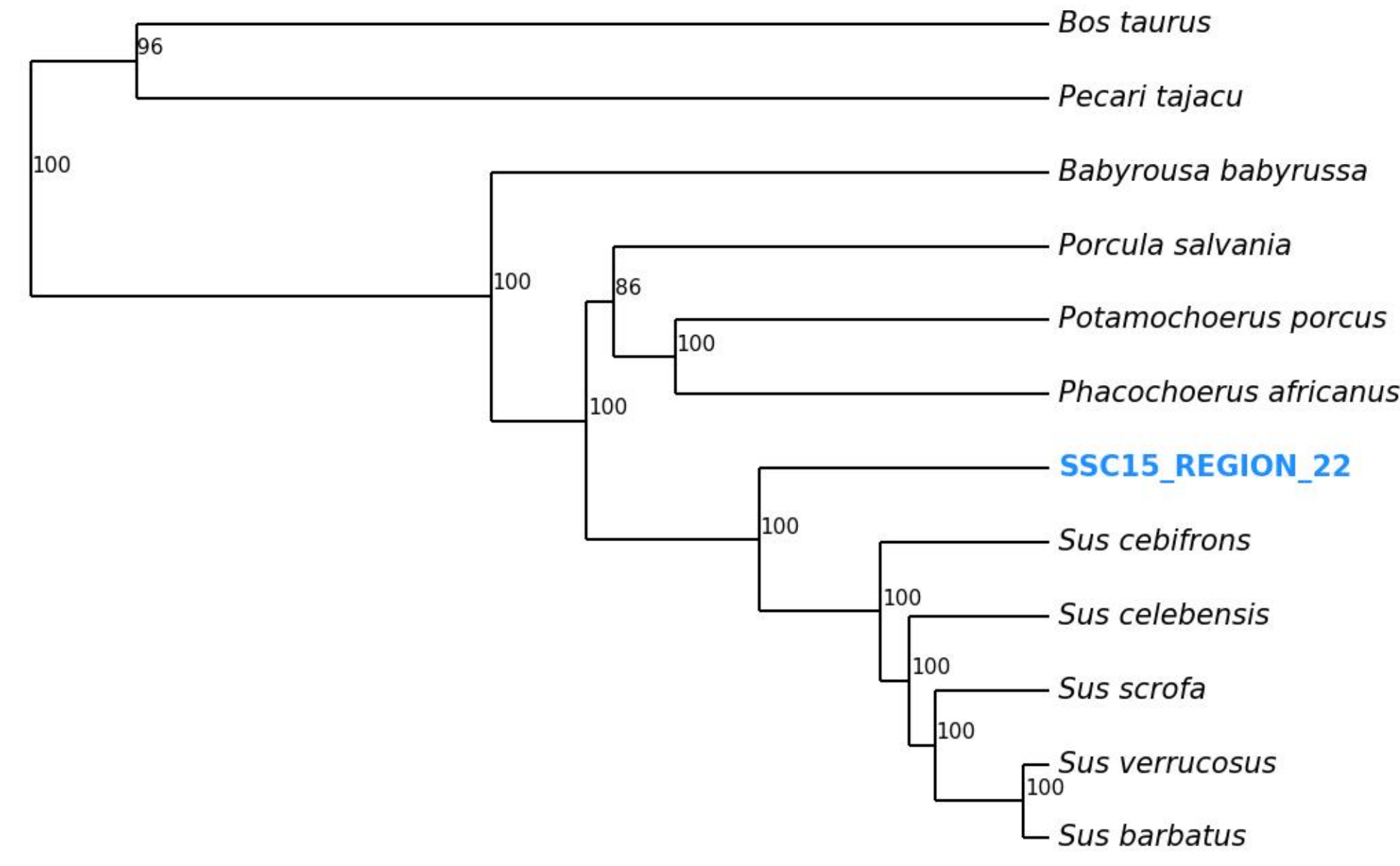
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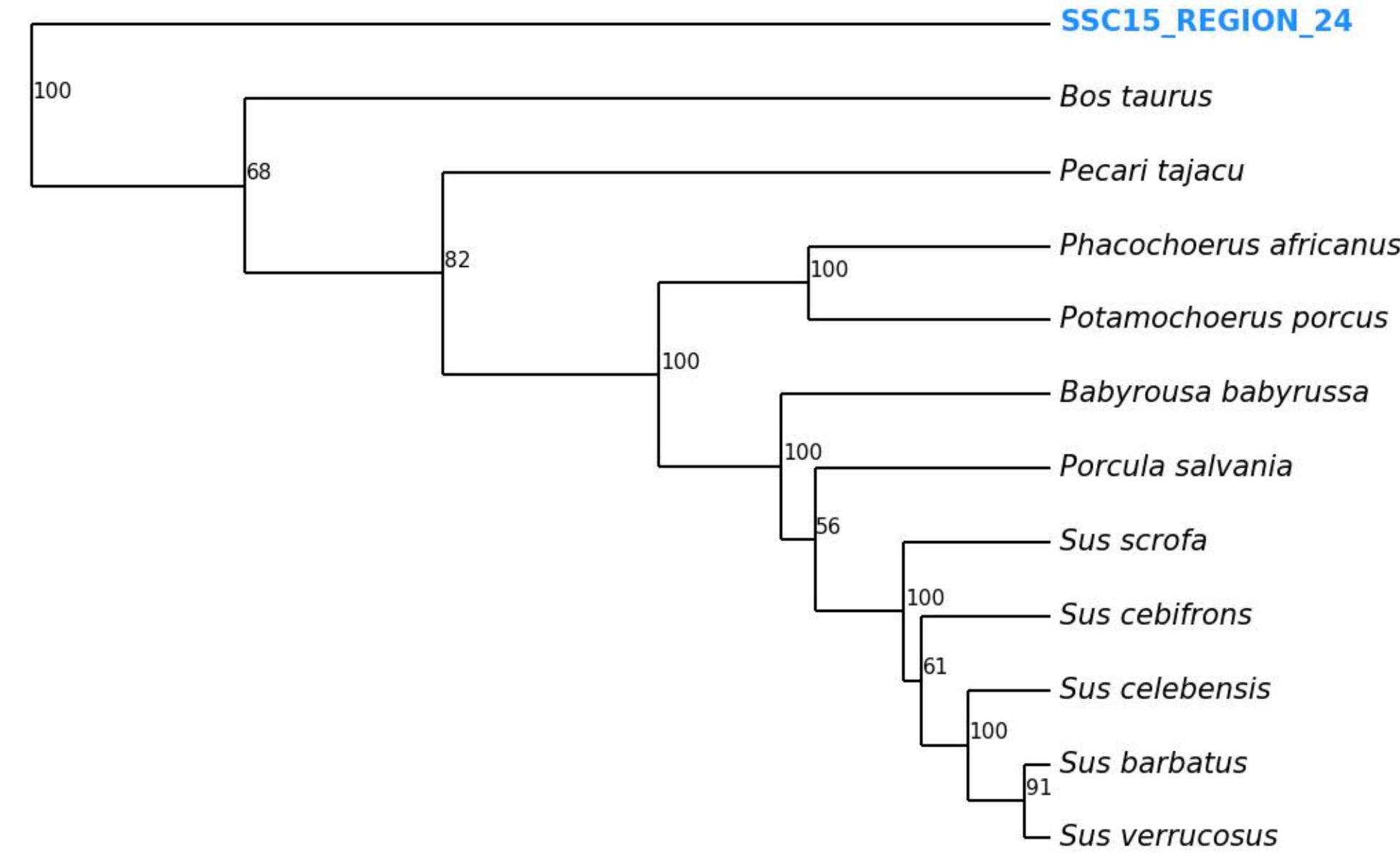
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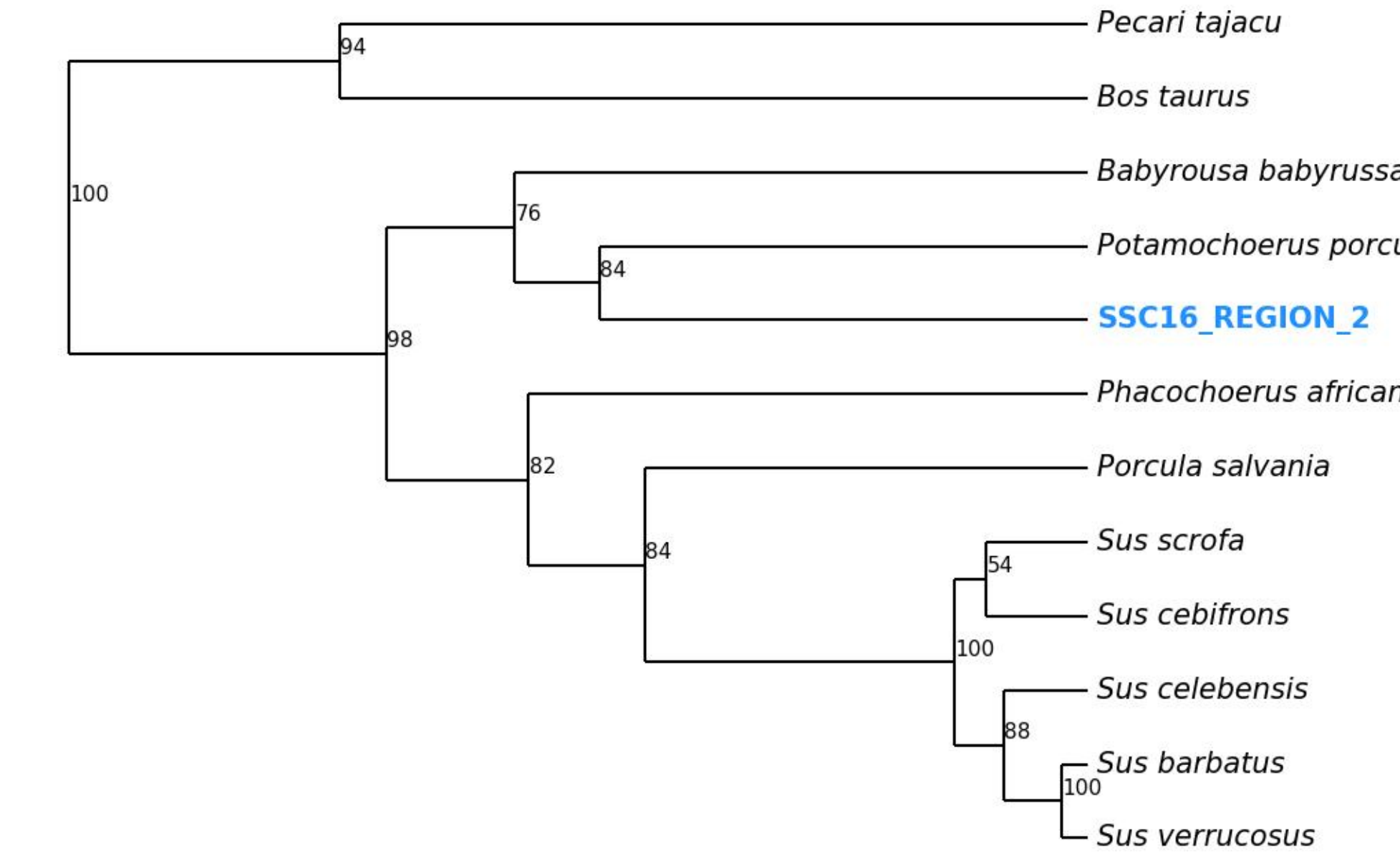
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SSC15_REGION_24



SSC16_REGION_2



SSC16_REGION_4

