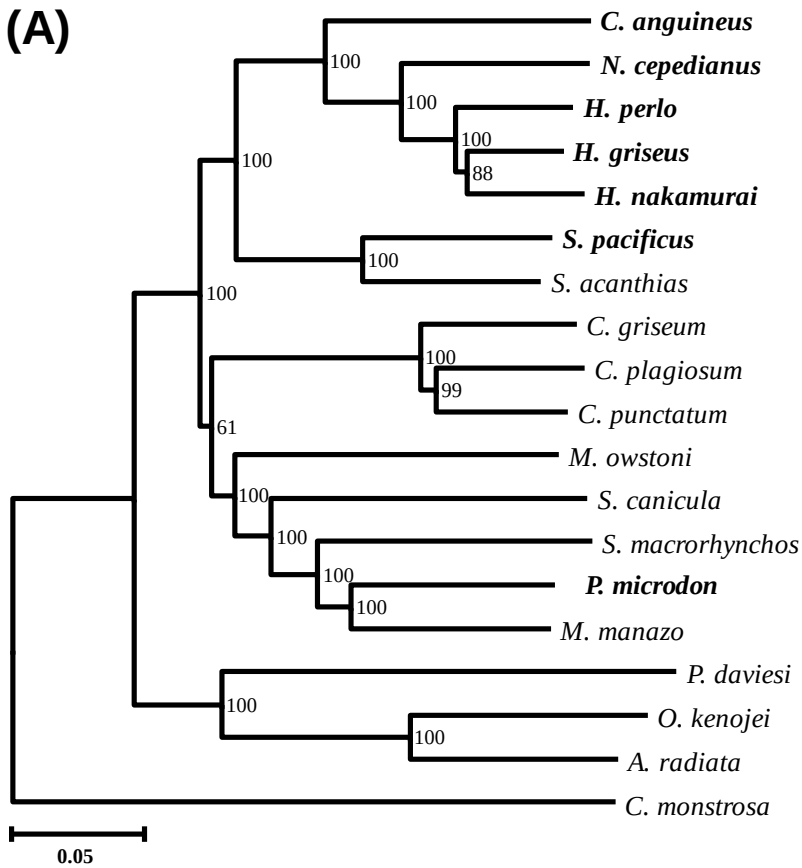
Supplementary figure 1

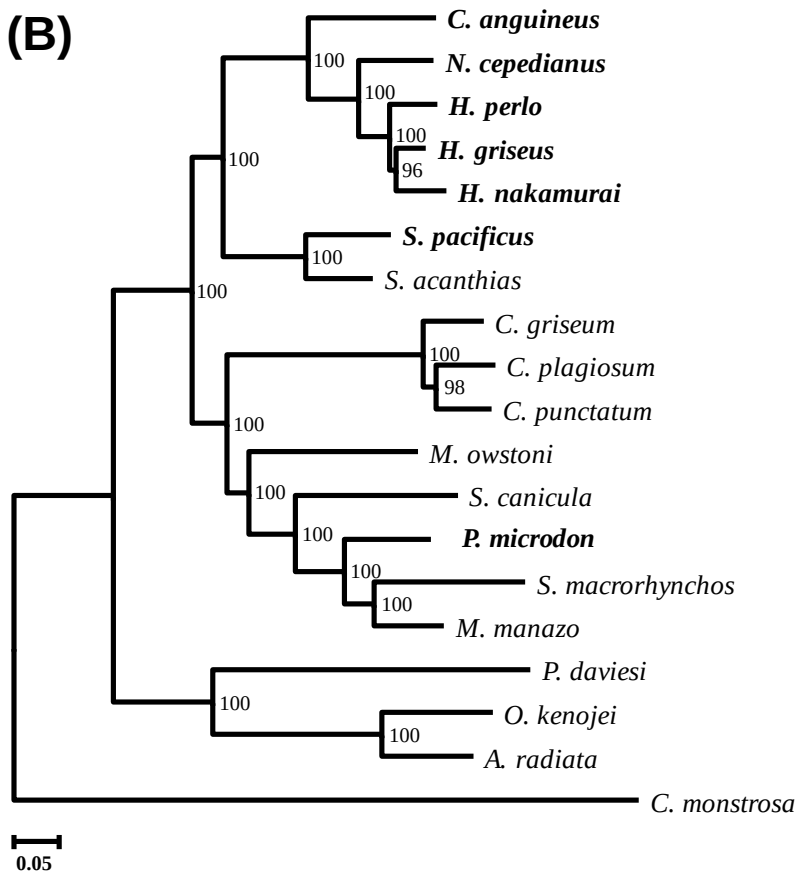
Neighbour-joining (A) and Bayesian inference (B) phylogenetic trees depicting genetic relationships among 19 Chondrichthyes species inferred from the whole mtDNA region. The 13,749 bp nucleotide alignment (Align_Set_1) was used for the analysis. Numbers showing on the branches are bootstrap support values in A and posterior probability in B. Bold letters indicate the nucleotide sequences of the species that we newly determined in this study.

Supplementary figure 2

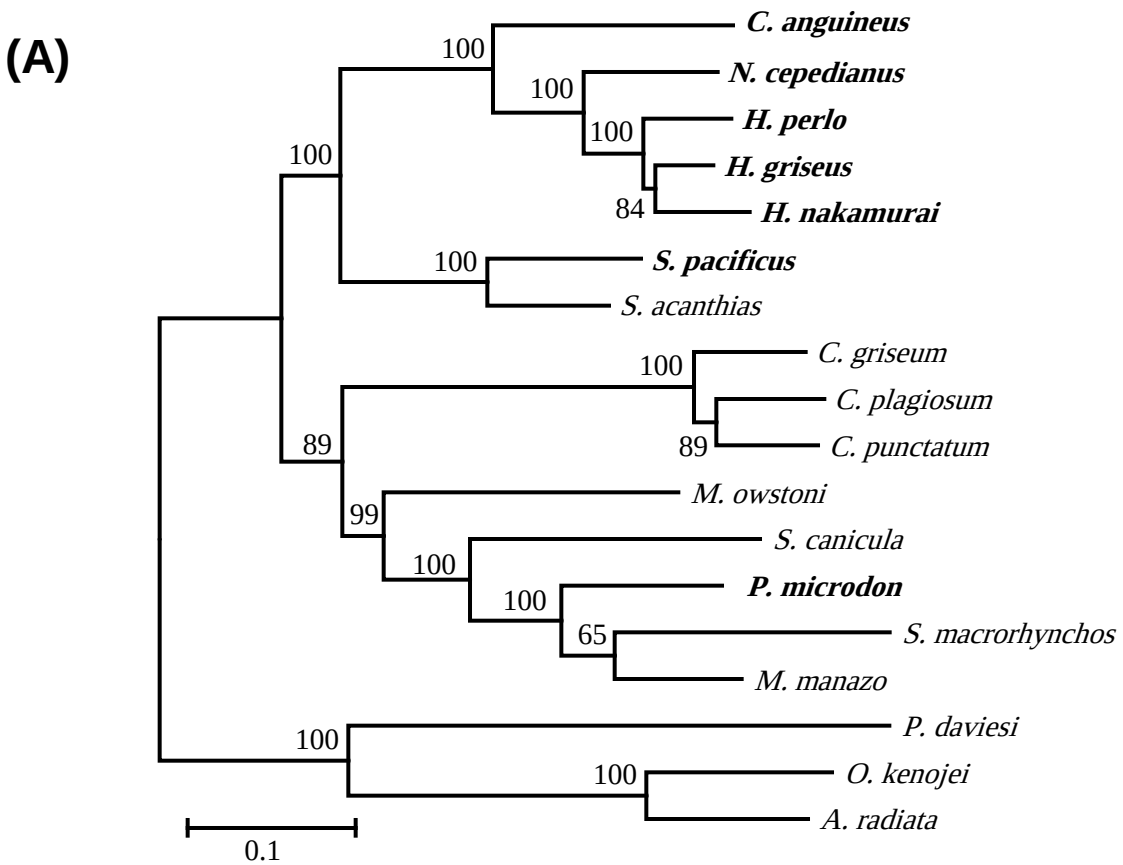
Maximum likelihood (A), Neighbour-joining (B) and Bayesian inference (C) phylogenies depicting genetic relationships among 18 Selachii and Batoidea species inferred from the whole mtDNA region. The 13,784 bp nucleotide alignment (Align_Set_2) was used for the analysis. Numbers showing on the branches are bootstrap support values in A and B and posterior probability in C. Bold letters indicate the nucleotide sequences of the species that we newly determined in this study.

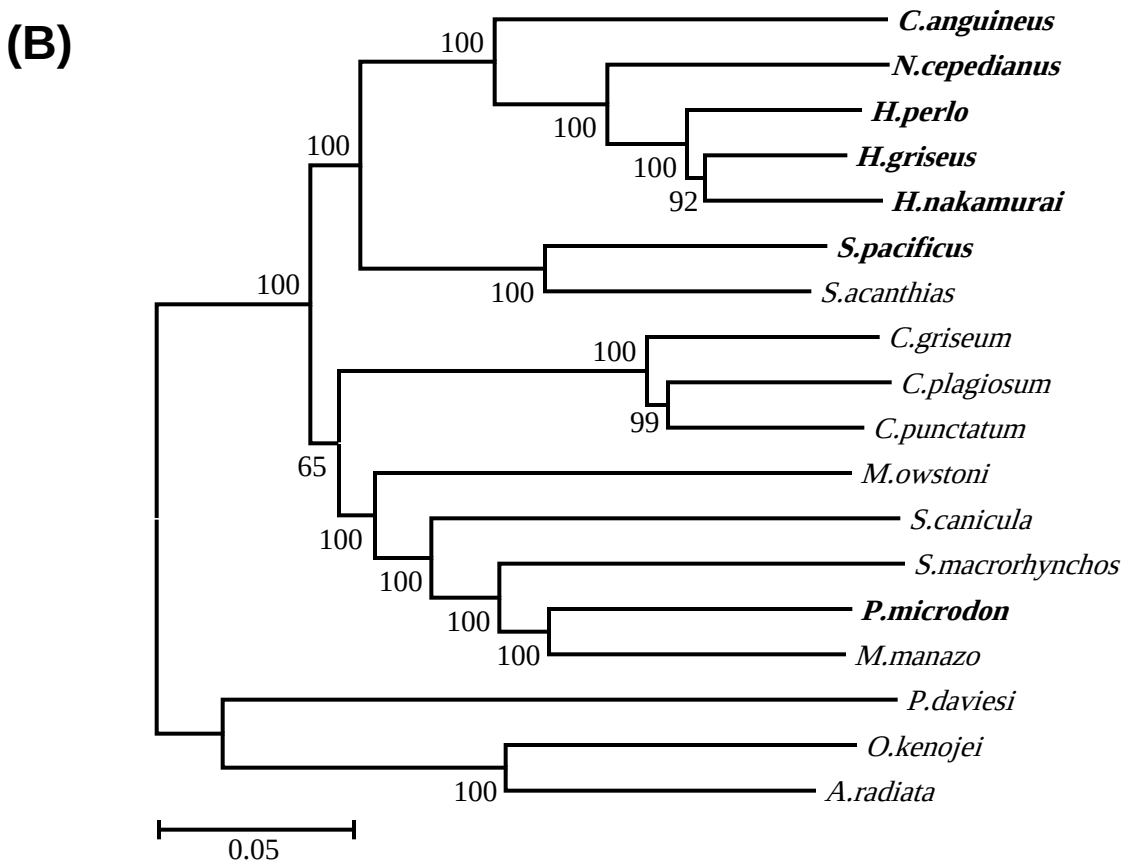
Supplementary figure 1

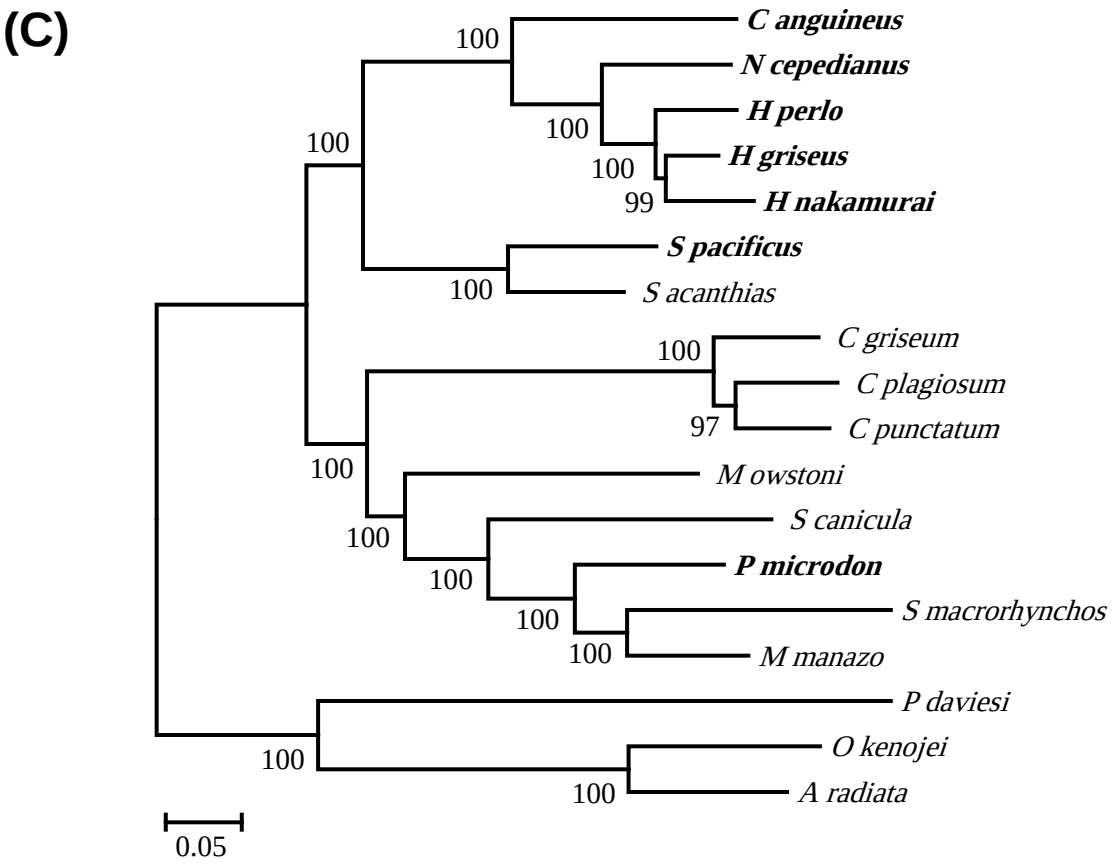




Supplementary figure 2






(C)
C anguineus
N cepedianus
H perlo
H griseus
H nakamurai
S pacificus
S acanthias
C griseum
C plagiosum
C punctatum
M owstoni
S canicula
P microdon
S macrorhynchos
M manazo
P daviesi
O kenojei
A radiata
100
100
100
100
99
100
100
100
97
100
100
100
100
100
100
0.05