

**Supplementary Table S3.** The beta-lactam biosynthesis proteins that were used to search for beta-lactam genes in the genome of the nematode *Plectus sambesii*. Abbreviations: IPNS: isopenicillin N synthase; IPN:AT: isopenicillin N N-acyltransferase; DAOC: deacetoxycephalosporin C; DAC deacetylcephalosporin.

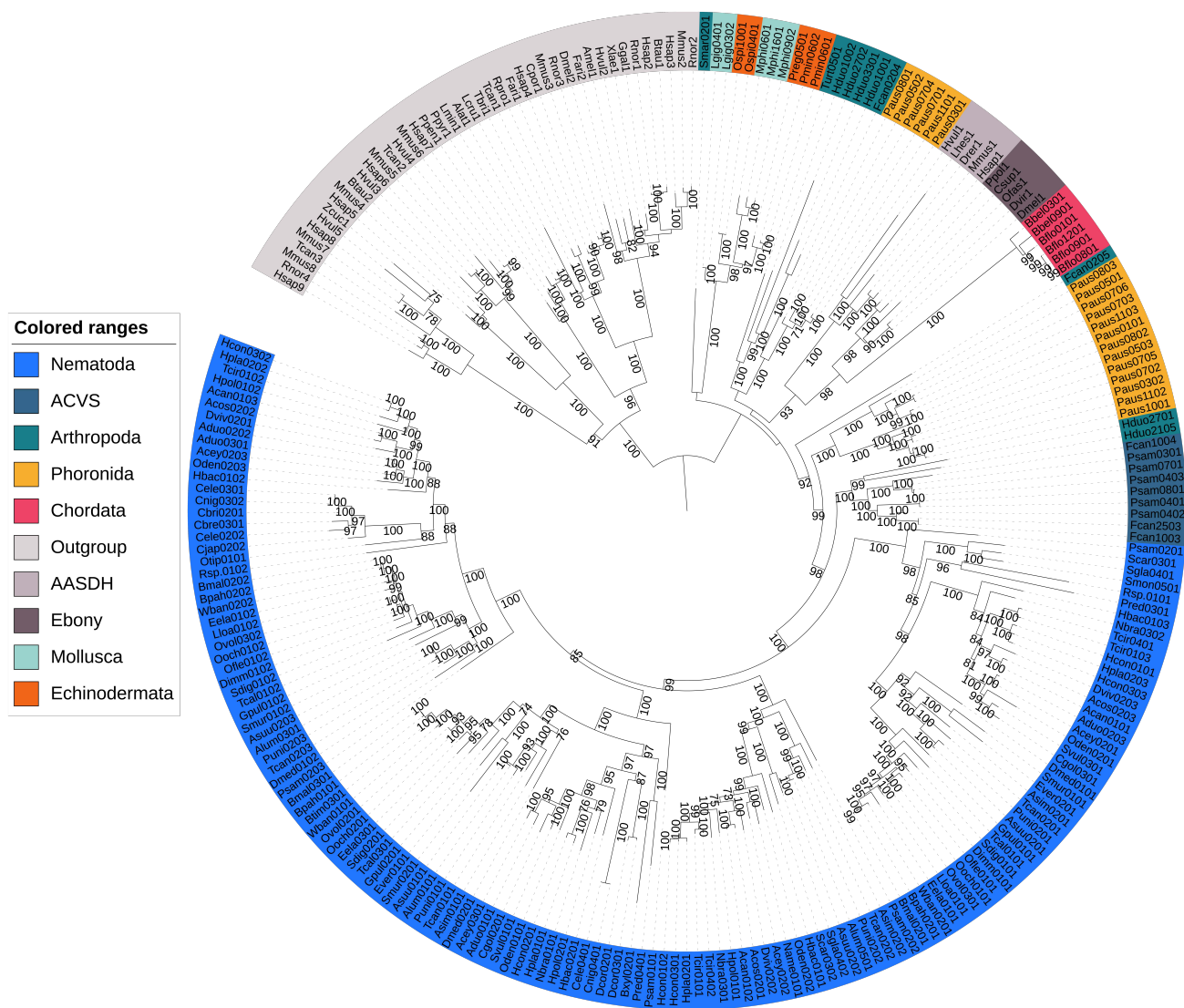
UniProt ID	Protein	Gene	Species
P18549	IPNS	pcbC	<i>Streptomyces clavuligerus</i>
P15802	IPN:AT	penDE	<i>Penicillium chrysogenum</i>
P18549	IPN: epimerase	cefD	<i>Streptomyces clavuligerus</i>
P18548	DAOC synthase	cefE	<i>Streptomyces clavuligerus</i>
P42220	DAOC hydroxylase	cefF	<i>Streptomyces clavuligerus</i>
P39058	DAC acetyltransferase	cefG	<i>Acremonium chrysogenum</i>
B5GZH3	3'-hydroxymethylcephem-O-carbamoyltransferase	cmcH	<i>Streptomyces clavuligerus</i>
NA <sup>1</sup>	O-carbamoyl DAC	cmcI	<i>Folsomia candida</i>
NA <sup>2</sup>	7-alpha-cephem-methoxylase	cmcJ	<i>Folsomia candida</i>

<sup>1</sup> Protein sequence:

MEPSTTNESKDLVEGNFVDLHRLRGLGDDPVYYPPILEDPRPLWPLDKWSSAPRDLGYDNFATEHWKGL  
RLLKDPETQSVYHNILWEIKPKTIIELGVYSGGSLVWFRDLTKAFKFPSRLIGIDIDLSRCQIPEGEMDMISLH  
QADCNNPESFAFLKDNVEHPILFIDDAHCNTFNVIKYAVNNFLKVGDFVMIEDTMGMWGRYSPKHLKS  
HLASFKDVMALDLLYSNVPCQLKDGVFQVIKSN

<sup>2</sup> Protein sequence:

MIKIKPGRDVQATINYSRSSTTEKWFIDTISCPNGNKITNAENDPISTTIHDLRGVEHNFSLDKNGFQAIFSP  
TSVPSNTLLSGGDVLKTVYYPEVEKLLMEVTGADKAVAFDHTIRQSQVNSETWLHRLPVMRAHVDQTPK  
SAWGRIALHSPEVQSFYRFQIINVWRPIVNIVDYDPLTMADFRSLNLHVDLMPTDLRYPEVWVKDKETYSV  
KWNRSRAWYWSCMTPDEVLMACYDSASQRLAEAYPLPLERGNRNLYCSESVAGLAPHTAFYDEKAS  
MKGSGRKSIEIRTLVFYK



**Supplementary Figure S1.** A phylogenetic tree of identified putative NRPS adenylation domains in animals including all nematode sequences. The nematodes form a monophyletic clade except for several *Plectus sambesii* sequences that cluster with ACVS proteins of the springtail *F. candida*. Compared to Figure 2, the Mollusca, Echinodermata and a group of Arthropoda have moved and diverge before AASDH and Ebony (but with low support). Bootstrap support >70% is shown. The adenylation domains of outgroup proteins (Supplementary Table S2) and putative NRPSs were aligned using Clustal Omega version 1.2.4 and columns with <70% coverage were trimmed. The phylogenetic tree was inferred with IQTREE version 2.0.6 (Minh et al., 2020) using the LG+F+R8 model with 1000 bootstrap replicates.