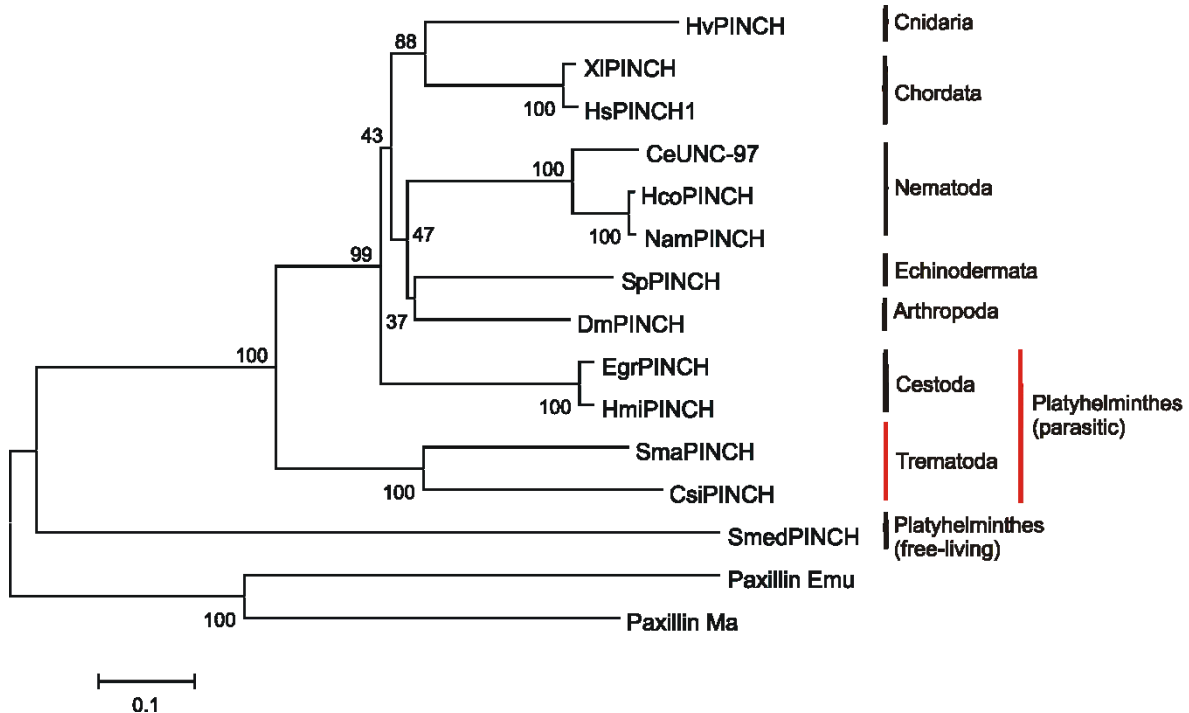


1 **Supplementary figure S2: Structure and phylogenetic analysis of SmpINCH**

2 **A**



3
4 **B**



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8 **Suppl. fig. S2**

9 **A**, Structure of SmPINCH (Smp_020540.2) analyzed by SMART showing five LIM domains.

10 **B**, Phylogenetic analysis using the Neighbor-Joining method [1-4]. In addition to SmpINCH
11 (SmaPINCH) the analysis involved the following 14 amino acid sequences of orthologs of
12 organisms of different phylogenetic origins such as *Hydra vulgaris* (HvPINCH;
13 XP_002164622), *Xenopus laevis* (XIPINCH; ABS17667), *Homo sapiens* (HsPINCH;
14 NP_001180413), *Caenorhabditis elegans* (CeUNC-97; CCD83467), *Haemonchus contortus*
15 (*HcoPINCH*; CDJ80147), *Necator americanus* (NamPINCH; ETN83005), *Strongylocentrotus*
16 *purpuratus* (SpPINCH; XP_793010), *Drosophila melanogaster* (DmPINCHs; NP_731242),
17 *Echinococcus granulosus* (EgrPINCH; EUB60965), *Hymenolepis microstoma* (HmiPINCH;
18 CDS30700), *Clonorchis sinensis* (CsiPINCH; GAA38790), *Schmidtea mediterranea* (SmedPINCH;
19 v31.005368) and the two amino acid sequences coding for LIM domain containing proteins of
20 *Echinococcus multilocularis* (Paxillin Emu; CDI97526) and *Mesocricetus auratus* (Paxillin Ma;
21 XP_005079036) serving as out-group. All positions containing gaps and missing data were
22 eliminated.

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