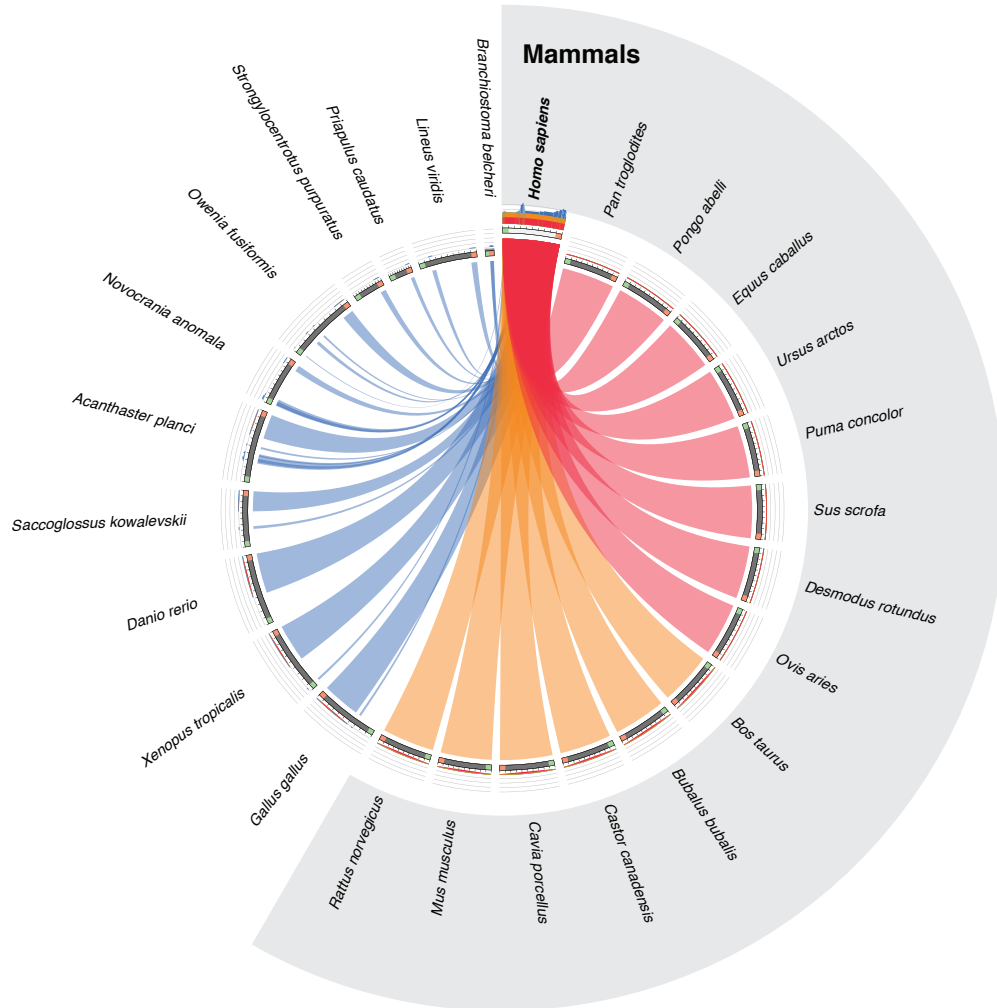


A



B

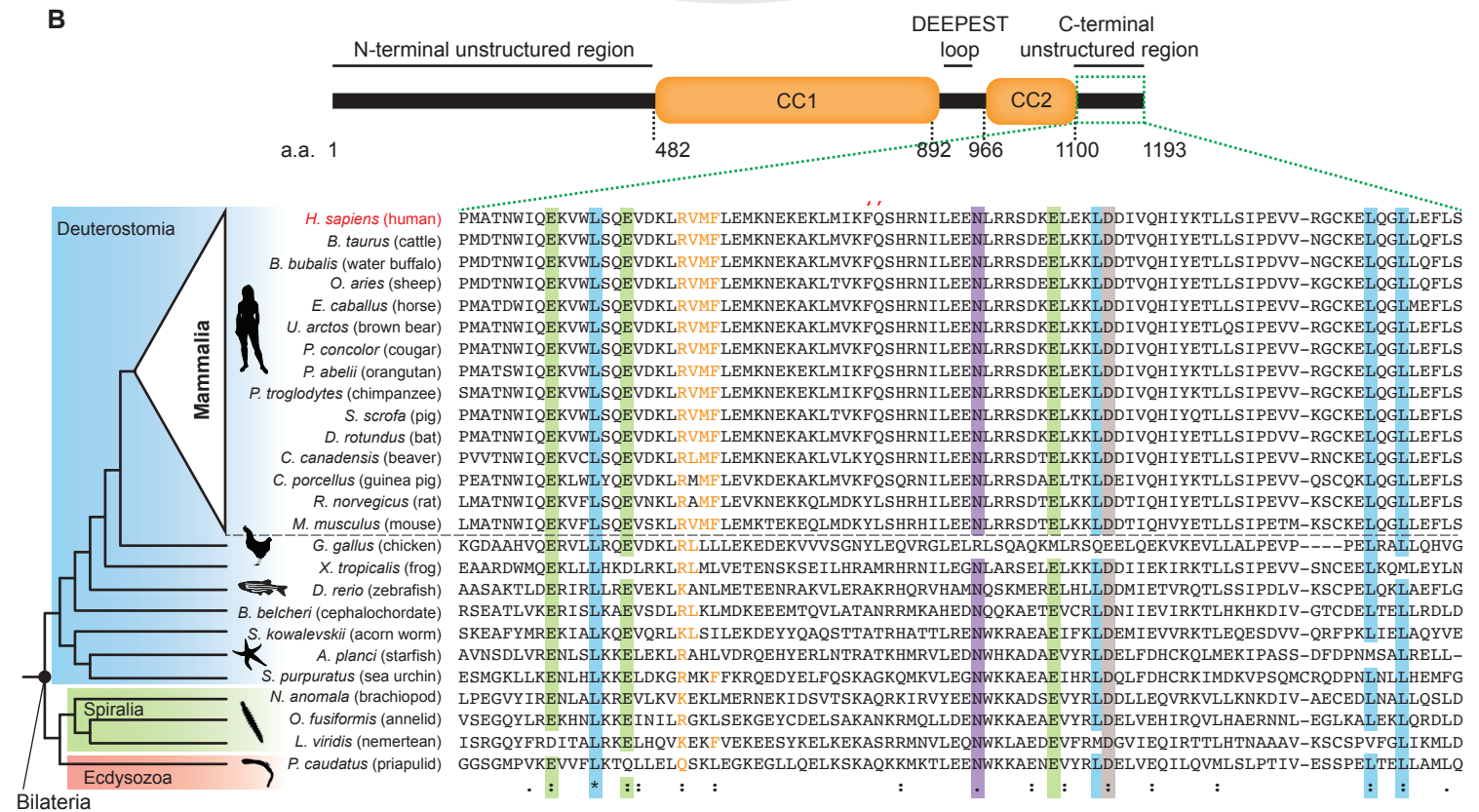


Figure 3 supplement 1. Evolutionary conservation of Astrin tail across Bilateria

(A) C- but not N-terminus of Astrin is evolutionarily conserved across Bilateria. Schematic of sequence similarity between representative Astrin proteins in bilaterians and mammals. While mammalian orthologs show high/medium similarity against human Astrin, non-mammalian orthologs are more divergent. However, all Astrin orthologs show similarity in the C-terminus region. Ribbon colour is based on % of sequence similarity, from red (highest) to blue (lowest). Diagram was built using Circioletto (Dazent, 2010). N and C-termini of the query sequence are highlighted in Green and Orange, respectively. **(B)** Schematic of key structural domains of human Astrin highlights the unstructured region analysed in the sequence alignment below. Protein sequence alignment generated using MAFFT demonstrates conservation of the tail region across bilaterian species (residues > 90% conservation are marked by coloured bands) and highlights high conservation of the putative PP1-binding motif RVxF and FQ (") (Choy et al. 2014; Bajaj et al. 2018) pocket across mammals. Identical (*), conservative (:) and similar (.) residues are marked. **Appendix File 1** includes all new Astrin orthologs identified using a published approach (van Hooff et al., 2017) and an extended database of animal proteomes.