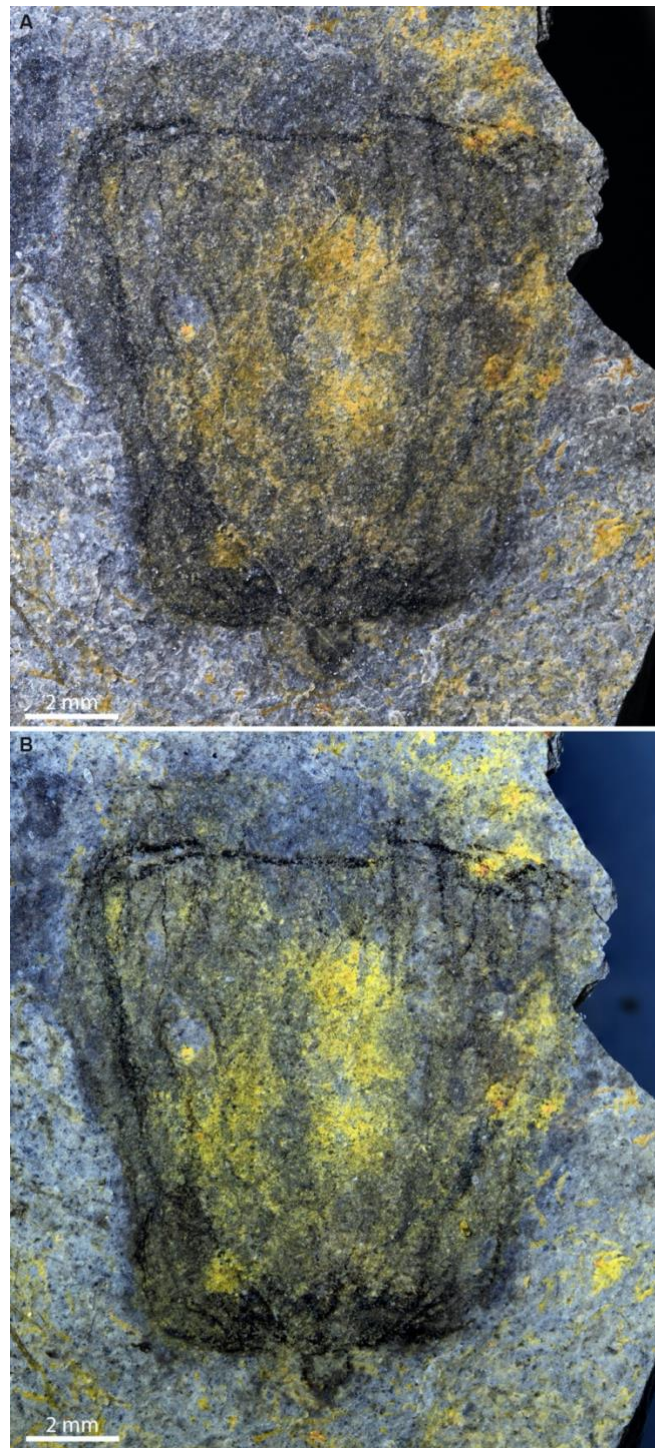**Supplemental information**

Cambrian comb jellies from Utah

illuminate the early evolution of nervous

and sensory systems in ctenophores

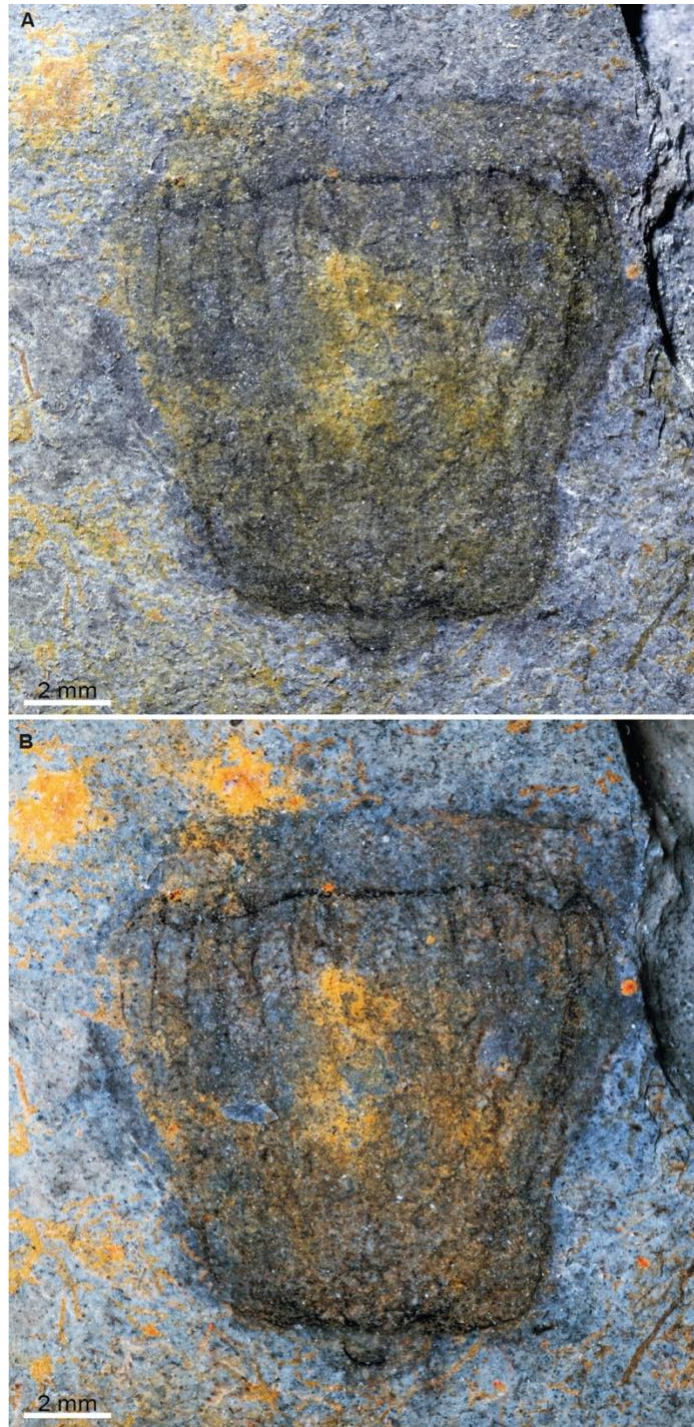Luke A. Parry, Rudy Lerosey-Aubril, James C. Weaver, and Javier Ortega-Hernández

Supplementary Figures

Fig. S1

Figure S1. Additional images of UMNH.IP.6125a, related to figure 2. A, specimen dry, with high angle, cross polarised light. **B,** specimen wet with high angle, cross polarised light.
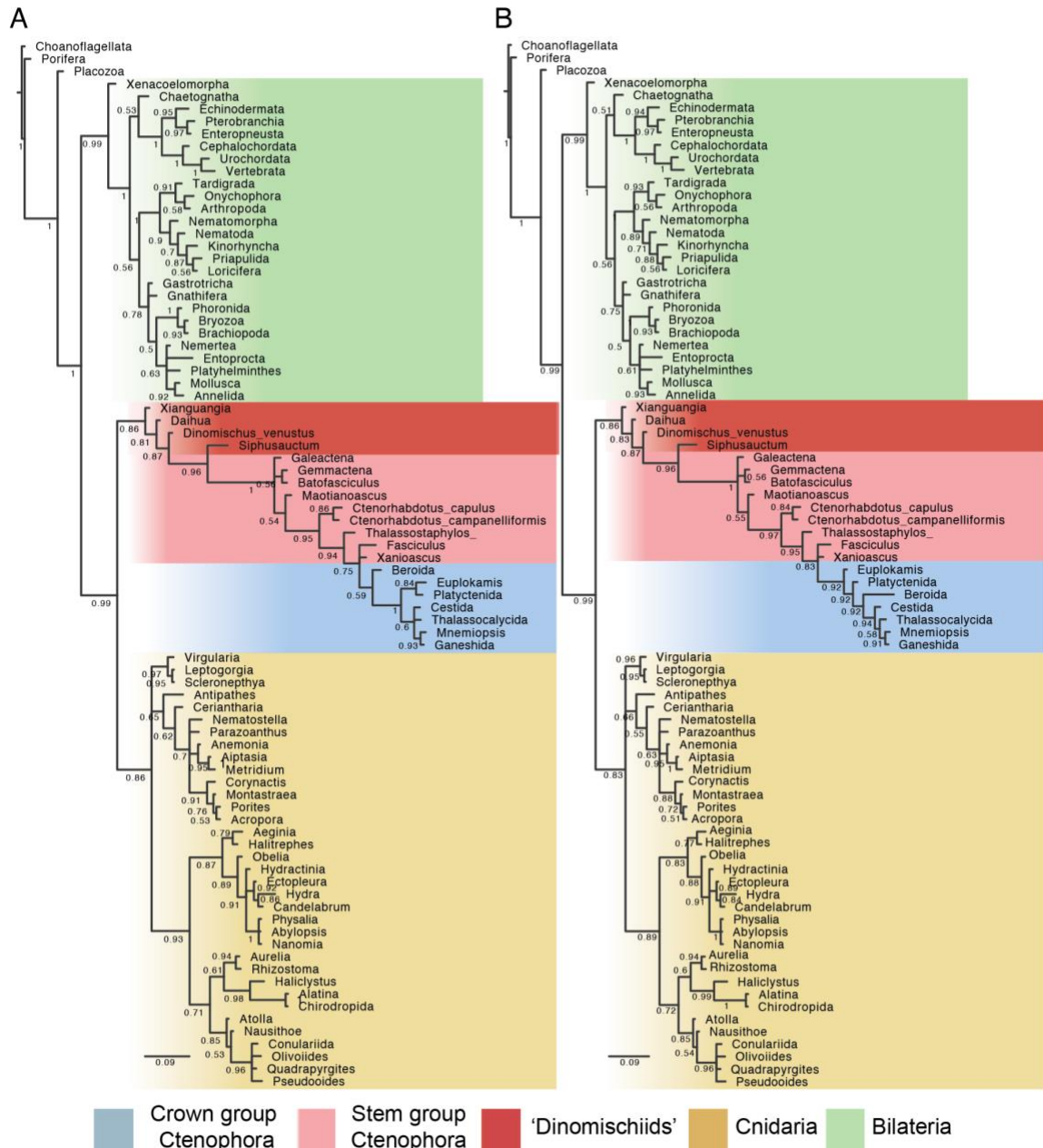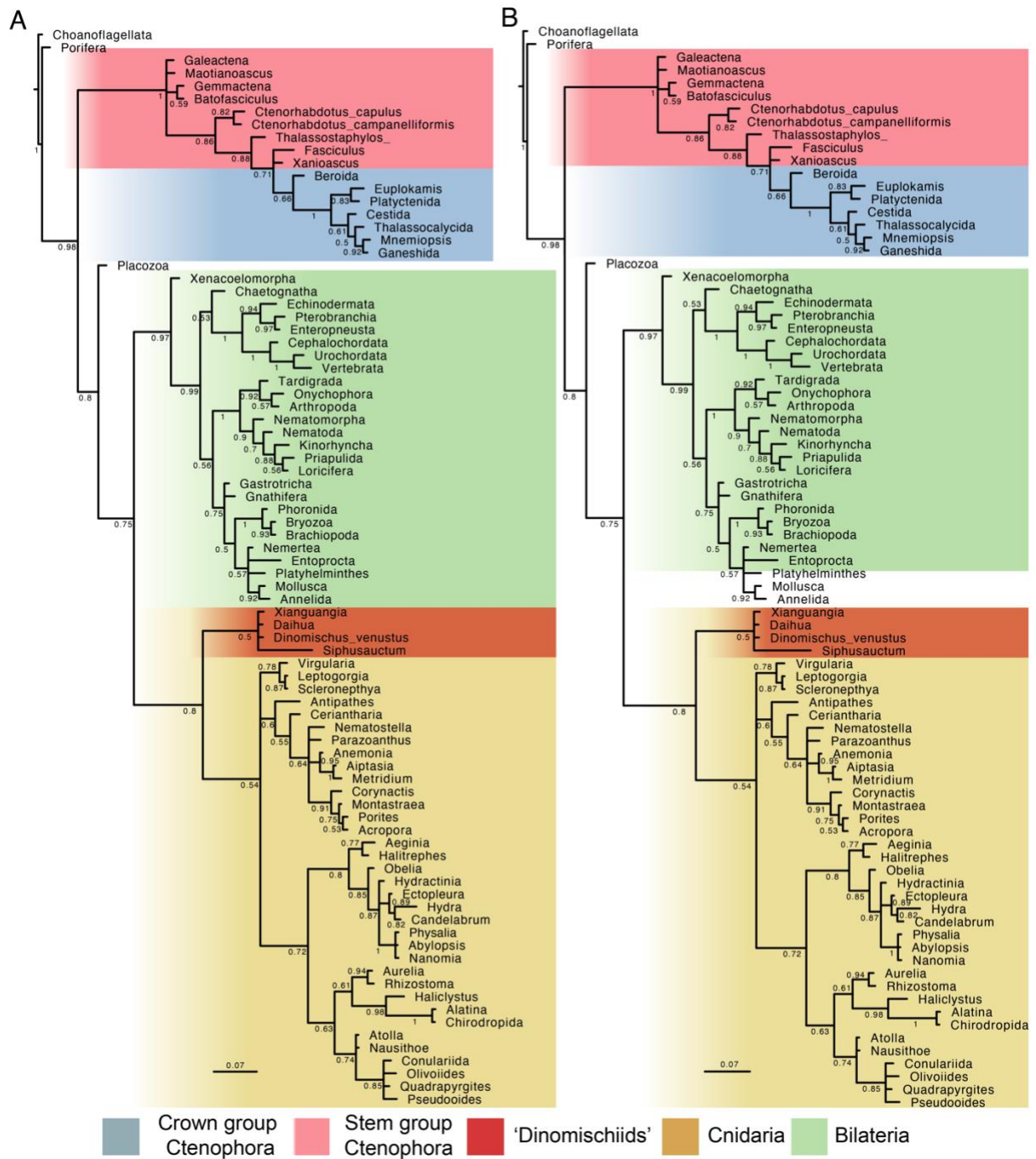
Fig. S2

Figure S2. Additional images of UMNH.IP.6125b, related to figure 2. A, specimen dry, with high angle, cross polarised light. **B,** specimen wet with high angle, cross polarised light.

Fig. S3

Crown group Ctenophora | Stem group Ctenophora | 'Dinomischiids' | Cnidaria | Bilateria

Figure S3. Additional phylogenetic results, related to figure 5. A, full results of the analysis with no topological constraints. **B,** full results of the analysis constraining relationships within the ctenophore crown group based on Whelan et al. [27] . Numbers at nodes are posterior probabilities and scale bars are in units of expected number of substitutions per site.

Fig. S4

Figure S4. Additional phylogenetic results, related to figure 5. A, results of the analysis where the monophyly of Parahoxozoa/Planulozoa. **B,** results of the analysis where ctenophores are constrained as the sister group of all other animals. Numbers at nodes are posterior probabilities and scale bars are in units of expected number of substitutions per site.

Table S1

SS run	Marg. Log Lik. H_0 = Coelenterata	Marg. Log Lik. H_1= Coelenterata Whelan	Marg. Log Lik. H_2 = Parahoxozoa	Marg. Log Lik. H_3 = Ctenosister
1	-2064.99	-2063.16	-2096.78	-2101.75
2	-2065.60	-2063.91	-2095.89	-2102.24
Mean	-2065.25	-2063.47	-2096.24	-2101.96

Table S1. Marginal likelihoods of different models estimated using two independent runs of steppingstone sampling. Related to Figure 5.

Table S2

	$2 \times \log_e B_{10}$	Interpretation
H_0 vs H_1	-1.78	Not worth more than a bare mention (i.e. some weak support for the Whelan *et al.* (2017) topology
H_0 vs H_2	30.99	Coelenterata very strongly supported
H_0 vs H_3	36.71	Coelenterata very strongly supported
H_2 vs H_3	5.72	Parahoxozoa positively supported

Table S2. Bayes factor comparison of the mean marginal likelihoods shown in Table S1, related to Figure 5.