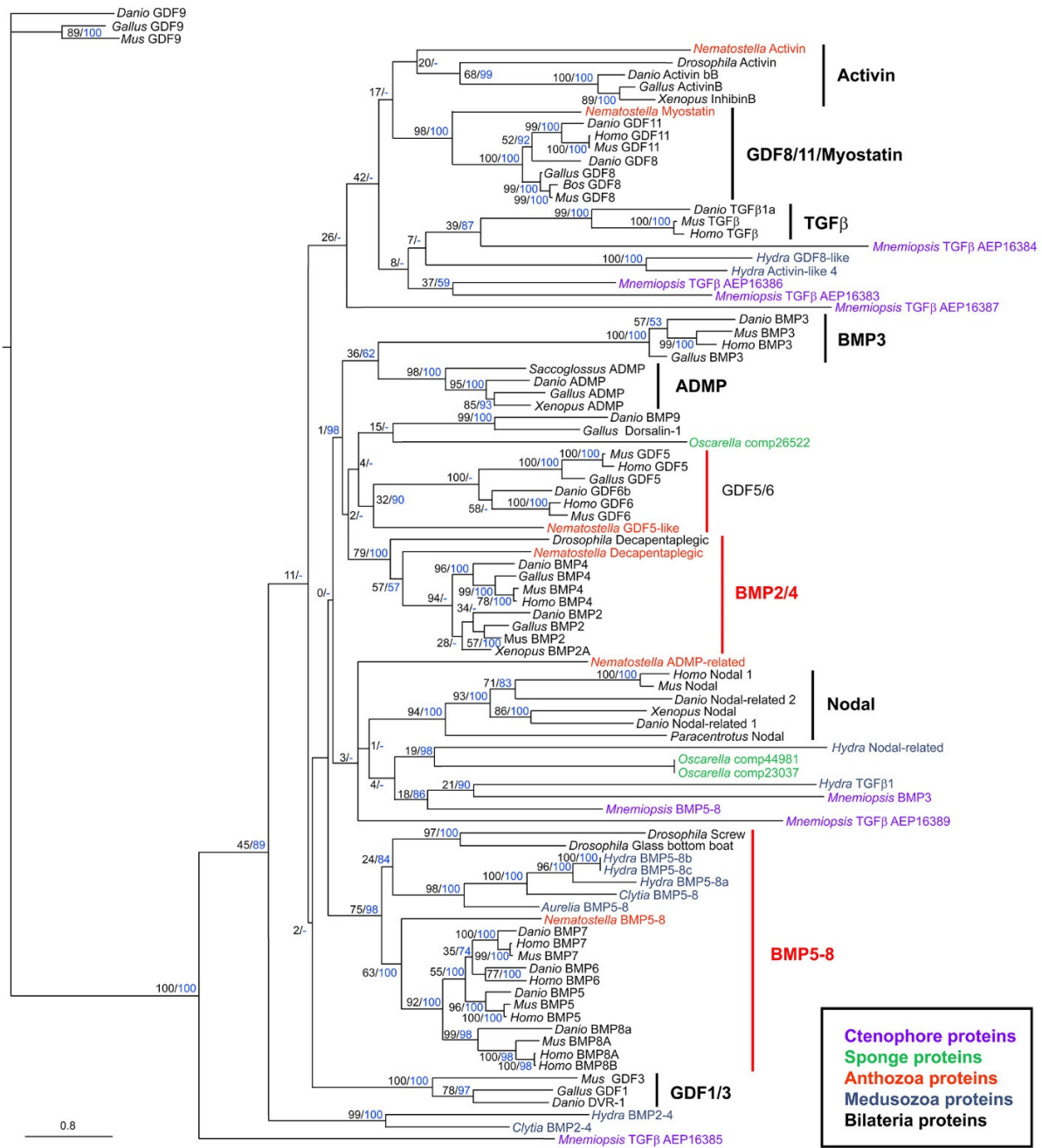


Supplementary Fig. 1. Phylogenetic analysis of TGF β and Chordin proteins.

(A) Maximum Likelihood tree of the bilaterian and cnidarian TGF β proteins (WAG+I+G4+F, bootstrap = 100, black values at nodes, best model selection and ML analysis performed with IQ-TREE (Trifinopoulos et al., 2016)). Posterior probabilities of the MrBayes analysis (WAG+I+G4, 500000 generations, burn-in = 6000 (Ronquist and Huelsenbeck, 2003)) are shown in percent in blue at nodes supported by both methods. Minuses stand for nodes not supported by MrBayes analysis. Some of the bootstrap values in the crown branches are not shown for the sake of space. Note long branches and low bootstrap support of medusozoan BMP2/4s and uncertain positions of *Hydra* TGF β 1, *Hydra* Nodal-related and *Nematostella* ADMP-related. The topology of the tree is affected by long-branch sequences, however, all main groups of TGF β molecules remain stable. Hydrozoan BMP2/4 sequences (*Hydra* BMP2/4 and *Clytia* BMP2/4) fall out of the BMP2/4 clade even in the absence of long branch sequences (*Hydra* Nodal-related, *Hydra* TGF β 1), once short-branch *Aurelia* BMP5-8 sequence is introduced into the alignment (see also Fig. S2). (B) Maximum Likelihood (WAG+I+G4+F, bootstrap = 100, black values at nodes) and MrBayes (WAG+I+G4, 500000 generations, burn-in = 1000, blue values at nodes show posterior probabilities in percent) analyses yield trees with identical topologies showing that *Hydra* Chordin-like does not group with *bona fide* metazoan Chordins.



Supplementary Fig. 2. Phylogenetic analysis of TGFβ proteins including sponge and ctenophore sequences.

Maximum Likelihood tree of the bilaterian, cnidarian, ctenophore and sponge TGFβ proteins (WAG+I+G4+F, bootstrap = 500, black values at nodes, best model selection and ML analysis)

performed with IQ-TREE (Trifinopoulos et al., 2016)). Posterior probabilities of the MrBayes analysis (WAG+I+G4, 50000 generations, burn-in = 10000 (Ronquist and Huelsenbeck, 2003)) are shown in blue at nodes supported by both ML and Bayesian analyses. Minuses stand for nodes not supported by MrBayes analysis. The topology of the tree is strongly affected by long-branch ctenophore, sponge and hydrozoan sequences, however, main groups of TGF β molecules remain stable. The affinity of ctenophore and sponge TGF β sequences to BMPs is not supported. Hydrozoan BMP2/4s fall out of the BMP2/4 clade.

References

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