

File S9. Estimates of evolutionary divergence between species.

The percent of base substitutions between sequences are shown. Analyses were run using the Kimura 2-parameter model (Kimura, 1980), a total of 394 positions in the analyzed dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al., 2018).

	<i>S. crosnieri</i>	<i>H. frontalis</i>	<i>H. glacialis</i>	<i>H. gracilis</i>	<i>A. quadrispinosa</i>	<i>E. ombango</i>	<i>H. microphthalma</i>	<i>K. corallina</i>	<i>M. longisulca</i>	<i>N. elegans</i>	<i>J. spinicauda</i>	<i>O. gracilirostris</i>	<i>S. pellucida</i>	<i>A. longirostris</i>
<i>Sclerodora crosnieri</i>														
<i>Hymenodora frontalis</i>	31.9													
<i>Hymenodora glacialis</i>	32.9	27.0												
<i>Hymenodora gracilis</i>	32.5	23.9	9.4											
<i>Acanthephyra quadrispinosa</i>	44.4	47.1	47.0	41.9										
<i>Ephyrina ombango</i>	51.5	52.4	55.9	53.0	23.9									
<i>Heterogenys microphthalma</i>	46.1	48.5	50.0	49.5	20.8	21.9								
<i>Kemphyra corallina</i>	50.7	49.8	54.7	54.0	21.4	21.5	17.9							
<i>Meningodora longisulca</i>	43.4	52.6	49.5	45.4	24.3	28.4	26.1	27.6						
<i>Notostomus elegans</i>	55.4	51.4	53.5	57.1	25.4	24.0	21.5	20.4	25.8					
<i>Janicella spinicauda</i>	50.9	53.0	54.1	50.6	26.7	24.5	26.3	25.6	28.3	26.0				
<i>Oplophorus gracilirostris</i>	44.8	49.2	48.4	45.0	24.5	21.9	26.2	27.9	23.6	27.0	24.4			
<i>Systellaspis pellucida</i>	49.6	51.3	51.2	49.7	26.6	26.4	23.5	26.1	27.8	25.9	28.9	23.3		
<i>Alvinocaris longirostris</i>	50.1	52.0	51.3	50.0	25.2	27.0	24.9	21.4	30.9	24.9	30.3	27.5	29.7	
<i>Pasiphaea sivado</i>	40.8	39.3	47.8	46.6	27.0	29.7	30.6	31.8	32.2	36.0	29.4	32.5	34.7	34.0