

## **Supplementary Figures**

# **Exploring prokaryotic communities in the guts and mucus of nudibranchs, and their similarity to sediment and seawater microbiomes**

**Journal: Current Microbiology**

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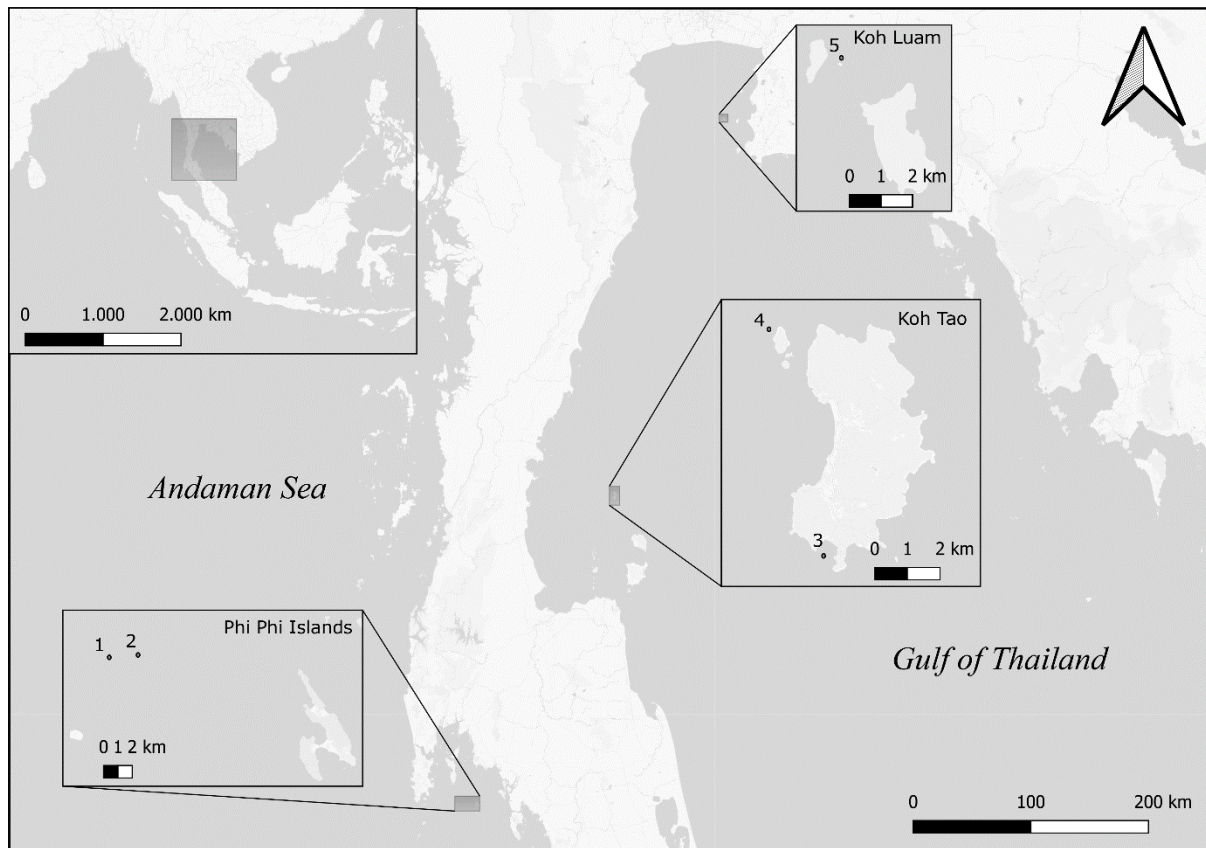
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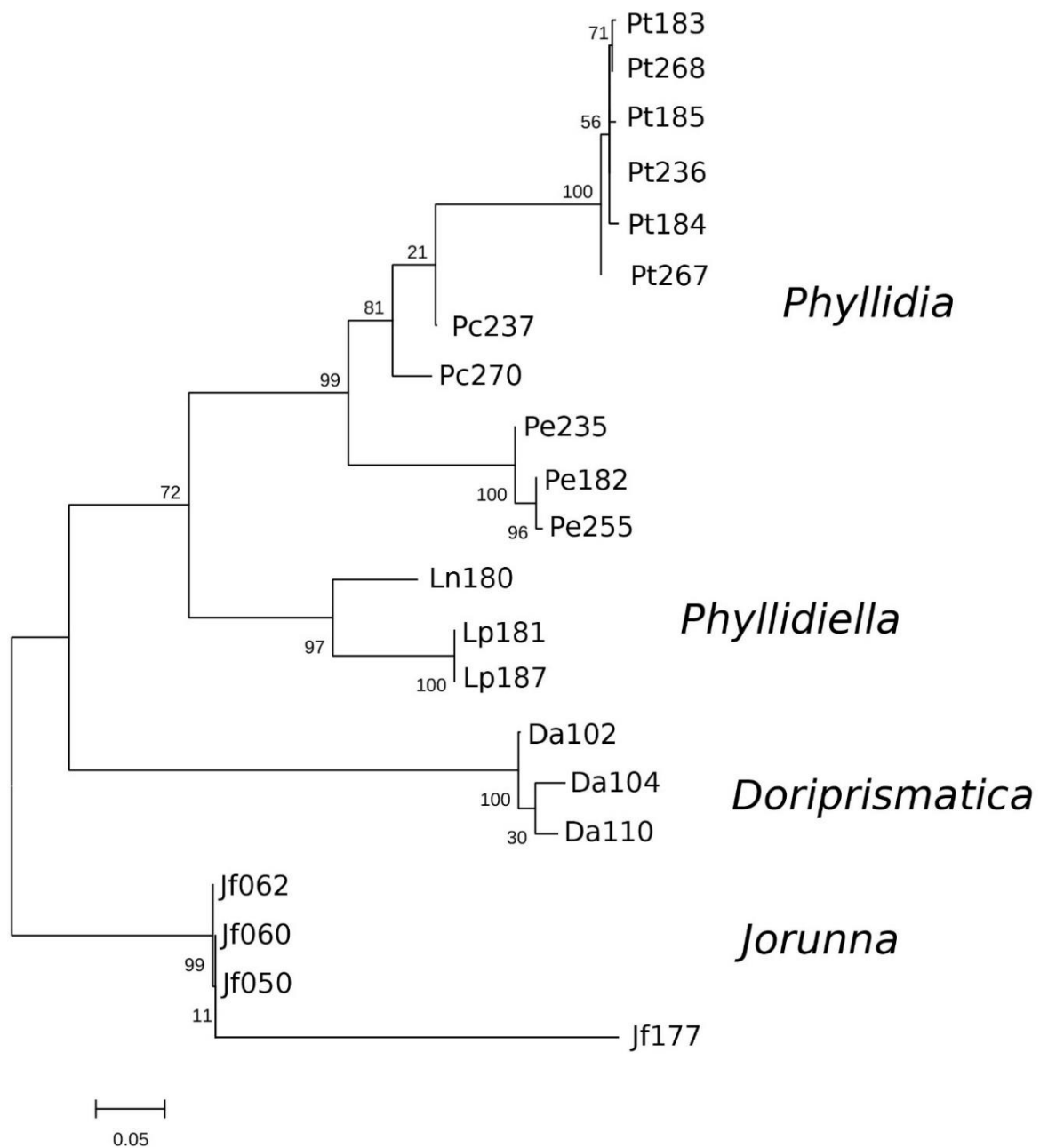
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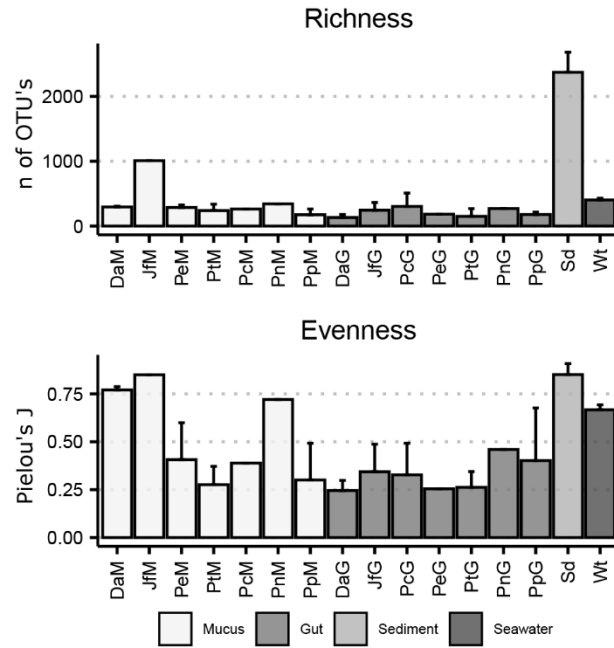
Email: [n.j.de.voogd@cml.leidenuniv.nl](mailto:n.j.de.voogd@cml.leidenuniv.nl) and/or [nicole.devoogd@naturalis.nl](mailto:nicole.devoogd@naturalis.nl)



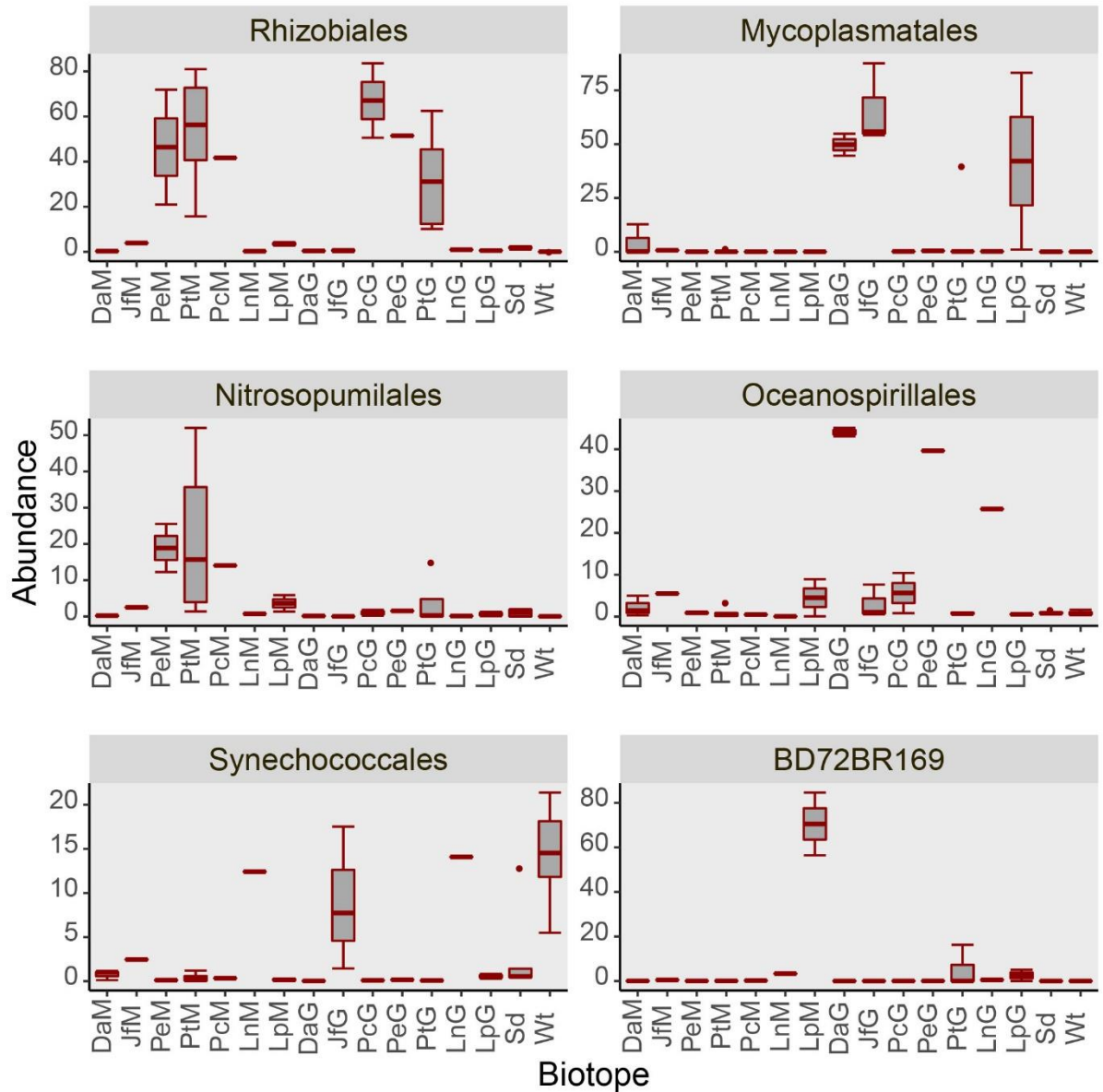
**Fig. S1.** Map of the study area (Andaman sea and gulf of Thailand) showing the three sample locations in higher scaled maps. Site 1 and 2: Phi Phi Islands; Site 3 and 4: Koh Tao; Site 5: Koh Luam.



**Fig. S2** Maximum likelihood phylogenetic tree based on nucleotide sequences of cytochrome oxidase I (COI) gene from the studied nudibranch specimens



**Fig. S3.** Barplots of alpha diversity measures of the prokaryotic communities observed in the mucus (xM) and gut (xG) of the nudibranch species: Da, *Doriprismatica atromarginata*; Jf, *Jorunna funebris*; Pe, *Phyllidia elegans*; Pt, *Phyllidia picta*; Pc, *Phyllidia carlsonhoffi*; Pn, *Phyllidiella nigra*; Pp, *Phyllidiella pustulosa*; Sd, sediment and Wt, seawater. a Evenness. b Richness. Error bars represent one standard deviation of the mean.



**Fig. S4** Boxplots of relative abundances of the most abundant prokaryotic orders observed in the guts (xG) and mantles (xM) of the nudibranch species: Da, *Doriprismatica atromarginata*; Jf, *Jorunna funebris*; Ln, *Phyllidiella nigra*; Lp, *Phyllidiella pustulosa*; Pc, *Phyllidia carlsonhoffi*; Pe, *Phyllidia elegans*; Pt, *Phyllidia picta*; Sd, sediment and Wt, seawater

