

## **Supporting Information for**

## Evidence for microbially-mediated tradeoffs between growth and defense throughout coral evolution

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## This PDF file includes:

Figures S1 to S4

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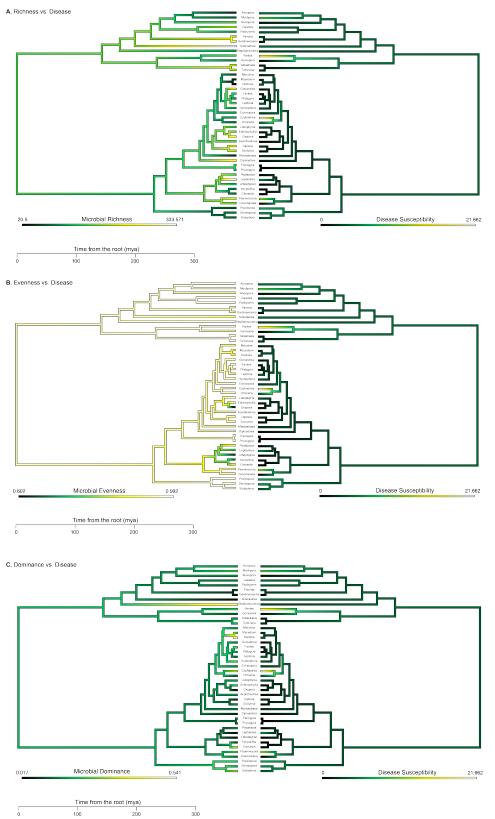
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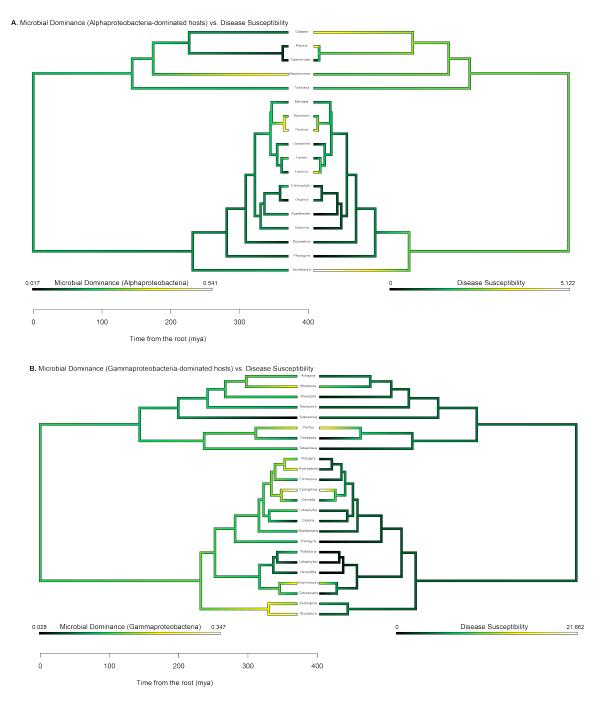
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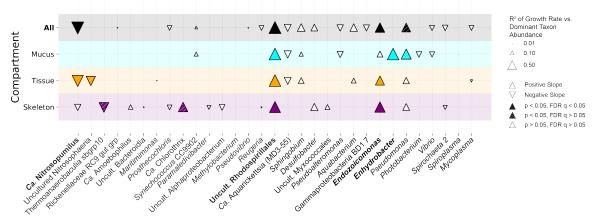
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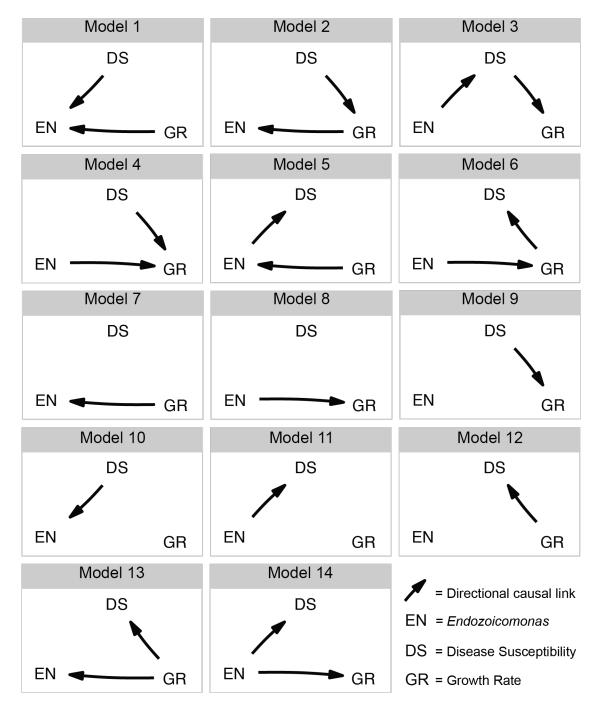
**Fig. S1.** Ancestral state reconstructions mirroring disease susceptibility and microbial alpha diversity metrics, including A) species richness, B) evenness (Gini Index), and C) dominance (Simpson's Index).



**Fig. S2.** Ancestral state reconstructions mirroring disease susceptibility and microbial dominance of A) Alphaproteobacteria only and B) Gammaproteobacteria only.



**Fig. S3. Growth rate vs. dominant taxon abundance (zeros excluded)**. R<sup>2</sup> of the correlations between average coral host growth rate and dominant taxon relative abundance in corals only where each taxon is present (zero counts excluded). Arrow direction indicates a positive or negative correlation, filled arrows refer to significant correlations, striped arrows indicate nominally significant correlations (did not pass multiple comparisons) and open arrows indicate insignificant correlations. Size of the arrow represents R<sup>2</sup> value (See Supplementary Data Table 9b for details).



**Fig. S4.** Model selection for phylogenetic causality analysis. These models represent the fourteen plausible causality pathways that were used in the phylogenetic causality analysis. EN = *Endozoicomonas* relative abundance, DS = coral disease susceptibility, and GR = coral growth rate.