Supplementary Figures for

Genomic insights into host-*Endozoicomonadaceae* cophylogeny

Author names

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Supplementary Figures

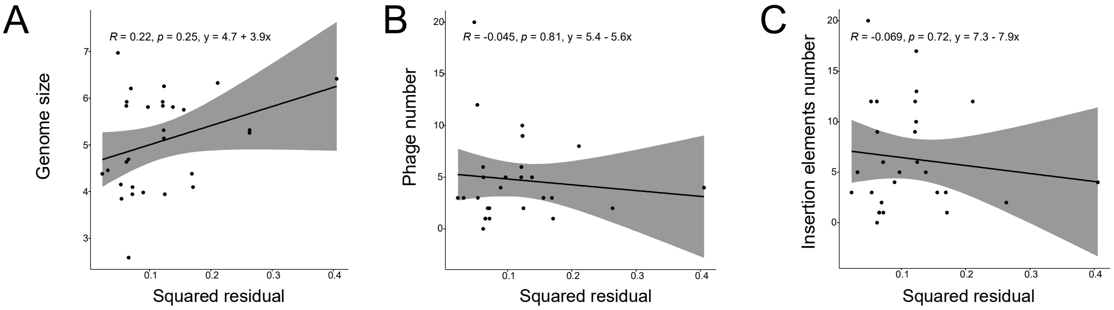

Fig. S1. The Spearman correlation of genome features with cophylogenetic squared residuals. A. The Spearman correlation between genome size and cophylogenetic squared residuals. B. The Spearman correlation between the number of phages and cophylogenetic squared residuals. C. The Spearman correlation between the number of insertion elements and cophylogenetic squared residuals. The gray shaded areas represent the 95% confidence intervals, and the straight lines represent the results of the linear regression.

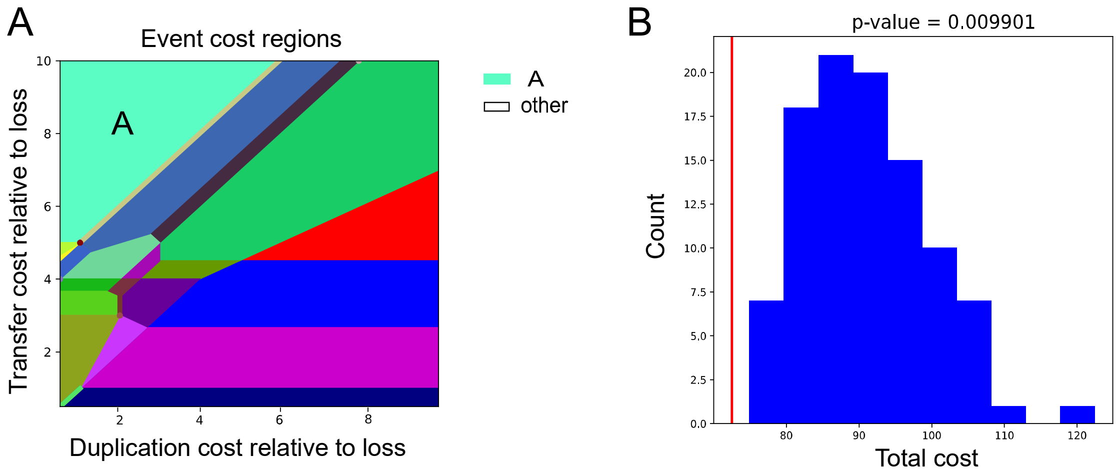

Fig. S2. Cophylogenetic event cost regions and significance of maximum parsimony reconciliation. A. Maximum parsimony reconciliation proposed for the cost region A (top left) and other regions. B. P-value histogram of maximum parsimony reconciliation under region A.