Supplementary Materials for:
Synonymous and Nonsynonymous Distances Help Untangle Convergent Evolution and Recombination

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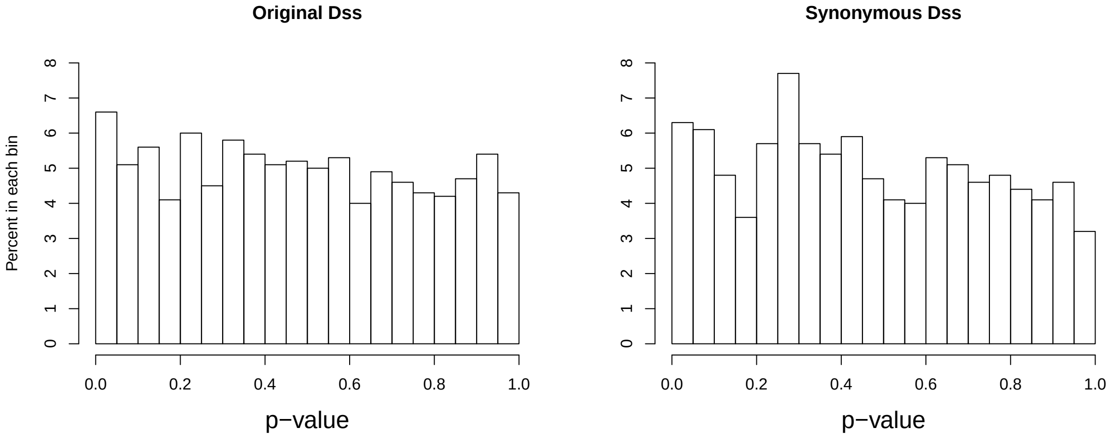

Figure S1: **Distribution of parametric bootstrap p-values under a null scenario**. This pair of histograms shows a simulated realization of the distribution of p-values, under a simulated null scenario. As expected, the p-values from both the original Dss and the synonymous Dss methods resemble a uniform distribution, confirming that they are well-behaved under the null hypothesis.

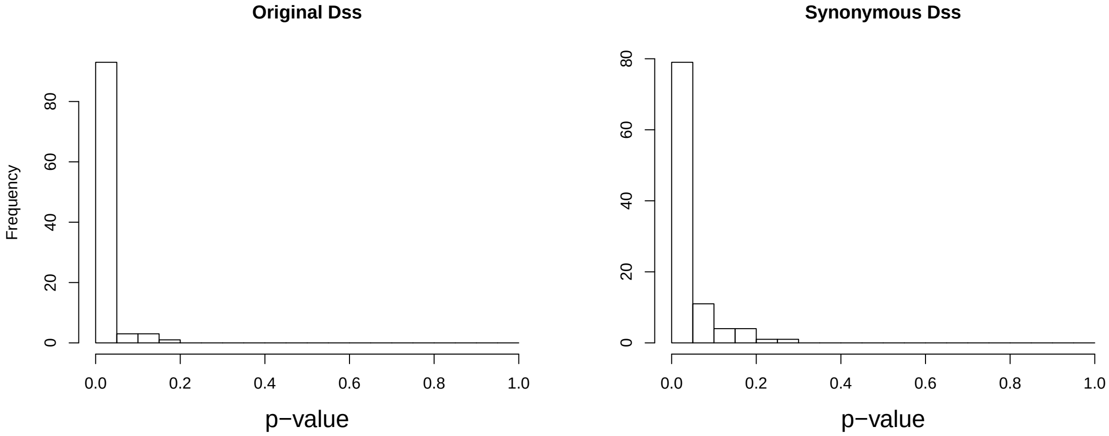

Figure S2: **Distribution of parametric bootstrap p-values under a recombination scenario**. This pair of histograms shows a simulated realization of the distribution of p-values, under a simulated recombination scenario. Since recombination has occurred, then the percentage of p-values that are below 0.05 would represent our power, under $\alpha = 0.05$. For the original Dss, we observe that 90% of the p-values are below 0.05, and for the synonymous Dss, we observe that 76% of the p-values are below 0.05. Thus, we observe a slight reduction in power when using the synonymous Dss statistic as compared to the original Dss statistic.

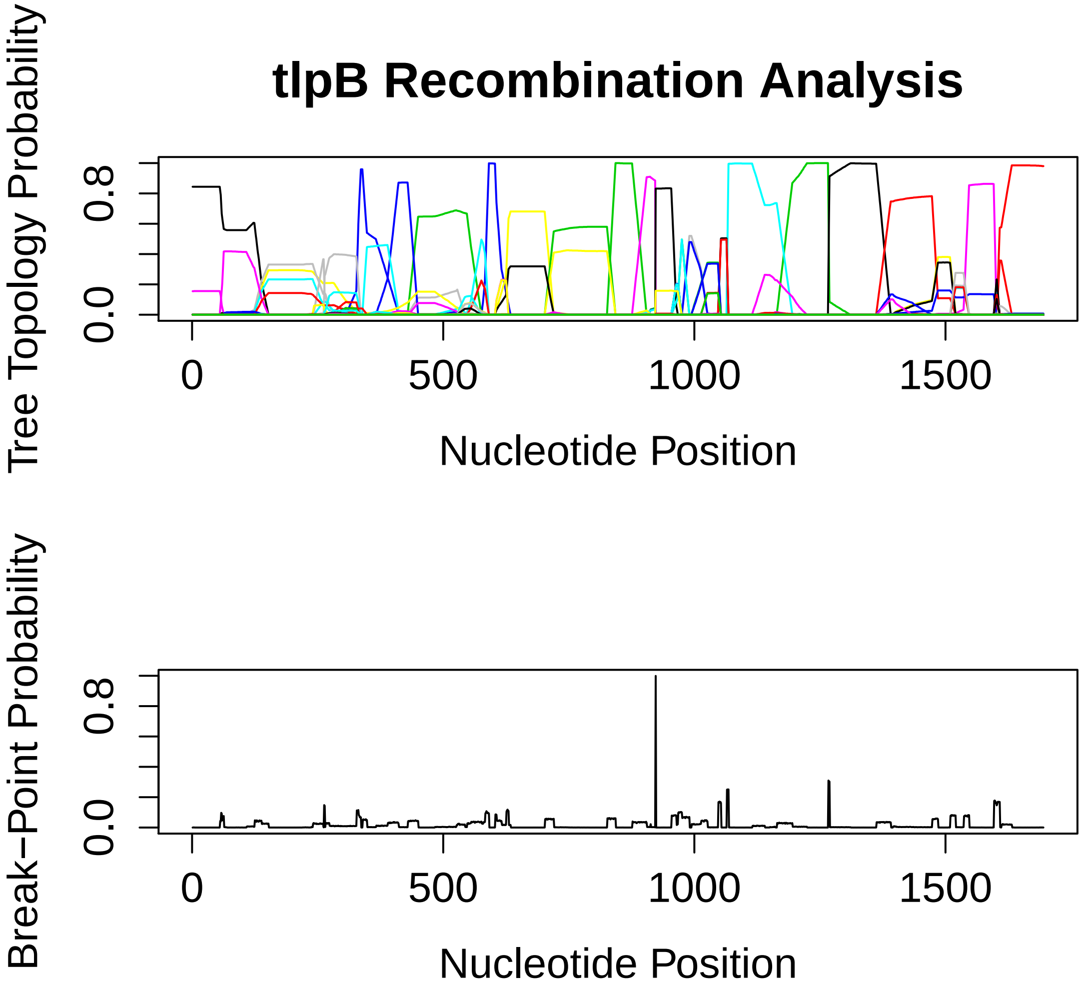

Figure S3: **Recombination breakpoint analysis on *H. pylori tlpB* gene with rbrothers I: prior=0.50**. In this analysis, the prior probability of at least one recombination breakpoint was set to 0.50. The top panel shows site-specific posterior probabilities for the most probable topologies, and the bottom panel shows the site-specific posterior probability of a breakpoint. The posterior mean number of recombination breakpoints was 29.

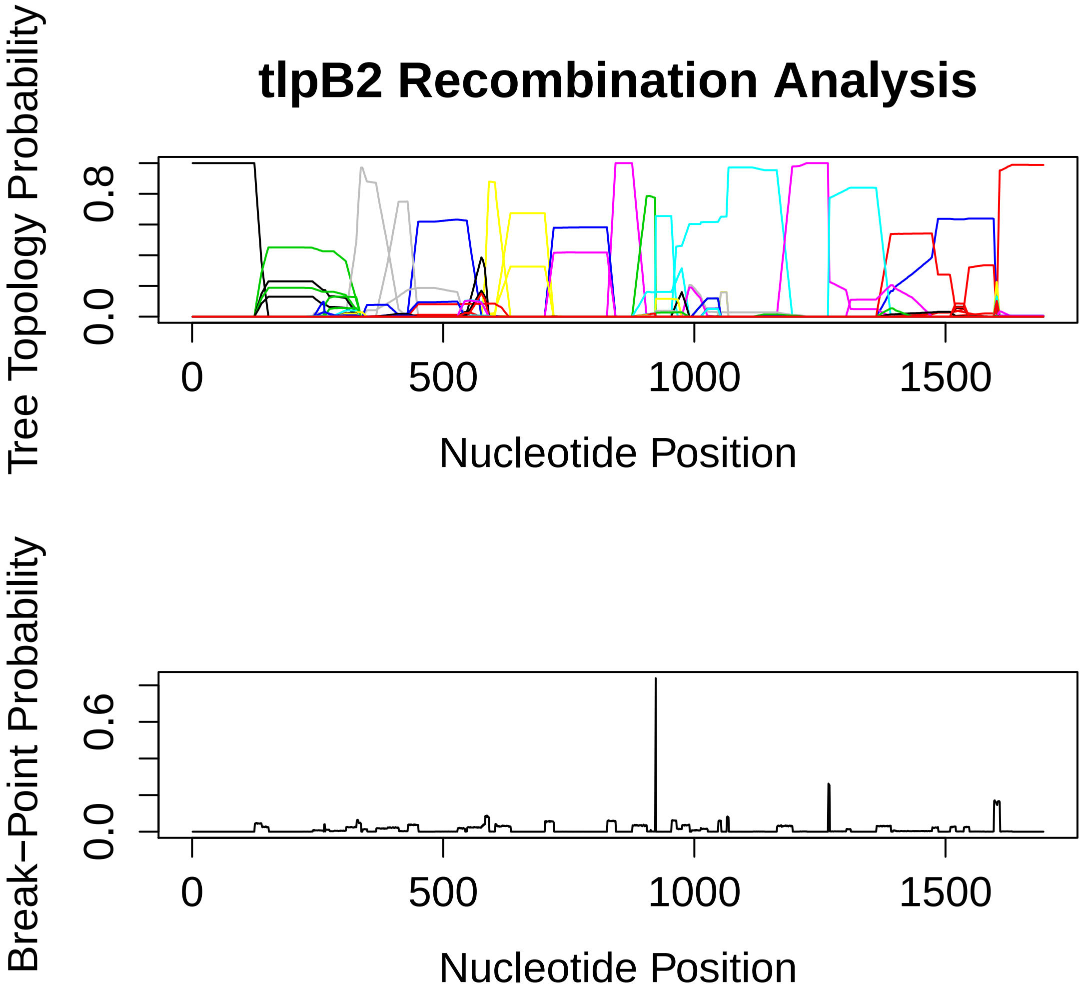

Figure S4: **Recombination breakpoint analysis on *H. pylori tlpB* gene with rbrothers II: prior=0.06**. Here, the prior probability of at least one recombination breakpoint was set to 0.06. Again, the top panel shows site-specific posterior probabilities for the most probable topologies, and the bottom panel shows the site-specific posterior probability of a breakpoint. The posterior mean number of recombination breakpoints was 19.

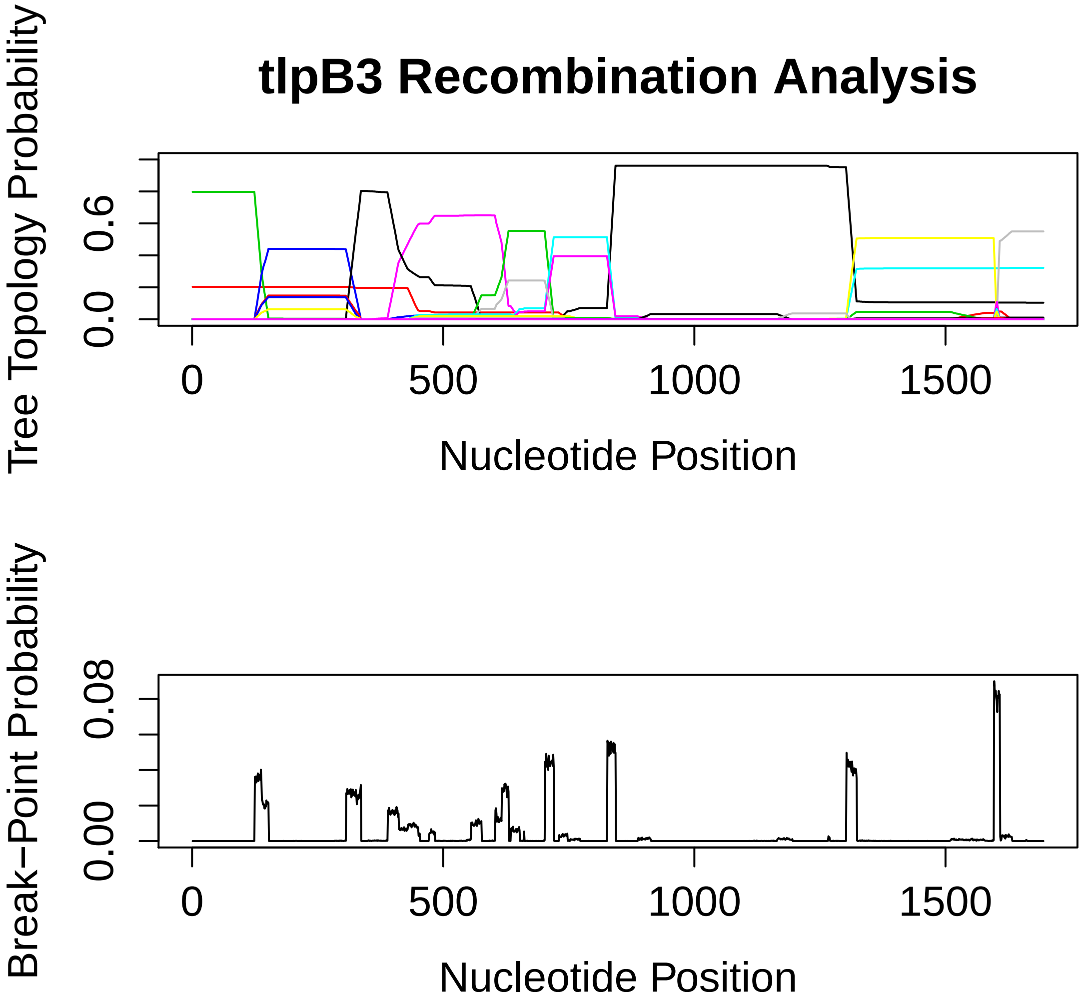

Figure S5: **Recombination breakpoint analysis on *H. pylori tlpB* gene with rbrothers III: prior=0.001**. Here, the prior probability of at least one recombination breakpoint was set to 0.001. The posterior mean number of recombination breakpoints was 7.