Table S2. Statistical analyses of LGT rates for Roseobacter branches. A) Analysis of covariance results of F-tests for ancestral compared to exterior branches. B) Deleted-t residuals analysis from regressions of gene loss rate, LGT rate, and gene duplication rate vs. amino acid substitution rate, conducted separately for ancestral and exterior branches.

A.

Phylogenetic method	**Factor**	**Dependent variable**		
		LGT	Losses	Duplications
P4	a.a. replacements[1]	0.002	< 0.001	N.S.
	branch category[2]	< 0.001	N.S.	< 0.001
	interaction	N.S.	N.S.	N.S.
RAxML	a.a. replacements[1]	0.003	< 0.001	N.S.
	branch category[2]	< 0.001	N.S.	< 0.001
	interaction	N.S.	N.S.	N.S.
PhyloBayes	a.a. replacements[1]	0.004	< 0.001	N.S.
	branch category[2]	< 0.001	N.S.	< 0.001
	interaction	N.S.	N.S.	N.S.

[1] Covariate

[2] Branches were categorized as ancestral or leaf.

N.S.: Not Significant

B.

Phylogenetic method	**Branch category**	**Dependent variable**	**Branch**	**Deleted-t residual**
P4	ancestral	**LGT**	**R37**	**12.84*** **
	leaf	Losses	CCS1	-3.54*
		Duplications	**OA238**	**7.77*** **
RAxML	ancestral	**LGT**	**R37**	**13.56*** **
		Duplications	R33	5.28***
	leaf	**Duplications**	**OA238**	**7.60*** **
PhyloBayes	ancestral	**LGT**	**R37**	**13.79*** **
		Duplications	R24	5.50***
	leaf	**Duplications**	**OA238**	**7.50*** **

[1] Significance levels were corrected for multiple testing by the Bonferroni method: * P < 0.05; *** P < 0.001. Boldface indicates patterns consistent across phylogenetic methods.