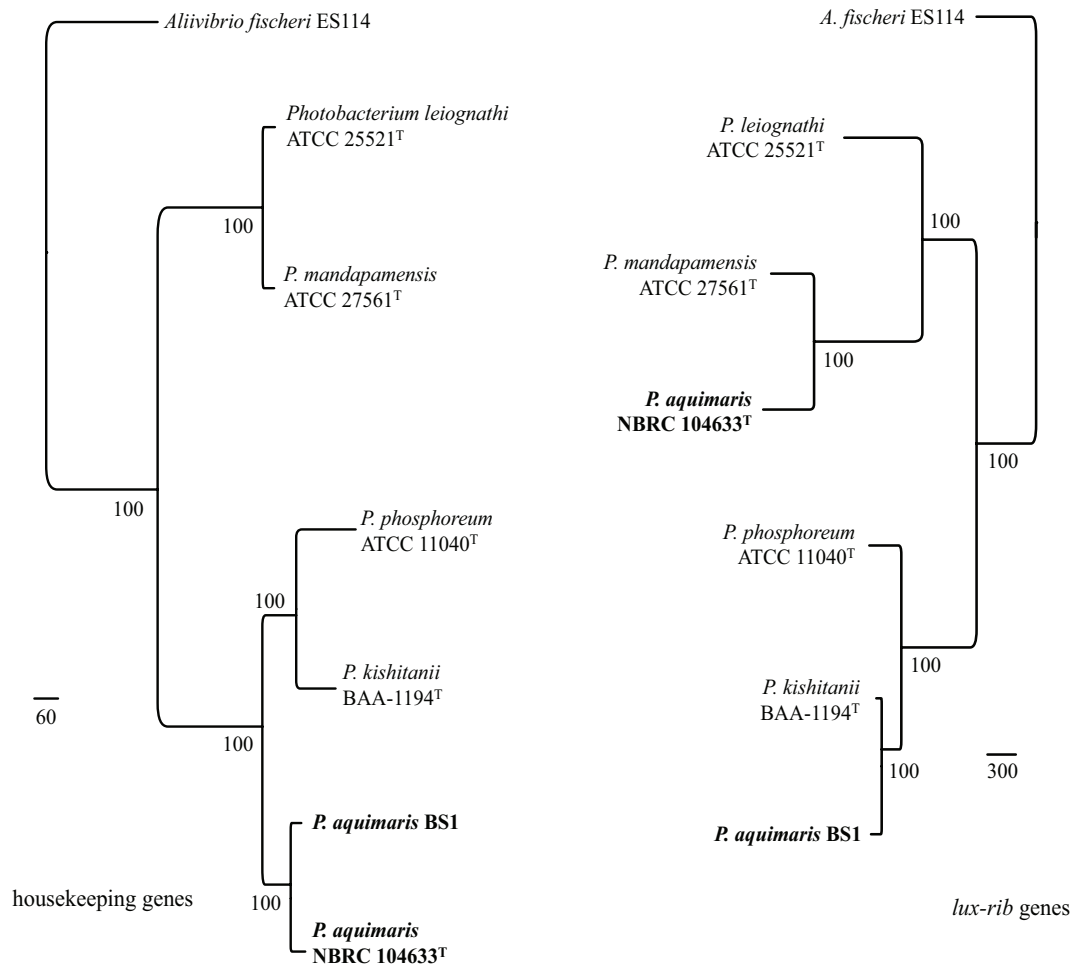


Supplementary Figure 1.

Natural Replacement of Vertically Inherited *lux-rib* Genes of *Photobacterium aquimaris* by Horizontally Acquired Homologs

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Relationship between luminous *Vibrionaceae* based on housekeeping genes (left tree) and *luxCDABFEG-ribEBHA* genes sequences (right tree).

The housekeeping tree was repeated from the Figure 1 for reference. For the *lux-rib* sequences analysis, only protein coding sequences were used. Sequence data were analyzed in PAUP* (Swofford, 2003) using the parsimony criterion. Treated as missing data were: *luxF*, absent in *P. leiognathi* and *A. fischeri*; *ribE*, absent in *P. phosphoreum*; and *ribEBHA*, absent in *A. fischeri*. The *lux-rib* sequence alignment had a total of 9453 characters, of which 2539 were phylogenetically informative. The analysis resulted in a single, most parsimonious tree, and analyses based on the individual genes gave the same phylogenetic placement. The trees were visualized using FigTree v. 1.3.1. Analysis of the housekeeping genes were also carried out using neighbor-joining and maximum-likelihood algorithms, as done by Yoshizawa *et al.* (2009), and the results were congruent with the parsimony analysis (data not shown). GenBank accession numbers for the sequences used in both analyses can be found in Table S1.