Figure S3. Comparison of cognate regulators and associated export systems in lipopeptide-synthesizing *Pseudomonas*. Maximum-likelihood trees inferred from amino acid sequence alignments of (A) LuxR-family regulators encoded by genes linked with the respective initiatory NRPS genes and (B) the components of tripartite MacA/MacB/OprM-like export systems (concatenated sequences; same phylogeny was obtained for the three individual sequence sets (data not shown)). Lipopeptide-specific codes as in Fig. 3, with the xantholysin-related ones in bold. The regulatory gene encoding SyrF (panel A) is located downstream of *syrE*. In panel B, the Syf and Arf systems are not included (no sequences available for the corresponding OprM-like protein). The scale bars represent 0.09 (panel A) and 0.04 (panel B) substitutions per site. The xantholysin cluster (blue) and viscosin cluster (green) are shown in different colors.