



Figure S2. Maximum-likelihood tree of thioesterase domains of characterized LP-producing *Pseudomonas* NRPSs. The clusters with tandemly organized domains TE1 (red) and TE2 (green) are shown in different colors. Lipopeptide-specific codes as in Fig. 3, with the xantholysin-related ones in bold. The tandem-TE domains of lysobactin synthetase LybB from *Lysobacter* sp. ATCC 53042 and the mono-TE domain of syringomycin synthetase SyrE from *P. syringae* pv. *syringae* B301D are included for comparison. The internal residue involved in cyclization with the carboxyterminal amino acid is specified for each TE1/TE domain (NA = not applicable for the linear syringafactins; OH-Phe = β -hydroxy phenylalanine). The scale bar represents 0.5 substitutions per site.