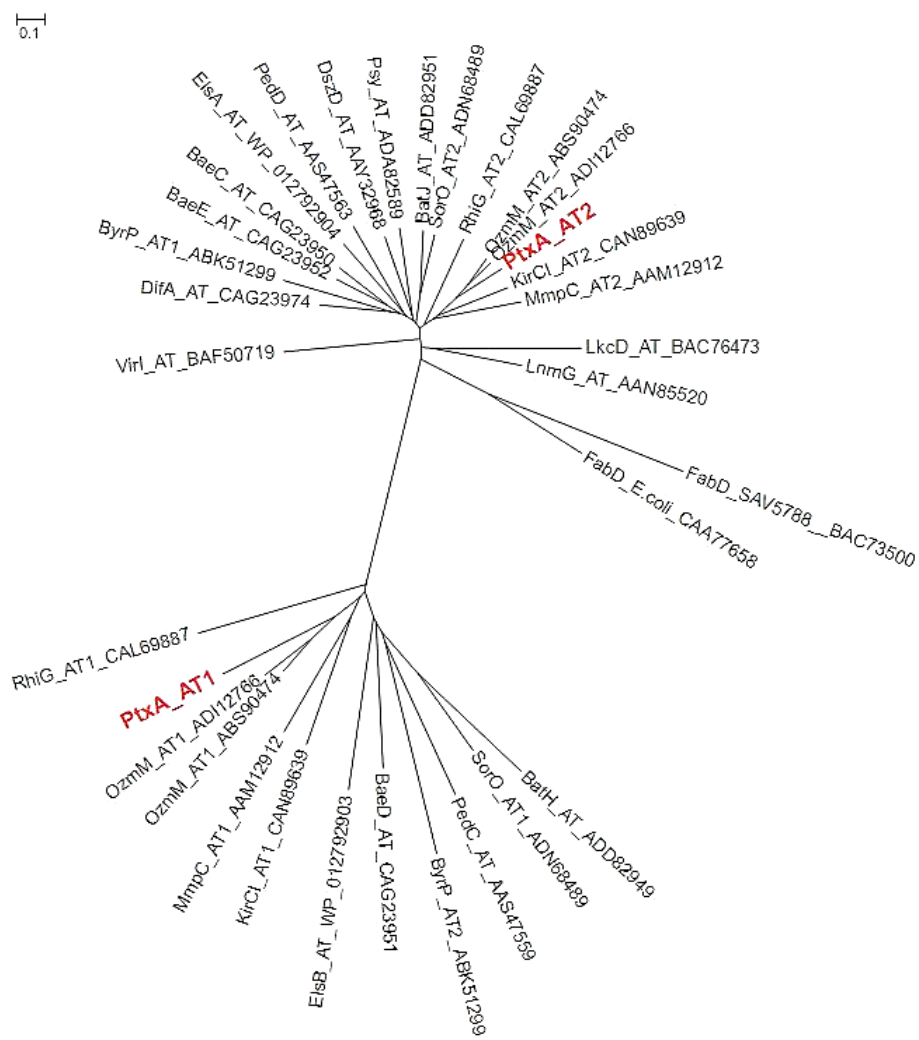


Clade B



Clade A

**S2 Fig. Phylogenetic analysis of AT domains of the *trans*-AT PKS system.** BaeC (CAG23950), BaeD (CAG23951), and BaeE (CAG23952) from *Bacillus amyloliquefaciens* FZB42; BatH (ADD82949) and BatJ (ADD82951) from *Pseudomonas fluorescens* BCCM\_ID9359; BryP (ABK51299) from *Candidatus endobugula sertula*; DifA (CAG23974) from *Bacillus amyloliquefaciens* FZB42; DszD (AAY32968) from *Sorangium cellulosum* So ce12; ElsA (WP\_012792904) and ElsB (WP\_012792903) from *Chitinophaga pinensis* DSM 2588; KirC1 (CAN89639) from *Streptomyces collinus* Tu 365; LnmG (AAN85520) from *Streptomyces atroolivaceus*; LkcD (BAC76473) from *Streptomyces rochei*; MmpC (AAM12912) from *P. fluorescens* NCIMB 10586; OzmM (ABS90474) from *S. albus* JA3453 and OzmM (ADI12766) from *Streptomyces bingchenggensis* BCW-1; PedC (AAS47559) and PedD (AAS47563) from symbiont bacterium of *Paederus fuscipes*; PsyH (ADA82589) from an unculturable symbiont of sponge *Psammocinia* aff. *Bulbosa*; RhiG (CAL69887) from *Burkholderia rhizoxina*; SorO (ADN68489) from *S. cellulosum* So ce12; VirI (BAF50719) from *Streptomyces virginiae*; FabD (CAA77658) form *E. coli*; and FabD SAV5788 (BAC73500) from *S. avermitilis*.