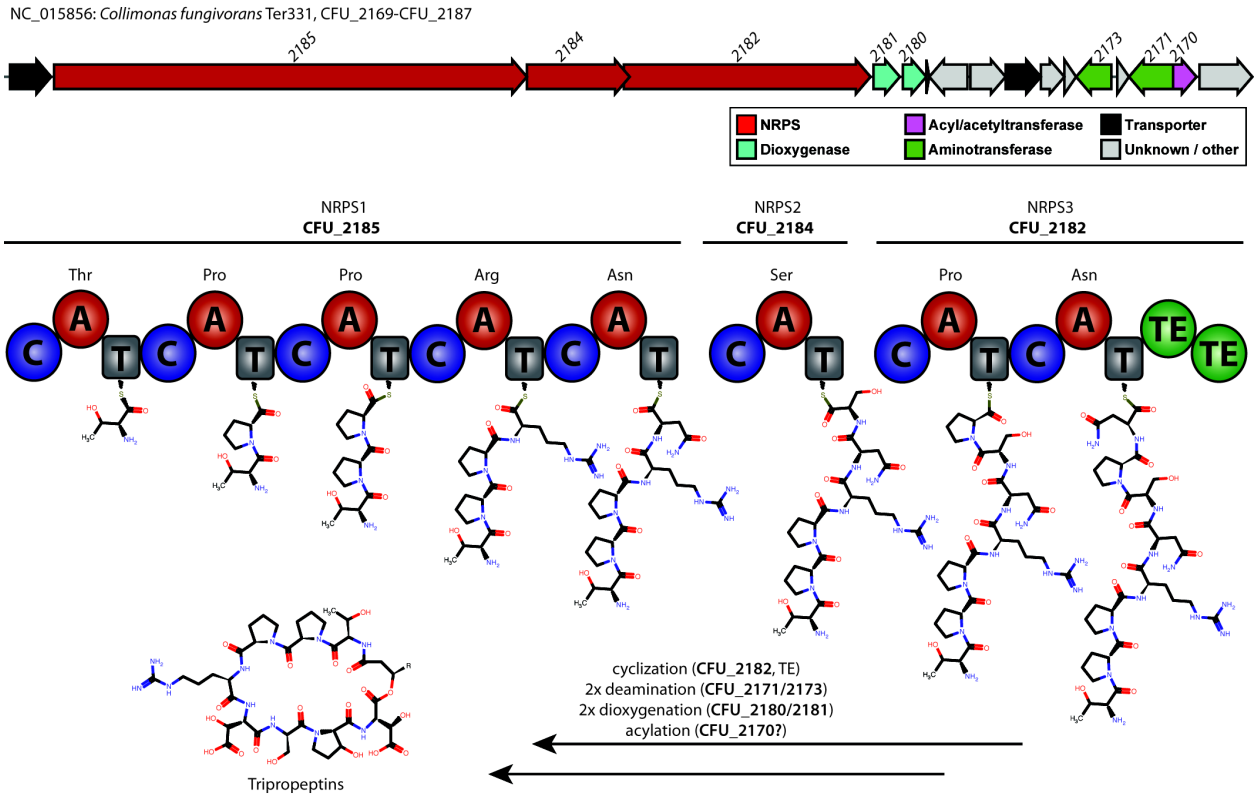

Figure S1: Gene cluster and predicted possible biosynthetic scheme for the production of tripropeptin-like molecules by *Collimonas fungivorans* Ter331. The gene cluster was identified by Pep2Path based on the raw amino acid sequence of compounds originally purified from *Lysobacter* sp. BMK333-48F3. The outline of the gene cluster and its encoded NRPS assembly-line above shows that the architecture of the gene cluster is consistent with the chemical structure of molecules highly similar to the tripropeptins that have been identified in *Lysobacter*. This BGC has eight NRPS modules, of which seven gave NRPSPredictor2 predictions exactly matching the tripropeptin A sequence in the right order, while the eighth prediction was only a near miss (ornithine predicted instead of arginine). This indicates that such a gene cluster might have undergone horizontal gene transfer at least once, from one subphylum to another. The peptides actually produced by *Collimonas* might have small differences in chemistry, compared to the *Lysobacter* tripropeptins, due to slight variations and/or promiscuity in the tailoring reactions and substrate acceptance.