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Supplementary Material

Identification of secondary metabolite gene clusters in the *Pseudovibrio* genus reveals a promising potential toward the discovery of novel bioactive compounds.

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Supplementary Figure Legends

Figure S1. Maximum Likelihood tree performed for the AMP-binding domains of the NRPS biosynthetic gene clusters. *Pseudovibrio* sequences were combined with those of other bacterial BGCs present in the MIBiG database.

Figure S2. Maximum Likelihood tree performed for the KS domains of the PKS biosynthetic gene clusters. *Pseudovibrio* sequences were combined with those other bacterial BGCs present in the MIBiG database.

Figure S3. Sub-tree containing *Pseudovibrio* sequences extracted from the AMP-binding domains. The subtrees were recovered from the tree shown in Figure S1. Only support values higher than 0.5 are shown.

Figure S4. Sub-tree containing *Pseudovibrio* sequences extracted from the KS domains. The subtrees were recovered from the tree shown in Figure S2. Only support values higher than 0.5 are shown.