## Title
Identification of secondary metabolite gene clusters in the Pseudovibrio genus reveals encouraging biosynthetic potential toward the production of novel bioactive compounds

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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.