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Author(s)	Naughton, Lynn M.; Romano, Stefano; O'Gara, Fergal; Dobson, Alan D. W.
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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.

Lynn M. Naughton¹§, Stefano Romano²§, Fergal O’Gara^{3,4} and Alan D.W. Dobson^{1*}

* **Correspondence:** Professor Alan Dobson: a.dobson@ucc.ie

§ These authors contributed equally to this work



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.