

**UCC Library and UCC researchers have made this item openly available.
Please [let us know](#) how this has helped you. Thanks!**

Title	Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus
Author(s)	Romano, Stefano; Fernández-Guerra, Antonio; Reen, F. Jerry; Glöckner, Frank O.; Crowley, Susan P.; O'Sullivan, Orla; Cotter, Paul D.; Adams, Claire; Dobson, Alan D. W.; O'Gara, Fergal
Publication date	2016-03-30
Original citation	Romano, S., Fernández-Guerra, A., Reen, F. J., Glöckner, F. O., Crowley, S. P., O'Sullivan, O., Cotter, P. D., Adams, C., Dobson, A. D. W. and O'Gara, F. (2016) 'Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus', <i>Frontiers in Microbiology</i> , 7, 387 (20pp.). doi: 10.3389/fmicb.2016.00387
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://journal.frontiersin.org/article/10.3389/fmicb.2016.00387/full http://dx.doi.org/10.3389/fmicb.2016.00387 Access to the full text of the published version may require a subscription.
Rights	© 2016, Romano, Fernández-Guerra, Reen, Glöckner, Crowley, O'Sullivan, Cotter, Adams, Dobson and O'Gara. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms https://creativecommons.org/licenses/by/4.0/
Item downloaded from	http://hdl.handle.net/10468/4114

Downloaded on 2021-05-12T03:01:09Z

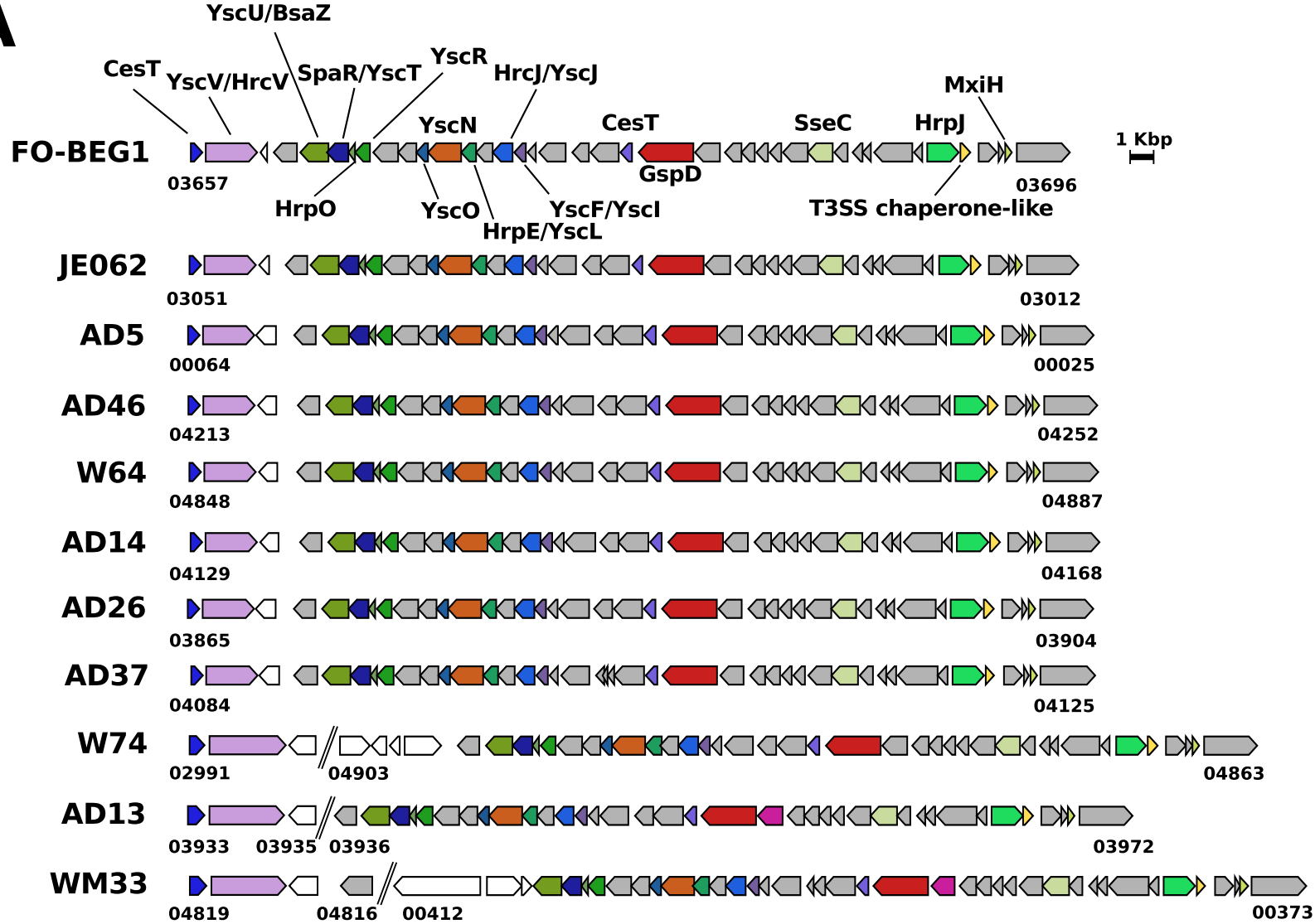
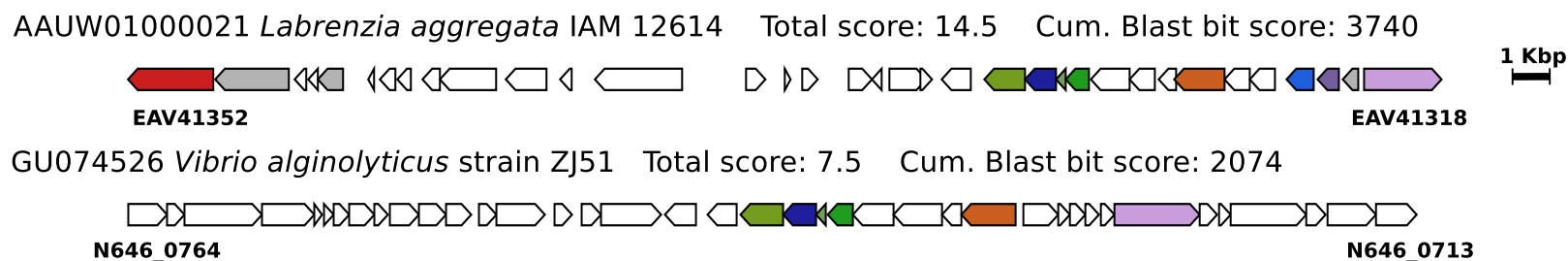
A**B**

Figure S4 Type 3 secretion system in the *Pseudovibrio* genus. In **A** are reported the gene clusters coding for the T3SS identified in the *Pseudovibrio* genomes. Forward slashes separate genes identified in separate contigs. A representative T3SS gene cluster for *Pseudovibrio* was then used as query against all available GeneBank bacterial genomes, with the aim of searching homologous clusters. Only the best two hits of this analysis are shown in **B**. For all gene clusters, similar colours indicates homologous genes. In gray are reported homologous genes shared amongst the strains, but not identified as part of the T3SS structure with the approach we used.