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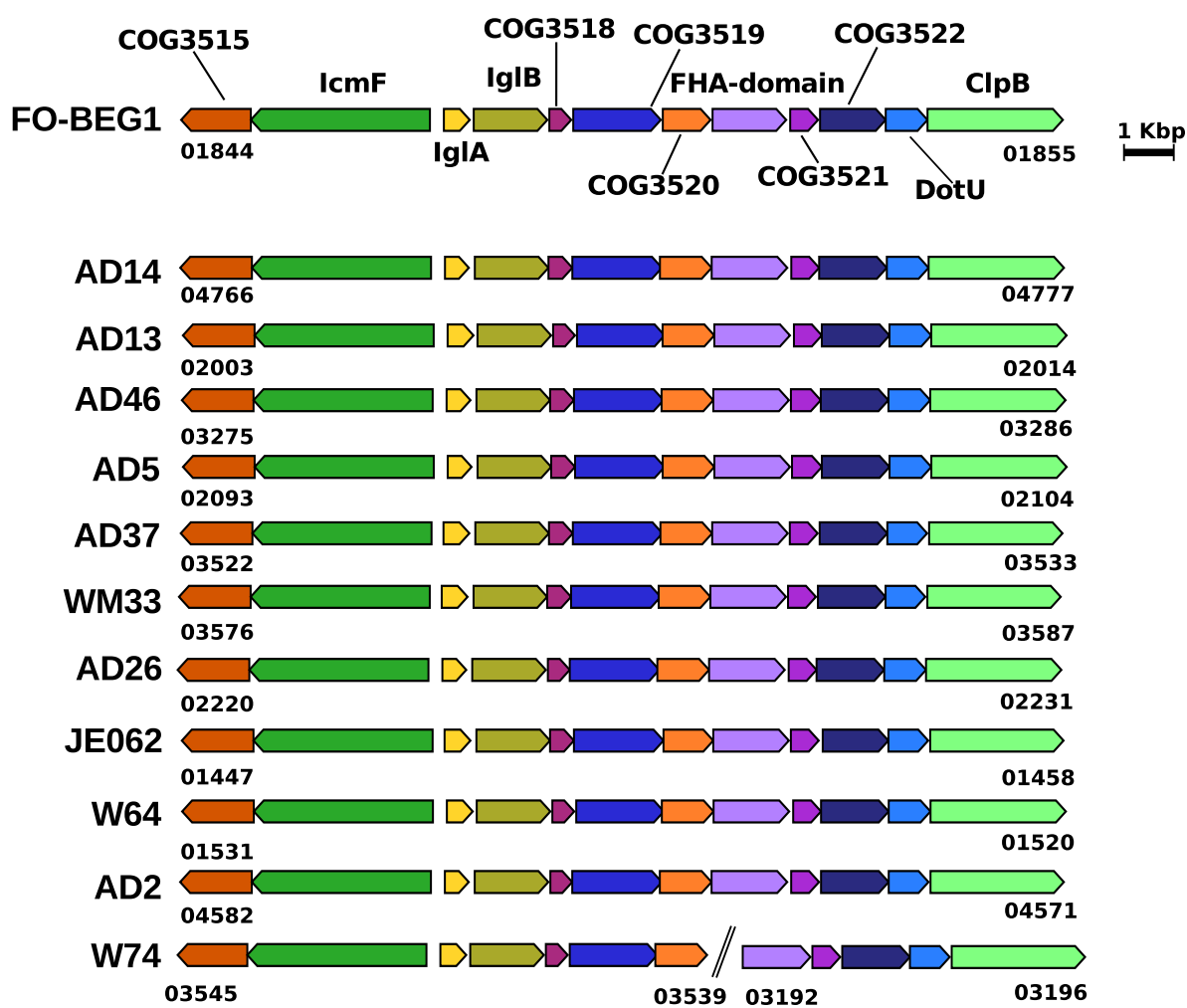
Title	Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus
Author(s)	Romano, Stefano; Fernàndez-Guerra, Antonio; Reen, F. Jerry; Glöckner, Frank O.; Crowley, Susan P.; O'Sullivan, Orla; Cotter, Paul D.; Adams, Claire; Dobson, Alan D. W.; O'Gara, Fergal
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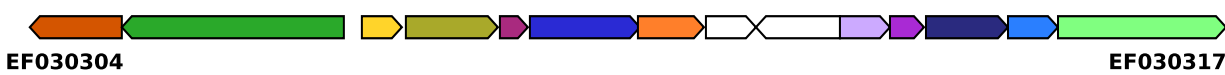


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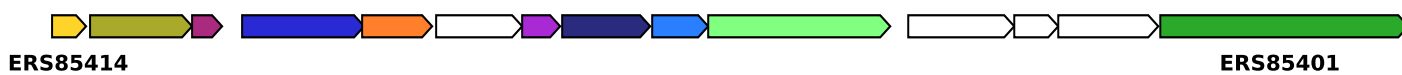
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

A**T6SS-I****B**

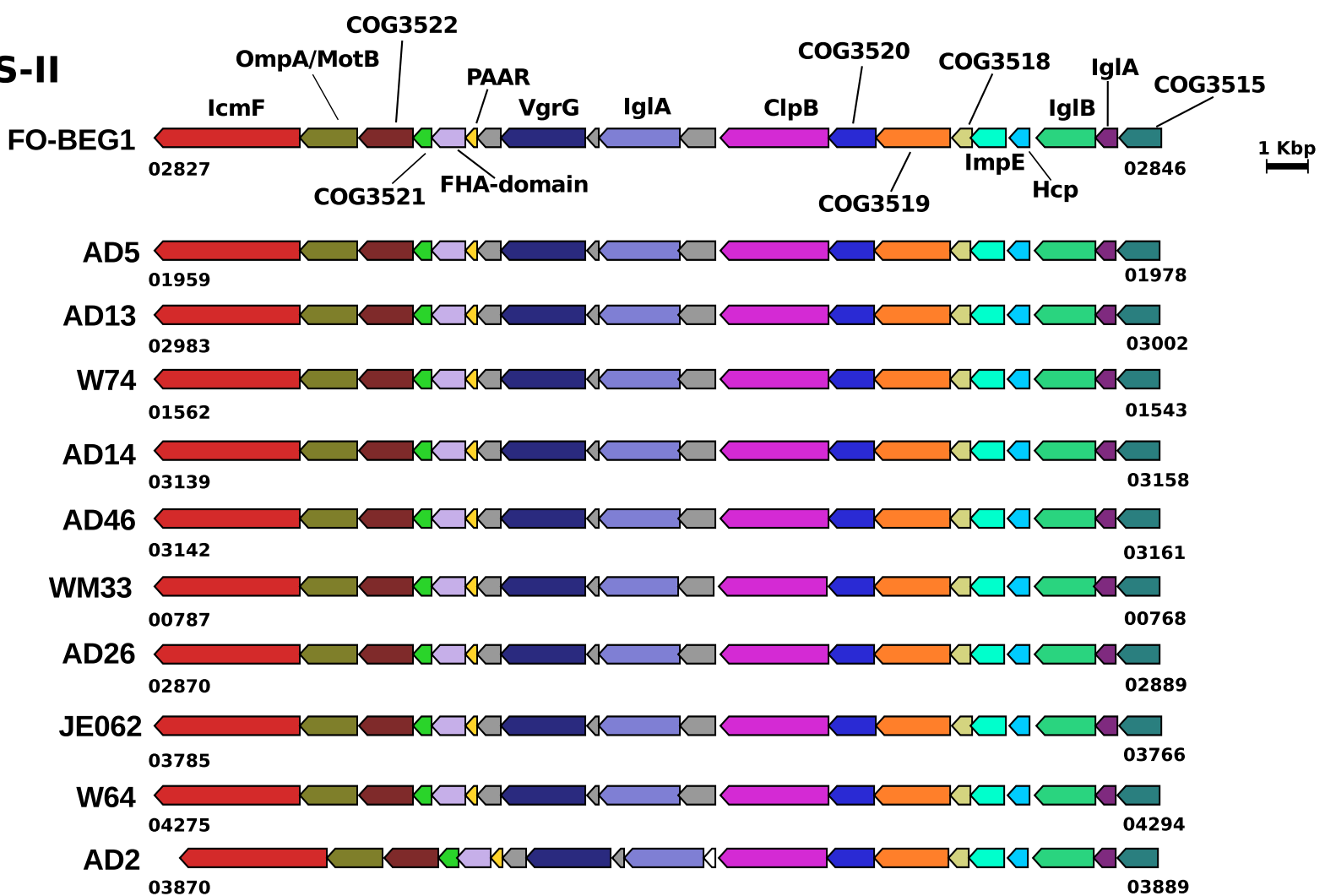
GL476319 *Roseibium* sp. TrichSKD4 genomic scaffold scf_1119120597020 Total score: 17.0 Cum. Blast bit score: 7083



AXCB01000017 *Marinobacter* sp. EVN1 Total score: 13.5 Cum. Blast bit score: 4037



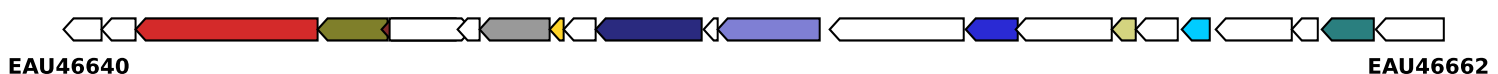
1 Kbp

C**T6SS-II****D**

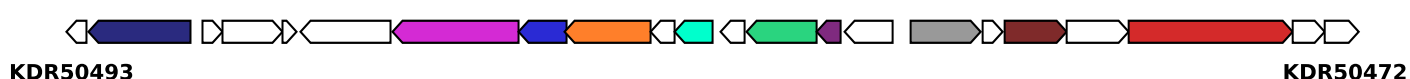
FO082060 *Methylobacterium alcaliphilum* str. 20Z chromosome Total score: 14.0 Cum. Blast bit score: 4395



CBTK010000028 *Pelagibaca bermudensis* HTCC2601 Total score: 12.0 Cum. Blast bit score: 3369



JJOD01000010 *Pseudomonas aeruginosa* strain PUPa3 Total score: 11.5 Cum. Blast bit score: 5031



1 Kbp

Figure S7 Type 6 secretion system in the *Pseudovibrio* genus. In **A** and **C** are reported the gene clusters coding for the T6SS-I and the T6SS-II identified in the *Pseudovibrio* genomes. Forward slashes separate genes identified in separate contigs. Representative T6SS gene clusters for *Pseudovibrio* were then used as query against all available GeneBank bacterial genomes, with the aim of searching homologous clusters. Of this analysis, only the best two hits for T6SS-I and three hits for T6SS-II are shown in **B** and **D**, respectively. 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 T6SS structure with the approach we used.