

# **In Silico Study of Cell Surface Structures of *Parabacteroides distasonis* Involved in Its Maintenance within the Gut Microbiota and Its Potential Pathogenicity**

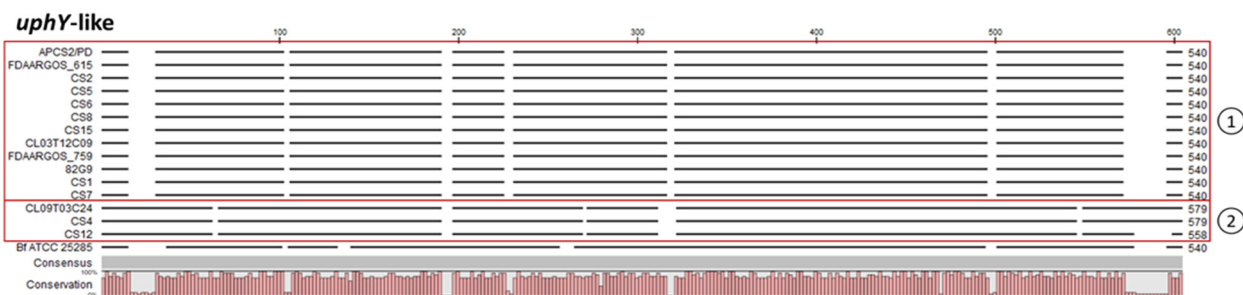
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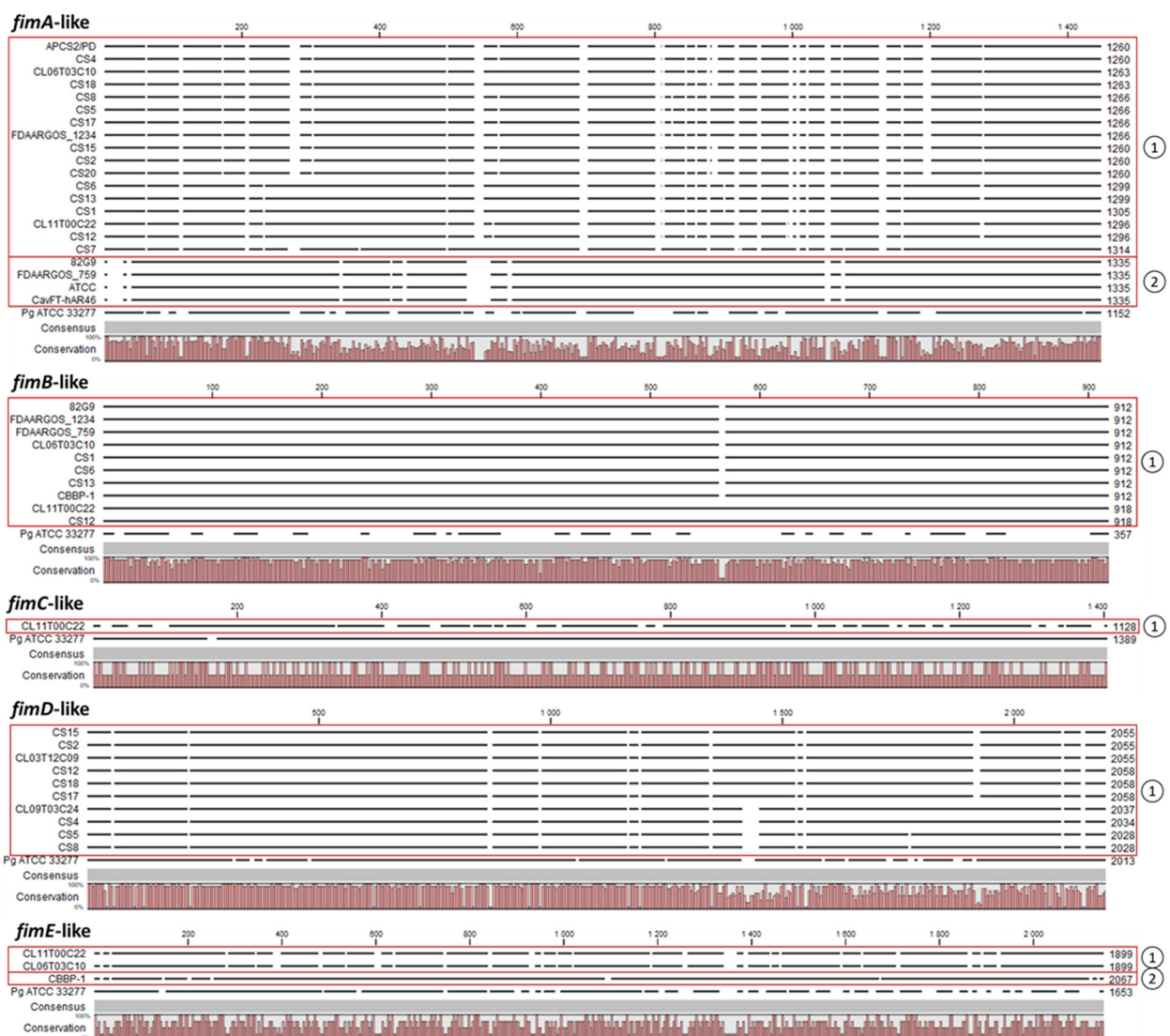
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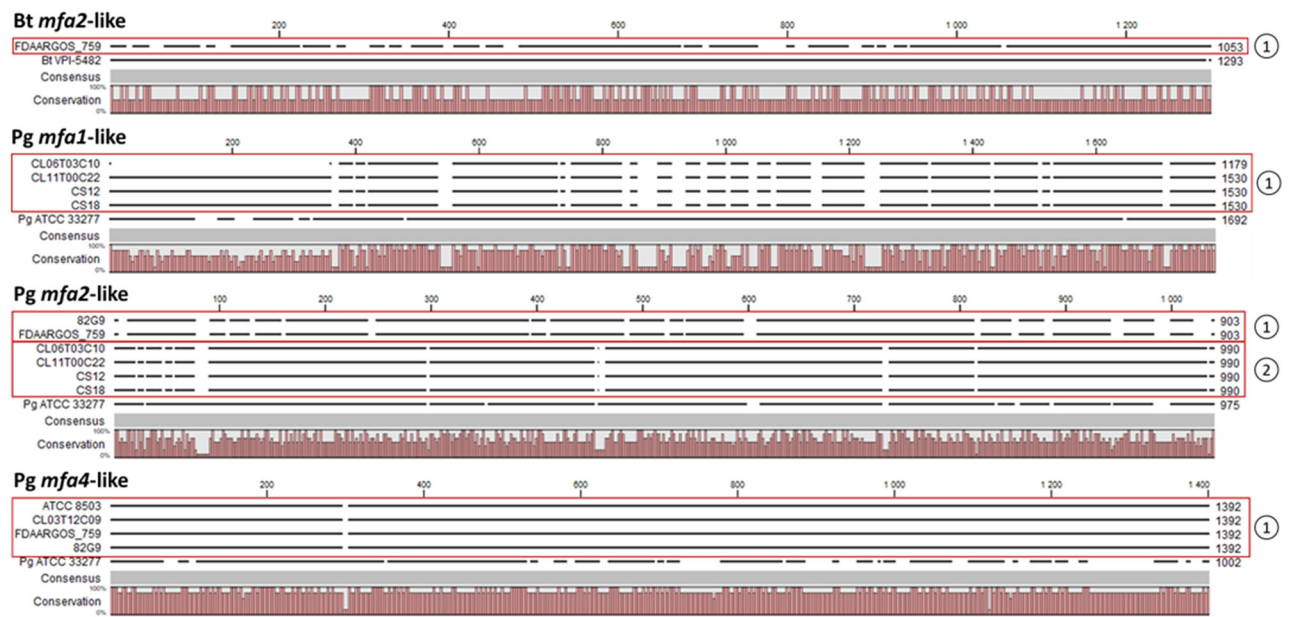
A



B



C



**Figure S1.** Multiple-sequence alignment of *P. distasonis* (A) *uphY*-like, (B) *fim*-like and (C) *mfa*-like genes listed in table 2. Each group of genes sharing similar patterns and sequences has been identified (red frame, 1 and 2) and aligned to generate a consensus sequence. As example, for *uphY*-like genes, two sequences have been generated: *uphY*-like 1 and *uphY*-like 2.