Species *Digestoria delfossei*[Ts]

Etymology
[del.fos.se'i] **N.L. gen. n.** *delfossei*, of Delfosse, named in honor of former group leader, Dr. Philippe Delfosse

Nomenclatural type
NCBI Assembly: GCA_056337095.1 [Ts]

Description
The genome of *Digestoria delfossei* in OTU_1 is complete and closed, 2.3 Mbp long, with a GC content of 54.3%, and it contains two rRNA operons. The species represents a distinct lineage defined by ANI ≥ 95% to its known relatives. Therefore, only the novel genus and species are formally established, while all higher-level ranks remain unnamed pending further phylogenomic resolution of the phylum. *D. delfossei* encodes a complete glycolysis pathway with exception for pyruvate kinase, previously shown to be replaced by pyruvate orthophosphate dikinase in *Cloacimonadota* genomes, and the microorganism can oxidize pyruvate further to acetyl-CoA and acetate. It is capable of beta-oxidation and protein degradation (i.e., encoding multiple peptidases) with a complete metabolism of histidine to glutamate.

Classification
Incertae sedis (Bacteria) » *Digestoria* » *Digestoria delfossei*[Ts]

References
Effective publication: Calusinska et al., 2026 [1]

Registry URL
https://seqco.de/i:55908

References

1. Calusinska et al. (2026). Phylum-wide propionate degradation and its potential connection to poly-gamma-glutamate biosynthesis in *Candidatus* Cloacimonadota phylum. *The ISME Journal*. DOI:10.1093/ismejo/wrag055