Species *Niallia hominis*

Etymology
[ho.mi'nis] **L. gen. n.** *hominis*, of a human being, pertaining to the human gut habitat, from where the type strain was isolated

Nomenclatural type
Strain sc|0043038 T

Description
The genome size is 4.9 Mbp, G+C percentage is 35.33%, with 92.24% completeness and 3.2% contamination. Strain CLA-SR-H024 was assigned to Niallia circulans (100%) based on 16S rRNA gene analysis. However, ANI suggested the isolate represents a novel species as comparison to all Niallia spp. were below 80%. GTDB-Tk classification of strain CLA-SR-H024 as 'Niallia sp001076885' confirmed that it represents a novel species. Functional analysis showed the strain has 244 transporters, 43 secretion genes, and predicted utilization of arbutin, salicin, cellobiose, starch, and dextran, along with production of L-glutamate, folate, and cobalamin. In total, 294 CAZymes were identified, with 34 different glycoside hydrolase families and 14 glycoside transferase families represented. The strain CLA-SR-H024 (phylum Bacillota, family Bacillaceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Bacilli* » *Bacillales* » *Bacillaceae* » *Niallia* » *Niallia hominis*

References
Effective publication: Hitch et al., 2025 [1]

Registry URL
https://seqco.de/i:48063

References

1. Hitch et al. (2025). HiBC: a publicly available collection of bacterial strains isolated from the human gut. *Nature Communications*. DOI: 10.1038/s41467-025-59229-9