**Figure 1:**

**Heatmap representation of ANI values using different assemblies.**

ANI values were calculated using Orthologous Average Nucleotide Identity Tool version 1.3 (Lee et al., 2016) and the values represented here are the orthoANI values.

**Table 1:**

**Assembly results of the *Vibrio aphrogenes* genome using reads from different platforms.**

Resulting assemblies were evaluated using QUAST v4.5 (Gurevich et al., 2013).

**Table 2:**

**Genome assemblies of five Rumoiensis clade species.**

The genomes of five species were reconstructed in two different methods; hybrid assembly and Nanopore-only assembly. Indels and mismatches in Nanopore-only assemblies were determined based on the differences from the hybrid assemblies. MinION read data shown here are those obtained after debarcoding and adaptor trimming with Porechop 0.2.2 (https://github.com/rrwick/Porechop).

**Table 3:**

**G+C content stability determined from different assemblies.**

G+C contents of the hybrid, Nanopore-only, and Illumina-only assemblies were calculated, respectively.

**Table 4:**

**Evaluation of protein coding gene sequences for MLSA retrieved from Nanopore-only assembly.**

Gene sequences from Nanopore-only assemblies were retrieved and compared with the genes from the hybrid assemblies.

**Figure S1**

**Heatmap representation of *in silico* DDH values using different assemblies.**

*in silico* DDH (DNA-DNA hybridization) values were estimated using Genome-to-Genome Distance Calculator (GGDC) 2.1 (Nelder & Wedderburn, 1972; Meier-Kolthoff et al., 2013) and the values represented here are calculated according to formula 2 (recommended).

**Figure S2**

**Phylogenetic reconstruction using eight protein-coding gene nucleotide sequences from hybrid and Nanopore-only assemblies.**

Trees were reconstructed using RAxML 8.2.11 (Stamatakis, 2014) with the GTRGAMMA model and 500 bootstrap replications. The final trees were prepared using FigTree v1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/).

**Table S1:**

**Data statistics for the reads used in *Vibrio aphrogenes* assemblies.**

Basic information of the data used to assemble *V. aphrogenes* genome. The genome was sequenced in four different methods; SMRT system from Pacific Biosciences (PacBio), MinION from Oxford Nanopore Technologies (MinION), mate-pair (MiSeq-MP) and paired-end (MiSeq-PE) reads from Illumina MiSeq. For MinION, the data shown here is after debarcoding with Porechop 0.2.2 (https://github.com/rrwick/Porechop) with --untrimmed option.