**Bacillus pumilus** is a Gram-positive rod-shaped spore-forming soil bacterium. *B. pumilus* and its spores are commonly resistant to extreme environmental conditions (1, 2). Therefore, *B. pumilus* contamination in industrial settings can be persistent. *B. pumilus* is also used beneficially in the production of industrially relevant compounds, such as xylanases (3), lipases (4), and proteases (5).

The five *B. pumilus* strains used in this study were grown overnight in 10 ml of brain heart infusion (BHI) broth (Difco) at 37°C and were harvested at the exponential growth phase after re inoculation. Following centrifugation, the cell pellet was resuspended in SET buffer (75 mM NaCl, 25 mM EDTA, 20 mM Tris-HCl [pH 7.5]) and incubated with lysozyme (2 mg/ml) and RNase (0.4 mg/ml) for 30 min at 37°C. Subsequently, the sample was treated with SDS (1% final concentration) and proteinase K (0.5 mg/ml) at 55°C for 60 min. Genomic DNA was extracted from the lysate with phenol-chloroform, precipitated with isopropanol (0.5 mg/ml) at 55°C for 60 min. Genomic DNA was sheared to 500-bp fragments in TE buffer. The isolated DNA was sheared to 500-bp fragments in a Covaris (KBiosciences) ultrasonicator device for preparing the NGS library using the paired-end NEBNext Ultra DNA library prep kit for Illumina. The isolated DNA was sheared to 500-bp fragments in a Covaris (KBiosciences) ultrasonicator device for preparing the NGS library using the paired-end NEBNext Ultra DNA library prep kit for Illumina. The libraries were 101 bases paired-end sequenced on an Illumina HiSeq 2000 by multiplexing 12 samples per flow cell. Velvet (6), in combination with VelvetOptimiser (https://github.com/Victorian-Bioinformatics-Consortium/VelvetOptimiser), was used to perform a de novo paired-end assembly on each of the five genomes, resulting in the draft genome sequences (Table 1). Annotation of the genomes was done using the following steps: (i) the scaffolds were uploaded to the RAST server (7) and automatically annotated using the SEED-based method on this server, (ii) the resulting annotated scaffolds were mapped using CONTIGuator (8) to their closest neighbor (as identified by RAST) to generate the pseudogene, (iii) locus tags were added to each feature using an in-house-developed perl script, according to the NCBI notation

**REFERENCES**


