The 4.3-Mb genome of *Lutibaculum baratangense* strain AMV1\textsuperscript{T}, isolated from a soil sample collected from a mud volcano in Andamans, India, is reported. The draft genome consists of 4,300,776 bp with a G+C content of 66.93 mol% and 4,198 predicted coding regions, including 56 RNAs.

L. *lutibaculum baratangense* AMV1\textsuperscript{T} is a Gram-staining negative, motile, oval-to-rod shaped bacterium isolated from a soil sample of a mud volcano in Baratang Island, Andamans, India (1). Because of their similarity to 16S rRNA gene sequences, *Tepidamorphus gemmatus* CB-27A\textsuperscript{T}, *Baulida consociate* 11T, *Afifella pfenningi* DSM 17143\textsuperscript{T}, and *Amorphus orientalis* YIM D10\textsuperscript{T}, with percent similarities of 95.03, 94.53, 94.43, and 94.08, respectively, are phylogenetically closely related. A Roche 454 (FLX titanium) pyrosequencing platform was used to perform the whole genome sequencing of *Lutibaculum baratangense* AMV1\textsuperscript{T}, which yielded a sequence of 70,392,118 bp in 163,500 reads, which is a 17-fold coverage of the genome. The CS De Novo Assembler (version 2.8) was used to perform assembly of the raw sequencing reads, which yielded a genome of 4,300,776 bp in 44 contigs with all contigs larger than 1,166 bp and with the largest contig being 670,712 bp. The calculated G+C content of the genome was 66.93 mol%.

Rapid annotation using subsystem technology was used to perform annotation of the assembled genome (2), tRNA was predicted in DDBJ/EMBL/GenBank under the accession number AWXZ0000000. The version described in this paper is version AWXZ0100000.

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**References**


