



# Draft Genome Sequence of *Romboutsia maritimum* sp. nov. Strain CCRI-22766<sup>T</sup>, Isolated from Coastal Estuarine Mud

Andrée F. Maheux,<sup>a</sup> Dominique K. Boudreau,<sup>a</sup> Ève Bérubé,<sup>a</sup> Maurice Boissinot,<sup>a</sup> Frédéric Raymond,<sup>a,b</sup> Stéphanie Brodeur,<sup>a</sup> Jacques Corbeil,<sup>a,b,c,d</sup> Gale Brightwell,<sup>e</sup> Dorota Broda,<sup>f</sup> Rabeea F. Omar,<sup>a,c</sup> Michel G. Bergeron<sup>a,c</sup>

Centre de Recherche en Infectiologie, Axe Maladies Infectieuses et Immunitaires, and Centre de Recherche du CHU de Québec, Université Laval, Québec City, Québec, Canada<sup>a</sup>; Centre de Recherche en Données Massives, Université Laval, Québec City, Québec, Canada<sup>b</sup>; Département de Microbiologie, Infectiologie et d'Immunologie, Faculté de Médecine, Université Laval, Québec City, Québec, Canada<sup>c</sup>; Département de Médecine Moléculaire, Université Laval, Québec City, Québec, Canada<sup>d</sup>; AgResearch Limited, Hamilton, New Zealand<sup>e</sup>; Half Moon Bay, Auckland, New Zealand<sup>f</sup>

**ABSTRACT** The *Romboutsia maritimum* sp. nov. CCRI-22766<sup>T</sup> strain was isolated from coastal estuarine mud in New Zealand. The genome assembly comprised 2,854,352 bp, with 27.1% G+C content. This is the first documentation that reports the genome sequence of *R. maritimum*.

*Romboutsia maritimum* (*Romboutsia maritimum* [ma.ri.ti'mum. N.L. masc. gen. n. *maritimum* of maritime, pertaining to the isolation source]) CCRI-22766<sup>T</sup> was isolated from a coastal estuarine mud sample in New Zealand. A comparative 16S rRNA gene sequence analysis showed that the closest cultured relative of strain CCRI-22766<sup>T</sup> was *Romboutsia ilealis* CRIB<sup>T</sup> (97.8% identity; GenBank accession number LN555523, positions 2388619 to 2390111) (1). The genome of *Romboutsia ilealis* CRIB<sup>T</sup> was also compared to that of strain CCRI-22766<sup>T</sup> for genomic relatedness assessment (accession number LN555523). The genomic average nucleotide identity obtained based on BLAST (ANiB) (2) was 77.7%. Since ANiB values around 95% corresponded to the 70% DNA-DNA hybridization cutoff value for species discrimination, strain CCRI-22766<sup>T</sup> represents a novel species of the genus *Romboutsia* (3).

*Romboutsia maritimum* is a rod-shaped, strictly anaerobic, and spore-forming bacterium. It grows on blood agar in 24 h at 35°C incubated under an anaerobic atmosphere, as previously described (4), forming 6-mm colonies. Genomic DNA was isolated using the BioSprint 15 DNA blood kit (Qiagen) automated with a KingFisher mL instrument (Thermo Fisher Scientific). Whole-genome sequencing of strain CCRI-22766<sup>T</sup> was performed on an Illumina HiSeq 2500 instrument using SBS version 4 to sequence a 126-bp paired-end library (Nextera XT [Illumina]). A total of 22,483,311 reads were assembled *de novo* in 95 contigs using the Ray software (version 2.3.0) (5). The total genome length is 2,854,352 bp ( $N_{50}$ , 77,093 bp), with an average G+C content of 27.1% (6). The draft genome sequence was annotated using NCBI GenBank annotation pipeline (version 4.2) and Rapid Annotations using Subsystems Technology (RAST) annotation server (version 2.0) (7). A total of 2,867 features were identified, including 36 rRNAs (complete or partial) and 56 tRNAs. Of the 2,729 putative protein-coding sequences, 1,006 were assigned as hypothetical proteins.

**Accession number(s).** This whole-genome shotgun project of *R. maritimum* CCRI-22766<sup>T</sup> has been deposited at DDBJ/ENA/GenBank under the accession number [NOJZ0000000](https://doi.org/10.1101/171000). The version described in this paper is version NOJZ01000000.

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Address correspondence to Rabeea F. Omar, [rabeea.omar@crchudequebec.ulaval.ca](mailto:rabeea.omar@crchudequebec.ulaval.ca), or Michel G. Bergeron, [michel.g.bergeron@crchudequebec.ulaval.ca](mailto:michel.g.bergeron@crchudequebec.ulaval.ca).

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