The draft genome has 1,634,278 bases in 24 contigs (N50, 33,800 bp) and a GC content of 42.6%. It contains 1,519 predicted tRNAs, with an average coverage of 47-fold. Annotation of genes and rRNA was performed using the Prokaryotic Genome Annotation Pipeline (PGAAP) (11). tRNAs were identified with tRNAscan-SE (12).

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**REFERENCES**