Correction for Props et al., “Gene Expansion and Positive Selection as Bacterial Adaptations to Oligotrophic Conditions”

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Data availability. Raw sequence reads are available on NCBI SRA under identifier (ID) or accession no. SRP142224. The coassembly and its annotation are available on IMG (https://img.jgi.doe.gov/) under taxon OID 3300014983, MAGs are available from IMG as specified by their taxon OIDs in Table 1, and raw sequences of the 16S V3-V4 rRNA gene amplicon surveys are available on NCBI SRA under ID SRP066190. The metagenome reconstructed 16S rRNA gene sequence of *R. aquaticus* LMG 30558 is available from NCBI GenBank under reference ID MW131457. The 16S rRNA gene sequence of the *R. aquaticus* LMG 30558T isolate is available from NCBI GenBank under reference ID MW138094. MAGs are also available from DDBJ/ENA/GenBank under accession IDs SAIV00000000 (*R. aquaticus*), SAIW00000000 (*Bacteroidetes* sp. MAG1), and SAIX00000000 (*Bacteroidetes* sp. MAG2). The versions described in this paper are versions SAIV01000000, SAIW01000000, and SAIX01000000. The draft genome assembly of the *R. aquaticus* LMG 30558T isolate is available from NCBI GenBank under ID JADDOJ000000000. Flow cytometry data are publicly available on FlowRepository under ID FR-FCM-ZYFM. The data analysis for this article is available at https://github.com/rprops/Ramlibacter-CW. The Anvi’o profile database is available at https://doi.org/10.6084/m9.figshare.6170420, and the Anvi’o pan-genome analysis is available at https://doi.org/10.6084/m9.figshare.6170117. Suplemental information and figures are available at https://doi.org/10.6084/m9.figshare.7577636. *R. aquaticus* LMG 30558T cultures are available from the BCCM (ID LMG 30558) and DSMZ (ID 110366) culture collections.


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