We present the draft genome of anammox bacterium “Candidatus Scalindua brodae,” which at 282 contigs is a major improvement over the highly fragmented genome assembly of related species “Ca. Scalindua profunda” (1,580 contigs) which was previously published.

Anammox bacteria are major players in the global nitrogen cycle, capable of anaerobically oxidizing ammonium to dinitrogen gas, using nitrite as the electron acceptor (1). All currently known anammox bacteria form the monophyletic order Brocadiales within the phylum Planctomycetes (2). Until now, draft genomes of four anammox species have been reported (3–6). The genome assemblies of “Candidatus Kuenenia stuttgartiensis” and “Ca. Jettenia caeni” are in 5 and 4 contigs, respectively, whereas the draft genome of “Ca. Brocadia fulgida” (411 contigs) is highly fragmented and the “Ca. Scalindua profunda” draft genome (1,580 contigs) is highly fragmented.

Despite advances in culturing techniques, no pure culture of anammox bacteria exists. This restricts genome-sequencing efforts to metagenomic sequencing and binning (7, 8). Here we present the draft genome of anammox bacterium “Candidatus Scalindua brodae,” which at 282 contigs is a major improvement over the highly fragmented genome assembly of related species “Ca. Scalindua profunda” (1,580 contigs) which was previously published.


