

Recovery of circular and high quality cable bacteria genomes from complex microbial communities

Sereika, Mantas; Petriglieri, Francesca; Nymann, Thomas; P. G. Marshall, Ian; Schramm, Andreas; Nielsen, Per Halkjær; Albertsen, Mads

Creative Commons License
GNU GPL

Publication date:
2022

Document Version
Publisher's PDF, also known as Version of record

[Link to publication from Aalborg University](#)

Citation for published version (APA):
Sereika, M., Petriglieri, F., Nymann, T., P. G. Marshall, I., Schramm, A., Nielsen, P. H., & Albertsen, M. (2022). *Recovery of circular and high quality cable bacteria genomes from complex microbial communities*. Poster presented at ISME18, Lausanne, Switzerland.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal -

Take down policy

If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.

Recovery of circular and high quality cable bacteria genomes from complex microbial communities

Mantas Sereika^a, Francesca Petriglieri^a, Thomas Bygh Nymann Jensen^a, Ian Marshall^b, Andreas Schramm^b, Per Halkjær Nielsen^a, Mads Albertsen^a

^aCenter for Microbial Communities, Aalborg University, Aalborg, Denmark

^bCenter for Electromicrobiology, Aarhus University, Denmark



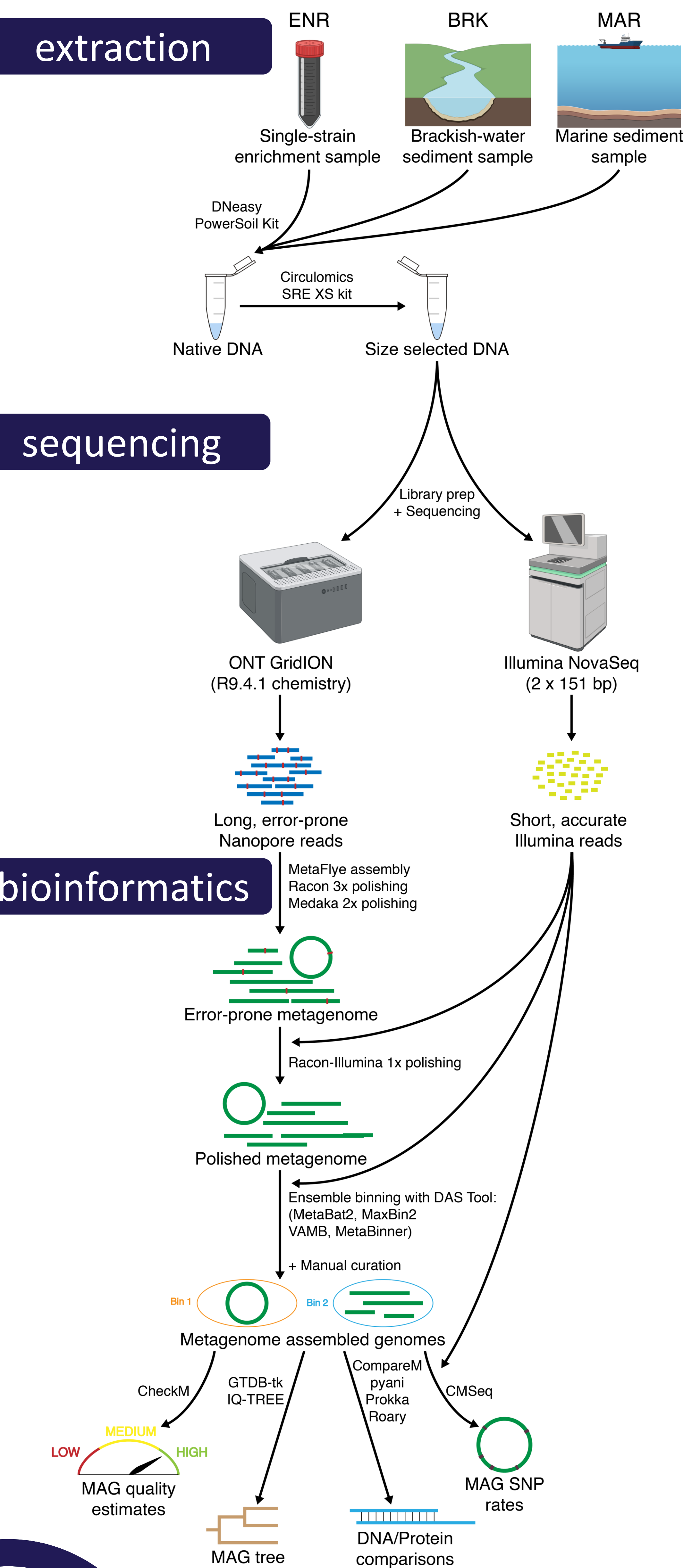
Introduction

Cable bacteria are centimeter-long filamentous bacteria that can conduct long-distance electron transfer through coupling of sulfide oxidation and oxygen reduction. To elucidate the unique physiology of cable bacteria, reliable genome reference sequences are required. Although publically available cable bacteria genomes are often fragmented and incomplete due to using short reads for genome-centric metagenomics, long-read DNA sequencing technologies, such as Nanopore sequencing, are yet to be applied for the recovery of cable bacteria genomes.

Aim

Recovery and characterization of circular or high quality cable bacteria genome drafts using long-read Nanopore sequencing.

Methods



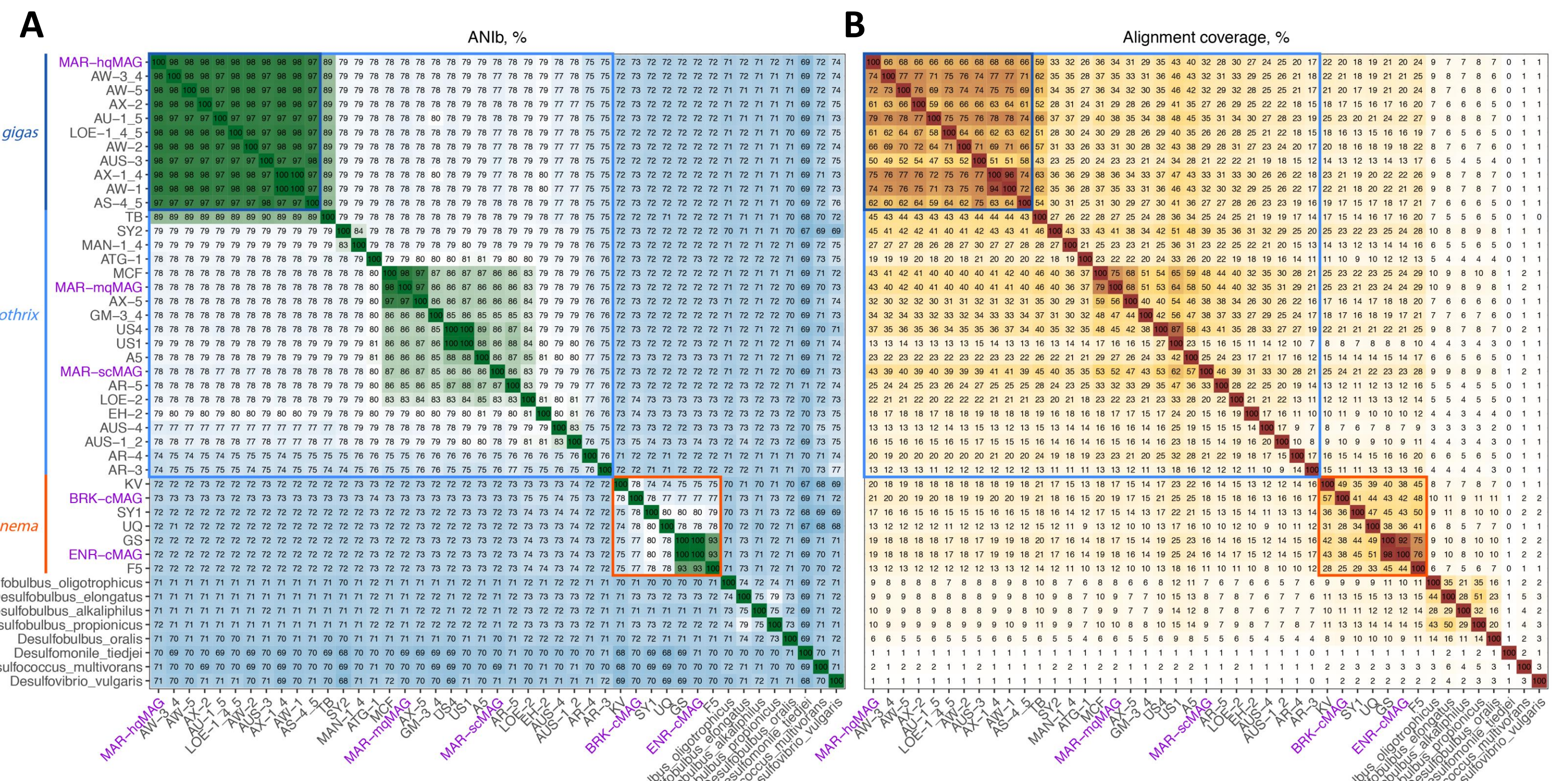
Conclusions

- 4 high quality genome drafts of cable bacteria were recovered (2 *Electronema*, 2 *Electrothrix*)
- Both *Electronema* genomes were circular, while one *Electrothrix* genome was single-contig
- The single-contig *Electrothrix* and 1 circular *Electronema* genomes were of novel species
- The novel species circular *Electronema* genome featured the most unique gene content and challenges the current definition of genus *Candidatus Electronema*

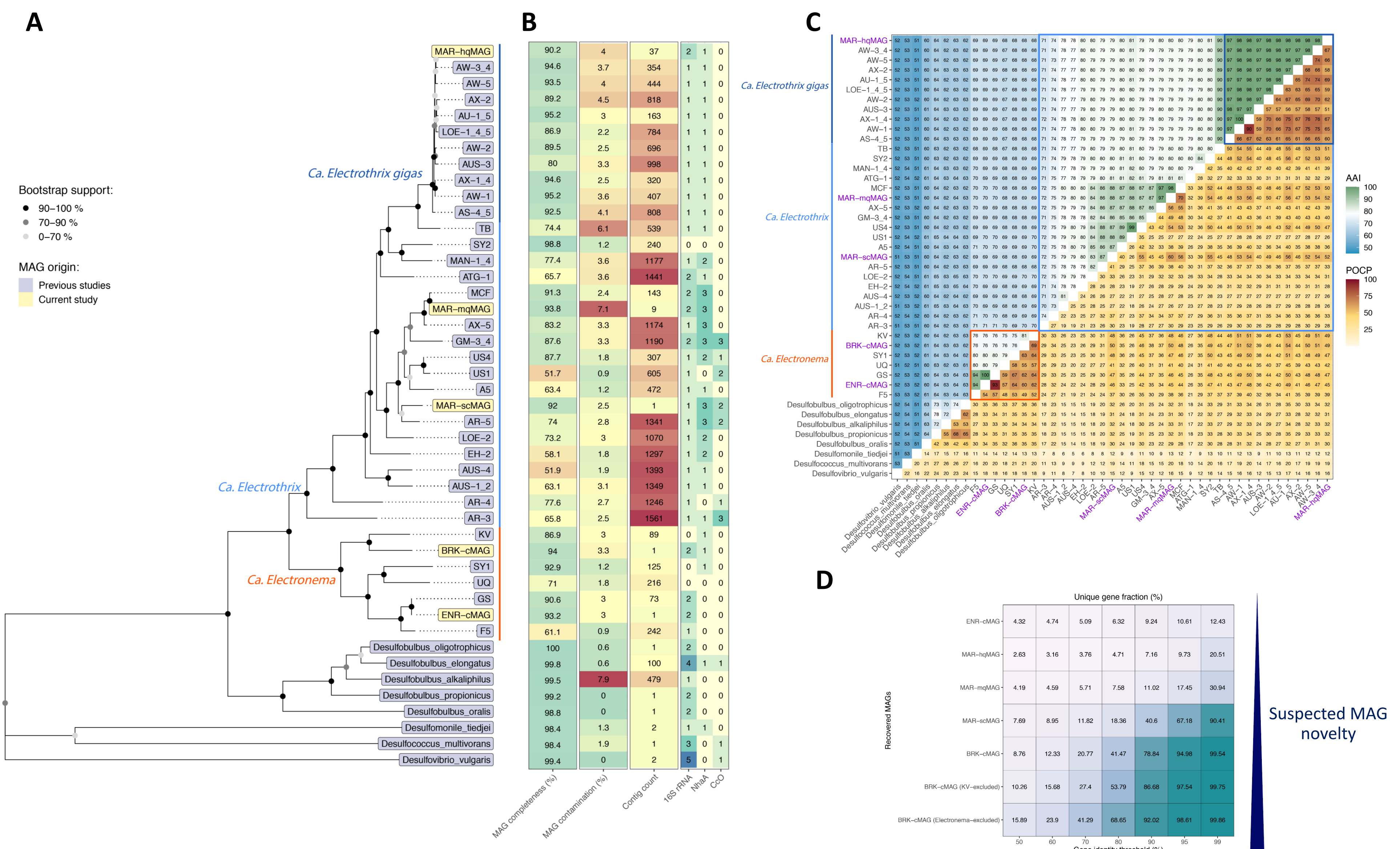
Results

Recovered cable bacteria MAG statistics

	ENR-cMAG	BRK-cMAG	MAR-scMAG	MAR-hqMAG	MAR-mqMAG
MAG Completeness, %	93.2	94.1	92.0	90.2	93.9
MAG Contamination, %	3.0	3.3	2.6	4.0	7.1
Contig count	1	1	1	37	9
SNP rate, %	0.002	0.03	0.8	1.4	1.0
CDS count	2,847	2,807	3,409	2,849	3,484
Hypothetical CDS, %	56.4	52.3	58.5	55.5	60.1
MIMAG quality ranking	HQ	HQ	HQ	HQ	MQ
Species taxonomy ranking	<i>Electronema</i> GS	Novel <i>Electronema</i>	Novel <i>Electrothrix</i>	<i>Electrothrix gigas</i>	<i>Electrothrix aarhusiensis</i>



Whole-genome-based comparisons for cable bacteria MAGs. HQ and MQ cable bacteria MAGs (and outgroups used for tree building) were compared to each other using BLAST-based average nucleotide identity (ANiB, **A**) and genome alignment fractions (**B**). Using ANi of 75-77 % as genus boundary, all cable bacteria MAGs from MAR sample were classified as *Candidatus Electrothrix*, while MAGs from BRK and ENR were attributed to *Candidatus Electronema*.



Gene-based comparisons of cable bacteria MAGs. **A)** Maximum-likelihood genome tree, built using 120 universal bacterial marker genes and 100 bootstraps for HQ, MQ cable bacteria MAGs, with multiple outgroups included. **B)** Selected features of cable bacteria MAGs: quality metrics and relevant gene contents. **C)** Average amino acid identity (AAI) and percentage of conserved proteins (POCP) between cable bacteria MAGs and outgroups. POCP of 50 % was used as genus boundary to further confirm the classification of BRK-cMAG as a member of *Candidatus Electronema*. **D)** Unique gene fractions for MAGs recovered in this study, compared to other cable bacteria MAGs (HQ and MQ), at different identity thresholds for gene clustering.