

Supplemental Figures and Tables

Antarctic *Pseudosulfitobacter pseudonitzschiae* BPC-C4-2: Genetic Analysis and Application in a Cold-Water Morphogenic *Ulva* System

Tia Wünschmann^{1,2}, Fatemeh Ghaderiardakani³, Timo Homeier-Bachmann⁴, Maria Lilliana Quartino⁵, Thomas Wichard^{3*}, Anne Busch^{1,2,*}

¹ Theoretical Microbial Ecology, Friedrich Schiller University, Jena, Germany

² Cluster of Excellence Balance of the Microverse, Friedrich Schiller University Jena, Jena, Germany

³ Institute for Inorganic and Analytical Chemistry, Friedrich Schiller University, Jena, Germany

⁴ Friedrich-Loeffler-Institute, Federal Research Institute for Animal Health, Institute of Epidemiology, Friedrich-Loeffler-Institute, Greifswald-Insel Riems, Germany.

⁵ Department of Coastal Biology, Argentinean Antarctic Institute, Buenos Aires, Argentina.

*Corresponding authors: thomas.wichard@uni-jena.de and anne.busch@uni-jena.de

Supplemental Table 1:

Strain	Acession Number 16S	Acession Number WGS
<i>Sulfitobacter aestuariivivens</i>	NR_181018	NZ_JACTAG010000000
<i>Sulfitobacter noctilucicola</i>	NR_134206	NZ_JASD01000001
<i>Sulfitobacter mediterraneus</i>	NR_026472	NZ_OMPT01000000
<i>Sulfitobacter litoralis</i>	NR_043547	NZ_JAXMOT010000000
<i>Sulfitobacter delicatus</i>	NR_025692	NZ_FNBP01000000
<i>Sulfitobacter aestuarii</i>	NR_179825	NZ_JBHUMP010000000
<i>Roseobacter litoralis</i>	NR_074143	NZ_CANLWU010000000
<i>Roseobacter denitrificans</i>	NR_102909	NZ_FOOO01000000
<i>Heliomarina baculiformis</i>	NR_181734	NZ_JAIMIC010000000
<i>Hypomonas beringensis</i>	/	NZ_AWFF01000000
<i>Hypomonas polymorpha</i>	AJ227813	/
<i>Pseudosulfitobacter pseudonitzschiae</i> strain H3	NR_178596	NZ_JAMD01000000

<i>Pseudosulfitobacter pseudonitzschiae strain SMR1</i>	Blast from WGS	CP022422
---	----------------	----------

Supplemental Table 1: Name and Accession Numbers of strains used in comparative genomic analysis.

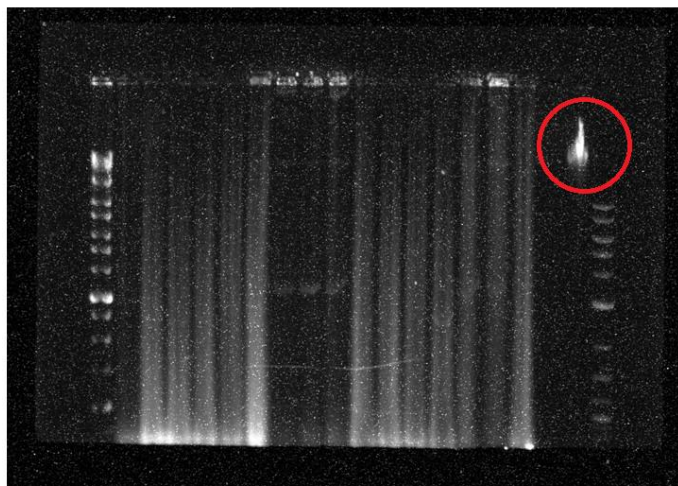
Supplemental Table 2:

	ONT/Illumina hybrid assembly	Illumina assembly
contigs	7	76
largest contig	3619192	758745
total length	5450390	5404620
N50	3619192	203213
N90	284771	56481
auN	2526817	302086
L50	1	8
L90	50	25
GC	58,98	58,99

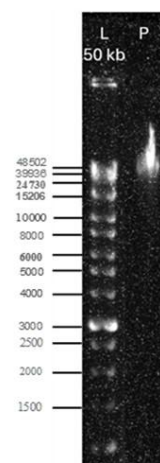
Supplemental Table 2: The table compares hybrid and Illumina assemblies, highlighting differences in contig count, total bases, scaffold sizes, GC content, and assembly metrics such as N50 and gaps, demonstrating the improved contiguity and accuracy of the hybrid assembly

Supplementary Figure 1

unmodified data:



modified data:

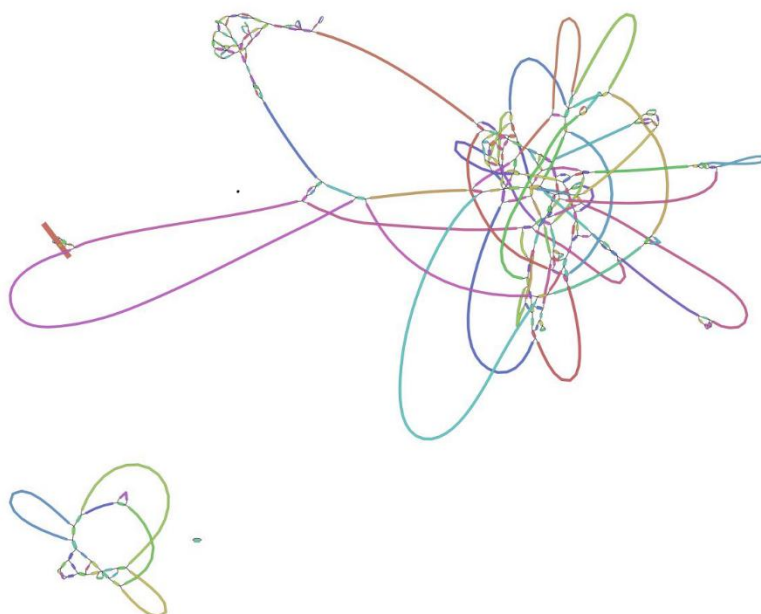


33

34 **Supplemental Figure 1:** Plasmid Preparation of *P. pseudonitzschiae* BPC-C4-2. Plasmid DNA
35 extracted from *P. pseudonitzschiae* BPC-C4-2 was resolved on a 0.5% agarose gel and
36 visualized by staining with ethidium bromide. A 1 kb ladder was run in parallel to serve as a
37 molecular weight reference, highlighting the estimated sizes of the plasmid bands.

38

39 **Supplementary Figure 2:**



40

Supplemental Figure 2: Bandage visualization of the hybrid genome assembly. A graphical representation of assembly graphs, enabling to explore contig connections, detect possible misassemblies, and assess overall assembly quality.

Supplementary Table 3:

Pseudosulfitobacter	contig 1	contig 2	contig 3	contig 4	contig 5	contig 6	contig 7
length (bp)	425393	292931	175267	284771	528791	3619192	124045
PlasmidFinder	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Plasflow	unclassified	Chromosome	Plasmid	Plasmid	unclassified	Chromosome	Plasmid

Supplementary Table 3: Summary of mobile element analysis including contig length (bp) and *in silico* plasmid predictions using PlasmidFinder and PlasFlow.

Supplementary Table 4:

Contig	GC Contig in %
1	58.3
2	58.8
3	59.7
4	58.4
5	53.7
6	59.9
7	53.7

Supplementary Table 4: Summary of GC contents in each contig in %.

Supplementary Table 5:

Assembly	Contigs	Genome Size (bp)	CDS	rRNA	tRNA	tmRNA	Circularisation
Unicycler	7	5,450,319	5,373	6	85	1	All contigs
Flye	7	5,450,390	5,380	6	85	1	All contigs
Canu	9	5,774,190	5,679	9	89	1	none

Supplementary Table 5: Comparison of *Pseudosulfitobacter pseudonitzschiae* BPC-C4-2 assembled by Unicycler, Flye and Canu across contig number, differences in base pairs, CDS, rRNA, tRNA, tmRNA, GC content and Circularisation.

Supplementary Table 6:

Assembly Comparison	DCJ Distance	SCJ Distance	Breakpoint Distance
Unicycler – Flye	19	70	35
Unicycler – Canu	13	70	35
Flye – Canu	20	70	35

Supplementary Table 6: Rearrangement distances between the three assemblies based on 35 shared LCBs.