

SUPPLEMENTARY INFORMATION

***Tenacibaculum platacis* sp. nov., *Tenacibaculum vairaonense* sp. nov. and *Tenacibaculum polynesiense* sp. nov. isolated from batfish (*Platax orbicularis*) in Tahiti Island, French Polynesia.**

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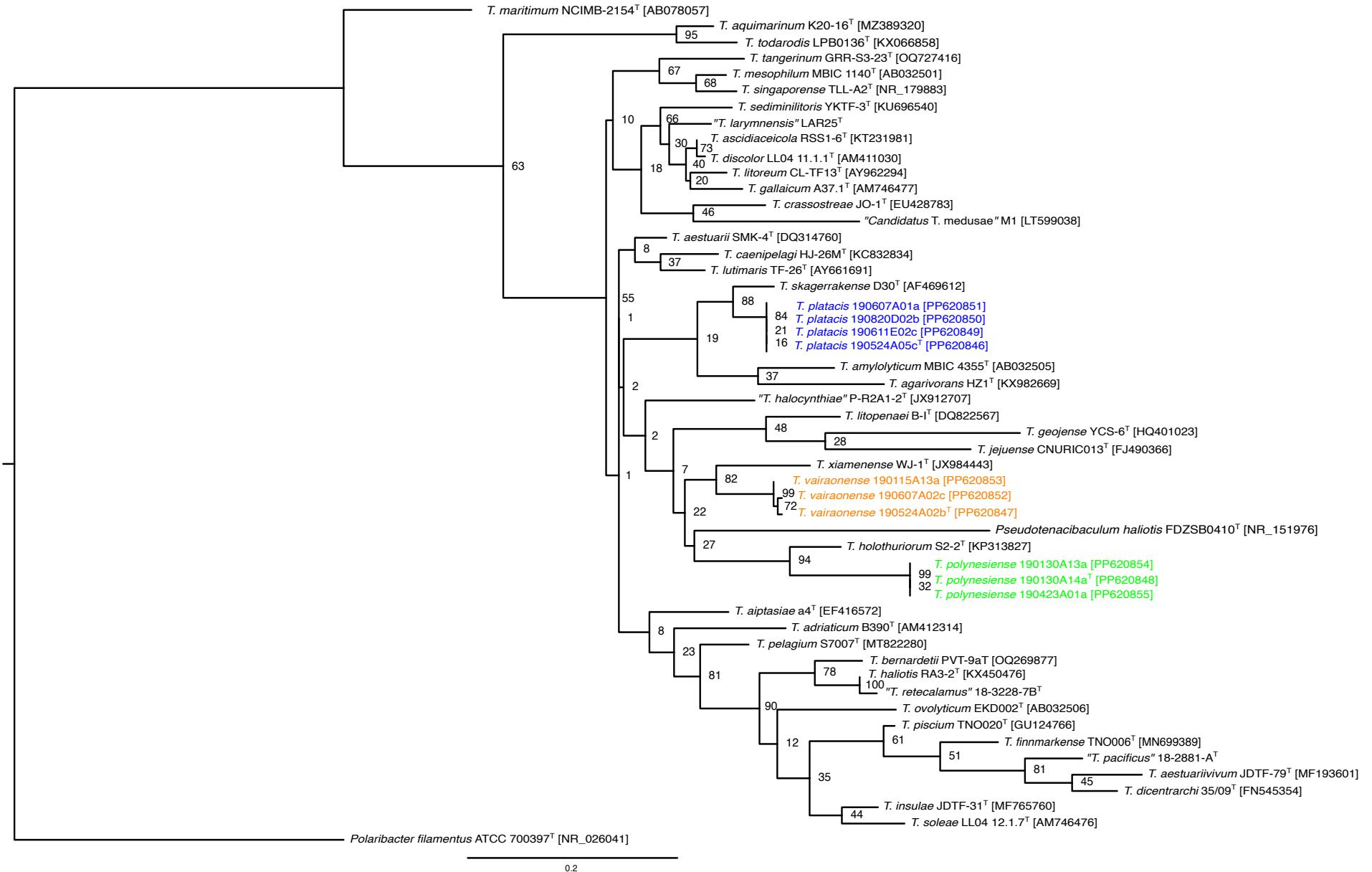
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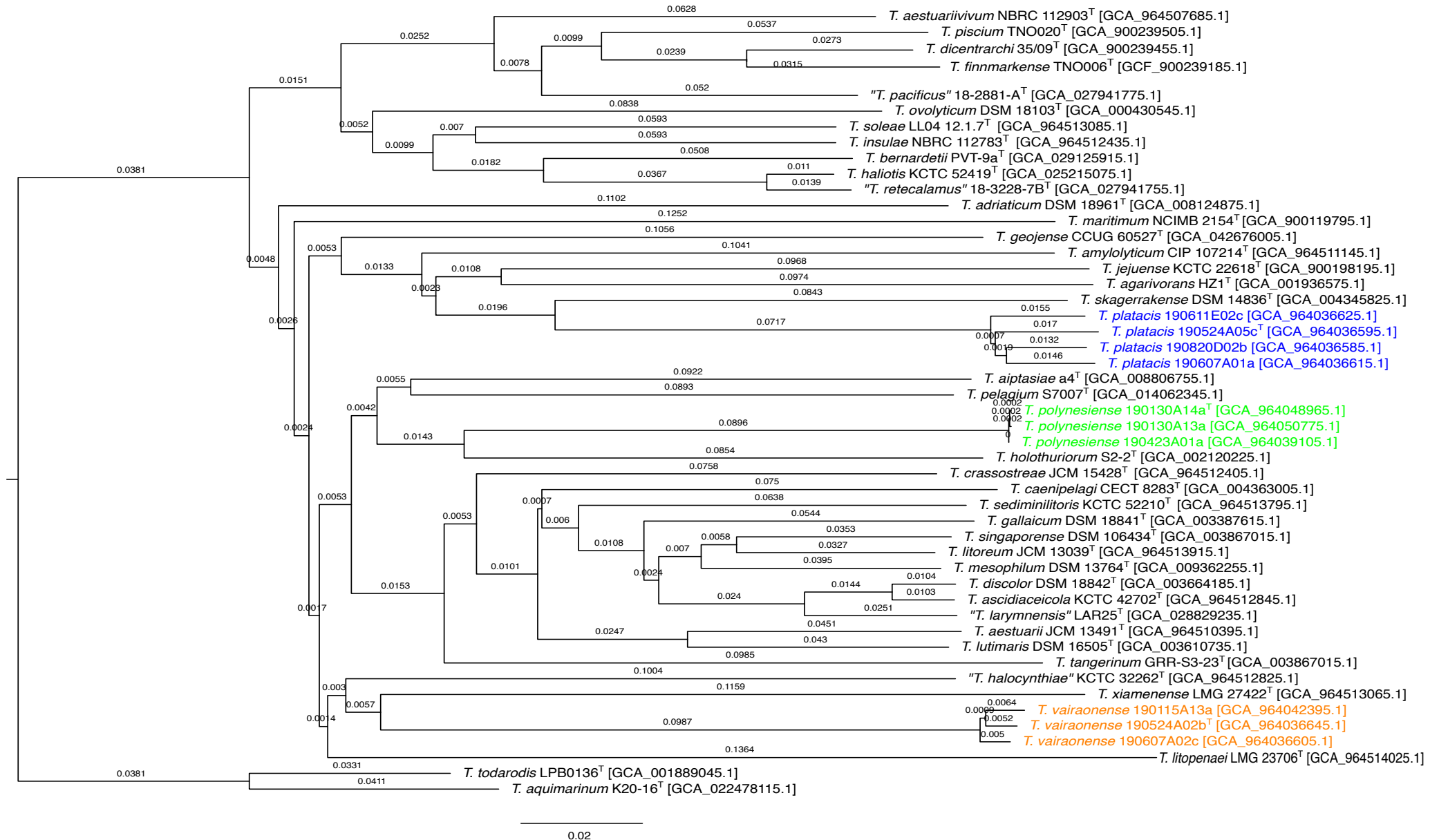
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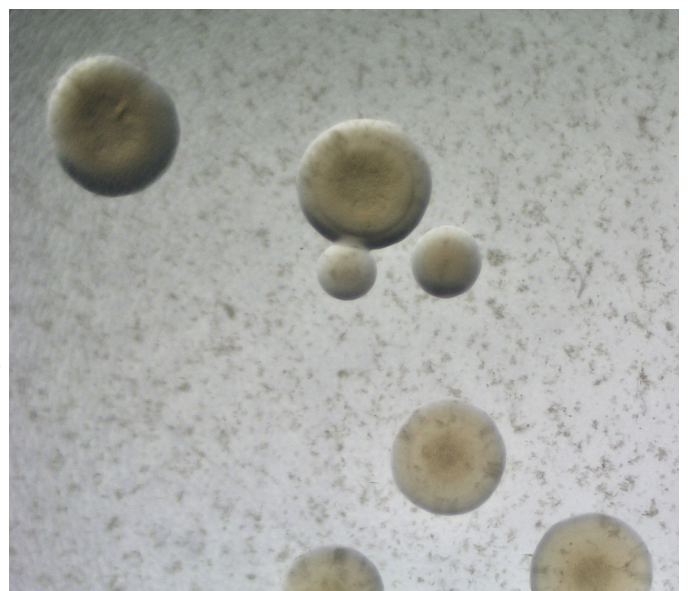
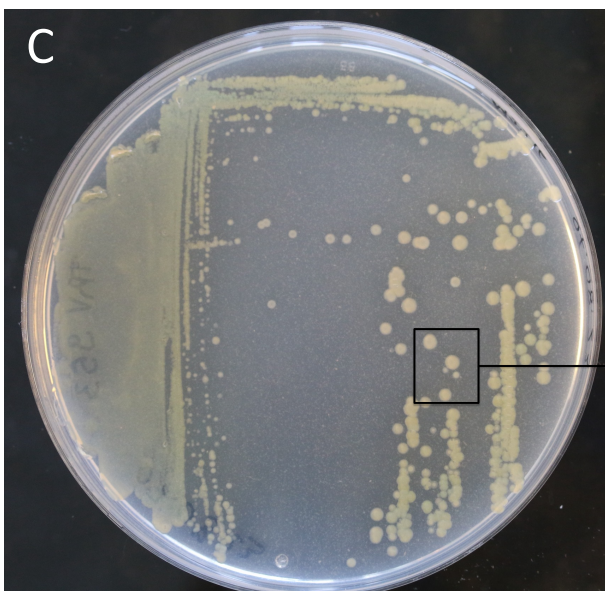
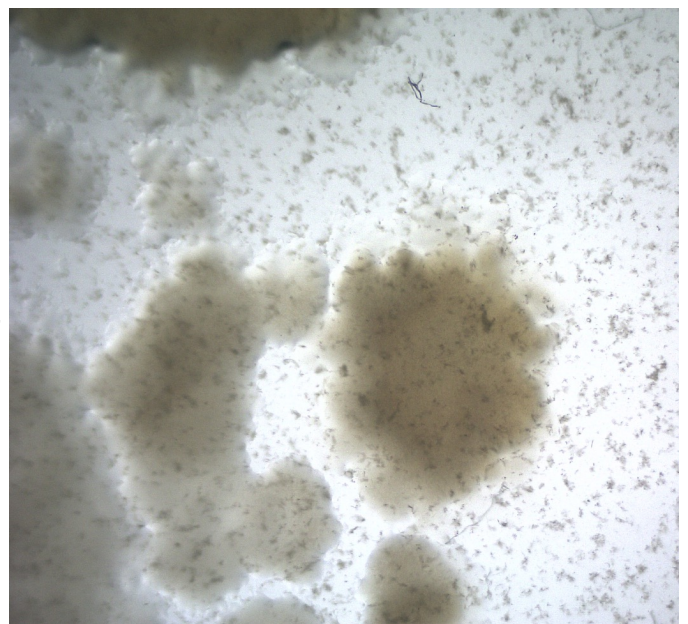
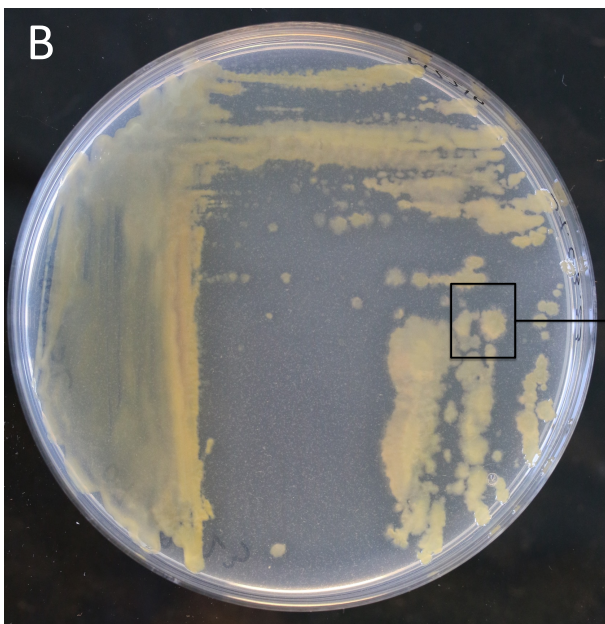
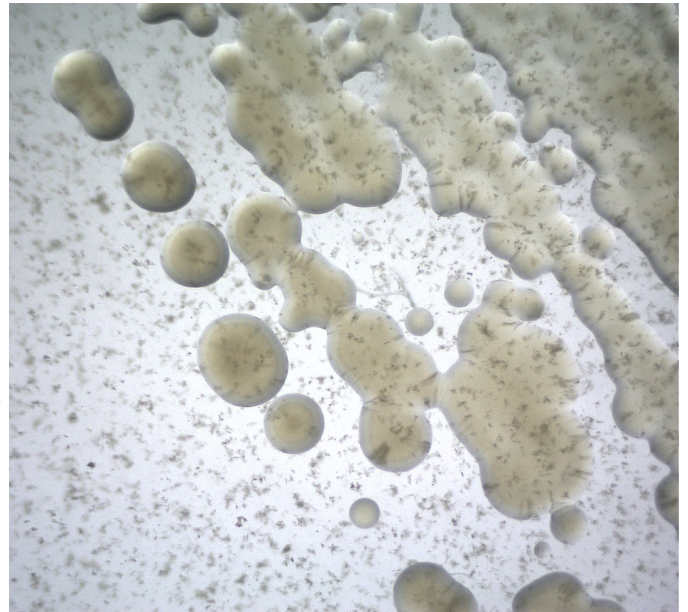
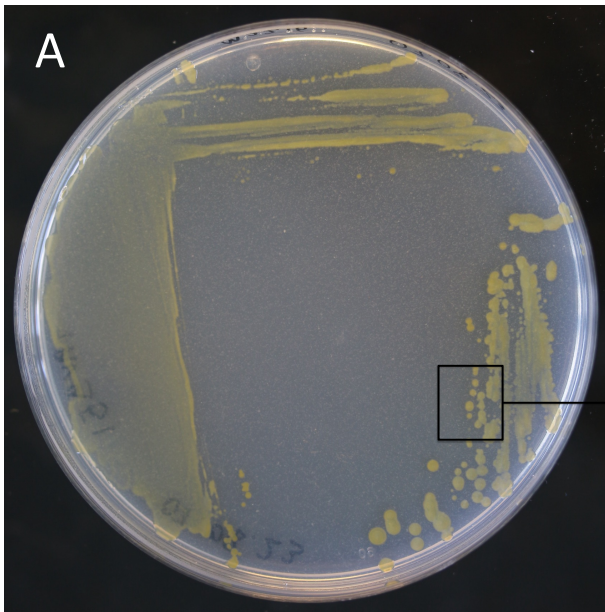
Supplementary Figure 1: Maximum-Likelihood 16S rRNA-based phylogeny. Phylogenetic tree inferred by PhyML using the 16S rRNA of *Tenacibaculum* species. The type strain of *Pseudotenacibaculum haliotis* has been included and the type strain of *Polaribacter filamentus* was used as an outgroup. Scale bar indicates estimated sequence divergence and bootstrap values are indicated at branch nodes. The 16S rRNA sequence of strains "*T. larymnensis*" LAR25^T, "*T. pacificus*" 18-2881-A^T and "*T. retecalamus*" 18-3228-7B^T have been retrieved from complete genomes accession number GCF_028829235.1, NZ_CP115917 and NZ_CP115916, respectively



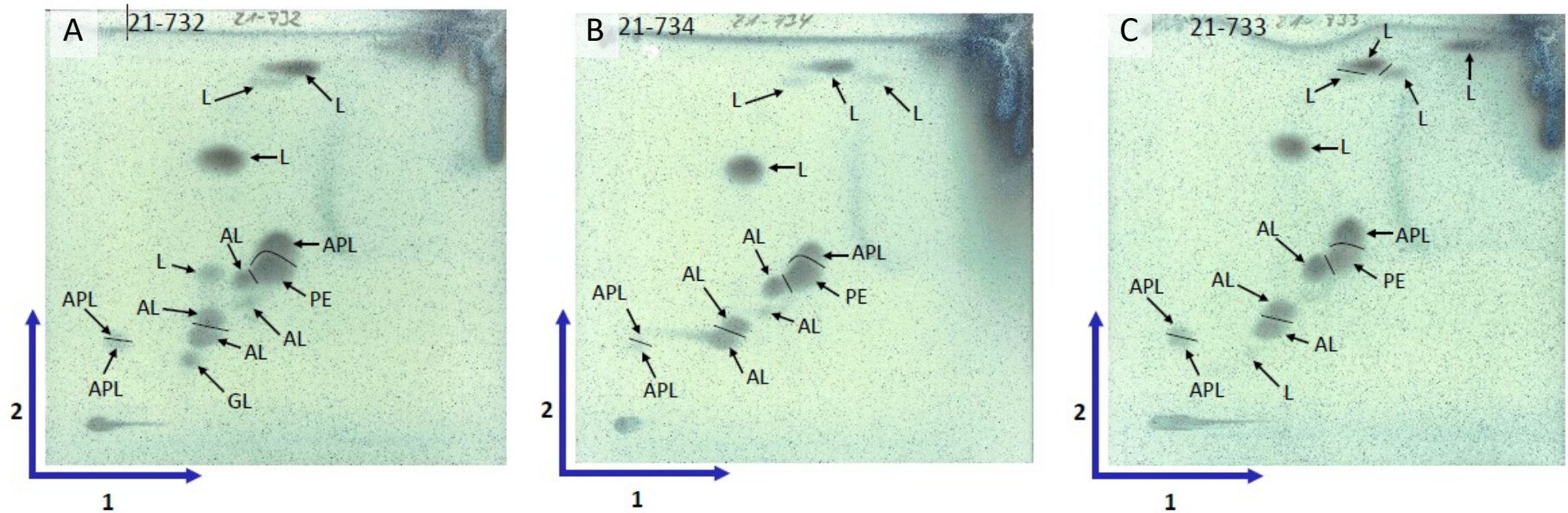
Supplementary figure 2: ANI-based phylogenetic tree. Genomic similarity was estimated using the Mash software that computes a distance between two genomes. A tree was constructed from all the pairwise distances of the genome set using the neighbour-joining Java script package V 1.0.4 (<https://github.com/biosustain/neighbor-joining>). MASH distances are indicated on tree branches.



Supplementary figure 3. Colony morphology of *Tenacibaculum* strains grown on MA plates for 24h at 28°C and observed by phase-contrast microscopy. (A) *T. platacis* sp. nov. 190524A05c^T, (B) *T. vairaonense* sp. nov. 190524A02b^T, (C) *T. polynesiense* sp. nov. 190130A14a^T.



Supplementary figure 4: Two-dimensional thin-layer chromatograms of the total polar lipids of strains 190130A14a^T (A), 190524A02b^T (B) and 190524A05c^T (C). AL, unidentified aminolipids; APL, unidentified aminophospholipids; GL, unidentified glycolipid; PE, phosphatidylethanolamine; PL, unidentified phospholipid; L, unidentified polar lipids.



Supplementary Table 1 : Genome characteristics

Species	Strain	Assembly size (bp)	G+C content (mol%)	Number of contigs (>2kb)	N50 (bp)	Completeness (%)	Contamination (%)	Average long read (Nanopore) coverage	Average short read (Illumina) coverage	Number of coding sequences (CDS)	Number of tRNA	Number of rRNA operons	ENA accession number
<i>Tenacibaculum platacis</i>	190524A05c ^T	4,130,482	31.48	1	4,130,482	99.6644	0.159795	149	750	3,615	54	3	GCA_964036595.1
	190611E02c	4,042,826	31.42	14	874,873	99.6644	0.243688		459	3,707	nd	nd	GCA_964036625.1
	190820D02b	4,011,514	31.46	19	455,254	99.6644	0.419463		542	3,652	nd	nd	GCA_964036585.1
	190607A01a	4,016,071	31.46	11	938,204	99.6644	0		427	3,622	nd	nd	GCA_964036615.1
<i>Tenacibaculum vairaonense</i>	190524A02b ^T	5,036,910	30.66	1	5,036,910	99.6644	1.566	97	346	4,085	68	6	GCA_964036645.1
	190115A13a	4,802,973	30.40	46	246,949	99.6644	1.00671		412	4,121	nd	nd	GCA_964042395.1
	190607A02c	4,767,073	30.40	41	258,17	99.6644	1.36465		374	4,096	nd	nd	GCA_964036605.1
<i>Tenacibaculum polynesiense</i>	190130A14a ^T	3,936,153	31.98	1	3,936,153	99.6644	1.59396	166	2,205	3,578	65	5	GCA_964048965.1
	190130A13a	3,843,691	31.73	18	569,163	99.6644	1.59396		460	3,700	nd	nd	GCA_964050775.1
	190423A01a	3,843,974	31.73	18	568,14	99.6644	1.59396		420	3,706	nd	nd	GCA_964039105.1

Supplementary Table 3: dDDH values between *T. platacis* 190524A05c^T; *T. polynesiense* 190130A14a^T; *T. vairaonense* 190524A02b^T and the *Tenacibaculum* type strains using Genome-to-Genome Distance Calculator 3.0 and Formula: 2 identities / HSP length. Quoted names have not been validly published.

	<i>T. platacis</i> 190524A05c ^T	<i>T. polynesiense</i> 190130A14a ^T	<i>T. vairaonense</i> 190524A02b ^T
<i>Polaribacter filamentus</i> ATCC 700397 ^T	18.90%	19.50%	20.20%
<i>Pseudotenacibaculum haliotis</i> FDZSB041 ^T	18.80%	18.70%	20.30%
" <i>T. halocynthiae</i> " KCTC 32262 ^T	19.00%	20.00%	21.40%
" <i>T. larymnensis</i> " LAR25 ^T	19.70%	20.70%	20.80%
" <i>T. pacificus</i> " 18-2881-A ^T	19.80%	20.50%	21.00%
" <i>T. retecalamus</i> " 18-3228-7B ^T	19.70%	20.20%	20.70%
<i>T. adriaticum</i> B390 ^T	19.20%	20.60%	20.40%
<i>T. aestuarii</i> SMK-4 ^T	20.00%	20.70%	21.00%
<i>T. aestuariivivum</i> NBRC 112903 ^T	20.00%	20.70%	21.00%
<i>T. agarivorans</i> HZ1 ^T	21.40%	19.80%	20.20%
<i>T. aiptasiae</i> a4 ^T	19.70%	20.70%	20.70%
<i>T. amylolyticum</i> CIP 107214 ^T	21.00%	20.30%	20.10%
<i>T. aquimarinum</i> K20-16 ^T	18.30%	19.40%	19.80%
<i>T. ascidiaceicola</i> KCTC 42702 ^T	19.90%	21.20%	21.10%
<i>T. bernardetii</i> PVT-9a ^T	18.60%	19.80%	20.40%
<i>T. caenipelagi</i> KCTC 32323 ^T	19.50%	20.90%	20.50%
<i>T. crassostreae</i> JO1 ^T	19.70%	22.00%	21.20%
<i>T. dicentrarchi</i> 35/09 ^T	20.70%	20.30%	21.20%
<i>T. discolor</i> DSM 18842 ^T	19.90%	21.20%	21.10%
<i>T. finnmarkense</i> TNO006 ^T	19.20%	19.70%	20.40%
<i>T. gallaicum</i> A37.1 ^T	19.60%	20.80%	20.90%
<i>T. geojense</i> YCS6 ^T	19.70%	19.80%	20.30%
<i>T. haliotis</i> NBRC 112382 ^T	19.70%	20.40%	20.70%
<i>T. holothuriorum</i> LMG 27758 ^T	19.60%	22.60%	20.40%
<i>T. insulae</i> NBRC 112783 ^T	19.10%	20.20%	21.00%
<i>T. jejuense</i> KCTC 22618 ^T	20.70%	19.70%	20.70%
<i>T. litopenaei</i> LMG 23706 ^T	18.80%	18.60%	18.50%
<i>T. litoreum</i> CL-TF13 ^T	19.70%	20.70%	21.10%
<i>T. lutimaris</i> TF-26 ^T	19.90%	20.70%	21.10%
<i>T. maritimum</i> NCIMB 2154 ^T	19.00%	19.70%	19.80%
<i>T. mesophilum</i> CIP 107215 ^T	20.00%	21.10%	21.10%
<i>T. ovolyticum</i> EKD002 ^T	19.30%	20.20%	21.10%
<i>T. platacis</i> 190524A05c ^T		19.90%	20.10%
<i>T. platacis</i> 190607A01a	69.20%	19.90%	20.10%
<i>T. platacis</i> 190611E02c	68.50%	19.70%	20.30%
<i>T. platacis</i> 190820D02b	69.20%	19.70%	20.20%
<i>T. pelagium</i> S7007 ^T	19.70%	20.90%	20.80%
<i>T. piscium</i> TNO020 ^T	19.80%	19.70%	20.60%
<i>T. polynesiense</i> 190130A14a ^T	19.70%		21.90%
<i>T. polynesiense</i> 190130A13a	19.70%	99.60%	21.70%
<i>T. polynesiense</i> 190423A01a	19.70%	99.50%	21.70%
<i>T. sediminilitoris</i> KCTC 52210 ^T	19.10%	20.60%	20.70%
<i>T. singaporense</i> DSM 106434 ^T	19.80%	21.20%	21.50%
<i>T. skagerrakense</i> DSM 14836 ^T	24.10%	19.70%	20.20%
<i>T. soleae</i> LL04 12.1.7 ^T	19.30%	20.10%	20.70%
<i>T. tangerinum</i> GRR-S3-23 ^T	19.60%	20.50%	20.60%
<i>T. todarodis</i> LPB0136 ^T	18.70%	19.50%	20.50%
<i>T. vairaonense</i> 190524A02b ^T	20.10%	21.90%	
<i>T. vairaonense</i> 190115A13a	19.60%	20.80%	89.00%
<i>T. vairaonense</i> 190607A02c	19.90%	21.00%	88.20%
<i>T. xiamenense</i> LMG 27422 ^T	19.60%	20.00%	19.80%