
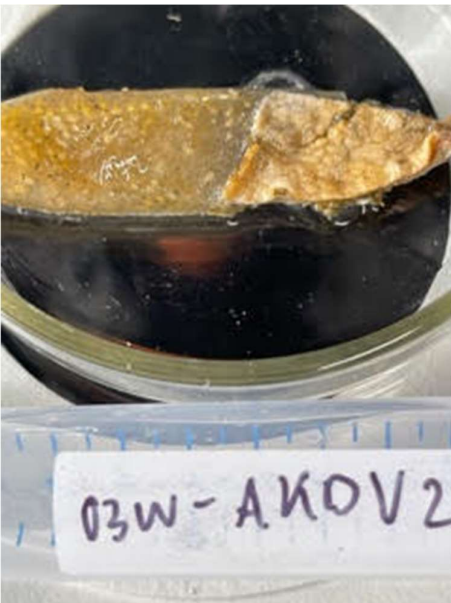


Supplementary material: The Microbiome of Colonial Ascidians.

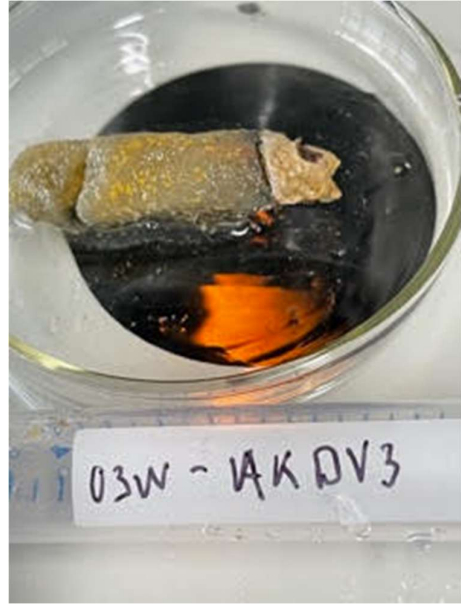
Table S1: Specimens pre- dissection including image and identifier name

Specimens name and date of dissection	Image
2503-AKDV1 5.7.21	
2503-AKDV2 5.7.21	



2503-AKDV3

5.7.21



1503-DVBL1

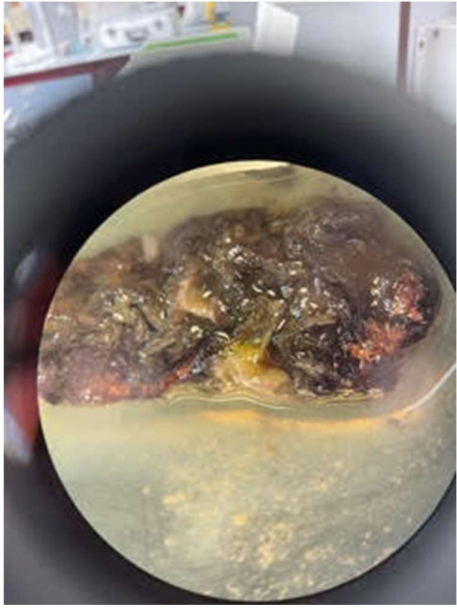
8.7.21



1503-DVBL2

8.7.21







1503-DVBL3

8.7.21





2503-DVAP1

13.7.21



2503-DVAP2

13.7.21



2503-DVAP3

13.7.21



2503-AKDI1

13.7.21



2503-AKDI2

16.07.21



2503-AKDI3

16.07.21



2503-AKAP1

16.07.21



2503-AKAP2

16.07.21



2503-AKAP3

19.07.21



1503-DVLN1

19.07.21



1503-DVLN2

19.07.21



1503-DVLN3

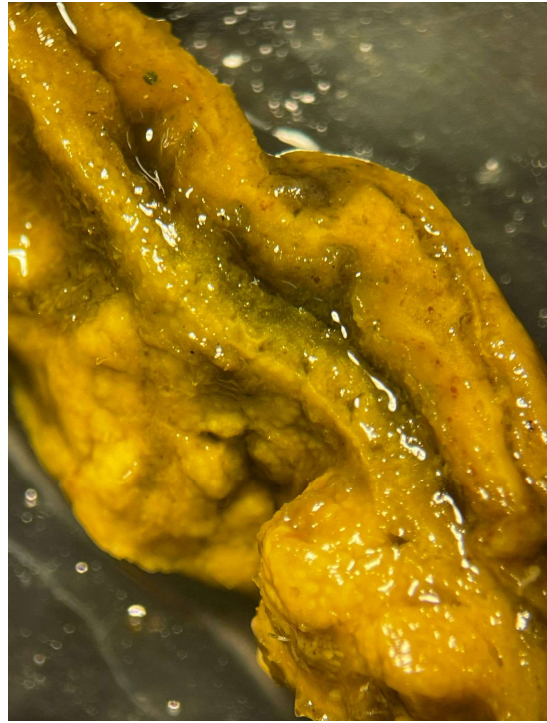
19.07.21



1802-DVDI1

21.07.21





1802-DVDI2

21.07.21



2503-DVDI3

21.07.21



1503-DV(S)1

21.07.21



1503-DV(S)2

21.07.21



1503-DV(S)3

21.07.21



1503-BL(S)1

22.07.21



1503-BL(S)2

22.07.21



1503-BL(S)3

22.07.21



2503-AK(S)1

22.07.21



2503-AK(S)2

22.07.21



2503-AK(S)3

22.07.21



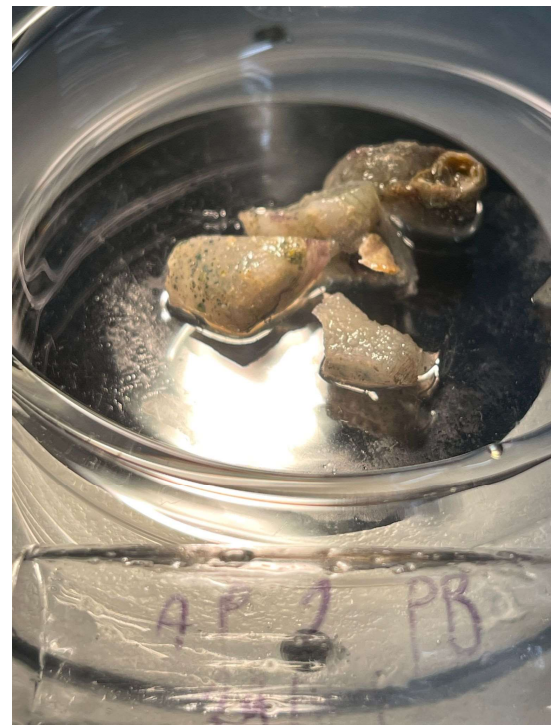
2904-AP(S)1

22.07.21



2904-AP(S)2

22.07.21



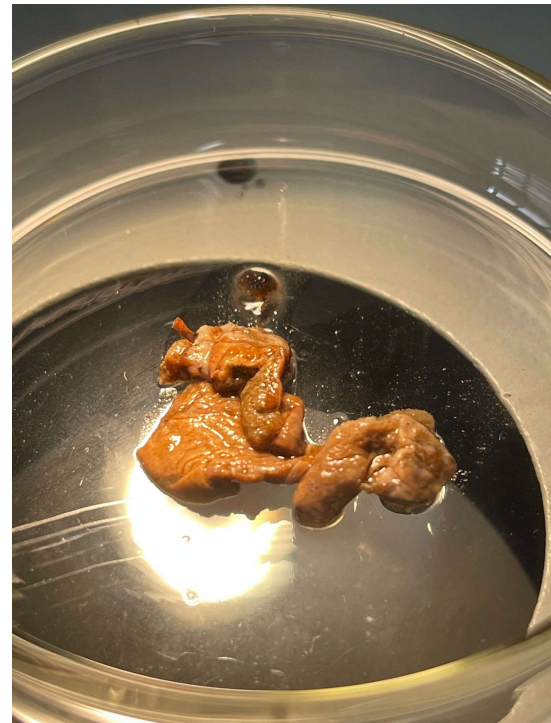
2904-AP(S)3

22.07.21



2503-DI(S)1

22.07.21



2503-DI(S)2

22.07.21



2503-DI(S)3

22.07.21



1503-LN(S)1

22.07.21



1503-LN(S)2

22.07.21



1503-LN(S)3

22.07.21



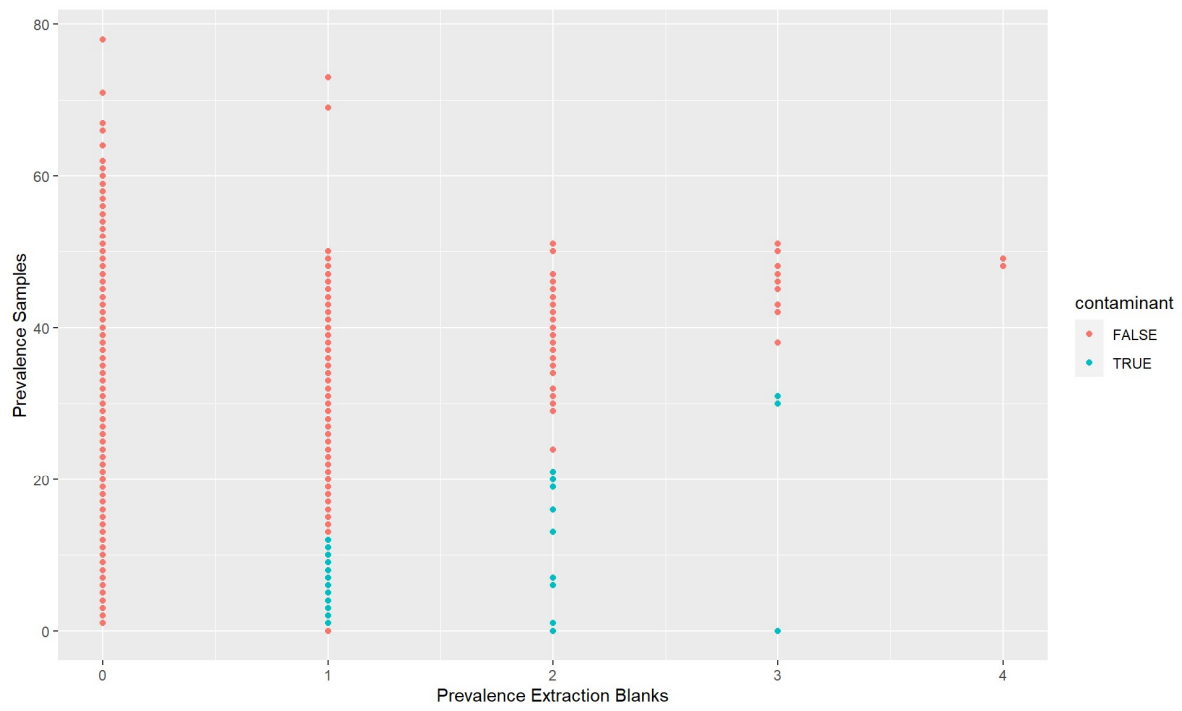


Figure S1: Prevalence plot decontam package

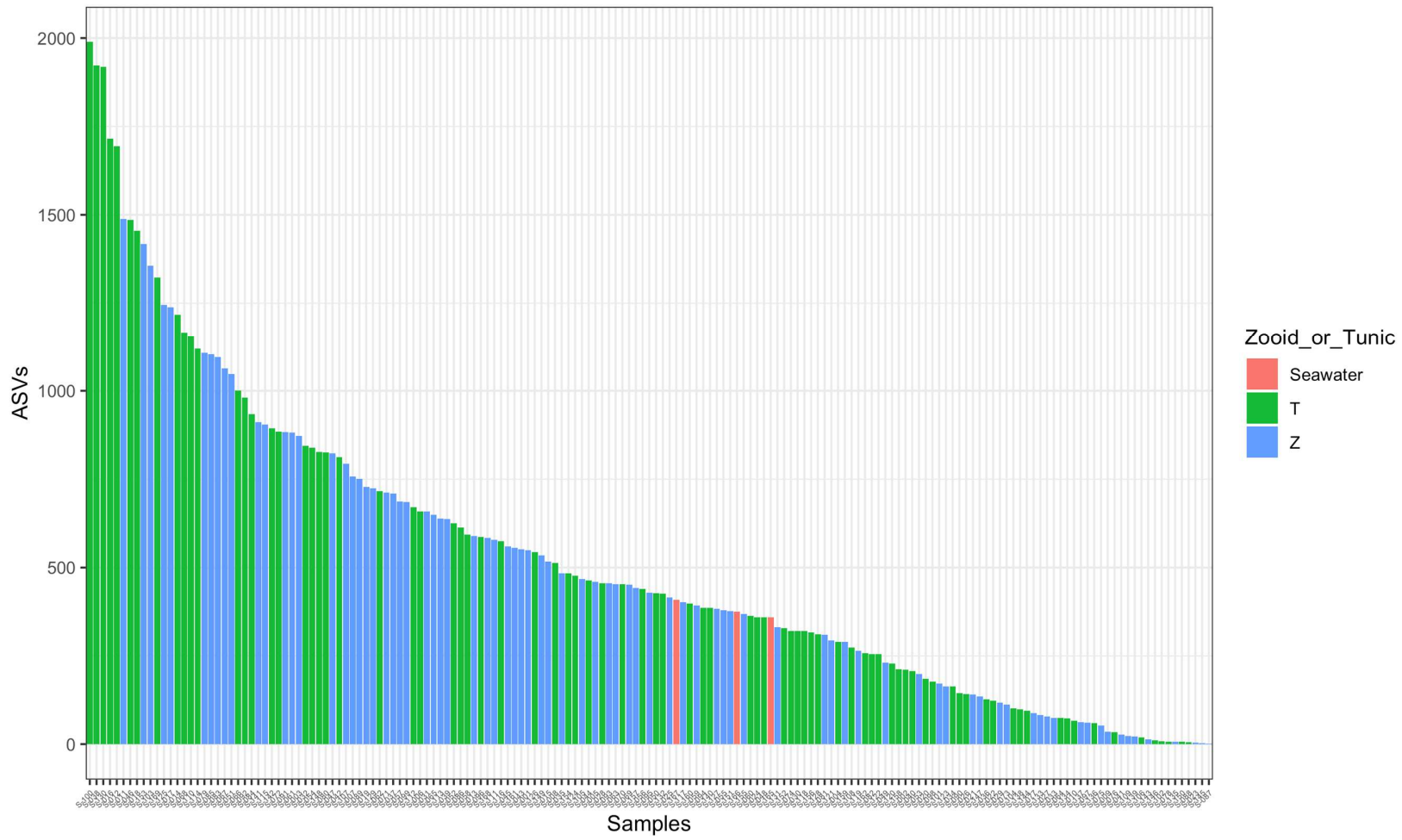


Figure S2: Numbers of ASVs per sample after quality control and filters

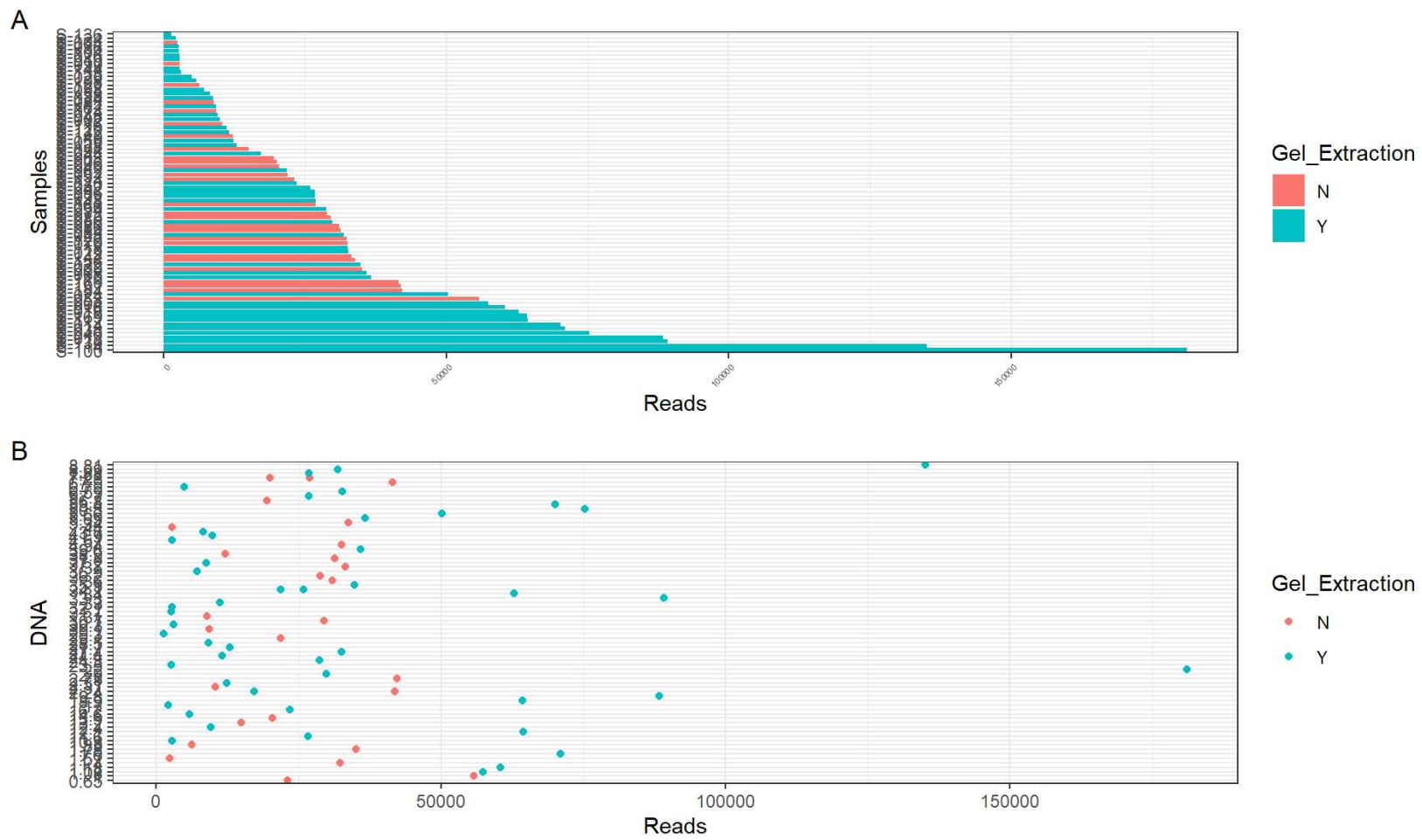


Figure S3: Number of reads per sample, by DNA initial concentration and/or whether the sample underwent gel extraction procedure.

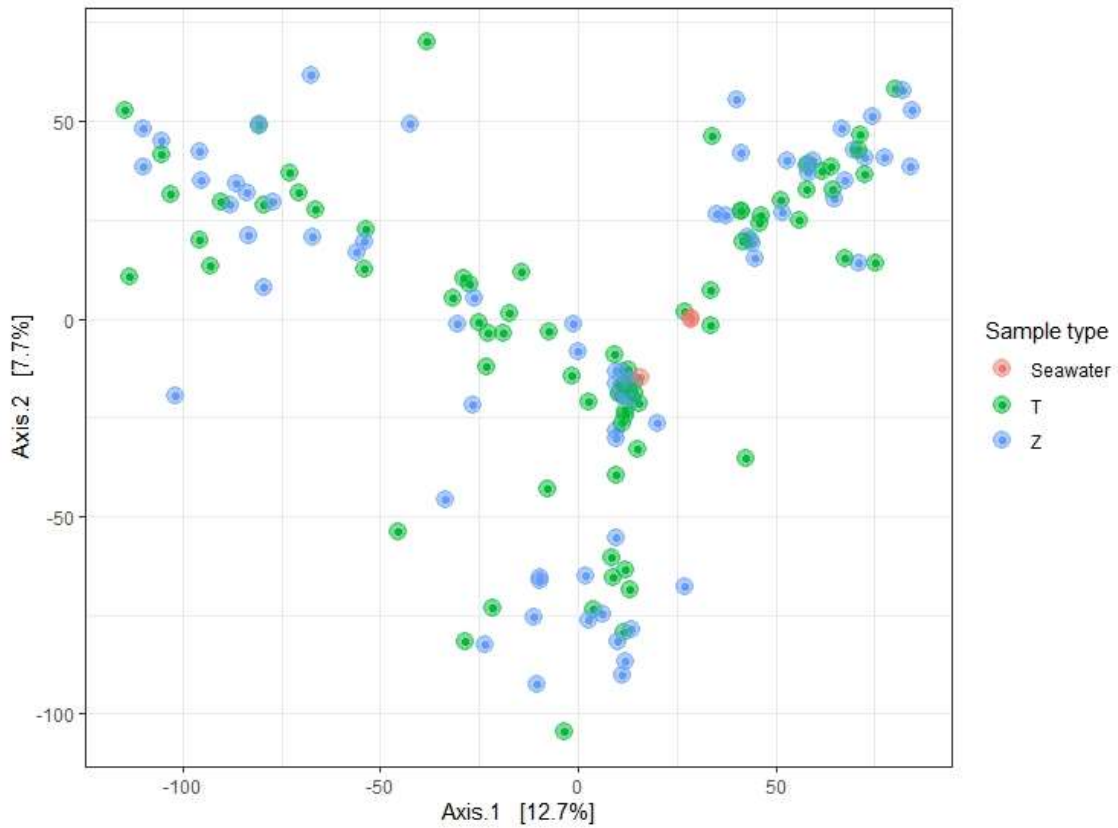


Figure S4: PCoA plot showing microbial community structure across tunic, zoid, and seawater samples, including erroneous taxonomy (chloroplast, and mitochondria).

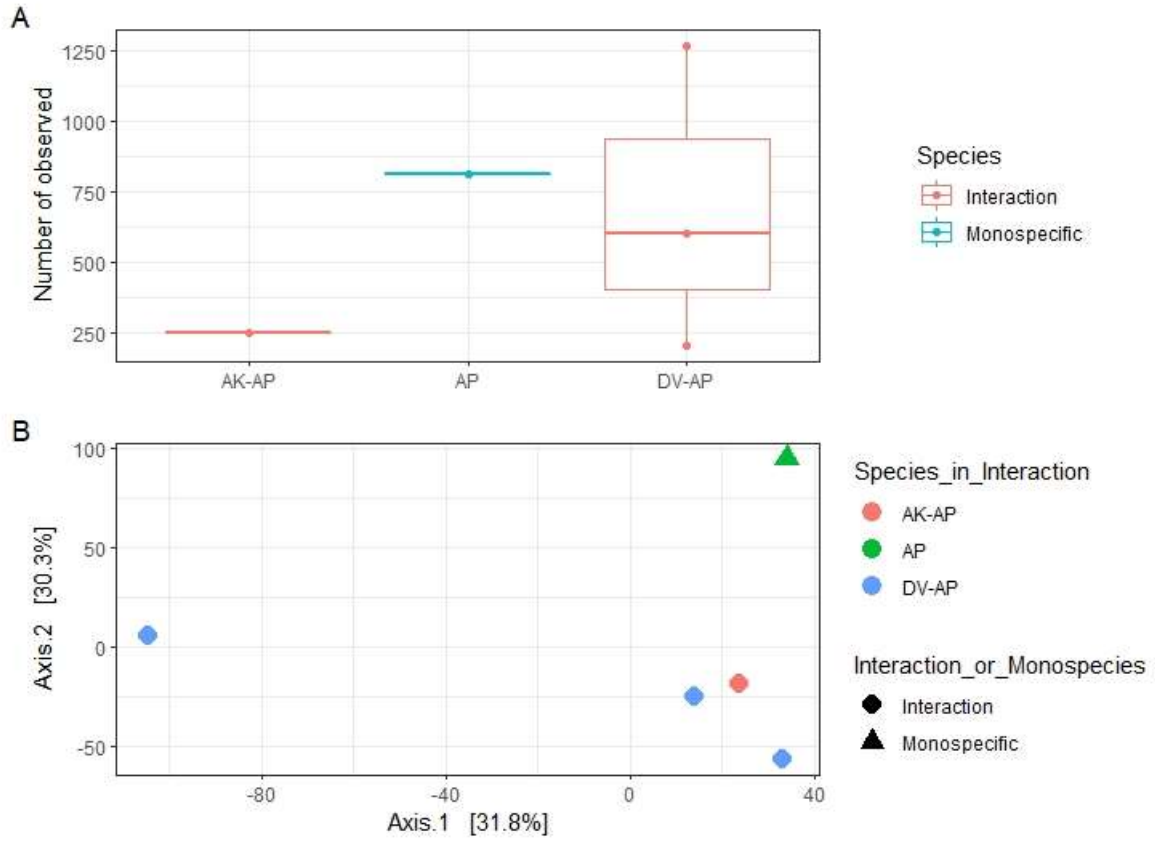


Figure S5: Alpha diversity using observed richness index (A), and PCoA plot (B) showing the differences between the monospecific and interacting forms of AP by each case study (no IB samples were included).

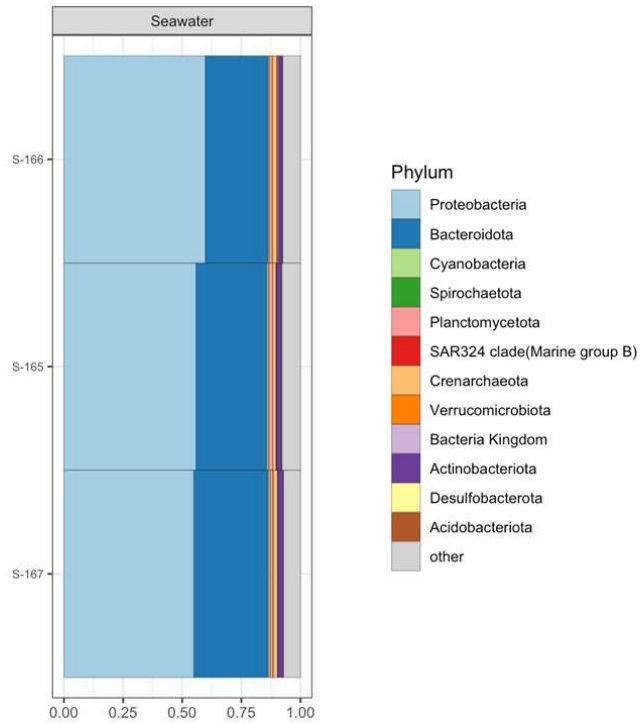


Figure S6: Taxonomic composition of seawater samples by each location. Sample S-165 was collected from Tauranga marine bridge marine precinct (37°40'27"S, 176°10'18"E) (Bridge), sample S-166 was collected from Tauranga Bridge Marina, Pier A (37°40'09"S, 176°10'44"E) (Pier A), and sample S-167 Salisbury wharf, Pilot Bay, Mount Maunganui (37°38'25"S, 176°10'52"E) Mount.

Table S2: Fusion primers barcodes (forward and reverse) used for DNA samples prior to amplification

	from Nextera XT v2			515FB = GTGYCAGCMGCCGCGGT AA							
Left arm P5 adapter	i5 na me	i5	Right arm P5 adapter	Forward Primer	Final nam e	Fusion sequence (5'-3')	Len gth	Hair pins	Sel f- di mer	To or de r	On ha nd
AATGATACGGCGACCA CCGAGATCTACAC	S5 01	TAGAT CGC	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S501 - 515F B	AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	46.6	6	5	
AATGATACGGCGACCA CCGAGATCTACAC	S5 02	CTCTC TAT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S502 - 515F B	AATGATACGGCGACCACCGAGATCTACACTCTCTATTTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	Low	Lo w		Ye s
AATGATACGGCGACCA CCGAGATCTACAC	S5 03	TATCC TCT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S503 - 515F B	AATGATACGGCGACCACCGAGATCTACACTATCCTCTTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	Low	Lo w		Ye s
AATGATACGGCGACCA CCGAGATCTACAC	S5 05	GTAAG GAG	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S505 - 515F B	AATGATACGGCGACCACCGAGATCTACACGTAAGGAGTCGTCGGCAGCGTCA GATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	Low	Lo w		Ye s
AATGATACGGCGACCA CCGAGATCTACAC	S5 06	ACTGC ATA	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S506 - 515F B	AATGATACGGCGACCACCGAGATCTACACTGCATATCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	Low	Lo w		Ye s
AATGATACGGCGACCA CCGAGATCTACAC	S5 07	AAGG AGTA	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S507 - 515F B	AATGATACGGCGACCACCGAGATCTACACAAGGAGTATCGTCGGCAGCGTCA GATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	47.7	6	6	
AATGATACGGCGACCA CCGAGATCTACAC	S5 08	CTAAG CCT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S508 - 515F B	AATGATACGGCGACCACCGAGATCTACACTAAGCCTTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCGCGGTAA	89	47.7	6	7	

AATGATACGGCGACCA CCGAGATCTACAC	S5 10	CGTCT AAT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S510 - S15F B	AATGATACGGCGACCACCGAGATCTACACCGTCTAATTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	8	
AATGATACGGCGACCA CCGAGATCTACAC	S5 11	TCTCT CCG	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S511 - S15F B	AATGATACGGCGACCACCGAGATCTACACTCTCCGTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	9	
AATGATACGGCGACCA CCGAGATCTACAC	S5 15	TTCTA GCT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S515 - S15F B	AATGATACGGCGACCACCGAGATCTACACTTCTAGCTTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	10	
AATGATACGGCGACCA CCGAGATCTACAC	S5 16	CCTAG AGT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S516 - S15F B	AATGATACGGCGACCACCGAGATCTACACCTAGAGTTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	44	6	11	
AATGATACGGCGACCA CCGAGATCTACAC	S5 17	GCGT AAGA	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S517 - S15F B	AATGATACGGCGACCACCGAGATCTACACCGTAAAGATCGTCGGCAGCGTCA GATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.1	6	12	
AATGATACGGCGACCA CCGAGATCTACAC	S5 18	CTATT AAG	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S518 - S15F B	AATGATACGGCGACCACCGAGATCTACACCTATTAAGTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	13	
AATGATACGGCGACCA CCGAGATCTACAC	S5 20	AAGG CTAT	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S520 - S15F B	AATGATACGGCGACCACCGAGATCTACACAAGGCTATTCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	14	
AATGATACGGCGACCA CCGAGATCTACAC	S5 21	GAGC CTTA	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S521 - S15F B	AATGATACGGCGACCACCGAGATCTACACGAGCCTTATCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	48.8	6	15	
AATGATACGGCGACCA CCGAGATCTACAC	S5 22	TTATG CGA	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAG	GTGYCAGCMGC CGCGGTAA	XF- S522 - S15F B	AATGATACGGCGACCACCGAGATCTACACTTATGCGATCGTCGGCAGCGTCAG ATGTGTATAAGAGACAGGTGYCAGCMGCCCGGTAA	89	47.7	6	16	

	from Nextera XT v2			926R = CCGYCAATTYMTT RAGTTT							
Left arm P7 adapter	i7 name	i7	Right arm P7 adapter	Reverse Primer	Final name	Fusion sequence (5'-3')	Le ng th	Hai rpi n	Self- dim er	To ord er	On han d
CAAGCAGAAGACGGC ATACGAGAT	N7 01	TCGC CTTA	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N701- 926R	CAAGCAGAAGACGGCATAACGAGATTCGCCTTAGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	Lo w	Low		Yes
CAAGCAGAAGACGGC ATACGAGAT	N7 02	CTAG TACG	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N702- 926R	CAAGCAGAAGACGGCATAACGAGATCTAGTACGGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	Lo w	Low		Yes
CAAGCAGAAGACGGC ATACGAGAT	N7 04	GCTC AGG A	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N704- 926R	CAAGCAGAAGACGGCATAACGAGATGCTCAGGAGTCTCGTGGGCTCGGAG ATGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	Lo w	Low		Yes
CAAGCAGAAGACGGC ATACGAGAT	N7 05	AGG AGTC C	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N705- 926R	CAAGCAGAAGACGGCATAACGAGATAGGAGTCCGTCTCGTGGGCTCGGAG ATGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	Lo w	Low		Yes
CAAGCAGAAGACGGC ATACGAGAT	N7 06	CATG CCTA	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N706- 926R	CAAGCAGAAGACGGCATAACGAGATCATGCCTAGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	5	
CAAGCAGAAGACGGC ATACGAGAT	N7 07	GTA GAG AG	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N707- 926R	CAAGCAGAAGACGGCATAACGAGATGTAGAGAGGTCTCGTGGGCTCGGAG ATGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	6	
CAAGCAGAAGACGGC ATACGAGAT	N7 10	CAG CCTC G	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N710- 926R	CAAGCAGAAGACGGCATAACGAGATCAGCCTCGGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	7	
CAAGCAGAAGACGGC ATACGAGAT	N7 11	TGCC TCTT	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N711- 926R	CAAGCAGAAGACGGCATAACGAGATTGCCTCTGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	8	
CAAGCAGAAGACGGC ATACGAGAT	N7 12	TCCT CTAC	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N712- 926R	CAAGCAGAAGACGGCATAACGAGATTCCTCTACGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	9	
CAAGCAGAAGACGGC ATACGAGAT	N7 14	TCAT GAG C	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N714- 926R	CAAGCAGAAGACGGCATAACGAGATTCATGAGCGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	10	
CAAGCAGAAGACGGC ATACGAGAT	N7 15	CCTG AGA T	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N715- 926R	CAAGCAGAAGACGGCATAACGAGATCCTGAGATGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	11	
CAAGCAGAAGACGGC ATACGAGAT	N7 16	TAGC GAG T	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N716- 926R	CAAGCAGAAGACGGCATAACGAGATTAGCGAGTGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6	12	

CAAGCAGAAGACGGC ATACGAGAT	N7 18	GTA GCTC C	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N718- 926R	CAAGCAGAAGACGGC ATACGAGATGTAGTCCGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 19	TACT ACG C	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N719- 926R	CAAGCAGAAGACGGC ATACGAGATTACTACGCTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 20	AGG CTCC G	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N720- 926R	CAAGCAGAAGACGGC ATACGAGATAGGCTCCGCTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 21	GCA GCG TA	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N721- 926R	CAAGCAGAAGACGGC ATACGAGATGCAGCTAGTCTCGTGGGCTCGGAGA ATGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 22	CTGC GCAT	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N722- 926R	CAAGCAGAAGACGGC ATACGAGATCTGCGCATGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 23	GAG CGCT A	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N723- 926R	CAAGCAGAAGACGGC ATACGAGATGAGCGCTAGTCTCGTGGGCTCGGAGA ATGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 24	CGCT CAGT	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N724- 926R	CAAGCAGAAGACGGC ATACGAGATCGCTCAGTGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 26	GTCT TAG G	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N726- 926R	CAAGCAGAAGACGGC ATACGAGATGTCTTAGGGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 27	ACTG ATCG	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N727- 926R	CAAGCAGAAGACGGC ATACGAGATACTGATCGGTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		
CAAGCAGAAGACGGC ATACGAGAT	N7 28	TAGC TGCA	GTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAG	CCGYCAATTYMTT RAGTTT	NR- N728- 926R	CAAGCAGAAGACGGC ATACGAGATTAGCTGCACTCTCGTGGGCTCGGAGA TGTGTATAAGAGACAGCCGYCAATTYMTTTRAGTTT	86	44	6		