

**Supplementary material**

**Bacteria in tropical floodplain soils are sensitive to changes in saltwater**

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**Table S1. Appearance and location of floodplain soils by site**

Visual image of soil	Site	Latitude	Longitude	Floodplain morphology	River zone
	1	12°44'15.32"S	132°31'3.74"E	Lower floodplain	Upstream
	2	12°45'1.53"S	132°30'6.66"E	Upper floodplain	Upstream
	3	12°45'48.35"S	132°28'58.97"E	Backwater swamp	Upstream
	4	12°42'6.42"S	132°30'29.64"E	Lower floodplain	Upstream
	5	12°42'33.81"S	132°30'28.95"E	Upper floodplain	Upstream
	6	12°42'37.60"S	132°30'21.26"E	Backwater swamp	Upstream
	7	12°37'19.95"S	132°29'22.25"E	Lower floodplain	Cuspate
	8	12°36'21.68"S	132°30'37.53"E	Upper floodplain	Cuspate
	9	12°35'28.43"S	132°31'43.28"E	Backwater swamp	Cuspate
	10	12°33'5.57"S	132°27'29.23"E	Lower floodplain	Cuspate
	11	12°33'33.19"S	132°29'23.26"E	Upper floodplain	Cuspate
	12	12°32'41.63"S	132°30'40.44"E	Backwater swamp	Cuspate
	13	12°26'18.63"S	132°26'8.62"E	Lower floodplain	Sinuuous
	14	12°25'28.47"S	132°27'34.19"E	Upper floodplain	Sinuuous
	15	12°25'46.54"S	132°29'17.94"E	Backwater swamp	Sinuuous
	16	12°23'31.23"S	132°23'56.09"E	Lower floodplain	Sinuuous
	17	12°22'37.25"S	132°26'31.63"E	Upper floodplain	Sinuuous
	18	12°22'13.26"S	132°29'56.18"E	Backwater swamp	Sinuuous

**Table S2. Relative abundance of phyla across all floodplain soil sites**

Average relative abundance of operational taxonomic units (OTUs) across floodplain soil sites  
classified to the level of phylum

Phyla	Average abundance	Cumulative abundance	Standard error
Unclassified	31.156	31.156	1.168
Proteobacteria	26.682	57.838	0.898
Chloroflexi	13.701	71.539	0.669
Acidobacteria	12.462	84.001	0.609
Verrucomicrobia	5.815	89.816	0.416
Actinobacteria	5.561	95.377	0.461
Firmicutes	2.962	98.340	0.296
Gemmatimonadetes	0.429	98.768	0.050
Planctomycetes	0.229	98.997	0.035
Chlamydiae	0.220	99.217	0.034
Armatimonadetes	0.193	99.410	0.017
Chlorobi	0.161	99.571	0.028
BRC1	0.153	99.724	0.012
WS3	0.148	99.872	0.022
Deinococcus–Thermus	0.038	99.909	0.013
Spirochaetes	0.033	99.943	0.006
Bacteroidetes	0.026	99.969	0.005
OD1	0.009	99.978	0.002
TM7	0.009	99.986	0.002
Fusobacteria	0.008	99.995	0.003
Tenericutes	0.003	99.997	0.001
Nitrospira	0.002	100.000	0.001
OP11	<0.001	100.000	<0.001

**Table S3. Abiotic variable measurements at replicate floodplain soil sites**

Abiotic variable values measured in floodplain soils were averaged across replicate sites. Standard deviation is shown in parentheses. Site-description categories of floodplain morphology and river zones are shown. TN, total nitrogen; TOC, total organic carbon

Site	Site description	pH	Salinity ( $\mu\text{S cm}^{-1}$ )	TN ( $\text{g kg}^{-1}$ )	TOC ( $\text{g kg}^{-1}$ )
Site 1	Lower floodplain, upstream	6.8 (0.4)	4670 (1431.6)	2.3 (0.4)	23.4 (2.5)
Site 2	Upper floodplain, upstream	4.7 (0.2)	492.8 (147)	3.3 (0.2)	33.6 (1.9)
Site 3	Backwater swamp, upstream	5.4 (0.2)	610.6 (152.2)	3.7 (0.3)	35.9 (2.6)
Site 4	Lower floodplain, upstream	5.6 (0.7)	1110.4 (517.1)	3.8 (1)	45.1 (11.5)
Site 5	Upper floodplain, upstream	4.8 (0.4)	426.9 (268)	1.9 (0.4)	23.8 (4.7)
Site 6	Backwater swamp, upstream	5.1 (0.2)	1845.2 (872.1)	2.6 (0.5)	32.5 (4.7)
Site 7	Lower floodplain, cusplate	6.3 (0.2)	8562 (1390.7)	3.1 (0.6)	32.7 (2.9)
Site 8	Upper floodplain, cusplate	5.6 (0.2)	54.6 (9.7)	1.1 (0.2)	11 (2.3)
Site 9	Backwater swamp, cusplate	4.1 (0.2)	3284.2 (1473.1)	4.5 (0.8)	42 (6.3)
Site 10	Lower floodplain, cusplate	4.8 (0.2)	739.3 (701.9)	3 (1.6)	34.2 (20.2)
Site 11	Upper floodplain, cusplate	5.6 (0.2)	18.6 (2.8)	1.1 (0.3)	13.3 (1.7)
Site 12	Backwater swamp, cusplate	4.9 (0.3)	107.9 (83.5)	4 (2.2)	35.8 (3.7)
Site 13	Lower floodplain, sinuous	5.2 (0.3)	7194 (2737.3)	5.6 (2.5)	69.2 (31.1)
Site 14	Upper floodplain, sinuous	4.8 (0.3)	1486.8 (499.9)	3 (0.4)	38.9 (4.4)
Site 15	Backwater swamp, sinuous	4.7 (0.1)	56.8 (17.9)	3.7 (0.8)	43.7 (7)
Site 16	Lower floodplain, sinuous	5.6 (0.3)	7798 (1477.1)	3.6 (0.9)	37.5 (11)
Site 17	Upper floodplain, sinuous	4.6 (0.3)	1203 (742.7)	2.7 (0.6)	34.4 (8.3)
Site 18	Backwater swamp, sinuous	3.8 (0.1)	2354.2 (143.5)	7.4 (1.1)	80.6 (10.5)

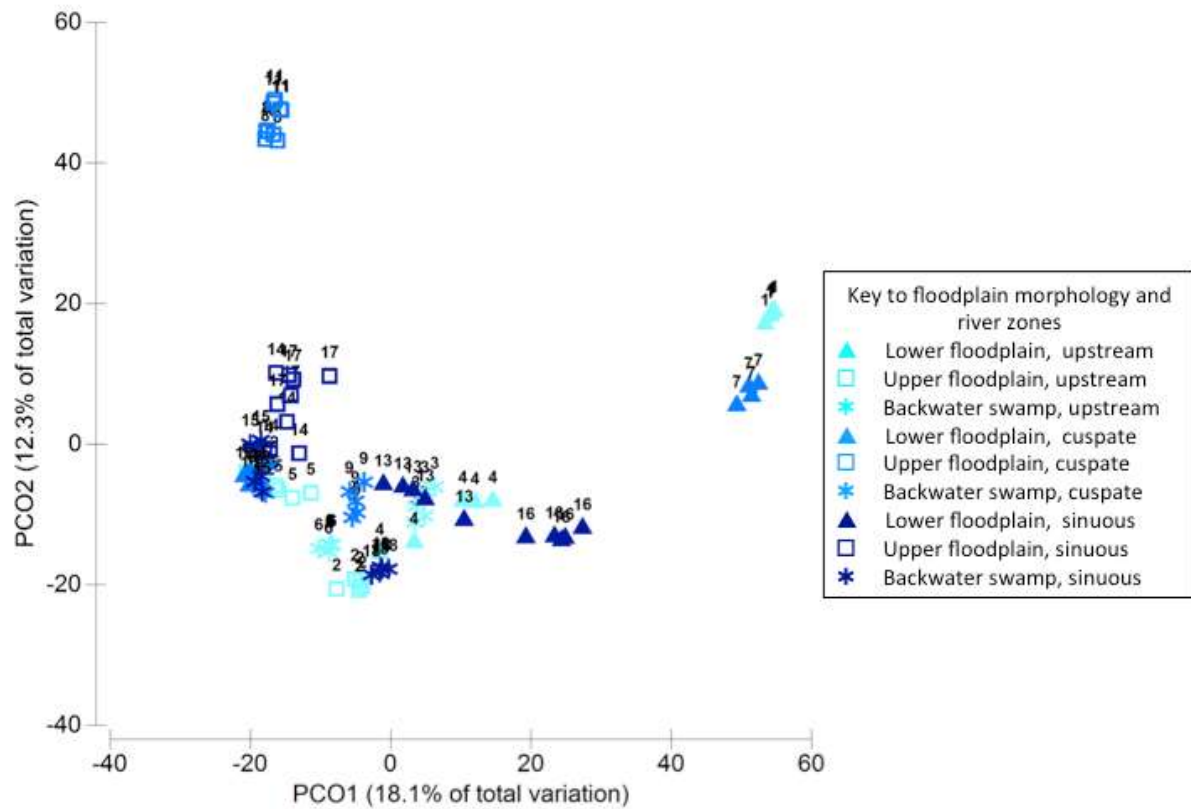
**Table S4. Bacterial taxa identified as responding to floodplain soil variables as indicated by threshold indicator taxa analysis (TITAN)**

TITAN was conducted for operational taxonomic units (OTUs) in response to soil variables, pH, salinity, total organic carbon (TOC) and total nitrogen (TN). Table data include genera classified to their highest level identified as responding either positively or negatively. The mark (x) denotes a response for that variable

Genera	Positive				Negative			
	pH	Salinity	TN	TOC	pH	Salinity	TN	TOC
<i>Acetobacter</i>	x							
<i>Acidisoma</i>		x				x	x	x
<i>Acidobacteria</i>	x	x	x	x	x	x	x	x
<i>Acidotherrmus</i>		x						
<i>Actinoallomurus</i>			x	x	x			x
<i>Actinomycetospora</i>					x			
<i>Actinospica</i>					x			
<i>Alicyclobacillus</i>	x				x			
<i>Alterococcus</i>		x						
<i>Anaeromyxobacter</i>					x	x	x	x
<i>Ancylobacter</i>	x	x						
<i>Anderseniella</i>	x							
<i>Aquicella</i>	x	x	x	x				
<i>Arenimonas</i>	x							
Armatimonadetes Group 2	x				x	x	x	x
<i>Asticcacaulis</i>		x						
<i>Bacillus</i>							x	x
<i>Bellilinea</i>	x	x						
BRC1	x	x					x	
<i>Burkholderia</i>						x		
<i>Bysovorax</i>			x	x				
<i>Caedibacter</i>					x			
<i>Caldilinea</i>	x	x				x		
<i>Catellibacterium</i>		x						
<i>Caulobacter</i>		x						
<i>Cellvibrio</i>			x					
Chthonomonas Armatimonadetes Group 3	x			x		x		
<i>Clostridium sensu stricto</i>	x	x						
<i>Clostridium XI</i>	x	x						
<i>Clostridium XIVb</i>	x							
<i>Conexibacter</i>	x				x	x	x	
<i>Coxiella</i>	x							
<i>Dehalogenimonas</i>		x						
<i>Demequina</i>	x							
<i>Dendrosporobacter</i>			x					
<i>Desulfobacterium</i>	x	x						x
<i>Desulfobacula</i>	x							
<i>Desulfobulbus</i>	x	x						x
<i>Desulfococcus</i>	x	x						
<i>Desulfomonile</i>		x		x	x			
<i>Desulfonema</i>	x	x						
<i>Desulfosarcina</i>	x	x						
<i>Desulfotomaculum</i>		x						
<i>Desulfovirga</i>		x						
<i>Desulfurivibrio</i>		x						

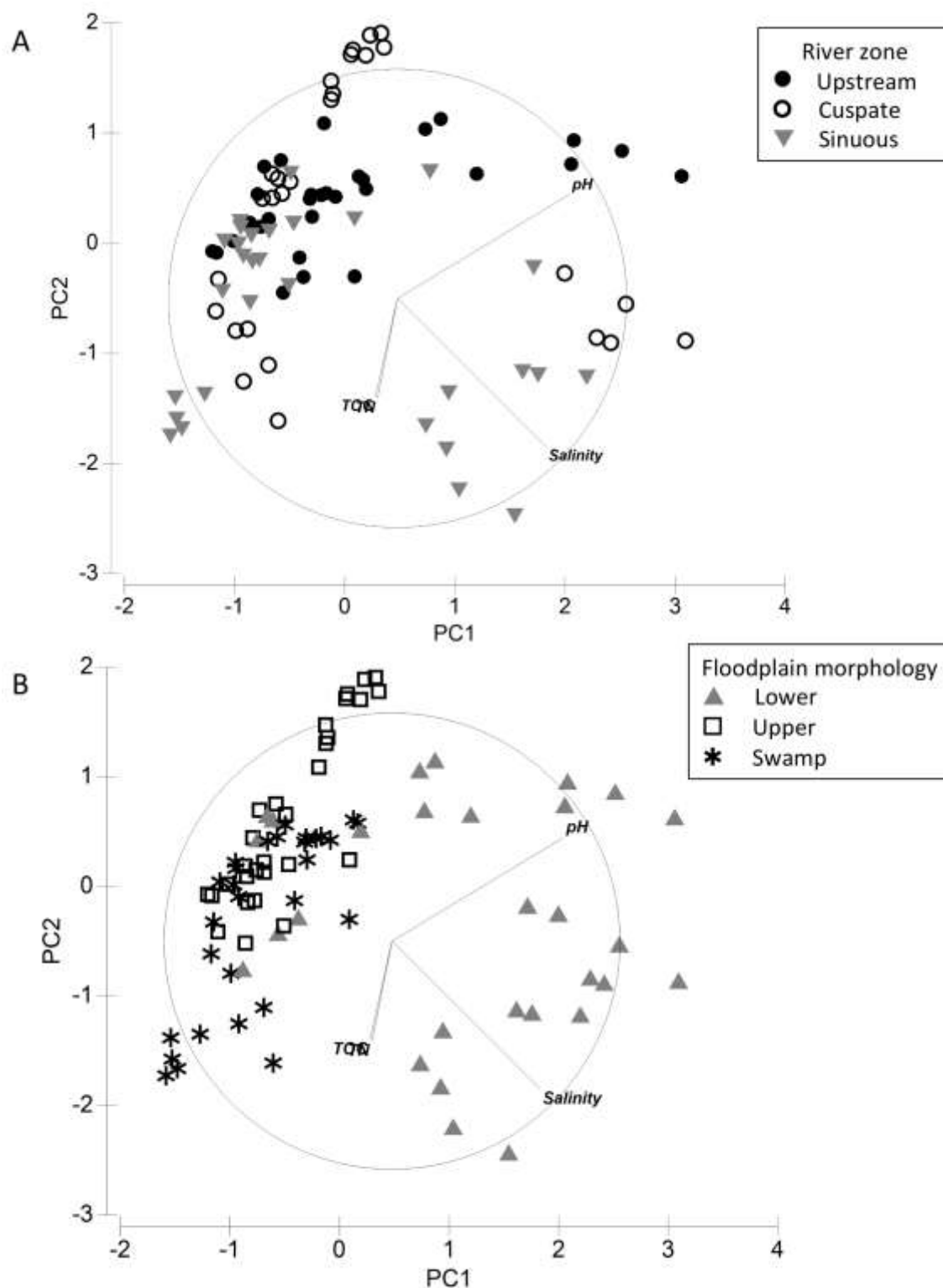
Genera	Positive				Negative			
	pH	Salinity	TN	TOC	pH	Salinity	TN	TOC
<i>Desulfuromonas</i>	x	x						
<i>Dongia</i>		x				x		
<i>Dyella</i>		x	x					
<i>Flavobacterium</i>	x	x						
<i>Fusibacter</i>		x						
<i>Gemmata</i>	x				x	x	x	x
<i>Gemmatimonas</i>		x	x	x	x	x	x	x
<i>Geobacter</i>		x				x		
<i>Halocella</i>	x							x
<i>Halomonas</i>		x						
<i>Halothiobacillus</i>	x							
<i>Heliothrix</i>			x					
<i>Holophaga</i>	x							
<i>Hydrogenophaga</i>	x	x						x
<i>Ignavibacterium</i>	x	x						
<i>Ilumatobacter</i>	x							x
<i>Ktedonobacter</i>	x				x	x	x	
<i>Labrys</i>						x		x
<i>Legionella</i>						x	x	
<i>Leptolinea</i>		x						
<i>Levilinea</i>					x			
<i>Longilinea</i>	x	x	x					
<i>Luteolibacter</i>	x	x						
<i>Magnetospirillum</i>					x			
<i>Marinobacter</i>		x						
<i>Marinomonas</i>	x							
<i>Massilia</i>						x		
<i>Mesorhizobium</i>	x	x						
<i>Methylobacterium</i>						x	x	x
<i>Methylocaldum</i>						x		
<i>Methylophilus</i>	x	x						
<i>Mycobacterium</i>			x		x			
<i>Nitrosococcus</i>	x	x						x
<i>Nocardia</i>						x		
<i>Nocardioides</i>	x	x	x	x	x			
<i>Opitutus</i>	x	x	x			x	x	x
<i>Orenia</i>	x	x						
<i>Oxobacter</i>		x						
<i>Paracoccus</i>		x						
<i>Paracraurococcus</i>						x	x	x
<i>Pedomicrobium</i>	x					x	x	x
<i>Pelagibius</i>	x	x						x
<i>Pelobacter</i>	x	x						
<i>Pelotomaculum</i>					x			
<i>Phaeobacter</i>	x	x						
<i>Phaselicystis</i>						x		
<i>Phenylobacterium</i>	x			x	x	x	x	x
<i>Planctomyces</i>		x						
<i>Porphyrobacter</i>				x				
<i>Propionicimonas</i>	x							
<i>Prostheco bacter</i>	x							
<i>Pseudolabrys</i>							x	x
<i>Pseudomonas</i>	x							
<i>Ralstonia</i>						x	x	
<i>Rheinheimera</i>		x						
<i>Rhizomicrobium</i>			x	x	x	x		

Genera	Positive				Negative			
	pH	Salinity	TN	TOC	pH	Salinity	TN	TOC
<i>Rhodobacter</i>		X						
<i>Rhodopila</i>				X	X	X		
<i>Roseomonas</i>	X	X				X	X	X
<i>Saccharofermentans</i>	X	X						
<i>Salisaeta</i>	X	X						
<i>Singulisphaera</i>			X	X	X			
<i>Skermanella</i>			X	X	X			
<i>Smithella</i>					X			
<i>Spartobacteria</i>	X					X	X	X
<i>Sphaerobacter</i>		X	X	X	X			
<i>Sphingobium</i>		X						
<i>Sphingomonas</i>					X			
<i>Sphingopyxis</i>		X						
<i>Spirochaeta</i>	X	X						
<i>Sporomusa</i>						X		
<i>Stappia</i>	X	X						X
<i>Sulfuricurvum</i>	X	X						
<i>Syntrophobacter</i>	X	X	X	X	X			
<i>Syntrophomonas</i>		X						
<i>Syntrophorhabdus</i>					X			
<i>Telmatospirillum</i>						X	X	X
<i>Thioalkalispira</i>	X	X						
<i>Thiobacillus</i>		X						
<i>Thiohalobacter</i>	X	X						
<i>Tistlia</i>		X						
<i>Treponema</i>		X						
<i>Truepera</i>	X	X						
<i>Tumebacillus</i>							X	
<i>Verrucomicrobia</i> Subdivision 3	X	X	X	X	X	X	X	X
<i>Verrucomicrobium</i>	X							
<i>Vibrio</i>	X	X						
WS3	X	X				X		
<i>Xanthobacter</i>	X	X						



**Fig. S1.** Dissimilarity of bacterial community on the South Alligator River floodplain labelled with sample site. Principal-coordinate analysis (PCoA) of bacterial operational taxonomic units (OTUs) of replicate floodplain soil sites. Each data point represents a soil sample, with site numbers indicated above the data points.





**Fig. S2.** Dissimilarity of floodplain soil abiotic variables. Principal-component analysis (PCA) displays dissimilarity between soil variables salinity, pH, total nitrogen (TN) and total organic carbon (TOC) in replicate soil samples coded for (a) floodplain morphology (FM) and (b) river zone (RZ). Data were normalised and transformed as necessary. Vectors display Pearson's correlation for included variables.