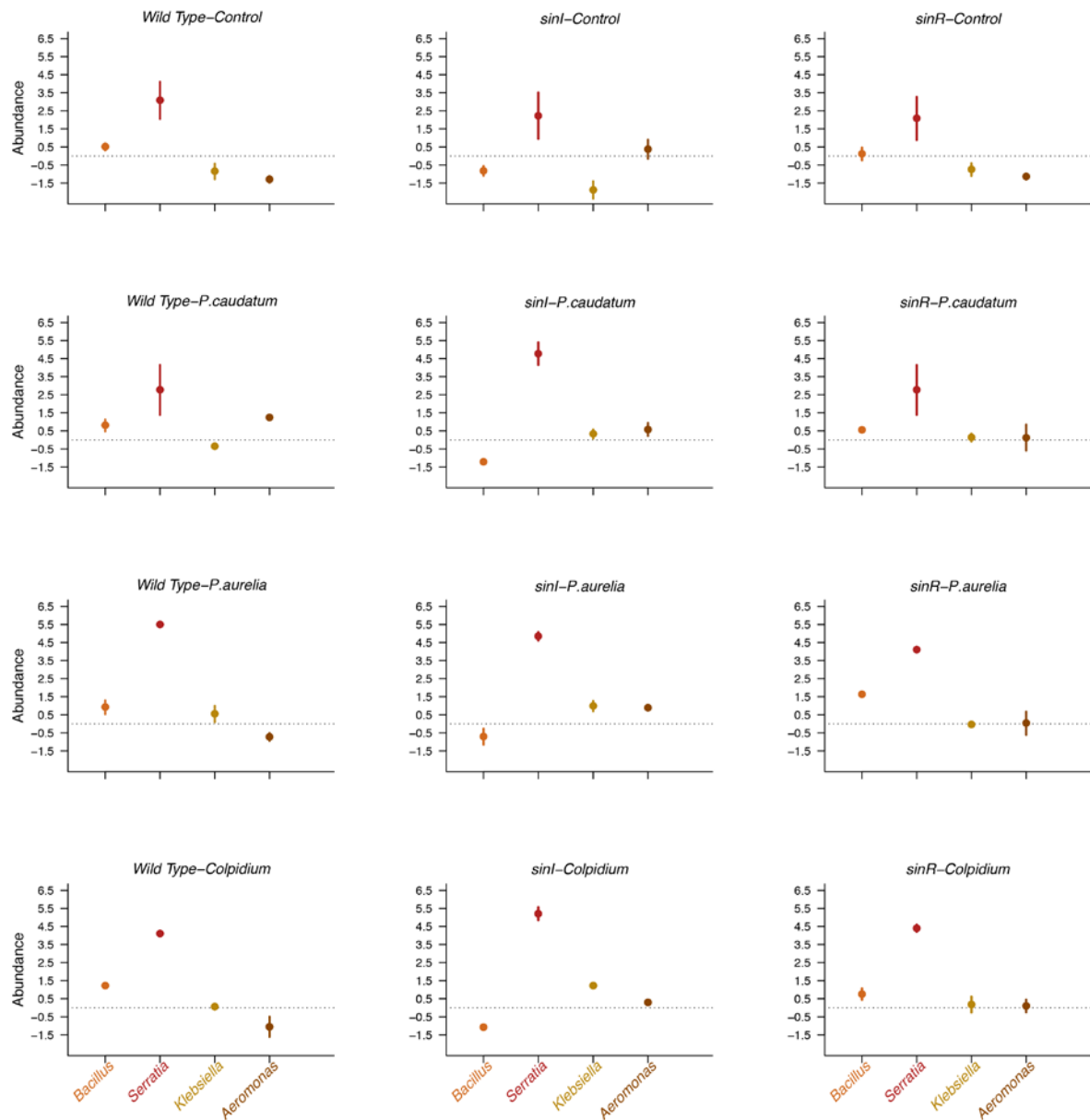
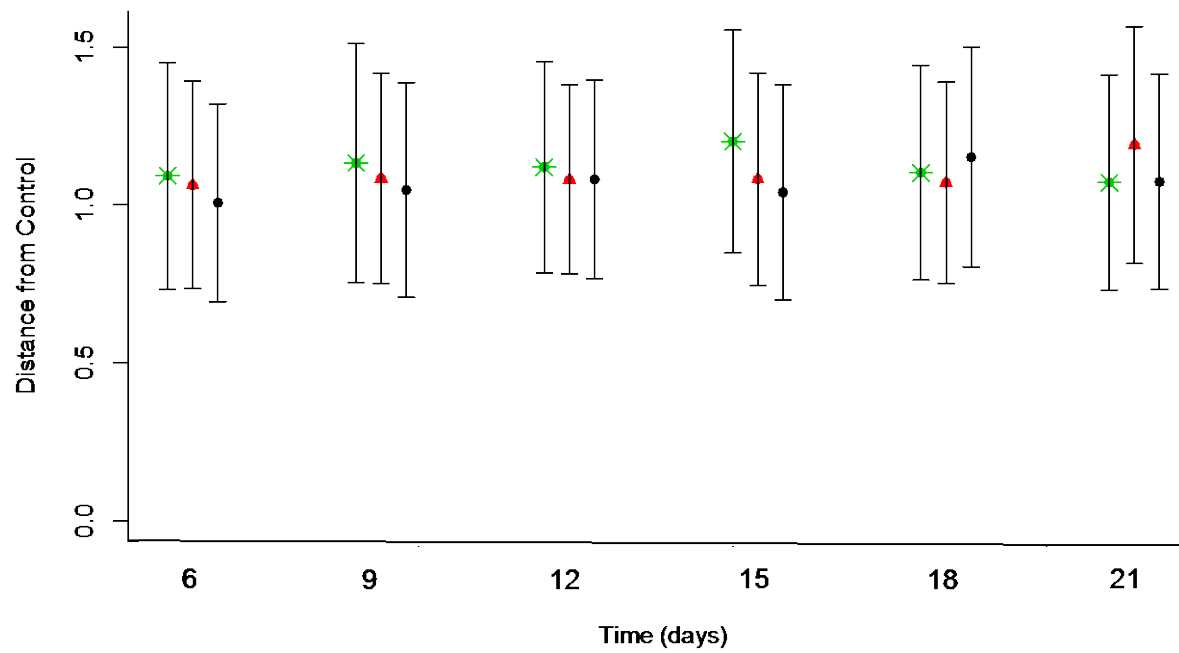




Supplementary Figure 1. Individual effects of each primary consumer species on bacterial community structure. Normalised (mean standardised) abundances (mean $\pm$ s.e.m, $n = 3$) of each bacterial species (*Bacillus*, *Serratia*, *Klebsiella* and *Aeromonas*) in microcosms containing no consumers ('Control') or one of the three primary consumer species used in the experiment (*P. caudatum* [second row from top], *P. Aurelia* [third row from top], *Colpidium* [bottom row]) across each of the three *Bacillus* treatments (wild type [left column], *sinI* [middle column], *sinR* [right column]).



Supplementary Figure 2. Euclidean distances between the centroid of the control treatment and each of the $\Delta sinI$ (black circles), $\Delta sinR$ (red triangles) and *Didinium* removed (green stars) treatments ($\pm$ bootstrapped sd. from 10^4 samples) across six time points (over 21 days) in pilot experiments.

Supplementary Table 1. Results of Spearman rank correlation tests for normalised densities of each species along a gradient of biofilm formation (see Fig. 4 in main text).

Species	rho	<i>P</i>
<i>B. subtilis</i>	0.604	< 0.001
<i>S. marcescens</i>	0.076	0.69
<i>Klebsiella</i>	0.191	0.31
<i>Aeromonas</i>	0.013	0.95
<i>P. aurelia</i>	0.113	0.55
<i>P. caudatum</i>	0.125	0.51
<i>Colpidium</i>	0.259	0.17
<i>Didinium</i>	-0.165	0.38

Supplementary Table 2. Bacterial strains used in the study.

Strain	Description	Source or reference
168 (<i>B.subtilis</i>)	<i>trpC2</i>	Laboratory stock
NCIB3610 (<i>B.subtilis</i>)	Wild-type isolate	BGSC 3A1
<i>Serratia marcescens</i>	Wild-type isolate	ATCC [®] 29632 [™]
LSB362 (<i>B.subtilis</i>)	<i>trpC2 ΔsinI::spc</i>	LFH →168
LSB363 (<i>B.subtilis</i>)	<i>trpC2 ΔsinR::spc</i>	LFH →168
LSB368 (<i>B.subtilis</i>)	<i>trpC2 ΔphoA::spc</i>	LFH →168
LSB369 (<i>B.subtilis</i>)	NCIB3610 <i>ΔsinI::spc</i>	SPP1 transduction →NCIB3610
LSB370 (<i>B.subtilis</i>)	NCIB3610 <i>ΔsinR::spc</i>	SPP1 transduction →NCIB3610
LSB377 (<i>B.subtilis</i>)	NCIB3610 <i>ΔphoA::spc</i>	SPP1 transduction →NCIB3610

Supplementary Table 3. Primers used in the study.

Primer #	Primer name	Primer sequence
oLS025	spc fwd	GACTGGCTCGCTAATAACGTAAACGTGACTGGCAAGAG
oLS026	spc rev	CGTAGCGAGGGCAAGGGTTTATTGTTTTCTAAAATCTG
oLS295	phoA up fwd	GCCGTTAATCGATAAAGTTTGTCC
oLS298	phoA do rev	GGAAACCAAGATTATGAATGAGG
oLS643	sinI up fwd	AAACAAAATGGGAGATTTACCAG
oLS646	sinI do rev	GCAAGCGGTAAAGTCAATGTAGC
oLS654	sinR do rev	TTAGTTGGAGGAGGAACATGGG
oLS785	sinI up rev (spc)	CGTTACGTTATTAGCGAGCCAGTCTTCTTCATGCAGTTTCTCCTCC
oLS786	sinI do fwd (spc)	CAATAAACCCCTTGCCCTCGCTACGCCGTAAATCCTTTCTGAATGTGC
oLS787	sinR up rev (spc)	CGTTACGTTATTAGCGAGCCAGTCTGGCCAATCAATGTCATCACC
oLS788	sinR do fwd (spc)	CAATAAACCCCTTGCCCTCGCTACGAGTAGTGCCTGAGCAGAGGC
oLS801	phoA up rev (spc)	CGTTACGTTATTAGCGAGCCAGTCAAGGACAGAAACAGCGGCGATTGG
oLS802	phoA do fwd (spc)	CAATAAACCCCTTGCCCTCGCTACGGATTGATTAAACAATACGGACCAGGC