

Supplementary information

Genetically similar temperate phages differentially affect the physiology of their shared host

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Table S1. Oligonucleotides used in this study

Primer name	Primer sequence (5'-3')	Gene target	Purpose/experiment
alaS_577for	GGAGAGAGTGACGCATGGAT	alanine tRNA hydrolase	Host reference gene
alaS_719rev	CAGCTGTCGAGATGGACGTA	alanine tRNA hydrolase	Host reference gene
map_164for	TCACGCAGATGATCGAAGAC	methionine aminopeptidase	Host reference gene
map_334rev	CATCGACAATTACGGTGACG	methionine aminopeptidase	Host reference gene
rpoC_3196for	AAAAAGTCCGTCGTGGTGAC	RNA polymerase	Host reference gene
rpoC_3356rev	AACGGCATGTCTTCCATAGG	RNA polymerase	Host reference gene
2047LexA_for	ACTCGATCTGCTGGCCTTTA	<i>lexA</i> transcriptional regulator	Host SOS response
2047LexA_rev	TCGGGCAGTTTCACTACCTC	<i>lexA</i> transcriptional regulator	Host SOS response
2047RecA_for	CTGATTTCCCAGCCTGACAC	recombinase <i>recA</i>	Host SOS response
2047RecA_rev	AGCCTGTCAGCTTACGCATT	recombinase <i>recA</i>	Host SOS response
Pro PEPG_for	CTATGAAGGCATGGGCGATA	endolysin	Φ-NYA Induction
Pro PEPG_rev	GGCGATCGATCCAACACT	endolysin	Φ-NYA Induction
Pro Rad_for	TGGCCCTCTACGACAAAGAC	Rad52/22 dsDNA break repair	Φ-NYA Induction
Pro Rad_rev	TCGTTTAGTTTCGTGCTGCAT	Rad52/22 dsDNA break repair	Φ-NYA Induction
Pro SSB_for	GCCTTGGAACGTCAATTCAT	ssDNA binding protein (<i>ssb</i>)	Φ-NYA Induction
Pro SSB_rev	ACAACGGCAAGGACAAGAAC	ssDNA binding protein (<i>ssb</i>)	Φ-NYA Induction
Pro rep_rev	CCGTGCCATTATTTGGCTAT	phage repressor	Φ-NYA Induction
Pro rep_rev	GCTAATGTGCTGGGCCTTAG	phage repressor	Φ-NYA Induction
int772_for	TGGGTCATTCTAACGCTGGT	integrase	Phage lysogeny establishment
int937_rev	ATTCCACAATCTCAAGCGCC	integrase	Phage lysogeny establishment
47AHTH_XRE_for	CAAAAGCTGACGCAGACTCA	phage repressor	Φ-47A lysogeny establishment
47AHTH_XRE_rev	ATATCCCGCATCAGCTCAAC	phage repressor	Φ-47A lysogeny establishment
47A PEPG_for	GTGTTTGCATAATCGGCAAG	endolysin	Φ-47A replication
47A PEPG_rev	CGGATCTGGAAAACCAGCTT	endolysin	Φ-47A replication
2047PP1_for	TATTCATAGCGAGGCGCAGT	endolysin	Φ-NYA enumeration
2047PP1_rev	ATACCTGCCCCAACGTCACAG	endolysin	Φ-NYA enumeration
2047A-C_for	CCCATGTGTATGTCGCCTCT	endolysin	Φ-47A enumeration
2047A-C_rev	CAGCGTTGAAAAAGGCTCTG	endolysin	Φ-47A enumeration

jxn761U_for	GGCCAGCATAACCGTTTCC	histidine kinase	Phage Integration site identification
int937_rev	ATTCCACAATCTCAAGCGCC	integrase	Phage Integration site identification
jxn1105D_rev	TGTCGCCAACACCTCTACC	HTH transcriptional regulator	Phage Integration site identification
jxn1105D_for	GGGAGGCATGAGCGTAGAA	hypothetical protein	Phage Integration site identification

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Table S2. Frequency (percentage) of Φ -A PCR positive colonies from superinfection studies (MOI 0.06)

Time (h.p.i.)	Replicate 1	Replicate 2	Replicate 3	Average
4	0	5	20	8
8	15	10	30	18

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38 Table S3. Comstat2 data analysis

	Biomass	Maximum thickness	Roughness coefficient	Thickness distribution	39
Organism name and Z stack field of view number	Biomass ($\mu\text{m}^3/\mu\text{m}^2$):	Maximum thickness (μm):	Roughness Coefficient (Ra^*):	Average thickness (Entire area) (μm):	Average thickness (Biomass) (μm): 40
<i>Sulfitobacter</i> sp. strain CB-A. Z stack field of view: 1	1.18876	5.4879	1.00278	2.46208	4.91842
<i>Sulfitobacter</i> sp. strain CB-A. Z stack field of view: 2	1.46763	6.1336	1.00804	2.03385	3.78813
<i>Sulfitobacter</i> sp. strain CB-A. Z stack field of view: 3	1.71986	5.4879	0.7344	3.01986	4.72083
<i>Sulfitobacter</i> sp. strain CB-A. Z stack field of view: 4	0.11164	13.2356	1.90794	0.32584	7.07645
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 1	0.53438	3.5706	1.28152	0.63001	1.73872
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 2	0.32996	5.6534	1.73059	0.60152	4.44958
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 3	0.53916	5.6534	1.36748	0.74707	2.34794
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 4	0.22374	5.6534	1.73358	0.66207	4.95401
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 5	2.31132	5.6534	0.22504	4.5969	4.82112
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 6	0.34321	5.6534	1.56043	0.39356	1.78002
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 7	0.14941	5.6534	1.85548	0.29573	4.09248
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 8	0.32476	5.6534	1.68187	0.73548	4.58514
<i>Sulfitobacter</i> sp. strain CB-D. Z stack field of view: 9	0.31593	5.6534	1.62062	0.47826	2.51737

42 **Table S4. Optical density (OD 540 nm) data for ϕ -A infected, ϕ -D infected, and uninfected, *Sulfitobacter* sp. CB-D cells as**
 43 **shown in Fig 2A**

	Control						Φ -A Infected						Φ -D Infected				
Time p.i. (h)	Rep 1	Rep 2	Rep 3	Average	Std dev		Rep 1	Rep 2	Rep 3	Average	Std Dev		Rep 1	Rep 2	Rep 3	Average	Std dev
0	0.170	0.170	0.173	0.171	0.002		0.183	0.172	0.171	0.175	0.007		0.171	0.170	0.172	0.171	0.001
1	0.238	0.234	0.237	0.236	0.002		0.247	0.237	0.234	0.239	0.007		0.221	0.220	0.219	0.220	0.001
2	0.291	0.294	0.289	0.291	0.003		0.300	0.286	0.285	0.290	0.008		0.274	0.273	0.272	0.273	0.001
3	0.348	0.346	0.350	0.348	0.002		0.362	0.340	0.341	0.348	0.012		0.327	0.323	0.325	0.325	0.002
4	0.411	0.411	0.414	0.412	0.002		0.426	0.404	0.411	0.414	0.011		0.390	0.384	0.386	0.387	0.003
5	0.482	0.480	0.479	0.480	0.002		0.484	0.462	0.466	0.471	0.012		0.456	0.451	0.452	0.453	0.003
6	0.537	0.541	0.536	0.538	0.003		0.524	0.506	0.505	0.512	0.011		0.509	0.505	0.506	0.507	0.002
7	0.585	0.581	0.577	0.581	0.004		0.554	0.532	0.538	0.541	0.011		0.551	0.546	0.545	0.547	0.003
8	0.636	0.631	0.640	0.636	0.005		0.527	0.503	0.506	0.512	0.013		0.598	0.586	0.584	0.589	0.008
9	0.630	0.626	0.625	0.627	0.003		0.457	0.438	0.439	0.445	0.011		0.643	0.645	0.630	0.639	0.008
10	0.622	0.614	0.618	0.618	0.004		0.431	0.410	0.413	0.418	0.011		0.640	0.634	0.642	0.639	0.004
11	0.613	0.617	0.618	0.616	0.003		0.410	0.397	0.392	0.400	0.009		0.637	0.624	0.634	0.632	0.007
12	0.612	0.613	0.616	0.614	0.002		0.398	0.380	0.377	0.385	0.011		0.637	0.624	0.633	0.631	0.007
24	0.595	0.594	0.599	0.596	0.003		0.248	0.231	0.221	0.233	0.014		0.614	0.604	0.609	0.609	0.005

53 **Table S5. Optical density (OD 540 nm) data for ϕ -A infected, ϕ -D infected, and uninfected, *Sulfitobacter* sp. CB-A cells as**
54 **shown in Fig 2B**

	Control						Φ -A Infected						Φ -D Infected				
Time p.i. (h)	Rep 1	Rep 2	Rep 3	Uninfected controls	Stdv		Rep 1	Rep 2	Rep 3	Φ -A infected	Stdv		Rep 1	Rep 2	Rep 3	Φ -D infected	Stdv
0	0.151	0.153	0.175	0.16	0.013		0.154	0.153	0.156	0.154	0.002		0.154	0.155	0.157	0.155	0.002
1	0.213	0.214	0.244	0.224	0.018		0.214	0.215	0.216	0.215	0.001		0.192	0.186	0.189	0.189	0.003
2	0.263	0.262	0.292	0.272	0.017		0.263	0.269	0.268	0.267	0.003		0.226	0.224	0.223	0.224	0.002
3	0.323	0.319	0.349	0.33	0.016		0.319	0.323	0.326	0.323	0.004		0.254	0.254	0.256	0.255	0.001
4	0.385	0.381	0.415	0.394	0.019		0.38	0.382	0.386	0.383	0.003		0.247	0.243	0.249	0.246	0.003
5	0.452	0.45	0.48	0.461	0.017		0.447	0.439	0.452	0.446	0.007		0.245	0.245	0.241	0.244	0.002
6	0.502	0.497	0.536	0.512	0.021		0.494	0.499	0.502	0.498	0.004		0.251	0.256	0.248	0.252	0.004
7	0.547	0.535	0.577	0.553	0.022		0.54	0.54	0.543	0.541	0.002		0.247	0.267	0.242	0.252	0.013
8	0.604	0.594	0.642	0.613	0.025		0.601	0.595	0.602	0.599	0.004		0.243	0.271	0.255	0.256	0.014
9	0.609	0.597	0.637	0.614	0.021		0.598	0.596	0.612	0.602	0.009		0.261	0.279	0.258	0.266	0.011
10	0.592	0.589	0.63	0.604	0.023		0.586	0.594	0.597	0.592	0.006		0.235	0.264	0.247	0.249	0.015
11	0.59	0.586	0.62	0.599	0.019		0.581	0.591	0.596	0.589	0.008		0.255	0.246	0.234	0.245	0.011
12	0.586	0.582	0.625	0.598	0.024		0.582	0.585	0.595	0.587	0.007		0.242	0.243	0.253	0.246	0.006
24	0.579	0.562	0.605	0.582	0.022		0.562	0.591	0.566	0.573	0.016		0.258	0.292	0.285	0.278	0.018

64 **Table S6. qPCR data (A phage primer set) for data shown in Fig 2C and D.**

Primer AC._										
			Rep A			Rep B			Rep C	
		Time	average	Stdv		average	Stdv		average	Stdv
CB-D	A only	T0	2.54E+07	3.35E+06		1.76E+07	3.83E+06		1.36E+07	4.14E+06
		T6	6.27E+10	3.71E+09		1.26E+10	3.10E+09		2.21E+10	1.73E+09
		T9	1.08E+12	9.20E+10		1.17E+11	2.14E+10		1.93E+11	7.07E+09
		T24	2.13E+12	2.88E+11		1.86E+11	1.31E+10		3.52E+11	5.09E+10
CB-A	A only	T0	1.92E+08	2.05E+07		1.32E+08	1.58E+07		7.09E+07	5.95E+06
		T6	2.96E+08	4.53E+07		2.57E+08	5.41E+07		1.81E+08	2.49E+07
		T9	1.63E+08	3.44E+07		7.47E+07	2.18E+07		8.14E+07	2.15E+07
		T24	1.61E+08	1.01E+07		9.69E+07	2.99E+07		4.40E+07	5.36E+06
CB-A	Control	T0	1.66E+08	1.37E+07		9.28E+07	2.65E+07		4.99E+07	1.82E+06
		T6	3.68E+08	1.91E+07		1.84E+08	1.88E+07		2.53E+08	1.52E+07
		T9	1.06E+08	5.31E+06		9.38E+07	8.96E+06		5.15E+07	6.81E+06
		T24	9.62E+07	1.34E+07		5.69E+07	3.38E+06		2.97E+07	3.47E+06
CB-A	D only	T0	1.49E+08	3.80E+07		3.21E+07	5.07E+06		3.40E+07	4.79E+06
		T6	1.36E+10	5.45E+08		7.78E+09	1.22E+09		4.61E+09	7.71E+07
		T9	4.54E+10	3.83E+09		7.23E+09	1.67E+09		1.30E+10	2.12E+09
		T24	4.43E+10	2.46E+09		8.87E+09	2.02E+09		6.99E+09	1.51E+08

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Table S7. qPCR data (D phage primer set) for data shown in Fig 2C and D.

Primer PP1										
			Rep A			Rep B			Rep C	
		time	average	Stdv		average	Stdv		average	Stdv
CB-D	A only	T0	1.74E+08	1.54E+07		5.97E+07	7.96E+06		1.31E+08	3.69E+07
		T6	1.97E+09	5.14E+08		1.21E+09	7.53E+07		1.65E+09	1.23E+08
		T9	1.49E+10	2.71E+09		1.68E+10	6.32E+08		1.18E+10	3.23E+08
		T24	2.37E+10	2.76E+09		2.38E+10	3.59E+09		1.53E+10	8.55E+08
CB-D	Control	T0	2.40E+08	2.66E+07		6.59E+07	6.65E+06		1.18E+08	7.95E+06
		T6	4.91E+08	1.08E+08		1.10E+08	1.53E+07		2.91E+08	4.22E+07
		T9	1.53E+08	3.11E+06		9.39E+07	1.26E+07		7.25E+07	7.97E+06
		T24	1.41E+08	1.42E+07		9.70E+07	6.63E+06		9.14E+07	6.05E+06
CB-D	D only	T0	1.22E+09	8.24E+07		3.26E+08	5.17E+07		4.65E+08	5.27E+07
		T6	1.52E+09	1.31E+08		4.25E+08	7.62E+07		5.85E+08	1.06E+08
		T9	1.05E+09	2.23E+08		5.70E+08	5.71E+07		4.86E+08	5.23E+07
		T24	1.17E+09	7.96E+07		6.77E+08	1.03E+08		4.48E+08	9.67E+07
CB-A	D only	T0	5.78E+08	6.59E+07		1.53E+08	1.28E+07		2.85E+08	3.16E+07
		T6	1.88E+11	2.75E+10		7.36E+10	4.61E+09		7.52E+10	1.23E+09
		T9	1.78E+11	4.15E+10		1.77E+11	1.63E+10		1.94E+11	2.46E+10
		T24	1.43E+11	3.55E+10		1.65E+11	1.43E+10		8.34E+10	6.09E+08

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84 **Table S8. RT qPCR data for Fig 3****phiA infected CB-D cultures**

time point (-rep)	gene	C(t)	time point (-rep)	gene	C(t)	time point (-rep)	gene	C(t)
T0-1	1 map	23.03	T3-1	1 map	22.9	T6-1	1 map	27.83
T0-1	1 map	22.49	T3-1	1 map	22.5	T6-1	1 map	27.68
T0-1	1 map	22.33	T3-1	1 map	22.5	T6-1	1 map	27.5
T0-1	2 alaS	23.67	T3-1	2 alaS	23.3	T6-1	2 alaS	28.03
T0-1	2 alaS	23.49	T3-1	2 alaS	23.2	T6-1	2 alaS	27.8
T0-1	2 alaS	23.10	T3-1	2 alaS	22.9	T6-1	2 alaS	27.77
T0-1	3 rpoC	17.99	T3-1	3 rpoC	20.1	T6-1	3 rpoC	24.32
T0-1	3 rpoC	17.68	T3-1	3 rpoC	20	T6-1	3 rpoC	24.22
T0-1	3 rpoC	17.66	T3-1	3 rpoC	20.1	T6-1	3 rpoC	24.27
T0-1	4 RecA	21.80	T3-1	4 RecA	20.5	T6-1	4 RecA	25.36
T0-1	4 RecA	21.69	T3-1	4 RecA	20.1	T6-1	4 RecA	25.13
T0-1	4 RecA	21.54	T3-1	4 RecA	20	T6-1	4 RecA	25.09
T0-1	5 LexA	24.65	T3-1	5 LexA	22.1	T6-1	5 LexA	26.74
T0-1	5 LexA	24.05	T3-1	5 LexA	21.4	T6-1	5 LexA	26.45
T0-1	5 LexA	23.50	T3-1	5 LexA	21.3	T6-1	5 LexA	25.94
T0-1	6 47A-PEPG	26.03	T3-1	6 47A-PEPG	16.2	T6-1	6 47A-PEPG	19.98
T0-1	6 47A-PEPG	25.66	T3-1	6 47A-PEPG	15.6	T6-1	6 47A-PEPG	19.35
T0-1	6 47A-PEPG	25.16	T3-1	6 47A-PEPG	15.2	T6-1	6 47A-PEPG	18.93
T0-1	7 47A-XRE	25.75	T3-1	7 47A-XRE	19.2	T6-1	7 47A-XRE	23.47
T0-1	7 47A-XRE	25.03	T3-1	7 47A-XRE	18.5	T6-1	7 47A-XRE	22.94
T0-1	7 47A-XRE	25.32	T3-1	7 47A-XRE	19.1	T6-1	7 47A-XRE	23.37
T0-1	8 47A-EXO	23.69	T3-1	8 47A-EXO	16.5	T6-1	8 47A-EXO	20.94

T0-1	8 47A-EXO	22.69	T3-1	8 47A-EXO	15.9	T6-1	8 47A-EXO	20.34
T0-1	8 47A-EXO	22.72	T3-1	8 47A-EXO	15.7	T6-1	8 47A-EXO	20.24
T0-1	9 Pro PEPG	23.05	T3-1	9 Pro PEPG	19	T6-1	9 Pro PEPG	22.66
T0-1	9 Pro PEPG	22.71	T3-1	9 Pro PEPG	18.6	T6-1	9 Pro PEPG	22.06
T0-1	9 Pro PEPG	22.36	T3-1	9 Pro PEPG	18.1	T6-1	9 Pro PEPG	21.85
T0-1	10 Pro Rad	25.41	T3-1	10 Pro Rad	19.8	T6-1	10 Pro Rad	23.75
T0-1	10 Pro Rad	24.59	T3-1	10 Pro Rad	18.9	T6-1	10 Pro Rad	22.89
T0-1	10 Pro Rad	24.83	T3-1	10 Pro Rad	19.1	T6-1	10 Pro Rad	23.14
T0-1	11 Pro SSB	25.19	T3-1	11 Pro SSB	18.7	T6-1	11 Pro SSB	23.07
T0-1	11 Pro SSB	24.72	T3-1	11 Pro SSB	18.3	T6-1	11 Pro SSB	22.51
T0-1	11 Pro SSB	24.34	T3-1	11 Pro SSB	18.2	T6-1	11 Pro SSB	22.28
T0-2	1 map	21.60	T3-2	1 map	21.9	T6-2	1 map	26.64
T0-2	1 map	21.17	T3-2	1 map	21.7	T6-2	1 map	26.71
T0-2	1 map	22.20	T3-2	1 map	22.3	T6-2	1 map	27.28
T0-2	2 alaS	22.69	T3-2	2 alaS	22.8	T6-2	2 alaS	27.27
T0-2	2 alaS	22.74	T3-2	2 alaS	22.9	T6-2	2 alaS	26.95
T0-2	2 alaS	22.92	T3-2	2 alaS	23	T6-2	2 alaS	27.11
T0-2	3 rpoC	17.13	T3-2	3 rpoC	19.7	T6-2	3 rpoC	23.38
T0-2	3 rpoC	16.78	T3-2	3 rpoC	19.4	T6-2	3 rpoC	22.92
T0-2	3 rpoC	16.97	T3-2	3 rpoC	19.7	T6-2	3 rpoC	23.37
T0-2	4 RecA	21.00	T3-2	4 RecA	19.9	T6-2	4 RecA	24.22
T0-2	4 RecA	20.72	T3-2	4 RecA	19.6	T6-2	4 RecA	24.21
T0-2	4 RecA	21.20	T3-2	4 RecA	20.1	T6-2	4 RecA	24.6
T0-2	5 LexA	23.47	T3-2	5 LexA	21.1	T6-2	5 LexA	25.33
T0-2	5 LexA	23.81	T3-2	5 LexA	21.4	T6-2	5 LexA	25.71
T0-2	5 LexA	23.48	T3-2	5 LexA	21.4	T6-2	5 LexA	25.13
T0-2	6 47A-PEPG	26.06	T3-2	6 47A-PEPG	15	T6-2	6 47A-PEPG	18.39
T0-2	6 47A-PEPG	25.86	T3-2	6 47A-PEPG	15	T6-2	6 47A-PEPG	18.35
T0-2	6 47A-PEPG	26.05	T3-2	6 47A-PEPG	15	T6-2	6 47A-PEPG	18.22
T0-2	7 47A-XRE	24.01	T3-2	7 47A-XRE	18.7	T6-2	7 47A-XRE	22.8
T0-2	7 47A-XRE	24.24	T3-2	7 47A-XRE	18.9	T6-2	7 47A-XRE	22.85

T0-2	7 47A-XRE	24.48	T3-2	7 47A-XRE	19.2	T6-2	7 47A-XRE	23.05
T0-2	8 47A-EXO	22.53	T3-2	8 47A-EXO	15.5	T6-2	8 47A-EXO	19.46
T0-2	8 47A-EXO	22.45	T3-2	8 47A-EXO	15.3	T6-2	8 47A-EXO	19.39
T0-2	8 47A-EXO	22.67	T3-2	8 47A-EXO	15.5	T6-2	8 47A-EXO	19.54
T0-2	9 Pro PEPG	22.82	T3-2	9 Pro PEPG	18.7	T6-2	9 Pro PEPG	21.75
T0-2	9 Pro PEPG	22.95	T3-2	9 Pro PEPG	18.9	T6-2	9 Pro PEPG	21.97
T0-2	9 Pro PEPG	22.95	T3-2	9 Pro PEPG	18.7	T6-2	9 Pro PEPG	21.82
T0-2	10 Pro Rad	24.85	T3-2	10 Pro Rad	18.7	T6-2	10 Pro Rad	22.79
T0-2	10 Pro Rad	24.09	T3-2	10 Pro Rad	18.5	T6-2	10 Pro Rad	21.92
T0-2	10 Pro Rad	24.95	T3-2	10 Pro Rad	19.2	T6-2	10 Pro Rad	22.68
T0-2	11 Pro SSB	24.79	T3-2	11 Pro SSB	18.6	T6-2	11 Pro SSB	22.18
T0-2	11 Pro SSB	24.56	T3-2	11 Pro SSB	18.2	T6-2	11 Pro SSB	21.86
T0-2	11 Pro SSB	24.68	T3-2	11 Pro SSB	18.5	T6-2	11 Pro SSB	22.08
T0-3	1 map	22.82	T3-3	1 map	23	T6-3	1 map	27.52
T0-3	1 map	23.34	T3-3	1 map	23.3	T6-3	1 map	27.9
T0-3	1map	23.08	T3-3	1 map	23.14	T6-3	1 map	27.71
T0-3	2 alaS	23.35	T3-3	2 alaS	23.2	T6-3	2 alaS	27.93
T0-3	2 alaS	23.74	T3-3	2 alaS	23.8	T6-3	2 alaS	27.72
T0-3	2 alaS	23.55	T3-3	2 alaS	23.52	T6-3	2 alaS	27.83
T0-3	3 rpoC	17.89	T3-3	3 rpoC	20.5	T6-3	3 rpoC	23.9
T0-3	3 rpoC	18.05	T3-3	3 rpoC	20.7	T6-3	3 rpoC	24.1
T0-3	3 rpoC	17.97	T3-3	3 rpoC	20.59	T6-3	3 rpoC	24.00
T0-3	4 RecA	23.08	T3-3	4 RecA	21.4	T6-3	4 RecA	25.4
T0-3	4 RecA	21.23	T3-3	4 RecA	20.2	T6-3	4 RecA	24.52
T0-3	4 RecA	22.03	T3-3	4 RecA	21.3	T6-3	4 RecA	25.13
T0-3	5 LexA	24.90	T3-3	5 LexA	21.9	T6-3	5 LexA	25.99
T0-3	5 LexA	23.99	T3-3	5 LexA	21.4	T6-3	5 LexA	25.61
T0-3	5 LexA	24.83	T3-3	5 LexA	21.8	T6-3	5 LexA	26.82
T0-3	6 47A-PEPG	27.53	T3-3	6 47A-PEPG	16.1	T6-3	6 47A-PEPG	18.77
T0-3	6 47A-PEPG	27.04	T3-3	6 47A-PEPG	15.6	T6-3	6 47A-PEPG	18.63
T0-3	6 47A-PEPG	27.62	T3-3	6 47A-PEPG	16.2	T6-3	6 47A-PEPG	19.05

T0-3	7 47A-XRE	23.70	T3-3	7 47A-XRE	18.2	T6-3	7 47A-XRE	22.08
T0-3	7 47A-XRE	24.90	T3-3	7 47A-XRE	19.4	T6-3	7 47A-XRE	23.49
T0-3	7 47A-XRE	25.38	T3-3	7 47A-XRE	19.9	T6-3	7 47A-XRE	23.62
T0-3	8 47A-EXO	23.37	T3-3	8 47A-EXO	15.8	T6-3	8 47A-EXO	19.7
T0-3	8 47A-EXO	23.36	T3-3	8 47A-EXO	16	T6-3	8 47A-EXO	19.89
T0-3	8 47A-EXO	24.51	T3-3	8 47A-EXO	17.2	T6-3	8 47A-EXO	20.77
T0-3	9 Pro PEPG	23.47	T3-3	9 Pro PEPG	19	T6-3	9 Pro PEPG	22.11
T0-3	9 Pro PEPG	23.76	T3-3	9 Pro PEPG	19.5	T6-3	9 Pro PEPG	22.29
T0-3	9 Pro PEPG	23.23	T3-3	9 Pro PEPG	18.8	T6-3	9 Pro PEPG	21.78
T0-3	10 Pro Rad	25.61	T3-3	10 Pro Rad	19.5	T6-3	10 Pro Rad	22.92
T0-3	10 Pro Rad	26.16	T3-3	10 Pro Rad	20.1	T6-3	10 Pro Rad	23.54
T0-3	10 Pro Rad	26.11	T3-3	10 Pro Rad	20.2	T6-3	10 Pro Rad	23.37
T0-3	11 Pro SSB	25.10	T3-3	11 Pro SSB	18.8	T6-3	11 Pro SSB	22.3
T0-3	11 Pro SSB	26.09	T3-3	11 Pro SSB	19.5	T6-3	11 Pro SSB	23.17
T0-3	11 Pro SSB	26.30	T3-3	11 Pro SSB	19.8	T6-3	11 Pro SSB	23.57

Non-infected controls

time point (-rep)	gene	C(t)	time point (-rep)	gene	C(t)	time point (-rep)	gene	C(t)
T0-1	1 map	26.34	T3-1	1 map	25.10	T6-1	1 map	25.25
T0-1	1 map	26.09	T3-1	1 map	24.98	T6-1	1 map	25.05
T0-1	1 map	26.03	T3-1	1 map	24.80	T6-1	1 map	24.95
T0-1	2 alaS	26.34	T3-1	2 alaS	26.23	T6-1	2 alaS	25.05
T0-1	2 alaS	25.72	T3-1	2 alaS	26.19	T6-1	2 alaS	24.58
T0-1	2 alaS	25.52	T3-1	2 alaS	26.19	T6-1	2 alaS	24.46
T0-1	3 rpoC	21.50	T3-1	3 rpoC	21.79	T6-1	3 rpoC	20.31
T0-1	3 rpoC	21.17	T3-1	3 rpoC	21.59	T6-1	3 rpoC	20.10
T0-1	3 rpoC	21.34	T3-1	3 rpoC	21.69	T6-1	3 rpoC	20.08
T0-1	4 RecA	25.32	T3-1	4 RecA	23.38	T6-1	4 RecA	23.55
T0-1	4 RecA	24.78	T3-1	4 RecA	23.19	T6-1	4 RecA	22.96

T0-1	4 RecA	24.83	T3-1	4 RecA	23.23	T6-1	4 RecA	23.20
T0-1	5 LexA	26.91	T3-1	5 LexA	26.92	T6-1	5 LexA	25.17
T0-1	5 LexA	26.27	T3-1	5 LexA	26.29	T6-1	5 LexA	24.80
T0-1	5 LexA	25.84	T3-1	5 LexA	25.45	T6-1	5 LexA	24.12
T0-1	8 47A-EXO	25.76	T3-1	8 47A-EXO	25.89	T6-1	8 47A-EXO	20.95
T0-1	8 47A-EXO	25.00	T3-1	8 47A-EXO	24.92	T6-1	8 47A-EXO	20.66
T0-1	8 47A-EXO	25.08	T3-1	8 47A-EXO	25.06	T6-1	8 47A-EXO	20.36
T0-1	9 Pro PEPG	25.01	T3-1	9 Pro PEPG	25.01	T6-1	9 Pro PEPG	21.49
T0-1	9 Pro PEPG	24.51	T3-1	9 Pro PEPG	24.48	T6-1	9 Pro PEPG	21.10
T0-1	9 Pro PEPG	24.32	T3-1	9 Pro PEPG	24.13	T6-1	9 Pro PEPG	20.47
T0-1	10 Pro Rad	27.14	T3-1	10 Pro Rad	27.84	T6-1	10 Pro Rad	24.24
T0-1	10 Pro Rad	26.26	T3-1	10 Pro Rad	26.99	T6-1	10 Pro Rad	23.79
T0-1	10 Pro Rad	26.39	T3-1	10 Pro Rad	27.57	T6-1	10 Pro Rad	24.23
T0-1	11 Pro SSB	26.71	T3-1	11 Pro SSB	28.06	T6-1	11 Pro SSB	23.88
T0-1	11 Pro SSB	25.85	T3-1	11 Pro SSB	27.11	T6-1	11 Pro SSB	23.32
T0-1	11 Pro SSB	25.67	T3-1	11 Pro SSB	26.58	T6-1	11 Pro SSB	23.29
T0-2	1 map	25.76	T3-2	1 map	23.49	T6-2	1 map	23.61
T0-2	1 map	25.49	T3-2	1 map	23.02	T6-2	1 map	23.39
T0-2	1 map	26.45	T3-2	1 map	24.11	T6-2	1 map	24.48
T0-2	2 alaS	26.19	T3-2	2 alaS	24.14	T6-2	2 alaS	23.69
T0-2	2 alaS	25.88	T3-2	2 alaS	24.24	T6-2	2 alaS	23.99
T0-2	2 alaS	26.04	T3-2	2 alaS	24.19	T6-2	2 alaS	23.92
T0-2	3 rpoC	21.00	T3-2	3 rpoC	20.61	T6-2	3 rpoC	19.58
T0-2	3 rpoC	20.98	T3-2	3 rpoC	20.19	T6-2	3 rpoC	19.44
T0-2	3 rpoC	21.13	T3-2	3 rpoC	20.45	T6-2	3 rpoC	19.61
T0-2	4 RecA	24.82	T3-2	4 RecA	21.95	T6-2	4 RecA	22.22
T0-2	4 RecA	24.79	T3-2	4 RecA	21.64	T6-2	4 RecA	23.25
T0-2	4 RecA	25.13	T3-2	4 RecA	22.22	T6-2	4 RecA	22.58
T0-2	5 LexA	26.12	T3-2	5 LexA	24.49	T6-2	5 LexA	23.50
T0-2	5 LexA	26.24	T3-2	5 LexA	25.02	T6-2	5 LexA	23.66
T0-2	5 LexA	26.80	T3-2	5 LexA	24.92	T6-2	5 LexA	23.64

T0-2	8 47A-EXO	25.33	T3-2	8 47A-EXO	23.99	T6-2	8 47A-EXO	20.98
T0-2	8 47A-EXO	25.15	T3-2	8 47A-EXO	23.70	T6-2	8 47A-EXO	21.02
T0-2	8 47A-EXO	25.33	T3-2	8 47A-EXO	23.79	T6-2	8 47A-EXO	21.00
T0-2	9 Pro PEPG	25.26	T3-2	9 Pro PEPG	23.64	T6-2	9 Pro PEPG	20.15
T0-2	9 Pro PEPG	25.37	T3-2	9 Pro PEPG	23.80	T6-2	9 Pro PEPG	20.00
T0-2	9 Pro PEPG	25.18	T3-2	9 Pro PEPG	23.79	T6-2	9 Pro PEPG	20.23
T0-2	10 Pro Rad	27.00	T3-2	10 Pro Rad	26.63	T6-2	10 Pro Rad	23.83
T0-2	10 Pro Rad	26.28	T3-2	10 Pro Rad	26.02	T6-2	10 Pro Rad	24.37
T0-2	10 Pro Rad	27.61	T3-2	10 Pro Rad	27.03	T6-2	10 Pro Rad	24.56
T0-2	11 Pro SSB	26.74	T3-2	11 Pro SSB	26.53	T6-2	11 Pro SSB	23.79
T0-2	11 Pro SSB	26.41	T3-2	11 Pro SSB	26.46	T6-2	11 Pro SSB	23.62
T0-2	11 Pro SSB	26.94	T3-2	11 Pro SSB	26.73	T6-2	11 Pro SSB	23.67
T0-3	1 map	23.66	T3-3	1 map	24.62	T6-3	1 map	24.20
T0-3	1 map	24.36	T3-3	1 map	24.77	T6-3	1 map	24.62
T0-3	1 map	24.01	T3-3	1 map	24.70	T6-3	1 map	24.17
T0-3	2 alaS	24.28	T3-3	2 alaS	24.68	T6-3	2 alaS	24.25
T0-3	2 alaS	24.60	T3-3	2 alaS	24.98	T6-3	2 alaS	24.86
T0-3	2 alaS	24.97	T3-3	2 alaS	25.20	T6-3	2 alaS	23.88
T0-3	3 rpoC	19.06	T3-3	3 rpoC	21.02	T6-3	3 rpoC	20.12
T0-3	3 rpoC	19.42	T3-3	3 rpoC	21.27	T6-3	3 rpoC	20.18
T0-3	3 rpoC	19.52	T3-3	3 rpoC	21.50	T6-3	3 rpoC	19.97
T0-3	4 RecA	23.38	T3-3	4 RecA	23.48	T6-3	4 RecA	22.14
T0-3	4 RecA	22.19	T3-3	4 RecA	22.53	T6-3	4 RecA	22.75
T0-3	4 RecA	22.93	T3-3	4 RecA	22.88	T6-3	4 RecA	24.45
T0-3	5 LexA	24.98	T3-3	5 LexA	25.84	T6-3	5 LexA	23.97
T0-3	5 LexA	24.52	T3-3	5 LexA	25.40	T6-3	5 LexA	25.16
T0-3	5 LexA	25.82	T3-3	5 LexA	26.12	T6-3	5 LexA	21.39
T0-3	8 47A-EXO	23.76	T3-3	8 47A-EXO	24.30	T6-3	8 47A-EXO	21.74
T0-3	8 47A-EXO	23.90	T3-3	8 47A-EXO	24.46	T6-3	8 47A-EXO	21.70
T0-3	8 47A-EXO	25.33	T3-3	8 47A-EXO	25.58	T6-3	8 47A-EXO	22.07
T0-3	9 Pro PEPG	23.30	T3-3	9 Pro PEPG	23.81	T6-3	9 Pro PEPG	20.84

T0-3	9 Pro PEPG	23.70
T0-3	9 Pro PEPG	23.98
T0-3	10 Pro Rad	26.44
T0-3	10 Pro Rad	27.15
T0-3	10 Pro Rad	26.92
T0-3	11 Pro SSB	26.06
T0-3	11 Pro SSB	26.82
T0-3	11 Pro SSB	26.91

T3-3	9 Pro PEPG	24.18
T3-3	9 Pro PEPG	24.52
T3-3	10 Pro Rad	27.21
T3-3	10 Pro Rad	27.82
T3-3	10 Pro Rad	27.95
T3-3	11 Pro SSB	26.83
T3-3	11 Pro SSB	27.89
T3-3	11 Pro SSB	27.85

T6-3	9 Pro PEPG	21.59
T6-3	9 Pro PEPG	25.34
T6-3	10 Pro Rad	25.44
T6-3	10 Pro Rad	25.91
T6-3	10 Pro Rad	25.64
T6-3	11 Pro SSB	24.60
T6-3	11 Pro SSB	25.97
T6-3	11 Pro SSB	22.01
No RT	SBG1	29.88
No RT	SBG1	28.14
No RT	SBG1	28.57
No RT	SBG1	28.88
No RT	SBG1	29.12
No RT	SBG1	28.31
No RT	SBG1	28.65
No RT	SBG1	29.09

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Table S9. Optical density (OD 540 nm) for Fig 4A

CB-D						CB-A					
Time (hours)	Rep 1	Rep 2	Rep 3	CB-D av	Stdev	Time	Rep 1	Rep 2	Rep 3	CB-A av	Stdev
-1	0.064	0.07	0.069	0.068	0.003	-1	0.063	0.065	0.077	0.068	0.008
-2	0.109	0.118	0.116	0.114	0.005	-2	0.105	0.106	0.117	0.109	0.007
0	0.173	0.187	0.179	0.180	0.007	0	0.168	0.164	0.166	0.166	0.002
1	0.267	0.275	0.275	0.272	0.005	1	0.248	0.242	0.245	0.245	0.003
2	0.359	0.388	0.384	0.377	0.016	2	0.325	0.325	0.319	0.323	0.003
3	0.465	0.512	0.506	0.494	0.026	3	0.417	0.441	0.406	0.421	0.018
4	0.63	0.646	0.664	0.647	0.017	4	0.525	0.567	0.523	0.538	0.025
5	0.748	0.792	0.766	0.769	0.022	5	0.628	0.659	0.615	0.634	0.023
6	0.852	0.893	0.866	0.870	0.021	6	0.758	0.791	0.712	0.754	0.040
7	0.928	0.966	0.957	0.950	0.020	7	0.835	0.843	0.776	0.818	0.037
8	1.018	1.054	1.016	1.029	0.021	8	0.9	0.914	0.848	0.887	0.035
27	1.426	1.445	1.46	1.444	0.017	27	0.967	0.978	0.981	0.975	0.007
28	1.448	1.451	1.452	1.450	0.002	28	1.182	0.952	0.951	1.028	0.133
29	1.45	1.46	1.452	1.454	0.005	29	1.228	0.941	0.935	1.035	0.167
30	1.448	1.454	1.432	1.445	0.011	30	1.224	0.946	0.923	1.031	0.168

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108 **Table S10. Optical density (OD 600 nm) for Fig 4B**

	CB-D	CB-A
Rep1	0.043	0.0873
	0.0442	0.0975
	0.0355	0.0682
Rep 2	0.0315	0.0769
	0.0464	0.0826
	0.0421	0.0689
Rep 3	0.0249	0.0917
	0.049	0.0839
	0.0481	0.0796

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Table S11. Optical density (OD 540nm) readings for Fig 5A.

	CB-A	CB-D	Co-Culture
	0.825	1.266	0.681
	0.807	1.122	0.863
	0.888	1.068	0.722
Av	0.84	1.152	0.7553
Stdv	0.02456	0.05909	0.05512

139 **Table S12. qPCR data for Fig 5A and B**

sample type	biological replicate	gene	C(t)	gene copies	gene	C(t)	gene copies
broth culture cell fraction	A	A phage	6.85	6.71E+07	D phage	7.89	3.70E+07
broth culture cell fraction	A	A phage	6.87	6.60E+07	D phage	8.15	3.10E+07
broth culture cell fraction	A	A phage	6.69	7.55E+07	D phage	7.92	3.64E+07
broth culture cell fraction	B	A phage	6.72	7.37E+07	D phage	9.34	1.37E+07
broth culture cell fraction	B	A phage	6.82	6.86E+07	D phage	9.09	1.63E+07
broth culture cell fraction	B	A phage	6.62	7.97E+07	D phage	9.03	1.70E+07
broth culture cell fraction	C	A phage	7.10	5.54E+07	D phage	9.43	1.29E+07
broth culture cell fraction	C	A phage	7.29	4.83E+07	D phage	8.94	1.81E+07
broth culture cell fraction	C	A phage	7.63	3.74E+07	D phage	9.24	1.48E+07
cell free filtrate	A	A phage	9.32	1.05E+07	D phage	12.69	1.39E+06
cell free filtrate	A	A phage	9.52	9.00E+06	D phage	12.56	1.52E+06
cell free filtrate	A	A phage	9.90	6.81E+06	D phage	12.61	1.47E+06
cell free filtrate	B	A phage	10.60	3.92E+06	D phage	12.95	1.16E+06
cell free filtrate	B	A phage	10.30	5.18E+06	D phage	12.87	1.23E+06
cell free filtrate	B	A phage	10.48	4.39E+06	D phage	13.05	1.09E+06
cell free filtrate	C	A phage	9.81	7.25E+06	D phage	13.47	8.18E+05
cell free filtrate	C	A phage	9.77	7.50E+06	D phage	13.03	1.10E+06
cell free filtrate	C	A phage	9.81	7.24E+06	D phage	13.42	8.47E+05
	Standard	A phage	27.08	10	D phage	28.86	10
	Standard	A phage	28.00	10	D phage	28.86	10
	Standard	A phage	24.82	100	D phage	26.66	100

Standard	A phage	24.10	100	D phage	27.34	100
Standard	A phage	21.68	1000	D phage	23.47	1000
Standard	A phage	22.30	1000	D phage	23.67	1000
Standard	A phage	18.70	1.00E+04	D phage	20.24	1.00E+04
Standard	A phage	18.40	1.00E+04	D phage	20.47	1.00E+04
Standard	A phage	16.10	1.00E+05	D phage	17.11	1.00E+05
Standard	A phage	15.70	1.00E+05	D phage	17.15	1.00E+05
Standard	A phage	12.40	1.00E+06	D phage	13.21	1.00E+06
Standard	A phage	12.60	1.00E+06	D phage	13.51	1.00E+06
Standard	A phage	9.41	1.00E+07	D phage	9.48	1.00E+07
Standard	A phage	9.64	1.00E+07	D phage	9.55	1.00E+07
Standard	A phage	5.58	1.00E+08	D phage	6.04	1.00E+08
Standard	A phage	6.33	1.00E+08	D phage	5.96	1.00E+08
Blank	A phage	30.50	1.33	D phage	28.70	24.48
Blank	A phage	30.20	1.683	D phage	28.81	22.67
Blank	A phage	29.30	3.352	D phage	28.13	36.22

biofilm	A	A phage	6.58	D phage	5.65
biofilm	A	A phage	5.41	D phage	5.78
biofilm	A	A phage	6.34	D phage	5.83
biofilm	B	A phage	4.77	D phage	4.27
biofilm	B	A phage	4.99	D phage	4.23
biofilm	B	A phage	4.61	D phage	5.38
biofilm	C	A phage	4.71	D phage	3.11
biofilm	C	A phage	4.59	D phage	2.95
biofilm	C	A phage	4.36	D phage	4.09

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145 **Table S13. Biofilm Crystal Violet assay optical density (OD 600nm) readings for Fig 5B.**

48hr biofilm assay												
rep	Neg-1	Neg-2	Neg-3	CB-D-1	CB-D-2	CB-D-3	CB-A-1	CB-A-2	CB-A-3	Comp-1	Comp-2	Comp-3
A	0.185	0.188	0.193	0.317	0.359	0.326	0.395	0.384	0.398	0.494	0.486	0.493
B	0.18	0.18	0.179	0.299	0.33	0.288	0.357	0.349	0.365	0.466	0.429	0.442
C	0.186	0.19	0.193	0.313	0.337	0.313	0.405	0.382	0.379	0.493	0.441	0.434
D	0.183	0.182	0.187	0.3	0.349	0.311	0.41	0.377	0.386	0.464	0.442	0.434
E	0.194	0.194	0.205	0.332	0.397	0.348	0.429	0.424	0.425	0.500	0.455	0.441
F	0.194	0.188	0.19	0.336	0.374	0.329	0.404	0.419	0.363	0.468	0.416	0.453
G	0.202	0.201	0.214	0.329	0.403	0.356	0.433	0.426	0.417	0.503	0.469	0.458
H	0.2	0.196	0.201	0.35	0.368	0.318	0.382	0.407	0.375	0.473	0.417	0.45

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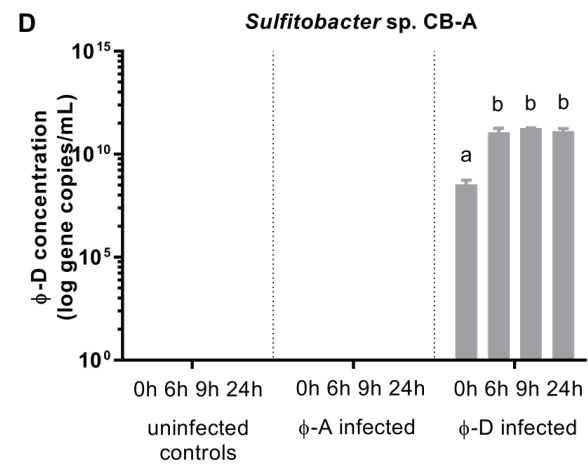
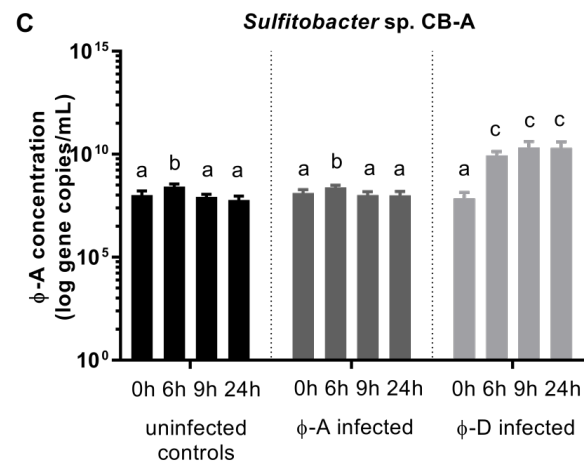
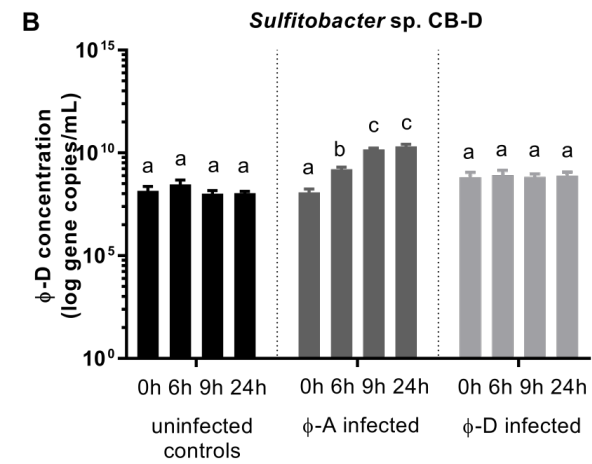
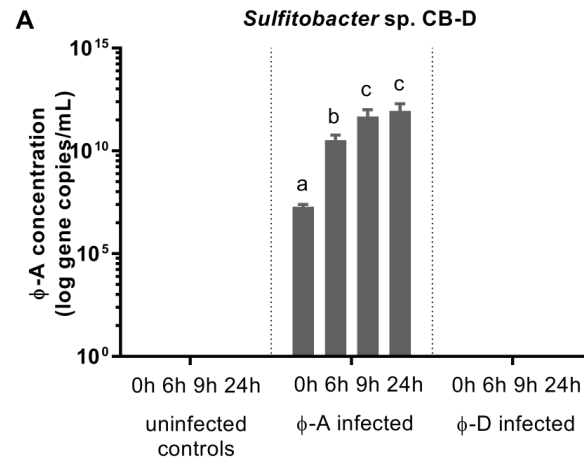
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180 **Fig S1.** Quantification of each phage during superinfection resistance tests. **(A)** ϕ -A and **(B)** ϕ -D gene copies during infection of
181 *Sulfitobacter* sp. strain CB-D. **(C)** ϕ -A and **(D)** ϕ -D gene copies during infection of *Sulfitobacter* sp. strain CB-A. Averages of biological
182 triplicates are reported for all treatments. Error bars represent the standard deviation of the mean. Different letters denote columns with
183 significantly different ($p < 0.05$) phage gene copy numbers within a given plot.

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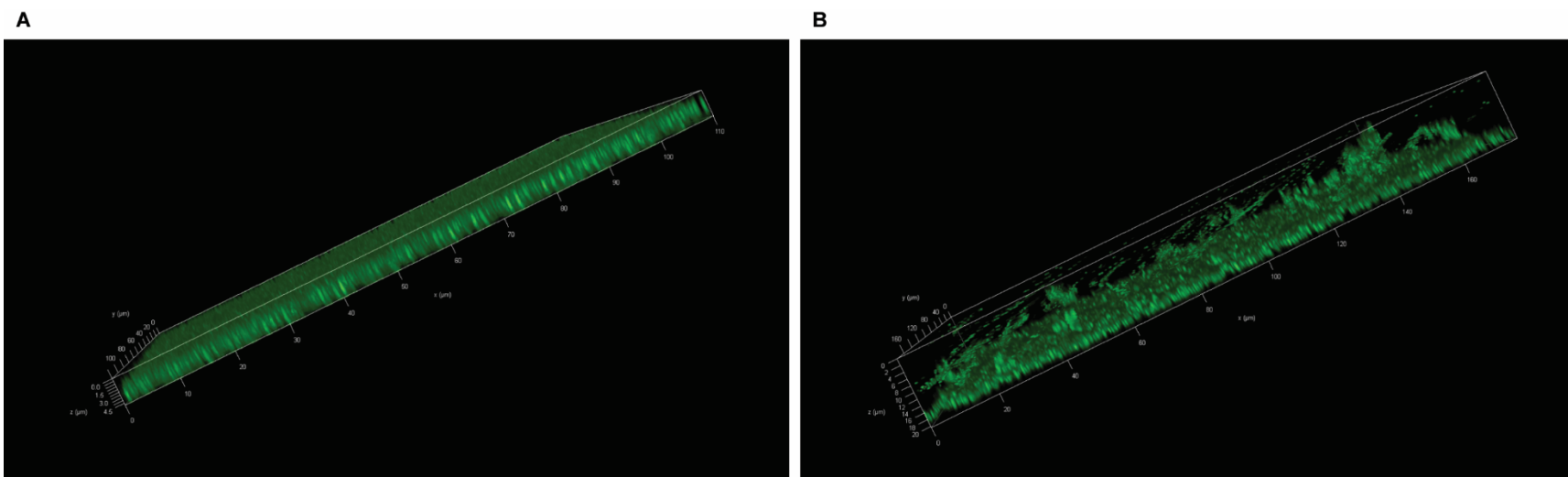


Fig S2. 3D analysis of **(A)** CB-D and **(B)** CB-A biofilms. Overnight cultures of each strain were sub-cultured, diluted, and grown to early exponential phase ($OD_{540nm} = 0.17$). 3 mL of each strain was added to FlouoroDish glass dishes (World Precision Instruments, Inc.) and incubated without agitation overnight at room temperature. Planktonic bacteria were removed by gentle inversion of the glass dishes and washed twice with standard marine media (SMM). Dishes were left to dry for 15 min, then stained with 3mL 25X SYBR Gold (ThermoFisher Scientific SYBRTM Gold Nucleic Acid Gel Stain) for 30 min. Images were generated using confocal laser microscopy and visualized using a Leica SP8 white light Laser Confocal System. Biofilm reconstruction was performed with the Leica Application Suite X (Las X) software. Confocal microscopy methods were greatly adapted from previously described literature (Townesley and Yildiz 2015) and data were analyzed using Comstat2 (Heydorn et al 2000, Vorregaard 2008). Images were taken from biological triplicate cultures and at least three images were generated per sample.

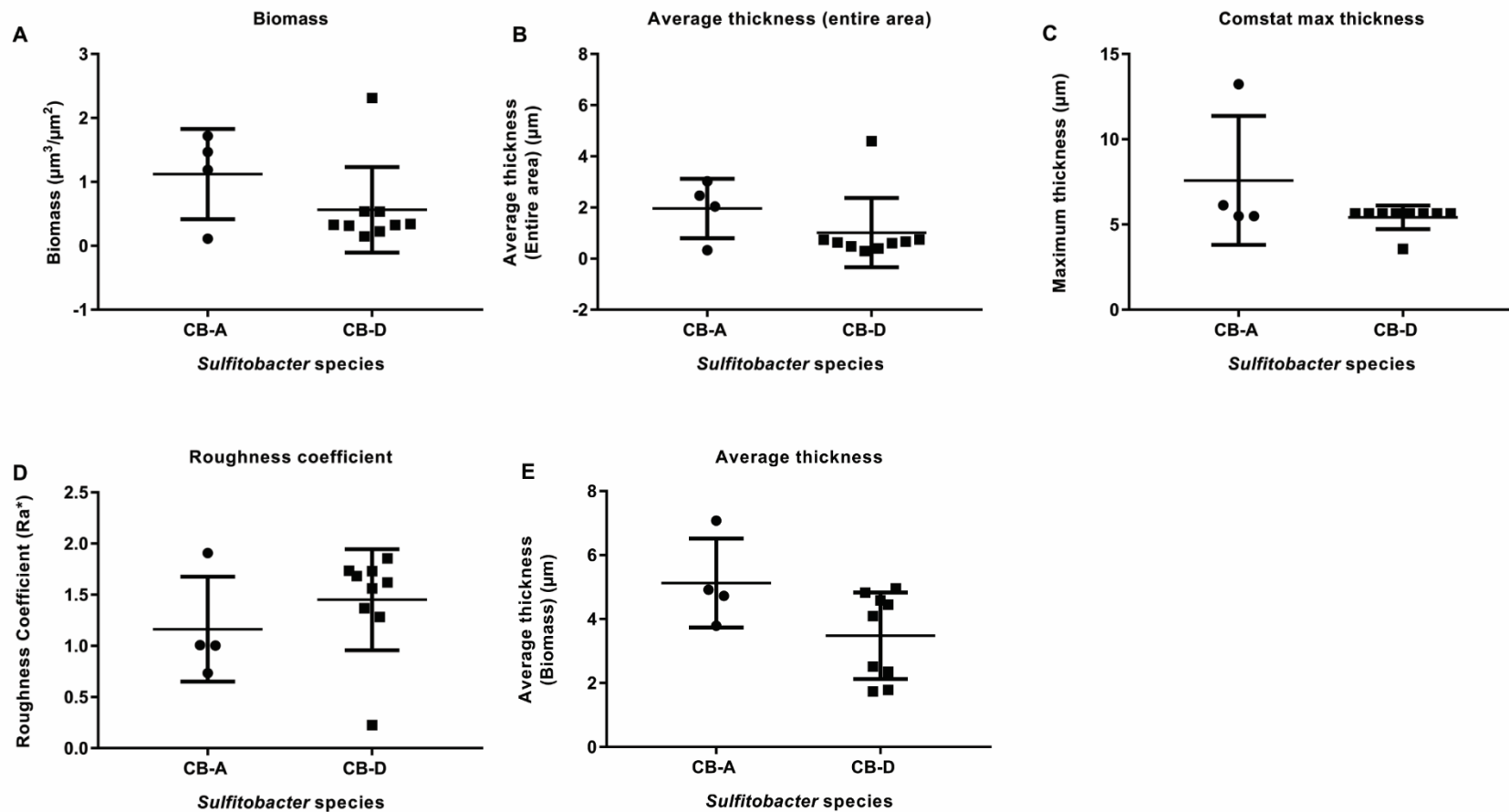
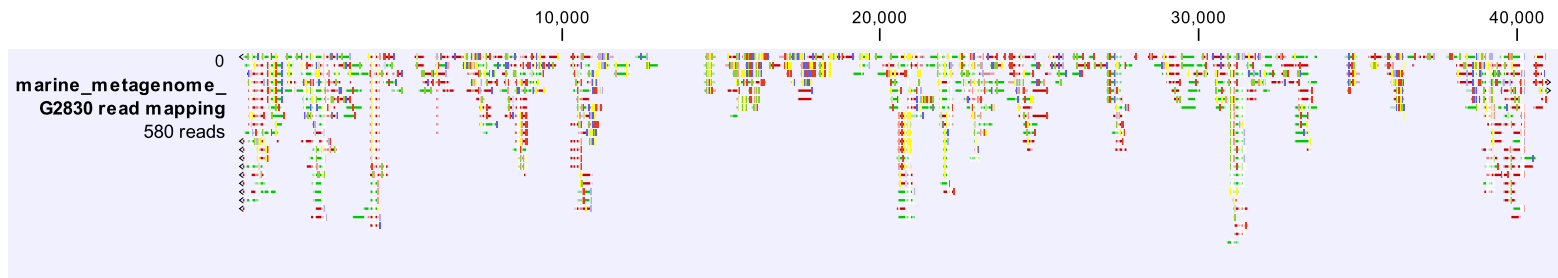


Fig S3. Comstat2 analysis of CB-D and CB-A biofilm confocal microscopy data. Biofilm (A) biomass, (B) average thickness, (C) Comstat max thickness, (D) roughness coefficient, and (E) average thickness. Each data point represents a separate Z stack field of view of the FlouroDish. All parameters showed no significant difference (Student's t-tests; $p < 0.05$).

ϕ -A



ϕ -D

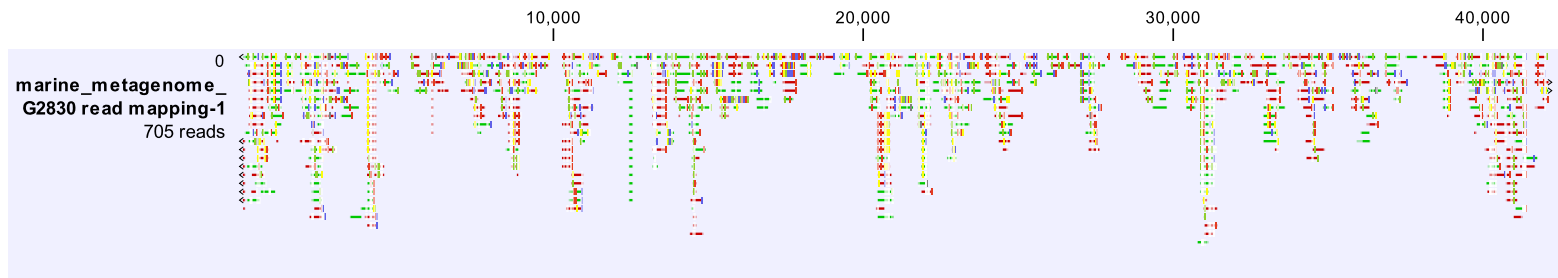


Fig S4. Recruitment of reads from ME-08-09 (~35kb size fraction virome reads) using either ϕ -A or ϕ -D as reference genomes. Read recruitments were done using CLC, default parameters. Single reads mapping in their forward direction are green. Those mapping in reverse direction are red. Non-specific matches are yellow.

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