Supplementary Information

Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere

mesocosm

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Supplementary Fig. 1 Bacterial and viral genome variation across the phytoplankton blooms. Bacteria (51 most abundant genomes), **a**, and viruses **b**, as determined by read based analysis on abundance trimmed data. Legends indicate species represented with dark gray circles denoting those that are labelled in the chart. Light gray circles on middle plot indicate day of sampling. Middle Plot shows phytoplankton abundance and bacterial abundance as reported in Figure 1. **a**, Orange portion of small pie charts above larger species pie charts represents 51 abundant genomes during the experiment and blue represents the remainder of the population. Abundance determined by number of samples above 0.5% of population and by sum of fraction of samples across blooms. Expanded pie charts demonstrate the identity and abundance of these species. Identities derived from bulk 0.2–3 µm samples. **b**, Virus species from 0.025–0.2 µm bulk samples. Error bars indicate s.d. and estimated error in aerosol measurements.



Supplementary Fig. 2 Abundance of draft genomes. 18 bacterial and 6 viral draft genomes determined by assembly based methods. Heatmap indicates fractional abundance of species in the sample. Day of sample is indicated on top columns. For each 9-square group size fraction is indicated from left to right: >3 µm, 0.02 – 3 µm, and 0.025 – 0.2 µm, and top to bottom: Aerosol, SSML, and bulk water compartments. Schematic in upper right corner indicates this sample arrangement. Blanks indicate samples below threshold limits.



Supplementary Fig. 3 Genome spatial coverage trimmed bacterial and viral populations aerosolization distribution. The ratio of fraction of genomes in aerosols to the fraction in bulk plotted against ratio of fraction of genomes in aerosols to those in sea surface is shown for bacteria, **a**, and viruses, **b**, in genome spatial coverage trimmed data sets on select days. The upper right quadrants of **a** and **b** indicate genomes enriched in aerosol relative to both bulk and SSML (A:B and A:S > 1); the lower left quadrants indicates genomes that are primarily waterborne (A:B and A:S < 1). The upper left quadrants indicates genomes enriched relative to bulk but not SSML (A:B > 1, A:S < 1), and the lower right indicates genomes enriched in aerosol relative to bulk (A:B < 1, A:S > 1). The data sets represent **a**, 76 bacterial genomes, and **b**, 30 viral genomes identified by read-based taxonomic assignments trimmed of species with low genome spatial coverage.



Supplementary Fig. 4 Population distribution of aerosolization and surface enrichment data sets. Histograms of all aerosolization factors (AFs) and surface enrichment factors (S:B) for bacteria, **a**–**c**, and viruses, **d**–**f** given by log values. **a**, **d** represent pooled AF and S:B values for abundance trimmed but not coverage trimmed data. **b**, **e** demonstrate day resolved variance in A:B distributions of these partially trimmed data sets. **c**, **f** show the pooled AF and S:B values for the fully trimmed data sets.

		Day	6	8	ŧ	19	2	4	5	28	3	34		0	8	19	24	28	34		
ISS	Phylum	Species AF	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	Avg AF	S:B	S:B	S:B	S:B	S:B	S:B	Avg S:B	Abundance
acterila Instituti	Bacteroidetes	Fusobacterium nucleatum Becteroides vulnatus	1.65	0.73	1.99	2.23	0.34	0,15	1.48	0.26	1.27	0.43	1.05	0.09	2.26	0.89	2.31	5.66	2.92	2.36	U .
hagia		Cyclobacterium marinum	0.22	0.33	0.13	0.13	0.64	0.76	2.11	2.23	0.39	0.54	0.75	2.36	0.66	0.97	0.84	0.95	0.72	1.06	
actenia		Nonlabens dokdonensis	0.14	0.17	0.26	0,27	0.36	0,32	1.00	1,51	0.24	0.68	0.50	1.95	0.82	0.96	1.11	0.66	0.36	0.98	1
		Croceibacter atlanticus	0.29	0.40	0.24	0.25	0.38	0,44	0.72	1.15	0.26	1.46	0.56	1.60	0.72	0.96	0.88	0.62	0.18	0.83	
		Flavobacterium indicum	0.20	0.27	0.20	0.20	0.22	0.24	0.89	1.24	0.25	1.16	0.49	2.32	0.74	0.95	0.91	0.72	0.21	0.98	
		Zunongwengie profunda Collulochaga algingia	0.22	0.30	0.30	0.34	0.31	0.32	0.86	1.14	0.26	0.64	0.47	2.48	0.72	0.89	0.99	0.75	0.41	1.04	
		Cellulophaga lytica	0.31	0.38	0.24	0.24	0.27	0.29	0.78	1.14	0.20	0.82	0.46	1.92	0.81	0.99	0.95	0.69	0.21	0.93	
		Prochlorococcus marinus	0.39	0.35	2.13	1.89	0.51	0.89	2.14	0.98	2.17	1.12	1.26	0.14	1.09	1.13	0.58	2.17	1.94	1.17	1
	Firmicutes	Streptococcus thermophilus	20.5	50.3	10.1	5.66	4.29	1.51	1.55	2.14	10,2	0.24	10.7	0.06	0.41	1.79	2.85	0,73	41.9	7.96	
	Firmicutes	Streptococcus suis	0,12	0.09	14.1	14.2	7.29	6.33	2,19	3.39	12.8	1.11	6.15	1,19	1.39	1.00	1.15	0,65	11.5	2.81	l
	Firmicutes	Staphylococcus epidermidis	7,74	7.40	5.11	3.36	2.87	1.85	1.02	0.97	2.12	0.31	3.27	1.04	1.05	1.52	1.56	1,05	6.87	2.18	í.
ciu Istileria	Antinobacteria	Nakamurella multipartita	0.86	0.79	3,90	3.61	2.52	2.91	2.90	2.74	6.33	2.67	25.7	2.88	1.09	0.00	0.76	1.05	2.57	1.54	i
		Cutibacterium acnes	38.5	26.9	20.5	16.8	12.2	3.15	23.6	10.2	14.4	0.60	16.7	2.38	1.43	1.22	3.89	2.31	23.9	5.86	
		Rothia mucilaginosa	1.05	4.78	212	246	3.96	4.45	19.0	3.87	3.26	0.03	49.8	0.53	0.22	0.85	0.89	4.90	129	22.70	
		Micrococcus luteus	13.9	9.00	26.4	18.7	10.8	6.03	1,40	1.71	9.20	1.01	9.82	0.48	1.54	1.41	1.79	0.82	9.07	2.52	
		Geodermatophilus obscurus	2.22	2.23	12.5	10.1	1.38	1.37	1.12	1.05	1.73	0.20	3.39	0.73	1.00	1.23	1.01	1.07	8.60	2.27	
		Blastococcus saxobsidens	2.33	1.93	24.2	25.5	2.47	3.23	1.55	1.32	2.58	0.21	6.53	1.76	1.21	0.95	0.76	1.18	12.5	3.05	1
		Bodococcus opecus	1,33	1.85	1,38	2.33	2.00	1.58	1.41	0.71	1.53	1.33	1.52	1.10	1.59	1.05	1.90	1,30	1.15	1.96	
acteria		Rhodococcus ervthropolis	5.68	3.35	2.26	2.36	2.04	1.81	3.70	2.03	14.9	10.0	4.82	3.16	1.70	0.96	1.12	1.82	1.49	1.71	
		Mycobacterium chubuense	3.54	5.35	7.41	10.8	2.91	2.95	0.49	0.56	9.05	2.02	4.51	1.67	0.66	0.69	0.99	0.83	4.47	1.55	
		Mycobacterium avium	5.56	6.05	11.2	10.7	3.14	6.25	0.53	1.08	5.27	1.90	5.17	0.92	0.92	1.05	0.50	0.49	2.78	1.11	
		Corynebacterium aurimucosum	9.49	9.00	14.0	14.8	2.41	1.74	2.19	6.85	3.73	0.19	6.44	2.64	1.05	0,95	1.38	0.32	19.9	4.38	
acteria	Actinobacteria	Corynebacterium kroppenstedtii	0.79	.0.49	0.29	0.25	0.17	0.28	0.63	0.69	0.40	0.17	0.41	1.47	1.62	1,18	0.62	0.91	2.39	1.36	
leobacteria	Proteobacteria	Sulturmonas denitriicans	0.10	0.07	2.05	1.04	0.15	0.16	1.90	4.05	0.86	1.11	1.15	1.65	1.50	1.97	0.98	0.47	0.78	1.08	1
obacteria	Proteobacteria	Paraburkholderia xenovorans	23.8	18.5	3.70	3.76	0.92	0.40	1.00	1.00	9.68	3.49	6.63	2.57	1.29	0.98	2 30	1.09	2.78	1.83	
obacteria	Proteobacteria	Ralstonia pickettii	0.89	0.89	1.49	1.39	0.83	0.91	0.91	0.72	1.11	0.93	1.01	1.70	1.01	1.07	0.91	1.26	1.19	1.19	i
teobacteria	Proteobacteria	Legionella pneumophila	1.74	2.69	0.84	0.74	0.36	0.29	1.03	0.91	0.75	0.29	0.96	1.24	0.64	1.14	1,24	1.12	2.55	1.32	1
teobacteria	Proteobacteria	Serratia marcescens	0.55	0.61	1.78	1.61	0.93	0.94	1,10	0.89	0.96	0.57	0.99	0.80	0.90	1.11	0.99	1.23	1.69	1.12	
teobacteria	Proteobacteria	Rahnella aquatilis	0.76	0.60	1.80	1.57	1.48	0.84	0.48	0.31	1.23	0.95	1.00	1.25	1.28	1.15	1.78	1,55	1.29	1.38	
leobacteria	Proteobacteria	Thalassolituus oleivorans	0.29	0.25	2.94	1.90	0.58	0.58	1.82	1.19	2.29	0.53	1.24	1.08	1.17	1.55	1.00	1,53	4.30	1.77	1
teobacteria teobacteria	Proteobacteria	Rhodapphacter denitrificans	16.4	1.94	12.92	11.1	0.73	1.13	1.35	1.44	1.01	0.75	5.82	1.45	1.07	1.29	1.00	1.30	1.48	1.36	i i
teobacteria	Proteobacteria	Stenotrophomonas maltophilia	1.88	2.04	4.24	3.73	0.89	1.00	0.98	0.74	1.00	0.37	1.69	1.58	0.92	1.14	0.89	1.33	2.69	1.43	ī
teobacteria	Proteobacteria	1ethylophaga nitratireducenticrescens	0.83	2.76	1.03	1,16	1.18	0.71	5.74	4,42	0.62	0.15	1.86	3,38	0,30	0.89	1.85	1,30	4.24	1.96	
teobacteria	Proteobacteria	Methylophaga frappieri	1,53	2.44	1.39	1.37	0.45	0.26	3.80	3.16	1.00	0.27	1.57	3,40	0.82	1.02	1.75	1.20	3.75	1.96	
teopacteria	Proteobacteria	Idiomarina loihiensis	0.61	0.56	0.64	0.40	0.34	0.20	0.76	0.54	0.70	0.54	0.53	1.04	1.10	1.60	1.68	1.40	1.31	1.36	
teobacteria	Proteobacteria	Alteromonas macleodii Marinobacter hydrocarbonoclasticus	1.37	1.15	5.04	4.49	0.56	0.28	1.37	1.19	1.15	0.40	1.89	0.98	1.19	1.34	1.99	1.15	5.20	1.97	
teobacteria	Proteobacteria	Marinobacter adhaerens	0.55	0.63	4.80	4.41	0.52	0.51	1.76	1.23	1.81	0.34	1.64	0.86	0.50	1.09	1.11	1.43	5.39	1.75	i i i
teobacteria	Proteobacteria	Moraxella catarrhalis	0.37	0.29	0.16	0,13	0.40	0,32	1.01	0.69	0.45	0.33	0.42	0.63	1.25	1.27	1.25	1.45	1.38	1.21	011-2
teobacteria	Proteobacteria	Acinetobacter calcoaceticus	19.2	60.4	3.22	2.99	2.71	2.92	1.61	2.23	1.36	0,89	9.76	1.01	0.32	1.08	0.93	0.72	1.53	0.93	
teobacteria	Proteobacteria	Pseudomonas fluorescens	1.84	1.61	3.75	2.69	0.79	0.76	0.89	0.71	1.61	0.43	1.51	1.52	1.15	1.40	1.03	1,25	3.73	1.68	
teobacteria	Proteobacteria	Pseudomonas mendocina	0.53	0.45	6.66	5.25	2.61	2.87	2.33	2.29	7.20	1.37	3.16	0.98	1.19	1.27	0.91	1.02	5.27	1.77	
teobacteria	Proteobacteria	Pseudomonas tulzen	0.70	0.51	9.32	1.62	0.85	0.77	0.70	0.58	1.03	0.39	1.70	1.64	1.28	1.19	1.11	1.27	1.33	1.58	
teobacteria	Proteobacteria	Pseudomonas putida	0.59	0.61	3.60	2.92	0.64	0.71	0.80	0.63	1.32	0.41	1.22	1/14	0.96	1.23	0.91	1.25	3.25	1.46	III
eobacteria	Proteobacteria	Polymorphum gilvum	0.59	0.71	0.62	0.65	1.15	1.24	1,45	1.36	0.79	0.84	0.94	3.31	0.83	0.95	0.93	1.07	0.94	1.34	0
eobacteria	Proteobacteria	Candidatus Puniceispirillum marinum	0.69	0.54	0.83	0.83	1.00	1.03	0.69	0,60	1.46	2.18	0.97	0.15	1.10	1.00	0.97	1,15	0.67	0.84	1
aobacteria	Proteobacteria	Bradyrhizobium diazoefficiens	3.33	3.78	1.84	1,86	1.13	1.09	3.18	2.88	2.29	1.51	2.29	3.06	88.0	0.99	1,04	1.11	1.51	1.43	
sobacteria	Proteobacteria	Methylobacterium radiotolerans	3.93	2.95	7.32	6.32	3.67	3,53	2.22	2.09	3.21	0,82	3.61	2,43	1.33	1.16	1.04	1,06	3.92	1.82	
eobacteria	Proteobacteria	alpha proteobacterium HIMB59	0.38	0.26	0.24	0.18	0.36	0.32	0,45	0.22	0.52	0.77	0.37	0.10	1,43	1.28	1.11	2.13	0.67	1.12	i.
obacteria	Proteobacteria	alpha proteobacterium HIMB5	0.78	0.67	1.28	0.88	0.79	0.22	2.25	0.36	0.86	0,40	0.85	0.11	1.16	1.45	3.60	6.29	2.14	2.46	i
eobacteria	Proteobacteria	Erythrobacter litoralis	0,59	0.82	0.41	0.50	0.16	0.22	0.46	0.58	0.44	0.73	0.49	1.79	0.71	0.82	0.71	0.78	0.61	0.90	
eobacteria	Proteobacteria	Sphingomonas wittichii	1.43	1.72	0.70	0.86	0.51	0.69	0,60	0.71	0.66	0.94	0.88	2.55	0.83	0.82	0.73	0.85	0.70	1.08	
eobacteria	Proteobacteria	Sphingobium japonicum	1.68	2.24	0.48	0.57	0.41	0.50	0.50	0.60	0.58	0.88	0.84	2.08	0.75	0.85	0.83	0.83	0.67	1.00	
eobacteria	Proteobacteria	Novosphingobium aromaticivorans	2.29	2.65	0.56	0.65	0.25	0.33	0.54	0.67	0.45	0.69	0.91	1.99	0.86	0.86	0.77	08.0	0.65	0.99	
eobacteria	Proteobacteria	Leisingera methylohalidivorans	0.76	1.20	0.50	0.61	1.76	1.70	1.25	1.19	1.00	1.38	1.14	3.08	0.63	0.82	1.04	1.05	0.72	1.22	
eobacteria	Proteobacteria	Ketogulonicigenium vulgare	0.68	1.01	0.52	0.68	1.23	1,14	1.11	1.09	0.73	1.04	0.92	2.33	0.67	0.77	1.08	1.02	0.70	1.09	
obacteria	Proteobacteria	Ruegeria pomeroyi	0.83	1.34	0.51	0.62	1.83	1.68	1.26	1.24	1.04	1.58	1.19	3.37	0.61	0.83	1.09	1.02	0.66	1.26	
sobacteria	Proteobacteria	Dinoroseobacter shibae	0.70	1.26	0.50	0.66	1.51	1.25	1.21	1.08	0.86	1.26	1.03	3.83	0.56	0.76	1.21	1.12	0.68	1.36	
eobacteria	Proteobacteria	Paracoccus denitrificans	0.69	1.07	0.60	0.72	1.28	1.29	1.18	1.15	0.79	1.12	0.99	3.85	0.65	0.83	1.00	1.03	0.71	1.34	
eobacteria	Proteobacteria	Phaeobacter gallaeciensis	0.80	1.37	0.52	0.68	1.68	1.33	1.29	1.19	0.91	1.41	1.12	3.41	0.59	0.76	1.28	1.09	0.65	1.29	
eobacteria	Proteobacteria	Phaeobacter inhibens Rhodobacter sobaersistos	0.76	1.12	0.59	0.69	1.96	1.82	1.18	1.22	0.75	1.36	1,17	3.60	88.0	0.85	1.07	1.05	0.75	1.12	
eobacteria	Proteobacteria	Rhodobacter capsulatus	0.70	1.07	0.45	0.55	1.33	1.21	1.16	1.09	0.86	1.21	0.96	3.15	0.65	0.81	1.10	1.06	0.71	1.25	
eobacteria	Proteobacteria	Roseobacter litoralis	0.71	1.15	0.55	0.67	1.41	1.42	1.12	1.15	0.73	1.18	1.01	1.93	0.62	0.83	0.99	0.97	0.62	0.99	
eobacteria	Proteobacteria	Roseobacter denitrificans	0.69	1.03	0.45	0.55	1.36	1.34	1.30	1.23	0.91	1.49	1.03	2.75	0.67	0.81	1.01	1.06	0.61	1,15	
sobacteria	Proteobacteria	Octadecabacter antarcticus	0.74	1.22	0.45	0.56	0,87	0.86	0.90	0.99	0.75	1.32	0.86	1.42	0.60	0.80	1.01	0.91	0.57	0.88	
eobacteria	Proteobacteria	Octadecabacter arcticus	0.71	1.00	0.53	0.65	0.85	1.00	0.88	0.98	0.68	1.29	0.86	1.44	0.71	0.81	0.85	0.90	0.53	0.87	
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Order

Cytophaga

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Thiotrichales Thiotrichales Alteromonadales Alteromonadales

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les > 0.5%

Supplementary Fig. 5 Bacterial aerosolization and surface enrichment. Taxonomy, aerosolization factors, and surface enrichment of bacterial genomes of spatial coverage and abundance trimmed data. Phylum, class, and orders are color coded to reflect species relationships. Genome annotation by read-based analysis, Heat map column labels indicate day and measurement. Aerosolization factor is expressed as the fraction of genomes in aerosol to bulk or surface (A:B or A:S). Surface enrichment is the fraction in SSML to the fraction in the bulk (S:B). Heat map values indicate ratio values (bottom legend). Species abundance is reported as the sum of fraction of the population across the experiment and as the number of samples above 0.5% of the population.



Supplementary Fig. 6 The genetic basis of bacterial and viral aerosolization in the abundance trimmed data set. Genome-based phylogenetic trees based on 197 bacterial genome sequences in **a** and 46 viral genomes in **b**. Sequences are derived from read-centric analysis of above 0.1% of the population but not trimmed of genomes with low spatial coverage. The bacteria are a subset of this data that contains 700 bacterial genomes total. The heatmaps display aerosolization factor (AF), A:B and A:S, on different days. AF intensity specified by the legend: Blue = Diminished aerosolization; Yellow = Neutral aerosolization; Red = Enhanced aerosolization a, Bacteria class is indicated on outer ring to further denote species and aerosolization relationships. Yellow highlights, i –iv indicate closely related species with differing aerosolization patterns. **b**, Line colors denote viral family and shading indicates order as shown by legend. Additionally, labels on the inner ring specify lipid-enveloped or non-enveloped classifications. Blanks indicate samples below threshold limits.

	Day		8		19	2	24		28	:	34		0	8	19	24	28	34		
Viral Draft genomes (0.025 µm fraction)	AF	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	Avg AF	S:B	S:B	S:B	S:B	S:B	S:B	Avg S:E	3 Abundance
JCVI_CAICE_NCLDV_1		3.18	11.2	2.82	2.11	0.60	0.83	0.85	0.60	0.68	0.28	2.3	2.60	0.28	1.33	0.72	1.41	2.42	1.5	
JCVI_CAICE_Phage_1		0.09	0.06	0.34	0.37	0.23	0.18	1.29	0.34	5.94	1.76	1.1	0.61	1.38	0.93	1.29	3.84	3.38	1.9	
JCVI_CAICE_Phage_2		0.35	0.35	0.82	0.53	0,40	0.31	1.40	0.26	2.17	0.80	0.7	0.19	1.01	1.54	1,29	5.32	2.71	2.0	
JCVI_CAICE_Phage_3		0.20	1.52	19.8	3.81	0.55	0.78	1.76	0.53	0.43	0.14	3.0	3.26	0.13	5.20	0.71	3.32	3.14	2.6	
JCVI_CAICE_Phage_4		2.48	10.7	0.84	0.76	0.44	0.20	0.72	0.17	0.63	0.24	1.7	1.06	0.23	1.11	2.15	4.30	2.60	1.9	
JCVI_CAICE_Phage_5		4.00	4.11	0.33	0.31	0.30	0.23	0.94	0.33	0.78	0.38	1.2	2.35	0.97	1.05	1.32	2.90	2.07	1.8	
Bacterial draft genomes (0.02 µm fraction)		8A:B	8A:S	19A:B	19A:S	24A:B	24A:S	28A:B	28A:S	34A:B	34A:S	Avg AF	0S:B	8S:B	19S:B	24S:B	28S:B	34S:B	Avg S:B	
JCVI_CAICE_Erythrobacter_1		0.36	0.53	0.31	0.38	0.19	0.23	0.45	0.65	0.31	0.67	0.4	1.56	0.69	0.82	0.82	0.69	0.46	0.8	
JCVI_CAICE_Novosphingobium_1		6.39	6.73	0.74	1.38	0.08	0.60	60.4	0.92	0.31	0.96	7.9	1.23	0.95	0.53	0.13	65.6	0.33	11.5	1
JCVI_CAICE_Methylophaga_1		3.50	6.53	1.26	1.70	0.31	0.21	12.6	1.20	0.28	0.23	2.8	1.56	0.54	0.74	1.52	10.4	1.21	2.7	
JCVI_CAICE_Gammaproteobacteria_	1	1.92	1.46	0.45	0.45	0,13	0.12	1.05	0.54	0.29	0.37	0.7	1.02	1.32	0.99	1.06	1.94	0.78	1.2	
JCVI_CAICE_Escherichia coli_1		1.55	0.47	5.69	0.58	3.47	1.79	3.27	2.43	0.25	0.88	2.0	1.53	3.29	9.89	1.93	1.35	0.28	3.0	
JCVI_CAICE_Legionella_1		3.83	5.49	0.97	0.86	1.17	0.28	4.94	3.03	1.1	0.23	2.2	3.87	0.70	1.12	4.17	1.63	4.80	2.7	
JCVI_CAICE_Polaribacter_1		1.82	1.49	0.11	0.11	0,40	0.23	2.86	3.55	0.38	1.43	1.2	7.99	1.22	1.00	1.73	0.81	0.27	2.2	
JCVI_CAICE_Deltaproteobacteria_1		5.84	7.89	0.81	1.65	0.02	0.30	58.8	0.82	0.13	0.91	7.7	1.15	0.74	0.49	0.06	71.3	0.14	12.3	
JCVI_CAICE_Diatom_1		2.19	0.66	4.12	3.37	0.83	3.51	6.78	25.1	6.16	8.23	6.1	15.2	3.32	1.22	0.24	0.27	0.75	3.5	
JCVI_CAICE_Roseobacter_1		0.63	0.69	0.68	0.81	1.97	1.67	0.90	1.17	1.10	1.41	1.1	3.32	0.91	0.85	1.18	0.77	0.78	1.3	
JCVI_CAICE_Roseovarius_1		1.21	1.81	1.75	1.89	14.3	11.5	2.41	2.93	4.54	4.62	4.7	1.94	0.67	0.92	1.25	0.82	0.98	1.1	
JCVI_CAICE_Roseobacter_fragments	5_1	0.14	0.08	1.79	6.04	0,49	1.01	0.42	1.91	1.53	0.77	1.4	0.31	1.72	0.30	0,49	0.22	2.00	0.8	
JCVI_CAICE_Roseobacter_fragments	3_2	0.32	0.42	1.20	1.66	12.6	2.82	0.21	2.42	8.36	1.34	3.1	2.78	0.76	0.72	4.49	0.09	6.22	2.5	
JCVI_CAICE_Roseobacter_fragments	5_3	1.35	2.13	0.55	0.67	1.84	1.48	1.28	1.31	0.69	1.35	1.3	3.89	0.63	0.82	1.24	0.97	0.51	1.3	
JCVI_CAICE_Roseobacter_fragments	5_4	0.09	0.08	0.30	0.20	0.29	0.17	0.53	0.49	0.36	0.93	0.3	1.57	1.12	1.52	1.70	1.07	0.38	1.2	1
JCVI_CAICE_Roseobacter_fragments	5_5	20.2	27.7	0.48	0.98	0.02	0.02	198	0.92	0.08	1.01	25.0	1.30	0.73	0.50	1.35	215	0.08	36.4	
JCVI_CAICE_Roseobacter_fragments	5_6	1.53	2.78	1.14	1.32	1.52	1.02	2.40	2.69	0.82	0.43	1.6	2.37	0.55	0.87	1.49	0.89	1.91	1.3	
JCVI_CAICE_Roseobacter_fragments	5_7	0.19	0.08	134	21.9	18.6	17.5	5.75	33.2	15.9	1.46	24.9	5.08	2.27	6.12	1.06	0.17	10.9	4.3	
JCVI_CAICE_Roseobacter_frag_conta	m	0.01	0.01	7.68	43.2	2.92	5.91	0.19	0.35	35.3	1.54	9.7	0.50	0.96	0.18	0.49	0.54	23.0	4.3	
					—Ae	eroso	lizatio	on—					-5	Surfac	ce Er	hand	eme	nt—		
						>5	0 15	. 50	10.15	0.67-1	0 02.	0.57 < 0	2							



Supplementary Fig. 7 Draft genome bacterial and viral aerosolization and surface enrichment. Taxonomy, aerosolization factors, and surface enrichment of assembled draft genomes. Heat map column labels indicate day and measurement. Aerosolization factor is expressed as the fraction of species in aerosol to bulk or surface (A:B or A:S). Surface enrichment is the fraction in SSML to the fraction in the bulk (S:B). Heat map values indicate ratio values (bottom legend). Genome abundance is reported as the sum of fraction of the population across the experiment and as the number of samples above 0.5% of the population.

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			10	>!	5.0	1	.5 - 5	.0	1.0 - 1.5	0.67	- 1.0	0.2 - 0.6	7	0.2	
						1.00	on oliv	ratio				Surface I	- abaaa		
Class	Phylum	Species	8A:8	8A:5	19A:8	Aer 194:57	24A:B 24	Lauo IA:S 28	A:8 28A:5 344	B 34A:5	05:B	85:8 195/8	245:B 285	8 345:B	AVG
Actinobacteria	Actinobacteria	Rhodococcus sp. (Rhodococcus erythropolis)	5.7	3,3	2.3	2.4	2.0 1	.8 3	7 2.0 14	.9 10.0	3,2	1.7 1.0	1.1 1.8	1.5	1.7.
	Actinobacteria	Corynebacterium sp. (Corynebacterium aurimucosum)	9.5	9.0	14.0	14.8	2.4 1	.7 2	2 6.9 3	7 0.2	2.6	1.1 1.0	14 0.3	19.9	4.4
	Actinobacteria	Clavibacter sp. (Clavibacter michiganensis)	5.1	7.6	8.8	77	1.5 1	2 2	0 2.7 3	0 0.8	1.0	0.7 11	0.8 0.3	3.9	14
	Actinobacteria	Leifsonia sp. (Leifsonia xyli) Propiopibactarium cp. (Propiopibactarium acport	18.5	10.2	3.1	3.0	117 3	11 2	35 102 14	4 0.6	2.4	0.6 1.0	3.9 7.3	73.9	5.9
Bacilli	Firmicutes	Strentococcus sp. (Streptococcus thermonhilus)	20.5	50.3	10.1	5.7	4.3 1	.5 1	6 2.1 10	2 0.2	0.1	0.4 1.8	2.8 0.3	41.9	8.0
phaproteobacteria	Proteobacteria	Methylobacterium sp. (Methylobacterium radiotolerans)	3.9	2.9	7.3	6.3	3.7 5	1.5 2	2 2.1 3.	2 0.8	2.4	1.3 1.2	1.0 1.1	3.9	1.8
Actinobacteria	Actinobacteria	Mycobacterium sp. (Mycobacterium avium)	5.6	6.0	11.2	10.7	3.1 6	i.3 0	5 1.1 5.	3 1.9	0.9	0.9 1.0	0.5 0.1	2.8	1.1
	Actinobacteria	Mycobacterium sp. (Mycobacterium abscessus)	4.6	3.3	6.5	6.9	10.6	1.4 1	2 1.9 5.	8 1.2	0.8	1.4 0.9	3.1 0.0	4,9	2.0
	Actinobacteria	Mycobacterium sp. (Mycobacterium chubuense)	3.5	5.3	7.4	10.8	2.9 3	1.0 0	5 0.6 9.	0 2.0	1.7	0.7 0.7	1.0 0.8	4.5	1.6
	Actinobacteria	Mycobacterium sp. (Mycobacterium vanbaalenii)	2.3	2.2	3.9	3.8	2.6 7	1.9 1	7 1.2 3.	8 1.2	0.1	1.1 1.0	0.9 1.4	3,1	1.3
	Actinobacteria	Blastococcus sp. (Blastococcus saxobsidens)	2.3	1.9	24.2	25.5	25 5	1.2. 1	6 13 2	6 0.2	1.8	1.2 0.9	0.8 1.	12.5	3.1
	Actinobacteria	Kotnia sp. (Kotnia muchaginosa) Micrococcus sp. (Micrococcus luteus)	13.9	9.0	212	187	10.8 6	10 1	4 37 9	2 1.0	8.5	15 14	18 05	9.1	25
	Actinobacteria	Cellulomonas sp. (Cellulomonas flaviaena)	2.4	1.9	8.5	6.0	2.1 3	L8 1	.0 1.2 5.	9 2.1	2.0	1.3 1.4	0.7 0.5	3.2	1.6
	Actinobacteria	Cellulomonas sp. (Cellulomonas fimi)	3.6	3.0	4.2	4.0	1.8 7	1.4 0	.8 0.9 3.	1 1.7	2.1	1.2 1.1	0.7 0.9	1.9	1.3
	Actinobacteria	Nakamurella sp. (Nakamurella multipartita)	0.9	0.8	3.6	3.6	2.5 2	1.9 2	9 2.7 6.	3 2.7	2.9	1.1 1.0	0.9 1.1	2.4	1.5
	Actinobacteria	Nocardioides sp. (Nocardioides sp. JS614)	3.9	43	7.7	8.7	1.6 1	.7 1	7 1.1 5.	1.1	2.2	0.9 0.9	1.0 1.5	4.8	1.9
	Actinobacteria	Saccharothrix sp. (Saccharothrix espanaensis)	2,2	2.4	4.9	6.1	1.8 4	12 0	1.9 1.2 4,	6 1.7	1.7	0.9 0.8	0.4 0.8	2.7	1.2
Actinobacteria	Actinobacteria	Actinosynnema sp. (Actinosynnema mirum)	2.5	1.5	3.9	4.2	1.4 1	5 2	.7 2.0 2.	7 0.7	2.6	1.6 0.9	0.9 1.	3,6	1.8
	Cyanobacteria	Synechococcus sp. (Synechococcus sp. CC9311)	1.9	16	9.4	2.7	0.5 1	19: 1	4 18 6	6 4 3	65	12 10	3.0 9.4	0,7	1.9
	Cvanobacteria	Calothrix sp. (Calothrix parietina)	1.3	1.5	2.9	23	0.6		1 2.9 2.	8 2.9	2.3	0.8 1.3	0.3 1.1	0.9	1.1
Bacilli	Firmicutes	Bacillus sp. (Bacillus cereus)	204	16.0	4.0	4.6	0.5 (9.7 4	6 10.0 9.	6 3.7	4.8	12.7 0.9	0.8 0.5	2,6	3.7
Phycisphaerae	Planctomycetes	Phycisphaera sp. (Phycisphaera mikurensis)	2.6	2.2	2,7	3.0	2.4 3	1.8 1	1 1.1 3.	5 4.5	1.9	1.2 0.9	0.9 1.0	0.8	1.1
phaproteobacteria	Proteobacteria	Bradyrhizobium sp. (Bradyrhizobium diazoefficiens)	3.3	3.8	1.8	1.9	1.1 1	1 3	2 2.9 2.	3 1.5	3.1	0.9 1.0	1.0 1.1	1.5	1.4
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia phytofirmans)	70.4	41.8	5.8	5.3	0.7	1.2 1	8 1.8 24	0 5.2	2.3	1.7 1.1	2.9 1.0	4,6	2.3
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia sp. CCGE1002)	14.4	16.6	5.0	4.8	0.9 0	1.6 2	3 2.1 7.	5 2.6	3.4	0.9 1.0	14 1.1	2.9	18
etaproteobacteria	Proteopacteria	Burkholderia sp. (Burkholderia cepacia)	4.9	5.4	3.7	35	65 1	5 1	0 06 8	1 8.7	0.5	1.4 0.9	15 1.	3.7	20
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia thailandensis)	6.3	4.5	2.1	1.8	1.5 1	5 1	5 0.9 3.	4 2.7	1.9	1.4 1.2	1.0 1.6	1.3	1.4
maproteobacteria	Proteobacteria	Candidatus sp. (Candidatus Hamiltonella defensa)	1.0	1.6	3.1	3.9	0.6	.8 3	8 2.4 4.	2 3.4	1.6	0.6 0.8	0.3 1.0	1.2	1.0
maproteobacteria	Proteobacteria	Acinetobacter sp. (Acinetobacter calcoaceticus)	19.2	60.4	3.Z	3.0	2.7	1.9 1	6 2.2 1.	4 0.9	1.0	0.3 1.1	0.9 0.3	1.5	0.9
imaproteobacteria	Proteobacteria	Cycloclasticus sp. (Cycloclasticus sp. P1)	0.7	0.6	3.5	2.9	3.3	1.3 1	.7 1.8 4/	0 2.7	2.8	1,2 1,2	1.4 0,5	1.4	1.5
	Actinobacteria	Intrasporangium sp. (Intrasporangium calvum)	2.8	1.8	4,7	5.3	1.7 1	2 1	1 0.8 2.	3 2.4	1.5	1.6 0.9	1.3 1.4	1.0	1.3
Actinobacteria	Actinobacteria	Nocardiopsis sp. (Nocardiopsis dassonvillei)	1.8	3.4	4,1	6.6	1.0 1	.7 7	2 14 1	9 1.2	0.7	0.5 0.6	0.6 1.6	5 1.6	0.9
Bacilli	Firmicutes	Stanhulococcus sn. (Stanhulococcus anidermidis)	10.x	7.4	5.1	3.6	2.9 1	8 1	0 10 2	1 0.3	1.0	10 15	1.6 10	1 69	2.0
	Firmicutes	Stephylococcus sp. (Staphylococcus epidermans) Streptococcus sp. (Streptococcus suis)	0.1	0.1	14.1	14.2	7.3 (.3 2	.2 3.4 12	.8 1.1	1.2	1.4 1.0	1.2 0.0	11.5	2.8
phaproteobacteria	Proteobacteria	Bradyrhizobium sp. (Bradyrhizobium japonicum)	3.1	3.2	2.2	2.0	1.2 1	2 2	3 1.8 1.	6 1.1	2.8	1.0 11	1.0 1.3	1.4	1.4
phaproteobacteria	Proteobacteria	Bradyrhizobium sp. (Bradyrhizobium sp. 523321)	3.0	2.9	1,7	1.6	1.4 1	Z 1	9 2.1 2.	5.1 0	2.7	1.0 1.0	1.2 0.5	1.6	1.4
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia phenoliruptrix)	24.5	15.5	4.9	4.9	1.7 0	0.7 0	16 0.4 19	2 4.8	0.3	1.6 1.0	2,2 1,8	4.0	1.8
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia cenocepacia)	8.3	7.7	2.9	2.8	1.1 1	.0 1	6 1.5 3.	7 2.3	1.7	1.1 1.0	1.1 1.1	1.6	1.3
etaproteobacteria	Proteobacteria	Acidovorax sp. (Acidovorax sp. KKS102)	2.4	2.6	2.7	2.4	14 1	.3 1	.6 1.6 1.	8 0.6	1.4	0.9 1.1	11 1.0	3.2	1.5
Actinobacteria	Actinobacteria	Mycobacterium sp. (Mycobacterium kansasii)	6.2	4.6	2.7	2.2	13 1	5 1	0 13 3	3 2.5	0.7	1.3 1.2	0.9 0.1	1.3	1.0
	Actinobacteria	Rhodococcus sp. (Rhodococcus opacus)	·Z.1	1.3	2.6	2.5	2.0 1	.5 1	3 0.7 4.	4 1.2	2.2	1.6 1.1	1.3 1.8	3.8	2.0
	Actinobacteria	Actinoplanes sp. (Actinoplanes missouriensis)	1.5	1.2	5.0	3.7	1.0 1	3 2	4 1.7 2.	7 1.0	1.3	13 13	0.8 1.4	2.8	1.5
	Actinobacteria	Kitasatospora sp. (Kitasatospora setae)	1.9	2.4	4.8	5.9	1.4 1	.5 1	A 0.7 3.	6 2.5	0.4	0.8 0.8	1.0 1.9	1.5	1.1
Actinobacteria	Actinobacteria	Streptosporangium sp. (Streptosporangium roseum)	1.4	1.5	3.2	3.0	0.9 1	1.6 1	1 15 4	4 3.2	2.0	0.9 1.0	0.6 0.8	1.4	1.1
Planctomycetia	Planctomycetes	Isosphaera sp. (Isosphaera pallida)	1.7	14	1.6	2.1	1.0 1	5 1	7 1.6 1.	4 4.4	1.9	1.2 0.7	0.6 0.8	0.3	0.9
proteobacteria ataproteobacteria	Proteobacteria	Brodyrnizobium sp. (Brodyrnizobium sp. UKS 278) Burkholderia sp. (Burkholderia sepovorans)	2.5	185	3.7	3.8	0.9 (x a 1	1 10 9	7 35	2.5	13 10	23. 1.1	1.9.8	18
eta proteobacteria	Proteobacteria	Burkholderig sp. (Burkholderig phymotum)	14.1	13.6	2.0	22	0.9 0	0.6 1	1 0.8 3.	2 1.8	2.2	1.0 0.9	14 14	1.7	1.5
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia sp. CCGE1003)	8.2	7.3	3.0	2.6	0.5	0.4 1	4 0.9 5.	1 2.5	1.7	1.1 1.2	1.5 1.6	5 2.0	1.5
Actinobacteria	Actinobacteria	Geodermatophilus sp. (Geodermatophilus obscurus)	2.2	2.2	12.5	10.1	1.4 1	.4 1	1 11 1	7 0.2	0.7	1.0 1.2	1.0 1.1	8.6	2.3
phaproteobacteria	Proteobacteria	Bradyrhizobium sp. (Bradyrhizobium oligotrophicum)	2.2	2.2	1,3	1.2	1.3 1	2 2	0 1.8 1.	6 1.3	2.4	1.0 1.1	1.0 1.1	1.1,2	1.3
etaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia sp. CCGE1001)	22.4	\$5.0	1.5	1.3	1.2 (0.9 1	9 1.8 6.	1 1.1	3.4	0.4 1.2	1.3 1.1	5.6	2.2
etaproteobacteria	Proteobacteria	Acidovorax sp. (Acidovorax sp. JS42)	11	14	2.2	1.8	1.8 2	0 1	8 12 1	2 0.3	11	0.8 1.2	0.9 1	3.5	1.5
maproteobacteria	Proteobacteria	Escherichia sp. (Escherichia coli) Alcanivorox sp. (Alcanivorax dieseloloi)	2.1	19	3.5	27	11	3 6	8 0.5 1	6 0.7	15	11 13	10 14	21	14
maproteobacteria	Proteobacteria	Pseudomonas so. (Pseudomonas stutzeri)	0.8	0.9	4,3	3.6	1.8 1	1.6. 1	1 0,9 1	6 0.4	0.9	0.8 1.7	1.2 1.3	4.1	1.6
maproteobacteria	Proteobacteria	Pseudomonas sp. (Pseudomonas fluorescens)	1.8	1.6	3.8	2.7	0.8 0	0.8 0	.9 0.7 1.	6 0,4	1.5	1.1 1.4	1.0 1.1	3.7	1.7
maproteobacteria	Proteobacteria	Xanthomonas sp. (Xanthomonas compestris)	0.9	0.7	2.6	2.2	0.4 (0.9 1	2 2.1 4	1 3,4	0.9	1.4 1.2	0.5 0.6	1.2	1.0
Actinobacteria	Actinobacteria	Gordonia sp. (Gordonia polyisoprenivorans)	1.3	1.8	1.4	23	1.4 1	.6. 1	4 1.1 1.	5 1.3	11	0,7 0.6	0.9 1.3	1.1	1.0

Species abundance

Supplementary Fig. 8 Bacterial aerosolization of abundance trimmed data set. Taxonomy, aerosolization factors, and surface enrichment of 197 bacterial genomes from abundance trimmed but not coverage trimmed data presented in three sets, **a**, **b**, **c**. Phylum, class, and orders are color coded to reflect genome relationships. Genome annotation by read-based analysis, exact assignment in parentheses. Heat map column labels indicate day and measurement as well as enrichment factor. Aerosolization factor is expressed as the fraction of a genome in aerosol to bulk or surface (A:B or A:S). Surface enrichment is the fraction in SSML to the fraction in the bulk (S:B). Heat map values indicate ratio values as given in legend. Bars on right indicate genome abundance (number of samples containing above 0.5% of the total population).

Order

Nakamurellales

Burkholderiales

Burkholderiales Burkholderiales Burkholderiales Burkholderiales Enterobacteriales Ga

Burkholderiales Burkholderiales

Micromonosporales

Burkholderiales Burkholderiales Burkholderiales

Burkholderiales Burkholderiales Enterobacteriales Ga

Pseudomonadales Pseudomonadales

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b				-				·I)	
~				3	> 5.0	1.5 - 5.0	1.0 - 1.5	0.67 - 1	.0 0.2 - 0.67	< 0.2	
							Non	_	Surface Fr	honcomo	
Order	Class	Phylum	Species	SA:B BA:S	19AB 19AS	24A:8 24A:5 2	8A:B 28A:S 34A:E	34A:5 05	- Sunace Er 5.8 85:8 195:8 245:	285:8 345:8	AVG
Chroococcales			Synechococcus sp. (Synechococcus sp. CC9902)	1.3 2.0	17.9 11.5	0.9 0.2	13.8 0.3 6.8	0.4 0	1 0.6 1.6 4.5	40.6 17.2	10.8
Prochlorales	Alobanroteobacteria	Cyanobacteria Protochacteria	Prochlorococcus sp. (Prochlorococcus marinus)	0.4 0.4	2.1 1.9	0.5 0.9	2.1 1.0 2.2	1.1 0	1 11 11 0.6	2.2 1.9	2.0
Burkholderiales	Betaproteobacteria	Proteobacteria	Burkholderia sp. (Burkholderia vietnamiensis)	8.2 6.1	1.3 1.2	0.6 0.5	0.4 0.5 5.7	5.8 0	1.6 1.3 1.1 1.0	0.9 1.0	1.0
Xanthomonadales	Gammaproteobacteria	Proteobacteria	Rhodanobacter sp. (Rhodanobacter denitrificans)	16.4 12.6	12.2 11.1	0.7 0.6	1.4 1.4 1.0	0.7 1	2 13 11 13	0.9 1.5	1.2
Xanthomonadales	Gammaproteobacteria	Proteobacteria	Stenotrophomonas sp. (Stenotrophomonas maltophilia)	1.9 2.0	4.2 3.7	0.9 1.0	1.0 0.7 1.0	0.4 1	.6 0.9 1.1 0.9	1.3 2.7	1.4
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Phaeobacter sp. (Phaeobacter innibens) Leisingera sp. (Leisingera methylohalidivorans)	0.8 1.1	0.5 0.6	1.8 1.7	12 1.2 10	1.4 2	1 0.6 0.8 1.0	1.0 0.7	12
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Ruegeria sp. (Ruegeria sp. TM1040)	0.9 1.5	0.6 0.7	1.5 1.5	1.1 1.0 1.0	1.3 2	.3 0.6 0.8 1.0	1.1 0.8	1.1
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Ruegeria sp. (Ruegeria pomeroyi)	0.8 1.3	0.5 0.6	1.8 1.7	1.3 1.2 1.0	1.6 3	4 0.6 0.8 1.1	1.0 0.7	1.3
Burkholderiales	Betaproteobacteria	Proteobacteria Proteobacteria	Acidovorax sp. (Acidovorax citrulli) Soranajum sp. (Soranajum cellulosum)	11 10	1.9 2.0	14 13	12 12 23 08 07 158	9.1 0	4 11 10 11	0.9 2.6	2.4
Rhizobiales	Alphaproteobacteria	Proteobacteria	Bartonella sp. (Bartonella henselae)	1.6 1.7	10 12	0.6 0.6	0.7 0.7 0.8	11 1	2 0.9 0.8 1.2	1.1 0.8	1.0
Legionellales	Gammaproteobacteria	Proteobacteria	Legionella sp. (Legionella pneumophila)	1.7 2.7	0.8 0.7	0.4 0.3	1.0 0.9 0.7	03 1	.2 0.6 1.1 1.2	1.1 2.6	1.3
Alteromonadales	Gammaproteobacteria	Proteobacteria	Alteromonas sp. (Alteromonas macleodii)	1.4 1.2	6.0 4.5	0.6 0.3	1.4 1.2 2.1	0,4 1	0 1.2 1.3 2.0	1.1 5.2	2.0
Vibrionales	Gammaproteobacteria	Proteobacteria	Methylophaga sp. (Methylophaga nitratireducenticrescens) Vibrio sp. (Vibrio sp. Ex25)	0.8 2.8	1.0 1.2	1.2 0.7	5.7 4.4 0.6 0.8 0.7 1.6	0.1 3	14 0.1 0.9 1.6 13 1.1 1.4 1.7	1.3 4.2 1.1 1.8	1.2
Alteromonadales	Gammaproteobacteria	Proteobacteria	Marinobacter sp. (Marinobacter adhaerens)	0.4 0.6	4.8 4.4	0.6 0.5	1.8 1.2 1.8	0.3 0	19 0.6 1.1 1.1	1.4 5.4	1.8
Oceanospirillales	Gammaproteobacteria	Proteobacteria	Thalassolituus sp. (Thalassolituus oleivorans)	E0 E0	2.9 1.9	0.6 0.6	1.8 1.2 2.3	0.5 1	.1 1.2 1,5 1.0	1.5 4.3	1,8
Thiotrichales	Gammaproteobacteria	Proteobacteria	Methylophaga sp. (Methylophaga frappieri)	1.5 2.4	1.4 1.4	0.4 0.3	3.8 3.2 1.0	0.3 3	1.4 0.6 1.0 1.7	1.2 3.8	2.0
Brachyspirales Pseudomopadales	Spirochaetia	Spirochaetes Proteobacteria	Brachyspira sp. (Brachyspira pilosicoli) Pseudomonas sp. (Pseudomonas sp. TKP)	0.5 0.4	2.7 2.0	0.5 0.5	1.0 0.6 5.5 0.7 0.6 1.0	1.8 0	1 14 13 10	1.7 1.1	1.2
	Gammaproteobacteria	Proteobacteria	Pseudomonas sp. (Pseudomonas sp. 1147) Pseudomonas sp. (Pseudomonas putida)	0.6 0.6	3.5 2.9	0.6 0.7	0.8 0.6 1.3	0.4 1	.1 1.0 1.2 0.9	1.3 3.3	15
	Gammaproteobacteria	Proteobacteria	Pseudomonas sp. (Pseudomonas entomophila)	0.6 0.7	2.1 2.1	0.7 0.8	0.7 0.6 1.1	0.8 2	7 0.5 1.0 0.8	1.1 1,4	1,3
Pseudomonadales	Gammaproteobacteria	Proteobacteria	Pseudomonas sp. (Pseudomonas fulva)	0.7 0.5	2.0 1.6	0.9 0.8	0.7 0.6 1.3	1.0 1	.6 1.3 1.7 1.1	1.2 1.1	13
Rhodobacterales Rhodobacterales	Alphaproteobacteria	Proteobacteria	Phaeobacter sp. (Phaeobacter gallaeciensis) Dinoroseobacter sp. (Dinoroseobacter shihae)	0.8 1.4	0.5 0.7	1.7 1.3	13 12 09 12 11 09	1.4 3	14 0.6 0.8 1.3	1.1 0.5	1.3
	Alphaproteobacteria	Proteobacteria	Candidatus sp. (Candidatus Puniceispirillum marinum)	0.6 0.5	0.8 0.8	1.0 1.0	0.7 0.6 1.5	2.2 0	12 1.1 1.0 1.0	1.1 0.7	0.8
	Alphaproteobacteria	Proteobacteria	alpha sp. (alpha proteobacterium HIMB5)	0.8 0.7	1.3 0.9	0.8 0.2	2.2 0.4 0.9	0.4 0	1 1.2 1.4 3.6	6.3 2.1	2.5
Burkholderiales	Betaproteobacteria	Proteobacteria	Polaromonas sp. (Polaromonas sp. 15666)	0.9 1.0	16 1.2	0.9 0.9	0.9 0.7 1.4	0.6 1	1 0.9 1.4 1.0	1.4 2.3	13
Planctomycetales	Planctomycetia	Planctomycetes	Planctomyces sp. (Planctomyces limnophilus)	0.6 1.2	1.1 1.4	0.6 1.2	0.6 0.6 1.7	0.8 1	4 0.5 0.8 0.5	1.0 2.0	1.0
Pasteurellales	Gammaproteobacteria	Proteobacteria	Actinobacillus sp. (Actinobacillus succinogenes)	1.4 2.1	0.5 0.5	0.3 0.4	2.5 1.3 0.5	0.5	.6 0.7 1.0 0.7	1.8 1.0	1.1
Aquificales	Aquificae	Aquificae	Sulfurihydrogenibium sp. (Sulfurihydrogenibium azorense)	1.9 1.9	0.0 0.0	0.4 0.2	1.8 1.5 0.3	2.7 4	.0 1.0 1.0 2.0	1.2 0.1	1,5
Sphingomonadales Sphingomonadales	Alphaproteobacteria	Proteobacteria Proteobacteria	Novosphingobium sp. (Novosphingobium aromaticivorans)	23 27	0.5 0.5	0.3 0.3	0.5 0.7 0.4	0.7 2	0 0.9 0.9 0.8	0.8 0.7	10
Burkholderiales	Betaproteobacteria	Proteobacteria	Variovorax sp. (Variovorax paradoxus)	1.1 1.1	2.0 1.8	1.0 1.1	1.1 1.0 1.5	0.7 1	.7 1.0 1.1 0.9	1.1 2.0	1.3
Burkholderiales	Betaproteobacteria	Proteobacteria	Janthinobacterium sp. (Janthinobacterium sp. Marseille)	0.8 0.6	2.6 2.0	0.5 0.4	0.7 0.6 1.2	0.6 0	1.3 1.3 1.1	1.2 1.9	1.3
Alteromonadales	Gammaproteobacteria	Proteobacteria	Marinobacter sp. (Marinobacter hydrocarbonoclasticus)	0.3 0.4	3.9 3.1	0.5 0.5	1.4 1.1 1.4	0.4 1	.4 0.9 1.3 1.0	1.3 3.5	1.6
Enterobacteriales	Gammaproteobacteria	Proteobacteria	Kannella sp. (Kannella aquatilis) Serratia sp. (Serratia marcescens)	0.8 0.6	1.8 1.6	0.9 0.9	11 0.9 1.0	0.5 0	8 0.9 1.1 1.0	1.5 1.1	1.1
Enterobacteriales	Gammaproteobacteria	Proteobacteria	Yersinia sp. (Yersinia pseudotuberculosis)	0.4 0.3	0.2 0.1	0.6 0.6	0.1 0.2 2.7	1.5 0	17 1.2 1.8 0.9	0.7 1.8	1,2
Rhizobiales	Alphaproteobacteria	Proteobacteria	Methylobacterium sp. (Methylobacterium nodulans)	0.8 1.2	0.7 0.8	1.0 0.9	1.5 1.3 0.8	0.8 1	.7 0.6 0.9 1.0	1.2 1.0	1.1
Rhizobiales	Alphaproteobacteria	Proteobacteria	Rhodopseudomonas sp. (Rhodopseudomonas palustris)	12 12	0.9 1.0	0.8 0.8	13 1.3 1.0	0.8 2	4 1.0 1.0 1.0	1.0 1.2	1,3
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Roseobacter sp. (Roseobacter denitrificans)	0.7 1.0	0.4 0.6	1.4 1.3	13 12 0.9	15 2	8 0.7 0.8 10	1.1 0.6	1.2
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Roseobacter sp. (Roseobacter litoralis)	0.7 1.2	0.5 0.7	1,4 1,4	1.1 1.2 0.7	1.2 1	9 0.6 0.8 1.0	1.0 0.6	1.0
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Rhodobacter sp. (Rhodobacter sphaeroides)	0.7 1.1	0.5 0.6	1.5 1.4	1.2 1.1 0.8	1.2 3	1.6 0.6 0.8 1.1	1.1 0.7	1.3
Rhodobacterales Rhodobacterales	Alphaproteobacteria	Proteobacteria Proteobacteria	Paracoccus sp. (Paracoccus denitrificans) Iannaschia sp. (Iannaschia sp. (CCS1)	0.7 11	0.6 0.7	13 13	12 12 0.8	11 3	8 0.6 0.8 1.0 7 0.6 0.8 1.1	1.0 0.7	13
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Rhodobacter sp. (Rhodobacter capsulatus)	0.7 1.1	0.4 0.6	1.3 1.2	1.2 1.1 0.9	12 3	Z 0.7 0.8 1.1	1.1 0.7	1.7
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Ketogulonicigenium sp. (Ketogulonicigenium vulgare)	0.7 1.0	0.5 0.7	1.2 1.1	1.1 1.1 0.7	1.0 2	.3 0.7 0.8 1.1	1.0 0.7	1.1
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Paracoccus sp. (Paracoccus aminophilus)	0.7 1.1	0.5 0.6	1.2 1.1	1.0 1.0 0.7	1.2 2	.4 0.6 0.8 1.0	0.9 0.6	11
Rhodobacterales	Alphaproteobacteria	Proteobacteria	Octadecabacter sp. (Octadecabacter antarcticus) Octadecabacter sp. (Octadecabacter arcticus)	0.7 1.2	0.5 0.7	0.9 0.9	0.9 1.0 0.7	13 1	4 0.6 0.8 1.0	0.9 0.5	0.9
Enterobacteriales	Gammaproteobacteria	Proteobacteria	Erwinia sp. (Erwinia amylovora)	11 11	1.4 1.4	0.5 0,4	1.7 1.0 1.0	0.5 1	3 1.0 1.0 1.3	1.6 2.1	1.4
Chlamydiales	Chlamydiia	Chlamydiae	Simkania sp. (Simkania negevensis)	1.7 1.1	0.2 0.1	0.3 0.3	1.8 1.7 1.3	1.3 8	15 1.4 0.9	1.0 1.0	2.4
Fusobacteriales	Fusobacteriia	Fusobacteria Protochasteria	Fusobacterium sp. (Fusobacterium nucleatum)	1.7 0.7	2.0 2.2	0.3 0.1	15 0.3 1.3	0.4 0	1 2.3 0.9 2.3 6 10 0.9 10	5.7 2.9	2.4
Campylobacterales	Epsilonproteobacteria	Proteobacteria	Desujopacula sp. (Desujopacula toluolică) Sulfurimonas sp. (Sulfurimonas denitrificans)	0.1 0.1	2.0 1.0	0.2 0.2	1.9 41 0.9	11 0	18 15 2.0 10	0.5 0.8	1.1
Rhodospirillales	Alphaproteobacteria	Proteobacteria	Azospirillum sp. (Azospirillum lipoferum)	0.5 0.5	0.5 0.5	0.8 1.0	1.2 1.0 0.8	0.7 2	.7 1.0 1.0 0.8	1.2 1.0	1.3
Rhodospirillales	Alphaproteobacteria	Proteobacteria	Magnetospirillum sp. (Magnetospirillum gryphiswaldense)	E.0 E.0	0.5 0.4	0.5 0.6	1.7 1.3 0.8	0.6 3	1.7 1.1 1.2 0.8	1.3 1.5	1.6
Sphingomonadales Sphingomonadales	Alphaproteobacteria	Proteobacteria Proteobactoria	Sphingomonas sp. (Sphingomonas wittichii) Sphingopuvis sp. (Sphingopuvis algeborgia)	14 17	0.7 0.9	0.5 0.7	0.6 0.7 0.7	0.9 2	0 07 08 07	0.8 0.7	1.0
Sphingomonadales	Alphaproteobacteria	Proteobacteria	Sphingomonas sp. (Sphingomonas sp. MM-1)	15 2.0	0.7 0.8	0.3 0.4	0.6 0.6 0.6	0.7 1	9 0.7 0.9 0.8	0.9 0.8	1.0
Sphingomonadales	Alphaproteobacteria	Proteobacteria	Novosphingobium sp. (Novosphingobium sp. PP1Y)	11 1.6	0.6 0.7	0.3 0.4	0.6 0.7 0.5	0.8 1	9 0.7 0.8 0.8	0.8 0.7	0.9

Species abundance

Supplementary Fig. 8 Bacterial aerosolization of abundance trimmed data set. (continued).

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Order	Class	Phylum
Sphingomonadales	Alphaproteobacteria	Proteobacteria
Sphingomonadales	Alphaproteobacteria	Proteobacteria
Cytophagales	Cytophagia	Bacteroidetes
Cytophagales	Cytophagia	Bacteroidetes
Flavobacteriales	Flavobacterija	Bacteroidetes
Natrialbales	Halobacteria	Euryarchaeota
Flavobacteriales		Bacteroidetes
Havobactenales	Havobactenia	Bacteroidetes
Sphingobacteriales	Sphingobacteriia	Bacteroidetes
Chiamydiales	Chiamydia	Chramyolae
Acidothermales		Actioobacteria
Corvneharteniales		Actinobacteria
	Gammaproteobacteria	Proteobacteria
	Epsilonproteobacteria	Proteobacteria
Magnetococcales	Alphaproteobacteria	Proteobacteria
Contract and the second second second	Alphaproteobacteria	Proteobacteria
	Alphaproteobacteria	Proteobacteria
Nitrosomonadales	Betaproteobacteria	Proteobacteria
Desulfovibrionales	Deltaproteobacteria	Proteobacteria
Desulfuromonadales	Deltaproteobacteria	Proteobacteria
Desulfuromonadales	Deltaproteobacteria	Proteobacteria
Desulfuromonadales	Deltaproteobacteria	Proteobacteria
Campylobacterales	Epsilonproteobacteria	Proteobacteria
Campylobacterales	Epsilonproteobacteria	Proteobacteria
Alteromonadales	Gammaproteobacteria	Proteobacteria
Alteromonadales	Gammaproteobacteria	Proteobacteria
Alteromonadales	Gammaproteobacteria	Proteobacteria
Enterobacteriales	Gammaproteobacteria	Proteobacteria
		Management Resources and
Legionellales	Gammaproteobacteria	Proteobacteria
Legionellales Pasteurellales	Gammaproteobacteria Gammaproteobacteria	Proteobacteria Proteobacteria
Legionellales Pasteurellales Pseudomonadales Thiotrichales	Gammaproteobacteria Gammaproteobacteria Gammaproteobacteria	Proteobacteria Proteobacteria Proteobacteria Proteobacteria
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	>	5.0		1.5 -	5.0	1	.0 - 1	1.5	0.67	7 - 1.0	0.2	- 0.6	7	<0	1.2	
	_		- Ae	eros	oliza	tion		_	-	_	Surf	ace	Enh	ance	emer	nt —
8A:B	8A:5	19A:B	19A-5	24A:8	24A:S	28A:8	28A:S	34A:8	34A:S	OS:B	85:B	195:B	24S:8	285:B	345:8	AVG
0.6	0.7	0.6	0.6	0.2	0.3	0.6	0.6	0.6	0.8	0.8	0.9	1.0	0.8	1.0	0.8	0.9
0.6	0.8	0,4	0.5	0.2	0.2	0.5	0.6	0.4	0.7	1.8	0.7	0.8	0.7	0.8	0.6	0,9
0.4	0.2	0.5	0.4	0,4	0.6	0.5	1.0	4,5	2.8	0.3	2.1	1.1	0.7	0.5	1.6	1.0
0.2	0.3	0.1	01	0.6	0.8	2.1	22	0,4	0.5	2.4	0,7	1.0	0.8	0.9	0.7	11
0.2	0.3	0.4	0.4	0.1	0.1	1.2	1.7	0.6	1.8	1.5	0.8	0.9	0,7	0.7	2.4	0.8
1.1	0.7	1.6	0.6	0,4	0.2	0.4	0.2	1.9	0,5	0.4	1.7	2.7	2.3	Z.4	3.8	2.2
0.2	0.3	0.1	0.1	0.5	0.4	1.3	2.0	0.6	1.0	2.5	0.9	1.0	1.2	0.7	0.6	1.1
1.0	2.3	0.4	0.5	0,4	0,4	0.2	0.4	0.1	0.4	0.8	0.4	0.9	0.9	0.7	0.3	0.7
E.O	0.4	01	0.1	0.4	0.4	1.4	15	03	1.1	1.8	0.9	1.1	11	0.9	0.3	1.0
0.2	0.3	0.1	0.1	0.2	0.2	0.8	13	02	23	3.1	0.9	1.0	1.0	0.6	0.1	11
0.3	0.3	0.7	0,2	0,4	0.3	1.0	1.6	ED	1.1	2.4	0.7	0.9	1.0	0.7	0.2	1.0
0.1	0.2	0.3	0.3	0.4	0.3	1.0	15	0.2	0.7	1.9	0.8	1.0	1.1	0.7	0.4	1.0
0.4	0.2	0.2	0.2	0.2	0.2	1.5	2.3	0.3	0.8	2.6	1.7	1.0	0.8	0.6	0.4	1.2
0.9	0.8	0.2	0.1	0.2	0.1	1.5	1.2	0.7	2.2	5.7	1.2	1.8	1.5	1.2	0.3	1.9
ē ē	01	0.6	0.6	0.2	0.2	1.5	0.8	0.2	0.1	3.7	1.1	1.0	1.2	1.9	23	1.8
0.4	0.3	0.9	0.8	0.5	0.4	03	04	03	0.2	0.8	1.5	12	11	0.8	11	11
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Species

Candidatus Azobacteroides sp. (Candidatus Azo

Zymomonas sp. (Zymomonas mobilis)

Erythrobacter sp. (Erythrobacter litoralis) Cytophaga sp. (Cytophaga hutchinsonii)

Species abundance

	1000000	100.007	12121	1000	-	100.000	24.6	12720	122	12025	1000	100.00	14121	10/20	12/21	1000	1000	
Cyclobacterium sp. (Cyclobacterium marinum)	0.2	0.3	0.1	0.1	0.6	0.8	2.1	22	0,4	0.5	2.4	0,7	1.0	0.8	0.9	0.7	11	
Capnocytophaga sp. (Capnocytophaga ochracea)	-9.2	0.3	0.4	0.4	0.1	0.1	1.2	17	0.6	1.8	1.5	0.8	0.9	0,7	0.7	2.4	0.8	
Halovivax sp. (Halovivax ruber)	11	0.7	1.6	0.6	0,4	0.2	0.4	0.2	1.9	0,5	0,4	1.7	27	2.3	2.4	3.8	2.2	
Zobellia sp. (Zobellia galactanivorans)	0.2	0.3	0,1	0.1	0.5	0,4	1.3	2.0	0.0	1.0	2.5	0,9	1.0	1.4	0.7	0,6	11	
Blattabacterium sp. (Mastotermes darwiniensis)	1.0	2.3	0.4	0.5	0,4	0,4	0.2	:0.4	0.1	0.4	0.8	0.4	0.9	0.9	0.7	0.3	0.7	
Ornithobacterium sp. (Ornithobacterium rhinotrocheale)	E.0	0,4	0.1	0.1	0.4	0.4	1.4	15	03	1.1	1.8	0.9	11	11	0.9	0.3	10	_
Polaribacter sp. (Polaribacter sp. MED152)	0.2	0.3	0.1	0.1	0.2	0.2	0.8	13	02	2.3	3.1	0.9	1.0	1.0	0.6	0.1	11	
Lacinutrix sp. (Lacinutrix sp. 5H-3-7-4)	0.3	0.3	0.7	0,2	0,4	0.3	1.0	1.5	03	1.1	2.4	0.7	0.9	1.0	0.7	0,7	1.0	
Nonlabens sp. (Nonlabens dokdonensis)	0.1	0.2	0.3	0.3	0,4	0.3	1.0	15	0.2	0.7	1,9	0.8	1.0	1,1	0.7	D.4	1.0	
Pedobacter sp. (Pedobacter saltans)	0.4	0.2	0.2	0.2	0.2	0,2	1.5	2.3	0.3	0.8	2,6	1.7	1.0	0.8	0.6	0.4	1.2	
Waddlia sp. (Waddlia chondrophila)	0.9	0.8	0.2	0.1	0.2	0.1	1.5	1.2	0.7	2.2	5.7	1.2	1.8	1.5	1.2	0.3	1.9	
Meiothermus sp. (Meiothermus silvanus)	03	0.1	0.6	0.6	.0.2	0.2	1.6	0.8	0.2	0.1	3.2	1.1	1.0	1.2	1.9	23	1.8	
Acidothermus sp. (Acidothermus cellulolyticus)	0.4	0.3	0.9	0.8	0.5	0.4	0.3	0.4	EG	0.9	0.8	1.5	12	1,1	0.8	1.1	1.1	
Corynebacterium sp. (Corynebacterium kroppenstedtii)	0.8	0.5	0.3	0.2	0.2	0.3	0.6	0.7	0,4	0.2	1.5	1.6	1.2	0.6	0.9	2.4	1,4	
Simiduia sp. (Simiduia agarivorans)	0.3	0.3	1.2	0.9	0,5	0.5	1.0	0.8	1.2	0.8	1.8	1.3	1.4	1.0	1.3	1.4	1.4	
Sulfurovum sp. (Sulfurovum sp. NBC37-1)	0.5	0.3	0.1	0.4	0.1	0.1	0.9	1.6	0.2	0.7	1.3	1.4	1.0	0.6	0.5	0.4	0.9	
Magnetococcus sp. (Magnetococcus marinus)	0.2	.0.1	0.5	0.5	.0.4	0.4	0.8	0.7	D.6	0.fi	2.6	1.2	1.1	0.9	1.3	1.0	1.4	
Polymorphum sp. (Polymorphum gilvum)	0.5	0.7	0.6	0.7	1.7	1.2	1.4	1.4	0.8	0.8	3.3	0.8	0.9	0.9	11	0.9	1.3	Π
alpha sp. (alpha proteobacterium HIMB59)	0.4	0.3	0.2	0.2	0,4	0.3	0.4	0.2	0.5	0.8	0.1	1.4	1.3	1.1	2.1	0.7	1.1	1
Nitrosospira sp. (Nitrosospira multiformis)	0.2	0.2	0.9	0.9	0.6	0.7	0.8	0.7	0.1	0.1	3.3	1.2	1.0	0.8	1.1	1.7	1.5	
Desulfohalobium sp. (Desulfohalobium retbaense)	0.6	0.4	0.6	0.7	0.5	0.5	0.6	0.5	0.5	0.5	1.8	1.6	0.9	1.0	1.1	1.0	1.2	
Geobacter sp. (Geobacter sulfurreducens)	0.2	0.2	11	1.1	0.5	0.5	0.9	0.7	0.9	0.5	2.3	1.0	0.9	1.0	1.4	1.8	1.4	
Geobacter sp. (Geobacter Joyan educens)	07	17	0.5	0.6	07	0.7	0.5	03	03	0 1	11	0.6	10	0.8	21	0.8	11	
Geobacter sp. (Geobacter Invieli)	0.2	0.2	0.3	0.0	0.2	0.4	0.5	0.5	05	0.8	10	0.0		0.0	10	87		
Nitratifastar co. (Nitratifastar solousiois)	0.0	0.2	0.0	0.9	0.6	0.5	0.0	0.0	0.3	0.7	0.5	1.2	1.0	1.7	1.0	0.7	0.0	
witratifractor sp. (witratifractor saisuginis)	0.6	0.2	0.9	0.9	0.0	0.5	0.2	0.2	(U.9)	0.7	0.3	4.5	1.0	4.0	1.0	0.7	0.9	
Arcobacter sp. (Arcobacter nitrofigiiis)	0.0	0.0	0.3	0.2	0,4	0.3	0.3	0.5	10.5	4.7	0.3	1.1	1.2	1.2	0.8	40.7	0.9	
Snewanella sp. (Snewanella sp. IVIK-7)	0.2	u.r	1.4	0.7	0.4	0.3	1.2	0.6	1.3	0.6	1.1	1.4	2.0	1.1	20	2.1	1.0	
Psychromonas sp. (Psychromonas sp. CNPT3)	0.5	0.6	0.7	0.4	0,5	0.4	0.6	0.5	0.6	Q.4	0,5	0.9	1.7	1,3	11	14	12	
Idiomarina sp. (Idiomarina loihiensis)	0.6	0.6	0.6	0.4	0,3	0.2	0.8	0,5	0,7	9,5	1.0	1.1	1.6	1.7	14	1.3	1.4	
Edwardsiella sp. (Edwardsiella ictaluri)	0.4	0.3	11	0.9	0,4	0.3	0.5	0,4	0,7	0.3	0,5	1.2	1.3	1.2	1.2	2.0	1.2	
Coxiella sp. (Coxiella burnetii)	0.6	0.6	1.0	0.6	0.2	0.4	0.6	0.8	0.4	0.4	1.1	1.0	1.6	0.5	0.8	1.0	1.0	
Haemophilus sp. (Haemophilus parasuis)	0.7	0.6	0.3	0.3	0.5	0.3	0.6	0.5	12	0.6	0.8	1.0	1.1	1.7	1.3	1.8	1.3	
Moraxella sp. (Moraxella catarrhalis)	0.4	0.3	0.2	0.1	0,4	0.3	1.0	0.7	0.5	0.3	0.5	1.3	1.3	1.3	1.5	1.4	1.2	
Francisella sp. (Francisella sp. TX077308)	0.5	0.6	0,6	0,5	0.5	0.5	0.7	0.9	0,4	0.2	0.7	0.8	1.4	1.0	0.8	2.3	1.2	
Ralstonia sp. (Ralstonia pickettii)	0.9	0.9	1.5	1,4	0.8	0.9	0.9	0.7	1.1	0.9	1.7	1.0	1.1	0.9	1.3	1,2	1.2	
Taylorella sp. (Taylorella asinigenitalis)	0.1	0.1	11	1.0	0.1	0.1	0.5	0.5	0.7	1.2	0.8	1.1	1.2	0.9	1.2	0.6	1.0	
Taylorella sp. (Taylorella equigenitalis)	6.0	0.2	0.2	01	0.3	0.6	8.0	0.6	0.1	0.2	0.8	1,7	1.3	0.4	13	0.8	1.1	
Bacteroides sp. (Bacteroides vulgatus)	0.5	0.8	0.8	0.7	0.5	0.7	0.6	0.8	0.3	0.1	1.5	0.7	1.1	0.8	0.7	2.2	1.2	
andidatus Azobacteroides sp. (Candidatus Azobacteroides pseudotrichonymphae)	0.8	0,3	0.6	0.5	0,4	0.4	0,4	0.5	0.7	0.6	1.0	2.5	1.1	0.8	0.7	1.1	1.2	
Bacteroides sp. (Bacteroides fragilis)	0.4	0.3	0.6	0.5	0.6	.0.4	6.7	0.4	0.5	0.9	1,4	1.5	1.2	1.6	1.6	0.6	1.3	
Paludibacter sp. (Paludibacter propionicigenes)	0.4	0.7	0.1	0.1	0.5	0.6	0.7	1.0	0.2	0.3	0.9	0.7	0.9	0.9	0.7	0.8	0.8	
Croceibacter sp. (Croceibacter atlanticus)	E.0	0.4	0.2	0.2	0.4	0.4	0.7	12	6ð	1.5	1.6	0.7	1.0	0.9	0.6	02	0.8	
Fluviicola sp. (Fluviicola taffensis)	0.4	0.4	0.5	0.5	0,3	0.4	1.0	12	02	0.5	1.3	1.0	1.0	0.9	0.8	0.4	0.9	
Blattabacterium sp. (Blattabacterium punctulatus)	0.5	0.3	0.5	0.6	0.1	0.3	0.9	1.5	0.2	E.0	1,2	1.5	0.9	0.6	0.6	0.9	1.0	
Dokdonia sp. (Dokdonia sp. 4H-3-7-5)	0.3	0.3	0.1	0.2	0,4	0.4	0.8	1.0	0.3	1.1	2.1	0.8	0.9	1.1	0.7	0.3	1.0	
Maribacter sp. (Maribacter sp. HTCC2170)	0.2	0.2	0:1	0.1	0.4	0.3	0.9	1,3	0.3	0.9	2.3	0.8	0.9	1.2	0.6	0.3	1.0	
Cellulophaga sp. (Cellulophaga alaicola)	0.2	0.3	0.2	0.2	0.3	0.3	0.8	11	03	1.2	1.8	0.9	1.1	1.0	0.7	02	1.0	
Flavobacterium sp. (Flavobacterium indicum)	.0.2	0.3	0.2	0.2	0.2	0.2	0.9	1.2	0.2	1.2	2.3	0.7	1.0	0.9	0.7	0.2	1.0	Π
Blattabacterium sp. (Blattella aermanica)	0.1	0.3	0.7	0.2	0.5	0.5	0.6	1.0	0.5	0.9	2.8	0.5	0.9	0.9	0.6	0.6	1.0	and .
Owenweeksig sp. (Owenweeksig hongkongensis)	0.2	0.2	0.2	0.2	0.3	0.3	0.7	1.0	0.4	1.3	1.8	0.8	0.9	0.9	0.7	0.3	0.9	
Aequorivita sp. (Aequorivita sublithincola)	0.1	0.2	0.3	0.3	0.4	0.3	0.8	12	0.4	0.8	15	0.8	1.0	11	0.7	0.5	0.9	
Zunonawanaja sp. (Zunonawanaja profunda)	0.2	0.1	0.7	0.3	0.3	0.3	6.9	11	03	0.5	2.5	0.7	0.9	1.0	0.R	0.4	1.0	
Cannosidanhaga sp. (Cannosidanhaga canimorsus)	0.1	0.2	0.2	0.2	na	0.2	1.0	14	03	07	21	0.7	0.9	1.2	0.7	0.5	1.0	
Cellulanhana ca. (Cellulanhana lutica)	0.2	0.4	0.2	0.2	0.2	0.2	0.2	11	0.2	0.5	1.0	0.2	1.0	0.0	0.7	0.7	0.5	-
Centrophaga sp. (Centrophaga Iyaca)	0.2	0.5	0.2	0.4	0.5	0.2	0.0	12	0.1	0.0	1.3	0.0	0.0	1.2	0.5	0.6	0.2	-
Springobacterium sp. (Springobacterium Sp. 21)	0.3	0.0	0.0	12.19	0.0	0.0	0.0	1.3	0.2	0.0	1.3	1.0	0.5	1.3	0.0	0.0	0.7	
Prostnecocnions sp. (Prostnecocnions destudrii)	10.2	(MAC)	0.8	U.D	0.0	0.5	0.0	0.9	.0.7	0.0	0.8	1.0	LA	LU	w.r	Contract of	11	
rerpetosipnon sp. (Herpetosipnon durantiacus)	0.3	O.d	0.3	0,6	0.2	0,4	0.9	0.8	0,4	0.1	1.5	1.1	0.0	0.5	12	4.6	1.1	
Geitlerinema sp. (Geitlerinema sp. PCC 7407)	E.0	0.3	0.8	0.5	0.6	0.7	0.6	93	83	0.1	0.9	1,2	1.8	0.9	17	2.0	1.4	
Deinococcus sp. (Deinococcus deserti)	0.4	0.3	0.3	0,2	0,7	0.6	0.5	0.4	0.7	0.4	1.8	1.2	11	1,2	1.2	0.6	1.2	
Meiothermus sp. (Meiothermus ruber)	0.6	0.4	0.5	0.5	0.2	0.2	0.9	0.7	0.5	0.6	1.0	1.5	1.2	0.9	1.4	0.7	11	
Exiguobacterium sp. (Exiguobacterium sp. AT1b)	0.2	0.3	0.3	02	0.4	0.2	03	0.4	0.6	0.6	1,2	0.6	1.3	1.7	0.8	11	11	
Streptococcus sp. (Streptococcus equi)	0.3	0.2	0,4	0.5	0.8	0.9	0.3	0.2	0.8	0.4	1.8	1.6	0.7	0.9	1.7	2.2	15	
Desulfotomaculum sp. (Desulfotomaculum kuznetsovii)	0.6	0.4	0.6	0.3	0.2	0.4	0.9	0.8	0.3	0.1	0.8	1.6	1.8	0,6	1.2	2.3	1.4	
lance trimmed data set. (continued).																		

Supplementary Fig. 8 Bacterial aerosolization of abundance trimmed data set. (

			Day	1	8		19	1	24	1	28		34		0	8	19	24	28	34		
Order	Family	Genus	Species AF	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	A:B	A:S	Avg AF	S:B	S:B	S:B	S:B	S:B	S:B	Avg S:B	, Abundance
Caudovirales	Myoviridae	T4likevirus	Klebsiella phage KP15	0.46	0.72	41.3	5.51	2.14	4.70	2.24	0.60	238	4.97	30.1	0.02	0.63	7.49	0.46	3.71	47.9	10.0	1
Caudovirales	Myoviridae		Klebsiella phage KP27	0.61	0.62	6.60	4.41	1.70	5.20	2.44	0.62	146	8.86	17.7	0.05	0.98	1.50	0.33	3,95	16.4	3.87	I
Caudovirales	Myoviridae	T4likevirus	Prochlorococcus phage P-SSM2	0.08	0.02	0.94	0.37	0.08	0.08	4.07	0.45	7.88	0.73	1.47	0.07	5.00	2.54	1.05	9.06	10.8	4.75	
Caudovirales	Myoviridae	T4likevirus	Synechococcus phage metaG-MbCM1	0.09	0.03	0.15	0.15	0.06	0.08	6,11	0.23	19.5	1.43	2.79	0.32	3,36	1.04	0.71	26.4	13.7	7.58	1
Caudovirales	Myoviridae	T4likevirus	Synechococcus phage S-MbCM100	0.11	0.02	0.89	0.55	0.19	0.34	1.36	0.69	10.3	0.73	1.52	0.43	4.62	1.64	0.56	1.98	14.1	3.89	1
Caudovirales	Myoviridae		Pelagibacter phage HTVC008M	0.11	0.03	0.30	0.24	0.17	0.10	3.03	0.26	6.70	0.34	1.13	0.35	3.49	1.23	1.67	11.7	19.8	6.37	
Caudovirales	Myoviridae		Prochlorococcus phage MED4-213	0.26	0.02	1.65	1.18	0.09	0.43	2.04	0.62	6.76	0.45	1.35	0.46	11.0	1.40	0.21	3.30	15.2	5.26	
Caudovirales	Myoviridae		Prochlorococcus phage P-SSM7	0.17	0.04	0.59	0.39	0.25	0.40	0.00	0.00	7.33	0.48	0.96	0.31	4.27	1.50	0.62	6.59	15.4	4.78	1
Caudovirales	Myoviridae		Synechococcus phage S-ShM2	0.15	0.02	0.90	0.81	0.11	0.08	3.06	1.85	10.8	0.44	1.82	0.24	7.86	1.11	1.44	1.65	24.7	6.16	
Caudovirales	Myoviridae		Synechococcus phage S-SM2	0.10	0.03	0.26	0.18	0.14	0.09	1.08	0.15	9.66	0.63	1.23	0.25	4.08	1.47	1.63	7.07	15.3	4.97	
Caudovirales	Myoviridae		Synechococcus phage S-SSM7	0.02	0.00	1.10	0.37	0.07	0.13			12.5	0.67	1.86	0,19	4.59	2.96	0.52	44.5	18.6	11.9	1
Caudovirales	Podoviridae	Phikmvlikevirus	Pseudomonas phage LKA1	1:13	1.68	19.5	6.42	3.62	8.22	1,90	0.63	196	7.05	24.6	0.09	0.68	3.04	0.44	3.01	27.8	5.84	
Caudovirales	Podoviridae		Pelagibacter phage HTVC010P	80.0	0.03	0.21	0.21	0,13	0.08	2.65	0.19	4,42	0.36	0.83	0.70	2.41	0.98	2.03	13.7	12.3	5.35	
Caudovirales	Podoviridae		Pelagibacter phage HTVC019P	0.05	0.03	0.17	0.20	0,16	0.12	2.72	0.17	7.36	0.87	1.19	0.39	2.92	0.87	1.30	15.7	8.43	4.93	1
Caudovirales	Podoviridae		Puniceispirillum phage HMO-2011	0.07	0.02	0.19	0.22	0.10	0.04	2.05	0.17	6.32	0.33	0.95	0.61	3.49	0.89	2.25	12.4	19,1	6.46	
Caudovirales	Podoviridae		Synechococcus phage S-RIP1	0.07	0.02	0.11	0.14	0.15	0.14	3.06	0.37	9.06	0.51	1.36	0.97	3.02	0.74	1.06	8.24	17.9	5.33	1
Caudovirales	Siphoviridae		Synechococcus phage S-SKS1	0.10	0.03	0.42	0.25	0.10	0.10	3.91	0.36	10.3	0.63	1.62	0.15	3.15	1.69	0.99	11.0	16.4	5.57	
Caudovirales			Prochlorococcus phage Syn1	0.09	0.03	0.52	0.29	0.05	0.05			22.4	2.14	3.19	0.28	3.50	1.80	1.10	7.69	10.5	4.14	1
Caudovirales			Prochlorococcus phage Syn33	0.11	0.03	0.26	0.20	0.06	0.14	1.63	0.25	12.4	1:43	1.65	0.30	3.28	1.29	0.44	8.59	8.70	3.43	1
	Inovirdae	Inovirus	Enterobacteria phage M13	0.66	2.87	0.15	0.22	3.76	1.54	0.04	0.46	0.11	0.13	0.99	0.22	0.23	0.68	2.43	0.08	0.85	0.75	1
			Prochlorococcus phage P-GSP1	0.05	0.01	0.50	0.46	0.06	0.05	6.11	0.21	5.34	0.28	1.31	0.11	3.72	1.11	1.17	29.7	19.4	9.19	1
	Phycodnaviridae	Prasinovirus	Ostreococcus lucimarinus virus OIV1	0.06	0.03	0.26	0.33	0.08	0.12	0.58	0.27	5.55	0.80	0.81	0.64	2.40	0.80	0.64	2.12	6.92	2.25	T I
	Phycodnaviridae	Prymnesiovirus	Phaeocystis globosa virus	5.42	6.65	0.29	0.53	1.58	0.59	1.45	1.06	6.17	1.10	2.48	1.97	0.82	0.55	2.69	1.37	5.62	2.17	0
	Polydnaviridae	Bracovirus	Cotesia congregata bracovirus	5.40	4.96	0.35	0.73	1.81	0.64	1.71	0.88	8.66	1.73	2.69	1.22	1.09	0.48	2.82	1.94	5.00	2.09	1
	Polydnaviridae	Ichnovirus	Glypta fumiferanae ichnovirus	5.26	7.24	0.41	0.48	2.27	0.66	1.85	1.23	4.75	0.99	2.51	2.23	0.73	0.85	3.43	1.51	4.78	2.26	
	Poxviridae	Molluscipoxvirus	s Molluscum contagiosum virus	7.33		0.83	0.81	2.31	0.46	0.94	0.41		1.25	1.79	1.59	0.27	1.01	5.07	2.28		2.04	
Herpesvirales	Alloherpesviridae	Cyprinivirus	Cyprinid herpesvirus 1	1.77	32.6	1.20	0.59	1.41	0.23	1.73	0.64	1.74	1.43	4.33	0.57	0.05	2.04	6.19	2.72	1.22	2.13	1
Herpesvirales	Alloherpesviridae	Cyprinivirus	Cyprinid herpesvirus 3	2.71	6.33	0.79	0.84	1.15	0.46	1.54	0.68	2.47	1.14	1.81	0.70	0.43	0.94	2.54	2.27	2.16	1.51	1
Herpesvirales	Alloherpesviridae	Ictalurivirus	Ictalurid herpesvirus 1	5.99	4.40	0.66	1.41	2.24	0.88	1.59	1.31	6.87	0.81	2.62	2.95	1.36	0.47	2.56	1.21	8.50	2.84	1
Herpesvirales	Herpesviridae	Roseolovirus	Human herpesvirus 6A	1	8.24	0.83	0.13		1.03	4.07	1.18	2.34	1.07	2.36	1.05		6.32		3.50	2.19	3.27	f -
							-A	eroso	olizati	on—						Surfa	ce Er	han	ceme	nt—		
								>5	0 1.5	- 5.0	10-15	0.67 -	1.0 0.2 -	0.67 <0.	2		_					
												-			•	Total f	raction	Same		84		
								Е	inriched	15	Ne	utral	D	iminished	200	. Start		Galige	ua - 0.5			

Supplementary Fig. 9 Viral aerosolization and surface enhancement. Taxonomy, aerosolization factors, and surface enrichment of viral genomes in the abundance and genome coverage trimmed data set. Heat map column labels indicate day and measurement. Aerosolization factor is expressed as the fraction of genomes in aerosol to bulk or surface (A:B or A:S). Surface enrichment is the fraction in SSML to the fraction in the bulk (S:B). Heat map values indicate ratio values (bottom legend). Genome abundance is reported as the sum of fraction of the population across the experiment and as the number of samples above 0.5% of the population. Blanks indicate samples below threshold limit.

2. Supplementary Tables

Supplementary Table 1 DNA extraction yields

Sample Date	Sample Type	Fraction	Total DNA recovered (ng)	Sample DNA concentration (ng mL ⁻¹)*	Sample Date	Sample Type	Fraction	Total DNA recovered (ng)	Sample DNA concentration (ng/mL ⁻¹)*
7/3/14	Bulk	3µm	1914.00	1.91	7/27/14	Bulk	3µm	1152.00	5.76E-01
7/3/14	Bulk	0.2µm	2850.00	1.43	7/27/14	Bulk	0.2µm	636.00	3.18E-01
7/3/14	Bulk	0.025µm	73.44	1.47E-01	7/27/14	Bulk	0.025µm	335.20	3.35E-01
7/3/14	SSML	Зµm	307.20	1.54	7/27/14	SSML	Зµm	765.60	3.83
7/3/14	SSML	0.2µm	628.80	3.14	7/27/14	SSML	0.2µm	1195.20	5.98
7/3/14	SSML	0.025µm	2.60	1.30E-02	7/27/14	SSML	0.025µm	251.33	1.26
7/5/14	Aerosol	3µm	0.75	5.22E-07	7/27/14	Aerosol	3µm	3.20	1.44E-06
7/5/14	Aerosol	0.2µm	0.80	5.53E-07	7/27/14	Aerosol	0.2µm	21.76	9.07E-06
7/5/14	Aerosol	0.025µm	8.01	3.66E-06	7/27/14	Aerosol	0.025µm	2.72	1.10E-06
7/11/14	Bulk	Зµm	554.40	2.77E-01	7/31/14	Bulk	Зµm	991.20	4.96E-01
7/11/14	Bulk	0.2µm	567.60	2.84E-01	7/31/14	Bulk	0.2µm	1248.00	8.91E-01
7/11/14	Bulk	0.025µm	4.61	4.61E-03	7/31/14	Bulk	0.025µm	344.40	3.44E-01
7/11/14	SSML	Зµm	244.80	1.22	7/31/14	SSML	Зµm	456.00	2.28
7/11/14	SSML	0.2µm	342.40	1.71	7/31/14	SSML	0.2µm	624.00	3.12
7/11/14	SSML	0.025µm	71.34	3.57E-01	7/31/14	SSML	0.025µm	305.87	1.53
7/11/14	Aerosol	3µm	6.09	2.78E-06	7/31/14	Aerosol	3µm	0.91	3.80E-07
7/11/14	Aerosol	0.2µm	220.73	7.93E-05	7/31/14	Aerosol	0.2µm	2.81	1.17E-06
7/11/14	Aerosol	0.025µm	3.38	1.45E-06	7/31/14	Aerosol	0.025µm	1.41	5.87E-07
7/22/14	Bulk	Зµm	559.20	2.80E-01	8/6/14	Bulk	3µm	583.20	2.92E-01
7/22/14	Bulk	0.2µm	1344.00	6.72E-01	8/6/14	Bulk	0.2µm	696.00	3.48E-01
7/22/14	Bulk	0.025µm	375.20	3.75E-01	8/6/14	Bulk	0.025µm	584.40	5.84E-01
7/22/14	SSML	3µm	274.40	1.37	8/6/14	SSML	3µm	122.64	6.13E-01
7/22/14	SSML	0.2µm	342.40	1.71	8/6/14	SSML	0.2µm	378.00	1.89
7/22/14	SSML	0.025µm	248.00	1.24	8/6/14	SSML	0.025µm	115.44	5.77E-01
7/22/14	Aerosol	3µm	3.02	1.26E-06	8/6/14	Aerosol	3µm	1.26	5.23E-07
7/22/14	Aerosol	0.2µm	5.53	2.30E-06	8/6/14	Aerosol	0.2µm	3.06	1.28E-06
7/22/14	Aerosol	0.025µm	2.59	1.20E-06	8/6/14	Aerosol	0.025µm	1.06	1.15E-06

*Bulk and SSML measurements are per mL of seawater, aerosol is per mL of air

Supplementary Table 2 Trimmed and filtered read statistics

Sample Name	Sequences (M)	Length (bp)	Percent GC	Sample Name	Sequences (M)	Length (bp)	Percent GC
03B0025_R1	1.7	138	46%	27B0025_R1	1.9	138	43%
03B0025_R2	1.7	147	46%	27B0025_R2	1.9	145	43%
03B02_R1	4.1	147	46%	27B3_R1	5.4	136	48%
03B02_R2	4.1	137	46%	27B3_R2	5.4	147	48%
03B3_R1	4.8	147	47%	27S0025_R1	4.2	137	44%
03B3_R2	4.8	138	47%	27S0025_R2	4.2	148	44%
03S0025_R1	1.3	136	46%	27S02_R1	5.4	148	51%
03S0025_R2	1.3	147	46%	27S02_R2	5.4	138	51%
03S02_R1	1.5	138	46%	27S3_R1	5.0	137	46%
03S02_R2	1.5	147	46%	27S3_R2	5.0	147	46%
03S3_R1	1.1	147	46%	31A0025_R1	1.1	147	48%
03S3_R2	1.1	138	46%	31A0025_R2	1.1	136	48%
05A0025_R1	0.8	137	48%	31A02_R1	1.3	147	48%
05A0025_R2	0.8	147	48%	31A02_R2	1.3	137	48%
05A02_R1	2.3	138	48%	31A3_R1	0.7	137	47%
05A02_R2	2.3	147	48%	31A3_R2	0.7	146	47%
05A3_R1	1.7	147	45%	31B0025_R1	1.4	147	47%
05A3_R2	1.7	137	45%	31B0025_R2	1.4	137	47%
11A0025_R1	1.0	147	46%	31B02_R1	6.4	148	49%
11A0025_R2	1.0	137	46%	31B02_R2	6.4	138	49%
11A02_R1	6.8	148	52%	31B3_R1	8.7	137	48%
11A02_R2	6.8	139	52%	31B3_R2	8.7	147	48%
11A3_R1	3.3	147	52%	31S0025_R1	2.3	136	45%
11A3_R2	3.3	138	52%	31S0025_R2	2.3	147	45%
11B0025_R1	0.7	138	44%	31S02_R1	10.7	148	51%
11B0025_R2	0.7	147	44%	31S02_R2	10.7	139	51%
11B02_R1	5.3	148	51%	31S3_R1	1.7	146	48%
11B02_R2	5.3	138	51%	31S3_R2	1.7	134	48%
11B3 R1	2.0	147	50%	86 27B02 R1	9.7	139	51%
11B3 R2	2.0	138	50%	86 27B02 R2	9.7	148	51%
11S0025_R1	5.7	148	43%	86A0025_R1	1.5	147	49%
11S0025 R2	5.7	140	43%	86A0025 R2	1.5	138	49%
11S02 R1	1.6	147	51%	86A02 R1	1.1	147	50%
11S02_R2	1.6	135	51%	86A02_R2	1.1	137	50%
11S3_R1	1.4	137	49%	86A3_R1	1.0	147	49%
11S3_R2	1.4	147	49%	86A3_R2	1.0	138	49%
18B3 02 R1	1.8	136	47%	86Ad R1	1.4	147	48%
18B3 02 R2	1.8	147	47%	86Ad R2	1.4	137	48%
22A0025 R1	0.7	147	45%	86B0025 R1	8.6	148	53%
22A0025 R2	0.7	137	45%	86B0025 R2	8.6	140	53%
22A02 R1	1.0	137	49%	86B3 R1	6.1	136	49%
22A02 R2	1.0	147	49%	86B3 R2	6.1	147	49%
22A3 R1	1.0	137	46%	86Bd R1	1.1	138	50%
22A3 R2	1.0	147	46%	86Bd R2	1.1	147	50%
22B0025 R1	2.5	137	43%	86S0025 R1	2.1	147	47%
22B0025 R2	2.5	148	43%	86S0025 R2	2.1	138	47%
22B02 R1	9.3	140	49%	86S02 R1	1.0	138	51%
22B02 R2	9.3	148	49%	86S02 R2	1.0	147	51%
22B3 R1	4.6	139	45%	86S3 R1	1.3	146	47%
22B3 R2	4.6	147	45%	86S3 R2	1.3	135	47%
22S0025 R1	4.7	148	43%	86Sd R1	1.3	137	48%
22S0025 R2	4.7	138	42%	86Sd R2	1.3	147	48%
22S02 R1	6.8	138	48%	87CA02 R1	0.6	137	46%
22S02 R2	6.8	148	49%	87CA02 R2	0.6	146	46%
22S3 R1	2.1	147	46%	87CA3 R1	4.7	147	51%
22S3 R2	2.1	137	46%	87CA3 R2	4.7	137	51%
27 86B02 R1	2.9	148	51%	88B02 R1	2.5	136	50%
27 86B02 R2	2.9	136	51%	88B02 R2	2.5	147	50%
27A0025 R1	1.0	137	47%	88B3 R1	1.0	138	47%
27A0025 R2	1.0	147	47%	88B3 R2	1.0	147	47%
27A02 R1	3.2	137	54%	88BS3 02 R1	1.6	147	48%
27A02 R2	3.2	147	54%	88BS3 02 R2	1.6	137	47%
27A3 R1	0.9	138	50%	mbla R1	1.7	138	49%
27A3 R2	0.9	147	50%	mbla R2	1.7	147	49%
····							
AVERAGE	3.0	142.3	47.9%				
MIN	0.6	134.0	42.0%				
MAX	10.7	148.0	54.0%	<u>.</u>			

Supplementary Table 3 Spatial coverage of scattolds to Kraken assigned genon
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Taxonomy	scaffold size	spatial coverage	spatial coverage	Taxonomy	scaffold size	spatial coverage	spatial coverage
Taxonomy	(nts)	(nts)	(%)	raxenenty	(nts)	(nts)	(%)
Acinetobacter calcoaceticus	4110074	17174	0.4%	Pelagibacter phage HTVC008M	147284	92310	62.7%
Alcanivorax dieselolei	4928223	203641	4.1%	Pelagibacter phage HTVC010P	34892	23275	66.7%
alpha proteobacterium HIMB5	1343202	4965	0.4%	Pelagibacter phage HTVC019P	42084	16404	39.0%
alpha proteobacterium HIMB59	1410127	21163	1.5%	Phaeobacter gallaeciensis	4061725	13031	0.3%
Alteromonas macleodii	4575623	1917348	41.9%	Phaeobacter inhibens	2041825.5	7261.5	0.5%
Bacillus cereus	5295158	186859	3.5%	Phaeocystis globosa virus	459984	826	0.2%
Bacteroides vulgatus	5163189	27842	0.5%	Polymorphum gilvum	4649365	18001	0.4%
Blastococcus saxobsidens	4875340	9395	0.2%	Prochlorococcus marinus	1657990	296810	17.9%
Bradvrhizobium diazoefficiens	9105828	10991	0.1%	Prochlorococcus phage MED4-213	180977	989	0.5%
Burkholderia xenovorans	3243713	13728	0.4%	Prochlorococcus phage P-GSP1	44945	1136	2.5%
Candidatus Pelagibacter ubique	1395018	27281	2.0%	Prochlorococcus phage P-SSM2	252407	300	0.1%
Candidatus Puniceispirillum marinum	2753527	33134	1.2%	Prochlorococcus phage P-SSM7	182180	3175	1.7%
Cellulophaga algicola	4888353	8416	0.2%	Prochlorococcus phage Syn1	191195	4277	2.2%
Cellulophaga lytica	3824196	20408	0.5%	Prochlorococcus phage Syn33	174285	4976	2.2%
Sonnebacterium aurimucosum	1/09613	23234	4.8%	Propionibacterium acres	2519002	2450832	97.3%
Convebacterium kronnenstedtii	2446804	4844	0.2%	Pseudomonas fluorescens	6143950	46014	0.7%
otesia congregata bracovirus	28766	157 5	0.2%	Pseudomonas fulva	4920769	6930	0.7 %
Proceibactor atlantique	20700	14005	0.7%	Pseudomonas mendocina	+920709	428758	9.5%
Noterbatter allanticus	2902902	15068	0.3%	Pseudomonas mendocina Recudomonas phago LKA1	41502	420/00	0.0%
	0221273	10900	0.3%		41593	13016	51.5%
Syprinia nerpesvirus 1	291144	1044	0.4%	Pseudomonas putida	6870827	408056	5.9%
Syprinia nerpesvirus 3	295146	316	0.1%	Pseudomonas stutzeri	4709064	1620871	34.4%
Dinoroseobacter shibae	869114.4	39816.4	25.4%	Puniceispirillum phage HMO-2011	55282	5830	10.5%
interobacteria phage M13	6407	636	9.9%	Rahnella aquatilis	2766562	3868	0.1%
rythrobacter litoralis	3251353	3890	0.1%	Ralstonia pickettii	1775243	10757	0.4%
lavobacterium indicum	2993089	5620	0.2%	Rhodanobacter denitrificans	4225490	10225	0.2%
usobacterium nucleatum	2443126	3274	0.1%	Rhodobacter capsulatus	1935960	2742.5	0.2%
Geodermatophilus obscurus	5322497	18786	0.4%	Rhodobacter sphaeroides	1461698	2004.33	0.3%
Glypta fumiferanae ichnovirus	3141	568	18.1%	Rhodococcus erythropolis	3297806	18933	0.4%
Gordonia polyisoprenivorans	2922149.5	1953	0.2%	Rhodococcus opacus	4229686.5	2595.5	0.1%
luman herpesvirus 6A	156714	363	0.2%	Roseobacter denitrificans	1081352.5	2596.25	1.8%
ctalurid herpesvirus 1	134226	321	0.2%	Roseobacter litoralis	1550624	6759	5.2%
diomarina loihiensis	2839759	13167	0.5%	Rothia mucilaginosa	2292716	311952	13.6%
<etoquloniciaenium td="" vulaare<=""><td>1516261</td><td>4392</td><td>0.4%</td><td>Ruegeria pomerovi</td><td>2300524</td><td>5500</td><td>0.2%</td></etoquloniciaenium>	1516261	4392	0.4%	Ruegeria pomerovi	2300524	5500	0.2%
(lebsiella phage KP15	174436	87598	50.2%	Serratia marcescens	5207023	16976	0.3%
(lebsiella phage KP27	174413	73104	41.9%	Sphingobium japonicum	884972.4	11099.8	4.6%
egionella pneumophila	3409143	55709	1.6%	Sphingomonas wittichii	1971748.7	14816	4.7%
eisingera methylobalidiyorans	1550332	5559 67	0.2%	Sphingopyxis alaskensis	1686856.5	34968 5	45.1%
Aarinobacter adhaerens	2304688	488703.5	17.6%	Stanhylococcus enidermidis	2454929	240828	9.8%
Aarinobacter bydrocarbonoclasticus	3080480	411335	10.3%	Stenotrophomonas maltophilia	4769156	56540	1.2%
Aethylobacterium radiotolerans	1685848	319342 25	10.3%	Streptococcus suis	2028815	54495	2.7%
Aethylophaga francieri	1372645	27145	3.5%	Streptococcus thermonhilus	17968/6	315310	17 5%
Aethylophaga nitretireducentiereseene	2127101	656087	20.0%	Sulfurimonas donitrificans	2201561	5509	0.3%
Aieropopous lutous	2501007	302046	20.9%	Sunannionas ucinitinitaris	172970	132029	76 404
	2501097	202940	12.1%	Synechococcus phage metaG-MbCM1	170429	152028	/0.4%
nonuscum contagiosum virus	190289	709	0.4%	Synechococcus phage S-IVIDCM100	170438	151/6	8.9%
ioraxella catarmalis	188/9/4	4629	0.2%	Synechococcus phage S-RIP1	44892	2/46	6.1%
nycobacterium avium	5011264	12848	0.3%	Synechococcus phage S-ShM2	1/9563	2432	1.4%
lycobacterium chubuense	3099500.5	1291.5	0.2%	Synechococcus phage S-SKS1	208007	44401	21.3%
lakamurella multipartita	6060298	245383	4.0%	Synechococcus phage S-SM2	190789	2506	1.3%
lonlabens dokdonensis	3914632	8829	0.2%	Synechococcus phage S-SSM7	232878	450	0.2%
Jovosphingobium aromaticivorans	1873023	17855	1.7%	Thalassolituus oleivorans	3764053	24088	0.6%
Octadecabacter antarcticus	4812600	5381	0.1%	Variovorax paradoxus	5626353	6430	0.1%
Octadecabacter arcticus	5200279	5393	0.1%	Zunongwangia profunda	5128187	52302	1.0%
Ostreococcus lucimarinus virus OIV1	194022	69241	35.7%				
Paragagua danitrifigana	2201180 5	9244 5	0.4%				

Supplementary Table 4 CheckM statistics of genome bins

Bin name	Label	BACT completeness	BACT contamination	BACT strain-heterogeneity	genome size (bp)	# scaffolds
np-bin7-pan.bin7_1	Legionella sp.	100	0	0	2886101	95
outliers	Roseobacter fragments	n/a	n/a	n/a		
np-bin4	<i>Methylophaga</i> sp.	100	1.72	100	2541903	61
pangenome_np-bin7_2-pan.bin7_2_14	Diatom fragment	12.93	0	0	146965	19
pangenome_np-bin7_2-pan.bin7_2_2	Polaribacter sp.	55.02	10.19	5.26	1354003	166
pangenome_np-bin7_2-pan.bin7_2_3	Phage 1	0	0	0	977327	76
pangenome_np-bin7_2-pan.bin7_2_13	Phage 2	0	0	0	356493	22
pangenome_np-bin7_2-pan.bin7_2_5	Erythrobacter sp.	97.96	0	0	2558218	49
pangenome_np-bin7_2-pan.bin7_2_6	Roseobacter fragments	12.85	3.45	52	543659	49
np-bin5	Escherichia coli	96.55	0	0	4486681	170
pangenome_np-bin7_2-pan.bin7_2_9	Roseobacter fragments	10.34	0	0	184708	27
pangenome_np-bin7_2-pan.bin7_2_8	Phage 3	0	0	0	416069	27
pangenome_np-bin7_2-pan.bin7_2_0	Roseobacter fragments	19.2	4.55	11.11	2970438	403
np-bin6	Delta proteobacteria	46.16	1.72	100	746461	86
np-bin3	Gamma proteobacteria	29.86	1.72	0	1709939	224
pangenome_np-bin7_2-pan.bin7_2_4	NCLDV	1.41	0	0	545842	57
pangenome_np-bin7_2-pan.bin7_2_7	Roseobacter fragments	1.72	0	0	178918	28
np-bin2	Novosphingobium sp.	5.8	0	0	282480	44
pangenome_np-bin7_2-pan.bin7_2_12	Roseobacter frags + contamina	ation 0	0	0	241080	24
pangenome_np-bin7_2-pan.bin7_2_10	Phage 4	0	0	0	490666	26
np-bin1	<i>Roseovarius</i> sp.	80.88	1.72	100	3387409	126
pangenome_np-bin7_2-pan.bin7_2_11	Phage 5	0	0	0	384320	24
pangenome_np-bin7_2-pan.bin7_2_1	Roseobacter sp.	74.61	0	0	4280636	394
np-bin8	Roseobacter fragments					
np-bin9	Roseobacter fragments					

Supplementary Table 5 Genome bin summaries

Genome bin	Annotation	Genome summary
NP1	Roseovarius sp.	The assembly is consistently annotated at <i>Roseovarius</i> based on ribosomal proteins and other conserved genes. The organism possesses microcompartments (ethanolamine) co-localized with polyamine uptake, which appears to be a novel system. Formate dehydrogenase suggests some C1 metabolism. This is the most abundant draft genome and is enriched in several aerosol samples.
NP2	Novosphingobium sp.	The assembly is consistently annotated as Novosphingobium but is an incomplete genome. It was very rare except at the beginning of the experiment.
NP3	Gamma proteobacteria 1	The genome is indicated as a SAR92/OM6 species, which possesses a Ni/Fe-dependent hydrogenase, a PQQ-dependent glucose dehydrogenase, and genes implicated in sulfur oxidization. It is relatively abundant throughout the experiment and generally evenly distributed between phases (bulk, SSML, and aerosol).
NP4	Methylophaga sp .	The assembly indicates a methylotroph, but unlike the closest reference genomes, it appears to lack NO reductase, dissimilatory nitrite reductase, and N ₂ O reductase. Instead it appears to have assimilatory nitrate and nitrite reductase. This species (bin) is most abundant early in the bloom.
NP5	Escherichia coli strain CAICE	The genome is annotated as <i>E. coli</i> but does not appear to have a Type III secretion system or many of the hallmarks of pathogenesis. It contains genes for capsular polysaccharide synthesis and multiple siderophore biosynthesis and uptake systems. The species is abundant in aerosols, particularly in the beginning of the experiment but is present throughout the experiment.
NP6	Delta proteobacteria 1	The genome indicates a basal deltaproteobacteria based on the phylogeny of r proteins.
NP8	Roseobacter fragments 1	This bin is annotated as a Roseobacter and is rare during the experiment.
NP9	Roseobacter fragments 2	This bin is very abundant particularly in the aerosol samples towards the end of the bloom. It contains a putative <i>rbcL /rbcS</i> gene cluster (carbon fixation via ribulose-bisphosphate carboxylase/oxygenase) and aerobic formate dehydrogenase-like protein (often can be hydrocarbon degrading).
7_1	<i>Legionella</i> sp.	Most ORFs have the highest amino acid similarity to Legionella pneumophila or drancourtii (70–80% identity) and represent a unique species, likely from a sister genus. The genome contains both Type II and Type IV secretion systems (Lsp and Dot/ICM respectively) as well as several ORFs with highest identity to eukaryotes. The genome also contains a Ni/Fe hydrogenase. The species is motile and compentent. It is most abundant early and found throughout the experiment.
7_2_0	Roseobacter fragments 6	This Roseobacter genome is most abundant in the water on day 8 of the experiment. It contains several elements of denitrification, including nitrite (Cu) reductase, nitric oxide reducatase. It is generally enriched in the aerosol phase.
7_2_1	Roseobacter sp.	The assembly yielded a moderately sized Roseobacter genome. It was abundant at the bloom peak, particularly in the aerosols. It contains a putative rbcL/rbcS gene cluster, in addition to nitrite reductase (Cu) and nitric oxide reductase. It may couple denitrification to carbon fixation.
7_2_2	Polaribacter sp.	The genome consistently suggests a basal Flavobacteria. It contains a Ni/Fe hydrogenase. It is mostly water-bourne and is most abundant during middle of the experiment.
7_2_3	Phage 1	The assembly is likely a Roseophage (phage of <i>Roseobacteria</i>) based on the similarity of auxillary metabolic proteins and the presence of clear orthologs for pelagiphage. The large size of the genome indicates this is probably not a single viral species and reflect many similar viral genomes.
7_2_4	NCLDV	This genome comprised a large bin with many hits to Marseillevirus.
7_2_5	Erythrobacter sp.	This species was abundant throughout the experiment, though most abundant towards the conclusion (Extended Data Fig. 5). It was generally found throughout all sample types.
7_2_6	Rosebacter fragments 3	This genome is abundant towards end of the experiment and was generally enriched in aerosols.
7_2_7	Rosebacter fragments 4	This assembly was rare throughout the experiment.
7_2_8	Phage 3	This assembly blooms at the end of the experiment in the 0.025 µm fraction. The abundance of Roseobacter and alpha-proteobacterial proteins, in addition to the clear phage genes (head, tail, baseplate wedge), indicate it a phage of these bacteria.
7_2_9	Rosebacter fragments 5	This assembly possibly contains a set of mobile genetic elements like plasmids. For example, much of the machinery for conjugal transfer (pilus, reverse transcriptase, resolvase, endonucleases, mate pair stabilization proteins), are present in this bin. It contains abundant <i>Roseobacter</i> elements and nitric oxide reductase and was present throughout the experiment.
7_2_10	Phage 4	Assembly indicates a phage with clear orthologs for tail, head, baseplate, but it is difficult to identify the host. A spike in abundance in the >3 µm fraction was followed by being very abundant in viral size fraction (0.025–0.2 µm) after the last two time points, with distributions in pretty much every substrate.
7_2_11	Phage 5	Assembly indicates a phage with clear orthologs for tail, head, baseplate, but it is difficult to identify the host. An abundance in the 0.025–0.2 µm fraction shifts to an increasing abundance in larger size fractions, and then reverts back to an increased amount in the 0.025–0.2 µm fraction indicating a possible transition from free hosts and then to a burst releasing process where the transition for the transition of the bast and then to a burst releasing process where the transition indicating a possible transition from free hosts.
7_2_13	Phage 2	Based on the similarity of auxillary metabolic proteins and the presence of clear orthologs for pelagiphage this assembly likely represents a phage for Resentant from later time notify the experiment and is nimarily absent from later time points.
7_2_14	Diatom fragment	This bin represents a diatom genome fragment. It includes several photosystem proteins, indicating it is likely a portion of the chloroplast genome, which is far more abundant than the nuclear chromosomes ⁷ . It is most abundant during the peak of the bloom in bulk, $>3 \mu m$ fraction samples.

Supplementary Table 6 Analysis of draft genomes using k-mer based taxonomic profiling

Draft genome	Kraken Assignment	Assembly characteristics	Genome size (bp)	No. of Contigs	% complete
JCVI_CAICE_Erythrobacter_1	Erythrobacter litoralis		2558218	49	97.96
JCVI_CAICE_Novosphingobium_1	Novosphingobium aromaticivorans		282480	44	5.8
JCVI_CAICE_Methylophaga_1 M	lethylophaga nitratireducenticrescen	s Many core methophaga genes	2541903	61	100
JCVI_CAICE_Gammaproteobacterium_1	Gammaproteobacterium HdN1	Basal gammaproteobacteria, SAR92	1709939	224	29.86
JCVI_CAICE_Escherichia coli_1	Escherichia coli		4486681	170	96.55
JCVI_CAICE_Legionella_1	Legionella pneumophila		2886101	95	100
JCVI_CAICE_Polaribacter_1	Polaribacter sp. MED152		1354003	166	55.02
JCVI_CAICE_Deltaproteobacterium_1	Candatus Babela massiliensis	Basal deltaproteobacteria	746461	86	46.16
JCVI_CAICE_Diatom_Fragment_1	Synechococcus sp. PCC_6312		146965	19	12.93
JCVI_CAICE_Roseobacter_1	Ruegeria pomeroyi		4280636	394	74.61
JCVI_CAICE_Roseovarius_1	Ruegeria pomeroyi		3387409	126	80.88
JCVI_CAICE_Roseobacter_fragments_1	-				
JCVI_CAICE_Roseobacter_fragments_2	Rhodobacter sphaeroides				
JCVI_CAICE_Roseobacter_fragments_3	Dinoroseobacter shibae		543659	49	12.85
JCVI_CAICE_Roseobacter_fragments_4	Bacillus infantis	Portion of roseobacter	178918	28	1.72
JCVI_CAICE_Roseobacter_fragments_5	Erythrobacter litoralis		184708	27	10.34
JCVI_CAICE_Roseobacter_fragments_6	Ruegeria pomeroyi	Missing core roseobacter genes	2970438	403	19.2
JCVI_CAICE_Roseobacter_fragments_7	Leisingera methylohalidivorans				
JCVI_CAICE_Roseobacter_fragments_contamination	Pseudomonas phage LKA1	Both alphaproteobacteria and roseobacter	r 241080	24	0
JCVI_CAICE_NCLDV_1	-		545842	57	1.41
JCVI_CAICE_Phage_1	Puniceispirillum phage HMO-2011	Large, T7-like	977327	76	0
JCVI_CAICE_Phage_2	Synecoccus phage ACG-2014c	Probable roseobacteria phage	356493	22	0
JCVI_CAICE_Phage_3	-		416069	27	0
JCVI_CAICE_Phage_4	Cotesia congregata bracovirus	Possible gammaproteobacteria phage	490666	26	0
JCVI_CAICE_Phage_5	-		384320	24	0

Taxonomic assignment of assembled metagenomics scaffolds using k-mer analysis (Kraken) with NCBI Refseq database. Assembled draft genomes identified utilizing APIS and manual curation. The assemblies were analyzed by Kraken to yield taxonomic assignments for comparison to raw read generated assignments. More complete genomes resulted in more accurate Kraken assignments. The diatom fragment derived from a chloroplast genome resulting in a cyanobacterial annotation in Kraken.

Supplementary Table 7 Population statistics for partially trimmed, fully trimmed, pooled, and day-resolved data sets

		AD - Value	P- Value	Skewness	Kurtosis	Mean	Std Dev	CV	Range	Minimum	Median	Maximum	N
	ALL A:B	25.91	<0.0050	0.726	2.184	-0.019	0.374	-1985	3.91	-1.59	-0.05	2.33	3550
Postorio	ALL A:S	17.25	<0.0050	0.537	2.287	-0.070	0.357	-512	4.02	-1.63	-0.08	2.39	3550
Bacteria	ALL AF	43.35	<0.0050	0.644	2.256	-0.044	0.367	-828	4.02	-1.63	-0.07	2.39	7100
	ALL S:B	-	<0.0050	0.328	4.848	0.057	0.243	423	3.31	-1.20	0.04	2.11	4260
	ALL A:B	4.47	<0.0050	0.945	1.765	0.097	0.501	516	3.31	-0.98	0.03	2.33	380
Bacteria	ALL A:S	3.54	<0.0050	0.737	2.214	0.036	0.482	1352	3.99	-1.60	0.02	2.39	380
Trimmed	ALL AF	7.70	<0.0050	0.848	1.981	0.066	0.492	742	3.99	-1.60	0.02	2.39	760
	ALL S:B	14.42	<0.0050	0.914	6.551	0.072	0.325	452	3.31	-1.20	0.03	2.11	456
	ALL A:B	4.85	<0.0050	-0.491	-0.473	-0.010	0.651	-6508	3.40	-1.78	0.21	1.62	224
Virus	ALL A:S	1.98	<0.0050	-0.300	0.257	-0.285	0.665	-233	3.95	-2.44	-0.23	1.51	223
virus	ALL AF	2.05	<0.0050	-0.380	-0.161	-0.147	0.672	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	447				
	ALL S:B	0.39	0.3826	-0.111	0.124	0.254	0.577	227	3.35	-1.67	0.22	1.68	263
	ALL A:B	1.58	<0.0050	0.219	-0.338	-0.008	0.827	-10183	4.16	-1.78	0.11	2.38	144
Virus	ALL A:S	1.03	0.0101	-0.128	0.068	-0.410	0.701	-171	3.95	-2.44	-0.35	1.51	146
Trimmed	ALL AF	0.47	0.250	0.196	0.045	-0.210	0.791	-376	4.82	-2.44	-0.21	2.38	290
	ALL S:B	0.30	0.5706	-0.204	0.034	0.276	0.629	228	3.38	-1.7	0.29	1.68	177
	day 8	12.53	<0.0050	1.353	4.175	-0.099	0.395	-400	3.34	-1.03	-0.16	2.31	710
	day 19	0.78	0.0434	0.122	1.290	0.092	0.436	471	3.91	-1.59	0.09	2.33	710
Bacteria A:B	day 24	0.87	0.0253	0.355	1.213	-0.160	0.288	-180	2.19	-1.10	-0.17	1.09	710
	day 28	5.46	<0.0050	0.508	3.723	-0.023	0.253	-1106	2.39	-1.02	-0.03	1.37	710
	day 34	8.40	<0.0050	0.619	0.765	0.095	0.393	413	2.62	-1.11	0.03	1.52	710
	day 8	6.08	<0.0050	0.902	2.142	-0.121	0.423	-348	2.96	-1.18	-0.17	1.78	710
	day 19	1.35	<0.0050	0.243	1.751	0.033	0.423	1264	4.02	-1.63	0.01	2.39	710
Bacteria A:S	day 24	0.68	0.0771	0.007	0.076	-0.137	0.282	-206	1.77	-0.97	-0.13	0.80	710
	day 28	1.47	<0.0050	0.331	1.595	-0.060	0.247	-412	1.97	-0.96	-0.06	1.01	710
	day 34	6.62	<0.0050	0.340	1.600	-0.064	0.350	-550	2.78	-1.60	-0.09	1.19	710
	day 0	7.93	<0.0050	-0.861	0.995	0.090	0.343	381	2.14	-1.20	0.14	0.93	710
	day 8	13.70	<0.0050	1.258	6.142	0.022	0.185	822	1.76	-0.66	0.01	1.11	710
Destaria C:D	day 19	5.46	<0.0050	1.154	5.543	0.059	0.122	206	1.34	-0.34	0.05	1.00	710
Dacteria 3.D	day 24	8.48	<0.0050	0.317	2.347	-0.023	0.179	-774	1.53	-0.68	-0.02	0.85	710
	day 28	*	<0.0050	1.933	16.100	0.037	0.160	429	2.10	-0.50	0.03	1.61	710
	day 34	3.81	<0.0050	0.286	2.932	0.159	0.332	209	3.11	-1.00	0.17	2.11	710
	day 8	1.85	<0.0050	0.049	-1.483	-0.230	0.823	-358	2.96	-1.78	-0.29	1.18	43
	day 19	1.64	<0.0050	1.726	4.575	-0.227	0.507	-224	2.59	-0.97	-0.25	1.62	44
Virus A:B	day 24	1.91	<0.0050	-0.244	-1.519	-0.322	0.648	-201	2.12	-1.54	-0.08	0.58	45
	day 28	2.10	<0.0050	-2.931	14.059	0.303	0.351	116	2.24	-1.45	0.31	0.79	44
	day 34	2.40	<0.0050	0.211	4.307	0.881	0.548	62	3.32	-0.94	0.86	2.38	41
	day 8	2.88	<0.0050	-0.020	-1.703	-0.417	1.168	-280	3.95	-2.44	-0.17	1.51	44
	day 19	0.67	0.077	0.526	-0.100	-0.224	0.474	-212	2.01	-1.20	-0.27	0.81	45
Virus A:S	day 24	0.97	0.0135	0.398	0.170	-0.483	0.538	-111	2.27	-1.35	-0.36	0.92	46
	day 28	0.29	0.6091	-0.100	-0.599	-0.214	0.376	-176	1.61	-1.04	-0.21	0.57	44
	day 34	0.91	0.019	0.695	1.589	-0.080	0.367	-457	1.82	-0.87	-0.10	0.95	44
	day 0	0.31	0.5526	-0.431	-0.023	-0.221	0.542	-245	2.43	-1.67	-0.22	0.76	46
	day 8	0.79	0.0362	-0.654	0.244	0.183	0.490	268	2.30	-1.26	0.29	1.04	42
Virue S.B	day 19	0.29	0.5923	0.333	0.720	0.000	0.327	-3.4x10 ¹⁸	1.58	-0.71	0.01	0.87	45
VIIUS 0.D	day 24	0.41	0.3244	-0.372	-0.447	0.172	0.352	204	1.49	-0.68	0.22	0.81	45
	day 28	0.60	0.1128	-0.289	1.711	0.532	0.497	93	2.77	-1.12	0.50	1.65	46
	day 34	1.68	<0.0050	-1.295	1.716	0.951	0.414	44	1.96	-0.28	1.03	1.68	39

Normality is tested by the Anderson–Darling (AD) normality test, skewness, kurtosis (excess), and inspection of histograms. For the AD test, p-values below 0.05 demonstrate data is significantly non-normal. Departure from zero indicates increasing non-normality in skewness and kurtosis values.

Supplementary Table 8 Percent of population in bacterial and viral reads in >3 µm, 3–0.2 µm, and 0.2–0.025 µm size fractions in bulk, SSML, and aerosol samples from read-based k-mer sequence analysis

_	Bulk	SSML	Aerosol	Bulk	SSML	Aerosol	Bulk	SSML	Aerosol
	> 3 µm	> 3 µm	> 3 μm	3 - 0.2 μm	3 - 0.2 μm	3 - 0.2 µm	0.2 - 0.025 μm	0.2 - 0.025 μm	0.2 - 0.025 μm
Bacteria	91.45	91.13	92.50	95.13	95.91	96.49	91.49	83.01	92.25
Viruses	7.28	7.72	6.86	4.27	3.63	3.03	8.00	16.15	7.18

3. Supplementary Notes

Supplementary Note 1: Bloom dynamics

Chlorophyll a peaked at 21.7 μ g L⁻¹ for bloom 1 and 30.0 μ g L⁻¹ for bloom 2 (Fig. 1. Supplementary Fig. 1). Major phytoplankton blooms at Scripps Pier generally have chlorophyll *a* levels in the range of $18 - 219 \mu g L^{-1}$, placing this on the low end of natural major bloom from the same source water. Bacteria counts were found to be in the range of 0.65 X $10^6 \pm 0.01$ X 10^6 to 3.98 X $10^6 \pm 0.02$ X 10^6 cells mL⁻¹ in bulk water, 0.36 X 10 $^6\pm$ 0.01 X 10 6 to 3.34 X 10 $^6\pm$ 0.03 X 10 6 cells mL $^{-1}$ in SSML, and 0.09 X 10 $^7\pm$ 0.06X 10⁷ to 5.83 X 10⁷ \pm 0.58 X 10⁷ cells m⁻³ in aerosol. Oceanic values for bacteria range from 10⁴ to 10⁶ cells mL^{-1 2}, making the values here on the high end of ocean concentrations. However, considering bacterial abundance increases linearly with chlorophyll ³ and under certain conditions oceanic concentrations have been found to up to 10⁸ cells mL⁻¹⁴, these values seem especially relevant. Aerosol bacteria concentrations are estimated to be $\sim 10^2$ to 10^4 cells m^{-3 5}. Virus abundances were found to be 1 X 10^7 to 8 X 10^7 cells mL⁻¹ in bulk and SSML and 0.3 X 10^7 to 7.7 X 10^7 cells m^{-3} in aerosol which is ~10-fold higher than water bacteria concentrations and approximately the same as bacterial concentrations in aerosol.

Supplementary Note 2: Genomic data analysis

DNA yields. DNA recovery and estimated original concentrations in native samples are given in Supplementary Table 1. DNA abundance was determined by Qubit[™] (ThermoFisher).

Metagenomic sequencing. A total of 625 million reads were trimmed and quality filtered generating on average 3.0 million sequence reads with lengths of 2 x 142 bp and GC content of 48% (Supplementary Table 2). Taxonomic profiling generated a total of 700 bacterial, 10 archaeal and 28 viral species in samples from the 0.02–3 μ m size fraction after data filtering. The >3 μ m and 0.025–0.2 μ m fraction were also trimmed similarly to generate 613 species (576 bacteria, 8 archaea, 29 viruses) and 627 species (585 bacteria, 7 archaea, 35 viruses), respectively. The viral species from the three fractions were pooled to yield 46 viral species.

Coverage analysis. 198 bacteria and 46 viral species identified using Kraken were further examined for genomic coverage. Scaffolds from species' assignments were examined against published genomes (Supplementary Table 3). This represented 28% of the species above abundance thresholds. Species below 0.1% spatial coverage were removed resulting in a coverage trimmed set of 76 bacterial and 30 viral species.

Genomic assembly and annotation. Sixty-two metagenomes resulted from assembly of shotgun reads. k-mer based binning (Vizbin) isolated seven bins (Np-bin1, 2, 3, 4, 5, 6, 8) and a mosaic bin (bin7). The remaining bin7 was a mosaic of genomes and thus was examined using sample-specific sequencing coverage vectors and hierarchical clustering, generating a further 14 bins. Completeness of bins was assessed using CheckM (Supplementary Table 4).

Genome bins, while mostly not complete, were recovered for Bacteria, Eukarya, and multiple viral lineages. The completeness appears to be mostly due to more conserved regions of the genome fragmenting during the secondary co-assembly, which did decrease large contigs. The low completeness (CheckM) for several genomes rather large in size is consistent with this. Annotation of genomes was performed by APIS and manual curation⁶. Summaries of genome bins are given in Supplementary Table 5. Additionally, the resulting draft genomes were run through read-based pipeline utilizing Kraken to detect similarity between the annotations of the different approaches. There was good agreement between annotations when genome coverage was adequate.

4. Supplementary References

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