Supplementary Information

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

Michaud *et al.*

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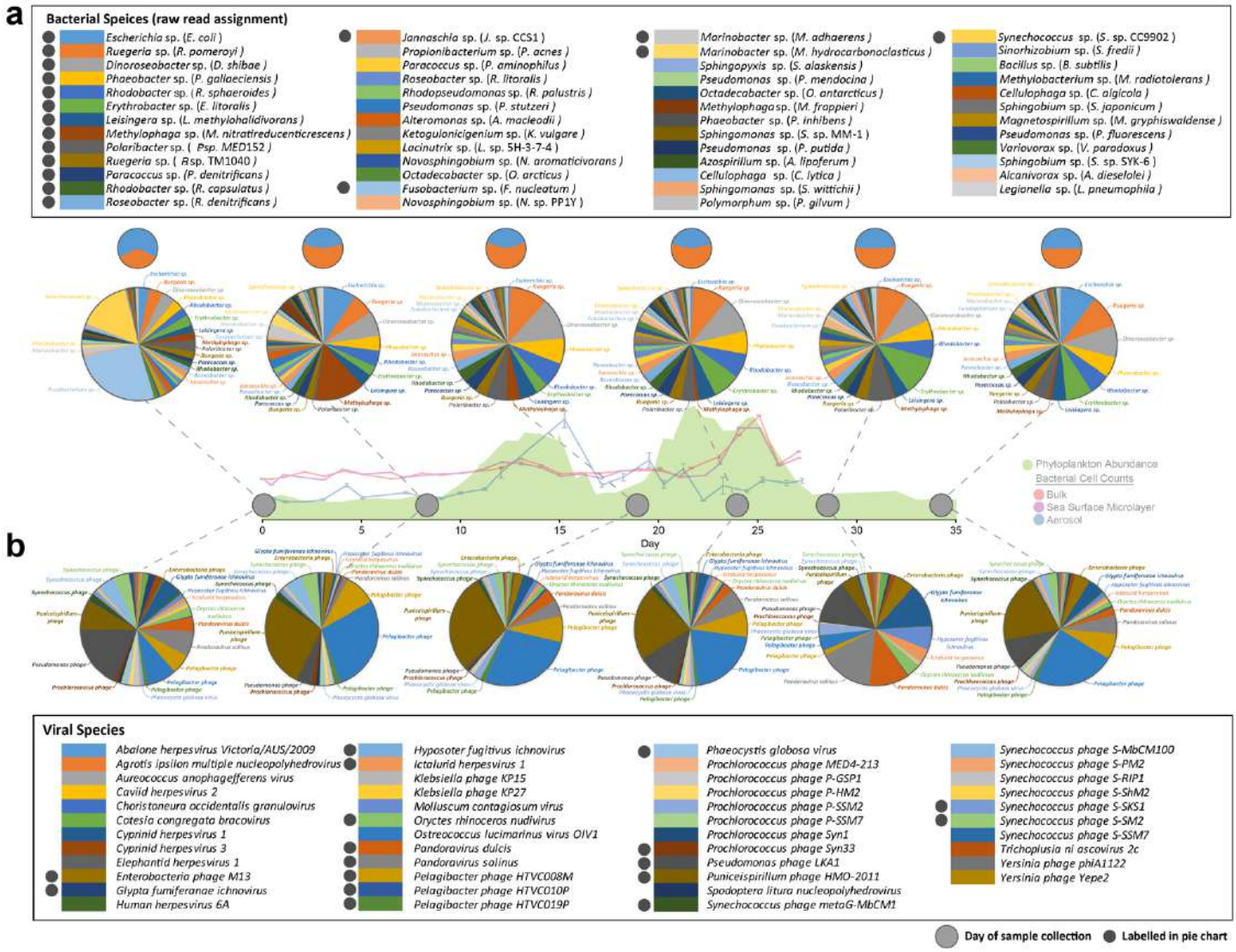
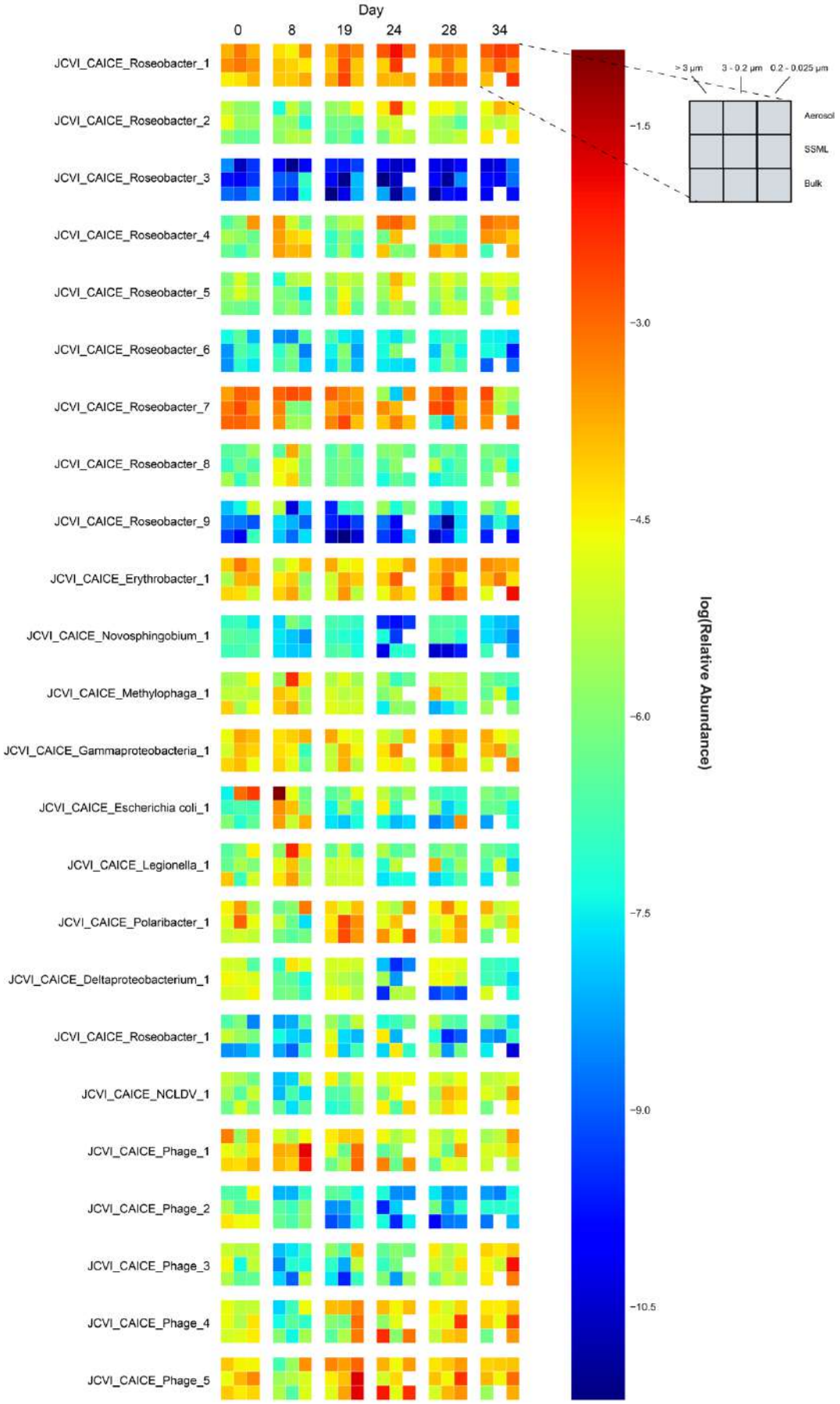
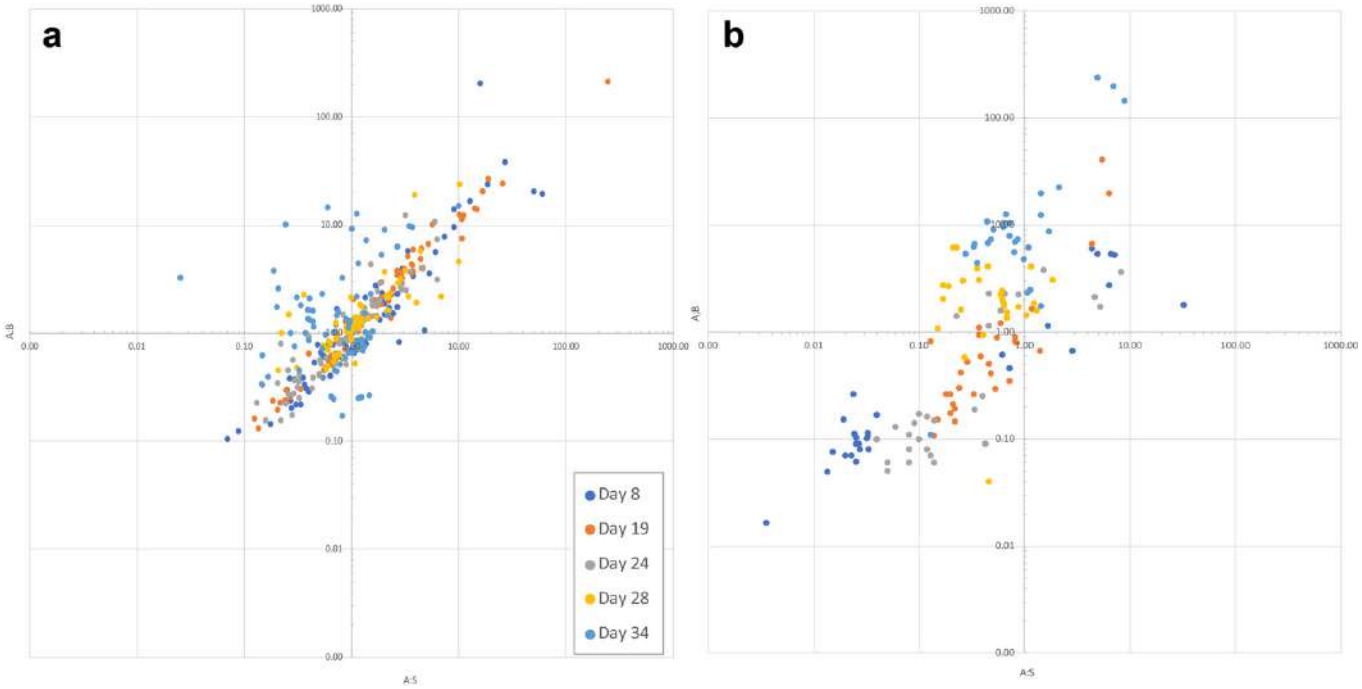
1. Supplementary Figures



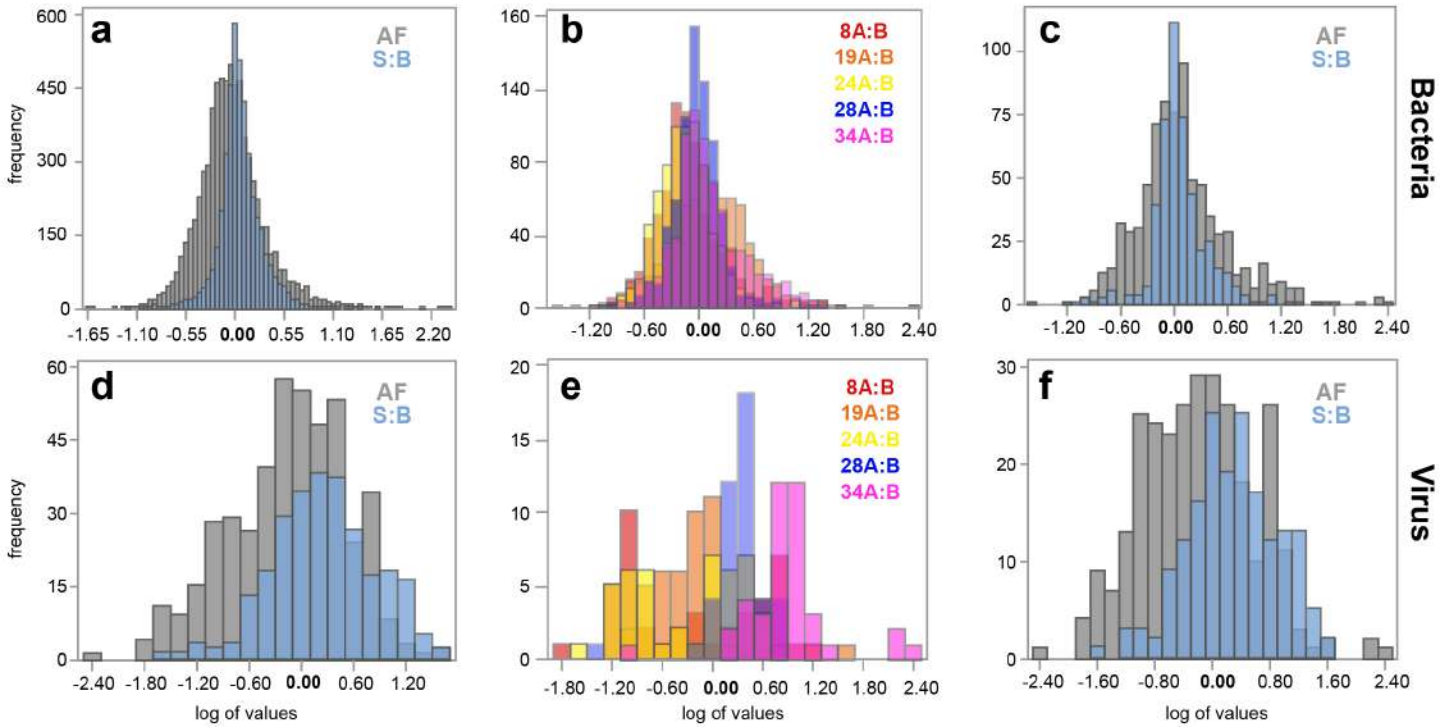
Supplementary Fig. 1 Bacterial and viral genome variation across the phytoplankton blooms. Bacteria (51 most abundant genomes), **a**, and viruses **b**, as determined by read based analysis on abundance trimmed data. Legends indicate species represented with dark gray circles denoting those that are 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.



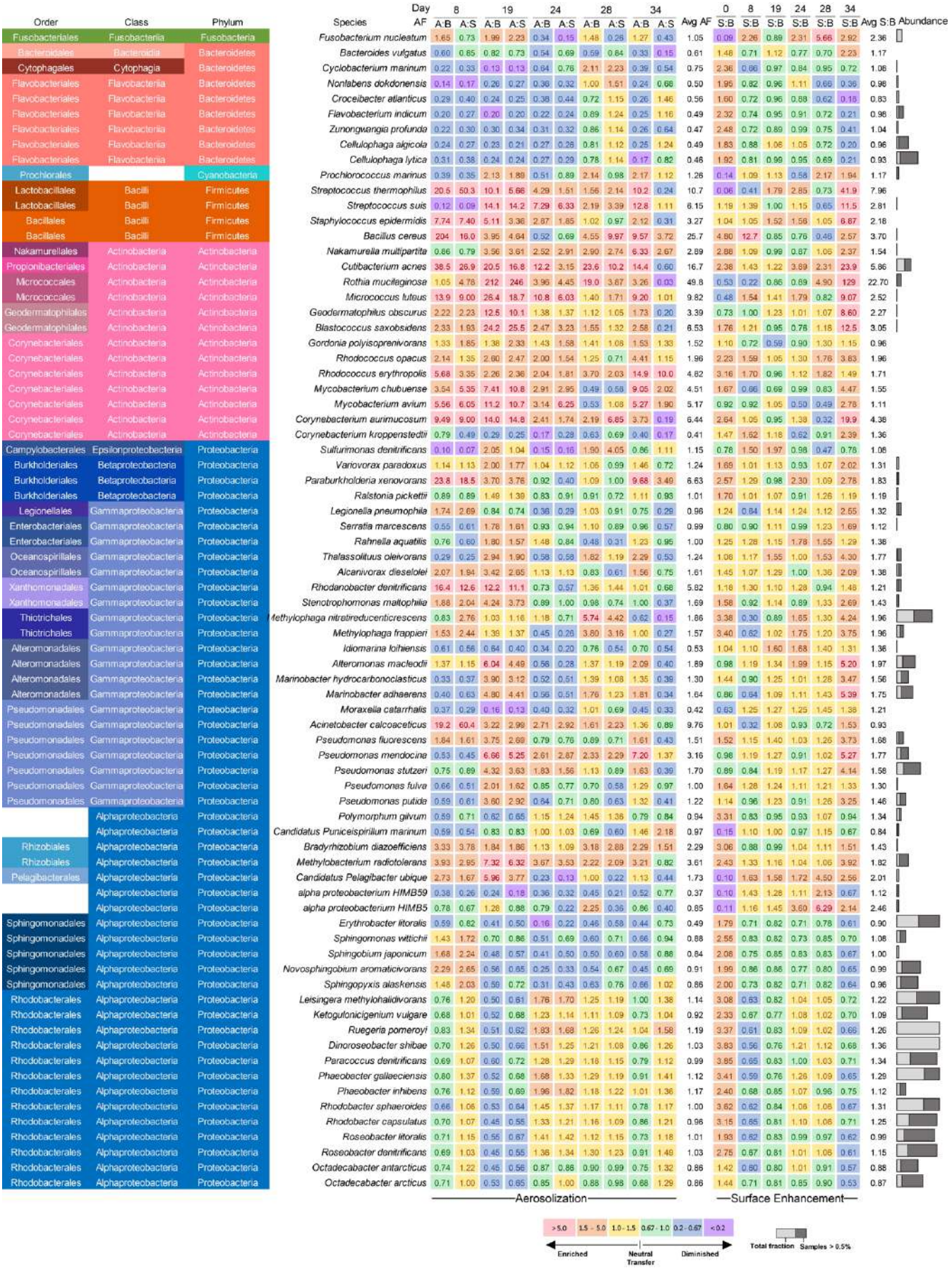
Supplementary Fig. 2 Abundance of draft genomes**.** 18 bacterial and 6 viral draft genomes determined by assembly based methods. Heatmap indicates fractional abundance of species in the sample. Day of sample is indicated on top columns. For each 9-square group size fraction is indicated from left to 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.



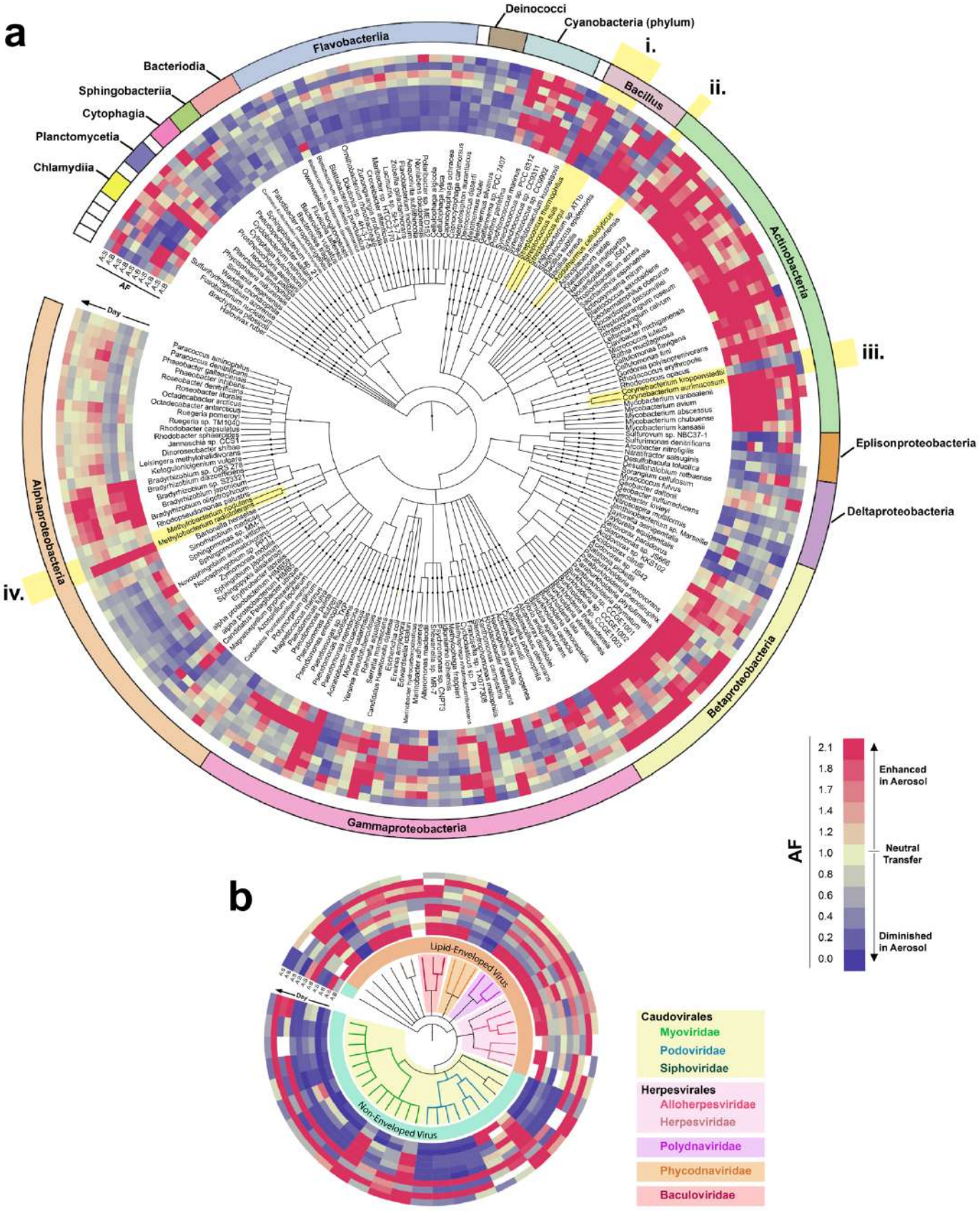
Supplementary Fig. 3 Genome spatial coverage trimmed bacterial and viral populations aerosolization distribution. The ratio of fraction of genomes in aerosols to the fraction in bulk plotted against ratio of fraction of genomes in aerosols to those in sea surface is shown for bacteria, **a**, and viruses, **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 the surface but not 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.



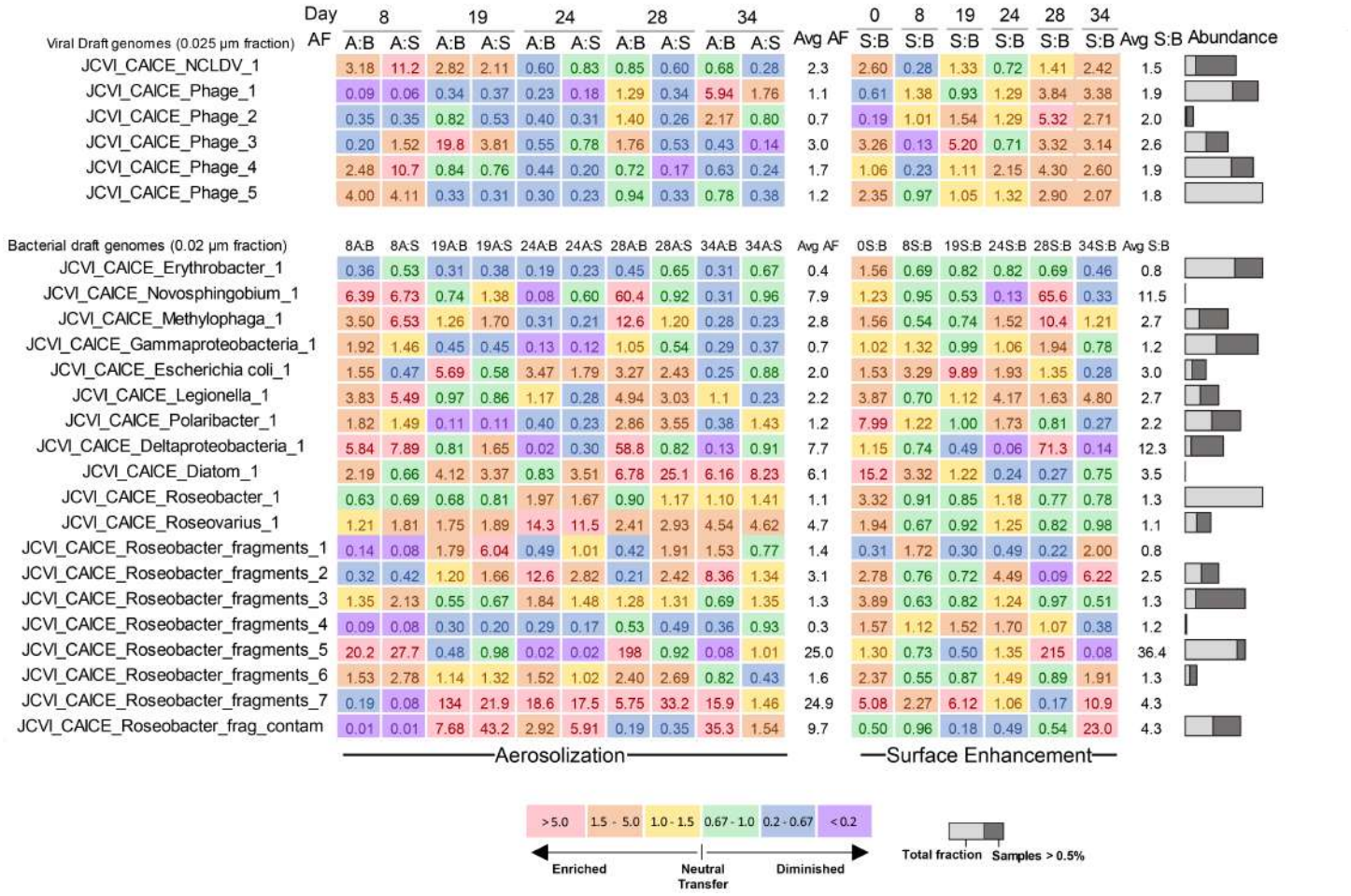
Supplementary Fig. 4 Population distribution of aerosolization and surface enrichment data sets. Histograms of all aerosolization factors (AFs) and surface enrichment factors (S:B) for bacteria, **a–c**, and viruses, **d–f** given by log values. **a, d** represent pooled AF and S:B values for abundance 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.



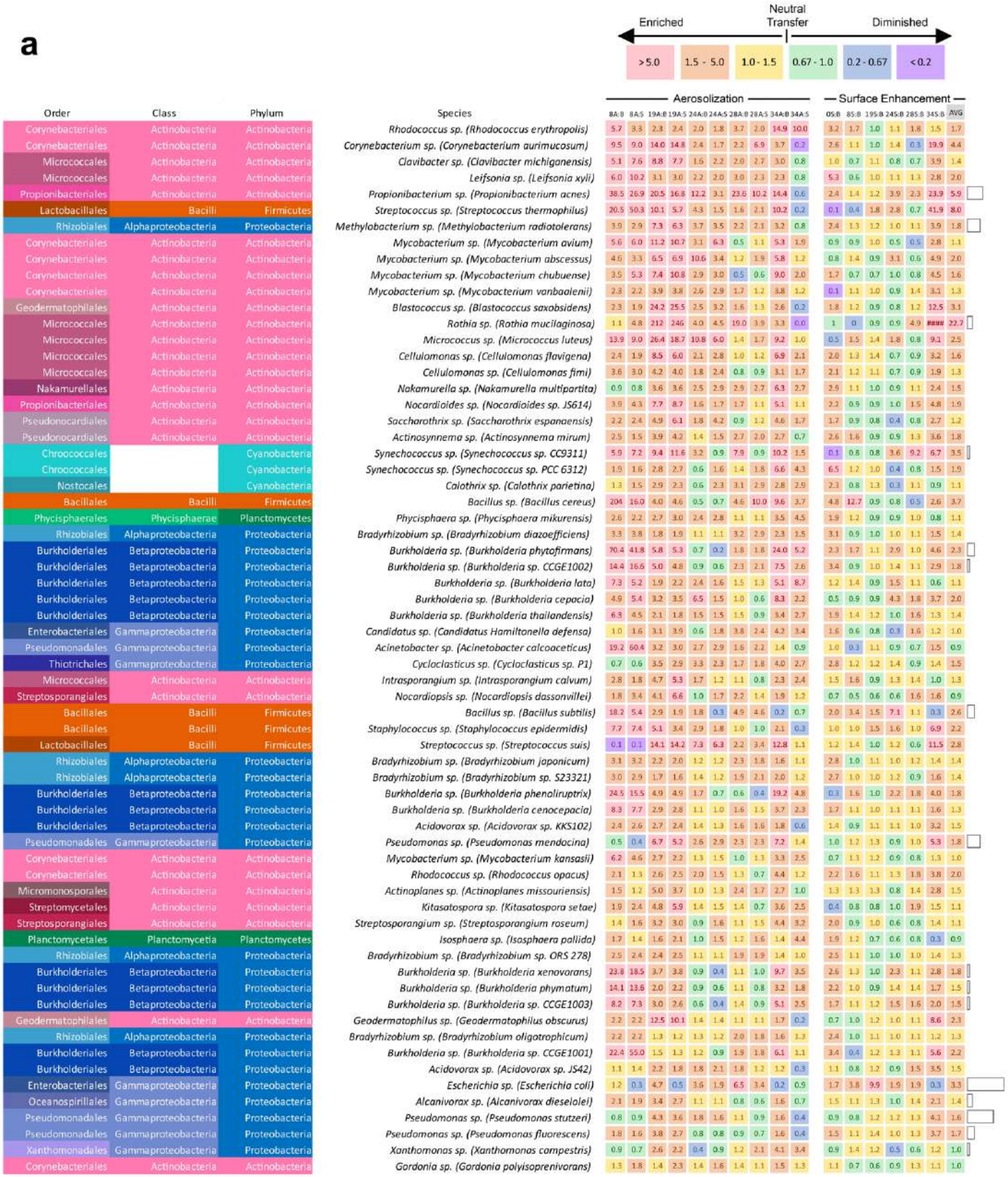
Supplementary Fig. 5 Bacterial aerosolization and surface enrichment. Taxonomy, aerosolization factors, and surface enrichment of bacterial genomes of spatial coverage and abundance trimmed data. Phylum, class, and orders are color coded to reflect species relationships. Genome annotation by read-based 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.



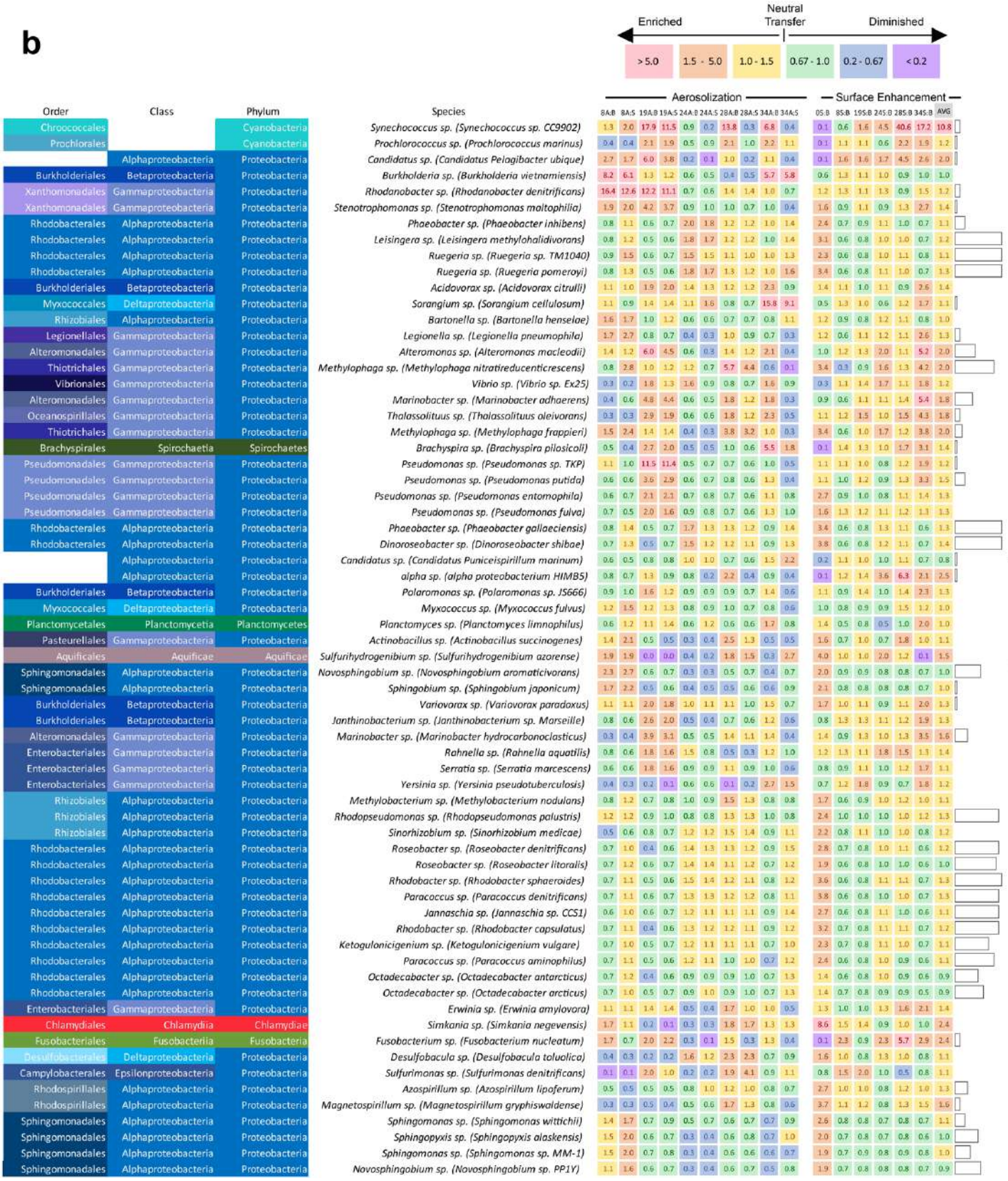
Supplementary Fig. 6 The genetic basis of bacterial and viral aerosolization in the abundance trimmed data set. Genome-based phylogenetic trees based on 197 bacterial genome sequences in **a** and 46 viral genomes in **b.** Sequences are derived from read-centric analysis of above 0.1% of the population 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.



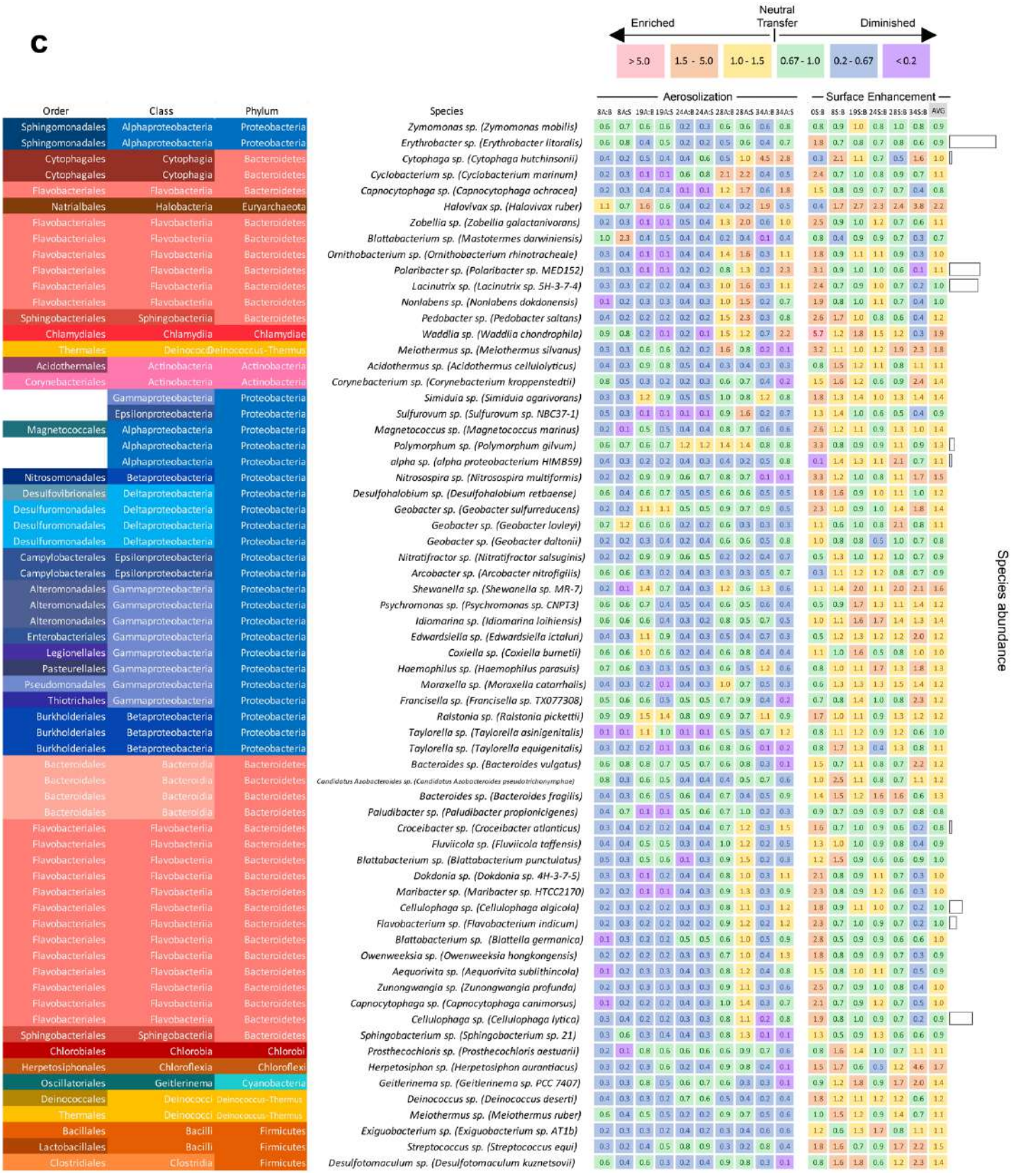
Supplementary Fig. 7 Draft genome bacterial and viral aerosolization and surface enrichment. Taxonomy, aerosolization factors, and surface enrichment of assembled draft genomes. Heat map column labels indicate day and measurement. Aerosolization factor is expressed as the fraction of species in aerosol 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.



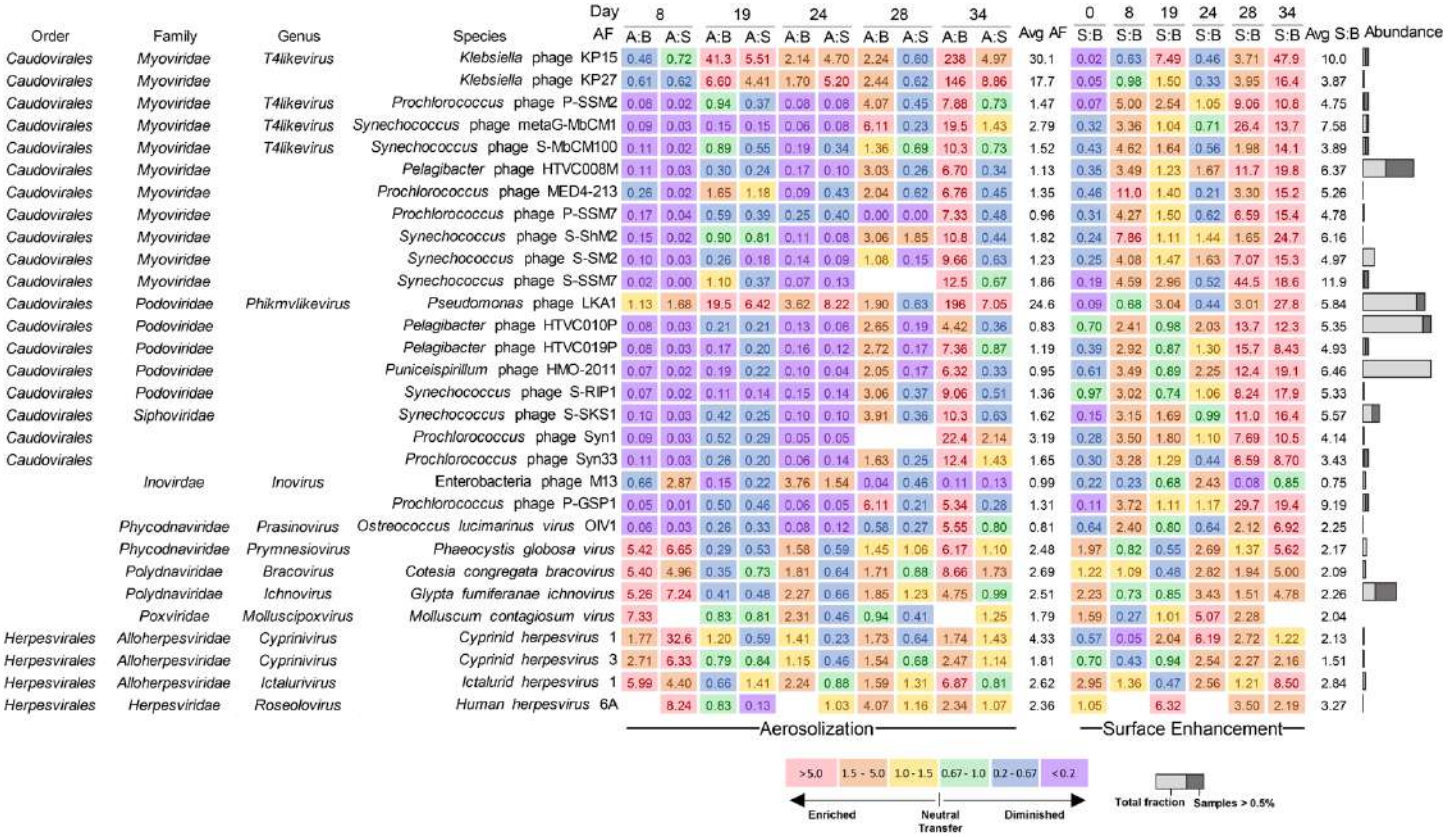
Supplementary Fig. 8 Bacterial aerosolization of abundance trimmed data set. Taxonomy, aerosolization factors, and surface enrichment of 197 bacterial genomes from abundance trimmed but not coverage trimmed data presented in three sets, **a**, **b**, **c**. Phylum, class, and orders are color coded to 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).



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



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



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	3µm	307.20	1.54	7/27/14	SSML	3µm	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	3µm	554.40	2.77E-01	7/31/14	Bulk	3µm	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	3µm	244.80	1.22	7/31/14	SSML	3µm	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	3µm	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%				

Supplementary Table 3 Spatial coverage of scaffolds to Kraken assigned genomes

Taxonomy	scaffold size (nts)	spatial coverage (nts)	spatial coverage (%)	Taxonomy	scaffold size (nts)	spatial coverage (nts)	spatial coverage (%)
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%
Bradyrhizobium 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	2.9%
Corynebacterium aurimucosum	1409613	23234	4.8%	*Propionibacterium acnes*	2519002	2450832	97.3%
Corynebacterium kroppenstedtii	2446804	4844	0.2%	*Pseudomonas fluorescens*	6143950	46014	0.7%
Cotesia congregata bracovirus	28766	157.5	0.7%	*Pseudomonas fulva*	4920769	6930	0.1%
Croceibacter atlanticus	2952962	14005	0.5%	*Pseudomonas mendocina*	5072807	428758	8.5%
Cyclobacterium marinum	6221273	15968	0.3%	Pseudomonas phage LKA1	41593	13016	31.3%
Cyprinid herpesvirus 1	291144	1044	0.4%	*Pseudomonas putida*	6870827	408056	5.9%
Cyprinid herpesvirus 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%
Enterobacteria phage M13	6407	636	9.9%	*Rahnella aquatilis*	2766562	3868	0.1%
Erythrobacter litoralis	3251353	3890	0.1%	*Ralstonia pickettii*	1775243	10757	0.4%
Flavobacterium indicum	2993089	5620	0.2%	*Rhodanobacter denitrificans*	4225490	10225	0.2%
Fusobacterium 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%
Human herpesvirus 6A	156714	363	0.2%	*Roseobacter denitrificans*	1081352.5	2596.25	1.8%
Ictalurid herpesvirus 1	134226	321	0.2%	*Roseobacter litoralis*	1550624	6759	5.2%
Idiomarina loihiensis	2839759	13167	0.5%	*Rothia mucilaginosa*	2292716	311952	13.6%
Ketogulonicigenium vulgare	1516261	4392	0.4%	*Ruegeria pomeroyi*	2300524	5500	0.2%
Klebsiella phage KP15	174436	87598	50.2%	*Serratia marcescens*	5207023	16976	0.3%
Klebsiella phage KP27	174413	73104	41.9%	*Sphingobium japonicum*	884972.4	11099.8	4.6%
Legionella pneumophila	3409143	55709	1.6%	*Sphingomonas wittichii*	1971748.7	14816	4.7%
Leisingera methylohalidivorans	1550332	5559.67	0.2%	*Sphingopyxis alaskensis*	1686856.5	34968.5	45.1%
Marinobacter adhaerens	2304688	488703.5	17.6%	*Staphylococcus epidermidis*	2454929	240828	9.8%
Marinobacter hydrocarbonoclasticus	3989480	411335	10.3%	*Stenotrophomonas maltophilia*	4769156	56540	1.2%
Methylobacterium radiotolerans	1685848	319342.25	10.3%	*Streptococcus suis*	2028815	54495	2.7%
Methylophaga frappieri	1372645	27145	3.5%	*Streptococcus thermophilus*	1796846	315319	17.5%
Methylophaga nitratireducenticrescens	3137191	656987	20.9%	*Sulfurimonas denitrificans*	2201561	5508	0.3%
Micrococcus luteus	2501097	302946	12.1%	*Synechococcus* phage metaG-MbCM1	172879	132028	76.4%
Molluscum contagiosum virus	190289	709	0.4%	*Synechococcus* phage S-MbCM100	170438	15176	8.9%
Moraxella catarrhalis	1887974	4629	0.2%	*Synechococcus* phage S-RIP1	44892	2746	6.1%
Mycobacterium avium	5011264	12848	0.3%	*Synechococcus* phage S-ShM2	179563	2432	1.4%
Mycobacterium chubuense	3099500.5	1291.5	0.2%	*Synechococcus* phage S-SKS1	208007	44401	21.3%
Nakamurella multipartita	6060298	245383	4.0%	*Synechococcus* phage S-SM2	190789	2506	1.3%
Nonlabens dokdonensis	3914632	8829	0.2%	*Synechococcus* phage S-SSM7	232878	450	0.2%
Novosphingobium 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 OlV1	194022	69241	35.7%				
Paracoccus denitrificans	2291189.5	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	*Methylophaga* 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 + contamination	0	0	0	241080	24
pangenome_np-bin7_2-pan.bin7_2_10	Phage 4	0	0	0	490666	26
np-bin1	*Roseovarius* 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 *Roseovarius* 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_2O 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 *E. coli* 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 *rbcL*/*rbcS* gene cluster (carbon fixation via ribulose-bisphosphate carboxylase/oxygenase) and aerobic formate dehydrogenase-like protein (often can be hydrocarbon degrading).
7_1	*Legionella* 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 *Roseobacteria*) 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 *Roseobacter* 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. This may indicate an early infection and burst event.
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 phage, to infection of the host, and then to a burst releasing progeny phage.
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 *Roseobacteria* . It is most abundant early in the experiment and is primarily 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 µm 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	Methylophaga nitratireducenticrescens	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	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
Bacteria	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
	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
	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
Bacteria Trimmed	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
	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
	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
Virus	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
	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
	ALL AF	2.05	<0.0050	-0.380	-0.161	-0.147	0.672	-456	4.06	-2.44	-0.09	1.62	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
Virus Trimmed	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
	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
	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
Bacteria A:B	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
	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
Bacteria A:S	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
	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
Bacteria S:B	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
	day 19	5.46	<0.0050	1.154	5.543	0.059	0.122	206	1.34	-0.34	0.05	1.00	710
	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
Virus A:B	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
	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
Virus A:S	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
	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
Virus S:B	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
	day 19	0.29	0.5923	0.333	0.720	0.000	0.327	-3.4×10^{18}	1.58	-0.71	0.01	0.87	45
	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 > 3 µm	SSML > 3 µm	Aerosol > 3 µm	Bulk 3 - 0.2 µm	SSML 3 - 0.2 µm	Aerosol 3 - 0.2 µm	Bulk 0.2 - 0.025 µm	SSML 0.2 - 0.025 µm	Aerosol 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 µg L^{-1} for bloom 1 and 30.0 µg 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 µg L^{-1} [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 10^7 to 5.83 X $10^7 \pm$ 0.58 X 10^7 cells m^{-3} in aerosol. Oceanic values for bacteria range from 10^4 to 10^6 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 10^8 cells mL^{-1} [4], these values seem especially relevant. Aerosol bacteria concentrations are estimated to be ~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 μm size fraction after data filtering. The >3 μm and 0.025–0.2 μm 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 curation[6]. 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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