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SUPPLEMENTARY INFORMATION

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Re-examination of the relationship between marine virus and microbial cell abundances

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Supplementary Text 1 – Operational definitions of viral and microbial abundances

The operational definitions "near-surface" and "sub-surface" are used to indicate predominantly euphotic and aphotic ocean depths [1]. We use the term virus abundance throughout this manuscript to denote estimates derived from culture-independent methods, including epiflourescence microscopy [2] or flow cytometry [3]. Viruses measured in these methods are generally thought to represent bacteriophage, consistent with the numerical dominance of bacteria in seawater [4]. Yet, currently available methods have potential limitations. For example, ssDNA viruses [5, 6], RNA viruses [7, 8], and giant viruses [9] are under-counted when estimates are made via epiflourescence microscopy with standard DNA based stains.

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Year	Observation	Reference
1894	Marine bacteria are first discussed by Certes, Fischer and Russell	Certes [10], Fischer [11], Russell [12], Fischer [13]
1915,1917	Bacteriophage are discovered	Twort [14], d'Hérelle [15]
1925	The presence of bacteriophage in seawater is noted	Arloing and Chavanne [16]
1946	ZoBell reports that bacteriophage occur only sporadically and in the littoral zone and concludes there is insufficient evidence for viruses to be considered as key to limiting open ocean bacteria	ZoBell [17], Carlucci and Pramer [18]
1947	The presence of bacteriophage described in the oceans	Kriss [19]
1979	Using transmission electronic microscopy, up to 10^4 ml^{-1} bacteriophage particles are observed in coastal water, an observations that sparked the rebirth of virus ecology a decade later.	Torrella and Morita [20]
1989	"Rebirth" of virus ecology across a series off papers begins with a report of virus and bacteria abundances for which VMRs range from 0.2 (Raunefjorden) to 50 (North Atlantic)	Bergh et al. [21]
1990	Report of virus particles ranging from 10^6 - 10^{11} per liter, infecting up to 7% of heterotrophic bacteria and each infected cell containing 10-100 mature virions	Proctor and Fuhrman [22]
1991-1993	Estimates of virus abundance exceeding bacteria abundance by 5-10 fold from a series of papers (this observation noted in Fuhrman and Suttle [23])	Hara et al. [24], Paul et al. [25], Wommack et al. [26], Cochlan et al. [27], Paul et al. [28]
1995	Maranger and Bird [29] survey 22 Quebec lakes and collect literature from 14 studies [21, 24, 26–28, 30–35] and report VMR higher in freshwater (20-25) than marine systems (1-5).	Maranger and Bird [29]
2000	Wommack and Colwell suggest that VMR typically ranges between 3 and 10, and note that VMR decreases as microbial abundance increases.	Wommack and Colwell [36]
2000	A VMR "roughly equal to 10" (attributed to Maranger and Bird [29] is designated as a target for parameterizing the Kill-the-Winner theory of virus-microbe interactions.	Thingstad [37]
2004	Consistency in VMR is attributed to the idea that most viruses are phage that infect bacteria. Notes a VMR of 10 in marine systems and attributes to Maranger and Bird [29].	Weinbauer [4]
2004	Chibani-Chennoufi and colleagues advance the notion that VMR is 10:1 in the ocean and that this is justified by the claim that each bacterial species can be infected by 10 different phage.	Chibani-Chennoufi et al. [38]
2008	VMR ratios reviewed in several publications that collate information from multiple studies, with a 10:1 consensus despite noted variation.	Clasen et al. [39], Wilhelm and Matteson [40]
2011	VMR reviewed across several regimes, with evidence for a linear relationship between viruses and microbes in the water column and a nonlinear relationship in sediment.	Danovaro et al. [41]
2014	The BioNumbers database, intended to facilitate quantitative analysis in the biosciences, lists VMR as 10.	Milo et al. [42]

TABLE S1: Origins and emerging consensus of the 10:1 ratio of virus abundance to microbial cell abundance in aquatic systems - from freshwater lakes to the global oceans.

Study	≤ 100m	> 100m	Total
ARCTICSBI	292	0	292
BATS	626	756	1382
BEDFORDBASIN	188	0	188
CASES03-04	199	46	245
ELA	85	0	85
FECYCLE1	31	0	31
FECYCLE2	15	0	15
GEOTRACES	141	631	772
GEOTRACES_LEG3	78	351	429
GREENLAND2012	78	46	124
INDIANOCEAN2006	42	10	52
KH04_5	159	383	542
KH05_2	117	238	355
MOVE	84	0	84
NASB2005	31	0	31
NORTHSEA2001	164	27	191
POWOW	9	0	9
RAUNEFJORD2000	95	0	95
SOG	67	0	67
STRATIPHYT1	89	24	113
STRATIPHYT2	59	34	93
SWAT	31	0	31
TABASCO	12	0	12
TROUT	47	0	47
USC MO	182	204	386
Total	2921	2750	5671

TABLE S2: Number of data points per study.

	≤ 100m		>100m	
Model	R^2	AIC	R^2	AIC
10:1	-0.16	-15305.83	-0.25	-14492.09
Power Law	0.15	-16301.81	0.64	-18313.82
Constrained Power Law	0.39	-17292.11	0.66	-18513.48
Power Law by Study	0.79	-20293.10	0.72	-18972.81

TABLE S3: Information theoretic comparison of alternative models of the relationship between virus and microbial cell abundances. The values of the Aikake Information Criteria (AIC) are defined in the Materials and Materials and Methods. The value of R^2 for each model denotes the relative amount of variance explained. Negative values of R^2 mean that a model explains less variance than does the overall mean.

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Study	Intercept	Std. Error	Group
ARCTICSBI	4.552594	0.1580157	A
FECYCLE1	4.552594	0.1837236	A
FECYCLE2	4.552594	0.1961546	A
MOVE	4.552594	0.1982541	A
Raunefjord	4.552594	0.1716625	A
StratiphytI	4.552594	0.1543207	A
USCMO	4.552594	0.1806831	A
KH05_2	4.513041	0.1683358	A
SOG	4.480697	0.1869220	A
POWOW	4.408948	0.2060002	B
StratiphytII	4.389658	0.1765001	B
KHO4	4.339907	0.1688285	B
CASES0304	4.339902	0.1669256	B
BEDFORDBASIN	4.336256	0.1825271	B
BATS	4.332784	0.1647363	B
ELA	4.332784	0.1885707	B
GEOTRACES	4.332784	0.1580225	B
GEOTRACES_LEG3	4.332784	0.1679548	B
GREENLAND2012	4.332784	0.1759093	B
INDIANOCEAN2006	4.332784	0.1820002	B
NASB2005	4.332784	0.1876671	B
NORTHSEA2001	4.332784	0.1770218	B
SWAT	4.332784	0.1945882	B
TABASCO	4.332784	0.2047635	B
TROUT	4.332784	0.2019569	B

TABLE S4: Variation in the estimate of the intercept, $\alpha_0^{(i)}$, for each study and associated standard error for the constrained power-law model as applied to surface ocean data. The common intercept in this model is $\alpha_0 = 4.44$ and the common slope is 0.42. The group column denotes whether the study-specific intercept exceeds that of the common intercept (denoted as group A) or is below that of the common intercept (denoted as group B). The table is sorted according to the lab-specific intercept estimates.

	≤ 100 m		> 100 m	
Study	R^2	p-value	R^2	p-value
ARCTICSBI	0.441	<1e-05		
BATS	0.045	<1e-05	0.504	<1e-05
BEDFORDBASIN	0.537	<1e-05		
CASES03-04	0.541	<1e-055	0.072	0.0718
ELA	0.343	<1e-05		
FECYCLE	0.146	0.0341		
FECYCLE2	0.004	0.813		
GEOTRACES	0.163	<1e-05	0.706	<1e-05
GEOTRACES_LEG3	0.043	0.0695	0.396	<1e-05
GREENLAND2012	0.868	<1e-05	0.333	2.7e-05
INDIANOCEAN2006	0.068	0.0955	0.288	0.11
KH04_5	0.325	<1e-05	0.703	<1e-05
KH05_2	0.122	0.000112	0.836	<1e-05
MOVE	0.24	<1e-05		
NASB2005	0.382	0.00021		
NORTHSEA2001	0.542	<1e-05	0.51	2.85e-05
POWOW	0.136	0.329		
RAUNEFJORD2000	0.349	<1e-05		
SOG	0.788	<1e-05		
STRATIPHYT1	0.448	<1e-05	0.471	0.000214
STRATIPHYT2	0.768	<1e-05	0.731	<1e-05
SWAT	0.026	0.389		
TABASCO	0.371	0.0354		
TROUT	0.687	<1e-05		
USC MO	0.229	<1e-05	0.462	<1e-05

TABLE S5: Explanatory power and significance of power-law fits for the model in which the power-law exponent is allowed to vary between studies. Empty cells in a row denote the absence of samples collected at depths > 100 m for the study denoted in the left-most column.

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	$\leq$ 100 m		$>$ 100 m	
Study	α_0	α_1	α_0	α_1
ARCTICSBI	2.13	0.97		
BATS	4.81	0.31	2.49	0.72
BEDFORDBASIN	1.32	0.91		
CASES03-04	2.40	0.77	2.80	0.65
ELA	2.38	0.66		
FECYCLE	1.29	1.05		
FECYCLE2	5.36	0.38		
GEOTRACES	4.40	0.41	3.63	0.52
GEOTRACES_LEG3	4.09	0.45	3.43	0.53
GREENLAND2012	0.98	0.97	2.05	0.76
INDIANOCEAN2006	4.97	0.28	2.75	0.66
KH04_5	4.04	0.48	3.00	0.64
KH05_2	4.66	0.40	2.48	0.76
MOVE	5.06	0.45		
NASB2005	1.80	0.69		
NORTHSEA2001	0.74	1.00	1.59	0.84
POWOW	5.14	0.30		
RAUNEFJORD2000	4.30	0.48		
SOG	-0.68	1.25		
STRATIPHYT1	3.42	0.71	4.53	0.45
STRATIPHYT2	2.93	0.68	2.96	0.67
SWAT	6.36	0.11		
TABASCO	3.73	0.49		
TROUT	1.83	0.78		
USC MO	4.37	0.49	2.18	0.79

TABLE S6: Power-law exponents, α_1, and intercepts, α_0, for each study from the mixed model allowing study-specific slopes and intercepts. Empty cells in a row denote the absence of samples collected at depths $>$ 100 m for the study denoted in the left-most column.

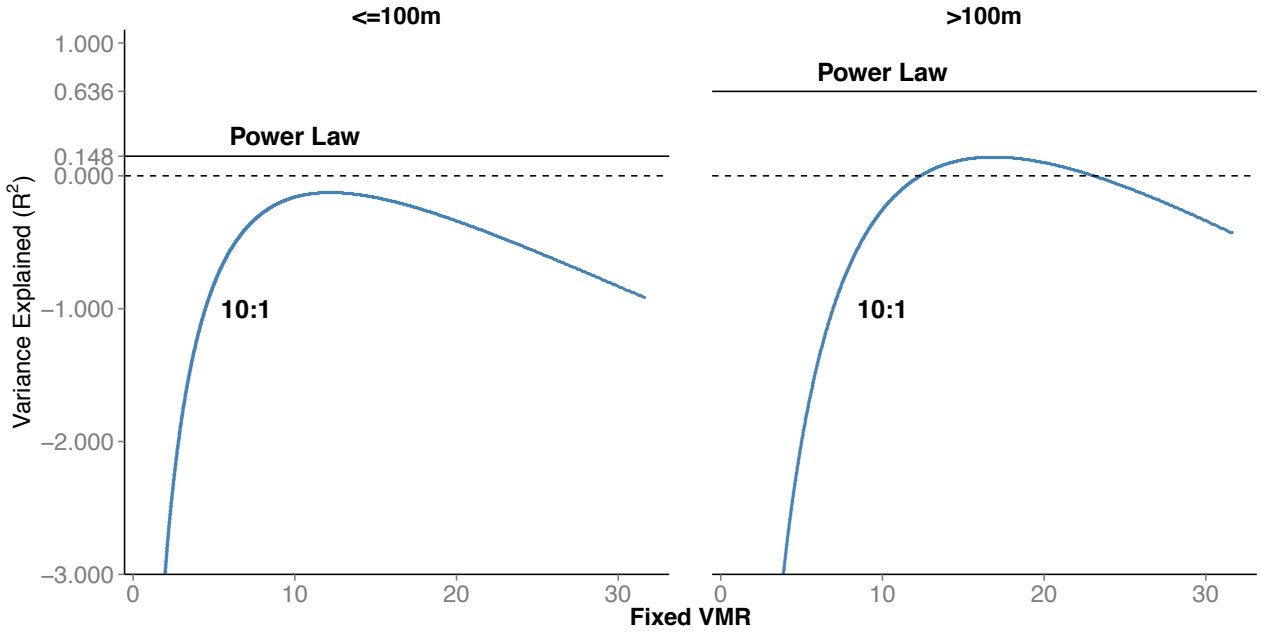

FIG. S1: Explanatory power of fixed VPR models in the surface ocean (left) and deeper water column (right). The x-axis denotes the value r in the model $V = rM$ where V denotes virus abundance and M denotes microbial abundance. The y-axis denotes the fraction of variance explained, R^2. Here, $R^2 = 1 - \mathrm{SSE}_{\mathrm{model}}/\mathrm{SSE}_{\mathrm{total}}$ where $\mathrm{SSE}_{\mathrm{model}}$ is the sum of squared errors for the model and $\mathrm{SSE}_{\mathrm{total}}$ is the sum of total squared errors.

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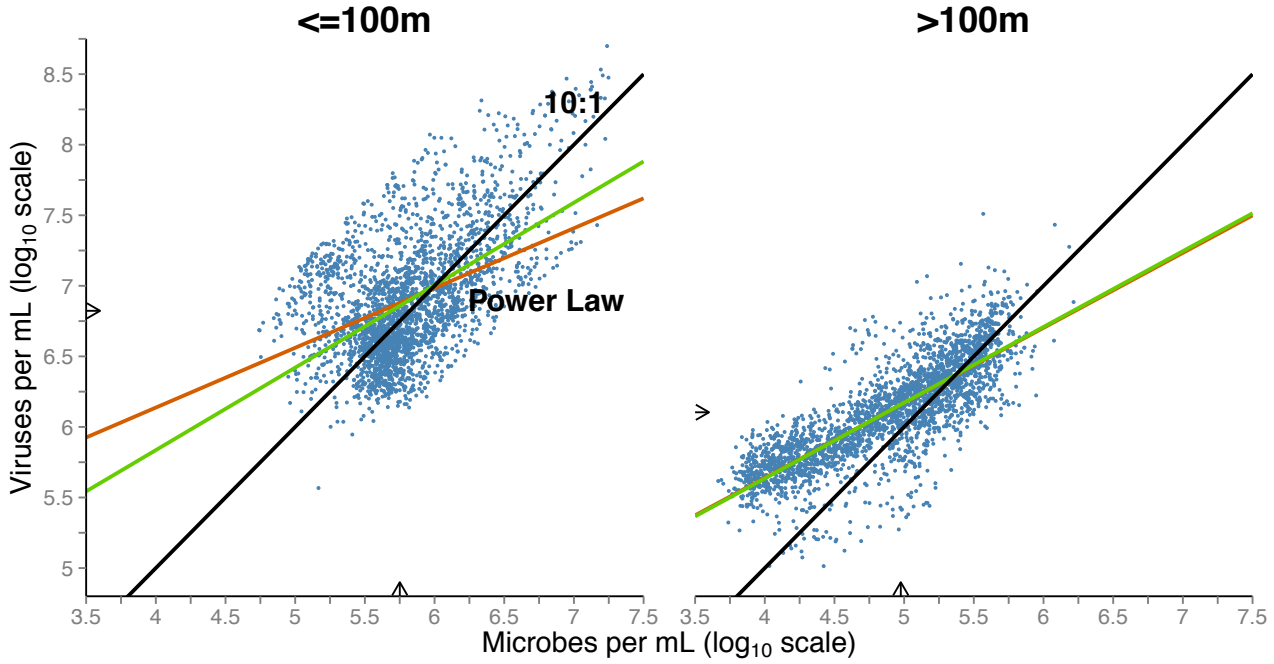

FIG. S2: Explanatory power of fixed VPR models in the near-surface and sub-surface with and without outliers. The three lines in each panel denote the 10:1 line (black), power-law fit (red) and power-law fit when removing outliers (green). The R^2 value for the power law fit for surface data excluding outliers is 0.30, has a slope of 0.58 and an intercept of 3.50. The R^2 value for the power law fit for sub-surface data excluding outliers is 0.65, has a slope of 0.54 and an intercept of 3.49.

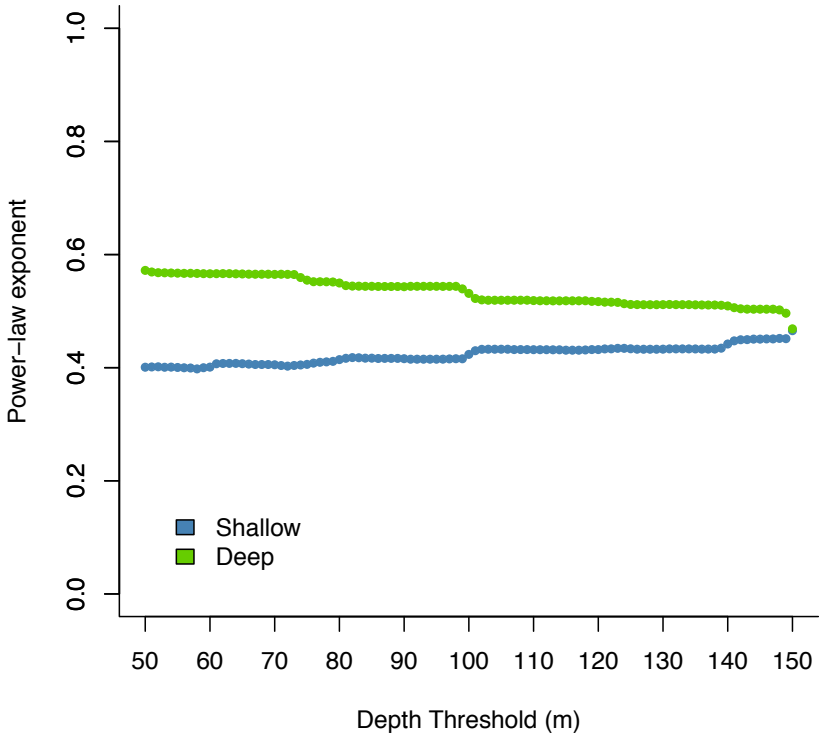

FIG. S3: Variation in estimated power-law exponent as a function of sampling depth cutoff, over the range 50m to 150m. In all cases power-law exponents were measured on log transformed data (see Materials and Methods). The slope varies from $0.40 - 0.47$ for near-surface samples, as compared to the CI of $0.39 - 0.46$ when using 100m cutoffs, i.e., nearly coinciding with the original uncertainty in the estimated slope. The slope varies from $0.47 - 0.57$ for sub-surface samples, as compared to the CI of $0.52 - 0.55$ when using 100m cutoffs. This represents an approximately 10% change in slope estimate. The trend in slope with changes in cutoff depth reflects the difference between near- and sub-surface scaling relationships which are shallower and steeper, respectively. Irrespective of cutoff, we conclude that power-law exponents are sublinear, close to that when estimated using a 100m cutoff.

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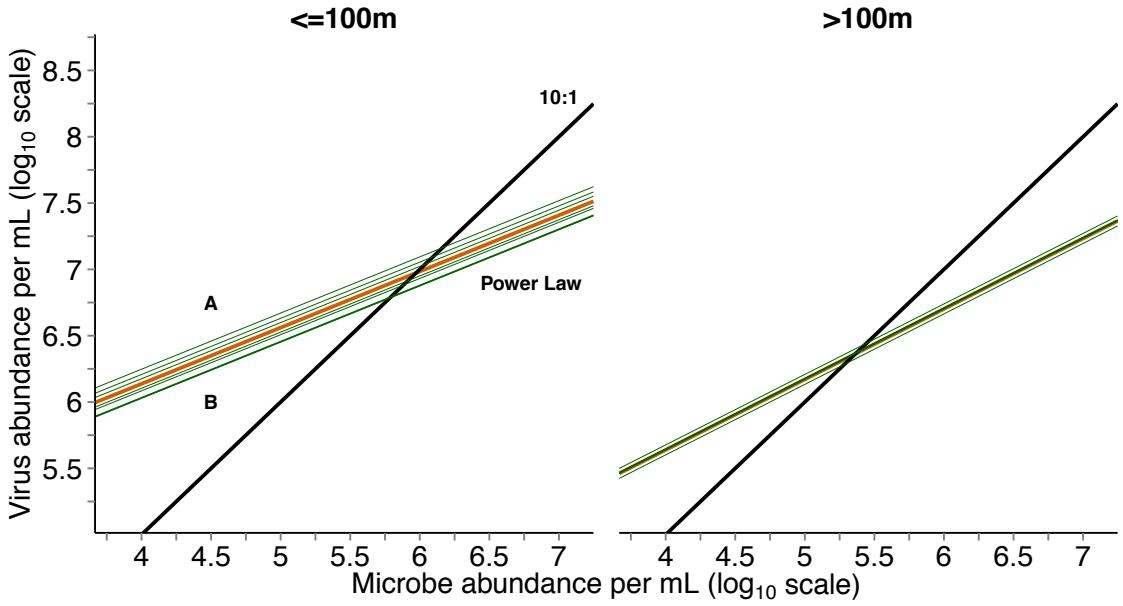

FIG. S4: Constrained regression model for samples taken at depths $\leq$ 100m (left) and $>$ 100m (right) where the intercept for each study was permitted to vary (see Materials and Methods). Blue line denotes the 10:1 relationships, the red line denotes the best-fitting power-law model, and the remainder of lines denote the variable intercept model with intercept values reported in Table S4.

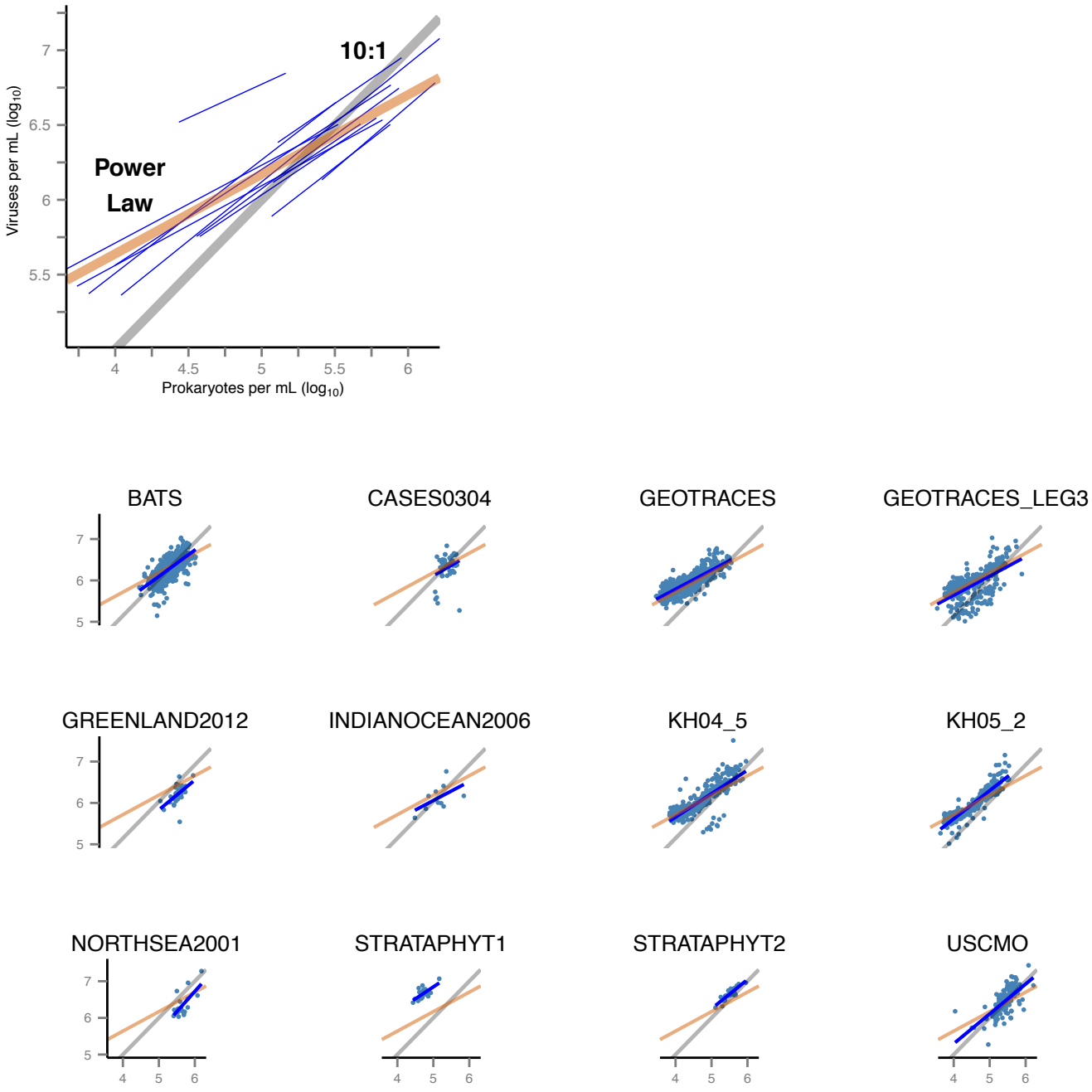

FIG. S5: Virus-microbe relationships given the variable slope and intercept mixed-effects model for samples taken at depths greater than 100m. (Upper-left) Best-fit power-law for each study (blue lines) plotted along with the best-fit power-law of the entire dataset (red line) and the 10:1 line (grey line). (Individual panels) Best-fit power-law model (blue line) on log-transformed data (blue points) for each study, with the power-law model regression (red) and 10:1 line (black) as reference. The power-law exponents and associated confidence intervals are shown in Figure S6,

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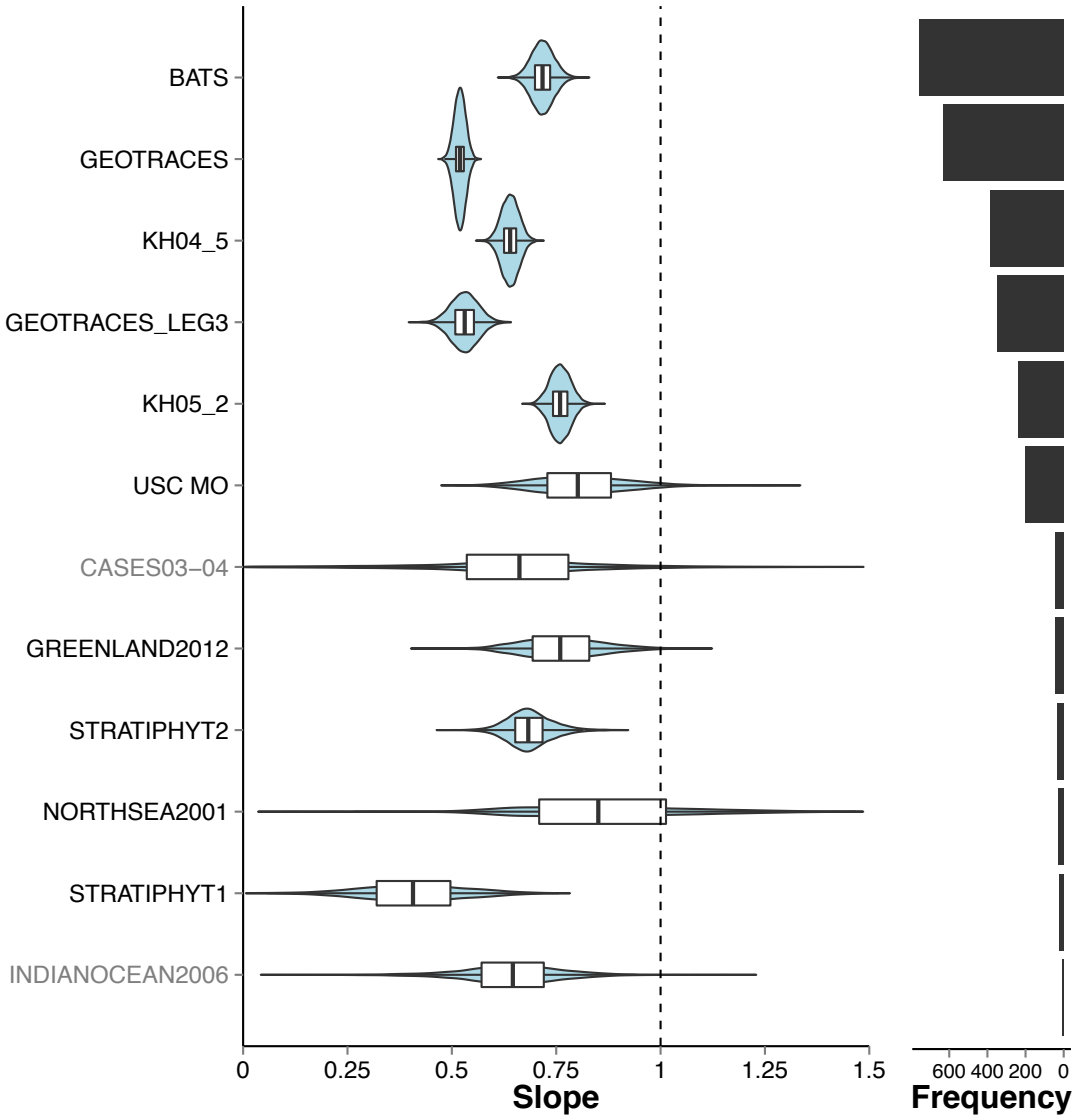

FIG. S6: Study-specific 95% confidence intervals of power-law exponents for relationships between virus and microbial cell abundance from samples taken at depths greater than 100m. The confidence intervals are plotting using "violin" plots including the median (center black line), 75% distribution (white bars) and 95% distribution (black line), with the distribution overlaid (blue shaded area). The number of points included as part of each study is displayed on the right-most bar plots. Study labels in black indicate those studies whose linear regression had a p-value less than .05/12 while labels in gray indicate a p-value above this threshold.

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