File Name: Supplementary Information
Description: Supplementary Figures, Supplementary Tables and Supplementary References

File Name: Supplementary Dataset 1
Description: Abundance profile of the MVCs and the reference phage genomes (rows) across the 121 marine viromes (columns).

File Name: Supplementary Dataset 2
Description: Functional and taxonomic annotation of the proteins encoded by the MVCs compared to the NCBI-nr database.

File Name: Supplementary Dataset 3
Description: Circular neighbour-joining clustering of the MVCs (blue) and the reference phage genomes (red) based on Dice distances depicting the true branch lengths.

File Name: Supplementary Dataset 4
Description: Circular neighbour-joining clustering of the MVCs (blue) and the reference phage genomes (red) based on Dice distances with the branch lengths omitted for better topology representation.

File Name: Supplementary Dataset 5
Description: A summary of all 5 approaches used for host prediction and their respective scores for each MVC.

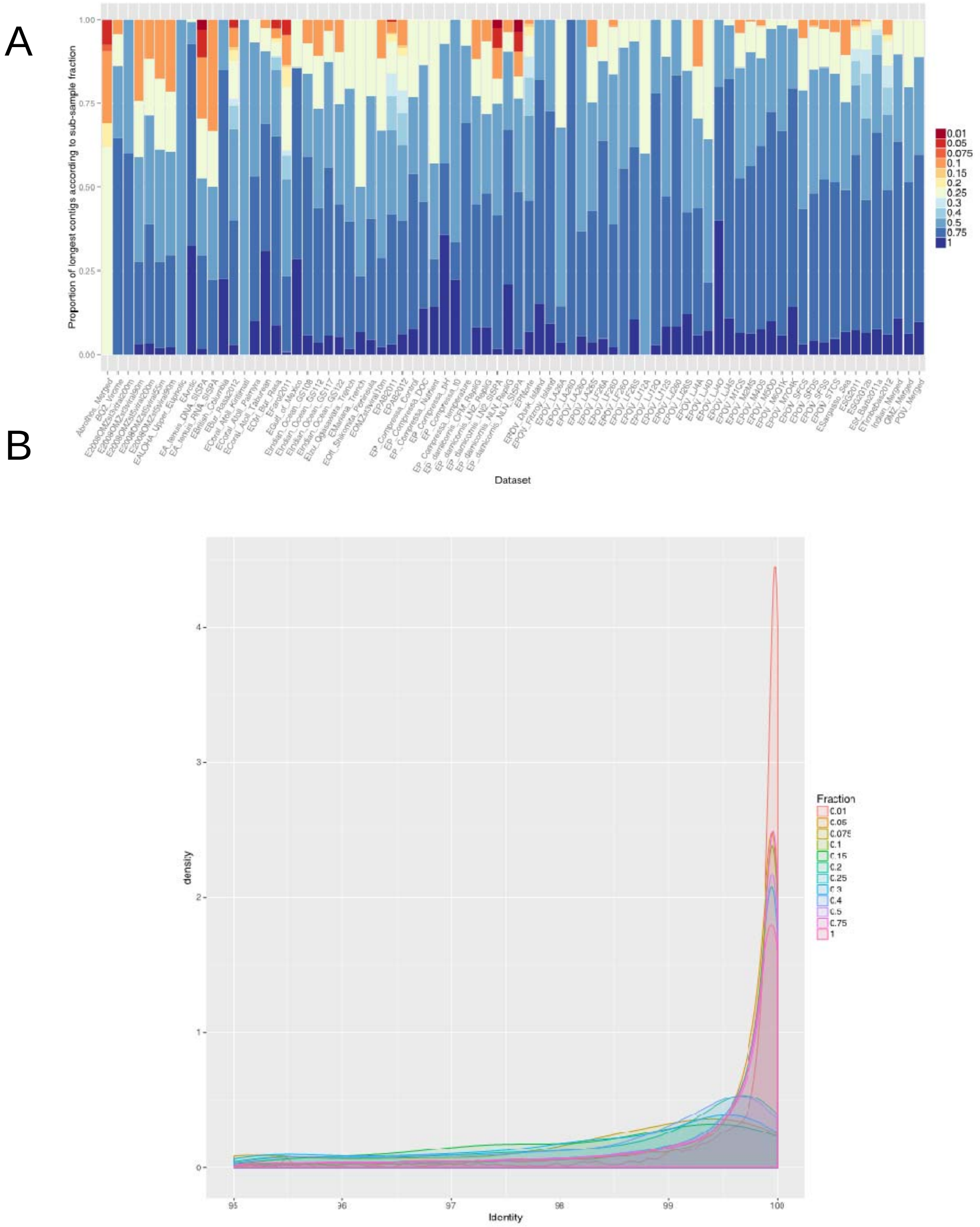
File Name: Supplementary Dataset 6
Description: The statistics of the abundance profiles of the MVCs and the reference viral genomes across the 121 marine viromes.

File Name: Supplementary Dataset 7
Description: Functional content derived from the MVCs and the reference phage genomes. The values represent the average number of occurrences of the KO in each group of phages according to the host phylum.

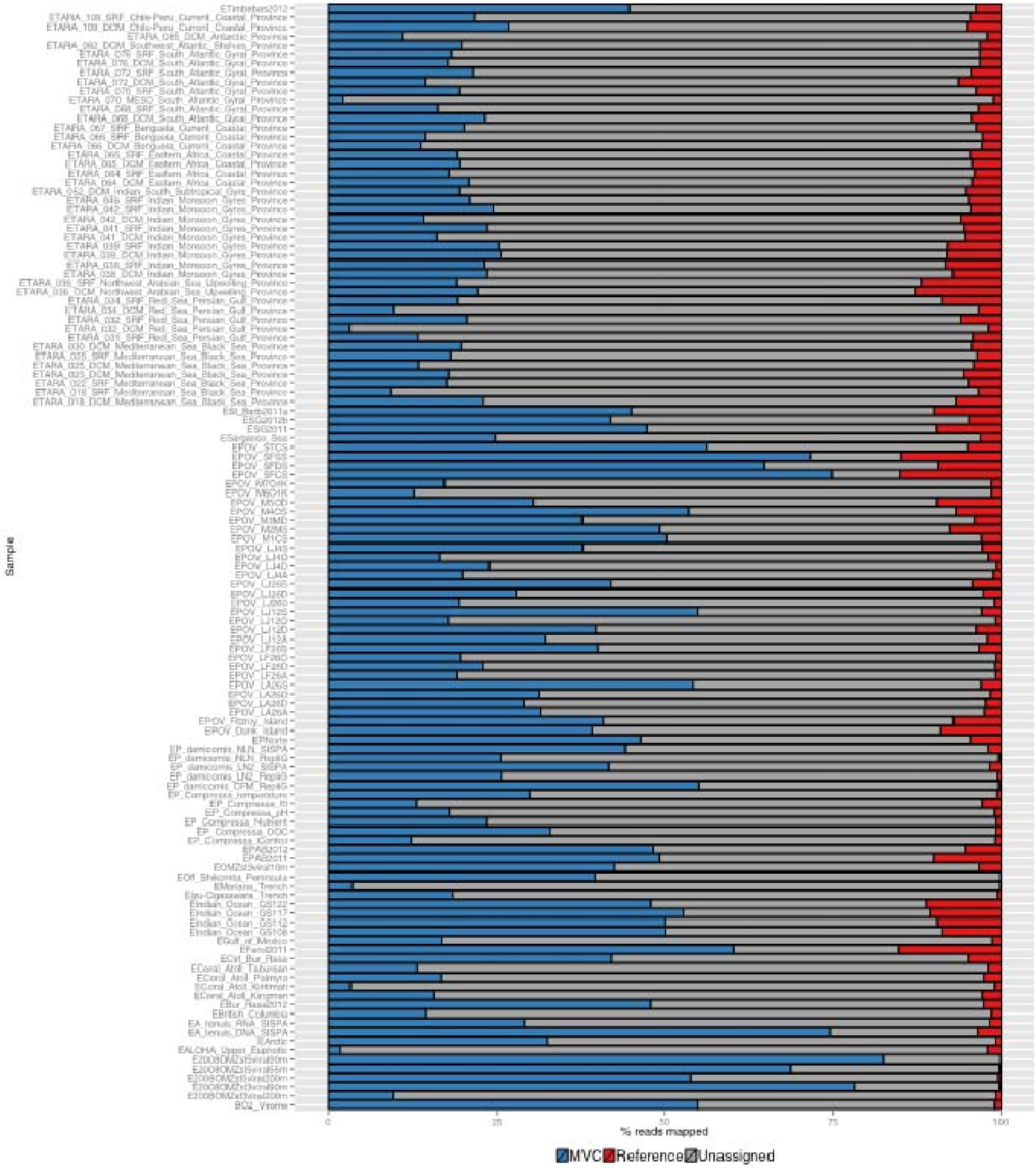
File Name: Supplementary Dataset 8
Description: A list of the MVCs and the reference phages enriched or depleted in abundance among the tested samples groups.

File Name: Supplementary Dataset 9
Description: A list of the KOs enriched or depleted in abundance among the tested samples groups.

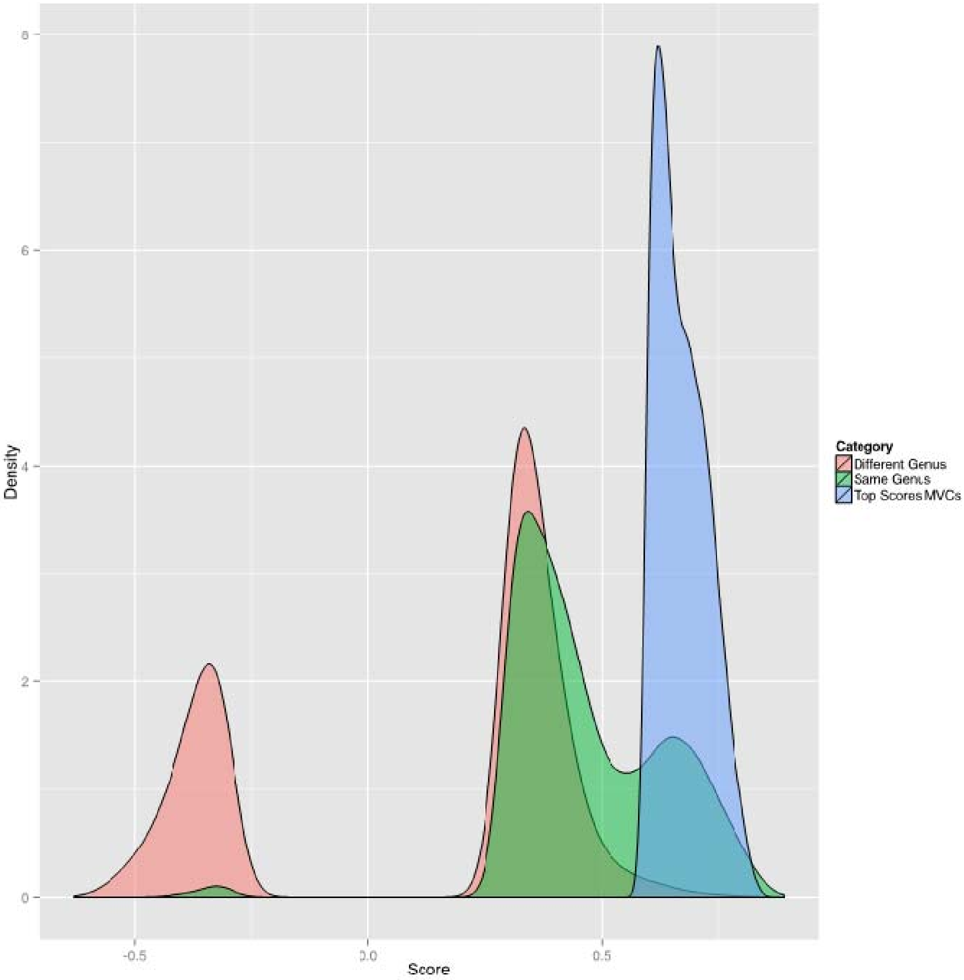
File Name: Supplementary Dataset 10
Description: A list of the bacterial and archaeal species enriched or depleted in abundance among the tested samples groups.



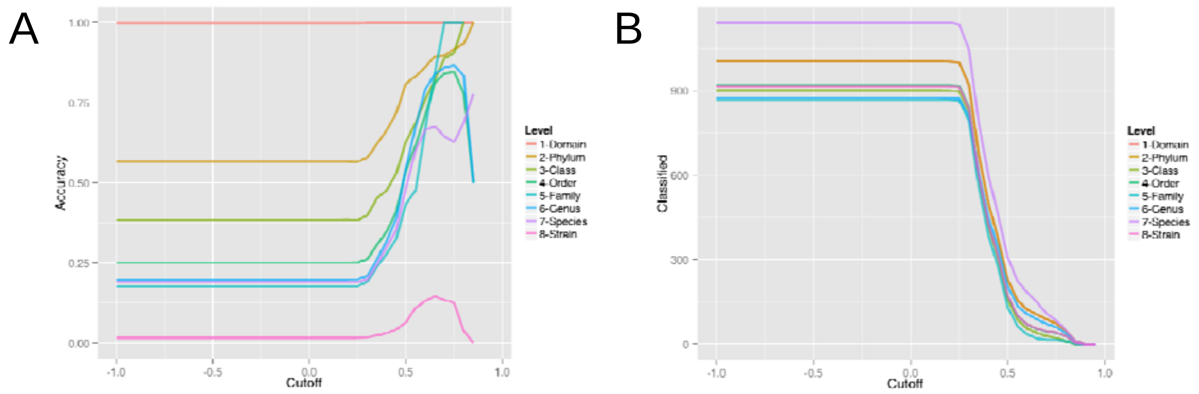
Supplementary Figure 1: Effect of random sub-sampling on virome assembly. Stacked bar plots displaying the proportion of contigs obtained for each sub-sample (color coded according to subsample size fractions) across each dataset. B) A density plot displaying the distribution of identity values of the contigs to the cluster representative according to the subsample fraction from which they are derived. The contigs from smaller subsamples displayed high identity (> 98%) to the cluster representative.



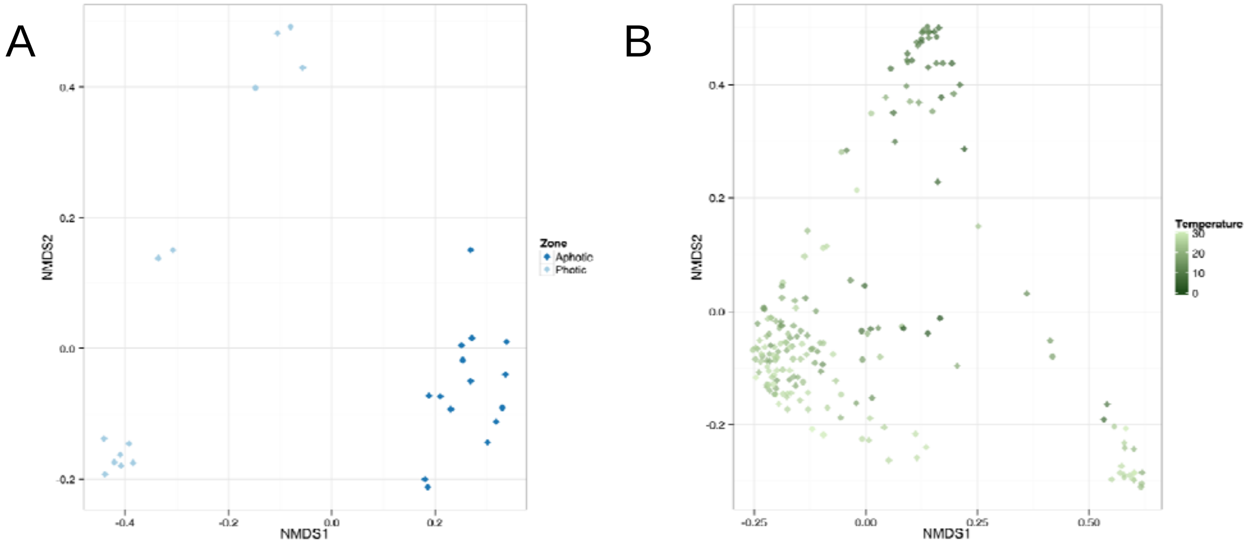
Supplementary Figure 2: Relative abundance of Unassigned reads (grey) or mapped to MVCs(blue) or Reference Phage Genomes (Red) in the 121 analysed marine viromes.



Supplementary Figure 3: Distribution of the SparCC correlation scores between prokaryotic viruses that infect a host of the same (green) or a different (red) genus. The top scores used to assign hosts to the MVCs are displayed in blue.



Supplementary Figure 4: Performance of the predictions based on the correlation scores for each taxonomic level. The X axis displays the minimum score of a correlation to be considered. A) The Y axis shows the accuracy of prediction. B) The Y axis shows the number of correlations in the network that fall within the established cut-off. The strongest scores detected (used for host prediction) were never below ~0.25. Hence, the lack of change in accuracy or the amount of predictions when the cut-off is set below the 0.25 threshold.



Supplementary Figure 5: Metagenome non-metric multidimensional scaling. The Manhattan distances were calculated based on prokaryote relative abundances estimated from cellular fraction microbial metagenomes and used as input for a NMDS analysis. The samples are colour coded according to their environmental features. A) SAO metagenomes. B) Tara oceans metagenomes.

Supplementary Table 1: Description of samples used to obtain the MVCs.

File	Reads	Bases	Average_read_length	Reference
EArctic.fasta	686209	68059812	99.1823365768	(Angly et al., 2006)
EBritish_Columbia.fasta	414964	42392364	102.1591366962	(Angly et al., 2006)
EGulf_of_Mexico.fasta	262501	26674941	101.6184357393	(Angly et al., 2006)
ESargasso_Sea.fasta	397939	41510756	104.3143697903	(Angly et al., 2006)
E2008OMZst3viral200m.fasta	96706	15866963	164.0742353112	(Cassman et al., 2012)
E2008OMZst3viral90m.fasta	361488	91589530	253.3681062719	(Cassman et al., 2012)
E2008OMZst5viral200m.fasta	163531	39736791	242.9924051097	(Cassman et al., 2012)
E2008OMZst5viral55m.fasta	226628	55711738	245.8290149496	(Cassman et al., 2012)
E2008OMZst5viral90m.fasta	300835	75835231	252.0824737813	(Cassman et al., 2012)
EOMZst3viral10m.fasta	128441	31647476	246.3969916148	(Cassman et al., 2012)
ECoral_Atoll_Kingman.fasta	93744	10159186	108.3715864482	(Dinsdale et al., 2008)
ECoral_Atoll_Kiritimati.fasta	279882	30957642	110.6096211975	(Dinsdale et al., 2008)
ECoral_Atoll_Palmyra.fasta	318178	33347087	104.8063882481	(Dinsdale et al., 2008)
ECoral_Atoll_Taburean.fasta	378475	39422223	104.1607054627	(Dinsdale et al., 2008)
EPOV_Dunk_Island.fasta	116855	28955563	247.7905352788	(Hurwitz & Sullivan, 2013)
EPOV_Fitzroy_Island.fasta	82739	20889623	252.4761358005	(Hurwitz & Sullivan, 2013)
EPOV_LA26A.fasta	42118	13594261	322.7660620162	(Hurwitz & Sullivan, 2013)
EPOV_LA26D.fasta	68516	18627549	271.8715190612	(Hurwitz & Sullivan, 2013)
EPOV_LA26O.fasta	70596	19933260	282.356790753	(Hurwitz & Sullivan, 2013)
EPOV_LA26S.fasta	165256	48389605	292.8160248342	(Hurwitz & Sullivan, 2013)
EPOV_LF26A.fasta	167616	48027477	286.5327713345	(Hurwitz & Sullivan, 2013)
EPOV_LF26D.fasta	125896	33423420	265.4843680498	(Hurwitz & Sullivan, 2013)
EPOV_LF26O.fasta	147537	40546266	274.8210008337	(Hurwitz & Sullivan, 2013)
EPOV_LF26S.fasta	192685	59738160	310.0301528401	(Hurwitz & Sullivan, 2013)
EPOV_LJ12A.fasta	58108	20543960	353.5478763681	(Hurwitz & Sullivan, 2013)
EPOV_LJ12D.fasta	49914	13188982	264.234122691	(Hurwitz & Sullivan, 2013)
EPOV_LJ12O.fasta	122565	45941366	374.83266838	(Hurwitz & Sullivan, 2013)
EPOV_LJ12S.fasta	92415	22582412	244.3587296435	(Hurwitz & Sullivan, 2013)
EPOV_LJ260.fasta	101179	28416547	280.8541989939	(Hurwitz & Sullivan, 2013)
EPOV_LJ26D.fasta	55332	14809960	267.6563290682	(Hurwitz & Sullivan, 2013)
EPOV_LJ26S.fasta	75036	19485257	259.6787808519	(Hurwitz & Sullivan, 2013)
EPOV_LJ4A.fasta	136876	44526523	325.305553932	(Hurwitz & Sullivan, 2013)
EPOV_LJ4D.fasta	98478	24169901	245.4345234469	(Hurwitz & Sullivan, 2013)
EPOV_LJ4O.fasta	97126	31475134	324.0649671561	(Hurwitz & Sullivan, 2013)
EPOV_LJ4S.fasta	107244	25738801	240.002247212	(Hurwitz & Sullivan, 2013)
EPOV_M1CS.fasta	303519	105200203	346.6017053298	(Hurwitz & Sullivan, 2013)
EPOV_M2MS.fasta	321754	92857788	288.5987058436	(Hurwitz & Sullivan, 2013)
EPOV_M3MD.fasta	31528	10927215	346.5876363867	(Hurwitz & Sullivan, 2013)
EPOV_M4OS.fasta	203238	52389322	257.7732609059	(Hurwitz & Sullivan, 2013)
EPOV_M5OD.fasta	156509	44009470	281.1944999968	(Hurwitz & Sullivan, 2013)
EPOV_M6O1K.fasta	225833	66311342	293.6299920738	(Hurwitz & Sullivan, 2013)
EPOV_M7O4K.fasta	144588	40451144	279.7683348549	(Hurwitz & Sullivan, 2013)
EPOV_SFCS.fasta	487339	191183563	392.3009711925	(Hurwitz & Sullivan, 2013)
EPOV_SFDS.fasta	645463	218687035	338.8064614083	(Hurwitz & Sullivan, 2013)
EPOV_SFSS.fasta	504826	173099948	342.8903186444	(Hurwitz & Sullivan, 2013)
EPOV_STCS.fasta	821404	246312846	299.8680868367	(Hurwitz & Sullivan, 2013)
BO2_Virome.fasta	2392879	855153008	357.3741121051	(Solonenko et al., 2013)
EP_Compressa_Control.fasta	39191	4065098	103.7252940726	(Vega Thurber et al., 2008)
EP_Compressa_DOC.fasta	35409	3620409	102.245446073	(Vega Thurber et al., 2008)
EP_Compressa_Nutrient.fasta	34139	3661593	107.2554263452	(Vega Thurber et al., 2008)
EP_Compressa_pH.fasta	49949	5234100	104.7888846624	(Vega Thurber et al., 2008)
EP_Compressa_t0.fasta	39113	3965136	101.3764221614	(Vega Thurber et al., 2008)
EP_Compressa_temperature.fasta	38482	4364749	113.4231328933	(Vega Thurber et al., 2008)
EA_tenuis_DNA_SISPA.fasta	1706540	528460555	309.6678396053	(Weynberg et al., 2014)
EA_tenuis_RNA_SISPA.fasta	734031	215417970	293.4725781336	(Weynberg et al., 2014)
EP_damicornis_CFM_RepliG.fasta	370135	100597355	271.785578235	(Weynberg et al., 2014)
EP_damicornis_LN2_RepliG.fasta	292476	82138284	280.8376892463	(Weynberg et al., 2014)
EP_damicornis_LN2_SISPA.fasta	2000000	585709573	292.8547865	(Weynberg et al., 2014)
EP_damicornis_NLN_RepliG.fasta	435494	122300721	280.8321607186	(Weynberg et al., 2014)
EP_damicornis_NLN_SISPA.fasta	2000000	604563712	302.281856	(Weynberg et al., 2014)
EIndian_Ocean_GS108.fasta	320104	125242428	391.2554294854	(Williamson et al., 2012)
EIndian_Ocean_GS112.fasta	494832	178668377	361.0687607107	(Williamson et al., 2012)
EIndian_Ocean_GS117.fasta	480375	194370437	404.6222992454	(Williamson et al., 2012)
EIndian_Ocean_GS122.fasta	341386	119422171	349.8156661375	(Williamson et al., 2012)
EIzu-Ogasawara_Trench.fasta	46458	15606815	335.9338542339	(Yoshida et al., 2013)
EMariana_Trench.fasta	49584	13814785	278.6137665376	(Yoshida et al., 2013)
EOff_Shikomita_Peninsula.fasta	76498	27935812	365.1835603545	(Yoshida et al., 2013)
EBur_Rasa2012.fasta	1943193	324123509	166.799442464	Silveira et al., 2016. In press
ECtrl_Bur_Rasa.fasta	2927179	565986037	193.3554582757	Silveira et al., 2016. In press
EFarol2011.fasta	5309048	1111783405	209.4129503067	Silveira et al., 2016. In press
EPAB2011.fasta	3353950	657983006	196.1815191043	Silveira et al., 2016. In press
EPAB2012.fasta	870827	182837271	209.9582018013	Silveira et al., 2016. In press

Sample	Abrolhos_Season	POV_Depth	TARA_Temp
BO2_Virome	ignore	ignore	ignore
E2008OMZst3viral200m	ignore	ignore	ignore
E2008OMZst3viral90m	ignore	ignore	ignore
E2008OMZst5viral200m	ignore	ignore	ignore
E2008OMZst5viral55m	ignore	ignore	ignore
E2008OMZst5viral90m	ignore	ignore	ignore
EALOHA_Upper_Euphotic	ignore	ignore	ignore
EA_tenuis_DNA_SISPA	ignore	ignore	ignore
EA_tenuis_RNA_SISPA	ignore	ignore	ignore
EArctic	ignore	ignore	ignore
EBritish_Columbia	ignore	ignore	ignore
EBur_Rasa2012	ignore	ignore	ignore
ECoral_Atoll_Kingman	ignore	ignore	ignore
ECoral_Atoll_Kiritimati	ignore	ignore	ignore
ECoral_Atoll_Palmyra	ignore	ignore	ignore
ECoral_Atoll_Taburean	ignore	ignore	ignore
ECtrl_Bur_Rasa	ignore	ignore	ignore
EFarol2011	2011	ignore	ignore
EGulf_of_Mexico	ignore	ignore	ignore
EIndian_Ocean_GS108	ignore	ignore	ignore
EIndian_Ocean_GS112	ignore	ignore	ignore
EIndian_Ocean_GS117	ignore	ignore	ignore
EIndian_Ocean_GS122	ignore	ignore	ignore
EIzu-Ogasawara_Trench	ignore	ignore	ignore
EMariana_Trench	ignore	ignore	ignore
EOMZst3viral10m	ignore	ignore	ignore
EOff_Shikomita_Peninsula	ignore	ignore	ignore
EPAB2011	2011	ignore	ignore
EPAB2012	2012	ignore	ignore
EPNorte	2012	ignore	ignore
EPOV_Dunk_Island	ignore	Photic	ignore
EPOV_Fitzroy_Island	ignore	Photic	ignore
EPOV_LA26A	ignore	Aphotic	ignore
EPOV_LA26D	ignore	Aphotic	ignore
EPOV_LA26O	ignore	Aphotic	ignore
EPOV_LA26S	ignore	Photic	ignore
EPOV_LF26A	ignore	Aphotic	ignore
EPOV_LF26D	ignore	Aphotic	ignore
EPOV_LF26O	ignore	Aphotic	ignore
EPOV_LF26S	ignore	Photic	ignore
EPOV_LJ12A	ignore	Aphotic	ignore
EPOV_LJ12D	ignore	Aphotic	ignore
EPOV_LJ12O	ignore	Aphotic	ignore
EPOV_LJ12S	ignore	Photic	ignore
EPOV_LJ260	ignore	Aphotic	ignore
EPOV_LJ26D	ignore	Aphotic	ignore
EPOV_LJ26S	ignore	Photic	ignore
EPOV_LJ4A	ignore	Aphotic	ignore
EPOV_LJ4D	ignore	Aphotic	ignore
EPOV_LJ4O	ignore	Aphotic	ignore
EPOV_LJ4S	ignore	Photic	ignore
EPOV_M1CS	ignore	Photic	ignore
EPOV_M2MS	ignore	Photic	ignore
EPOV_M3MD	ignore	Photic	ignore
EPOV_M4OS	ignore	Photic	ignore
EPOV_M5OD	ignore	Photic	ignore
EPOV_M6O1K	ignore	Aphotic	ignore
EPOV_M7O4K	ignore	Aphotic	ignore
EPOV_SFCS	ignore	Photic	ignore
EPOV_SFDS	ignore	Photic	ignore
EPOV_SFSS	ignore	Photic	ignore
EPOV_STCS	ignore	Photic	ignore

Supplementary Table 2: Listing of sample groupings used for the enrichment analyzes.

EP_Compressa_Control	ignore	ignore	ignore
EP_Compressa_DOC	ignore	ignore	ignore
EP_Compressa_Nutrient	ignore	ignore	ignore
EP_Compressa_pH	ignore	ignore	ignore
EP_Compressa_t0	ignore	ignore	ignore
EP_Compressa_temperature	ignore	ignore	ignore
EP_damicornis_CFM_RepliG	ignore	ignore	ignore
EP_damicornis_LN2_RepliG	ignore	ignore	ignore
EP_damicornis_LN2_SISPA	ignore	ignore	ignore
EP_damicornis_NLN_RepliG	ignore	ignore	ignore
EP_damicornis_NLN_SISPA	ignore	ignore	ignore
ESG2011	2011	ignore	ignore
ESG2012b	2012	ignore	ignore
ESargasso_Sea	ignore	ignore	ignore
ESt_Barb2011a	2011	ignore	ignore
ETARA_018_DCM_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_018_SRF_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_022_SRF_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_023_DCM_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_025_DCM_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_025_SRF_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_030_DCM_Mediterranean_Sea_Black_Sea_Province	ignore	ignore	Cold
ETARA_031_SRF_Red_Sea_Persian_Gulf_Province	ignore	ignore	Warm
ETARA_032_DCM_Red_Sea_Persian_Gulf_Province	ignore	ignore	Warm
ETARA_032_SRF_Red_Sea_Persian_Gulf_Province	ignore	ignore	Warm
ETARA_034_DCM_Red_Sea_Persian_Gulf_Province	ignore	ignore	Warm
ETARA_034_SRF_Red_Sea_Persian_Gulf_Province	ignore	ignore	Warm
ETARA_036_DCM_Northwest_Arabian_Sea_Upwelling_Province	ignore	ignore	Warm
ETARA_036_SRF_Northwest_Arabian_Sea_Upwelling_Province	ignore	ignore	Warm
ETARA_038_DCM_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_038_SRF_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_039_DCM_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_039_SRF_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_041_DCM_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_041_SRF_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_042_DCM_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_042_SRF_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_046_SRF_Indian_Monsoon_Gyres_Province	ignore	ignore	Warm
ETARA_052_DCM_Indian_South_Subtropical_Gyre_Province	ignore	ignore	Warm
ETARA_064_DCM_Eastern_Africa_Coastal_Province	ignore	ignore	Warm
ETARA_064_SRF_Eastern_Africa_Coastal_Province	ignore	ignore	Warm
ETARA_065_DCM_Eastern_Africa_Coastal_Province	ignore	ignore	Warm
ETARA_065_SRF_Eastern_Africa_Coastal_Province	ignore	ignore	Warm
ETARA_066_DCM_Benguela_Current_Coastal_Province	ignore	ignore	Cold
ETARA_066_SRF_Benguela_Current_Coastal_Province	ignore	ignore	Cold
ETARA_067_SRF_Benguela_Current_Coastal_Province	ignore	ignore	Cold
ETARA_068_DCM_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_068_SRF_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_070_MESO_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_070_SRF_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_072_DCM_South_Atlantic_Gyral_Province	ignore	ignore	Warm
ETARA_072_SRF_South_Atlantic_Gyral_Province	ignore	ignore	Warm
ETARA_076_DCM_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_076_SRF_South_Atlantic_Gyral_Province	ignore	ignore	Cold
ETARA_082_DCM_Southwest_Atlantic_Shelves_Province	ignore	ignore	Cold
ETARA_085_DCM_Antarctic_Province	ignore	ignore	Cold
ETARA_109_DCM_Chile-Peru_Current_Coastal_Province	ignore	ignore	Warm
ETARA_109_SRF_Chile-Peru_Current_Coastal_Province	ignore	ignore	Warm
ETimbebas2012	2012	ignore	ignore

Supplementary Table 3: Correlation scores between the viruses and the hosts across the Tara Oceans samples calculated at the genus level.

Microbe	Spearman_Score_Abundance	p_value_Abundance	Spearman_Score_VHR	p_value_VHR	Intercept	Coefficient	Median_VHR
Acholeplasma	-0.0897435897	0.6551148366	-0.7918192918	2.77485041906018E-006	2.6390947056	-221.356320944	0.0006731856
Burkholderia	0.0706766917	0.7673301273	-0.7518796992	0.0002005705	0.3933706386	-0.4911575602	0.0778090613
Candidatus_Pelagibacter	0.7207207207	1.91486869488262E-006	-0.5933075933	0.0001825509	7.0776174966	-0.206169233	0.5096964592
Candidatus_Puniceispirillum	0.0535714286	0.8525093768	-0.7178571429	0.0035697913	0.8253670301	-0.482693615	0.4417823791
Clostridium	0.1605616606	0.421987618	-0.8424908425	1.63711885751082E-006	1.5244503504	-2.4583227373	0.0886579336
Croceibacter	0.2295652174	0.2792184609	-0.8695652174	2.51572197322635E-006	0.7746601981	-30.9133058485	0.0011361179
Exiguobacterium	-0.0457368718	0.8403574467	-0.7312252964	0.0001678697	0.3507201017	-4.4213806776	0.0005415427
Fusobacterium	0.3415384615	0.0882030026	-0.8618803419	1.88156236780931E-006	0.1832144858	-0.3048264016	0.1021796689
Haloquadratum	-0.0336122076	0.8412189805	-0.0697196446	0.6774607402	3.3308065431	-13789.8936628182	0
Leptospira	-0.0012870013	0.994621753	-0.7292149292	1.41832304552279E-006	1.8757868748	-10.1811706671	0.0117860692
Leuconostoc	0.3081554461	0.1107833117	-0.741652983	1.15855424126558E-005	0.7661340972	-21.4115177414	0.0034241717
Magnetospirillum	-0.2631578947	0.2751840936	-0.601754386	0.0075105622	0.3000664676	-0.516229263	0.0062252617
Marinomonas	-0.1168831169	0.6127360376	-0.6662337662	0.0013002749	1.1968707761	-599.2463695185	0.0003126992
Methanobacterium	-0.0222305556	0.8976015663	-0.2011528456	0.2394372755	1.3199809909	-851.2545217336	2.33084931317066E-005
Myxococcus	0.0298584299	0.8626206951	-0.502960103	0.0020146217	0.6104927701	-19.9990135023	0.0007479578
Porphyromonas	0.0887507633	0.6945000219	-0.2560770433	0.2500183316	0.289146152	-2.8836058149	0.0009241011
Prochlorococcus	0.4062753036	0.0107797241	0.0253036437	0.8783670412	15.8161328076	-2.2742458066	0.1961558333
Rhodobacter	-0.5	0.1214291558	-0.7818181818	0.0070121129	0.2041216285	-0.091966454	0.0504024325
Rhodopirellula	-0.0207715235	0.9250525748	-0.5548964139	0.0059921124	0.790250522	-96.4408425634	0.000504267
Spiroplasma	0.2393162393	0.2282881749	-0.7490842491	1.24966777067635E-005	1.7682111785	-29.3523367065	0.0064639359
Staphylococcus	-0.0931451613	0.6169586777	-0.9116935484	7.55137262061412E-008	1.238667744	-2.5510849631	0.0835727133
Streptococcus	-0.3128851541	0.0676570391	-0.943977591	0	1.8591246303	-11.8458256952	0.0416806827
Sulfolobus	-0.4138904574	0.0566759494	-0.9480519481	3.97738009413851E-006	1.2540135467	-62.4437065058	0.0013793744
Synechococcus	0.4864957265	0.0126122509	-0.4844444444	0.0130342351	2.4460221709	-0.0702163975	4.9054168419
Leptotrichia	-0.0285714286	1	-0.9428571429	0.0166666667	0.6836752584	-15.1989367014	0.0186075988
Ruegeria	0.103030303	0.785018104	-0.4666666667	0.1782193293	0.2487522074	-3.1218398561	0.0124057428
Atopobium	-0.358554489	0.1018781887	-0.8430265387	0.000000871	0.6696239452	-4.4327296023	0.0028153489
Bifidobacterium	0.2	0.4100098244	-0.601754386	0.0075105622	0.3162132879	0.1084235625	0.0109659178
Lactobacillus	-0.0303030303	0.9457098084	-0.9757575758	0	0.9724045537	-1.4384026105	0.1180761148
Mycoplasma	0.3552419355	0.0505457136	-0.8524193548	4.8258055809074E-007	0.9993676428	-33.7842023949	0.003027669
Prevotella	-0.1823529412	0.4979213725	-0.9764705882	0	2.3123656689	-64.3651237005	0.0024500631
Shewanella	-0.1	0.95	-0.9	0.0833333333	0.7163509017	-0.9440151482	0.0276617615
Spirochaeta	0.0285714286	1	-0.0857142857	0.9194444444	0.1415578274	-13.1350742861	0.0013635406
Corynebacterium	-0.0714285714	0.9063492063	-0.3571428571	0.4444444444	0.3798208917	1.3208445271	0.0049118479
Flavobacterium	0.1281761717	0.568312186	-0.8927159797	3.19706976253081E-006	1.1341277571	-0.1239339403	0.6624901891
Neisseria	-0.2142857143	0.6615079365	-0.6428571429	0.1388888889	0.1934000597	-0.6000173031	0.046770624
Vibrio	-0.3696969697	0.2956040892	-0.9757575758	0	1.0898577702	-4.3502075622	0.0343918727
Brachyspira	0	1	-0.75	0.0662698413	0.6816891301	-26.8040952435	0.0062675438
Coprococcus	-0.0286978514	0.9224205467	-0.7483516645	0.0020787303	0.5972249469	-128.5141800102	0.000224633
Treponema	-0.6666666667	0.0830853175	-0.9523809524	0.001140873	1.2788442978	-393.2300271252	0.000489972
Thermus	0.6967032967	0.007343265	-0.5912087912	0.0288937236	0.2070740535	-1.7042496078	0.0525676916
Haloferax	0.1644325947	0.5581408249	-0.2252011623	0.4196781971	0.4128272456	-7.3942072781	0.0029201669
Olsenella	-0.7181818182	0.0167992341	-0.8	0.0052015025	0.3364084675	-4.7355863648	0.0018903593
Selenomonas	-0.1428571429	0.8027777778	-0.7714285714	0.1027777778	1.0847197092	-75.1076237115	0.0036546489
Cellulophaga	0.6	0.2416666667	-0.9428571429	0.0166666667	1.6722300243	-9.2681555217	0.0513465397
Desulfovibrio	-0.2	0.7138888889	-0.6	0.2416666667	0.1042627889	-0.2308270493	0.064935013
Bacillus	0.6428571429	0.1388888889	-0.8928571429	0.0123015873	0.8440946301	-0.1930062559	0.2958520169
Xylella	0.6428571429	0.1388888889	-0.8928571429	0.0123015873	1.0002495561	-28.2940329388	0.0048490512

Supplementary Table 4: Correlation scores between the viruses and the hosts across the Tara Oceans samples calculated at the phylum level.

Microbe	Spearman_Score_Abundance	p_value_Abundance	Spearman_Score_VHR	p_value_VHR	Intercept	Coefficient	Median_VHR
Bacteroidetes	0.487854251	0.0018440462	-0.0587044534	0.7218046355	6.5718123628	-0.8691127829	0.2942114454
Proteobacteria	0.5700404858	0.0001969337	0.0714574899	0.6645328164	41.6510547139	-2.8456391386	0.4728114824
Chlamydiae	0.224785273	0.4824316437	-0.3408034784	0.2783436757	1.3054541352	-1125.5415903991	0.0001312777
Cyanobacteria	0.4287449393	0.0068892257	-0.1935222672	0.2369237852	21.7154380513	-1.5670240917	1.631312893
Nitrospirae	-0.1552539658	0.4393705456	-0.2415941814	0.2247315758	0.692990787	-757.9028606154	0
Chloroflexi	0.1402597403	0.5427637571	-0.687012987	0.0008070563	0.4365735353	-17.4971416845	0.0012303541
Synergistetes	-0.5303759999	0.0932731105	-0.8560454736	0.0007716582	0.4207727833	-77.497439152	0.0006656232
Firmicutes	0.0495951417	0.7636823368	-0.5718623482	0.0001862272	7.1450479718	-10.3560829904	0.1007878894
Planctomycetes	0.0298719772	0.8585100099	-0.644162381	2.0270257907871E-005	1.1593147267	-20.0764366062	0.0053903494
Euryarchaeota	-0.3380566802	0.03586063	-0.6386639676	1.9170771177978E-005	11.0498598531	-1047.2704950545	0.0007424886
Spirochaetes	0.2519969362	0.1267868461	-0.6544479702	1.37698760641859E-005	2.3641307508	-19.8223758252	0.0128895901
Crenarchaeota	0.0786738155	0.6376082776	-0.7439544808	4.98082163215247E-007	2.1539224633	-108.6354586489	0.0013896698
Actinobacteria	-0.1083451873	0.5218849548	-0.7598387862	4.2867457596182E-007	2.1527612906	-1.161736751	0.2030214715
Deinococcus-Thermus	0.0512091038	0.7627878024	-0.8477951636	1.14534805773338E-008	0.5870313379	-4.3343088481	0.0229846302
Fusobacteria	-0.0440967283	0.7950393182	-0.9229492651	0	0.9894272934	-2.9219067318	0.0236006339
Tenericutes	-0.14048583	0.3922637652	-0.8967611336	0	3.4383676516	-11.5564472183	0.0044451534

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