A novel method to create efficient phage cocktails via use of phage-resistant bacteria

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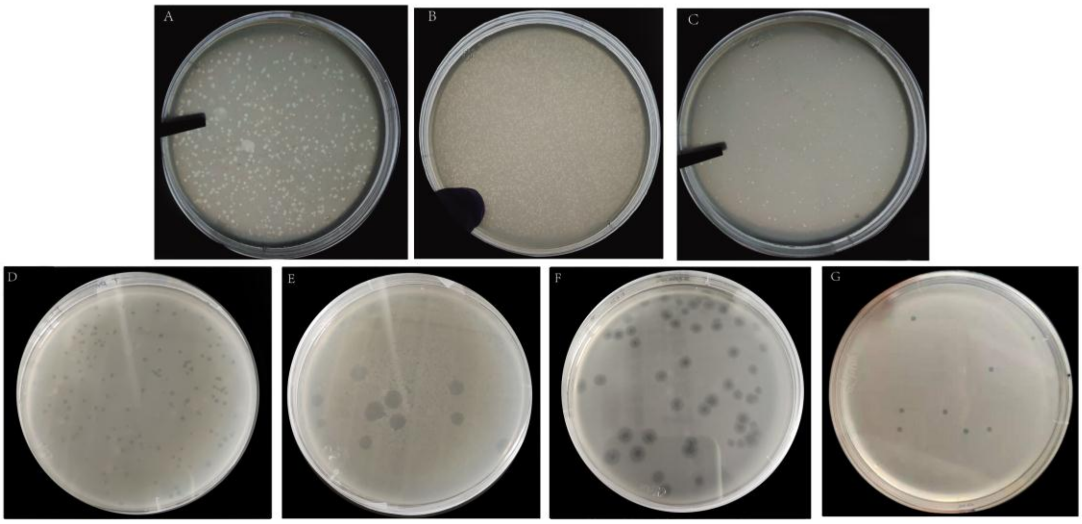

Fig. S1 Phage plaques of Va1(A), Va2 (B), Va3 (C), VP1 (D), VP2 (E), VP3 (F), and VP4 (G) formed in double-layer agar plates.

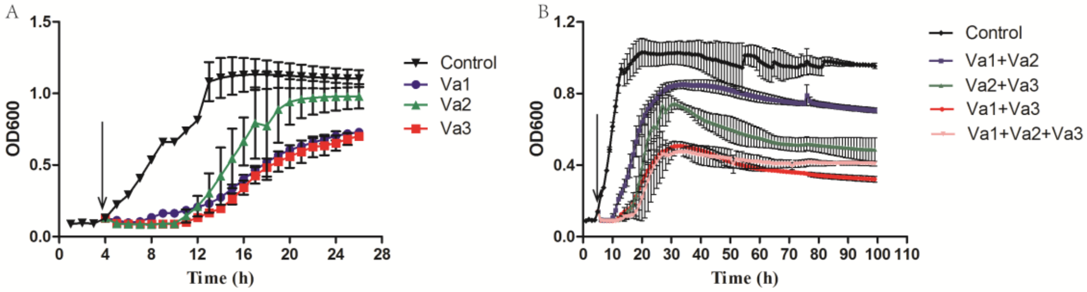

Fig. S2 Growth curves of (A) *V. alginolyticus* 283T infected by Va1, Va2, and Va3 alone and (B) combinations of these three phages at an MOI = 10. These experiments were performed simultaneously with that in Figure 4A and 4B, therefore their control was same. The arrows indicate the time point when the phages were added in the bacterial medium. The data are shown as mean ± SD, and the *P*-values (calculated by one-way ANOVA and Student's t-test) are shown in Table S8-S9.

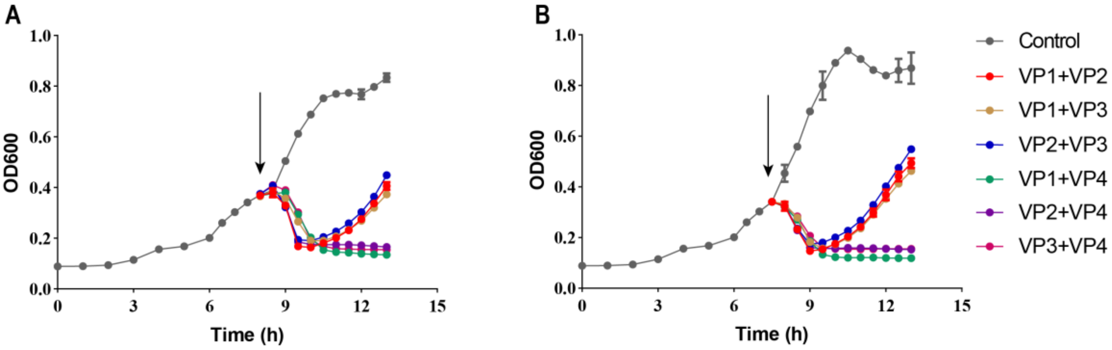

Fig. S3 The growth curves of *Vibrio parahaemolyticus* MCS (VP) infected by the combination of phages VP1, VP2, VP3, and VP4 at MOIs of 1 (A) and 10 (B). VP1, VP2, and VP3 were isolated using the wild strain (*Vibrio parahaemolyticus* MCS), and VP4 was isolated using a mutant strain evolved under the stress of VP1. The arrows indicate the time point when the phages were added in the bacterial medium. The data are shown as mean ±

SD, and the *P*-values (calculated by one-way ANOVA and Student's t-test) are shown in Table S10-S11.

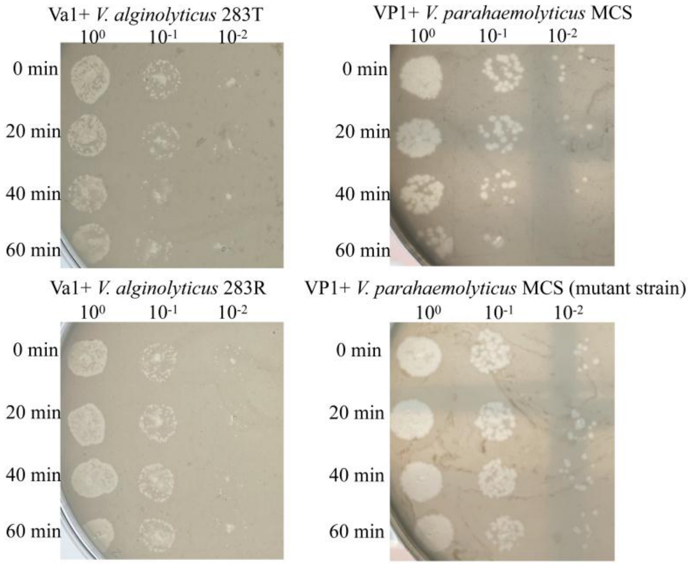

Figure S4. Phage adsorption assay. When the host bacteria grew to the early exponential phase, phages were added to the culture at MOI 0.01. Samples were taken at the indicated time points and the number of extracellular phages were determined by spot assay. The decreased number of extracellular phages over time (eg. Va1 + *V. alginolyticus* 283T and VP1 + *V. parahaemolyticus* MCS) revealed that phages gradually adsorbed to the host. While the unchanged number of extracellular phages (eg. Va1 + *V. alginolyticus* 283R and VP1 + *V. parahaemolyticus* MCS mutant strain) indicated that phages failed to adsorb to the host.

Table S1 Functionally-annotated ORFs of the genome of phage Va1.

ORF no.	Best hit organism	Accession No.	E value	Identity(%)	Putative Product
10	Acinetobacter tandoii	WP_016166803.1	1.55E-65	45.349	protease SohB
21	Sulfurovum sp. NBC37-1	WP_083760521.1	1.46E-30	53	DUF2493 domain-containing protein
28	Capnocytophaga gingivalis	WP_002670075.1	0	65.546	anaerobic ribonucleoside-triphosphate reductase
29	Capnocytophaga sp. H2931	WP_095893997.1	1.14E-36	46.207	anaerobic ribonucleoside-triphosphate reductase activating protein
39	Clostridium scatologenes	WP_029159783.1	2.94E-74	36.658	adenylosuccinate synthase
40	Vibrio phage PWH3a-P1	YP_007675972.1	8.01E-63	53.591	exonuclease
55	Pseudoalteromonas sp. TMED43	OUX93577.1	1.84E-75	78.358	glycerol-3-phosphate cytidylyltransferase
60	uncultured Clostridium sp.	SCG88662.1	5.19E-22	46.465	Thioredoxin
65	Clostridium	WP_042396253.1	4.31E-54	46.073	MULTISPECIES: ATP-dependent Clp endopeptidase, proteolytic subunit ClpP
95	Campylobacter virus CP21	YP_007005208.1	2.51E-75	42.208	putative sliding clamp loader (T4-like DNA polymerase accessory factor)
101	Campylobacter virus CP220	YP_009169249.1	6.67E-86	33.766	Possible phage DNA polymerase
103	Sinorhizobium phage phiN3	YP_009212557.1	3.19E-10	27.57	MobE homing endonuclease
105	Campylobacter virus CP220	YP_009169249.1	3.59E-76	43.119	Possible phage DNA polymerase
113	Campylobacter phage PC5	ANH51266.1	4.10E-08	27.966	putative clamp loader subunit
121	Deferribacter desulfuricans	WP_013008544.1	2.36E-06	26.49	phosphoesterase
130	Campylobacter virus CPt10	YP_009169066.1	1.95E-114	43.077	Possible phage ATP-dependent primase-helicase
136	Campylobacter virus CP21	YP_007005197.1	2.09E-64	48.4	putative terminase (T4 gp17-like)
137	Campylobacter virus CPt10	YP_009168939.1	1.01E-61	49.289	Putative phage DNA packaging protein (terminase)

145	Escherichia phage 4MG	YP_008857319.1	1.51E-88	48.355	putative RNA ligase 1/tail attachment protein
153	Shewanella sp. phage 1/4	YP_009100402.1	1.38E-138	47.797	multifunctional tRNA nucleotidyl transferase
171	Vibrio phage nt-1	YP_008125493.1	2.11E-46	58.784	gp36+37 fusion long tail fiber distal subunit
173	Campylobacter virus CPt10	YP_009169114.1	1.97E-35	37.727	Possible phage tail sheath completion protein
175	Campylobacter virus IBB35	AEI88223.1	3.63E-81	36.638	gp39 topoisomerase II
180	Campylobacter virus IBB35	AEF56840.1	4.21E-89	39.002	gp52 DNA topoisomerase II
184	Arcobacter anaerophilus	WP_044419043.1	1.72E-138	46.482	phosphate starvation protein PhoH
186	Vibrio sinaloensis	WP_008072846.1	1.08E-50	43.925	serine protease
190	Campylobacter virus CP21	YP_007005117.1	1.48E-112	52.848	MreB-like ATPase protein
198	Campylobacter virus CPt10	YP_009169063.1	2.47E-32	33.028	Possible sliding clamp
199	Campylobacter virus IBB35	AEF56815.1	2.50E-85	47.5	gp32 single-stranded DNA binding protein
200	Campylobacter virus CP21	YP_007005209.1	1.23E-73	40.663	putative RNaseH
202	Campylobacter virus CP220	YP_009169143.1	5.67E-44	31.285	Putative DNA primase subunit
209	Tenacibaculum phage pT24	BAV39295.1	3.98E-12	64.706	DNA ligase 1
210	Enterobacter cloacae	WP_084833038.1	1.44E-32	58.763	transcriptional regulator
226	Campylobacter virus IBB35	AEF56843.1	2.68E-105	40.443	DNA helicase UvsW
234	Clostridium paraputrificum	WP_027097998.1	4.46E-16	32.973	restriction endonuclease subunit M
235	Mycoplasma iowae	WP_004025021.1	9.92E-112	50.294	ribonucleoside-diphosphate reductase subunit beta
236	Mycoplasma iowae	WP_004025022.1	0	54.594	ribonucleoside-diphosphate reductase subunit alpha
243	Mitsuaria chitosanitabida	WP_084453285.1	7.49E-24	35.795	class I SAM-dependent methyltransferase
249	Sulfuricurvum sp. PC08-66	KIM11589.1	2.19E-07	31.818	molecular chaperone GroES
253	Campylobacter virus IBB35	AEI88261.1	6.79E-34	30.672	gp13 neck protein
254	Rhizobium phage vB_RleM_P10VF	YP_009099829.1	9.10E-31	45.794	head completion protein
256	Campylobacter virus IBB35	AEI88197.1	4.03E-126	44.737	gp20 portal vertex protein of head
258	Campylobacter virus CPX	YP_004956875.1	5.68E-151	42.284	gp18 tail sheath protein

259	Vibrio tritonius	WP_068716942.1	0	65.326	chaperonin GroEL
260	Campylobacter virus IBB35	AEI88177.1	1.11E-28	30.888	gp19 tail tube protein
261	Campylobacter virus CP220	YP_009169309.1	3.73E-63	42.629	Possible phage tail tube protein
262	Campylobacter virus CPt10	YP_009168994.1	2.89E-62	48.187	Possible phage tail tube protein
264	Campylobacter virus CP21	YP_007005136.1	4.77E-38	44.304	putative DNA end protector protein (T4 gp02-like)
266	Campylobacter virus CP220	YP_009169327.1	1.72E-69	66.867	Probable phage prohead core protein precursor
267	Campylobacter virus CP220	YP_009169184.1	7.98E-14	37.5	Possible prohead core scaffold protein
268	Campylobacter virus IBB35	AEF56742.1	1.53E-146	50.216	gp23 major capsid protein
269	Klosneuvirus KNV1	ARF12305.1	1.07E-30	40.102	csr/MutH/archaeal HJR family nuclease
271	Paenibacillus sp. oral taxon 786	WP_009226174.1	4.04E-24	34.483	dihydrofolate reductase
273	Neptuniibacter caesariensis	WP_007021383.1	4.28E-149	69.55	thymidylate synthase
274	Chrysiogenes arsenatis	WP_051321624.1	1.24E-19	35.714	DUF1353 domain-containing protein
277	Campylobacter virus CPt10	YP_009168940.1	2.90E-12	26.749	Putative base plate hub assembly catalyst
278	Campylobacter phage PC5	ANH51291.1	1.37E-19	33.854	putative peptidase
279	Campylobacter virus IBB35	AEF56804.1	3.53E-14	25.926	gp48 T4-like baseplate tail tube cap
284	Campylobacter virus IBB35	AEI88187.1	8.53E-15	37.374	gp25 baseplate wedge subunit
285	Campylobacter virus CPX	YP_004957005.1	1.19E-80	30.866	putative baseplate wedge protein
289	Campylobacter virus NCTC12673	YP_004421661.1	2.48E-11	25.166	gp3 tail completion and sheath stabilizer protein
293	Proteus phage PM16	YP_009147859.1	9.97E-14	35.659	putative DNA endonuclease VII
319	Enterobacteria phage T4	NP_049745.2	1.26E-50	45.57	SegB homing endonuclease

Table S2. Functionally-annotated ORFs of the genome of phage Va2.

ORF no.	Best hit organism	Accession No.	E value	Identity(%)	Putative Product

1	Vibrio phage RYC	ADX89528.1	2.4e-216	54.2	Anaerobic nucleoside diphosphate reductase
6	Capnocytophaga sp. H2931	AUR83180.1	7.1e-124	45.4	Helicase superfamily 1/2 ATP-binding domain protein
8	Acinetobacter guillouiae	AUR83013.1	1.5e-165	35.0	Coil containing protein
10	Saudi moumouvirus	AUR83031.1	1.4e-123	41.7	P-loop containing nucleoside triphosphate hydrolase
14	Desulfocapsa sulfexigens	WP_039458044	6.3e-19	31.1	SDR family oxidoreductase
15	Yersinia phage phiR1-37	WP_020404777	4.4e-15	31.3	SDR family oxidoreductase
16	Verrucomicrobia bacterium 61-8	WP_071216967	6.4e-14	36.3	ribonuclease HI family protein
23	Alphaproteobacteria bacterium TMED194	AUR83174.1	7.0e-145	45.2	Terminase large subunit
27	Vibrio phage jenny 12G5	AUR83170.1	3.1e-113	47.6	Major capsid protein
31	Vibrio phage S4-7	AUR83162.1	5.8e-35	42.6	SWIM-type zinc finger protein
36	Vibrio nigripulchritudo	AUR83155.1	1.7e-147	41.6	Tail sheath protein
40	Sinorhizobium phage phiN3	AXY86112.1	9.6e-37	40.4	Putative glycoside hydrolase
44	Pseudoalteromonas phage H103	CP035107_389	2.9e-10	31.9	Rhs element Vgr protein
46	Aureimonas ureilytica	WP_091362230	8.7e-11	42.1	type VI secretion system PAAR protein
52	Campylobacter virus CPt10	AUR83137.1	1.6e-7	47.1	Cold-shock DNA-binding domain protein
53	Vibrio phage eugene 12A10	AUR83178.1	7.7e-12	33.1	Beta-like DNA polymerase
60	Vibrio phage qdvp001	SCN43224.1	1.5e-2	25.7	YD repeat
63	Candidatus Pelagibacter sp. TMED203	PWB34328.1	6.7e-3	29.2	Thioredoxin
65	Vibrio phage eugene 12A10	EMBL:AUR83119.1	8.3e-153	46.9	P-loop containing nucleoside triphosphate hydrolase
74	Campylobacter virus CPt10	RU004279	4.9e-271	44.0	DNA-directed RNA polymerase subunit
86	Campylobacter virus CP220	WP_133955757	2.1e-5	51.8	elongation factor Tu

97	Candidatus Kaiserbacteria bacterium	AUR83018.1	2.2e-26	25.9	PIN domain-like protein
99	Vibrio campbellii	WP_029300088	4.0e-8	49.3	DUF1653 domain-containing protein
103	Rhizobium phage vB_RleM_P10VF	AQT28046.1	7.7e-44	51.1	Deoxyuridine 5'-triphosphate nucleotidohydrolase
107	Vibrio tritonius	WP_013554351	7.7e-65	42.3	thiamine pyrophosphate-binding protein
108	Campylobacter virus IBB35	WP_039553247	0	77.2	ribonucleoside-diphosphate reductase subunit alpha
109	Campylobacter virus CP220	KII80920.1	1.4e-154	70.9	Ribonucleotide-diphosphate reductase subunit beta
110	Campylobacter virus CPt10	WP_105080778	1.1e-13	29.1	phosphoenolpyruvate mutase
112	Campylobacter virus CP220	WP_129033863	1.0e-52	38.2	NAD-dependent epimerase/dehydratase family protein
115	Klosneuvirus KNV1	ASZ78959.1	3.7e-26	38.1	Metallophosphatase
117	Paenibacillus sp. oral taxon 786	WP_028950958	1.1e-20	30.8	exodeoxyribonuclease III
128	Campylobacter virus CPt10	PWB88064.1	3.9e-43	42.2	Phosphodiesterase
136	Pseudomonas phage Lu11	PYG50685.1	2.3e-6	71.4	FtsH-binding integral membrane protein

Table S3. Functionally-annotated ORFs of the genome of phage Va3.

ORF no.	Best hit organism	Accession No.	E value	Identity(%)	Putative Product
2	Vibrio phage VH7D	YP_009006096.1	0	100	RNA ligase 2
4	Vibrio phage ValKK3	YP_009201232.1	1.08E-121	99.41	recombination endonuclease VII
6	Vibrio phage VH7D	YP_009006093.1	9.20E-74	100	capsid assembly protein
11	Vibrio phage VH7D	YP_009006088.1	1.81E-177	100	7-cyano-7-deazaguanine synthase
12	Vibrio phage VH7D	YP_009006087.1	0	100	NADPH-dependent 7-cyano-7-deazaguanine reductase
14	Vibrio phage VH7D	YP_009006085.1	3.13E-165	100	GTP cyclohydrolase 1

15	Vibrio phage ValKK3	YP_009201243.1	0	99.68	6-pyruvoyl tetrahydropterin synthase-like protein
16	Vibrio phage ValKK3	YP_009201244.1	4.93E-108	100	deoxycytidylate deaminase
44	Vibrio phage VH7D	YP_009006385.1	0	96.72	polynucleotide kinase
49	Vibrio phage VH7D	YP_009006379.1	0	100	RNA ligase
51	Vibrio phage phi-ST2	ALP47342.1	0	99.88	DNA polymerase
54	Vibrio phage nt-1	YP_008125278.1	1.03E-87	99.21	RegA translational repressor protein
55	Vibrio phage VH7D	YP_009006373.1	5.94E-117	100	polymerase accessory protein 62
56	Vibrio phage VH7D	YP_009006372.1	0	100	DNA polymerase accessory protein 44
57	Vibrio phage VH7D	YP_009006371.1	2.96E-159	100	DNA polymerase processivity component
60	Vibrio phage phi-Grn1	ALP46964.1	0	99.87	recombination-related endonuclease
62	Vibrio phage VH7D	YP_009006366.1	0	100	exonuclease subunit 1
63	Vibrio phage VH7D	YP_009006365.1	2.63E-122	100	putative 5'(3')-deoxyribonucleotidase
70	Vibrio phage VH7D	YP_009006358.1	3.66E-125	100	RNA polymerase sigma factor
71	Vibrio phage ValKK3	YP_009201301.1	0	100	head vertex protein
72	Vibrio phage ValKK3	YP_009201302.1	6.50E-53	100	glutaredoxin
75	Vibrio phage ValKK3	YP_009201305.1	0	99.45	RNA polymerase-ADP-ribosyltransferase
77	Vibrio phage phi-Grn1	ALP46988.1	0	99.78	DNA ligase
91	Vibrio phage VH7D	YP_009006338.1	0	100	DNA topoisomerase large subunit
92	Vibrio phage VH7D	YP_009006337.1	0	99.61	NAD-dependent deacetylase
104	Vibrio phage VH7D	YP_009006325.1	0	100	thymidylate synthase
112	Vibrio phage phi-ST2	ALP47434.1	2.21E-171	100	exonuclease A
114	Vibrio phage phi-ST2	ALP47489.1	3.4E-115	100	deoxyuridine 5'-triphosphate nucleotidohydrolase
115	Vibrio phage ValKK3	YP_009201345.1	0	100	DNA primase subunit
120	Vibrio phage VH7D	YP_009006309.1	5.04E-114	99.37	anaerobic ribonucleoside-triphosphate reductase-activating protein
123	Vibrio phage phi-Grn1	ALP46970.1	0	100	ribonucleoside-triphosphate reductase

124	Vibrio phage ValKK3	YP_009201354.1	1.41E-51	98.77	hypothetical protein
125	Vibrio phage ValKK3	YP_009201355.1	0	100	DNA primase-helicase subunit
127	Vibrio phage VH7D	YP_009006302.1	0	100	recombination and repair protein
128	Vibrio phage VH7D	YP_009006301.1	3.23E-178	100	ATP-dependent Clp protease proteolytic subunit 2
129	Vibrio phage ValKK3	YP_009201359.1	3.18E-132	100	dihydrofolate reductase
130	Vibrio phage phi-Grn1	ALP47019.1	0	100	single stranded DNA-binding protein
131	Vibrio phage ValKK3	YP_009201361.1	4.97E-134	99.46	loader of DNA helicase
132	Vibrio phage phi-Grn1	ALP47199.1	3.43E-68	100	transcriptional regulator
133	Vibrio phage VH7D	YP_009006296.1	1.22E-59	100	double-stranded DNA-binding protein
134	Vibrio phage VH7D	YP_009006295.1	0	100	ribonuclease H
135	Vibrio phage phi-ST2	ALP47338.1	0	99.76	short tail fiber protein
136	Vibrio phage phi-ST2	ALP47341.1	0	97.99	tail connector protein
137	Vibrio phage ValKK3	YP_009201367.1	3.38E-95	100	recombination, repair and single-stranded DNA binding protein
142	Vibrio phage VH7D	YP_009006294.1	0	100	ATP-dependent DNA helicase
152	Vibrio phage ValKK3	YP_009201382.1	9.43E-110	96.97	prohead protease inhibitor
153	Vibrio phage KVP40	NP_899611.1	0	86.78	hypothetical protein KVP40.0366
154	Vibriophage phi-pp2	AFN37597.1	1.96E-76	95.58	hypothetical protein pp2_365
155	Vibrio phage phi-Grn1	ALP47001.1	0	96.71	tRNA nucleotidyltransferase
156	Vibrio phage ValKK3	YP_009201384.1	0	99.81	major capsid protein precursor
157	Vibrio phage VH7D	YP_009006290.1	0	100	major prohead-scaffolding core protein
158	Vibrio phage VH7D	YP_009006289.1	7.42E-154	100	prohead core protein protease
159	Vibrio phage VH7D	YP_009006288.1	2.35E-109	100	prohead core protein protease
161	Vibrio phage VH7D	YP_009006286.1	0	100	structural protein of head
162	Vibrio phage VH7D	YP_009006285.1	8.72E-121	100	tail tube protein
163	Vibrio phage VH7D	YP_009006284.1	0	99.85	tail sheath protein

164	Vibrio phage ValKK3	YP_009201392.1	0	100	large terminase protein
165	Vibrio phage VH7D	YP_009006282.1	7.86E-130	100	DNA-packaging protein
167	Vibrio phage phi-Grn1	ALP47013.1	0	99.69	tail assembly protein
168	Vibrio phage VH7D	YP_009006279.1	0	100	neck protein
169	Vibrio phage VH7D	YP_009006278.1	0	100	neck protein
170	Vibrio phage VH7D	YP_009006277.1	0	99.29	fibritin
171	Vibrio phage VH7D	YP_009006276.1	0	99.79	short tail fiber protein
174	Vibrio phage VH7D	YP_009006273.1	0	100	baseplate structural protein
175	Vibrio phage VH7D	YP_009006272.1	0	99.69	baseplate structural protein
176	Vibrio phage phi-ST2	ALP47388.1	0	99.71	baseplate wedge subunit
177	Vibrio phage phi-ST2	ALP47339.1	0	99.74	baseplate wedge subunit
178	Vibrio phage VH7D	YP_009006269.1	0	100	baseplate structural protein
179	Vibrio phage VH7D	YP_009006268.1	9.61E-97	100	tail lysozyme
182	Vibrio phage phi-Grn1	ALP47208.1	6.22E-63	98.98	putative phospholipase
184	Vibrio phage VH7D	YP_009006265.1	0	99.51	tail-associated lysozyme
186	Vibrio phage VH7D	YP_009006263.1	9.68E-140	100	baseplate structural protein
187	Vibrio phage VH7D	YP_009006262.1	0	100	tail-tube assembly protein
188	Vibrio phage ValKK3	YP_009201416.1	1.77E-108	100	head completion protein
189	Vibrio phage ValKK3	YP_009201417.1	2.00E-145	100	DNA end protector protein
190	Vibrio phage ValKK3	YP_009201418.1	0	100	baseplate-tail tube initiator
194	Vibrio phage phi-Grn1	ALP47091.1	8.21E-131	100	tail completion protein
195	Vibrio phage phi-Grn1	ALP47061.1	5.09E-156	100	deoxynucleotide monophosphate kinase
217	Vibrio phage ValKK3	YP_009201449.1	0	96.09	tail fiber
219	Vibrio phage ValKK3	YP_009201451.1	0	78.66	long tail fiber distal subunit
220	Vibrio phage phi-ST2	ALP47337.1	0	92.44	tail fibers protein
227	Vibrio phage VH7D	YP_009006252.1	3.62E-173	100	PhoH-like protein

237	Vibrio phage VH7D	YP_009006242.1	0	100	DNA topoisomerase medium subunit
238	Vibrio phage phi-Grn1	ALP47011.1	0	100	thioredoxin
241	Vibrio phage VH7D	YP_009006238.1	1.88E-65	98.99	glutaredoxin
242	Vibrio phage VH7D	YP_009006237.1	0	100	ribonucleoside-diphosphate reductase 1 subunit beta
243	Vibrio phage VH7D	YP_009006236.1	0	100	ribonucleoside-diphosphate reductase subunit alpha
252	Vibrio phage VH7D	YP_009006228.1	0	99.6	nicotinamide phosphoribosyl transferase
291	Vibrio phage ValKK3	YP_009201132.1	2.54E-161	98.66	nicotinamide riboside transporter
295	Vibrio phage ValKK3	YP_009201136.1	0	98.77	trifunctional NAD biosynthesis/regulator protein
302	Vibrio phage ValKK3	YP_009201143.1	6.09E-99	97.86	endonuclease V
323	Vibrio phage VH7D	YP_009006157.1	8.21E-140	100	thymidine kinase
357	Vibrio phage phi-ST2	ALP47387.1	0	99.41	nicotinamide-nucleotide adenylyltransferase NadM family/ ADP-ribose pyrophosphatase
363	Vibrio phage VH7D	YP_009006117.1	0	99.76	ATP-dependent DNA helicase
372	Vibrio phage ValKK3	YP_009201217.1	8.43E-165	98.24	potassium voltage-gated channel subfamily A member 1 protein
375	Vibrio phage VH7D	YP_009006106.1	0	100	protein rIIB
376	Vibrio phage VH7D	YP_009006105.1	0	100	protein rIIA

Table S4. Host range of phages cocktails against 15 Vibrio sp. isolates

Strain	Most closely related strain	Origin	Va1+Va2	Va1+Va3	Va2+Va3	Va1+Va2+Va3
VIB283	*Vibrio alginolyticus*	Donated[#]	+	+	+	+
LMG 19158(T)	*Vibrio scophthalmi*	Collection	+	+	+	+
NBRC 104587(T)	*Vibrio azureus*	Collection	+	+	+	+
VIB 283 R	*Vibrio alginolyticus*	Collection	-	+	+	+

NBRC15630(T)	*Vibrio alginolyticus*	Collection	-	+	+	+
CAIM 1831(T)	*Vibrio alfacsensis*	Collection	-	-	-	-
CAIM 25(T)	*Vibrio gigantis*	Collection	-	-	-	-
E20121(T)	*Vibrio zhuhaiensis*	Collection	-	-	-	-
Vb 11.11(T)	*Vibrio atlanticus*	Collection	-	-	-	-
E20121(T)	*Vibrio zhuhaiensis*	Collection	-	-	-	-
R-3712(T)	*Vibrio chagasii*	Collection	-	-	-	-
18	*Vibrio campbellii*	Donated*	-	-	-	-
20160303005-1	*Vibrio parahemolyticus*	Donated*	-	-	-	-
VIB 72	*Vibrio anguillarum*	Donated[#]	-	-	-	-
VIB 645	*Vibrio harveyi*	Donated[#]	-	-	-	-

Table S5. Results of one-way ANOVA on the OD600 of *V. alginolyticus* 283T treated with different phages at MOI=1, and of a *posteriori* pairwise multiple comparisons for the OD600 of *V. alginolyticus* 283T (Student's t-test).

Sources of variation	**P**
Factor (OD600 of *V. alginolyticus* 283T)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. Va1	< 0.001
Control vs. Va2	< 0.001
Control vs. Va3	< 0.001

Va1 vs.Va2	0.155
Va2 vs.Va3	0.148
Va1vs.Va3	0.675

Table S6. Results of one-way ANOVA on the OD600 of *V. alginolyticus* 283T treated with different phage cocktails at MOI=1, and of a *posteriori* pairwise multiple comparisons for the OD600 of *V. alginolyticus* 283T (Student's t-test).

Sources of variation	**P**
Factor (number of *V. alginolyticus* 283T)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. Va1/Va2	< 0.001
Control vs. Va2/Va3	< 0.001
Control vs. Va1/Va3	< 0.001
Control vs. Va1//Va2/Va3	< 0.001
Va1/Va2 vs.Va2/Va3	< 0.001
Va1/Va2 vs.Va1/Va3	< 0.001
Va1/Va2 vs.Va1//Va2/Va3	< 0.001
Va2/Va3 vs.Va1/Va3	< 0.001
Va2/Va3 vs.Va1//Va2/Va3	< 0.001
Va1/Va3 vs.Va1//Va2/Va3	< 0.001

Table S7. Results of one-way ANOVA on the number of *V. alginolyticus* 283T treated with different phage cocktails at MOI=1, and of a *posteriori* pairwise multiple comparisons for the number of *V. alginolyticus* 283T (Student's t-test).

Sources of variation	**P**

Factor (number of *V. alginolyticus* 283T)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. Va1/Va2	< 0.001
Control vs. Va2/Va3	< 0.001
Control vs. Va1/Va3	< 0.001
Control vs. Va1//Va2/Va3	< 0.001
Va1/Va2 vs.Va2/Va3	< 0.001
Va1/Va2 vs.Va1/Va3	< 0.001
Va1/Va2 vs.Va1//Va2/Va3	< 0.001
Va2/Va3 vs.Va1/Va3	< 0.001
Va2/Va3 vs.Va1//Va2/Va3	< 0.001
Va1/Va3 vs.Va1//Va2/Va3	< 0.001

Table S8. Results of one-way ANOVA on the OD600 of *V. alginolyticus* 283T treated with different phages at MOI=10, and of a *posteriori* pairwise multiple comparisons for the OD600 of *V. alginolyticus* 283T (Student's t-test).

Sources of variation	**P**
Factor (OD600 of *V. alginolyticus* 283T)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. Va1	< 0.001
Control vs. Va2	< 0.001
Control vs. Va3	< 0.001
Va1 vs.Va2	< 0.001
Va2 vs.Va3	0.007

Va1vs.Va3	0.244

Table S9. Results of one-way ANOVA on the OD600 of *V. alginolyticus* 283T treated with different phage cocktails at MOI=10, and of a *posteriori* pairwise multiple comparisons for the OD600 of *V. alginolyticus* 283T (Student's t-test).

Sources of variation	**P**
Factor (number of *V. alginolyticus* 283T)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. Va1/Va2	< 0.001
Control vs. Va2/Va3	< 0.001
Control vs. Va1/Va3	< 0.001
Control vs. Va1//Va2/Va3	< 0.001
Va1/Va2 vs.Va2/Va3	< 0.001
Va1/Va2 vs.Va1/Va3	< 0.001
Va1/Va2 vs.Va1//Va2/Va3	< 0.001
Va2/Va3 vs.Va1/Va3	< 0.001
Va2/Va3 vs.Va1//Va2/Va3	< 0.001
Va1/Va3 vs.Va1//Va2/Va3	< 0.001

Table S10. Results of one-way ANOVA on the OD600 of *Vibrio parahaemolyticus* MCS treated with different phages at MOI=1, and of a *posteriori* pairwise multiple comparisons for the OD600 of *Vibrio parahaemolyticus* MCS (Student's t-test).

Sources of variation	**P**
Factor (OD600 of *Vibrio parahaemolyticus* MCS)	< 0.001
***A posteriori* pairwise comparisons**	**P**

Control vs. VP1+VP2	< 0.001
Control vs. VP2+VP4	< 0.001
Control vs. VP3+VP4	< 0.001
Control vs. VP1+VP4	0.02
Control vs. VP2+VP3	0.008
Control vs. VP1+VP3	0.004
VP1+VP2 vs.VP2+VP4	< 0.001
VP1+VP2 vs.VP3+VP4	0.02
VP1+VP2 vs.VP3+VP4	< 0.001
VP1+VP2vs.VP2+VP3	0.298
VP1+VP2vs.VP1+VP3	0.596
VP2+VP4vs.VP3+VP4	0.669
VP2+VP4vs.VP1+VP4	0.906
VP2+VP4vs.VP2+VP3	0.001
VP2+VP4vs.VP1+VP3	0.005
VP3+VP4vs.VP1+VP4	0.608
VP3+VP4vs.VP2+VP3	0.012
VP3+VP4vs.VP1+VP3	0.031
VP1+VP4vs.VP2+VP3	0.002
VP1+VP4vs.VP1+VP3	0.006
VP2+VP3vs.VP1+VP3	0.548

Table S11. Results of one-way ANOVA on the OD600 of *Vibrio parahaemolyticus* MCS treated with different phages at MOI=10, and of a *posteriori* pairwise multiple comparisons for the OD600 of *Vibrio parahaemolyticus* MCS (Student's t-test).

Sources of variation	**P**

Factor (OD600 of *Vibrio parahaemolyticus* MCS)	< 0.001
***A posteriori* pairwise comparisons**	**P**
Control vs. VP1+VP2	< 0.001
Control vs. VP2+VP4	< 0.001
Control vs. VP3+VP4	< 0.001
Control vs. VP1+VP4	0.02
Control vs. VP2+VP3	0.001
Control vs. VP1+VP3	< 0.001
VP1+VP2 vs.VP2+VP4	< 0.001
VP1+VP2 vs.VP3+VP4	0.02
VP1+VP2 vs.VP3+VP4	< 0.001
VP1+VP2vs.VP2+VP3	0.372
VP1+VP2vs.VP1+VP3	0.994
VP2+VP4vs.VP3+VP4	0.642
VP2+VP4vs.VP1+VP4	0.321
VP2+VP4vs.VP2+VP3	< 0.001
VP2+VP4vs.VP1+VP3	< 0.001
VP3+VP4vs.VP1+VP4	0.167
VP3+VP4vs.VP2+VP3	< 0.001
VP3+VP4vs.VP1+VP3	< 0.001
VP1+VP4vs.VP2+VP3	< 0.001
VP1+VP4vs.VP1+VP3	< 0.001
VP2+VP3vs.VP1+VP3	0.341