

Table S1. Host range of phage vB_VnaS-L3.

Strains	Best matched species (% Identity of 16S rDNA)	GenBank ID	Source and location	Susceptibility to phage vB_VnaS-L3 1
AbY-1805	<i>Vibrio natriegens</i> (100)	OP247638	Cells of <i>Haliotis discus hannai</i> Ino, China	+
AbY-1806	<i>Vibrio natriegens</i> (99.93)	OP268245	Cells of <i>Haliotis discus hannai</i> Ino, China	+
AbY-1807	<i>Vibrio natriegens</i> (99.86)	OP268246	Larval rearing water, China	+
MCCC 1A14388	<i>Vibrio natriegens</i> (99.93)		Shrimp farm water, China	-
MCCC 1K03861	<i>Vibrio natriegens</i> (99.93)		Sediment of oyster farming area, China	-
MCCC 1H000251	<i>Vibrio natriegens</i> (100)		Type strain	-
ScY-2105	<i>Vibrio alginolyticus</i> (99.72)	OP268247	Cells of <i>Mizuhopecten yessoensis</i> , China	-
ScY-2106	<i>Vibrio alginolyticus</i> (99.93)	OP268248	Cells of <i>Azumapecten farreri</i> , China	-
ScY-2108	<i>Vibrio alginolyticus</i> (99.93)	OP268249	Cells of <i>Azumapecten farreri</i> , China	-
WaY-2220	<i>Vibrio alginolyticus</i> (99.72)	OP268250	Larval rearing water, China	-
ScY-2203	<i>Vibrio splendidus</i> (99.93)	OP268251	Cells of <i>Azumapecten farreri</i> , China	-
ScY-2204	<i>Vibrio splendidus</i> (99.93)	OP268252	Cells of <i>Azumapecten farreri</i> , China	-
ScG-2206	<i>Vibrio splendidus</i> (100.00)	OP268253	Cells of <i>Azumapecten farreri</i> , China	-
WaY-2207	<i>Vibrio splendidus</i> (100.00)	OP268254	Coastal seawater, China	-

ScY-2109	<i>Vibrio atlanticus</i> (99.93)	OP268255	Cells of <i>Azumapecten farreri</i> , China	-
ScG-2110	<i>Vibrio atlanticus</i> (99.92)	OP268256	Cells of <i>Azumapecten farreri</i> , China	-
AbG-1906	<i>Vibrio chagasii</i> (100.00)	OP268257	Cells of <i>Haliotis discus hannai</i> Ino, China	-
AbG-1907	<i>Vibrio chagasii</i> (100.00)	OP268258	Cells of <i>Haliotis discus hannai</i> Ino, China	-
WaY-2101	<i>Vibrio chagasii</i> (99.51)	OP268259	Larval rearing water, China	-
AbY-1902	<i>Vibrio mediterranei</i> (99.86)	OP268260	Cells of <i>Haliotis discus hannai</i> Ino, China	-
AbY-1905	<i>Vibrio mediterranei</i> (100.00)	OP268261	Cells of <i>Haliotis discus hannai</i> Ino, China	-
AbY-2104	<i>Vibrio mediterranei</i> (100.00)	OP268262	Cells of <i>Haliotis discus hannai</i> Ino, China	-
ScG-2205	<i>Vibrio crassostreae</i> (99.78)	OP268263	Cells of <i>Azumapecten farreri</i> , China	-
AbY-2219	<i>Vibrio crassostreae</i> (99.79)	OP268264	Cells of <i>Haliotis discus hannai</i> Ino, China	-
AbY-1901	<i>Vibrio owensii</i> (100.00)	OP268265	Cells of <i>Haliotis discus hannai</i> Ino, China	-
WaY-2217	<i>Vibrio parahaemolyticus</i> (99.79)	OP268266	Coastal seawater, China	-
AbY-1904	<i>Vibrio neocaledonicus</i> (100.00)	OP268267	Cells of <i>Haliotis discus hannai</i> Ino, China	-
ScG-2111	<i>Vibrio celticus</i> (100.00)	OP268268	Cells of <i>Azumapecten farreri</i> , China	-
WaG-2102	<i>Shewanella japonica</i> (99.93)	OP268269	Larval rearing water, China	-
AbG-2103	<i>Shewanella japonica</i> (100.00)	OP268270	Cells of <i>Haliotis discus hannai</i> Ino, China	-
ScG-2112	<i>Shewanella japonica</i> (99.93)	OP268271	Cells of <i>Azumapecten farreri</i> , China	-

AbG-1908	<i>Shewanella waksmanii</i> (99.93)	OP268272	Cells of <i>Haliotis discus hannai</i> Ino, China	-
ScG-2113	<i>Shewanella colwelliana</i> (100.00)	OP268273	Cells of <i>Azumapecten farreri</i> , China	-
AbY-1903	<i>Photobacterium jeanii</i> (99.78)	OP268274	Cells of <i>Haliotis discus hannai</i> Ino, China	-
ScY-2107	<i>Photobacterium rosenbergii</i> (99.84)	OP268275	Cells of <i>Azumapecten farreri</i> , China	-
Wa-1801	<i>Idiomarina</i> sp. (99.93)	OP268276	Surface seawater, Yellow sea, China	-
Wa-1802	<i>Pseudoalteromonas</i> sp. (100.00)	OP268277	Surface seawater, Yellow sea, China	-
Wa-1803	<i>Pseudoalteromonas marina</i> (99.93)	OP268278	Surface seawater, Yellow sea, China	-
Wa-1804	<i>Sulfitobacter</i> sp. (99.97)	OP268279	Larval rearing water, China	-

1. +, susceptible; -, resistant.

Table S2. Antimicrobial resistance and susceptibility of *V. natriegens* AbY-1805

Antibiotic class/group	Antibiotic name	Concentration (µg disc ⁻¹)	Standard of inhibition zone (mm)			Diameter of inhibition zone	Interpretive category result
			Resistant	Intermediate	Sensitive		
β-Lactam/β-Lactamase Inhibitor	Penicillin G	10 U	≤ 11	12~15	≥ 16	15	I
	Oxacillin	1	≤ 10	11~12	≥ 13	No zone	R
	Ampicillin	10	≤ 13	14~16	≥ 17	17	S
	Carbenicillin	100	≤ 19	20~22	≥ 23	14	R
	Piperacillin	100	≤ 17	18~20	≥ 21	21	S
Cephalosporin/Cephem	Cefalexin	30	≤ 14	15~17	≥ 18	13	R
	Cefazolin	30	≤ 14	15~17	≥ 18	12	R
	Cefradine	30	≤ 14	15~17	≥ 18	12	R

	Cefuroxime	30	≤ 14	15~22	≥ 23	14	R
	Ceftazidime	30	≤ 14	15~17	≥ 18	17	I
	Ceftriaxone	30	≤ 13	14~20	≥ 21	20	I
	Cefoperazone	75	≤ 15	16~20	≥ 21	19	I
Aminoglycosides	Amikacin	30	≤ 14	15~16	≥ 17	9	R
	Gentamicin	10	≤ 12	13~14	≥ 15	10	R
	Kanamycin	30	≤ 13	14~17	≥ 18	9	R
	Neomycin	30	≤ 12	13~16	≥ 17	10	R
Tetracycline	Tetracycline	30	≤ 14	15~18	≥ 19	No zone	R
	Oxytetracycline	30	≤ 14	12~18	≥ 19	21	S
	Minocycline	30	≤ 14	15~18	≥ 19	No zone	R
	Doxycycline	30	≤ 12	13~15	≥ 16	No zone	R
Macrolides	Erythrocine	15	≤ 13	14~22	≥ 23	10	R
	Medemycin	30	≤ 13	14~17	≥ 18	11	R
Fluoroquinolones	Norfloxacin	10	≤ 12	13~16	≥ 17	19	S
	Ofloxacin	5	≤ 12	13~15	≥ 16	19	S
	Ciprofloxacin	5	≤ 15	16~20	≥ 21	22	S
Glycopeptides	Vancomycin	30	≤ 14	15~16	≥ 17	No zone	R
polymyxins	Polymyxin B	300 IU	≤ 8	9~11	≥ 12	13	S
Folate Pathway Inhibitor	Sulfamethoxazole-trimethoprim	23.75/1.25	≤ 12	13~15	≥ 16	22	S
Nitrofurans	Furazolidone	300	≤ 14	15~16	≥ 17	12	S
Phenicol	Chloramphenicol	30	≤ 12	13~17	≥ 18	24	S
Lincosamide	Clindamycin	2	≤ 14	15~20	≥ 21	No zone	R
Fluorfenicol	Florfenicol	30	≤ 12	13~17	≥ 18	17	I

Note: S = susceptible; I = intermediate; R = resistant. The susceptibility of the strain AbY-1805 to antibiotics (Hangwei, Hangzhou, China, except for oxytetracycline and florfenicol)

was tested by using disk-diffusion method followed Kirby-Bauer disk diffusion method and the standard techniques of the Clinical and Laboratory Standard Institute (CLSI) [102,103]. Briefly, the disks were dispensed on the surface of the RO agar medium that was mixed with the strain AbY-1805, and incubated at 28 °C for 24 h. Diameters of the inhibition zone were interpreted according to the Hangwei antibiotic susceptible zone interpretation chart and the M45 guideline for *Vibrio* spp. (not *V. cholerae*) of CLSI [103], except for oxytetracycline that was interpreted according to the M2-A8 guideline of CLSI [104].

Table S3. Genome annotation of *V. natriegens* AbY-1805-infecting phage vB_VnaS-L3

ORF	Start	Stop	Strand	Putative function	CD accession no.	Best matched species	Identity (%)
1	46	528	+	Hypothetical protein	AAW67525.1	Listonella phage ϕ HSIC	96.9
2	540	944	+	Hypothetical protein	AAW67526.1	Listonella phage ϕ HSIC	92.5
3	1034	4273		Putative tail tape measure			
			+	protein	AAW67528.1	Listonella phage ϕ HSIC	77.9
4	4273	5859	+	Hypothetical protein	AAW67529.1	Listonella phage ϕ HSIC	83.9
5	5913	8096	+	Hypothetical protein	AUG88486.1	Vibrio phage Vp-R1	47.7
7	8313	8627	+	Hypothetical protein	AGN34328.1	Vibrio phage pYD38-B	96.8
8	8727	9059	-	Hypothetical protein	AUR86940.1	Vibrio phage 1.091.O.-10N.286.52.B12	81.5
9	9196	9402	-	Hypothetical protein	AGN34330.1	Vibrio phage pYD38-B	91.2
11	9610	9816	-	Hypothetical protein	AUR92455.1	Vibrio phage 1.172.O.-10N.261.52.F5	69.1
12	10180	10389	-	Hypothetical protein	AGN34331.1	Vibrio phage pYD38-B	73.9
13	10386	10538	-	Hypothetical protein	AGN34332.1	Vibrio phage pYD38-B	86
14	10602	11060	-	Putative phage lysozyme	AAW67534.1	Listonella phage ϕ HSIC	90.1
15	11057	11236	-	Hypothetical protein	AVR75884.1	Vibrio phage ValSw3-3	97
17	11328	11876	-	hypothetical protein	AGN34334.1	Vibrio phage pYD38-B	77.5
18	11873	12052	-	hypothetical protein	AGN34335.1	Vibrio phage pYD38-B	94.9
19	12049	12255	-	Hypothetical protein	AGN34336.1	Vibrio phage pYD38-B	89.7
20	12248	12547	-	Hypothetical protein	ADM26694.1	Pseudoalteromonas phage H105/1	53.5
21	12540	12725	-	Hypothetical protein	AZF88631.1	Vibrio phage P23	95.1

22	12750	12965	+	Hypothetical protein	AAW67537.1	Listonella phage ϕ HSIC	69
23	12991	13374	-	hypothetical protein	AAW67538.1	Listonella phage ϕ HSIC	96.8
24	13371	15230	-	Putative helicase	AAW67539.1	Listonella phage ϕ HSIC	83.4
25	15199	15849	-	Hypothetical protein	AIM40751.1	Idiomarinaceae phage 1N2-2	34.9
26	15849	16403	-	Hypothetical protein	AAW67540.1	Listonella phage ϕ HSIC	95.6
27	16388	17242	-	Hypothetical protein	AGH16091.1	Vibrio phage pYD21-A	62.3
28	17280	17813	-	Hypothetical protein	AAW67542.1	Listonella phage ϕ HSIC	93.8
29	17820	18530	-	Putative helicase subunit	AAW67543.1	Listonella phage ϕ HSIC	96.2
31	18922	21234	-	Putative DNA primase/polymerase	QXO10371.1	Proteus phage vB_PmiM_ZX7	41.4
32	21711	22262	+	Putative DNA polymerase III beta subunit	AAW67499.1	Listonella phage ϕ HSIC	92.9
33	22265	22405	+	Hypothetical protein	AVR75863.1	Vibrio phage ValSw3-3	80.4
34	22544	23059	+	Coil containing protein	QGZ13264.1	Vibrio phage NF	64.6
35	23139	23312	+	Protein of unknown function DUF551	AUR89397.1	Vibrio phage 1.122.B.-10N.286.46.F8	83.6
36	23309	23461	+	Hypothetical protein	AZF88614.1	Vibrio phage P23	67.4
37	23458	23760	+	Hypothetical protein	AVR75857.1	Vibrio phage ValSw3-3	81.8
38	23790	24635	+	DNA-binding domain protein	AUR99418.1	Vibrio phage 1.265.O.-10N.286.52.F6	52.9
39	24632	24844	+	Hypothetical protein	AGN34354.1	Vibrio phage pYD38-B	87.1
40	24841	25125	+	Hypothetical protein	AZF88608.1	Vibrio phage P23	93.6
41	25184	25648	+	DNA-packaging protein	AZF88606.1	Vibrio phage P23	98.7
42	25635	27233	+	Terminase large subunit	AZF88605.1	Vibrio phage P23	97.6
43	27353	27805	+	Hypothetical protein	AGH16106.1	Vibrio phage pYD21-A	83.3
44	28012	28464	+	Hypothetical protein	AAW67508.1	Listonella phage ϕ HSIC	88.9
45	28529	29023	+	Hypothetical protein	AVR75852.1	Vibrio phage ValSw3-3	45.6

46	29079	30509	+	Hypothetical protein	AGN34361.1	Vibrio phage pYD38-B	95
48	31096	32166		Putative NAD-asparagine	AAW67511.1		94.5
			+	ribosyltransferase		Listonella phage ϕ HSIC	
49	32264	32578	+	Hypothetical protein	AGN34363.1	Vibrio phage pYD38-B	84
50	32575	32763	+	Hypothetical protein	AGN34365.1	Vibrio phage pYD38-B	82.3
52	33459	34208	+	DNA methylase, partial	AUR81467.1	Vibrio phage 1.007.O.-10N.261.55.F9	68.5
53	34302	34976	+	Hypothetical protein	AGN34367.1	Vibrio phage pYD38-B	95.5
54	34987	35934	+	Major capsid protein	AVR75838.1	Vibrio phage ValSw3-3	97.4
55	35965	36555	+	Hypothetical protein	AAW67516.1	Listonella phage ϕ HSIC	83.8
56	36861	37358	+	Hypothetical protein	AGN34370.1	Vibrio phage pYD38-B	92.1
57	37362	38159	+	Putative DNA methylase	AIM40744.1	Idiomarinaceae phage 1N2-2	67.2
58	38159	38560	+	Head-closure protein	AZF88585.1	Vibrio phage P23	92.4
59	38565	39035	+	Hypothetical protein	AVR75833.1	Vibrio phage ValSw3-3	95.5
60	39035	39418	+	Hypothetical protein	AAW67523.1	Listonella phage ϕ HSIC	91.3
61	39489	39965	+	Hypothetical protein	AAW67524.1	Listonella phage ϕ HSIC	98.7
