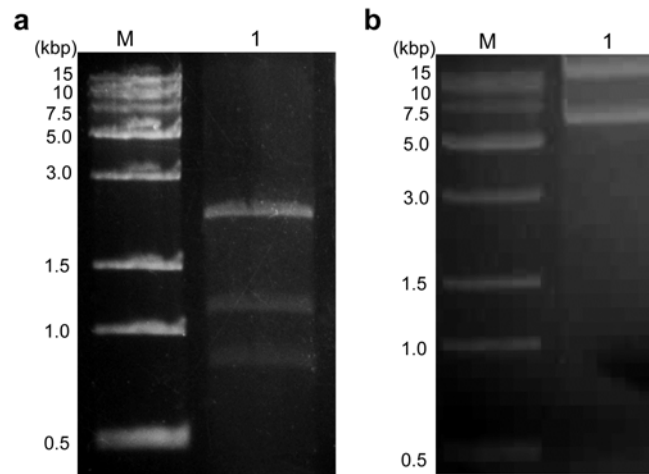
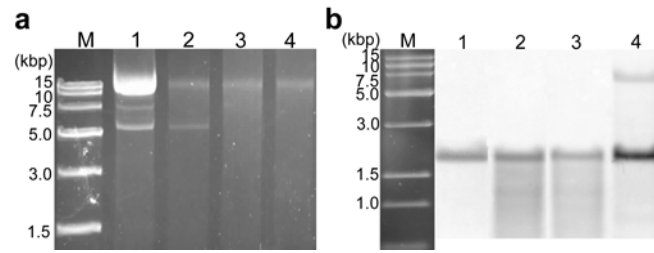


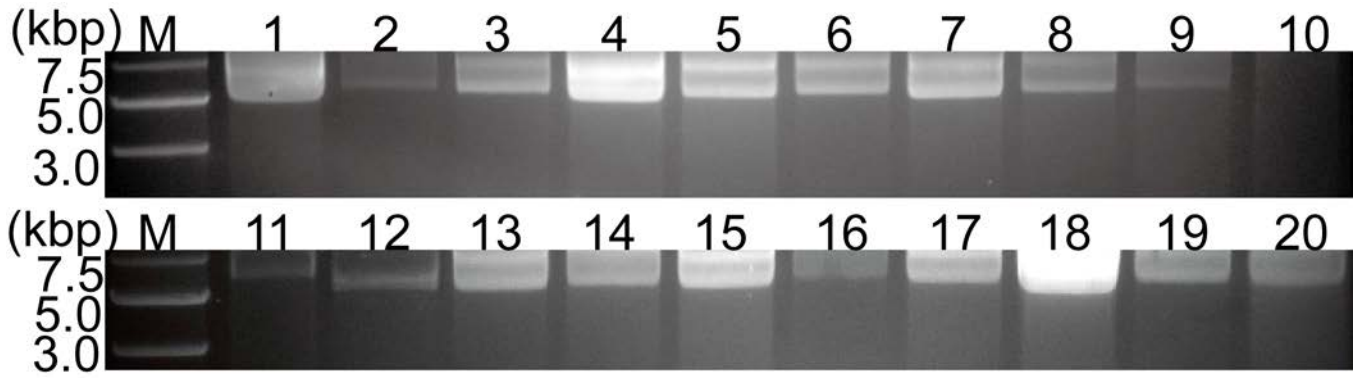
## Supplementary Information



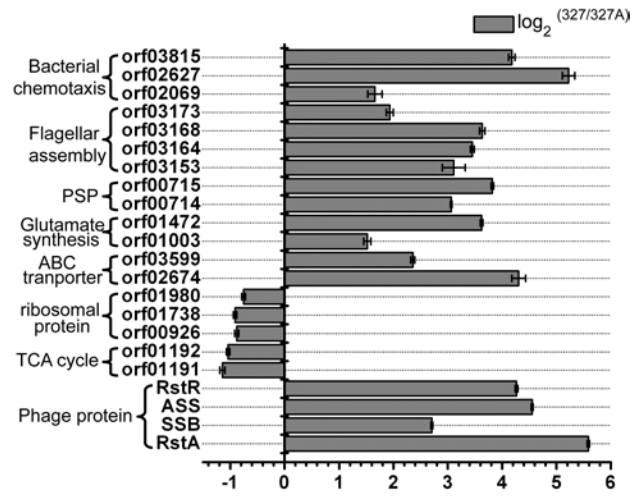
**Figure S1.** Agarose gel electrophoresis analysis of the digested RF327 by *Hind*III. (a) Digested RF327. Lanes: M, *Trans*15K DNA marker; 1, RF327 digested by *Hind*III. (b) Untreated RF327. Lanes: M, *Trans*15K DNA marker; 1, RF327.



**Figure S2.** Verification of the RF327-cured host. (a) Agarose gel electrophoresis analysis of RF327 extracted from the RF-cured host strains. Lanes: M, *Trans15K* DNA marker (TransGen, China); 1, RF327 extracted from strain BSi20327 as the positive control; 2-4, RF327 extracted from high temperature treated host strains, showing that 3 and 4 had no RF327 detected. (b) Southern blot hybridization of BSi20327 and its RF-cured strain BSi20327A with ORF386 as a probe. Lanes: M, *Trans15K* DNA marker; 1, genomic DNA of BSi20327A treated with S1 nuclease prior to be digested by *HindIII*; 2, genomic DNA of BSi20327A digested by *HindIII*; 3, genomic DNA of BSi20327 treated with S1 nuclease prior to be digested by *HindIII*; 4, genomic DNA of BSi20327 digested by *HindIII*. The results indicate that phage ssDNA is not detectable in the RF-cured host strain BSi20327A.



**Figure S3.** Agarose gel electrophoresis analysis of the replicative forms of phage isolated from 19 phage gene-containing strains. Lanes 1-20 were BSi20327, BSi20335, BSi20381, BSi20465, BSi20401, BSi20514, BSi20407, BSi20357, BSi20436, BSi20670, BSi20366, BSi20340, BSi20455, BSi20447, BSi20462, BSi20451, BSi20464, BSi20341, BSi20437 and BSi20439, respectively. Strain BSi20670 harboring no phage gene was used as the negative control.



**Figure S4.** Verification of the whole-transcriptomes results by Real time-qPCR. Twenty two genes were selected to perform the verification. RstR, ASS, SSB, RstA were phage protein of f327.

They represent ORF37, ORF448, ORF116 and ORF386, respectively.

**Table S1. *Pseudoalteromonas* strains used in this study.**

<b>Identification Number</b>	<b>Sampling Sites</b>	<b>Location of Sampling Sites</b>	<b>Identification Number</b>	<b>Sampling Sites</b>	<b>Location of Sampling Sites</b>
BSi20316	CNIS7	78°23'14"N 149°06'55"W	BSi20597	CNIS7	78°23'14"N 149°06'55"W
BSi20319	CNIS7	78°23'14"N 149°06'55"W	BSi20612	CNIS7	78°23'14"N 149°06'55"W
BSi20324	CNIS7	78°23'14"N 149°06'55"W	BSi20613	CNIS7	78°23'14"N 149°06'55"W
BSi20325	CNIS7	78°23'14"N 149°06'55"W	BSi20424	IS2	74°41'11"N 164°04'28"W
BSi20326	CNIS7	78°23'14"N 149°06'55"W	BSi20428	IS2	74°41'11"N 164°04'28"W
BSi20327	CNIS7	78°23'14"N 149°06'55"W	BSi20430	IS2	74°41'11"N 164°04'28"W
BSi20335	CNIS7	78°23'14"N 149°06'55"W	BSi20434	IS2	74°41'11"N 164°04'28"W
BSi20339	CNIS7	78°23'14"N 149°06'55"W	BSi20436	IS2	74°41'11"N 164°04'28"W
BSi20340	CNIS7	78°23'14"N 149°06'55"W	BSi20437	IS2	74°41'11"N 164°04'28"W
BSi20341	CNIS7	78°23'14"N 149°06'55"W	BSi20439	IS2	74°41'11"N 164°04'28"W
BSi20343	CNIS7	78°23'14"N 149°06'55"W	BSi20447	IS3	75°28'52"N 152°51'18"W
BSi20347	CNIS7	78°23'14"N 149°06'55"W	BSi20451	IS3	75°28'52"N 152°51'18"W
BSi20354	CNIS7	78°23'14"N 149°06'55"W	BSi20489	IS3	75°28'52"N 152°51'18"W
BSi20357	CNIS7	78°23'14"N 149°06'55"W	BSi20496	IS3	75°28'52"N 152°51'18"W
BSi20359	CNIS7	78°23'14"N 149°06'55"W	BSi20514	IS3	75°28'52"N 152°51'18"W
BSi20366	CNIS7	78°23'14"N 149°06'55"W	BSi20453	IS5	77°30'59"N 152°52'04"W
BSi20370	CNIS7	78°23'14"N 149°06'55"W	BSi20454	IS5	77°30'59"N 152°52'04"W
BSi20372	CNIS7	78°23'14"N 149°06'55"W	BSi20455	IS5	77°30'59"N 152°52'04"W
BSi20381	CNIS7	78°23'14"N 149°06'55"W	BSi20456	IS5	77°30'59"N 152°52'04"W
BSi20382	CNIS7	78°23'14"N 149°06'55"W	BSi20462	IS5	77°30'59"N 152°52'04"W
BSi20391	CNIS7	78°23'14"N 149°06'55"W	BSi20464	IS5	77°30'59"N 152°52'04"W
BSi20398	CNIS7	78°23'14"N 149°06'55"W	BSi20465	IS9	80°11'50"N 146°46'10"W
BSi20401	CNIS7	78°23'14"N 149°06'55"W	BSi20578	IS9	80°11'50"N 146°46'10"W
BSi20407	CNIS7	78°23'14"N 149°06'55"W	BSi20472	IS10	79°17'36"N 151°50'49"W
BSi20410	CNIS7	78°23'14"N 149°06'55"W	BSi20474	IS10	79°17'36"N 151°50'49"W
BSi20581	CNIS7	78°23'14"N 149°06'55"W	BSi20670	IS13	77°30'03"N 162°29'22"W
BSi20584	CNIS7	78°23'14"N 149°06'55"W			

Gray background represents the strains containing filamentous phage.

**Table S2.** Analysis of the ORFs on RF327 from *Pseudoalteromonas* sp. BSi20327

ORF	Homologous protein (source species, accession no.)	Identity	Similarity
ORF63 <sup>a</sup>	transcriptional regulator ( <i>Marinobacter</i> sp. ES-1, WP 022988450)	36% (12/33) <sup>b</sup>	61% (20/33) <sup>b</sup>
ORF386	Replication initiation factor family ( <i>Vibrio harveyi</i> , ZP 01985526)	40% (155/383)	54% (209/383)
	RstA phage-related replication protein ( <i>Vibrio cholerae</i> , ZP 04416969)	37% (134/367)	56% (208/367)
ORF116	putative ssDNA binding protein ( <i>Vibrio</i> phage KSF-1phi, YP 087071)	39% (31/80)	57% (46/80)
	RstB phage-related integrase ( <i>Vibrio splendidus</i> , ZP 12592573)	43% (48/111)	65% (73/111)
ORF65	conserved hypothetical protein ( <i>Vibrio cholerae</i> , ZP 07008260)	32% (19/60)	48% (29/60)
ORF74	coat protein F ( <i>Haloplasma contractile</i> , WP 008825221)	29% (19/65)	49% (32/65)
ORF461	Conserved hypothetical protein ( <i>Shewanella piezotolerans</i> , ACJ29305)	38% (52/137)	46% (64/137)
ORF103	minor coat protein ( <i>Ralstonia solanacearum</i> , YP 003745721)	34% (36/106)	51% (55/106)
	integral membrane protein ( <i>Neisseria flavescens</i> , ZP 04757926)	30% (25/84)	59% (50/84)
ORF448	zonular occludens toxin ( <i>Vibrio scophthalmi</i> , ZP 08749162)	41% (132/320)	55% (179/320)
	putative phage assembly protein ( <i>Ralstonia syzygii</i> , CCA84653)	31% (55/179)	45% (81/179)
ORF37	phage replication repressor RstR ( <i>Vibrio</i> phage CTXΦ, AAM70438)	46% (17/37)	75% (28/37)
	RstR-like phage repressor protein ( <i>Haemophilus influenzae</i> , YP 001291604)	51% (19/37)	75% (28/37)

<sup>a</sup> Number indicates the number of amino acids in the encoded protein.

<sup>b</sup> The ratio in the bracket indicates the number of amino acids with identity or similarity/total number of amino acids in the homologous region.

**Table S3. Identity of proteins between the phages from BSi20327 and BSi20439**

ORF in BSi20327	Identity <sup>a</sup>
ORF63	98%
ORF386	99%
ORF116	68%
ORF65	100%
ORF74	85%
ORF461	74%
ORF103	89%
ORF448	93%

<sup>a</sup> The ratio is the number of amino acids with identity or similarity/total number of amino acids in the homologous region.

**Table S4. Annotation of the differently expressed genes between BSi20327 and BSi20327A.**

ORF number	Description	ORF number	Description
orf4084	major capsid protein of f327	orf03163	flagellar hook-length control protein FliK
orf4085	ssDNA binding protein of f327	orf03164	flagellar protein FliJ
orf4087	replication protein of f327	orf03165	flagellum-specific ATP synthase FliI
orf4088	transcriptional regulator of f327	orf03166	flagellar assembly protein FliH
orf01191	succinyl-CoA synthetase beta subunit	orf03168	flagellar MS-ring protein FliF
orf01192	succinyl-CoA synthetase subunit alpha	orf03169	flagellar hook-basal body complex protein FliE
orf01188	succinate dehydrogenase iron-sulfur subunit	orf03170	sigma-54 dependent response regulator FlrC
orf01186	succinate dehydrogenase membrane anchor subunit	orf03171	Flagellar assembly sensory box sensor histidine kinase FlrB
orf02045	transcription elongation factor	orf03173	Flagellar regulatory protein FlrA
orf00432	50S ribosomal protein L19	orf03177	flagellar hook-associated protein FliD
orf00484	30S ribosomal subunit protein S15	orf03955	flagellar basal body rod protein FlgF
orf00892	50S ribosomal protein L20	orf03956	flagellar basal body rod protein FlgG
orf00926	small subunit ribosomal protein S1	orf03958	flagellar P-ring protein precursor FlgI
orf01736	large subunit ribosomal protein L7/L12	orf03962	flagellar hook-associated protein FlgK
orf01738	large subunit ribosomal protein L1	orf03963	flagellar hook-associated protein FlgL
orf01739	50S ribosomal protein L11	orf00154	chemotaxis protein CheY
orf01824	30S ribosomal protein S3	orf00438	diguanylate phosphodiesterase
orf01980	large subunit ribosomal protein L17	orf00458	diguanylate phosphodiesterase
orf01985	50S ribosomal protein L36	orf00583	GGDEF domain protein
orf01987	large subunit ribosomal protein L15	orf01012	response regulator
orf01991	large subunit ribosomal protein L6	orf01313	signaling protein ykoW



ORF number	Description	ORF number	Description
orf01994	large subunit ribosomal protein L5	orf01527	hemolysin secretion protein
orf01995	50S ribosomal protein L24	orf01563	methyl-accepting chemotaxis protein
orf01996	50S ribosomal protein L14	orf01564	methyl-accepting chemotaxis protein
orf02674	polar amino acid transport system permease protein	orf01699	methyl-accepting chemotaxis protein
orf01862	branched-chain amino acid transport system substrate-binding protein	orf02069	chemotaxis protein CheW
orf01003	glutamate synthase	orf02071	CheA signal transduction histidine kinase
orf01472	glutamate-5-semialdehyde dehydrogenase	orf02500	methyl-accepting chemotaxis protein
orf00714	phage shock protein A	orf02516	methyl-accepting chemotaxis protein
orf00715	phage shock protein C	orf02627	methyl-accepting chemotaxis protein
orf03442	transcriptional activator of the Psp operon with PspB	orf02855	CheB/CheR fusion protein
orf03443	phage shock protein B	orf02923	sensor kinase CheA
orf02824	flagellar motor switch protein FliG	orf03022	biofilm dispersion protein BdlA
orf02825	flagellar assembly protein FliH	orf03144	chemotaxis protein MotB
orf03145	flagellar motor protein MotA/chemotaxis protein MotA	orf03146	response regulator CheB
orf03153	flagellar biosynthesis protein FlhA	orf03324	CheB/CheR fusion protein
orf03154	flagellar biosynthesis protein FlhB	orf03516	methyl-accepting chemotaxis protein
orf03155	flagellar biosynthesis protein FliR	orf03815	EAL domain protein
orf03157	flagellar biosynthetic protein FliP		

**Table S5. Primers used in this study**

Primer	Sequence (5'-3')	Primer	Sequence (5'-3')
386F	ATGAATTATCAATATAGTGACCG TGC	orf00714R	GCTTGTGTTTATTGCTTATTG
448R	AAATTGAGCTAGGTATATATTTT TACC	orf00715F	TGTCTGTAGTGGGTTAGC
70F	ACGACTGACCCGGTACGCATGTA YATGMGNGARATGGGNACNGT	orf00715R	GACAACAGTGTGCGATTA
70R	ATAGAAATAACCAGACGTAAGT TNGCYTCNACCATYTCYTTYTT	orf03164F	ACGCTGGCTTACTACTTG
rpoDF	TTCTTCTTCGTCTTCATCATC	orf03164R	AGGTCAATCGGGCTTATC
rpoDR	CTTAGCGACATTATCTCTGG	orf03168F	CACGGACACACTTATTCTG
orf01191F	ACACCAGAACTTATCCACAA	orf03168R	TACCTGAAGATGCGATGG
orf01191R	GTTGCCAAGACCCATAAAG	orf03153F	CAAGTCCTGGTTCTATTCC
orf01192F	TCCTGGTGAGACTAAGATTG	orf03153R	AAGATGCTGTTGGTATGTC
orf01192R	CCAACACAAGAAGACTGAC	orf03173F	ATCACGCTCCATCAGTTC
orf01738F	TTTAGGGTTTGGCATTAGAC	orf03173R	GCTGGCTAATCTTGTTGAG
orf01738R	GCTGAATTAGTAGGCATGGAA	orf03815F	AAGGCGTTCTTTCCACTG
orf01980F	GCGTCTTCTTGAACCTCTTC	orf03815R	GCACTTGGCGTAAATAGC
orf01980R	AATCGGTCCTCGTAATGC	orf02627F	ACCACTTCACTGTAATAATCAC
orf00926F	TGTGAAGAGCAAGAGACT	orf02627R	TAGATAACGCACTGAGACAA
orf00926R	TACTGGACGAACATCAACA	orf02069F	AATCAATTAAGGCGACCATT
orf02674F	ATGTCGTCCATCACAATATG	orf02069R	GCAGTGGCAGATGTTTATAG
orf02674R	CACAGTCAGCCATTATTTCT	RstAF	TTAGCCAGTAGAGTGAAGTG
orf03599F	GCCTTGTTGCTCAGTAAT	RstAR	GGTGTTAGGTATATCCAAAGAC
orf03599R	GCGGTGCTCAATACTTAG	SSBF	AAGAGCCTTTAGCAATTAAC
orf01003F	TTAGTGCGATGCGATAGC	SSBR	AACAGGTATGATTTCAACAAC
orf01003R	GTCTTGATTGCGGTAACC	ASSF	TGAGATTTGCCAAGACTATG
orf01472F	TCGGTTGTTATGGTTAATGC	ASSR	TCATCATCACCGATAAGAATAG
orf01472R	TTCAGTGGTTAATGACTCAAG	RstRF	AGTCGTCTTCGGTGATTAC
orf00714F	AACTACTTAATTTGATGCTAACC	RstRR	CGTGGAGGAAAGTGGAAC

Gray background represents the primers used in real time-qPCR.