

## Supplemental Materials

# **Phylogenomic Network and Comparative Genomics Reveals a Diverged Member of the $\Phi$ KZ-related group, Marine *Vibrio* phage JM-2012**

Ho Bin Jang, Fernand F. Fagutao, Seong Won Nho, Seong Bin Park, In Seok Cha, Jong Earn Yu, Jung Seok Lee, Se Pyeong Im, Takashi Aoki and Tae Sung Jung

This file contains

Supplementary Table S1-S3

**Table S1. Putative open reading frames (ORFs) of  $\Phi$ JM-2012.** Putative functions of ORFs of  $\Phi$ JM-2012 (only best hits with probability >90% and/or E-value <10<sup>-4</sup> are included), transcription terminators (loops are in red color and stems in blue one), and promoters are presented.

ORF	Query					HHpred best matches					BLASTp best matches	
	Size (aa)	Start	Stop	Strand	GC (%)	PDB <sup>a</sup>	Description	P <sup>b</sup> (%)	E-value	HMM alignment (Q/T) <sup>c</sup>	Putative annotation	Species
1	233	68	769	+	34.8						Ribonuclease H	<i>Pseudomonas</i> phage phiKZ
2	136	753	1163	+	32.4	3k8u	Putative ABC transporter	99.9	1.7e-22	2-132/5-143	ORF0015, hypothetical	<i>Shigella</i> phage phiSboM-AG3
3	317	1174	2127	+	37.3	4edh	DTMP kinase	99.9	3.9e-32	1-216/3-209	Possible dTMP kinase	<i>Anaerococcus</i> tetradius
Promoter P4 (range: 2130-2149, strand: +) [TATTATATCTATATATTATA]												
4	143	2260	2691	+	32.6							
5	94	2693	2977	+	33.3							
6	297	2993	3886	+	36.7							
7	173	3949	4470	+	33.9							
8	861	4575	7160	+	32.6	3auy	RAD50 ATPase	99.93	5.4e-24	14-840/3-368	ORF165, hypothetical	<i>Pseudomonas</i> phage phiKZ
9	121	7150	7515	+	33.6							
Promoter P10 (range: 7523-7542, strand: +) [ATTTACACTCCTATATTATA]												
10	151	7791	8246	+	34.9							
11	118	8321	8677	+	37.8							
12	76	8692	8922	+	34.2							
Transcription terminator (range: 8927-8970, strand: -, stability $\Delta$ G: -13.60) [ATCAAAAAAGAGTAGCCCGAAGGCTACTCTTTTTAACCCGTA]												
Transcription terminator (range: 8929-8971, strand: +, stability $\Delta$ G: -17.40) [CGGGTTAAAAAGAGTAGCCTTCGGGCTACTCTTTTTTTTGATC]												
13	439	8993	10312	-	39.0							
14	448	10423	11769	-	40.7							
15	210	11819	12451	-	35.7							
16	300	12455	13357	-	36.0						ORF152, structural	<i>Pseudomonas</i> phage 201phi2-1
17	348	13385	14431	-	38.9						ORF089, structural	<i>Pseudomonas</i> phage phiKZ
18	382	14488	15636	-	38.1						ORF150, structural	<i>Pseudomonas</i> phage 201phi2-1
19	960	15652	18534	-	33.3						ORF149, structural	<i>Pseudomonas</i> phage 201phi2-1
20	506	18583	20103	-	36.3							
21	105	20110	20427	-	34.0							
22	140	20446	20868	-	34.0							
23	426	20876	22156	-	37.7	4aw6	CAAX prenyl protease 1, ZMPSTE24	100.0	1e-41	52-352/188-481	ORF045, structural	<i>Salmonella</i> phage SPN3US
24	574	22233	23957	+	35.9	3iay	DNA polymerase delta catalytic subunit	100.0	6.6e-66	1-573/43-607	ORF044, hypothetical	<i>Salmonella</i> phage SPN3US
25	51	23991	24146	+	32.7							
26	178	24237	24773	+	33.0							
27	117	24782	25135	+	37.9							
28	239	25183	25902	-	39.0							
Promoter P29 (range: 25987-26006, strand: +) [GATTACATCTATATATTATA]												
29	156	26054	26524	+	33.5							
30	130	26524	26916	+	33.6							
Transcription terminator (range: 26917-26962, strand: -, stability $\Delta$ G: -14.00) [GAAGTTAAATAGACCACGACGTAATGTCGTGGTCTATTATTATGTT]												
Transcription terminator (range: 26917-26966, strand: +, stability $\Delta$ G: -12.80) [AACATAATAATAGACCACGACATTACGTCGTGGTCTaTTTAACTTCGATT]												
31	413	26974	28215	-	36.4	2a6h	DNA-directed RNA polymerase $\beta$ ' subunit	100.0	3.5e-75	47-407/801-1248	ORF139, hypothetical	<i>Pseudomonas</i> phage 201phi2-1
32	277	28212	29045	-	33.7							
33	134	29193	29597	+	37.8							

34	517	29600	31153	+	35.2						ORF077, hypothetical	<i>Pseudomonas</i> phage phiPA3
35	115	31192	31539	+	32.5							
Promoter P36 (range: 31592-31611, strand: +) [ATTTATACCTATATATAATA]												
36	342	31819	32847	+	42.2							
37	543	32909	34540	+	36.6						ORF139, hypothetical	<i>Pseudomonas</i> phage phiPA3
38	768	34811	37117	+	36.8							
39	215	37253	37900	+	36.0							
40	177	37972	38505	+	32.4							
41	203	38502	39113	+	32.2							
Transcription terminator (range: 39136-39182, strand: +, stability ΔG: -12.00) [GCGACTTAAAGAGTAGGGTGTGAACCCTACTTCTTTTTTTTTTACT]												
42	807	39186	41609	-	36.0						ORF148, structural	<i>Pseudomonas</i> phage phiPA3
43	626	41782	43662	+	32.1						Kinase-associated domain I	<i>Pseudomonas</i> phage phiKZ
44	288	43662	44528	+	36.4						ORF139, hypothetical	<i>Pseudomonas</i> phage phiKZ
45	198	44528	45124	+	36.3	lhj	Holliday junction resolvase	98.7	3.6e-09	1-181/1-148		
46	191	45099	45674	+	37.8							
47	161	45682	46167	+	38.9							
Transcription terminator (range: 46172-46214, strand: +, stability ΔG: -11.50) [ATTATATAAGAAGCTGGGGTAATTCCTAGTCTTATTGACCC]												
48	331	47031	48026	+	34.1	lyre	Hypothetical protein PA3270	96.6	0.024	15-142/16-148	ORF082, hypothetical	<i>Yersinia</i> phage phiR1-37
49	123	48054	48425	+	37.9							
50	163	49079	49570	+	29.9							
51	199	49592	50191	+	37.8	2nr7	Secretion activator protein	100.0	3.6e-57	4-196/5-194	Hypothetical CR3_210	<i>Cronobacter</i> phage CR3
Transcription terminator (range: 50197-50238, strand: -, stability ΔG: -12.20) [ATAATAATCAACCTACCGATATCGGTAGGTTGATTATTATCT]												
Transcription terminator (range: 50199-50239, strand: +, stability ΔG: -12.20) [ATAATAATCAACCTACCGATATCGGTAGGTTGATTATTATC]												
52	245	50249	50986	-	33.1						Hypothetical protein	<i>Methylosinus trichosporium</i> OB3b
53	702	50991	53099	-	35.4	lzmB	Acetylxyylan esterase related enzyme	100.0	2.3e-43	316-599/2-268	Hypothetical protein	<i>Methylosinus trichosporium</i> OB3b
Transcription terminator (range: 53117-53159, strand: +, stability ΔG: -11.10) [TAATCGGGTAACTGGGTAFTTTTTTACCCAGTTATTTATAATA]												
54	933	53169	55970	-	36.9	2vpt	Lipolytic enzyme; esterase	99.79	4.2e-19	644-932/2-199	Hypothetical Arad_2315	<i>Argobacterium radiobacter</i> K84
55	292	55970	56848	-	34.4						ORF154, structural	<i>Pseudomonas</i> phage phiPA3
56	243	56862	57593	-	36.6	2xgf	Long tail fiber protein P37	94.1	0.05	183-241/29-80	ORF153, structural	<i>Pseudomonas</i> phage phiPA3
Promoter P57 (range: 57644-57663, strand: +) [AAATACATCTATATATTATA]												
57	199	57719	58318	+	30.8							
58	528	58387	59973	+	38.5	1kp8	Groel protein	100.0	4e-105	6-524/2-527	Chaperonin GroEL	<i>Cardiobacterium hominis</i>
Transcription terminator (range: 59979-60021, strand: +, stability ΔG: -11.60) [TATAAAAATAGAGTGGCTTCGAGCTACTCTTTTTTTGTTT]												
59	347	60059	61102	+	32.5							
60	89	61136	61405	-	38.5							
61	434	61470	62774	+	34.9						ORF243, structural	<i>Pseudomonas</i> phage 201phi2-1
62	200	62776	63378	+	32.5						ORF245, hypothetical	<i>Pseudomonas</i> phage 201phi2-1
63	143	63418	63849	-	35.0							
64	278	63871	64707	-	34.2							
65	485	64814	66271	+	38.6	3io5	RECA like protein	99.91	1.7e-23	27-406/7-312	ORF175, UvsX protein	<i>Pseudomonas</i> phage phiPA3
66	92	66292	66570	+	36.6							
67	223	66580	67251	+	36.0						ORF149, hypothetical	<i>Pseudomonas</i> phage phiKZ
68	238	67273	67989	+	33.5						ORF170, hypothetical	<i>Pseudomonas</i> phage phiPA3
Promoter P69 (range: 67992-68011, strand: +) [TATTACATCTATATATTATA]												

69	157	68046	68519	+	30.2														
70	308	68534	69460	+	34.5														
71	89	69462	69731	+	33.0														
72	247	69748	70491	+	38.2														
73	131	70463	70858	+	31.1														
74	699	70948	73047	+	37.7								ORF182, hypothetical					<i>Pseudomonas</i> phage phiKZ	
75	2278	73093	79929	-	36.9	3t21	Murein lytic transglycosylase	99.78	9.7e-24	1939-2102/17-204			Lytic murein transglycosylase					<i>Bacillus</i> sp. m3-13	
76	1292	80126	84004	+	35.1	2a6h	DNA-directed RNA polymerase $\beta$ subunit	100.0	9.4e-120	675-1290/253-910			ORF178, hypothetical					<i>Pseudomonas</i> phage phiKZ	
77	60	84001	84183	+	33.9														
78	464	84187	85581	+	36.3														
79	233	85593	86294	+	35.3														
80	267	86297	87100	+	39.4														
Promoter P81 (range: 87150-87169, strand: +) [TTTATAACCCCTATATTATA]																			
81	135	87219	87626	+	31.6														
82	346	87663	88703	-	31.8														
Promoter P83 (range: 88767-88786, strand: +) [AAATACACCTATATATTATA]																			
83	87	88829	89092	+	29.9														
84	149	89089	89538	+	34.0														
85	116	89540	89890	+	31.3									ORF174, hypothetical					<i>Pseudomonas</i> phage phiPA3
86	144	89950	90384	+	32.4														
87	118	90381	90737	+	34.5														
88	203	90749	91360	+	35.1														
89	356	91386	92456	+	32.6	2hvq	Hypothetical protein in GP24-HOC	100.0	1.8e-56	4-352/2-329			RnlB RNA ligase 2						<i>Salmonella</i> phage PVP-SE1
90	163	92477	92968	+	30.5														
91	249	93052	93801	+	36.4														
92	154	93785	94249	+	34.2														
93	427	94256	95539	+	35.2	3maj	DNA processing chain A	100.0	2.2e-35	4-237/95-366			Hypothetical protein						<i>Paenibacillus</i> sp. HGF7
Promoter P94 (range: 95597-95616, strand: +) [ATTTATAAGCCTATATTATA]																			
94	262	95706	96494	+	33.3														
Transcription terminator (range: 96494-96541, strand: -, stability $\Delta$ G: -10.90) [ATAATTATATACTACCTACTCATTACGAGTAGGTAGTATATTATACGT]																			
95	295	96556	97443	-	38.0	1hw4	Thymidylate synthase	100.0	3.2e-96	1-295/72-355			Thymidylate synthase						<i>Haemophilus parainfluenza</i>
96	140	97529	97951	+	32.2								Hypothetical protein						<i>Roseovarius</i> sp. 217 phage 1
97	131	97972	98367	+	36.9														
98	190	98354	98926	+	30.0														
99	289	98957	99826	-	35.3									ORF008, hypothetical					<i>Salmonella</i> phage SPN3U5
100	191	100156	100731	+	33.9														
101	172	100761	101279	-	31.2														
102	312	101372	102310	+	39.3	3r4v	PhuZ; <i>Pseudomonas</i> 201 $\Phi$ 2-1	100.0	2.0e-47	1-311/3-314			ORF016, hypothetical						<i>Pseudomonas</i> phage phiEL
Promoter P103 (range: 102357-102376, strand: +) [ATTTACAACCTATATATTATA]																			
103	219	102415	103074	+	31.7														
104	117	103081	103434	+	32.8														
105	93	103425	103706	+	33.0														
106	38	103848	103964	+	41.0														
107	116	103968	104318	+	35.6	1opc	OMPR, OMPC; transcription regulation	92.50	0.16	39-116/9-104									
108	94	104311	104595	+	37.5														



145	196	137829	138419	+	33.5															
146	199	138416	139015	+	33.7															
Promoter P147 (range: 139080-139099, strand: +) [TTTACACCTATATATCATT]																				
147	147	139158	139601	+	31.8															
148	369	139614	140723	+	33.1	3g06	SSPH2; leucine-rich repeat protein	92.64	0.0019	32-270/31-267										
149	271	140751	141566	+	34.3	3cvr	Invasion plasmid antigen;IpaH3	99.87	4.3e-21	42-220/59-243	Leucine-rich repeat protein								Salmonella enterica BAA-1581	
150	251	141597	142352	+	33.1	1j15	YOPM; leucine-rich repeat	99.84	4.7e-07	17-246/85-326										
151	500	142427	143929	+	35.2						ORF062, hypothetical								Pseudomonas phage phiPA3	
152	509	143913	145442	+	38.4						ORF063, hypothetical								Pseudomonas phage phiPA3	
153	398	145499	146695	+	37.4						ORF064, hypothetical								Pseudomonas phage phiPA3	
154	148	146783	147229	+	34.0															
155	140	147230	147652	+	34.5															
156	109	147714	148043	-	32.4															
Promoter P157 (range: 148046-148065, strand: +) [TTTATACCTATATATTATA]																				
157	671	148136	150151	+	38.2	3lu0	DNA-directed RNA polymerase β subunit	100.0	2e-130	4-663/660-1338	ORF129, hypothetical								Pseudomonas phage 201phi2-1	
158	662	150151	152139	+	36.8	2a6h	DNA-directed RNA polymerase β ' subunit	100.0	2.1e-78	73-426/904-1286	DNA-directed RNA polymerase (β)								Pseudomonas phage phiKZ	
159	44	152293	152427	+	35.6															
160	470	152608	154020	+	35.0	2db3	ATP-dependent DNA helicase UVSW	100.0	1.1e-36	38-456/60-490	ORF075								Pseudomonas phage phiEL	
161	164	154138	154632	+	38.0															
162	84	154645	154899	+	32.5															
163	136	154930	155340	+	34.8															
Transcription terminator (range: 155450-155493, strand: +, stability ΔG: -17.40) [TAAAAAAAAAGAGTAGCCTTCGGGCTACTCTTTTGGCTGCTGC]																				
Transcription terminator (range: 155452-155494, strand: +, stability ΔG: -13.60) [AGCAGCAAAAAGAGTAGCCGGAAGGCTACTCTTTTTTTTTAC]																				
164	702	155514	157622	-	40.7															
165	193	157662	158243	-	34.5															
166	516	158260	159810	+	36.2	3bgw	DNAB-like replicative helicase	100.0	6.1e-49	29-494/30-443	ORF197, DnaB helicase								Pseudomonas phage 201phi2-1	
167	293	159836	160717	+	35.9															
168	183	160738	161289	+	33.9															
169	203	161282	161893	+	33.8	3kbb	Phosphorylated carbohydrates phosphatase	99.9	1.5e-21	20-203/1-200	ORF248, hypothetical								Salmonella phage SPN3U5	
170	359	161929	163008	-	34.5						ORF249, hypothetical								Pseudomonas phage 201phi2-1	
171	434	163161	164465	-	34.2						ORF106, structural								Pseudomonas phage phiPA3	
172	206	164481	165101	-	35.9															
173	444	165116	166450	-	36.2						ORF104, structural								Pseudomonas phage phiPA3	

<sup>a</sup>PDB, Protein Data Bank; <sup>b</sup>Probability is the most sensitive measure, a value > 95% indicates almost certain homology; <sup>c</sup>Q/T, Query/Template.

**Table S2.** Summary of pair-wise relationship of  $\Phi$ JM-2012 using the ACALME database.

Query	MGE ID/Name/Type	Hosts	FuncAnnot	E-value	Ident (%)	ProtFamilies	GbkAnnot
ORF1	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-10	31	F:v_p:763	ORF155
ORF3	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-07	29	F:v_p:5814	putative thymidylate kinase
ORF8	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-49	23	F:v_p:5808	ORF165
ORF8	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-23	22	F:v_p:5808	hypothetical protein
ORF17	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		6.00E-18	25	F:v_p:5791	ORF089
ORF17	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-15	27	F:v_p:5791	hypothetical protein
ORF18	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-29	28	F:v_p:5790	ORF088
ORF18	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		8.00E-18	26	F:v_p:5790	hypothetical protein
ORF19	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		9.00E-61	23	F:v_p:5789	ORF087
ORF19	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		5.00E-26	18	F:v_p:5789	hypothetical protein
ORF23	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-11	24	F:v_p:14261	ORF084
ORF24	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-42	33	F:v_p:5788	ORF082
ORF24	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-35	23	F:v_p:5788	hypothetical protein
ORF31	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-30	27	F:v_p:5787	hypothetical protein
ORF31	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-30	28	F:v_p:5787	ORF080
ORF34	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		4.00E-15	22	F:v_p:5786	ORF077
ORF37	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		9.00E-35	25	F:v_p:5797	ORF123
ORF37	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		7.00E-13	21	F:v_p:5797	hypothetical protein
ORF42	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-32	23	F:v_p:5799	ORF129
ORF42	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		4.00E-07	21	F:v_p:5799	hypothetical protein
ORF43	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		5.00E-31	37	F:v_p:5798	ORF128
ORF43	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		6.00E-22	23	F:v_p:5798	hypothetical protein
ORF44	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		6.00E-26	32	F:v_p:5801	ORF139
ORF44	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-18	29	F:v_p:5801	hypothetical protein
ORF51	mge:1628/VP882/virus	<i>Vibrio parahaemolyticus</i>		7.00E-14	29	F:v_p:244	conserved phage-related protein
ORF51	mge:2727/prophinder:43169/prophage	<i>Shewanellasp. W3-18-1</i>	phage function unknown	7.00E-13	28	F:v_p:244	hypothetical protein
ORF51	mge:182/VHML/ virus	<i>Vibrio Harveyi</i>		3.00E-11	28	F:v_p:244	ORF19
ORF51	mge:2092/prophinder:44877/prophage	<i>Thiomicrospiracrunogena</i>	phage function unknown	3.00E-10	29	F:v_p:244	hypothetical protein
ORF51	mge:2337/prophinder:43976/prophage	<i>Pectobacteriumatrosepticum</i>	phage function unknown	7.00E-09	29	F:v_p:244	hypothetical protein
ORF51	mge:1586/N4/ virus	<i>Escherichia coli</i>		4.00E-06	25	F:v_p:244	N-acetylmuramidase
ORF51	mge:2516/prophinder:47278/prophage	<i>Acinetobacterbaumannii</i>	phage function unknown	1.00E-05	27	F:v_p:244	hypothetical protein
ORF51	mge:2517/prophinder:47278/prophage	<i>Acinetobacterbaumannii</i>	phage function unknown	2.00E-05	27	F:v_p:244	hypothetical protein
ORF53	mge:2661/prophinder:43496/prophage	<i>Acinetobacterbaumannii</i>		1.00E-67	35	F:v_p:1992	hypothetical protein
ORF53	mge:2138/prophinder:44372/prophage	<i>Pseudomonas putida</i>		4.00E-19	24	F:v_p:1992	hypothetical protein
ORF53	mge:2139/prophinder:44374/prophage	<i>Pseudomonas putida</i>		1.00E-18	23	F:v_p:1992	hypothetical protein
ORF58	mge:2667/prophinder:46184/prophage	<i>Nitrobacterwinogradskyi</i>		2.00E-61	31	F:v_p:2808	chaperoninGroEL
ORF58	mge:2393/prophinder:42783/prophage	<i>Psychromonasingrahamii</i>		1.00E-58	31	F:v_p:2808	GroEL, large subunit of GroESL
ORF58	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-26	25	F:v_p:2808	GroEL-like chaperonine protein
ORF61	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-17	22	F:v_p:5805	ORF157
ORF61	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-10	20	F:v_p:5805	hypothetical protein
ORF62	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-05	24	F:v_p:5806	ORF161
ORF64	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		7.00E-06	19	F:v_p:14300	ORF153
ORF65	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		4.00E-50	29	F:v_p:5804	ORF152
ORF65	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-16	24	F:v_p:5804	hypothetical protein
ORF67	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-25	34	F:v_p:5803	ORF149
ORF67	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-11	24	F:v_p:5803	hypothetical protein
ORF68	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-08	21	F:v_p:14296	ORF147

ORF74	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		6.00E-44	26	F:v_p:5813	ORF182
ORF74	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		8.00E-19	28	F:v_p:5813	hypothetical protein
ORF75	mge:13/SPBc2/virus	<i>Bacillus subtilis</i>		3.00E-23	39	F:v_p:1	putative transglycosylase
ORF75	mge:2378/prophinder:45715/prophage	<i>Bacillus subtilis</i>	phage tail tape measure protein	3.00E-23	39	F:v_p:1	hypothetical protein
ORF75	mge:2343/prophinder:46721/prophage	<i>Erythrobacter litoralis</i>	lytic transglycosylase; phage DNA translocation	5.00E-21	53	F:v_p:351	lytic transglycosylase
ORF75	mge:2339/prophinder:46016/prophage	<i>Acidobacteria bacterium</i>	lytic transglycosylase; phage DNA translocation	4.00E-18	36	F:v_p:351	lytic transglycosylase, catalytic
ORF75	mge:1600/PR772/virus	<i>Salmonella typhimurium</i>		9.00E-18	53	F:v_p:351	transglycosylase
ORF75	mge:1526/PR5/virus	<i>Salmonella typhimurium</i>		6.00E-17	51	F:v_p:351	transglycosylase
ORF75	mge:47/PRD1/virus	<i>Escherichia coli</i>		6.00E-17	51	F:v_p:351	transglycosylase
ORF75	mge:1663/PR4/virus	<i>Salmonella typhimurium</i>		1.00E-15	47	F:v_p:351	transglycosylase
ORF75	mge:1464/L17/virus	<i>Salmonella typhimurium</i>		1.00E-15	47	F:v_p:351	transglycosylase
ORF75	mge:1596/PR3/virus	<i>Salmonella typhimurium</i>		1.00E-15	47	F:v_p:351	transglycosylase
ORF75	mge:1597/F8/virus	<i>Pseudomonas aeruginosa</i>		1.00E-13	48	F:v_p:351	ORF038
ORF75	mge:2066/prophinder:43828/prophage	<i>Photorhabdus luminescens</i>		4.00E-13	43	F:v_p:2492	hypothetical protein
ORF75	mge:2767/prophinder:47162/prophage	<i>Shewanella pealeana</i>	lytic transglycosylase	1.00E-12	35	F:v_p:649	lytic transglycosylase catalytic
ORF75	mge:2492/prophinder:46883/prophage	<i>Xanthobacter autotrophicus</i>	phage DNA translocation; lytic transglycosylase	4.00E-12	34	F:v_p:351	lytic transglycosylase catalytic
ORF75	mge:2389/prophinder:43931/prophage	<i>Mesorhizobium sp. BNC1</i>	lytic transglycosylase; phage DNA translocation	4.00E-12	37	F:v_p:351	lytic transglycosylase, catalytic
ORF75	mge:2040/prophinder:42908/prophage	<i>Clostridium botulinum</i>	lytic transglycosylase	5.00E-11	34	F:v_p:649	SLT domain protein
ORF75	mge:2638/prophinder:45720/prophage	<i>Clostridium botulinum</i>	lytic transglycosylase	5.00E-11	34	F:v_p:649	SLT domain-containing protein
ORF75	mge:2205/prophinder:44548/prophage	<i>Clostridium botulinum</i>	lytic transglycosylase	5.00E-11	34	F:v_p:649	SLT domain-containing protein
ORF75	mge:2162/prophinder:45074/prophage	<i>Shigella dysenteriae</i>	lytic transglycosylase; phage DNA translocation	7.00E-10	29	F:v_p:351	putative transglycosylase
ORF75	mge:2749/prophinder:44935/prophage	<i>Shigella flexneri</i>	phage DNA translocation; lytic transglycosylase	8.00E-10	29	F:v_p:351	putative transglycosylase
ORF75	mge:2687/prophinder:46938/prophage	<i>Shigella flexneri</i>	phage DNA translocation; lytic transglycosylase	8.00E-10	29	F:v_p:351	putative transglycosylase
ORF75	mge:2715/prophinder:46778/prophage	<i>Shigella flexneri</i>	phage DNA translocation; lytic transglycosylase	8.00E-10	29	F:v_p:351	putative transglycosylase
ORF75	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>	lytic transglycosylase	4.00E-09	18	F:v_p:649	ORF181
ORF75	mge:2595/prophinder:44805/prophage	<i>Enterobacter sp. 638</i>	phage prohead/capsid assembly; phage DNA translocation; lytic transglycosylase; phage head/capsid internal protein	4.00E-09	37	F:v_p:102	lytic transglycosylase, catalytic
ORF75	mge:2254/prophinder:45501/prophage	<i>Magnetospirillum magneticum</i>	phage release by lysis; endolysin activity	3.00E-08	36	F:v_p:380	hypothetical protein
ORF75	mge:2562/prophinder:43459/prophage	<i>Pseudomonas putida</i>	phage prohead/capsid assembly; phage DNA translocation; lytic transglycosylase; phage head/capsid internal protein	1.00E-07	31	F:v_p:102	phage internal core protein
ORF75	mge:31/phiYeO3-12/virus	<i>Yersinia enterocolitica</i>		2.00E-07	31	F:v_p:102	internal virion protein D
ORF75	mge:2020/prophinder:47260/prophage	<i>Acinetobacter baumannii</i>	phage tail tape measure protein	3.00E-07	46	F:v_p:1	putative bacteriophage protein
ORF75	mge:49/T7/virus	<i>Escherichia coli</i>		5.00E-07	33	F:v_p:102	internal virion protein D
ORF75	mge:184/phiA1122/virus	<i>Yersinia pestis</i>		8.00E-07	32	F:v_p:102	internal virion protein
ORF75	mge:2436/prophinder:47561/prophage	<i>Salmonella enterica</i>	phage prohead/capsid assembly; phage DNA translocation; lytic transglycosylase; phage head/capsid internal protein	9.00E-07	34	F:v_p:102	hypothetical protein
ORF75	mge:161/gh-1/virus	<i>Pseudomonas putida</i>		9.00E-07	36	F:v_p:102	internal virion protein D
ORF75	mge:1512/P1/virus	<i>Escherichia coli</i>		2.00E-06	28	F:v_p:2492	Sit
ORF75	mge:67/T3/virus	<i>Escherichia coli</i>		3.00E-06	31	F:v_p:102	internal virion protein D
ORF75	mge:2093/prophinder:43102/prophage	<i>Campylobacter hominis</i>		3.00E-06	32	F:v_p:3636	regulatory protein dnir
ORF75	mge:1516/Berlin/virus	<i>Yersinia pestis</i>		5.00E-06	34	F:v_p:102	Internal virion protein D
ORF75	mge:2586/prophinder:47421/prophage	<i>Bartonella tribocorum</i>		9.00E-05	33	F:v_p:2690	lytic transglycolase
ORF76	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-130	31	F:v_p:3449	ORF178
ORF76	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-61	28	F:v_p:3449	hypothetical protein
ORF76	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-31	28	F:v_p:3449	hypothetical protein
ORF79	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-20	26	F:v_p:5811	ORF176
ORF79	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		9.00E-07	22	F:v_p:5811	hypothetical protein



ORF80	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		5.00E-13	28	F:v_p:5810	ORF175
ORF80	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-11	31	F:v_p:5810	hypothetical protein
ORF85	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		7.00E-15	37	F:v_p:14299	ORF151
ORF93	mge:119/KVP40/virus	<i>Vibrio parahaemolyticus</i>		5.00E-10	35	F:v_p:485	conserved hypothetical protein
ORF93	mge:149/Bxz2/virus	<i>Mycobacterium smegmatis</i>		5.00E-09	33	F:v_p:485	gp62
ORF93	mge:1656/Che12/virus	<i>Mycobacterium tuberculosis</i>		1.00E-08	36	F:v_p:485	gp66
ORF93	mge:1466/C-St/virus	<i>Clostridium botulinum</i>		3.00E-08	36	F:v_p:485	putative guanylate kinase
ORF93	mge:52/D29/virus	<i>Mycobacterium tuberculosis</i>		5.00E-08	34	F:v_p:485	hypothetical protein
ORF93	mge:89/L5/virus	<i>Mycobacterium tuberculosis</i>		1.00E-07	33	F:v_p:485	predicted 14.2 protein
ORF93	mge:2386/prophinder:42520/prophage	<i>Shewanellabaltica</i>		8.00E-06	23	F:v_p:2806	oligoribonuclease
ORF95	mge:2672/prophinder:42587/prophage	<i>Rhizobium leguminosarum</i>	thymidylate synthase activity	1.00E-31	31	F:v_p:273	thymidylate synthase
ORF95	mge:1667/RB43/virus	<i>Enterobacteriaceae</i>		2.00E-26	30	F:v_p:273	Td thymidylatesynthetase
ORF95	mge:142/T4/virus	<i>Escherichia coli</i>		4.00E-25	31	F:v_p:273	dTMP (thymidylate) synthase
ORF95	mge:1474/Aeh1/virus	<i>Aeromonashydrophila</i>		1.00E-24	31	F:v_p:273	dTMP synthase
ORF95	mge:1542/RB32/virus	<i>Enterobacteriaceae</i>		2.00E-24	31	F:v_p:273	thymidylatesynthetase
ORF95	mge:2002/JS98/virus	<i>Escherichia coli</i>		2.00E-24	30	F:v_p:273	dTMPthymidylate synthase
ORF95	mge:119/KVP40/virus	<i>Vibrio parahaemolyticus</i>		3.00E-24	32	F:v_p:273	dTMP (thymidylate) synthase
ORF95	mge:1580/31/virus	<i>Aeromonassalmonicida</i>		4.00E-24	29	F:v_p:273	dTMP (thymidylate) synthase
ORF95	mge:1892/Geobacillus virus E2/virus	<i>Geobacillus</i>		8.00E-24	29	F:v_p:273	putative thymidylate synthase
ORF95	mge:1582/44R2.8t/virus	<i>Aeromonassalmonicida</i>		2.00E-23	29	F:v_p:273	dTMP (thymidylate) synthase
ORF95	mge:140/RB69/virus	<i>Escherichia coli</i>		2.00E-23	30	F:v_p:273	dTMP (thymidylate) synthase
ORF95	mge:1488/25/virus	<i>Aeromonassalmonicida</i>		7.00E-23	29	F:v_p:273	thymidylatesynthetase
ORF95	mge:1504/T5/virus	<i>Escherichia coli</i>		1.00E-18	29	F:v_p:273	putative thymidylate synthase
ORF95	mge:2262/prophinder:43410/prophage	<i>Staphylococcus epidermidis</i>	thymidylate synthase activity	3.00E-15	24	F:v_p:273	thymidylate synthase
ORF95	mge:1561/Felix01/virus	<i>Salmonella</i>		2.00E-13	25	F:v_p:273	Thymidylate synthase
ORF95	mge:1885/phiEF24C/virus	<i>Enterococcus faecalis</i>		8.00E-12	29	F:v_p:273	putative thymidylate synthase
ORF95	mge:139/RB49/virus	<i>Escherichia coli</i>		3.00E-06	27	F:v_p:273	dTMP (thymidylate) synthase
ORF96	mge:122/PY54/virus	<i>Yersinia enterocolitica</i>		8.00E-31	48	F:v_p:851	hypothetical protein
ORF96	mge:52/D29/virus	<i>Mycobacterium tuberculosis</i>		9.00E-31	57	F:v_p:851	gp64
ORF96	mge:155/Omega/virus	<i>Mycobacterium smegmatis</i>		1.00E-29	57	F:v_p:851	gp120
ORF96	mge:89/L5/virus	<i>Mycobacterium tuberculosis</i>		9.00E-29	53	F:v_p:851	predicted 14.0Kd protein
ORF96	mge:1656/Che12/virus	<i>Mycobacterium tuberculosis</i>		6.00E-28	53	F:v_p:851	gp70
ORF96	mge:1623/Twort/virus	<i>Staphylococcus aureus</i>		6.00E-15	37	F:v_p:851	ORF101
ORF96	mge:109/Sfi21/virus	<i>Streptococcus thermophilus</i>		9.00E-14	35	F:v_p:851	Hypothetical protein
ORF96	mge:2702/prophinder:43072/prophage	<i>Lactococcuslactis</i>	phage function unknown	1.00E-11	39	F:v_p:851	prophage pi1 protein 29
ORF96	mge:21/bIL309/virus	<i>Lactococcuslactis</i>		1.00E-11	39	F:v_p:851	Orf34
ORF96	mge:105/7201/virus	<i>Streptococcus thermophilus</i>		1.00E-05	35	F:v_p:851	ORF14
ORF99	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		4.00E-20	29	F:v_p:5779	ORF042
ORF99	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-11	25	F:v_p:5779	hypothetical protein
ORF102	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-14	27	F:v_p:5778	hypothetical protein
ORF102	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-12	24	F:v_p:5778	ORF039
ORF110	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		7.00E-06	31	F:v_p:14240	ORF049
ORF112	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		5.00E-25	27	F:v_p:5776	ORF030
ORF112	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-08	21	F:v_p:5776	hypothetical protein
ORF113	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-30	23	F:v_p:5775	ORF029
ORF113	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		9.00E-13	23	F:v_p:5775	hypothetical protein
ORF116	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-35	25	F:v_p:5773	ORF026
ORF116	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-21	24	F:v_p:5773	hypothetical protein
ORF117	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	2.00E-95	30	F:v_p:686	ORF025
ORF117	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	5.00E-46	27	F:v_p:686	ATP-dependent DNA helicase
ORF119	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		4.00E-70	32	F:v_p:5812	ORF180

ORF119	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-64	35	F:v_p:5812	hypothetical protein
ORF129	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		5.00E-37	26	F:v_p:5777	hypothetical protein
ORF129	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		6.00E-29	23	F:v_p:5777	ORF032
ORF132	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-68	27	F:v_p:5780	ORF050
ORF132	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		4.00E-42	24	F:v_p:5780	hypothetical protein
ORF134	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-08	17	F:v_p:5792	ORF098
ORF136	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-22	26	F:v_p:5781	ORF055
ORF140	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		7.00E-31	28	F:v_p:5783	ORF065
ORF140	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-22	31	F:v_p:5783	hypothetical protein
ORF141	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		7.00E-13	34	F:v_p:5784	ORF066
ORF141	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-12	26	F:v_p:5784	hypothetical protein
ORF149	mge:2718/prophinder:46816/prophage	<i>Shigella flexneri</i>	interaction with host via protein secreted by type III secretion system	4.00E-06	37	F:v_p:1198	invasion plasmid antigen
ORF149	mge:2315/prophinder:44082/prophage	<i>Shigella boydii</i>	interaction with host via protein secreted by type III secretion system	4.00E-06	37	F:v_p:1198	invasion plasmid antigen
ORF149	mge:2162/prophinder:45074/prophage	<i>Shigella dysenteriae</i>	interaction with host via protein secreted by type III secretion system	5.00E-06	23	F:v_p:1198	invasion plasmid antigen
ORF149	mge:2715/prophinder:46778/prophage	<i>Shigella flexneri</i>	interaction with host via protein secreted by type III secretion system	5.00E-06	23	F:v_p:1198	invasion plasmid antigen
ORF149	mge:2749/prophinder:44935/prophage	<i>Shigella flexneri</i>	interaction with host via protein secreted by type III secretion system	5.00E-06	23	F:v_p:1198	invasion plasmid antigen
ORF149	mge:2687/prophinder:46938/prophage	<i>Shigella flexneri</i>	interaction with host via protein secreted by type III secretion system	5.00E-06	23	F:v_p:1198	invasion plasmid antigen
ORF151	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		4.00E-06	22	F:v_p:14254	ORF068
ORF151	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-05	22	F:v_p:14522	hypothetical protein
ORF152	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		6.00E-07	20	F:v_p:14255	ORF069
ORF153	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-13	25	F:v_p:5785	ORF070
ORF153	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		3.00E-05	22	F:v_p:5785	hypothetical protein
ORF157	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-27	27	F:v_p:3444	ORF071
ORF157	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-20	21	F:v_p:3444	hypothetical protein
ORF157	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-09	26	F:v_p:3444	ORF073
ORF158	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	2.00E-51	28	F:v_p:686	ORF074
ORF158	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	3.00E-11	22	F:v_p:686	ATP-dependent DNA helicase
ORF160	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	1.00E-29	27	F:v_p:686	ATP-dependent DNA helicase
ORF160	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>	helicase activity	4.00E-28	24	F:v_p:686	ORF075
ORF164	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		1.00E-23	22	F:v_p:5796	ORF120
ORF164	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		7.00E-05	21	F:v_p:5796	hypothetical protein
ORF166	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		4.00E-26	23	F:v_p:5795	hypothetical protein
ORF166	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		3.00E-25	23	F:v_p:5795	ORF118
ORF170	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-24	28	F:v_p:5807	ORF164
ORF170	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		5.00E-07	23	F:v_p:5807	putative structural protein
ORF171	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		2.00E-15	22	F:v_p:5794	ORF101
ORF171	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		2.00E-06	21	F:v_p:5794	hypothetical protein
ORF173	mge:163/phiKZ/virus	<i>Pseudomonas aeruginosa</i>		5.00E-13	22	F:v_p:5793	ORF099
ORF173	mge:1500/phiEL/virus	<i>Pseudomonas aeruginosa</i>		1.00E-09	22	F:v_p:5793	hypothetical protein

**Table S3.** The matrix displaying the list of protein families assigned to  $\Phi$ JM-2012 and  $\Phi$ KZ-related phages (E-value <0.0001).

Families <sup>a</sup>	Functions <sup>b</sup>	Gene product (gp) pairs of $\Phi$ KZ-related phages					
		$\Phi$ JM-2012	$\Phi$ PA3	$\Phi$ KZ	201 $\phi$ 2-1	$\Phi$ EL	$\Phi$ OBP
F:v_p:1 <sup>c</sup>	Tail tape measure protein	ORF75					
F:v_p:20	Phage capsid assembly						ORF244
F:v_p:23	Phage release by lysis		ORFs166,167,169	ORF146	ORF230	ORF156	
F:v_p:27	Deoxyribonuclease I activity		210	56,72,179		25,185	
F:v_p:32	Phage release by lysis						279
F:v_p:141	Phage function unknown				35		
F:v_p:175	Ribonucleoside-diphosphate reductase		378	306	467		
F:v_p:238	Thiol-disulfide exchange						12
F:v_p:239	Ribonucleoside-diphosphate reductase		377	305	457		211
F:v_p:243	Transcription repressor activity					163	
F:v_p:244	Phage function unknown	51					
F:v_p:273	Thymidylate synthase activity	95	274	235	350		
F:v_p:318	Transpositional DNA recombination					37	
F:v_p:400	Phage release by lysis				229		
F:v_p:485	Phage function unknown	93					
F:v_p:497	Dihydrofolate reductase activity		3	4	3		241
F:v_p:499	Thymidine kinase activity						249
F:v_p:635	Phage function unknown						61
F:v_p:649	Lytic transglycosylase activity		163,213	144,181	276	183	149,276
F:v_p:686	Helicase activity	117,158,160	7,65,233	25,74,75,203	5,130,131,300	11,39,40,166	6,74,84,263
F:v_p:758	Phage function unknown					100	
F:v_p:763	Exoribonuclease H activity	1	178	155	240	124	158
F:v_p:767	Phage function unknown		96,217	184	280		60
F:v_p:769	Phage function unknown		88		147		
F:v_p:820	Phage function unknown					154	
F:v_p:851	Phage function unknown	96					
F:v_p:933	DNA binding			114			
F:v_p:941	Phage function unknown						229
F:v_p:990	ATPase activity		347	286			
F:v_p:1020	Phage function unknown		5		4		
F:v_p:1043	Phage function unknown					15	
F:v_p:1094	Phage function unknown					188	
F:v_p:1133	Phage function unknown		150-154	131-135	216-220	113-115	142-144
F:v_p:1182	dCTP deaminase activity		255	214	331		
F:v_p:1193	Phage function unknown		241	245	315		
F:v_p:1198	Protein related type III secretion system	149					
F:v_p:1200	Phage DNA replication		257		333	122	153
F:v_p:1238	Phage function unknown		249	207	321		
F:v_p:1607	Deoxyribonuclease I activity			296			
F:v_p:1860	Phage function unknown		229	197			
F:v_p:1910	5'-3' exonuclease activity			35			
F:v_p:1992	Not assigned <sup>d</sup>	53					
F:v_p:2099	Not assigned		164,165	145			
F:v_p:2808	Not assigned	58				146	246
F:v_p:2944	Not assigned					125	
F:v_p:3044	Not assigned		289		355		
F:v_p:3175	Not assigned						7,98
F:v_p:3184	Not assigned				306		27
F:v_p:3444	Not assigned	157		71,73	129	38	73
F:v_p:3445	Not assigned		80,81,82,83	83	452,456	153	
F:v_p:3446	Phage function unknown		97,98,99,100	93,94,95	155,156,157		
F:v_p:3447	Not assigned		116	113,115		85	
F:v_p:3449	Not assigned	76	211	178	273,274	186,187	278
F:v_p:4444	Not assigned					157	
F:v_p:4626	Not assigned						161
F:v_p:5409	Not assigned		286	40	62		
F:v_p:5770	Not assigned			10		101	
F:v_p:5771	Not assigned			13		98	
F:v_p:5772	Not assigned		122	14		99	
F:v_p:5773	Not assigned	116	8	26	27	9	5
F:v_p:5774	Not assigned		9	27	28	8	4
F:v_p:5775	Not assigned	113	11	29	30	6	2
F:v_p:5776	Not assigned	112	12	30	32	5	1
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F:v_p:5778	Not assigned	102	28	39	59	16	47
F:v_p:5779	Not assigned	99	37	42	73	14	10
F:v_p:5780	Not assigned	132	47	50	83	21	55
F:v_p:5781	Not assigned	136	54	55	107	24	58
F:v_p:5782	Not assigned		55	59	114	27	59
F:v_p:5783	Not assigned	140	59	65	121	30	65
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F:v_p:14632	Not assigned					111	
F:v_p:14633	Not assigned					116	145
F:v_p:14634	Not assigned					88	
F:v_p:14635	Not assigned					119	
F:v_p:14636	Not assigned					120	
F:v_p:14637	Not assigned					121	
F:v_p:14638	Not assigned					123	
F:v_p:14639	Not assigned					126	
F:v_p:14640	Not assigned					139	
F:v_p:14838	Not assigned				308		
<b>Uncharacterized protein families (UPFs)</b>		<b><math>\phi</math>JM-2012</b>	<b><math>\phi</math>PA3</b>	<b><math>\phi</math>KZ</b>	<b>201<math>\phi</math>2-1</b>	<b><math>\phi</math>EL</b>	<b><math>\phi</math>OBP</b>
UPF56		ORF91					ORF286
UPF335		48			ORF266		
UPF402-410		2,4,5-7,9-14					
UPF411		15					272
UPF412-501		20-22,25-30,32, 33,35,36,38-41,45- 50,52,54-57,59,60, 63,66,69-73,77,78, 81-84,86-92,94,97, 98,100,101,103-109 ,111,114,115,118, 120-128,130,131, 133,135,137-139, 142,148,150,154, 155					
UPF502		156					72
UPF503-511		159,161-163,165, 167-169,172					

<sup>a, b</sup>Protein families and (putative) functions defined in the ACLAME

<sup>c</sup>‘F:v-P’ indicates ‘Family:vir\_proph’.

<sup>d</sup>protein family those unassigned for reasons associated with the algorithm is denoted as “not assigned.”