SUPPLEMENTAL MATERIAL

Table S1. Summary of indels in the phage genomes relative to the genome of PaMx43.

#	Coordinates (PaMx43)	Length (bp)[1]	Phage[2]	ORF[3]
1	52	-1	33, 35, 41, 46, PaP2	nc[4]
2	126	+1	35, 41, 46, 119X	nc
3	285	-21	41	nc
4	297	-10/+1	33, 35, 46/ PaP2	nc
5	**1183**	**-175**	**119X**	**a**
6	2058	-1	41	nc
7	20091	-1	35, 41	nc
8	2265	+1	119X	nc
9	2991	-21	35, 41	6
10	9844	+12	33, 46	12
11	11841	+1	PaP2	17
12	24060	+1	33, 46	nc
13	24081	+1	33, 46	nc
14	**24386**	**+300**	**119X**	**24**
15	24890	+1	119X	nc
16	25006	+6	119X	nc
17	25023	-1	119X	nc
18	25631	-9	119X	27
19	27635	+1	41	29
20	30238	+1	41, 119X	nc
21	30238	+1	41, 119X	nc
22	**30753**	**+547**	**PaP2**	**31**
23	34777	+3	33, 35, 41, 46	38
24	36040	+6/+12	35/ 33, 46, PaP2	40
25	37249	-3	35, 119X	45
26	37835	-18	35	47
27	37914	+6	35	47
28	37963	+3	35	47
29	38074	+9/-15	35/119X	47
30	**38202**	**+303/+506**	**41/ 35**	**b1, b2**
31	38316	+1	41	48
32	38431	+15	35	48
33	38575	+3	35	49
34	38591	+12	35	49
35	42963	+12	119X	53
36	43108	+23	33, 46, 119X	nc
37	43141	+1	33, 46	nc
38	43171	-1	41, 119X	nc
39	43198	+1	41, 119X	nc

[1] (+) insertions and (-) deletions relative to PaMx43 genome.

[2] Except for PaP2 and 119X, digits correspond to the specific name of PaMx phages.

[3] ORFs affected by the respective indel; nc indicates that the respective indel is located in non-coding regions.

Indels larger than 175 bp are in **bold**; ORFs inside these regions are named **a**, **b** and **c** as in Fig. 1.

Table S2. Pairwise single nucleotide polymorphisms (SNP) between phage genomes.

	119X	**PaP2**	**PaMx43**	**PaMx46**	**PaMx33**	**PaMx41**	**PaMx35**
119X	0						
PaP2	1733	0					
PaMx43	1804	610	0				
PaMx46	2239	1326	1407	0			
PaMx33	2270	1348	1429	25	0		
PaMx41	1873	1001	1089	1479	1499	0	
PaMx35	1965	1176	1300	1582	1605	1306	0

The values indicate the number of one base pair substitutionfor a given pair of phage genomes.

Table S3. Functional annotation ORFS families.

ORF	**Length (aa)**	**BlastP, most significant matches [organism; e-value]**	**Conserved Domains**[1]	**Structural similarity**[2] **[organism; e-value]**	**Function**
ORF_1	212	XP_001621223.1 [*Nematostella vectensis*; 1e-15]	–	–	Hypothetical protein
ORF_a	65	No significant similarity found	–	–	Hypothetical protein (ORFan)
ORF_2	99	No significant similarity found	–	–	Hypothetical protein
ORF_3	69	No significant similarity found	–	–	Hypothetical protein
ORF_4	194	EKD22471.1 [uncultured bacterium, groundwater metagenome; 3e-11]*	Coiled-coil domain	4DYQ, Small terminase [Bacteriophage Sf6; 0.3]	Putative Small terminase
ORF_5	48	No significant similarity found	–	–	Hypothetical protein
ORF_6	529	AEI70966.1 [EBPR podovirus 3; 2e-117]*	–	4BIJ, Large terminase [Bacteriophage T7; 8.4e-54]	Putative Large terminase
ORF_7	666	EKD22468.1 [uncultured bacterium, groundwater metagenome; 3e-134]*	–	3LJ5, Portal protein [bacteriophage P22; 1e-7]	Putative Portal protein (virion protein)
ORF_8	189	WP_028627490.1 [*Pseudomonas resinovorans*; 7e-11]	P-loop containing nucleoside triphosphate hydrolase (IPR027417)	3TUI, ATP-binding domain of Methionine import [E. coli, 3.3e-29]	Nucleotide monophosphate kinase
ORF_9	122	No significant similarity found	–	–	Hypothetical protein
ORF_10	248	EKD22466.1 [uncultured bacterium, groundwater metagenome; 2e-17]*	–	–	Hypothetical protein (virion protein)
ORF_11	418	AEI70970.1 [EBPR podovirus 3; 4e-99]*	–	1OHG, major capsid protein [Bacteriophage HK97; 26]	Major capsid protein (virion protein)
ORF_12	138	No significant similarity found	–	–	Hypothetical protein
ORF_13	217	No significant similarity found	–	–	Hypothetical protein (virion protein)
ORF_14	115	No significant similarity found	3 Transmenbrane domains, non-cytoplasmic domain	–	Hypothetical protein
ORF_15	133	No significant similarity found	3 Transmenbrane domains, non-cytoplasmic domain	–	Putative Holyn
ORF_16	116	WP_011192942.1 [*Yersinia pseudotuberculosis*; 4e-32]	D-alanyl-D-alanine carboxypeptidase (SSF55166)	2MXZ, Endolysin [Bacteriophage T5; 3.9-33]	Putative Endolysin
ORF_17	128	No significant similarity found	Transmenbrane domain, non-cytoplasmic domain	–	Putative Rz-like
ORF_18	98	No significant similarity found	Non-cytoplasmic domain, Lipoprotein signal	–	Putative Rz1-like

ORF_19	123	No significant similarity found	–	–	Hypothetical protein
ORF_20	1031	EKD22434.1 [uncultured bacterium, groundwater metagenome; 4e-39]*	–	–	Hypothetical protein (virion protein)
ORF_21	305	EKD22433.1 [uncultured bacterium, groundwater metagenome; 4e-16]*	–	–	Hypothetical protein (virion protein)
ORF_22	577	No significant similarity found	–	–	Hypothetical protein (virion protein)
ORF_23	1849	AEI70980.1 [EBPR podovirus 3; 0.0]*	–	–	Hypothetical protein (virion protein)
ORF_24	93	WP_004859226.1 [*Acinetobacter gerneri*; 5e-27]	–	–	Phage conserved Hypothetical protein
ORF_25	166	WP_044767099.1 [*Streptococcus suis*; 0.03]	–	–	Hypothetical protein
ORF_26	84	No significant similarity found	–	–	Hypothetical protein
ORF_27	296	WP_003356576.1 [*Pseudomonas fluorescens*; 4e-14]	–	2Q73, MazG [*Vibrio* sp. DAT 722; 1.2e-20]	Putative MazG-like protein
ORF_28	417	EKD22461.1 [uncultured bacterium, water metagenome; 2e-82]*	DUF3987	1W5S, Origin Recognition Complex Protein 2 [*Aeropyrum pernix*; 0.0016]	Putative Primase
ORF_29	801	AEI70990.1 [EBPR podovirus 3; 2e-174]*	DNA_pol_A (PF00476)	2KFN, Klenow Fragment DNA Polymerase I [*E. coli*, 3e-116]	Putative DNA polymerase
ORF_30	109	No significant similarity found	–	–	Hypothetical protein
ORF_31	171	EKD22459.1 [uncultured bacterium, groundwater metagenome; 2e-12]*	Coiled-coil domain	–	Hypothetical protein
ORF_32	318	EKD22458.1 [uncultured bacterium, groundwater metagenome; 9e-66]*	AAA+ ATPase (PF13479)	2CVH, Rad51 homologue [*Thermococcus kodakaraensis*; 8.4e-4]	Putative DNA repair and recombination protein
ORF_33	85	WP_007341107.1 [Neisseria bacilliformis; 2e-4]	–	–	Hypothetical protein
ORF_34	155	WP_030031775.1 [*Clostridium botulinum*; 2e-7]	–	–	Hypothetical protein
ORF_35	78	YP_006382361.1 [Escherichia phage bV_EcoS_AKFV33; 1e-11]	–	–	Phage conserved protein
ORF_36	224	No significant similarity found	Ribonuclease H-like domain (IPR012337)	1W0H, 3'-5'-exoribonuclease [Homo sapiens, 1.5e-5]	Putative 3'-5'-exoribonuclease
ORF_37	341	EKD22454.1 [uncultured bacterium, groundwater metagenome; 1e-59]*	PDDEXK_1 nuclease family (PF12705)	3U4Q, Helicase/nuclease subunit A [*Bacillus subtilis*; 8.4e-3]	Helicase/nuclease
ORF_38	107	No significant similarity found	–	–	Hypothetical protein
ORF_39	61	No significant similarity found	–	–	Hypothetical protein

ORF_40	236	AEI71000.1 [EBPR podovirus 3; 1e-6]*	–	–	Hypothetical protein
ORF_41	100	No significant similarity found	–	–	Hypothetical protein
ORF_42	145	No significant similarity found	–	–	Hypothetical protein
ORF_43	97	No significant similarity found	2 Transmenbrane domains, non-cytoplasmic domain	–	Hypothetical protein
ORF_44	85	No significant similarity found	–	–	Hypothetical protein
ORF_45	108	No significant similarity found	–	–	Hypothetical protein
ORF_46	108	No significant similarity found	–	–	Hypothetical protein
ORF_47	139	No significant similarity found	–	–	Hypothetical protein
ORF_b-1	97	No significant similarity found	–	–	Hypothetical protein (ORFan)
ORF_b.2	51	No significant similarity found	–	–	Hypothetical protein (ORFan)
ORF_48	114	No significant similarity found	–	–	Hypothetical protein
ORF_49	78	No significant similarity found	–	–	Hypothetical protein
ORF_50	683	EKD22442.1 [uncultured bacterium, groundwater metagenome; 6e-121]*	DNA2/NAM helicase (PTHR10887; 6.6E-25), UvrD-like helicase C-terminal domain (PF13538; 6.6-17)	3E1S, RecD2 [*Deinococcus radiodurans*; 1.3e-58]	Putative Helicase
ORF_51	110	No significant similarity found	–	–	Hypothetical protein
ORF_52	342	No significant similarity found	–	–	Hypothetical protein
ORF_53	227	EKD99106.1 [uncultured bacterium, groundwater metagenome; 1e-44]*	–	–	Hypothetical protein

1 Conserved domains search was performed with InterPro.

2 HHpred structural similarity predictions.

* Sequences from metagenomic data.

Gray highlighted lines indicate genes encoding virion proteins.

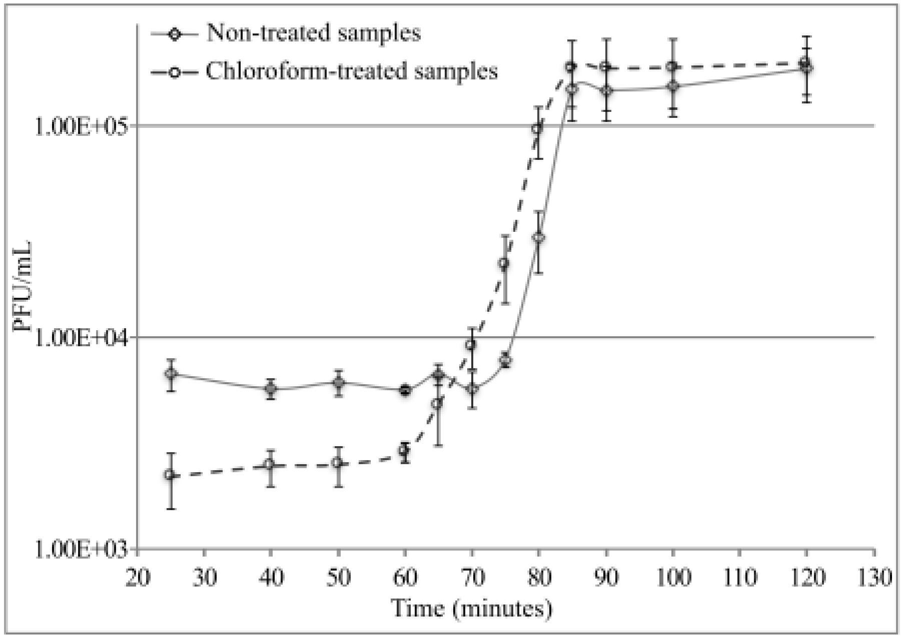

FIG S1. One-step growth curve of PaMx41 infecting the clinical strain Ps26. Infections were carried out in LB media at 37°C (see Methods). PFU/mL were quantified at the indicated times after infection, each quantification represents the average of three independent experiments, error bars indicate standard deviation.

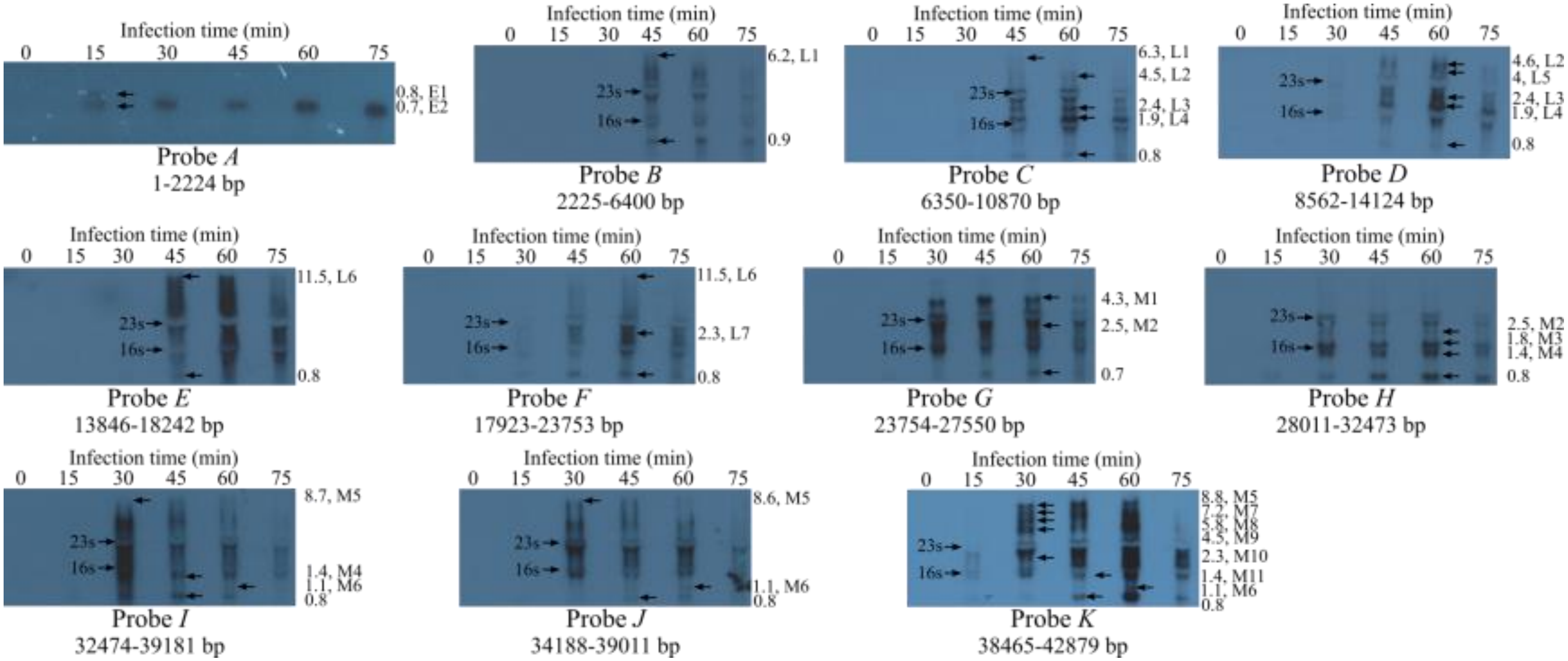

FIG S2. Northern blot set of the viral mRNA identification during PaMx41 infection. Northern blots of total RNA isolated from Ps26 infected cells at the indicated time after infection. RNA samples were hybridized with the indicated probes described in figure 5B, the position covered by each probe is indicated. Each detected signal is indicated with a black arrow, their estimated sizes are given in kbs. The 0-minutes sample is total RNA isolated from uninfected cells.