TABLE S1. Host spectrum of phage KHP30 among *H. pylori* strains.

***H. pylori* strain**	**Sensitivity to phage KHP30**[a]	**Description of *H. pylori* strain**	**Reference**	**Typing by RFLP**[b]	
				UreAB PCR/HaeIII	**FlaA PCR/HhaI**
KMT7	-	Isolated at Kochi, Japan	This study	A	1
KMT9	+	Isolated at Kochi, Japan	This study	B	2
KMT15	-	Isolated at Kochi, Japan	This study	C	3
KMT16	-	Isolated at Kochi, Japan	This study	C	3
KMT17	-	Isolated at Kochi, Japan	This study	D	2
KMT18	+	Isolated at Kochi, Japan	This study	E	3
KMT19	-	Isolated at Kochi, Japan	This study	D	2
KMT28	-	Isolated at Kochi, Japan	This study	F	1
KMT84	+	Isolated at Kochi, Japan	This study	C	2
KMT85	+	Isolated at Kochi, Japan	This study	I	3
KMT86	+	Isolated at Kochi, Japan	This study	C	2
KMT87	+	Isolated at Kochi, Japan	This study	C	1
KMT88	-	Isolated at Kochi, Japan	This study	J	6
KMT89	+	Isolated at Kochi, Japan	This study	D	3
KMT90	-	Isolated at Kochi, Japan	This study	K	7
KMT114	+	Isolated at Kochi, Japan	This study	L	3
KMT117	-	Isolated at Kochi, Japan	This study	G	1
KMT124	-	Isolated at Kochi, Japan	This study	F	1
KMT126	+	Isolated at Kochi, Japan	This study	L	2
KMT130	+	Isolated at Kochi, Japan	This study	K	3
NY1	-	Isolated at Yamaguchi, Japan	This study	L	5
NY2	+	Isolined in Yamaguchi, Japan	This study	M	1
NY3	+	Isolined in Yamaguchi, Japan	This study	C	6
NY4	+	Isolined in Yamaguchi, Japan	This study	C	6
NY5	+	Isolined in Yamaguchi, Japan	This study	N	2
NY6	+	Isolined in Yamaguchi, Japan	This study	N	2
NY9	+	Isolined in Yamaguchi, Japan	This study	H	2
NY10	-	Isolined in Yamaguchi, Japan	This study	D	7
NY11	+	Isolined in Yamaguchi, Japan	This study	O	8
NY12	+	Isolined in Yamaguchi, Japan	This study	O	8
NY23	+	Isolined in Yamaguchi, Japan	This study	H	5
NY24	-	Isolined in Yamaguchi, Japan	This study	J	2
NY31	-	Isolined in Yamaguchi, Japan	This study	D	5
NY37	+	Isolined in Yamaguchi, Japan	This study	G	4
NY38	+	Isolined in Yamaguchi, Japan	This study	H	5
NY43	-	Isolined in Yamaguchi, Japan	This study	P	7
NY44	+	Isolined in Yamaguchi, Japan	This study	P	7
NY50	+	Isolined in Yamaguchi, Japan	This study	No PCR amplification	3
3401	+	Isolined in Yamaguchi, Japan	17	I	5
26695	+	Isolated in the United Kingdom	18	A	1
SS-1	+	Isolated in Australia	19	I	5
NCTC 11637	+	Isolated in USA	20	F	1
PY1	+	Hyogo, Japan	21	A	1
TK1402	-	Kanagawa, Japan	22	K	3

[a], "+" and "-" indicate that phage can and cannot form plaques, respectively.

[b], RFLP, restriction fragment length polymorphism.

[b], RFLP types are described in Fig. S1.

TABLE S2. List of *Helicobacter* spp. and phages used in the in silico analysis.

Organism	**Genbank accession No.**
Helicobacter pylori F16	AP011940
Helicobacter pylori F30	AP011941
Helicobacter pylori F32	AP011943
Helicobacter pylori F57	AP011945
Helicobacter pylori 35A	CP002096
Helicobacter pylori 51	CP000012
Helicobacter pylori 83	CP002605
Helicobacter pylori 52	CP001680
Helicobacter pylori v225d	CP001582
Helicobacter pylori Cuz20	CP002076
Helicobacter pylori PeCan4	CP002074
Helicobacter pylori Shi470	CP001072
Helicobacter pylori Sat464	CP002071
Helicobacter pylori 26695	AE000511
Helicobacter pylori B8	FN598874
Helicobacter pylori B38	FM991728
Helicobacter pylori G27	CP001173
Helicobacter pylori HPAG1	CP000241
Helicobacter pylori India7	CP002331
Helicobacter pylori P12	CP001217
Helicobacter pylori Lithuania75	CP002334
Helicobacter pylori SJM180	CP002073
Helicobacter pylori 2017	CP002571
Helicobacter pylori 2018	CP002572
Helicobacter pylori J99	AE001439
Helicobacter pylori 908	CP002184
Helicobacter pylori Gambia94/24	CP002332
Helicobacter pylori SouthAfrica7	CP002336
Helicobacter felis ATCC 49179	FQ670179
Helicobacter hepaticus ATCC 51449	AE017125
Helicobacter bizzozeronii CIII-1	FR871757
Helicobacter mustelae 12198	FN555004
Helicobacter acinonychis str. Sheeba	AM260522
Helicobacter phage KHP30	AB647160
Helicobacter phage KHP40	AB731695
Helicobacter phage 1961P	JQ617284
Helicobacter phage phiHP33	JF734911

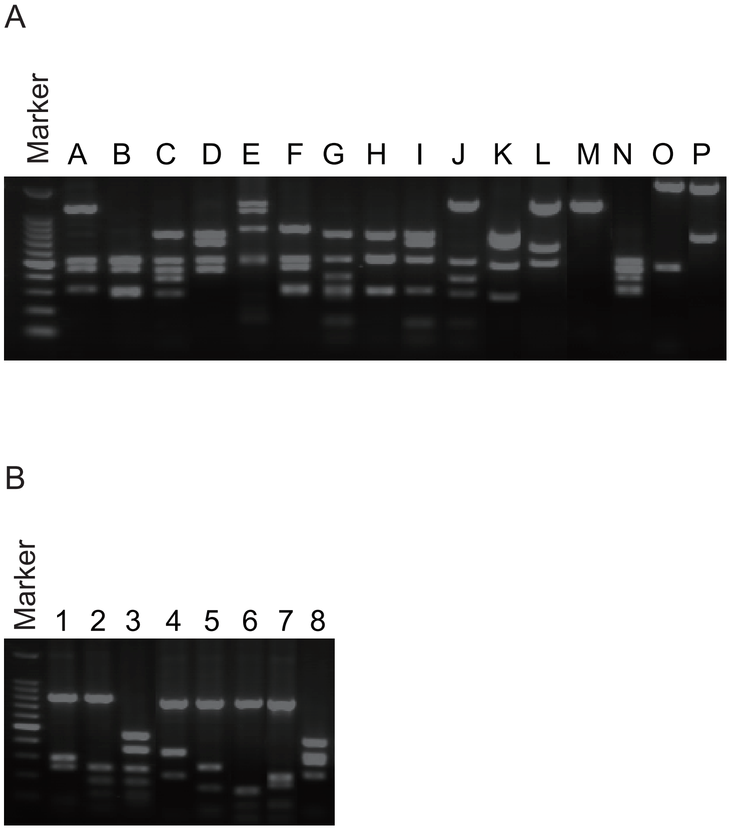


FIG. S1. Restriction fragment length polymorphism analysis of *H. pylori* strains used in this study. Representative restriction patterns of the restriction fragment length polymorphisms are shown. The 100 bp DNA ladder (Takara Bio) was electrophoresed in the leftmost lane of each panel, designated as “Marker”. (A) Restriction patterns of UreAB digested by HaeIII. (B) Restriction patterns of FlaA digested by HhaI.

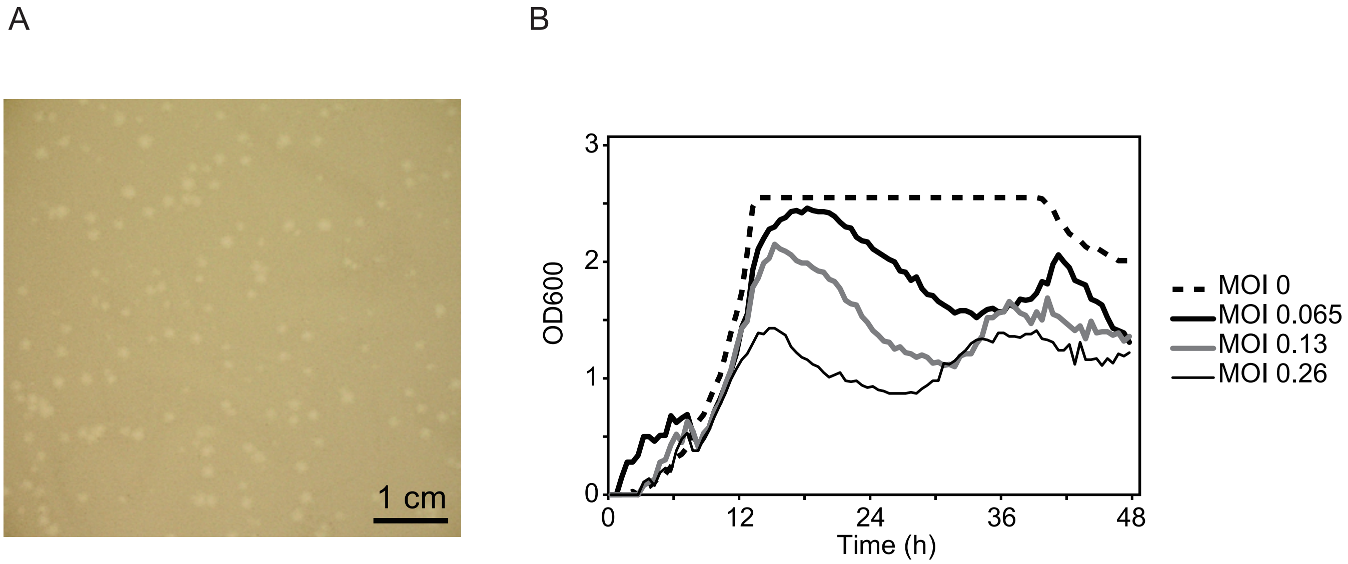


FIG. S2. (A) Photograph of phage plaques. Phage KHP30 was incubated with *H. pylori* strain 3401 for 2 days. (B) Lytic activity of phage KHP30 in liquid medium. *H. pylori* strain 3401 was added to BEV broth at a final concentration of 3.1×10^7 bacteria/ml. Phage KHP30 was added to the BEV medium containing *H. pylori* strain 3401 at MOIs of 0.065, 0.13, and 0.26. A no-phage culture was used as the control. The cultures (5 ml) were incubated in glass tubes with shaking, and bacterial growth was measured as the optical density at a wavelength of 600 nm using an automated turbidity meter (OD-Monitor C & T; Titec Co., Saitama, Japan).

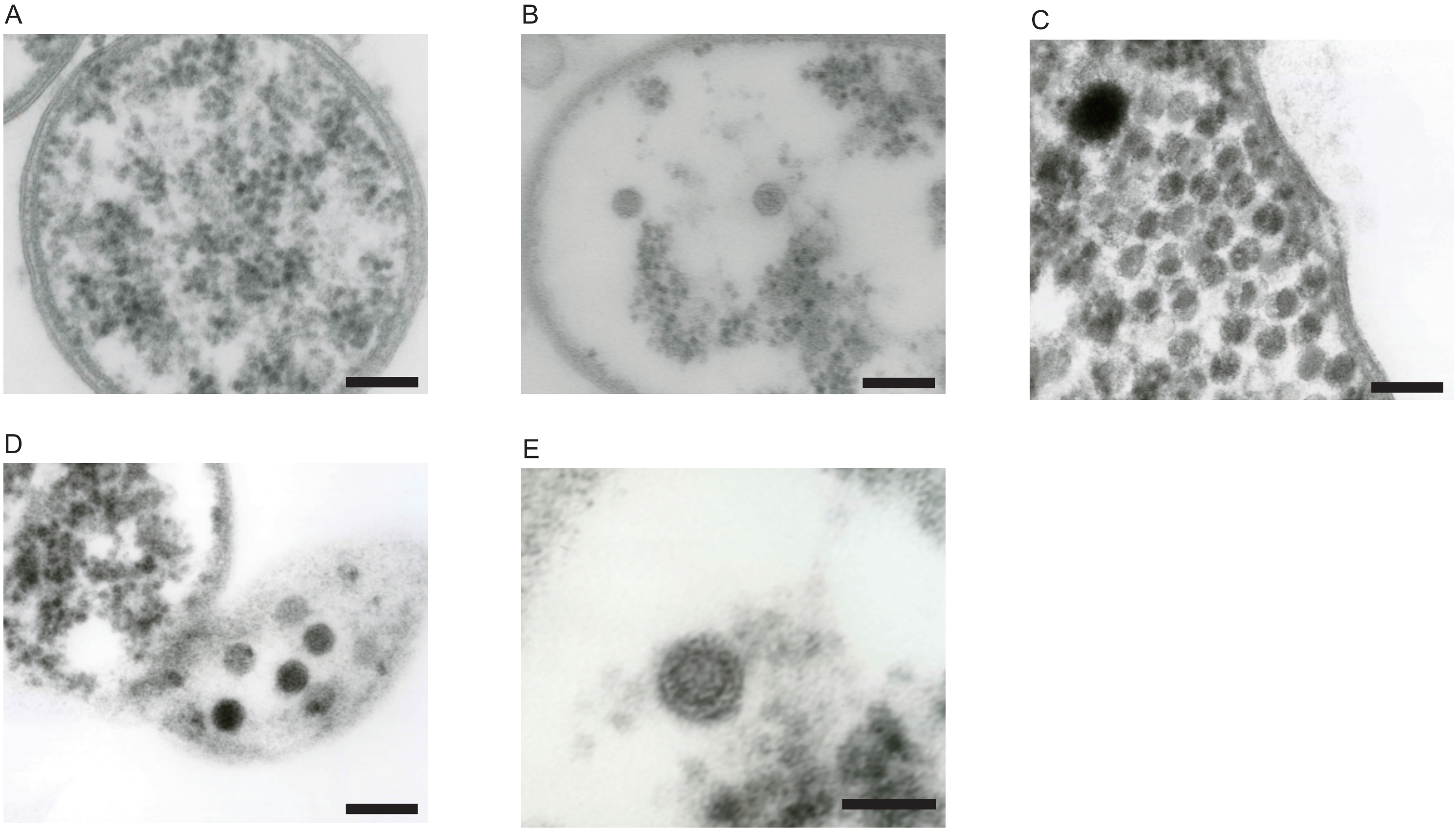
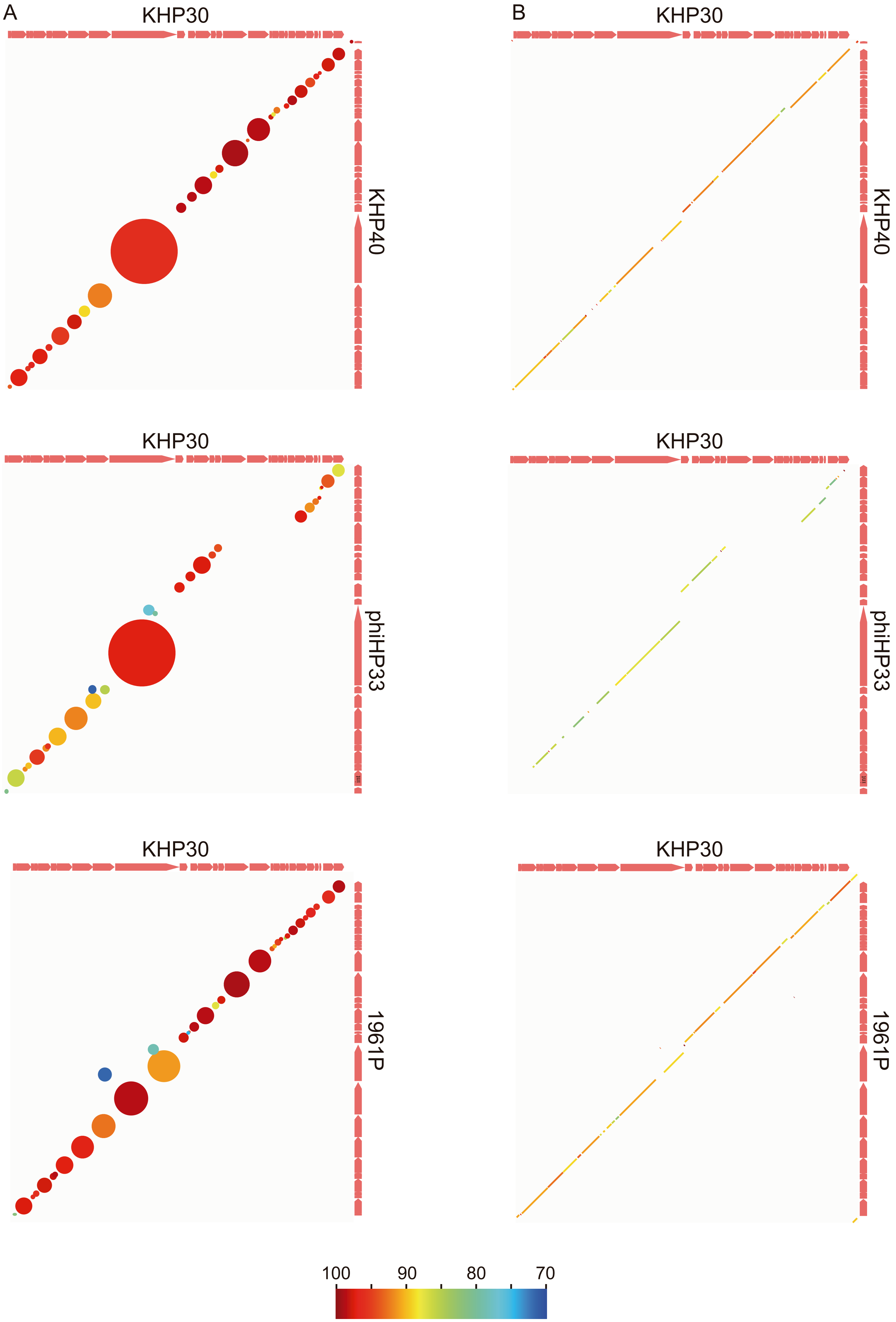


FIG. S3. Electron microscopic observation of thin sections of *H. pylori* and phage-infected *H. pylori*. (A) Thin section of *H. pylori* strain 3401. (B-E) Thin section of *H. pylori* strain 3401 infected with phage KHP30. *H. pylori* was infected with phage, and the thin sections were observed at B 140 min and C, D, E 280 min after phage infection. The observations were made with transmission electron microscopy. Phage particles were seen in B. The phage accumulated inside the cells, which are about to burst in C. Cell burst and phage release are shown in D. The possible layered structure of *H. pylori* phage KHP30 is visible in E. The bars indicate 100 nm in A–D and 50 nm in E.

Supplemental Material- Figure S4

FIG. S4. *In silico* analysis of potential integrated phages in the *H. pylori* genome. *H. pylori* whole genomes were analyzed with BLASTp against using GenomeMatcher, to identify sequences that could be aligned with the KHP30-like phage protein sequences. In each elongated rectangular panel, the vertical and horizontal axes indicate the *H. pylori* genome and the phage genome, respectively. The names of the *H. pylori* strains are listed on the top of the panel. The *H. pylori* strains were grouped into geographical types according to an *in silico* multiple-locus sequence analysis. Red circles, which contain similar ORF alignments to phage KHP30, indicate the possible integration of the phage. The bar on the right indicates the degree of similarity.



Supplemental Material- Figure S5

FIG. S5. BLAST analysis of phage KHP30 against the other *H. pylori* phages. *H. pylori* phages ϕHP33, KHP40, and 1961P were used for this analysis. The analysis was performed with GenomeMatcher. In each panel, the horizontal and vertical axes indicate phage KHP30 and another *H. pylori* phage, respectively. The bar on the bottom indicates the degree of similarity. (A) BLASTp analysis. (B) BLASTn analysis. These phages are highly similar.

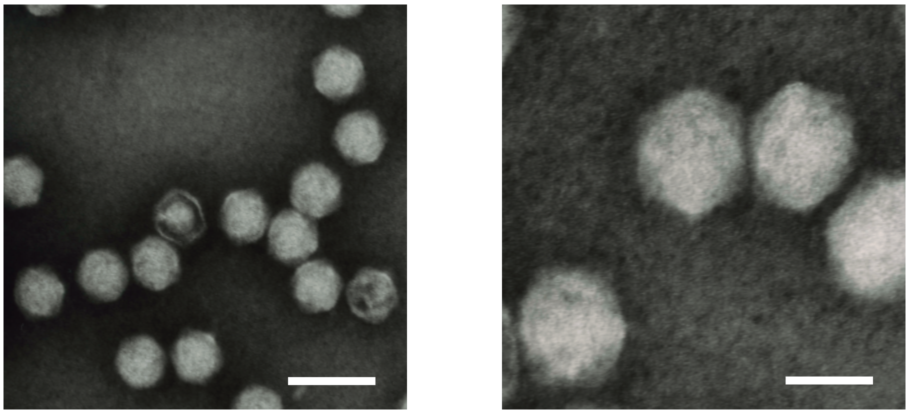


FIG. S6. Morphology of phage KHP40. Phage KHP40 was isolated from *H. pylori* strain KMT83, which was taken from a patient at Kochi University Hospital, Kochi, Japan. The purified phage was observed with transmission electron microscopy. The bars indicate 100 nm (left) and 50 nm (right). Phage KHP40 is a spherical phage with a diameter of 69.4 ± 2.3 nm (mean ± SD; n = 11).