

Figure S1

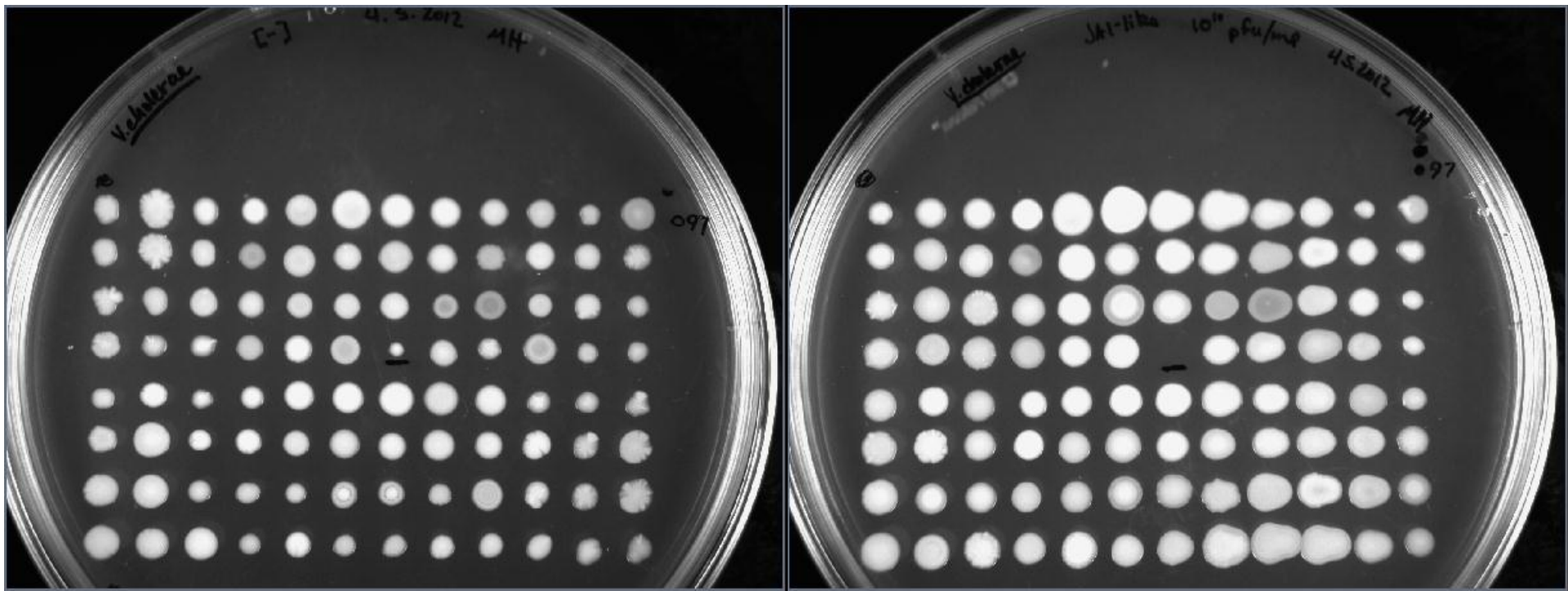
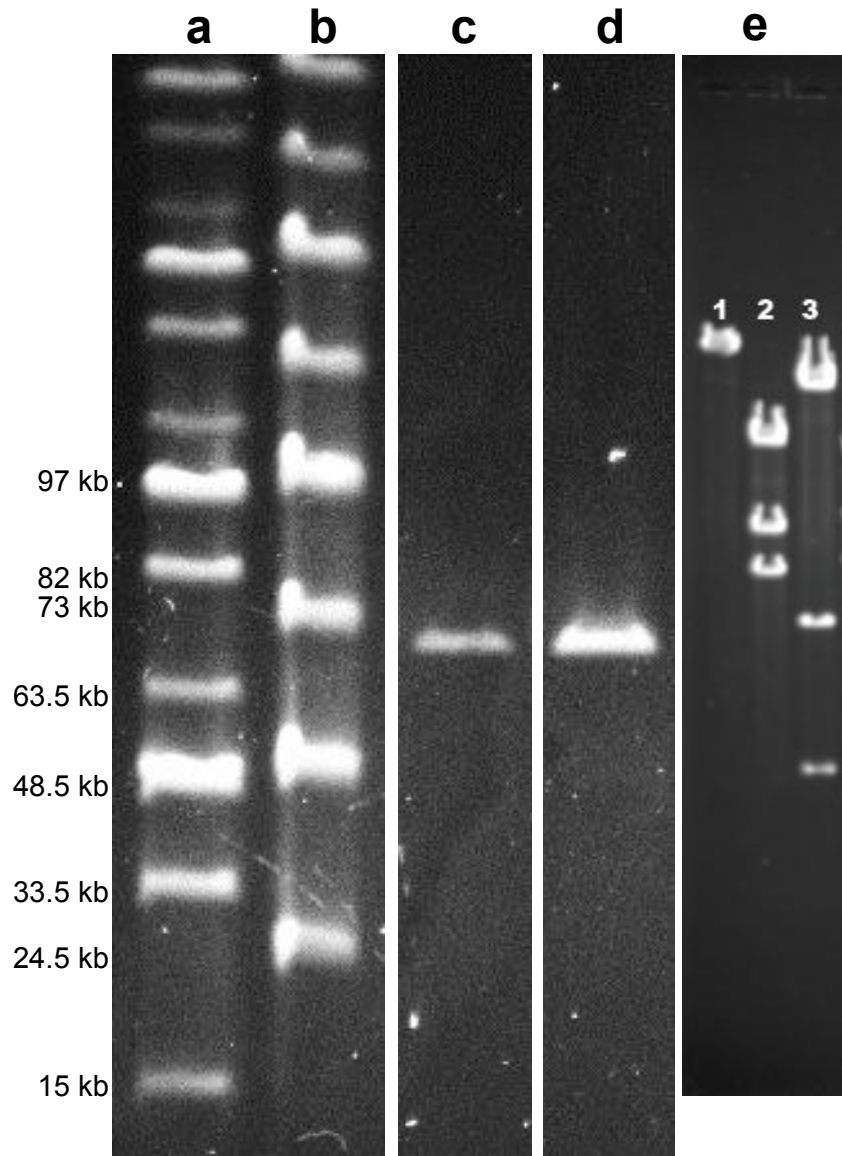


Figure S2

A.



B.

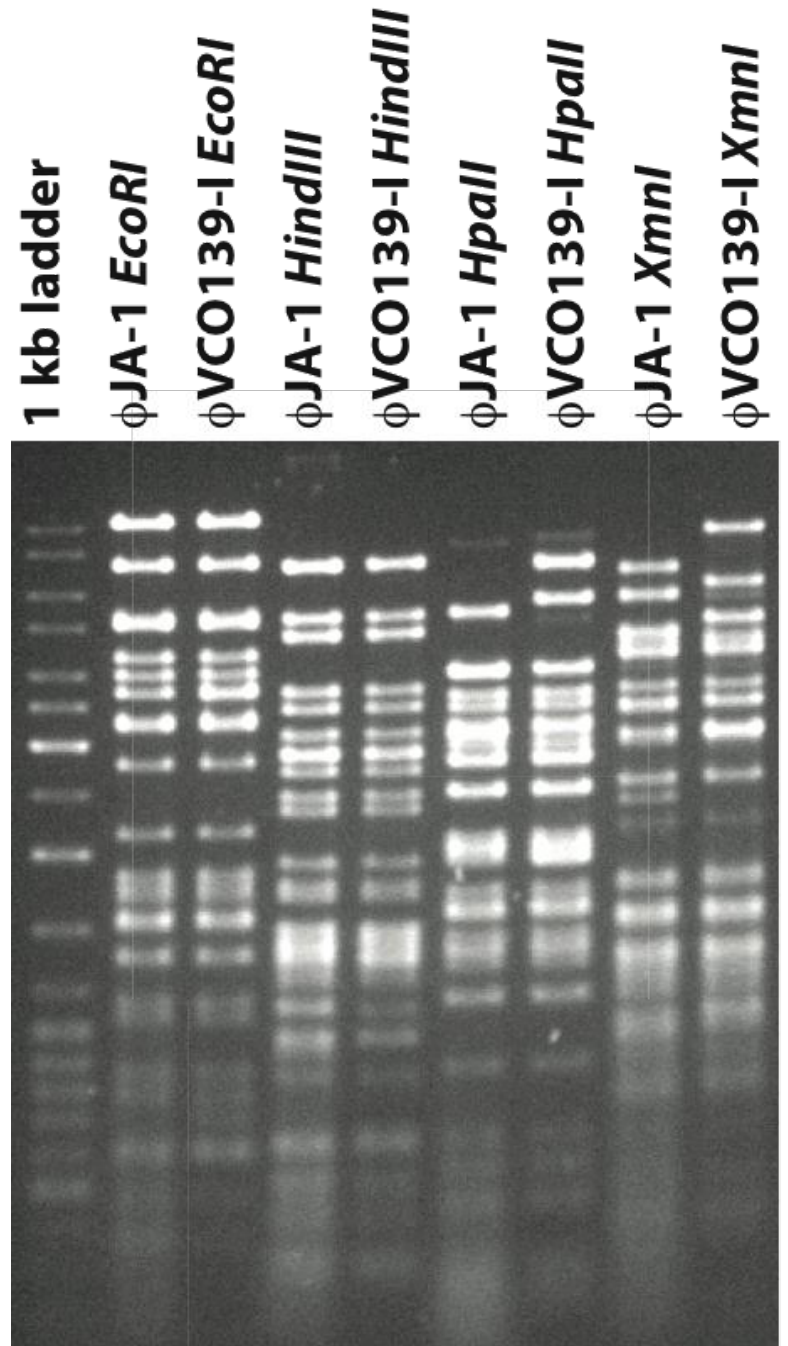
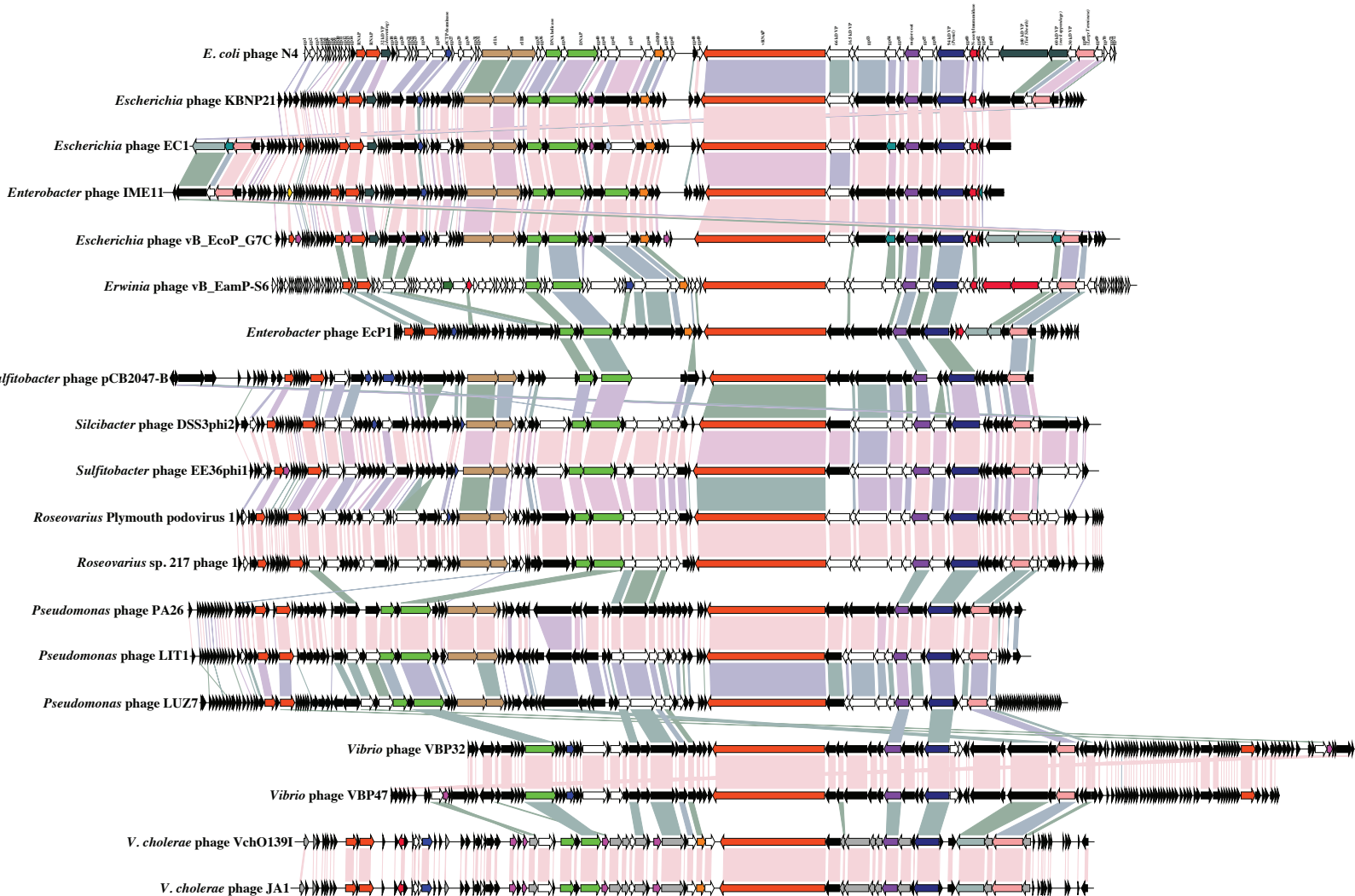


Figure S4



Capsid structural components and assembly	Tail and baseplate assembly	DNA metabolism
<ul style="list-style-type: none"> large terminase major capsid portal other 	<ul style="list-style-type: none"> structural protein tail component 	<ul style="list-style-type: none"> replication DNA binding nucleotides
	Host cell lysis	Other
	<ul style="list-style-type: none"> endolysin/lysin holin lysis inhibition 	<ul style="list-style-type: none"> transcription conserved hypothetical hypothetical protein intron/intein other (not defined)
<p>BLASTP 100 35% identity</p>		

Table S3. Comparison of Miscellaneous features between N4-like Phages and Coliphages

Phage	Accession	Size (bp)	Length of DTRs (bp)	# tRNAs	tRNA type*	#homing endo	#>5 polyA	#>5 polyT	#>5 polyG	#>5 polyC	Total	#HT/bp	pA/#	pT/#	pG/#	pC/#
<i>E. coli</i> phage KBNP21	JX415535	69855	Not Determined	1	Ile	1	11	11	2	1	25	0.000357884	7/1	7/3	6/2	7/1
<i>E. coli</i> phage N4	EF056009	70153	390-440 + 3' ss extension	4	Asn,Ser,Thr,Pro	1	11	13	0	1	25	0.000356364	8/1	7/2	0	9/1
<i>E. coli</i> phage EC1	KC206276	70831	Not Determined	0	NA	2	9	13	4	3	29	0.000409425	6/9	7/3	6/4	7/1
<i>E. coli</i> phage vB_EcoP_G7C	HQ259105	72917	1160	0	NA	5	11	11	2	5	29	0.000397712	6/11	7/3	6/2	7/2
<i>Enterobacter</i> phage EcP1	HQ641380	59080	Not Determined	3	Asn,Pro,Met	0	37	37	0	2	76	0.001286391	8/1	10/1	0	9/1
<i>Enterobacter</i> phage IME11	JX880034	72570	Not Determined	2	Undet, Ile	0	12	8	6	1	27	0.000372055	7/2	6/8	7/2	6/1
<i>Erwinia</i> phage vB_EamP-S6	HQ728266	74669	396	0	NA	0	8	12	0	2	22	0.000294634	7/1	8/1	0	9/2
<i>Pseudomonas</i> phage PA26	JX194238	72321	Not Determined	0	NA	1	5	6	2	2	15	0.000207409	7/1	7/3	7/1	7/1
<i>Pseudomonas</i> phage LIT1	FN422399	72544	632-665	0	NA	1	6	5	2	2	15	0.000206771	7/1	11/1	6/2	7/2
<i>Pseudomonas</i> phage LUZ7	FN422398	74901	632-665	0	NA	0	4	5	2	4	15	0.000200264	7/1	7/1	6/2	7/3
<i>Roseovarius</i> sp. 217 phage 1	FR682616	74583	Not Determined	3	Pro,Ile,Gln	1	9	8	2	2	21	0.000281566	6/9	6/8	7/1	7/1
<i>Roseovarius</i> Plymouth podovirus 1	FR719956	74704	Not Determined	3	Pro,Ile,Gln	1	8	7	2	3	20	0.000267723	6/8	6/7	7/1	7/1
<i>Silicibacter</i> phage DSS3phi2	FJ591093	74611	Not Determined	3	Pro,Met,Ser	1	18	11	6	4	39	0.000522711	9/1	7/2	6/6	6/4
<i>Sulfitobacter</i> phage EE36phi1	FJ591094	73325	Not Determined	3	Pro,Ile,Ser	1	20	12	3	10	45	0.000613706	7/2	7/2	6/3	7/4
<i>Sulfitobacter</i> phage pCB2047-B	HQ317387	74480	Not Determined	13	Met,Tyr,Trp,Leu,Cys,Thr,Pro,Asn,Ile,Lys,Phe,Gln,Arg	0	8	11	4	4	27	0.000362513	6/8	6/11	7/2	7/1
<i>Vibrio</i> phage VBP32	HQ634196	76718	Not Determined	1	Trp	3	11	13	3	1	28	0.000364973	10/1	7/2	9/1	6/1
<i>Vibrio</i> phage VBP47	HQ634194	76705	Not Determined	1	Trp	3	13	12	1	3	29	0.000378072	7/2	10/1	6/1	10/1
<i>V. cholerae</i> phage JA1	JA1	69755	1974	1	Arg	4	19	19	2	3	43	0.000616443	8/1	11/1	6/2	7/1
<i>V. cholerae</i> phage VchO139I	VchO139I	68964	1974	1	Arg	4	18	18	2	3	41	0.000594513	8/1	12/1	6/2	7/1
Lambda	JO2459	48502	cos	0	NA	?	40	36	5	2	83	0.00171127	8/2	8/1	7/1	6/2
Mu	AF083977	36717	variable	0	NA	?	30	16	6	3	55	0.001497944	7/4	7/3	6/6	7/1
P1	AF234172	94800	circular	3	Asn,Thr,Met	?	60	71	3	5	139	0.001466245	8/5	8/2	6/3	8/1
T1	AY216660	48836		0	NA	1	35	29	2	0	66	0.001351462	7/6	8/2	7/1	0
T4	AF158101	168903	circular permutation and terminal redundant	8	Gln,Leu,Gly,Pro,Ser,Thr,Met,Arg	15	79	112	0	0	191	0.001130827	8/1	7/2	0	0
T5	AY543070	121750		23	Arg,Ser,Met,Tyr,Glu,Phe,Cys,Asn,Asp,Pro,Lys,Val,Ala,Leu,Gln,Gly,Thr,Ile	?	33	63	0	4	100	0.000821355	6/33	7/1	0	0
T7	GU071091	39778		0	NA	?	0	1	0	0	1	2.51395E-05	0	6/1	0	0

Homopolymeric Tracts > 9 nucleotides

Highest number of homopolymeric nucleotides