

Figure S1

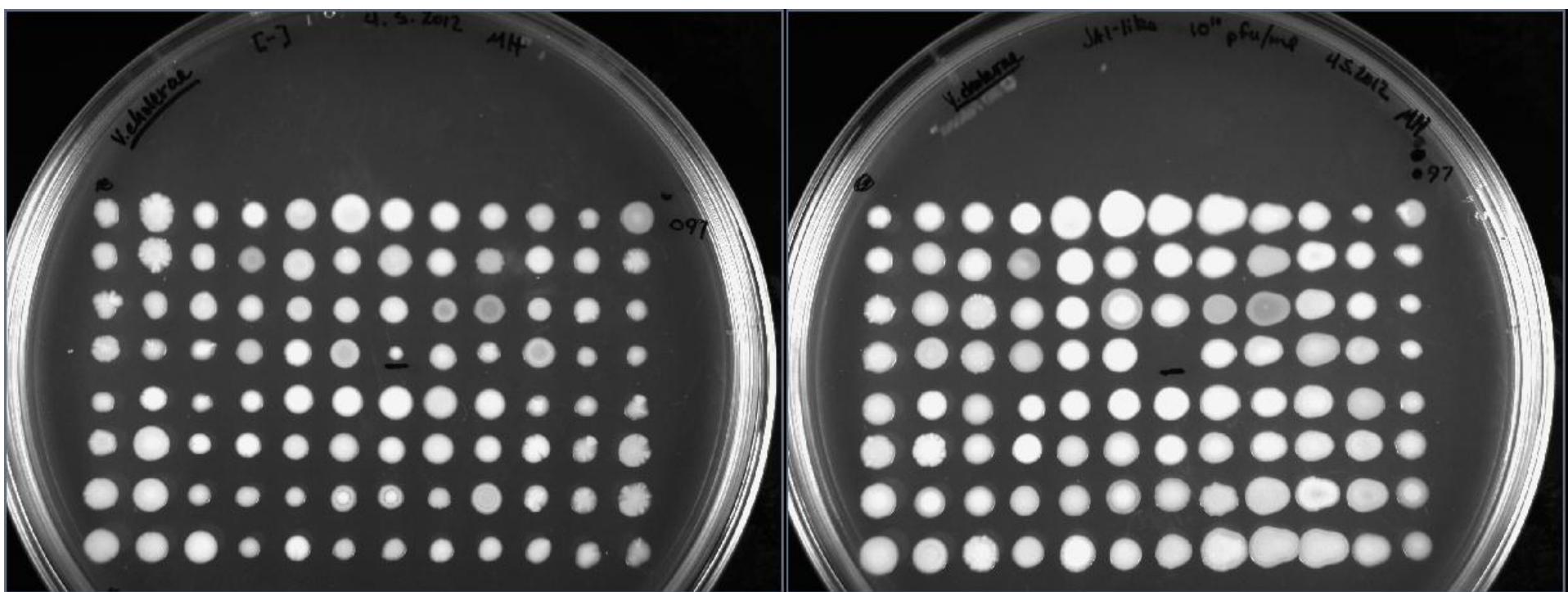
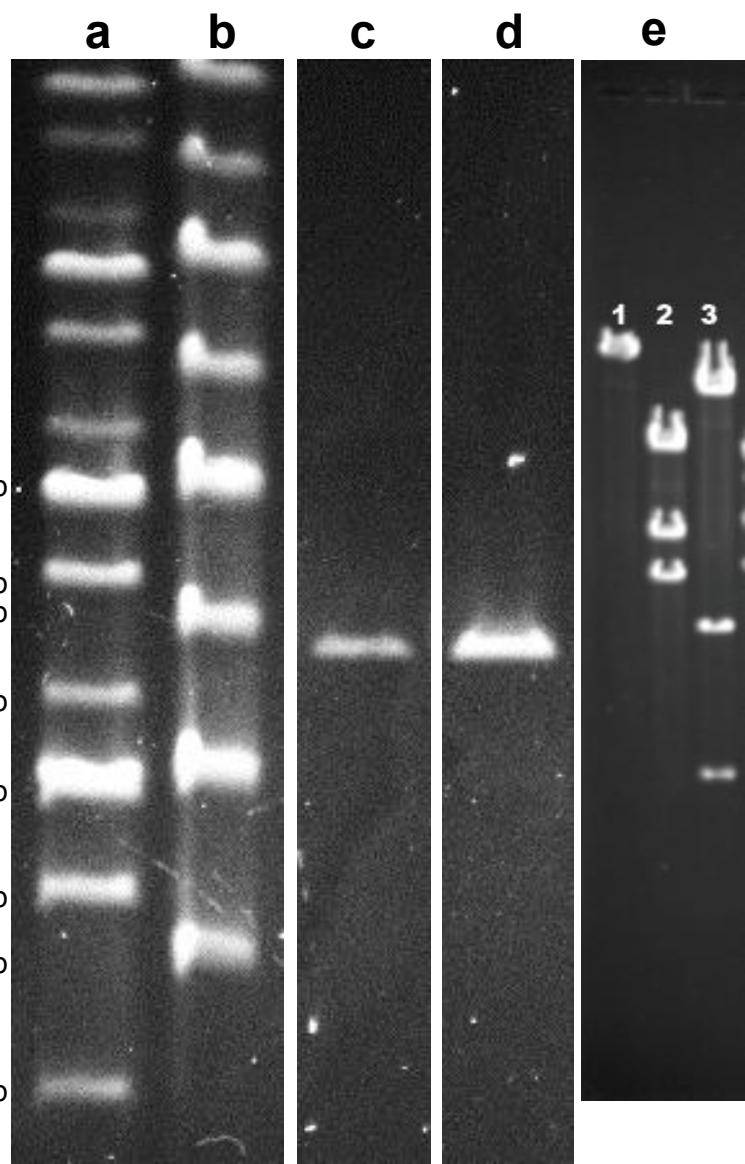


Figure S2

A.



B.

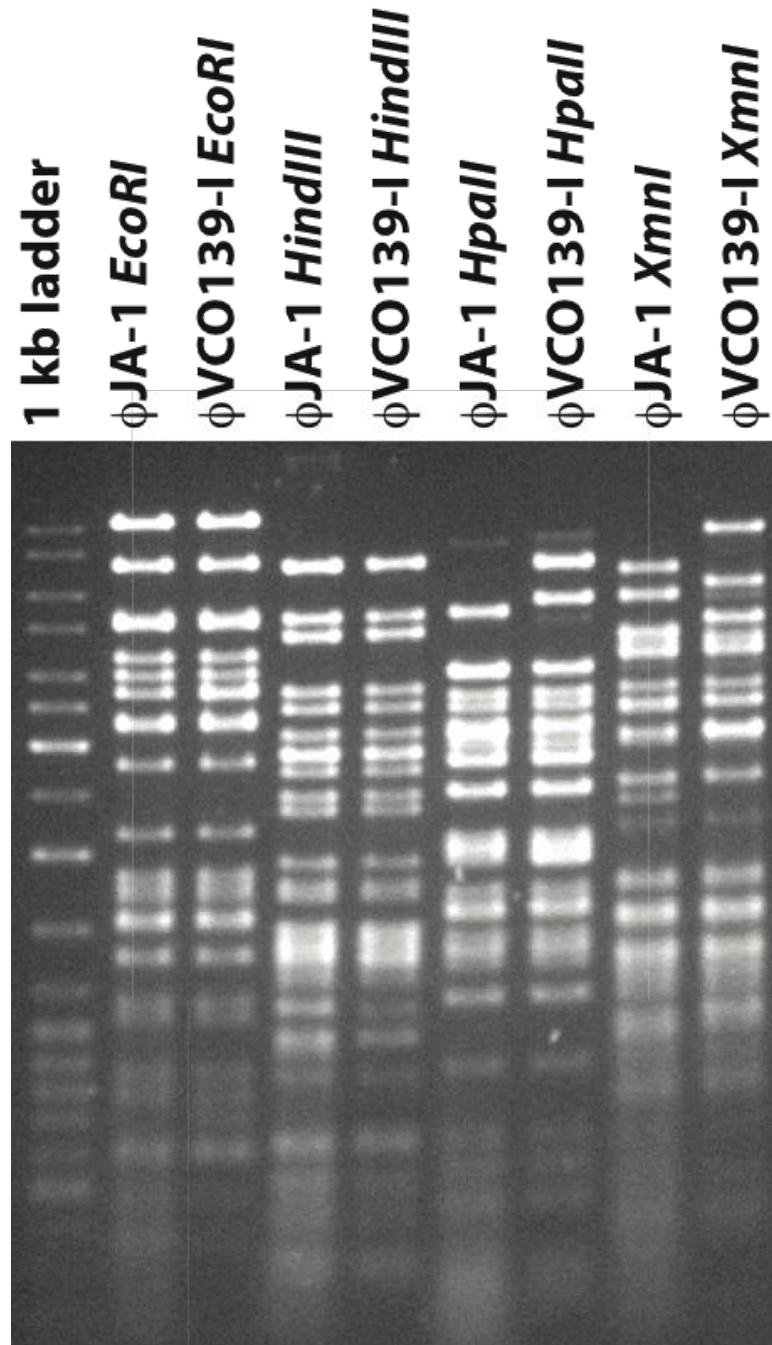


Figure S3

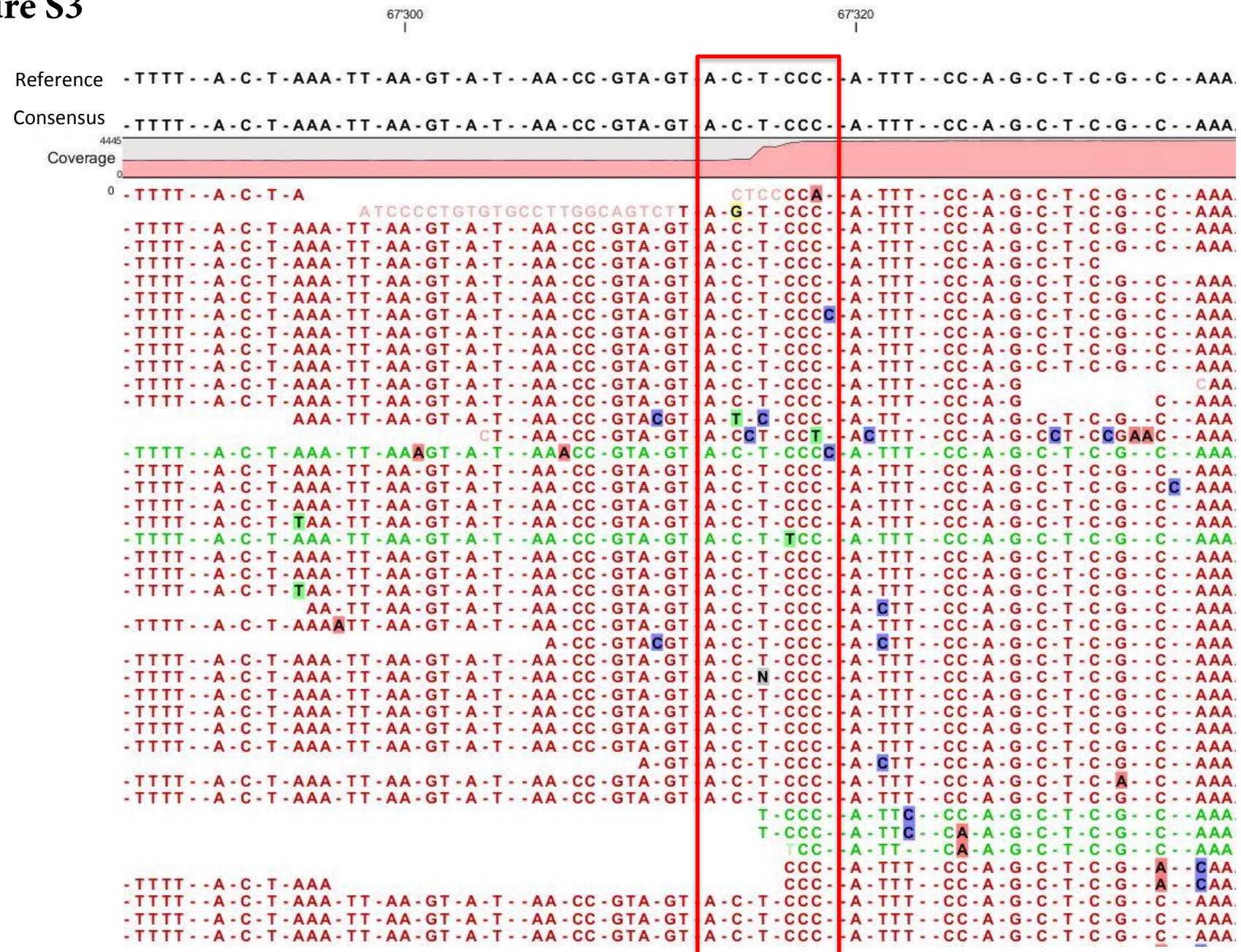


Figure S4

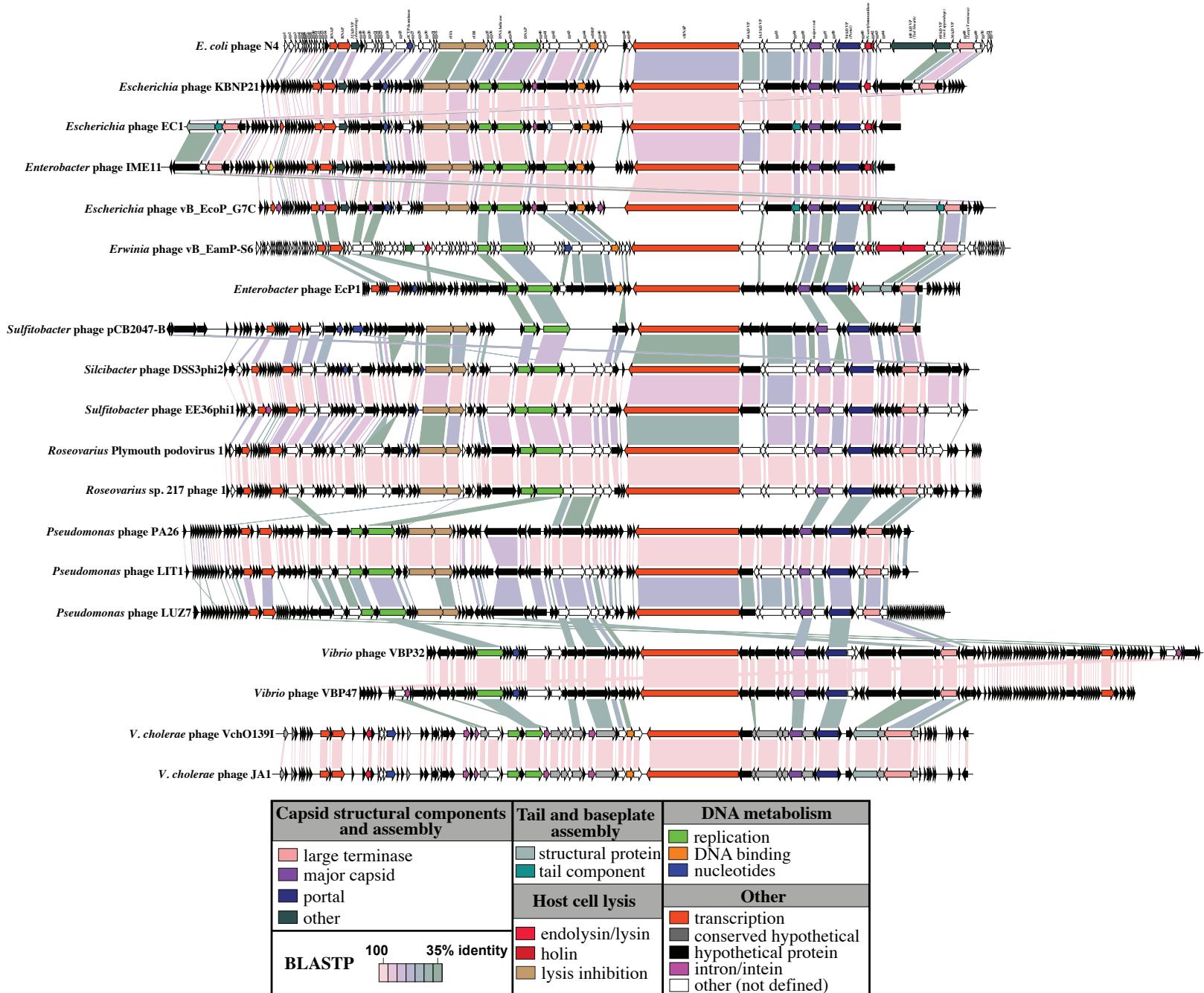


Table S1. Comparison of Bacteriophages vB_VchP_JA1 and vB_VchP_VchO139-I

Locus	Annotation	vB_VchP_JA1		Mol. Wt.	vB_VchP_VchO139-I		Mol. Wt.	BLASTP	BLASTN	SNPs		
		Size (bp)	(kDa)	Locus	Annotation	Size (bp)	(kDa)	% id	%id	S	NS	Total (S + NS)
JA1_0001	conserved hypothetical protein	411	15.2	VCO139_0001	conserved hypothetical protein	411	15.2	100	100			
JA1_0002	hypothetical protein	228	9.1									
JA1_0003	conserved hypothetical protein	279	10.6	VCO139_0002	conserved hypothetical protein	279	10.6	100	100			
JA1_0004	hypothetical protein	237	9.1	VCO139_0003	hypothetical protein	237	9.1	100	100			
JA1_0005	hypothetical protein	258	10.0	VCO139_0004	hypothetical protein	258	10.0	100	100			
JA1_0006	hypothetical protein	189	7.4	VCO139_0005	hypothetical protein	189	7.4	100	100			
JA1_0007	hypothetical protein	189	7.3	VCO139_0006	hypothetical protein	189	7.3	100	100			
JA1_0008	hypothetical protein	234	8.6	VCO139_0007	hypothetical protein	234	8.6	100	100			
JA1_0009	hypothetical protein	267	9.6	VCO139_0008	hypothetical protein	267	9.6	100	100			
JA1_0010	DNA-directed RNA polymerase RNAP1	942	36.4	VCO139_0009	DNA-directed RNA polymerase RNAP1	942	36.4	100	100			
JA1_0011	hypothetical protein	216	8.7	VCO139_0010	hypothetical protein	216	8.7	100	100			
JA1_0012	DNA-directed RNA polymerase RNAP2	1227	46.4	VCO139_0011	DNA-directed RNA polymerase RNAP2	1227	46.5	99.3	98.5	15	4	19
JA1_0013	hypothetical protein	189	7.5	VCO139_0012	hypothetical protein	189	7.5	100	100			
JA1_0014	N-acetylmuramoyl-L-alanine amidase	525	19.4	VCO139_0013	N-acetylmuramoyl-L-alanine amidase	525	19.4	100	99.8	1	0	1
JA1_0015	hypothetical protein	273	10.3	VCO139_0014	hypothetical protein	273	10.3	100	100			
JA1_0016	hypothetical protein	297	11.2	VCO139_0015	hypothetical protein	297	11.2	96.9	96.3	6	5	11
JA1_0017	conserved hypothetical protein	129	5.0	VCO139_0016	conserved hypothetical protein	129	5.0	100	100			
JA1_0018	PF10947 family protein	420	16.2	VCO139_0017	PF10947 family protein	420	16.2	100	98.3	5	0	5
JA1_0019	putative lipoprotein	303	11.7	VCO139_0018	putative lipoprotein	303	11.7	100	100			
JA1_0020	thymidylate synthase	852	32.6	VCO139_0019	thymidylate synthase	852	32.6	100	100			
JA1_0021	hypothetical protein	159	6.2	VCO139_0020	hypothetical protein	159	6.2	100	100			
JA1_0022	hypothetical protein	216	7.9	VCO139_0021	hypothetical protein	216	7.9	100	100			
JA1_0023	conserved hypothetical protein	327	12.6	VCO139_0022	conserved hypothetical protein	327	12.7	99.1	99.7	0	1	1
JA1_0025	hypothetical protein	312	11.3	VCO139_0024	hypothetical protein	312	11.3	100	100			
JA1_0026	hypothetical protein	399	15.4	VCO139_0025	hypothetical protein	399	15.4	100	100			
JA1_0080	hypothetical protein	141	5.7	VCO139_0026	hypothetical protein	141	5.7	100	100			
JA1_0027	hypothetical protein	456	18.1	VCO139_0027	hypothetical protein	456	18.1	100	100			
JA1_0028	PF11753 family protein	294	11.5	VCO139_0028	PF11753 family protein	294	11.5	100	100			
JA1_0029	hypothetical protein	183	7.1	VCO139_0029	hypothetical protein	183	7.1	100	100			
JA1_0030	hypothetical protein	642	23.5	VCO139_0030	hypothetical protein	642	23.4	99.5	99.8	0	1	1
JA1_0031	hypothetical protein	456	17.7	VCO139_0031	hypothetical protein	456	17.7	100	99.8	1	0	1
JA1_0032	putative HNH homing endonuclease	576	22.3	VCO139_0032	putative HNH homing endonuclease	576	22.3	100	99.8	1	0	1
JA1_0033	hypothetical protein	321	11.7	VCO139_0033	hypothetical protein	321	11.7	100	100			
JA1_0034	putative HNH homing endonuclease	387	14.4	VCO139_0034	putative HNH homing endonuclease	387	14.4	100	100			
JA1_0035	conserved hypothetical protein	732	27.1	VCO139_0035	conserved hypothetical protein	732	27.1	100	100			
JA1_0036	metallopeptidase domain protein	1230	46.7	VCO139_0036	metallopeptidase domain protein	1230	46.7	100	100			
JA1_0037	hypothetical protein	168	7.1	VCO139_0037	hypothetical protein	168	7.1	100	100			
JA1_0038	DNA helicase	1191	45.3	VCO139_0038	DNA helicase	1191	45.3	100	100			
JA1_0039	hypothetical protein	450	17.6	VCO139_0039	hypothetical protein	450	17.6	99.3	99.6	1	1	2
JA1_0040	DNA polymerase	1680	63.8	VCO139_0040	DNA polymerase	1680	63.8	99.8	99.6	6	1	7
JA1_0041	putative HNH homing endonuclease	534	20.4	VCO139_0041	putative HNH homing endonuclease	534	20.4	100	100			
JA1_0042	conserved hypothetical protein	999	38.1	VCO139_0042	conserved hypothetical protein	999	38.1	100	100			
JA1_0043	conserved hypothetical protein	609	23.4	VCO139_0043	conserved hypothetical protein	609	23.4	100	100			
JA1_0044	phosphoribosyl-ATP diphosphatase	450	16.9	VCO139_0044	phosphoribosyl-ATP diphosphatase	450	16.9	100	100			
JA1_0045	conserved hypothetical protein	1014	38.1	VCO139_0045	conserved hypothetical protein	1014	38.1	100	100			
JA1_0046	hypothetical protein	243	8.9	VCO139_0046	hypothetical protein	243	8.9	100	100			
JA1_0047	putative HNH homing endonuclease	636	23.9	VCO139_0047	putative HNH homing endonuclease	636	23.9	100	100			
JA1_0048	conserved hypothetical protein	1923	73.5	VCO139_0048	conserved hypothetical protein	1923	73.5	100	100			
JA1_0049	hypothetical protein	288	10.6	VCO139_0049	hypothetical protein	288	10.6	100	99.7	1	0	1
JA1_0050	AAA domain protein	738	28.0	VCO139_0050	AAA domain protein	738	28.0	100	100			
JA1_0051	ssDNA binding protein	723	26.1	VCO139_0051	ssDNA binding protein	723	26.1	100	100			
JA1_0052	crossover junction endodeoxyribonuclease RusA	798	30.5	VCO139_0052	crossover junction endodeoxyribonuclease RusA	798	30.5	98.1	99.1	2	5	7
JA1_0053	viron-encapsulated RNA polymerase	9069	335.3	VCO139_0054	viron-encapsulated RNA polymerase	9069	335.4	99.3	99.1	58	21	79
JA1_0054	hypothetical protein	1269	47.2	VCO139_0055	hypothetical protein	1269	47.2	99.3	98.8	12	3	15
JA1_0055	conserved domain protein	408	15.3	VCO139_0056	conserved domain protein	408	15.3	100	100			
JA1_0056	conserved domain protein	2109	79.6	VCO139_0057	conserved domain protein	2109	79.6	99.9	99.7	6	1	7
JA1_0057	conserved hypothetical protein	477	17.1	VCO139_0058	conserved hypothetical protein	477	17.1	100	100			
JA1_0058	conserved hypothetical protein	585	22.2	VCO139_0059	conserved hypothetical protein	585	22.2	100	98.6	8	0	8
JA1_0059	major capsid protein, N4-gp56 family	1314	47.0	VCO139_0060	major capsid protein, N4-gp56 family	1314	47.0	100	100			
JA1_0060	conserved hypothetical protein	1092	40.4	VCO139_0061	conserved hypothetical protein	1092	40.4	99.4	99.5	3	2	5
JA1_0061	hypothetical protein	312	11.7	VCO139_0062	hypothetical protein	312	11.7	98.1	98.1	4	2	6
JA1_0062	portal protein	2118	79.3	VCO139_0063	portal protein	2118	79.3	99.6	99.6	5	3	8
JA1_0063	hypothetical protein	288	11.0	VCO139_0064	hypothetical protein	288	10.9	96.8	99	0	3	3
JA1_0064	hypothetical protein	624	23.4	VCO139_0065	hypothetical protein	624	23.4	99.5	99.8	0	1	1
JA1_0065	putative phage minor structural protein	2427	87.3	VCO139_0066	putative phage minor structural protein	2427	87.4	99.5	99.8	1	5	6
JA1_0066	conserved domain protein	687	25.8	VCO139_0067	conserved hypothetical protein	687	25.9	99.1	99.3	3	2	5
JA1_0067	terminase, large subunit (intein-containing)	2613	99.5	VCO139_0068	terminase, large subunit (intein-containing)	2613	99.5	100	100			
JA1_0068	conserved hypothetical protein	678	25.2	VCO139_0069	conserved hypothetical protein	678	25.2	100	100			
JA1_0069	hypothetical protein	138	5.4	VCO139_0070	hypothetical protein	138	5.4	97.8	99.3	0	1	1
JA1_0070	hypothetical protein	183	7.3	VCO139_0071	hypothetical protein	183	7.3	100	100			
JA1_0071	hypothetical protein	114	4.6	VCO139_0072	hypothetical protein	114	4.6	100	100			
JA1_0072	hypothetical protein	174	7.2	VCO139_0073	hypothetical protein	174	7.2	100	100			
JA1_0073	hypothetical protein	207	8.2	VCO139_0074	hypothetical protein	207	8.2	98.5	99.5	0	1	1
JA1_0074	hypothetical protein	192	7.5	VCO139_0075	hypothetical protein	192	7.5	100	100			
JA1_0075	hypothetical protein	126	5.0	VCO139_0076	hypothetical protein	126	5.0	100	100			
JA1_0076	hypothetical protein	240	9.2	VCO139_0077	hypothetical protein	240	9.2	100	100			
JA1_0077	hypothetical protein	222	8.6	VCO139_0078	hypothetical protein	222	8.6	100	100			
JA1_0078	hypothetical protein	114	4.7	VCO139_0080	hypothetical protein	114	4.7	100	100			
JA1_0079	hypothetical protein	534	20.3	VCO139_0081	hypothetical protein	534	20.3	100	100			

Average: 699

Average: 698

Totals: 139 63 202

proteins 19 19
 Synonymous SNPs 139
 Non-synonymous SNPs 63
 intergenic SNPs 96
 total SNPs 298

Table S2. Average Percent Identity of N4-like Phages at the Amino Acid Level

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
Enterobacter 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
Enterobacter 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
Erwinia phage vB_Eamp-S6	HQ728266	74669	396	0	NA	0	8	12	0	2	22	0.000294634	7/1	8/1	0	9/2
Pseudomonas phage PA26	JX194238	72321	Not Determined	0	NA	1	5	6	2	2	15	0.000207409	7/1	7/3	7/1	7/1
Pseudomonas phage LIT1	FN422399	72544	632-665	0	NA	1	6	5	2	2	15	0.000206771	7/1	11/1	6/2	7/2
Pseudomonas phage LU27	FN422398	74901	632-665	0	NA	0	4	5	2	4	15	0.000200264	7/1	7/1	6/2	7/3
Roseovarius 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
Roseovarius Plymooth 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
Silicibacter phage DSSphi2	FJ591093	74611	Not Determined	3	Pro,Met,Ser	1	18	11	6	4	39	0.000522711	9/1	7/2	6/6	6/4
Sulfitobacter 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
Sulfitobacter 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	6/6	6/11	7/2	7/1
Vibrio phage VBP32	HQ634196	76718	Not Determined	1	Trp	3	11	13	3	1	28	0.000364973	10/1	7/2	9/1	6/1
Vibrio 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	J02459	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