## **Supplementary Materials**

## Isolation and Characterization T4- and T7-like Phages that Infect the Bacterial Plant Pathogen, *Agrobacterium tumefaciens*

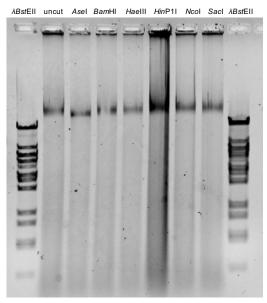
Hedieh Attai † and Pamela J.B. Brown \*

Division of Biological Sciences, University of Missouri, Columbia, MO 65211 USA

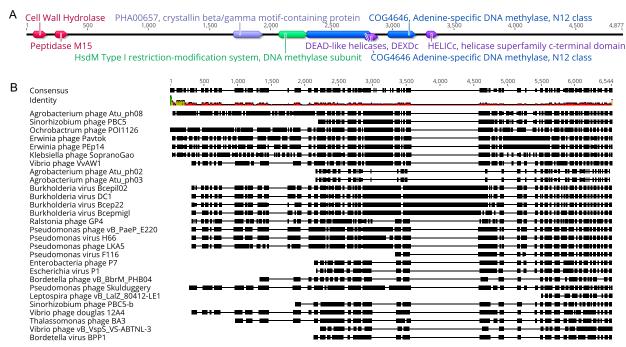
<sup>†</sup>Present address: Department of Pathology, University of California at San Diego, La Jolla, CA92093; hattai@ucsd.edu

\*Correspondence: brownpb@missouri.edu; Tel.: (+1-573-884-0214)

## SUPPLEMENTARY FIGURES



**Supplementary Figure S1**: Restriction fragment analysis of digested Atu\_ph04 genomic DNA. DNA is loaded onto a 0.7% agarose gel.



**Supplementary Figure S2**: Analysis of DarB-like protein in Atu\_ph08. (A) Domain structure of DarB-like protein in Atu\_ph08. (B) ClustalW alignment of DarB-like proteins in other T7-like phages. Dark black blocks indicate regions of synteny.

## SUPPLEMENTARY TABLES

**Supplementary Table S1**: Atu\_ph04 genes organized by predicted function.

CDS	RAST annotated function	Updated assigned	Length	Category
#	To to 1 annotated function	function	(bp)	category
1	hypothetical protein CDS	putative T7-like tail	186	Structural
	ny podredicar protein ego	fiber protein	100	Structurar
2	hypothetical protein CDS	process	600	Hypothetical
3	hypothetical protein CDS		321	Hypothetical
4	hypothetical protein CDS		246	Hypothetical
5	hypothetical protein CDS		210	Hypothetical
6	UDP-galactopyranose		1173	Other/Bacterial
	mutase (EC 5.4.99.9) CDS			
7	hypothetical protein CDS		315	Hypothetical
8	hypothetical protein CDS		159	Hypothetical
9	hypothetical protein CDS		354	Hypothetical
10	N-acetylmuramoyl-L-alanine		942	Lysis
	amidase (EC 3.5.1.28) CDS			
11	hypothetical protein CDS		216	Hypothetical
12	hypothetical protein CDS		516	Hypothetical
13	hypothetical protein CDS		366	Hypothetical
14	Phage protein CDS		351	Hypothetical
15	hypothetical protein CDS		399	Hypothetical
16	hypothetical protein CDS		213	Hypothetical
17	Phosphohydrolase		588	Nucleotide
	(MutT/nudix family protein)			metabolism
	CDS			
18	hypothetical protein CDS		600	Hypothetical
19	hypothetical protein CDS		249	Hypothetical
20	hypothetical protein CDS		309	Hypothetical
21	hypothetical protein CDS		546	Hypothetical
22	hypothetical protein CDS		198	Hypothetical
23	hypothetical protein CDS	putative	282	Nucleotide
		glutaredoxin		metabolism
24	Ribonucleotide reductase of		1662	Nucleotide
	class Ia (aerobic), alpha			metabolism
	subunit (EC 1.17.4.1) CDS			

25	Ribonucleotide reductase of		1053	Nucleotide		
20	class Ia (aerobic), beta		1000	metabolism		
	subunit (EC 1.17.4.1) CDS			Trettae Offort		
26	Phage-associated DNA		1041	DNA		
	primase (EC 2.7.7) #gp61			replication		
	CDS			•		
27	hypothetical protein CDS		339	Hypothetical		
28	hypothetical protein CDS		402	Hypothetical		
29	hypothetical protein CDS		354	Hypothetical		
30	hypothetical protein CDS		297	Hypothetical		
31	hypothetical protein CDS		510	Hypothetical		
32	hypothetical protein CDS		480	Hypothetical		
33	hypothetical protein CDS	putative uracil	468	DNA repair		
		DNA glycosylase				
34	hypothetical protein CDS		273	Hypothetical		
35	hypothetical protein CDS		405	Hypothetical		
36	hypothetical protein CDS		255	Hypothetical		
37	hypothetical protein CDS		219	Hypothetical		
38	hypothetical protein CDS		291	Hypothetical		
39	hypothetical protein CDS		207	Hypothetical		
40	Phage DNA end protector		627	DNA		
	during packaging CDS			associated		
41	hypothetical protein CDS	putative baseplate	537	Structural		
		tail tube initiator				
42	Phage baseplate hub subunit		702	Structural		
	# T4-like gp26 CDS					
43	hypothetical protein CDS	putative baseplate	177	Structural		
		hub assembly				
		catalyst				
44	hypothetical protein CDS		381	Hypothetical		
45	hypothetical protein CDS		1812	Hypothetical		
46	hypothetical protein CDS		273	Hypothetical		
47	Single stranded DNA-		1011	DNA		
	binding protein, phage-			replication		
	associated CDS					
48	hypothetical protein CDS		555	Hypothetical		
49	hypothetical protein CDS		312	Hypothetical		

50	hypothetical protein CDS		288	Hypothetical
51	hypothetical protein CDS		540	Hypothetical
52	hypothetical protein CDS	putative homing	654	DNA
		endonuclease		replication
53	Phage terminase, large subunit #T4-like phage Gp17 CDS		1734	Structural
54	T4-like phage baseplate hub + tail lysozyme CDS		2562	Structural
55	hypothetical protein CDS		126	Hypothetical
56	hypothetical protein CDS		285	Hypothetical
57	hypothetical protein CDS		507	Hypothetical
58	T4-like phage protein, T4 GC1630 CDS	putative homing endonuclease	459	DNA replication
59	probable ATP-dependent helicase CDS		1614	DNA replication
60	Phage endonuclease CDS	denV endonuclease V, N-glycosylase UV repair enzyme	318	DNA repair
61	hypothetical protein CDS	•	264	Hypothetical
62	hypothetical protein CDS		414	Hypothetical
63	Phage ribonuclease H (EC 3.1.26.4) #T4-like phage Rnh #T4 GC0870 CDS		909	DNA replication
64	hypothetical protein CDS		720	Hypothetical
65	hypothetical protein CDS		438	Hypothetical
66	hypothetical protein CDS	tail completion and sheath stabilizer protein	522	Structural
67	Single stranded DNA- binding protein, phage- associated #T4-like phage Gp32 CDS		486	DNA replication
68	hypothetical protein CDS	putative homing endonuclease	765	DNA replication
69	Phage head completion protein CDS		459	Structural

70	Phage tail sheath CDS		2517	Structural
71	hypothetical protein CDS	putative tail tube	627	Structural
		monomer		
72	Phage portal vertex of the		1575	Structural
	head #T4-like phage Gp20			
	CDS			
73	hypothetical protein CDS		153	Hypothetical
74	Phage prohead core protein CDS		666	Structural
75	MJ0042 family finger-like protein CDS		1131	Hypothetical
76	Phage major capsid protein		1332	Structural
70	of Caudovirales CDS		1002	Structurur
77	hypothetical protein CDS		183	Hypothetical
78	DNA helicase, phage-		1503	DNA
	associated CDS			replication
79	hypothetical protein CDS		324	Hypothetical
80	hypothetical protein CDS	putative terminase	504	DNA
		DNA packaging		associated
		enzyme small		
		subunit		
81	hypothetical protein CDS		186	Hypothetical
82	hypothetical protein CDS	putative base plate wedge subunit	387	Structural
83	gp6 baseplate wedge subunit CDS		1782	Structural
84	hypothetical protein CDS	baseplate wedge	3114	Structural
		subunit-like protein		
85	hypothetical protein CDS		1227	Hypothetical
86	Phage protein CDS		1545	Hypothetical
87	Phosphate starvation-		783	Other/Bacterial
	inducible protein PhoH,			
	predicted ATPase CDS			
88	hypothetical protein CDS		348	Hypothetical
89	RNA polymerase ECF-type		483	Transcription
	sigma factor CDS			
90	hypothetical protein CDS		294	Hypothetical

91	hypothetical protein CDS		345	Hypothetical
92	hypothetical protein CDS		150	Hypothetical
93	hypothetical protein CDS	putative baseplate	780	Structural
		tail tube cap		
94	hypothetical protein CDS	putative base plate	579	Structural
		wedge component		
95	hypothetical protein CDS		414	Hypothetical
96	Phage recombination protein		1164	DNA
	CDS			associated
97	hypothetical protein CDS	DNA	1434	DNA
		primase/helicase		replication
98	hypothetical protein CDS	putative holliday	624	DNA
		junction resolvase		associated
99	hypothetical protein CDS		435	Hypothetical
100	hypothetical protein CDS	5'-	621	DNA
		deoxynucleotidase		associated
101	hypothetical protein CDS	putative	786	DNA
		deoxynucleotide		associated
		monophosphate		
		kinase		
102	hypothetical protein CDS		363	Hypothetical
103	hypothetical protein CDS		465	Hypothetical
104	Deoxycytidylate 5-		744	DNA
	hydroxymethyltransferase			modification
	(EC 2.1.2.8) CDS			
105	hypothetical protein CDS		1017	Hypothetical
106	hypothetical protein CDS		642	Hypothetical
107	hypothetical protein CDS		594	Hypothetical
108	hypothetical protein CDS		423	Hypothetical
109	hypothetical protein CDS		378	Hypothetical
110	Phage DNA topoisomerase		1938	DNA
	large subunit (EC 5.99.1.3)			replication
	#T4-like gp60 #T4 GC1464			
	CDS			
111	hypothetical protein CDS		306	Hypothetical
112	hypothetical protein CDS		552	Hypothetical

113	Topoisomerase IV subunit A		1365	DNA	
	(EC 5.99.1) CDS			replication	
114	hypothetical protein CDS		120	Hypothetical	
115	hypothetical protein CDS		336	Hypothetical	
116	COG1896: Predicted		723	Lysis	
	hydrolases of HD				
	superfamily CDS				
117	hypothetical protein CDS		336	Hypothetical	
118	hypothetical protein CDS		360	Hypothetical	
119	hypothetical protein CDS	sigma factor for late	513	Transcription	
		transcription			
120	hypothetical protein CDS	recombination	951	DNA	
		endonuclease		associated	
		subunit			
121	Phage recombination-related		1647	DNA	
	endonuclease Gp46 CDS			associated	
122	hypothetical protein CDS	sliding clamp DNA	729	DNA	
		polymerase		replication	
100		accessory protein	0.40	DATA	
123	Replication factor C small	Sliding clamp	948	DNA	
101	subunit CDS	loader subunit	405	replication	
124	hypothetical protein CDS	putative clamp	405	DNA	
105		loader subunit	100	replication	
125	hypothetical protein CDS		177	Hypothetical	
126	hypothetical protein CDS		159	Hypothetical	
127	hypothetical protein CDS		267	Hypothetical	
128	hypothetical protein CDS		690	Hypothetical	
129	hypothetical protein CDS		258	Hypothetical	
130	hypothetical protein CDS		381	Hypothetical	
131	hypothetical protein CDS		210	Hypothetical	
132	hypothetical protein CDS		234	Hypothetical	
133	DNA polymerase (EC 2.7.7.7), phage-associated		2640	DNA	
	#T4-like phage gp43 #T4			replication	
	GC0178 CDS				
134	hypothetical protein CDS		768	Hypothetical	
135	hypothetical protein CDS		120	Hypothetical	
100	Try podiedcar protein CD3		120	Trypometical	

136	hypothetical protein CDS		303	Hypothetical
137	hypothetical protein CDS		546	Hypothetical
138	DNA ligase, phage-		1257	DNA
	associated CDS			replication
139	hypothetical protein CDS		336	Hypothetical
140	hypothetical protein CDS		213	Hypothetical
141	hypothetical protein CDS		189	Hypothetical
142	hypothetical protein CDS		201	Hypothetical
143	hypothetical protein CDS		594	Hypothetical
144	hypothetical protein CDS		165	Hypothetical
145	Phage protein CDS	predicted	984	Nucleotide
		alternative		metabolism
		thymidylate		
		synthase		
146	hypothetical protein CDS		282	Hypothetical
147	hypothetical protein CDS		165	Hypothetical
148	hypothetical protein CDS	putative GT1	1164	Nucleotide
		glycosyltransferase		metabolism
		protein		
149	hypothetical protein CDS		405	Hypothetical
150	FIG00451076: hypothetical		255	Hypothetical
	protein CDS			
151	hypothetical protein CDS	putative homing	714	DNA
		endonuclease		associated
152	hypothetical protein CDS	putative ParB-like	450	DNA
		nuclease domain		associated
		containing protein		
153	hypothetical protein CDS		474	Hypothetical
154	hypothetical protein CDS		216	Hypothetical
155	hypothetical protein CDS		303	Hypothetical
156	hypothetical protein CDS		303	Hypothetical
157	hypothetical protein CDS		267	Hypothetical
158	hypothetical protein CDS		183	Hypothetical
159	hypothetical protein CDS		246	Hypothetical
160	hypothetical protein CDS		501	Hypothetical
161	hypothetical protein CDS		156	Hypothetical
162	hypothetical protein CDS		357	Hypothetical

163	Glycine-rich cell wall structural protein 1.8		657	Other/Bacterial
	precursor CDS			
164	hypothetical protein CDS		480	Hypothetical
165	hypothetical protein CDS		489	Hypothetical
166	hypothetical protein CDS		279	Hypothetical
167	hypothetical protein CDS		555	Hypothetical
168	hypothetical protein CDS		135	Hypothetical
169	hypothetical protein CDS	DNA repair	489	DNA repair
		exonuclease		
170	hypothetical protein CDS		267	Hypothetical
171	hypothetical protein CDS		207	Hypothetical
172	hypothetical protein CDS		195	Hypothetical
173	hypothetical protein CDS		198	Hypothetical
174	hypothetical protein CDS		201	Hypothetical
175	hypothetical protein CDS		417	Hypothetical
176	hypothetical protein CDS		363	Hypothetical
177	hypothetical protein CDS		300	Hypothetical
178	hypothetical protein CDS		198	Hypothetical
179	hypothetical protein CDS		225	Hypothetical
180	hypothetical protein CDS	von Willebrand	702	Other/Bacterial
		factor type A		
		domain containing		
		protein		
181	hypothetical protein CDS		225	Hypothetical
182	hypothetical protein CDS		303	Hypothetical
183	hypothetical protein CDS		207	Hypothetical
184	hypothetical protein CDS		276	Hypothetical
185	Polymerase epsilon subunit		858	DNA
	CDS			associated
186	hypothetical protein CDS		285	Hypothetical
187	hypothetical protein CDS		291	Hypothetical
188	hypothetical protein CDS		264	Hypothetical
189	dCMP deaminase (EC		600	DNA
	3.5.4.12); Late competence			associated
	protein ComEB CDS			
190	hypothetical protein CDS		510	Hypothetical

191	hypothetical protein CDS		210	Hypothetical
192	hypothetical protein CDS		234	Hypothetical
193	hypothetical protein CDS		462	Hypothetical
194	Phage protein CDS	putative	825	DNA
174	Thage protein CD3	exonuclease	023	associated
195	hypothetical protein CDS	DNA primase	531	DNA
193	Try potitetical protein CD3	DIVA primase	331	replication
196	hypothetical protein CDS		282	Hypothetical
197	hypothetical protein CDS		363	Hypothetical
198	hypothetical protein CDS		372	Hypothetical
199	hypothetical protein CDS		231	Hypothetical
200	hypothetical protein CDS		234	Hypothetical
201	hypothetical protein CDS		261	Hypothetical
	<u> </u>		423	
202	hypothetical protein CDS			Hypothetical
203	hypothetical protein CDS		300	Hypothetical
204	hypothetical protein CDS		330	Hypothetical
205	hypothetical protein CDS		744	Hypothetical
206	hypothetical protein CDS		609	Hypothetical
207	hypothetical protein CDS		231	Hypothetical
208	hypothetical protein CDS		201	Hypothetical
209	hypothetical protein CDS		435	Hypothetical
210	hypothetical protein CDS		510	Hypothetical
211	hypothetical protein CDS		579	Hypothetical
212	hypothetical protein CDS		1347	Hypothetical
213	T4-like phage baseplate hub +		876	Structural
	tail lysozyme CDS			
214	hypothetical protein CDS		297	Hypothetical
215	Phage neck protein #Gp13		756	Structural
	CDS			
216	Gp14 neck protein CDS		843	Structural
217	hypothetical protein CDS		360	Hypothetical
218	Phage tail assembly CDS		882	Structural
219	hypothetical protein CDS	baseplate wedge	1461	Structural
220	Phage virulence-associated	VrlC protein	5088	Structural
	VriC protein CDS			
221	hypothetical protein CDS		207	Hypothetical
222	Phage tail fibers CDS		1791	Structural

223	FIG00920814:	hypothetical	1149	Hypothetical
	protein CDS			

Supplementary Table S2: Comparative analysis of Atu\_ph04 gene products with related phages.

gp #	Functional annotation	vB_RleM_ P10VF	phiM9	Cr30	syn9	syn30	syn33	T4	Atu_ph07	phiM12	Ccr Colossus	phiN3	KVP 40	Melville
	UDP-	3.00E-125	1.00E-128											
6	galactopyranose													
	mutase													
9	hypothetical	9.00E-22												
10	N-acetylmuramoyl- L-alanine amidase	4.00E-90	1.00E-87											
11	hypothetical	6.00E-12	5.00E-14											
12	hypothetical	1.00E-31	2.00E-38											
13	hypothetical		4.00E-27											
14	hypothetical	1.00E-26	1.00E-21											
15	hypothetical	9.00E-17								4.00E-11				
	Phosphohydrolase			7.00E-						5.00E-23	9.00E-24	6.00E-23		
17	(MutT/nudix family			16										
	protein)													
20	hypothetical										2.00E-11			
23	hypothetical	2.00E-23	1.00E-20											
	Ribonucleotide	0	0		3.00E-	2.00E-	2.00E-	9.00E-	0		5.00E-70		2.00	1.00E-16
24	reductase of class Ia				17	16	16	17					E-17	
24	(aerobic), alpha													
	subunit													
	Ribonucleotide	4.00E-156	1.00E-162						3.00E-104					
25	reductase of class Ia													
23	(aerobic), beta													
	subunit													

26	Phage-associated	3.00E-87	2.00E-108		4.00E-	1.00E-	8.00E-	2.00E-	1.00E-37	8.00E-37	7.00	9.00E-34
	DNA primase				42	41	34	37			E-22	
27	hypothetical	1.00E-32	1.00E-43									
28	hypothetical	6.00E-29	3.00E-36									
29	hypothetical	9.00E-10	1.00E-23									
30	hypothetical	3.00E-24	4.00E-21									
33	hypothetical	1.00E-17	1.00E-19									
36	hypothetical	1.00E-06										
	Phage DNA end	3.00E-102	3.00E-100	2.00E-				6.00E-	2.00E-25			3.00E-28
40	protector during			17				29				
	packaging											
	putative baseplate	7.00E-56	3.00E-67		3.00E-		6.00E-				2.00	
41	tail tube initiator				06		08				E-08	
	Phage baseplate	1.00E-80	3.00E-84								3.00	9.00E-07
42	hub subunit										E-05	
		3.00E-18	5.00E-13	3.00E-								
43	hypothetical			04								
44	hypothetical	8.00E-17	2.00E-19	01								
45	hypothetical	2.00E-122	1.00E-141									
		2.00E-122										
46	hypothetical		7.00E-07									
	Single stranded	6.00E-125	4.00E-105	1.00E-		3.00E-	7.00E-		3.00E-24	2.00E-24	5.00	
47	DNA-binding			25		26	28				E-16	
	protein											
48	hypothetical	7.00E-12	2.00E-16									
49	hypothetical	5.00E-20	7.00E-14									
50	hypothetical	5.00E-16	1.00E-14							 		

			1						1	I	1			I
51	hypothetical	4.00E-66	9.00E-70											
		5.00E-22	2.00E-36	6.00E-				2.00E-		2.00E-07		3.00E-07		
52	hypothetical			10				13						
	Phage terminase,	0	0	2.00E-	9.00E-	7.00E-	1.00E-	2.00E-	3.00E-33	5.00E-		8.00E-	2.00	2.00E-
53	large subunit			114	114	117	112	105		120		120	E-99	108
	T4-like phage	0	0	8.00E-				6.00E-		6.00E-18		2.00E-17	7.00	7.00E-16
54	baseplate hub + tail			16				14					E-20	
	lysozyme													
	putative homing	4.00E-79	2.00E-66							3.00E-72	6.00E-60	2.00E-71	2.00	7.00E-60
58	endonuclease												E-57	
	probable ATP-	0	0											
59	dependent helicase													
		1.00E-31	4.00E-37					2.00E-					2.00	
60	Phage endonuclease							18					E-07	
62	hypothetical	8.00E-36	2.00E-32						7.00E-20		1.00E-24			
	Phage ribonuclease	2.00E-135	8.00E-140	1.00E-						3.00E-32				
63	Н			28										
64	hypothetical	6.00E-53	3.00E-56											
65	hypothetical	9.00E-16	2.00E-27											
	tail completion and	3.00E-55	9.00E-55					2.00E-						7.00E-12
66	sheath stabilizer	0.002 00	7.002 00					08						7.002 12
00	protein													
	Single stranded	4.00E-52	5.00E-48			1.00E-	3.00E-	3.00E-		9.00E-15				1.00E-11
67	DNA-binding	T.00E-02	J.00E-40			1.0012-	3.00E-	08		7.00E-13				1.002-11
07	_					14	14	00						
	protein													
68	hypothetical		2.00E-23											

	1	ı	1	1		Т	1		1	ı	1		1	
69	Phage head	1.00E-76	2.00E-77	9.00E-	5.00E-	6.00E-	6.00E-	5.00E-	1.00E-25	4.00E-36			2.00	1.00E-41
	completion protein			08	36	35	37	34					E-40	
70	Phage tail sheath	0	0	6.00E-	2.00E-	1.00E-	4.00E-	3.00E-		4.00E-61		3.00E-61	3.00	2.00E-33
	_			47	46	43	42	31					E-34	
71	putative tail tube monomer	5.00E-87	2.00E-98		3.00E- 14	2.00E- 16	7.00E- 18							
72	Phage portal vertex	0	0	9.00E-	3.00E-	7.00E-	3.00E-	5.00E-	7.00E-19	3.00E-87		4.00E-87	4.00	3.00E-93
	of the head			98	109	113	76	97					E-86	
74	Phage prohead core	7.00E-93	7.00E-94	3.00E-	8.00E-	5.00E-	3.00E-	1.00E-		3.00E-38		3.00E-38	2.00	2.00E-16
71	protein			26	34	34	33	14					E-30	
75	MJ0042 family finger-like protein	2.00E-52	4.00E-55											
76	Phage major capsid	0	0	2.00E- 71	1.00E- 83	4.00E- 81	9.00E- 85	5.00E- 48	5.00E-31	1.00E-92		1.00E-92	2.00 E-55	3.00E-48
78	DNA helicase	0	0	2.00E- 78	1.00E- 68	3.00E-	7.00E- 65	2.00E-	3.00E-18	2.00E-67		4.00E-66	2.00 E-72	1.00E-71
80	putative terminase  DNA packaging  enzyme small  subunit	6.00E-48	2.00E-43											
82	putative base plate wedge subunit	5.00E-58	2.00E-57											
83	baseplate wedge subunit	0	0	2.00E- 54	5.00E- 46	2.00E- 46	1.00E- 43			1.00E-55		2.00E-56		
84	baseplate wedge subunit-like protein	0	0							5.00E-06		5.00E-06		
85	hypothetical		0.001											

					I		1	1	I		I	1		
	Phosphate starvation-inducible	2.00E-99	2.00E-111	1.00E- 23	1.00E- 21	2.00E- 21	1.00E- 22		2.00E-54		8.00E-29	1.00E-17	3.00 E-29	
87	protein PhoH,													
	predicted ATPase													
92	hypothetical	1.00E-05												
93	putative baseplate tail tube cap	5.00E-123	5.00E-135											
94	putative base plate wedge component	2.00E-60	4.00E-66											
95	hypothetical	2.00E-28	2.00E-27											
96	Phage recombination protein	0	0	7.00E- 55				2.00E- 71	5.00E-17	8.00E-65		5.00E-65	5.00 E-72	5.00E-71
97	DNA primase/helicase	0	0	6.00E-	4.00E- 83	5.00E- 84	1.00E- 84	2.00E- 56	1.00E-27	9.00E-76		1.00E-74	1.00 E-68	2.00E-56
98	putative holliday junction resolvase	3.00E-63	8.00E-51	1.00E- 13										
100	hypothetical	1.00E-70	1.00E-59											
101	putative deoxynucleotide monophosphate kinase	6.00E-58	4.00E-66											
103	hypothetical	4.00E-71	3.00E-65											
104	Deoxycytidylate 5- hydroxymethyltran sferase	9.00E-79	2.00E-85											
105	hypothetical	5.00E-89	9.00E-91											

		1	I			1			1	1	1		1	
106	hypothetical	3.00E-10	7.00E-20											
107	hypothetical			3.00E-			8.00E-							
	71			09			16							
109	hypothetical	1.00E-28												
	Phage DNA	0	0					5.00E-	3.00E-146				2.00	5.00E-53
110	topoisomerase large subunit							26					E-49	
113	Topoisomerase IV	0	0					8.00E-	1.00E-98				2.00	3.00E-31
	subunit A							33					E-37	
119	sigma factor for late transcription	1.00E-47	2.00E-51											
	recombination	1.00E-67	4.00E-70											
120	endonuclease													
	subunit													
	Phage	6.00E-164	2.00E-173	9.00E-	7.00E-	1.00E-	5.00E-	6.00E-		4.00E-59		8.00E-59	5.00	1.00E-59
	recombination-			56	59	59	62	65					E-28	
121	related													
	endonuclease													
	sliding clamp DNA	6.00E-58	8.00E-70											
122	polymerase													
	accessory protein													
	Replication factor C	5.00E-128	4.00E-117					7.00E-	2.00E-31				7.00	6.00E-04
123	small subunit							05					E-51	
	putative clamp	4.00E-50	4.00E-48	3.00E-	5.00E-	3.00E-								
124	loader subunit			09	05	05								
129	hypothetical	2.00E-36	2.00E-30		7-									
131	hypothetical	2.002.00	2.00E-05											
131	пуротенсат	1	2.00E-03		1	<u> </u>	1	1	1	<u> </u>	<u> </u>	1		

	DNA polymerase	0	0	3.00E-	2.00E-	6.00E-	1.00E-	2.00E-	8.00E-23	8.00E-		9.00E-	6.00	2.00E-80
133	(EC 2.7.7.7), phage-			89	109	103	105	81		104		104	E-74	
	associated													
134	hypothetical	2.00E-90	5.00E-102											
	DNA ligase, phage-	8.00E-145	1.00E-153										6.00	
138	associated												E-26	
139	hypothetical	2.00E-21	3.00E-14											
		1.00E-43	7.00E-38										6.00	
143	hypothetical												E-13	
	predicted										3.00E-39			
1.45	alternative													
145	thymidylate													
	synthase													
	putative GT1	2.00E-127	1.00E-118											
148	glycosyltransferase													
	protein													
	FIG00451076:	7.00E-22	8.00E-20	1.00E-										
150	hypothetical protein			22										
	putative homing		4.00E-41											
151	endonuclease													
	putative ParB-like	1.00E-22	5.00E-19											
152	nuclease domain													
	containing protein													
153	hypothetical	3.00E-61	2.00E-59											
157	hypothetical	2.00E-08												
159	hypothetical	4.00E-12	3.00E-13						3.00E-23					
160	hypothetical	8.00E-07												
				1										

		1	1						1		1		1	1
164	hypothetical	7.00E-13	2.00E-23											
165	hypothetical	3.00E-30	4.00E-37											
166	hypothetical		0.001						2.00E-04					
167	hypothetical	1.00E-09												
168	hypothetical	4.00E-04												
169	DNA repair exonuclease	1.00E-25	2.00E-33						3.00E-16	2.00E-31		1.00E-31		
180	von Willebrand factor type A domain containing protein	1.00E-81												
182	hypothetical								6.00E-16	7.00E-27			4.00 E-04	
185	Polymerase epsilon subunit	7.00E-112	3.00E-112						7.00E-28					
188	hypothetical	5.00E-14												
189	dCMP deaminase (EC 3.5.4.12); Late competence protein ComEB	1.00E-49	1.00E-49					9.00E- 10					3.00 E-14	4.00E-11
190	hypothetical	2.00E-09	1.00E-10											
192	hypothetical	0.001	7.00E-04											
194	putative exonuclease	7.00E-112	1.00E-100	1.00E- 26	6.00E- 22	5.00E- 21	1.00E- 21		2.00E-14			3.00E-22		
201	hypothetical	2.00E-07	7.00E-07											
202	hypothetical	3.00E-27												
206	hypothetical	6.00E-14							2.00E-12					

207	hypothetical	2.00E-06												
209	hypothetical	2.00E-11	3.00E-20											
		0	0				2.00E-							
212	hypothetical						06							
	T4-like phage	3.00E-147	3.00E-141	2.00E-	8.00E-	3.00E-	4.00E-	3.00E-		4.00E-12		4.00E-12		9.00E-16
213	baseplate hub + tail			18	13	13	14	15						
	lysozyme													
		4.00E-106	3.00E-106	3.00E-	4.00E-	7.00E-		7.00E-		5.00E-24		2.00E-24	5.00	4.00E-06
215	Phage neck protein			25	24	20		09					E-04	
		3.00E-122	7.00E-109	1.00E-	1.00E-					2.00E-15		3.00E-15		
216	Gp14 neck protein			14	08									
217	hypothetical	8.00E-37	6.00E-31											
		1.00E-82	3.00E-106	7.00E-	9.00E-	6.00E-	2.00E-			2.00E-18			5.00	
218	Phage tail assembly	1.00L-02	3.00L-100	24	24	19	26			2.00L-10			E-14	
		4.005.445	2.005.450		24	19	20						E-14	
219	baseplate wedge	4.00E-147	2.00E-170	7.00E-										
				09										
	Phage virulence-	0	0	3.00E-	6.00E-	4.00E-	2.00E-			9.00E-69		4.00E-67		
220	associated VriC			28	41	43	42							
	protein													
221	have a that it as I		7.00E-17	9.00E-										
221	hypothetical			05										
222	Phage tail fibers	8.00E-175	2.00E-167											2.00E-06
	FIG00920814:	5.00E-66	7.00E-76											
223	hypothetical protein													
	TOTAL	115	109	32	23	23	24	25	22	30	7	25	29	26

**Supplementary Table S3**: T4 core proteins found in Atu\_ph04.

T4 protein	T4 protein function	Match in Atu_ph04*	Identity (%)	E- value	Query cover (%)	Atu_ph04 protein name	Atu_ph04 gp #
P	hage morphogenesis						
gp4	head completion protein	yes	39	1e-35	96	Head completion protein	69
	baseplate lysozyme hub		45	2e-16	17	T4-like phage baseplate hub + tail lysozyme	213
gp5	component	yes	30	1e-15	32	T4-like phage baseplate hub + tail lysozyme	54
gp13	head completion protein	unresolved	21	6e-08	99	Neck protein	215
gp15	tail completion protein	yes	25	1e-11	74	Phage tail assembly	218
gp17	subunit of the terminase for DNA packaging	yes	37	7e-107	81	Terminase large subunit	53
gp18	tail tube subunit	yes	28	9e-32	91	Tail sheath	70
gp20	head portal vertex protein	yes	36	2e-98	85	Portal vertex of the head	72
gp21	prohead core protein and protease	yes	33	6e-16	66	Prohead core protein	74
gp22	prohead core protein	no					
gp23	precursor of major head protein	yes	34	4e-17	96	Major capsid protein	76
gp25	base plate wedge subunit	no					
gp34	proximal tail fiber protein subunit	no					
gp36	small distal tail fiber protein subunit	no					
DNA	A replication, repair, and recombination						

gp43	DNA polymerase	yes	28	7e-83	97	DNA polymerase	133
gp44	sliding clamp loader complex tetramer	yes	32	6e-47	99	Replication factor C small subunit	123
gp41	helicase-primer complex hexamer	no					
gp46	subunit of a recombination nuclease complex	yes	29	2e-66	99	Phage recombination-related endonuclease	121
gp47	subunit of a recombination nuclease complex	no					
UvsW	recombination DNA-RNA helicase, DNA-dependent ATPase	yes	33	8e-71	82	DNA helicase	78
A	Auxillary metabolism						
nrdA	subunit of an aerobic ribonucleotide reductase complex	yes	23	4e-18	58	Ribonucleotide reductase of 1a (aerobic), alpha subunit	24
nrdB	subunit of an aerobic ribonucleotide reductase complex	no					
	Gene expression						
gp55	sigma factor for late transcription	no					

<sup>\*</sup>Atu\_ph04 matches with E-values above 1E-10 are considered "yes" matches and those between 1E-10 and 1E-03 are "unresolved." Matches with E-values lower than 1E-03 were not considered significant.

**Supplementary Table S4**: Atu\_ph08 genes organized by predicted function.

CDS	RAST annotated	Updated assigned	Lengt	
#	function	function	h (bp)	Category
1	Phage protein CDS	XRE transcriptional regulator	300	Transcription
2	hypothetical protein CDS		297	Hypothetical
3	Phage protein CDS		417	Hypothetical
4	FIG00451076: hypothetical protein CDS	DUF2312 domain- containing protein	396	Hypothetical
5	hypothetical protein CDS	GcrA cell cycle regulator	588	Transcription
6	hypothetical protein CDS		495	Hypothetical
7	C-5 cytosine-specific DNA methylase CDS		1866	DNA modification
8	hypothetical protein CDS		351	Hypothetical
9	hypothetical protein CDS	putative PRK12775- containing protein	246	Posttranslationa l modification
10	hypothetical protein CDS	NERD domain- containing protein	741	DNA processing
11	Phage protein CDS		627	Hypothetical
12	Phage protein CDS		804	Hypothetical
13	probable terminase large subunit CDS		1557	Structural
14	Phage protein CDS		429	Hypothetical
15	Phage portal protein CDS		2232	Structural
16	Phage protein CDS		1011	Hypothetical
17	hypothetical protein CDS		195	Hypothetical
18	hypothetical protein CDS		294	Hypothetical
	hypothetical protein		_	

20	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein) CDS		786	Other/Bacterial
21	helicase, Snf2 family CDS	Adenine-specific DNA methylase, N12 class; DarB-like protein	14634	DNA modification
22	Phage protein CDS		1311	Hypothetical
23	Phage protein CDS	tail fiber domain- containing protein	1161	Structural
24	Phage protein CDS	N-acetyltransferase	450	DNA modification
25	hypothetical protein CDS		246	Hypothetical
26	Phage protein CDS	putative virion structural protein	1740	Structural
27	hypothetical protein CDS	DUF4376 domain- containing protein	603	Hypothetical
28	Phage tail fibers CDS	-	1074	Structural
29	Phage protein CDS		279	Hypothetical
30	hypothetical protein CDS		312	Hypothetical
31	Phage protein CDS	major capsid protein	417	Structural
32	Phage protein CDS	DUF4238 domain- containing protein	627	Hypothetical
33	Phage protein CDS		702	Hypothetical
34	hypothetical protein CDS		363	Hypothetical
35	Phage protein CDS		462	Hypothetical
36	Phage protein CDS	N4-gp56 family major capsid protein	1131	Structural
37	protein of unknown function DUF847 CDS	secretion activator protein; lysozyme-like protein	753	Lysis
38	hypothetical protein CDS	Holin of 3TMs, for gene- transfer release	525	Lysis
39	Phage protein CDS		333	Hypothetical

40	hypothetical protein CDS	AlpA family phage regulatory protein	231	Transcription
41	Integrase CDS		1299	DNA recombination
42	hypothetical protein CDS	Arc family DNA-binding protein	192	DNA-associated
43	hypothetical protein CDS		402	Hypothetical
44	hypothetical protein CDS		498	Hypothetical
45	hypothetical protein CDS		189	Hypothetical
46	hypothetical protein CDS	DUF551 domain- containing protein	186	Hypothetical
47	hypothetical protein CDS		324	Hypothetical
48	hypothetical protein CDS		219	Hypothetical
49	hypothetical protein CDS	3'-5' exoribonuclease	705	DNA-associated
50	hypothetical protein CDS		264	Hypothetical
51	hypothetical protein CDS		645	Hypothetical
52	Phage protein CDS		330	Hypothetical
53	Phage DNA modification methyltransferase CDS		753	DNA modification
54	hypothetical protein CDS		219	Hypothetical
55	Bacteriophage protein gp37 CDS	DUF5131 family protein	921	Hypothetical
56	COG1896: Predicted hydrolases of HD superfamily CDS	metal-dependent phosphohydrolase	606	DNA modification
57	Phage protein CDS		687	Hypothetical

58	hypothetical protein CDS		426	Hypothetical
59	Phage-related protein CDS	morphogenetic protein	708	Structural
60	Phage protein CDS		399	Hypothetical
61	hypothetical protein CDS		231	Hypothetical
62	hypothetical protein CDS		525	Hypothetical
63	hypothetical protein CDS		159	Hypothetical
64	Phage protein CDS	C4-dicarboxylate ABC transporter substrate-binding protein	882	Other/Bacterial
65	Transcriptional regulator CDS	C2-like repressor protein	417	Transcription
66	hypothetical protein CDS		219	Hypothetical
67	hypothetical protein CDS	class I SAM-dependent methyltransferase	582	DNA modification
68	hypothetical protein CDS		288	Hypothetical
69	Phage protein CDS		309	Hypothetical
70	hypothetical protein CDS		123	Hypothetical
71	Predicted periplasmic protein CDS	Clp protease	651	Posttranslationa l modification
72	hypothetical protein CDS	XRE family transcriptional regulator	306	Transcription
73	hypothetical protein CDS		240	Hypothetical
74	hypothetical protein CDS		243	Hypothetical
75	hypothetical protein CDS		207	Hypothetical

Supplementary Table S5: Comparative analysis of Atu\_ph08 gene products with related phages.

Sup	<b>Supplementary Table 55</b> : Comparative analysis of Atu_pho8 gene products with related phages.										
gp #	Functional annotation	PBC5	POI1126	Soprano Gao	Pavtok	DC1	Bcep22	PS-1	phiKMV	T7	Atu_ph03
1	XRE transcriptional regulator	7.00E-44									
3	Hypothetical	4.00E-26	1.00E-10								
4	Hypothetical	1.00E-38	5.00E-20								
10	NERD domain-containing protein		1.00E-32								
11	Hypothetical	8.00E-66									
12	Hypothetical	1.00E-77									
13	probable terminase large subunit	0	0	1.00E-143	5.00E-145	2.00E-127	1.00E-127	2.00E-100			
14	Hypothetical	6.00E-72	2.00E-40	3.00E-17	1.00E-17		9.00E-15				
15	Phage portal protein	0	0	0	0	0	0				
16	Hypothetical	7.00E-79	6.00E-07	9.00E-11	2.00E-18	4.00E-18	2.00E-19				
17	Hypothetical					6.00E-05					
21	Adenine-specific DNA methylase, N12 class; helicase, Snf2 family	0	0	0	0	0	0				5.00E-48
22	Hypothetical	1.00E-106	2.00E-45	5.00E-08	2.00E-20						
23	tail fiber domain-containing protein	0	4.00E-160	1.00E-110	2.00E-114	1.00E-75	3.00E-73				
24	N-acetyltransferase	3.00E-84	2.00E-43	9.00E-36	1.00E-35	3.00E-41	1.00E-39				
25	Hypothetical		2.00E-13			5.00E-08	2.00E-08				
26	putative virion structural protein	0	0	2.00E-140	1.00E-148	0.00E+00	1.00E-179				
28	Phage tail fibers	2.00E-31	3.00E-28	9.00E-23	4.00E-17	1.00E-26	2.00E-26				
29	Hypothetical	7.00E-38	1.00E-31			2.00E-18	3.00E-18				
31	major capsid protein	1.00E-46	5.00E-49			2.00E-36	6.00E-38				
32	Hypothetical	4.00E-76	6.00E-28	7.00E-30	1.00E-33	8.00E-45	2.00E-37				
33	Hypothetical	6.00E-105	2.00E-54	4.00E-45	2.00E-38	8.00E-29	9.00E-23				
34	Hypothetical		3.00E-12								

35	Hypothetical		2.00E-31	4.00E-12		2.00E-24	5.00E-34				
36	N4-gp56 family major capsid protein	0	0	2.00E-155	0	3.00E-179	0				
37	secretion activator protein;		7.00E-61								
38	Holin of 3TMs, for gene-transfer release		8.00E-18								
39	Hypothetical	7.00E-26									
41	Integrase	3.00E-179									
42	Arc family DNA-binding protein		1.00E-22								
52	Hypothetical	5.00E-31									
55	Hypothetical	2.00E-89	7.00E-34								
59	morphogenetic protein	8.00E-29	1.00E-27								
60	Hypothetical	2.00E-32									
64	C4-dicarboxylate ABC transporter substrate-binding protein	2.00E-165									
65	Transcriptional regulator	7.00E-39									
67	class I SAM-dependent methyltransferase	7.00E-91									
69	Hypothetical	1.00E-21									
72	XRE family transcriptional regulator		8.00E-14								
	TOTAL	30	27	14	13	16	16	1	0	0	1

**Supplementary Table S6**: Atu\_ph08 gene products present in other *Agrobacterium* 

phages.

Atu_ph08 gene product	Atu_ph08 protein function	Phage Match	Identity (%)	E- value	Query cover (%)	Protein name	Phage gp #
gp4	Hypothetical	7-7-1	81	9e-40	59	Hypothetical protein	15
		Atu_ph03	36	4e-48	6	Cell wall hydrolyse	35
gp21	Helicase	Atu_ph02	36	4e-48	6	Cell wall hydrolyse	32
		Atu_ph07	31	3e-18	3	Mega protein	42
gp37	protein of unknown function DUF847	7-7-1	28	6e-28	91	Putative membrane protein	10
gp56	Predicted hydrolases of HD superfamily	Atu_ph04	29	3e-20	92	putative HD superfamily hydrolase	116
gp65	Transcriptional regulator	7-7-1	47	2e-17	47	Putative transcriptional regulator	68
gp67	Hypothetical protein	Atu_ph07	33	1e-20	80	Hypothetical protein	599