

Table S1. Putative *Agrobacterium pho* boxes used to generate a weight matrix in this study.

Gene	Distance	Score	Pho box motif	Description
Atu0421	-151	0.37	TTGACATTTCCCATTTCAT	pstC, ABC transporter, membrane spanning protein
Atu0420	-117	0.54	TTGTCACAAATCTTTCGT	pstS, ABC transporter, substrate binding protein [phosphate]
	-106	0.36	CTTTCGTCAAAGTGACAT	
Atu0181	-67	0.47	ATGTCACACGCTTGTCAT	phnG, hypothetical protein
Atu0174	-48	0.36	CTGACACTCCCGCTTCAC	phnC, ABC transporter, nucleotide binding ATPase [phosphonate]
	-59	0.37	TCTTCATCAAACCTGACAC	
	-70	0.36	ATGTAATATTTTCTTCAT	
Atu6108	-81	0.37	CTGTCAGAACACCTGAT	phnA, alkylphosphonate uptake protein
Atu0419	-58	0.36	ATGATGAATCTCTGTCAT	phoR, two component sensor kinase
	-47	0.38	CTGTCATGAAGCTGGCCT	
Atu5058	-75	0.47	CTGTCATCAAAACGTCGC	ugpB, ABC transporter, substrate binding protein
	-29	0.37	TTGCTAGACAGCCGTCAT	
Atu0305	-76	0.44	GTGTAATAAATCTGACAC	ugpA, ABC transporter, substrate binding protein
	-87	0.47	CTGACACGGAACCTGCAA	
	-98	0.63	CTGTCAAAGAGGCGTCAT	
Atu1263	-51	0.59	ATGTCATGCCACTGTCAC	Conserved hypothetical protein
Atu2119	-44	0.58	CTGTCATCAAACCTGTAGC	Hypothetical protein (btaA-like)
Atu1144	-84	0.46	CTGTCACAGTTCCGTCGT	ppk polyphosphate kinase
	-73	0.39	CCGTCGTCAAACCTGTTAT	
Atu2147	-63	0.39	TTGCAATCCAACCGTCAC	ABC transporter, substrate binding protein
Atu0202	-66	0.37	CTGGCATCCATCCGATAT	ABC transporter, substrate binding protein (iron)
Atu2014	-46	0.54	CTGTCACATACATGTTAT	afuA2, ABC transporter, substrate binding
Atu2329	-161	0.51	CGGTCACACGCCTGTCAT	Conserved hypothetical protein
Atu1649	-64	0.51	CTGTCATGTTGCTGAAAC	Conserved hypothetical protein
Atu4642	-133	0.37	TAGTCATCTTCATGACAG	katA, bifunctional catalase/peroxidase HPI
Atu6138	-77	0.43	TTGCAACAAAACCTGTCAC	accA, ABC transporter, substrate binding protein
	-66	0.76	CTGTCACCAAACCTTTCAT	

*Distance : distance from the start codon

Table S2. Weight matrix used for the *pho* box analysis in this study.

A	4	1	0	4	4	24	2	12	11	16	11	3	1	0	6	2	22	1
C	15	2	0	3	21	0	9	9	7	5	6	19	9	1	0	21	1	9
G	1	2	25	1	0	3	2	4	3	2	4	3	0	21	1	1	4	1
T	7	23	2	19	2	0	14	2	6	4	6	2	17	5	20	3	0	16

Table S3. Genes associated with putative *pho* box sequences in *Agrobacterium tumefaciens* strain C58

gene						pho -box					
locus tag ^a	gene	5'-end	3'-end	product	replicon	strand ^b	start ^c	end ^c	putative <i>pho</i> box sequence ^d	score ^e	ln(P) ^f
Atu0052	<i>hrpB</i>	56078	53592	helicase	chromosome-circular	D	-277	-260	TCGTCAAAAACTGACAT	12.33	-14.87
Atu0058		62235	62492	hypothetical protein	chromosome-circular	R	-157	-140	CTGTCAATATTCTACAC	8.76	-10.96
Atu0110	<i>polA</i>	113127	116222	DNA polymerase I	chromosome-circular	R	-111	-94	TTTTCACAAAGCCCTCGT	8	-10.27
Atu0111		116299	117018	hypothetical protein	chromosome-circular	D	-58	-41	ATGTCATTGCTTTGTCTG	8.29	-10.53
Atu0123	tRNA-Ser	128502	128410	tRNA-Ser	chromosome-circular	D	-104	-87	ATTTCAAAAACTGTCAG	10.73	-12.97
Atu0124		128715	129041	hypothetical protein	chromosome-circular	R	-126	-109	ATTTCAAAAACTGTCAG	10.73	-12.97
Atu0174	<i>phnC</i>	179342	178482	ABC transporter, nucleotide binding/ATPase protein [phosphonate]	chromosome-circular	D	-76	-59	TCTTCATCAAAGTACAC	10.52	-12.75
Atu0174	<i>phnC</i>	179342	178482	ABC transporter, nucleotide binding/ATPase protein [phosphonate]	chromosome-circular	D	-87	-70	ATGTAATATTTCTTCAT	10.02	-12.21
Atu0182		185020	185757	transcriptional regulator, GntR family	chromosome-circular	R	-16	1	ATGTCACACGCTTGTCTG	10.79	-13.04
Atu0183	<i>dapB</i>	186579	185767	dihydrodipicolinate reductase	chromosome-circular	R	-34	-17	TTTTCACTCACTTTTCAT	8.93	-11.13
Atu0201	<i>rirA</i>	205949	205479	iron-responsive transcriptional regulator	chromosome-circular	R	-93	-76	CTGGCATCCATCCGATAT	9.55	-11.74
Atu0202		206108	207172	ABC transporter, substrate binding protein [iron]	chromosome-circular	D	-83	-66	CTGGCATCCATCCGATAT	9.55	-11.74
Atu0210		215252	215596	hypothetical protein	chromosome-circular	D	-206	-189	TTGCAATAAACTGGCAC	10.6	-12.83
Atu0234		235199	234324	conserved hypothetical protein, membrane protein	chromosome-circular	R	-85	-68	ATATCAATAAACTGTTAT	8.05	-10.32
Atu0235		235316	236704	transcriptional regulator, GntR family	chromosome-circular	D	-49	-32	ATATCAATAAACTGTTAT	8.05	-10.32
Atu0237		237647	237189	hypothetical protein	chromosome-circular	D	-71	-54	TAGTCACGCAACTTATAT	8.35	-10.58
Atu0238		237802	238695	oxidoreductase	chromosome-circular	R	-101	-84	TAGTCACGCAACTTATAT	8.35	-10.58
Atu0237		237647	237189	hypothetical protein	chromosome-circular	D	-112	-95	TTTTCATGAACTTATAT	10.94	-13.2
Atu0238		237802	238695	oxidoreductase	chromosome-circular	R	-60	-43	TTTTCATGAACTTATAT	10.94	-13.2
Atu0288		283478	282201	hypothetical protein	chromosome-circular	D	-79	-62	TTGACACAAGTTTGTGAT	8.24	-10.48
Atu0300		293562	292969	methyltransferase	chromosome-circular	R	-42	-25	TTGTCAAAAATTGTTAC	12.02	-14.47
Atu0305	<i>ugpA</i>	297124	298422	ABC transporter, substrate binding protein [sn-glycerol 3-phosphate]	chromosome-circular	D	-93	-76	GTGTAATAAATCTGACAC	12.03	-14.49
Atu0305	<i>ugpA</i>	297124	298422	ABC transporter, substrate binding protein [sn-glycerol 3-phosphate]	chromosome-circular	D	-71	-54	CTGTCAAAGAGCGTCAT	10.8	-13.05
Atu0305	<i>ugpA</i>	297124	298422	ABC transporter, substrate binding protein [sn-glycerol 3-phosphate]	chromosome-circular	D	-82	-65	CTGACACGGAAGTGTCAA	10.42	-12.63
Atu0344		335816	336697	hypothetical protein	chromosome-circular	D	-68	-51	TTGTCATATTCTGTGCG	10.61	-12.84
Atu0344		335816	336697	hypothetical protein	chromosome-circular	R	-48	-31	CTGTCATAAATCACTAAT	10.53	-12.76
Atu0350		346223	345888	hypothetical protein	chromosome-circular	D	-74	-57	CTGACATGATAATTACAT	10.55	-12.78
Atu0351		346382	346945	hypothetical protein	chromosome-circular	R	-102	-85	CTGACATGATAATTACAT	10.55	-12.78
Atu0391		384107	385138	ABC transporter, nucleotide binding/ATPase protein	chromosome-circular	D	-192	-175	GTGTCATAGAAGTTTCCC	9.14	-11.33
Atu0396		389380	390876	coenzyme A transferase	chromosome-circular	R	-33	-16	CTGTCATCAGATGGCAC	9.38	-11.56
Atu0418		414581	413700	hypothetical protein	chromosome-circular	R	-185	-168	CTGTCATGAAGCTGGCCT	9.24	-11.43
Atu0419	<i>phoR</i>	414813	416081	two component sensor kinase	chromosome-circular	D	-64	-47	CTGTCATGAAGCTGGCCT	9.24	-11.43
Atu0420		416277	417311	ABC transporter, substrate binding protein [phosphate]	chromosome-circular	D	-134	-117	TTGTCACAAATCTTTCGT	13.63	-16.63
Atu0420		416277	417311	ABC transporter, substrate binding protein [phosphate]	chromosome-circular	D	-123	-106	CTTTCGTCAAAGTACAT	10.39	-12.6
Atu0421	<i>pstC</i>	417570	419084	ABC transporter, membrane spanning protein	chromosome-circular	D	-168	-151	TTGACATTTCCCATTCAT	8.1	-10.36
Atu0438	<i>intD</i>	434858	433830	phage-related integrase	chromosome-circular	R	-294	-277	CTGAAATCAGGCCGACAT	9.11	-11.3
Atu0597		582974	581613	hypothetical protein	chromosome-circular	D	-87	-70	TTGTCATGCGGCTGTGAT	9.3	-11.48
Atu0602	<i>glnA</i>	590152	588758	glutamine synthetase	chromosome-circular	D	-97	-80	TTGTCAAACTACGGTTAT	8.1	-10.36
Atu0603		590321	591505	hypothetical protein	chromosome-circular	R	-89	-72	TTGTCAAACTACGGTTAT	8.1	-10.36
Atu0607	<i>aceA</i>	594585	593281	isocitrate lyase	chromosome-circular	D	-204	-187	CTGTTACAAACTCGTCAG	9.06	-11.25
Atu0608		594821	596236	transcriptional regulator	chromosome-circular	R	-49	-32	CTGTTACAAACTCGTCAG	9.06	-11.25

Atu0607	<i>aceA</i>	594585	593281	isocitrate lyase	chromosome-circular	D	-145	-128	CTGTCACGCACCCTACAG	8.22	-10.47
Atu0608		594821	596236	transcriptional regulator	chromosome-circular	R	-108	-91		8.22	-10.47
Atu0668		665046	664387	hypothetical protein	chromosome-circular	D	-65	-48	CTGTCATTCAACTGTTAT	14.41	-17.83
Atu0683	<i>groES</i>	678332	678036	co-chaperonin GroES	chromosome-circular	R	-146	-129		8.3	-10.54
Atu0684		678585	679550	hypothetical protein	chromosome-circular	D	-124	-107	CTGCCGGAAAAATTTCCAC	8.3	-10.54
Atu0731		730944	729949	divalent cation transporter	chromosome-circular	D	-111	-94		16.23	-21.15
Atu0732	<i>mmgC</i>	731154	732938	acyl-CoA dehydrogenase	chromosome-circular	R	-116	-99	TTGTTATAAAACTGTCAT	16.23	-21.15
Atu0754	<i>aroC</i>	752724	751627	chorismate synthase	chromosome-circular	D	-234	-217		8.03	-10.29
Atu0755		753120	753422	hypothetical protein	chromosome-circular	R	-179	-162	CTTTTACAATTCGTCAC	8.03	-10.29
Atu0802		801242	800271	hypothetical protein	chromosome-circular	D	-203	-186		9.59	-11.77
Atu0803	<i>ppdK</i>	801469	804195	pyruvate phosphate dikinase	chromosome-circular	R	-41	-24	TTGTCATTTTCTATCAT	9.59	-11.77
Atu0826		825843	824032	hypothetical protein	chromosome-circular	D	-137	-120	CCGTTACAAAACCTTCAT	11.01	-13.29
Atu0837		836752	836237	transcriptional regulator, MarR family	chromosome-circular	R	-74	-57		8.33	-10.57
Atu0838		836900	838423	MFS permease	chromosome-circular	D	-91	-74	ATGTCAAAAACTTGCCAT	8.33	-10.57
Atu0837		836752	836237	transcriptional regulator, MarR family	chromosome-circular	D	-91	-74		9.82	-12.01
Atu0838		836900	838423	MFS permease	chromosome-circular	R	-74	-57	TTGGCATATATATGTCAA	9.82	-12.01
Atu0851		852876	852454	hypothetical protein	chromosome-circular	D	-64	-47	ATGTCATCCGGCCGTGCGC	8.3	-10.54
Atu0878		875145	874405	hypothetical protein	chromosome-circular	R	-41	-24		8.52	-10.74
Atu0879	<i>rhtB</i>	875271	875915	RhtB family transporter	chromosome-circular	D	-102	-85	CTGACACAACGTTGTCAG	8.52	-10.74
Atu0916	<i>ros</i>	905207	905635	transcriptional regulator	chromosome-circular	R	-106	-89	TTGAAACCAACGTGAAAT	8.06	-10.32
Atu0921		908753	910285	two component sensor kinase	chromosome-circular	D	-180	-163	CCGTCGCTTACCGTCAT	8.2	-10.45
Atu0924		913336	913530	hypothetical protein	chromosome-circular	R	-86	-69	ATGTCATCACCATCACAT	9.01	-11.2
Atu0988		984418	982991	molecular chaperone, Hsp70 family	chromosome-circular	R	-213	-196		8.76	-10.97
Atu0989		984701	985678	hypothetical protein	chromosome-circular	D	-87	-70	GTGAAATAAATTTTTAT	8.76	-10.97
Atu0991		986670	987590	cation efflux system component	chromosome-circular	D	-16	1	AGGTCAAATACACGTCAT	8.42	-10.65
Atu1021		1013849	1014946	outer membrane protein	chromosome-circular	D	-135	-118	CTGCTTCCCTTTGTGCAT	8.43	-10.66
Atu1084	<i>dnaC</i>	1076077	1074581	replicative DNA helicase	chromosome-circular	D	-249	-232		9.21	-11.4
Atu1085	<i>slyA</i>	1076390	1076845	transcriptional regulator, MarR family	chromosome-circular	R	-81	-64	TTTTCAAGTTTCTTTCAT	9.21	-11.4
Atu1105		1094532	1093585	hypothetical protein	chromosome-circular	D	-178	-161	CTTTCAACAACCGACAC	10.7	-12.95
Atu1144	<i>ppk</i>	1132881	1135079	polyphosphate kinase	chromosome-circular	D	-90	-73	CCGTCGTCAAAGTGTAT	11.16	-13.46
Atu1144	<i>ppk</i>	1132881	1135079	polyphosphate kinase	chromosome-circular	D	-101	-84	CTGTCACAGTCCGTCGT	10.98	-13.25
Atu1148		1139873	1138515	hypothetical protein	chromosome-circular	D	-97	-80	ATTTTCATCAAAGCTTCAA	8.45	-10.68
Atu1210	<i>cpdB</i>	1205624	1203636	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase bifunctional periplasi	chromosome-circular	D	-96	-79	CTGTCACGGCTTGTGCAT	9.44	-11.62
Atu1211		1205775	1206200	hypothetical protein	chromosome-circular	R	-72	-55		9.44	-11.62
Atu1210	<i>cpdB</i>	1205624	1203636	2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase bifunctional periplasi	chromosome-circular	R	-44	-27	CTGTCAGGAAAACGACAG	8.25	-10.49
Atu1211		1205775	1206200	hypothetical protein	chromosome-circular	D	-124	-107		8.25	-10.49
Atu1221		1214752	1215195	hypothetical protein	chromosome-circular	D	-54	-37	TTGTCGCTAAATTGTCAC	10.43	-12.65
Atu1226	<i>exoD</i>	1218204	1217560	exoD protein	chromosome-circular	R	-206	-189	ATGTAACGAAGCTTACAT	10.51	-12.74
Atu1254		1242255	1241941	transcriptional regulator, ArsR family	chromosome-circular	R	-55	-38		10.78	-13.02
Atu1255		1242358	1243116	oxidoreductase	chromosome-circular	D	-65	-48	TTTTAATAAAAACCGAAAT	10.78	-13.02
Atu1263		1252117	1254315	hypothetical protein	chromosome-circular	D	-68	-51	ATGTCATGCCACTGTCAC	12.79	-15.47
Atu1348		1344362	1337895	hypothetical protein	chromosome-circular	D	-177	-160		10.19	-12.39
Atu1349		1344719	1345087	hypothetical protein	chromosome-circular	R	-197	-180	CTGTTAAAAAGCCGACAC	10.19	-12.39
Atu1349		1344719	1345087	hypothetical protein	chromosome-circular	R	-50	-33	ATGTCACATATGTGTCGT	11.73	-14.13
Atu1349		1344719	1345087	hypothetical protein	chromosome-circular	D	-50	-33	ACGACACATATGTGACAT	8.36	-10.6

Atu1372		1366762	1366292	hypothetical protein	chromosome-circular	R	-32	-15	TTGTTGTAATCCTTCAA	8.61	-10.83
Atu1373		1366879	1367721	hypothetical protein	chromosome-circular	D	-102	-85		8.61	-10.83
Atu1375	<i>tsf</i>	1369042	1369968	elongation factor Ts	chromosome-circular	D	-193	-176	TCTTCATAACGCTGTCAC	9.5	-11.68
Atu1492		1481481	1481128	transcriptional regulator, ArsR family	chromosome-circular	D	-107	-90	TTGATATATAGATGTTAT	9.88	-12.06
Atu1526	<i>gnd</i>	1518951	1517521	6-phosphogluconate dehydrogenase	chromosome-circular	D	-100	-83	GCGTCATCAAAATTTAAT	8.32	-10.56
Atu1555	tRNA-Leu	1543361	1543274	tRNA-Leu	chromosome-circular	D	-90	-73		12.7	-15.34
Atu1556	<i>lipB</i>	1543582	1544283	lipoyltransferase	chromosome-circular	R	-148	-131	ATTTCAAAAACTGTAC	12.7	-15.34
Atu1615		1599366	1597438	hypothetical protein	chromosome-circular	R	-258	-241		8.58	-10.8
Atu1616	<i>fumC</i>	1599703	1601196	fumarate hydratase	chromosome-circular	D	-96	-79	CCGTAGTAAAAATGACAC	8.58	-10.8
Atu1615		1599366	1597438	hypothetical protein	chromosome-circular	R	-131	-114		8.15	-10.41
Atu1616	<i>fumC</i>	1599703	1601196	fumarate hydratase	chromosome-circular	D	-223	-206	AAGCCATAAAAACGTAAT	8.15	-10.41
Atu1621		1606678	1605797	hypothetical protein	chromosome-circular	R	-96	-79		8.85	-11.05
Atu1622	<i>gyrB</i>	1606898	1609036	DNA topoisomerase IV subunit B	chromosome-circular	D	-141	-124	CTGACACAATCGTGCCAT	8.85	-11.05
Atu1649		1633804	1632974	hypothetical protein	chromosome-circular	D	-81	-64	CTGTCATGTTGCTGAAAC	9.69	-11.87
Atu1657	<i>nadE</i>	1643233	1641554	NAD(+) synthase	chromosome-circular	D	-165	-148		15.1	-18.98
Atu1658		1643603	1645396	hypothetical protein	chromosome-circular	R	-222	-205	TTGTCATGTAAGTGTAC	15.1	-18.98
Atu1657	<i>nadE</i>	1643233	1641554	NAD(+) synthase	chromosome-circular	D	-176	-159		9.85	-12.04
Atu1658		1643603	1645396	hypothetical protein	chromosome-circular	R	-211	-194	ACGTCGCAAAATTTGCAT	9.85	-12.04
Atu1678	<i>queA</i>	1666685	1665585	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	chromosome-circular	R	-203	-186	TTGTCACCAATGTGAAAC	10.23	-12.43
Atu1706	<i>tata</i>	1691454	1691242	twin arginine translocase protein A	chromosome-circular	D	-49	-32	CTTTCAAACGTCTTACAT	8.58	-10.79
Atu1716		1703406	1703089	hypothetical protein	chromosome-circular	R	-162	-145	TCGTCACAAAACCTTCGG	8.57	-10.79
Atu1744		1731200	1730613	nitroreductase family protein	chromosome-circular	R	-22	-5		8.98	-11.18
Atu1745		1731304	1732284	hypothetical protein	chromosome-circular	D	-99	-82	CTTCCATTCTGCTGTCAT	8.98	-11.18
Atu1767		1750785	1751825	transcriptional regulator, AraC family	chromosome-circular	D	-145	-128	TTGTCGCAAAATTTGCAT	8.95	-11.15
Atu1777		1762007	1761663	hypothetical protein	chromosome-circular	D	-106	-89	ATGTAACGAAACGGACAT	8.43	-10.66
Atu1819		1799121	1798732	hypothetical protein	chromosome-circular	R	-109	-92	CTGTCAAAATCGCGTCAG	8.53	-10.75
Atu1835		1818555	1818749	hypothetical protein	chromosome-circular	R	-195	-178	CTGATATATATTCGAAAT	8.05	-10.31
Atu1855		1834617	1835825	MFS permease	chromosome-circular	D	-44	-27	CTGTGACAGAACTTTCAC	9.76	-11.95
Atu1882	<i>usg</i>	1862640	1862888	usg protein	chromosome-circular	R	-134	-117	CCGTCACAAATTTGTTAT	11.05	-13.33
Atu1908		1886142	1885321	hypothetical protein	chromosome-circular	R	-39	-22	TTGTCACAAACATGTGAC	11.14	-13.43
Atu2014		1976961	1975978	ABC transporter, substrate binding protein	chromosome-circular	D	-63	-46	CTGTCACATACATGTTAT	13.16	-15.97
Atu2049		2007140	2007475	tmRNA	chromosome-circular	D	-60	-43	TTTTTCATGGAATTTGCAT	11.22	-13.52
Atu2072	<i>prmA</i>	2033770	2033045	ribosomal protein L11 methyltransferase	chromosome-circular	R	-210	-193	TTGCCACAAAACCTTCAT	13.08	-15.86
Atu2073	<i>sco1</i>	2034611	2034003	sco1 protein homolog	chromosome-circular	R	-130	-113	TTGTCACAAAGCCGCAAT	8.4	-10.64
Atu2078		2037904	2037002	transcriptional regulator, LysR family	chromosome-circular	D	-149	-132		10.1	-12.29
Atu2079		2038103	2039032	ABC transporter, membrane spanning protein	chromosome-circular	R	-67	-50	CTGCCATCCACCCGATAT	10.1	-12.29
Atu2085	<i>lpxC</i>	2046758	2045802	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	chromosome-circular	D	-137	-120	TTGTCGTGACACCTTCAT	10.7	-12.95
Atu2114	<i>djlA</i>	2078748	2077996	molecular chaperone, DnaJ family	chromosome-circular	D	-83	-66		9.47	-11.66
Atu2115	<i>pfp</i>	2078840	2080279	diphosphate--fructose-6-phosphate 1-phosphotransferase	chromosome-circular	R	-26	-9	CTGAAGCAAAACTGTCCG	9.47	-11.66
Atu2121	<i>lyc</i>	2084652	2085503	glycosyl hydrolase/lysozyme	chromosome-circular	R	-22	-5	TGGTAACAAACTGATAT	8.38	-10.61
Atu2146		2111487	2111299	hypothetical protein	chromosome-circular	R	-21	-4		11.22	-13.53
Atu2147		2111571	2112677	ABC transporter, substrate binding protein	chromosome-circular	D	-80	-63	TTGCAATCCAACCGTCAC	11.22	-13.53
Atu2146		2111487	2111299	hypothetical protein	chromosome-circular	R	-32	-15		9.17	-11.35
Atu2147		2111571	2112677	ABC transporter, substrate binding protein	chromosome-circular	D	-69	-52	CCGTCACATTAGCTTCAT	9.17	-11.35
Atu2155	<i>metH</i>	2123789	2120016	methionine synthase	chromosome-circular	D	-133	-116	CTGTCAGCGATATTTCTG	8.88	-11.08

Atu2156		2123981	2125228	hypothetical protein	chromosome-circular	R	-76	-59	CTGTACGCATATTTCG	8.88	-11.08
Atu2157		2125980	2125420	tyrosine/serine protein phosphatase	chromosome-circular	R	-179	-162	TTTTCAAATCCCGTGAT	8.05	-10.31
Atu2201		2174776	2174132	hydrolase	chromosome-circular	D	-81	-64	CTGGCATCTTTCCGTCGC	8.11	-10.37
Atu2202		2174913	2174981	hypothetical protein	chromosome-circular	R	-73	-56	CTGGCATCTTTCCGTCGC	8.11	-10.37
Atu2218	<i>prsA</i>	2186242	2187174	ribose-phosphate pyrophosphokinase	chromosome-circular	D	-205	-188	AAGTCATAGAGATTTTCAC	8.25	-10.49
Atu2222		2190893	2190054	dolichol-phosphate mannosyltransferase	chromosome-circular	D	-56	-39	CCGTAATAAAACTGCAAT	8.03	-10.3
Atu2223	<i>mcpA</i>	2191092	2193356	methyl-accepting chemotaxis protein	chromosome-circular	R	-160	-143	CCGTAATAAAACTGCAAT	8.03	-10.3
Atu2241		2213654	2211771	ABC transporter, nucleotide binding/ATPase protein	chromosome-circular	D	-89	-72	CTTTCATTTTCCTGACGT	8.54	-10.76
Atu2297		2272088	2273137	glycosyltransferase	chromosome-circular	D	-93	-76	CTGACATGATCCTGTAAC	10.32	-12.53
Atu2329		2304306	2303599	hypothetical protein	chromosome-circular	D	-85	-68	ACGTCGTTAATCTGTCAC	9.18	-11.37
Atu2435		2405882	2406397	acetyltransferase	chromosome-circular	D	-70	-53	CTTTCCTATACCTGTCAC	9.08	-11.27
Atu2489		2458677	2457859	hypothetical protein	chromosome-circular	D	-153	-136	TTTTCAATTGGCTGTCAT	8.17	-10.42
Atu2491		2460309	2459926	hypothetical protein	chromosome-circular	R	-40	-23	CTGTCACTCTGATGTCAC	10.01	-12.2
Atu2492	<i>mtbA</i>	2460472	2462316	MFS permease [sugar]	chromosome-circular	D	-140	-123	CTGTCACTCTGATGTCAC	10.01	-12.2
Atu2502	<i>hemO</i>	2470987	2470376	heme oxygenase	chromosome-circular	R	-285	-268	ATGCCATCAATCCGTTGT	9.57	-11.75
Atu2503	<i>dapA</i>	2471294	2472178	dihydrodipicolinate synthase	chromosome-circular	D	-39	-22	ATGCCATCAATCCGTTGT	9.57	-11.75
Atu2525		2499620	2498271	MFS permease	chromosome-circular	D	-133	-116	CTTCTATCAATATTTTCAT	8.71	-10.92
Atu2541		2512997	2512788	hypothetical protein	chromosome-circular	R	-205	-188	CTGTCAATATTCCTACAC	8.76	-10.96
Atu2548	<i>hemH</i>	2519121	2520071	phosphoribosylaminoimidazole-succinocarboxamide synthase	chromosome-circular	D	-196	-179	TCGTCAAAAACTGACAT	12.33	-14.87
Atu2577		2549950	2552667	ABC transporter, nucleotide binding/ATPase protein	chromosome-circular	D	-18	-1	AGGTCATAGAAGTTTTAT	8.38	-10.61
Atu2579		2553340	2554218	metal dependant beta lactamase protein	chromosome-circular	D	-118	-101	TTGCAATATAAATGAAAT	9.68	-11.87
Atu2626		2609704	2609372	hypothetical protein	chromosome-circular	D	-108	-91	CTGTGCGTACCCTGTCAT	10.33	-12.54
Atu2702		2686375	2685629	hypothetical protein	chromosome-circular	R	-89	-72	TTGATAAAATATTGTCAC	8.77	-10.98
Atu2703	<i>rplS</i>	2686644	2687183	50S ribosomal protein L19	chromosome-circular	D	-197	-180	TTGATAAAATATTGTCAC	8.77	-10.98
Atu2741		2737992	2739152	hypothetical protein	chromosome-circular	R	-76	-59	CTGACAACCTAATCTCAT	8.01	-10.28
Atu2757	<i>glnK</i>	2757161	2757511	nitrogen regulatory protein PII	chromosome-circular	D	-139	-122	CCGTCATATAATCTTTAT	9.86	-12.04
Atu2757	<i>glnK</i>	2757161	2757511	nitrogen regulatory protein PII	chromosome-circular	D	-150	-133	TTTTCAGACGCCCGTCAT	8.64	-10.85
Atu2785	<i>rplU</i>	2789144	2788830	50S ribosomal protein L21	chromosome-circular	R	-238	-221	TTGAAAAGTAACTGTAAC	8.63	-10.84
Atu2786		2789477	2789917	hypothetical protein	chromosome-circular	D	-112	-95	TTGAAAAGTAACTGTAAC	8.63	-10.84
Atu2788	<i>citE</i>	2791022	2790138	citrate lyase, beta subunit	chromosome-circular	D	-56	-39	ATGTCACAAAAGCTTGAC	9.18	-11.37
Atu2789		2791160	2791390	hypothetical protein	chromosome-circular	R	-99	-82	ATGTCACAAAAGCTTGAC	9.18	-11.37
Atu2806		2809754	2809335	hypothetical protein	chromosome-circular	R	-181	-164	CTATCAACACCCTGTCAC	8	-10.27
Atu2826	<i>hpx</i>	2832148	2831183	heat shock protein HtpX	chromosome-circular	R	-104	-87	ATTTCATATCCCGTCAT	8.59	-10.81
Atu2827		2832265	2832477	hypothetical protein	chromosome-circular	D	-30	-13	ATTTCATATCCCGTCAT	8.59	-10.81
Atu3105		114149	113220	hypothetical protein	chromosome-linear	R	-90	-73	TTGTCATAAAGCCGTAGC	10.84	-13.1
Atu3114		124940	123651	ABC transporter, substrate binding protein [sugar]	chromosome-linear	D	-78	-61	ATGTAACCAATTAGTTAT	8.32	-10.56
Atu3115		125058	125756	transcriptional regulator, TetR family	chromosome-linear	R	-57	-40	ATGTAACCAATTAGTTAT	8.32	-10.56
Atu3180		190735	189902	ABC transporter, nucleotide binding/ATPase protein	chromosome-linear	R	-190	-173	ATGTCGCACATATGTAAT	9.65	-11.83
Atu3181		191036	192238	hypothetical protein	chromosome-linear	D	-128	-111	ATGTCGCACATATGTAAT	9.65	-11.83
Atu3191		201234	200548	outer membrane protein	chromosome-linear	D	-200	-183	TTGTTGCGCAATTGTCAC	8	-10.27
Atu3297	<i>dctB</i>	324887	323046	two component sensor kinase for C4-dicarboxylate transport	chromosome-linear	R	-98	-81	CTTCAATAAAAACTACAT	8.43	-10.65
Atu3298	<i>dctA</i>	325124	326470	C4-dicarboxylate transport protein	chromosome-linear	D	-156	-139	CTTCAATAAAAACTACAT	8.43	-10.65
Atu3312		343954	343097	hypothetical protein	chromosome-linear	R	-110	-93	TTGTTATCTGCATGACAC	8.09	-10.35
Atu3318		350134	349337	transcriptional regulator, LuxR family	chromosome-linear	R	-88	-71	ATGTCAACTATCATTAAAT	8.3	-10.54
Atu3319		350330	350623	hypothetical protein	chromosome-linear	D	-125	-108	ATGTCAACTATCATTAAAT	8.3	-10.54

Atu3334		369564	369331	hypothetical protein	chromosome-linear	D	-155	-138	ATGTCATGCAACTTTCCA	8.43	-10.65
Atu3335		369811	370392	3-methyladenine DNA glycosylase	chromosome-linear	R	-109	-92		8.43	-10.65
Atu3353	<i>manC</i>	388556	387126	mannose-1-phosphate guanylyltransferase (GDP)	chromosome-linear	D	-133	-116	CATTCACCAAGCTTTCCAC	8.61	-10.83
Atu3363		403148	401412	sensory methylation accepting chemotaxis protein	chromosome-linear	R	-271	-254	CTTTCATCCAAACGGCAT	9.34	-11.52
Atu3364		403463	404716	D-amino acid dehydrogenase	chromosome-linear	D	-61	-44		9.34	-11.52
Atu3363		403148	401412	sensory methylation accepting chemotaxis protein	chromosome-linear	R	-228	-211	TTGCCACAGTGCTGATAT	8.09	-10.35
Atu3364		403463	404716	D-amino acid dehydrogenase	chromosome-linear	D	-104	-87		8.09	-10.35
Atu3515		563428	563114	hypothetical protein	chromosome-linear	R	-135	-118	TTTTCACGAAGCTGTGAC	8.66	-10.87
Atu3565		619497	618517	hypothetical protein	chromosome-linear	D	-169	-152	ATGTCATAAAGCTGTAAA	11.73	-14.12
Atu3699		779273	778764	hypothetical protein	chromosome-linear	R	-168	-151	TTGTCATTTCTCTGTTGC	9.18	-11.37
Atu3700	tRNA-Gly	779527	779604	tRNA-Gly	chromosome-linear	D	-103	-86		9.18	-11.37
Atu3702	tRNA-Met	780880	780801	tRNA-Met	chromosome-linear	D	-29	-12	CAGTCACATGACTGTGAC	10.75	-12.99
Atu3704		783602	782412	hypothetical protein	chromosome-linear	D	-200	-183	TTTTCATTCATCTGTCAT	12.92	-15.65
Atu3717	<i>tolQ</i>	800084	799365	tolQ Protein	chromosome-linear	D	-221	-204	CTGTAACTCCTTTAAC	9.4	-11.59
Atu3752		835937	835761	hypothetical protein	chromosome-linear	D	-78	-61	ATGTCACATTGCCGTCGT	10.36	-12.57
Atu3753		836171	836374	hypothetical protein	chromosome-linear	R	-173	-156		10.36	-12.57
Atu3752		835937	835761	hypothetical protein	chromosome-linear	D	-67	-50	CCGTCGTAACCTGAAAC	8.34	-10.58
Atu3753		836171	836374	hypothetical protein	chromosome-linear	R	-184	-167		8.34	-10.58
Atu3767		850035	849127	GGDEF family protein	chromosome-linear	R	-188	-171	CCGTCATATGTCCGTCAT	11.17	-13.47
Atu3768		850295	851740	homospermidine synthase	chromosome-linear	D	-89	-72		11.17	-13.47
Atu3778	<i>galU</i>	861704	860817	UTP-glucose-1-phosphate uridylyltransferase	chromosome-linear	R	-132	-115	TTGACATTCTTTTGTAT	8.83	-11.03
Atu3779	<i>mltB</i>	861900	863120	murein hydrolase	chromosome-linear	D	-81	-64		8.83	-11.03
Atu3781		864671	865345	two component response regulator	chromosome-linear	R	-194	-177	CGGTCCTCAAAGTGTGAT	9.68	-11.87
Atu3818	<i>rhsA</i>	914307	915806	ABC transporter, nucleotide binding/ATPase protein [ribose]	chromosome-linear	D	-35	-18	ATGTAACAAAACCTTGAA	9.11	-11.3
Atu3818	<i>rhsA</i>	914307	915806	ABC transporter, nucleotide binding/ATPase protein [ribose]	chromosome-linear	D	-55	-38	TTGCCACAATTATTATAT	8.09	-10.35
Atu3824		921399	920416	hypothetical protein	chromosome-linear	R	-40	-23	CCGATATAAACCTGAAAT	8.32	-10.55
Atu3868		960823	961926	hypothetical protein	chromosome-linear	R	-77	-60	CCGTCATCATGCCGAAAT	8.27	-10.51
Atu3882	tRNA-Val	978026	977949	tRNA-Val	chromosome-linear	D	-78	-61	CTCTCAAAAAACCTTCAC	9.16	-11.35
Atu3942		1047365	1047556	hypothetical protein	chromosome-linear	R	-223	-206	CTGTCAATATTCTACAC	8.76	-10.96
Atu3947	<i>ordL</i>	1050290	1048980	oxidoreductase	chromosome-linear	D	-273	-256	CTGTAGCCCATACGACAT	8.31	-10.54
Atu3948		1050590	1051735	hypothetical protein	chromosome-linear	R	-44	-27		8.31	-10.54
Atu3951		1055082	1054168	transcriptional regulator, LysR family	chromosome-linear	D	-65	-48	TTGTAGCCAACCTGTCCT	8.75	-10.96
Atu3952		1055268	1056596	oxidoreductase	chromosome-linear	R	-138	-121		8.75	-10.96
Atu4020		1133850	1132183	hypothetical protein	chromosome-linear	R	-132	-115	CTGTCACGAAAGTGTGAT	14.4	-17.82
Atu4047	<i>cvgS</i>	1161200	1163668	two component sensor kinase/response regulator hybrid	chromosome-linear	R	-156	-139	ATGTGCGCATGAGCGTCAT	8.6	-10.81
Atu4185		1309692	1309991	hypothetical protein	chromosome-linear	R	-157	-140	CTGTCAATATTCTACAC	8.76	-10.96
Atu4207		1330789	1329641	transcriptional regulator, ROK family	chromosome-linear	R	-44	-27	ATGTCATGACTTTTGTAC	9.78	-11.96
Atu4208		1330879	1332252	ABC transporter, substrate binding protein [sugar]	chromosome-linear	D	-63	-46		9.78	-11.96
Atu4214	<i>cspA</i>	1336994	1336791	cold shock protein	chromosome-linear	R	-152	-135	ATGATAAAGATCCTTCAT	8.06	-10.33
Atu4319		1447185	1448084	transcriptional regulator, AraC family	chromosome-linear	D	-146	-129	CTGACAAAAAAGTCAA	8.4	-10.63
Atu4411		1546895	1546032	transcriptional regulator, LysR family	chromosome-linear	R	-177	-160	TTGTTAAGAAATCGTCAT	10.13	-12.33
Atu4412	<i>rzxA</i>	1547245	1553079	rhizobiocin/RTX toxin	chromosome-linear	D	-190	-173		10.13	-12.33
Atu4519	<i>livJ</i>	1666730	1665558	ABC transporter, substrate binding protein [branched amino acid]	chromosome-linear	D	-86	-69	ATTTTCATTTTACTTTGAT	8.07	-10.33
Atu4537		1684383	1683715	ABC transporter, membrane spanning protein [amino acid]	chromosome-linear	D	-178	-161	TTGACACAAAAATGAACT	8.07	-10.33
Atu4567		1716080	1714932	transcriptional regulator, ROK family	chromosome-linear	R	-89	-72	CTGTCACAAATATTACAC	12.49	-15.07

Atu4568		1716226	1717455	ABC transporter, substrate binding protein	chromosome-linear	D	-74	-57	CTGTACAAATATTCAC	12.49	-15.07
Atu4567		1716080	1714932	transcriptional regulator, ROK family	chromosome-linear	R	-78	-61	TTTTCACTGGACTGTCAC	8.57	-10.79
Atu4568		1716226	1717455	ABC transporter, substrate binding protein	chromosome-linear	D	-85	-68		8.57	-10.79
Atu4606		1752664	1751054	hypothetical protein	chromosome-linear	R	-79	-62	TATTCATAATTCTGTGCG	8.15	-10.4
Atu4634		1784966	1784322	hypothetical protein	chromosome-linear	R	-61	-44	TTGTCATAAAAACGTGCAT	18.1	-26.03
Atu4635		1785080	1785619	hypothetical protein	chromosome-linear	D	-70	-53		18.1	-26.03
Atu4803		1980211	1979558	two component response regulator	chromosome-linear	D	-39	-22	TTATCACCGAACTTTCAT	9.52	-11.71
Atu4804		1980285	1980650	hypothetical protein	chromosome-linear	R	-52	-35		9.52	-11.71
Atu4841	<i>deoR</i>	2021333	2020602	transcriptional regulator, DeoR family	chromosome-linear	D	-93	-76	TTGTTATTCTTCTGTCAA	9.14	-11.33
Atu4842		2021671	2022717	ABC transporter, substrate binding protein [sugar]	chromosome-linear	R	-262	-245		9.14	-11.33
Atu4850		2032246	2032770	hypothetical protein	chromosome-linear	D	-223	-206	TTTTAATAAAAAATTAT	8.29	-10.53
Atu5031		32477	31458	hypothetical protein	pATC58	R	-271	-254	CTGTTATGTCGCTGTTAC	9.2	-11.39
Atu5058	<i>ugpB</i>	56951	58210	ABC transporter, substrate binding protein [glycerol-3-phosphate]	pATC58	D	-92	-75	CTGTCATCAAAACGTCGC	12.35	-14.89
Atu5058	<i>ugpB</i>	56951	58210	ABC transporter, substrate binding protein [glycerol-3-phosphate]	pATC58	D	-46	-29	TTGCTAGACAGCCGTCAT	8.62	-10.84
Atu5117		124902	123961	hypothetical protein	pATC58	D	-82	-65	TTGCCAGCAAAGTGTGAT	8.46	-10.69
Atu5125	<i>atrA</i>	132964	132275	transcriptional regulator, GntR family	pATC58	R	-54	-37	ATGTCACAAAAATGGAAT	10.32	-12.53
Atu5126	<i>attA1</i>	133170	134282	ABC transporter, nucleotide binding/ATPase protein[putrescine]	pATC58	D	-169	-152		10.32	-12.53
Atu5279		277978	278568	hypothetical protein	pATC58	D	-100	-83	ATGAAATATTTCTTTCAT	11.28	-13.6
Atu5279		277978	278568	hypothetical protein	pATC58	R	-100	-83	ATGAAAGAAATATTTTCAT	9.61	-11.79
Atu5442		434495	436435	methyl-accepting chemotaxis protein	pATC58	D	-106	-89	TTGTTATATAACTTTTAT	13.15	-15.95
Atu5442		434495	436435	methyl-accepting chemotaxis protein	pATC58	R	-101	-84	CTGTAATAAAAAGTTATAT	11.78	-14.19
Atu5443		437082	436534	transcriptional regulator, TetR family	pATC58	D	-42	-25	TGTCATATAAAAGTCAA	8.13	-10.39
Atu5444		437193	437981	short-chain dehydrogenase	pATC58	R	-86	-69		8.13	-10.39
Atu5503		495422	493965	hypothetical protein	pATC58	R	-284	-267	TTGTCAGCGAATTGTCAT	11.8	-14.21
Atu5504		495746	496201	hypothetical protein	pATC58	D	-57	-40		11.8	-14.21
Atu5529	<i>amiC</i>	522874	524025	two component sensor kinase	pATC58	D	-102	-85	CTGACATCATCCTTTCGC	9.91	-12.09
Atu6004	<i>geneD</i>	7578	8273	D protein	pTiC58	D	-239	-222	ATGTCATTCACATGTCAA	10.04	-12.23
Atu6004	<i>geneD</i>	7578	8273	D protein	pTiC58	R	-239	-222	TTGACATGTGAATGACAT	9.61	-11.79
Atu6007	<i>mas1</i>	11383	10349	agrociniopine synthesis reductase	pTiC58	D	-68	-51	GTGTTAAATCTCTGTTAT	8.05	-10.32
Atu6012	<i>ipt</i>	19337	20059	isopentenyl transferase	pTiC58	R	-187	-170	TTGAAAGCAATTTGTCAC	9.14	-11.33
Atu6014	<i>gene6b</i>	22241	21618	protein 6b	pTiC58	D	-135	-118	ATGCTATCAATCTGTCGT	10.21	-12.41
Atu6043	<i>repA</i>	52233	53450	replication protein A	pTiC58	R	-52	-35	TTGCCATTTATCCGTGAC	8.26	-10.5
Atu6090		108998	107937	ATP-dependent DNA ligase	pTiC58	D	-241	-224	ATGTCGTGCAAATGTCAA	8.88	-11.08
Atu6091		109282	110034	hypothetical protein	pTiC58	R	-60	-43		8.88	-11.08
Atu6094		115339	116079	hypothetical protein	pTiC58	R	-80	-63	CTGCAAGAAAACGTGCGA	8.18	-10.43
Atu6108	<i>phnA</i>	129931	129626	alkylphosphonate uptake protein	pTiC58	D	-98	-81	CTGTCAGAACACCCTGAT	8.08	-10.34
Atu6137		157232	156936	hypothetical protein	pTiC58	R	-166	-149	CTGTCACCAAACTTTCAT	15.93	-20.54
Atu6138	<i>accR</i>	157464	158240	transcriptional regulator	pTiC58	D	-83	-66		15.93	-20.54
Atu6137		157232	156936	hypothetical protein	pTiC58	R	-155	-138	TTGCAACAAAACGTGCAC	12.92	-15.65
Atu6138	<i>accR</i>	157464	158240	transcriptional regulator	pTiC58	D	-94	-77		12.92	-15.65
Atu6178	<i>virG</i>	193546	194307	two component response regulator	pTiC58	D	-148	-131	TTGTCATCAAACGGAGAC	8.03	-10.29

^a Locus tags highlighted yellow are associated with multiple *pho* boxes.

^b Symbols: D, the same strand; R, the other strand

^c Coordinates counted from the start codon

^d Sequences boxed are shared by two genes

^c Significance measures provided by patser