

Table S1. Strain names and 16S BLAST results of SWI strains.

Strain name and Genus	Strain name and Genus
F16_33-1 <i>Bacillus</i> spp.	F17_19-1 <i>Lysinibacillus</i> spp.
F16_34-2 <i>Pseudomonas</i> spp.	F17_20-1 <i>Paenibacillus</i> spp.
F16_35-1 <i>Bacillus</i> spp.	F17_21-1 <i>Bacillus</i> spp.
F16_35-2 <i>Pseudomonas</i> spp.	F17_22-1 <i>Bacillus</i> spp.
F16_36-1 <i>Pseudomonas</i> spp.	F17_22-2 <i>Pseudomonas</i> spp.
F16_36-2 <i>Pseudomonas</i> spp.	F17_23-1 <i>Bacillus</i> spp.
F16_37-2 <i>Pseudomonas</i> spp.	F17_23-2 <i>Pseudomonas</i> spp.
F16_38-1 <i>Bacillus</i> spp.	F17_24-2 <i>Pseudomonas</i> spp.
F16_38-2 <i>Pseudomonas</i> spp.	F17_28-2 <i>Pseudomonas</i> spp.
F16_39-1 <i>Bacillus</i> spp.	F17_SWI6 <i>Pseudomonas</i> spp.
F16_39-2 <i>Pseudomonas</i> spp.	S18_1-1 <i>Bacillus</i> spp.
F16_40-1 <i>Bacillus</i> spp.	S18_1-2 <i>Pseudomonas</i> spp.
F16_40-2 <i>Pseudomonas</i> spp.	S18_3-1 <i>Pseudomonas</i> spp.
F16_41-1 <i>Bacillus</i> spp.	S18_3-2 <i>Pseudomonas</i> spp.
F16_41-2 <i>Pseudomonas</i> spp.	S18_4-1 <i>Pseudomonas</i> spp.
F16_42-1 <i>Bacillus</i> spp.	S18_4-2 <i>Pseudomonas</i> spp.
F16_43-1 <i>Bacillus</i> spp.	S18_6-2 <i>Pseudomonas</i> spp.
F16_43-2 <i>Pseudomonas</i> spp.	S18_8-1 <i>Bacillus</i> spp.
F16_44-1 <i>Bacillus</i> spp.	S18_8-2 <i>Pseudomonas</i> spp.
F16_45-1 <i>Bacillus</i> spp.	S18_9-1 <i>Bacillus</i> spp.
F16_46-1 <i>Bacillus</i> spp.	S18_9-2 <i>Pseudomonas</i> spp.

F16_46-2 <i>Pseudomonas</i> spp.	S18_10-1 <i>Bacillus</i> spp.
F16_47-1 <i>Bacillus</i> spp.	S18_10-2 <i>Pseudomonas</i> spp.
F16_47-2 <i>Pseudomonas</i> spp.	S18_11-1 <i>Bacillus</i> spp.
F16_48-1 <i>Pseudomonas</i> spp.	S18_12-2 <i>Pseudomonas</i> spp.
F16_48-2 <i>Pseudomonas</i> spp.	S18_13-1 <i>Bacillus</i> spp.
F16_50-2 <i>Pseudomonas</i> spp.	S18_13-2 <i>Pseudomonas</i> spp.
F16_51-1 <i>Bacillus</i> spp.	S18_15-2 <i>Pseudomonas</i> spp.
F16_52-1 <i>Bacillus</i> spp.	S18_16-1 <i>Bacillus</i> spp.
F16_53-1 <i>Bacillus</i> spp.	S18_16-2 <i>Pseudomonas</i> spp.
F16_53-2 <i>Pseudomonas</i> spp.	S18_17-1 <i>Bacillus</i> spp.
F16_54-1 <i>Bacillus</i> spp.	S18_17-2 <i>Serratia</i> spp.
F16_54-2 <i>Pseudomonas</i> spp.	S18_18-1 <i>Pseudomonas</i> spp.
F16_55-1 <i>Bacillus</i> spp.	S18_18-2 <i>Pseudomonas</i> spp.
F16_55-2 <i>Serratia</i> spp.	S18_19-1 <i>Citrobacter</i> spp.
F16_56-1 <i>Bacillus</i> spp.	S18_19-2 <i>Pseudomonas</i> spp.
F16_56-2 <i>Pseudomonas</i> spp.	S18_21-1 <i>Pseudomonas</i> spp.
F16_SWI44 <i>Pseudomonas</i> spp.	S18_22-2 <i>Pseudomonas</i> spp.
F17_1-1 <i>Bacillus</i> spp.	S18_24-2 <i>Pseudomonas</i> spp.
F17_1-2 <i>Pseudomonas</i> spp.	S18_25-1 <i>Bacillus</i> spp.
F17_2-1 <i>Bacillus</i> spp.	S18_25-2 <i>Pseudomonas</i> spp.
F17_2-2 <i>Pseudomonas</i> spp.	S18_33-2 <i>Pseudomonas</i> spp.
F17_3-1 <i>Bacillus</i> spp.	S18_34-1 <i>Pseudomonas</i> spp.
F17_3-2 <i>Pseudomonas</i> spp.	S18_34-2 <i>Pseudomonas</i> spp.

F17_4-1 <i>Bacillus</i> spp.	S18_37-2 <i>Pseudomonas</i> spp.
F17_4-2 <i>Pseudomonas</i> spp.	S18_41-2 <i>Pseudomonas</i> spp.
F17_5-1 <i>Pseudomonas</i> spp.	S18_42-1 <i>Bacillus</i> spp.
F17_6-1 <i>Lysinibacillus</i> spp.	S18_42-2 <i>Pseudomonas</i> spp.
F17_7-1 <i>Bacillus</i> spp.	S18_43-2 <i>Pseudomonas</i> spp.
F17_7-2 <i>Pseudomonas</i> spp.	S18_44-1 <i>Bacillus</i> spp.
F17_8-2 <i>Pseudomonas</i> spp.	S18_44-2 <i>Pseudomonas</i> spp.
F17_9-1 <i>Bacillus</i> spp.	S18_48-2 <i>Pseudomonas</i> spp.
F17_9-2 <i>Pseudomonas</i> spp.	S18_49-2 <i>Pseudomonas</i> spp.
F17_10-1 <i>Pseudomonas</i> spp.	S18_50-1 <i>Pseudomonas</i> spp.
F17_10-2 <i>Pseudomonas</i> spp.	S18_52-2 <i>Pseudomonas</i> spp.
F17_11-2 <i>Pseudomonas</i> spp.	S18_54-2 <i>Pseudomonas</i> spp.
F17_12-1 <i>Bacillus</i> spp.	S18_55-1 <i>Bacillus</i> spp.
F17_12-2 <i>Bacillus</i> spp.	S18_57-2 <i>Pseudomonas</i> spp.
F17_13-1 <i>Bacillus</i> spp.	S18_BC-2 <i>Pseudomonas</i> spp.
F17_14-1 <i>Bacillus</i> spp.	S18_MD-1 <i>Bacillus</i> spp.
F17_14-2 <i>Pseudomonas</i> spp.	S18_MD-2 <i>Pseudomonas</i> spp.
F17_15-1 <i>Bacillus</i> spp.	S18_SS-1 <i>Bacillus</i> spp.
F17_15-2 <i>Pseudomonas</i> spp.	S18_SS-2 <i>Pseudomonas</i> spp.
F17_16-2 <i>Pseudomonas</i> spp.	S18_SWI7 <i>Pseudomonas</i> spp.
F17_18-2 <i>Pseudomonas</i> spp.	SWI36 <i>Pseudomonas</i> spp.

Table S2. BGCs identified by JGI IMG in SWI44_{WT}.

BGC	From bp	To bp	Length	Predicted Product
1	311,568	355,175	43,608	arylpolyene
2	564,316	606,657	42,342	thiopeptide
3	1,413,052	1,428,017	14,966	NAGGN
4	2,132,818	2,153,234	20,417	phenazine
5	2,946,528	2,987,254	40,727	NRPS-like
6	3,576,460	3,587,305	10,846	bacteriocin
7	3,982,122	4,073,153	91,032	NRPS

Table S3. BGCs identified by JGI IMG in SWI6_{WT}

BGC	From bp	To bp	Length	Predicted Product
1	2,042,474	2,133,503	91,030	NRPS
2	2,524,761	2,535,606	10,846	bacteriocin
3	2,873,580	2,916,387	42,808	NRPS-like
4	3,627,484	3,647,900	20,417	phenazine
5	4,351,262	4,366,227	14,966	NAGGN
6	5,149,350	5,191,694	42,345	thiopeptide
7	5,403,567	5,447,174	43,608	arylpolyene

Table S4. BGCs identified by JGI IMG in SWI7_{WT}.

BGC	From bp	To bp	Length	Predicted product
1	258,018	272,845	14,827	NAGGN
2	504,289	600,124	95,835	NRPS
3	1,087,797	1,111,436	23,639	terpene
4	1,428,494	1,508,635	80,141	NRPS
5	4,104,237	4,147,845	43,608	arylpolyene

Table S5. Transposon insertions in SWI44_{LOI} mutants.

SWI44 mutant	Gene ID	BGC ID	Location of Tn insertion (bp)	Predicted Function
1	2717929146	2716925891.Ga0172617 11.region2	574,981	glutathione-regulated potassium-efflux system ancillary protein KefG
2	2717929148	2716925891.Ga0172617 11.region2	576,124	A-factor biosynthesis hotdog domain-containing protein
3	2717929151	2716925891.Ga0172617 11.region2	579,269	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family
4	2717929836	-	1,322,000	<i>gacS</i> , two-component system, sensor histidine kinase
5	2717929836	-	1,320,750	<i>gacS</i> , two-component system, sensor histidine kinase

6	2717929836	-	1,321,500	<i>gacS</i> , two-component system, sensor histidine kinase
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Table S6. Transposon insertions in SWI6_{LOI} mutants.

SWI6 mutant	Gene ID	BGC ID	Location of Tn insertion (bp)	Predicted Function
1	2771388066	2770957150.Ga0255654 11.region6	5176564	NAD(P)-dependent dehydrogenase
2	2771387398	-	4458161	<i>gacS</i> sensor kinase

Table S7. Transposon insertions in SWI7_{LOI} mutant.

SWI6 mutant	Gene ID	DNA cluster coordinates	Location of Tn insertion (bp)	Predicted Function
1	2791818508	-	2541253	hypothetical

Table S8. Predicted ORFs in SWI44_{WT} and SWI6_{WT} BGC.

ORF #	^a JGI locus tag	AA length	Predicted function
1	11499	86	tRNA dimethylallyl-transferase
2	11501	433	GTP-binding protein HflX
3	11502	390	Protease FtsH subunit HflK
4	11503	289	Protease FtsH subunit HflC
5	11504	395	ATP phosphor- ribosyltransferase regulatory subunit
6	11505	430	Adenylosuccinate synthetase
7	11506	644	Methyl-accepting chemotaxis protein
8	11507	237	LuxR family transcriptional regulator
9	11508	206	N-acyl-L-homoserine lactone synthetase

10	11509	198	Potassium-efflux system ancillary protein KefG
11	11510	173	Protein of unknown function
12	11511	403	A-factor biosynthesis hotdog domain- containing protein
13	11512	379	2,4-dienoyl-CoA reductase
14	11513	257	NAD(P)-dependent dehydrogenase
15	11514	245	NAD(P)-dependent dehydrogenase
16	-	143	Hypothetical protein
17	11516	521	iron(III) transport system permease protein
18	11517	337	iron(III) transport system substrate-binding protein
19	-	84	tRNA
20	-	84	tRNA
21	11520	858	RNAse R
22	11521	248	23S rRNA methyltransferase

23	11522	141	SSU ribosomal protein
24	11523	76	SSU ribosomal protein
25	11524	287	hypothetical
26	11525	148	LSU ribosomal protein
27	11526	465	DNA helicase
28	11527	541	ATP-binding cassette
29	11528	384	ribosomal protein
30	11529	42	hypothetical
31	11530	765	SAM protein
32	11531	195	hypothetical
33	11532	29	hypothetical
34	11533	149	azurin
35	11534	275	NH(3)-dependent NAD(+) synthetase
36	11535	401	phosphoribosyltransferase
37	11536	378	amino acid ABC transporter
38	11537	304	amino acid ABC transporter
39	11538	432	amino acid ABC transporter

38 11539 291 amino acid ABC
transporter

41 115430 238 amino acid ABC
transporter

Table S9. Gene regions in SWI6 genome that are absent in SWI44.

Region	Chromosome	Gene			
	coordinates	No.	Locus Tag	Predicted function	Gene coordinates
1	129346- 198529	1	C4Q28_00630	hypothetical protein	130471-130920
		2	C4Q28_00635	hypothetical protein	130933-132400
		3	C4Q28_00640	hypothetical protein	132590-133117
		4	C4Q28_00645	hypothetical protein	133219-133542
		5	C4Q28_00650	DNA-binding response regulator	133660-134334
		6	C4Q28_00655	outer membrane porin, OprD family	134823-136166
		7	C4Q28_00660	TolC family protein	136657-137841
		8	C4Q28_00665	efflux RND transporter periplasmic adaptor subunit	137910-139160
		9	C4Q28_00670	CusA/CzcA family heavy metal efflux RND transporter	139185-142346
		10	C4Q28_00675	DUF2790 domain- containing protein	142509-142832

11	C4Q28_00680	heavy metal translocating P-type ATPase	143035-145032
12	C4Q28_00685	hypothetical protein	145125-145349
13	C4Q28_00690	hypothetical protein	145477-146502
14	C4Q28_00695	porin	146801-148108
15	C4Q28_00700	LysR family transcriptional regulator	148319-149287
16	C4Q28_00705	GtrA family protein	149545-149964
17	C4Q28_00710	glycosyltransferase	149930-150913
18	C4Q28_00715	phospholipid carrier-dependent glycosyltransferase	150907-152361
19	C4Q28_00720	hypothetical protein	152444-152665
20	C4Q28_00725	hypothetical protein	152932-153519
21	C4Q28_00730	two-component sensor histidine kinase	153577-154995
22	C4Q28_00735	DNA-binding response regulator	154992-155666
23	C4Q28_00740	DUF2790 domain- containing protein	156356-156682

24	C4Q28_00745	hypothetical protein	156715-157065
25	C4Q28_00750	cation transporter	157223-158128
26	C4Q28_00755	zinc ribbon domain- containing protein	158183-158521
27	C4Q28_00760	phosphoethanolami ne transferase	159012-160709
28	C4Q28_00765	hypothetical protein	161104-161310
29	C4Q28_00770	hypothetical protein	161325-161534
30	C4Q28_00775	hypothetical protein	161755-161952
31	C4Q28_00780	IS3 family transposase	162011-163161
32	C4Q28_00785	transposase	163178-163423
33	C4Q28_00790	hypothetical protein	163446-163754
34	C4Q28_00795	hypothetical protein	163812-164108
35	C4Q28_00800	hypothetical protein	164167-164823
36	C4Q28_00805	NAD-dependent deacylase	165030-165818
37	C4Q28_00810	DUF4325 domain- containing protein	166136-166441
38	C4Q28_00815	ATP-binding protein	166565-167185
39	C4Q28_00820	transcriptional regulator	168116-168322

40	C4Q28_00825	copper-translocating P-type ATPase	168734-171121
41	C4Q28_00830	cation transporter	171459-171659
42	C4Q28_00835	hypothetical protein	171925-172947
43	C4Q28_00840	hypothetical protein	173086-173541
44	C4Q28_00845	DUF2933 domain- containing protein	173567-173842
45	C4Q28_00850	isoprenylcysteine carboxylmethyltrans ferase family protein	173839-174498
46	C4Q28_00855	IS5/IS1182 family transposase	174618-175598
47	C4Q28_00860	polyamine ABC transporter substrate-binding protein	175734-175877
48	C4Q28_00865	heat-shock protein HtpX	176109-176456
49	C4Q28_00870	CusA/CzcA family heavy metal efflux RND transporter	176453-179611

50	C4Q28_00875	efflux RND transporter periplasmic adaptor subunit	179608-181074
51	C4Q28_00880	ToIC family protein	181071-182324
52	C4Q28_00885	hypothetical protein	182411-182758
53	C4Q28_00890	HAMP domain- containing protein	182795-184201
54	C4Q28_00895	DNA-binding response regulator	184201-184878
55	C4Q28_00900	hypothetical protein	185045-185251
56	C4Q28_00905	copper resistance system multicopper oxidase	185434-187392
57	C4Q28_00910	hypothetical protein	187389-187730
58	C4Q28_00915	copper resistance protein B	187720-188835
59	C4Q28_00920	cytochrome c	188845-189624
60	C4Q28_00925	DUF411 domain- containing protein	189614-190069
61	C4Q28_00930	DUF2790 domain- containing protein	190167-190499

		62	C4Q28_00935	transcriptional regulator	190871-191230
		63	C4Q28_00940	hypothetical protein	191287-193203
		64	C4Q28_00945	AAA family ATPase	193279-194238
		65	C4Q28_00950	integrase	194235-196193
		66	C4Q28_00955	transposase	196174-196812
		67	C4Q28_00960	IS30 family transposase	197442-198470
2	652042- 705805	68	C4Q28_03055	DNA methylase	652338-654035
		69	C4Q28_03060	hypothetical protein	654762-655859
		70	C4Q28_03065	histidine kinase	655849-658236
		71	C4Q28_03070	plasmid mobilization relaxosome protein MobC	658969-659484
		72	C4Q28_03075	type IV secretion system protein VirB5	659903-660667
		73	C4Q28_03080	hypothetical protein	660669-661160
		74	C4Q28_03085	hypothetical protein	661157-661411

75	C4Q28_03090	type IV secretion system protein VirB6	661414-662493
76	C4Q28_03095	hypothetical protein	662780-662989
77	C4Q28_03100	DUF4917 domain- containing protein	663172-664179
78	C4Q28_03105	hypothetical protein	664870-665766
79	C4Q28_03110	hypothetical protein	666173-666397
80	C4Q28_03115	Site-specific recombinase	666612-667673
81	C4Q28_03120	hypothetical protein	668199-669800
82	C4Q28_03125	hypothetical protein	669838-670809
83	C4Q28_03130	hypothetical protein	670782-671486
84	C4Q28_03135	DNA-binding protein	671483-672031
85	C4Q28_03140	hypothetical protein	672028-672951
86	C4Q28_03145	hypothetical protein	672948-673655
87	C4Q28_03150	hypothetical protein	673663-674709
88	C4Q28_03155	phage tail protein	674893-676059
89	C4Q28_03160	phage tail protein	676068-676592
90	C4Q28_03165	Phage protein gp47	676589-677761
91	C4Q28_03170	DUF2590 domain- containing protein	677758-678075

92	C4Q28_03175	phage tail tape measure protein	678075-680438
93	C4Q28_03180	Tail assembly chaperone	680613-680900
94	C4Q28_03185	lysis protein	680897-681394
95	C4Q28_03190	lysozyme	681391-681921
96	C4Q28_03195	hypothetical protein	681918-682124
97	C4Q28_03200	conjugal transfer protein TraR	682121-682339
98	C4Q28_03205	DUF2597 domain- containing protein	682339-682788
99	C4Q28_03210	DUF2586 domain- containing protein	682795-683910
100	C4Q28_03215	virion morphogenesis protein	683922-684602
101	C4Q28_03220	phage tail completion protein	684592-685047
102	C4Q28_03225	head completion protein	685044-685505
103	C4Q28_03230	terminase	685604-686329
104	C4Q28_03235	phage major capsid protein, P2 family	686326-687345

105	C4Q28_03240	capsid scaffolding protein	687345-688307
106	C4Q28_03245	terminase	688468-690456
107	C4Q28_03250	phage portal protein	690350-691282
108	C4Q28_03255	transcriptional regulator	691355-691609
109	C4Q28_03260	hypothetical protein	692061-692294
110	C4Q28_03265	DNA-binding protein	692291-692548
111	C4Q28_03270	hypothetical protein	692559-692798
112	C4Q28_03275	hypothetical protein	692865-693131
113	C4Q28_03280	hypothetical protein	693564-696257
114	C4Q28_03285	hypothetical protein	696267-696482
115	C4Q28_03290	XRE family transcriptional regulator	696577-696813
116	C4Q28_03295	integrase	696817-697887
117	C4Q28_03300	tRNA-Met	697949-698025
118	C4Q28_03305	bifunctional diguanylate cyclase/phosphodies terase	698042-701785

		119	C4Q28_03310	RNA polymerase RpoD-like protein	701905-703755
		120	C4Q28_03315	DNA primase	703823-705805
3	1007790- 1023145	121	C4Q28_04825	hypothetical protein	1007746-1007975
		122	C4Q28_04830	hypothetical protein	1008255-1009274
		121	C4Q28_04835	hypothetical protein	1009267-1010316
		122	C4Q28_04840	IS30 family transposase	1010358-1011374
		123	C4Q28_04845	hypothetical protein	1011322-1012074
		124	C4Q28_04850	hypothetical protein	1013953-1014278
		125	C4Q28_04855	XRE family transcriptional regulator	1014242-1014634
		126	C4Q28_04860	DDE transposase	1014730-1015565
		127	C4Q28_04865	hypothetical protein	1015876-1016730
		128	C4Q28_04870	hypothetical protein	1016814-1017434
		129	C4Q28_04875	hypothetical protein	1017608-1018096
		130	C4Q28_04880	preprotein translocase subunit SecA	1018481-1020814
		131	C4Q28_04885	hypothetical protein	1021612-1022463

4	1272390- 1308485	132	C4Q28_05995	glycine/betaine ABC transporter substrate-binding protein	1272305-1273216
		133	C4Q28_06000	ABC transporter permease	1273230-1273943
		134	C4Q28_06005	hypothetical protein	1274322-1274900
		135	C4Q28_06010	integrase	1275253-1276497
		136	C4Q28_06015	addiction module toxin RelE	1276558-1276926
		137	C4Q28_06020	transcriptional regulator	1276919-1277248
		138	C4Q28_06025	hypothetical protein	1277329-1277580
		139	C4Q28_06030	hypothetical protein	1277797-1278036
		140	C4Q28_06035	hypothetical protein	1278073-1278345
		141	C4Q28_06040	site-specific integrase	1278363-1279538
		142	C4Q28_06045	hypothetical protein	1279867-1280466
		143	C4Q28_06050	DNA-binding protein	1280994-1281176
		144	C4Q28_06055	helicase	1281194-1284403
		145	C4Q28_06060	DUF4391 domain- containing protein	1284418-1285197

146	C4Q28_06065	site-specific DNA- methyltransferase	1285212-1287059
147	C4Q28_06070	restriction endonuclease subunit R	1287072-1290086
148	C4Q28_06075	SIR2 family protein	1290202-1291215
149	C4Q28_06080	ATPase	1291225-1292955
150	C4Q28_06085	transcriptional regulator	1293092-1293454
151	C4Q28_06090	hypothetical protein	1293477-1293656
152	C4Q28_06095	anti-restriction protein ArdA	1294238-1294750
153	C4Q28_06100	hypothetical protein	1295123-1295905
154	C4Q28_06105	hypothetical protein	1296012-1297910
155	C4Q28_06110	hypothetical protein	1298268-1298717
156	C4Q28_06115	hypothetical protein	1298801-1299130
157	C4Q28_06120	hypothetical protein	1299245-1299574
158	C4Q28_06125	hypothetical protein	1299647-1300333
159	C4Q28_06130	hypothetical protein	1300432-1301304
160	C4Q28_06135	hypothetical protein	1301486-1301743
161	C4Q28_06140	TRAG family protein	1301754-1303178
162	C4Q28_06145	hypothetical protein	1303604-1303813

		163	C4Q28_06150	hypothetical protein	1304542-1304829
		164	C4Q28_06155	relaxase	1304826-1306415
		165	C4Q28_06160	hypothetical protein	1306489-1306995
		166	C4Q28_06165	hypothetical protein	1307026-1307511
		167	C4Q28_06170	hypothetical protein	1307540-1308370
5	2538588- 2547684	168	C4Q28_12015	four-helix bundle copper-binding protein	2538592-2539044
		169	C4Q28_12020	TonB-dependent receptor	2539153-2541213
		170	C4Q28_12025	hypothetical protein	2541292-2541696
		171	C4Q28_12030	DUF2946 domain- containing protein	2541828-2542148
		172	C4Q28_12035	nickel import ATP- binding protein NikE	2542263-2543078
		173	C4Q28_12040	nickel import ATP- binding protein NikD	2543075-2543845
		174	C4Q28_12045	nickel ABC transporter permease subunit NikC	2543846-2544691

		175	C4Q28_12050	nickel ABC transporter permease subunit NikB	2544688-2545629
		176	C4Q28_12055	nickel ABC transporter, nickel/metallophore periplasmic binding protein	2545631-2547205
		179	C4Q28_12060	nickel-responsive transcriptional regulator NikR	2547293-2547718
6	3654735- 3678798	180	C4Q28_17100	LysR family transcriptional regulator	3654863-3655738
		181	C4Q28_17105	MFS transporter	3656143-3657441
		182	C4Q28_17110	aminotransferase	3657423-3658103
		183	C4Q28_17115	outer membrane porin, OprD family	3658246-3659598
		184	C4Q28_17120	hypothetical protein	3659699-3659974
		185	C4Q28_17125	hypothetical protein	3661611-3662066

186	C4Q28_17130	aldehyde dehydrogenase PuuC	3662077-3663591
187	C4Q28_17135	amino acid permease	3663661-3665112
188	C4Q28_17140	glutamine amidotransferase	3665182-3666048
189	C4Q28_17145	ferredoxin	3666067-3666261
190	C4Q28_17150	cytochrome P450	3666275-3667435
191	C4Q28_17155	glutamine synthetase	3667498-3668877
192	C4Q28_17160	4Fe-4S dicluster domain-containing protein	3668940-3669260
193	C4Q28_17165	ferredoxin-- NADP(+) reductase	3669261-3670244
194	C4Q28_17170	KR domain- containing protein	3670604-3671356
195	C4Q28_17175	helix-turn-helix domain-containing protein	3671685-3672230
196	C4Q28_17180	hypothetical protein	3672315-3673091

		197	C4Q28_17185	succinate- semialdehyde dehydrogenase	3673088-3674470
		198	C4Q28_17190	glutamine amidotransferase	3674565-3675467
		199	C4Q28_17195	IS66 family insertion sequence hypothetical protein	3675812-3676132
		200	C4Q28_17200	IS66 family insertion sequence hypothetical protein	3676129-3676461
		201	C4Q28_17205	IS66 family transposase	3676519-3677979
		202	C4Q28_17210	porin	3678275-3679603
7	3682759- 3697545	203	C4Q28_17220	GMC family oxidoreductase	3681040-3682806
		204	C4Q28_17225	dehydrogenase	3682824-3683546
		205	C4Q28_17230	LacI family DNA- binding transcriptional regulator	3683788-3684816
		206	C4Q28_17235	hypothetical protein	3684919-3685251

207	C4Q28_17240	IclR family transcriptional regulator	3685361-3686134
208	C4Q28_17245	DUF1656 domain- containing protein	3686230-3686439
209	C4Q28_17250	efflux RND transporter periplasmic adaptor subunit	3686436-3687317
210	C4Q28_17255	hypothetical protein	3687314-3689086
211	C4Q28_17260	AraC family transcriptional regulator	3689098-3690153
212	C4Q28_17265	amino acid permease	3690446-3691873
213	C4Q28_17270	phytanoyl-CoA dioxygenase	3691910-3692791
214	C4Q28_17275	polyketide cyclase	3692839-3693231
215	C4Q28_17280	nitrilotriacetate monooxygenase	3693301-3693837
216	C4Q28_17285	LacI family DNA- binding	3693959-3694156

			transcriptional regulator	
		217	C4Q28_17290 DoxX family membrane protein	3694258-3695160
		218	C4Q28_17295 hypothetical protein	3695173-3695685
		219	C4Q28_17300 hypothetical protein	3695750-3696223
		220	C4Q28_17305 glyoxalase	3696364-3697551
8	3704939- 3718588	221	C4Q28_17335 alcohol dehydrogenase	3704186-3705493
		222	C4Q28_17340 outer membrane porin, OprD family	3705582-3706826
		223	C4Q28_17345 galactonate dehydratase	3706980-3708512
		224	C4Q28_17350 enolase	3708578-3709765
		225	C4Q28_17355 MFS transporter	3709782-3711167
		226	C4Q28_17360 LacI family DNA- binding transcriptional regulator	3711449-3712486
		227	C4Q28_17365 steryl acetyl hydrolase	3712499-3713401
		228	C4Q28_17370 outer membrane porin, OprD family	3713444-3714724

229	C4Q28_17375	hypothetical protein	3714764-3715633
230	C4Q28_17380	mandelate racemase/muconate lactonizing enzyme family protein	3715715-3716803
231	C4Q28_17385	NAD(P)-dependent oxidoreductase	3716800-3717609
232	C4Q28_17390	MFS transporter	3717644-3718933
233	C4Q28_17415	IclR family transcriptional regulator	3722280-3723845
234	C4Q28_17420	hypothetical protein	3723910-3724182
235	C4Q28_17425	cation/acetate symporter ActP	3724643-3726208
236	C4Q28_17430	hypothetical protein	3726198-3726488
237	C4Q28_17435	aliphatic nitrilase	3726569-3727639
238	C4Q28_17440	LysR family transcriptional regulator	3727958-3728869
239	C4Q28_17445	CoA transferase	3729137-3730324
240	C4Q28_17450	methylmalonyl-CoA decarboxylase	3730360-3731160

		241	C4Q28_17455	succinate- semialdehyde dehydrogenase (NADP(+))	3731485-3731674
		242	C4Q28_17460	hypothetical protein	3731976-3732713
		243	C4Q28_17465	AlpA family phage regulatory protein	3732827-3733042
9	3750938- 3753781	244	C4Q28_17575	DUF3800 domain- containing protein	3751029-3752150
		245	C4Q28_17580	hypothetical protein	3752219-3753055
		246	C4Q28_17585	molecular chaperone Tir	3753126-3753635
10	3771417- 3777674	247	C4Q28_17690	hypothetical protein	3771779-3772855
		248	C4Q28_17695	hypothetical protein	3772855-3773820
		249	C4Q28_17700	hypothetical protein	3774150-3775226
		250	C4Q28_17705	IS3 family transposase	3775313-3776463
		251	C4Q28_17710	tRNA-Pro	3777731-3777807
11	3976780- 3980761	252	C4Q28_18645	carbon-nitrogen hydrolase family protein	3976866-3977627
		253	C4Q28_18650	MFS transporter	3977678-3979051

		254	C4Q28_18655	hypothetical protein	3979078-3979569
		255	C4Q28_18660	LysR family transcriptional regulator	3979750-3980685
12	4298450- 4322513	256	C4Q28_20150	dTDP-4- dehydrorhamnose reductase	4298338-4299243
		257	C4Q28_20155	dTDP-glucose 4,6- dehydratase	4299240-4300340
		258	C4Q28_20160	hypothetical protein	4300493-4302496
		259	C4Q28_20165	aminotransferase	4302589-4303767
		260	C4Q28_20170	acetyltransferase	4303864-4304487
		261	C4Q28_20175	sugar transferase	4304484-4305080
		262	C4Q28_20180	glycosyltransferase family 1 protein	4305122-4306246
		263	C4Q28_20185	glycosyl transferase	4306357-4307492
		264	C4Q28_20190	asparagine synthase (glutamine- hydrolyzing)	4307486-4309366
		265	C4Q28_20195	hypothetical protein	4309390-4310616
		266	C4Q28_20200	serine acetyltransferase	4310649-4311173

267	C4Q28_20205	glycosyl transferase family 2	4311170-4312078
268	C4Q28_20210	polysaccharide biosynthesis protein	4312080-4313615
269	C4Q28_20215	UDP-4-amino-4, 6- dideoxy-N-acetyl- beta-L-altrosamine N-acetyltransferase	4313581-4314120
270	C4Q28_20220	hypothetical protein	4315087-4315785
271	C4Q28_20225	aminotransferase	4315785-4316897
272	C4Q28_20230	Vi polysaccharide biosynthesis UDP- N- acetylglucosaminur onic acid C-4 epimerase TviC	4317109-4318134
273	C4Q28_20235	Vi polysaccharide biosynthesis UDP- N- acetylglucosamine C-6 dehydrogenase TviB	4318196-4319473

		274	C4Q28_20240	chain-length determining protein	4319774-4321078
		275	C4Q28_20245	hypothetical protein	4321297-4322346
13	5039533- 5058869	276	C4Q28_23550	hypothetical protein	5039637-5040428
		277	C4Q28_23555	integrase	5040613-5040942
		278	C4Q28_23560	restriction endonuclease subunit R	5041083-5043470
		279	C4Q28_23565	hypothetical protein	5043478-5043660
		280	C4Q28_23570	restriction endonuclease subunit S	5043674-5044786
		281	C4Q28_23575	type I restriction endonuclease subunit M	5044783-5046237
		282	C4Q28_23580	hypothetical protein	5047770-5048012
		283	C4Q28_23585	hypothetical protein	5048121-5048384
		284	C4Q28_23590	hypothetical protein	5049016-5049225
		285	C4Q28_23595	DUF726 domain- containing protein	5049217-5052462
		286	C4Q28_23600	labile enterotoxin output A	5052462-5054165

287	C4Q28_23605	hypothetical protein	5054502-5054759
288	C4Q28_23610	WYL domain- containing protein	5054879-5055754
289	C4Q28_23615	hypothetical protein	5055914-5056120
290	C4Q28_23620	hypothetical protein	5056147-5056347
291	C4Q28_23625	hypothetical protein	5056682-5058163
292	C4Q28_23630	GABA permease	5058478-5059869

Table S10. Predicted ORF functions of putative prophage.

CDS	coordinates	AA Size	^a Locus Tag	Function
1	666612-667673	353	11631	Site specific recombinase XerD
2	667800-667844	-	-	<i>attL</i>
3	668199-669800	533	11632	hypothetical protein
4	669838-670809	323	11633	hypothetical protein
5	670782-671486	234	11634	hypothetical protein
6	671483-672031	182	11635	DNA-binding protein
7	672028-672951	307	11636	hypothetical protein
8	672948-673655	235	11637	hypothetical protein
9	673663-674709	348	11638	hypothetical protein
10	674893-676059	388	11638	phage tail protein
11	676068-676592	174	11639	phage tail protein
12	676589-677761	390	11640	Phage protein gp47
13	677758-678075	105	11641	DUF2590 domain-containing protein
14	678075-680438	787	11642	phage tail tape measure protein
15	680613-680900	95	11643	tail assembly chaperone
16	680897-681394	165	11644	lysis protein
17	681391-681921	176	11645	lysozyme
18	681918-682124	68	11646	hypothetical protein
19	682121-682339	72	11647	conjugal transfer protein TraR
20	682339-682788	149	11648	DUF2597 domain-containing protein

21	682795-683910	371	11649	DUF2586 domain-containing protein
22	683922-684602	226	11650	virion morphogenesis protein
23	684592-685047	151	11651	phage tail completion protein
24	685044-685505	153	11652	head completion protein
25	685604-686329	241	11653	terminase
26	686326-687345	339	11654	phage major capsid protein, P2 family
27	687345-688307	320	11655	capsid scaffolding protein
28	688468-690456	680	11656	terminase
29	690350-691282	245	11657	phage portal protein
30	692061-692294	77	11658	hypothetical protein
31	692291-692548	85	11659	DNA-binding protein
32	692559-692798	79	11660	hypothetical protein
33	692865-693104	79	11661	hypothetical protein
34	693564-696257	897	11662	Toprim domain-containing protein
35	696577-696813	78	11664	XRE family transcriptional regulator
36	696817-697887	356	11665	Site specific recombinase XerD
37	697952-698025	74	11666	tRNA-Met
38	697949-697993	-	-	<i>attR</i>
39	698042-701785	1247	11667	bifunctional diguanylate cyclase/phosphodiesterase
40	701905-703755	616	11668	RNA polymerase sigma factor
41	703823-705805	660	11669	DNA primase

^a JGI locus tags numbers begin with Ga0255654_

Table S11. Predicted genes that encode for antibiotic resistance.

Resistance to	Number of genes in:				
	SWI36	SWI44	SWI6	SWI7	PAO1
Lactams	9	10	10	7	5
Chloramphenicol	6	4	4	3	1
Macrolides	2	2	2	3	1
Vancomycin	0	0	0	0	1
Aminoglycosides	2	1	1	1	2
Efflux pumps	15	11	11	12	12
Total	34	28	28	26	22