Table S1. Annotation of ORFs in a novel 124 Kb *P. aeruginosa* gene island (from 5’ to 3’)

ORF	Start	End	Length (bp)	Accession Number	Gene Name	Annotation (highest nucleotide sequence homology)
1*	1	501	501	CP000352		*Cupriavidus metallidurans* – putative membrane protein
2*	766	1698	933	CP000352		*C. metallidurans* – conserved hypothetical protein
3*	1817	2029	213	CP000352	*alpA*	*C. metallidurans* – DNA-binding transcriptional activator
4*	2072	2947	876	CP000352	*soj*	*C. metallidurans* – ATPase involved in plasmid partitioning Soj
5*	2931	3200	270	CP000352		*C. metallidurans* – conserved hypothetical protein
6*	3193	4872	1680	CP000352		*C. metallidurans* – putative regulator
7*	4887	5447	561	CP000352		*C. metallidurans* – putative regulator
8*	5451	6689	1239	CP000352		*C. metallidurans* – conserved hypothetical protein
9*	7119	7910	792	CP000352		*C. metallidurans* – conserved hypothetical protein
10*	7907	8434	528	CP000352	*inrR*	*C. metallidurans* – integrase regulator R
11*	8508	8948	441	CP000352	*ssb2*	C. metallidurans – single-stranded DNA binding protein
12*	8957	9097	141	CP000352		*C. metallidurans* – transposon:CH34 genomic island CMGI-1
13*	9310	11340	2031	CP000352	*topB2*	*C. metallidurans* – DNA topoisomerase III
14*	12064	12699	636	CP000352		*C. metallidurans* – cation efflux system protein
15*	13084	13320	237	CP000352		*C. metallidurans* – conserved hypothetical protein
16*	13520	13708	189	CP000352		*C. metallidurans* – hypothetical protein
17*	13776	14174	399	CP000352	*pbrR2*	*C. metallidurans* – transcriptional regulator, MerR-family
18*	14266	17178	2913	CP000352	*cadA*	*C. metallidurans* – lead/cadmium-transporting ATPase
19*	17182	17682	501	CP000352	*pbrC2*	*C. metallidurans* – prolipoprotein signal peptidase
20*	18082	18330	249	CP000352		*C. metallidurans* – conserved hypothetical protein
21*	18668	18880	213	CP000352		*C. metallidurans* – conserved hypothetical protein
22	18902	19294	393	CP000774		*Parvibaculum lavamentivorans* - conserved hypothetical protein
23	19508	20245	738	CP000774		*P. lavamentivorans* - conserved hypothetical protein
24	20342	20620	279	CP000774		*P. lavamentivorans* - conserved hypothetical protein
25	20908	21720	813	CP000774		*P. lavamentivorans* - conserved hypothetical protein
26	21862	22215	354	CP000774		*P. lavamentivorans* - conserved hypothetical protein
27	22582	23511	930	CP000774		*P. lavamentivorans* - conserved hypothetical protein
28	23570	24259	690	CP000774		*P. lavamentivorans* - conserved hypothetical protein
29	24354	24680	327	CP000774		*P. lavamentivorans* - conserved hypothetical protein
30	24783	25124	342	CP000774		*P. lavamentivorans* - conserved hypothetical protein
31	25211	25861	651	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
32	25887	27035	1149	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
33*	27086	27406	321	CP000352		*C. metallidurans* – conserved hypothetical protein
34	27663	27803	141	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
35*	27940	30219	2280	CP000352		*C. metallidurans* – putative plasmid-related DNA/RNA helicase
36	30278	31000	723	CP000539		*Acidovorax sp. JS42* - NADPH-dependent FMN reductase
37	30993	31415	423	CP002287	*arsC1*	*Achromobacter xylosoxidans* - arsenate reductase (glutaredoxin) 1
38	31432	32508	1077	CP002287		*A. xylosoxidans* - sodium bile acid symporter family protein 1
39	32520	33050	531	CP002287		*A. xylosoxidans* - low molecular weight phosphotyrosine protein phosphatase family protein
40	33017	33337	321	CP000539		*Acidovorax sp. JS42* - transcriptional regulator, ArsR family
41	33506	34084	579	CP000539		*Acidovorax sp. JS42* - putative secreted protein
42	34081	34725	645	AM902716		*Bordetella petrii* - putative membrane protein
43	34738	35463	726	AM902716		*B. petrii* - conserved protein, putatively exported
44	35445	36047	603	CP002449		*Alicycliphilus denitrificans* - Lytic transglycosylase catalytic
45	36044	36592	549	CP000539		*Acidovorax sp. JS42* - putative secreted protein
46*	36597	38789	2193	CP000352	*virD4*	*C. metallidurans* – Type IV secretory pathway, VirD4 components
47	38786	39535	750	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
48*	39576	42200	2625	CP000352		*C. metallidurans* – conserved hypothetical protein
49*	42210	42935	726	CP000352		*C. metallidurans* – conserved hypothetical protein
50*	42974	43876	903	CP000352		*C. metallidurans* – conserved hypothetical protein
51*	43876	44376	501	CP000352		*C. metallidurans* – conserved hypothetical protein
52*	44373	44843	471	CP000352		*C. metallidurans* – conserved hypothetical protein
53*	44840	45754	915	CP000352		*C. metallidurans* – putative AAA ATPase
54*	45772	46275	504	CP000352		*C. metallidurans* – conserved hypothetical protein

55*	46344	46814	471	CP000352		*C. metallidurans* – putative excisionase
56*	47018	47401	384	CP000352		*C. metallidurans* – conserved hypothetical protein
57	47398	47631	234	CP002287		*A. xylosoxidans* - hypothetical protein
58	47648	48007	360	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
59	48019	48417	399	CP002287		*A. xylosoxidans* - hypothetical protein
60	48414	49106	693	CP002287		*A. xylosoxidans* - hypothetical protein
61	49103	50014	912	CP002287		*A. xylosoxidans* - hypothetical protein
62	50004	51422	1419	CP002287		*A. xylosoxidans* - hypothetical protein
63	51403	51858	456	CP000539		*Acidovorax sp. JS42* - putative secreted protein
64*	51858	54758	2901	CP000352		*C. metallidurans* – Type IV secretory pathway, VirB4 components
65*	54783	55550	768	CP000352		*C. metallidurans* – putative exported protein
66*	55726	56220	495	CP000352	*radC*	*C. metallidurans* – DNA binding protein
67	56433	56831	399	CP000539		*Acidovorax sp. JS42* - protein of unknown function DUF1525
68	56828	57778	951	CP002287		*A. xylosoxidans* - hypothetical protein
69	57788	59182	1395	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
70	59179	59538	360	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
71	59552	61072	1521	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
72	61084	61449	366	CP000539		*Acidovorax sp. JS42* - conserved hypothetical protein
73	61530	62162	633	AM902716		*B. petrii* - conserved hypothetical protein
74	62175	62801	627	AM902716		*B. petrii* - conserved hypothetical protein
75	62769	62969	201	AM902716		*B. petrii* - conserved hypothetical protein
76	63193	64929	1737	CP000539		*Acidovorax sp. JS42* - relaxase
77	64911	65021	111			No significant similarity
78	65071	65184	114			No significant similarity
79	65253	65408	156			No significant similarity
80	65431	66726	1296			No significant similarity
81	66763	67227	465			No significant similarity
82	68072	69298	1227	CP000744		*Pseudomonas aeruginosa* PA7 – transposase, Mutator family
83	69301	71631	2331	CP000884		*Delftia acidovorans*- heavy metal translocating P-type ATPase
84	71745	72017	273	CP002287		*A. xylosoxidans* - hypothetical protein
85	72051	72536	486	CP002287		*A. xylosoxidans* - hypothetical protein
86	72574	73554	981	CP000539		*Acidovorax sp. JS42* - copper resistance B precursor
87	73580	75341	1762	CP000539		A. xylosoxidans - copper resistance protein, CopA family
88	75743	76447	705	CP000539		*Acidovorax sp. JS42* - two component heavy metal response transcriptional regulator, winged helix family
89	76419	77855	1437	CP002287		*A. xylosoxidans* - sensor kinase CusS
90	78405	78515	111			No significant similarity
91	78490	78816	327			No significant similarity
92	78835	79134	300			No significant similarity
93	79143	80810	1668	CP002657		*A. denitrificans* - hypothetical protein
94	80881	81093	213			No significant similarity
95	81106	82239	1134			No significant similarity
96	82457	82909	453			No significant similarity
97	83064	84380	1317	CP000539		*Acidovorax sp. JS42* - Cyclopropane-fatty-acyl-phospholipid synthase
98	84498	86927	2430	CP000539		*Acidovorax sp. JS42* - D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase
99	87105	87707	603			No significant similarity
100	87824	88654	831	AB022919	*psbB*	*Rhodopseudomonas palustris* – oxidoreductase involved in aerobic degradation of para-substituted benzoate derivatives
101	88663	89925	1263			No significant similarity
102	89922	90977	1056	CP000539		*Acidovorax sp. JS42* - glyceraldehyde-3 phosphate dehydrogenase
103	91005	92627	1623	CP000539		*Acidovorax sp. JS42* - 2-octaprenylphenol hydroxylase
104	92624	93655	1032	CP000539		*Acidovorax sp. JS42* - D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding protein
105	93652	93906	255			No significant similarity
106	93903	94547	645	CP000539		*Acidovorax sp. J S42* - conserved hypothetical protein
107	94601	95500	900	CP000539		*Acidovorax sp. JS42* - ribose-phosphate pyrophosphokinase

108	95497	97050	1554	CP000539		*Acidovorax sp. JS42* - putative thymidine phosphorylase
109	97047	98408	1362	CP000539		*Acidovorax sp. JS42* - beta-lactamase domain protein
110	98434	98925	492	CP002657		*A. denitrificans* - protein of unknown function DUF477
111	98933	99820	888			No significant similarity
112	99840	100451	612	CP000539		*Acidovorax sp. JS42* - LemA family protein
113	100448	101773	1326	CP002657		*A. denitrificans* - major facilitator superfamily MFS 1
114	101787	104252	2466	CP002657		*A. denitrificans* - copper translocating P-type ATPase
115	104285	105148	864	CP000539		*Acidovorax sp. JS42* - protein of unknown function DUF344
116	105159	105317	159			No significant similarity
117	105319	105969	651			No significant similarity
118	105966	106205	240			No significant similarity
119	106217	106618	402			No significant similarity
120	106830	107354	525			No significant similarity
121	107339	107743	405			No significant similarity
122	107746	108972	1227	CP000744		*P. aeruginosa* PA7 – transposase, Mutator family
123	109005	109229	225	CP002287		*A. xylosoxidans* – copper-translocating P-type ATPase 2
124	109371	109757	387	CP002287	*copC*	*A. xylosoxidans* - copper resistance protein C
125	109762	110688	927	CP002287	*copD*	*A. xylosoxidans* - copper resistance protein D
126	110817	111101	285	CP002287		*A. xylosoxidans* - hypothetical protein
127	111335	112225	891	CP002287		*A. xylosoxidans* - transcriptional regulator 2
128	112230	112349	120	CP002287		*A. xylosoxidans* - helix-turn-helix family protein 2
129	112350	112568	219	CP002287		*A. xylosoxidans* - helix-turn-helix family protein 2
130	112760	113284	525	CP002287		*A. xylosoxidans* - bacterial regulatory helix-turn-helix protein, LysR family protein 34
131	113313	113417	105	CP002287		*A. xylosoxidans* - hypothetical protein
132	113571	113882	312	CP002287		*A. xylosoxidans* - hypothetical protein
133	113958	115265	1308	CP002287		*A. xylosoxidans* - heavy metal RND efflux outer membrane protein, CzcC family
134	115281	116798	1518	CP002287		*A. xylosoxidans* - efflux transporter, RND family, MFP subunit 3
135	116795	119914	3120	CP000539		*Acidovorax sp. JS42* - heavy metal efflux pump, CzcA family
136	120073	121170	1098	AP008229	*XOO4197*	*Xanthomonas oryzae* - ISXoo14 transposase
137	122005	123909	1905	CP000539		*Acidovorax sp. JS42* - phage integrase family protein

***Also found on *Pseudomonas aeruginosa* gene island PAGI-2(C)**

Origin of DNA

🟨	**Cupriavidus**	🟦	**Achromobacter**	🟪	**Pseudomonas**	🟦	**Xanthomonas**
🟩	**Parvibaclum**	🟧	**Bordetella**	⬜	**Rhodopseudomonas**	⬜	**No homology**
🟩	**Acidovorax**	🟧	**Alicycliphilus**	🟪	**Delftia**		

Table S2. Potential Deletions in PA Strain 3

Size of Deletion (bp)	Putative Gene Function of Deletion Site
1	putative Rossman fold nucleotide-binding
7	No gene
1	No gene
1	*MoeA1*, Molydopterin biosynthesis enzyme
4	putative sodium/hydrogen exchanger
2	single-stranded-DNA-specific exonuclease RecJ
2	putative transcriptional regulator, AraC family
3	conserved hypothetical protein
1	conserved hypothetical protein
3	putative oxidase
7	cytochrome C Snr1
3	putative molybdopterin-guanine dinucleotide
3	putative diacylglycerol kinase
3	putative ABC transporter, permease protein
5	conserved hypothetical protein
1	putative chemotaxis transducer
6	gluconokinase
2	hpothetical protein
7	putative DNA helicase
5	No gene
8	glutaminyl-tRNA synthetase
10	No gene
1	putative transcriptional regulator
1	No gene
2	hypothetical protein
2	alkaline protease secretion protein AprD
2	probable MFS transporter
3	No gene
7	No gene
18	putative MFS transporter
1	conserved hypothetical protein
5	putative 3-hydroxyacyl-CoA dehydrogenase
1	putative ABC transporter ATP-binding