

Table S1 MICs ($\mu\text{g/ml}$) to four aminoglycosides of selected transposon insertion library mutants of *P. aeruginosa* PA14.

Mutant	TOB	STR	AMK	KAN	PAO1 orthologue of mutant gene	Gene name	Gene description
PA14	0.75	8	1	24	-		
1	1	16	3	16	<i>PA5130</i>		hypothetical protein
2	1	12	1.5	32	<i>PA5150</i>		dehydrogenase
3	1	128	4	≥ 256	<i>PA5183</i>		hypothetical protein
4	0.5	3	1	16	<i>PA5469</i>		hypothetical protein
5	1.5	32	8	48	<i>PA5471</i>	<i>armZ</i>	<i>mexZ</i> anti-repressor
6	1	32	6	64	<i>PA4999</i>	<i>waaL</i>	O-antigen ligase
7	0.5	8	1	12	<i>PA0770</i>	<i>rnc</i>	ribonuclease III
8	1	12	1.5	24	<i>PA1316</i>		probable MFS transporter
9	1	192	8	≥ 256	<i>PA1440</i>		hypothetical protein
10	0.5	16	1.5	16	<i>PA2659</i>		hypothetical protein
11	3	24	8	64	<i>PA3247</i>		hypothetical protein
12	1	12	1	32	<i>PA3433</i>		transcriptional regulator
13	3	16	4	32	<i>PA3844</i>		hypothetical protein
14	0.75	16	3	32	<i>PA4441</i>		hypothetical protein
15	0.75	96	3	≥ 256	<i>PA4874</i>		conserved hypothetical protein
16	1.5	16	6	48	<i>PA0479</i>		transcriptional regulator
17	0.75	16	3	32	<i>PA1411</i>		hypothetical protein
18	1	12	1.5	48	<i>PA1442</i>		conserved hypothetical protein
19	3	24	4	48	<i>PA3704</i>		chemotaxis sensor
20	0.75	12	2	32	<i>PA3983</i>		conserved hypothetical protein
21	0.38	8	0.75	16	<i>PA5016</i>	<i>aceF</i>	dihydrolipoamide acetyltransferase
22	1	24	3	32	<i>PA5003</i>		Mig-14-like protein
23	1	12	1.5	32	<i>PA1167</i>		hypothetical protein
24	1	12	2	48	<i>PA1452</i>	<i>flhA</i>	flagellar biosynthesis protein
25	0.75	8	0.5	12	<i>PA4465</i>		conserved hypothetical protein
26	1	12	2	16	<i>PA5193</i>	<i>yrfl</i>	heat shock protein
27	2	32	6	96	<i>PA14_15600</i>		hypothetical protein
28	3	32	6	64	<i>PA14_28520</i>		hypothetical protein
29	0.5	12	1.5	48	<i>PA1375</i>	<i>pdxB</i>	dehydrogenase
30*	0.38	3	0.25	6	<i>PA3016</i>		hypothetical protein
31	0.5	4	1	24	<i>PA3032</i>		cytochrome C

32	2	24	8	64	<i>PA3259</i>		hypothetical protein
33	1.5	16	1	32	<i>PA4496</i>		transporter ABC binding protein
34	0.5	16	1.5	32	<i>PA4740</i>	<i>pnp</i>	polynucleotide phosphorylase
35	0.75	16	2	16	<i>PA5368</i>	<i>pstC</i>	phosphate transporter
36	0.5	6	0.5	32	<i>PA2965</i>	<i>fabF1</i>	3-oxoacyl-ACP synthase
37	3	32	6	64	<i>PA4402</i>	<i>argJ</i>	glutamate N-acetyltransferase
38	0.75	8	0.5	16	<i>PA3160</i>	<i>wzz</i>	O-antigen chain length regulator
39	4	64	8	96	<i>PA2621</i>	<i>clpS</i>	protease
40	3	32	8	96	<i>PA452</i>	<i>pilC</i>	fimbrial biogenesis protein
41	0.38	8	0.75	24	<i>PA0590</i>	<i>apaH</i>	diadenosine tetraphosphatase
42	0.75	8	0.75	16	<i>PA2876</i>	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase
43	1	16	1.5	32	<i>PA3350</i>		hypothetical protein
44	1.5	8	1.5	32	<i>PA5470</i>		probable peptide chain release factor
45	0.5	6	1.5	16	<i>PA0427</i>	<i>oprM</i>	outer membrane protein
46	1	16	1	32	<i>PA0104</i>		hypothetical protein
47	1	16	6	32	<i>PA1809</i>	<i>nppB</i>	ABC permease
48	1	12	8	48	<i>PA2020</i>	<i>mexZ</i>	<i>mexXY</i> repressor
49	1	64	6	128	<i>PA2970</i>	<i>rpmF</i>	50S ribosomal protein L32
50	0.75	6	0.75	16	<i>PA4069</i>		hypothetical protein
51*	0.25	4	0.75	8	<i>PA4942</i>	<i>hflK</i>	protease
52	2	24	8	48	<i>PA5443</i>	<i>uvrD</i>	DNA helicase II
53	1.5	48	6	48	<i>PA14_23420</i>		zinc binding dehydrogenase
54	0.5	12	2	32	<i>PA14_06490</i>		hypothetical protein
55	2	48	8	64	<i>PA14_43090</i>		hypothetical protein
56	0.75	8	0.75	24	<i>PA0407</i>	<i>gshB</i>	glutathione synthetase
57	1	8	0.75	32	<i>PA2017</i>		hypothetical protein
58	0.38	4	0.75	12	<i>PA3584</i>	<i>glpD</i>	dehydrogenase
59	0.75	8	0.75	16	<i>PA4269</i>	<i>rpoC</i>	RNA polymerase subunit beta
60	0.5	12	0.5	24	<i>PA5203</i>	<i>gshA</i>	glutamate—cysteine ligase
61	0.5	12	2	24	<i>PA14_49010</i>		hypothetical protein
62	0.38	4	0.5	32	<i>PA2018</i>	<i>mexY</i>	RND multidrug efflux transporter
63*	0.25	3	0.5	16	<i>PA3658</i>	<i>glnD</i>	PII uridylyl transferase

64	1	12	1.5	32	<i>PA5263</i>	<i>argH</i>	argininosuccinate lyase
65	0.75	16	1.5	12	<i>PA5332</i>	<i>crc</i>	catabolite repression control protein
66	1	12	1.5	16	<i>PA402</i>	<i>pyrB</i>	aspartate carbamoyltransferase
67	0.5	12	1.5	32	<i>PA1005</i>		conserved hypothetical protein
68	0.5	12	2	48	<i>PA1080</i>	<i>flgE</i>	flagellar hook protein
69	0.75	12	2	32	<i>PA1081</i>	<i>flgF</i>	flagellar basal-body rod protein
70	3	16	3	32	<i>PA1083</i>	<i>flgH</i>	flagellar L-ring protein
71	1.5	12	3	48	<i>PA1084</i>	<i>flgI</i>	flagellar P-ring protein
72	2	16	1.5	48	<i>PA1085</i>	<i>flgJ</i>	flagellar rod assembly protein
73	1	12	1	32	<i>PA1777</i>	<i>oprF</i>	outer membrane protein
74	2	32	6	64	<i>PA2023</i>	<i>galU</i>	UTP-glucose-1-phosphate uridylyltransferase
75	0.38	6	0.5	16	<i>PA2615</i>	<i>ftsK</i>	cell division protein
76	1	16	1.5	24	<i>PA3244</i>	<i>minD</i>	cell division inhibitor
77	0.75	16	3	32	<i>PA3391</i>	<i>nosR</i>	regulatory protein
78	1	12	1.5	48	<i>PA4954</i>	<i>motA</i>	flagellar motor protein
79	0.5	8	0.75	12	<i>PA5558</i>	<i>atpF</i>	ATP synthase subunit B
80	1	16	1	32	<i>PA14_22270</i>		probable recombinase
81	0.5	8	2	32	<i>PA0420</i>	<i>bioA</i>	transaminase
82	0.5	6	0.75	16	<i>PA3194</i>	<i>edd</i>	phosphoenolpyruvate dehydratase
83	0.5	12	2	32	<i>PA3351</i>		hypothetical protein
84*	0.25	3	0.75	16	<i>PA4463</i>		conserved hypothetical protein
85	0.5	16	2	48	<i>PA5197</i>		ribosomal protein S6
86	0.75	16	2	32	<i>PA0026</i>		hypothetical protein
87	0.75	8	1.5	16	<i>PA0401</i>		non-catalytic dihydroorotase-like protein
88	1	8	1	24	<i>PA0503</i>	<i>bioC</i>	probable biotin synthesis protein
89	1	16	1.5	32	<i>PA1086</i>	<i>flgK</i>	flagellar hook-associated protein
90	1	12	1	24	<i>PA1195</i>		hypothetical protein
91	0.75	16	3	48	<i>PA1770</i>	<i>ppsA</i>	phosphoenolpyruvate synthase
92	0.75	8	1.5	12	<i>PA3050</i>	<i>pyrD</i>	dihydroorotate dehydrogenase
93	3	12	1.5	32	<i>PA3108</i>	<i>purF</i>	amidophosphoribosyltransferase
94	0.75	12	1	16	<i>PA4462</i>	<i>rpoN</i>	RNA polymerase sigma-54 factor
95	0.5	8	1.5	12	<i>PA4748</i>	<i>tpiA</i>	triosephosphate isomerase

96	3	24	6	48	<i>PA5000</i>	<i>wapR</i>	alpha-1,3-rhamnosyltransferase
97	1	12	1.5	32	<i>PA5174</i>		probable beta-ketoacyl synthase
98	1	16	2	48	<i>PA3145</i>	<i>wbpL</i>	glycosyltransferase
99	0.25	8	0.75	48	<i>PA0766</i>	<i>mucD</i>	serine protease
100	1	16	0.75	48	<i>PA3109</i>		hypothetical protein
101	0.75	12	2	32	<i>PA3649</i>		conserved hypothetical protein
102	0.5	12	2	48	<i>PA4343</i>		probable MFS transporter
103	1	16	2	48	<i>PA5005</i>		probable carbamoyl transferase
104	1	8	1.5	32	<i>PA5038</i>	<i>aroB</i>	3-dehydroquinate synthase
105	1.5	16	2	48	<i>PA5300</i>	<i>cycB</i>	cytochrome c5
106	0.19	6	0.38	12	<i>PA5199</i>	<i>amgS</i>	two-component sensor
107	3	32	6	64	<i>PA5001</i>	<i>ssg</i>	cell surface sugar
108	2	24	8	128	<i>PA4946</i>	<i>mutL</i>	DNA mismatch repair protein
109	2	24	3	64	<i>PA4429</i>		cytochrome c1
110	1.5	48	6	96	<i>PA3818</i>	<i>suhB</i>	extragenic suppressor protein
111	2	32	8	64	<i>PA3667</i>		pyridoxal-phosphate dependent enzyme
112	1.5	32	6	48	<i>PA3620</i>	<i>mutS</i>	DNA mismatch repair protein
113	3	32	8	48	<i>PA3589</i>		probable acyl-CoA thiolase
114	2	12	4	48	<i>PA2648</i>	<i>nuoM</i>	NADH dehydrogenase I chain M
115	2	16	2	48	<i>PA2644</i>	<i>nuoI</i>	NADH dehydrogenase I chain J
116	2	16	4	48	<i>PA1553</i>	<i>ccoOI</i>	cytochrome c oxidase, ccoO subunit
117	0.75	12	1.5	24	<i>PA0392</i>		hypothetical protein
118	2	24	3	48	<i>PA0337</i>	<i>ptsP</i>	phosphotransferase
119	1	12	1.5	32	<i>PA3014</i>	<i>faoA</i>	fatty-acid oxidation complex alpha-subunit
120	0.75	8	0.75	16	<i>PA5366</i>	<i>pstB</i>	phosphate transporter
121	0.75	8	1	24	<i>PA2797</i>		probable two-component sensor
122*	0.19	4	0.19	8	<i>PA2798</i>		probable two-component response regulator
123	1	8	1	32	<i>PA0113</i>		probable cytochrome c oxidase assembly factor
124	1.5	8	1.5	32	<i>PA0393</i>	<i>proC</i>	pyrroline-5-carboxylate reductase
125	1	8	1	48	<i>PA1622</i>		probable hydrolase
126	3	24	3	64	<i>PA1767</i>		hypothetical membrane protein
127	2	8	1	32	<i>PA4609</i>	<i>radA</i>	DNA repair protein

128	2	12	1.5	32	<i>PA1856</i>	<i>ccoN-2</i>	cbb3-type cytochrome c oxidase subunit I
129	1.5	48	1.5	32	<i>PA2997</i>	<i>nqrC</i>	NADH quinone reductase
130	2	12	3	48	<i>PA3003</i>		hypothetical protein
131	1	8	1	32	<i>PA3114</i>	<i>truA</i>	tRNA pseudouridine synthase
132	1	8	1.5	32	<i>PA3232</i>		probable nuclease
133	1	8	1	32	<i>PA3233</i>		hypothetical protein
134	1.5	6	2	32	<i>PA5067</i>	<i>hisE</i>	phosphoribosyl-ATP pyrophosphatase
135	2	16	1.5	24	<i>PA0149</i>		RNA polymerase ECF-subfamily sigma-70 factor
136	1	12	1.5	32	<i>PA4882</i>	<i>gatC</i>	aspartyl/glutamyl-tRNA amidotransferase subunit C
137	1	8	4	32	<i>PA5147</i>	<i>mutM</i>	formamidopyrimidine-DNA glycosylase
138	1	16	3	32	<i>PA5438</i>		probable transcriptional regulator
139	1	12	1.5	64	<i>PA5309</i>	<i>paub4</i>	FAD-dependent oxidoreductase
140	1.5	12	2	32	<i>PA4673</i>		conserved hypothetical protein
141	1.5	24	1.5	24	<i>PA3002</i>	<i>mfd</i>	transcription-repair coupling factor
142	1	16	1.5	48	<i>PA0227</i>		coA transferase subunit B
143	1	16	3	48	<i>PA3492</i>		hypothetical protein
144	1	12	1.5	32	<i>PA0151</i>		probable TonB-dependent receptor
145	1	8	1	32	<i>PA0228</i>	<i>pcaF</i>	beta-ketoacyl CoA thiolase
146	2	16	2	64	<i>PA1549</i>		type P ATPase
147	1	12	1.5	32	<i>PA4496</i>	<i>dppA1</i>	ABC transporter
148	1	24	4	32	<i>PA2647</i>	<i>nuoL</i>	NADH dehydrogenase I chain L
149	1	12	0.75	32	<i>PA5349</i>		rubredoxin reductase
150	0.75	16	4	32	<i>PA1320</i>	<i>cyoD</i>	cytochrome o ubiquinol oxidase subunit IV
151	1.5	8	1.5	64	<i>PA1554</i>	<i>ccoN</i>	cytochrome c oxidase subunit
152	2	12	3	32	<i>PA2643</i>	<i>nuoH</i>	NADH dehydrogenase I chain H
153	0.75	8	2	24	<i>PA0305</i>	<i>hacB</i>	acylhomoserine lactone acylase B
154	1	8	1.5	32	<i>PA0306</i>		transcriptional regulator
155	1.5	12	2	48	<i>PA0307</i>		conserved hypothetical protein
156	1	16	1.5	48	<i>PA1768</i>		conserved hypothetical protein
157	1.5	12	2	32	<i>PA3394</i>	<i>nuoF</i>	NADH dehydrogenase I chain F
158	1.5	16	2	32	<i>PA3405</i>	<i>hasE</i>	metalloprotease secretion protein

159	0.75	12	1.5	24	<i>PA4430</i>		cytochrome b
160	1.5	12	1.5	48	<i>PA4695</i>	<i>ilvH</i>	acetolactate synthase 3 regulatory subunit
161	0.75	12	3	16	<i>PA0023</i>	<i>qor</i>	quinone oxidoreductase
162	1	12	1.5	24	<i>PA0071</i>		conserved hypothetical protein
163	3	12	2	64	<i>PA1551</i>		probable ferredoxin
164	1.5	12	3	64	<i>PA2640</i>	<i>nuoE</i>	NADH dehydrogenase I chain E
165	1.5	12	1.5	32	<i>PA1556</i>	<i>ccoO2</i>	cbb3-type cytochrome c oxidase subunit II
166	1	16	2	32	<i>PA3406</i>	<i>hasD</i>	transport protein
167	1	16	3	48	<i>PA3115</i>	<i>fimV</i>	pilus assembly protein
168	1.5	12	1.5	48	<i>PA4112</i>		sensor/response regulator hybrid
169	1	12	2	48	<i>PA4640</i>	<i>mgo</i>	malate:quinone oxidoreductase
170	1	16	2	32	<i>PA5448</i>	<i>wbpY</i>	glycosyltransferase
171	1.5	12	1.5	32	<i>PA0072</i>	<i>tagS1</i>	permease
172	1.5	16	2	32	<i>PA0150</i>		anti-sigma factor
173	1.5	16	2	48	<i>PA1480</i>	<i>ccmF</i>	cytochrome C-type biogenesis protein
174	0.75	16	1.5	24	<i>PA1734</i>		cytochrome c protein
175	1.5	16	3	64	<i>PA2641</i>	<i>nuoF</i>	NADH dehydrogenase I chain F
176	1	12	3	64	<i>PA2993</i>		thiamine biosynthesis lipoprotein
177	0.75	16	2	32	<i>PA2994</i>	<i>nqrF</i>	NADH:quinone oxidoreductase
178	1.5	16	2	48	<i>PA2996</i>	<i>nqrD</i>	NADH:uniquinone oxidoreductase
179	1	16	1.5	32	<i>PA3393</i>	<i>nosD</i>	copper ACB transporter
180	0.75	12	2	24	<i>PA3976</i>	<i>thiE</i>	thiamin-phosphate pyrophosphorylase
181	1	16	1.5	32	<i>PA5066</i>	<i>hisI</i>	phosphoribosyl-AMP cyclohydrolase
182	1	16	2	32	<i>PA1321</i>	<i>cyoE</i>	cytochrome
183	1.5	24	3	64	<i>PA1548</i>		conserved hypothetical protein
184	1.5	12	3	64	<i>PA2638</i>	<i>nuoB</i>	NADH dehydrogenase I chain B
185	1	12	1	48	<i>PA2992</i>		conserved hypothetical protein
186	1	12	1.5	24	<i>PA3814</i>	<i>iscS</i>	L-cysteine desulfurase
187	1	12	2	48	<i>PA4863</i>		hypothetical protein
188	0.75	16	2	32	<i>PA5530</i>		probable MFS transporter
189	1	16	2	32	<i>PA1588</i>	<i>sucC</i>	succinyl-CoA synthetase beta chain
190	1	12	2	24	<i>PA1589</i>	<i>sucD</i>	succinyl-CoA synthetase alpha chain

191	1.5	8	2	48	<i>PA1688</i>		conserved hypothetical protein
192	0.75	12	1.5	24	<i>PA2642</i>	<i>nuoG</i>	NADH dehydrogenase I chain G
193	0.75	12	2	48	<i>PA2960</i>	<i>pilZ</i>	fimbrial biogenesis protein
194	1.5	12	2	48	<i>PA2995</i>	<i>nqrE</i>	NADH:quinone oxidoreductase
195	1.5	12	1.5	48	<i>PA3392</i>	<i>nosZ</i>	nitrous-oxide reductase precursor
196	0.75	12	2	32	<i>PA4253</i>	<i>rplN</i>	50S ribosomal protein L14
197	1	16	2	48	<i>PA4696</i>	<i>ilvI</i>	acetolactate synthase large subunit
198	1.5	16	2	128	<i>PA4916</i>	<i>nrtR</i>	Nudix-related transcriptional regulator
199	1	16	2	48	<i>PA5312</i>	<i>pauC</i>	aldehyde dehydrogenase
200	1	12	1.5	24	<i>PA5450</i>	<i>wzt</i>	ABC subunit A-band LPS efflux transporter
201	1	8	2	24	<i>PA5451</i>	<i>wzm</i>	membrane subunit A-band LPS efflux transporter
202	1.5	12	1.5	24	<i>PA0114</i>	<i>senC</i>	copper binding protein
203	1.5	8	3	32	<i>PA1483</i>	<i>cycH</i>	cytochrome c-type biogenesis protein
204	1.5	12	3	48	<i>PA1550</i>		conserved hypothetical protein
205	1	12	1	24	<i>PA1883</i>		plastoquinone oxidoreductase
206	2	24	3	48	<i>PA2645</i>	<i>nuoJ</i>	NADH dehydrogenase I chain J
207	1	6	2	24	<i>PA2963</i>		hypothetical protein
208	1.5	12	1	32	<i>PA4234</i>	<i>uvrA</i>	excinuclease ABC subunit A
209	0.75	12	2	24	<i>PA4543</i>		conserved hypothetical protein
210	1	12	2	32	<i>PA4571</i>		probable cytochrome c
211	1.5	12	1	24	<i>PA5350</i>	<i>rubA2</i>	rubredoxin 2
212	1.5	12	3	48	<i>PA1689</i>		membrane protein
213	1	12	1.5	32	<i>PA1621</i>		probable hydrolase
214	1	8	1	32	<i>PA1689</i>		membrane protein
215	1	16	2	32	<i>PA1766</i>		conserved hypothetical protein
216	1.5	16	1.5	32	<i>PA1882</i>		probable transporter
217	1.5	12	1.5	32	<i>PA3274</i>		conserved hypothetical protein
218	1.5	16	3	32	<i>PA3395</i>	<i>nosY</i>	multi-copper enzyme maturation
219	1	12	1.5	24	<i>PA3407</i>	<i>hasAp</i>	heme acquisition protein
220	1.5	12	2	32	<i>PA3493</i>		hypothetical protein
221	0.75	12	2	24	<i>PA3495</i>	<i>nth</i>	endonuclease III
222	2	24	2	48	<i>PA4431</i>		iron-sulfur subunit of cytochrome c reductase

223	1.5	24	2	48	<i>PA4544</i>	<i>rluD</i>	pseudouridine synthase
224	1	16	3	24	<i>PA4833</i>		conserved hypothetical protein
225	1	12	1.5	24	<i>PA4868</i>	<i>ureC</i>	urease alpha subunit
226	0.75	16	2	32	<i>PA4917</i>	<i>nadD2</i>	nicotinate mononucleotide adenylyltransferase
227	2	12	3	64	<i>PA5070</i>	<i>tatC</i>	transport protein
228	1.5	24	2	32	<i>PA5315</i>	<i>rpmG</i>	50S ribosomal protein L33
229	1	8	1.5	32	<i>PA5334</i>	<i>rph</i>	Ribonuclease PH
230	1	12	1.5	32	<i>PA5452</i>	<i>wbpW</i>	phosphomannose isomerase
231	1.5	16	2	48	<i>PA0338</i>		hypothetical protein
232	1	12	1.5	32	<i>PA0382</i>	<i>micA</i>	DNA mismatch repair protein
233	1	12	1	24	<i>PA0432</i>	<i>sahH</i>	S-adenosyl-L-homocysteine hydrolase
234	1	12	1.5	48	<i>PA1555</i>	<i>ccoP2</i>	cytochrome c oxidase
235	1	16	1	24	<i>PA3231</i>		conserved hypothetical protein
236	1	12	1	32	<i>PA3408</i>	<i>hasR</i>	Heme uptake outer membrane receptor
237	1.5	16	2	48	<i>PA3816</i>	<i>cysE</i>	O-acetylserine synthase
238	1	16	2	32	<i>PA3975</i>	<i>thiD</i>	phosphomethylpyrimidine kinase
239	1.5	12	1.5	32	<i>PA5145</i>		probable dehydrogenase
240	1.5	16	3	48	<i>PA2639</i>	<i>nuoD</i>	NADH dehydrogenase I chain C,D
241	0.75	16	2	32	<i>PA3817</i>		probable methyltransferase
242	1	12	1.5	32	<i>PA5447</i>	<i>wbpZ</i>	glycosyltransferase
243	1	16	3	32	<i>PA2999</i>	<i>nqrA</i>	NADH:ubiquinone oxidoreductase

*: aminoglycoside hypersusceptible mutants that were chosen for further characterization.

The genes that are identified with a UCBPP-PA14 code do not have an orthologue in *P. aeruginosa* PAO1 strain. TOB: tobramycin, STR: streptomycin, AMK: amikacin, KAN: kanamycin.

Table S2 Primers used to verify transposon insertion in hypersusceptible mutants

Mutants	Tn insertion position	Primer fw (5'-3')	Primer rv (5'-3')
PA3016	330/435	CTATTGGCAGAATACCCC	CGCGCTGGCGGAGAAACT
<i>hpf</i>	55/309	ACTGGTGTGACGTTGATC	GGCTTCGATCTTCTGCTT
PA2798	5/1185	AGTACCGTCTGCGCCTTG	AATCGCAAATGACCAGGT
<i>hflK</i>	359/1203	TCTGGCTGTACAACGCCA	AGCGGCACTTCGACGATGTT
<i>glnD</i>	377/2703	ATCACCCCTGGTCGCCGT	TGGCCAGGAAGAACTCCTT

Nucleotide position in which transposon is inserted/ Gene length.