Supplemental Table 1. Non-synonymous mutations unique to each isolate.

Variant calls for all strains were made using PA01 as the reference strain. Non-synonmyous mutations found only in a single strain are reported for each isolate A) BSL5, B) BSL9, and C) BSL15, respectively.

A) Present in BSL5, but not BSL9 or BSL15

POS[a]	REF	ALT	EFFECT	NUCLEOTIDE CHANGE[b]	AMINO ACID CHANGE	GENE LOCI[c]
53877	CTG	TCT	upstream_gene_variant	c.-4909_-4907delCTGinsTCT	-	PA0044
264708	A	C	upstream_gene_variant	c.-1908A>C	-	PA0236
283003	G	T	missense_variant	c.551C>A	p.Thr184Asn	PA0251
283010	GCCT	CTTC	missense_variant	c.541_544delAGGCinsGAAG	p.ArgLeu181GluVal	PA0251
283023	CTCGAGGTGTTCCTTGACG	TTCCAGATGCTTGTTCACT	missense_variant	c.513_531delCGTCAAGGAACACCTCGAGinsAGTGAACAAGCATCTGGAA	p.AsnValLysGlu171LysValAsnLys	PA0251
358851	T	G	upstream_gene_variant	c.-2374A>C	-	PA0316
795611	GTGA	ATCT	missense_variant	c.1111_1114delGTGAinsATCT	p.ValSer371IleCys	PA0727
999921	T	TTCTA	upstream_gene_variant	c.-92_-91insTCTA	-	PA0917
1013762	GGCCGTCCGGA	G	frameshift_variant	c.1981_1990delTCCGGACGGC	p.Ser661fs	PA0928
1335571	T	C	upstream_gene_variant	c.-4188A>G	-	PA1229
1400468	G	GT	frameshift_variant	c.37dupA	p.Thr13fs	PA1288
2110105	CGATGCGG	TGCCGCGA	upstream_gene_variant	c.-601_-594delCCGCATCGinsTCGCGGCA	-	PA1928
2419167	GC	AT	missense_variant	c.445_446delGCinsAT	p.Ala149Met	PA2200
2419175	CA	TT	missense_variant	c.453_454delCAinsTT	p.Thr152Ser	PA2200
2464659	A	G	missense_variant	c.664A>G	p.Thr222Ala	PA2239
2568794	A	G	upstream_gene_variant	c.-510T>C	-	PA2326
2641547	CAGCGCG	TACGGCC	missense_variant	c.513_519delCAGCGCGinsTACGGCC	p.Ser172Thr	PA2388
2687979	CA	GG	missense_variant	c.483_484delCAinsGG	p.Ile162Val	PA2403
2775335	G	T	missense_variant	c.3470C>A	p.Ala1157Asp	PA2462
2776508	T	G	missense_variant	c.2297A>C	p.Lys766Thr	PA2462
2897386	A	G	upstream_gene_variant	c.-3558T>C	-	PA2559
2922557	A	C	missense_variant	c.13T>G	p.Leu5Val	PA2583
2922563	C	T	missense_variant	c.7G>A	p.Ala3Thr	PA2583
3642284	ACGCCG	GCGCCA	missense_variant	c.546_551delCGGCGTinsTGGCGC	p.Val184Ala	PA3256
3889920	G	A	upstream_gene_variant	c.-936C>T	-	PA3475
3979685	T	TCCAA	upstream_gene_variant	c.-175_-174insCCAA	-	PA3552
4214613	TCGCCCC	CCGCCCT	downstream_gene_variant	c.*925_*931delGGGGCGAinsAGGGCGG	-	PA3763
5071899	G	C	upstream_gene_variant	c.-2368C>G	-	PA4525
5139031	CCTCTA	TCTCTG	upstream_gene_variant	c.-282_-277delTAGAGGinsCAGAGA	-	PA4588
5825796	A	G	upstream_gene_variant	c.-339A>G	-	PA5174
5898737	ACAAG	GCAGA	missense_variant	c.54_58delCTTGTinsTCTGC	p.Ser20Pro	PA5238
6241614	G	A	upstream_gene_variant	c.-3364C>T	-	PA5544

[a]Position in reference to *P. aeruginosa* PAO1 chromosome

[b]Numbering indicates nucleotide from start codon, * indicates number of nucleotides from the end of the stop codon

[c]Gene loci references homologous gene in PAO1 chromosome

B) Present in BSL9, but not BSL5 or BSL15

POS[a]	REF	ALT	EFFECT	NUCLEOTIDE CHANGE[b]	AMINO ACID CHANGE	GENE LOCI[c]
53982	GCC	ACA	upstream_gene_variant	c.-4804_-4802delGCCinsACA	-	PA0044
353654	TCTCGGG	CCTCGGA	upstream_gene_variant	c.-4609_-4603delCCCGAGAinsTCCGAGG	-	PA0307
1061189	C	T	upstream_gene_variant	c.-1732C>T	-	PA0981
1267001	T	G	upstream_gene_variant	c.-3835A>C	-	PA1163
1447192	G	GCGCCCCA	upstream_gene_variant	c.-2742_-2741insTGGGGCG	-	PA1331
2077042	C	T	downstream_gene_variant	c.*4104C>T	-	PA1901
2558822	TGC	CGCG	upstream_gene_variant	c.-4974_-4972delGCAinsCGCG	-	PA2315
2568823	AC	GT	upstream_gene_variant	c.-540_-539delGTinsAC	-	PA2326
2632977	C	CGCGCAG	conservative_inframe_insertion	c.217_222dupCTGCGC	p.Arg74_Val75insLeuArg	PA2380
2639068	T	A	missense_variant	c.1192A>T	p.Ser398Cys	PA2386
2688442	A	G	missense_variant	c.946A>G	p.Ser316Gly	PA2403
2704358	G	GA	upstream_gene_variant	c.-3254_-3253insT	-	PA2417
2704370	TC	CT	upstream_gene_variant	c.-3266_-3265delGAinsAG	-	PA2417
2760310	C	T	upstream_gene_variant	c.-223G>A	-	PA2459
3043419	A	G	upstream_gene_variant	c.-3002A>G	-	PA2692
3136982	T	C	upstream_gene_variant	c.-4952A>G	-	PA2773
3528364	T	C	upstream_gene_variant	c.-1686A>G	-	PA3141
3528373	A	G	upstream_gene_variant	c.-1695T>C	-	PA3141
4008781	C	T	upstream_gene_variant	c.-4025C>T	-	PA3581
4008790	T	C	upstream_gene_variant	c.-4016T>C	-	PA3581
4304575	GCCGTTTTTT	ACCGTTTTTC	upstream_gene_variant	c.-82_-73delAAAAAACGGCinsGAAAAACGGT	-	PA3841
4305503	AGGCCT	GGGCCG	upstream_gene_variant	c.-1006_-1001delAGGCCTinsCGGCCC	-	PA3841
4725273	C	T	stop_gained	c.1529G>A	p.Trp510*	PA4221
4831147	GAA	ACC	missense_variant	c.184_186delGAAinsACC	p.Glu62Thr	PA4306
4831229	A	G	upstream_gene_variant	c.-4041T>C	-	PA4302
4831248	GTAA	ATGC	upstream_gene_variant	c.-4063_-4060delTTACinsGCAT	-	PA4302
5050710	G	GACGCCA	upstream_gene_variant	c.-4047_-4046insTGGCGT	-	PA4507
5189697	T	C	missense_variant	c.3179A>G	p.Asn1060Ser	PA4625
5446395	G	GCGGCCACCT	conservative_inframe_insertion	c.217_218insCGGCCACCT	p.Ala73_Ala74insAlaThrSer	PA4851
5727408	T	C	missense_variant	c.2069A>G	p.Glu690Gly	PA5089
5994736	CTCCA	TCCC	upstream_gene_variant	c.-1300_-1296delCTCCAinsTCCC	-	PA5325
6188000	A	G	upstream_gene_variant	c.-1475T>C	-	PA5493

[a]Position in reference to *P. aeruginosa* PAO1 chromosome

[b]Numbering indicates nucleotide from start codon, * indicates number of nucleotides from the end of the stop codon

[c]Gene loci references homologous gene in PAO1 chromosome

C) Present in BSL15, but not BSL5 or BSL9

POS[a]	REF	ALT	EFFECT	NUCLEOTIDE CHANGE[b]	AMINO ACID CHANGE	GENE LOCI[c]
184126	CTCGGAC	TTCGGAG	upstream_gene_variant	c.-468_-462delCTCGGACinsTTCGGAG	-	PA0162
321949	CCTGG	TGA	upstream_gene_variant	c.-4164_-4160delCCAGGinsTCA	-	PA0283
473432	A	C	missense_variant	c.242A>C	p.Glu81Ala	PA0426
750530	C	G	missense_variant	c.574C>G	p.Leu192Val	PA0690
750652	GG	CA	missense_variant	c.696_697delGGinsCA	p.Asp233Asn	PA0690
994768	C	CAGGCTGC	conservative_inframe_insertion	c.70_71insAGGCTGCCGGGAGTGTCGTCGAGACGGGGCAAG	p.Gln24_Ala25insAlaAlaGlySerValValGluThrGlyGlnGlu	PA0911
1243402	A	C	upstream_gene_variant	c.-902T>G	-	PA1148
1527020	GTTCGGGC	G	upstream_gene_variant	c.-2204_-2190delGTGGGGTCCCCCGAA	-	PA1401
1566317	CG	TT	missense_variant	c.2351_2352delCGinsTT	p.Ser784Phe	PA1436
2216029	CCTACCT	TCTACCC	upstream_gene_variant	c.-659_-653delCCTACCTinsTCTACCC	-	PA2025
2262929	C	T	missense_variant	c.154G>A	p.Ala52Thr	PA2064
2263733	GC	AT	missense_variant	c.1244_1245delGCinsAT	p.Ser415Asn	PA2065
2486179	T	G	upstream_gene_variant	c.-1677T>G	-	PA2259
2568691	A	G	upstream_gene_variant	c.-407T>C	-	PA2326
2640875	G	A	upstream_gene_variant	c.-2070C>T	-	PA2385
2647470	AAC	CAG	missense_variant	c.939_941delGTTinsCTG	p.Phe314Cys	PA2392
2685507	C	T	missense_variant	c.1672G>A	p.Val558Ile	PA2402
2761459	C	T	upstream_gene_variant	c.-1372G>A	-	PA2459
3099269	CCCAA	TCCAG	upstream_gene_variant	c.-3221_-3217delTTGGGinsCTGGA	-	PA2734
3099280	TA	CT	upstream_gene_variant	c.-3229_-3228delTAinsAG	-	PA2734
3596196	GCGCCTGC	G	conservative_inframe_deletion	c.256_294delCGCCTGGTCGACGGCACCTACCTGCCGCGCCCCCACCAC	p.Arg86_His98del	PA3206
3605482	TGGCC	CGGCCG	upstream_gene_variant	c.-202_-198delTGGCCinsCGGCCG	-	PA3217
3686843	G	T	missense_variant	c.1808C>A	p.Thr603Lys	PA3294
3773983	CGG	GGT	upstream_gene_variant	c.-2505_-2503delCCGinsACC	-	PA3359
3808278	C	CCGGCGCC	upstream_gene_variant	c.-4936_-4935insCCCGGCGCGCCG	-	PA3397
4133900	T	C	upstream_gene_variant	c.-3508A>G	-	PA3687
4305586	A	G	upstream_gene_variant	c.-1084T>C	-	PA3841
4305591	G	T	upstream_gene_variant	c.-1089C>A	-	PA3841
4407702	TCCGG	CCCGGT	upstream_gene_variant	c.-2808_-2804delCCGGAinsACCGGG	-	PA3929
4476328	A	G	missense_variant	c.374A>G	p.His125Arg	PA3995
4591101	GTGC	CTGA	upstream_gene_variant	c.-2928_-2925delGTGCinsCTGA	-	PA4110
4699809	C	CGTCGAGC	upstream_gene_variant	c.-3775_-3774insAACGCTCGAC	-	PA4197
4732282	G	T	missense_variant	c.4517C>A	p.Pro1506Gln	PA4225
4925171	GCGACGTT	CCGACGTT	upstream_gene_variant	c.-1865_-1857delGCGACGTTTinsCCGACGTTC	-	PA4397
5361311	G	A	upstream_gene_variant	c.-2760G>A	-	PA4776
5471532	T	C	upstream_gene_variant	c.-1292T>C	-	PA4876
5471545	A	G	upstream_gene_variant	c.-1279A>G	-	PA4876
5726546	AGTC	GGCT	missense_variant	c.690_693delGACTinsAGCC	p.Thr231Ala	PA5088
5944026	CA	C	frameshift_variant	c.422delA	p.His141fs	PA5279
6187938	C	T	upstream_gene_variant	c.-1413G>A	-	PA5493
6187946	CGGA	TGG	upstream_gene_variant	c.-1424_-1421delTCCGinsCCA	-	PA5493

[a]Position in reference to *P. aeruginosa* PAO1 chromosome

[b]Numbering indicates nucleotide from start codon

[c]Gene loci references homologous gene in PAO1 chromosome