Supplementary 6: Mutati	ion prome of	us genes for	12 isolates											
Strain:	Gene	Start	Stop	Match_Type	Description	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length	Match_Length	Target_Length	Strand
A17	PAO1_lasR	139500	140220	Mutant	L110P,	1	1	0	0.9958	0.9986	1	720	720	+
	PAO1_lasI	140583	141189	Native	No coding mutations	0	0	0	1	1	1	606	606	
	PAO1_rhIR	111501	112227	Native	No coding mutations	0		0	_	0.9959	1	726	726	
	PAO1_rhll	110716	111322	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	
	PAO1_pqsA	266692	268246		N180T,	1	3	2	0.9981	0.9981	1	1554	1554	_
	PAO1_pqsB	265847		Mutant	P200L,	1	3	0	0.9965	0.9965	1		852	
	PAO1_pqsC	264808 263752	265855	Native Mutant	No coding mutations E176D,	1	6	2	0.997	0.9933 0.9941	1	1047 1014	1047 1014	
	PAO1_pqsD	262853	263759			0	0	0		0.9941	1	906	906	
	PAO1_pqsE	202033	203739	ivative	No coding mutations 223 SNPs in 1-1054,96 coding	U	U	U	1	1	1	900	900	-
				Contig Edge	mutations,truncation at codon									
	PAO1_pqsH	0	1054	(truncation)	268 (of 351 codons)	128	318	148	0.6658	0.7232	0.9173	1054	1149	L
	PAO1_pqsL	246548		Mutant	E330G,	120	4	0	0.9975	0.9967	1	1197	1197	
	PAO1_pqsR	259613	260612	Mutant	R289L,	1	2	1	0.997	0.998	1	999	999	
	PAO1_qscR	1815	2529	Native	No coding mutations	0	2	0	1	0.9972	1	714	714	-
	PAO1_rsaL	140209	140452	Native	No coding mutations	0	0	0	1	1	1	243	243	-
	PAO1_vqsR	6714		Native	No coding mutations	0	1	0	1	0.9988	1	807	807	-
Strain:	Gene	Start	Stop	Match_Type	Description	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length	Match_Length	Target_Length	Strand
SWPA15J = NSWPA15a	PAO1_lasR	82843	83563	Native	No coding mutations	0	0	0	1	1	1	720	720	-
	PAO1_lasI	81874	82480	Native	No coding mutations	0		0	1	1	1	606	606	
Ī	PAO1_rhIR	593582	594308	Native	No coding mutations	0		1	1	0.9931	1	726	726	
	PAO1_rhll	594487	595093		S62G,D83E,	2	8	3	0.9901	0.9868	1	000	606	
	PAO1_pqsA	330200	331754	Native	No coding mutations	0	4	1	1	0.9974	1	1554	1554	+
	PAO1_pqsB	331747	332599		No coding mutations	0	2	0	1	0.9977	1	852	852	
	PAO1_pqsC	332591	333638		L58P,	1	4	0	0.9971	0.9962	1	1047	1047	
	PAO1_pqsD	333680	334694		E176D,	1	6	2	0.997	0.9941	1	1014	1014	-
	PAO1_pqsE	334687	335593		S257P,	1	5	1	0.9967	0.9945	1	500	906	
	PAO1_pqsH	196503	197652	Native	No coding mutations	0		0		0.9956	1	1149	1149	
	PAO1_pqsL	50584	51781	Native	No coding mutations	0	,	0		0.9975	1	1137	1197	
	PAO1_pqsR	337835	338834		No coding mutations	0		0	-	0.999	1	999	999	
	PAO1_qscR	2085	2799		No coding mutations	0	3	0	1	0.9958	1	714	714	
	PAO1_rsaL	82611	82854	Native	No coding mutations	0	0	0	1	1	1	243	243	+
													007	
Churcher	PAO1_vqsR	190036	190843		No coding mutations	0	1 DD Characa	0	Coden Demont	0.9988	1	807	807	
Strain:	Gene Gene		190843 Stop		Description	Codon_Changes	BP_Changes	Transversions	1 Codon_Percent		Percent_Length			
Strain: CND03					Description 11 bp Deletion at	Codon_Changes	BP_Changes	Transversions	Codon_Percent		Percent_Length			
				Match_Type	Description 11 bp Deletion at 440,truncation at codon 229	0 Codon_Changes	BP_Changes	Transversions	Codon_Percent		Percent_Length			
	Gene	Start	Stop	Match_Type Indel	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding					BP_Percent		Match_Length	Target_Length	Strand
			Stop 51430	Match_Type	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations	Codon_Changes	BP_Changes	Transversions 10	0.6375		Percent_Length 0.9847			Strand +
	Gene PAO1_lasR	Start 50721	51430 52399	Match_Type Indel Truncation	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding	87	24 1	10		BP_Percent 0.9667		Match_Length 709	Target_Length 720	Strand + +
	PAO1_lasR PAO1_lasI	50721 51793	51430 52399	Match_Type Indel Truncation Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations	87 0	24 1	10 0	0.6375	0.9667 0.9983		Match_Length 709 606	Target_Length 720 606	+ +
	PAO1_lasR PAO1_lasI PAO1_rhIR	50721 51793 109740	51430 52399 110466	Indel Truncation Native Nonstop	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations	87 0	24 1 36	10 0	0.6375 1 0.938	0.9667 0.9983 0.9504		709 606 726	720 606 726	+ + -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII	50721 51793 109740 109019	51430 52399 110466 109625	Match_Type Indel Truncation Native Nonstop Mutant Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G,	87 0	24 1 36	10 0	0.6375 1 0.938 0.995	0.9667 0.9983 0.9504 0.9868		709 606 726 606	720 606 726	+ + - -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA	50721 51793 109740 109019 171136	51430 52399 110466 109625 172690	Match_Type Indel Truncation Native Nonstop Mutant Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q,	87 0 15 1 2	24 1 36 8	10 0	0.6375 1 0.938 0.995 0.9961	0.9667 0.9983 0.9504 0.9868 0.9897		709 606 726 606 1554	720 606 726 606 1554	+ + - - -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA PAO1_pqsB	50721 51793 109740 109019 171136 170291	51430 52399 110466 109625 172690 171143	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V871,A208D,A281V,	87 0 15 1 2	24 1 36 8 16	10 0	0.6375 1 0.938 0.995 0.9961	0.9667 0.9983 0.9504 0.9868 0.9897 0.9883		709 606 726 606 1554 852	720 606 726 606 1554	+ + - - - -
	PAO1 lasR PAO1 lasI PAO1 rhlR PAO1 rhlR PAO1 pgsA PAO1 pgsB PAO1 pgsC	50721 51793 109740 109019 171136 170291 169252	51430 52399 110466 109625 172690 171143 170299	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87IA,208D,A281V, T311A,	87 0 15 1 2	24 1 36 8 16 10 19	10 0	0.6375 1 0.938 0.995 0.9961 0.9894	0.9667 0.9983 0.9504 0.9868 0.9897 0.9883 0.9819		709 606 726 606 1554 852	720 606 726 606 1554 852	+ + - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhlR PAO1 rhlR PAO1 pgsA PAO1 pgsC PAO1 pgsD	50721 51793 109740 109019 171136 170291 169252 168196	51430 52399 110466 109625 172690 171143 170299 169210	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87I,A208D,A281V, T3311A, A243V,	87 0 15 1 2 3 1	24 1 36 8 16 10 19	10 0 21 1 6 1 3	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971	0.9667 0.9983 0.9504 0.9868 0.9897 0.9883 0.9819	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047	720 606 726 606 1554 852 1047	+ + - - - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhlR PAO1 rhlI PAO1 pqsA PAO1 pqsB PAO1 pqsC PAO1 pqsC	50721 51793 109740 109019 171136 170291 169252 168196	51430 52399 110466 109625 172690 171143 170299 169210 168203	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, Pp63A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations	87 0 15 1 2 3 3 1 1	24 1 36 8 16 10 19	10 0 21 1 6 1 3	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 0.997	0.9667 0.9983 0.9504 0.9868 0.9897 0.9883 0.9819 0.9842	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014	720 606 726 606 1554 852 1047 1014	+ + - - - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhIR PAO1 pqsA PAO1 pqsA PAO1 pqsC PAO1 pqsC PAO1 pqsC PAO1 pqsC	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924	51430 52399 110466 109625 172690 171143 170299 169210 168203 175073	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations No coding mutations	87 0 15 1 2 3 3 1 1	24 1 36 8 16 10 19 16 3	10 0 21 1 6 1 3 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997	0.9667 0.9983 0.9504 0.9868 0.987 0.9883 0.9819 0.9842 0.9967	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906	720 606 726 606 1554 852 1047 1014 906	+ + - - - - - - -
	PAO1 lasR PAO1 lasR PAO1 lasR PAO1 mlR PAO1 mlR PAO1 mgsA PAO1 mgsA PAO1 mgsB PAO1 mgsB	50721 51793 109740 171136 170291 169252 168196 167297 173924	\$1430 \$2399 \$10466 \$172690 \$171143 \$170299 \$169210 \$168203 \$175073	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Native Native Nonstop	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations S62G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P	87 0 155 1 2 3 1 1 0 0	24 1 36 8 16 10 19	10 0 21 1 6 1 3	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1	0.9667 0.9983 0.9504 0.9886 0.9897 0.9883 0.9819 0.9942 0.9967	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 1554 852 1047 1014 906 1149	+ + - - - - - - - +
	PAO1 IasR PAO1 Iasr PAO1 Iasr PAO1 Iasr PAO1 Insr	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924	\$1430 \$1339 \$10466 \$109625 \$172690 \$171143 \$170299 \$169210 \$168203 \$175073	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Native Native Nonstop Nonstop	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P,A314V,	87 0 15 1 2 2 3 1 1 0 0	24 1 36 8 166 100 19 16 3 3 7	10 0 21 1 6 6 1 3 3 1 1 0 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997	0.9667 0.9667 0.9983 0.9504 0.9883 0.9819 0.9842 0.9967 0.9939	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 1554 852 1047 1014 906 1149	+ + - - - - - - - - +
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhIR PAO1 pSO1 PAO1 pqSD PAO1 pqSD PAO1 pqSD PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSR PAO1 pqSR PAO1 pqSR	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924	51430 51430 52399 110466 109625 172690 171143 170299 169210 168203 175073	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Native Native Nonstop Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, PP63A,R347O, V87I,A208D,A281V, T311A, A243V, No coding mutations	87 0 15 1 2 3 1 1 0 0	24 1 36 8 166 10 19 166 3 3 7	10 0 21 1 6 1 3 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1	0.9667 0.9983 0.9504 0.9886 0.9897 0.9883 0.9819 0.9942 0.9967	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714	720 606 726 606 1554 852 1047 1014 906 1149	+ + - - - - - - - - + + +
	PAO1 lasR PAO1 lasI PAO1 lasI PAO1 rhiR PAO1 rhiR PAO1 rhiR PAO1 rhiS	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 181144	51430 51430 52399 110466 109625 1771630 177143 170299 169210 175173 66443 155056 25288 51662	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Native Native Native Native Native Native Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P , A314V, No coding mutations No coding mutations No coding mutations	87 0 15 1 2 2 3 1 1 0 0	24 1 366 8 8 16 100 19 16 3 3 7 7	10 0 21 1 6 6 1 3 3 1 1 0 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 1	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9819 0.9842 0.9967 0.9983 0.99741 0.998	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243	+ + + - - - - - - + + + +
CND03	PAO1 Jask PAO1 risk	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 1814 51419 167457	\$1430 \$1399 \$10466 \$109625 \$172690 \$17143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2528 \$16626 \$16826	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Native Native Nonstop Mutant Native Nonstop Mutant Native Mutant Native Mutant Native Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V87II,A208D,A281V, T311A, A243V, No coding mutations No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P, A314V, No coding mutations	87 0 15 1 2 3 3 1 1 0 0 0	24 1 366 8 8 166 100 199 166 3 7 7	10 0 21 1 6 6 3 1 1 0 0 1 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9974	0.96677 0.9983 0.9504 0.9888 0.9897 0.9883 0.9819 0.9842 0.9967 0.9939 0.9741 0.998 0.993	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243	+ + - - - - - - - + + - - - - - - - - -
CND03	PAO1 lasR PAO1 lasI PAO1 lasI PAO1 rhil	50721 51793 109740 109019 170291 169252 168196 167297 173924 65246 164057 1814 51419 167457 Start	\$1430 \$2399 \$10466 \$19625 \$172690 \$171143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2528 \$51662 \$168264 \$\$505	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Native Native Nonstop Mutant Native Native Nonstop Mutant Native Native Mutant Native Native Mutant Native Native Mutant Mutant Native Native Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 9263A,8347O, V87I,A208D,A281V, 7311A, A243V, No coding mutations	87 0 15 1 2 3 1 1 0 0	24 1 366 8 8 166 100 199 166 3 7 7	10 0 21 1 6 6 3 1 1 0 0 1 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9974	0.96677 0.9983 0.9504 0.9888 0.9897 0.9883 0.9819 0.9842 0.9967 0.9939 0.9741 0.998 0.993	0.9847 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 8007 Target_Length	+ + - - - - - - + + + + - - - - - - - -
CND03	PAO1 lasR PAO1 lasI PAO1 lasI PAO1 rhiR PAO1 rhiR PAO1 rhiR PAO1 rhiS	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 181141 51419 167457 Start 21434	51430 51430 52399 110466 109625 1771630 177143 170299 169210 168203 175073 66443 165056 52282 51662 168264 Stop	Match_Type Indel Truncation Native Nonstop Mutant Native Mutant Mutant Native Native Native Native Mutant Match_Type Native Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 5626, P263A,R347Q, V871,A208D,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A2325,R240C,A3 95S,P396L,L397E,G398A,*399P , A314V, No coding mutations No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P , A314V, No coding mutations D41H,R631,V66I,T116A, Description No coding mutations	87 00 15 1 2 3 3 1 1 0 0 0 9 11 0 4 Codon_Changes	24 1 366 8 8 16 100 199 16 3 3 7 7	10 0 21 1 6 11 3 3 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9974	0.96677 0.9983 0.9504 0.9888 0.9897 0.9883 0.9819 0.9842 0.9967 0.9939 0.9741 0.998 0.993	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 1554 852 1047 1014 906 1149 1197 399 714 243 807 Target_Length	+ + + + + Strand +
CND03	PAO1 lasR PAO1 lasr PAO1 lasr PAO1 lasr PAO1 rhil rhil PAO1 rhil rhil PAO1 rhil	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 1814 51419 167457 5tart 21434 22517	\$1430 \$13399 \$10466 \$109625 \$172690 \$17143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2128 \$1662 \$168264 \$16926 \$168264 \$212154	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutiant Mutant Mutant Mutant Native Native Mutant Mutant Native Native Mutant Mutant Native Native Mutant Mutant Native Mutant Match_Type Native Native Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations S62G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,L397E,G398A,*399P, A314V, No coding mutations D41H,R63I,V66I,T116A, Description No coding mutations	87 0 15 1 2 3 3 1 1 0 0 0 9 1 1 0 0 4 Codon_Changes 0 0	24 1 366 8 16 100 19 16 3 7 7 31 2 2 5 0 0	10 0 0 21 1 6 1 1 3 3 1 1 0 0 1 1 2 1 2 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 0.9851 Codon_Percent 1	0.96677 0.9983 0.9504 0.9868 0.9837 0.9838 0.9819 0.9842 0.9967 0.9939 0.9741 0.9988 4 BP_Percent	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	+ + + + + + + + + + +
CND03	PAO1 lasR PAO1 lasI PAO1 lasI PAO1 mil mil PAO1 mil PAO1 mil PAO1 mil PAO1 mil PAO1	50721 51793 109740 109019 170291 169252 168196 167297 173924 55246 51419 167457 586980	\$1430 \$1339 \$110466 \$19625 \$17690 \$171143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2528 \$1662 \$168264 \$Stop \$22154 \$23123 \$587706	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Native Native Native Nonstop Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 562G, P263A,8347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations	87 0 155 1 1 2 2 3 3 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	24 1 36 88 166 10 19 16 3 7 31 2 5 0 11 BP_Changes	10 0 21 1 6 11 3 3 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9851 Codon_Percent 1 1 1 1	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.98879 0.9883 0.9819 0.9941 0.9942 0.9948 0.9939 1 0.9848 BP_Percent 1 1 0.9972	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606	+ + + + + + + + + + + + + + + +
CND03	PAO1 IasR PAO1 Iasl	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 18144 51419 167457 Start 21434 22517 586980 587885	51430 51430 52399 110466 109625 172690 17143 170299 169210 168203 175073 66443 165056 2528 51662 168264 500 22154 23123 587706 588491	Match_Type Indel Truncation Native Nonstop Mutant Native Native Native Native Mutant Native Mutant Match_Type Native Native Mutant Native Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 5626, P263A,8347Q, V871,A2080,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A2325,R240C,A3 955,P396L,L397E,G398A,*399P, A314V, No coding mutations	87 00 15 1 2 3 3 1 1 0 0 0 9 1 1 Codon_Changes 0 0 0 2	24 1 366 8 8 16 100 199 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9	10 0 0 21 1 6 1 1 3 3 1 1 0 0 1 1 2 1 2 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 0.9851 Codon_Percent 1	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9819 0.9842 0.9967 0.9983 0.9939 0.9941 0.9986 BP_Percent 1 1 0.9972 0.9887	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length 720 606 726 606	+ + + + + + + + + + + + + + + +
CND03	PAO1 lasR PAO1 lasR PAO1 lasR PAO1 rhiR	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 1314 51419 167457 5tart 21434 22517 586980 587885 242065	\$1430 \$13399 \$10466 \$109625 \$172690 \$17143 \$170299 \$169210 \$168203 \$175073 \$66443 \$155056 \$2128 \$51662 \$168264 \$23123 \$58706 \$22154 \$23123 \$587706	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutie Native Native Native Mutant Native Native Mutant Native Mutant Native Mutant Native Mutant Mutant Native Mutant Match_Type Native Mutant Mutant Native Native Mutant Mutant Native Native Native Native Native Native Native Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations S62G, P263A,R347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A2325,R240C,A3 95S,P396L,L397E,G398A,*399P, A314V, No coding mutations No coding mutations D41H,R63I,V66I,T116A, Description No coding mutations	87 0 155 1 2 3 1 1 0 0 0	24 1 366 8 8 16 100 199 16 3 7 7 31 2 2 5 0 0 11 BP_Changes 0 0 2 2 9 9	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9851 Codon_Percent 1 1 0.9901	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.98879 0.9883 0.9819 0.9941 0.9942 0.9948 0.9939 1 0.9848 BP_Percent 1 1 0.9972	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	+ + + + + + + + + + + + + + + + +
CND03	PAO1 lasR PAO1 lasI PAO1 lasI PAO1 rhil	50721 51793 109740 109019 170291 169252 168196 167297 173924 55246 164057 1814 51419 167457 5tart 21434 22517 586980 587885 242065	51430 51430 52399 110466 109625 171690 171143 170299 169210 168203 175073 66443 165056 2528 51662 2154 5top 22154 58706 588491 242072	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 15 coding mutations 9263A,8347Q, 987I,A208D,A281V, 7311A, A243V, No coding mutations	87 0 15 1 2 3 1 1 0 0 0 9 1 1 0 0 0 0 0 4 Codon_Changes 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	24 1 36 88 16 10 19 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9 2 0 0	10 0 0 21 1 6 1 1 3 3 1 1 0 0 1 1 2 1 2 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9851 Codon_Percent 1 1 0.9901	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9887 0.9883 0.9819 0.9842 0.9967 0.9939 1 0.9844 BP_Percent 1 0.9985 0.9939 1 0.9844 0.99864	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 606 1554 852	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 714 243 807 Target_Length 720 606 606 1554 852	+ + + + + + + + + + + + + + + + +
CND03	PAO1 IasR PAO1 Iasl	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 18141 51419 167457 Start 21434 22517 586980 587885 242065 241220 240181	51430 51430 52399 110466 109625 172690 171143 170299 169210 168203 175073 66443 165056 2528 51662 168264 52154 23123 587706 588491 244072 241228	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 15 coding mutations 9263A,8347Q, 9871,A208D,A281V, 7311A, A243V, No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,1397E,G398A,*399P, A314V, No coding mutations No coding mutations D41H,R63I,V66I,T116A, Description No coding mutations	87 0 155 1 2 3 1 1 0 0 0	24 1 36 88 16 10 19 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9 2 0 0	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997 1 1 1 0.9774 0.997 1 1 1 1 0.9851 Codon_Percent 1 1 0.9901 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9819 0.9842 0.9967 0.9983 0.9939 1.0.9984 0.99864 BP_Percent 1.1 1.0.9982 0.9987 0.9987 1.0.9987	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 1554 852 1047	720 606 726 606 1554 852 1047 1014 906 1149 1197 724 243 807 7Target_Length 606 726 606 1554 852 1047 1047 1197 1197 1197 1197 1197 1197 1197 11	+ + + + Strand + + + +
CND03	PAO1 lasR PAO1 risR	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 65246 164057 18114 51419 167457 Start 21434 22517 586980 587885 242065 241220 240181 239125	51430 51430 52399 110466 109625 172690 171143 170299 169210 168203 175073 66443 165056 2528 51662 168264 Stop 22154 23123 58706 588491 243619 242072 241228 240129	Match_Type Indel Truncation Native Nonstop Mutant Native Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 562G, P263A,R347Q, V871,A208D,A281V, T311A, A243V, No coding mutations No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,1397E,G398A,*399P, A314V, No coding mutations D175E,R179H,A232S,R140,A3 D175E,R179H,A232S,R240C,A3 D175E,R179H,A232S	87 00 155 11 22 33 11 10 00 00 91 11 00 00 00 00 00 00 00 00 00 00 00 00	24 1 36 88 16 10 19 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9 2 0 0	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9894 0.9971 1 1 0.9774 0.997 1 1 0.9851 Codon_Percent 1 1 0.9901	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9887 0.9883 0.9819 0.9842 0.9967 0.9939 1 0.9844 BP_Percent 1 0.9985 0.9939 1 0.9844 0.99864	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 605 1554 852 1047	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 726 606 1554 852 1047	+ + + + + + + + +
CND03	PAO1 IasR PAO1 Iasl	50721 51793 109740 109019 170291 169252 168196 167297 173924 55246 164057 1814 51419 167457 5Start 21434 22517 586980 587885 242065 241220 240181 2439125 238226	\$1430 \$1339 \$110466 \$19625 \$17690 \$171143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2528 \$16602 \$168264 \$\$2154 \$21154 \$21154 \$23123 \$587706 \$588491 \$242072 \$241228 \$240139 \$239132	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 15 coding mutations P263A,8347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations	87 0 15 1 2 3 1 1 0 0 0 9 1 1 0 0 0 0 0 4 Codon_Changes 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	24 1 36 88 16 10 19 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9 2 0 0	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997 1 1 1 0.9774 0.997 1 1 1 1 0.9851 Codon_Percent 1 1 0.9901 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9887 0.9883 0.9819 0.9842 0.9967 0.9939 1 1 0.9868 BP_Percent 1 1 0.9972 0.9851 0.9987 1 0.9987 1 0.9987 1 0.9993	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 709 606 726 606 1554 852 1047 1014 906 1149 714 243 807 Match_Length 720 606 726 606 1554 852 1047 1014	Target_Length 720 666 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 606 1554 852 1047 1014	+ + + + + + + + +
CND03	PAO1 IasR	50721 51793 109740 109019 171136 170291 169252 168196 167297 173924 55246 164057 1814 51419 167457 58art 21434 22517 586980 587885 242065 241220 240181 239125 238226	51430 51430 52399 110466 109625 17143 170299 171143 175073 66443 165056 2528 51662 168264 5top 22154 23123 587706 588491 244072 241228 240139 249132	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Native Native Native Native Native Native Mutant Mutant Native Native Mutant Mutant Native Native Mutant Native Native Native Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 15 coding mutations P263A,R347Q, V871,A208D,A281V, T311A, A243V, No coding mutations No coding mutations D175E,R179H,A232S,R240C,A3 95S,P396L,1397E,G398A,*399P, A314V, No coding mutations	87 00 15 1 2 3 3 1 1 1 0 0 0 0 9 1 1 Codon_Changes 0 0 0 2 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0	24 1 36 88 16 10 19 16 3 7 31 2 5 0 11 BP_Changes 0 0 2 9 9 2 0 0	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997 1 1 1 0.9774 0.997 1 1 1 1 0.9881 Codon_Percent 1 1 0.9901 1 1 0.9901 1 1 1 1 1 0.9901	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9887 0.9883 0.9819 0.99842 0.9967 0.99839 1 1 1 1 1 1 0.9972 0.9851 0.9987 1 0.9987 1 0.9993 0.9993 0.9993 0.9993 0.9993 0.9993 0.9993 0.9993 0.9993 0.9994 0.9993	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	709 606 726 606 726 606 1554 852 1047 1014 906 1149 714 243 807 Match_Length 852 606 726 606 1554 852 1047 1014 906	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 714 243 807 7Target_Length 720 606 1554 852 1047 1014 906	# + +
CND03	PAO1 IasR PAO1 Iasl	50721 51793 109740 109019 170291 169252 168196 167297 173924 55246 164057 1814 51419 167457 5Start 21434 22517 586980 587885 242065 241220 240181 2439125 238226	\$1430 \$1339 \$110466 \$19625 \$17690 \$171143 \$170299 \$169210 \$168203 \$175073 \$66443 \$165056 \$2528 \$16602 \$168264 \$\$2154 \$21154 \$21154 \$23123 \$587706 \$588491 \$242072 \$241228 \$240139 \$239132	Match_Type Indel Truncation Native Nonstop Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Mutant	Description 11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations No coding mutations 15 coding mutations 15 coding mutations 15 coding mutations P263A,8347Q, V87I,A208D,A281V, T311A, A243V, No coding mutations	87 00 155 11 22 33 11 10 00 00 91 11 00 00 00 00 00 00 00 00 00 00 00 00	24 1 366 8 8 16 100 19 16 3 7 7 31 2 2 5 5 0 0 11 11 BP_Changes 0 0 0 2 2 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	10 0 21 1 6 11 3 1 1 0 11 1 12 11 0 0 0 0 0 0 0 0 0 3 1	0.6375 1 0.938 0.995 0.9961 0.9971 0.997 1 1 1 0.9774 0.997 1 1 1 0.9851 Codon_Percent 1 1 1 0.9901 1 1 1 1 0.9901 1 1 1 0.9907	BP_Percent 0.96677 0.9983 0.9504 0.9868 0.9887 0.9883 0.9819 0.9842 0.9967 0.9939 1 1 0.9868 BP_Percent 1 1 0.9972 0.9851 0.9987 1 0.9987 1 0.9987 1 0.9993	0.9847 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 709 606 726 606 1554 852 1047 1014 906 1149 714 243 807 Match_Length 720 606 726 606 1554 852 1047 1014	Target_Length 720 666 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 606 1554 852 1047 1014	* + + + + + + + + + + + + + + + + + + +

Ī	2121 2	5400	5005		Lo 407W				0.0050	0.0050		744		1.
	PAO1_qscR	5192		Mutant	G197X,	1	3	0	0.9958	0.9958	1	714	714	+
	PAO1_rsaL	22143	22386	Native	No coding mutations	0	0	0	1	0.0000	1	243	243	<u> -</u>
	PAO1_vqsR	24329		Native	No coding mutations		1		1	0.9988	_ 1	807	807	
Strain: Co398373	Gene	Start	Stop	Match_Type	Description	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length			Strand
C0398373	PAO1_lasR	82710	83430	Native	No coding mutations	0	0	0	1	1	1	720	720	-
	PAO1_lasI	81741	82347	Native	No coding mutations	0		0	1	1	1	606	606	
	PAO1_rhIR	46340		Native	No coding mutations	0		1	1	0.9917	1	726	726	
	PAO1_rhlI	45555		Mutant	S62G,D83E,	2		3	0.9901	0.9851	1	606	606	<u> -</u>
	PAO1_pqsA	163393	164947		No coding mutations	0		1 0	1	0.9987	1	1554	1554	-
	PAO1_pqsB	162548		Native	No coding mutations	0	-	0	1	2 2274	1	852	852	<u> -</u>
	PAO1_pqsC	161509	162556		No coding mutations	0	3	1	1	0.9971	1	1047	1047	-
	PAO1_pqsD	160453	161467	Mutant	E176D,	1	5	2	0.997	0.9951	1	1014	1014	-
	PAO1_pqsE	159554	160460	Native	No coding mutations	0	1	1	1	0.9989	1	906	906	-
	PAO1_pqsH	24290		Native	No coding mutations	0	5	0	1	0.9956	1	1149	1149	+
	PAO1_pqsL	30827	32024	Mutant	R30H,	1	2	0	0.9975	0.9983	1	1197	1197	-
	PAO1_pqsR	156313	157312	Native	No coding mutations	0	2	1	1	0.998	1	999	999	+
	PAO1_qscR	1815	2529	Native	No coding mutations	0	_	0	1	0.9958	1	714	714	-
	PAO1_rsaL	82478	82721	Native	No coding mutations	0	0	0	1	1	1	243	243	
	PAO1_vqsR	17823			No coding mutations	0	1	0	1	0.9988	1	807	807	
Strain:	Gene	Start	Stop		Description	Codon_Changes	BP_Changes	Transversions			Percent_Length			
CPHL2000	PAO1_lasR	798489		Mutant	E196G,	1	2	1	0.9958	0.9972	1	720	720	
1	PAO1_lasI	799572		Native	No coding mutations	0	2	0	_	0.9967	1	606	606	+
1	PAO1_rhIR	658430		Native	No coding mutations	0	4	0		0.9945	1	726	726	-
1	PAO1_rhlI	657645		Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	<u> -</u>
1	PAO1_pqsA	330679		Mutant	P263A,	1	3	2	0.9981	0.9981	1	1554	1554	+
	PAO1_pqsB	332226	333078	Native	No coding mutations	0	1	0	1	0.9988	1	852	852	+
1	PAO1_pqsC	333070		Native	No coding mutations	0	3	1	1	0.9971	1	1047	1047	+
	PAO1_pqsD	334159	335173	Mutant	H103P,E176D,	2	7	3	0.9941	0.9931	1	1014	1014	+
	PAO1_pqsE	335166	336072	Native	No coding mutations	0	1	1	1	0.9989	1	906	906	+
	PAO1_pqsH	161904	163053	Native	No coding mutations	0	1	0	1	0.9991	1	1149	1149	+
	PAO1_pqsL	25594	26791	Native	No coding mutations	0	2	0	1	0.9983	1	1197	1197	-
					truncation at codon 14 (of 333									
	PAO1_pqsR	338314	339313	Truncation	codons),2 coding mutations	2	3	1	0.994	0.997	1	999	999	-
	PAO1_qscR	1119	1833	Native	No coding mutations	0	2	0	1	0.9972	1	714	714	-
	PAO1_rsaL	799198	799441	Native	No coding mutations	0	0	0	1	1	1	243	243	-
I	PAO1_vqsR	155437	156244	Mutant	R23Q,	1	2	0	0.9963	0.9975	1	807	807	+
Strain:	PAO1_vqsR Gene	155437 Start	156244 Stop		R23Q, Description	1 Codon_Changes	2 BP_Changes	0	0.9963 Codon_Percent		1 Percent_Length		807 Target_Length	
Strain: Jp238			156244 Stop 83542	Mutant Match_Type Native	Description	Codon_Changes 0	BP_Changes	0			Percent_Length 1			_
	Gene	Start	Stop 83542	Match_Type	•	Codon_Changes 0 0	BP_Changes 0	0			Percent_Length 1	Match_Length	Target_Length	Strand -
	Gene PAO1_lasR PAO1_lasI	Start 82822	83542 82459	Match_Type Native Native	Description No coding mutations No coding mutations	0	0	0			Percent_Length 1 1 1 1 1 1	Match_Length 720 606	Target_Length 720 606	Strand -
	Gene PAO1_lasR	Start 82822 81853	Stop 83542	Match_Type Native	Description No coding mutations	0	0	0		BP_Percent 1	1 Percent_Length 1 1 1 1 1 1	Match_Length 720	Target_Length 720	Strand -
	Gene PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII	82822 81853 791947	83542 82459 792673 791768	Match_Type Native Native Native Mutant	Description No coding mutations No coding mutations No coding mutations S62G,D83E,	0 0	0	0 Transversions 0 0	Codon_Percent 1 1 1	BP_Percent 1 1 0.9917	1 1 1	720 606 726	720 606 726	Strand -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA	82822 81853 791947 791162 542456	83542 82459 792673 791768 544010	Match_Type Native Native Native Mutant Native	Description No coding mutations No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations	0 0 0 2	0	0 Transversions 0 0 1 3	2 Codon_Percent 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994	1 1 1	Match_Length 720 606 726 606 1554	720 606 726 606 726	Strand -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA PAO1_pqsB	82822 81853 791947 791162	83542 82459 792673 791768 544010 542463	Match_Type Native Native Native Mutant	Description No coding mutations No coding mutations No coding mutations Se2G, D83E, No coding mutations A50V,	0 0 0 2	0 0 6 8 1 1	0 Transversions 0 0 1 3	Codon_Percent 1 1 1	BP_Percent 1 1 0.9917 0.9868	1 1 1 1 1	Match_Length 720 606 726 606	720 606 726 606	Strand -
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA PAO1_pqsB PAO1_pqsC	82822 81853 791947 791162 542456 541611	83542 82459 792673 791768 544010 542463 541619	Match_Type Native Native Native Mutant Native Mutant	Description No coding mutations No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations	0 0 0 2 0	0 0 6 8 1 1 3	0 Transversions 0 0 1 3	2 Codon_Percent 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988	1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852	Target_Length 720 606 726 606 1554 852	Strand -
	Gene PAO1 lasR PAO1 lasl PAO1 rhlR PAO1 rhlI PAO1 pqsA PAO1 pqsB PAO1 pqsC PAO1 pqsD	82822 81853 791947 791162 542456 541611 540572	83542 82459 792673 791768 544010 542463 541619	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F,E176D,	0 0 0 2 0 1	0 0 6 8 1 1 3	0 Transversions 0 0 1 3	Codon_Percent 1 1 0.9901 0.9965 1 0.9941	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971	1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047	720 606 726 606 726 606 1554 852	Strand -
	Gene PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhII PAO1 pqsA PAO1 pqsB PAO1 pqsC PAO1 pqsE PAO1	82822 81853 791947 791162 542456 541611 540572 539516 538617	83542 82459 792673 791768 544010 542463 541619 540530 539523	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations	0 0 0 2 2 0 1 1 0 2	0 0 6 8 1 1 3	0 Transversions 0 0 1 1 3 0 0 0 1 1 3 3	Codon_Percent 1 1 0.9901 0.9965 1 0.9941	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971	1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906	Target_Length 720 606 726 606 1554 852 1047 1014	Strand
	Gene PAO1 lasR PAO1 lasI PAO1 rhil PAO1 rhil PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsC PAO1	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635	83542 82459 792673 791768 544010 542463 541619 540530 539523 109784	Match_Type Native Native Native Mutant	Description No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations ASOV, No coding mutations L120F,E176D, No coding mutations L120F,E176D, No coding mutations N915,	0 0 0 2 2 0 1 1 0 2	0 0 6 8 1 1 1 3 7 0 6	0 Transversions 0 0 1 1 3 0 0 0 1 1 3 3	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 0.9974	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948	1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149	Target_Length 720 606 726 606 1554 852 1047 1014 906	Strand
	Gene PAO1 lasR PAO1 lasI PAO1 rhill PAO1 pqsA PAO1 pqsA PAO1 pqsC PAO1	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199	83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations L120F,E176D, No coding mutations	0 0 0 2 0 1 0 0 2 2 0 1 1 0 1	0 0 6 8 1 1 3 7 0 6 6	0 Transversions 0 0 0 0 0 1 1 3 3 0 0 0 1 1	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 0.9941 1 0.9974	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931	1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 726 606 1554 852 1047 1014	Strand
	Gene PAO1 lasR PAO1 lasR PAO1 rill PAO1 pqsA PAO1 pqsA PAO1 pqsB PAO1 pqsC PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsR PAO1	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635	83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375	Match_Type Native Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native	Description No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations ASOV, No coding mutations L120F,E176D, No coding mutations L120F,E176D, No coding mutations N915,	0 0 0 2 2 0 1 1 0 2 0 0	0 0 6 8 1 1 3 7 0 6 6 2 2	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 1 0.9901 0.9965 1 0.9964 0.9941 1 0.9974 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9998 0.9971 0.9931 1 0.9948 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 1554 852 1047 1014 906 1149	Strand
	Gene PAO1 lasR PAO1 lasI PAO1 rhill PAO1 pqsA PAO1 pqsA PAO1 pqsC PAO1	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199	83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations N91S, No coding mutations N91S, No coding mutations No coding mutations No coding mutations	0 0 0 2 0 0 1 0 0 2 2 0 0 0 0 0 0 0 0 0	0 6 8 1 1 3 7 0 6 2 2	0 Transversions 0 1 3 0 0 0 1 1 3 3 0 0	Codon_Percent 1 1 0.9901 0.9965 1 0.9941 0.9974 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9983 0.9998	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197	Strand
	Gene	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376	\$150p 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 336375 2529 82833	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations ASOV, No coding mutations L12OF,E17ED, No coding mutations	0 0 0 2 0 1 1 0 2 2 0 0 1 1 0 0 0 1 1 0 0 0 0	0 6 8 1 1 3 7 0 6 2 2	0 Transversions 0 0 0 1 1 3 3 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 0	Codon_Percent 1 1 0.9901 0.9965 1 0.9941 0.9974 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9983 0.9998	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999	Strand
Jp238	Gene	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168	\$top 83542 82459 792673 791768 544010 542463 541619 54053 539523 109784 185396 536375 25299 82833 102975	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Nutant Native Native Native Native Native Native	Description No coding mutations No coding mutations No coding mutations S62G, B83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F, £176D, No coding mutations N91S, No coding mutations	0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 6 8 1 1 1 3 7 0 6 6 2 2 2 2 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 0.9901 0.9905 1 0.9941 0.9941 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9948 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807	Target_Length 720 6606 726 6606 1554 852 1047 1011 906 1149 1197 999 714 243	Strand
Jp238 Strain:	Gene	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815	\$150p 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 336375 2529 82833	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native Native	Description No coding mutations No coding mutations No coding mutations S626,D83E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations N91S, No coding mutations Description	0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 6 8 1 1 1 3 7 0 6 6 2 2 2 2 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 0.9901 0.9905 1 0.9941 0.9941 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9948 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807	Target_Length 720 6606 726 6606 1554 852 1047 1011 906 1149 1197 999 714 243	Strand
Jp238	Gene	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168	\$top 83542 82459 792673 791768 544010 542463 541619 54053 539523 109784 185396 536375 25299 82833 102975	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Nutant Native Native Native Native Native Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations L120F,E176D, No coding mutations Description 11 bp Deletion at	0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 6 8 1 1 1 3 7 0 6 6 2 2 2 2 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 0.9901 0.9905 1 0.9941 0.9941 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9948 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807	Target_Length 720 6606 726 6606 1554 852 1047 1011 906 1149 1197 999 714 243	Strand
Jp238 Strain:	Gene	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168	\$top 83542 82459 792673 791768 544010 542463 541619 54053 539523 109784 185396 536375 25299 82833 102975	Match_Type Native Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations N91S, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229	0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0	0 0 6 8 1 1 1 3 7 0 6 6 2 2 2 2 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 0.9901 0.9905 1 0.9941 0.9941 1 1 1 1 1 1 1 1 1	BP_Percent 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9948 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807	Target_Length 720 6606 726 6606 1554 852 1047 1011 906 1149 1197 999 714 243	Strand
Jp238 Strain:	Gene PAO1 lasR PAO1 rhlR PAO1 rhlR PAO1 rhlR PAO1 rhlR PAO1 rhlD PAO1 pgsA PAO1 pgsA PAO1 pgsB PAO1 pgsD PAO1 pgsD PAO1 pgsD PAO1 pgsB PAO1 pgsL PAO1 pgsR PAO1 qscR PAO1 rsaL PAO1 rsaL PAO1 rsaL	82822 81853 791947 791162 542456 541611 540572 108635 184199 533576 1815 82590 102168 Start	\$top 83542 82459 792673 791768 544010 542463 541619 540530 54053	Match_Type Native Native Native Mutant Native Native Native Native Native Native Native Native Indel	Description No coding mutations No coding mutations No coding mutations S626,083E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations N91S, No coding mutations N91S, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),151 coding	0 0 0 2 0 1 1 0 2 0 0 1 1 0 0 0 0 0 0 0	0 0 6 8 8 1 1 3 7 7 0 6 2 2 2 2 0 0 BP_Changes	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 0.9974 1 1 1 1 1 Codon_Percent	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9931 1 0.9948 0.9983 0.9972 1 1 BP_Percent	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	Strand
Jp238 Strain:	Gene PAO1 lasR PAO1 shill PAO1 psA PAO1 psA PAO1 psA PAO1 psA PAO1 pgSA PAO1 pgSC PAO1	82822 818533 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168 Start	83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 2529 82833 102975 Stop	Match_Type Native Native Native Mutant Native Indive Native Native Native Native Indive Indel Iruncation	Description No coding mutations No coding mutations No coding mutations S626, B83E, No coding mutations S626, B83E, No coding mutations L120F, E176D, No coding mutations L120F, E176D, No coding mutations Not coding mutations Not coding mutations No coding mutations Description 11 bp Deletion at 197, truncation at codon 229 (of 240 codons), 161 coding mutations	0 0 0 0 1 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0	0 0 6 8 1 1 1 3 7 0 6 6 2 2 2 2 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 0.9901 0.9905 1 0.9941 0.9941 1 1 1 1 1 1 1 1 1	BP_Percent 1 1.0.9917 0.9868 0.9994 0.9988 0.9971 0.9981 0.9983 0.9972 1 1 BP_Percent 0.9722	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	Strand + + + Strand
Jp238 Strain:	Gene PAO1 lasR PAO1 gsR PAO1 psB PAO1 psB PAO1 psB PAO1 psB PAO1 pgSB	Start 82822 81853 791947 791162 5242456 541611 540572 539516 538617 108635 184199 535376 8155 82590 102168 Start	83542 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 828333 102975 Stop	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Mutant Native Mutant Native Native Native Native Native Native Native Native Indel Iruncation Native	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations L12OF,E175D, No coding mutations N91S, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations	0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 Codon_Changes	0 0 6 8 8 1 1 3 7 7 0 6 2 2 2 2 0 0 BP_Changes	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 0 0 1 1 0 0 Transversions	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 0.9974 1 1 1 1 1 Codon_Percent	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9991 1 0.9943 0.9933 0.9983 0.9972 1 BP_Percent 0.9722 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 97 1197 999 714 243 807 Match_Length	Target_Length 720 606 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	\$tart 82822 81853 791947 791162 542456 541611 540572 108635 184199 533576 1815 82590 102168 \$tart 365051 364082 10191	\$top 83542 83459 792673 791768 544010 542463 541619 540530 530523 109784 185396 2529 82833 102975 \$top 365760 364688 10917	Match_Type Native Native Native Mutant Native Native Native Native Native Native Match_Type Indel Truncation Native Native Native	Description No coding mutations No coding mutations No coding mutations S62G,083E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations	0 0 0 0 2 0 1 1 0 0 2 0 0 0 0 0 0 0 0 0	0 0 6 8 8 1 1 3 7 7 0 6 2 2 2 2 0 0 BP_Changes	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 0 0 1 1 0 0 Transversions	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 1 1 1 1 1 1 1 1 Codon_Percent	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9981 0.9983 0.9972 1 1 BP_Percent BP_Percent	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length	Strand
Jp238 Strain:	Gene PA01 IasR PA01 rail	82822 81853 791947 791162 542456 542451 540572 539516 538617 108635 184199 535376 1815 82590 102168 Start	\$top 83542 82459 792673 791768 544010 542463 541619 540530 109784 185396 2529 82833 109275 \$top 365760 364688 10917 11702	Match_Type Native Native Native Mutant Native Indel Truncation Native Native Native Mutant Native Native Native Native Match_Type	Description No coding mutations No coding mutations No coding mutations S626, D83E, No coding mutations S626, D83E, No coding mutations L120F, £176D, No coding mutations L120F, £176D, No coding mutations Description 11 bp Deletion at 197, truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutation at codon 229 (of 240 codons),161 coding mutations No coding mutations R22L,5626,	0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 Codon_Changes	0 0 6 8 8 1 1 3 7 7 0 6 2 2 2 2 0 0 BP_Changes	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 0 0 1 1 0 0 Transversions	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 1 0.9974 1 1 1 1 Codon_Percent 0.3292 1 1 0.9901	BP_Percent 1 1.0.9917 0.9868 0.9994 0.9988 0.9971 0.9983 0.9983 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9993	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 709 606 726 606	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	Strand +
Jp238 Strain:	Gene PAO1 lasR PAO1 grain PAO1 profile PAO1	Start 82822 81853 791947 791162 542456 542456 541611 540572 539516 538617 108635 184199 535376 8155 82590 102168 Start 365051 364082 10191 11090 836864	\$top 83542 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 828333 102975 \$top 365760 364688 10917 11702 838418	Match_Type Native Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Mutant Mutant Mutant Mutant	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L12OF,E176D, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations	0 0 0 0 0 1 1 0 0 1 0 0 0 1 0 0 0 0 0 0	0 0 6 8 8 1 1 3 7 7 0 6 6 2 2 2 2 2 0 0 8 BP_Changes	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9941 1 1 1 1 1 Codon_Percent 0.3292 1 1 0.9901 0.9901	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9972 1 1BP_Percent 0.9722 0.9983 0.9959 0.9959 0.9984	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 999 714 243 307 Match_Length 709 606 726 606 606	Target_Length 720 6606 726 6606 1554 852 1047 1014 906 1149 1197 999 714 2443 807 Target_Length 720 660 606	Strand + + + + + + + + + + +
Jp238 Strain:	Gene PAO1 IasR PAO1 risR	Start 82822 81853 791947 791162 542456 541611 540572 108635 184199 533676 1815 82590 102168 Start 365051 10991 11096 836864 836019	\$top 83542 83549 792673 791768 54010 542463 541619 540530 539523 109784 109784 109784 109784 109784 109784 109784 109784 109784 109795 109795 109784	Match_Type Native Native Native Mutant Native Native Native Native Native Mutant Native Native Native Mutant Mutant Mutant Mutant Mutant Mutant Mutant	Description No coding mutations No coding mutations So2G,D83E, No coding mutations So2G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations N91S, No coding mutations Not coding mutations No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations Poscription 11 by Deletion at 107,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations R22L,562G, P263A,R347Q, G279E,	0 0 0 0 0 2 0 0 1 1 0 0 0 1 1 0 0 0 0 0	0 0 6 8 8 1 1 1 3 3 7 0 6 6 2 2 2 2 2 2 0 0 9 8 BP_Changes	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 1 0.9974 1 1 1 1 Codon_Percent 0.3292 1 1 0.9901	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9988 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 709 606 726 606 726 606 1554	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 714 243 807 Target_Length	Strand + + + + + + + + + + +
Jp238 Strain:	Gene PAO1 IasR PAO1 rill P	82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 535376 102168 Start	\$top 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 2529 82833 102975 \$top 365760 364688 10917 11702 838418 836871 836027	Match_Type Native Native Native Mutant Native Indel Iruncation Native Mutant Native Mutant Native Native Native Native Match_Type Indel Iruncation Native Mutant Mutant Mutant Mutant Mutant Native	Description No coding mutations No coding mutations So2G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations Description 11 bp Deletion at 197, truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations R0 coding mutations No coding mutations No coding mutations No coding mutations No coding mutations R22L,S62G, P263A,R347Q, G279E, No coding mutations	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 6 8 8 1 1 3 7 0 6 6 2 2 2 2 2 0 0 8 BP_Changes 2 2 3 7 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 1 0.9965 1 0.9941 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9965 0.9965	BP_Percent 1 10.9917 0.9868 0.9994 0.9988 0.9971 0.9981 0.9983 0.99972 1 1 BP_Percent 0.9983 0.9999 0.9884 0.9916 0.99884 0.9916 0.9981	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 709 606 726 606 1554 852	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length 720 606 726 606 1554 852 1047	Strand
Jp238 Strain:	Gene PAO1 lasR PAO1 asl PAO1 rhlR PAO1 pqsB PAO1 rpsB	Start 82822 81853 791947 791162 5242456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168 Start 365051 364082 10191 11096 836864 836019 834980 834924	83542 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 828333 102975 Stop 365760 364688 10917 11702 838418 836871 836027 8363627	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Mutant Mutant Mutant Mutant Native Match_Type Indel Truncation Native Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Mutant Mutant Mutant Mutant	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L12OF,E176D, No coding mutations No15, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations	0 0 0 0 0 1 1 0 0 1 0 0 0 1 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 0 0 1 1 0 0 Transversions 6 0 0 0 1 1 0 0 1 1 0 0 0 0 1 1 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9974 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9905 0.9905 1 0.9905	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9993 0.9972 0.9983 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 999 714 243 307 Match_Length 709 606 726 606 605 606 1554 852 1047	Target_Length 720 6606 726 6606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 606 1554 852 1047 1014	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	\$tart 82822 81853 791947 791162 542456 541641 540572 539516 538617 108635 108163 102168 \$tart 365051 364082 10191 11096 836864 836019 834980 834980 834980 833924	\$top 83542 83459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 \$2529 \$364688 10917 11702 836418 836871 836927 836938 833931	Match_Type Native Native Native Mutant Native Native Native Native Native Native Native Mutant Mutant Mutant Mutant Mutant Native Native Native Mutant Mutant Mutant Mutant Native Mutant Mutant Mutant Native Mutant Native Mutant Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations N91S, No coding mutations N91S, No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations A243V, No coding mutations	0 0 0 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 3 0 0 1 1 0 0 Transversions 6 0 0 0 2 4 4 1 3 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9974 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9905 0.9905 1 0.9905	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9982 1 1 1BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916 0.9941 0.9838 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 909 714 243 3807 Match_Length 709 606 726 606 1554 852 1047 1014	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length 720 606 726 606 1554 852 1047 1044	Strand
Jp238 Strain:	Gene PAO1 lasR PAO1 asl PAO1 rhlR PAO1 pqsB PAO1 rpsB	Start 82822 81853 791947 791162 5242456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168 Start 365051 364082 10191 11096 836864 836019 834980 834924	\$top 83542 83459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 \$2529 \$364688 10917 11702 836418 836871 836927 836938 833931	Match_Type Native Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Mutant Mutant Mutant Mutant Native Match_Type Indel Truncation Native Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant Mutant Native Mutant Mutant Mutant Mutant	Description No coding mutations No coding mutations No coding mutations S62G, B93E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations Description 11 bp Deletion at 117,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations R22L,562G, P263A,R347O, G279E, No coding mutations No coding mutations No coding mutations No coding mutations	0 0 0 0 0 1 1 0 0 1 0 0 0 1 1 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 0 0 1 1 0 0 Transversions 6 0 0 0 1 1 0 0 1 1 0 0 0 0 1 1 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9974 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9905 0.9905 1 0.9905	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9993 0.9972 0.9983 0.9983 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 999 714 243 307 Match_Length 709 606 726 606 605 606 1554 852 1047	Target_Length 720 6606 726 6606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 606 1554 852 1047 1014	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	\$tart 82822 81853 791947 791162 542456 541641 540572 539516 538617 108635 108163 102168 \$tart 365051 364082 10191 11096 836864 836019 834980 834980 834980 833924	\$top 83542 83459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 \$2529 \$364688 10917 11702 836418 836871 836927 836938 833931	Match_Type Native Native Native Mutant Native Native Native Native Native Native Native Mutant Mutant Mutant Mutant Mutant Native Native Native Mutant Mutant Mutant Mutant Native Mutant Mutant Mutant Native Mutant Native Mutant Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L12OF,E175D, No coding mutations Do coding mutations No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations A243V, No coding mutations D175E,5206A,A232S,T378A,A3	0 0 0 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 3 0 0 1 1 0 0 0 Transversions 6 0 0 0 2 4 4 1 3 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9974 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9905 0.9905 1 0.9905	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9982 1 1 1BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916 0.9941 0.9838 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 909 714 243 3807 Match_Length 709 606 726 606 1554 852 1047 1014	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length 720 606 726 606 1554 852 1047 1044	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	Start 82822 81853 791947 791162 542456 541611 540572 108635 108635 11815 2590 102168 Start 365051 364082 10191 11096 834980 834980 834980 833924 833924 58848	\$top 83542 83545 792673 791768 54010 542463 541619 540530 539523 109784 109784 109784 109784 109784 109784 109784 109784 109784 10997 11702 8364688 10917 11702 838481 836871 836027 839997	Match_Type Native Native Native Mutant Native Native Native Native Native Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S62G, B93E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations Description 11 bp Deletion at 117,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations No coding mutations No coding mutations R22L,562G, P263A,R347O, G279E, No coding mutations No coding mutations No coding mutations No coding mutations	0 0 0 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 1 0.9901 0.9965 1 1 0.9941 1 1 1 1 1 1 Codon_Percent 1 1 0.9965 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9948 0.9948 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916 0.9941 0.9938 0.9948 0.9959 0.9884 0.9959 0.9884 0.9959	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Match_Length 709 606 726 606 605 1554 852 1047 1047 1049 1040 1149	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1149 714 243 807 Target_Length 720 606 726 606 1554 852 1047 1014 906	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	\$tart 82822 81853 791947 791162 542456 541611 540572 539516 538617 108635 184199 535376 1815 82590 102168 \$tart 365051 11096 836864 83602 83692 833924 833025 58848	\$top 83542 83459 792673 791768 544010 54263 541619 540530 539523 109784 185396 2529 82833 102975 \$top 365760 365760 8364188 369478 11702 838418 836871 11702 838418 59997	Match_Type Native Native Native Mutant Native Native Native Native Native Mutant Native Match_Type Indel Truncation Native Mutant Mutant Mutant Mutant Mutant Mutant Native Mutant Native Mutant Native Native Native Native Native Mutant Native	Description No coding mutations No coding mutations No coding mutations S626, B93E, No coding mutations A50V, No coding mutations L120F,E176D, No coding mutations R22L,562G, P263A,R347O, G279E, No coding mutations No soding mutations No coding mutations No coding mutations No soding mutations	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 1 1 3 0 0 0 1 1 3 3 0 0 1 1 0 0 0 Transversions 6 0 0 0 2 4 4 1 3 3 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 0.9901 0.9901 1 0.9941 1 1 0.9974 1 1 1 Codon_Percent 0.3292 1 0.9901 0.9905 0.9905 1 0.9905	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 1 0.9948 0.9982 1 1 1BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916 0.9941 0.9838 0.9983	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 709 606 726 606 1554 852 1047 1014 906 1149	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 7arget_Length 720 606 726 606 1554 852 1047 1014 906	Strand
Jp238 Strain:	Gene PAO1 IasR PAO1	Start 82822 81853 791947 791162 542456 541611 540572 108635 108635 11815 2590 102168 Start 365051 364082 10191 11096 834980 834980 834980 833924 833924 58848	\$top 83542 83542 82459 792673 791768 544010 542463 541619 540530 539523 109784 185396 536375 2529 828333 102975 \$top 365760 364688 10917 11702 836027 836938 833931 59997	Match_Type Native Native Native Mutant Native Native Native Native Native Native Mutant Native	Description No coding mutations No coding mutations S62G,D83E, No coding mutations S62G,D83E, No coding mutations A50V, No coding mutations A50V, No coding mutations L12OF,E175D, No coding mutations Do coding mutations No coding mutations Description 11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations No coding mutations A243V, No coding mutations D175E,5206A,A232S,T378A,A3	0 0 0 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Transversions 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Codon_Percent 1 1 1 0.9901 0.9965 1 1 0.9941 1 1 1 1 1 1 Codon_Percent 1 1 0.9965 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BP_Percent 1 1 0.9917 0.9868 0.9994 0.9988 0.9971 0.9948 0.9948 0.9972 1 1 BP_Percent 0.9722 0.9983 0.9959 0.9884 0.9916 0.9941 0.9938 0.9948 0.9959 0.9884 0.9959 0.9884 0.9959	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Match_Length 720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Match_Length 709 606 726 606 605 1554 852 1047 1047 1049 1040 1149	Target_Length 720 606 726 606 1554 852 1047 1014 906 1149 1149 714 243 807 Target_Length 720 606 726 606 1554 852 1047 1014 906	Strand

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	PAO1_rsaL	364819	365062		No coding mutations	0	0	0	1	1	1	243	243	
	PAO1_vqsR	65657		Mutant	R63I,V66I,T116A,	3	10	_ 1	0.9888	0.9876	_ 1	807	807	
Strain: W15Dec14	Gene	Start	Stop	Match_Type	Description	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length			Strand
W15Dec14	PAO1_lasR PAO1_lasI	83344 82375	84064 82981	Native Native	No coding mutations No coding mutations	0	0	0	1	1	1	720 606	720 606	1 -
	PAO1_lasi	728506	729232	Native	No coding mutations	0	2	0	-	0.9972	1	726	726	
	PAO1_IIIIK	729412	730018		S62G,D83E,	2	9	3	0.9901	0.9868	1	606	606	
	PAO1_pqsA	561139	562693		No coding mutations	0		0		0.9981	1	1554	1554	
	PAO1_pqsB	560294		Native	No coding mutations	0		0		0.9977	1	852	852	
	PAO1_pqsC	559255			No coding mutations	0		1		0.9952	1	1047	1047	
	PAO1_pqsD	558199		Mutant	E176D,	1	7	2	0.997	0.9931	1	1014	1014	_
	PAO1_pqsE	557300		Mutant	H71X,E103G,	2	4	1	0.9934	0.9956	1	906	906	-
	PAO1_pqsH	196286	197435		No coding mutations	0	3	1	1	0.9974	1	1149	1149	+
	PAO1_pqsL	50331	51528		H75D,T378A,	2	6	1	0.995	0.995	1	1197	1197	
	PAO1_pqsR	554059	555058	Native	No coding mutations	0	2	1	1	0.998	1	999	999	+
	PAO1_qscR	421613	422327	Native	No coding mutations	0	2	0	1	0.9972	1	714	714	+
	PAO1_rsaL	83112	83355	Native	No coding mutations	0	0	0	1	1	1	243	243	
	PAO1_vqsR	189819	190626	Native	No coding mutations	0	1	0		0.9988	1	807	807	
Strain:	Gene	Start	Stop	Match_Type	Description	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length		Target_Length	
Aa249	PAO1_lasR	85774		Native	No coding mutations	0	0	0	1	1	1	720	720	_
	PAO1_lasI	84805	85411		No coding mutations	0	0	0	-	1	1	606	606	
	PAO1_rhIR	111501	112227	Native	No coding mutations	0	3	0		0.9959	1	726	726	
1	PAO1_rhII	110716	111322	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	
I	PAO1_pqsA	563765		Native	No coding mutations	0	2	1	1 0 0000	0.9987	1	1554	1554	_
1	PAO1_pqsB	562920			P200L,	0	3	0		0.9965 0.9933	1	852 1047	852 1047	
	PAO1_pqsC	561881		Native	No coding mutations	1	6	2			1			_
	PAO1_pqsD PAO1_pqsE	560825 559926		Mutant Native	E176D, No coding mutations	0	Ŭ	0		0.9941	1	1014 906	1014 906	
	PAO1_pqsE	91040		Native	No coding mutations	0	-	0		0.9956	1	1149	1149	
	PAO1_pqsh PAO1_pqsL	225165	226362	Mutant	E330G,	1	3	0		0.9956	1	1149	1149	_
	PAO1_pqsR	489416	490415	Native	No coding mutations	0	1	0		0.999	1	999	999	
	PAO1_qscR	1815	2529	Native	No coding mutations	0		0		0.9972	1	714	714	
	PAO1_rsaL	85542	85785		No coding mutations	0		0	1	1	1	243	243	
	PAO1_vqsR	97849		Native	No coding mutations	0	1	0	1	0.9988	1	807	807	_
Strain:	Gene	Start	Stop	Match Type	Description	Codon Changes	BP Changes	Transversions	Codon Percent	BP Percent	Percent Length	Match Length	Target Length	Strand
Strain: PT31M	Gene	Start	Stop	Match_Type	Description 13 bp Deletion at	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length	Match_Length	Target_Length	Strand
	Gene	Start	Stop	Match_Type		Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length	Match_Length	Target_Length	Strand
	Gene	Start	Stop	Match_Type Indel	13 bp Deletion at	Codon_Changes	BP_Changes	Transversions	Codon_Percent	BP_Percent	Percent_Length	Match_Length	Target_Length	Strand
	PAO1_lasR	46184	46891	Indel Truncation	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations	Codon_Changes	BP_Changes	Transversions 6	Codon_Percent 0.5542	0.9694	Percent_Length 0.9819	707	720	1+
	PAO1_lasR PAO1_lasI	46184 47254	46891 47860	Indel Truncation Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations	107 0	22 2	Transversions 6		0.9694 0.9967	0.9819 1	707 606	720 606) + i +
	PAO1_lasR PAO1_lasI PAO1_rhIR	46184 47254 219207	46891 47860 219933	Indel Truncation Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations	107 0 0	22 2	Transversions 6 1	0.5542 1 1	0.9694 0.9967 0.9931	0.9819 1 1	707 606 726	720 606 726) + i +
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII	46184 47254 219207 218422	46891 47860 219933 219028	Indel Truncation Native Native Mutant	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E,	107 0 0	22 2 5	6 1 1 3		0.9694 0.9967 0.9931 0.9851	0.9819 1 1	707 606 726 606	720 606 726 606	+
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA	46184 47254 219207 218422 286400	46891 47860 219933 219028 287954	Indel Truncation Native Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations Se2G,D83E, No coding mutations	107 0 0 2	22 2 5	6 1 1 3 2	0.5542 1 1 0.9901	0.9694 0.9967 0.9931 0.9851 0.9987	0.9819 1 1 1 1	707 606 726 606 1554	720 606 726 606 1554	+
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA PAO1_pqsB	46184 47254 219207 218422 286400 285555	46891 47860 219933 219028 287954 286407	Indel Truncation Native Native Mutant Native Mutant	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations \$626,D83E, No coding mutations	107 0 0 2 2 0	22 2 5 9 2	6 1 1 3 2 0	0.5542 1 1 0.9901 1 0.9965	0.9694 0.9967 0.9931 0.9851 0.9987	0.9819 1 1 1 1 1	707 606 726 606 1554 852	720 606 726 606 1554 852	+
	PAO1_lasR PAO1_lasI PAO1_rhIR PAO1_rhII PAO1_pqsA PAO1_pqsB PAO1_pqsC	46184 47254 219207 218422 286400 285555 284516	46891 47860 219933 219028 287954 286407 285563	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations	107 0 0 2 0 1	22 2 5 9 2	6 1 1 3 2	0.5542 1 1 0.9901 1 0.9965	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977	0.9819 1 1 1 1 1 1	707 606 726 606 1554 852	720 606 726 606 1554 852	+ +
	PAO1 lasR PAO1 rhIR PAO1 rhII PAO1 pqsA PAO1 pqsA PAO1 pqsC PAO1 pqsD	46184 47254 219207 218422 286400 285555 284516 283460	46891 47860 219933 219028 287954 286407 285563 284474	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant	13 bp Deletion at 380,truncation at codon 173 (0f 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D,	107 0 0 2 0 1 0	22 2 5 9 2	6 1 1 3 2 0 0	0.5542 1 1 0.9901 1 0.9965 1 0.997	0.9694 0.9967 0.9931 0.9851 0.9987	0.9819 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047	720 606 726 606 1554 852 1047	+ +
	PAO1 lask PAO1 rhiR PAO1 rhiR PAO1 pqsA PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsD PAO1 pqsD	46184 47254 219207 218422 286400 285555 284516 283460 282561	46891 47860 219933 219028 287954 286407 285563 284474 283467	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 2 2 0 1 1 0 1	22 2 5 9 2	6 1 1 3 2 0	0.5542 1 1 0.9901 1 0.9965 1 1 0.9967	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971	0.9819 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014	720 606 726 606 1554 852 1047 1014	+ + - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhII PAO1 rhII PAO1 pqsA PAO1 pqsC PAO1 pqsC PAO1 pqsC	46184 47254 219207 218422 286400 285555 284516 283460 282561 151924	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073	Indel Truncation Native Native Mutant Native Mutant Mutant Mutant Mutant Native Mutant Native Mutant Native Mutant	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 0	22 2 5 9 2 2 2 3 6 0 7	6 1 1 3 2 0 0	0.5542 1 1 0.9901 1 0.9965 1 0.997 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 1 0.9939	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906	720 606 726 606 1554 852 1047 1014 906	+ + +
	PAO1 lasR PAO1 lasl PAO1 rhlR PAO1 rhlI PAO1 rhlI PAO1 pqsA PAO1 pqsC PAO1 pqsC PAO1 pqsE PAO1 pqsE PAO1 pqsE	46184 47254 219207 218422 286400 285555 284516 283460 282561 151924 25330	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Mutant Native Mutant Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 1 0 1 1 0	22 2 5 9 2 2 2 3 6 0 0 7	6 1 1 3 2 0 0 0 2 2	0.5542 1 1 1 0.9901 1 0.9965 1 0.997 1 0.9974 1 0.9974	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9941 1 0.9939 0.9967	0.9819 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149	720 606 726 606 1554 852 1047 1014 906 1149	+ + - - - - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhII PAO1 rhII PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsL PAO1 pqsL	46184 47254 219207 218422 286400 285555 284516 283460 282561 25330 279320	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527 280319	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations Sc2G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 0 1 1 0 0	22 2 5 9 2 2 3 6 0 7 4	6 1 1 3 2 2 0 0 2 2 0 0 2 0 0	0.5542 1 1 0.9901 1 0.9965 1 1 0.997 1 0.997 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 1 0.9939	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197	720 606 726 606 1554 852 1047 1014 906 1149 1197 999	+ + - - - - - - - - - - -
	PAO1 lasR PAO1 lasl PAO1 rllR PAO1 rllR PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsC PAO1 pqsB PAO1 pqsE PAO1 pqsE PAO1 pqsH PAO1 pqsR PAO1 pqsR PAO1 pqsR PAO1 pqsR	46184 47254 219207 218422 286400 285555 284516 283460 282561 151924 25330 279320 424624	46891 47860 219933 219928 287954 286407 285563 284474 283467 153073 26527 280319 425338	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 1 0 1 1 0	22 2 5 9 2 2 2 3 6 6 0 7 7 4 1	66 11 13 3 2 0 0 0 2 2 0 0	0.5542 1 1 0.9901 1 0.9965 1 1 0.9974 1 1 1 1 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9941 1 0.9939 0.9967	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714	720 606 726 606 1554 852 1047 1014 906 1149 1197 999	+ + - - - - - - - - - - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhII PAO1 rhII PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsB PAO1 pqsL PAO1 pqsL	46184 47254 219207 218422 286400 285555 284516 283460 282561 25330 279320	46891 47860 219933 219028 287954 286407 285563 285474 283467 153073 26527 280319 425338 47123	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations Sc2G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 0 0 2 2 0 0 1 1 0 0 1 1 0 0 0 0 0 0	22 2 5 9 2 2 2 3 6 6 0 7 7 4 1	6 1 1 3 2 0 0 0 2 2 0 0 2 0 0	0.5542 1 1 0.9901 1 0.9965 1 1 0.9974 1 1 1 1 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 1 0.9939 0.9967	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197	720 606 726 606 1554 852 1047 1014 906 1149 1197 999	+ + - - - - - - - - - - - - - -
	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhIR PAO1 pqSA PAO1 pqSB PAO1 pqSC PAO1 pqSD PAO1 pqSD PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSL PAO1 pqSR	46184 47254 219207 218422 285400 285555 284516 282561 151924 25330 279320 424624 46880	46891 47860 219933 219028 287954 286407 285563 285474 283467 153073 26527 280319 425338 47123	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Nutant Native Native Native Native Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0 0 0	22 2 5 9 9 2 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0	6 1 1 3 2 0 0 0 2 2 0 0 2 0 0	0.5542 1 1 0.9901 2 0.9965 1 0.997 1 0.9974 1 1 1 1 1 1 1 1 1 1	0.9694 0.9967 0.9987 0.9987 0.9977 0.9971 0.9941 1 0.9939 0.9967 0.9999 1 0.9959 0.9959	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 999 714 243 807	720 606 726 606 1554 852 1047 1014 906 1149 999 714	+ + + + + +
РТ31М	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhIR PAO1 pgsA PAO1 pgsB PAO1 pgsC PAO1 pgsC PAO1 pgsC PAO1 pgsH PAO1 pgsH PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR	46184 47254 219207 218427 286400 285555 284516 283460 282561 25330 279320 424624 46888 158733	46891 47860 219933 219038 287954 285407 285563 284474 283467 153073 265272 280319 425338 47123 159540	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Nutant Native Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 2 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0 0 0	22 2 5 9 9 2 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0	6 1 1 3 2 2 0 0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0	0.5542 1 1 0.9901 2 0.9965 1 0.997 1 0.9974 1 1 1 1 1 1 1 1 1 1	0.9694 0.9967 0.9987 0.9987 0.9977 0.9971 0.9941 1 0.9939 0.9967 0.9999 1 0.9959 0.9959	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 999 714 243 807	720 606 726 606 1554 852 1047 1014 906 1149 91197 999 714 243 807	+ + + + +
PT31M	PAO1 lasR PAO1 lasl PAO1 rhil PAO1 rhil PAO1 pgsA PAO1 pgsB PAO1 pgsB PAO1 pgsE PAO1 pgsE PAO1 pgsE PAO1 pgsE PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 pgsR PAO1 gsR PAO1 gsR PAO1 gsR PAO1 gsR PAO1 gsR	46184 47254 219207 218422 286400 285555 284516 151924 25330 279320 424624 46880 158733 Start	46891 47860 219933 219938 219928 287954 286407 285563 284474 283467 153073 26527 280319 425338 47123 159540 Stop	Indel Truncation Native Mutant Native Mative Native Native Native Native Native Math_Type	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations Description	107 0 0 2 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0 0 0	22 2 5 9 9 2 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0	6 1 1 3 2 2 0 0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0	0.5542 1 1 0.9901 1 0.9965 1 0.9967 1 1 0.9974 1 1 1 1 1 1 Codon_Percent 1	0.9694 0.9967 0.9987 0.9987 0.9977 0.9971 0.9941 1 0.9939 0.9967 0.9999 1 0.9959 0.9959	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	+ + + +
PT31M	PAO1 lasR PAO1 asl PAO1 whR PAO1 whR PAO1 whR PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 pgsP PAO1 pgsP PAO1 pgsR PAO1 pgsR	46184 47254 219207 218422 286400 285555 284516 233460 279320 479320 46880 158733 5tart	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527 280319 42538 47123 159540 Stop	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Nutant Native Nutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations Not coding mutations Not coding mutations No coding mutations	107 0 0 0 1 1 0 1 1 0 0 1 1 0 0 0 0 0 Codon_Changes	22 2 5 9 2 2 2 3 3 6 6 0 0 7 7 4 1 1 1 1 7 8 P_Changes 0 0	6 1 1 3 3 2 0 0 0 2 2 0 0 0 0 1 Transversions	0.5542 1 1 0.9901 1 0.9965 1 0.9967 1 1 0.9974 1 1 1 1 1 1 Codon_Percent 1	0.9694 0.9967 0.9987 0.9987 0.9977 0.9971 0.9941 1 0.9939 0.9967 0.9999 1 0.9959 0.9959	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length	+ + + Strand + + + +
PT31M	PAO1 lasR PAO1 lasI PAO1 rhIR PAO1 rhIR PAO1 pqSA PAO1 pqSA PAO1 pqSC PAO1 pqSC PAO1 pqSC PAO1 pqSC PAO1 pqSR PAO1 qsCR PAO1 qsCR PAO1 qsCR PAO1 qsCR PAO1 qsCR PAO1 qsCR PAO1 sqSCR PAO1 sqSCR	46184 47254 219207 218422 286400 285555 284516 233460 222561 279320 424624 46880 158733 Start	46891 47860 219933 219028 287954 285407 285563 284474 23346 153073 26527 280319 425338 47123 159540 Stop 319522 320491 800210	Indel Truncation Native Mutant Native Mative Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0	22 2 5 9 2 2 2 3 3 6 6 0 0 7 7 4 1 1 1 1 7 8 P_Changes 0 0	6 1 1 3 3 2 0 0 0 2 2 0 0 0 0 1 Transversions	0.5542 1 1 0.9901 1 0.9965 1 0.9967 1 1 0.9974 1 1 1 1 1 1 Codon_Percent 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 0.9941 1 1 0.9959 0.9967 0.9999 1 1 0.9959 0.9999 0.9913 BP_Percent 1	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 Percent_Length	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606	720 606 726 606 1554 852 1047 1014 906 1149 919 714 243 807 Target_Length 720 606	+ + + Strand + +
PT31M	PAO1 lasR PAO1 lasI PAO1 mill PAO1 mill PAO1 mill PAO1 pgsA PAO1 pgsC PAO1 pscC	46184 47254 219207 218422 286400 285555 284516 151924 25330 279320 424624 46880 158733 Start 318802 318802 799345	46891 47860 219933 219028 287954 284577 285563 284474 153073 26527 280319 45338 47123 159540 Stop 319522 320491 800210 799305	Indel Truncation Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations P31S, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 Codon_Changes	22 2 5 5 9 9 2 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 7 8P_Changes	6 1 1 3 3 2 0 0 0 2 2 0 0 0 0 1 Transversions	0.5542 1 1 0.9901 1 0.9965 1 1 0.9965 1 1 1 0.9974 1 1 1 1 1 1 Codon_Percent 1 1 1 0.9901	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9939 0.9967 0.9999 1 0.9999 1 0.9999 1 0.9999 1 0.9999 0.9999 0.9999	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606	+ + +
PT31M	PAO1 asR PAO1 asR PAO1 asI PAO1 rhil PAO1 pg3A PAO1 pg3A PAO1 pg3E PAO1 pg5E PAO1 pg5E PAO1 pg5E PAO1 pg5E PAO1 pg5E PAO1 pg5E PAO1 yg5E PAO1 yg5E PAO1 yg5E PAO1 yg5E PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 jasR PAO1 pg5A PAO1 rhil PAO1 rhil PAO1 pg5A	46184 47254 219207 218422 286400 285555 284516 283460 282561 151924 25330 2793220 424624 46880 158733 Start 318802 318882 798484 798699	46891 47860 219933 219028 287954 285407 285563 284474 23346 153073 26527 280319 425338 47123 159540 Stop 319522 320491 800210 799305 19766	Indel Truncation Native Mutant Native Native Native Native Native Native Native Mutant Native Mutant Native Mutant Mutant Mutant Mutant	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V,	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0	22 2 5 5 9 9 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 7 8 P_ Changes 0 0 0 0 6 6 1 1 0 1 2 2 1 1 1	6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.5542 1 1 0.9901 1 0.9905 1 1 0.9974 1 1 1 1 1 1 1 1 Codon_Percent 1 1 0.9901 0.9981	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 0.9941 1 0.9959 1 0.9959 1 0.9959 1 0.9959 1 0.9959 0.9913 BP_Percent 1 0.9917 0.9937 0.9938	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 1554 852	720 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Target_Length 720 606 606 1554	+ + +
PT31M	PAO1 lasR PAO1 lasI PAO1 rhII PAO1 rhII PAO1 pgsA PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 gsL PAO1 gsL PAO1 gsL PAO1 gsR PAO1 rsaL PAO1 rsaL PAO1 lasR PAO1 lasR PAO1 rhII PAO1 rhII PAO1 rhII PAO1 rpsB PAO1 rpsB PAO1 rpsB PAO1 rpsB PAO1 rpsB PAO1 pgsB PAO1 pgsB PAO1 pgsB PAO1 pgsB	46184 47254 219207 218422 286400 285555 284516 283460 283460 279320 424624 46880 158733 5tart 318802 319885 799484 798699 190222	46891 47860 219933 219928 287954 284677 285563 284474 153073 26527 26527 26527 319540 5top 319522 320491 799305 191776	Indel Truncation Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native Native Native Native Mutant Native Native Native Mutant Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 1 1 0 0 0 0	22 2 5 5 9 9 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 7 8 P_ Changes 0 0 0 0 6 6 1 1 0 1 2 2 1 1 1	6 1 1 3 3 2 0 0 0 2 2 0 0 0 0 1 Transversions 0 1 1 2 0 0 0 1	0.5542 1 1 0.9901 1 0.9965 1 1 0.9974 1 1 1 1 1 1 1 1 1 1 0.9901 0.9981 0.9985 1 0.9965	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9937 0.9967 0.9996 1 1 0.9939 0.9959 0.9913 BP_Percent 1 0.9935 0.9937 0.9998 0.9938	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 1554 852	720 606 726 606 1554 852 1047 1014 906 1149 1199 714 243 807 Target_Length 720 606 726 606 1554 852	+ + +
PT31M	PAO1 lasR PAO1 asI PAO1 rhIR PAO1 rhIR PAO1 pqsA PAO1 pqsA PAO1 pqsB PAO1 pqsB PAO1 pqsC	46184 47254 219207 218422 286400 282561 283460 282561 25330 279320 424624 46880 158733 Start 318802 319885 798484 798699 190222 191769	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527 280319 425338 47123 159540 Stop 319522 320491 800210 799305 191776 192621 193660 194716	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations D47N, No coding mutations E176D, No coding mutations S62G,D83E, P356L, No coding mutations E176D,	107 0 0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0	22 2 5 9 9 2 2 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 7 BP_Changes 0 0 6 6 100 2 1 1 6 6 6	6 11 33 22 00 00 22 00 00 00 11 Transversions 00 11 22 00 00 01 12 10 11 12 12 12 13 14 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	0.5542 1 1 0.9901 1 0.9965 1 0.9974 1 1 1 1 1 1 1 1 1 0.9901 0.9981 0.9965 1 1 0.9978	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 0.9941 1 0.9959 1 0.9959 1 0.9959 1 0.9959 1 0.9959 0.9913 BP_Percent 1 0.9917 0.9937 0.9938	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 1554 852 1047	720 606 726 606 1554 852 1047 1014 906 61149 1197 999 714 243 807 Target_Length 720 606 1554 852 1047	+ + + + + + + + + + + + + + + + +
PT31M	PAO1 lasR PAO1 lasI PAO1 mill PAO1 m	46184 47254 219207 218422 286400 285555 284516 283460 283561 151924 282561 151924 424624 46880 158733 Start 318802 319885 799484 798699 192613 193702	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527 280319 425338 47123 159540 Stop 319522 320491 800210 799305 191776 192621 193660 193660 194716	Indel Truncation Native Mutant Native Native Native Native Native Native Mutant Native Mutant Mutant Mutant Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V, No coding mutations E176D, No coding mutations E176D, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0	22 2 5 9 9 2 2 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 7 BP_Changes 0 0 6 6 100 2 1 1 6 6 6	6 1 1 3 3 3 2 2 0 0 0 0 0 0 1 1 2 2 0 0 0 0 1 1 2 2 0 0 0 0	0.5542 1 10.9901 11 0.9905 11 0.9974 11 11 11 11 11 11 10 Codon_Percent 11 0.9901 0.99081 0.9905 10 0.99681	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 0.9941 1 0.9959 1 1 0.9959 0.9913 BP_Percent 1 1 0.9917 0.9835 0.9988 0.9943 0.9988	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1154 852 1047 1014 906 1149 1197 714 243 807 Match_Length 720 606 606 1554 852 1047 1014	720 606 726 606 1554 852 1047 1014 906 1149 1197 714 243 807 Target_Length 720 606 605 1554 852 1047 1014	+ + + + + + + + + + + + + + +
PT31M	PAO1 lasR PAO1 lasR PAO1 lasI PAO1 rhII PAO1 rhII PAO1 pgsA PAO1 pgsB PAO1 rsaL PAO1 rsaL PAO1 rsaL PAO1 rsaL PAO1 rsaL PAO1 pgsB	46184 47254 219207 218422 286400 285555 284516 283460 283460 1519244 285251 313802 474624 48880 15873 Start 318802 319885 199232 191769 192613 193702 194709	46891 47860 219933 219028 287954 285407 285563 284474 283467 153073 26527 280319 425338 47123 159540 5top 799305 191776 192621 193660 194716 195615 195615	Indel Truncation Native Native Mutant Native Mative Native Mative Mative Mative Mative Mative Mative Mutant Mutant Mutant Native Native Native Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations P15G, No coding mutations S62G,D83E, P356L, A50V, No coding mutations E176D, No coding mutations No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 0	22 2 2 5 5 9 9 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 1 1 7 7 BP_Changes 0 0 0 6 6 10 10 2 2 1 1 1 1 1 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0	66 1 1 1 3 3 2 0 0 0 2 2 0 0 0 0 1 Transversions 0 0 0 1 1 2 0 0 0 1 1 2 0 0 0 1 1 1 2 0 0 1 1 1 1	0.5542 1 1 0.9901 1 0.9965 1 1 0.9965 1 1 1 0.9974 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.9901 0.9981 0.9985 1 0.9997 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9939 0.9967 1 0.9999 1 1 0.9999 1 1 0.9999 1 1 1 0.9913 0.9987 0.9987 0.9987	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 726 606 1554 852 1047 1014 906	720 606 726 606 1554 852 1047 1014 906 1149 1199 714 243 807 Target_Length 720 606 1554 852 1047 1014 9066	+ + + + + + + + + + + +
PT31M	PAO1 lasR PAO1 asI PAO1 with PAO1 with PAO1 pgsB PAO1 rgsB PAO1 rgsB PAO1 rgsB PAO1 rgsB PAO1 pgsB	46184 47254 219207 218422 286400 282555 284516 283460 282561 25330 279320 424624 46880 158733 Start 318802 319885 79484 798699 190222 191769 19261 193702	46891 47860 219933 219028 287954 286407 285563 284474 283467 153073 26527 280319 47533 47123 159540 Stop 319522 320491 800210 799305 191776 192621 193660 194716 195615 195615 195615 195615 195615	Indel Truncation Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations D47N, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V, No coding mutations E176D, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 0	22 2 5 5 9 2 2 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 7 BP_Changes 0 0 0 6 6 100 2 2 1 1 6 6 7 7 7 7 0 0 3 3	66 11 33 22 00 00 22 00 00 00 1 Transversions 0 00 1 2 00 00 1 2 00 00 00 00 00 00 00 00 00 00 00 00 0	0.5542 1 1 0.9901 1 0.9965 1 0.9967 1 1 1 1 1 1 1 1 1 1 0.9901 0.9981 0.9965 1 1 0.9974	0.9694 0.9967 0.9931 0.9851 0.9987 0.9977 0.9971 0.9941 1 0.9959 1 1 0.9959 0.9913 BP_Percent 1 1 0.9917 0.9835 0.9988 0.9943 0.9988	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 1554 852 1047 1014 906 1154 852 1047 1014	720 606 726 606 1554 852 1047 1014 906 61149 1197 720 606 726 606 1554 852 1047 1014 906 1149	+ + + + + + + + + + + + + + + + +
PT31M	PAO1 lasR PAO1 lasI PAO1 msl PAO1 msl PAO1 msl PAO1 msl PAO1 msl PAO1 pgsA PAO1 pgsC PAO1 msl	46184 47254 219207 218422 286400 285555 284516 283460 283561 151924 282561 151924 424624 46880 158733 Start 318802 319885 799484 798699 192769 192761 193702 194709 150411 187133	46891 47860 219933 219028 287954 284070 285563 284474 283467 153073 26527 280319] 425338 47123 159540 Stop 319522 320491 800210 799305 191776 192621 193660 193600 193600 193600 193600 193600 193600 193600 193600 193600	Indel Truncation Native Mutant Native Native Native Native Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V, No coding mutations E176D, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0	22 5 9 9 2 2 3 6 0 7 4 4 1 1 7 8 9 9 2 2 3 3 6 0 0 0 1 1 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9	6 1 1 3 3 3 2 2 0 0 0 0 0 0 0 1 1 2 2 0 0 0 1 1 2 2 0 0 0 0	0.5542 1 10.9965 110.9965 110.9965 1110.9967 1110.9961 1110.9961 110.9961 10.9961 10.9961 10.9961 10.9961 10.9961 10.9961	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9959 1 0.9959 1 0.9959 0.9913 BP_Percent 1 0.9937 0.9987 0.9983 0.9943 0.9943 0.9943 0.9943 0.9995	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 744 243 807 Match_Length 720 606 606 1554 852 1047 1014 1149 1197	720 606 726 606 1554 852 1047 1014 906 1149 1197 720 606 726 606 1554 852 1047 1014 906 1149	+ +
PT31M	PAO1 lasR PAO1 lasR PAO1 lasI PAO1 rhII PAO1 pqsA PAO1 pqsA PAO1 pqsB PAO1 pqsL PAO1 pqsR PAO1 lasI PAO1 pqsA PAO1 pqsB	46184 47254 219207 218422 286400 285555 284516 283460 283460 283460 319867 318802 319885 79948 798699 190222 191769 192613 193702 194769 195011 187133 197857 829886	46891 47860 219933 219028 287954 285607 285563 284474 283467 153073 26527 280319 425338 47123 159540 5top 319522 320491 799305 191776 192621 193660 194716 195615 1	Indel Truncation Native Mutant Native Mative Native Mative Mative Mative Mative Mative Mutant Mutant Mutant Mutant Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations	107 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	22 2 2 5 5 9 9 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0 0 0 6 6 1 10 2 2 1 1 6 6 7 7 0 0 3 3 6 6 0 0 0 0 7 7 8 7 9	66 11 13 33 22 00 00 22 00 00 00 11 Transversions 0 00 11 22 00 01 11 20 00 01 00 01 00 01 01 00 01 01 01 01 01	0.5542 1 1 0.9901 1 0.9965 1 1 0.9974 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.9901 0.9981 1 0.9965 1 1 0.9974 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9939 0.9967 1 0.9999 1 1 0.9999 1 1 0.9999 1 1 1 0.9913 0.9987 0.9987 0.9987	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 999 714 243 807 Match_Length 720 606 606 1554 852 1047 1014 906 1149 1197 999 1149	720 606 726 606 1554 852 1047 1014 906 1149 1197 734 243 807 7arget_length 720 606 606 1554 852 1047 1014 1199 1199 1199	+ + + + + + + + + + + + + +
PT31M	PAO1 lasR PAO1 lasI PAO1 msl PAO1 msl PAO1 msl PAO1 msl PAO1 msl PAO1 pgsA PAO1 pgsC PAO1 msl	46184 47254 219207 218422 286400 285555 284516 283460 283561 151924 282561 151924 424624 46880 158733 Start 318802 319885 799484 798699 192769 192761 193702 194709 150411 187133	46891 47860 219933 219028 287954 285607 285563 284474 283467 153073 26527 280319 425338 47123 159540 5top 319522 320491 799305 191776 192621 193660 194716 195615 1	Indel Truncation Native Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Mutant Native Native Native Native Native Native Native Native Mutant Native Mutant Native	13 bp Deletion at 380,truncation at codon 173 (of 240 codons),107 coding mutations No coding mutations No coding mutations S62G,D83E, No coding mutations D47N, No coding mutations E176D, No coding mutations E176D, No coding mutations S62G,D83E, P356L, A50V, No coding mutations E176D, No coding mutations	107 0 0 0 0 1 1 0 0 1 1 0 0 0 0 0 0 0 0	22 2 2 5 5 9 9 2 2 3 3 6 6 0 0 7 7 4 4 1 1 0 0 1 1 1 7 8P_Changes 0 0 0 6 6 100 100 2 2 1 1 6 6 7 7 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 1 1 3 3 3 2 2 0 0 0 0 0 0 0 1 1 2 2 0 0 0 1 1 2 2 0 0 0 0	0.5542 1 1 0.9965 1 0.9965 1 0.9974 1 1 1 1 1 1 1 1 1 1 0.9965 1 1 1 1 0.9901 0.9981 0.9965 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.9694 0.9967 0.9931 0.9851 0.9987 0.9971 0.9941 1 0.9959 1 0.9959 1 0.9959 0.9913 BP_Percent 1 0.9937 0.9987 0.9983 0.9943 0.9943 0.9943 0.9943 0.9995	0.9819 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	707 606 726 606 1554 852 1047 1014 906 1149 1197 744 243 807 Match_Length 720 606 606 1554 852 1047 1014 1149 1197	720 606 726 606 1554 852 1047 1014 906 1149 1197 720 606 726 606 1554 852 1047 1014 906 1149	+ + + + + + +