

Supplementary 6: Mutation profile of QS 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_rhlR	111501	112227	Native	No coding mutations	0	3	0	1	0.9959	1	726	726	-
	PAO1_rhlI	110716	111322	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	-
	PAO1_pqsA	266692	268246	Mutant	N180T,	1	3	2	0.9981	0.9981	1	1554	1554	-
	PAO1_pqsB	265847	266699	Mutant	P200L,	1	3	0	0.9965	0.9965	1	852	852	-
	PAO1_pqsC	264808	265855	Native	No coding mutations	0	7	1	1	0.9933	1	1047	1047	-
	PAO1_pqsD	263752	264766	Mutant	E176D,	1	6	2	0.997	0.9941	1	1014	1014	-
	PAO1_pqsE	262853	263759	Native	No coding mutations	0	0	0	1	1	1	906	906	-
	PAO1_pqsH	0	1054	Contig Edge (truncation)	223 SNPs in 1-1054,96 coding mutations,truncation at codon 268 (of 351 codons)	128	318	148	0.6658	0.7232	0.9173	1054	1149	-
	PAO1_pqsL	246548	247745	Mutant	E330G,	1	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	7521	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	0	1	1	1	606	606	-
	PAO1_rhlR	593582	594308	Native	No coding mutations	0	5	1	1	0.9931	1	726	726	+
	PAO1_rhlI	594487	595093	Mutant	S62G,D83E,	2	8	3	0.9901	0.9868	1	606	606	+
	PAO1_pqsA	330200	331754	Native	No coding mutations	0	4	1	1	0.9974	1	1554	1554	+
	PAO1_pqsB	331747	332599	Native	No coding mutations	0	2	0	1	0.9977	1	852	852	+
	PAO1_pqsC	332591	333638	Mutant	L58P,	1	4	0	0.9971	0.9962	1	1047	1047	+
	PAO1_pqsD	333680	334694	Mutant	E176D,	1	6	2	0.997	0.9941	1	1014	1014	+
	PAO1_pqsE	334687	335593	Mutant	S257P,	1	5	1	0.9967	0.9945	1	906	906	+
	PAO1_pqsH	196503	197652	Native	No coding mutations	0	5	0	1	0.9956	1	1149	1149	+
	PAO1_pqsL	50584	51781	Native	No coding mutations	0	3	0	1	0.9975	1	1197	1197	+
	PAO1_pqsR	337835	338834	Native	No coding mutations	0	1	0	1	0.999	1	999	999	-
	PAO1_qscR	2085	2799	Native	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	+
	PAO1_vqsR	190036	190843	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
CND03	PAO1_lasR	50721	51430	Indel	11 bp Deletion at 440,truncation at codon 229 (of 240 codons),87 coding mutations	87	24	10	0.6375	0.9667	0.9847	709	720	+
	PAO1_lasI	51793	52399	Native	No coding mutations	0	1	0	1	0.9983	1	606	606	+
	PAO1_rhlR	109740	110466	Nonstop	15 coding mutations	15	36	21	0.938	0.9504	1	726	726	-
	PAO1_rhlI	109019	109625	Mutant	S62G,	1	8	1	0.995	0.9868	1	606	606	-
	PAO1_pqsA	171136	172690	Mutant	P263A,R347Q,	2	16	6	0.9961	0.9897	1	1554	1554	-
	PAO1_pqsB	170291	171143	Mutant	V87I,A208D,A281V,	3	10	1	0.9894	0.9883	1	852	852	-
	PAO1_pqsC	169252	170299	Mutant	T311A,	1	19	3	0.9971	0.9819	1	1047	1047	-
	PAO1_pqsD	168196	169210	Mutant	A243V,	1	16	1	0.997	0.9842	1	1014	1014	-
	PAO1_pqsE	167297	168203	Native	No coding mutations	0	3	0	1	0.9967	1	906	906	-
	PAO1_pqsH	173924	175073	Native	No coding mutations	0	7	1	1	0.9939	1	1149	1149	+
	PAO1_pqsL	65246	66443	Nonstop	D175E,R179H,A232S,R240C,A395S,P396L,L397E,G398A,*399P	9	31	12	0.9774	0.9741	1	1197	1197	+
	PAO1_pqsR	164057	165056	Mutant	A314V,	1	2	1	0.997	0.998	1	999	999	+
	PAO1_qscR	1814	2528	Native	No coding mutations	0	5	0	1	0.993	1	714	714	-
	PAO1_rsaL	51419	51662	Native	No coding mutations	0	0	0	1	1	1	243	243	-
	PAO1_vqsR	167457	168264	Mutant	D41H,R63I,V66I,T116A,	4	11	2	0.9851	0.9864	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
5BR2	PAO1_lasR	21434	22154	Native	No coding mutations	0	0	0	1	1	1	720	720	+
	PAO1_lasI	22517	23123	Native	No coding mutations	0	0	0	1	1	1	606	606	+
	PAO1_rhlR	586980	587706	Native	No coding mutations	0	2	0	1	0.9972	1	726	726	+
	PAO1_rhlI	587885	588491	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	+
	PAO1_pqsA	242065	243619	Native	No coding mutations	0	2	1	1	0.9987	1	1554	1554	-
	PAO1_pqsB	241220	242072	Native	No coding mutations	0	0	0	1	1	1	852	852	-
	PAO1_pqsC	240181	241228	Native	No coding mutations	0	7	1	1	0.9933	1	1047	1047	-
	PAO1_pqsD	239125	240139	Mutant	E176D,	1	6	2	0.997	0.9941	1	1014	1014	-
	PAO1_pqsE	238226	239132	Native	No coding mutations	0	0	0	1	1	1	906	906	-
	PAO1_pqsH	17520	18669	Native	No coding mutations	0	6	1	1	0.9948	1	1149	1149	-
	PAO1_pqsL	14990	16187	Mutant	D175E,E330G,	2	5	1	0.995	0.9958	1	1197	1197	+
	PAO1_pqsR	234986	235985	Native	No coding mutations	0	1	0	1	0.999	1	999	999	+

	PAO1_qscR	5192	5906	Mutant	G197X,	1	3	0	0.9958	0.9958	1	714	714	+
	PAO1_rsaL	22143	22386	Native	No coding mutations	0	0	0	1	1	1	243	243	-
	PAO1_vqsR	24329	25136	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
Co398373	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	0	1	1	1	606	606	-
	PAO1_rhlR	46340	47066	Native	No coding mutations	0	6	1	1	0.9917	1	726	726	-
	PAO1_rhlI	45555	46161	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	-
	PAO1_pqsA	163393	164947	Native	No coding mutations	0	2	1	1	0.9987	1	1554	1554	-
	PAO1_pqsB	162548	163400	Native	No coding mutations	0	0	0	1	1	1	852	852	-
	PAO1_pqsC	161509	162556	Native	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	25439	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	3	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	18630	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
CPHL2000	PAO1_lasR	798489	799209	Mutant	E196G,	1	2	1	0.9958	0.9972	1	720	720	+
	PAO1_lasI	799572	800178	Native	No coding mutations	0	2	0	1	0.9967	1	606	606	+
	PAO1_rhlR	658430	659156	Native	No coding mutations	0	4	0	1	0.9945	1	726	726	-
	PAO1_rhlI	657645	658251	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	-
	PAO1_pqsA	330679	332233	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	+
	PAO1_pqsC	333070	334117	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	-
	PAO1_pqsR	338314	339313	Truncation	truncation at codon 14 (of 333 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	-
	PAO1_vqsR	155437	156244	Mutant	R23Q,	1	2	0	0.9963	0.9975	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
Jp238	PAO1_lasR	82822	83542	Native	No coding mutations	0	0	0	1	1	1	720	720	-
	PAO1_lasI	81853	82459	Native	No coding mutations	0	0	0	1	1	1	606	606	-
	PAO1_rhlR	791947	792673	Native	No coding mutations	0	6	1	1	0.9917	1	726	726	-
	PAO1_rhlI	791162	791768	Mutant	S62G,D83E,	2	8	3	0.9901	0.9868	1	606	606	-
	PAO1_pqsA	542456	544010	Native	No coding mutations	0	1	0	1	0.9994	1	1554	1554	-
	PAO1_pqsB	541611	542463	Mutant	A50V,	1	1	0	0.9965	0.9988	1	852	852	-
	PAO1_pqsC	540572	541619	Native	No coding mutations	0	3	1	1	0.9971	1	1047	1047	-
	PAO1_pqsD	539516	540530	Mutant	L120F,E176D,	2	7	3	0.9941	0.9931	1	1014	1014	-
	PAO1_pqsE	538617	539523	Native	No coding mutations	0	0	0	1	1	1	906	906	-
	PAO1_pqsH	108635	109784	Mutant	N91S,	1	6	1	0.9974	0.9948	1	1149	1149	+
	PAO1_pqsL	184199	185396	Native	No coding mutations	0	2	0	1	0.9983	1	1197	1197	+
	PAO1_pqsR	535376	536375	Native	No coding mutations	0	2	1	1	0.998	1	999	999	+
	PAO1_qscR	1815	2529	Native	No coding mutations	0	2	0	1	0.9972	1	714	714	-
	PAO1_rsaL	82590	82833	Native	No coding mutations	0	0	0	1	1	1	243	243	+
	PAO1_vqsR	102168	102975	Native	No coding mutations	0	0	0	1	1	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
Jp1155				Indel	11 bp Deletion at 197,truncation at codon 229 (of 240 codons),161 coding mutations									
	PAO1_lasR	365051	365760	Truncation		161	20	6	0.3292	0.9722	0.9847	709	720	-
	PAO1_lasI	364082	364688	Native	No coding mutations	0	1	0	1	0.9983	1	606	606	-
	PAO1_rhlR	10191	10917	Native	No coding mutations	0	3	0	1	0.9959	1	726	726	+
	PAO1_rhlI	11096	11702	Mutant	R22L,S62G,	2	7	2	0.9901	0.9884	1	606	606	+
	PAO1_pqsA	836864	838418	Mutant	P263A,R347Q,	2	13	4	0.9961	0.9916	1	1554	1554	-
	PAO1_pqsB	836019	836871	Mutant	G279E,	1	5	1	0.9965	0.9941	1	852	852	-
	PAO1_pqsC	834980	836027	Native	No coding mutations	0	17	3	1	0.9838	1	1047	1047	-
	PAO1_pqsD	833924	834938	Mutant	A243V,	1	14	1	0.997	0.9862	1	1014	1014	-
	PAO1_pqsE	833025	833931	Native	No coding mutations	0	6	0	1	0.9934	1	906	906	-
	PAO1_pqsH	58848	59997	Native	No coding mutations	0	9	2	1	0.9922	1	1149	1149	-
					D175E,S206A,A232S,T378A,A395S,P396L,L397E,G398A,*399P									
	PAO1_pqsL	22214	23411	Nonstop		9	31	13	0.9774	0.9741	1	1197	1197	-
	PAO1_pqsR	829785	830784	Native	No coding mutations	0	0	0	1	1	1	999	999	+
	PAO1_qscR	1983	2697	Mutant	S64N,	1	5	0	0.9958	0.993	1	714	714	-

	PAO1_rsaL	364819	365062	Native	No coding mutations	0	0	0	1	1	1	243	243	+
	PAO1_vqsR	65657	66464	Mutant	R63I,V66I,T116A,	3	10	1	0.9888	0.9876	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
W15Dec14	PAO1_lasR	83344	84064	Native	No coding mutations	0	0	0	1	1	1	720	720	+
	PAO1_lasI	82375	82981	Native	No coding mutations	0	0	0	1	1	1	606	606	-
	PAO1_rhlR	728506	729232	Native	No coding mutations	0	2	0	1	0.9972	1	726	726	+
	PAO1_rhlI	729412	730018	Mutant	S62G,D83E,	2	8	3	0.9901	0.9868	1	606	606	+
	PAO1_pqsA	561139	562693	Native	No coding mutations	0	3	0	1	0.9981	1	1554	1554	-
	PAO1_pqsB	560294	561146	Native	No coding mutations	0	2	0	1	0.9977	1	852	852	-
	PAO1_pqsC	559255	560302	Native	No coding mutations	0	5	1	1	0.9952	1	1047	1047	-
	PAO1_pqsD	558199	559213	Mutant	E176D,	1	7	2	0.997	0.9931	1	1014	1014	-
	PAO1_pqsE	557300	558206	Mutant	H71X,E103G,	2	4	1	0.9934	0.9956	1	906	906	-
	PAO1_pqsH	196286	197435	Native	No coding mutations	0	3	1	1	0.9974	1	1149	1149	+
	PAO1_pqsL	50331	51528	Mutant	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	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
Aa249	PAO1_lasR	85774	86494	Native	No coding mutations	0	0	0	1	1	1	720	720	+
	PAO1_lasI	84805	85411	Native	No coding mutations	0	0	0	1	1	1	606	606	-
	PAO1_rhlR	111501	112227	Native	No coding mutations	0	3	0	1	0.9959	1	726	726	-
	PAO1_rhlI	110716	111322	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	-
	PAO1_pqsA	563765	565319	Native	No coding mutations	0	2	1	1	0.9987	1	1554	1554	-
	PAO1_pqsB	562920	563772	Mutant	P200L,	1	3	0	0.9965	0.9965	1	852	852	-
	PAO1_pqsC	561881	562928	Native	No coding mutations	0	7	1	1	0.9933	1	1047	1047	-
	PAO1_pqsD	560825	561839	Mutant	E176D,	1	6	2	0.997	0.9941	1	1014	1014	-
	PAO1_pqsE	559926	560832	Native	No coding mutations	0	0	0	1	1	1	906	906	-
	PAO1_pqsH	91040	92189	Native	No coding mutations	0	5	0	1	0.9956	1	1149	1149	-
	PAO1_pqsL	225165	226362	Mutant	E330G,	1	4	0	0.9975	0.9967	1	1197	1197	+
	PAO1_pqsR	489416	490415	Native	No coding mutations	0	1	0	1	0.999	1	999	999	+
	PAO1_qscR	1815	2529	Native	No coding mutations	0	2	0	1	0.9972	1	714	714	-
	PAO1_rsaL	85542	85785	Native	No coding mutations	0	0	0	1	1	1	243	243	+
	PAO1_vqsR	97849	98656	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
PT31M					13 bp Deletion at 380, truncation at codon 173 (of 240 codons), 107 coding mutations	107	22	6	0.5542	0.9694	0.9819	707	720	+
	PAO1_lasR	46184	46891	Indel Truncation										
	PAO1_lasI	47254	47860	Native	No coding mutations	0	2	1	1	0.9967	1	606	606	+
	PAO1_rhlR	219207	219933	Native	No coding mutations	0	5	1	1	0.9931	1	726	726	-
	PAO1_rhlI	218422	219028	Mutant	S62G,D83E,	2	9	3	0.9901	0.9851	1	606	606	-
	PAO1_pqsA	286400	287954	Native	No coding mutations	0	2	2	1	0.9987	1	1554	1554	-
	PAO1_pqsB	285555	286407	Mutant	D47N,	1	2	0	0.9965	0.9977	1	852	852	-
	PAO1_pqsC	284516	285563	Native	No coding mutations	0	3	0	1	0.9971	1	1047	1047	-
	PAO1_pqsD	283460	284474	Mutant	E176D,	1	6	2	0.997	0.9941	1	1014	1014	-
	PAO1_pqsE	282561	283467	Native	No coding mutations	0	0	0	1	1	1	906	906	-
	PAO1_pqsH	151924	153073	Mutant	N91S,	1	7	2	0.9974	0.9939	1	1149	1149	-
	PAO1_pqsL	25330	26527	Native	No coding mutations	0	4	0	1	0.9967	1	1197	1197	-
	PAO1_pqsR	279320	280319	Native	No coding mutations	0	1	0	1	0.999	1	999	999	+
	PAO1_qscR	424624	425338	Native	No coding mutations	0	0	0	1	1	1	714	714	+
	PAO1_rsaL	46880	47123	Native	No coding mutations	0	1	0	1	0.9959	1	243	243	-
	PAO1_vqsR	158733	159540	Native	No coding mutations	0	7	1	1	0.9913	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
JD303	PAO1_lasR	318802	319522	Native	No coding mutations	0	0	0	1	1	1	720	720	+
	PAO1_lasI	319885	320491	Native	No coding mutations	0	0	0	1	1	1	606	606	+
	PAO1_rhlR	799484	800210	Native	No coding mutations	0	6	1	1	0.9917	1	726	726	-
	PAO1_rhlI	798699	799305	Mutant	S62G,D83E,	2	10	2	0.9901	0.9835	1	606	606	-
	PAO1_pqsA	190222	191776	Mutant	P356L,	1	2	0	0.9981	0.9987	1	1554	1554	+
	PAO1_pqsB	191769	192621	Mutant	A50V,	1	1	0	0.9965	0.9988	1	852	852	+
	PAO1_pqsC	192613	193660	Native	No coding mutations	0	6	1	1	0.9943	1	1047	1047	+
	PAO1_pqsD	193702	194716	Mutant	E176D,	1	7	2	0.997	0.9931	1	1014	1014	+
	PAO1_pqsE	194709	195615	Native	No coding mutations	0	0	0	1	1	1	906	906	+
	PAO1_pqsH	150411	151560	Native	No coding mutations	0	3	1	1	0.9974	1	1149	1149	-
	PAO1_pqsL	187133	188330	Native	No coding mutations	0	6	0	1	0.995	1	1197	1197	+
	PAO1_pqsR	197857	198856	Native	No coding mutations	0	0	0	1	1	1	999	999	-
	PAO1_qscR	829886	830600	Native	No coding mutations	0	1	0	1	0.9986	1	714	714	+
	PAO1_rsaL	319511	319754	Native	No coding mutations	0	0	0	1	1	1	243	243	-
	PAO1_vqsR	157220	158027	Native	No coding mutations	0	0	0	1	1	1	807	807	-