

Supplementary Table S7. Regions of genomic plasticity surrounding the *lecA* locus and identified by ACT comparisons in *P. aeruginosa* PAO1, PA7, and EML strains sequenced in this work.

Location in PAO1 (length in bp)	RGP	Location in PA7 (length in bp / ID% according to PAO1)	Location in EML528 (length in bp / ID% according to PA7)	Location in EML545 (length in bp / ID% according to PA7)	Location in EML548 (length in bp / ID% according to PA7)	Inserted near tRNA	Conserved CDS codes	CDS number and/or inferred function (COG)
2862110..2863981 (1871)	RGP90	2717953..2717952 (0 / 0%)	2740069..2740068 (0 / 0%)	2539106..2537236 (35102 / 0%)	2729558..2727577 (1982 / 0%)	no	PAO1 (PA) 2534-2535 PA7 No indel found EML528 No indel found EML545 140229 - 140189 140188 - 140187 EML548 480006-480005	PAO1, EML548 Transcriptional regulator (0583) Oxidoreductase (0667) EML545 In order: ORF 3, 5, 7-10, 16, 23-41, and 44-58 of Bacteriophage B3 (Supplementary Figure S10)
2877475..2878918 (1443)	RGP91	2704472..2703030 (1443 / 98%)	2725480..2724038 (1443 / 99%)	2523814..2522642 (1173 / 0%)	2714173..2713001 (1173 / 0%)	no	PAO1 (PA) PA2546-2547 PA7 (PSPA7)* 2691-2690 EML528* 140493-140492 EML545 140176 EML548 470136	PAO1, PA7, EML528 Ring-cleaving dioxygenase (0346) Transcriptional regulator (0583) EML545 HP (3422) EML548 HP (3422)
2904733..2905942 (1209)	RGP26^c	2677165..2668018 (9148 / 0%)	2698191..2689043 (9148 / 99%)	2496777..2485105 (11673 / 98%)	2687137..2675473 (11665 / 98%)	tRNA ^{Leu} (left)	PAO1 (PA) 2570-2571 PA7 (PSPA7) 2661-2648 EML528** 1404663-140453 EML545** 140148-140129 + 2.5kb inserted between PASPA7_2657 and 2656 (140144-140138) EML548** 470107-470088 + 2.5kb inserted between PASPA7_2657 and 2656 (470103-470097)	PAO1 PA lectin A PA7, EML528 2661-2650: HP 2649/2648: Phage integrase family proteins (no/0582) EML545 insertion: 140144, 140141-140138: HP 140143/140142: Lytic enzymes (3772/3179) EML548 insertion: 470103, 470101-470097: HP 470102 / 470101: Lytic enzymes (3772/3179)
2916749..2917152 (403)	RGP92	2657270..2656322 (949 / 0%)	2678298..2677348 (949)	2474353..2471430 (2923 / 0%)	2664727..2661827 (2901 / 0%)	no	PAO1 No indel found (+ 403 nt) PA7 (PSPA7) 2635 EML528* 140437 EML545 140116-140115 EML548*** 470077-470076	PA7, EML528 HP EML545, EML548 Fimbrial protein (3539) Transcriptional regulator, MerR family (0789)
2918196..2918556 (360)	RGP72^y	2655278..2654441 (838 / 0%)	2676307..2675469 (838 / 99%)	2470411..2469576 (836 / 98%)	2660788..2659954 (835 / 98%)	tRNA ^{Cys} (left)	PAO1 2581 PA7 (PSPA7) 2633-2632 EML528** 140435-140434 EML545** 140113-140112 EML548** 470074-470073	PA7, EML528, EML545, EML548 EF hand domain-containing protein HP

Continued next page

Table S7. *cont'd*

Location in PAO1 (length in bp)	RGP	Location in PA7 (length in bp / ID% according to PAO1)	Location in EML528 (length in bp / ID% according to PA7)	Location in EML545 (length in bp / ID% according to PA7)	Location in EML548 (length in bp / ID% according to PA7)	Inserted near tRNA	Conserved CDS codes	Gene class /COG
2918812..2919524 (712)	RGP72[‡]	2654166..2641296 (12870 / 0%)	2675194..2662324 (12870 / 99%)	2469302..2451833 (17470 / 99%)	2659679..2642206 (17474 / 99%)	tRNA ^{Cys} (right)	PAO1 2582 PA7 (PSPA7) 2630-2621 EML528** 140435-140426 EML545** 140113-140099 + 4.8kb inserted between PASPA7_2622 and 2621 (140104-140100) EML548** 470074-470058 + 4.8kb inserted between PASPA7_2622 and 2621 (470064-470060)	PA7, EML528 TetR family transcriptional regulator (1309) Beta-glucosidase (2723) Glycine betaine transmethylese HP Sulfatase (3119) HP Arylsulfatase (3119) Sulfatase-modifying factor (1262) Sugar transporter, glycoside-pentoside-hexuronide (2211) EML545, EML548 Insertion: 140104/470064: 2-keto-3 dextralactono-kinase (3734) 140102/470062: 2-oxo-3-deoxygalactono-6-phosphate aldolase (0800) 140101/470061: galactonate dehydratase (4948) 140100/470060: Short-chain dehydrogenase/ reductase SDR (1028)
2919573..2923218 (3645)	RGP27[‡]	2640759..2635979 (4781 / 0%)	2657003..2551974 (105029 / 99%)	2451291..2446420 (4872 / 99%)	2641669..2636809 (4861 / 99%)	tRNA ^{Gly} (left)	PAO1 (PA) 2583-2584 PA7 (PSPA7) 2620-2616 EML528 (PAGI-2) 140420-140306 EML545** 140098-140095 EML548** 470057-470054	PAO1 PA2583: Sensor/response regulator hybrid (0642) PA7, EML545, EML548 PSPA7_2620: Thioredoxin domain-containing protein (3531) PSPA7_2619: HP (4319) PSPA7_2618: Putative HTH-type transcriptional regulator YafC (0583) PSPA7_2617: EAL domain-containing protein (4943) EML528 (RGP29) (See Supplementary Figure S9A)
2929523..2933615 (4092)	RGP93	2629633..2629525 (109 / 0%)	2545706..2545598 (108 / 100%)	2440074..2439966 (109 / 99%)	2630463..2630356 (108 / 98%)	no	PAO1 (PA) 2589-2590 PA7 No indel found (+ 108 nt) EML528 No indel found (+ 108 nt) EML545 No indel found (+ 109 nt) EML548 No indel found (+ 108 nt)	PAO1 HP (0477) HP (1629)
2936423..2947544 (11121)	RGP94	2626730..2626598 (132 / 0%)	2542802..2542670 (133 / 98%)	2437171..2437039 (133 / 98%)	2627560..2578071 (49490 / 98%)	tRNA ^{Ser} (left)	PAO1 (PA) PA2594-2603 PA7 No indel found (+ 132 nt) EML528 No indel found (+ 133 nt) EML545 No indel found (+ 133 nt) EML548 470043-460051	PAO1 PA2594-2696, 2699: HP (0715) PA2597 HP (1960) PA2598, 2600: HP (2141) PA2601 Transcriptional regulator (0583) PA2602 HP (5553) PA2603 Thiosulfate sulfurtransferase (0607) EML548 <i>Pseudomonas</i> phage P52: 53% of query cover (see Supplementary Figure S11)

HP = hypothetical protein.

ID = identity between two compared RGP sequences.

nt=nucleotides.

* Conserved in PAO1.

** Conserved in PA7.

*** Conserved in EML545.

[‡] According to Mathee et al., (2008).[‡] According to Roy et al., (2010).