

Figure S1: *pel* promoter region

Alignment of *pel* promoter regions from *P. aeruginosa* strains PAO1, 2192, 39016, B136-33, C3719, DK2, LESB58, M18, NCGM2.S1, PA7, PACS2, RP73, UCBPP-PA14. The numbers on the right indicate the number of bases upstream of the translation start site of the *pelA* orthologs. The stars under the sequences indicate that the bases are conserved at this position. The FleQ consensus sequences are boxed (A). Gene organization of the *pel* operon in *P. aeruginosa* PAO1 or *P. protegens* CHAO or Pf-5. The *pelA* orthologs are boxed in black. The figure was taken from the *Pseudomonas* genome database (<http://www.pseudomonas.com>) (B). *pel* promoter alignments of strains *P. protegens* CHAO and Pf5 in addition to a few *P. aeruginosa* strains. The FleQ consensus sequences are boxed. For *P. protegens* CHAO and Pf5, the FleQ boxes are located 224 bases upstream of the *pelA* translation start site, for strains 39016, M18, PA7 and NCGM2.S1, the FleQ boxes are located 153 bases upstream of the *pelA* ATG and for the remaining 9 strains, the FleQ boxes are located 126 bases upstream of the *pelA* translation start site. The stars below the sequences indicate that the bases are conserved at this position (C).

Figure S2: *lapA*-like gene alignments

Multiple alignments of the promoter regions of *lapA*-like genes from *Pseudomonas denitrificans* ATCC 13867, *Pseudomonas fulva* 12-X, *Pseudomonas brassicacearum* subsp. *brassicacearum* NFM421, *Pseudomonas fluorescens* Pf0-1, *Pseudomonas entomophila* L48 and *Pseudomonas putida* BIRD-1.

Figure S3: identification of a new exopolysaccharide biosynthesis operon preceded by a FleQ binding site.

A new exopolysaccharide synthesis operon in *P. brassicacearum* subsp. *brassicacearum* NFM421 (A). The figure was taken from the *Pseudomonas* Genome Database. Sequence of the putative *psl* operon promoter region of *P. brassicacearum* subsp. *brassicacearum* NFM421. The putative FleQ consensus sequences and the translation start site of *PSEBR\_a3747* are in bold (B).

A

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PA2G_02478      -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
G655_09465     -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PA14_24480     -CAAAGGACACTATTTCCGCATGGGTGTCCTAAAAATTGACAGTTCCCGCTTAAAAA 283
PA39016_001330085 -CAAAGGACACCATGGCGCCATGTGCGGCCTAAAAATTGACAGTTTCCGCTTAAAAA 256
NGCM2_4184     -CAAAGGACACCATGGCGCCATGTGCGGCCTAAAAATTGACAGTTTCCGCTTAAAAA 256
PAM18_1896    -CAAAGGACACCATGGCGCCATGTGTCGCCTAAAAATTGACAGTTTCCGCTTAAAAA 256
PA3064         -CAAAGGACACCATGGCGTCATGTGTCGCCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PaerPA_01003677 -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PADK2_09015   -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
M062_16375    -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PALES_19961   -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PACG_01993    -CAAAGGACACCATGGCGTCATGTATGCGCTAAAAATTGACAGTTTCCGCTTAAAAA 283
PSPA7_2073    CTTCGGGAATTTTCATT-CGGCATGTA-GCGCTAAAAATTGACAGTATCCGGTTGAAAAT 257

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PA2G_02478      TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
G655_09465     TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
PA14_24480     TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
PA39016_001330085 TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 435
NGCM2_4184     TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 435
PAM18_1896    TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 435
PA3064         TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
PaerPA_01003677 TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
PADK2_09015   TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
M062_16375    TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCCG 462
PALES_19961   TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCTG 462
PACG_01993    TTAGCAATTAGCATATTTGTCATTAGATTGACSTTAATCGCCTGCGGCTGCTTTGGCTG 462
PSPA7_2073    TTACCAATTAGCATATGTTGTCATTAGATTGACSTTGGTCGCTGGAATCCCTTCGGCTA 435

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C

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PA14_24480     -TCACGGGGAGGCAAGAACAGGCAAAAGGACACTATTTCCGCATGGGTGTCCTAAAAA
PAM18_1896    -TCACGGGGAGGCAAGAGCAGGCAAAAGGACACCATGGCGCCATGTGTGGCCTAAAAA
PA3064        -CCTGCAAAGCGTCACGGGCAGGCAAAAGGACACCATGGCGTCATGTGTGGCCTAAAAA
PALES_19961   -CCTGCAAAGCGTCACGGGCAGGCAAAAGGACACCATGGCGTCATGTGTGGCCTAAAAA
PSPA7_2073    GAGGGGGCGGACGTTCCGGCAGGGCTTCGGGAATTTTCATTCGGCATGTA-GCCTCCAAAAA
PFL_2971      -ATGGCATGTGGCCAGCTACGGCGGGCTTTTCAGCGCTTTATGCTAGGCAASTCAATATA
PFLCHA0_c30140 -ATGGCATGTGGCCAGCTACGGCGGGCTTTTCAGCGCTTTATGCTAGGCAASTCAATATA

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PA14_24480     TTGACAGTTTCCGCTTAAAAAATTAGCAATTAGCATATTTATCATTAGATTGACSTTAA
PAM18_1896    TTGACAGTTTCCGCTTAAAAAATTAGCAATTAGCATATTTATCATTAGATTGACSTTAA
PA3064        TTGACAGTTTCCGCTTAAAAAATTAGCAATTAGCATATTTATCATTAGATTGACSTTAA
PALES_19961   TTGACAGTTTCCGCTTAAAAAATTAGCAATTAGCATATTTATCATTAGATTGACSTTAA
PSPA7_2073    TTGACAGTATCCGGTTGAAAAATTACCAATTAGCATATGTAATCATTAGATTGACSTTGG
PFL_2971      TTGACCTATTTTCTGCGCTTAAATAATCAACAAATATCAGCGCATTATTGACGATTT
PFLCHA0_c30140 TTGACCTATTTTCTGCGCTTAAATAATCAACAAATATCAGCGCATTATTGACGATTT

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PA14_24480     TCGCCTGCGGCTGCTTTGGCCGTGCCCGCACTGTCAGGGATTTCGA
PAM18_1896    TCGCCTGCGGCTGCTTTGGCCGTACCCGCACTGCCAGGGATTTCGA
PA3064        TCGCCTGCGGCTGCTTTGGCCGTGCCCGCACTGTCAGGGATTTCGA
PALES_19961   TCGCCTGCGGCTGCTTTGGCTGTCGCCCGCACTGTCAGGGATTTCGA
PSPA7_2073    TCGCCTGGAATCCCTTCGGCTATACCCAGAGAGTCAGGGACTTCGA
PFL_2971      TGCTTTTCTGACCCAGTATGTCGGCGCTGAGCGATTGATTATCTT
PFLCHA0_c30140 TGCTTTTCTGACCCAGTATGTCGGCGCTGAGCGATTGATTATCTT

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B

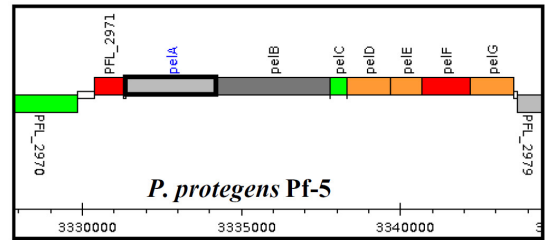
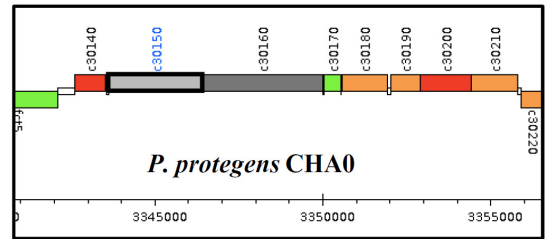
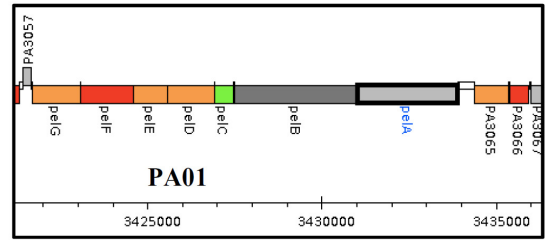


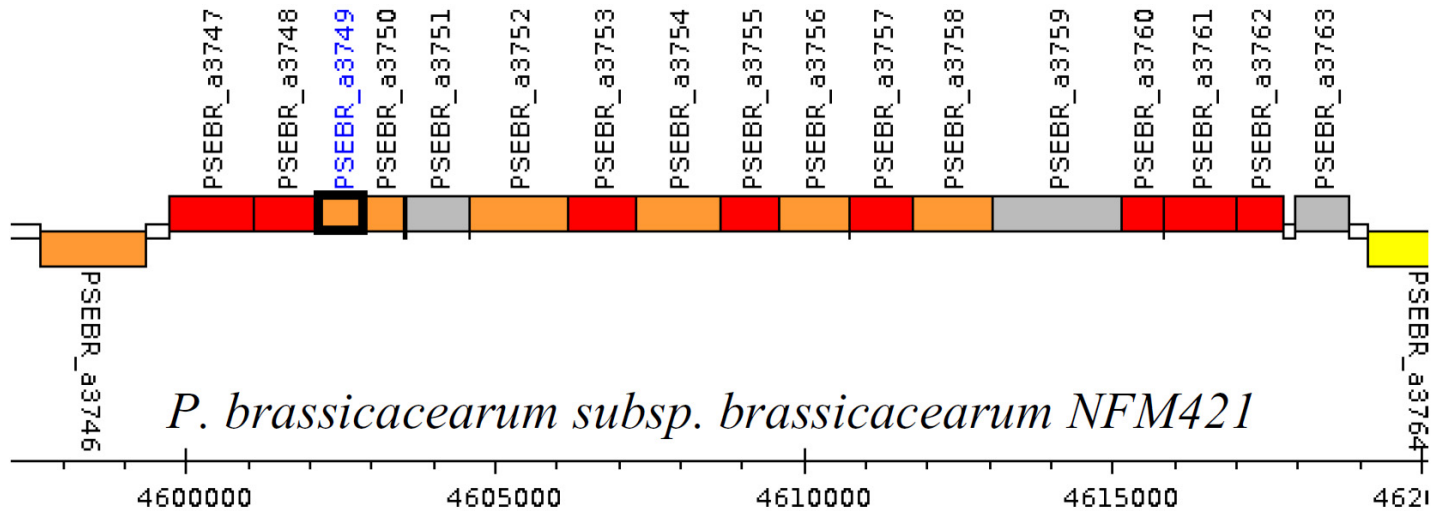
Figure S1

	370	380	390	400	410	420
H681_06575	GC-CAATTGTTTAGGATGACACGCGAATCGTCAATACATTGGCCATATACACAATATCCAT					
Psefu_3263	GTGCGATTGTTTATGATCGGACCCGAAGCGTCAATACTCTGGCCGGAAGC-CTTTGGACAA					
PSEBR_a206	GG-CGATTGTTTAGGATGGCCGGCAGAAACGTCAATAGTTTGGCCACAAACAAAATAATTGA					
Pf101_0133	GG-CGATTGTTTAGGATGGCAGCCAGAAACGTCAATAGTTTGGCCATAAAGTTAATAGC-GA					
PFL_0133	GG-CGATTGTTTAGGATGGCGTCCATAAACGTCAATAGTTTGGCCATAAAGTTAATACC-CA					
PSEEN0141	GG-CGATTGTTTAGGATGGCAGCCAGAAACGTCAATAGTTTGGCCATAAAGTTAATTGC-CA					
PPUBIRD1_0199	GC-CGATTGTTTAGGATGGCATGTATAAACGTCAATAGTTTGGCCAGTCAGGCAATTCC-AA					
	* * ***** **		* ***** **			*
Prim.cons.	GGGCGATTGTTTAGGATGGCAGCCAGAAAGGTCAATAGTTTGGCCATAAAGT2AATAGCCAA					
	430	440	450	460	470	480
H681_06575	TTGGAATAAGCCAAGTTATTGACG-TCAGATATTTTCGCTCT-----GAATGACAGG-					
Psefu_3263	TAAATTTAGCCCAAACATATGACG-CCATGTTTTTAGC-----A-----					
PSEBR_a206	GAAACACAGCCAAAATATTGACATGTAAAAGCGTCAAATA-ACCTTACTTTGTGAACA-					
Pf101_0133	AAGAATCTAGCCAAAATATTGACCAATAGCAGCGTCAACTTTGTTTCACCTTTTTTTAA-					
PFL_0133	AAAAATATAGCCAAACTTTTACG-ATAGATCTGTCAATTACCCGTTCCCAATTACACAC					
PSEEN0141	ATCGTTATAGACGTAAAATTGACACTTTAACGTGTCAAAA-----CATTTTGA-					
PPUBIRD1_0199	AAAGTTATAGACGGAAATATTGACG-TCAAAACGTCAAGAG-----ATCATCTACATA-					
	* *	****		*		
Prim.cons.	AAAAATATAGCCAAAATATTGACG3TTA2A2GTGTCAA2TA23C3TTACCATTTACA2AC					

Figure S2



A



B

>PSEBR\_a3747

ATTCCCGTTAAGCCCAATAAAAACAGCCACTTTACTAAGACAG  
**TCAAGGACTTGAT**ATCAAAAGGCCCGATTTCACTTGAATTGC  
 CAACACTGACAAC**TGTCATTTTGCTGAC**ACGCTTTTTCTGAAG  
 CTGCGCTATACCCCTCTAAACAGTTTCATCCGAGTTACATCA  
 ACCGGTTTACGAGGCGCGCCAAAA**ATG**

Figure S3