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).

Figure S1

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              370        380        390        400        410        420
               |          |          |          |          |          |
H681_06575     GC-CAATTGTTTAGGATGACACGCGAATC GTCAATACATTGGC ATATACACAATATCCAT
Psefu_3263     GTGCGATTGTTTATGATCGGACCCGAAGC GTCAATACTCTGGC GGAAGC-CTTTGGACAA
PSEBR_a206     GG-CGATTGTTTAGGATGGCCGGCAGAAC GTCAATAGTTTGGC ACAAACAAAATAATTGA
Pfl01_0133     GG-CGATTGTTTAGGATGGCACCCAGAAC GTCAATAGTTTGGC ATAAAGTTAATAGC-GA
PFL_0133       GG-CGATTGTTTAGGATGGCGTCCATAAC GTCAATAGTTTGGC ATAAAGTTAATACC-CA
PSEEN0141      GG-CGATTGTTTAGGATGGCAGCCAGAAC GTCAATAGTTTGGC ATAAAGTTAATTGC-CA
PPUBIRD1_0199  GC-CGATTGTTTAGGATGGCATGTATAAC GTCAATAGTTTGGC AGTCAGGCAATTCC-AA
               *    *  ******** *** *      * ******* ****         *
Prim.cons.     GGGCGATTGTTTAGGATGGCACCCAGAAGGTCAATAGTTTGGCATAAAGT2AATAGCCAA


              430        440        450        460        470        480
               |          |          |          |          |          |
H681_06575     TTGGAATAA GCCAAGTTATTGACG -TCAGATATTCGCTCT---------GAATGACAGG-
Psefu_3263     TAAATTTAC GCCAAACATATGACG -CCATGTTTTTAGC------------------A-----
PSEBR_a206     GAAAACACA GCCAAAATATTGAC ATGTAAAAGCGTCAAATA-ACCTTACTTTGTGAACA-
Pfl101_0133    AAGAATCTA GCCAAAATATTGAC GAATAGCAGCGTCAACTTTGTTTCACCTTTTTTTAA-
PFL_0133       AAAAATATA GCCAAACTTTTGACG -ATAGATCTGTCAATTACCCGTTCCCAATTACACAC
PSEEN0141      ATCGTTATA GACGTAAAATTGAC ACTTTAACGTGTCAAAAA--------CATTTTTGAA-
PPUBIRD1_0199  AAAGTTATA GACGGAATATTGACG -TCAAAAACGTCAAGAG------ATCATCTACATA-
               * *      ****        *
Prim.cons.     AAAAATATAGCCAAAATATTGACG3TTA2A2GTGTCAA2TA23C3TTACCATTTACA2AC
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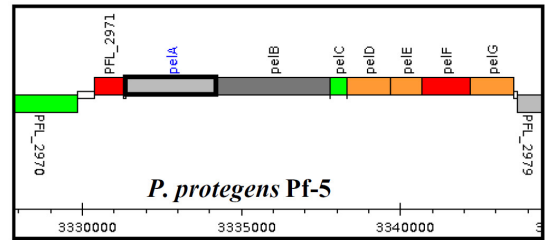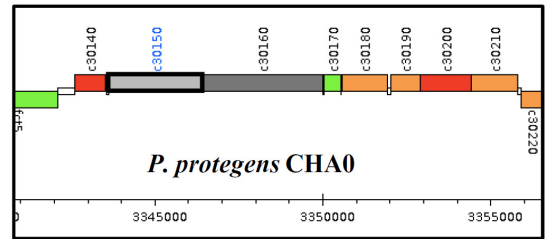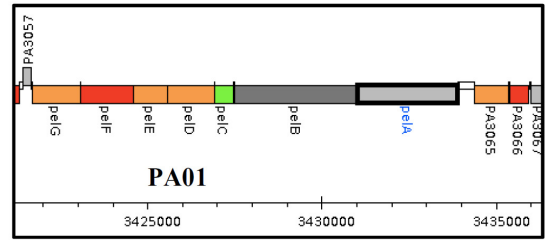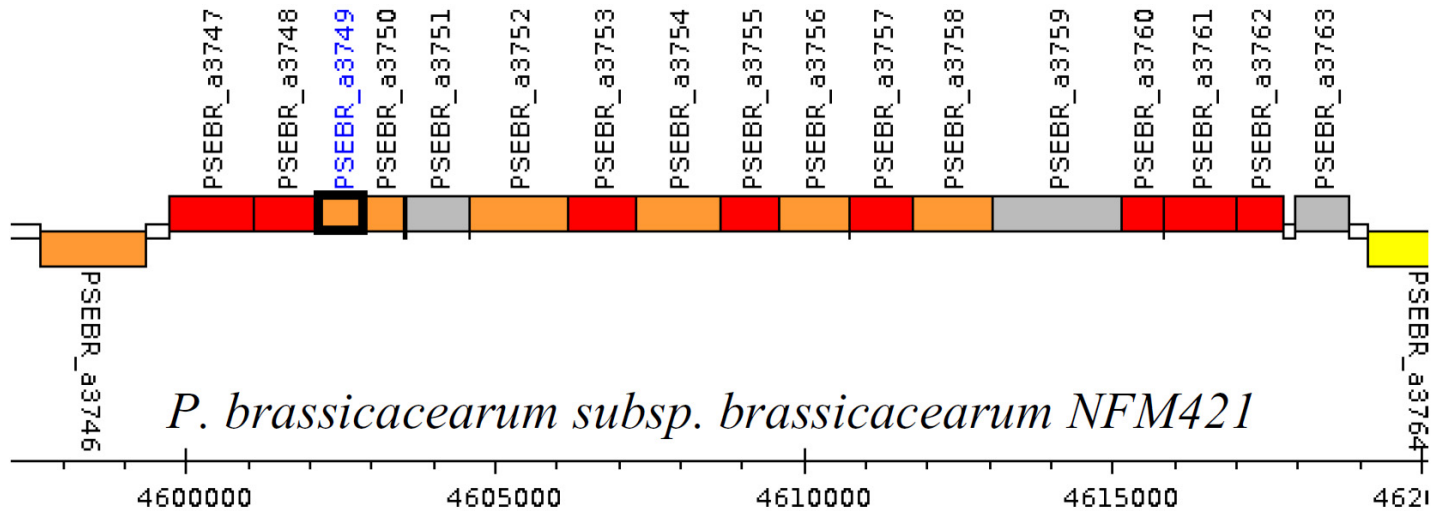
Figure S2

A

B

>**PSEBR_a3747**

ATTCCCGTTAAGCCCAATAAAACAGCCACTTTACTAAGACA**G**
TCAAGGACTTGATATCAAAAGGCCCGATTTCACTTGAATTGC
CAACACTGACAACT**GTCATTTTGCTGAC**ACGCTTTTCTGAAG
CTGCGCTATACCCCTCTAAACAGTTTCATCCGAGTTACATCA
ACCGGTTTACGAGGCGCGCCAAAA**ATG**

Figure S3