

## Supplementary Information

# Genome analysis of *Paenibacillus polymyxa* A18 gives insights into the features associated with its adaptation to the termite gut environment

Nandita Pasari<sup>1,2</sup>, Mayank Gupta<sup>1,2</sup>, Danish Eqbal<sup>1</sup>, Syed Shams Yazdani<sup>1,2,\*</sup>

### Supplementary information provided with this submission:

**Figure S1.** Comparative analyses of Carbohydrate-active enzyme (CAZymes) numbers across the members of the genus *Paenibacillus*.

**Figure S2.** Comparative analyses of genes involved in nitrogen fixation and dissimilatory nitrate reduction across the members of the genus *Paenibacillus*.

**Figure S3.** Zoom map of circular representation of *P. polymyxa* A18 CDSs and their alignment with CDSs of members of the genus *Paenibacillus* for regions R2, R3 and R7 as mentioned in Figure 4.

**Figure S4.** Comparative analyses of genes encoding for CRISPR/Cas and CRISPR/cmr across the members of the genus *Paenibacillus*. The colored box represents the presence of a gene within the genome and white box indicates the absence of a gene.

**Table S1:** General features of *P. polymyxa* A18 genome

**Table S2:** Horizontal Gene Transfers in *P. polymyxa* A18 genome

**Table S3:** Genome features of members belonging to genus *Paenibacillus*

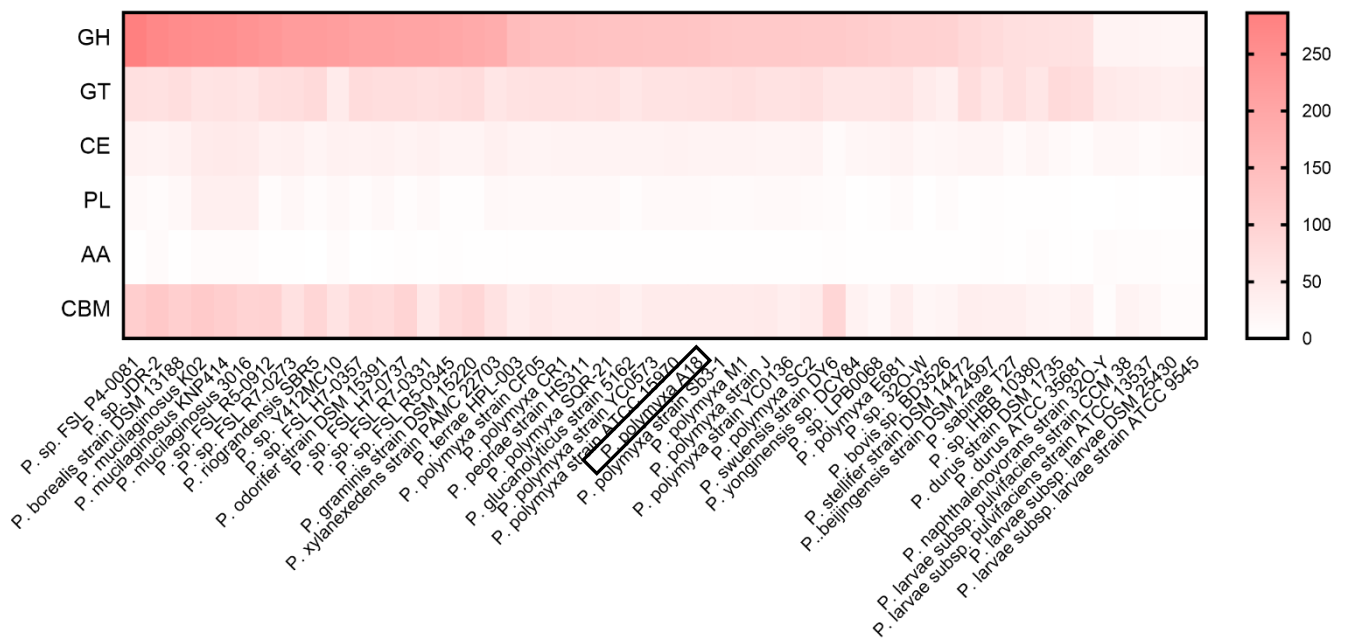
**Table S4:** Categorization of CAZy genes encoded in *P. polymyxa* A18 according to their functions

**Table S5:** Genes encoding for antibiotic synthesizing polypeptides in *P. polymyxa* A18

**Table S6.** Concentration of antibiotics used for susceptibility testing

**Additional file1:** Annotation of *P. polymyxa* A18 ORFs

**Additional file2:** Annotation of CAZy genes in *P. polymyxa* A18



|                                                               | nifB | nifH | nifD | nifK | nifE | nifN | nifX | hesA | nifU | narG | narH | narJ | narI | nirB | nirD | nirB | nirD |
|---------------------------------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| <i>P. polymyxa</i> A18                                        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> CF05                                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> SQR21                                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> M1                                         |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> SC2                                        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> Sb3-1                                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. peoriae</i> HS311                                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> strain ATCC 15970                          |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> strain YC0573                              |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> strain J                                   |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> CR1                                        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> strain YC0136                              |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> E681                                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. polymyxa</i> strain HPL-003                             |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. xylanexedens</i> strain PAMC 22703                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. riograndensis</i> SBR5                                  |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL H7-0357</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. graminis</i> strain DSM 15220                           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL P4-0081</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL R7-0273</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. borealis</i> strain DSM 13188                           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. odorifer</i> strain DSM 15391                           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL R7-0331</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL R5-0912</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL H7-0737</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. bovis</i> sp. BD3526                                    |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. Y412MC10</i>                                        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. FSL R5-0345</i>                                     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. glucanolyticus</i> strain 5162                          |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. IHBB 10380</i>                                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. durus</i> strain DSM 1735                               |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. mucilaginosus</i> K02                                   |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. durus</i> ATCC 35681                                    |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. stellifer</i> strain DSM 14472                          |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. mucilaginosus</i> KNP414                                |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sabiniae</i> T27                                        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. mucilaginosus</i> 3016                                  |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. yonginensis</i> sp. DCY84                               |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. LPB0068</i>                                         |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. JDR-2</i>                                           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. beijingensis</i> strain DSM 24997                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. swuensis</i> strain DY6                                 |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. sp. 320-W</i>                                           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. naphthalenovorans</i> strain 320-Y                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain CCM 38     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. larvae</i> subsp. <i>larvae</i> DSM 25430               |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. larvae</i> subsp. <i>larvae</i> strain ATCC 9545        |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain ATCC 13537 |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |

**Figure S2. Comparative analyses of genes involved in nitrogen fixation and dissimilatory nitrate reduction across the members of the genus *Paenibacillus*.** The colored box represents the presence of a gene within a genome and white box indicates the absence of a gene.

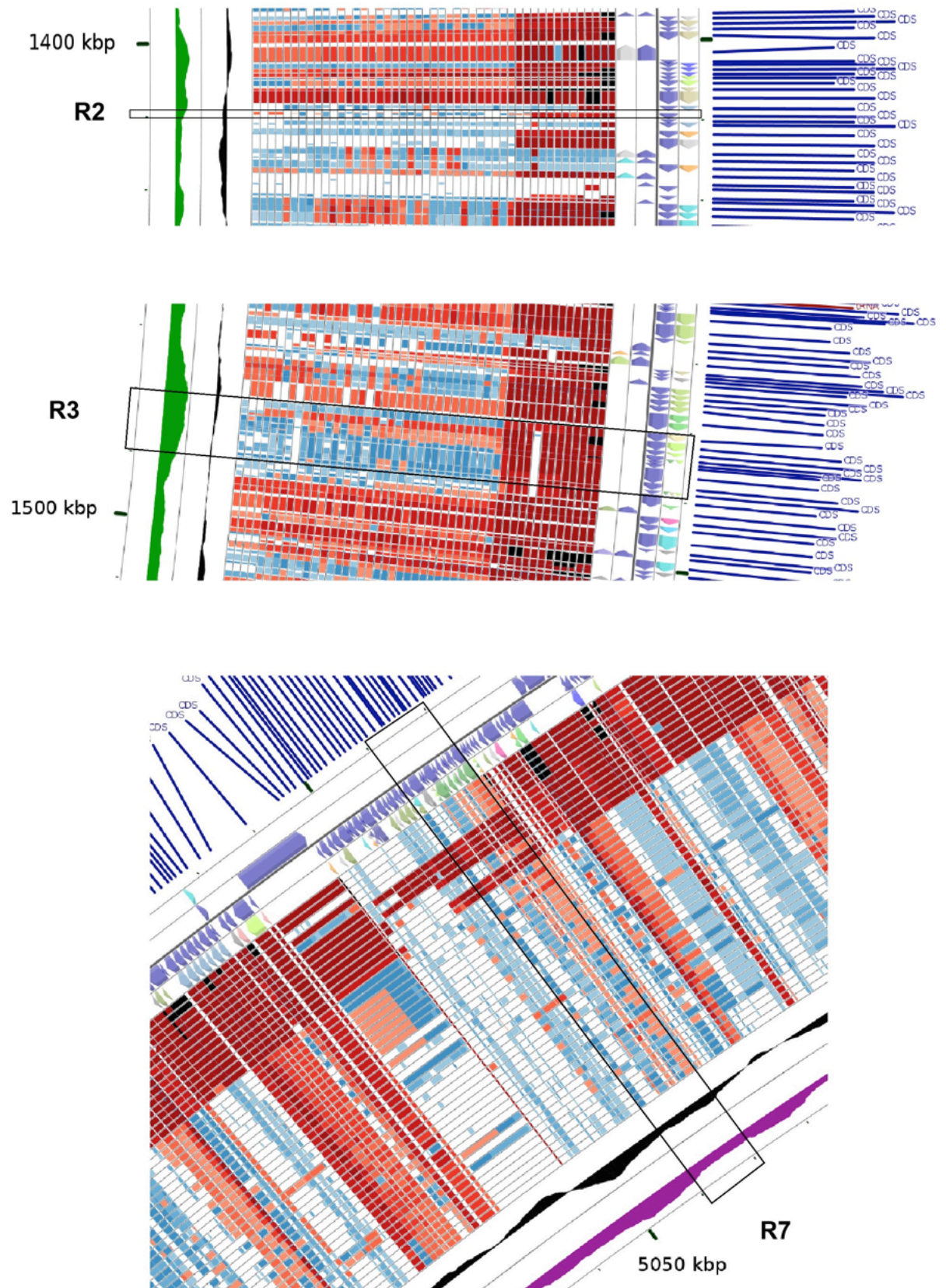


**Figure S3. Zoom map of circular representation of *P. polymyxa* A18 CDSs and their alignment with CDSs of members of the genus *Paenibacillus* for regions R2, R3 and R7 as mentioned in Figure 4.**

|                                                               | Cas1 | Cas2 | Cas3 | Cas4 | Cas5d | Cas8c | Cas7 | Cmr1 | Cmr2 | Cmr3 | Cmr4 | Cmr5 |
|---------------------------------------------------------------|------|------|------|------|-------|-------|------|------|------|------|------|------|
| <i>P. polymyxa</i> A18                                        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> CF05                                       | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> SQR21                                      | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> M1                                         | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> SC2                                        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> Sb3-1                                      | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. peoriae</i> HS311                                       | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> strain ATCC 15970                          | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> strain YC0573                              | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> strain J                                   | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> CR1                                        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> strain YC0136                              | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> E681                                       | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. polymyxa</i> strain HPL-003                             | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. xylanexedens</i> strain PAMC 22703                      | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. riograndensis</i> SBR5                                  | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL H7-0357</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. graminis</i> strain DSM 15220                           | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL P4-0081</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL R7-0273</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. borealis</i> strain DSM 13188                           | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. odorifer</i> strain DSM 15391                           | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL R7-0331</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL R5-0912</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL H7-0737</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. bovis</i> sp. BD3526                                    | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. Y412MC10</i>                                        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. FSL R5-0345</i>                                     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. glucanolyticus</i> strain 5162                          | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. IHBB 10380</i>                                      | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. durus</i> strain DSM 1735                               | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. mucilaginosus</i> K02                                   | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. durus</i> ATCC 35681                                    | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. stellifer</i> strain DSM 14472                          | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. mucilaginosus</i> KNP414                                | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sabiniae</i> T27                                        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. mucilaginosus</i> 3016                                  | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. yonginensis</i> sp. DCY84                               | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. LPB0068</i>                                         | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. JDR-2</i>                                           | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. beijingensis</i> strain DSM 24997                       | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. swuensis</i> strain DY6                                 | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. sp. 320-W</i>                                           | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. naphthalenovorans</i> strain 320-Y                      | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain CCM 38     | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. larvae</i> subsp. <i>larvae</i> DSM 25430               | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. larvae</i> subsp. <i>larvae</i> strain ATCC 9545        | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |
| <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain ATCC 13537 | ■    | ■    | ■    | ■    | ■     | ■     | ■    | ■    | ■    | ■    | ■    | ■    |

**Figure S4. Comparative analyses of genes encoding for CRISPR/Cas and CRISPR/cmr across the members of the genus *Paenibacillus*.** The colored box represents the presence of a gene within the genome and white box indicates the absence of a gene.

**Table S1: General features of *P. polymyxa* A18 genome**

|                                    |           |
|------------------------------------|-----------|
| Sequencing platform                | Roche 454 |
| Genome size                        | 5.72 Mb   |
| Number of contigs                  | 682       |
| Number of scaffolds                | 28        |
| Sequencing coverage                | 16.5x     |
| GC content (%)                     | 46.2      |
| Predicted CDS                      | 4608      |
| tRNAs                              | 105       |
| Mobile element genes/ transposases | 23        |

**Table S2: Horizontal Gene Transfers in *P. polymyxa* A18 genome**

| Island start | Island end | Length | Gene start | Gene end | Product                                                                       |
|--------------|------------|--------|------------|----------|-------------------------------------------------------------------------------|
| 333544       | 340568     | 7024   | 333544     | 334965   | arylsulfatase regulator                                                       |
|              |            |        | 334955     | 335833   | ABC transporter ATP-binding protein                                           |
|              |            |        | 335838     | 336527   | hypothetical protein                                                          |
|              |            |        | 336524     | 337669   | hypothetical protein                                                          |
|              |            |        | 337736     | 339583   | Lipid A export ATP-binding/permease protein MsbA                              |
|              |            |        | 340362     | 340568   | hypothetical protein                                                          |
| 512341       | 536062     | 23721  | 512502     | 513248   | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)                     |
|              |            |        | 513741     | 514949   | Mobile element protein                                                        |
|              |            |        | 515161     | 515322   | hypothetical protein                                                          |
|              |            |        | 515555     | 515980   | hypothetical protein                                                          |
|              |            |        | 516572     | 516754   | hypothetical protein                                                          |
|              |            |        | 516825     | 517922   | Spore germination protein GerKB                                               |
|              |            |        | 517951     | 519177   | Spore germination protein GerKC                                               |
|              |            |        | 519190     | 520806   | Spore germination protein GerKA                                               |
|              |            |        | 521056     | 521184   | hypothetical protein                                                          |
|              |            |        | 522225     | 522620   | unknown                                                                       |
|              |            |        | 523774     | 524685   | Transcriptional regulator, AraC family                                        |
|              |            |        | 524799     | 525092   | hypothetical protein                                                          |
|              |            |        | 525043     | 525609   | putative short-chain dehydrogenase/oxidoreductase                             |
|              |            |        | 525820     | 526647   | AP endonuclease, family 2                                                     |
|              |            |        | 526664     | 528010   | Fructoselysine transporter FrIA, cationic amino acid permease                 |
|              |            |        | 528171     | 529184   | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) |
|              |            |        | 529279     | 530061   | Fructoselysine kinase (EC 2.7.1.-)                                            |
|              |            |        | 530125     | 530853   | Transcriptional regulator of fructoselysine utilization operon FrIR           |
|              |            |        | 531125     | 531775   | hypothetical protein                                                          |
|              |            |        | 532132     | 533115   | kelch-like 1                                                                  |
|              |            |        | 533325     | 533558   | hypothetical protein                                                          |
|              |            |        | 533687     | 534502   | hypothetical protein                                                          |

|         |         |      |         |         |                                                                                       |
|---------|---------|------|---------|---------|---------------------------------------------------------------------------------------|
|         |         |      | 534705  | 535247  | Ribosomal protein S5p alanine acetyltransferase                                       |
|         |         |      | 535718  | 536062  | Dienelactone hydrolase family                                                         |
| 897034  | 901038  | 4004 | 897034  | 898581  | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
|         |         |      | 898578  | 899840  | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)           |
|         |         |      | 899842  | 901038  | Anticodon nuclease                                                                    |
| 1730296 | 1738714 | 8418 | 1730296 | 1731372 | 6 kDa early secretory antigenic target ESAT-6 (EsxA)                                  |
|         |         |      | 1731384 | 1731605 | hypothetical protein                                                                  |
|         |         |      | 1732278 | 1732736 | hypothetical protein                                                                  |
|         |         |      | 1732912 | 1733160 | hypothetical protein                                                                  |
|         |         |      | 1733814 | 1733978 | hypothetical protein                                                                  |
|         |         |      | 1734127 | 1734399 | hypothetical protein                                                                  |
|         |         |      | 1734552 | 1734719 | hypothetical protein                                                                  |
|         |         |      | 1734732 | 1734974 | hypothetical protein                                                                  |
|         |         |      | 1734976 | 1735089 | hypothetical protein                                                                  |
|         |         |      | 1735211 | 1735498 | hypothetical protein                                                                  |
|         |         |      | 1735884 | 1736429 | hypothetical protein                                                                  |
|         |         |      | 1737097 | 1738305 | Mobile element protein                                                                |
| 1731384 | 1736429 | 5045 | 1731384 | 1731605 | hypothetical protein                                                                  |
|         |         |      | 1732278 | 1732736 | hypothetical protein                                                                  |
|         |         |      | 1732912 | 1733160 | hypothetical protein                                                                  |
|         |         |      | 1733814 | 1733978 | hypothetical protein                                                                  |
|         |         |      | 1734127 | 1734399 | hypothetical protein                                                                  |
|         |         |      | 1734552 | 1734719 | hypothetical protein                                                                  |
|         |         |      | 1734732 | 1734974 | hypothetical protein                                                                  |
|         |         |      | 1734976 | 1735089 | hypothetical protein                                                                  |
|         |         |      | 1735211 | 1735498 | hypothetical protein                                                                  |
|         |         |      | 1735884 | 1736429 | hypothetical protein                                                                  |
| 2115218 | 2121318 | 6100 | 2115218 | 2115742 | hypothetical protein                                                                  |
|         |         |      | 2115739 | 2116386 | hypothetical protein                                                                  |
|         |         |      | 2116794 | 2117135 | Drug resistance transporter EmrB/QacA subfamily                                       |
|         |         |      | 2117506 | 2117625 | hypothetical protein                                                                  |
|         |         |      | 2117581 | 2118279 | SSU ribosomal protein S2p (SAe)                                                       |
|         |         |      | 2118412 | 2119062 | Translation elongation factor Ts                                                      |
|         |         |      | 2119183 | 2119911 | Uridine monophosphate kinase (EC 2.7.4.22)                                            |
|         |         |      | 2119911 | 2120465 | Ribosome recycling factor                                                             |
|         |         |      | 2120551 | 2121318 | Undecaprenyl diphosphate synthase (EC 2.5.1.31)                                       |
| 2334173 | 2341097 | 6924 | 2334173 | 2334295 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                                     |
|         |         |      | 2334438 | 2335025 | Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.-)                            |
|         |         |      | 2334998 | 2335174 | hypothetical protein                                                                  |
|         |         |      | 2335167 | 2335718 | hypothetical protein                                                                  |
|         |         |      | 2335735 | 2336304 | putative integral membrane protein                                                    |
|         |         |      | 2336329 | 2337495 | 1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)                               |
|         |         |      | 2337526 | 2338227 | Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.-)                            |
|         |         |      | 2338250 | 2339383 | diglucosyldiacylglycerol synthase                                                     |

|         |         |       |         |         |                                                                                                      |
|---------|---------|-------|---------|---------|------------------------------------------------------------------------------------------------------|
|         |         |       | 2339380 | 2340606 | Multidrug-efflux transporter                                                                         |
|         |         |       | 2340789 | 2341097 | Alkaline phosphatase like protein                                                                    |
| 2419508 | 2461861 | 42353 | 2419508 | 2461861 | Bacitracin synthetase 3 (BA3)                                                                        |
| 2669891 | 2682305 | 12414 | 2669891 | 2670901 | Two-component response regulator yesN                                                                |
|         |         |       | 2671332 | 2672312 | Beta-galactosidase (EC 3.2.1.23)                                                                     |
|         |         |       | 2672328 | 2673701 | PTS system, beta-glucoside-specific IIB component (EC 2.7.1.69) / PTS system, beta-glucoside-specifi |
|         |         |       | 2673736 | 2676159 | Beta-glucosidase (EC 3.2.1.21)                                                                       |
|         |         |       | 2676291 | 2677472 | Beta-lactamase class C                                                                               |
|         |         |       | 2677530 | 2678399 | Gluconolactonase (EC 3.1.1.17)                                                                       |
|         |         |       | 2679006 | 2681672 | Possible DNA-binding protein                                                                         |
|         |         |       | 2681760 | 2682305 | PTS system, beta-glucoside-specific IIB component (EC 2.7.1.69)                                      |
| 3026847 | 3038959 | 12112 | 3026920 | 3027102 | hypothetical protein                                                                                 |
|         |         |       | 3027099 | 3027287 | hypothetical protein                                                                                 |
|         |         |       | 3027410 | 3027598 | hypothetical protein                                                                                 |
|         |         |       | 3027722 | 3027940 | hypothetical protein                                                                                 |
|         |         |       | 3027965 | 3028192 | hypothetical protein                                                                                 |
|         |         |       | 3028189 | 3028503 | hypothetical protein                                                                                 |
|         |         |       | 3028454 | 3028972 | Hypothetical protein, Lmo2306 homolog [Bacteriophage A118]                                           |
|         |         |       | 3028973 | 3030091 | DNA polymerase III beta subunit (EC 2.7.7.7)                                                         |
|         |         |       | 3030220 | 3031176 | Helicase loader DnaI                                                                                 |
|         |         |       | 3031183 | 3032193 | Phage replication initiation                                                                         |
|         |         |       | 3032228 | 3032650 | hypothetical protein                                                                                 |
|         |         |       | 3032643 | 3033803 | Phage protein                                                                                        |
|         |         |       | 3033864 | 3034262 | hypothetical protein                                                                                 |
|         |         |       | 3034253 | 3034609 | hypothetical protein                                                                                 |
|         |         |       | 3034727 | 3035158 | hypothetical protein                                                                                 |
|         |         |       | 3035155 | 3036276 | Chromosome (plasmid) partitioning protein ParB                                                       |
|         |         |       | 3036483 | 3036749 | hypothetical protein                                                                                 |
|         |         |       | 3036762 | 3036881 | hypothetical protein                                                                                 |
|         |         |       | 3037205 | 3037594 | transcriptional regulator, XRE family                                                                |
|         |         |       | 3037704 | 3038891 | Phage integrase                                                                                      |
| 3757106 | 3769706 | 12600 | 3757082 | 3757198 | hypothetical protein                                                                                 |
|         |         |       | 3757584 | 3757697 | hypothetical protein                                                                                 |
|         |         |       | 3757782 | 3758432 | hypothetical protein                                                                                 |
|         |         |       | 3758605 | 3758820 | hypothetical protein                                                                                 |
|         |         |       | 3759272 | 3759421 | hypothetical protein                                                                                 |
|         |         |       | 3760101 | 3761093 | hypothetical protein                                                                                 |
|         |         |       | 3761099 | 3761932 | CRISPR-associated RAMP Cmr6                                                                          |
|         |         |       | 3761952 | 3762323 | CRISPR-associated RAMP Cmr5                                                                          |
|         |         |       | 3762320 | 3763279 | CRISPR-associated RAMP Cmr4                                                                          |
|         |         |       | 3763269 | 3764558 | CRISPR-associated RAMP Cmr3                                                                          |
|         |         |       | 3764527 | 3766347 | CRISPR-associated RAMP Cmr2                                                                          |
|         |         |       | 3766347 | 3767900 | CRISPR-associated RAMP Cmr1                                                                          |
|         |         |       | 3768679 | 3769359 | hypothetical protein                                                                                 |

|         |         |       |         |         |                                                                         |
|---------|---------|-------|---------|---------|-------------------------------------------------------------------------|
| 3810554 | 3822720 | 12166 | 3810554 | 3810703 | hypothetical protein                                                    |
|         |         |       | 3810954 | 3811577 | Methyltransferase (EC 2.1.1.-)                                          |
|         |         |       | 3811599 | 3812054 | Conserved domain protein                                                |
|         |         |       | 3812401 | 3813123 | Methyltransferase (EC 2.1.1.-)                                          |
|         |         |       | 3813133 | 3813276 | Methyltransferase (EC 2.1.1.-)                                          |
|         |         |       | 3813325 | 3813588 | hypothetical protein                                                    |
|         |         |       | 3813910 | 3814350 | hypothetical protein                                                    |
|         |         |       | 3814422 | 3815045 | hypothetical protein                                                    |
|         |         |       | 3815065 | 3815643 | hypothetical protein                                                    |
|         |         |       | 3817658 | 3818509 | Possible aminoglycoside phosphotransferase                              |
|         |         |       | 3818503 | 3818952 | hypothetical protein                                                    |
|         |         |       | 3819061 | 3819951 | hypothetical protein                                                    |
|         |         |       | 3820090 | 3820536 | hypothetical protein                                                    |
|         |         |       | 3820743 | 3821282 | hypothetical protein                                                    |
|         |         |       | 3821470 | 3821883 | Histone acetyltransferase HPA2                                          |
|         |         |       | 3821973 | 3822422 | GCN5-related N-acetyltransferase                                        |
|         |         |       | 3822583 | 3822720 | hypothetical protein                                                    |
| 3829120 | 3842427 | 13307 | 3829120 | 3829629 | hypothetical protein                                                    |
|         |         |       | 3829767 | 3830411 | hypothetical protein                                                    |
|         |         |       | 3830585 | 3830797 | hypothetical protein                                                    |
|         |         |       | 3831202 | 3831384 | Ubiquinone/menaquinone biosynthesis methyltransferase UBIE (EC 2.1.1.-) |
|         |         |       | 3831398 | 3832015 | Ubiquinone/menaquinone biosynthesis methyltransferase UBIE (EC 2.1.1.-) |
|         |         |       | 3832211 | 3832936 | hypothetical protein                                                    |
|         |         |       | 3833938 | 3835179 | hypothetical protein                                                    |
|         |         |       | 3835433 | 3836584 | hypothetical protein                                                    |
|         |         |       | 3836656 | 3836934 | hypothetical protein                                                    |
|         |         |       | 3837344 | 3838303 | putative cytoplasmic protein                                            |
|         |         |       | 3838463 | 3838951 | hypothetical protein                                                    |
|         |         |       | 3839126 | 3839764 | hypothetical protein                                                    |
|         |         |       | 3839983 | 3840186 | hypothetical protein                                                    |
|         |         |       | 3840708 | 3841319 | hypothetical protein                                                    |
|         |         |       | 3841454 | 3841681 | Phage integrase                                                         |
|         |         |       | 3841678 | 3841854 | hypothetical protein                                                    |
|         |         |       | 3842047 | 3842427 | hypothetical protein                                                    |
| 3962011 | 3972716 | 10705 | 3962011 | 3962316 | hypothetical protein                                                    |
|         |         |       | 3962827 | 3964182 | hypothetical protein                                                    |
|         |         |       | 3964336 | 3966060 | ATPase involved in DNA repair                                           |
|         |         |       | 3966265 | 3967248 | hypothetical protein                                                    |
|         |         |       | 3967472 | 3968158 | SII1429 protein                                                         |
|         |         |       | 3968422 | 3968637 | hypothetical protein                                                    |
|         |         |       | 3968686 | 3969729 | ankyrin repeat protein, putative                                        |
|         |         |       | 3970588 | 3971730 | hypothetical protein                                                    |
|         |         |       | 3971865 | 3972716 | hypothetical protein                                                    |
| 4167992 | 4213959 | 45967 | 4168136 | 4173100 | beta-ketoacyl synthase                                                  |

|         |         |       |         |         |                                                                     |
|---------|---------|-------|---------|---------|---------------------------------------------------------------------|
|         |         |       | 4173093 | 4180103 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4180118 | 4180237 | hypothetical protein                                                |
|         |         |       | 4180213 | 4181043 | Chaperone protein DnaK                                              |
|         |         |       | 4181262 | 4181924 | Chaperone protein DnaK                                              |
|         |         |       | 4182136 | 4189719 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4189761 | 4194407 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4194380 | 4197388 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4197385 | 4199682 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4199676 | 4199837 | hypothetical protein                                                |
|         |         |       | 4199936 | 4200079 | hypothetical protein                                                |
|         |         |       | 4200184 | 4201230 | O-methyltransferase                                                 |
|         |         |       | 4201212 | 4201946 | Aspartate racemase (EC 5.1.1.13)                                    |
|         |         |       | 4202020 | 4205814 | Peptide synthetase                                                  |
|         |         |       | 4205851 | 4209216 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)         |
|         |         |       | 4209473 | 4210084 | Transcription antitermination protein NusG                          |
|         |         |       | 4210512 | 4211114 | Transcriptional regulator, TetR family                              |
|         |         |       | 4211396 | 4213753 | Phosphoenolpyruvate synthase (EC 2.7.9.2)                           |
| 4310402 | 4318130 | 7728  | 4310402 | 4311934 | Radical SAM domain protein                                          |
|         |         |       | 4311900 | 4313573 | ABC-type multidrug/protein/lipid transport system, ATPase component |
|         |         |       | 4313820 | 4314467 | hypothetical protein                                                |
|         |         |       | 4314461 | 4315789 | Arylsulfatase regulator (Fe-S oxidoreductase)                       |
|         |         |       | 4316031 | 4316144 | hypothetical protein                                                |
|         |         |       | 4316275 | 4317111 | response regulator                                                  |
|         |         |       | 4317117 | 4318130 | two-component sensor histidine kinase                               |
| 4821202 | 4855690 | 34488 | 4821202 | 4821432 | hypothetical protein                                                |
|         |         |       | 4821879 | 4823249 | Bacitracin synthetase 3 (BA3)                                       |
|         |         |       | 4823209 | 4832796 | FIG01233961: hypothetical protein                                   |
|         |         |       | 4833027 | 4834760 | Lipid A export ATP-binding/permease protein MsbA                    |
|         |         |       | 4834757 | 4836583 | Lipid A export ATP-binding/permease protein MsbA                    |
|         |         |       | 4836573 | 4839881 | Siderophore biosynthesis non-ribosomal peptide synthetase modules   |
|         |         |       | 4840036 | 4855029 | hypothetical protein                                                |
|         |         |       | 4855105 | 4855290 | hypothetical protein                                                |
|         |         |       | 4855577 | 4855690 | hypothetical protein                                                |

**Table S3. Genome features of members belonging to genus *Paenibacillus***

| Sl no. | Name                                     | Genome assembly ID | Location of isolation              | Ecological occurrence | References    | Genome size (Mb) | GC content (%) | Total Genes* | Total Proteins* |
|--------|------------------------------------------|--------------------|------------------------------------|-----------------------|---------------|------------------|----------------|--------------|-----------------|
| 1.     | <i>P. polymyxa</i> A18                   | NZ_JWJJ00000000.1  | Termite gut, India                 | Gut                   | Current Study | 5.72             | 46.2           | 5066         | 4,805           |
| 2.     | <i>P. polymyxa</i> CF05                  | NZ_CP009909.1      | Cryptomeria fortunei tree, China   | Rhizosphere           | 1             | 5.76             | 45.5           | 4,928        | 4,715           |
| 3.     | <i>P. polymyxa</i> SQR-21                | NZ_CP006872.1      | Watermelon rhizosphere             | Rhizosphere           | 2             | 5.82             | 45.64          | 5,030        | 4,768           |
| 4.     | <i>P. polymyxa</i> M1                    | NC_017542.1        | Wheat roots, China                 | Rhizosphere           |               | 6.23             | 44.8           | 5,596        | 5,372           |
| 5.     | <i>P. polymyxa</i> SC2                   | NC_014622.2        | Pepper rhizosphere, Guizhou, China | Rhizosphere           | 3             | 6.24             | 44.58          | 5,747        | 5,474           |
| 6.     | <i>P. polymyxa</i> Sb3-1                 | NZ_CP010268.1      | Agricultural soil, Egypt           | Rhizosphere           | 4             | 5.82             | 45.37          | 5,050        | 4,802           |
| 7.     | <i>P. peoriae</i> HS311                  | NZ_CP011512.1      | Korea                              | Rhizosphere           | unpublished   | 6.01             | 45.7           | 5,507        | 5,365           |
| 8.     | <i>P. polymyxa</i> strain ATCC 15970     | NZ_CP011420.1      | Soil, Belgium                      | Rhizosphere           | unpublished   | 6.09             | 45.6           | 5,325        | 4,991           |
| 9.     | <i>P. polymyxa</i> strain YC0573         | NZ_CP017968.2      | rhizosphere of tobacco, China      | Rhizosphere           | unpublished   | 6.12             | 45.6           | 5,334        | 5,194           |
| 10.    | <i>P. polymyxa</i> strain J              | NZ_CP015423.1      | China                              | NA                    | unpublished   | 5.75             | 45.7           | 5,175        | 5,023           |
| 11.    | <i>P. polymyxa</i> CR1                   | NC_023037.2        | Corn roots, Canada                 | Rhizosphere           | 5             | 6.01             | 45.6           | 5,301        | 5,029           |
| 12.    | <i>P. polymyxa</i> strain YC0136         | NZ_CP017967.1      | Rhizosphere of Tobacco, China      | Rhizosphere           | unpublished   | 5.62             | 45.7           | 4,937        | 4,808           |
| 13.    | <i>P. polymyxa</i> E681                  | NC_014483.2        | Barley rhizosphere, South Korea    | Rhizosphere           | 6             | 5.39             | 45.8           | 4,796        | 4,528           |
| 14.    | <i>P. terrae</i> HPL-003                 | NC_016641.1        | Forest residue, Iraq               | Rhizosphere           | 7             | 6.08             | 46.77          | 5,396        | 5,137           |
| 15.    | <i>P. xylanexedens</i> strain PAMC 22703 | NZ_CP018620.1      | Sediments, Russia                  | Rhizosphere           | unpublished   | 7.05             | 46             | 6,208        | 6,066           |
| 16.    | <i>P. riograndensis</i> SBR5             | NZ_LN831776        | Wheat field, Brazil                | Soil                  | unpublished   | 7.5              | 51             | 7,326        | 7,286           |
| 17.    | <i>P. sp.</i> FSL H7-0357                | NZ_CP009241.1      | Pasteurized milk, USA              | NA                    | unpublished   | 7.7              | 49.1           | 6,857        | 6,741           |
| 18.    | <i>P. graminis</i> strain DSM 15220      | NZ_CP009287.1      | Maize rhizosphere, France          | Rhizosphere           | unpublished   | 7.16             | 50.6           | 5,763        | 5,584           |
| 19.    | <i>P. sp.</i> FSL P4-0081                | NZ_CP009280.1      | heat treated raw milk, USA         | NA                    | unpublished   | 8.42             | 51.1           | 7,302        | 7,183           |
| 20.    | <i>P. sp.</i> FSL R7-0273                | NZ_CP009283.1      | Milk, USA                          | NA                    | unpublished   | 7.18             | 51.9           | 6,231        | 6,180           |

|     |                                         |               |                                                          |             |             |      |       |       |       |
|-----|-----------------------------------------|---------------|----------------------------------------------------------|-------------|-------------|------|-------|-------|-------|
| 21. | <i>P. borealis</i> strain DSM 13188     | NZ_CP009285.1 | Spruce forest humus, Finland                             | NA          | unpublished | 8.15 | 51.4  | 6,382 | 6,213 |
| 22. | <i>P. odorifer</i> strain DSM 15391     | NZ_CP009428.1 | Radioactive waste repository, Finland                    | NA          | unpublished | 6.81 | 44.2  | 5,593 | 5,431 |
| 23. | <i>P. sp.</i> FSL R7-0331               | NZ_CP009284.1 | Pasteurized fat milk, USA                                | NA          | unpublished | 6.93 | 51.2  | 6,066 | 5,947 |
| 24. | <i>P. sp.</i> FSL R5-0912               | NZ_CP009282.1 | Pasteurized fat milk, USA                                | NA          | unpublished | 7.71 | 51.1  | 6,662 | 6,540 |
| 25. | <i>P. sp.</i> FSL H7-0737               | NZ_CP009279.1 | Pasteurized milk, USA                                    | NA          | unpublished | 6.76 | 43.7  | 5,961 | 5,836 |
| 26. | <i>P. bovis sp.</i> BD3526              | NZ_CP013023.1 | Yak milk, China                                          | NA          | unpublished | 5.35 | 47.3  | 4,567 | 4,450 |
| 27. | <i>P. sp.</i> Y412MC10                  | NC_013406.1   | Hot Spring, Montana, USA                                 | Intestine   | 8           | 7.12 | 51.2  | 6,302 | 6,152 |
| 28. | <i>P. sp.</i> FSL R5-0345               | NZ_CP009281.1 | Pasteurized fat milk, USA                                | NA          | unpublished | 6.78 | 43.7  | 6,037 | 5,914 |
| 29. | <i>P. glucanolyticus</i> strain 5162    | NZ_CP015286.1 | Soil                                                     | NA          | unpublished | 5.89 | 49.2  | 5,285 | 5,184 |
| 30. | <i>P. sp.</i> IHBB 10380                | NZ_CP010976.1 | Soil, India                                              | NA          | unpublished | 5.77 | 41.29 | 5,313 | 5,185 |
| 31. | <i>P. durus</i> strain DSM 1735         | NZ_CP009288.1 | marine sediment                                          | NA          | unpublished | 6.03 | 50.8  | 5,453 | 5,338 |
| 32. | <i>P. mucilaginosus</i> K02             | NC_017672.3   | Soil                                                     | NA          | 9           | 8.81 | 58.3  | 7,403 | 7,209 |
| 33. | <i>P. durus</i> ATCC 35681              | NZ_CP011114.1 | NA                                                       | NA          | 10          | 5.57 | 50.8  | 5,308 | 5,179 |
| 34. | <i>P. stellifer</i> strain DSM 14472    | NZ_CP009286.1 | Paperboard, Finland                                      | NA          | 11          | 5.65 | 53.5  | 4,675 | 4,464 |
| 35. | <i>P. mucilaginosus</i> KNP414          | NC_015690.1   | Soil of Tianmu Mountain, China                           | Rhizosphere | 12          | 8.66 | 58.38 | 7,173 | 6,909 |
| 36. | <i>P. sabinae</i> T27                   | NZ_CP004078.1 | rhizosphere soil                                         | Rhizosphere | 13          | 5.27 | 52.6  | 4,904 | 4,792 |
| 37. | <i>P. mucilaginosus</i> 3016            | NC_016935.1   | rhizosphere soil                                         | Rhizosphere | 14          | 8.73 | 58.3  | 7,442 | 7,221 |
| 38. | <i>P. yonginensis sp.</i> DCY84         | NZ_CP014167.1 | humus soil, South Korea                                  | NA          | 15          | 4.98 | 51    | 4,558 | 4,441 |
| 39. | <i>P. sp.</i> LPB0068                   | NZ_CP017770.1 | Pacific oyster ( <i>Crassostrea gigas</i> ), South Korea | NA          | 16          | 4.62 | 40    | 4,461 | 4,336 |
| 40. | <i>P. sp.</i> JDR-2                     | NC_012914.1   | Sweet gum stem, USA                                      | Rhizosphere | 17          | 7.18 | 50.28 | 6,322 | 6,128 |
| 41. | <i>P. beijingensis</i> strain DSM 24997 | NZ_CP011058.1 | Jujube rhizosphere soil, China                           | Rhizosphere | 18          | 5.74 | 52.5  | 5,215 | 4,728 |
| 42. | <i>P. swuensis</i> strain DY6           | NZ_CP011388.1 | Soil, South Korea                                        | NA          | 19          | 5.01 | 48.9  | 4,551 | 4,430 |
| 43. | <i>P. sp.</i> 32O-W                     | NZ_CP013653.1 | Soil, USA                                                | NA          | 20          | 5.37 | 56.3  | 4,844 | 4,754 |

|     |                                                               |               |                           |                    |    |      |       |       |       |
|-----|---------------------------------------------------------------|---------------|---------------------------|--------------------|----|------|-------|-------|-------|
| 44. | <i>P. naphthalenovorans</i> strain 32O-Y                      | NZ_CP013652.1 | Soil, USA                 | NA                 | 20 | 5.2  | 49.7  | 5,135 | 5,004 |
| 45. | <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain CCM 38     | NZ_CP020327   | NA                        | NA                 | NA | 4.33 | 44.19 | 4,611 | 4,504 |
| 46. | <i>P. larvae</i> subsp. <i>larvae</i> DSM 25430               | NC_023134.1   | Honey bee broods, Tunisia | Honey bee pathogen | 21 | 4.05 | 45    | 3,993 | 3,683 |
| 47. | <i>P. larvae</i> subsp. <i>larvae</i> strain ATCC 9545        | NZ_CP019687   | NA                        | Honey bee pathogen | NA | 4.28 | 44.2  | 4,496 | 4,388 |
| 48. | <i>P. larvae</i> subsp. <i>pulvifaciens</i> strain ATCC 13537 | NZ_CP019794   | NA                        | NA                 | NA | 4.41 | 44.19 | 4,778 | 4,671 |

NA-Not Available

\*The total genes and proteins represented here are based on NCBI annotation

**Table S4: Categorization of CAZy genes encoded in *P. polymyxa* A18 according to their functions**

| Enzyme                                         | EC Number | CAZy Family | RAST ID                     | NCBI ID        |
|------------------------------------------------|-----------|-------------|-----------------------------|----------------|
| <b>1.Cellulose-degrading enzymes</b>           |           |             |                             |                |
| Cellobiohydrolase                              | 3.2.1.14  | GH6         | fig 6666666.120009.peg.1002 | WP_016821398.1 |
| $\beta$ -1,3-endoglucanase                     |           | GH81        | fig 6666666.120009.peg.4288 | WP_017425583.1 |
| $\beta$ -1,4-endoglucanase                     |           | GH5         | fig 6666666.120009.peg.2467 | WP_017426982.1 |
|                                                | 3.2.1.4   | GH5         | fig 6666666.120009.peg.5008 | WP_038978163.1 |
|                                                | 3.2.1.4   | GH5         | fig 6666666.120009.peg.3617 | WP_017426793.1 |
|                                                |           | GH5         | fig 6666666.120009.peg.3481 | WP_017428294.1 |
|                                                |           | GH48        | fig 6666666.120009.peg.2298 |                |
|                                                | 3.2.1.3   | GH26        | fig 6666666.120009.peg.4472 | WP_017427072.1 |
|                                                | 3.2.1.4   | GH44        | fig 6666666.120009.peg.4472 | WP_017427072.1 |
| Xyloglucan-specific $\beta$ -1,4-endoglucanase |           | GH74        | fig 6666666.120009.peg.2569 | WP_017427741.1 |
| $\beta$ -1,3(4)-endoglucanase                  | 3.2.1.73  | GH16        | fig 6666666.120009.peg.2386 | WP_017426919.1 |
| $\beta$ -glucosidase                           | 3.2.1.21  | GH1         | fig 6666666.120009.peg.1624 | WP_017425890.1 |
|                                                | 3.2.1.21  | GH1         | fig 6666666.120009.peg.3835 | WP_026065451.1 |
|                                                | 3.2.1.21  | GH1         | fig 6666666.120009.peg.3948 | WP_017427334.1 |
|                                                | 3.2.1.21  | GH1         | fig 6666666.120009.peg.4226 | WP_017425532.1 |
|                                                | 3.2.1.21  | GH1         | fig 6666666.120009.peg.4845 | WP_026065363.1 |
|                                                | 3.2.1.21  | GH3         | fig 6666666.120009.peg.903  | WP_017426284.1 |
|                                                | 3.2.1.21  | GH3         | fig 6666666.120009.peg.1068 | WP_017426395.1 |

|                                                             |          |      |                             |                |
|-------------------------------------------------------------|----------|------|-----------------------------|----------------|
|                                                             | 3.2.1.21 | GH3  | fig 6666666.120009.peg.2390 | WP_038978010.1 |
|                                                             | 3.2.1.21 | GH3  | fig 6666666.120009.peg.2427 | WP_017426950.1 |
|                                                             | 3.2.1.21 | GH3  | fig 6666666.120009.peg.285  | WP_038978231.1 |
|                                                             | 3.2.1.21 | GH3  | fig 6666666.120009.peg.3484 | WP_017428297.1 |
|                                                             | 3.2.1.21 | GH3  | fig 6666666.120009.peg.4693 | WP_017428582.1 |
| <b>2. Hemicellulose-degrading enzymes</b>                   |          |      |                             |                |
| $\alpha$ -galactosidase                                     | 3.2.1.22 | GH27 | fig 6666666.120009.peg.2230 | WP_017428506.1 |
|                                                             | 3.2.1.22 | GH36 | fig 6666666.120009.peg.2321 | WP_017426877.1 |
|                                                             | 3.2.1.22 | GH36 | fig 6666666.120009.peg.2477 | WP_016820825.1 |
|                                                             | 3.2.1.22 | GH36 | fig 6666666.120009.peg.516  | WP_017428015.1 |
|                                                             | 3.2.1.22 | GH36 | fig 6666666.120009.peg.691  | WP_016819342.1 |
|                                                             | 3.2.1.22 | GH4  | fig 6666666.120009.peg.1001 | WP_016821399.1 |
|                                                             | 3.2.1.22 | GH4  | fig 6666666.120009.peg.964  | WP_026065381.1 |
| $\beta$ -1,4-endoxylanase                                   | 3.2.1.8  | GH5  | fig 6666666.120009.peg.3656 | WP_026065408.1 |
|                                                             | 3.2.1.8  | GH5  | fig 6666666.120009.peg.2343 | WP_016818773.1 |
|                                                             |          | GH10 | fig 6666666.120009.peg.4954 | WP_013373834.1 |
|                                                             | 3.2.1.8  | GH10 | fig 6666666.120009.peg.4797 | WP_017426140.1 |
|                                                             |          | GH11 | fig 6666666.120009.peg.4323 | WP_017425612.1 |
|                                                             |          | GH30 | fig 6666666.120009.peg.610  | WP_017425752.1 |
|                                                             | 3.2.1.8  | GH43 | fig 6666666.120009.peg.2385 | WP_017426918.1 |
| $\beta$ -1,4-xylosidase                                     | 3.2.1.37 | GH43 | fig 6666666.120009.peg.3200 | WP_017428110.1 |
|                                                             |          | GH43 | fig 6666666.120009.peg.4843 | WP_017426115.1 |
|                                                             | 3.2.1.37 | GH52 | fig 6666666.120009.peg.4822 | WP_017426124.1 |
| $\alpha$ -arabinofuranosidase                               |          | GH43 | fig 6666666.120009.peg.269  | WP_017425677.1 |
|                                                             | 3.2.1.55 | GH43 | fig 6666666.120009.peg.1753 | WP_017425805.1 |
|                                                             | 3.2.1.55 | GH51 | fig 6666666.120009.peg.188  | WP_038978238.1 |
|                                                             | 3.2.1.55 | GH51 | fig 6666666.120009.peg.296  | WP_038978229.1 |
|                                                             | 3.2.1.55 | GH51 | fig 6666666.120009.peg.3030 | WP_017427480.1 |
| $\alpha$ -1,5-endoarabinosidase                             | 3.2.1.99 | GH43 | fig 6666666.120009.peg.796  | WP_017426194.1 |
|                                                             | 3.2.1.99 | GH43 | fig 6666666.120009.peg.1752 | WP_017425806.1 |
| Mannanase                                                   |          | GH5  | fig 6666666.120009.peg.576  | WP_017427981.1 |
| $\beta$ -1,4-mannosidase                                    | 3.2.1.78 | GH26 | fig 6666666.120009.peg.522  | WP_017428011.1 |
|                                                             | 3.2.1.78 | GH26 | fig 6666666.120009.peg.635  | WP_017425735.1 |
|                                                             | 3.2.1.78 | GH26 | fig 6666666.120009.peg.3186 | WP_017428102.1 |
|                                                             |          | GH26 | fig 6666666.120009.peg.1157 | WP_017426461.1 |
| $\alpha$ -1,5-exoarabinanase/endo- $\beta$ -1,4-galactanase |          | GH53 | fig 6666666.120009.peg.3141 | WP_017427835.1 |
| Polygalacturonase                                           | 3.2.1.15 | GH28 | fig 6666666.120009.peg.3203 | WP_017428113.1 |
| Acetyl xylan esterase                                       |          | CE1  | fig 6666666.120009.peg.4249 | WP_017425551.1 |
|                                                             |          | CE1  | fig 6666666.120009.peg.4482 | WP_017427076.1 |
| xylanase deacetylase                                        | 3.5.1.-  | CE4  | fig 6666666.120009.peg.2340 | WP_017426884.1 |
|                                                             |          | CE8  | fig 6666666.120009.peg.4307 | WP_017425600.1 |
| <b>3. Pectin-degrading enzymes</b>                          |          |      |                             |                |

|                             |          |       |                             |                |
|-----------------------------|----------|-------|-----------------------------|----------------|
| Pectinesterase              |          |       | fig 6666666.120009.peg.3201 | WP_017428111.1 |
| Pectin lyase                | 4.2.2.10 | PL1   | fig 6666666.120009.peg.1417 | WP_017426635.1 |
| Pectate lyase               | 4.2.2.2  | PL1   | fig 6666666.120009.peg.3626 | WP_016821905.1 |
|                             | 4.2.2.2  | PL1   | fig 6666666.120009.peg.4834 | WP_017426120.1 |
|                             | 4.2.2.2  | PL1   | fig 6666666.120009.peg.4834 | WP_017426120.1 |
|                             | 4.2.2.2  | PL1   | fig 6666666.120009.peg.210  | WP_017425629.1 |
|                             |          | PL10  | fig 6666666.120009.peg.1582 | WP_017425913.1 |
|                             |          | PL3   | fig 6666666.120009.peg.870  | WP_016819868.1 |
|                             |          | PL9   | fig 6666666.120009.peg.2463 | WP_017426980.1 |
| Rhamnogalacturonanendolyase |          | PL11  | fig 6666666.120009.peg.1582 | WP_017425913.1 |
|                             |          | PL11  | fig 6666666.120009.peg.985  | WP_017426343.1 |
|                             |          | PL9   | fig 6666666.120009.peg.2463 | WP_017426980.1 |
|                             |          | PL27  | fig 6666666.120009.peg.963  | WP_038978105.1 |
| $\alpha$ -rhamnosidase      | 3.2.1.40 | GH78  | fig 6666666.120009.peg.3499 | WP_017428310.1 |
|                             |          | GH106 | fig 6666666.120009.peg.2393 | WP_038978012.1 |
| Endo-apiosidase             | 3.2.1.-  | GH140 | fig 6666666.120009.peg.3943 | WP_026065445.1 |
|                             |          | GH140 | fig 6666666.120009.peg.4110 | WP_017428672.1 |
| $\alpha$ -L-fucosidase      | 3.2.1.51 | GH141 | fig 6666666.120009.peg.3588 | WP_017426818.1 |

**Table S5: Annotation of antibiotic synthesizing polypeptides in *P. polymyxa* A18**

| Antibiotics synthesized | Protein involved in synthesis                                | NCBI Protein ID             |
|-------------------------|--------------------------------------------------------------|-----------------------------|
| Polymyxin               | Polymyxin synthetase A, pmx A                                | WP_017427759.1              |
|                         | Polymyxin synthetase B, pmxB                                 | WP_038978210.1              |
|                         | Polymyxin synthetase C, pmxC, transporter                    | WP_017428090.1              |
|                         | Polymyxin synthetase D, pmxD, transporter                    | WP_017428091.1              |
|                         | Polymyxin synthetase E, pmx E                                | fig 6666666.120009.CDS.4336 |
| Paenibacillin           | PaeA, paenibacillin prepropeptide                            |                             |
|                         | PaeP, peptidase                                              | WP_016819874.1              |
|                         | PaeB, lantibiotic dehydratase                                | WP_038978102.1<br>52..667   |
|                         | PaeC, lantibiotic cyclase                                    | WP_017426262.1<br>46..419   |
|                         | PaeI, putative immunity protein                              |                             |
|                         | PaeT, transporter                                            | WP_026065373.1              |
|                         | AgrB, accessory gene regulator B, processing signal molecule | WP_019686238.1              |
|                         | AgrD, autoinducing peptide (AIP)                             | fig 6666666.120009.CDS.881  |
|                         | AgrC, histidine kinase                                       | WP_017426266.1              |
|                         | AgrA, response regulator                                     | WP_017426267.1              |
|                         | PaeN, putative acetylase                                     | WP_017426268.1              |
|                         |                                                              |                             |
| Tridecaptin             | TrbA thioestrerase                                           | WP_017428487.1              |
|                         | TrbB ABC transporter                                         | WP_038978247.1              |

|             |                      |                |
|-------------|----------------------|----------------|
|             | TrbC ABC transporter | WP_017428489.1 |
|             | TrbD NRPS            | WP_038978246.1 |
|             | TrbE NRPS            | WP_026065510.1 |
| Fusaricidin | FusA                 | WP_017427039.1 |
|             | FusB                 | WP_017427040.1 |
|             | FusC                 | WP_016818887.1 |
|             | FusD                 | WP_017427041.1 |
|             | FusE                 | WP_017427883.1 |
|             | FusF                 | WP_017427042.1 |
|             | FusG                 | WP_017427043.1 |

**Table S6. Concentration of antibiotics used for susceptibility testing**

| Antibiotic tested | Range (µg/ml) | Concentration used for testing (µg/ml)                                          |
|-------------------|---------------|---------------------------------------------------------------------------------|
| Tetracycline      | 1-150         | 1, 2.5, 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 |
| Erythromycin      | 1-25          | 1, 2.5, 5, 10, 15, 20, 25                                                       |
| Kanamycin         | 10-150        | 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150                |
| Chloramphenicol   | 10-150        | 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150                |
| Penicillin        | 10-100        | 10, 20, 30, 40, 50, 60, 70, 80, 90, 100                                         |
| Vancomycin        | 10-90         | 10, 20, 30, 40, 50, 60, 70, 80, 90                                              |

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