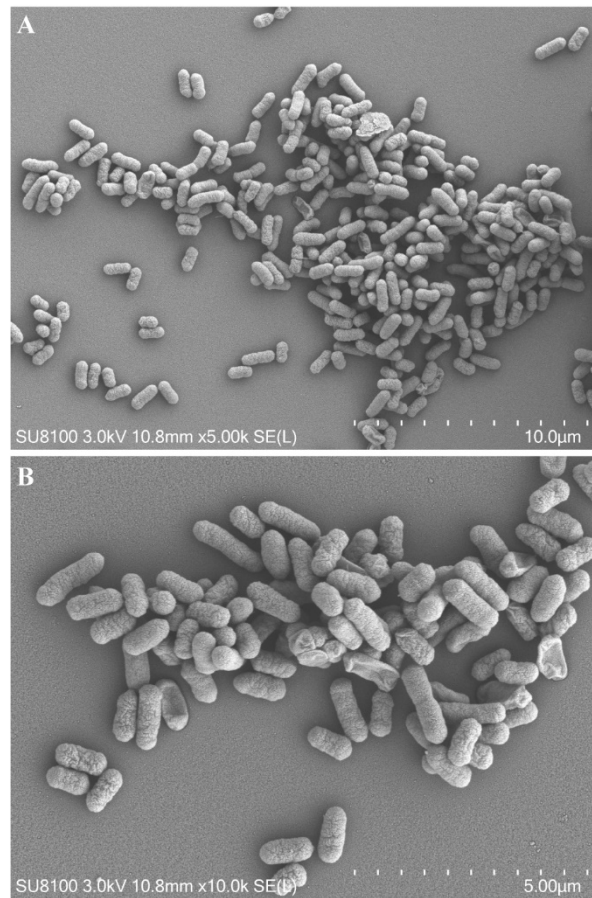
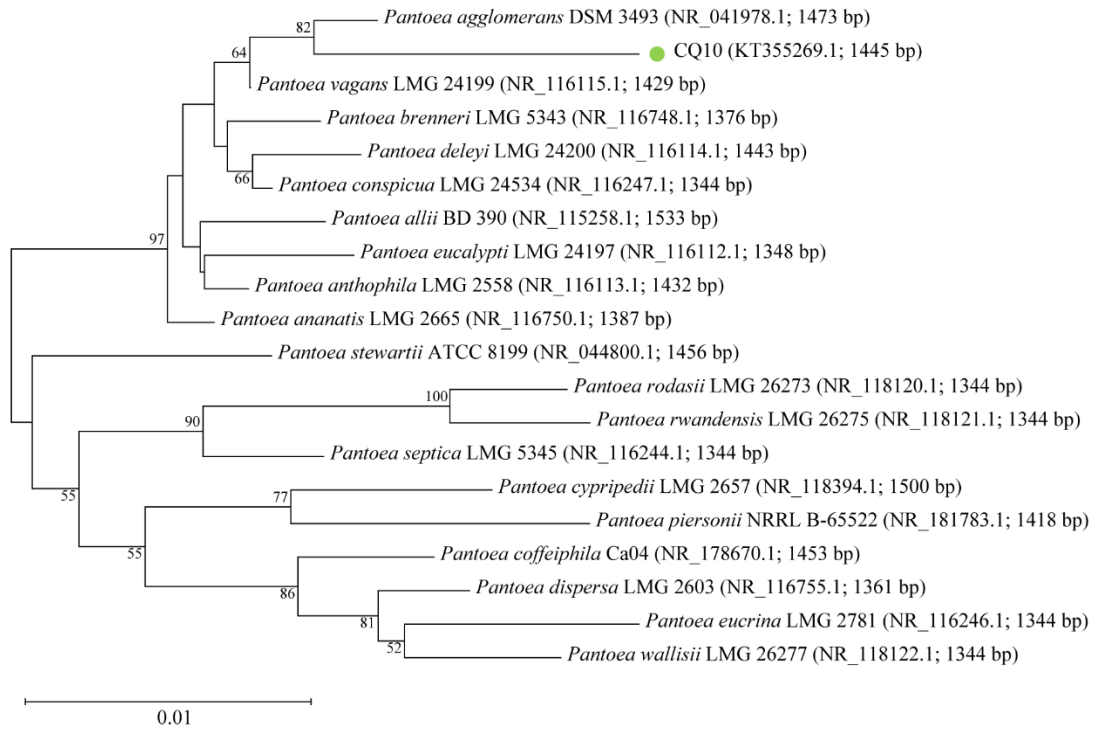


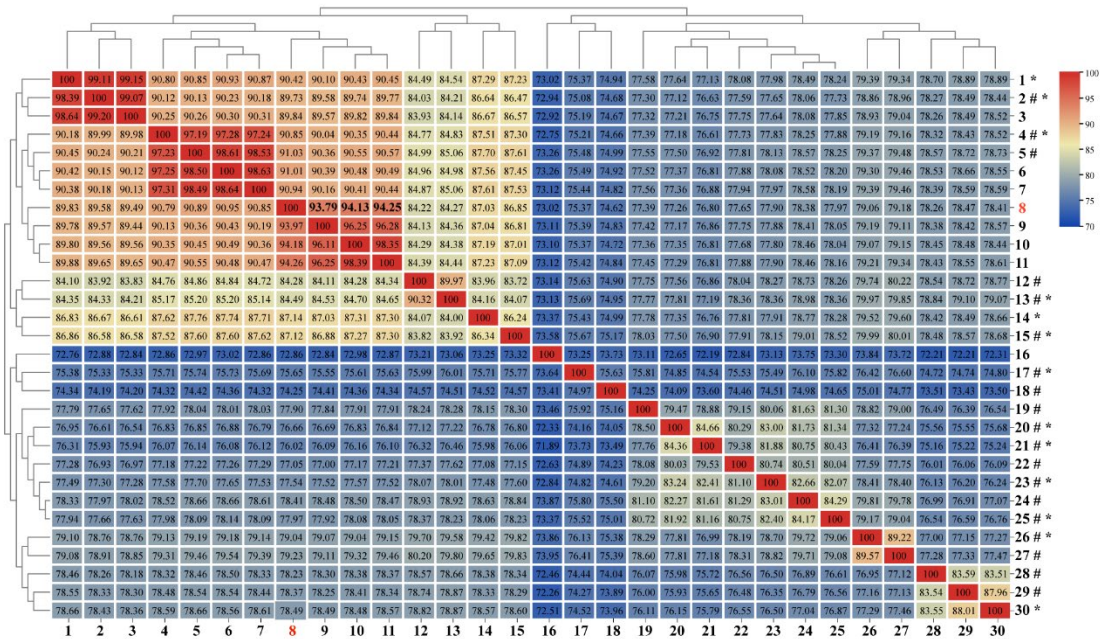
**Figure S1** Photograph of colonial morphology of strain CQ10 grown on LB agar plates (A) NB agar plates (B) and TSB agar plates (C) for 48 h at 30°C. Single colony of strain CQ10 on (D) LB agar plates, (E) NB agar plates, and (F) TSB agar plates.



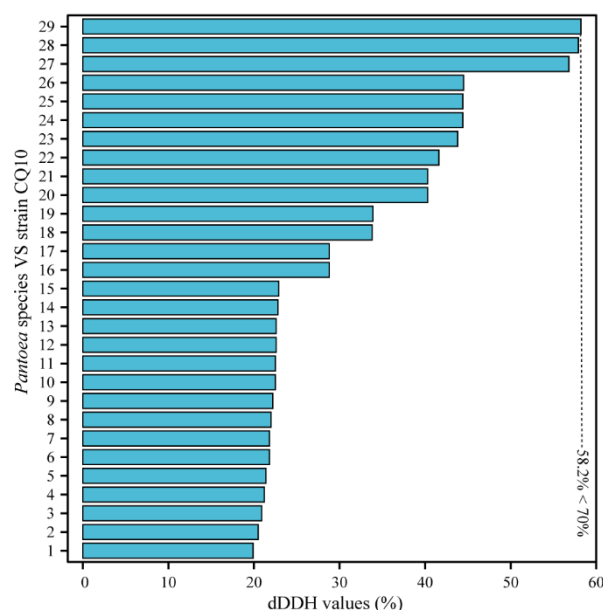
**Figure S2** Scanning electron microscopy (SEM) imaging of strain CQ10. (A) Scale bar = 10.0  $\mu$ M. (B) Scale bar = 5.0  $\mu$ M.



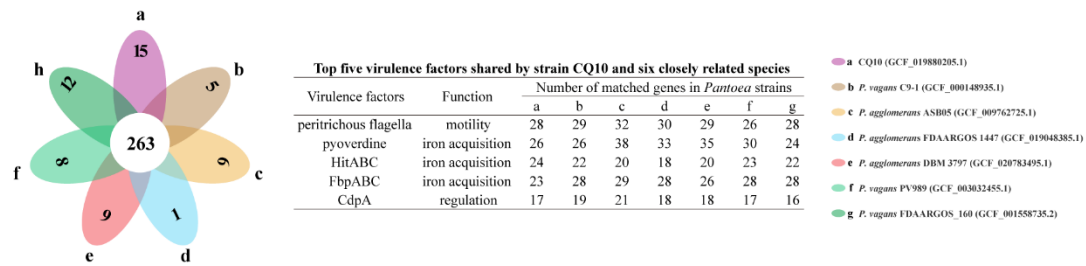
**Figure S3** Neighbor-Joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between strain CQ10 and closely related 19 species (GenBank accession numbers and sequence lengths of the nucleotide sequences are given in parentheses). Numbers at branching points are bootstrap values > 50% (1000 replicates). Bar, 0.01 substitution per site. Green spot indicates strain CQ10. Evolutionary analyses were conducted in MEGA11.



**Figure S4** Heatmap showing ANI (average nucleotide identity) of representative *Pantoea* species. Numbers 1-30 represent *Pantoea* strains: <sup>1</sup>*P. hericii* JZB 2120024, <sup>2</sup>*P. eucalypti* LMG 24197, <sup>3</sup>*P. jilinensis* D25, <sup>4</sup>*P. pleuroti* JZB 2120015, <sup>5</sup>*P. agglomerans* FDAARGOS 1447, <sup>6</sup>*P. agglomerans* ASB05, <sup>7</sup>*P. agglomerans* DBM 3797, <sup>8</sup>CQ10, <sup>9</sup>*P. vagans* FDAARGOS\_160, <sup>10</sup>*P. vagans* C9-1, <sup>11</sup>*P. vagans* PV989, <sup>12</sup>*P. brenneri* IIFCSG-B1, <sup>13</sup>*P. conspicua* LMG 24534, <sup>14</sup>*P. anthophila* LMG 2558, <sup>15</sup>*P. deleyi* LMG 24200, <sup>16</sup>*P. sesami* Si-M154, <sup>17</sup>*P. alhagi* LTYR-11Z, <sup>18</sup>*P. coffeiphila* 1480, <sup>19</sup>*P. eucrinea* XL123, <sup>20</sup>*P. rodasii* DSM 26611, <sup>21</sup>*P. rwandensis* LMG 26275, <sup>22</sup>*P. cypripedii* WS4375, <sup>23</sup>*P. endophytica* 596, <sup>24</sup>*P. dispersa* Lsch, <sup>25</sup>*P. wallisii* LMG 26277, <sup>26</sup>*P. latae* AS1, <sup>27</sup>*P. septica* MGYG-HGUT-02423, <sup>28</sup>*P. stewartii* ZJ-FGZX1, <sup>29</sup>*P. allii* PNA 200-10, <sup>30</sup>*P. ananatis* LMG 2665. # Represents reference genome in the NCBI genome database, \* represents type strain.



**Figure S5** Analysis of the digital DNA-DNA hybridisation (dDDH, species cut-off  $\geq 70\%$ ) values of strain CQ10 versus 29 *Pantoea* species. Numbers 1-29 indicates: <sup>1</sup>*P. sesami* Si-M154, <sup>2</sup>*P. coffeiphila* 1480, <sup>3</sup>*P. alhagi* LTYR-11Z, <sup>4</sup>*P. rwandensis* LMG 26275, <sup>5</sup>*P. rodasii* DSM 26611, <sup>6</sup>*P. endophytica* 596, <sup>7</sup>*P. eucrina* XL123, <sup>8</sup>*P. cypripedii* WS4375, <sup>9</sup>*P. wallisii* LMG 26277, <sup>10</sup>*P. allii* PNA 200-10, <sup>11</sup>*P. ananatis* LMG 2665, <sup>12</sup>*P. dispersa* Lsch, <sup>13</sup>*P. stewartii* ZJ-FGZX1, <sup>14</sup>*P. latae* AS1, <sup>15</sup>*P. septica* MGYG-HGUT-02423, <sup>16</sup>*P. brenneri* IIFCSG-B1, <sup>17</sup>*P. conspicua* LMG 24534, <sup>18</sup>*P. deleyi* LMG 24200, <sup>19</sup>*P. anthophila* LMG 2558, <sup>20</sup>*P. eucalypti* LMG 24197, <sup>21</sup>*P. jilinensis* D25, <sup>22</sup>*P. hericii* JZB 2120024, <sup>23</sup>*P. pleuroti* JZB 2120015, <sup>24</sup>*P. agglomerans* ASB05, <sup>25</sup>*P. agglomerans* DBM 3797, <sup>26</sup>*P. agglomerans* FDAARGOS 1447, <sup>27</sup>*P. vagans* FDAARGOS\_160, <sup>28</sup>*P. vagans* C9-1, <sup>29</sup>*P. vagans* PV989.



**Figure S6** Petal diagram of virulence factors of *Pantoea* strains. The numbers of common virulence factors in seven *Pantoea* strains was represented in the center and unique virulence factors in the petals. Latest Refseq accession numbers for strains are indicated in the legend in parentheses.

**Table S1** General genome features of strain CQ10

| Feature    | Size (bp) | GC content (%) | CDS  | tRNAs | rRNAs | misc_RNAs | tmRNAs |
|------------|-----------|----------------|------|-------|-------|-----------|--------|
| Chromosome | 3,973,606 | 55.45          | 3591 | 78    | 22    | 82        | 1      |
| Plasmid 1  | 235,469   | 51.92          | 234  | 0     | 0     | 1         | 0      |
| Plasmid 2  | 160,986   | 52.33          | 136  | 0     | 0     | 0         | 0      |
| Plasmid 3  | 143,561   | 52.57          | 140  | 0     | 0     | 1         | 0      |
| Plasmid 4  | 137,838   | 55.59          | 120  | 0     | 0     | 2         | 0      |
| Plasmid 5  | 89,114    | 50.72          | 99   | 3     | 0     | 2         | 0      |
| Plasmid 6  | 4,424     | 40.71          | 5    | 0     | 0     | 0         | 0      |
| Plasmid 7  | 2,709     | 62.24          | 4    | 0     | 0     | 0         | 0      |
| Plasmid 8  | 2,495     | 47.82          | 1    | 0     | 0     | 0         | 0      |

**Table S2** COG classification of CQ10 genes

| Category code | Category name   | CQ10 gene number | Percentage (%) |
|---------------|---|------------------|----------------|
| E             | Amino acid transport and metabolism                             | 295              | 11.29%         |
| G             | Carbohydrate transport and metabolism                           | 234              | 8.96%          |
| J             | Translation, ribosomal structure and biogenesis                 | 210              | 8.04%          |
| M             | Cell wall/membrane/envelope biogenesis                          | 190              | 7.27%          |
| C             | Energy production and conversion                                | 181              | 6.93%          |
| P             | Inorganic ion transport and metabolism                          | 173              | 6.62%          |
| K             | Transcription   | 151              | 5.78%          |
| R             | General function prediction only                                | 150              | 5.74%          |
| H             | Coenzyme transport and metabolism                               | 143              | 5.47%          |
| S             | Function unknown  | 134              | 5.13%          |
| T             | Signal transduction mechanisms                                  | 116              | 4.44%          |
| L             | Replication, recombination and repair                           | 113              | 4.33%          |
| O             | Posttranslational modification, protein turnover,<br>chaperones | 106              | 4.06%          |
| F             | Nucleotide transport and metabolism                             | 89               | 3.41%          |
| I             | Lipid transport and metabolism                                  | 80               | 3.06%          |
| N             | Cell motility   | 78               | 2.99%          |
| V             | Defense mechanisms  | 56               | 2.14%          |
| D             | Cell cycle control, cell division, chromosome<br>partitioning   | 43               | 1.65%          |
| Q             | Secondary metabolites biosynthesis, transport and<br>catabolism | 38               | 1.45%          |
| U             | Intracellular trafficking, secretion, and vesicular transport   | 27               | 1.03%          |
| W             | Extracellular structures  | 2                | 0.08%          |
| X             | Mobilome: prophages, transposons                                | 2                | 0.08%          |
| A             | RNA processing and modification                                 | 1                | 0.04%          |



**Table S3** The ANI and dDDH values between strain CQ10 and other *Pantoea* species

| Species                                  | ANI (%) | dDDH (%) |
|--|---------|----------|
| <i>Pantoea vagans</i> PV989              | 94.25   | 58.2     |
| <i>Pantoea vagans</i> C9-1               | 94.13   | 57.9     |
| <i>Pantoea vagans</i> FDAARGOS_160       | 93.79   | 56.8     |
| <i>Pantoea agglomerans</i> ASB05         | 90.95   | 44.4     |
| <i>Pantoea agglomerans</i> FDAARGOS 1447 | 90.89   | 44.5     |
| <i>Pantoea agglomerans</i> DBM 3797      | 90.85   | 44.4     |
| <i>Pantoea pleuroti</i> JZB 2120015      | 90.79   | 43.8     |
| <i>Pantoea hericii</i> JZB2120024        | 89.83   | 41.6     |
| <i>Pantoea eucalypti</i> LMG 24197       | 89.58   | 40.3     |
| <i>Pantoea jilinensis</i> D25            | 89.49   | 40.3     |
| <i>Pantoea anthophila</i> LMG 2558       | 87.03   | 33.9     |
| <i>Pantoea deleyi</i> LMG 24200          | 86.85   | 33.8     |
| <i>Pantoea conspicua</i> LMG 24534       | 84.27   | 28.8     |
| <i>Pantoea brenneri</i> IIFCSG-B1        | 84.22   | 28.8     |
| <i>Pantoea septica</i> MGYG-HGUT-02423   | 79.18   | 22.9     |
| <i>Pantoea latae</i> AS1                 | 79.06   | 22.8     |
| <i>Pantoea allii</i> PNA 200-10          | 78.47   | 22.5     |
| <i>Pantoea ananatis</i> LMG 2665         | 78.41   | 22.5     |
| <i>Pantoea dispersa</i> Lsch             | 78.38   | 22.6     |
| <i>Pantoea stewartii</i> ZJ-FGZX1        | 78.26   | 22.6     |
| <i>Pantoea wallisii</i> LMG 26277        | 77.97   | 22.2     |
| <i>Pantoea endophytica</i> 596           | 77.9    | 21.8     |
| <i>Pantoea cypripedii</i> WS4375         | 77.65   | 22       |
| <i>Pantoea eucrina</i> XL123             | 77.39   | 21.8     |
| <i>Pantoea rodasii</i> DSM 26611         | 77.26   | 21.4     |
| <i>Pantoea rwandensis</i> LMG 26275      | 76.8    | 21.2     |
| <i>Pantoea alhagi</i> LTYR-11Z           | 75.37   | 20.9     |
| <i>Pantoea coffeiphila</i> 1480          | 74.62   | 20.5     |
| <i>Pantoea sesami</i> Si-M154            | 73.02   | 19.9     |

**Table S4** Correlation analysis of physiological indices in roots, stems, and leaves of alfalfa

| PI  | RPI        | Correlation | Absolute value of r | Significance | SPI        | Correlation | Absolute value of r | Significance | LPI        | Correlation | Absolute value of r | Significance |
|-----|------------|-------------|---------------------|--------------|------------|-------------|---------------------|--------------|------------|-------------|---------------------|--------------|
| SOD | <b>PAL</b> | -           | <b>0.83</b>         | *            | <b>PAL</b> | -           | <b>0.94</b>         | **           | <b>PAL</b> | +           | <b>0.94</b>         | **           |
|     | MDA        | -           | 0.89                | *            | MDA        | -           | 0.94                | **           | CAT        | -           | 0.89                | *            |
|     | <b>APX</b> | +           | <b>0.94</b>         | **           | <b>POD</b> | +           | <b>0.83</b>         | *            | <b>POD</b> | -           | <b>0.83</b>         | *            |
|     | SP         | +           | 0.83                | *            | PPO        | -           | 1.00                | ***          | SS         | +           | 1.00                | ***          |
| CAT | PPO        | +           | 0.83                | *            | PPO        | -           | 0.94                | **           | SOD        | -           | 0.89                | *            |
|     | <b>SS</b>  | +           | <b>0.94</b>         | **           | <b>SP</b>  | +           | <b>0.83</b>         | *            | <b>SS</b>  | -           | <b>0.89</b>         | *            |
|     | /          | /           | /                   | /            | PAL        | -           | 0.83                | *            | PAL        | -           | 0.94                | **           |
|     | /          | /           | /                   | /            | MDA        | -           | 0.89                | *            | POD        | +           | 0.89                | *            |
| APX | <b>POD</b> | +           | <b>0.89</b>         | *            | POD        | +           | 0.89                | *            | MDA        | +           | 0.94                | **           |
|     | SOD        | +           | 0.94                | **           | SP         | +           | 0.94                | **           | SP         | -           | 0.94                | **           |
|     | /          | /           | /                   | /            | /          | /           | /                   | /            | PPO        | -           | 0.83                | *            |
| POD | APX        | +           | 0.89                | *            | APX        | +           | 0.89                | *            | CAT        | +           | 0.89                | *            |
|     | /          | /           | /                   | /            | SOD        | +           | 0.83                | *            | SOD        | -           | 0.83                | *            |
|     | /          | /           | /                   | /            | SP         | +           | 0.94                | **           | SS         | -           | 0.83                | *            |
|     | /          | /           | /                   | /            | PPO        | -           | 0.83                | *            | PAL        | -           | 0.94                | **           |
| MDA | SOD        | -           | 0.89                | *            | SOD        | -           | 0.94                | **           | APX        | +           | 0.94                | **           |
|     | <b>SP</b>  | -           | <b>0.89</b>         | *            | <b>CAT</b> | -           | <b>0.89</b>         | *            | <b>SP</b>  | -           | <b>1.00</b>         | ***          |
|     | PAL        | +           | 0.83                | *            | /          | /           | /                   | /            | /          | /           | /                   | /            |
| PAL | SOD        | -           | 0.83                | *            | SOD        | -           | 0.94                | **           | SOD        | +           | 0.94                | **           |
|     | MDA        | +           | 0.83                | *            | CAT        | -           | 0.83                | *            | CAT        | -           | 0.94                | **           |
|     | SP         | -           | 0.89                | *            | /          | /           | /                   | /            | POD        | -           | 0.94                | **           |
|     | /          | /           | /                   | /            | /          | /           | /                   | /            | SS         | +           | 0.94                | **           |

**Table S4** Correlation analysis of physiological indices in roots, stems, and leaves of alfalfa (continued)

| PI  | RPI | Correlation | Absolute value of r | Significance | SPI | Correlation | Absolute value of r | Significance | LPI | Correlation | Absolute value of r | Significance |
|-----|-----|-------------|---------------------|--------------|-----|-------------|---------------------|--------------|-----|-------------|---------------------|--------------|
| PPO | CAT | +           | 0.83                | *            | CAT | -           | 0.94                | **           | APX | -           | 0.83                | *            |
|     | /   | /           | /                   | /            | SOD | -           | 1.00                | ***          | /   | /           | /                   | /            |
|     | /   | /           | /                   | /            | POD | -           | 0.83                | *            | /   | /           | /                   | /            |
| SS  | CAT | +           | 0.94                | **           | SP  | -           | 0.83                | *            | CAT | -           | 0.89                | *            |
|     | /   | /           | /                   | /            | /   | /           | /                   | /            | SOD | +           | 1.00                | ***          |
|     | /   | /           | /                   | /            | /   | /           | /                   | /            | PAL | +           | 0.94                | **           |
|     | /   | /           | /                   | /            | /   | /           | /                   | /            | POD | -           | 0.83                | *            |
| SP  | SOD | +           | 0.83                | *            | APX | +           | 0.94                | **           | APX | -           | 0.94                | **           |
|     | MDA | -           | 0.89                | *            | POD | +           | 0.94                | **           | MDA | -           | 1.00                | ***          |
|     | PAL | -           | 0.89                | *            | CAT | +           | 0.83                | *            | /   | /           | /                   | /            |
|     | /   | /           | /                   | /            | SS  | -           | 0.83                | *            | /   | /           | /                   | /            |

PI, physiological indices; RPI, root physiological indices; SPI, stem physiological indices; LPI, leaf physiological indices. + represent positive correlation, - represent negative correlation, r represent correlation coefficient. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .

**Table S5** COG classification of core genes in each orthologous group

| COG Categories                     | COG Subcategories   | Category code | Number of Matched Genes | Percentage (%) |
|------------------------------------|---|---------------|-------------------------|----------------|
| Poorly characterized               | Function unknown  | S             | 703                     | 19.41          |
| Metabolism                         | Amino acid transport and metabolism                           | E             | 325                     | 8.98           |
|                                    | Inorganic ion transport and metabolism                        | P             | 316                     | 8.73           |
|                                    | Carbohydrate transport and metabolism                         | G             | 278                     | 7.68           |
|                                    | Energy production and conversion                              | C             | 214                     | 5.91           |
|                                    | Coenzyme transport and metabolism                             | H             | 193                     | 5.33           |
|                                    | Nucleotide transport and metabolism                           | F             | 98                      | 2.71           |
|                                    | Lipid transport and metabolism                                | I             | 96                      | 2.65           |
|                                    | Secondary metabolites biosynthesis, transport and catabolism  | Q             | 56                      | 1.55           |
| Cellular processes and signaling   | Cell wall/membrane/envelope biogenesis                        | M             | 223                     | 6.16           |
|                                    | Signal transduction mechanisms                                | T             | 140                     | 3.87           |
|                                    | Posttranslational modification, protein turnover, chaperones  | O             | 98                      | 2.71           |
|                                    | Cell motility   | N             | 91                      | 2.51           |
|                                    | Intracellular trafficking, secretion, and vesicular transport | U             | 86                      | 2.38           |
|                                    | Cell cycle control, cell division, chromosome partitioning    | D             | 50                      | 1.38           |
|                                    | Defense mechanisms  | V             | 38                      | 1.05           |
| Information storage and processing | Transcription   | K             | 303                     | 8.37           |
|                                    | Translation, ribosomal structure and biogenesis               | J             | 183                     | 5.05           |
|                                    | Replication, recombination and repair                         | L             | 130                     | 3.59           |

**Table S6** COG classification of strain unique genes in each orthologous group

| COG Categories                     | COG Subcategories   | Category code | a    |      | b    |      | c    |      | d    |      |
|------------------------------------|---|---------------|------|------|------|------|------|------|------|------|
|                                    |   |               | Num. | Pct. | Num. | Pct. | Num. | Pct. | Num. | Pct. |
| Poorly characterized               | Function unknown  | S             | 1    | 3.8  | 7    | 19.4 | 9    | 18.4 | 18   | 27.3 |
| Metabolism                         | Amino acid transport and metabolism                           | E             | 1    | 3.8  | 1    | 2.8  | 1    | 2.0  | 3    | 4.5  |
|                                    | Inorganic ion transport and metabolism                        | P             | 3    | 11.5 | 0    | 0.0  | 0    | 0.0  | 2    | 3.0  |
|                                    | Carbohydrate transport and metabolism                         | G             | 2    | 7.7  | 3    | 8.3  | 1    | 2.0  | 3    | 4.5  |
|                                    | Energy production and conversion                              | C             | 1    | 3.8  | 0    | 0.0  | 2    | 4.1  | 2    | 3.0  |
|                                    | Coenzyme transport and metabolism                             | H             | 2    | 7.7  | 0    | 0.0  | 0    | 0.0  | 3    | 4.5  |
|                                    | Nucleotide transport and metabolism                           | F             | 1    | 3.8  | 3    | 8.3  | 1    | 2.0  | 1    | 1.5  |
|                                    | Lipid transport and metabolism                                | I             | 1    | 3.8  | 1    | 2.8  | 1    | 2.0  | 6    | 9.1  |
|                                    | Secondary metabolites biosynthesis, transport and catabolism  | Q             | 2    | 7.7  | 1    | 2.8  | 1    | 2.0  | 5    | 7.6  |
| Cellular processes and signaling   | Cell wall/membrane/envelope biogenesis                        | M             | 2    | 7.7  | 2    | 5.6  | 3    | 6.1  | 4    | 6.1  |
|                                    | Signal transduction mechanisms                                | T             | 1    | 3.8  | 1    | 2.8  | 1    | 2.0  | 2    | 3.0  |
|                                    | Posttranslational modification, protein turnover, chaperones  | O             | 2    | 7.7  | 0    | 0.0  | 0    | 0.0  | 2    | 3.0  |
|                                    | Cell motility   | N             | 1    | 3.8  | 1    | 2.8  | 1    | 2.0  | 0    | 0.0  |
|                                    | Intracellular trafficking, secretion, and vesicular transport | U             | 2    | 7.7  | 0    | 0.0  | 2    | 4.1  | 0    | 0.0  |
|                                    | Cell cycle control, cell division, chromosome partitioning    | D             | 1    | 3.8  | 1    | 2.8  | 1    | 2.0  | 2    | 3.0  |
|                                    | Defense mechanisms  | V             | 0    | 0.0  | 2    | 5.6  | 7    | 14.3 | 2    | 3.0  |
| Information storage and processing | Transcription   | K             | 2    | 7.7  | 7    | 19.4 | 9    | 18.4 | 6    | 9.1  |
|                                    | Translation, ribosomal structure and biogenesis               | J             | 0    | 0.0  | 0    | 0.0  | 1    | 2.0  | 0    | 0.0  |
|                                    | Replication, recombination and repair                         | L             | 1    | 3.8  | 6    | 16.7 | 8    | 16.3 | 5    | 7.6  |

**Table S6** COG classification of strain unique genes in each orthologous group (continued)

| COG Categories                     | COG Subcategories   | Category code | e    |      | f    |      | g    |      | h    |      |
|------------------------------------|---|---------------|------|------|------|------|------|------|------|------|
|                                    |   |               | Num. | Pct. | Num. | Pct. | Num. | Pct. | Num. | Pct. |
| Poorly characterized               | Function unknown  | S             | 26   | 22.6 | 55   | 41.0 | 51   | 35.4 | 69   | 36.7 |
| Metabolism                         | Amino acid transport and metabolism                           | E             | 11   | 9.6  | 8    | 6.0  | 2    | 1.4  | 16   | 8.5  |
|                                    | Inorganic ion transport and metabolism                        | P             | 8    | 7.0  | 8    | 6.0  | 0    | 0.0  | 13   | 6.9  |
|                                    | Carbohydrate transport and metabolism                         | G             | 10   | 8.7  | 12   | 9.0  | 5    | 3.5  | 8    | 4.3  |
|                                    | Energy production and conversion                              | C             | 2    | 1.7  | 3    | 2.2  | 1    | 0.7  | 6    | 3.2  |
|                                    | Coenzyme transport and metabolism                             | H             | 3    | 2.6  | 3    | 2.2  | 0    | 0.0  | 4    | 2.1  |
|                                    | Nucleotide transport and metabolism                           | F             | 4    | 3.5  | 1    | 0.7  | 2    | 1.4  | 2    | 1.1  |
|                                    | Lipid transport and metabolism                                | I             | 2    | 1.7  | 3    | 2.2  | 8    | 5.6  | 3    | 1.6  |
|                                    | Secondary metabolites biosynthesis, transport and catabolism  | Q             | 4    | 3.5  | 3    | 2.2  | 2    | 1.4  | 1    | 0.5  |
| Cellular processes and signaling   | Cell wall/membrane/envelope biogenesis                        | M             | 2    | 1.7  | 2    | 1.5  | 15   | 10.4 | 8    | 4.3  |
|                                    | Signal transduction mechanisms                                | T             | 6    | 5.2  | 7    | 5.2  | 0    | 0.0  | 10   | 5.3  |
|                                    | Posttranslational modification, protein turnover, chaperones  | O             | 2    | 1.7  | 2    | 1.5  | 6    | 4.2  | 4    | 2.1  |
|                                    | Cell motility   | N             | 4    | 3.5  | 2    | 1.5  | 5    | 3.5  | 5    | 2.7  |
|                                    | Intracellular trafficking, secretion, and vesicular transport | U             | 4    | 3.5  | 3    | 2.2  | 13   | 9.0  | 8    | 4.3  |
|                                    | Cell cycle control, cell division, chromosome partitioning    | D             | 1    | 0.9  | 1    | 0.7  | 2    | 1.4  | 2    | 1.1  |
|                                    | Defense mechanisms  | V             | 2    | 1.7  | 3    | 2.2  | 9    | 6.3  | 2    | 1.1  |
| Information storage and processing | Transcription   | K             | 9    | 7.8  | 14   | 10.4 | 12   | 8.3  | 20   | 10.6 |
|                                    | Translation, ribosomal structure and biogenesis               | J             | 4    | 3.5  | 0    | 0.0  | 1    | 0.7  | 0    | 0.0  |
|                                    | Replication, recombination and repair                         | L             | 11   | 9.6  | 4    | 3.0  | 10   | 6.9  | 7    | 3.7  |

Num. represent number of matched core genes. Pct. represent percentage (%). a, *Pantoea alfaiae* CQ10. b, *Pantoea agglomerans* FDAARGOS 1447. c, *Pantoea agglomerans* DBM 3797. d, *Pantoea agglomerans* ASB05. e, *Pantoea vagans* C9-1. f, *Pantoea pleuroti* JZB 2120015. g, *Pantoea vagans* PV989. h, *Pantoea vagans* FDAARGOS\_160.

**Table S7** The collinearity analysis of the strain CQ10 genome and the closest *Pantoea* genomes

| Query Species                            | Query sequence location | Subject sequence location | Number of collinearity region | Percentage of total collinearity region (%) |
|--|-------------------------|---------------------------|-------------------------------|---|
| <i>Pantoea agglomerans</i> DBM 3797      | Chromosome              |                           | 2199                          |   |
|  | Plasmid pPA_DBM3797_1   | Chromosome_CQ10           | 60                            | 93.66                                       |
|  | Plasmid pPA_DBM3797_2   |                           | 1                             |   |
|  | Chromosome              |                           | 3                             |   |
|  | Plasmid pPA_DBM3797_1   | Plasmid p1_CQ10           | 49                            | 2.20  |
|  | Plasmid pPA_DBM3797_2   |                           | 1                             |   |
|  | Chromosome              | Plasmid p2_CQ10           | 2                             | 1.28  |
|  | Plasmid pPA_DBM3797_2   |                           | 29                            |   |
|  | Chromosome              |                           | 8                             |   |
|  | Plasmid pPA_DBM3797_1   | Plasmid p3_CQ10           | 22                            | 1.28  |
|  | Plasmid pPA_DBM3797_2   |                           | 1                             |   |
|  | Chromosome              | Plasmid p4_CQ10           | 21                            | 1.37  |
|  | Plasmid pPA_DBM3797_1   |                           | 12                            |   |
|  | Chromosome              | Plasmid p5_CQ10           | 1                             | 0.08  |
|  | Plasmid pPA_DBM3797_2   |                           | 1                             |   |
|  | Chromosome              | Plasmid p6_CQ10           | 1                             | 0.04  |
|  | Plasmid pPA_DBM3797_1   | Plasmid p8_CQ10           | 2                             | 0.08  |
| <i>Pantoea agglomerans</i> FDAARGOS 1447 | Chromosome              |                           | 2190                          |   |
|  | Plasmid unnamed1        | Chromosome_CQ10           | 2                             | 93.89                                       |
|  | Plasmid unnamed2        |                           | 53                            |   |
|  | Chromosome              |                           | 5                             |   |
|  | Plasmid unnamed1        | Plasmid p1_CQ10           | 1                             | 2.17  |
|  | Plasmid unnamed2        |                           | 46                            |   |

**Table S7** The collinearity analysis of the strain CQ10 genome and the closest *Pantoea* genomes (continued)

| Query Species                            | Query sequence location | Subject sequence location | Number of collinearity region | Percentage of total collinearity region |
|--|-------------------------|---------------------------|-------------------------------|---|
| <i>Pantoea agglomerans</i> FDAARGOS 1447 | Chromosome              | Plasmid p2_CQ10           | 3                             | 1.30                                    |
|  | Plasmid unnamed1        |                           | 28                            |   |
|  | Chromosome              | Plasmid p3_CQ10           | 7                             | 1.30                                    |
|  | Plasmid unnamed1        |                           | 2                             |   |
|  | Plasmid unnamed2        |                           | 22                            |   |
|  | Chromosome              | Plasmid p4_CQ10           | 17                            | 1.17                                    |
|  | Plasmid unnamed2        |                           | 11                            |   |
|  | Plasmid unnamed1        | Plasmid p5_CQ10           | 2                             | 0.13                                    |
|  | Plasmid unnamed2        |                           | 1                             |   |
|  | Plasmid unnamed2        | Plasmid p8_CQ10           | 1                             | 0.04                                    |
| <i>Pantoea agglomerans</i> ASB05         | Chromosome              | Chromosome_CQ10           | 2162                          | 93.43                                   |
|  | Plasmid pASB05p1        |                           | 9                             |   |
|  | Plasmid pASB05p2        |                           | 2                             |   |
|  | Plasmid pASB05p3        |                           | 2                             |   |
|  | Chromosome              | Plasmid p1_CQ10           | 3                             | 2.19                                    |
|  | Plasmid pASB05p1        |                           | 47                            |   |
|  | Plasmid pASB05p2        |                           | 1                             |   |
|  | Chromosome              | Plasmid p2_CQ10           | 1                             | 1.29                                    |
|  | Plasmid pASB05p2        |                           | 29                            |   |
|  | Chromosome              | Plasmid p3_CQ10           | 8                             | 1.25                                    |
|  | Plasmid pASB05p1        |                           | 19                            |   |
|  | Plasmid pASB05p2        |                           | 1                             |   |
|  | Plasmid pASB05p3        |                           | 1                             |   |



**Table S7** The collinearity analysis of the strain CQ10 genome and the closest *Pantoea* genomes (continued)

| Query Species                    | Query sequence location | Subject sequence location | Number of collinearity region | Percentage of total collinearity region |
|----------------------------------|-------------------------|---------------------------|-------------------------------|---|
| <i>Pantoea agglomerans</i> ASB05 | Chromosome              | Plasmid p4_CQ10           | 21                            | 1.33                                    |
|                                  | Plasmid pASB05p1        |                           | 10                            |   |
|                                  | Plasmid pASB05p2        | Plasmid p5_CQ10           | 3                             | 0.47                                    |
|                                  | Plasmid pASB05p3        |                           | 8                             |   |
|                                  | Plasmid pASB05p1        | Plasmid p8_CQ10           | 1                             | 0.04                                    |
| <i>Pantoea vagans</i> PV989      | Chromosome              | Chromosome_CQ10           | 2108                          | 94.75                                   |
|                                  | Plasmid pPV989-167      |                           | 3                             |   |
|                                  | Plasmid pPV989-508      |                           | 70                            |   |
|                                  | Plasmid pPV989-94       |                           | 1                             |   |
|                                  | Chromosome              | Plasmid p1_CQ10           | 2                             | 1.13                                    |
|                                  | Plasmid pPV989-508      |                           | 24                            |   |
|                                  | Chromosome              | Plasmid p2_CQ10           | 1                             | 1.17                                    |
|                                  | Plasmid pPV989-167      |                           | 25                            |   |
|                                  | Plasmid pPV989-508      |                           | 1                             |   |
|                                  | Chromosome              | Plasmid p3_CQ10           | 3                             | 1.22                                    |
|                                  | Plasmid pPV989-167      |                           | 1                             |   |
|                                  | Plasmid pPV989-508      |                           | 22                            |   |
|                                  | Plasmid pPV989-94       |                           | 2                             |   |
|                                  | Chromosome              | Plasmid p4_CQ10           | 22                            | 1.26                                    |
|                                  | Plasmid pPV989-508      |                           | 7                             |   |
|                                  | Plasmid pPV989-94       | Plasmid p5_CQ10           | 9                             | 0.39                                    |
|                                  | Plasmid pPV989-508      | Plasmid p8_CQ10           | 2                             | 0.09                                    |

**Table S7** The collinearity analysis of the strain CQ10 genome and the closest *Pantoea* genomes (continued)

| Query Species                      | Query sequence location | Subject sequence location | Number of collinearity region | Percentage of total collinearity region |
|------------------------------------|-------------------------|---------------------------|-------------------------------|---|
| <i>Pantoea vagans</i> FDAARGOS_160 | Chromosome              | Chromosome_CQ10           | 2112                          | 94.10                                   |
|                                    | Plasmid unnamed2        |                           | 9                             |   |
|                                    | Chromosome              | Plasmid p1_CQ10           | 1                             | 1.29                                    |
|                                    | Plasmid unnamed1        |                           | 1                             |   |
|                                    | Plasmid unnamed2        |                           | 27                            |   |
|                                    | Chromosome              | Plasmid p2_CQ10           | 3                             | 1.46                                    |
|                                    | Plasmid unnamed2        |                           | 1                             |   |
|                                    | Plasmid unnamed3        |                           | 29                            |   |
|                                    | Chromosome              | Plasmid p3_CQ10           | 4                             | 1.29                                    |
|                                    | Plasmid unnamed1        |                           | 1                             |   |
|                                    | Plasmid unnamed2        |                           | 24                            |   |
|                                    | Chromosome              | Plasmid p4_CQ10           | 12                            | 0.98                                    |
|                                    | Plasmid unnamed2        |                           | 10                            |   |
|                                    | Plasmid unnamed1        | Plasmid p5_CQ10           | 17                            | 0.80                                    |
|                                    | Plasmid unnamed3        |                           | 1                             |   |
|                                    | Plasmid unnamed2        | Plasmid p8_CQ10           | 2                             | 0.09                                    |
| <i>Pantoea vagans</i> C9-1         | Chromosome              | Chromosome_CQ10           | 1927                          | 94.32                                   |
|                                    | Plasmid pPag2           |                           | 3                             |   |
|                                    | Plasmid pPag3           |                           | 64                            |   |
|                                    | Chromosome              | Plasmid p1_CQ10           | 1                             | 1.32                                    |
|                                    | Plasmid pPag2           |                           | 2                             |   |
|                                    | Plasmid pPag3           |                           | 25                            |   |

**Table S7** The collinearity analysis of the strain CQ10 genome and the closest *Pantoea* genomes (continued)

| Query Species              | Query sequence location | Subject sequence location | Number of collinearity region | Percentage of total collinearity region |
|----------------------------|-------------------------|---------------------------|-------------------------------|---|
| <i>Pantoea vagans</i> C9-1 | Chromosome              |                           | 1                             |   |
|                            | Plasmid pPag1           | Plasmid p2_CQ10           | 24                            | 1.23                                    |
|                            | Plasmid pPag3           |                           | 1                             |   |
|                            | Chromosome              |                           | 3                             |   |
|                            | Plasmid pPag2           | Plasmid p3_CQ10           | 1                             | 1.14                                    |
|                            | Plasmid pPag3           |                           | 20                            |   |
|                            | Chromosome              | Plasmid p4_CQ10           | 20                            |   |
|                            | Plasmid pPag3           |                           | 7                             | 1.28                                    |
|                            | Plasmid pPag2           | Plasmid p5_CQ10           | 12                            | 0.57                                    |
|                            | Chromosome              | Plasmid p6_CQ10           | 1                             | 0.05                                    |
|                            | Plasmid pPag3           | Plasmid p8_CQ10           | 2                             | 0.09                                    |

**Table S8** Analysis of unique virulence factors for strain CQ10 and other species of genus *Pantoea*

| Species                          | Location of the query sequence | Start   | End     | VFs                     | Function                                     |
|----------------------------------|--------------------------------|---------|---------|-------------------------|--|
| CQ10                             | chromosome                     | 802581  | 803135  | F1C fimbriae            | Biofilm                                      |
|                                  | chromosome                     | 804018  | 806624  | Type 1 fimbriae         | Biofilm                                      |
|                                  | chromosome                     | 806664  | 807623  | Type 3 fimbriae         | Biofilm                                      |
|                                  | chromosome                     | 1197506 | 1199890 | F1 antigen              | Immune modulation                            |
|                                  | chromosome                     | 1199944 | 1200651 | Haemagglutinating pili  | Adherence                                    |
|                                  | chromosome                     | 1670197 | 1671402 | Flagella                | Motility                                     |
|                                  | chromosome                     | 2065798 | 2066361 | Type 1 fimbriae         | Biofilm                                      |
|                                  | chromosome                     | 2066374 | 2067438 | Type 1 fimbriae         | Biofilm                                      |
|                                  | chromosome                     | 2071495 | 2072052 | Type 1 fimbriae         | Biofilm                                      |
|                                  | plasmid_1                      | 84815   | 86050   | CAI-1                   | Biofilm                                      |
|                                  | plasmid_1                      | 186711  | 188699  | Flagella                | Motility                                     |
|                                  | plasmid_3                      | 74875   | 76035   | MtrCDE                  | Antimicrobial activity/Competitive advantage |
|                                  | plasmid_4                      | 76819   | 77292   | Polar flagella          | Motility                                     |
|                                  | plasmid_5                      | 42803   | 44905   | Polar flagella          | Motility                                     |
|                                  | plasmid_6                      | 1864    | 2793    | Capsule                 | Immune modulation                            |
| <i>Pantoea agglomerans</i> ASB05 | chromosome                     | 443659  | 444432  | Exe T2SS                | Effector delivery system                     |
|                                  | chromosome                     | 619149  | 627734  | C $\beta$ G             | Immune modulation                            |
|                                  | plasmid_2                      | 160988  | 162469  | Pyoverdine              | Nutritional/Metabolic factor                 |
|                                  | plasmid_2                      | 169832  | 170695  | Phenazines biosynthesis | -  |
|                                  | plasmid_2                      | 170695  | 172524  | Phenazines biosynthesis | -  |
|                                  | plasmid_2                      | 172592  | 173221  | Phenazines biosynthesis | -  |
|                                  | plasmid_2                      | 173355  | 173831  | Phenazines biosynthesis | -  |
|                                  | plasmid_3                      | 39266   | 39889   | Polar flagella          | Motility                                     |
|                                  | plasmid_3                      | 55328   | 56044   | TcpC                    | Immune modulation                            |

**Table S8** Analysis of unique virulence factors for strain CQ10 and other species of genus *Pantoea* (continued)

| Species                                  | Location of the query sequence | Start   | End     | VFs   | Function                     |
|--|--------------------------------|---------|---------|---|------------------------------|
| <i>Pantoea agglomerans</i> DBM 3797      | chromosome                     | 2440903 | 2443026 | TTSS  | Effector delivery system     |
|  | chromosome                     | 2447277 | 2447930 | TTSS  | Effector delivery system     |
|  | chromosome                     | 2447938 | 2448198 | TTSS  | Effector delivery system     |
|  | chromosome                     | 2448198 | 2449013 | TTSS  | Effector delivery system     |
|  | chromosome                     | 2449010 | 2450095 | TTSS  | Effector delivery system     |
|  | chromosome                     | 3059010 | 3059513 | Afimbrial adhesin, AfaE-VIII                        | -                            |
|  | chromosome                     | 3059529 | 3062093 | Afimbrial adhesin, AFA-I, mannose-resistant adhesin | -                            |
|  | chromosome                     | 3062090 | 3062797 | Afimbrial adhesin, AfaE-VIII                        | -                            |
|  | plasmid_1                      | 147372  | 148892  | Lateral flagella                                    | Motility                     |
| <i>Pantoea agglomerans</i> FDAARGOS 1447 | chromosome                     | 3380417 | 3381889 | Capsule   | Immune modulation            |
| <i>Pantoea vagans</i> C9-1               | chromosome                     | 2057889 | 2058782 | Rhamnolipid biosynthesis                            | -                            |
|  | plasmid_1                      | 81144   | 82571   | Sat   | Effector delivery system     |
|  | plasmid_2                      | 33286   | 35376   | Aerobactin  | Nutritional/Metabolic factor |
|  | plasmid_2                      | 104268  | 106007  | pyoverdine  | Nutritional/Metabolic factor |
|  | plasmid_2                      | 109232  | 111055  | LPS   | Immune modulation            |
| <i>Pantoea vagans</i> FDAARGOS_160       | chromosome                     | 581583  | 584105  | F1C fimbriae  | Biofilm                      |
|  | chromosome                     | 3089419 | 3091341 | SpA   | Exotoxin                     |
|  | chromosome                     | 3555820 | 3556851 | Shu   | Nutritional/Metabolic factor |
|  | chromosome                     | 3539544 | 3540539 | Tap type IV pili                                    | Adherence                    |
|  | plasmid_1                      | 37370   | 37903   | LEE encoded T3SS                                    | -                            |
|  | plasmid_3                      | 32619   | 33635   | Yersiniabactin                                      | Nutritional/Metabolic factor |
|  | plasmid_3                      | 70496   | 72649   | TTSS  | Effector delivery system     |
|  | plasmid_3                      | 76831   | 77484   | TTSS  | Effector delivery system     |

**Table S8** Analysis of unique virulence factors for strain CQ10 and other species of genus *Pantoea* (continued)

| Species                            | Location of the query sequence | Start   | End     | VFs          | Function                 |
|------------------------------------|--------------------------------|---------|---------|--------------|--------------------------|
| <i>Pantoea vagans</i> FDAARGOS_160 | plasmid_3                      | 77492   | 77752   | T3SS1        | Effector delivery system |
|                                    | plasmid_3                      | 77755   | 78552   | TTSS         | Effector delivery system |
|                                    | plasmid_3                      | 78554   | 79636   | T3SS         | Effector delivery system |
|                                    | plasmid_3                      | 96830   | 100786  | Pic          | Effector delivery system |
| <i>Pantoea vagans</i> PV989        | chromosome                     | 3430499 | 3432181 | Flagella     | Motility                 |
|                                    | plasmid_167                    | 69950   | 73909   | Tsh          | Effector delivery system |
|                                    | plasmid_94                     | 39010   | 41196   | Dot/Icm T4SS | Effector delivery system |
|                                    | plasmid_94                     | 64994   | 66160   | Dot/Icm T4SS | Effector delivery system |
|                                    | plasmid_94                     | 67592   | 68986   | Type IV pili | Adherence                |
|                                    | plasmid_94                     | 70805   | 71920   | Type IV pili | Adherence                |
|                                    | plasmid_94                     | 71913   | 73436   | Type IV pili | Adherence                |
|                                    | plasmid_94                     | 75320   | 76951   | Type IV pili | Adherence                |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10

| PHI categories                       | Genes                | Numbers of matched genes in strain CQ10 |
|--------------------------------------|----------------------|---|
| increased virulence (hypervirulence) | raxB                 | 97                                      |
|                                      | kdpE                 | 56                                      |
|                                      | ShvR (BCAS0225)      | 37                                      |
|                                      | rcsC11               | 36                                      |
|                                      | bcam1160             | 34                                      |
|                                      | bcam1161             | 34                                      |
|                                      | MorA                 | 34                                      |
|                                      | rpfR (bcam0580)      | 33                                      |
|                                      | cdpA (bcal1069)      | 30                                      |
|                                      | tcrX                 | 29                                      |
|                                      | luxO                 | 28                                      |
|                                      | gigX4                | 26                                      |
|                                      | tlp2 (Cjj81176_0180) | 26                                      |
|                                      | gigX5                | 24                                      |
|                                      | THR                  | 24                                      |
|                                      | AlHK1                | 23                                      |
|                                      | bcal1635             | 23                                      |
|                                      | CovR                 | 23                                      |
|                                      | PmrA                 | 23                                      |
|                                      | QseB                 | 23                                      |
|                                      | atsR                 | 22                                      |
|                                      | ECA2008              | 22                                      |
|                                      | gcpA (Dda3937_03858) | 22                                      |
|                                      | tcrY                 | 22                                      |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes    | Numbers of matched genes in strain CQ10 |
|--------------------------------------|----------|---|
| increased virulence (hypervirulence) | bcal0430 | 21                                      |
|                                      | bcam1670 | 21                                      |
|                                      | bcam2256 | 21                                      |
|                                      | bcam2836 | 21                                      |
|                                      | ccpE     | 21                                      |
|                                      | kdpD     | 21                                      |
|                                      | raxR     | 21                                      |
|                                      | bcal0621 | 20                                      |
|                                      | bcal1975 | 20                                      |
|                                      | bcal2852 | 20                                      |
|                                      | bcam0748 | 20                                      |
|                                      | bcam1554 | 20                                      |
|                                      | bcam2822 | 20                                      |
|                                      | bcas0398 | 20                                      |
|                                      | BphP1    | 20                                      |
|                                      | egsB     | 20                                      |
|                                      | dgcA     | 20                                      |
|                                      | GdpX1    | 20                                      |
|                                      | bcal0652 | 19                                      |
|                                      | bcam0158 | 19                                      |
|                                      | bcam2426 | 19                                      |
|                                      | ssrB     | 19                                      |
|                                      | bcal1100 | 18                                      |
|                                      | CovRS    | 18                                      |



**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes                 | Numbers of matched genes in strain CQ10 |
|--------------------------------------|-----------------------|---|
| increased virulence (hypervirulence) | CovS                  | 18                                      |
|                                      | vraR                  | 16                                      |
|                                      | treS                  | 15                                      |
|                                      | BfiS                  | 13                                      |
|                                      | BfvR (YPO1737)        | 13                                      |
|                                      | glbC                  | 13                                      |
|                                      | PhoQ                  | 13                                      |
|                                      | raxH                  | 13                                      |
|                                      | App                   | 11                                      |
|                                      | dosR (devR)           | 11                                      |
|                                      | Opp                   | 11                                      |
|                                      | RpiRc                 | 11                                      |
|                                      | bcas0263              | 10                                      |
|                                      | LacR                  | 10                                      |
|                                      | GntR                  | 8                                       |
|                                      | hns                   | 8                                       |
|                                      | HxfA (PD_2118) (pspA) | 8                                       |
|                                      | VEDA_05196            | 8                                       |
|                                      | Lmo0866               | 7                                       |
|                                      | Lmo1246               | 6                                       |
|                                      | Lmo1450               | 6                                       |
|                                      | Lmo1722               | 6                                       |
|                                      | lon                   | 6                                       |
|                                      | lrp                   | 6                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes               | Numbers of matched genes in strain CQ10 |
|--------------------------------------|---------------------|---|
| increased virulence (hypervirulence) | PKS                 | 6                                       |
|                                      | raxQ                | 6                                       |
|                                      | rpfF                | 6                                       |
|                                      | spxB                | 6                                       |
|                                      | AOL_s00215g283      | 5                                       |
|                                      | EAMY_3025           | 5                                       |
|                                      | Ohmm                | 5                                       |
|                                      | pchD                | 5                                       |
|                                      | phuR                | 5                                       |
|                                      | VEDA_05198          | 5                                       |
|                                      | bcal2749            | 4                                       |
|                                      | EAMY_3224           | 4                                       |
|                                      | esaN                | 4                                       |
|                                      | Rv0462 (lpdC)       | 4                                       |
|                                      | Rv1773c             | 4                                       |
|                                      | Rv3213c             | 4                                       |
|                                      | sidN                | 4                                       |
|                                      | ymoA                | 4                                       |
|                                      | AS87_RS09170 (bioF) | 3                                       |
|                                      | bcas0378            | 3                                       |
|                                      | BfeA (PD_1198)      | 3                                       |
|                                      | Can2                | 3                                       |
|                                      | CD3284              | 3                                       |
|                                      | EAMY_3005           | 3                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes     | Numbers of matched genes in strain CQ10 |
|--------------------------------------|-----------|---|
| increased virulence (hypervirulence) | EAMY_3222 | 3                                       |
|                                      | gigX10    | 3                                       |
|                                      | htrA      | 3                                       |
|                                      | LysX      | 3                                       |
|                                      | mgtC      | 3                                       |
|                                      | PA3242    | 3                                       |
|                                      | pecS      | 3                                       |
|                                      | pknH      | 3                                       |
|                                      | ptsI      | 3                                       |
|                                      | raxC      | 3                                       |
|                                      | Rho       | 3                                       |
|                                      | UgeB      | 3                                       |
|                                      | adeN      | 2                                       |
|                                      | BcFKBP12  | 2                                       |
|                                      | bcsA      | 2                                       |
|                                      | CdpR      | 2                                       |
|                                      | crcI      | 2                                       |
|                                      | EAMY_3004 | 2                                       |
|                                      | EAMY_3010 | 2                                       |
|                                      | EAMY_3011 | 2                                       |
|                                      | EAMY_3012 | 2                                       |
|                                      | EAMY_3015 | 2                                       |
|                                      | EAMY_3020 | 2                                       |
|                                      | EAMY_3023 | 2                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes                      | Numbers of matched genes in strain CQ10 |
|--------------------------------------|----------------------------|---|
| increased virulence (hypervirulence) | EAMY_3028                  | 2                                       |
|                                      | EAMY_3227                  | 2                                       |
|                                      | EF-P                       | 2                                       |
|                                      | feoB                       | 2                                       |
|                                      | fliC                       | 2                                       |
|                                      | fliB                       | 2                                       |
|                                      | gigX1                      | 2                                       |
|                                      | katE                       | 2                                       |
|                                      | NTH1                       | 2                                       |
|                                      | NTH2                       | 2                                       |
|                                      | Pat                        | 2                                       |
|                                      | picC                       | 2                                       |
|                                      | PrsA                       | 2                                       |
|                                      | RsmA                       | 2                                       |
|                                      | Rv2220 (glnA1)             | 2                                       |
|                                      | S5nA                       | 2                                       |
|                                      | treA                       | 2                                       |
|                                      | tslA                       | 2                                       |
|                                      | ACC deaminase (VDAG 10392) | 1                                       |
|                                      | Acp1 (PA1869)              | 1                                       |
|                                      | AI-2                       | 1                                       |
|                                      | ampG                       | 1                                       |
|                                      | ANP1                       | 1                                       |
|                                      | BbbqrA                     | 1                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes          | Numbers of matched genes in strain CQ10 |
|--------------------------------------|----------------|---|
| increased virulence (hypervirulence) | Bsi            | 1                                       |
|                                      | cmaA2          | 1                                       |
|                                      | croI           | 1                                       |
|                                      | Dmt (PD_1542)  | 1                                       |
|                                      | EAMY_3003      | 1                                       |
|                                      | EAMY_3006      | 1                                       |
|                                      | EAMY_3007      | 1                                       |
|                                      | EAMY_3008      | 1                                       |
|                                      | EAMY_3009      | 1                                       |
|                                      | EAMY_3019      | 1                                       |
|                                      | EAMY_3021      | 1                                       |
|                                      | EAMY_3022      | 1                                       |
|                                      | EAMY_3027      | 1                                       |
|                                      | EAMY_3201      | 1                                       |
|                                      | EAMY_3213      | 1                                       |
|                                      | EAMY_3214      | 1                                       |
|                                      | EAMY_3216      | 1                                       |
|                                      | EAMY_3226      | 1                                       |
|                                      | EAMY_3228      | 1                                       |
|                                      | essC (lmo0061) | 1                                       |
|                                      | fur            | 1                                       |
|                                      | gigX3          | 1                                       |
|                                      | gluP (PD_0681) | 1                                       |
|                                      | GroEL          | 1                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                       | Genes             | Numbers of matched genes in strain CQ10 |
|--------------------------------------|-------------------|---|
| increased virulence (hypervirulence) | HmbR              | 1                                       |
|                                      | hrcC              | 1                                       |
|                                      | HSP90             | 1                                       |
|                                      | katG              | 1                                       |
|                                      | L7052             | 1                                       |
|                                      | mce1R             | 1                                       |
|                                      | Mgt2 (CNAG_03502) | 1                                       |
|                                      | modA10            | 1                                       |
|                                      | Ndk               | 1                                       |
|                                      | Oma1              | 1                                       |
|                                      | PA0005            | 1                                       |
|                                      | PA0336 (RppH)     | 1                                       |
|                                      | PepN              | 1                                       |
|                                      | PKR1              | 1                                       |
|                                      | pvdA              | 1                                       |
|                                      | PXO_00049         | 1                                       |
|                                      | raxA              | 1                                       |
|                                      | raxP (cysD)       | 1                                       |
|                                      | rcsA              | 1                                       |
|                                      | rsmS (ECA1172)    | 1                                       |
|                                      | rssC              | 1                                       |
|                                      | Rv0652 (rpIL)     | 1                                       |
|                                      | Rv1093 (glyA1)    | 1                                       |
|                                      | Rv1837c (glcB)    | 1                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                          | Genes                        | Numbers of matched genes in strain CQ10 |
|---|------------------------------|---|
| increased virulence (hypervirulence)    | secA2                        | 1                                       |
|   | secY                         | 1                                       |
|   | Uge3                         | 1                                       |
|   | UmaA1                        | 1                                       |
|   | vfr                          | 1                                       |
|   | vraS                         | 1                                       |
| effector (plant avirulence determinant) | BP1026B_II1587               | 16                                      |
|   | VasH                         | 9                                       |
|   | ACE1                         | 7                                       |
|   | EAMY_3223                    | 6                                       |
|   | LpdA                         | 6                                       |
|   | TssL                         | 5                                       |
|   | EAMY_3024                    | 4                                       |
|   | Hcp                          | 4                                       |
|   | Stk (ORF: z1444)             | 3                                       |
|   | ClpV                         | 3                                       |
|   | EAMY_3026                    | 2                                       |
|   | EAMY_3220                    | 2                                       |
|   | TssA                         | 2                                       |
|   | HopI1                        | 2                                       |
|   | ipx10                        | 2                                       |
|   | Me23                         | 2                                       |
|   | pagC                         | 2                                       |
|   | pip (proline iminopeptidase) | 2                                       |

**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                          | Genes         | Numbers of matched genes in strain CQ10 |
|---|---------------|---|
| effector (plant avirulence determinant) | sssB          | 2                                       |
|   | TssC          | 2                                       |
|   | TssB          | 1                                       |
|   | TssD          | 1                                       |
|   | TssE          | 1                                       |
|   | TssF          | 1                                       |
|   | TssG          | 1                                       |
|   | TssJ          | 1                                       |
|   | TssK          | 1                                       |
|   | TssM          | 1                                       |
|   | VasK          | 1                                       |
|   | avrAC (XopAC) | 1                                       |
|   | bsaO          | 1                                       |
|   | bsaZ          | 1                                       |
|   | BtpB          | 1                                       |
|   | EAMY_3211     | 1                                       |
|   | esx-3         | 1                                       |
|   | katN          | 1                                       |
|   | Mg1LysM       | 1                                       |
|   | Mg3LysM       | 1                                       |
|   | spaP          | 1                                       |
|   | sseB          | 1                                       |
|   | T3SS          | 1                                       |
|   | VgrG          | 1                                       |



**Table S9** Pathogen-host interaction (PHI) analysis of strain CQ10 (continued)

| PHI categories                          | Genes   | Numbers of matched genes in strain CQ10 |
|---|---------|---|
| effector (plant avirulence determinant) | XC_3703 | 1                                       |
|   | xrp8    | 1                                       |
|   | ysaC    | 1                                       |

**Table S10** Carbohydrate active enzymes (CAZymes) analysis of strain CQ10

| HMMER         | dbCAN_sub | DIAMOND | Categories |
|---------------|-----------|---------|------------|
| GT9(87-308)   | GT9_e292  | GT9     | GTs        |
| GT9(85-322)   | GT9_e18   | GT9     | GTs        |
| GT9(77-300)   | GT9_e71   | GT9     | GTs        |
| GT9(76-316)   | GT9_e14   | GT9     | GTs        |
| GT9(69-305)   | GT9_e84   | GT9     | GTs        |
| GT9(103-331)  | GT9_e213  | GT9     | GTs        |
| GT83(5-520)   | GT83_e0   | GT83    | GTs        |
| GT81(117-322) | GT81_e1   | GT81    | GTs        |
| GT8(4-251)    | GT8_e175  | GT8     | GTs        |
| GT8(23-268)   | GT8_e20   | GT8     | GTs        |
| GT56(2-348)   | GT56_e0   | GT56    | GTs        |
| GT51(63-226)  | GT51_e71  | GT51    | GTs        |
| GT51(61-225)  | GT51_e0   | GT51    | GTs        |
| GT51(54-229)  | GT51_e130 | GT51    | GTs        |
| GT51(208-378) | GT51_e28  | GT51    | GTs        |
| GT5(2-474)    | GT5_e31   | GT5     | GTs        |
| GT4(226-371)  | GT4_e731  | GT4     | GTs        |
| GT4(223-374)  | GT4_e91   | GT4     | GTs        |
| GT4(203-336)  | GT4_e3707 | GT4     | GTs        |
| GT4(200-341)  | GT4_e1381 | GT4     | GTs        |
| GT4(170-320)  | GT4_e2087 | GT4     | GTs        |
| GT35(91-798)  | GT35_e0   | GT35    | GTs        |
| GT35(91-798)  | GT35_e0   | GT35    | GTs        |
| GT35(101-810) | GT35_e0   | GT35    | GTs        |

**Table S10** Carbohydrate active enzymes (CAZymes) analysis of strain CQ10 (continued)

| HMMER         | dbCAN_sub | DIAMOND | Categories |
|---------------|-----------|---------|------------|
| GT30(32-210)  | GT30_e0   | GT30    | GTs        |
| GT28(183-339) | GT28_e46  | GT28    | GTs        |
| GT26(62-231)  | GT26_e141 | GT26    | GTs        |
| GT25(2-100)   | GT25_e93  | -       | GTs        |
| GT20(2-457)   | GT20_e1   | GT20    | GTs        |
| GT20(13-449)  | GT20_e18  | GT20    | GTs        |
| GT2(9-133)    | GT2       | GT2     | GTs        |
| GT2(9-118)    | GT2       | GT2     | GTs        |
| GT2(8-128)    | GT2       | GT2     | GTs        |
| GT2(7-127)    | GT2       | GT2     | GTs        |
| GT2(7-119)    | GT2       | GT2     | GTs        |
| GT2(4-166)    | GT2       | GT2     | GTs        |
| GT2(4-166)    | GT2       | GT2     | GTs        |
| GT2(3-99)     | GT2       | GT2     | GTs        |
| GT2(276-447)  | GT2+GT2   | GT2     | GTs        |
| GT2(253-435)  | GT2       | GT2     | GTs        |
| GT2(130-301)  | GT2+GT2   | GT2     | GTs        |
| GT2(11-172)   | GT2       | GT2     | GTs        |
| GT2(10-132)   | GT2       | GT2     | GTs        |
| GT19(8-365)   | GT19_e17  | GT19    | GTs        |
| GT101(55-280) | GT101_e11 | GT101   | GTs        |
| GT1(8-414)    | GT1_e11   | GT1     | GTs        |
| -             | GT4_e3814 | GT4     | GTs        |
| -             | GT4_e3218 | GT4     | GTs        |

**Table S10** Carbohydrate active enzymes (CAZymes) analysis of strain CQ10 (continued)

| HMMER          | dbCAN_sub | DIAMOND | Categories |
|----------------|-----------|---------|------------|
| -              | GT2       | GT2     | GTs        |
| -              | GT2       | GT2     | GTs        |
| GH8(27-328)    | GH8_e29   | GH8     | GHs        |
| GH77(146-684)  | GH77_e27  | GH77    | GHs        |
| GH77(141-680)  | GH77_e27  | GH77    | GHs        |
| GH73(762-888)  | GH73_e162 | GH73    | GHs        |
| GH73(165-301)  | GH73_e114 | GH73    | GHs        |
| GH53(37-396)   | GH53_e15  | GH53    | GHs        |
| GH43_26(7-306) | GH43_e105 | GH43_26 | GHs        |
| GH42(19-391)   | GH42_e20  | GH42    | GHs        |
| GH37(71-546)   | GH37_e6   | GH37    | GHs        |
| GH37(64-540)   | GH37_e6   | GH37    | GHs        |
| GH33(39-376)   | GH33_e0   | GH33    | GHs        |
| GH32(31-336)   | GH32_e57  | GH32    | GHs        |
| GH31(236-682)  | GH31_e60  | GH31    | GHs        |
| GH3(98-319)    | GH3_e1    | GH3     | GHs        |
| GH3(59-283)    | GH3_e19   | GH3     | GHs        |
| GH28(30-357)   | GH28_e5   | GH28    | GHs        |
| GH28(29-400)   | GH28_e13  | GH28    | GHs        |
| GH24(30-161)   | GH24_e283 | -       | GHs        |
| GH24(29-160)   | GH24_e190 | -       | GHs        |
| GH23(61-207)   | GH23_e734 | GH23    | GHs        |
| GH23(485-616)  | GH23_e96  | GH23    | GHs        |
| GH23(298-447)  | GH23_e225 | GH23    | GHs        |

**Table S10** Carbohydrate active enzymes (CAZymes) analysis of strain CQ10 (continued)

| HMMER            | dbCAN_sub | DIAMOND | Categories |
|------------------|-----------|---------|------------|
| GH23(207-352)    | GH23_e150 | GH23    | GHs        |
| GH23(108-252)    | GH23_e819 | GH23    | GHs        |
| GH20(328-763)    | GH20_e0   | GH20    | GHs        |
| GH20(152-582)    | GH20_e52  | GH20    | GHs        |
| GH2(41-919)      | GH2_e92   | GH2     | GHs        |
| GH15(238-597)    | GH15_e9   | GH15    | GHs        |
| GH15(222-588)    | GH15_e13  | GH15    | GHs        |
| GH13_9(274-574)  | GH13_e200 | GH13_9  | GHs        |
| GH13_5(31-373)   | GH13_e245 | GH13_5  | GHs        |
| GH13_26(25-309)  | GH13_e105 | GH13_26 | GHs        |
| GH13_18(82-422)  | GH13_e137 | GH13_18 | GHs        |
| GH13_11(188-536) | GH13_e48  | GH13_11 | GHs        |
| GH13_11(172-522) | GH13_e48  | GH13_11 | GHs        |
| GH13_10(123-436) | GH13_e85  | GH13_10 | GHs        |
| GH109(1-347)     | GH109_e5  | -       | GHs        |
| GH105(60-376)    | GH105_e57 | GH105   | GHs        |
| GH103(62-351)    | GH103_e0  | GH103   | GHs        |
| GH102(126-259)   | GH102_e2  | GH102   | GHs        |
| GH1(7-465)       | GH1_e42   | GH1     | GHs        |
| GH1(6-476)       | GH1_e0    | GH1     | GHs        |
| GH1(51-345)      | GH1_e19   | GH1     | GHs        |
| GH1(4-472)       | GH1_e85   | GH1     | GHs        |
| GH1(31-357)      | GH1_e73   | GH1     | GHs        |
| GH1(2-459)       | GH1_e85   | GH1     | GHs        |

**Table S10** Carbohydrate active enzymes (CAZymes) analysis of strain CQ10 (continued)

| HMMER          | dbCAN_sub  | DIAMOND | Categories |
|----------------|------------|---------|------------|
| CBM48(17-107)  | CBM48_e3   | CBM48   | CBMs       |
| CBM48(125-211) | CBM48_e2   | CBM48   | CBMs       |
| CBM48(10-98)   | CBM48_e3   | CBM48   | CBMs       |
| -              | CBM50_e657 | CBM50   | CBMs       |
| -              | CBM50_e567 | CBM50   | CBMs       |
| -              | CBM50_e486 | CBM50   | CBMs       |
| -              | CBM50_e126 | CBM50   | CBMs       |
| -              | CBM48_e0   | CBM48   | CBMs       |
| AA6(3-195)     | AA6_e2     | -       | AAs        |
| AA3_2(2-532)   | AA3_e57    | AA3_2   | AAs        |
| AA1(66-524)    | AA1_e20    | -       | AAs        |
| -              | AA2_e1     | AA0     | AAs        |
| CE9(5-376)     | CE9_e0     | CE9     | CEs        |
| CE11(4-276)    | CE11_e22   | CE11    | CEs        |
| -              | CE4_e177   | CE4     | CEs        |

*HMMER: the results of the HMMER run versus the dbCAN database. dbCAN\_sub: the results of the HMMER run versus the dbCAN-sub database. DIAMOND: the results of the DIAMOND blast versus the CAZy database. GTs: GlycosylTransferases. GHs: Glycoside Hydrolases. CBMs: Carbohydrate-Binding Modules. AAs: Auxiliary Activities. CEs: Carbohydrate Esterases.*

**Table S11** Biosynthetic gene clusters (BGCs) predicted by antiSMASH 6.1 softwares in the genome of strain CQ10

| Region     | Location   | Type       | Comounds          | MIBiG reference | Organism   | Similarity score |
|------------|------------|------------|-------------------|-----------------|--|------------------|
| Region 1.1 | Chromosome | saccharide | jinggangmycin     | BGC0000701.1    | <i>Streptomyces hygroscopicus</i> subsp. <i>yingchengensis</i> | 0.61             |
| Region 1.2 | Chromosome | RiPP       | WGK               | BGC0001929.1    | <i>Streptococcus ferus</i>                                     | 0.55             |
| Region 1.3 | Chromosome | other      | cycloserine       | BGC0000896.1    | <i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i>        | 0.49             |
| Region 1.4 | Chromosome | saccharide | O-antigen         | BGC0000784.1    | <i>Pseudomonas aeruginosa</i>                                  | 0.58             |
| Region 1.5 | Chromosome | NRP        | bacillibactin     | BGC0001185.1    | <i>Bacillus velezensis</i> FZB42                               | 0.67             |
| Region 2.1 | Plasmid    | other      | bacilysin         | BGC0001184.1    | <i>Bacillus velezensis</i> FZB42                               | 0.62             |
| Region 4.1 | Plasmid    | other      | desferrioxamine E | BGC0001572.1    | <i>Pantoea agglomerans</i>                                     | 0.90             |
| Region 5.1 | Plasmid    | terpene    | carotenoid        | BGC0000638.1    | <i>Pantoea ananatis</i>  | 0.85             |