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Supplementary Figure 1: Experimental design of the bioassay. Two batches were tested with 9 composts each where compost H was included in both batches. Three replicates for metabarcoding (red circles) and three replicates of cress biomass (green triangles) were sampled. In total, 174 samples were obtained for metabarcoding including 54 compost samples (2 batches x 9 composts x 3 replicates), 3 matrix samples, 108 rhizoplane samples of cress grown in compost substrate (2 batches x 2 inoculation levels x 9 composts x 3 replicates) and 12 rhizoplane samples of cress grown in control matrix (2 batches x 2 inoculation levels x 3 replicates). In total, 240 cress biomass samples were obtained including 182 samples from plants grown in compost substrates (2 batches x 9 composts x 4 inoculation levels x 3 replicates) and 24 samples from plants grown in the control matrix (2 batches x 4 inoculation levels x 3 replicates).
Supplementary Figure 2: Correlations of mean percent growth promotion and mean compost characteristics such as nitrate \([\text{mg N (kg dry weight)}^{-1}]\), inorganic nitrogen \([\text{mg N (kg dry weight)}^{-1}]\), salinity \([\text{g KCl eq (kg dry weight)}^{-1}]\), age \([\text{d}]\), ammonia \([\text{mg N (kg dry weight)}^{-1}]\), dry matter \([\%]\), content of soluble humic substances \((\text{OD 550})\) and pH. Plots were ordered according to the absolute value of the strength of the Spearman correlation (\(\text{rho}\)) and a linear trendline was added only for significant correlations \((p < 0.05)\). Correlations were based on 17 composts, except for age only 12 were available. Statistics of correlations are also presented in Supplementary Table 4. Mean growth promotion was defined as the percent increase in shoot weight of plants that were grown in compost substrates compared to the control matrix both without inoculation with the pathogen.
Supplementary Figure 3: Disease suppression among compost substrates (A-Q) and the control matrix (m) inoculated with either 0.25, 0.5 or 1 g of *P. ultimum*-millet-mix (L of substrate)$^{-1}$ of the first (A) and the second (B) batch of composts. Percent disease suppression was defined as the relative shoot weight of *P. ultimum*-inoculated and uninoculated cress plants for each compost treatment and the control matrix. Letters show significant differences among substrates (TukeyHSD-tests, p < 0.05). ANOVA was performed separately for each experiment and inoculation-level and overall statistics for 0.25, 0.5 and 1 g L$^{-1}$ were $F = 1.2$ and $p = 0.358$, $F = 2.6$ and $p = 0.038$ as well as $F = 19.8$ and $p = 4 \times 10^{-8}$ in batch one (A) and $F = 3.0$ and $p = 0.019$, $F = 7.2$ and $p = 0.0001$ as well as $F = 8.0$ and $p = 6 \times 10^{-8}$ in batch 2 (B). Compost H was tested in both experiments.
Supplementary Figure 4: Correlation plots of mean percent disease suppression and compost characteristics such as age [d], nitrate [mg N (kg dry weight)^-1], inorganic nitrogen [mg N (kg dry weight)^-1], dry matter [%], content of soluble humic substances (OD 550), ammonia [mg N (kg dry weight)^-1], pH and salinity [g KCl eq (kg dry weight)^-1]. Plots were ordered according to the absolute value of the strength of the Spearman correlation (rho) and a linear trendline was added only for significant results (p < 0.05). Correlations were based on 17 composts, except for age only 12 were available. Statistics of correlations are also presented in Supplementary Table 4. Percent disease suppression was defined as the relative shoot weight of *P. ultimum*-inoculated and uninoculated cress plants for each compost treatment.
Supplementary Figure 5: Partitioning of robustly detected SVs among substrates and rhizoplanes. (A) Venn diagram displaying the occurrence of SVs in each compartment, i.e., compost (brown), matrix (black), rhizoplanes of cress plants grown in compost substrate (“rhizo c”, pink dashed line) and rhizoplanes of cress plants grown in the matrix (“rhizo m”, blue dashed line). Rhizoplane data derived from plants inoculated with P. ultimum are presented. The numbers outside of the circles of the Venn diagram show the number of SVs and the mean percentage of SVs in each compartment. The numbers in the different areas of the Venn diagram correspond to mean percentages of SVs from the 17 composts, the matrix, the corresponding rhizoplanes and their intersections. Standard deviations are presented in parenthesis. Data were obtained using a subsampling procedure to 18,743 sequences with 100 iterations. (B) Partitioning of SVs in rhizoplanes of plants grown in compost substrates (“rhizo c”). Percentages correspond to SVs that were also found in compost (“c”), in compost and the matrix (“c+m”), the matrix (“m”) and in rhizoplanes of plants grown in the control matrix (“rhizo m”), or that were only detected in rhizoplanes of plants grown in the compost substrates (“rhizo c”).
Supplementary Figure 6: Partitioning of robustly detected SVs among substrates and rhizoplanes of the most and the least growth promoting (A) and disease suppressing (B) composts. The numbers in the different areas of the Venn diagram correspond to mean percentages of SVs. The first number is the mean percentage of SVs in the 5 most active and the second number the 5 least active compost for growth promotion (A) and disease suppression (B). Colours represent different compartments, i.e., compost (brown), matrix (black), rhizoplanes of cress plants grown in compost substrate ("rhizopl. compost", pink dashed line) and rhizoplanes of cress plants grown in the matrix ("rhizopl. matrix", blue dashed line). Rhizoplane data derived from uninoculated plants (A) and plants inoculated with P. ultimum (B) are presented. Data were obtained using a subsampling procedure to 18,743 (A) and 13,173 (B) sequences with 100 iterations. The Asterisk represents a significant difference of percentage of SVs of the five most active and least active composts (p < 0.05). Statistics of all Student t-tests are presented in Supplementary Table 9.
**Supplementary Table 1: Composition of starting materials in percent used in the composting process of each of the 17 composts obtained from different commercial compost providers.**

| Compost Provider | Plant residues<sup>a</sup> | Soil / humus | Fibre chalk<sup>b</sup> | Mature compost | Manure<sup>c</sup> | Wet biomass | Biochar and/or additives |
|------------------|-----------------------------|--------------|--------------------------|----------------|-------------------|-------------|--------------------------|
| A                | A                           | 60           | 10                       | 0              | 10                | 15          | 0                       |
|                  |                              |              |                          |                |                   |             | (biochar, leonardit, biolit, betonit) |
| B                | A                           | 40           | 8                        | 0              | 8                 | 33          | 0                       |
|                  |                              |              |                          |                |                   |             | (biochar, biolit)        |
| C                | A                           | 58           | 8                        | 0              | 8                 | 25          | 0                       |
|                  |                              |              |                          |                |                   |             | (biochar, biolit)        |
| D                | A                           | 40           | 8                        | 0              | 8                 | 40          | 0                       |
|                  |                              |              |                          |                |                   |             | (biochar, biolit)        |
| E                | A                           | 45           | 8                        | 0              | 10                | 33          | 0                       |
| F                | B                           | 90           | 0                        | 10             | 0                 | 0           | 0                       |
| G                | C                           | 75           | 10                       | 0              | 10                | 5           | 0                       |
| H                | C                           | 80           | 10                       | 0              | 10                | 0           | 0                       |
| I                | C                           | 75           | 10                       | 0              | 10                | 5           | 0                       |
| J                | D                           | NA           | NA                       | NA             | NA                | NA          | NA                      |
| K                | D                           | NA           | NA                       | NA             | NA                | NA          | NA                      |
| L                | E                           | NA           | NA                       | NA             | NA                | NA          | NA                      |
| M                | E                           | NA           | NA                       | NA             | NA                | NA          | NA                      |
| N                | B                           | NA           | NA                       | NA             | NA                | NA          | NA                      |
| O                | B                           | 100          | 0                        | 0              | 0                 | 0           | 0                       |
| P                | B                           | 95           | 2                        | 0              | 0                 | 0           | 0                       |
| Q                | B                           | 70           | 0                        | 0              | 0                 | 0           | 30                      |

<sup>a</sup> Plant residues included leaves, twigs, roots, green waste, grass and hay

<sup>b</sup> Fibre chalk from a paper production company

<sup>c</sup> Manure from cow, horse, pig, chicken

NA not available
Supplementary Table 2: Compost characteristics of the 17 composts that were used to define different qualities such as age, dry matter, pH, salinity, content of soluble humic substances of the extract (OD 550), total inorganic nitrogen, nitrate and ammonia.

| Compost | Age [d] | Dry matter content [%] | pH | Salinity [g KCl eq⁻¹ (kg dry weight)⁻¹] | OD 550 [nm] | Nmin [mg N (kg dry weight)⁻¹] | NO₃⁻ [mg N (kg dry weight)⁻¹] | NH₄⁺ [mg N (kg dry weight)⁻¹] |
|---------|---------|------------------------|----|----------------------------------------|-------------|-------------------------------|-------------------------------|-------------------------------|
| A       | 199     | 62.4                   | 7.2| 10.1                                   | 0.04        | 589.9                         | 579.5                         | 10.3                          |
| B       | 260     | 65.0                   | 8.0| 7.0                                    | 0.16        | 68.3                          | 65.7                          | 2.6                           |
| C       | 320     | 67.7                   | 7.2| 5.6                                    | 0.05        | 446.5                         | 444                           | 2.5                           |
| D       | 290     | 64.9                   | 7.2| 12.5                                   | 0.12        | 759.9                         | 749.4                         | 10.5                          |
| E       | 260     | 63.7                   | 7.6| 11.1                                   | 0.10        | 634.4                         | 629.9                         | 4.5                           |
| F       | 141     | 42.5                   | 7.2| 7.3                                    | 0.42        | 360.5                         | 236.4                         | 124.1                         |
| G       | 155     | 63.2                   | 8.0| 6.9                                    | 0.13        | 118.3                         | 100.3                         | 18                            |
| H       | 65      | 47.6                   | 8.0| 8.6                                    | 0.16        | 9.9                           | 0                             | 9.9                           |
| I       | 106     | 49.0                   | 8.0| 8.6                                    | 0.16        | 8.3                           | 0                             | 8.3                           |
| J       | NA      | 67.9                   | 7.9| 7.4                                    | 0.09        | 217.7                         | 214.4                         | 3.3                           |
| K       | NA      | 37.2                   | 7.7| 7.4                                    | 0.27        | 14.2                          | 0                             | 14.2                          |
| L       | NA      | 64.1                   | 7.6| 6.6                                    | 0.32        | 17.1                          | 0                             | 17.1                          |
| M       | NA      | 60.7                   | 8.2| 7.5                                    | 0.25        | 16.6                          | 9.3                           | 7.3                           |
| N       | NA      | 40.0                   | 7.5| 6.9                                    | 0.46        | 56.5                          | 44.6                          | 11.9                          |
| O       | 203     | 65.9                   | 7.3| 11.3                                   | 0.39        | 387.9                         | 380.3                         | 7.6                           |
| P       | 147     | 44.1                   | 7.3| 8.6                                    | 0.48        | 359.2                         | 232.6                         | 126.6                         |
| Q       | 35      | 41.9                   | 7.7| 10.2                                   | 0.20        | 196.1                         | 106.1                         | 90                            |

1 potassium chloride equivalent
2 inorganic nitrogen, sum of ammonia and nitrate
NA not available
Supplementary Table 3: Cress shoot weight (mean and standard deviation) and disease symptoms (median) of plants grown in compost substrate (A-Q) or the control matrix (m). Bioassays were conducted in two batches including nine compost substrates each. Compost A-I were tested in the first batch, compost J-Q were tested in the second batch and compost H (H1 and H2) and the control matrix (m1 and m2) were included in both batches. Plants were inoculated with 1 g of *P. ultimum*-millet-mix (L substrate). The severity of disease symptoms of damping-off was classified in five categories according to the severity of disease, i.e., plants showing yellowing of leaves and growth reduction.

| substrate | inoculation with *P. ultimum* | cress shoot weight [g] | disease symptoms<sup>a</sup> |
|-----------|-------------------------------|-------------------------|----------------------------|
|           |                               | mean    | SD     | median |
| A         | no                            | 7.97    | 0.89   | 0      |
| A         | yes                           | 2.25    | 0.73   | 2      |
| B         | no                            | 8.22    | 0.54   | 0      |
| B         | yes                           | 2.82    | 0.69   | 1      |
| C         | no                            | 8.48    | 0.41   | 0      |
| C         | yes                           | 3.58    | 0.20   | 1      |
| D         | no                            | 9.10    | 0.51   | 0      |
| D         | yes                           | 2.44    | 1.20   | 2      |
| E         | no                            | 9.26    | 0.30   | 0      |
| E         | yes                           | 3.33    | 0.63   | 1      |
| F         | no                            | 7.37    | 0.34   | 0      |
| F         | yes                           | 3.40    | 0.74   | 1      |
| G         | no                            | 7.83    | 0.64   | 0      |
| G         | yes                           | 2.90    | 0.73   | 1.5    |
| H1        | no                            | 6.44    | 0.36   | 0      |
| H1        | yes                           | 5.15    | 0.22   | 0      |
| I         | no                            | 7.55    | 0.15   | 0      |
| I         | yes                           | 5.04    | 0.68   | 0      |
| m1        | no                            | 5.77    | 0.49   | 0      |
| m1        | yes                           | 0.30    | 0.10   | 3.5    |
| H2        | no                            | 5.82    | 0.53   | 0      |
| H2        | yes                           | 3.61    | 0.55   | 1      |
| J         | no                            | 7.47    | 1.96   | 0      |
| J         | yes                           | 4.56    | 0.53   | 0.5    |
| K         | no                            | 4.68    | 0.14   | 0      |
| K         | yes                           | 3.98    | 0.62   | 0.5    |
| L         | no                            | 5.59    | 0.19   | 0      |
| L         | yes                           | 3.80    | 0.27   | 1      |
| M         | no                            | 8.20    | 0.20   | 0      |
| M         | yes                           | 3.19    | 1.71   | 1      |
| N         | no                            | 7.40    | 0.07   | 0      |
| N         | yes                           | 2.65    | 1.66   | 2      |
| O         | no                            | 8.34    | 1.18   | 0      |
| O         | yes                           | 3.78    | 1.07   | 1      |
| P         | no                            | 6.74    | 0.21   | 0      |
| P         | yes                           | 2.73    | 0.31   | 1      |
| Q         | no                            | 7.89    | 0.31   | 0      |
| Q         | yes                           | 6.76    | 0.55   | 0      |
| m2        | no                            | 4.86    | 0.44   | 0      |
| m2        | yes                           | 0.99    | 0.77   | 3      |

<sup>a</sup> Ordinal scale for severity of disease symptoms: 0 = no symptoms, 1 = few symptoms, 2 = medium symptoms, 3 = strong symptoms, 4 = no germination
Supplementary Table 4: Spearman correlations of mean disease suppression or mean growth promotion with compost characteristics of the 17 composts. Percent disease suppression was defined as the relative shoot weight of *P. ultimum*-inoculated and un-inoculated cress plants for each compost treatment. Mean growth promotion was defined as the percent increase in shoot weight of plants that were grown in compost substrates compared to the control matrix both without inoculation with the pathogen. Results from a correlation of mean disease suppression with mean growth promotion was also included.

| Factor                               | Correlation with suppression | Correlation with growth promotion |
|--------------------------------------|-------------------------------|-----------------------------------|
|                                      | rho  | p-value | n   | rho  | p-value | n   |
| age at arrival [d]                   | -0.75 | 0.005*  | 12  | 0.45 | 0.140   | 12  |
| dry matter content [%]               | -0.31 | 0.224   | 17  | 0.35 | 0.168   | 17  |
| pH                                   | 0.10  | 0.697   | 17  | 0.02 | 0.933   | 17  |
| Salinity [g KCl eq (kg dry weight)⁻¹] | -0.10 | 0.714   | 17  | 0.46 | 0.063   | 17  |
| soluble humic substances (OD 550)    | 0.28  | 0.276   | 17  | -0.12| 0.659   | 17  |
| nitrate [mg N (kg dry weight)⁻¹]     | -0.56 | 0.019*  | 17  | 0.52 | 0.034*  | 17  |
| ammonia [mg N (kg dry weight)⁻¹]     | 0.24  | 0.358   | 17  | -0.38| 0.133   | 17  |
| Inorganic N [mg N (kg dry weight)⁻¹]b| -0.54 | 0.026*  | 17  | 0.47 | 0.060   | 17  |
| Growth promotion [%]                 | -0.34 | 0.178   | 17  | NA   | NA      | NA  |

* p-value smaller than 0.05
a Potassium chloride equivalent
b sum of ammonia and nitrate
NA not available
Supplementary Table 5: Sequences assigned to plant organelles such as chloroplasts and mitochondria as well as to bacteria. Mean and standard deviation of numbers for each compartment including composts, control matrix and rhizoplanes of cress plants grown in either compost substrates or the untreated control matrix. Percentages of sequences assigned to chloroplast and mitochondria of all sequences. Plant organelle sequences were removed from the dataset for all following analyses.

| compartment       | chloroplasts |          | mitochondria |          | bacteria |          | chloroplasts [%] |          | mitochondria [%] |          |
|-------------------|--------------|----------|--------------|----------|----------|----------|-----------------|----------|------------------|----------|
|                   | mean  SD     | mean  SD | mean  SD     | mean  SD | mean  SD | mean  SD | mean  SD        | mean  SD | mean  SD          | mean  SD |
| compost           | 1.9 2.3      | 3.4 5.1  | 29,738.0 2,490.6 | 0.006 0.008 | 0.010 0.020 |
| matrix            | 0.7 0.6      | 0       | 24,825.3 5,637.0 | 0.003 0.002 | 0 0 |
| Rhizopl. of compost | 1,071.1 1,413.5 | 394.4 442.4 | 28,862.4 4,879.3 | 3.489 4.487 | 1.290 1.420 |
| Rhizopl. of matrix | 2,792.9 5,175.8 | 1,015.4 1,764.9 | 27,543.9 5,633.9 | 7.946 13.737 | 2.910 4.690 |
Supplementary Table 6: Differences of bacterial community structures among composts and the matrix as well as rhizoplanes grown in different substrates, i.e., composts or matrix, with or without inoculation with the pathogen. Tests were performed using PERMANOVA and Bray Curtis dissimilarities of relative abundances. Compost and rhizoplane communities included three replicates for each treatment. Except, the rhizoplanes of plants grown in H and in the matrix, included six replicates which originated from two experimental batches.

|                                      | Pseudo-F | p-value |
|--------------------------------------|----------|---------|
| Compost communities                  | 36.7     | 0.0001  |
| Rhizoplanes communities inoculated with *P. ultimum* | 6.3      | 0.0001  |
| Rhizoplane communities not inoculated with *P. ultimum* | 7.3      | 0.0001  |
Supplementary Table 7: Number and percentage of 15,236 SVs occurring in increasing combinations from one to 17 different composts. Only robustly detected SVs, i.e., that occurred in at least two of the three replicates of each compost, were selected.

| Compost combinations | number of SVs | Cumulative number of SVs | Percentage of SVs | cumulative percentage of SVs |
|----------------------|--------------|-------------------------|------------------|-----------------------------|
| 1                    | 2,447        | 2,447                   | 16.1             | 16.1                        |
| 2                    | 2,635        | 5,082                   | 17.3             | 33.4                        |
| 3                    | 2,279        | 7,361                   | 15.0             | 48.3                        |
| 4                    | 1,807        | 9,168                   | 11.9             | 60.2                        |
| 5                    | 1,366        | 10,534                  | 9.0              | 69.1                        |
| 6                    | 1,041        | 11,575                  | 6.8              | 76.0                        |
| 7                    | 816          | 12,391                  | 5.4              | 81.3                        |
| 8                    | 587          | 12,978                  | 3.9              | 85.2                        |
| 9                    | 478          | 13,456                  | 3.1              | 88.3                        |
| 10                   | 376          | 13,832                  | 2.5              | 90.8                        |
| 11                   | 316          | 14,148                  | 2.1              | 92.9                        |
| 12                   | 243          | 14,391                  | 1.6              | 94.5                        |
| 13                   | 199          | 14,590                  | 1.3              | 95.8                        |
| 14                   | 174          | 14,764                  | 1.1              | 96.9                        |
| 15                   | 148          | 14,912                  | 1.0              | 97.9                        |
| 16                   | 145          | 15,057                  | 1.0              | 98.8                        |
| 17                   | 179          | 15,236                  | 1.2              | 100.0                       |
Supplementary Table 8: Effect of disease suppression, growth promotion and compost characteristics on bacterial community structures in different compartments. Bacterial communities were assessed in composts, rhizoplanes grown in different compost substrates and in rhizoplanes including only compost-derived rhizoplane SVs. Bacterial community structures were based on Bray-Curtis dissimilarities using mean relative abundances of robustly detected SVs for each substrate or rhizoplane. For compost H, means across both experiments were used. Dissimilarity based linear models were performed with PERMANOVA including explained variation (expl. var.), pseudo F-statistic (F) and p-value (p).

| Factor                              | Compost communities | Rhizoplane communities derived from compost<sup>a</sup> |
|-------------------------------------|---------------------|--------------------------------------------------------|
|                                     | expl. var. | F     | p     | expl. var. | F         | p     |
| Disease suppression                 | 14.7       | 2.6   | 0.0093 | 10.8       | 1.8       | 0.0206 |
| Growth promotion                    | 11.5       | 1.9   | 0.0457 | 9.1        | 1.5       | 0.0711 |
| Nitrate                             | 11.6       | 2.0   | 0.0419 | NA         | NA        | NA     |
| Disease suppression with nitrate as covariate | 9.5       | 1.7   | 0.0765 | NA         | NA        | NA     |
| Growth promotion with nitrate as covariate | 6.9       | 1.8   | 0.2698 | NA         | NA        | NA     |
| Inorganic nitrogen                  | 10.4       | 1.7   | 0.0698 | NA         | NA        | NA     |
| age<sup>b</sup>                     | 17.6       | 2.1   | 0.0335 | NA         | NA        | NA     |

NA not available

<sup>a</sup> for the correlations of rhizoplanes inoculated with <i>P. ultimum</i> with mean percent suppression 11,207 SVs derived from composts were used for the calculation of the Bray-Curtis dissimilarity while for the correlations of rhizoplanes without inoculation with <i>P. ultimum</i> with mean growth promotion 11,359 SVs were included.

<sup>b</sup> data on age was available for 12 composts.
Supplementary Table 9: Partitioning of SVs among five most and least active composts. Mean and standard deviation (in parentheses) of percentage of number of SVs in each area of the Venn diagram between the five compost with least growth promotion (compost F, H, I, K and L) and the five compost with the largest growth promotion (compost D, E, M, N and Q) as well as between the five composts with least (compost A, B, D, E and N) and the five compost with the largest disease suppression against *P. ultimum* (compost H, I, K, L and Q) were presented. Student t-tests were performed and p-values adjusted using the Benjamini Hochberg correction. Menas are also presented in Supplementary Figure 6.

| Trait                        | Area in Venn | Mean and standard deviation of percentage of SVs in five compost with strongest activity | Mean and standard deviation of percentage of SVs in five composts with least activity | T-test statistic | BH adjusted p-value |
|------------------------------|--------------|-----------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-----------------|---------------------|
| Growth promotion             | a1           | 12.78 (2.69)                                                                            | 12.24 (2.42)                                                                         | 0.35            | 0.827               |
|                              | a2           | 8.5 (1.68)                                                                              | 8.65 (1.6)                                                                           | -0.15           | 0.881               |
|                              | a3           | 19.71 (3.45)                                                                            | 18.35 (1.98)                                                                         | 0.78            | 0.771               |
|                              | a4           | 0.12 (0.1)                                                                              | 0.15 (0.17)                                                                          | -0.30           | 0.827               |
|                              | a5           | 0.03 (0.02)                                                                             | 0.04 (0.02)                                                                          | -0.34           | 0.827               |
|                              | a6           | 0.23 (0.05)                                                                             | 0.26 (0.14)                                                                          | -0.49           | 0.827               |
|                              | a7           | 4.78 (1.67)                                                                             | 3.49 (1.32)                                                                          | 1.40            | 0.755               |
|                              | a8           | 0.4 (0.27)                                                                              | 0.23 (0.2)                                                                           | 1.14            | 0.771               |
|                              | a9           | 21.06 (5.5)                                                                             | 22.58 (3.74)                                                                         | -0.52           | 0.827               |
|                              | a10          | 0.05 (0.02)                                                                             | 0.06 (0.02)                                                                          | -0.82           | 0.771               |
|                              | a11          | 0.07 (0.02)                                                                             | 0.09 (0.02)                                                                          | -1.46           | 0.755               |
|                              | a12          | 0.94 (0.69)                                                                             | 1.61 (0.74)                                                                          | -1.56           | 0.755               |
|                              | a13          | 5.45 (1.86)                                                                             | 3.42 (1.23)                                                                          | 2.08            | 0.755               |
|                              | a14          | 11.4 (1.32)                                                                             | 12.08 (0.97)                                                                         | -0.95           | 0.771               |
|                              | a15          | 14.47 (4.31)                                                                            | 16.75 (3.02)                                                                         | -1.00           | 0.771               |
| Disease suppression          | a8           | 0.35 (0.12)                                                                             | 0.71 (0.15)                                                                          | -4.43           | 0.038               |
|                              | a9           | 22.92 (4.16)                                                                            | 28.44 (3.21)                                                                         | -2.48           | 0.098               |
|                              | a10          | 0.08 (0.03)                                                                             | 0.13 (0.04)                                                                          | -2.07           | 0.145               |
|                              | a11          | 0.13 (0.03)                                                                             | 0.08 (0.03)                                                                          | 2.69            | 0.098               |
|                              | a12          | 1.84 (1.06)                                                                             | 0.51 (0.38)                                                                          | 2.84            | 0.098               |
|                              | a13          | 3.52 (1.12)                                                                             | 5.04 (0.98)                                                                          | -2.41           | 0.098               |
|                              | a14          | 10.65 (0.85)                                                                            | 10.51 (1.78)                                                                         | 0.16            | 0.903               |
|                              | a15          | 17.94 (3.48)                                                                            | 13.6 (5.85)                                                                          | 1.46            | 0.290               |
Supplementary Table 10: Relative abundance and taxonomy of SVs associated with growth promoting composts, i.e., D, E, M, N and Q. Potentially growth promoting SVs were selected by comparing robustly detected SVs of the five most and the five least growth promoting composts using indicator species analysis with point biserial correlation coefficient larger than 0.7 as a selection criterion. A literature research was performed to assess if the genera have been mentioned in relation to compost bacteria or plant growth promotion (end October 2020).

| SV       | Rpb | rho / p / n | highly growth promoting composts | weakly growth promoting composts | rhizoplanes grown in substrates with high growth promotion matrix | rhizoplanes grown in the matrix | phylum               | lowest possible taxonomic classification | comparison to literature related to compost plant growth promotion |
|----------|-----|-------------|----------------------------------|----------------------------------|---------------------------------------------------------------|---------------------------------|---------------------|-----------------------------------------|---------------------------------------------------------------|
| SV-11330 | 0.84| NA          | 1.7E-03                          | 0                                | 0                                                              | 0                               | 0                   | Proteobacteria o_Rhizobiales            | NA                                              |
| SV-21591 | 0.81| NA          | 8.8E-04                          | 0                                | 3.9E-04                                                        | 0                               | 0                   | Proteobacteria g_Panacagri monas         | No reference                                    |
| SV-2745  | 0.80| NA          | 1.3E-02                          | 9.3E-04                          | 1.1E-02                                                        | 0                               | 0                   | Actinobacteria c_Actinobacteria          | NA                                              |
| SV-12568 | 0.78| NA          | 2.8E-03                          | 2.1E-04                          | 5.5E-04                                                        | 0                               | 0                   | Chloroflexi c_OLB14                      | NA                                              |
| SV-4513  | 0.78| 0.23 / 0.38 / 13 | 2.3E-03                          | 6.9E-04                          | 4.2E-03                                                        | 0                               | 0                   | Proteobacteria g_Microvirga              | [1, 2] [reviewed in 3, 4]                         |
| SV-6616  | 0.77| NA          | 1.5E-03                          | 0                                | 7.2E-04                                                        | 0                               | 0                   | Gemmatimonadetes f_Gemmimonadaceae       | NA                                              |
| SV-11998 | 0.77| NA          | 1.5E-03                          | 0                                | 1.5E-03                                                        | 0                               | 0                   | Proteobacteria o_Rhizobiales            | NA                                              |
| SV-12378 | 0.77| NA          | 5.1E-03                          | 1.6E-03                          | 0                                                              | 0                               | 0                   | unclassified                            | unclassified                                    |
| SV-5145  | 0.76| 0.66 / 0.03 / 15 | 7.5E-03                          | 2.2E-03                          | 3.4E-03                                                        | 0                               | 0                   | Chloroflexi c_JG30-KF-CM66              | NA                                              |
| SV-2659  | 0.75| 0.36 / 0.20 / 14 | 8.0E-03                          | 1.2E-03                          | 2.0E-02                                                        | 0                               | 0                   | Actinobacteria c_Actinobacteria          | NA                                              |
| SV-7153  | 0.75| NA          | 1.3E-03                          | 2.3E-04                          | 0                                                              | 0                               | 0                   | Proteobacteria g_Acinetobacter           | [5, 6] [7, 8]                                    |
| SV-2059  | 0.74| 0.51 / 0.09 / 13 | 5.6E-03                          | 6.8E-04                          | 2.8E-02                                                        | 1.5E-02                         | 2.7E-02 | Actinobacteria g_Streptomyces            | [9, 10] [reviewed in 11, 12]                     |
| SV-14393 | 0.74| NA          | 1.9E-03                          | 0                                | 0                                                              | 0                               | 0                   | unclassified                            | unclassified                                    |
| SV-10345 | 0.74| 0.3 / 0.29 / 11 | 1.9E-03                          | 4.9E-04                          | 1.0E-03                                                        | 0                               | 0                   | Chloroflexi o_SAR202_clade              | NA                                              |
| SV-8795  | 0.73| NA          | 4.4E-03                          | 2.6E-03                          | 0                                                              | 0                               | 0                   | Chloroflexi c_OLB14                     | NA                                              |
| SV-15304 | 0.73| NA          | 2.4E-03                          | 4.2E-04                          | 2.3E-04                                                        | 0                               | 0                   | Proteobacteria c_Gamma proteobacteria    | NA                                              |
| SV-1147  | 0.73| 0.69 / 0.03 / 17 | 3.6E-02                          | 2.0E-02                          | 3.5E-02                                                        | 0                               | 1.9E-03 | Proteobacteria g_Hyphomicrobium         | [13, 14] No reference                           |
| SV-3208  | 0.73| 0.27 / 0.32 / 12 | 1.2E-03                          | 7.1E-04                          | 5.9E-03                                                        | 0                               | 0                   | Acidobacteria c_Subgroup_6              | NA                                              |
| SV-6142  | 0.72| NA          | 2.4E-03                          | 2.5E-03                          | 0                                                              | 0                               | 0                   | Gemmatimonadetes c_S0134_ terrestrial_group | NA                                              |
| SV-9424  | 0.72| NA          | 1.9E-03                          | 2.4E-04                          | 3.2E-03                                                        | 0                               | 0                   | Proteobacteria g_Pereidibacter           | [15] No reference                               |
| SV-31    | 0.72| 0.6 / 0.06 / 13 | 1.0E-02                          | 2.1E-03                          | 2.6E-01                                                        | 3.9E+00                         | 1.4E+00 | Proteobacteria g_Bradyrhizobium         | No reference [reviewed in 16, 17]               |
| SV-61    | 0.72| 0.58 / 0.06 / 17 | 6.6E-01                          | 1.6E-01                          | 1.6E-01                                                        | 2.1E-03                         | 0                   | Gemmatimonadetes c_S0134_ terrestrial_group | NA                                              |
| SV-5197  | 0.72| 0.49 / 0.11 / 13 | 9.0E-03                          | 2.6E-03                          | 4.1E-04                                                        | 0                               | 0                   | Proteobacteria g_Brevundimonas          | [18, 19] [20]                                  |
| SV-2097  | 0.72| 0.77 / 0.01 / 14 | 7.4E-03                          | 1.7E-03                          | 3.2E-02                                                        | 0                               | 0                   | Firmicutes f_Bacillaceae                | NA                                              |
| SV-7098  | 0.71| NA          | 3.5E-03                          | 2.4E-04                          | 3.2E-03                                                        | 0                               | 0                   | unclassified                            | unclassified                                    |
| SV-16762 | 0.70| NA          | 1.5E-03                          | 1.6E-03                          | 0                                                              | 0                               | 0                   | Proteobacteria c_Gamma proteobacteria    | NA                                              |
| SV-13305 | 0.70| NA          | 1.5E-03                          | 2.3E-04                          | 1.0E-03                                                        | 6.1E-03                         | 0                   | Proteobacteria o_Rhizobiales            | NA                                              |
| SV-4136  | 0.70| NA          | 2.2E-03                          | 1.6E-02                          | 0                                                              | 0                               | 0                   | Firmicutes g_Bacillus                   | [21, reviewed in 22] [23, 24]                  |

1 point biserial correlation coefficient
2 Spearman correlation of the relative abundance of an SV with mean growth promotion including all 17 composts; with Benjamini Hochberg adjusted p-value.
3 letter preceding the lowest possible taxonomic classification corresponds to the taxonomic rank (g for genus, f for family, o for order, c for class)
NA not available
Supplementary Table 11: Relative abundance, occurrence and taxonomy of 75 SVs associated to strongly suppressive composts, i.e., H, I, K, L and Q. Potentially disease suppressive SVs were selected by comparing robustly detected SVs of the five most and the five least suppressive composts using indicator species analysis with point biserial correlation coefficient larger than 0.7 as a selection criterion. Mean relative sequence abundance of each SV was correlated with mean disease suppression including all 17 composts. For each SV, which was assigned to a genus, evidence from literature about its occurrence in composts and involvement in suppression against soil borne fungal and oomycete diseases was assessed (end October 2020).

| SV    | $R_{ee}^{1}$ | rho / p / n$^{2}$ | mean sequence abundance [%] in phylum | lowest taxonomic classification$^{2}$ | comparison to literature related to compost suppression |
|-------|--------------|------------------|----------------------------------------|--------------------------------------|-----------------------------------------------------|
|       |              |                  | highly suppr. composts | Phyllosaphe s of highly suppr. composts + Pu$^{3}$ | subst r ate | Rhizoplanes of substrate + Pu |                              |
| SV-437 | 0.95        | 0.57 / 0.031 / 16 | 6.9E-02 | 8.9E-03 | 1.0E-01 | 0 | 0 | Chloroflexi | c_OLB14 | NA | NA |
| SV-48  | 0.95        | 0.65 / 0.017 / 17 | 2.9E-01 | 8.6E-02 | 5.8E-01 | 0 | 1.9E-03 | Proteobacteria | o_Rhizobiales | NA | NA |
| SV-1095 | 0.90       | 0.78 / 0.007 / 17 | 3.5E-02 | 4.0E-03 | 3.6E-02 | 0 | 8.2E-03 | Proteobacteria | c_Gammaproteobacteria | NA | NA |
| SV-1471 | 0.89       | 0.65 / 0.017 / 17 | 6.4E-02 | 9.0E-03 | 4.2E-02 | 0 | 0 | Firmicutes | g_Ureibacillus | [25, 26] | No reference |
| SV-754  | 0.88        | 0.55 / 0.035 / 16 | 5.6E-02 | 9.3E-03 | 2.3E-02 | 0 | 5.9E-04 | Gemmatimonadetes | f_Gemmatimonadaceae | NA | NA |
| SV-25590 | 0.88    | NA | 1.9E-03 | 0 | 9.4E-04 | 0 | 0 | Proteobacteria | c_Gammaproteobacteria | NA | NA |
| SV-142  | 0.88        | 0.53 / 0.04 / 17 | 1.6E-01 | 2.7E-02 | 2.5E-01 | 0 | 5.6E-03 | Proteobacteria | c_Gammaproteobacteria | NA | NA |
| SV-2226 | 0.87        | 0.64 / 0.017 / 11 | 1.2E-02 | 4.0E-03 | 4.5E-02 | 0 | 1.1E-03 | Firmicutes | g_Ureibacillus | [25, 26] | No reference |
| SV-6646 | 0.87        | 0.68 / 0.013 / 11 | 2.6E-03 | 2.0E-04 | 1.8E-03 | 0 | 0 | Firmicutes | f_Limnochordaceae | NA | NA |
| SV-757  | 0.83        | 0.4 / 0.112 / 17 | 3.8E-02 | 1.2E-02 | 5.2E-02 | 0 | 6.3E-04 | Proteobacteria | c_Alphaproteobacteria | NA | NA |
| SV-11381 | 0.83      | NA | 5.8E-03 | 2.3E-04 | 4.2E-03 | 0 | 1.2E-03 | Firmicutes | g_Ureibacillus | [25, 26] | No reference |
| SV-458  | 0.82        | 0.64 / 0.017 / 17 | 8.6E-02 | 1.1E-02 | 5.3E-02 | 0 | 0 | Proteobacteria | o_Rhizobiales | NA | NA |
| SV-23516 | 0.82      | NA | 9.5E-04 | 0 | 8.3E-04 | 0 | 0 | Proteobacteria | c_Gammaproteobacteria | NA | NA |
| SV-2932 | 0.81        | 0.64 / 0.017 / 13 | 4.8E-02 | 2.9E-03 | 5.9E-03 | 0 | 0 | Proteobacteria | c_Gammaproteobacteria | NA | NA |
| SV-5576 | 0.80        | 0.63 / 0.017 / 14 | 6.8E-03 | 1.3E-03 | 2.1E-03 | 0 | 0 | Bacteroidetes | g_Natronofoxus | No reference | No reference |
| SV-6245 | 0.79        | NA | 2.6E-03 | 0 | 3.1E-03 | 0 | 0 | Firmicutes | f_Thermoactinomycetaceae | NA | NA |
| SV-162  | 0.79        | 0.57 / 0.033 / 17 | 1.4E-01 | 1.8E-02 | 5.7E-02 | 0 | 0 | Proteobacteria | c_Gammaphageae | [28, 29] | [30, 31] |
| SV-2898 | 0.79        | NA | 2.2E-02 | 4.9E-04 | 2.7E-03 | 0 | 0 | Firmicutes | o_Dadabacteriales | NA | NA |
| SV-3619 | 0.79        | NA | 2.1E-03 | 2.2E-04 | 1.1E-02 | 0 | 0 | Firmicutes | f_JG30-KF-CM45 | NA | NA |
| SV-3061 | 0.78        | 0.55 / 0.035 / 12 | 1.7E-02 | 1.3E-03 | 7.8E-03 | 0 | 0 | Gemmatimonadetes | f_Gemmatimonadaceae | NA | NA |
| SV-64   | 0.78        | 0.68 / 0.013 / 14 | 9.1E-02 | 5.1E-03 | 4.4E-02 | 1.1E-03 | 6.4E-03 | Bacteroidetes | g_Algoriphagus | [32, 33] | No reference |
| SV-13552 | 0.78      | NA | 1.6E-03 | 0 | 1.8E-04 | 0 | 0 | Actinobacteria | g_CL502-29_marine_group | NA | NA |
| SV-19698 | 0.78     | NA | 1.6E-03 | 0 | 1.9E-04 | 0 | 0 | Hydrogenobacte ria | f_Hydrogenobacteriales | NA | NA |
| SV-12   | 0.77        | 0.64 / 0.017 / 17 | 1.7E+00 | 5.5E-01 | 1.9E+00 | 4.2E-03 | 3.6E-03 | Chloroflexi | f_A4b | NA | NA |
| SV-5594 | 0.77        | NA | 3.7E-03 | 2.2E-04 | 4.5E-03 | 0 | 0 | Proteobacteria | c_Alphaproteobacteria | NA | NA |
| SV-1974 | 0.77        | 0.83 / 0.003 / 16 | 1.1E-02 | 1.6E-03 | 2.1E-02 | 0 | 0 | Firmicutes | f_Symbiobacterium | [34, 35] | No reference |
| SV-1477 | 0.77        | NA | 1.4E-02 | 2.3E-04 | 1.5E-02 | 0 | 0 | Gemmatimonadetes | c_S0134_ terrestrial_group | NA | NA |
| SV-5032 | 0.76        | NA | 4.5E-03 | 4.5E-04 | 2.5E-03 | 0 | 0 | Firmicutes | f_Limnochordaceae | NA | NA |
| SV-630  | 0.76        | NA | 4.5E-03 | 2.1E-04 | 1.3E-02 | 0 | 0 | Proteobacteria | c_Gammaphageae | [36, 37] | No reference |
| SV-9181 | 0.76        | NA | 2.6E-03 | 0 | 1.7E-03 | 0 | 0 | Firmicutes | g_Caldalkalibacillus | [38, 39] | No reference |
| SV-19508 | 0.76      | NA | 1.1E-03 | 0 | 0 | 0 | 0 | Proteobacteria | g_Bdellovibrio | [40, 41] | No reference |
| SV-13855 | 0.76      | NA | 1.1E-03 | 0 | 1.6E-03 | 0 | 0 | Firmicutes | f_Thermoanerobacterales_Family_III | NA | NA |
| SV-3867 | 0.76        | NA | 7.9E-03 | 1.1E-03 | 1.2E-02 | 0 | 0 | Proteobacteria | o_Rhizobiales | NA | NA |
| SV-3338 | 0.76        | NA | 1.4E-03 | 0 | 2.3E-03 | 0 | 0 | Proteobacteria | f_Xanthomonadaceae | NA | NA |
| SV      | 1 point biserial correlation coefficient | 2 Spearman correlation of the relative abundance of an SV with mean growth promotion including all 17 composts; with Benjamini Hochberg adjusted p-value. | 3 letter preceding the lowest possible taxonomic classification corresponds to the taxonomic rank (g for genus, f for family, o for order, c for class) |
|---------|-----------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------|
| SV-1081 | 0.76 0.53 / 0.04 / 17 5.5E-02 8.6E-03 1.6E-02 0 0 Proteobacteria o_Betaproteobacteriales NA NA |
| SV-6670 | 0.75 NA 8.7E-03 2.3E-04 4.7E-04 0 0 Proteobacteria g_Salinipirillum No reference No reference |
| SV-6347 | 0.75 NA 3.1E-03 0 1.6E-03 0 0 Firmicutes f_Limnochromaceae NA NA |
| SV-1760 | 0.75 0.59 / 0.025 / 16 1.5E-02 3.2E-03 2.4E-02 0 0 Gemmatimonadetes c_SO134_terrestrial_group NA NA |
| SV-3512 | 0.75 0.5 / 0.045 / 11 4.5E-03 1.8E-03 7.1E-03 0 0 Proteobacteria c_Deltaproteobacteria NA NA |
| SV-10781| 0.74 NA 2.6E-03 0 1.2E-03 0 0 Bacteroidetes g_Flavobacterium [18, 42] [43, 44] |
| SV-478 | 0.74 0.62 / 0.02 / 17 1.4E-01 1.1E-02 3.7E-02 0 0 Proteobacteria [45] No reference No reference |
| SV-658 | 0.74 NA 3.1E-03 0 1.6E-03 0 0 Firmicutes f_Limnochordaceae NA NA |
| SV-133 | 0.74 0.71 / 0.013 / 12 3.4E-02 7.1E-04 2.6E-01 0 0 Proteobacteria f_Burkholderiaceae NA NA |
| SV-2107 | 0.74 0.69 / 0.013 / 13 2.7E-02 1.1E-03 9.8E-03 0 0 Planctomycetes g_Pirellula [46, 47] No reference |
| SV-998 | 0.73 0.54 / 0.035 / 15 1.1E-01 3.5E-03 2.5E-02 0 0 Proteobacteria f_Burkholderiaceae NA NA |
| SV-3316 | 0.73 NA 3.9E-03 0 1.9E-03 0 0 Firmicutes g_Ruminiclostridium [48, 49] |
| SV-529 | 0.73 0.28 / 0.28 / 16 5.7E-02 2.2E-02 7.2E-03 0 0 Bacteroidetes g_Flavobacterium [42] |
| SV-5435 | 0.73 NA 2.4E-03 0 5.3E-03 0 0 Firmicutes c_Bacteroidia NA NA |
| SV-7931 | 0.72 0.51 / 0.042 / 14 4.2E-03 9.1E-04 6.7E-04 0 0 Proteobacteria o_R7C24 NA NA |
| SV-3861 | 0.72 NA 4.4E-03 0 2.0E-03 0 0 Bacteroidetes f_A4b NA NA |
| SV-2995 | 0.72 0.69 / 0.013 / 13 5.6E-03 2.4E-04 8.8E-03 0 0 Proteobacteria f_Devosiaceae NA NA |
| SV-2082 | 0.72 0.55 / 0.035 / 14 1.4E-02 1.6E-03 1.5E-02 0 0 Bacteroidetes f_Chitinophagaceae NA NA |
| SV-1543 | 0.72 0.67 / 0.017 / 15 5.4E-02 6.5E-03 2.0E-02 0 0 Bacteroidetes f_NS11-12_marine_group NA NA |
| SV-260 | 0.72 NA 1.4E-02 2.0E-04 1.3E-01 0 0 Firmicutes p_Firmicutes NA NA |
| SV-395 | 0.72 0.44 / 0.083 / 17 1.3E-01 5.4E-02 3.3E-02 0 0 Bacteroidetes o_R7C24 NA NA |
| SV-6873 | 0.71 NA 5.1E-03 0 5.2E-03 0 0 Bacteroidetes g_Pedobacter [50] [51, 52] |
| SV-1154 | 0.72 0.67 / 0.017 / 15 5.4E-02 6.5E-03 2.0E-02 0 0 Bacteroidetes f_Chitinophagaceae NA NA |
| SV-260 | 0.72 NA 1.4E-02 2.0E-04 1.3E-01 0 0 Firmicutes p_Firmicutes NA NA |
| SV-395 | 0.72 0.44 / 0.083 / 17 1.3E-01 5.4E-02 3.3E-02 0 0 Bacteroidetes o_R7C24 NA NA |
| SV-6873 | 0.71 NA 5.1E-03 0 5.2E-03 0 0 Bacteroidetes g_Pedobacter [50] [51, 52] |
| SV-1154 | 0.72 0.67 / 0.017 / 15 5.4E-02 6.5E-03 2.0E-02 0 0 Bacteroidetes f_Chitinophagaceae NA NA |
| SV-260 | 0.72 NA 1.4E-02 2.0E-04 1.3E-01 0 0 Firmicutes p_Firmicutes NA NA |
| SV-395 | 0.72 0.44 / 0.083 / 17 1.3E-01 5.4E-02 3.3E-02 0 0 Bacteroidetes o_R7C24 NA NA |
| SV-6873 | 0.71 NA 5.1E-03 0 5.2E-03 0 0 Bacteroidetes g_Pedobacter [50] [51, 52] |
| SV-1154 | 0.72 0.67 / 0.017 / 15 5.4E-02 6.5E-03 2.0E-02 0 0 Bacteroidetes f_Chitinophagaceae NA NA |
| SV-260 | 0.72 NA 1.4E-02 2.0E-04 1.3E-01 0 0 Firmicutes p_Firmicutes NA NA |
| SV-395 | 0.72 0.44 / 0.083 / 17 1.3E-01 5.4E-02 3.3E-02 0 0 Bacteroidetes o_R7C24 NA NA |
| SV-6873 | 0.71 NA 5.1E-03 0 5.2E-03 0 0 Bacteroidetes g_Pedobacter [50] [51, 52] |
| SV-1154 | 0.72 0.67 / 0.017 / 15 5.4E-02 6.5E-03 2.0E-02 0 0 Bacteroidetes f_Chitinophagaceae NA NA |
| SV-260 | 0.72 NA 1.4E-02 2.0E-04 1.3E-01 0 0 Firmicutes p_Firmicutes NA NA |
| SV-395 | 0.72 0.44 / 0.083 / 17 1.3E-01 5.4E-02 3.3E-02 0 0 Bacteroidetes o_R7C24 NA NA |
| SV-6873 | 0.71 NA 5.1E-03 0 5.2E-03 0 0 Bacteroidetes g_Pedobacter [50] [51, 52] |
Supplementary References

1. Vajna B, Szili D, Nagy A, Márialigeti K: An improved sequence-aided T-RFLP analysis of bacterial succession during oyster mushroom substrate preparation. *Microbial Ecology* 2012, 64:702-713.

2. Chen R, Wang Y, Wei S, Wang W, Lin X: Windrow composting mitigated CH$_4$ emissions: Characterization of methanogenic and methanotrophic communities in manure management. *FEMS Microbiology Ecology* 2014, 90:575-586.

3. Martínez-Hidalgo P, Hirsch A: The nodule microbiome: N$_2$-fixing rhizobia do not live alone. *Phytobiomes* 2017, 1:13.

4. Ardley JK, Parker MA, De Meyer SE, Trengove RD, O’Hara GW, Reeve WG, Dilworth MJ, Willems A, Howieson JG: *Microvirga lupini* sp. nov., *Microvirga lotononidis* sp. nov. and *Microvirga zambeziensis* sp. nov. are alphaproteobacterial root-nodule bacteria that specifically nodulate and fix nitrogen with geographically and taxonomically separate legume hosts. *International Journal of Systematic and Evolutionary Microbiology* 2012, 62:2579-2588.

5. Zhu L, Zhao Y, Zhang W, Zhou H, Chen X, Li Y, Wei D, Wei Z: Roles of bacterial community in the transformation of organic nitrogen toward enhanced bioavailability during composting with different wastes. *Bioresource Technology* 2019, 285:121326.

6. Cayuela ML, Mondini C, Insam H, Sinicco T, Franke-Whittle I: Plant and animal wastes composting: Effects of the N source on process performance. *Bioresource Technology* 2009, 100:3097-3106.

7. Sokhakhkh-Zamin F, Sachdev D, Kazemi-Pour N, Engineer A, Pardesi KR, Zinjarde S, Dhakephalkar PK, Chopade BA: Characterization of plant-growth-promoting traits of *Acinetobacter* species isolated from rhizosphere of *Pennisetum glaucum*. *J Microbiol Biotechnol* 2011, 21:556-566.

8. Kotoky R, Das S, Singha LP, Pandey P, Singh KM: Biodegradation of Benzo(a)pyrene by biofilm forming and plant growth promoting *Acinetobacter* sp. strain PDB4. *Environmental Technology & Innovation* 2017, 8:256-268.

9. Salamoni SP, Mann MB, Campos FS, Franco AC, Germani JC, Van Der Sand ST: Preliminary characterization of some Streptomyces species isolated from a composting process and their antimicrobial potential. *World Journal of Microbiology and Biotechnology* 2010, 26:1847-1856.

10. Kandasamy S, P D, Chendrayan, Uthandi S: Laccase producing streptomyces bikiniensis CSC12 isolated from compost. *Journal of microbiology, biotechnology and food sciences* 2016, 6:794-798.

11. Olanrewaju OS, Babalola OO: Streptomyces: implications and interactions in plant growth promotion. *Applied Microbiology and Biotechnology* 2019, 103:1179-1188.

12. Kamal R, Sharma A: Control of Fusarium wilt using biological agent Streptomyces sp.CPP-53 isolated from compost with plant growth promoting effect on tomato under greenhouse condition. *Journal of Microbiology and Antimicrobials* 2014, 6:97-103.

13. Carrasco J, Tello ML, de Toro M, Tkacz A, Poole P, Pérez-Clavijo M, Preston G: Casing microbiome dynamics during button mushroom cultivation: implications for dry and wet bubble diseases. *Microbiology* 2019, 165:611-624.

14. Tumuhairwe JB, Tenywa J: Bacterial community changes during composting of municipal crop waste using low technology methods as revealed by 16S rRNA. *African Journal of Environmental Science and Technology* 2018, 12:209-221.

15. Munoz-Ucros J, Panke-Buisse K, Robe J: Bacterial community composition of vermicompost-treated tomato rhizospheres. *PLOS ONE* 2020, 15:e0230577.

16. Mehboob I, Naveed M, Zahir ZA: Rhizobial association with non-Legumes: Mechanisms and applications. *Critical Reviews in Plant Sciences* 2009, 28:432-456.

17. Antoun H, Beauchamp CJ, Goussard N, Chabot R, Lalande R: Potential of *Rhizobium* and *Bradyrhizobium* species as plant growth promoting rhizobacteria on non-legumes: Effect on radishes (*Raphanus sativus* L.). *Plant and Soil* 1998, 204:57-67.

18. Sun Y, Men M, Xu B, Meng Q, Bello A, Xu X, Huang X: Assessing key microbial communities determining nitrogen transformation in composting of cow manure using illumina high-throughput sequencing. *Waste Management* 2019, 92:59-67.
19. Vivas A, Moreno B, García-Rodríguez S, Benítez E: Assessing the impact of composting and vermicomposting on bacterial community size and structure, and microbial functional diversity of an olive-mill waste. *Bioresource Technology* 2009, 100:1319-1326.

20. Singh N, Marwa N, Mishra Sk, Mishra J, Verma PC, Rathaur S, Singh N: *Brevundimonas diminuta* mediated alleviation of arsenic toxicity and plant growth promotion in *Oryza sativa* L. *Ecotoxicology and Environmental Safety* 2016, 125:25-34.

21. Lin Y, Du D, Si C, Zhao Q, Li Z, Li P: Potential biocontrol *Bacillus* sp. strains isolated by an improved method from vinegar waste compost exhibit antibiosis against fungal pathogens and promote growth of cucumbers. *Biological Control* 2014, 71:7-15.

22. Lutz S, Thuerig B, Oberhaensli T, Mayerhofer J, Fuchs JG, Widmer F, Freimoser FM, Ahrens CH: Harnessing the microbiomes of suppressive composts for plant protection: From metagenomes to beneficial microorganisms and reliable diagnostics. *Frontiers in Microbiology* 2020, 11.

23. Ghosh S, Penterman JN, Little RD, Chavez R, Glick BR: Three newly isolated plant growth-promoting bacilli facilitate the seedling growth of canola, *Brassica campestris*. *Plant Physiology and Biochemistry* 2003, 41:277-281.

24. Santoyo G, Orozco-Mosqueda MdC, Govindappa M: Mechanisms of biocontrol and plant growth-promoting activity in soil bacterial species of *Bacillus* and *Pseudomonas*: a review. *Biocontrol Science and Technology* 2012, 22:855-872.

25. Wang Y, Gong J, Li J, Xin Y, Hao Z, Chen C, Li H, Wang B, Ding M, Li W, et al: Insights into bacterial diversity in compost: Core microbiome and prevalence of potential pathogenic bacteria. *Science of The Total Environment* 2020, 718:137304.

26. Weon HY, Lee SY, Kim BY, Noh HJ, Schumann P, Kim JS, Kwon SW: *Ureibacillus composti* sp. nov. and *Ureibacillus thermophilus* sp. nov., isolated from livestock-manure composts. *International Journal of Systematic and Evolutionary Microbiology* 2007, 57:2908-2911.

27. Zhong XZ, Li XX, Zeng Y, Wang SP, Sun ZY, Tang YQ: Dynamic change of bacterial community during dairy manure composting process revealed by high-throughput sequencing and advanced bioinformatics tools. *Bioresource Technology* 2020, 306:123091.

28. Li M, Xu J, Jiang Z, Li Q: Molecular understanding of autotrophic CO2-fixing bacterial communities in composting based on RuBisCO genes analysis. *Journal of Biotechnology* 2020, 320:36-43.

29. Tian W, Sun Q, Xu D, Zhang Z, Chen D, Li C, Shen Q, Shen B: Succession of bacterial communities during composting process as detected by 16S rRNA clone libraries analysis. *International Biodeterioration & Biodegradation* 2013, 78:58-66.

30. Fujiwara K, Iida Y, Someya N, Takano M, Ohnishi J, Terami F, Shinohara M: Emergence of antagonism against the pathogenic fungus *Fusarium oxysporum* by interplay among non-antagonistic bacteria in a hydroponics using multiple parallel mineralization. *Journal of Phytopathology* 2016, 164:853-862.

31. Klein E, Ofek M, Katan J, Minz D, Gamliel A: Soil suppressiveness to *Fusarium* disease: Shifts in root microbiome associated with reduction of pathogen root colonization. *Phytopathology* 2013, 103:23-33.

32. Cai L, Gong X, Sun X, Li S, Yu X: Comparison of chemical and microbiological changes during the aerobic composting and vermicomposting of green waste. *PloS one* 2018, 13:e0207494-e0207494.

33. Ohno M, Shiratori H, Park MJ, Saitoh Y, Kumon Y, Yamashita N, Hirata A, Nishida H, Ueda K, Beppu T: *Symbiobacterium thermophilum* gen. nov., sp. nov., a symbiotic thermophile that depends on co-culture with a *Bacillus* strain for growth. *International Journal of Systematic and Evolutionary Microbiology* 2000, 50:1829-1832.

34. Williams LE, Kleinschmidt CE, Mecca S: Bacterial communities in the digester bed and liquid effluent of a microflush composting toilet system. *PeerJ* 2018, 6:e6077-e6077.

35. Williams LE, Kleinschmidt CE, Mecca S: Bacterial communities in the digester bed and liquid effluent of a microflush composting toilet system. *PeerJ* 2018, 6:e6077-e6077.

36. Ohno M, Shiratori H, Park MJ, Saitoh Y, Kumon Y, Yamashita N, Hirata A, Nishida H, Ueda K, Beppu T: *Symbiobacterium thermophilum* gen. nov., sp. nov., a symbiotic thermophile that depends on co-culture with a *Bacillus* strain for growth. *International Journal of Systematic and Evolutionary Microbiology* 2000, 50:1829-1832.
37. Obi L, Atagana H, Adeleke R, Maila M, Bamuza-Pemu E: Potential microbial drivers of biodegradation of polycyclic aromatic hydrocarbons in crude oil sludge using a composting technique. *Journal of Chemical Technology & Biotechnology* 2020, 95:1569-1579.

38. Chi CP, Chu S, Wang B, Zhang D, Zhi Y, Yang X, Zhou P: Dynamic bacterial assembly driven by *Streptomyces griseorubens* JSD-1 inoculants correspond to composting performance in swine manure and rice straw co-composting. *Bioresource Technology* 2020, 313:123692.

39. Kong W, Sun B, Zhang J, Zhang Y, Gu L, Bao L, Liu S: Metagenomic analysis revealed the succession of microbiota and metabolic function in corn cob composting for preparation of cultivation medium for *Pleurotus ostreatus*. *Bioresource Technology* 2020, 306:123156.

40. Koval SF, Hynes SH, Flannagan RS, Pasternak Z, Davidov Y, Jurkevitch E: *Bdellovibrio exovorus* sp. nov., a novel predator of *Caulobacter crescentus*. *International Journal of Systematic and Evolutionary Microbiology* 2013, 63:146-151.

41. Lei L, Gu J, Wang X, Song Z, Yu J, Wang J, Dai X, Zhao W: Effects of phosphogypsum and medical stone on nitrogen transformation, nitrogen functional genes, and bacterial community during aerobic composting. *Science of The Total Environment* 2021, 753:141746.

42. Kim J-J, Kanaya E, Weon H-Y, Koga Y, Takano K, Dunfield PF, Kwon S-W, Kanaya S: *Flavobacterium compostarboris* sp. nov., isolated from leaf-and-branch compost, and emended descriptions of *Flavobacterium hercynium*, *Flavobacterium resistens* and *Flavobacterium johnsoniae*. *International Journal of Systematic and Evolutionary Microbiology* 2012, 62:2018-2024.

43. Kwok OCH, Fahy PC, Hoitink HJ, Kuter GA: Interactions between bacteria and *Trichoderma hamatum* in suppression of *Rhizoctonia* damping-off in bark compost media. *Phytopathology* 1987, 77:1206-1212.

44. Sang MK, Kim KD: The volatile-producing *Flavobacterium johnsoniae* strain GSE09 shows biocontrol activity against *Phytophthora capsici* in pepper. *Journal of Applied Microbiology* 2012, 113:383-398.

45. Akyol Ç, Ince O, Ince B: Crop-based composting of lignocellulosic digestates: Focus on bacterial and fungal diversity. *Bioresource Technology* 2019, 288:121549.

46. De Gannes V, Eudoxie G, Hickey WJ: Prokaryotic successions and diversity in composts as revealed by 454-pyrosequencing. *Bioresource Technology* 2013, 133:573-580.

47. Sukhumavasi J, Ohmiya K, Shimizu S, Ueno K: *Clostridium josui* sp. nov., a cellulolytic, moderate thermophilic species from Thai compost. *International Journal of Systematic and Evolutionary Microbiology* 1988, 38:179-182.

48. Cao G, Song T, Shen Y, Jin Q, Feng W, Fan L, Cai W: Diversity of bacterial and fungal communities in wheat straw compost for *Agaricus bisporus* cultivation. *HortScience* 2019, 54:100-109.

49. Lee H-G, Kim S-G, Im W-T, Oh H-M, Lee S-T: *Pedobacter composti* sp. nov., isolated from compost. *International Journal of Systematic and Evolutionary Microbiology* 2009, 59:345-349.

50. Weon HY, Kim BY, Kwon SW, Park IC, Cha IB, Tindall BJ, Stackebrandt E, Trüper HG, Go SJ: *Leadbetterella byssophilica* gen. nov., sp. nov., isolated from cotton-waste composts for the cultivation of oyster mushroom. *Int J Syst Evol Microbiol* 2005, 55:2297-2302.
56. Kalinovskaya NI, Romanenko LA, Kalinovsky AI: Antibacterial low-molecular-weight compounds produced by the marine bacterium Rheinheimera japonica KMM 9513T. Antonie van Leeuwenhoek 2017, 110:719-726.

57. Wang C, Dong D, Wang H, Müller K, Qin Y, Wang H, Wu W: Metagenomic analysis of microbial consortia enriched from compost: new insights into the role of Actinobacteria in lignocellulose decomposition. Biotechnology for Biofuels 2016, 9:22.

58. Krishnan Y, Bong CPC, Azman NF, Zakaria Z, Othman NA, Abdullah N, Ho CS, Lee CT, Hansen SB, Hara H: Co-composting of palm empty fruit bunch and palm oil mill effluent: Microbial diversity and potential mitigation of greenhouse gas emission. Journal of Cleaner Production 2017, 146:94-100.

59. Yin Y, Gu J, Wang X, Song W, Zhang K, Sun W, Zhang X, Zhang Y, Li H: Effects of copper addition on copper resistance, antibiotic resistance genes, and intI1 during swine manure composting. Frontiers in Microbiology 2017, 8.

60. Vida C, Bonilla N, de Vicente A, Cazorla FM: Microbial profiling of a suppressiveness-induced agricultural soil amended with composted almond shells. Frontiers in Microbiology 2016, 7.

61. Wang G, Govinden R, Chenia HY, Ma Y, Guo D, Ren G: Suppression of Phytophthora blight of pepper by biochar amendment is associated with improved soil bacterial properties. Biology and Fertility of Soils 2019, 55:813-824.

62. Zhang X, Zhong Y, Yang S, Zhang W, Xu M, Ma A, Zhuang G, Chen G, Liu W: Diversity and dynamics of the microbial community on decomposing wheat straw during mushroom compost production. Bioresource Technology 2014, 170:183-195.