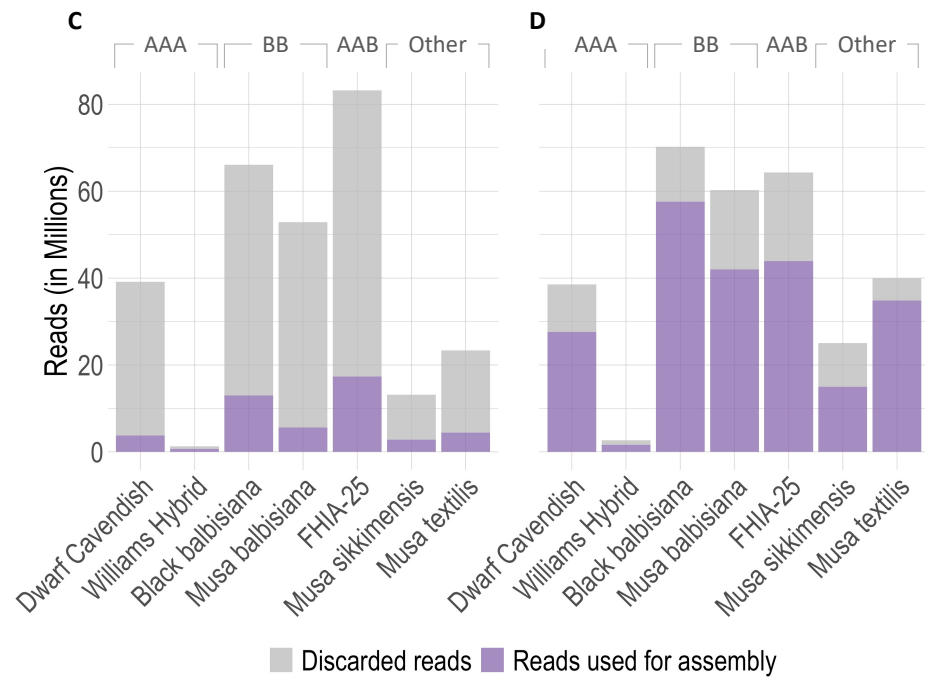
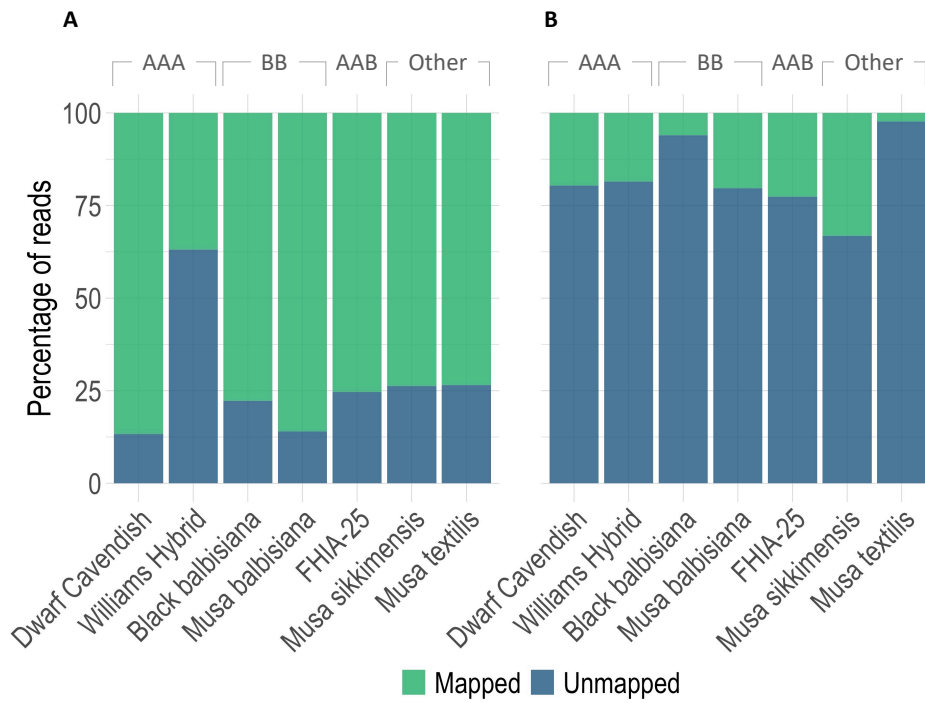


Supplementary Tables and Figures

Supplementary Table 1: Comparison of number of sequenced reads that mapped to *Musa acuminata* and *Musa balbisiana* reference genomes for endophytic microbiomes from 14 sampled *Musa* cultivars and tissues. Sample names refer to the 14 *Musa* samples listed in **Table 1**.

| Sample | <i>Musa acuminata</i> | | | <i>Musa balbisiana</i> | | |
|--------|-----------------------|------------|-------------|------------------------|------------|-------------|
| | Merged | Paired | Total | Merged | Paired | Total |
| BBC | 46 450 660 | 20 273 696 | 66 724 356 | 45 917 687 | 20 032 633 | 65 950 320 |
| BBL | 16 244 953 | 4 218 444 | 20 463 397 | 11 503 987 | 3 254 487 | 14 758 474 |
| DCL | 3 175 932 | 907 304 | 4 083 236 | 4 280 926 | 923 967 | 5 204 893 |
| DCR | 24 507 376 | 6 431 093 | 30 938 469 | 24 614 729 | 6 389 508 | 31 004 237 |
| FHC | 38 130 315 | 13 726 480 | 51 856 795 | 36 695 875 | 13 055 913 | 49 751 788 |
| FHL | 16 325 027 | 5 962 142 | 22 287 169 | 15 305 348 | 5 207 791 | 20 513 139 |
| MBL | 8 252 147 | 4 251 722 | 12 503 869 | 4 596 796 | 2 815 348 | 7 412 144 |
| MBR | 37 300 884 | 12 572 584 | 49 873 468 | 35 905 426 | 12 101 084 | 48 006 510 |
| MSL | 2 705 870 | 929 858 | 3 635 728 | 2 613 297 | 850 979 | 3 464 276 |
| MSR | 13 652 914 | 3 374 732 | 17 027 646 | 13 413 921 | 3 292 485 | 16 706 406 |
| MTC | 30 968 791 | 8 183 841 | 39 152 632 | 30 863 830 | 8 155 691 | 39 019 521 |
| MTL | 5 630 295 | 2 609 028 | 8 239 323 | 4 071 599 | 2 108 008 | 6 179 607 |
| WHC | 833 453 | 1 394 276 | 2 227 729 | 830 678 | 1 362 416 | 2 193 094 |
| WHL | 544 241 | 248 538 | 792 779 | 556 956 | 248 001 | 804 957 |
| Sum | 244 722 858 | 85 083 738 | 329 806 596 | 231 171 055 | 79 798 311 | 310 969 366 |

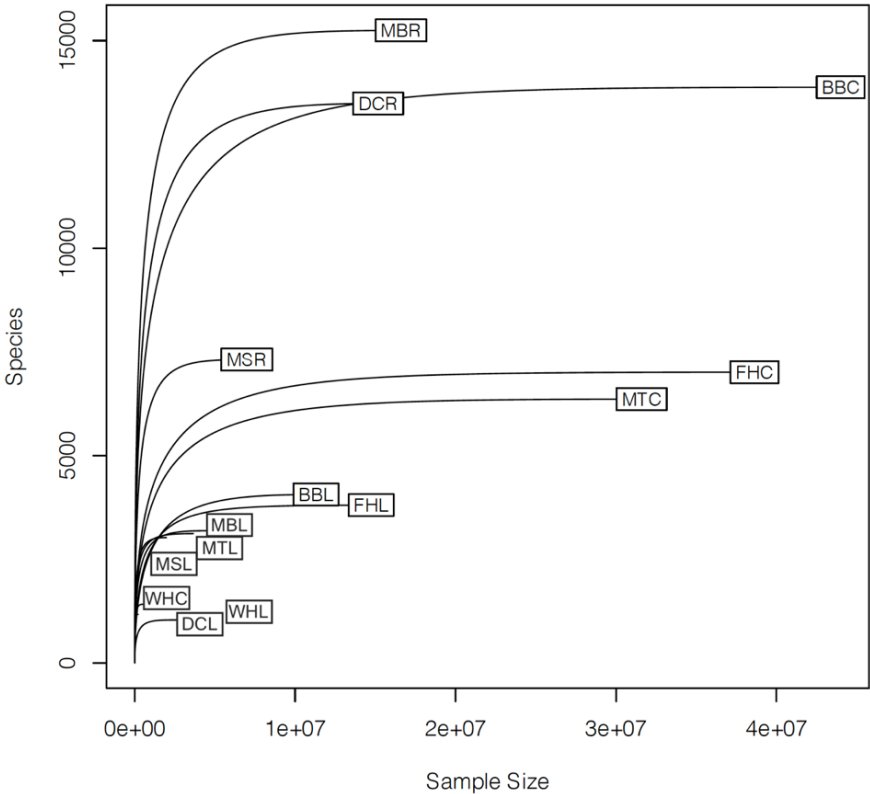
Supplementary Figure 1: Reads obtained from endophytic microbiomes from 14 sampled *Musa* cultivars and tissues, for (A) and (B) percentage of reads that mapped to 11 chromosomes of *Musa balbisiana* (DH-PKW), comparing samples grouped according to (A) leaf to (B) root tissues, and for (C) and (D) remaining reads (in millions) after quality-filtering and mapping to remove *Musa* reads for endophytic microbiomes for (C) leaf and (B) root (sequenced reads are represented by respective bar length whereas reads used for assembly are displayed as purple portions). Sample names and host genotypes are described on the x-axis.



Supplementary Table 2: Assembly statistics for metagenomes generated from endophytic microbiomes for 14 sampled *Musa* cultivars and tissues, assessed using QUAST. Sample names refer to the 14 *Musa* samples listed in **Table 1**.

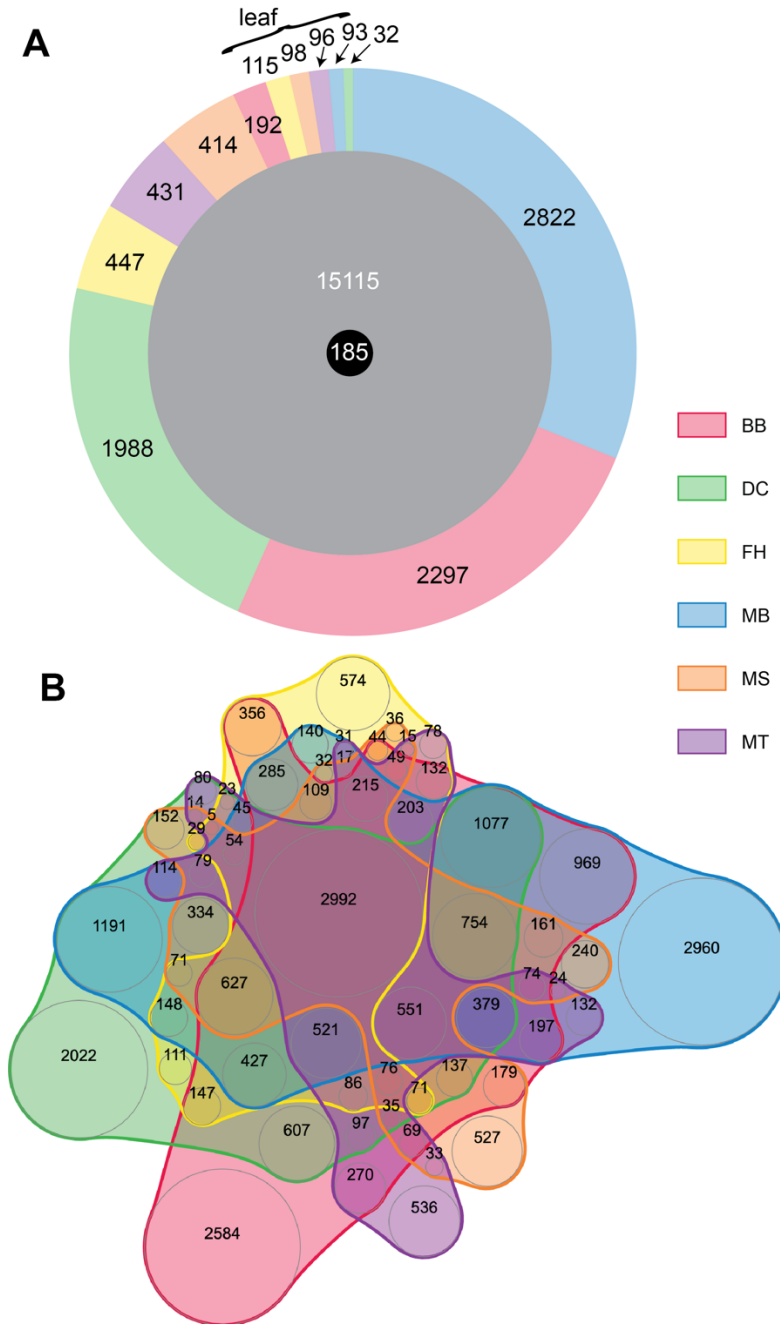
| Sample | N50 | Total length (Mb) | # Scaffolds | # Scaffolds >10kb | # Scaffolds >50kb | Largest scaffold (kbp) |
|--------|-------|-------------------|-------------|-------------------|-------------------|------------------------|
| BBC | 1 829 | 495.81 | 493 020 | 3299 | 268 | 610.05 |
| BBL | 4 956 | 59.45 | 46 779 | 606 | 62 | 663.95 |
| DCL | 1 111 | 28.51 | 45 011 | 11 | 0 | 13.95 |
| DCR | 995 | 326.34 | 429 726 | 721 | 159 | 571.3 |
| FHC | 2 818 | 173.18 | 150 230 | 1 301 | 140 | 960.09 |
| FHL | 1 769 | 86.53 | 91 272 | 552 | 87 | 433.94 |
| MBL | 3 749 | 70.71 | 52 600 | 552 | 84 | 672.24 |
| MBR | 956 | 335.36 | 455 985 | 1 068 | 69 | 550.14 |
| MSL | 1 616 | 63.33 | 63 091 | 234 | 2 | 74.77 |
| MSR | 1 228 | 118.88 | 142 412 | 326 | 33 | 240.6 |
| MTC | 4 162 | 190.37 | 145 440 | 2 025 | 271 | 642.9 |
| MTL | 3 125 | 63.05 | 46 243 | 449 | 75 | 276.32 |
| WHC | 1 506 | 15.3 | 16 001 | 163 | 0 | 39.05 |
| WHL | 857 | 7.36 | 10 902 | 0 | 0 | 9.6 |

Supplementary Figure 2: Alpha rarefaction curves representing the observed number of OTUs versus the number of sampled sequences for endophytic microbiomes from 14 sampled Musa cultivars and tissues. Letters in boxes refer to the 14 Musa samples listed in **Table 1**.



Supplementary Table 3: List of normalized read abundances of taxa detected with DIAMOND blastx in metagenomes assembled from 12 *Musa* samples (see additional excel file) showing unfiltered results, filtering for separate kingdoms, and showing taxon overlap results used in Venn diagrams.

Supplementary Figure 3: Number of shared and unshared taxa at lowest taxonomic levels (mostly species and strains) for endophytic microbiomes from 12 sampled *Musa* listed in **Table 1**, with (A) leaf and root compared individually, showing few universal ‘core’ taxa (black circle) occurring in every sample, compared to ‘shell’ taxa shared among two or more samples (grey circle) and unique unshared ‘cloud’ taxa (colored), and (B) communities for each *Musa* genotype combining tissues, leaf and root, showing each shared or unshared group via proportional area Venn drawing. Color legend for (A) and (B) indicates sampled genotypes BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*.



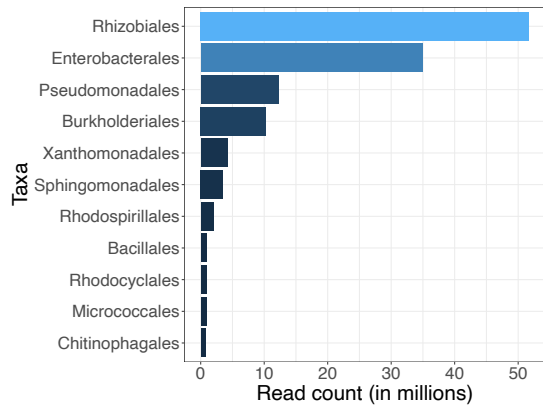
Supplementary Table 4: Pan-community analysis (see additional excel file) comparing the samples with the largest numbers of unique ‘cloud’ taxa, MBR, BBC, and DCR (which comprise BB and AAA genotypes), showing taxon overlap results used in Venn diagrams.

Supplementary Table 5: Taxonomic distribution of shotgun sequencing reads from endophytic microbiomes of 14 sampled *Musa* cultivars and tissues classified by proportion of reads mapping to scaffolds classified to superkingdom level by DIAMOND blast matches to the NCBI nr database. Sample names refer to the 14 *Musa* samples listed in **Table 1**.

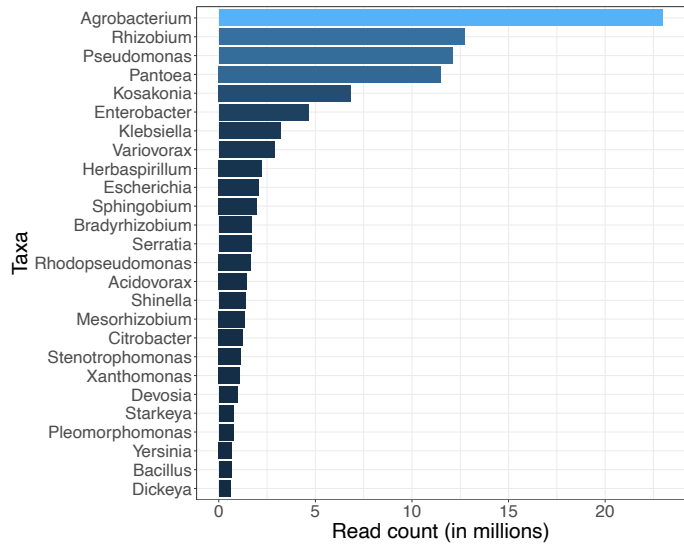
| Sample | Archaea | Bacteria | Fungi | Eukaryota (excluding fungi) | Viruses | Unclassified |
|--------|---------|-------------|-----------|-----------------------------------|---------|--------------|
| BBC | 762 | 37 771 951 | 570 279 | 1 403 106 | 8 429 | 4 257 053 |
| BBL | 14 | 5 909 428 | 4 848 | 2 023 489 | 19 484 | 3 340 617 |
| DCL | 6 | 40 593 | 997 | 586 878 | 12 364 | 1 945 959 |
| DCR | 23 250 | 12 418 597 | 59 511 | 505 411 | 2 909 | 2 167 819 |
| FHC | 68 | 20 915 106 | 1943 539 | 6 983 485 | 23 193 | 8 771 237 |
| FHL | 21 | 2 712 599 | 11 024 | 4 087 313 | 23 582 | 7 903 883 |
| MBL | 15 | 2 373 711 | 74 181 | 923 341 | 9 007 | 1 069 717 |
| MBR | 2 380 | 11 516 114 | 157 361 | 1 287 650 | 15 588 | 3 619 918 |
| MSL | 3 | 1 108 830 | 28 600 | 155 063 | 10 496 | 675 843 |
| MSR | 1 482 | 4 249 519 | 75 777 | 557 496 | 12 804 | 2 091 792 |
| MTC | 104 | 26 814 612 | 961 989 | 1 492 809 | 5 335 | 2 326 017 |
| MTL | 0 | 1 975 112 | 16 039 | 522 302 | 6 511 | 1 137 460 |
| WHC | 0 | 311 502 | 17 399 | 53 204 | 23 | 186 095 |
| WHL | 0 | 183 971 | 16 | 4 891 | 32 | 23 600 |
| Sum | 28 105 | 128 301 645 | 3 921 560 | 20 586 438 | 149 757 | 39 517 010 |

Supplementary Figure 4: Bacterial read counts from endophytic microbiomes of 14 sampled *Musa* cultivars and tissues for all samples (non-normalized) that were taxonomically assigned to level of (A) order or (B) genus by mapping to scaffolds classified based on DIAMOND blastn to the nr database, showing only taxa with more than 0.5% abundance.

A



B



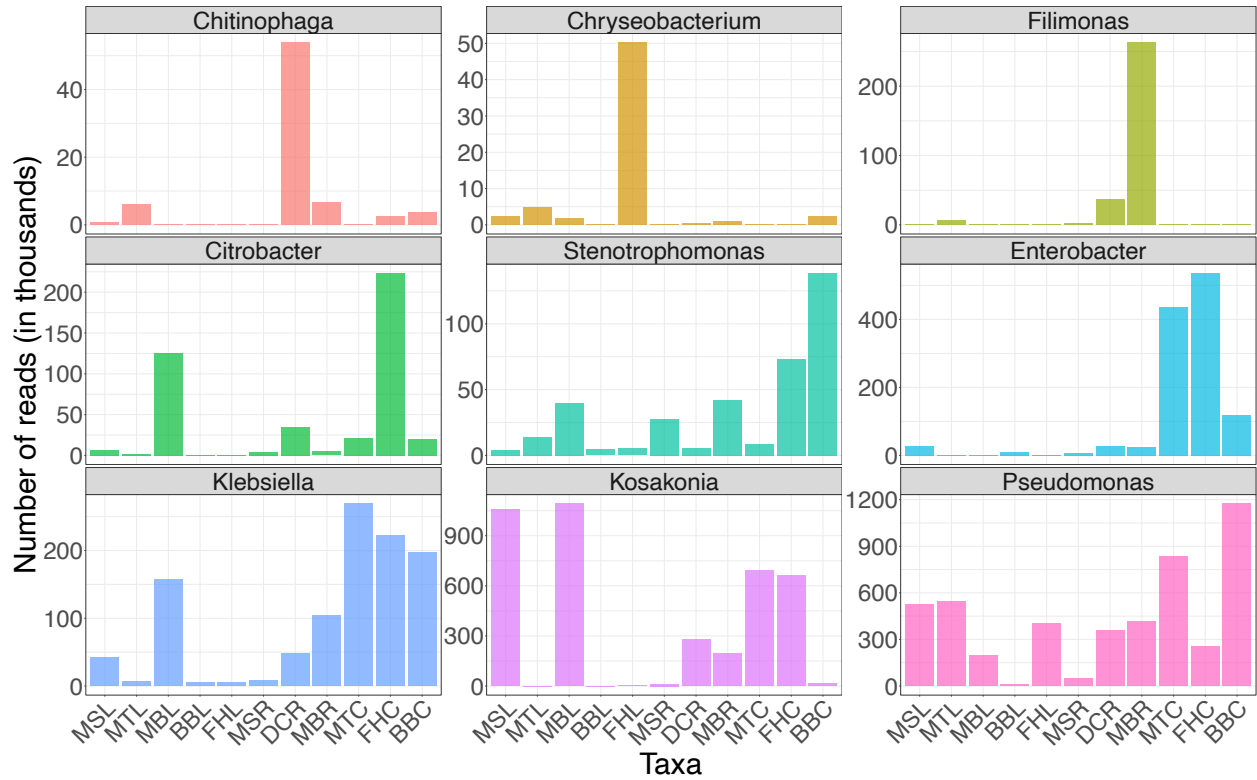
Supplementary Table 6: Bacterial taxa that were more abundant in below-ground (root) than above-ground (leaf) from endophytic microbiomes from sampled *Musa* cultivars and tissues for *Musa* samples listed in **Table 1** excluding DCL, WHC and WHL due to low sample sizes. P-values were from Welch's two sample t-tests analyzed *post hoc* following statistically significant ANOVA comparison between groups. Only taxa present in all samples were compared.

| Class | Order | Family | Genus | t-value | p-value |
|---------------------|-------------------|----------------------|-----------------------|---------|---------|
| Actinomycetia | Corynebacteriales | N/A | N/A | 3.56 | 0.01 |
| Actinomycetia | Corynebacteriales | Mycobacteriaceae | N/A | 3.47 | 0.02 |
| Alphaproteobacteria | Hyphomicrobiales | Parvibaculaceae | N/A | 2.82 | 0.04 |
| Alphaproteobacteria | Hyphomicrobiales | Methylobacteriaceae | N/A | 2.33 | 0.05 |
| Alphaproteobacteria | Hyphomicrobiales | Pleomorphomonadaceae | <i>Methylobrevis</i> | 2.51 | 0.04 |
| Alphaproteobacteria | Hyphomicrobiales | Beijerinckiaceae | N/A | 2.65 | 0.04 |
| Alphaproteobacteria | Hyphomicrobiales | Stappiaceae | <i>Stappia</i> | 2.71 | 0.04 |
| Alphaproteobacteria | Hyphomicrobiales | Kiastiaceae | <i>Kaistia</i> | 3.52 | 0.02 |
| Alphaproteobacteria | Hyphomicrobiales | Methylobacteriaceae | <i>Microvirga</i> | 2.58 | 0.04 |
| Alphaproteobacteria | Hyphomicrobiales | Bradyrhizobiaceae | <i>Bradyrhizobium</i> | 2.94 | 0.03 |
| Alphaproteobacteria | Hyphomicrobiales | Bradyrhizobiaceae | <i>Afipia</i> | 2.67 | 0.04 |
| Alphaproteobacteria | Hyphomonadales | N/A | N/A | 2.43 | 0.04 |
| Alphaproteobacteria | Hyphomonadales | Hyphomonadaceae | N/A | 2.43 | 0.04 |
| Alphaproteobacteria | Rhodospirillales | N/A | N/A | 2.72 | 0.04 |
| Alphaproteobacteria | Rhodospirillales | Azospirillaceae | <i>Nitrospirillum</i> | 3.39 | 0.02 |
| Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | N/A | 2.7 | 0.04 |
| Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | <i>Granulibacte</i> | 3.21 | 0.02 |
| Betaproteobacteria | Burkholderiales | Comamonadaceae | <i>Variovorax</i> | 3.18 | 0.02 |
| Betaproteobacteria | Burkholderiales | Comamonadaceae | N/A | 3.07 | 0.03 |
| Betaproteobacteria | Burkholderiales | Burkholderiaceae | <i>Ralstonia</i> | 3.57 | 0.02 |
| Betaproteobacteria | Burkholderiales | Burkholderiaceae | <i>Cupriavidus</i> | 3.05 | 0.03 |
| Gammaproteobacteria | Xanthomonadales | Rhodanobacteraceae | <i>Dyella</i> | 3.14 | 0.03 |

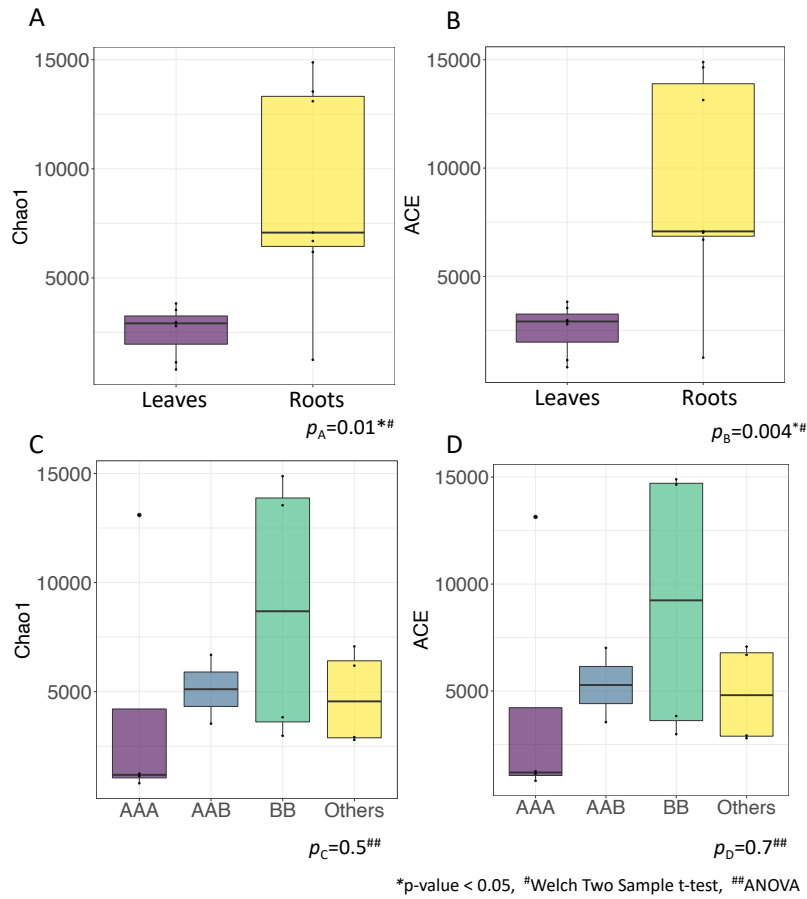
Supplementary Table 7: Bacterial taxa that were differentially abundant among BB and AAB and other *Musa* genotypes from endophytic microbiomes from sampled *Musa* cultivars and tissues for *Musa* samples listed in **Table 1**, showing ANOVA results and Welch’s t-tests from *post hoc* comparisons among taxa. Moraxellaceae, *Luteimonas*, and *Solimonas* were more abundant in *M. balbisiana* BB samples whereas Rhizobiales, *Hoeflea*, and *Neorhizobium* were more abundant in *M. sikkimensis* and *M. textilis* compared to FHIA-25 (AAB).

| Order | Family | Genus | ANOVA p-value | Pairwise t-test p-value | | |
|------------------|--------------------|-----------------------|---------------|-------------------------|-----------|----------|
| | | | | AAB-BB | AAB-Other | BB-Other |
| Rhizobiales | N/A | N/A | 0.25 | | 0.005 | |
| Hyphomicrobiales | Phyllobacteriaceae | <i>Hoeflea</i> | 0.21 | | 0.03 | |
| Hyphomicrobiales | Rhizobiaceae | <i>Neorhizobium</i> | 0.43 | | 0.05 | |
| Pseudomonadales | Moraxellaceae | N/A | 0.002 | | | |
| Myxococcales | Myxococcaceae | <i>Coralloccoccus</i> | 0.56 | | 0.01 | |
| Nevskiales | Sinobacteraceae | <i>Solimonas</i> | 0.04 | | | |
| Xanthomadales | Xanthomonadaceae | <i>Luteimonas</i> | 0.005 | 0.01 | | 0.02 |

Supplementary Figure 5: Normalized abundances between samples for specific genera of Bacteroidetes and Gammaproteobacteria from endophytic microbiomes from sampled *Musa* cultivars that were previously observed to potentially inhibit *Fusarium oxysporum* f. sp. *cubense* activity. Letters on the horizontal axis refer to the 14 *Musa* samples listed in **Table 1**. Samples DCL, WHC and WHL were excluded due to small sample size.



Supplementary Figure 6: Comparison of alpha diversity in endophytic microbiomes of 14 sampled *Musa* cultivars and tissues grouped according to (A, B) tissue location (leaves or roots) or (C, D) plant genotype (*M. acuminata* Dwarf Cavendish and Williams Hybrid = AAA, *M. acuminata* FHIA-25 = AAB, *M. balbisiana* and *M. balbisiana* ‘Thai Black’ = BB, *M. sikkimensis* and *M. textilis* = Others). Diversity was calculated by either the Chao1-index or ACE-index based on shotgun sequence reads mapped to taxonomically classified scaffolds.



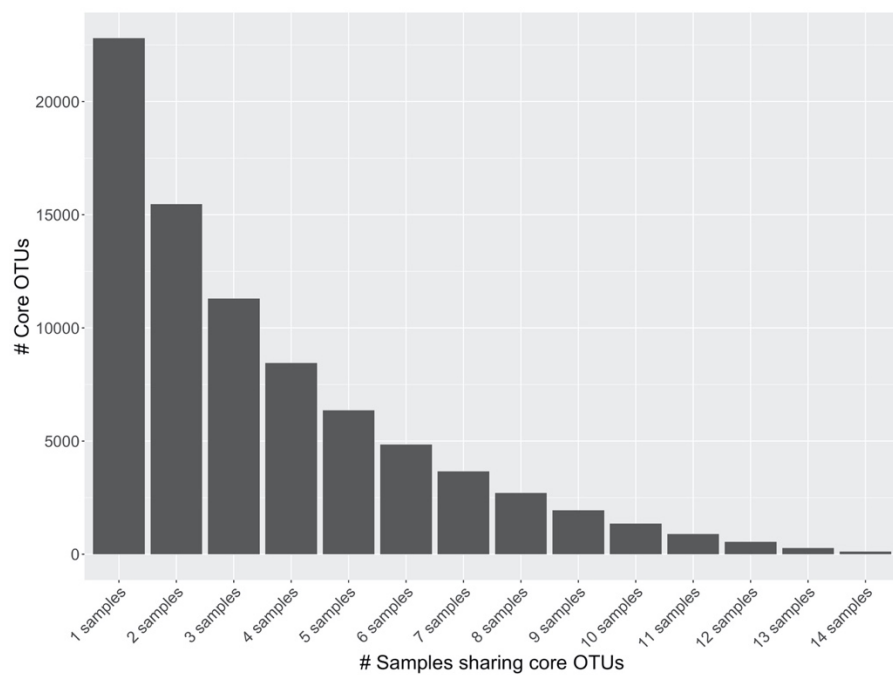
Supplementary Table 8: Alpha diversity indices for endophytic microbiomes of 14 sampled *Musa* cultivars and tissues for samples listed in **Table 1**. SVs are sequence variants generated in phyloseq based on shotgun sequence reads mapped to taxonomically classified scaffolds.

| Sample | Observed SVs | Chao1 | se.chao1 | ACE | se.ACE | Shannon | Simpson | InvSimpson | Fisher |
|--------|--------------|----------|----------|----------|--------|---------|---------|------------|---------|
| BBC | 13543 | 14649.26 | 67.97 | 14704.98 | 59.79 | 5.4 | 0.98 | 50.24 | 1567.62 |
| BBL | 3829 | 3829 | 0.04 | 3829.52 | 30.89 | 2.31 | 0.77 | 4.28 | 387.93 |
| DCL | 804 | 804 | 0 | 804 | 4.63 | 0.25 | 0.05 | 1.06 | 69.75 |
| DCR | 13097 | 13139.73 | 8.25 | 13190.43 | 56.4 | 5.26 | 0.97 | 30.34 | 1509.49 |
| FHC | 6692 | 7016.95 | 31.93 | 7098.06 | 41.34 | 3.78 | 0.91 | 10.63 | 723.85 |
| FHL | 3536 | 3542.53 | 3.1 | 3550.54 | 29.46 | 1.79 | 0.45 | 1.81 | 360.17 |
| MBL | 2979 | 2979 | 0 | 2979 | 21.97 | 3.42 | 0.88 | 8.57 | 294.65 |
| MBR | 14877 | 14896.92 | 5.42 | 14921.87 | 59.55 | 5.28 | 0.94 | 16.47 | 1754.49 |
| MSL | 2794 | 2794 | 0 | 2794 | 9.68 | 3.48 | 0.84 | 6.39 | 269.99 |
| MSR | 7077 | 7077 | 0 | 7077 | 36.66 | 3.89 | 0.88 | 8.01 | 759.73 |
| MTC | 6195 | 6691.71 | 45.74 | 6691.48 | 40.32 | 4.29 | 0.97 | 28.99 | 652.07 |
| MTL | 2919 | 2919 | 0 | 2919 | 15.81 | 3.62 | 0.86 | 6.94 | 285.58 |
| WHC | 1247 | 1247 | 0 | NA | NA | 3.04 | 0.83 | 5.75 | 111.15 |
| WHL | 1133 | 1133 | 0 | NA | NA | 3.47 | 0.82 | 5.47 | 99.33 |

Supplementary Table 9: Ordination values based on Bray-Curtis dissimilarity among endophytic microbiomes from 14 sampled *Musa* cultivars and tissues listed in **Table 1** based on shotgun sequence reads mapped to taxonomically classified scaffolds.

| Sample | Axis.1 | Axis.2 | Axis.3 | Axis.4 | Axis.5 | Axis.6 |
|--------|-----------|-----------|-----------|-----------|-----------|-----------|
| BBC | 0.372814 | 0.019434 | 0.000112 | -0.131983 | -0.140008 | 0.198154 |
| BBL | -0.191006 | 0.056104 | -0.028594 | 0.160933 | -0.21589 | 0.11076 |
| DCL | -0.401249 | 0.037994 | 0.060917 | -0.234468 | 0.122027 | 0.057081 |
| DCR | 0.289755 | 0.051271 | -0.24421 | -0.051957 | 0.12364 | 0.00951 |
| FHC | 0.088003 | -0.257474 | 0.179089 | 0.033634 | 0.008093 | -0.099456 |
| FHL | -0.301147 | 0.082167 | 0.061513 | -0.132139 | 0.122938 | 0.082725 |
| MBL | -0.089589 | -0.255576 | 0.025574 | 0.257816 | 0.114559 | 0.071626 |
| MBR | 0.11496 | -0.081341 | -0.288359 | -0.00685 | 0.080999 | 0.013922 |
| MSL | -0.153009 | 0.025109 | 0.023791 | 0.082092 | 0.073175 | -0.182239 |
| MSR | -0.112102 | -0.042066 | -0.247677 | -0.043689 | -0.134868 | -0.200375 |
| MTC | 0.409345 | -0.134091 | 0.218502 | -0.073084 | 0.052607 | -0.02376 |
| MTL | -0.15055 | 0.046771 | 0.005088 | 0.124905 | -0.045134 | 0.167899 |
| WHC | -0.078847 | -0.025762 | 0.114971 | -0.125905 | -0.220134 | -0.11467 |
| WHL | 0.202621 | 0.477459 | 0.119283 | 0.140694 | 0.057996 | -0.091178 |
| | | | | | | |
| Sample | Axis.7 | Axis.8 | Axis.9 | Axis.10 | Axis.11 | Axis.12 |
| BBC | 0.206746 | -0.068856 | -0.069413 | -0.048225 | -0.030924 | 0.016586 |
| BBL | -0.197525 | -0.043527 | -0.144383 | 0.01662 | -0.049931 | -0.011659 |
| DCL | -0.003421 | 0.018027 | -0.098426 | 0.013255 | 0.026544 | -0.0099 |
| DCR | -0.163942 | -0.026203 | 0.00297 | -0.112797 | 0.083233 | 0.081647 |
| FHC | 0.001119 | 0.085112 | -0.044053 | 0.073704 | -0.056141 | 0.145312 |
| FHL | 0.000178 | -0.006376 | 0.030049 | 0.032342 | -0.012866 | 0.008576 |
| MBL | 0.10162 | 0.060832 | -0.062779 | -0.072351 | 0.106608 | -0.054369 |
| MBR | 0.003398 | 0.162338 | 0.038725 | 0.050311 | -0.145388 | -0.067642 |
| MSL | 0.056137 | -0.205117 | 0.024865 | -0.124742 | -0.118988 | -0.007131 |
| MSR | 0.092794 | -0.081807 | -0.019753 | 0.126772 | 0.101182 | -0.006289 |
| MTC | -0.12902 | -0.112499 | 0.037568 | 0.08368 | 0.024649 | -0.098746 |
| MTL | 0.012681 | -0.04876 | 0.246896 | 0.058003 | 0.021738 | 0.042455 |
| WHC | -0.034852 | 0.16468 | 0.097771 | -0.139675 | 0.02847 | -0.033914 |
| WHL | 0.054086 | 0.102157 | -0.040038 | 0.043102 | 0.021813 | -0.004926 |

Supplementary Figure 7. Comparison of OTUs shared between endophytic microbiomes of 14 sampled *Musa* cultivars and tissues listed in **Table 1**.



Supplementary Table 10: Number of predicted genes from endophytic microbiomes from 12 sampled *Musa* listed in **Table 1**, after normalizing scaffolds among samples, showing numbers of genes before and after removing redundant paralogs and genes of unknown function denoted ‘hypothetical protein’ by Prokka or ‘group_#’ by Roary.

| Sample | Total Number of Genes Annotated | Number of Redundant Genes (i.e., Variants or Paralogs) | Number of Nonredundant Genes Including Genes of Unknown Function | Number of Genes of Unknown Function Denoted “group_#” | Number of Nonredundant Genes with Annotated Function |
|--------|---------------------------------|--|--|---|--|
| DCL | 27 963 | 219 | 27 744 | 26 878 | 1 085 |
| BBL | 46 007 | 17 309 | 28 698 | 23 783 | 22 224 |
| FHL | 49 216 | 16 243 | 32 973 | 28 060 | 21 156 |
| MSL | 52 065 | 14 704 | 37 361 | 32 056 | 20 009 |
| MTL | 55 484 | 20 457 | 35 027 | 29 919 | 25 565 |
| MBL | 58 149 | 22 984 | 35 165 | 29 668 | 28 481 |
| FHC | 87 640 | 44 869 | 42 771 | 36 432 | 51 208 |
| MTC | 113 305 | 61 033 | 52 272 | 45 788 | 67 517 |
| MSR | 121 442 | 27 694 | 93 748 | 87 779 | 33 663 |
| MBR | 148 078 | 54 121 | 93 957 | 86 901 | 61 177 |
| DCR | 158 841 | 58 841 | 100 000 | 92 762 | 66 079 |
| BBC | 201 024 | 100 889 | 100 135 | 92 318 | 108 706 |

Supplementary Table 11: List of all predicted genes (see additional excel file) across metapangenomes endophytic microbiomes from 12 sampled *Musa*, by genotype, including full gene clusters and consolidated genes with duplicate copies and unannotated genes removed, showing additional root/leaf and pairwise genotype Venn data.

Supplementary Table 12: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the total root metapangenomes from 6 *Musa* genotypes shown in **Table 1** (BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*), i.e., genes not shared with leaf metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 588 | 344 | 151.57 | < 1e-30 |
| GO:0015074 | DNA integration | 515 | 276 | 132.75 | < 1e-30 |
| GO:0030435 | sporulation resulting in formation of a cellular spore | 124 | 73 | 31.96 | 2.1e-16 |
| GO:0006352 | DNA-templated transcription, initiation | 349 | 137 | 89.96 | 6.7e-09 |
| GO:0022904 | respiratory electron transport chain | 158 | 61 | 40.73 | 1.2e-05 |
| GO:0043709 | cell adhesion involved in single-species biofilm formation | 28 | 18 | 7.22 | 2.0e-05 |
| GO:0009847 | spore germination | 9 | 8 | 2.32 | 0.00013 |
| GO:0016051 | carbohydrate biosynthetic process | 234 | 39 | 60.32 | 0.00032 |
| GO:0030153 | bacteriocin immunity | 11 | 8 | 2.84 | 0.00147 |
| GO:0008152 | metabolic process | 5290 | 1402 | 1363.62 | 0.00157 |
| GO:0032196 | transposition | 609 | 355 | 156.98 | 0.00280 |
| GO:0030420 | establishment of competence for transformation | 25 | 12 | 6.44 | 0.00391 |
| GO:0030436 | asexual sporulation | 10 | 7 | 2.58 | 0.00421 |
| GO:0031222 | arabinan catabolic process | 8 | 6 | 2.06 | 0.00497 |
| GO:0046336 | ethanolamine catabolic process | 6 | 5 | 1.55 | 0.00534 |
| GO:0045493 | xylan catabolic process | 18 | 10 | 4.64 | 0.00679 |
| GO:0006032 | chitin catabolic process | 9 | 6 | 2.32 | 0.01166 |
| GO:0006707 | cholesterol catabolic process | 7 | 5 | 1.8 | 0.01472 |
| GO:0044571 | [2Fe-2S] cluster assembly | 7 | 5 | 1.8 | 0.01472 |
| GO:0006591 | ornithine metabolic process | 14 | 6 | 3.61 | 0.01750 |
| GO:0071704 | organic substance metabolic process | 4651 | 1221 | 1198.9 | 0.03657 |
| GO:0042742 | defense response to bacterium | 29 | 12 | 7.48 | 0.04808 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 2319 | 633 | 555.6 | 1.2e-11 |
| GO:0005576 | extracellular region | 274 | 105 | 65.65 | 1.9e-08 |
| GO:0009289 | pilus | 44 | 27 | 10.54 | 1.2e-07 |
| GO:0031160 | spore wall | 11 | 9 | 2.64 | 0.00078 |
| GO:0042601 | endospore-forming forespore | 5 | 4 | 1.2 | 0.01327 |
| GO:0030076 | light-harvesting complex | 11 | 7 | 2.64 | 0.02257 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 587 | 344 | 147.67 | < 1e-30 |
| GO:0003677 | DNA binding | 1681 | 625 | 422.89 | < 1e-30 |
| GO:0003676 | nucleic acid binding | 2161 | 788 | 543.65 | 1.4e-24 |
| GO:0016987 | sigma factor activity | 336 | 135 | 84.53 | 4.8e-10 |
| GO:0009055 | electron transfer activity | 340 | 109 | 85.53 | 0.00046 |
| GO:0008061 | chitin binding | 10 | 7 | 2.52 | 0.00362 |
| GO:0046558 | arabinan endo-1,5-alpha-L-arabinosidase activity | 8 | 6 | 2.01 | 0.00436 |
| GO:0031176 | endo-1,4-beta-xylanase activity | 9 | 6 | 2.26 | 0.01029 |
| GO:0005509 | calcium ion binding | 44 | 18 | 11.07 | 0.01559 |

| | | | | | |
|------------|--|------|-----|--------|---------|
| GO:0005355 | glucose transmembrane transporter activity | 6 | 5 | 1.51 | 0.01595 |
| GO:0004534 | 5'-3' exoribonuclease activity | 5 | 4 | 1.26 | 0.01597 |
| GO:0016491 | oxidoreductase activity | 1634 | 385 | 411.07 | 0.02562 |
| GO:0008810 | cellulase activity | 16 | 8 | 4.03 | 0.02801 |
| GO:0004252 | serine-type endopeptidase activity | 53 | 20 | 13.33 | 0.02866 |

Supplementary Table 13: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the total leaf metapangenomes from 6 *Musa* genotypes shown in **Table 1** (BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*), i.e., genes not shared with root metapangenomes.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 588 | 37 | 9.23 | 3.2e-14 |
| GO:0015074 | DNA integration | 515 | 33 | 8.08 | 7.4e-13 |
| GO:0019441 | tryptophan catabolic process to kynurenine | 10 | 2 | 0.16 | 0.010 |
| GO:0032196 | transposition | 609 | 39 | 9.56 | 0.023 |
| GO:0006310 | DNA recombination | 662 | 40 | 10.39 | 0.049 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 2319 | 37 | 27.38 | 0.0064 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 587 | 37 | 9.13 | 6.0e-14 |
| GO:0003677 | DNA binding | 1681 | 49 | 26.14 | 2.4e-06 |
| GO:0004322 | ferroxidase activity | 5 | 2 | 0.08 | 0.0023 |
| GO:0004061 | arylformamidase activity | 7 | 2 | 0.11 | 0.0048 |
| GO:0008199 | ferric iron binding | 15 | 2 | 0.23 | 0.0221 |
| GO:0003676 | nucleic acid binding | 2161 | 60 | 33.61 | 0.0299 |
| GO:0016746 | acyltransferase activity | 259 | 5 | 4.03 | 0.0333 |
| GO:0004803 | transposase activity | 587 | 37 | 9.13 | 6.0e-14 |
| GO:0003677 | DNA binding | 1681 | 49 | 26.14 | 2.4e-06 |
| GO:0004322 | ferroxidase activity | 5 | 2 | 0.08 | 0.0023 |
| GO:0004061 | arylformamidase activity | 7 | 2 | 0.11 | 0.0048 |
| GO:0008199 | ferric iron binding | 15 | 2 | 0.23 | 0.0221 |
| GO:0003676 | nucleic acid binding | 2161 | 60 | 33.61 | 0.0299 |
| GO:0016746 | acyltransferase activity | 259 | 5 | 4.03 | 0.0333 |

Supplementary Table 14: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were universally shared among root samples from 6 *Musa* genotypes shown in **Table 1** (BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*), i.e., core genes among root metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|---|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006412 | translation | 159 | 124 | 79.82 | 3.2e-09 |
| GO:0055085 | transmembrane transport | 340 | 226 | 170.69 | 2.2e-08 |
| GO:0008643 | carbohydrate transport | 131 | 80 | 65.77 | 7.5e-06 |
| GO:0044780 | bacterial-type flagellum assembly | 22 | 20 | 11.04 | 3.2e-05 |
| GO:0009432 | SOS response | 22 | 20 | 11.04 | 6.4e-05 |
| GO:0008033 | tRNA processing | 52 | 45 | 26.11 | 0.00011 |
| GO:0006099 | tricarboxylic acid cycle | 42 | 33 | 21.09 | 0.00014 |
| GO:0043093 | FtsZ-dependent cytokinesis | 28 | 24 | 14.06 | 0.00028 |
| GO:0006541 | glutamine metabolic process | 41 | 31 | 20.58 | 0.00029 |
| GO:0008652 | cellular amino acid biosynthetic process | 211 | 157 | 105.93 | 0.00036 |
| GO:0009245 | lipid A biosynthetic process | 18 | 16 | 9.04 | 0.00069 |
| GO:0015833 | peptide transport | 45 | 35 | 22.59 | 0.00079 |
| GO:0000160 | phosphorelay signal transduction system | 113 | 75 | 56.73 | 0.00095 |
| GO:0019380 | 3-phenylpropionate catabolic process | 10 | 10 | 5.02 | 0.00101 |
| GO:0007049 | cell cycle | 105 | 79 | 52.71 | 0.00127 |
| GO:0045892 | negative regulation of transcription, DNA-templated | 94 | 63 | 47.19 | 0.00163 |
| GO:0009082 | branched-chain amino acid biosynthetic process | 28 | 23 | 14.06 | 0.00199 |
| GO:0001522 | pseudouridine synthesis | 12 | 12 | 6.02 | 0.00201 |
| GO:0043165 | Gram-negative-bacterium-type cell outer membrane assembly | 9 | 9 | 4.52 | 0.00201 |
| GO:0009086 | methionine biosynthetic process | 31 | 24 | 15.56 | 0.00215 |
| GO:0006189 | 'de novo' IMP biosynthetic process | 16 | 14 | 8.03 | 0.00217 |
| GO:0051301 | cell division | 109 | 81 | 54.72 | 0.00254 |
| GO:0006749 | glutathione metabolic process | 33 | 27 | 16.57 | 0.00306 |
| GO:0006096 | glycolytic process | 25 | 20 | 12.55 | 0.00345 |
| GO:0006865 | amino acid transport | 105 | 72 | 52.71 | 0.00381 |
| GO:0017004 | cytochrome complex assembly | 16 | 14 | 8.03 | 0.00383 |
| GO:0009061 | anaerobic respiration | 21 | 16 | 10.54 | 0.00393 |
| GO:0009435 | NAD biosynthetic process | 16 | 14 | 8.03 | 0.00400 |
| GO:0032297 | negative regulation of DNA-dependent DNA replication initiation | 8 | 8 | 4.02 | 0.00402 |
| GO:0045893 | positive regulation of transcription, DNA-templated | 71 | 49 | 35.64 | 0.00424 |
| GO:0006260 | DNA replication | 95 | 68 | 47.69 | 0.00517 |
| GO:0009246 | enterobacterial common antigen biosynthetic process | 11 | 10 | 5.52 | 0.00605 |
| GO:0009228 | thiamine biosynthetic process | 14 | 12 | 7.03 | 0.00670 |
| GO:0009229 | thiamine diphosphate biosynthetic process | 14 | 12 | 7.03 | 0.00670 |
| GO:0006355 | regulation of transcription, DNA-templated | 394 | 241 | 197.8 | 0.00708 |
| GO:0009116 | nucleoside metabolic process | 43 | 34 | 21.59 | 0.00974 |
| GO:0000917 | division septum assembly | 22 | 18 | 11.04 | 0.00993 |

| | | | | | |
|-----------------------------|--|------|------|---------|---------|
| GO:0010124 | phenylacetate catabolic process | 19 | 15 | 9.54 | 0.00998 |
| GO:0000105 | histidine biosynthetic process | 16 | 13 | 8.03 | 0.01102 |
| GO:0031564 | transcription antitermination | 10 | 9 | 5.02 | 0.01106 |
| GO:0071973 | bacterial-type flagellum-dependent cell motility | 47 | 34 | 23.6 | 0.01359 |
| GO:0046777 | protein autophosphorylation | 24 | 18 | 12.05 | 0.01380 |
| GO:0042128 | nitrate assimilation | 27 | 20 | 13.55 | 0.01506 |
| GO:0009236 | cobalamin biosynthetic process | 48 | 32 | 24.1 | 0.01542 |
| GO:0000270 | peptidoglycan metabolic process | 96 | 61 | 48.19 | 0.01569 |
| GO:0006261 | DNA-dependent DNA replication | 37 | 29 | 18.57 | 0.01576 |
| GO:0000028 | ribosomal small subunit assembly | 6 | 6 | 3.01 | 0.01597 |
| GO:0015920 | lipopolysaccharide transport | 6 | 6 | 3.01 | 0.01597 |
| GO:0000162 | tryptophan biosynthetic process | 6 | 6 | 3.01 | 0.01597 |
| GO:0006744 | ubiquinone biosynthetic process | 19 | 15 | 9.54 | 0.01598 |
| GO:0045454 | cell redox homeostasis | 23 | 17 | 11.55 | 0.01803 |
| GO:0009306 | protein secretion | 75 | 41 | 37.65 | 0.01817 |
| GO:0009447 | putrescine catabolic process | 9 | 8 | 4.52 | 0.02004 |
| GO:0008360 | regulation of cell shape | 77 | 48 | 38.66 | 0.02094 |
| GO:0009058 | biosynthetic process | 2225 | 1279 | 1117.01 | 0.02578 |
| GO:0006974 | cellular response to DNA damage stimulus | 185 | 124 | 92.87 | 0.02698 |
| GO:0006520 | cellular amino acid metabolic process | 427 | 287 | 214.36 | 0.02847 |
| GO:0006351 | transcription, DNA-templated | 750 | 358 | 376.52 | 0.03150 |
| GO:0006119 | oxidative phosphorylation | 27 | 21 | 13.55 | 0.03160 |
| GO:0015846 | polyamine transport | 10 | 10 | 5.02 | 0.03172 |
| GO:0008616 | queuosine biosynthetic process | 8 | 8 | 4.02 | 0.03177 |
| GO:0006072 | glycerol-3-phosphate metabolic process | 10 | 9 | 5.02 | 0.03177 |
| GO:0019634 | organic phosphonate metabolic process | 12 | 9 | 6.02 | 0.03182 |
| GO:0035999 | tetrahydrofolate interconversion | 5 | 5 | 2.51 | 0.03184 |
| GO:2000144 | positive regulation of DNA-templated transcription, initiation | 5 | 5 | 2.51 | 0.03184 |
| GO:0018104 | peptidoglycan-protein cross-linking | 5 | 5 | 2.51 | 0.03184 |
| GO:0006101 | citrate metabolic process | 5 | 5 | 2.51 | 0.03184 |
| GO:0070301 | cellular response to hydrogen peroxide | 5 | 5 | 2.51 | 0.03184 |
| GO:0036460 | cellular response to cell envelope stress | 5 | 5 | 2.51 | 0.03184 |
| GO:0019301 | rhamnose catabolic process | 5 | 5 | 2.51 | 0.03184 |
| GO:0090071 | negative regulation of ribosome biogenesis | 5 | 5 | 2.51 | 0.03184 |
| GO:0006979 | response to oxidative stress | 70 | 50 | 35.14 | 0.03285 |
| GO:0009097 | isoleucine biosynthetic process | 19 | 14 | 9.54 | 0.03287 |
| GO:0016226 | iron-sulfur cluster assembly | 27 | 17 | 13.55 | 0.03297 |
| GO:0010212 | response to ionizing radiation | 17 | 14 | 8.53 | 0.03345 |
| GO:0006526 | arginine biosynthetic process | 17 | 13 | 8.53 | 0.03352 |
| GO:0005978 | glycogen biosynthetic process | 12 | 10 | 6.02 | 0.03356 |
| GO:0006826 | iron ion transport | 34 | 21 | 17.07 | 0.03590 |
| GO:0006298 | mismatch repair | 8 | 7 | 4.02 | 0.03597 |
| GO:0006212 | uracil catabolic process | 8 | 7 | 4.02 | 0.03597 |
| GO:0009088 | threonine biosynthetic process | 8 | 7 | 4.02 | 0.03597 |
| GO:0009252 | peptidoglycan biosynthetic process | 66 | 43 | 33.13 | 0.03751 |
| GO:0055072 | iron ion homeostasis | 75 | 41 | 37.65 | 0.03846 |
| GO:0031460 | glycine betaine transport | 16 | 12 | 8.03 | 0.03960 |
| GO:1990961 | xenobiotic detoxification by transmembrane export across the plasma membrane | 21 | 15 | 10.54 | 0.04054 |
| GO:0006935 | chemotaxis | 50 | 33 | 25.1 | 0.04181 |
| GO:0009314 | response to radiation | 44 | 29 | 22.09 | 0.04704 |
| Cellular Components: | | | | | |

| | | | | | |
|-----------------------------|---|------|------|--------|---------|
| GO:0005829 | cytosol | 442 | 343 | 239.64 | 7.1e-21 |
| GO:0005737 | cytoplasm | 1410 | 948 | 764.45 | 5.2e-15 |
| GO:0005887 | integral component of plasma membrane | 266 | 182 | 144.22 | 2.7e-06 |
| GO:0043190 | ATP-binding cassette (ABC) transporter complex | 71 | 57 | 38.49 | 3.6e-06 |
| GO:0022625 | cytosolic large ribosomal subunit | 23 | 22 | 12.47 | 1.5e-05 |
| GO:0032153 | cell division site | 22 | 20 | 11.93 | 0.00043 |
| GO:0009425 | bacterial-type flagellum basal body | 20 | 18 | 10.84 | 0.00238 |
| GO:0032993 | protein-DNA complex | 51 | 41 | 27.65 | 0.00393 |
| GO:0045261 | proton-transporting ATP synthase complex, catalytic core F(1) | 7 | 7 | 3.8 | 0.01372 |
| GO:0005840 | ribosome | 71 | 61 | 38.49 | 0.01401 |
| GO:0022627 | cytosolic small ribosomal subunit | 17 | 14 | 9.22 | 0.01562 |
| GO:0009326 | formate dehydrogenase complex | 6 | 6 | 3.25 | 0.02533 |
| GO:0005886 | plasma membrane | 1756 | 1023 | 952.04 | 0.03032 |
| GO:0030288 | outer membrane-bounded periplasmic space | 122 | 76 | 66.14 | 0.04179 |
| Metabolic Functions: | | | | | |
| GO:0005524 | ATP binding | 801 | 508 | 399.2 | 2.9e-16 |
| GO:0003735 | structural constituent of ribosome | 68 | 58 | 33.89 | 8.8e-10 |
| GO:0019843 | rRNA binding | 58 | 51 | 28.91 | 2.0e-09 |
| GO:0003700 | DNA-binding transcription factor activity | 602 | 289 | 300.02 | 2.3e-09 |
| GO:0000049 | tRNA binding | 43 | 39 | 21.43 | 1.3e-08 |
| GO:0042626 | ATPase-coupled transmembrane transporter activity | 181 | 129 | 90.21 | 4.9e-07 |
| GO:0042802 | identical protein binding | 235 | 158 | 117.12 | 9.0e-07 |
| GO:0022857 | transmembrane transporter activity | 908 | 586 | 452.53 | 1.0e-06 |
| GO:0000287 | magnesium ion binding | 228 | 149 | 113.63 | 1.2e-06 |
| GO:0000976 | transcription cis-regulatory region binding | 87 | 66 | 43.36 | 5.8e-06 |
| GO:0008270 | zinc ion binding | 186 | 121 | 92.7 | 1.7e-05 |
| GO:0003723 | RNA binding | 230 | 173 | 114.63 | 3.6e-05 |
| GO:0015293 | symporter activity | 73 | 52 | 36.38 | 5.0e-05 |
| GO:0008408 | 3'-5' exonuclease activity | 22 | 19 | 10.96 | 0.00012 |
| GO:0001216 | DNA-binding transcription activator activity | 37 | 29 | 18.44 | 0.00034 |
| GO:0005525 | GTP binding | 79 | 54 | 39.37 | 0.00063 |
| GO:0046872 | metal ion binding | 1762 | 977 | 878.14 | 0.00066 |
| GO:0003924 | GTPase activity | 37 | 28 | 18.44 | 0.00118 |
| GO:0050660 | flavin adenine dinucleotide binding | 201 | 113 | 100.17 | 0.00127 |
| GO:0000166 | nucleotide binding | 1360 | 856 | 677.79 | 0.00156 |
| GO:0015344 | siderophore uptake transmembrane transporter activity | 13 | 12 | 6.48 | 0.00164 |
| GO:0038023 | signaling receptor activity | 50 | 25 | 24.92 | 0.00166 |
| GO:0051287 | NAD binding | 100 | 65 | 49.84 | 0.00344 |
| GO:0002161 | aminoacyl-tRNA editing activity | 12 | 11 | 5.98 | 0.00379 |
| GO:0050661 | NADP binding | 76 | 51 | 37.88 | 0.00439 |
| GO:0000156 | phosphorelay response regulator activity | 31 | 23 | 15.45 | 0.00500 |
| GO:0043023 | ribosomal large subunit binding | 11 | 10 | 5.48 | 0.00566 |
| GO:0030145 | manganese ion binding | 53 | 36 | 26.41 | 0.00579 |
| GO:0043022 | ribosome binding | 14 | 12 | 6.98 | 0.00622 |
| GO:0003681 | bent DNA binding | 7 | 7 | 3.49 | 0.00762 |
| GO:0052591 | sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity | 7 | 7 | 3.49 | 0.00762 |
| GO:0042803 | protein homodimerization activity | 42 | 29 | 20.93 | 0.00908 |
| GO:0046933 | proton-transporting ATP synthase activity, rotational mechanism | 10 | 9 | 4.98 | 0.01042 |

| | | | | | |
|------------|--|------|-----|--------|---------|
| GO:0003774 | cytoskeletal motor activity | 10 | 9 | 4.98 | 0.01042 |
| GO:1904680 | peptide transmembrane transporter activity | 25 | 20 | 12.46 | 0.01077 |
| GO:0009982 | pseudouridine synthase activity | 11 | 11 | 5.48 | 0.01524 |
| GO:0004362 | glutathione-disulfide reductase (NADPH) activity | 6 | 6 | 2.99 | 0.01530 |
| GO:0015220 | choline transmembrane transporter activity | 6 | 6 | 2.99 | 0.01530 |
| GO:0008753 | NADPH dehydrogenase (quinone) activity | 6 | 6 | 2.99 | 0.01530 |
| GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 28 | 20 | 13.95 | 0.01696 |
| GO:0001217 | DNA-binding transcription repressor activity | 12 | 10 | 5.98 | 0.01870 |
| GO:0030955 | potassium ion binding | 9 | 8 | 4.49 | 0.01903 |
| GO:0008863 | formate dehydrogenase (NAD+) activity | 9 | 8 | 4.49 | 0.01903 |
| GO:0047834 | D-threo-aldose 1-dehydrogenase activity | 17 | 13 | 8.47 | 0.02365 |
| GO:0003887 | DNA-directed DNA polymerase activity | 27 | 19 | 13.46 | 0.02493 |
| GO:0003678 | DNA helicase activity | 24 | 20 | 11.96 | 0.02757 |
| GO:0003684 | damaged DNA binding | 16 | 12 | 7.97 | 0.02780 |
| GO:0043546 | molybdopterin cofactor binding | 29 | 20 | 14.45 | 0.02930 |
| GO:0042910 | xenobiotic transmembrane transporter activity | 33 | 25 | 16.45 | 0.03036 |
| GO:0008198 | ferrous iron binding | 24 | 17 | 11.96 | 0.03065 |
| GO:0019808 | polyamine binding | 6 | 6 | 2.99 | 0.03069 |
| GO:0008695 | 3-phenylpropionate dioxygenase activity | 5 | 5 | 2.49 | 0.03071 |
| GO:0003857 | 3-hydroxyacyl-CoA dehydrogenase activity | 5 | 5 | 2.49 | 0.03071 |
| GO:0019003 | GDP binding | 5 | 5 | 2.49 | 0.03071 |
| GO:0043565 | sequence-specific DNA binding | 160 | 111 | 79.74 | 0.03176 |
| GO:0015276 | ligand-gated ion channel activity | 11 | 9 | 5.48 | 0.03185 |
| GO:0050136 | NADH dehydrogenase (quinone) activity | 36 | 27 | 17.94 | 0.03407 |
| GO:0043531 | ADP binding | 8 | 7 | 3.99 | 0.03439 |
| GO:0003697 | single-stranded DNA binding | 16 | 12 | 7.97 | 0.03720 |
| GO:0016787 | hydrolase activity | 1513 | 790 | 754.04 | 0.04133 |

Supplementary Table 15: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were universally shared among leaf samples from 6 *Musa* genotypes shown in **Table 1** (BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*), i.e., core genes among leaf metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|---|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006412 | translation | 146 | 35 | 16.34 | 2.5e-06 |
| GO:0000028 | ribosomal small subunit assembly | 6 | 5 | 0.67 | 9.4e-05 |
| GO:0055085 | transmembrane transport | 285 | 50 | 31.9 | 0.00035 |
| GO:0042773 | ATP synthesis coupled electron transport | 9 | 5 | 1.01 | 0.00148 |
| GO:0006310 | DNA recombination | 296 | 20 | 33.13 | 0.00177 |
| GO:0000105 | histidine biosynthetic process | 15 | 6 | 1.68 | 0.00394 |
| GO:0006605 | protein targeting | 12 | 7 | 1.34 | 0.00405 |
| GO:0006164 | purine nucleotide biosynthetic process | 42 | 14 | 4.7 | 0.00494 |
| GO:0009252 | peptidoglycan biosynthetic process | 53 | 13 | 5.93 | 0.00537 |
| GO:0008360 | regulation of cell shape | 61 | 14 | 6.83 | 0.00629 |
| GO:0071978 | bacterial-type flagellum-dependent swarming motility | 12 | 5 | 1.34 | 0.00698 |
| GO:0071973 | bacterial-type flagellum-dependent cell motility | 40 | 12 | 4.48 | 0.00778 |
| GO:0051301 | cell division | 98 | 23 | 10.97 | 0.00832 |
| GO:0010125 | mycothiol biosynthetic process | 5 | 3 | 0.56 | 0.01173 |
| GO:0043953 | protein transport by the Tat complex | 5 | 3 | 0.56 | 0.01173 |
| GO:0019285 | glycine betaine biosynthetic process from choline | 9 | 4 | 1.01 | 0.01234 |
| GO:0019877 | diaminopimelate biosynthetic process | 9 | 4 | 1.01 | 0.01234 |
| GO:0043952 | protein transport by the Sec complex | 9 | 4 | 1.01 | 0.01234 |
| GO:0006189 | 'de novo' IMP biosynthetic process | 14 | 5 | 1.57 | 0.01460 |
| GO:0007049 | cell cycle | 95 | 23 | 10.63 | 0.01585 |
| GO:0009116 | nucleoside metabolic process | 41 | 9 | 4.59 | 0.01679 |
| GO:0046855 | inositol phosphate dephosphorylation | 7 | 4 | 0.78 | 0.02143 |
| GO:0046718 | viral entry into host cell | 6 | 3 | 0.67 | 0.02152 |
| GO:0075713 | establishment of integrated proviral latency | 6 | 3 | 0.67 | 0.02152 |
| GO:0044826 | viral genome integration into host DNA | 6 | 3 | 0.67 | 0.02152 |
| GO:0043093 | FtsZ-dependent cytokinesis | 27 | 7 | 3.02 | 0.02553 |
| GO:0019646 | aerobic electron transport chain | 11 | 4 | 1.23 | 0.02695 |
| GO:0006099 | tricarboxylic acid cycle | 40 | 9 | 4.48 | 0.02951 |
| GO:0044780 | bacterial-type flagellum assembly | 22 | 6 | 2.46 | 0.02982 |
| GO:0045892 | negative regulation of transcription, DNA-templated | 81 | 15 | 9.07 | 0.03305 |
| GO:0065002 | intracellular protein transmembrane transport | 9 | 4 | 1.01 | 0.03444 |
| GO:0019740 | nitrogen utilization | 10 | 4 | 1.12 | 0.03446 |
| GO:0009088 | threonine biosynthetic process | 7 | 3 | 0.78 | 0.03457 |
| GO:0006268 | DNA unwinding involved in DNA replication | 7 | 3 | 0.78 | 0.03457 |
| GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | 5 | 3 | 0.56 | 0.03464 |
| GO:0009432 | SOS response | 23 | 6 | 2.57 | 0.03666 |
| GO:0006351 | transcription, DNA-templated | 558 | 62 | 62.46 | 0.04965 |
| Cellular Components: | | | | | |

| | | | | | |
|-----------------------------|---|------|-----|--------|---------|
| GO:0009425 | bacterial-type flagellum basal body | 19 | 10 | 2.39 | 0.00016 |
| GO:0022625 | cytosolic large ribosomal subunit | 23 | 9 | 2.89 | 0.00116 |
| GO:0005887 | integral component of plasma membrane | 224 | 44 | 28.14 | 0.00284 |
| GO:0005840 | ribosome | 68 | 25 | 8.54 | 0.00317 |
| GO:0005737 | cytoplasm | 1189 | 191 | 149.38 | 0.00359 |
| GO:0045261 | proton-transporting ATP synthase complex, catalytic core F(1) | 7 | 4 | 0.88 | 0.00630 |
| GO:0022627 | cytosolic small ribosomal subunit | 16 | 6 | 2.01 | 0.01005 |
| GO:0033281 | TAT protein transport complex | 5 | 3 | 0.63 | 0.01620 |
| GO:0032993 | protein-DNA complex | 46 | 14 | 5.78 | 0.02405 |
| GO:0009376 | HslUV protease complex | 6 | 3 | 0.75 | 0.02941 |
| GO:0005618 | cell wall | 89 | 17 | 11.18 | 0.03749 |
| GO:0005829 | cytosol | 394 | 73 | 49.5 | 0.03846 |
| GO:1990077 | primosome complex | 7 | 3 | 0.88 | 0.04675 |
| Metabolic Functions: | | | | | |
| GO:0003735 | structural constituent of ribosome | 64 | 24 | 6.59 | 6.2e-09 |
| GO:0019843 | rRNA binding | 53 | 23 | 5.46 | 4.0e-08 |
| GO:0005524 | ATP binding | 692 | 106 | 71.24 | 7.8e-06 |
| GO:0046933 | proton-transporting ATP synthase activity, rotational mechanism | 10 | 7 | 1.03 | 1.1e-05 |
| GO:0003924 | GTPase activity | 35 | 13 | 3.6 | 2.2e-05 |
| GO:0005525 | GTP binding | 73 | 20 | 7.52 | 3.0e-05 |
| GO:0003774 | cytoskeletal motor activity | 9 | 6 | 0.93 | 7.4e-05 |
| GO:0003899 | DNA-directed 5'-3' RNA polymerase activity | 11 | 7 | 1.13 | 0.00017 |
| GO:0000049 | tRNA binding | 41 | 11 | 4.22 | 0.00223 |
| GO:0031419 | cobalamin binding | 16 | 6 | 1.65 | 0.00377 |
| GO:0001217 | DNA-binding transcription repressor activity | 12 | 5 | 1.24 | 0.00487 |
| GO:0043022 | ribosome binding | 13 | 5 | 1.34 | 0.00725 |
| GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 24 | 7 | 2.47 | 0.00859 |
| GO:0071916 | dipeptide transmembrane transporter activity | 9 | 4 | 0.93 | 0.00918 |
| GO:0004129 | cytochrome-c oxidase activity | 14 | 5 | 1.44 | 0.01033 |
| GO:0001216 | DNA-binding transcription activator activity | 32 | 8 | 3.29 | 0.01356 |
| GO:0008955 | peptidoglycan glycosyltransferase activity | 11 | 4 | 1.13 | 0.02035 |
| GO:0003700 | DNA-binding transcription factor activity | 430 | 48 | 44.27 | 0.02544 |
| GO:0003681 | bent DNA binding | 7 | 3 | 0.72 | 0.02769 |
| GO:0000976 | transcription cis-regulatory region binding | 75 | 14 | 7.72 | 0.03461 |
| GO:0003746 | translation elongation factor activity | 13 | 4 | 1.34 | 0.03736 |
| GO:0042626 | ATPase-coupled transmembrane transporter activity | 162 | 31 | 16.68 | 0.04361 |
| GO:0047834 | D-threo-aldose 1-dehydrogenase activity | 14 | 4 | 1.44 | 0.04817 |
| GO:0003684 | damaged DNA binding | 14 | 4 | 1.44 | 0.04817 |

Supplementary Table 16: Enriched GO category results (see additional excel file) of shared and unshared root and leaf metapangenomes and core (shared) metapangenomes of root and leaf endophytic microbiomes from 6 *Musa* genotypes used in Venn diagrams.

Supplementary Table 17: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from diploid ‘wild’ genotypes *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*) compared to cultivated triploid genotypes *Musa* (DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25)) shown in **Table 1**, i.e., genes not shared with root triploid and triploid+diploid metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|----------|
| Biological Processes: | | | | | |
| GO:0030435 | sporulation resulting in formation of a cellular spore | 119 | 35 | 9.6 | 5.50E-13 |
| GO:0022904 | respiratory electron transport chain | 156 | 37 | 12.59 | 1.60E-09 |
| GO:0006352 | DNA-templated transcription, initiation | 262 | 43 | 21.14 | 5.40E-06 |
| GO:0030420 | establishment of competence for transformation | 25 | 9 | 2.02 | 2.10E-05 |
| GO:0009847 | spore germination | 9 | 5 | 0.73 | 0.00032 |
| GO:0042742 | defense response to bacterium | 27 | 8 | 2.18 | 0.00095 |
| GO:0015979 | photosynthesis | 38 | 14 | 3.07 | 0.00338 |
| GO:0006032 | chitin catabolic process | 9 | 4 | 0.73 | 0.0038 |
| GO:0030436 | asexual sporulation | 10 | 4 | 0.81 | 0.00593 |
| GO:0019835 | cytolysis | 30 | 7 | 2.42 | 0.00844 |
| GO:0019253 | reductive pentose-phosphate cycle | 12 | 4 | 0.97 | 0.01227 |
| GO:0036070 | light-independent bacteriochlorophyll biosynthetic process | 7 | 3 | 0.56 | 0.01428 |
| GO:0019941 | modification-dependent protein catabolic process | 7 | 3 | 0.56 | 0.01428 |
| GO:0018298 | protein-chromophore linkage | 13 | 4 | 1.05 | 0.01662 |
| GO:0030153 | bacteriocin immunity | 8 | 3 | 0.65 | 0.0215 |
| GO:0019684 | photosynthesis, light reaction | 8 | 3 | 0.65 | 0.0215 |
| GO:0010498 | proteasomal protein catabolic process | 9 | 3 | 0.73 | 0.03035 |
| GO:0015995 | chlorophyll biosynthetic process | 16 | 7 | 1.29 | 0.03433 |
| GO:0019685 | photosynthesis, dark reaction | 16 | 6 | 1.29 | 0.03448 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 1944 | 204 | 166.98 | 4.40E-07 |
| GO:0030076 | light-harvesting complex | 11 | 9 | 0.94 | 8.90E-06 |
| GO:0005576 | extracellular region | 235 | 39 | 20.19 | 2.70E-05 |
| GO:0019866 | organelle inner membrane | 7 | 3 | 0.6 | 0.01693 |
| GO:0005886 | plasma membrane | 1690 | 156 | 145.16 | 0.01884 |
| Metabolic Functions: | | | | | |
| GO:0009055 | electron transfer activity | 309 | 56 | 23.96 | 7.90E-09 |
| GO:0016987 | sigma factor activity | 251 | 42 | 19.46 | 1.20E-06 |
| GO:0003677 | DNA binding | 956 | 91 | 74.13 | 0.00032 |
| GO:0008233 | peptidase activity | 246 | 36 | 19.08 | 0.0005 |
| GO:0004252 | serine-type endopeptidase activity | 46 | 10 | 3.57 | 0.00229 |
| GO:0016984 | ribulose-bisphosphate carboxylase activity | 9 | 3 | 0.7 | 0.02735 |
| GO:0008061 | chitin binding | 10 | 3 | 0.78 | 0.03686 |
| GO:0042834 | peptidoglycan binding | 10 | 3 | 0.78 | 0.03686 |
| GO:0004803 | transposase activity | 11 | 3 | 0.85 | 0.04784 |

Supplementary Table 18: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from cultivated triploid genotypes *Musa* (DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25)) compared to diploid ‘wild’ genotypes *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*) shown in **Table 1**, i.e., genes not shared with root diploid and triploid+diploid metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0009399 | nitrogen fixation | 34 | 5 | 0.91 | 0.0019 |
| GO:0017000 | antibiotic biosynthetic process | 68 | 7 | 1.82 | 0.0021 |
| GO:0042203 | toluene catabolic process | 13 | 3 | 0.35 | 0.0044 |
| GO:0010207 | photosystem II assembly | 5 | 2 | 0.13 | 0.0067 |
| GO:0042549 | photosystem II stabilization | 5 | 2 | 0.13 | 0.0067 |
| GO:0006352 | DNA-templated transcription, initiation | 262 | 14 | 7 | 0.0098 |
| GO:0006265 | DNA topological change | 7 | 2 | 0.19 | 0.0136 |
| GO:0032259 | methylation | 103 | 7 | 2.75 | 0.0197 |
| Cellular Components: | | | | | |
| GO:0005576 | extracellular region | 235 | 15 | 6.14 | 0.0034 |
| GO:0031676 | plasma membrane-derived thylakoid membrane | 5 | 2 | 0.13 | 0.0064 |
| GO:0009654 | photosystem II oxygen evolving complex | 5 | 2 | 0.13 | 0.0064 |
| GO:0033644 | host cell membrane | 12 | 2 | 0.31 | 0.0376 |
| Metabolic Functions: | | | | | |
| GO:0051538 | 3 iron, 4 sulfur cluster binding | 14 | 3 | 0.39 | 0.00616 |
| GO:0010242 | oxygen evolving activity | 5 | 2 | 0.14 | 0.00729 |
| GO:0016987 | sigma factor activity | 251 | 14 | 6.99 | 0.01001 |
| GO:0003690 | double-stranded DNA binding | 108 | 5 | 3.01 | 0.01717 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity | 24 | 3 | 0.67 | 0.02794 |
| GO:0031177 | phosphopantetheine binding | 26 | 3 | 0.72 | 0.03447 |
| GO:0004144 | diacylglycerol O-acyltransferase activity | 11 | 2 | 0.31 | 0.03592 |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 113 | 7 | 3.14 | 0.03768 |
| GO:0005507 | copper ion binding | 47 | 4 | 1.31 | 0.04091 |

Supplementary Table 19: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from diploid ‘wild’ genotypes *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*) compared to cultivated triploid genotypes *Musa* (DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25)) shown in **Table 1**, i.e., genes not shared with leaf triploid and triploid+diploid metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|---|------------|--------------|----------|----------|
| Biological Processes: | | | | | |
| GO:0009401 | phosphoenolpyruvate-dependent sugar phosphotransferase system | 51 | 32 | 13.03 | 1.90E-08 |
| GO:0022904 | respiratory electron transport chain | 95 | 44 | 24.27 | 1.30E-07 |
| GO:0017000 | antibiotic biosynthetic process | 46 | 25 | 11.75 | 0.00014 |
| GO:0043709 | cell adhesion involved in single-species biofilm formation | 10 | 7 | 2.55 | 0.00396 |
| GO:0030254 | protein secretion by the type III secretion system | 8 | 6 | 2.04 | 0.00472 |
| GO:0045490 | pectin catabolic process | 15 | 9 | 3.83 | 0.00484 |
| GO:0000272 | polysaccharide catabolic process | 57 | 34 | 14.56 | 0.00571 |
| GO:0015979 | photosynthesis | 30 | 16 | 7.66 | 0.0063 |
| GO:0019290 | siderophore biosynthetic process | 19 | 12 | 4.85 | 0.00838 |
| GO:0009297 | pilus assembly | 15 | 9 | 3.83 | 0.01165 |
| GO:0009399 | nitrogen fixation | 28 | 13 | 7.15 | 0.01326 |
| GO:0045493 | xylan catabolic process | 7 | 5 | 1.79 | 0.01412 |
| GO:1902201 | negative regulation of bacterial-type flagellum-dependent cell motility | 7 | 5 | 1.79 | 0.01412 |
| GO:0071805 | potassium ion transmembrane transport | 6 | 5 | 1.53 | 0.01658 |
| GO:0030494 | bacteriochlorophyll biosynthetic process | 10 | 7 | 2.55 | 0.01679 |
| GO:0030980 | alpha-glucan catabolic process | 5 | 4 | 1.28 | 0.01689 |
| GO:0006352 | DNA-templated transcription, initiation | 160 | 51 | 40.87 | 0.02416 |
| GO:0006071 | glycerol metabolic process | 26 | 10 | 6.64 | 0.02712 |
| GO:0019605 | butyrate metabolic process | 8 | 5 | 2.04 | 0.02978 |
| GO:0000746 | conjugation | 12 | 7 | 3.07 | 0.03766 |
| GO:0015977 | carbon fixation | 14 | 8 | 3.58 | 0.0402 |
| GO:1901848 | nicotinate catabolic process | 6 | 4 | 1.53 | 0.04044 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 1483 | 456 | 389.52 | 5.40E-10 |
| GO:0005576 | extracellular region | 147 | 64 | 38.61 | 2.20E-06 |
| GO:0005886 | plasma membrane | 1346 | 386 | 353.54 | 0.00024 |
| GO:0015627 | type II protein secretion system complex | 13 | 7 | 3.41 | 0.03131 |
| Metabolic Functions: | | | | | |
| GO:0008982 | protein-N(PI)-phosphohistidine-sugar phosphotransferase activity | 26 | 18 | 6.78 | 2.10E-06 |
| GO:0009055 | electron transfer activity | 211 | 79 | 54.99 | 7.20E-05 |
| GO:0016984 | ribulose-bisphosphate carboxylase activity | 8 | 7 | 2.08 | 0.0005 |
| GO:0051536 | iron-sulfur cluster binding | 251 | 99 | 65.41 | 0.00057 |
| GO:0015473 | fimbrial usher porin activity | 9 | 7 | 2.35 | 0.00174 |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 131 | 49 | 34.14 | 0.00254 |
| GO:0004556 | alpha-amylase activity | 10 | 7 | 2.61 | 0.00449 |
| GO:0016163 | nitrogenase activity | 6 | 5 | 1.56 | 0.00562 |
| GO:0030570 | pectate lyase activity | 6 | 5 | 1.56 | 0.00562 |

| | | | | | |
|------------|--|------|-----|--------|---------|
| GO:0016298 | lipase activity | 18 | 7 | 4.69 | 0.00564 |
| GO:0046872 | metal ion binding | 1306 | 369 | 340.36 | 0.00822 |
| GO:0008234 | cysteine-type peptidase activity | 11 | 8 | 2.87 | 0.01226 |
| GO:0031177 | phosphopantetheine binding | 17 | 9 | 4.43 | 0.01621 |
| GO:0004190 | aspartic-type endopeptidase activity | 12 | 7 | 3.13 | 0.01788 |
| GO:0004494 | methylmalonyl-CoA mutase activity | 5 | 4 | 1.3 | 0.01821 |
| GO:2001070 | starch binding | 5 | 4 | 1.3 | 0.01821 |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 92 | 33 | 23.98 | 0.0231 |
| GO:0016987 | sigma factor activity | 150 | 50 | 39.09 | 0.02692 |
| GO:0005506 | iron ion binding | 117 | 34 | 30.49 | 0.02764 |
| GO:0005509 | calcium ion binding | 24 | 11 | 6.25 | 0.02849 |
| GO:0030976 | thiamine pyrophosphate binding | 30 | 13 | 7.82 | 0.02969 |
| GO:0004497 | monooxygenase activity | 98 | 35 | 25.54 | 0.03785 |
| GO:0008047 | enzyme activator activity | 8 | 6 | 2.08 | 0.04323 |
| GO:0008564 | protein-exporting ATPase activity | 6 | 4 | 1.56 | 0.04339 |
| GO:0103025 | alpha-amylase activity (releasing maltohexaose) | 6 | 4 | 1.56 | 0.04339 |
| GO:0042602 | riboflavin reductase (NADPH) activity | 6 | 4 | 1.56 | 0.04339 |

Supplementary Table 20: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from cultivated triploid genotypes *Musa* (DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25)) compared to diploid ‘wild’ genotypes *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*) shown in **Table 1**, i.e., genes not shared with leaf diploid and triploid+diploid metapangenomes.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006048 | UDP-N-acetylglucosamine biosynthetic process | 5 | 2 | 0.09 | 0.0032 |
| GO:0010207 | photosystem II assembly | 6 | 2 | 0.11 | 0.0048 |
| GO:0042549 | photosystem II stabilization | 6 | 2 | 0.11 | 0.0048 |
| GO:0030163 | protein catabolic process | 24 | 3 | 0.44 | 0.0193 |
| Cellular Components: | | | | | |
| GO:0031676 | plasma membrane-derived thylakoid membrane | 6 | 2 | 0.08 | 0.0026 |
| GO:0009654 | photosystem II oxygen evolving complex | 6 | 2 | 0.08 | 0.0026 |
| GO:0005615 | extracellular space | 13 | 2 | 0.18 | 0.0126 |
| Metabolic Functions: | | | | | |
| GO:0052874 | FMN reductase (NADH) activity | 5 | 2 | 0.09 | 0.00314 |
| GO:0010242 | oxygen evolving activity | 6 | 2 | 0.11 | 0.00465 |
| GO:0051213 | dioxygenase activity | 74 | 5 | 1.34 | 0.00979 |
| GO:0008199 | ferric iron binding | 14 | 2 | 0.25 | 0.02567 |

Supplementary Table 21: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from BB-genotype *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*) compared to AAA-genotype *Musa* (DC = *M. acuminata* Dwarf Cavendish) shown in **Table 1**, i.e., genes not shared with root AAA and AAA+BB metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0022904 | respiratory electron transport chain | 152 | 52 | 23.55 | 3.5e-10 |
| GO:0030435 | sporulation resulting in formation of a cellular spore | 119 | 41 | 18.44 | 5.0e-08 |
| GO:0043709 | cell adhesion involved in single-species biofilm formation | 26 | 15 | 4.03 | 9.1e-07 |
| GO:0006352 | DNA-templated transcription, initiation | 253 | 67 | 39.2 | 2.8e-06 |
| GO:0009401 | phosphoenolpyruvate-dependent sugar phosphotransferase system | 64 | 21 | 9.91 | 0.00041 |
| GO:0030420 | establishment of competence for transformation | 25 | 10 | 3.87 | 0.00210 |
| GO:0006032 | chitin catabolic process | 8 | 5 | 1.24 | 0.00328 |
| GO:0019835 | cytolysis | 28 | 10 | 4.34 | 0.00328 |
| GO:0030254 | protein secretion by the type III secretion system | 12 | 6 | 1.86 | 0.00542 |
| GO:0009847 | spore germination | 9 | 5 | 1.39 | 0.00645 |
| GO:0034220 | ion transmembrane transport | 91 | 14 | 14.1 | 0.00658 |
| GO:0046336 | ethanolamine catabolic process | 6 | 4 | 0.93 | 0.00660 |
| GO:0042742 | defense response to bacterium | 24 | 9 | 3.72 | 0.00716 |
| GO:0030436 | asexual sporulation | 10 | 5 | 1.55 | 0.01126 |
| GO:0019941 | modification-dependent protein catabolic process | 7 | 4 | 1.08 | 0.01353 |
| GO:0008219 | cell death | 15 | 3 | 2.32 | 0.02404 |
| GO:0030153 | bacteriocin immunity | 5 | 3 | 0.77 | 0.02901 |
| GO:0071555 | cell wall organization | 145 | 31 | 22.46 | 0.03459 |
| GO:0010498 | proteasomal protein catabolic process | 9 | 4 | 1.39 | 0.03764 |
| Cellular Components: | | | | | |
| GO:0009289 | pilus | 37 | 21 | 6.21 | 3.5e-08 |
| GO:0005576 | extracellular region | 224 | 68 | 37.58 | 7.2e-08 |
| GO:0016021 | integral component of membrane | 1897 | 362 | 318.29 | 2.9e-06 |
| GO:0009986 | cell surface | 31 | 12 | 5.2 | 0.0029 |
| GO:0030430 | host cell cytoplasm | 14 | 7 | 2.35 | 0.0047 |
| Metabolic Functions: | | | | | |
| GO:0009055 | electron transfer activity | 299 | 82 | 44.94 | 1.8e-08 |
| GO:0016987 | sigma factor activity | 242 | 66 | 36.37 | 4.0e-07 |
| GO:0003677 | DNA binding | 942 | 170 | 141.57 | 2.5e-05 |
| GO:0004252 | serine-type endopeptidase activity | 46 | 16 | 6.91 | 0.00069 |
| GO:0008233 | peptidase activity | 239 | 56 | 35.92 | 0.00539 |
| GO:0008982 | protein-N(PI)-phosphohistidine-sugar phosphotransferase activity | 32 | 11 | 4.81 | 0.01755 |
| GO:0090563 | protein-phosphocysteine-sugar phosphotransferase activity | 11 | 5 | 1.65 | 0.02138 |
| GO:0008061 | chitin binding | 8 | 4 | 1.2 | 0.02142 |
| GO:0003951 | NAD ⁺ kinase activity | 8 | 4 | 1.2 | 0.02142 |
| GO:0008236 | serine-type peptidase activity | 88 | 26 | 13.23 | 0.02260 |
| GO:0016757 | glycosyltransferase activity | 154 | 30 | 23.14 | 0.02532 |
| GO:0005355 | glucose transmembrane transporter activity | 6 | 4 | 0.9 | 0.02664 |

| | | | | | |
|------------|---|----|---|------|---------|
| GO:0004298 | threonine-type endopeptidase activity | 5 | 3 | 0.75 | 0.02670 |
| GO:2001070 | starch binding | 5 | 3 | 0.75 | 0.02670 |
| GO:0052593 | tryptamine:oxygen oxidoreductase (deaminating) activity | 5 | 3 | 0.75 | 0.02670 |
| GO:0052594 | aminoacetone:oxygen oxidoreductase(deaminating) activity | 5 | 3 | 0.75 | 0.02670 |
| GO:0052595 | aliphatic-amine oxidase activity | 5 | 3 | 0.75 | 0.02670 |
| GO:0052596 | phenethylamine:oxygen oxidoreductase (deaminating) activity | 5 | 3 | 0.75 | 0.02670 |
| GO:0008131 | primary amine oxidase activity | 5 | 3 | 0.75 | 0.02670 |
| GO:0008658 | penicillin binding | 14 | 5 | 2.1 | 0.04690 |

Supplementary Table 22: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from AAA-genotype *Musa* (DC = *M. acuminata* Dwarf Cavendish) compared to BB-genotype *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*) shown in **Table 1**, i.e., genes not shared with root BB and AAA+BB metapangenomes.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0042203 | toluene catabolic process | 13 | 5 | 0.43 | 3.8e-05 |
| GO:0009399 | nitrogen fixation | 34 | 6 | 1.12 | 0.00072 |
| GO:0045926 | negative regulation of growth | 16 | 4 | 0.53 | 0.00151 |
| GO:0030245 | cellulose catabolic process | 17 | 4 | 0.56 | 0.00192 |
| GO:0045927 | positive regulation of growth | 12 | 3 | 0.39 | 0.00617 |
| GO:0006352 | DNA-templated transcription, initiation | 253 | 16 | 8.32 | 0.00856 |
| GO:0016075 | rRNA catabolic process | 6 | 2 | 0.2 | 0.01477 |
| GO:0017000 | antibiotic biosynthetic process | 62 | 6 | 2.04 | 0.01551 |
| GO:0006265 | DNA topological change | 7 | 2 | 0.23 | 0.02024 |
| GO:0042203 | toluene catabolic process | 13 | 5 | 0.43 | 3.8e-05 |
| GO:0009399 | nitrogen fixation | 34 | 6 | 1.12 | 0.00072 |
| GO:0045926 | negative regulation of growth | 16 | 4 | 0.53 | 0.00151 |
| GO:0030245 | cellulose catabolic process | 17 | 4 | 0.56 | 0.00192 |
| GO:0045927 | positive regulation of growth | 12 | 3 | 0.39 | 0.00617 |
| GO:0006352 | DNA-templated transcription, initiation | 253 | 16 | 8.32 | 0.00856 |
| GO:0016075 | rRNA catabolic process | 6 | 2 | 0.2 | 0.01477 |
| GO:0017000 | antibiotic biosynthetic process | 62 | 6 | 2.04 | 0.01551 |
| GO:0006265 | DNA topological change | 7 | 2 | 0.23 | 0.02024 |
| Cellular Components: | | | | | |
| GO:0005576 | extracellular region | 224 | 20 | 6.84 | 0.00011 |
| GO:0005615 | extracellular space | 17 | 3 | 0.52 | 0.01381 |
| GO:0033644 | host cell membrane | 12 | 2 | 0.37 | 0.04996 |
| Metabolic Functions: | | | | | |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 107 | 11 | 3.59 | 0.00086 |
| GO:0008810 | cellulase activity | 15 | 4 | 0.5 | 0.00126 |
| GO:0016987 | sigma factor activity | 242 | 16 | 8.12 | 0.00714 |
| GO:0051538 | 3 iron, 4 sulfur cluster binding | 14 | 3 | 0.47 | 0.01033 |
| GO:0003690 | double-stranded DNA binding | 108 | 6 | 3.63 | 0.02788 |
| GO:0004521 | endoribonuclease activity | 35 | 4 | 1.17 | 0.02865 |
| GO:0004144 | diacylglycerol O-acyltransferase activity | 10 | 2 | 0.34 | 0.04226 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity | 24 | 3 | 0.81 | 0.04494 |

Supplementary Table 23: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from BB-genotype *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*) compared to AAA-genotype *Musa* (DC = *M. acuminata* Dwarf Cavendish) shown in **Table 1**, i.e., genes not shared with leaf AAA and AAA+BB metapangenomes.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--------------------------------------|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0022904 | respiratory electron transport chain | 87 | 78 | 73.31 | 1.2e-05 |
| GO:0019439 | aromatic compound catabolic process | 221 | 201 | 186.22 | 0.013 |
| GO:0009636 | response to toxic substance | 62 | 56 | 52.24 | 0.016 |
| GO:0045454 | cell redox homeostasis | 20 | 20 | 16.85 | 0.032 |
| GO:0017000 | antibiotic biosynthetic process | 36 | 35 | 30.33 | 0.038 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 1354 | 1153 | 1127.5 | 0.00013 |
| GO:0005576 | extracellular region | 128 | 116 | 106.59 | 0.00742 |
| Metabolic Functions: | | | | | |
| GO:0009055 | electron transfer activity | 186 | 164 | 158.01 | 0.00071 |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 75 | 71 | 63.71 | 0.00780 |
| GO:0046872 | metal ion binding | 1151 | 999 | 977.77 | 0.02046 |
| GO:0003824 | catalytic activity | 3380 | 2901 | 2871.31 | 0.02234 |
| GO:0004519 | endonuclease activity | 82 | 75 | 69.66 | 0.03079 |
| GO:0016491 | oxidoreductase activity | 971 | 845 | 824.86 | 0.04479 |
| GO:0051536 | iron-sulfur cluster binding | 218 | 192 | 185.19 | 0.04592 |

Supplementary Table 24: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from AAA-genotype *Musa* (DC = *M. acuminata* Dwarf Cavendish) compared to BB-genotype *Musa* (BB = *M. balbisiana* ‘Thai Black’, MB = *M. balbisiana*) shown in **Table 1**, i.e., genes not shared with leaf BB and AAA+BB metapangenomes.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0070814 | hydrogen sulfide biosynthetic process | 5 | 1 | 0.02 | 0.0237 |
| GO:0035435 | phosphate ion transmembrane transport | 6 | 1 | 0.03 | 0.0284 |
| GO:0001666 | response to hypoxia | 6 | 1 | 0.03 | 0.0284 |
| GO:0010039 | response to iron ion | 8 | 1 | 0.04 | 0.0377 |
| GO:0006276 | plasmid maintenance | 8 | 1 | 0.04 | 0.0377 |
| GO:0000103 | sulfate assimilation | 8 | 1 | 0.04 | 0.0377 |
| GO:0030091 | protein repair | 9 | 1 | 0.04 | 0.0424 |
| GO:0042773 | ATP synthesis coupled electron transport | 9 | 1 | 0.04 | 0.0424 |
| GO:0006414 | translational elongation | 14 | 2 | 0.07 | 0.0446 |
| Cellular Components: | | | | | |
| GO:0005618 | cell wall | 76 | 2 | 0.33 | 0.0415 |
| Metabolic Functions: | | | | | |
| GO:0042802 | identical protein binding | 185 | 4 | 0.98 | 0.0154 |
| GO:0070402 | NADPH binding | 8 | 1 | 0.04 | 0.0417 |
| GO:0070404 | NADH binding | 8 | 1 | 0.04 | 0.0417 |

Supplementary Table 25: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. balbisiana* ‘Thai Black’ (BB), i.e., genes not shared with the leaf metapangenome of BB.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|--|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0030435 | sporulation resulting in formation of a cellular spore | 122 | 35 | 7.54 | 5.6e-16 |
| GO:0022904 | respiratory electron transport chain | 158 | 33 | 9.77 | 1.9e-10 |
| GO:0006313 | transposition, DNA-mediated | 551 | 64 | 34.06 | 3.5e-07 |
| GO:0030420 | establishment of competence for transformation | 25 | 9 | 1.55 | 2.9e-06 |
| GO:0015074 | DNA integration | 482 | 53 | 29.8 | 2.0e-05 |
| GO:0009847 | spore germination | 9 | 5 | 0.56 | 9.0e-05 |
| GO:0030436 | asexual sporulation | 10 | 4 | 0.62 | 0.0022 |
| GO:0019941 | modification-dependent protein catabolic process | 7 | 3 | 0.43 | 0.0068 |
| GO:0006352 | DNA-templated transcription, initiation | 345 | 33 | 21.33 | 0.0076 |
| GO:0010498 | proteasomal protein catabolic process | 9 | 3 | 0.56 | 0.0149 |
| GO:0042742 | defense response to bacterium | 28 | 5 | 1.73 | 0.0266 |
| GO:0006741 | NADP biosynthetic process | 5 | 2 | 0.31 | 0.0336 |
| GO:0070395 | lipoteichoic acid biosynthetic process | 5 | 2 | 0.31 | 0.0336 |
| GO:0006769 | nicotinamide metabolic process | 5 | 2 | 0.31 | 0.0336 |
| GO:0019835 | cytolysis | 31 | 5 | 1.92 | 0.0396 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 2287 | 181 | 140.8 | 5.4e-09 |
| GO:0005886 | plasma membrane | 1756 | 124 | 108.11 | 0.0017 |
| GO:0005576 | extracellular region | 272 | 28 | 16.75 | 0.0048 |
| GO:0031160 | spore wall | 11 | 4 | 0.68 | 0.0330 |
| Metabolic Functions: | | | | | |
| GO:0003677 | DNA binding | 1635 | 139 | 91.85 | 2.0e-10 |
| GO:0009055 | electron transfer activity | 336 | 44 | 18.88 | 1.1e-08 |
| GO:0004803 | transposase activity | 550 | 64 | 30.9 | 1.1e-08 |
| GO:0003676 | nucleic acid binding | 2104 | 175 | 118.2 | 0.00017 |
| GO:0016987 | sigma factor activity | 332 | 33 | 18.65 | 0.00094 |
| GO:0004252 | serine-type endopeptidase activity | 53 | 7 | 2.98 | 0.02772 |
| GO:0008976 | polyphosphate kinase activity | 5 | 2 | 0.28 | 0.02812 |
| GO:0017108 | 5'-flap endonuclease activity | 5 | 2 | 0.28 | 0.02812 |

Supplementary Table 26: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. balbisiana* ‘Thai Black’ (BB), i.e., genes not shared with the root metapangenome of BB.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|---|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0015074 | DNA integration | 239 | 22 | 6.81 | 7.6e-07 |
| GO:0006313 | transposition, DNA-mediated | 244 | 22 | 6.95 | 1.1e-06 |
| GO:0043709 | cell adhesion involved in single-species biofilm formation | 10 | 3 | 0.28 | 0.0023 |
| GO:0006065 | UDP-glucuronate biosynthetic process | 7 | 2 | 0.2 | 0.0154 |
| GO:0042026 | protein refolding | 7 | 2 | 0.2 | 0.0154 |
| GO:0006542 | glutamine biosynthetic process | 10 | 2 | 0.28 | 0.0312 |
| GO:0019605 | butyrate metabolic process | 12 | 2 | 0.34 | 0.0441 |
| Cellular Components: | | | | | |
| GO:0009289 | pilus | 17 | 3 | 0.41 | 0.0071 |
| GO:0016021 | integral component of membrane | 1690 | 49 | 40.46 | 0.0189 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 243 | 22 | 6.66 | 6.2e-07 |
| GO:0003677 | DNA binding | 1057 | 46 | 28.96 | 0.00037 |
| GO:0004494 | methylmalonyl-CoA mutase activity | 6 | 2 | 0.16 | 0.01041 |
| GO:0008745 | N-acetylmuramoyl-L-alanine amidase activity | 7 | 2 | 0.19 | 0.01432 |
| GO:0030246 | carbohydrate binding | 78 | 6 | 2.14 | 0.01665 |
| GO:0042803 | protein homodimerization activity | 38 | 4 | 1.04 | 0.01945 |
| GO:0051082 | unfolded protein binding | 23 | 3 | 0.63 | 0.02393 |
| GO:0004497 | monooxygenase activity | 116 | 8 | 3.18 | 0.04540 |
| GO:0106310 | protein serine kinase activity | 13 | 2 | 0.36 | 0.04776 |

Supplementary Table 27: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. balbisiana* (MB), i.e., genes not shared with the leaf metapangenome of MB.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 551 | 69 | 16.86 | 3.6e-26 |
| GO:0015074 | DNA integration | 482 | 56 | 14.75 | 2.5e-19 |
| GO:0032196 | transposition | 570 | 72 | 17.45 | 0.0079 |
| GO:0008152 | metabolic process | 5211 | 189 | 159.5 | 0.0252 |
| Cellular Components: | | | | | |
| GO:0030430 | host cell cytoplasm | 15 | 2 | 0.3 | 0.035 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 550 | 69 | 16.67 | 1.1e-25 |
| GO:0003677 | DNA binding | 1635 | 96 | 49.56 | 1.0e-12 |
| GO:0003676 | nucleic acid binding | 2104 | 125 | 63.78 | 5.4e-11 |
| GO:0016798 | hydrolase activity, acting on glycosyl bonds | 256 | 12 | 7.76 | 0.0022 |
| GO:2001070 | starch binding | 6 | 2 | 0.18 | 0.0127 |
| GO:0005509 | calcium ion binding | 44 | 4 | 1.33 | 0.0434 |

Supplementary Table 28: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. balbisiana* (MB), i.e., genes not shared with the root metapangenome of MB.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 244 | 26 | 8.8 | 4.3e-07 |
| GO:0030254 | protein secretion by the type III secretion system | 8 | 5 | 0.29 | 3.0e-06 |
| GO:0015074 | DNA integration | 239 | 21 | 8.62 | 0.00012 |
| GO:0015675 | nickel cation transport | 12 | 4 | 0.43 | 0.00064 |
| GO:0015628 | protein secretion by the type II secretion system | 15 | 4 | 0.54 | 0.00163 |
| GO:0017000 | antibiotic biosynthetic process | 48 | 6 | 1.73 | 0.00704 |
| GO:0045227 | capsule polysaccharide biosynthetic process | 7 | 2 | 0.25 | 0.02408 |
| GO:0006829 | zinc ion transport | 8 | 2 | 0.29 | 0.03136 |
| GO:0022904 | respiratory electron transport chain | 97 | 8 | 3.5 | 0.03402 |
| GO:0006824 | cobalt ion transport | 10 | 2 | 0.36 | 0.04808 |
| Cellular Components: | | | | | |
| GO:0005576 | extracellular region | 169 | 21 | 6.66 | 4.9e-06 |
| GO:0015627 | type II protein secretion system complex | 13 | 5 | 0.51 | 8.9e-05 |
| GO:0016021 | integral component of membrane | 1690 | 83 | 66.65 | 0.0012 |
| GO:0030430 | host cell cytoplasm | 11 | 4 | 0.43 | 0.0139 |
| GO:0030257 | type III protein secretion system complex | 5 | 2 | 0.2 | 0.0143 |
| GO:0043657 | host cell | 21 | 7 | 0.83 | 0.0380 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 243 | 26 | 8.58 | 3.2e-07 |
| GO:0003677 | DNA binding | 1057 | 54 | 37.33 | 0.00069 |
| GO:0008775 | acetate CoA-transferase activity | 8 | 3 | 0.28 | 0.00213 |
| GO:0030570 | pectate lyase activity | 6 | 2 | 0.21 | 0.01696 |
| GO:0008564 | protein-exporting ATPase activity | 6 | 2 | 0.21 | 0.01696 |
| GO:0004252 | serine-type endopeptidase activity | 33 | 4 | 1.17 | 0.02778 |
| GO:0016298 | lipase activity | 23 | 4 | 0.81 | 0.02984 |
| GO:0008800 | beta-lactamase activity | 8 | 2 | 0.28 | 0.03021 |

Supplementary Table 29: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. textilis* (MT), i.e., genes not shared with the leaf metapangenome of MT.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|------------------------------------|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 551 | 32 | 4.22 | 1.1e-22 |
| GO:0015074 | DNA integration | 482 | 23 | 3.69 | 1.0e-13 |
| GO:0019383 | (+)-camphor catabolic process | 5 | 1 | 0.04 | 0.038 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 2287 | 18 | 9.92 | 0.00012 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 550 | 32 | 3.9 | 6.9e-23 |
| GO:0003677 | DNA binding | 1635 | 33 | 11.6 | 6.8e-10 |
| GO:0003676 | nucleic acid binding | 2104 | 39 | 14.93 | 0.0028 |
| GO:0004333 | fumarate hydratase activity | 5 | 1 | 0.04 | 0.0350 |
| GO:0015643 | toxic substance binding | 5 | 1 | 0.04 | 0.0350 |
| GO:0102483 | scopolin beta-glucosidase activity | 5 | 1 | 0.04 | 0.0350 |

Supplementary Table 30: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. textilis* (MT), i.e., genes not shared with the root metapangenome of MT.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|---|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 244 | 26 | 7.1 | 4.6e-09 |
| GO:0015074 | DNA integration | 239 | 24 | 6.95 | 6.3e-08 |
| GO:0051692 | cellular oligosaccharide catabolic process | 6 | 2 | 0.17 | 0.0117 |
| GO:0030980 | alpha-glucan catabolic process | 7 | 2 | 0.2 | 0.0160 |
| GO:0044179 | hemolysis in other organism | 8 | 2 | 0.23 | 0.0210 |
| GO:0017000 | antibiotic biosynthetic process | 48 | 5 | 1.4 | 0.0297 |
| GO:0008654 | phospholipid biosynthetic process | 70 | 6 | 2.04 | 0.0410 |
| Cellular Components: | | | | | |
| GO:0009507 | chloroplast | 6 | 2 | 0.14 | 0.0078 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 243 | 26 | 7.2 | 8.4e-09 |
| GO:0003676 | nucleic acid binding | 1374 | 59 | 40.69 | 0.00031 |
| GO:0004556 | alpha-amylase activity | 13 | 4 | 0.39 | 0.00043 |
| GO:0003677 | DNA binding | 1057 | 46 | 31.3 | 0.00043 |
| GO:0103025 | alpha-amylase activity (releasing maltohexaose) | 8 | 3 | 0.24 | 0.00128 |
| GO:0009881 | photoreceptor activity | 11 | 2 | 0.33 | 0.04025 |
| GO:0005509 | calcium ion binding | 26 | 3 | 0.77 | 0.04031 |
| GO:0004497 | monooxygenase activity | 116 | 7 | 3.44 | 0.04226 |

Supplementary Table 31: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. acuminata* FHIA-25 (FH), i.e., genes not shared with the leaf metapangenome of FH.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0015074 | DNA integration | 482 | 18 | 3.91 | 1.8e-08 |
| GO:0006313 | transposition, DNA-mediated | 551 | 17 | 4.46 | 8.0e-07 |
| GO:0032259 | methylation | 117 | 4 | 0.95 | 0.015 |
| GO:0046168 | glycerol-3-phosphate catabolic process | 5 | 1 | 0.04 | 0.040 |
| GO:0051085 | chaperone cofactor-dependent protein refolding | 5 | 1 | 0.04 | 0.040 |
| GO:0015074 | DNA integration | 482 | 18 | 3.91 | 1.8e-08 |
| GO:0006313 | transposition, DNA-mediated | 551 | 17 | 4.46 | 8.0e-07 |
| GO:0032259 | methylation | 117 | 4 | 0.95 | 0.015 |
| GO:0046168 | glycerol-3-phosphate catabolic process | 5 | 1 | 0.04 | 0.040 |
| GO:0051085 | chaperone cofactor-dependent protein refolding | 5 | 1 | 0.04 | 0.040 |
| Cellular Components: | | | | | |
| GO:0009289 | pilus | 44 | 2 | 0.29 | 0.033 |
| GO:0009331 | glycerol-3-phosphate dehydrogenase complex | 6 | 1 | 0.04 | 0.038 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 550 | 17 | 4.76 | 3.1e-06 |
| GO:0003676 | nucleic acid binding | 2104 | 31 | 18.22 | 0.00014 |
| GO:0003677 | DNA binding | 1635 | 21 | 14.16 | 0.02396 |

Supplementary Table 32: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. acuminata* FHIA-25 (FH), i.e., genes not shared with the root metapangenome of FH.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--------------------------------|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 244 | 33 | 6.22 | 4.1e-16 |
| GO:0015074 | DNA integration | 239 | 30 | 6.09 | 9.0e-14 |
| GO:0030163 | protein catabolic process | 24 | 3 | 0.61 | 0.0357 |
| Cellular Components: | | | | | |
| GO:0016021 | integral component of membrane | 1690 | 38 | 28.09 | 0.0027 |
| GO:0005615 | extracellular space | 16 | 2 | 0.27 | 0.0281 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 243 | 33 | 5.73 | 6.3e-17 |
| GO:0003677 | DNA binding | 1057 | 48 | 24.94 | 2.5e-07 |
| GO:0003676 | nucleic acid binding | 1374 | 60 | 32.42 | 5.9e-05 |
| GO:0052874 | FMN reductase (NADH) activity | 5 | 2 | 0.12 | 0.0053 |
| GO:0008239 | dipeptidyl-peptidase activity | 6 | 2 | 0.14 | 0.0078 |
| GO:0008199 | ferric iron binding | 15 | 2 | 0.35 | 0.0475 |

Supplementary Table 33: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. acuminata* Dwarf Cavendish (DC), i.e., genes not shared with the leaf metapangenome of DC.

| GO_ID | Term | Annot-ated | Signif-icant | Expected | P-value |
|------------------------------|----------------------------------|------------|--------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 551 | 61 | 19.18 | 5.1e-17 |
| GO:0015074 | DNA integration | 482 | 47 | 16.78 | 4.3e-11 |
| GO:0009399 | nitrogen fixation | 37 | 5 | 1.29 | 0.0086 |
| GO:0042203 | toluene catabolic process | 13 | 3 | 0.45 | 0.0092 |
| GO:0017000 | antibiotic biosynthetic process | 72 | 7 | 2.51 | 0.0122 |
| GO:0006265 | DNA topological change | 7 | 2 | 0.24 | 0.0226 |
| GO:0044571 | [2Fe-2S] cluster assembly | 7 | 2 | 0.24 | 0.0226 |
| GO:0030153 | bacteriocin immunity | 10 | 2 | 0.35 | 0.0452 |
| Cellular Components: | | | | | |
| GO:0005576 | extracellular region | 272 | 24 | 7.08 | 2.2e-07 |
| GO:0033644 | host cell membrane | 13 | 2 | 0.34 | 0.043 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 550 | 61 | 18.86 | 5.9e-17 |
| GO:0003677 | DNA binding | 1635 | 93 | 56.05 | 8.4e-09 |
| GO:0003676 | nucleic acid binding | 2104 | 121 | 72.13 | 0.00016 |
| GO:0051538 | 3 iron, 4 sulfur cluster binding | 15 | 3 | 0.51 | 0.01336 |
| GO:0031177 | phosphopantetheine binding | 29 | 4 | 0.99 | 0.01635 |
| GO:0051536 | iron-sulfur cluster binding | 340 | 16 | 11.66 | 0.01962 |
| GO:0003690 | double-stranded DNA binding | 109 | 4 | 3.74 | 0.03420 |
| GO:0031071 | cysteine desulfurase activity | 10 | 2 | 0.34 | 0.04395 |

Supplementary Table 34: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. acuminata* Dwarf Cavendish (DC), i.e., genes not shared with the root metapangenome of DC.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0070814 | hydrogen sulfide biosynthetic process | 5 | 1 | 0.01 | 0.0060 |
| GO:0006048 | UDP-N-acetylglucosamine biosynthetic process | 5 | 1 | 0.01 | 0.0060 |
| GO:0000103 | sulfate assimilation | 8 | 1 | 0.01 | 0.0095 |
| GO:0042773 | ATP synthesis coupled electron transport | 9 | 1 | 0.01 | 0.0107 |
| Cellular Components: | | | | | |
| Metabolic Functions: | | | | | |
| GO:0031177 | phosphopantetheine binding | 19 | 1 | 0.03 | 0.0326 |
| GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 24 | 1 | 0.04 | 0.0411 |

Supplementary Table 35: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the root metapangenome from *M. sikkimensis* (MS), i.e., genes not shared with the leaf metapangenome of MS.

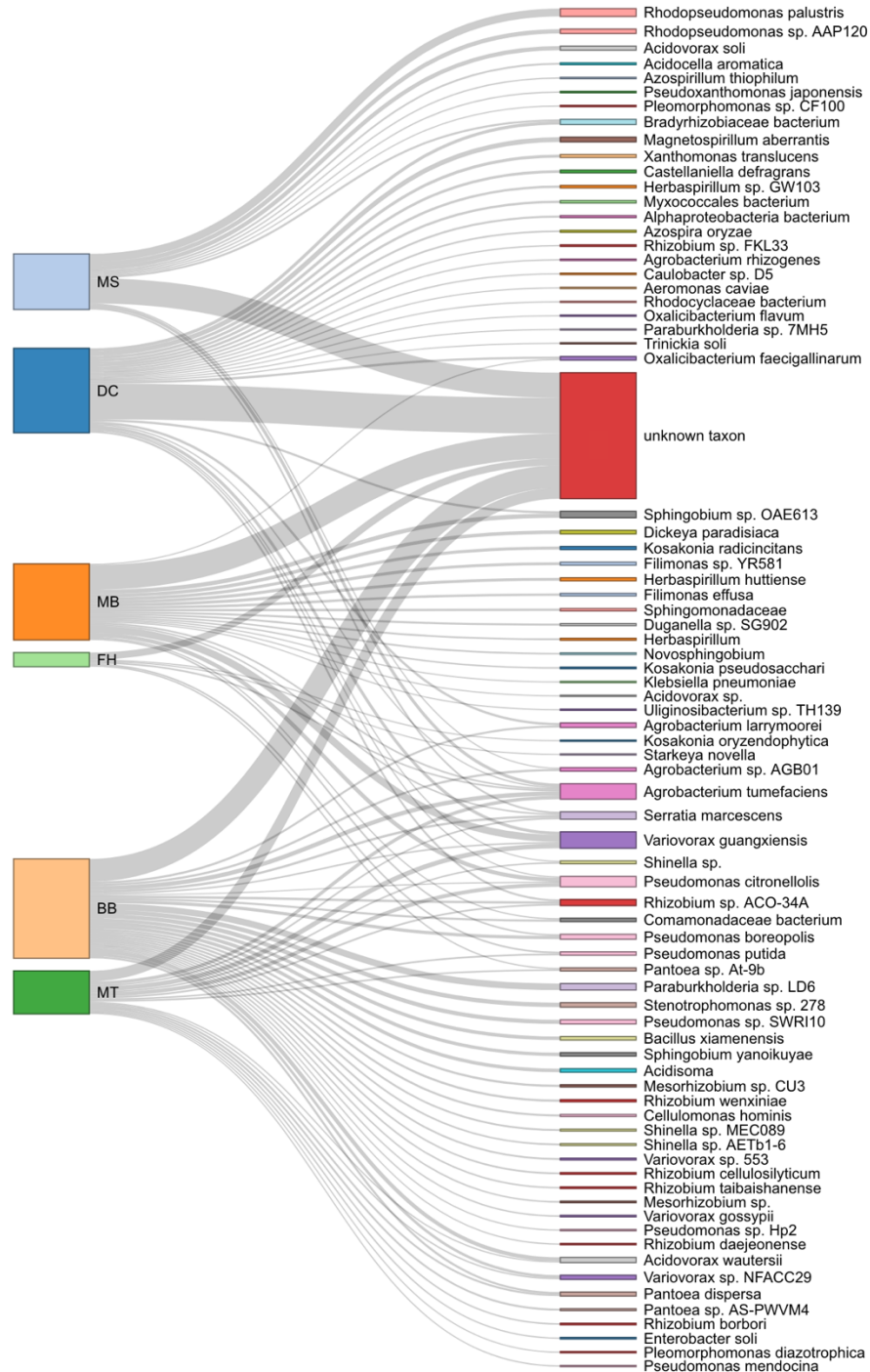
| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|---|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0006313 | transposition, DNA-mediated | 551 | 21 | 7.44 | 9.4e-06 |
| GO:0019684 | photosynthesis, light reaction | 5 | 3 | 0.07 | 2.3e-05 |
| GO:0015979 | photosynthesis | 38 | 11 | 0.51 | 2.8e-05 |
| GO:0018298 | protein-chromophore linkage | 15 | 3 | 0.2 | 0.00096 |
| GO:0015995 | chlorophyll biosynthetic process | 16 | 6 | 0.22 | 0.00097 |
| GO:0030494 | bacteriochlorophyll biosynthetic process | 12 | 4 | 0.16 | 0.00168 |
| GO:0019685 | photosynthesis, dark reaction | 18 | 4 | 0.24 | 0.00169 |
| GO:0036070 | light-independent bacteriochlorophyll biosynthetic process | 7 | 2 | 0.09 | 0.00362 |
| GO:0019441 | tryptophan catabolic process to kynurenine | 8 | 2 | 0.11 | 0.00479 |
| GO:0015074 | DNA integration | 482 | 14 | 6.51 | 0.00488 |
| GO:0019253 | reductive pentose-phosphate cycle | 13 | 2 | 0.18 | 0.01277 |
| Cellular Components: | | | | | |
| GO:0030076 | light-harvesting complex | 11 | 9 | 0.12 | 2.9e-11 |
| GO:0019866 | organelle inner membrane | 7 | 3 | 0.08 | 4.6e-05 |
| Metabolic Functions: | | | | | |
| GO:0004803 | transposase activity | 550 | 21 | 7.41 | 1.1e-05 |
| GO:0004568 | chitinase activity | 5 | 2 | 0.07 | 0.0018 |
| GO:0004061 | arylformamidase activity | 5 | 2 | 0.07 | 0.0018 |
| GO:0046872 | metal ion binding | 1762 | 37 | 23.74 | 0.0019 |
| GO:0016636 | oxidoreductase activity, acting on the CH-CH group of donors, iron-sulfur protein as acceptor | 9 | 3 | 0.12 | 0.0036 |
| GO:0016984 | ribulose-bisphosphate carboxylase activity | 9 | 2 | 0.12 | 0.0061 |
| GO:0016730 | oxidoreductase activity, acting on iron-sulfur proteins as donors | 32 | 3 | 0.43 | 0.0089 |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 179 | 6 | 2.41 | 0.0336 |
| GO:0030145 | manganese ion binding | 53 | 3 | 0.71 | 0.0343 |
| GO:0003677 | DNA binding | 1635 | 30 | 22.03 | 0.0405 |

Supplementary Table 36: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that were unique to the leaf metapangenome from *M. sikkimensis* (MS), i.e., genes not shared with the root metapangenome of MS.

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|---|----------------|------------------|----------|---------|
| Biological Processes: | | | | | |
| GO:0015979 | photosynthesis | 28 | 9 | 0.81 | 1.2e-06 |
| GO:0015074 | DNA integration | 239 | 18 | 6.95 | 0.00017 |
| GO:0036070 | light-independent bacteriochlorophyll biosynthetic process | 5 | 3 | 0.15 | 0.00023 |
| GO:0015977 | carbon fixation | 14 | 4 | 0.41 | 0.00044 |
| GO:0015995 | chlorophyll biosynthetic process | 13 | 7 | 0.38 | 0.00232 |
| GO:0019439 | aromatic compound catabolic process | 275 | 22 | 8 | 0.00316 |
| GO:0018298 | protein-chromophore linkage | 14 | 3 | 0.41 | 0.00693 |
| GO:0030494 | bacteriochlorophyll biosynthetic process | 10 | 5 | 0.29 | 0.00763 |
| GO:0006558 | L-phenylalanine metabolic process | 14 | 3 | 0.41 | 0.00785 |
| GO:0000917 | division septum assembly | 22 | 3 | 0.64 | 0.02474 |
| GO:0042203 | toluene catabolic process | 9 | 2 | 0.26 | 0.02644 |
| GO:0030245 | cellulose catabolic process | 10 | 2 | 0.29 | 0.03243 |
| GO:0019509 | L-methionine salvage from methylthioadenosine | 12 | 2 | 0.35 | 0.04579 |
| Cellular Components: | | | | | |
| Metabolic Functions: | | | | | |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | 100 | 13 | 3.15 | 1.3e-05 |
| GO:0016984 | ribulose-bisphosphate carboxylase activity | 8 | 4 | 0.25 | 6.1e-05 |
| GO:0031419 | cobalamin binding | 16 | 4 | 0.5 | 0.00129 |
| GO:0004497 | monooxygenase activity | 116 | 13 | 3.66 | 0.00588 |
| GO:0047125 | delta1-piperidine-2-carboxylate reductase activity | 5 | 2 | 0.16 | 0.00928 |
| GO:0052595 | aliphatic-amine oxidase activity | 5 | 2 | 0.16 | 0.00928 |
| GO:0008131 | primary amine oxidase activity | 5 | 2 | 0.16 | 0.00928 |
| GO:0004494 | methylmalonyl-CoA mutase activity | 6 | 2 | 0.19 | 0.01364 |
| GO:0003676 | nucleic acid binding | 1374 | 39 | 43.3 | 0.01455 |
| GO:0004300 | enoyl-CoA hydratase activity | 9 | 2 | 0.28 | 0.03075 |
| GO:0016705 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 126 | 13 | 3.97 | 0.04260 |
| GO:0016730 | oxidoreductase activity, acting on iron-sulfur proteins as donors | 28 | 3 | 0.88 | 0.04489 |
| GO:0009881 | photoreceptor activity | 11 | 2 | 0.35 | 0.04508 |
| GO:0046872 | metal ion binding | 1417 | 56 | 44.66 | 0.04699 |

Supplementary Table 37: List of taxon matches and gene matches for which there was a signature of phyllosymbiosis (see additional excel file) from for endophytic microbiomes of *Musa* samples, showing gene and taxon lists, counts, and complete DIAMOND blastx output.

Supplementary Figure 8: Associations between *Musa* genotypes (left) and dominant endophytic microbiome strains that displayed signatures of phylosymbiosis with their hosts (center). Size of block indicates relative abundance. Host *Musa* genotypes correspond to those listed in **Table 1** (BB = *M. balbisiana* ‘Thai Black’, DC = *M. acuminata* Dwarf Cavendish, FH = *M. acuminata* (FHIA-25), MB = *M. balbisiana*, MS = *M. sikkimensis*, MT = *M. textilis*). For display purposes, microbes with fewer than 18 occurrences in the gene clusters were omitted.



Supplementary Table 38: Significantly enriched gene ontology (GO) categories of the endophytic microbiome genes that showed signatures of phylosymbiosis with host genotype from all tissues from 12 sampled *Musa* listed in **Table 1** (*M. balbisiana* ‘Thai Black’, *M. acuminata* Dwarf Cavendish, *M. acuminata* (FHIA-25), *M. balbisiana*, *M. sikkimensis*, *M. textilis*).

| GO_ID | Term | Annot- ated | Signif- icant | Expected | P-value |
|------------------------------|--|----------------|------------------|----------|----------|
| Biological Processes: | | | | | |
| GO:0006351 | transcription, DNA-templated | 757 | 13 | 15.36 | 0.0035 |
| GO:0001123 | transcription initiation from bacterial-type RNA polymerase promoter | 5 | 2 | 0.1 | 0.0039 |
| GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | 5 | 2 | 0.1 | 0.0039 |
| GO:0006412 | translation | 159 | 12 | 3.23 | 0.0047 |
| GO:0017038 | protein import | 6 | 2 | 0.12 | 0.0058 |
| GO:0042026 | protein refolding | 7 | 2 | 0.14 | 0.008 |
| GO:0019430 | removal of superoxide radicals | 8 | 2 | 0.16 | 0.0106 |
| GO:0019619 | 3,4-dihydroxybenzoate catabolic process | 8 | 2 | 0.16 | 0.0106 |
| GO:0006099 | tricarboxylic acid cycle | 43 | 4 | 0.87 | 0.0108 |
| GO:0019288 | isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | 10 | 2 | 0.2 | 0.0165 |
| GO:0043213 | bacteriocin transport | 11 | 2 | 0.22 | 0.0199 |
| GO:0006541 | glutamine metabolic process | 41 | 4 | 0.83 | 0.02 |
| GO:0017004 | cytochrome complex assembly | 16 | 2 | 0.32 | 0.0407 |
| GO:0006094 | gluconeogenesis | 16 | 2 | 0.32 | 0.0407 |
| GO:0006189 | 'de novo' IMP biosynthetic process | 16 | 2 | 0.32 | 0.0407 |
| GO:0006353 | DNA-templated transcription, termination | 17 | 2 | 0.34 | 0.0455 |
| Cellular Components: | | | | | |
| GO:0005829 | cytosol | 443 | 23 | 9.8 | 0.0032 |
| GO:0005737 | cytoplasm | 1417 | 52 | 31.33 | 0.0127 |
| GO:0022625 | cytosolic large ribosomal subunit | 23 | 3 | 0.51 | 0.0135 |
| GO:0005886 | plasma membrane | 1763 | 50 | 38.98 | 0.0331 |
| Metabolic Functions: | | | | | |
| GO:0005524 | ATP binding | 803 | 36 | 16.11 | 2.70E-06 |
| GO:0003924 | GTPase activity | 38 | 6 | 0.76 | 9.70E-05 |
| GO:0005525 | GTP binding | 79 | 8 | 1.59 | 0.00017 |
| GO:0003735 | structural constituent of ribosome | 68 | 6 | 1.36 | 0.00234 |
| GO:0046872 | metal ion binding | 1789 | 47 | 35.89 | 0.00242 |
| GO:0003899 | DNA-directed 5'-3' RNA polymerase activity | 14 | 3 | 0.28 | 0.00245 |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 180 | 10 | 3.61 | 0.0033 |
| GO:0008948 | oxaloacetate decarboxylase activity | 9 | 2 | 0.18 | 0.01313 |
| GO:0046933 | proton-transporting ATP synthase activity, rotational mechanism | 10 | 2 | 0.2 | 0.0162 |
| GO:0004176 | ATP-dependent peptidase activity | 11 | 2 | 0.22 | 0.01954 |
| GO:0042626 | ATPase-coupled transmembrane transporter activity | 183 | 14 | 3.67 | 0.02094 |
| GO:0019843 | rRNA binding | 58 | 5 | 1.16 | 0.02232 |
| GO:0043022 | ribosome binding | 14 | 2 | 0.28 | 0.03109 |
| GO:0051538 | 3 iron, 4 sulfur cluster binding | 16 | 2 | 0.32 | 0.03994 |
| GO:0003746 | translation elongation factor activity | 16 | 2 | 0.32 | 0.03994 |