SUP\_Permanova\_table\_a: PERMANOVA table of community composition including all ASVs of all samples. SumOfSqs = Sum of Squares, R2 = explained variance, Df = degrees of freedom, asterisks indicate significant differences

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | SumOfSqs | R2 | F value | P value |  |
| Stress treatment | 3 | 0.4586 | 0.0362 | 1.6211 | 0.006 | \*\* |
| Plant species | 1 | 1.2735 | 0.10051 | 13.5032 | 0.001 | \*\*\* |
| Sample type | 1 | 2.0913 | 0.16506 | 22.1755 | 0.001 | \*\*\* |
| Block | 5 | 0.8289 | 0.06542 | 1.7579 | 0.001 | \*\*\* |
| Stress treatment:Plant species | 3 | 0.5193 | 0.04098 | 1.8354 | 0.003 | \*\* |
| Stress treatment:Sample type | 3 | 0.2254 | 0.01779 | 0.7968 | 0.906 |  |
| Plant species:Sample type | 1 | 0.2616 | 0.02064 | 2.7734 | 0.001 | \*\*\* |
| Stress treatment:Plant species:Sample type | 3 | 0.2214 | 0.01747 | 0.7825 | 0.924 |  |
| Residual | 72 | 6.7902 | 0.53592 |  |  |  |
| Total | 92 | 12.6702 | 1 |  |  |  |

SUP\_Permanova\_table\_b: PERMANOVA table of community composition including all ASVs of each sample partition. SumOfSqs = Sum of Squares, R2 = explained variance, Df = degrees of freedom, asterisks indicate significant differences

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Plant species | Sample type | Effect | Df | SumOfSqs | R2 | F value | P value |  |
| *A. thaliana* | Endosphere | Stress treatment | 3 | 0.3774 | 0.1601 | 1.2018 | 0.0165 | \* |
|  |  | Block | 5 | 0.6188 | 0.2625 | 1.1823 | 0.0171 | \* |
|  |  | Residual | 13 | 1.3609 | 0.5773 |  |  |  |
|  |  | Total | 21 | 2.3571 | 1 |  |  |  |
|  |  |  |  |  |  |  |  |  |
|  | Rhizosphere | Stress treatment | 3 | 0.3210 | 0.1416 | 1.1673 | 0.0068 | \*\* |
|  |  | Block | 5 | 0.5704 | 0.2516 | 1.2443 | 0.0068 | \*\* |
|  |  | Residual | 15 | 1.3751 | 0.6067 |  |  |  |
|  |  | Total | 23 | 2.2665 | 1 |  |  |  |
|  |  |  |  |  |  |  |  |  |
| *B. oleracea* | Endosphere | Stress treatment | 3 | 0.3968 | 0.1840 | 1.454 | 0.0012 | \*\* |
|  |  | Block | 5 | 0.4863 | 0.2255 | 1.0693 | 0.0011 | \*\* |
|  |  | Residual | 14 | 1.2735 | 0.5905 |  |  |  |
|  |  | Total | 22 | 2.1566 | 1 |  |  |  |
|  |  |  |  |  |  |  |  |  |
|  | Rhizosphere | Stress treatment | 3 | 0.3256 | 0.1442 | 1.1689 | 0.0622 |  |
|  |  | Block | 5 | 0.5392 | 0.2389 | 1.1615 | 0.0622 |  |
|  |  | Residual | 15 | 1.3927 | 0.6169 |  |  |  |
|  |  | Total | 23 | 2.2575 | 1 |  |  |  |

SUP\_Pairwise\_permanova\_table: Pairwise comparisons of full microbial community compositions in each data partition (based on adonis.pair function of the EcolUtils R package).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Plant sp. | Sample type | Pairwise comparison | | | SumsOfSqs | MeanSqs | F.Model | R2 | P.value | P.value.corrected |
| AT | Endosphere | control | <-> | MeJA\_0.1 | 0.07971894 | 0.07971894 | 0.8675067 | 0.07982574 | 0.886113886 | 0.88611389 |
| AT | Endosphere | control | <-> | MeJA\_1.0 | 0.16033695 | 0.16033695 | 1.3096952 | 0.11580287 | 0.053946054 | 0.16183816 |
| AT | Endosphere | control | <-> | oral\_secretion | 0.09732527 | 0.09732527 | 0.9952997 | 0.11064664 | 0.438561439 | 0.60899101 |
| AT | Endosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.17836589 | 0.17836589 | 1.4895962 | 0.12964739 | 0.003996004 | 0.02397602 |
| AT | Endosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.09371623 | 0.09371623 | 0.9924162 | 0.11036146 | 0.507492507 | 0.60899101 |
| AT | Endosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.13716067 | 0.13716067 | 1.0344459 | 0.11450021 | 0.376623377 | 0.60899101 |
|  |  |  |  |  |  |  |  |  |  |  |
| AT | Rhizosphere | control | <-> | MeJA\_0.1 | 0.10874737 | 0.10874737 | 1.121378 | 0.10083085 | 0.11488511 | 0.2757243 |
| AT | Rhizosphere | control | <-> | MeJA\_1.0 | 0.11279697 | 0.11279697 | 1.085294 | 0.09790392 | 0.1988012 | 0.2982018 |
| AT | Rhizosphere | control | <-> | oral\_secretion | 0.09945722 | 0.09945722 | 1.040184 | 0.09421801 | 0.35064935 | 0.4207792 |
| AT | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.12093265 | 0.12093265 | 1.22237 | 0.1089226 | 0.03896104 | 0.2337662 |
| AT | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.09082385 | 0.09082385 | 1.002296 | 0.09109883 | 0.43156843 | 0.4315684 |
| AT | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.10931898 | 0.10931898 | 1.1204 | 0.10075174 | 0.13786214 | 0.2757243 |
|  |  |  |  |  |  |  |  |  |  |  |
| BO | Endosphere | control | <-> | MeJA\_0.1 | 0.15383848 | 0.15383848 | 1.458853 | 0.139485 | 0.02697303 | 0.05394605 |
| BO | Endosphere | control | <-> | MeJA\_1.0 | 0.18031721 | 0.18031721 | 1.957544 | 0.1786481 | 0.01398601 | 0.05394605 |
| BO | Endosphere | control | <-> | oral\_secretion | 0.13052097 | 0.13052097 | 1.436418 | 0.1376351 | 0.08291708 | 0.0995005 |
| BO | Endosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.12343402 | 0.12343402 | 1.310282 | 0.1158488 | 0.02097902 | 0.05394605 |
| BO | Endosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.11611524 | 0.11611524 | 1.247469 | 0.1109111 | 0.05394605 | 0.08091908 |
| BO | Endosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.09498452 | 0.09498452 | 1.171539 | 0.1048682 | 0.16783217 | 0.16783217 |
|  |  |  |  |  |  |  |  |  |  |  |
| BO | Rhizosphere | control | <-> | MeJA\_0.1 | 0.11114605 | 0.11114605 | 1.134862 | 0.10191972 | 0.14385614 | 0.2877123 |
| BO | Rhizosphere | control | <-> | MeJA\_1.0 | 0.1478538 | 0.1478538 | 1.4978239 | 0.13027021 | 0.02397602 | 0.1438561 |
| BO | Rhizosphere | control | <-> | oral\_secretion | 0.10271213 | 0.10271213 | 0.9583681 | 0.08745536 | 0.51248751 | 0.6883117 |
| BO | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.10931434 | 0.10931434 | 1.2708375 | 0.11275449 | 0.06493506 | 0.1948052 |
| BO | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.08937762 | 0.08937762 | 0.9460037 | 0.08642457 | 0.68831169 | 0.6883117 |
| BO | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.09077754 | 0.09077754 | 0.953009 | 0.08700888 | 0.58741259 | 0.6883117 |

SUP\_table\_alpha\_diversity\_tests : ANOVA table of Shannon diversity indexes across the different treatments, plant species and sample types. SumOfSqs = Sum of Squares, Df = degrees of freedom, asterisks indicate significant differences

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | SumOfSqs | F value | P value |  |
| Block | 5 | 0.597 | 1.7681 | 0.130323 |  |
| Plant species | 1 | 0.0526 | 0.7782 | 0.380634 |  |
| Treatment | 3 | 0.5908 | 2.9161 | 0.039974 | \* |
| Sample type | 1 | 8.6669 | 128.3363 | 2.20E-16 | \*\*\* |
| Plant species:Treatment | 3 | 0.34 | 1.6783 | 0.179269 |  |
| Plant species:Sample type | 1 | 0.9281 | 13.7431 | 0.000409 | \*\*\* |
| MeJA treatment:Sample type | 3 | 0.218 | 1.076 | 0.364794 |  |
| Plant species:Treatment:Sample type | 3 | 0.1909 | 0.9424 | 0.424793 |  |
| Residuals | 72 | 4.8624 |  |  |  |

SUP\_table\_alpha\_diversity\_pairwise (missing until Aug/31): Post-hoc test of Shannon’s Shannon diversity indexes across the different treatments, plant species, and sample types

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatment | Plant Species | Plant compartment | Shannon Diversity | Tukey post-hoc groups |
| control | Arabidopsis thaliana | Rhizosphere | 5.657 | a |
| MeJA\_0.1 | Arabidopsis thaliana | Rhizosphere | 5.648 | a |
| oral\_secretion | Arabidopsis thaliana | Rhizosphere | 5.628 | a |
| MeJA\_0.1 | Brassica oleraceae | Rhizosphere | 5.598 | a |
| MeJA\_1.0 | Arabidopsis thaliana | Rhizosphere | 5.590 | a |
| oral\_secretion | Brassica oleraceae | Rhizosphere | 5.495 | ab |
| MeJA\_1.0 | Brassica oleraceae | Rhizosphere | 5.446 | abc |
| control | Brassica oleraceae | Rhizosphere | 5.399 | abc |
| oral\_secretion | Brassica oleraceae | Endosphere | 5.230 | abc |
| MeJA\_0.1 | Brassica oleraceae | Endosphere | 5.153 | abc |
| MeJA\_1.0 | Brassica oleraceae | Endosphere | 5.013 | bcd |
| MeJA\_0.1 | Arabidopsis thaliana | Endosphere | 4.955 | bcd |
| control | Arabidopsis thaliana | Endosphere | 4.922 | cd |
| oral\_secretion | Arabidopsis thaliana | Endosphere | 4.899 | cd |
| control | Brassica oleraceae | Endosphere | 4.877 | cd |
| MeJA\_1.0 | Arabidopsis thaliana | Endosphere | 4.495 | d |

#colors & treatments

color\_treatments <- c("#999999", "#E69F00", "#56B4E9", "#009E73")

#names(color\_treatments) <- c("Control", "MeJA 0.1mM", "MeJA 1mM", "P. brassicae OS")

#color\_treatments <- hcl.colors(4,palette="Geyser")

#color\_treatments <- c("#E6C186", "#B8CDAE", "#008585", "#C7522B")

#color\_species <- c("#146627ff", "#1fb695ff") #at & bo, respectively

#color\_samples<- c("#e7b083ff", "#905423ff") #endo & rhizo, respectively

Table\_Permanovas\_above\_neutral: PERMANOVA results of rhizosphere community composition of AT and BO, for both the full microbial communities and the sub-community composed of ASVs occurring above expectations of Sloan’s Neutral model. Treat = treatment effect on community composition, Block = Block effect on community composition

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Plant sp. | Factor | P value | | R2 | | F value | |
|  |  | Full community | Above-neutral subset | Full community | Above-neutral subset | Full community | Above-neutral subset |
| AT | Treat | 0.0068 | >0.001 | 0.1416 | 0.6568 | 1.1673 | 14.152 |
|  | Block | 0.0068 | >0.001 | 0.2516 | 0.111 | 1.2443 | 1.436 |
| BO | Treat | 0.0622 | >0.001 | 0.1442 | 0.6911 | 1.1689 | 15.528 |
|  | Block | 0.0622 | >0.001 | 0.2388 | 0.0862 | 1.1615 | 1.162 |

SUP\_Pairwise\_permanova\_table\_neutral: Pairwise comparisons of above-neutral microbial sub-community compositions in each data partition (based on adonis.pair function of the EcolUtils R package).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Plant sp. | Sample type | Pairwise comparison | | | SumsOfSqs | MeanSqs | F.Model | R2 | P.value | P.value.corrected |
| BO | Rhizosphere | control | <-> | MeJA\_0.1 | 0.7283925 | 0.7283925 | 17.79959 | 0.6402825 | 0.000999001 | 0.001998 |
| BO | Rhizosphere | control | <-> | MeJA\_1.0 | 0.6963898 | 0.6963898 | 16.23748 | 0.6188659 | 0.001998002 | 0.001998 |
| BO | Rhizosphere | control | <-> | oral\_secretion | 0.5043068 | 0.5043068 | 11.84432 | 0.5422152 | 0.001998002 | 0.001998 |
| BO | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.6235926 | 0.6235926 | 16.06228 | 0.6163037 | 0.001998002 | 0.001998 |
| BO | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.6031414 | 0.6031414 | 15.66049 | 0.6102959 | 0.001998002 | 0.001998 |
| BO | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.4880576 | 0.4880576 | 12.05691 | 0.5466274 | 0.000999001 | 0.001998 |
|  |  |  |  |  |  |  |  |  |  |  |
| AT | Rhizosphere | control | <-> | MeJA\_0.1 | 0.4690952 | 0.4690952 | 11.37724 | 0.5322128 | 0.000999001 | 0.001998 |
| AT | Rhizosphere | control | <-> | MeJA\_1.0 | 0.5867515 | 0.5867515 | 12.9454 | 0.5641828 | 0.001998002 | 0.001998 |
| AT | Rhizosphere | control | <-> | oral\_secretion | 0.4864118 | 0.4864118 | 11.46948 | 0.5342226 | 0.001998002 | 0.001998 |
| AT | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.5972128 | 0.5972128 | 15.16373 | 0.6026026 | 0.001998002 | 0.001998 |
| AT | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.4694965 | 0.4694965 | 12.87405 | 0.5628234 | 0.001998002 | 0.001998 |
| AT | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.5223843 | 0.5223843 | 12.8785 | 0.5629083 | 0.000999001 | 0.001998 |

SUP\_Table\_Artefact\_check: p, R2 and F values of 100 permanovas picking random ASVs found within each treatment based on CSS normalization or rarefied data. The number of Picked ASVs is the same as the number of ASVs found as above neutral by the neutral models. Norm = normalization method, CSS = Cumulative Sum Scaling, Raref = Rarefaction

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | p values | | R2 values | | F value | |
|  | Norm. | A. thaliana | B. oleraceae | A. thaliana | B. oleraceae | A. thaliana | B. oleraceae |
| Max | CSS | 0.6689 | 0.5233 | 0.1552 | 0.1627 | 1.3111 | 1.3880 |
| Mean |  | 0.0758 | 0.1368 | 0.1412 | 0.1423 | 1.1615 | 1.1509 |
| Min |  | 0.0016 | 0.0045 | 0.1232 | 0.1274 | 0.9635 | 0.9868 |
| St.Dev |  | 0.1029 | 0.0988 | 0.0068 | 0.0069 | 0.0688 | 0.0699 |
| Median |  | 0.0419 | 0.1075 | 0.1409 | 0.1422 | 1.1576 | 1.1545 |
|  |  |  |  |  |  |  |  |
| Max | Raref | 0.3228 | 0.3496 | 0.2020 | 0.1984 | 1.9547 | 1.7299 |
| Mean |  | 0.0297 | 0.0949 | 0.1623 | 0.1597 | 1.3991 | 1.3118 |
| Min |  | 0.0011 | 0.0003 | 0.1283 | 0.1323 | 1.0509 | 1.0548 |
| St.Dev |  | 0.0508 | 0.0976 | 0.0157 | 0.0153 | 0.1699 | 0.1549 |
| Median |  | 0.0103 | 0.0573 | 0.1604 | 0.1589 | 1.3835 | 1.3076 |

SUP\_ **Table\_RF\_output:** Summary of Random Forest models performance. Sample partition = plant species and sample type; Sample Size = number of samples in each partition; Model = Whether the full community or the Boruta-selected features were utilized as an input; input ASVs = number of ASVs in the input dataset ; Accuracy and Kappa are defined in the methods section.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Plant Species | Sample type | Sample Size | Model | input ASVs | Accuracy | Kappa |
| *A. thaliana* | endosphere | 22 | Full community RF | 2690 | 0.3282 | 0.1097 |
|  |  | 22 | Boruta-selected RF | 11 | 0.8086 | 0.7426 |
|  | rhizosphere | 24 | Full community RF | 3124 | 0.3571 | 0.1750 |
|  |  | 24 | Boruta-selected RF | 7 | 0.8204 | 0.7609 |
| *B.oleracea* | endosphere | 23 | Full community RF | 2421 | 0.4898 | 0.3350 |
|  |  | 23 | Boruta-selected RF | 16 | 0.8911 | 0.8533 |
|  | rhizosphere | 24 | Full community RF | 2558 | 0.3533 | 0.0908 |
|  |  | 24 | Boruta-selected RF | 6 | 0.6784 | 0.6714 |

SUP\_ table\_confusion\_matrix: Confusion matrix performance of the random forest model when using only the Boruta-selected features. Values outside the diagonals indicate misclassifications by the Random forest algorithm.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **AT Endo (n=22)** | | **Reference** | | | |  | **AT Rhizo (n=24)** | | **Reference** | | | |
| **11 of 2690 ASVs** | | Control | MeJA 0.1 | MeJA 1.0 | Oral |  | **7 of 3124 ASVs** | | Control | MeJA 0.1 | MeJA 1.0 | Oral |
| **Prediction** | Control | 22 | 5.1 | 2.8 | 5.3 |  | **Prediction** | Control | 20.8 | 4.2 | 1.2 | 0.4 |
| MeJA 0.1 | 0.3 | 21.3 | 0 | 0 |  | MeJA 0.1 | 0.3 | 15.1 | 0.6 | 0.7 |
| MeJA 1.0 | 0 | 0.8 | 24.5 | 0 |  | MeJA 1.0 | 3.9 | 3.2 | 21.8 | 0 |
| Oral | 4.8 | 0.1 | 0 | 13 |  | Oral | 0 | 2.5 | 1.4 | 24 |
|  |  | *Accuracy: 0.8086* | | *Kappa: 0.7426* | |  |  |  | *Accuracy: 0.8167* | | *Kappa: 0.7609* | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BO Endo (n=23)** | | **Reference** | | | |  | **BO Rhizo (n=24)** | | **Reference** | | | |
| **16 of 2421 ASVs** | | Control | MeJA 0.1 | MeJA 1.0 | Oral |  | **6 of 2558 ASVs** | | Control | MeJA 0.1 | MeJA 1.0 | Oral |
| **Prediction** | Control | 19 | 0.3 | 0 | 3.3 |  | **Prediction** | Control | 19.5 | 0 | 0 | 5.1 |
| MeJA 0.1 | 0.4 | 25.8 | 0 | 0.1 |  | MeJA 0.1 | 0.1 | 21.5 | 4 | 1.4 |
| MeJA 1.0 | 0 | 0 | 26.1 | 4.3 |  | MeJA 1.0 | 1.2 | 3.5 | 14 | 5.8 |
| Oral | 2.4 | 0 | 0 | 18 |  | Oral | 4.82 | 0 | 7 | 13 |
|  |  | *Accuracy: 0.8911* | | *Kappa: 0.8533* | |  |  |  | *Accuracy: 0.6784* | | *Kappa: 0.6714* | |

SUP\_ table\_rf\_taxonomies: Taxonomies and mean importance of ASVs tagged as important by Boruta for each data partition.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Plant species | Sample type | ASV ID | Phylum | Class | Order | Family | Genus | Mean Importance |
| *A. thaliana* | **Endosphere** | ASV\_74 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | g\_\_Massilia | 19.092 |
|  |  | ASV\_114 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Chitinophagales | f\_\_Chitinophagaceae | g\_\_Niastella | 11.331 |
|  |  | ASV\_143 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Chitinophagales | f\_\_Chitinophagaceae | g\_\_Ferruginibacter | 14.558 |
|  |  | ASV\_178 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Chitinophagales | f\_\_Chitinophagaceae | g\_\_Niastella | 20.855 |
|  |  | ASV\_192 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Rubrivivax | 13.01 |
|  |  | ASV\_198 | p\_\_Acidobacteriota | c\_\_Holophagae | o\_\_Holophagales | f\_\_Holophagaceae | g\_\_Holophaga | 11.313 |
|  |  | ASV\_483 | p\_\_Myxococcota | c\_\_Polyangia | o\_\_Polyangiales | f\_\_Polyangiaceae | g\_\_Pajaroellobacter | 10.025 |
|  |  | ASV\_512 | p\_\_Spirochaetota | c\_\_Leptospirae | o\_\_Leptospirales | f\_\_Leptospiraceae | g\_\_Leptospira | 15.829 |
|  |  | ASV\_553 | p\_\_Chloroflexi | c\_\_Ktedonobacteria | o\_\_Ktedonobacterales | f\_\_Ktedonobacteraceae | g\_\_uncultured | 12.509 |
|  |  | ASV\_608 | p\_\_Myxococcota | c\_\_Polyangia | o\_\_Polyangiales | f\_\_BIrii41 | g\_\_BIrii41 | 13.888 |
|  |  | ASV\_1387 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | g\_\_Massilia | 14.411 |
|  |  |  |  |  |  |  |  |  |
|  | **Rhizosphere** | ASV\_5 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Rhizobacter | 15.401 |
|  |  | ASV\_29 | p\_\_Proteobacteria | c\_\_Alphaproteobacteria | o\_\_Rhizobiales | f\_\_Xanthobacteraceae | g\_\_Bradyrhizobium | 21.212 |
|  |  | ASV\_191 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | g\_\_Massilia | 19.722 |
|  |  | ASV\_192 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Rubrivivax | 20.851 |
|  |  | ASV\_407 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Chitinophagales | f\_\_Chitinophagaceae | g\_\_Ferruginibacter | 19.078 |
|  |  | ASV\_473 | p\_\_Proteobacteria | c\_\_Alphaproteobacteria | o\_\_Rhizobiales | f\_\_Xanthobacteraceae | g\_\_uncultured | 25.946 |
|  |  | ASV\_909 | p\_\_Proteobacteria | c\_\_Alphaproteobacteria | o\_\_Caulobacterales | f\_\_Caulobacteraceae | g\_\_Asticcacaulis | 26.75 |
|  |  |  |  |  |  |  |  |  |
| *B. oleracea* | **Endosphere** | **ASV\_10** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Acidovorax | 12.037 |
|  |  | **ASV\_67** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | NA | 18.616 |
|  |  | **ASV\_83** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | NA | 15.693 |
|  |  | ASV\_100 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Sphingobacteriales | f\_\_Sphingobacteriaceae | g\_\_Pedobacter | 12.396 |
|  |  | ASV\_106 | p\_\_Verrucomicrobiota | c\_\_Chlamydiae | o\_\_Chlamydiales | f\_\_Parachlamydiaceae | g\_\_Candidatus\_Protochlamydia | 12.973 |
|  |  | **ASV\_123** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Rhizobacter | 14.055 |
|  |  | **ASV\_240** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Leptothrix | 21.175 |
|  |  | **ASV\_291** | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | g\_\_Leptothrix | 10.406 |
|  |  | ASV\_293 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | NA | 12.844 |
|  |  | ASV\_318 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Burkholderiaceae | g\_\_Burkholderia-Caballeronia-Paraburkholderia | 16.645 |
|  |  | ASV\_413 | p\_\_Chloroflexi | c\_\_Ktedonobacteria | o\_\_C0119 | f\_\_C0119 | g\_\_C0119 | 11.519 |
|  |  | ASV\_782 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Cytophagales | f\_\_Cytophagaceae | g\_\_Cytophaga | 14.745 |
|  |  | ASV\_799 | p\_\_Planctomycetota | c\_\_Planctomycetes | o\_\_Planctomycetales | f\_\_uncultured | g\_\_uncultured | 12.979 |
|  |  | ASV\_959 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Flavobacteriales | f\_\_Flavobacteriaceae | g\_\_Flavobacterium | 11.165 |
|  |  | ASV\_962 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Rhodocyclaceae | g\_\_Uliginosibacterium | 10.344 |
|  |  | ASV\_1091 | p\_\_Bdellovibrionota | c\_\_Oligoflexia | o\_\_0319-6G20 | f\_\_0319-6G20 | g\_\_0319-6G20 | 16.545 |
|  |  | ASV\_1385 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | NA | 12.486 |
|  |  |  |  |  |  |  |  |  |
|  | **Rhizosphere** | ASV\_12 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Comamonadaceae | NA | 16.5 |
|  |  | ASV\_61 | p\_\_Proteobacteria | c\_\_Gammaproteobacteria | o\_\_Burkholderiales | f\_\_Oxalobacteraceae | g\_\_Massilia | 18.569 |
|  |  | ASV\_97 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Sphingobacteriales | f\_\_Sphingobacteriaceae | g\_\_Mucilaginibacter | 19.327 |
|  |  | ASV\_101 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Sphingobacteriales | f\_\_Sphingobacteriaceae | g\_\_Pedobacter | 16.441 |
|  |  | ASV\_410 | p\_\_Actinobacteriota | c\_\_Actinobacteria | o\_\_Propionibacteriales | f\_\_Nocardioidaceae | g\_\_Nocardioides | 19.108 |
|  |  | ASV\_496 | p\_\_Bacteroidota | c\_\_Bacteroidia | o\_\_Sphingobacteriales | f\_\_Sphingobacteriaceae | g\_\_Mucilaginibacter | 16.534 |

SUP\_table\_random\_networks: Comparison of global network metrics from calculated real networks and 1000 random networks with the same number of nodes and edges. Real ≠ Random = indicates if the real network metric is outside the mean±2 standard deviations of the random networks. No AT = A. thaliana, BO = B. oleraceae, Endo = Endosphere, Rhizo = Rizosphere

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Plant sp. | Sample type | Network | Centralized betweenness | Centralized closeness | Centralized eigenvector | Network transitivity | Network mean shortest path | Network modularity | Mean node betweenness | Mean edge betweenness |
| *AT* | Endo | Real network | 0.0371 | 0.1295 | 0.9675 | 0.3333 | 0.1724 | 0.7315 | 209.5 | 316.4 |
|  |  | Random network mean | 0.1053 | 0.0898 | 0.9601 | 0.0038 | 0.3422 | 0.8597 | 691.0 | 1002.7 |
|  |  | Random network sd | 0.0297 | 0.0168 | 0.0155 | 0.0049 | 0.0511 | 0.0150 | 131.5 | 182.3 |
|  |  | Real ≠ Random | Yes | Yes | No | Yes | Yes | Yes | Yes | Yes |
|  |  |  |  |  |  |  |  |  |  |  |
|  | Rhizo | Real network | 0.0612 | 0.1880 | 0.9538 | 0.2461 | 0.1338 | 0.6294 | 1361.2 | 937.0 |
|  |  | Random network mean | 0.0409 | 0.0999 | 0.8410 | 0.0057 | 0.1384 | 0.5821 | 1774.5 | 1236.2 |
|  |  | Random network sd | 0.0084 | 0.0106 | 0.0348 | 0.0024 | 0.0036 | 0.0063 | 60.3 | 38.4 |
|  |  | Real ≠ Random | Yes | Yes | Yes | Yes | No | Yes | Yes | Yes |
|  |  |  |  |  |  |  |  |  |  |  |
| *BO* | Endo | Real network | 0.0447 | 0.1709 | 0.9688 | 0.3327 | 0.1415 | 0.7571 | 261.0 | 384.3 |
|  |  | Random network mean | 0.1035 | 0.0876 | 0.9633 | 0.0032 | 0.3288 | 0.8612 | 860.0 | 1223.9 |
|  |  | Random network sd | 0.0274 | 0.0159 | 0.0139 | 0.0044 | 0.0442 | 0.0129 | 149.4 | 203.0 |
|  |  | Real ≠ Random | Yes | Yes | No | Yes | Yes | Yes | Yes | Yes |
|  |  |  |  |  |  |  |  |  |  |  |
|  | Rhizo | Real network | 0.0604 | 0.1918 | 0.9537 | 0.2103 | 0.1236 | 0.5976 | 1082.7 | 699.6 |
|  |  | Random network mean | 0.0381 | 0.1019 | 0.8191 | 0.0065 | 0.1221 | 0.5513 | 1591.5 | 1035.0 |
|  |  | Random network sd | 0.0077 | 0.0109 | 0.0364 | 0.0023 | 0.0028 | 0.0061 | 50.0 | 29.4 |
|  |  | Real ≠ Random | Yes | Yes | Yes | Yes | No | Yes | Yes | Yes |

SUP\_Alpha\_diversity\_comamonadace: ANOVA tables for Shannon diversity index in the full comamonadaceae community (left), the comomonadaceae detected as above neutral (center), and the commamonadaceae tagged as “important” (right)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | All Comamonadaceae | | | | Above Neutral ASVs | | | | “Important” ASVs | | | |
|  | SumOfSqs | Df | F value | P value | SumOfSqs | Df | F value | P value | SumOfSqs | Df | F value | P value |
| Block | 0.1521 | 5 | 0.534 | 0.74987 | 0.01734 | 5 | 0.2646 | 0.929355 | 0.6639 | 5 | 1.7669 | 0.1306 |
| Plant sp. | 0.0285 | 1 | 0.4996 | 0.48196 | 0.51887 | 1 | 39.5861 | 3.19E-07\*\*\* | 2.3884 | 1 | 31.7804 | 3.16E-07\*\*\* |
| Stress treatment | 0.2829 | 3 | 1.6548 | 0.1844 | 0.26359 | 3 | 6.7033 | 0.001079\*\* | 2.0255 | 3 | 8.9839 | 3.95E-05\*\*\* |
| Sample type | 0.4237 | 1 | 7.4348 | 0.0080\*\* | - | - | - | - | 11.3968 | 1 | 151.647 | 2.20E-16\*\*\* |
| Plant sp.:Stress treatment | 0.3072 | 3 | 1.797 | 0.15542 | 1.17516 | 3 | 29.8855 | 9.17E-10\*\*\* | 0.3363 | 3 | 1.4917 | 0.2241 |
| Plant sp:Sample type | 0.1904 | 1 | 3.3411 | 0.07171 | - | - | - | - | 0.0175 | 1 | 0.2324 | 0.6312 |
| Stress treatment:Sample type | 0.147 | 3 | 0.8599 | 0.46597 | - | - | - | - | 1.9112 | 3 | 8.4767 | 6.76E-05\*\*\* |
| Plant sp.:Stress treatment:Sample type | 0.1034 | 3 | 0.6051 | 0.6138 | - | - | - | - | 0.226 | 3 | 1.0026 | 0.3967 |
| Residuals | 4.1029 | 72 |  |  | 0.45876 | 35 |  |  | 5.4111 | 72 |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Levene's test of homogeniety of variance |  | 15 | 1.6816 | 0.07246 |  | 7 | 1.2466 | 0.3011 |  | 15 | 0.9115 | 0.5549 |

(incorporate these significance letters on the figure! We won’t publish this table)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| All comamonadaceae | shannon | groups |  | Above neutral comma | shannon | groups |  | Imporntat comma | shannon | groups |
| control\_VS\_Arabidopsis\_thaliana\_Soil | 3.415237 | a |  | oral\_secretion\_VS\_Arabidopsis\_thaliana | 2.906176 | a |  | MeJA\_1.0mM\_VS\_Brassica\_oleraceae\_Soil | 1.911945 | a |
| oral\_secretion\_VS\_Arabidopsis\_thaliana\_Soil | 3.388189 | ab |  | MeJA\_0.1mM\_VS\_Arabidopsis\_thaliana | 2.770747 | b |  | MeJA\_0.1mM\_VS\_Brassica\_oleraceae\_Soil | 1.86083 | a |
| MeJA\_1.0mM\_VS\_Arabidopsis\_thaliana\_Soil | 3.362565 | abc |  | MeJA\_1.0mM\_VS\_Brassica\_oleraceae | 2.711727 | bc |  | oral\_secretion\_VS\_Brassica\_oleraceae\_Soil | 1.813785 | a |
| oral\_secretion\_VS\_Brassica\_oleraceae\_Root | 3.336245 | abc |  | MeJA\_0.1mM\_VS\_Brassica\_oleraceae | 2.601288 | cd |  | control\_VS\_Brassica\_oleraceae\_Soil | 1.764686 | ab |
| MeJA\_0.1mM\_VS\_Arabidopsis\_thaliana\_Soil | 3.306795 | abc |  | control\_VS\_Arabidopsis\_thaliana | 2.557185 | d |  | MeJA\_0.1mM\_VS\_Arabidopsis\_thaliana\_Soil | 1.748341 | ab |
| oral\_secretion\_VS\_Brassica\_oleraceae\_Soil | 3.29956 | abc |  | MeJA\_1.0mM\_VS\_Arabidopsis\_thaliana | 2.537444 | de |  | oral\_secretion\_VS\_Arabidopsis\_thaliana\_Soil | 1.669271 | abc |
| MeJA\_0.1mM\_VS\_Brassica\_oleraceae\_Soil | 3.281881 | abc |  | control\_VS\_Brassica\_oleraceae | 2.417862 | e |  | MeJA\_1.0mM\_VS\_Arabidopsis\_thaliana\_Soil | 1.447608 | bcd |
| MeJA\_1.0mM\_VS\_Brassica\_oleraceae\_Soil | 3.271901 | abc |  | oral\_secretion\_VS\_Brassica\_oleraceae | 2.208915 | f |  | MeJA\_0.1mM\_VS\_Brassica\_oleraceae\_Root | 1.390838 | cde |
| MeJA\_1.0mM\_VS\_Brassica\_oleraceae\_Root | 3.270013 | abc |  |  |  |  |  | control\_VS\_Arabidopsis\_thaliana\_Soil | 1.322109 | def |
| MeJA\_0.1mM\_VS\_Arabidopsis\_thaliana\_Root | 3.25965 | abcd |  |  |  |  |  | control\_VS\_Brassica\_oleraceae\_Root | 1.302309 | def |
| MeJA\_0.1mM\_VS\_Brassica\_oleraceae\_Root | 3.23721 | abcde |  |  |  |  |  | oral\_secretion\_VS\_Brassica\_oleraceae\_Root | 1.219447 | defg |
| oral\_secretion\_VS\_Arabidopsis\_thaliana\_Root | 3.206546 | abcde |  |  |  |  |  | oral\_secretion\_VS\_Arabidopsis\_thaliana\_Root | 1.049925 | efgh |
| control\_VS\_Brassica\_oleraceae\_Soil | 3.125934 | bcde |  |  |  |  |  | control\_VS\_Arabidopsis\_thaliana\_Root | 1.023148 | fgh |
| control\_VS\_Arabidopsis\_thaliana\_Root | 3.103044 | cde |  |  |  |  |  | MeJA\_0.1mM\_VS\_Arabidopsis\_thaliana\_Root | 0.918047 | gh |
| MeJA\_1.0mM\_VS\_Arabidopsis\_thaliana\_Root | 2.996386 | de |  |  |  |  |  | MeJA\_1.0mM\_VS\_Brassica\_oleraceae\_Root | 0.769873 | h |
| control\_VS\_Brassica\_oleraceae\_Root | 2.963253 | e |  |  |  |  |  | MeJA\_1.0mM\_VS\_Arabidopsis\_thaliana\_Root | 0.272206 | i |