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 |

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 |

Table\_Permanovas\_above\_neutral: PERMANOVA table of community composition including only the ASVs classified as above-neutral in at least one treatment. 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* | Rhizosphere | Stress treatment | 3 | 0.11377 | 0.22789 | 2.1067 | 1.00E-04 | \*\* |
|  |  | Block | 5 | 0.11544 | 0.23123 | 1.2826 | 1.00E-04 | \*\* |
|  |  | Residual | 13 | 0.27001 | 0.54087 |  |  |  |
|  |  | Total | 21 | 0.49922 | 1 |  |  |  |
|  |  |  |  |  |  |  |  |  |
| *B. oleracea* | Rhizosphere | Stress treatment | 3 | 0.12263 | 0.2259 | 1.9829 | 1.00E-04 | \*\* |
|  |  | Block | 5 | 0.111 | 0.20448 | 1.0769 | 1.00E-04 | \*\* |
|  |  | Residual | 14 | 0.30921 | 0.56962 |  |  |  |
|  |  | Total | 22 | 0.54283 | 1 |  |  |  |

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** |
| **AT** | Rhizosphere | control | <-> | MeJA\_0.1 | 0.037789 | 0.037789 | 2.060087 | 0.170819 | 0.003996 | 0.005994006 |
| **AT** | Rhizosphere | control | <-> | MeJA\_1.0 | 0.042581 | 0.042581 | 1.970279 | 0.164598 | 0.003996 | 0.005994006 |
| **AT** | Rhizosphere | control | <-> | oral\_secretion | 0.032141 | 0.032141 | 1.633714 | 0.140429 | 0.006993 | 0.006993007 |
| **AT** | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.044273 | 0.044273 | 2.346015 | 0.190022 | 0.003996 | 0.005994006 |
| **AT** | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.030214 | 0.030214 | 1.784259 | 0.15141 | 0.002997 | 0.005994006 |
| **AT** | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.040539 | 0.040539 | 2.006745 | 0.167135 | 0.006993 | 0.006993007 |
|  |  |  |  |  |  |  |  |  |  |  |
| **BO** | Rhizosphere | control | <-> | MeJA\_0.1 | 0.043274 | 0.043274 | 2.052011 | 0.170263 | 0.002997 | 0.008991009 |
| **BO** | Rhizosphere | control | <-> | MeJA\_1.0 | 0.058428 | 0.058428 | 2.608005 | 0.206853 | 0.006993 | 0.013986014 |
| **BO** | Rhizosphere | control | <-> | oral\_secretion | 0.038074 | 0.038074 | 1.49277 | 0.129888 | 0.064935 | 0.064935065 |
| **BO** | Rhizosphere | MeJA\_0.1 | <-> | MeJA\_1.0 | 0.042295 | 0.042295 | 2.56103 | 0.203887 | 0.002997 | 0.008991009 |
| **BO** | Rhizosphere | MeJA\_0.1 | <-> | oral\_secretion | 0.027824 | 0.027824 | 1.418373 | 0.124219 | 0.025974 | 0.038961039 |
| **BO** | Rhizosphere | MeJA\_1.0 | <-> | oral\_secretion | 0.035359 | 0.035359 | 1.689276 | 0.144515 | 0.033966 | 0.040759241 |