Supplementary Data

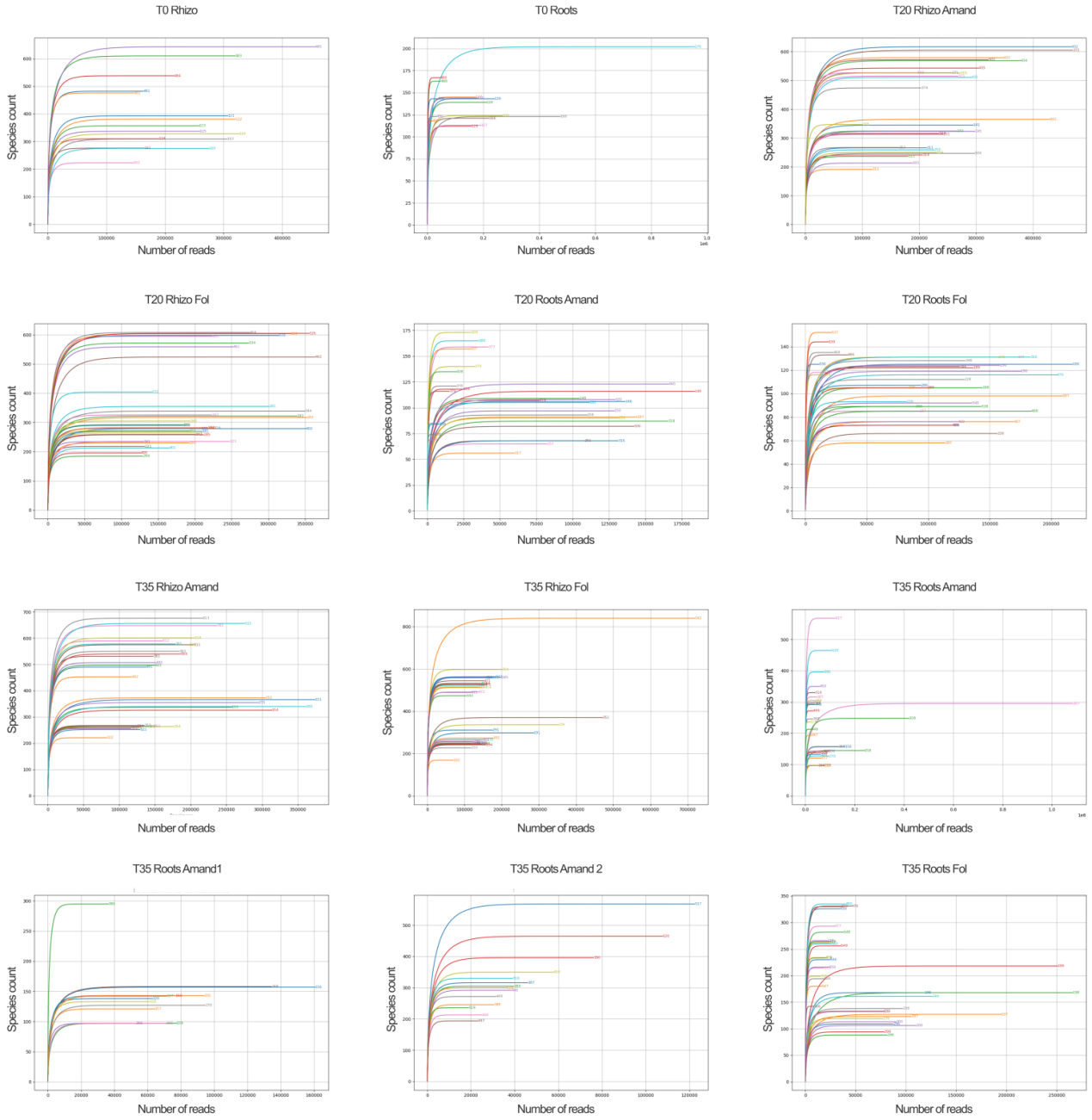

Figure S1: Rarefaction curves of all samples for targeted genomics analysis from Rhizospheric (Rhizo) and Endospheric (Roots) samples at T0, T20 and T35 after biostimulant application through Amendment (Amend) or Foliar (Fol) applications.

Table S1: Samples analysed for targeted genomic analysis. CM = Culture media biostimulants, BM = biomass extract biostimulants, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

Rhizosphere	**Reads count for rarefaction**	**Roots**	**Reads count for rarefaction**
CMRhizoA	40.312	CMRootsA	4.705
CMRhizoF	65.089	CMRootsF	5.019
BMRhizoA	100.576	BMRootsA	4.801
BMRhizoF	78.201	BMRootsF	11.368

Script S1: Python Script for Rarefaction Analysis

```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import os
from tqdm import tqdm
from scipy.stats import sem, t

print("Starting script execution.")

# Prompt the user for the path to the .txt file
file_path = input("Please enter the path to the .txt file (e.g., data.txt): ")
print(f"Provided file path: {file_path}")

# Extract the base name of the file to use in titles and output names
base_name = os.path.splitext(os.path.basename(file_path))[0]

# Check if the file exists
if not os.path.isfile(file_path):
    print(f"Error: The file {file_path} does not exist.")
    exit()

# Read data from the .txt file
try:
    print("Reading data from the .txt file...")
    data = pd.read_csv(file_path, sep="\t")  # Modify the separator if necessary
    print(f"Data read successfully. Data size: {data.shape}")
    print("Preview of raw data:")
    print(data.head())
except Exception as e:
    print(f"Error reading the file: {e}")
    exit()

# Keep only numeric columns and handle individual rarefaction
numeric_data = data.iloc[:, 1:]  # Assuming the first column is a non-numeric label

# Convert data to numeric values
try:
    print("Converting data to numeric values...")
    numeric_data = numeric_data.apply(pd.to_numeric, errors='coerce')
    # Drop rows with all NaN values after conversion
    numeric_data = numeric_data.dropna(how='all')
```

```python
    # Drop rows where the sum of values is zero
    numeric_data = numeric_data[numeric_data.sum(axis=1) > 0]
    print("Data cleaning completed.")
except Exception as e:
    print(f"Error during data conversion: {e}")
    exit()

print("Preview of numeric data after cleaning:")
print(numeric_data.head())
print(f"Size of numeric data: {numeric_data.shape}")

# Define a rarefaction function specifically for individual rarefaction
def individual_rarefy(sample, num_repetitions=1000, confidence=0.95):
    individuals = np.repeat(np.arange(len(sample)), sample)  # Flatten counts into individual occurrences
    max_depth = len(individuals)
    depths = np.linspace(1, max_depth, num=200).astype(int)
    rarefied_means = []
    lower_bounds = []
    upper_bounds = []

    for depth in tqdm(depths, desc="Calculating individual rarefaction curve", unit="depth"):
        richness_estimates = []
        for _ in range(num_repetitions):
            subsample = np.random.choice(individuals, depth, replace=False)
            richness = len(np.unique(subsample))  # Count unique species
            richness_estimates.append(richness)

        mean_richness = np.mean(richness_estimates)
        rarefied_means.append(mean_richness)

        # Calculate confidence intervals
        std_err = sem(richness_estimates)
        h = std_err * t.ppf((1 + confidence) / 2, num_repetitions - 1)
        lower_bounds.append(mean_richness - h)
        upper_bounds.append(mean_richness + h)

    return rarefied_means, depths, lower_bounds, upper_bounds

# Plot the individual rarefaction curves for each sample with confidence intervals
plt.figure(figsize=(12, 8))

```

```python
for idx, column in enumerate(numeric_data.columns):
    print(f"Calculating individual rarefaction curve for sample {column} ({idx + 1} of {len(numeric_data.columns)})...")
    sample = numeric_data[column].values

    if sample.sum() > 1:
        rarefied_means, depths, lower_bounds, upper_bounds = individual_rarefy(sample)
        line, = plt.plot(depths, rarefied_means, label=f'{column}')
        plt.fill_between(depths, lower_bounds, upper_bounds, color=line.get_color(), alpha=0.2)
        plt.text(depths[-1], rarefied_means[-1], column, fontsize=8, ha='left', va='center', color=line.get_color())

plt.ylabel('Taxa S (95% confidence)')
plt.xlabel('Specimens')
plt.title(base_name)  # Use the base name of the file as the title
plt.grid(True)

# Create the PNG file path in the same directory as the .txt file
output_dir = os.path.dirname(file_path)
png_file_path = os.path.join(output_dir, f"RarefactionCurves-{base_name}.png")
plt.savefig(png_file_path)
print(f"Rarefaction curve saved as: {png_file_path}")

# Show the plot
plt.show()
print("Execution completed.")
```

Table S2: Reads number for each sample. Sample excluded in red. CM = Culture media biostimulants, BM = biomass extract biostimulants, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

Rhizosphere			Roots		
Manip	**Sample**	**Reads number**	**Manip**	**Sample**	**Reads number**
CMRhizoA	121	204149	CMRootsA	126	45407
CMRhizoA	122	202763	CMRootsA	127	43682
CMRhizoA	123	150405	CMRootsA	128	31875
CMRhizoA	124	106375	CMRootsA	129	18124
CMRhizoA	125	169408	CMRootsA	130	65896
CMRhizoA	141	176446	CMRootsA	146	16439
CMRhizoA	142	285455	CMRootsA	147	14888
CMRhizoA	143	168978	CMRootsA	148	19395
CMRhizoA	144	138116	CMRootsA	149	27394
CMRhizoA	145	166411	CMRootsA	150	14686
CMRhizoA	151	193915	CMRootsA	156	47047
CMRhizoA	152	165196	CMRootsA	157	13115
CMRhizoA	153	144147	CMRootsA	158	22871
CMRhizoA	154	167370	CMRootsA	159	8879
CMRhizoA	155	149066	CMRootsA	160	20494
CMRhizoA	251	177814	CMRootsA	256	8515
CMRhizoA	252	154908	CMRootsA	257	6814
CMRhizoA	253	103100	CMRootsA	258	15513
CMRhizoA	254	147790	CMRootsA	259	18542

Rhizosphere			Roots		
Manip	**Sample**	**Reads number**	**Manip**	**Sample**	**Reads number**
CMRhizoA	255	135659	CMRootsA	260	44635
CMRhizoA	261	63478	CMRootsA	266	13564
CMRhizoA	262	82186	CMRootsA	267	199646
CMRhizoA	263	72856	CMRootsA	268	24891
CMRhizoA	264	92984	CMRootsA	269	11706
CMRhizoA	265	219133	CMRootsA	270	28528
CMRhizoA	311	153288	CMRootsA	316	7127
CMRhizoA	312	73980	CMRootsA	317	4705
CMRhizoA	313	130354	CMRootsA	318	15165
CMRhizoA	314	142472	CMRootsA	319	11292
CMRhizoA	321	70927	CMRootsA	320	18338
CMRhizoA	322	40312	CMRootsA	326	15167
CMRhizoA	323	77172	CMRootsA	327	18624
CMRhizoA	324	67301	CMRootsA	328	82414
CMRhizoA	325	70266	CMRootsA	329	17568
			CMRootsA	330	19181
CMRhizoF	161	100384	CMRootsF	166	88296
CMRhizoF	162	104454	CMRootsF	167	50746
CMRhizoF	163	210010	CMRootsF	168	135319
CMRhizoF	164	232683	CMRootsF	169	73658
CMRhizoF	165	204081	CMRootsF	170	199506
CMRhizoF	181	120939	CMRootsF	186	22189
CMRhizoF	182	200188	CMRootsF	187	13077
CMRhizoF	183	185978	CMRootsF	188	13385
CMRhizoF	184	116876	CMRootsF	189	26769
CMRhizoF	185	127112	CMRootsF	190	41650
CMRhizoF	191	139821	CMRootsF	196	22300
CMRhizoF	192	37850	CMRootsF	197	17701
CMRhizoF	193	69235	CMRootsF	198	30122
CMRhizoF	194	83240	CMRootsF	199	50713
CMRhizoF	195	69069	CMRootsF	200	9435
CMRhizoF	281	157804	CMRootsF	286	11962
CMRhizoF	282	103182	CMRootsF	287	5019
CMRhizoF	283	106430	CMRootsF	288	11529
CMRhizoF	284	65089	CMRootsF	289	15303
CMRhizoF	285	115660	CMRootsF	290	30310
CMRhizoF	291	97411	CMRootsF	296	12313
CMRhizoF	292	97823	CMRootsF	297	14544
CMRhizoF	293	77454	CMRootsF	298	8351
CMRhizoF	294	78421	CMRootsF	299	7364
CMRhizoF	295	75041	CMRootsF	300	8895
CMRhizoF	341	72340	CMRootsF	346	25659
CMRhizoF	342	103126	CMRootsF	347	31160
CMRhizoF	343	111931	CMRootsF	348	25818
CMRhizoF	344	214414	CMRootsF	349	22830
CMRhizoF	345	110752	CMRootsF	350	26358
CMRhizoF	351	239732	CMRootsF	356	8608
CMRhizoF	352	76538	CMRootsF	357	18416
CMRhizoF	353	71319	CMRootsF	358	17996
CMRhizoF	354	200496	CMRootsF	359	14143
CMRhizoF	355	174577	CMRootsF	360	25776
BMRhizoA	371	257226	BMRootsA	376	15076
BMRhizoA	372	469805	BMRootsA	377	41891
BMRhizoA	373	267752	BMRootsA	378	19833
BMRhizoA	374	203147	BMRootsA	379	32652
BMRhizoA	375	100576	BMRootsA	380	35220
BMRhizoA	381	147461	BMRootsA	386	36452
BMRhizoA	382	236330	BMRootsA	387	46015
BMRhizoA	383	183606	BMRootsA	388	30108
BMRhizoA	384	197807	BMRootsA	389	39537
BMRhizoA	385	178257	BMRootsA	390	76020
BMRhizoA	431	291540	BMRootsA	436	8298
BMRhizoA	432	467374	BMRootsA	437	29503
BMRhizoA	433	347649	BMRootsA	438	20047
BMRhizoA	434	378418	BMRootsA	439	24540
BMRhizoA	435	304386	BMRootsA	440	45274
BMRhizoA	441	137325	BMRootsA	446	38468
BMRhizoA	442	117128	BMRootsA	447	23188
BMRhizoA	443	149571	BMRootsA	448	24829
BMRhizoA	444	185792	BMRootsA	449	31440
BMRhizoA	445	151142	BMRootsA	450	57741
BMRhizoA	501	102029	BMRootsA	506	12484
BMRhizoA	502	321337	BMRootsA	508	4801
BMRhizoA	503	196776	BMRootsA	509	30039
BMRhizoA	504	172869	BMRootsA	510	6139
BMRhizoA	505	272573	BMRootsA	516	38739
BMRhizoA	511	203912	BMRootsA	517	122378
BMRhizoA	512	160714	BMRootsA	518	36336
BMRhizoA	513	216922	BMRootsA	519	18845
BMRhizoA	514	204986	BMRootsA	520	107697

Rhizosphere			Roots		
Manip	**Sample**	**Reads number**	**Manip**	**Sample**	**Reads number**
BMRhizoA	515	275399	BMRootsA	486	36419
BMRhizoA	481	488892	BMRootsA	487	17888
BMRhizoA	482	440661	BMRootsA	488	47167
BMRhizoA	483	958191	BMRootsA	489	45175
BMRhizoA	484	646371	BMRootsA	490	32802
BMRhizoA	485	1368825			
BMRhizoF	401	91551	BMRootsF	406	12823
BMRhizoF	402	204420	BMRootsF	407	23578
BMRhizoF	403	115644	BMRootsF	408	23135
BMRhizoF	404	104165	BMRootsF	409	33890
BMRhizoF	405	78201	BMRootsF	410	17462
BMRhizoF	411	156837	BMRootsF	416	34419
BMRhizoF	412	136852	BMRootsF	417	22608
BMRhizoF	413	143282	BMRootsF	418	23998
BMRhizoF	414	143049	BMRootsF	419	35072
BMRhizoF	415	117010	BMRootsF	420	21749
BMRhizoF	461	251905	BMRootsF	466	34525
BMRhizoF	462	363678	BMRootsF	467	16824
BMRhizoF	463	222822	BMRootsF	468	22911
BMRhizoF	464	274301	BMRootsF	469	14858
BMRhizoF	465	98369	BMRootsF	470	25593
BMRhizoF	471	152193	BMRootsF	476	45965
BMRhizoF	472	137132	BMRootsF	477	28945
BMRhizoF	473	153181	BMRootsF	478	19776
BMRhizoF	474	153645	BMRootsF	479	20124
BMRhizoF	475	142675	BMRootsF	480	39854
BMRhizoF	481	162964	BMRootsF	486	36419
BMRhizoF	482	146887	BMRootsF	487	17888
BMRhizoF	483	319397	BMRootsF	488	47167
BMRhizoF	484	215457	BMRootsF	489	45175
BMRhizoF	485	456275	BMRootsF	490	32802
BMRhizoF	531	141965	BMRootsF	536	11368
BMRhizoF	532	314437	BMRootsF	537	21114
BMRhizoF	533	330227	BMRootsF	538	17513
BMRhizoF	534	273442	BMRootsF	539	18791
BMRhizoF	535	355225	BMRootsF	540	21478
BMRhizoF	541	184418	BMRootsF	546	24553
BMRhizoF	542	718849	BMRootsF	547	16403
BMRhizoF	543	104344	BMRootsF	548	38083
BMRhizoF	544	150235	BMRootsF	549	35296
BMRhizoF	545	199592	BMRootsF	550	23558

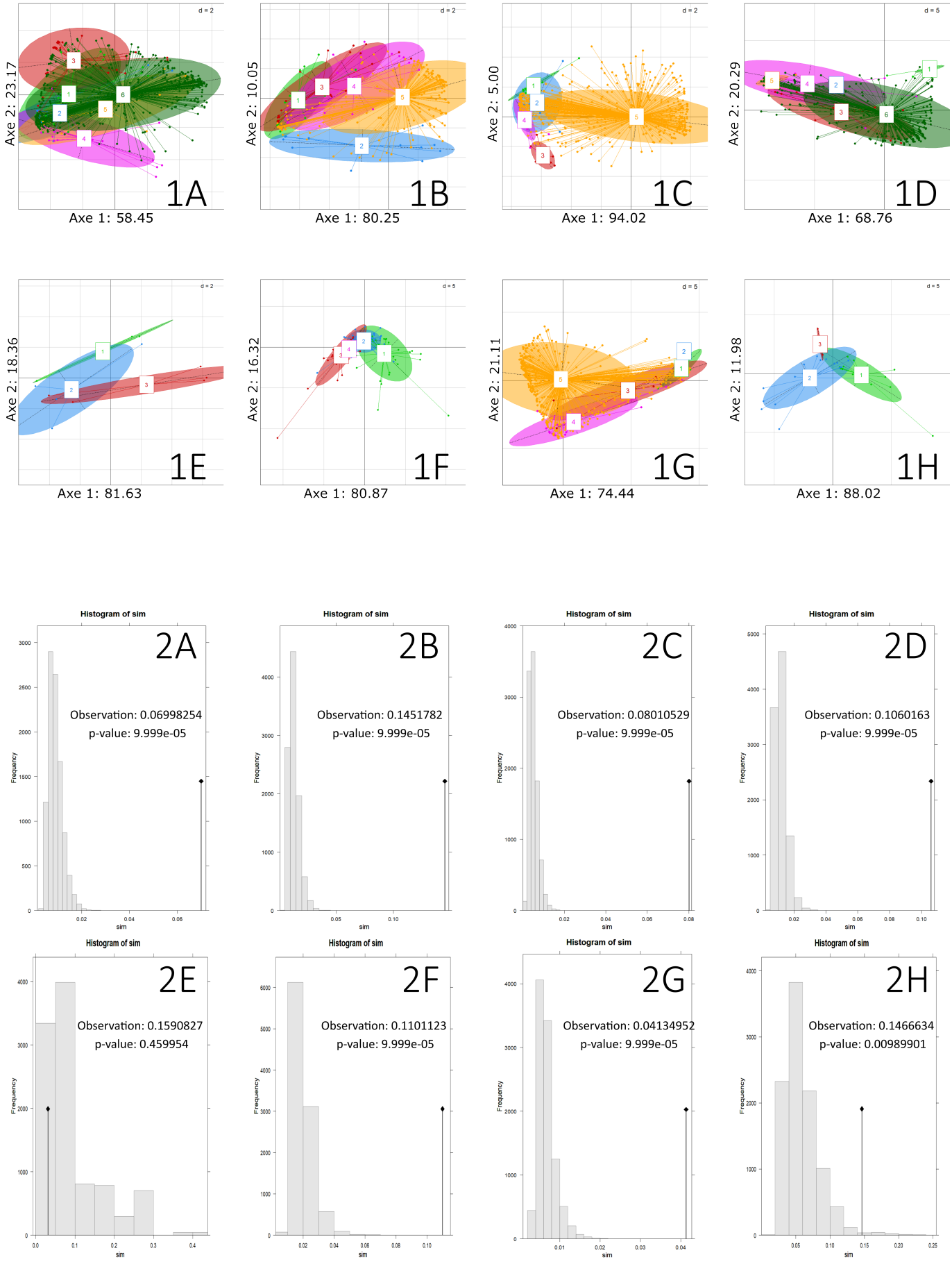

Figure S2: Validity of the RGs by (1A to 1H) BCA followed by (2A to 2H) a null model Monte-Carlo simulation with all the genera and 100 000 group permutations. A=CMRhizoA, B=CMRootsA, C=CMRhizoF, D=CMRootsF, E=BMRhizoA, F=BMRootsA, G=BMRhizoF, H=BMRootsF. CM = Culture media biostimulants, BM = biomass extract biostimulants, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

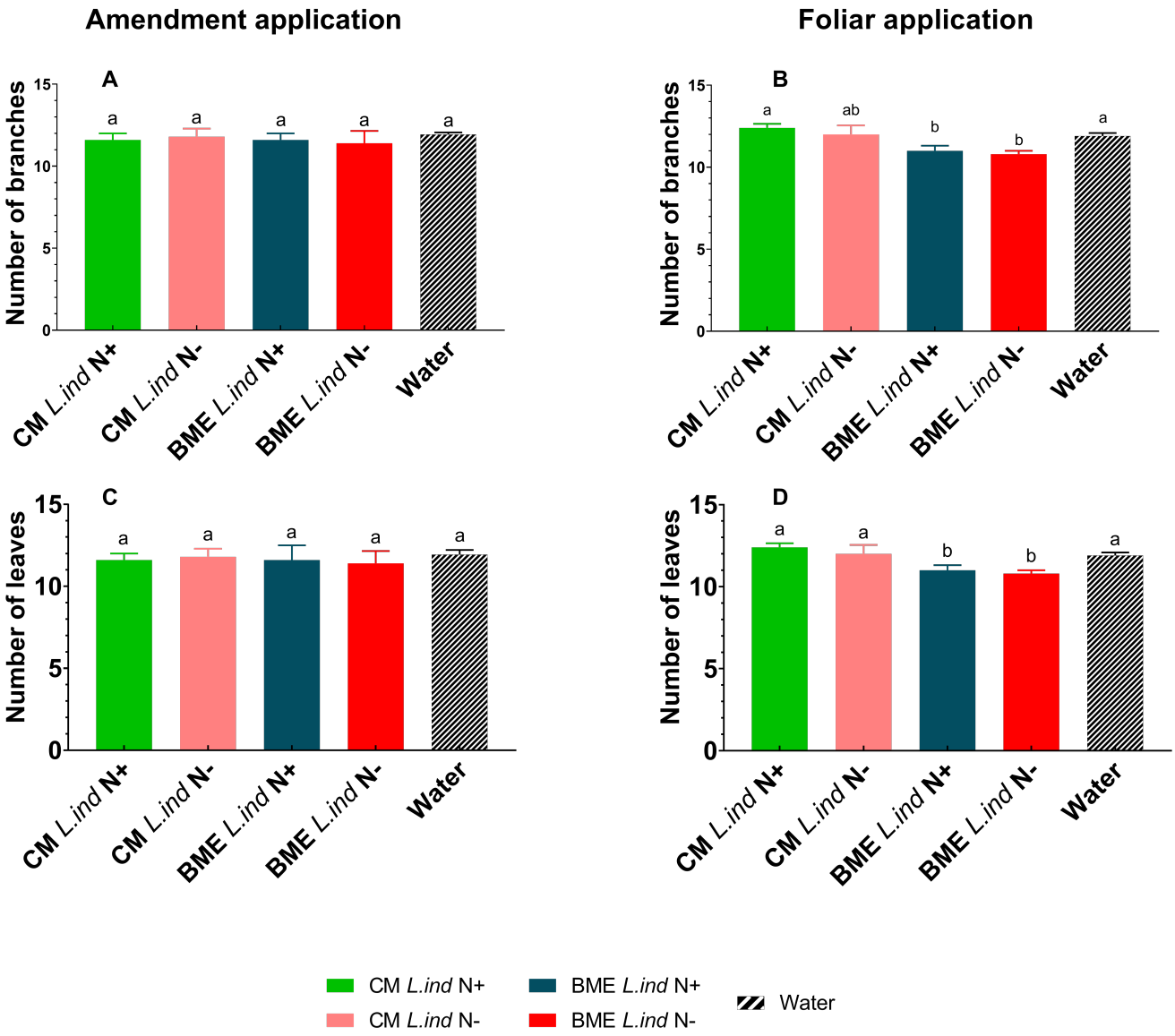

Figure S3: *Solanum lycopersicum* ramifications (A and B) and leaves (C and D) (unit per plant) under amendment (A and C) and foliar (B and D) biostimulant applications at day 35. The values are shown as mean ± SEM. Statistical significance was tested using a t-test, n=5. CM = Culture media biostimulants, BM = biomass extract biostimulants.

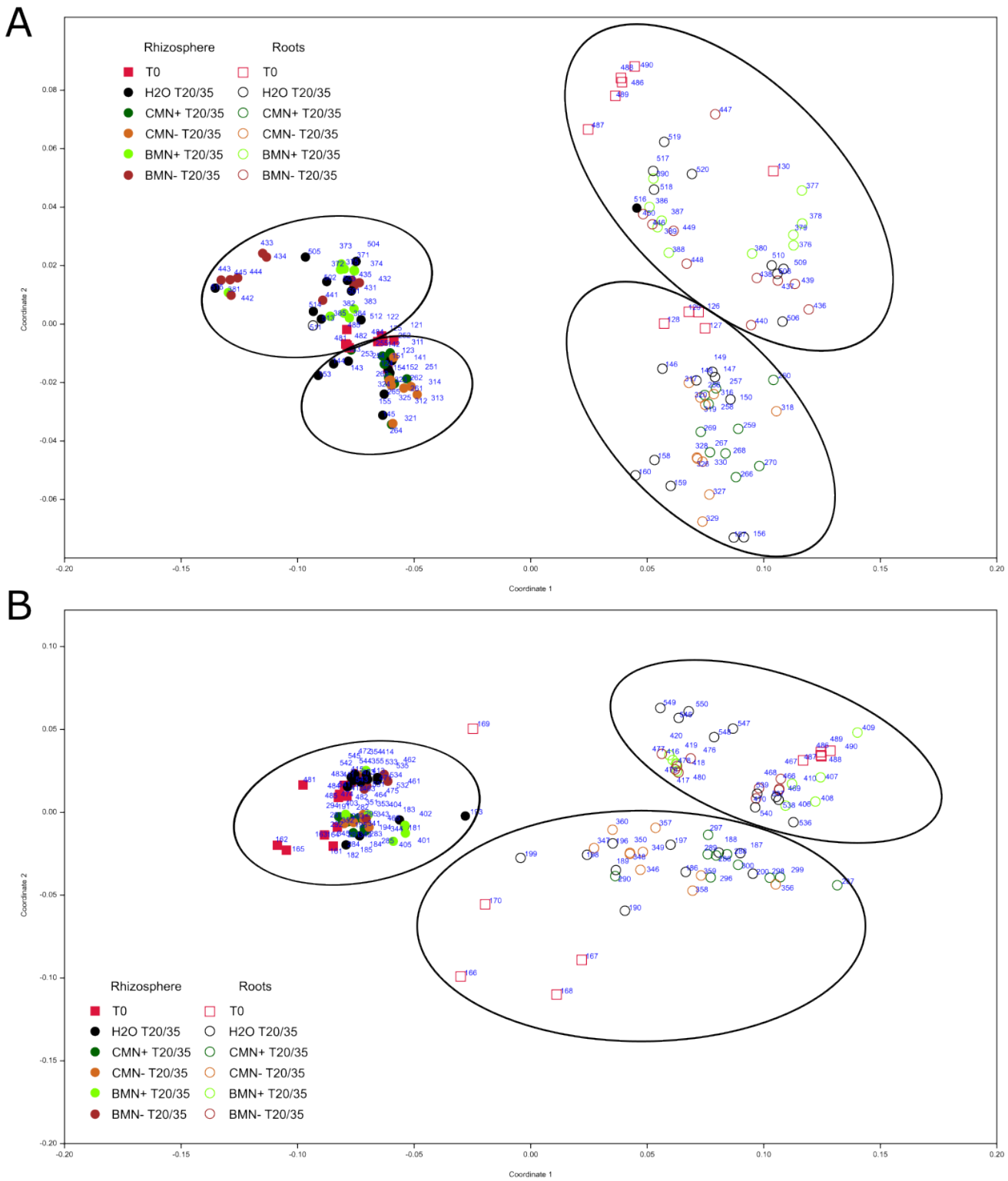

Figure S4: (A) NMDS profile of the pairwise community dissimilarity of samples treated by biostimulant through amendment application and (B) NMDS profile of the pairwise community dissimilarity of samples treated by biostimulant through foliaire application. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days.

Table S3: PERMANOVA analysis using Bray-Curtis dissimilarity with 10,000 permutations. A two-way PERMANOVA was carried out on the following factors: Conditions (H_2O, CMN^+, CMN^-) and Time (T0, T20, T35). Significance: *, *p-value*<0.05; **, *p-value*<0.01; ***, *p-value*<0.001. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

Data Set	**Factors tested**	***p-value***	**r^2**	**Signif.**
2 Rhizo F	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	5,00E-05	0.37509	***
2 Roots F	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	1,00E-05	0.78547	***
3 Rhizo A	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	1,00E-05	0.52625	***
3 Rhizo F	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	1,00E-05	0.56155	***
3 Roots A	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	1,00E-05	0.4309	***
3 Roots F	Two-way PERMANOVA (Bray-Curtis dissimilarity, 10,000 permutations): Conditions (H_2O, CMN+, CMN-) * Time (T0, T20, T35)	1,00E-05	0.67005	***

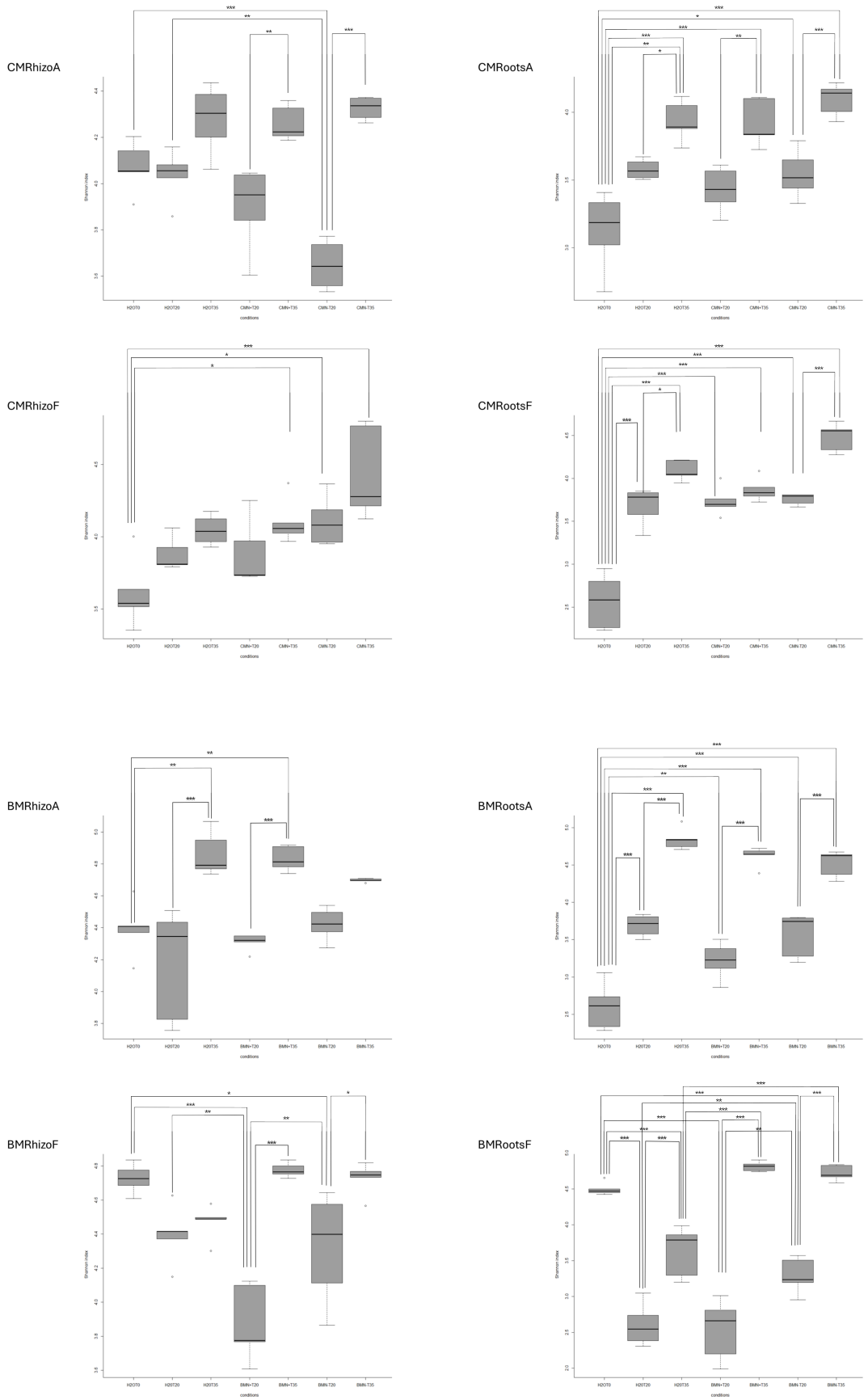

Figure S5: Alpha diversity measured by Shannon diversity index in all data sets. For clarity, statistical significance are shown only within a same biostimulant condition or same time point. * $= p-value < 0.05$, ** $= p-value < 0.01$, *** $= p-value < 0.001$. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

Table S4: Shannon index statistical analysis. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

CMRhizoA			CMRootsA		
Sample	*p-value*		**Sample**	*p-value*	
CMN-T35-CMN-T20	5,00E-07	***	CMN-T35-CMN-T20	6,13E-04	***
CMN+T20-CMN-T20	6,97E-02		CMN+T20-CMN-T20	9,43E-01	
CMN+T35-CMN-T20	1,20E-06	***	CMN+T35-CMN-T20	3,08E-02	*
H2OT0-CMN-T20	3,72E-04	***	H2OT0-CMN-T20	1,23E-02	*
H2OT20-CMN-T20	1,16E-03	**	H2OT20-CMN-T20	1,00E+00	
H2OT35-CMN-T20	7,00E-07	***	H2OT35-CMN-T20	2,33E-02	*
CMN+T20-CMN-T35	3,07E-04	***	CMN+T20-CMN-T35	3,97E-05	***
CMN+T35-CMN-T35	9,81E-01		CMN+T35-CMN-T35	7,20E-01	
H2OT0-CMN-T35	5,94E-02		H2OT0-CMN-T35	0,00E+00	***
H2OT20-CMN-T35	2,17E-02	*	H2OT20-CMN-T35	1,40E-03	**
H2OT35-CMN-T35	9,96E-01		H2OT35-CMN-T35	7,87E-01	
CMN+T35-CMN+T20	1,25E-03	**	CMN+T35-CMN+T20	2,37E-03	**
H2OT0-CMN+T20	2,93E-01		H2OT0-CMN+T20	1,26E-01	
H2OT20-CMN+T20	5,58E-01		H2OT20-CMN+T20	8,28E-01	
H2OT35-CMN+T20	7,00E-04	***	H2OT35-CMN+T20	1,74E-03	**
H2OT0-CMN+T35	2,24E-01		H2OT0-CMN+T35	1,70E-06	***
H2OT20-CMN+T35	9,14E-02		H2OT20-CMN+T35	6,25E-02	
H2OT35-CMN+T35	1,00E+00		H2OT35-CMN+T35	1,00E+00	
H2OT20-H2OT0	9,99E-01		H2OT20-H2OT0	5,63E-03	**
H2OT35-H2OT0	1,49E-01		H2OT35-H2OT0	1,30E-06	***
H2OT35-H2OT20	5,67E-02		H2OT35-H2OT20	4,80E-02	*

CMRhizoF			CMRootsF		
Sample	*p-value*		**Sample**	*p-value*	
CMN-T35-CMN-T20	2,04E-01		CMN-T35-CMN-T20	2,46E-05	***
CMN+T20-CMN-T20	6,05E-01		CMN+T20-CMN-T20	1,00E+00	
CMN+T35-CMN-T20	1,00E+00		CMN+T35-CMN-T20	9,65E-01	
H2OT0-CMN-T20	1,14E-02	*	H2OT0-CMN-T20	0,00E+00	***
H2OT20-CMN-T20	5,88E-01		H2OT20-CMN-T20	9,92E-01	
H2OT35-CMN-T20	9,99E-01		H2OT35-CMN-T20	1,03E-01	
CMN+T20-CMN-T35	4,15E-03	**	CMN+T20-CMN-T35	1,47E-05	***
CMN+T35-CMN-T35	1,87E-01		CMN+T35-CMN-T35	2,92E-04	***
H2OT0-CMN-T35	1,84E-05	***	H2OT0-CMN-T35	0,00E+00	***
H2OT20-CMN-T35	3,88E-03	**	H2OT20-CMN-T35	4,10E-06	***
H2OT35-CMN-T35	1,11E-01		H2OT35-CMN-T35	3,80E-02	*
CMN+T35-CMN+T20	6,34E-01		CMN+T35-CMN+T20	9,15E-01	
H2OT0-CMN+T20	3,90E-01		H2OT0-CMN+T20	0,00E+00	***
H2OT20-CMN+T20	1,00E+00		H2OT20-CMN+T20	9,99E-01	
H2OT35-CMN+T20	9,01E-01		H2OT35-CMN+T20	6,84E-02	
H2OT0-CMN+T35	1,28E-02	*	H2OT0-CMN+T35	0,00E+00	***
H2OT20-CMN+T35	6,18E-01		H2OT20-CMN+T35	6,74E-01	
H2OT35-CMN+T35	1,00E+00		H2OT35-CMN+T35	4,93E-01	
H2OT20-H2OT0	4,05E-01		H2OT20-H2OT0	0,00E+00	***
H2OT35-H2OT0	5,60E-02		H2OT35-H2OT0	0,00E+00	***
H2OT35-H2OT20	8,92E-01		H2OT35-H2OT20	2,22E-02	*

BMRhizoA			BMRootsA		
Sample	*p-value*		**Sample**	*p-value*	
BMN-T35-BMN-T20	1,63E-01		BMN-T35-BMN-T20	5,10E-06	***
BMN+T20-BMN-T20	9,35E-01		BMN+T20-BMN-T20	2,24E-01	
BMN+T35-BMN-T20	9,06E-03	**	BMN+T35-BMN-T20	9,00E-07	***
H20T20-BMN-T20	2,58E-01		H20T20-BMN-T20	9,73E-01	
H20T35-BMN-T20	4,38E-03	**	H20T35-BMN-T20	0,00E+00	***
H2OT0-BMN-T20	1,00E+00		H2OT0-BMN-T20	5,40E-06	***
BMN+T20-BMN-T35	1,58E-02	*	BMN+T20-BMN-T35	0,00E+00	***
BMN+T35-BMN-T35	8,54E-01		BMN+T35-BMN-T35	9,93E-01	
H20T20-BMN-T35	5,67E-04	***	H20T20-BMN-T35	1,35E-04	***
H20T35-BMN-T35	7,02E-01		H20T35-BMN-T35	2,80E-01	
H2OT0-BMN-T35	9,32E-02		H2OT0-BMN-T35	0,00E+00	***
BMN+T35-BMN+T20	5,75E-04	***	BMN+T35-BMN+T20	0,00E+00	***
H20T20-BMN+T20	8,52E-01		H20T20-BMN+T20	5,08E-02	
H20T35-BMN+T20	2,68E-04	***	H20T35-BMN+T20	0,00E+00	***
H2OT0-BMN+T20	9,85E-01		H2OT0-BMN+T20	2,96E-03	**
H20T20-BMN+T35	1,86E-05	***	H20T20-BMN+T35	2,54E-05	***
H20T35-BMN+T35	1,00E+00		H20T35-BMN+T35	6,72E-01	
H2OT0-BMN+T35	4,44E-03	**	H2OT0-BMN+T35	0,00E+00	***
H20T35-H20T20	8,80E-06	***	H20T35-H20T20	5,00E-07	***
H2OT0-H20T20	3,99E-01		H2OT0-H20T20	1,60E-06	***
H2OT0-H20T35	2,11E-03	**	H2OT0-H20T35	0,00E+00	***

BMRhizoF			BMRootsF		
Sample	*p-value*		**Sample**	*p-value*	
BMN-T35-BMN-T20	1,54E-02	*	BMN-T35-BMN-T20	0,00E+00	***
BMN+T20-BMN-T20	6,72E-03	**	BMN+T20-BMN-T20	1,57E-03	**
BMN+T35-BMN-T20	5,03E-03	**	BMN+T35-BMN-T20	0,00E+00	***
H20T20-BMN-T20	9,92E-01		H20T20-BMN-T20	4,74E-03	**
H20T35-BMN-T20	8,15E-01		H20T35-BMN-T20	4,35E-01	
H2OT0-BMN-T20	1,55E-02	*	H2OT0-BMN-T20	1,30E-06	***
BMN+T20-BMN-T35	5,00E-07	***	BMN+T20-BMN-T35	0,00E+00	***
BMN+T35-BMN-T35	9,99E-01		BMN+T35-BMN-T35	9,98E-01	
H20T20-BMN-T35	7,56E-02		H20T20-BMN-T35	0,00E+00	***
H20T35-BMN-T35	2,75E-01		H20T35-BMN-T35	7,00E-06	***
H2OT0-BMN-T35	1,00E+00		H2OT0-BMN-T35	8,24E-01	
BMN+T35-BMN+T20	2,00E-07	***	BMN+T35-BMN+T20	0,00E+00	***
H20T20-BMN+T20	1,12E-03	**	H20T20-BMN+T20	9,99E-01	
H20T35-BMN+T20	1,85E-04	***	H20T35-BMN+T20	7,70E-06	***
H2OT0-BMN+T20	5,00E-07	***	H2OT0-BMN+T20	0,00E+00	***
H20T20-BMN+T35	2,77E-02	*	H20T20-BMN+T35	0,00E+00	***
H20T35-BMN+T35	1,22E-01		H20T35-BMN+T35	1,70E-06	***
H2OT0-BMN+T35	9,99E-01		H2OT0-BMN+T35	5,04E-01	
H20T35-H20T20	9,93E-01		H20T35-H20T20	2,35E-05	***
H2OT0-H20T20	7,62E-02		H2OT0-H20T20	0,00E+00	***
H2OT0-H20T35	2,77E-01		H2OT0-H20T35	2,49E-04	***

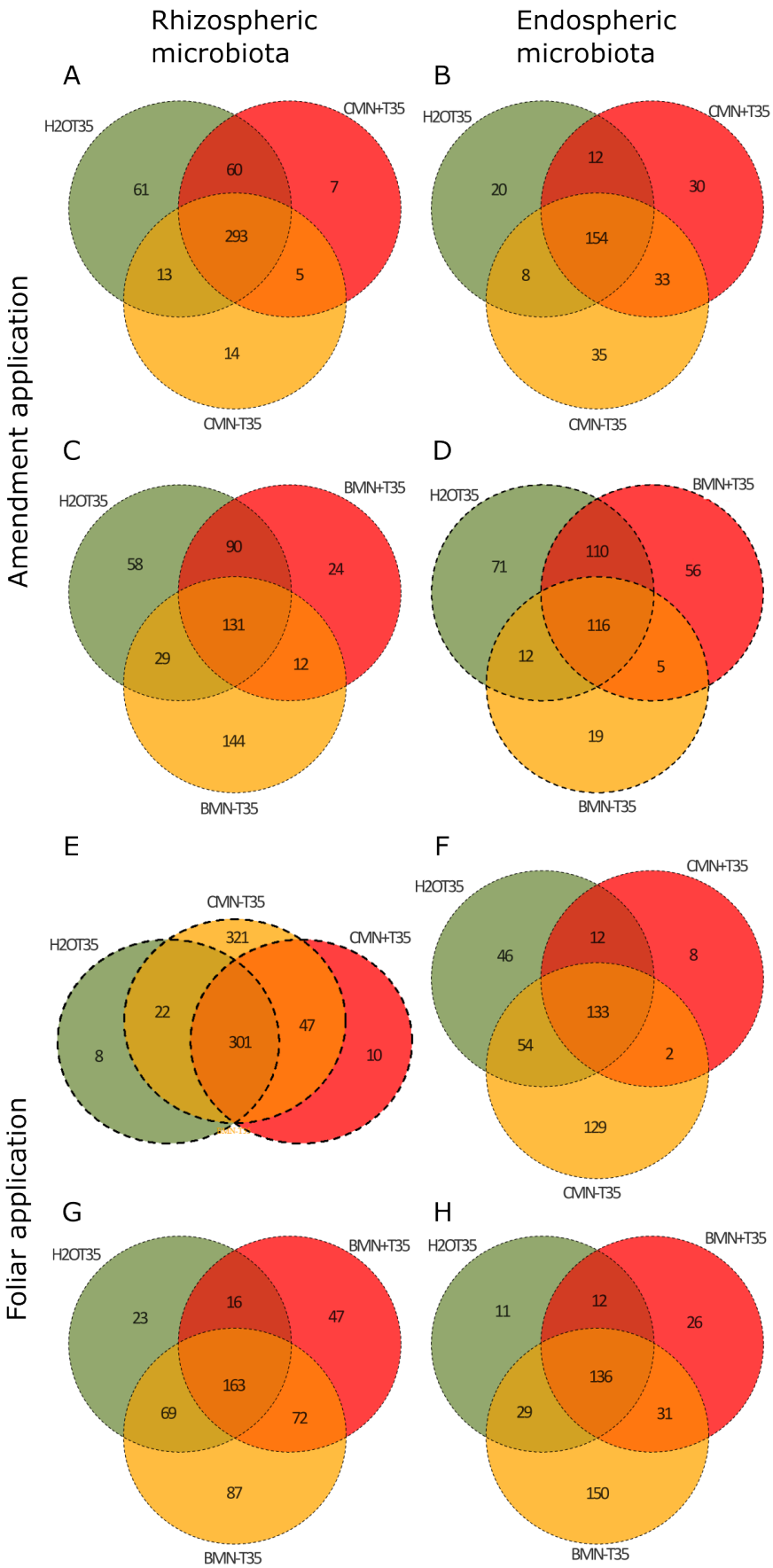

Figure S6: Distinctness of the microbial communities of the rhizospheric microbiota (A, C, E and G) and endospheric microbiota (B, D, F and H) on samples after 35 days of growth with amendment (A to D) and foliar (E to H) applications. NMDS profile of the pairwise community dissimilarity of samples treated by biostimulant (CM (A, B, E, and F) and BM (C, D, G and H)) through amendment application and (B) NMDS profile of the pairwise community dissimilarity of samples treated by biostimulant through foliaire application. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days, Rhizo = rhizosphere, Roots = endosphere, A = amendment treatment, F = foliar treatment.

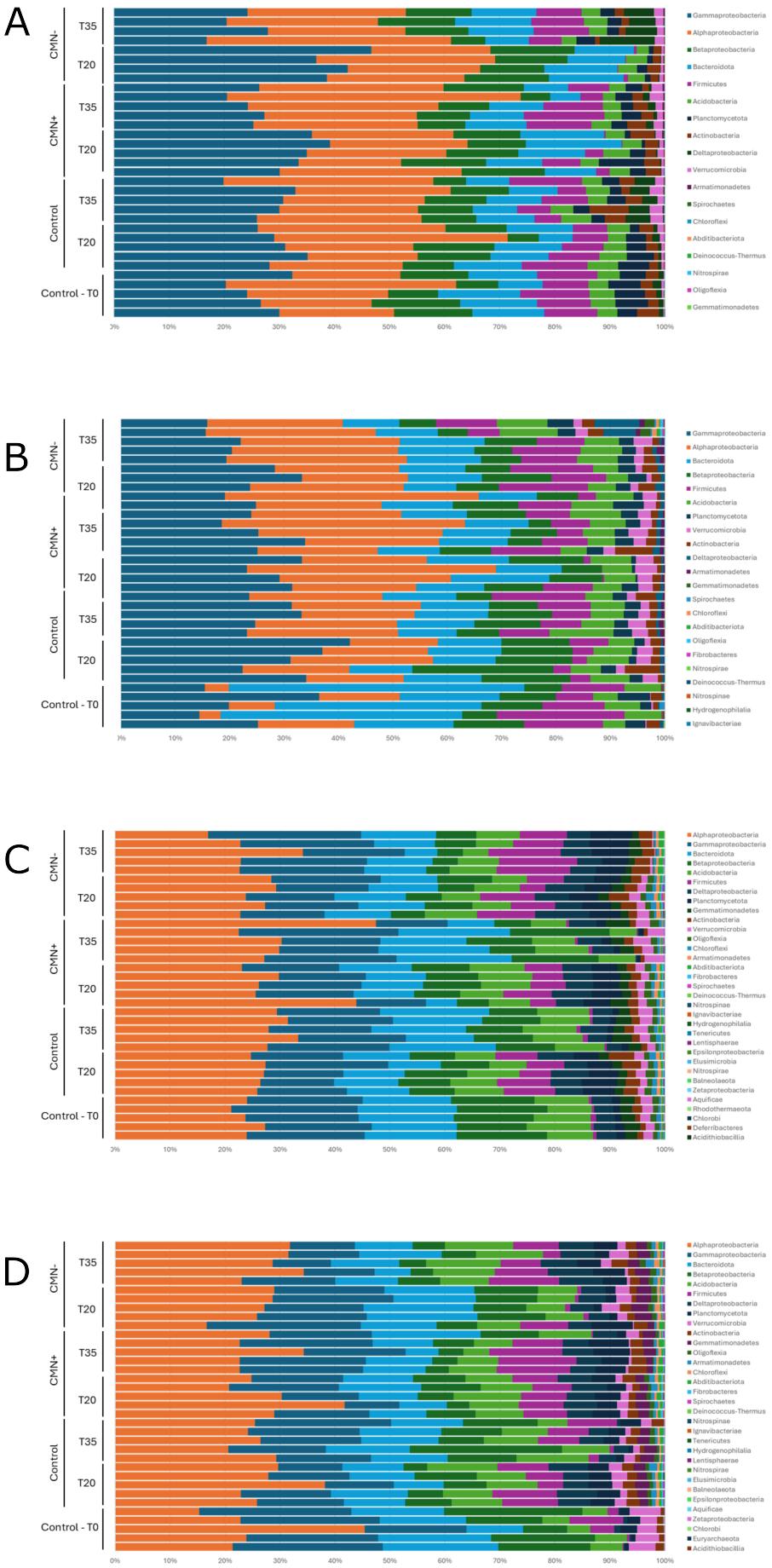

Figure S7: Phyla composition of the rhizospheric microbial community after amendment application (A and C) and foliar application (B and D) on samples after 0, 20 and 35 days of biostimulant application (CM N^+, CM N^-). CM = Culture media biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days.

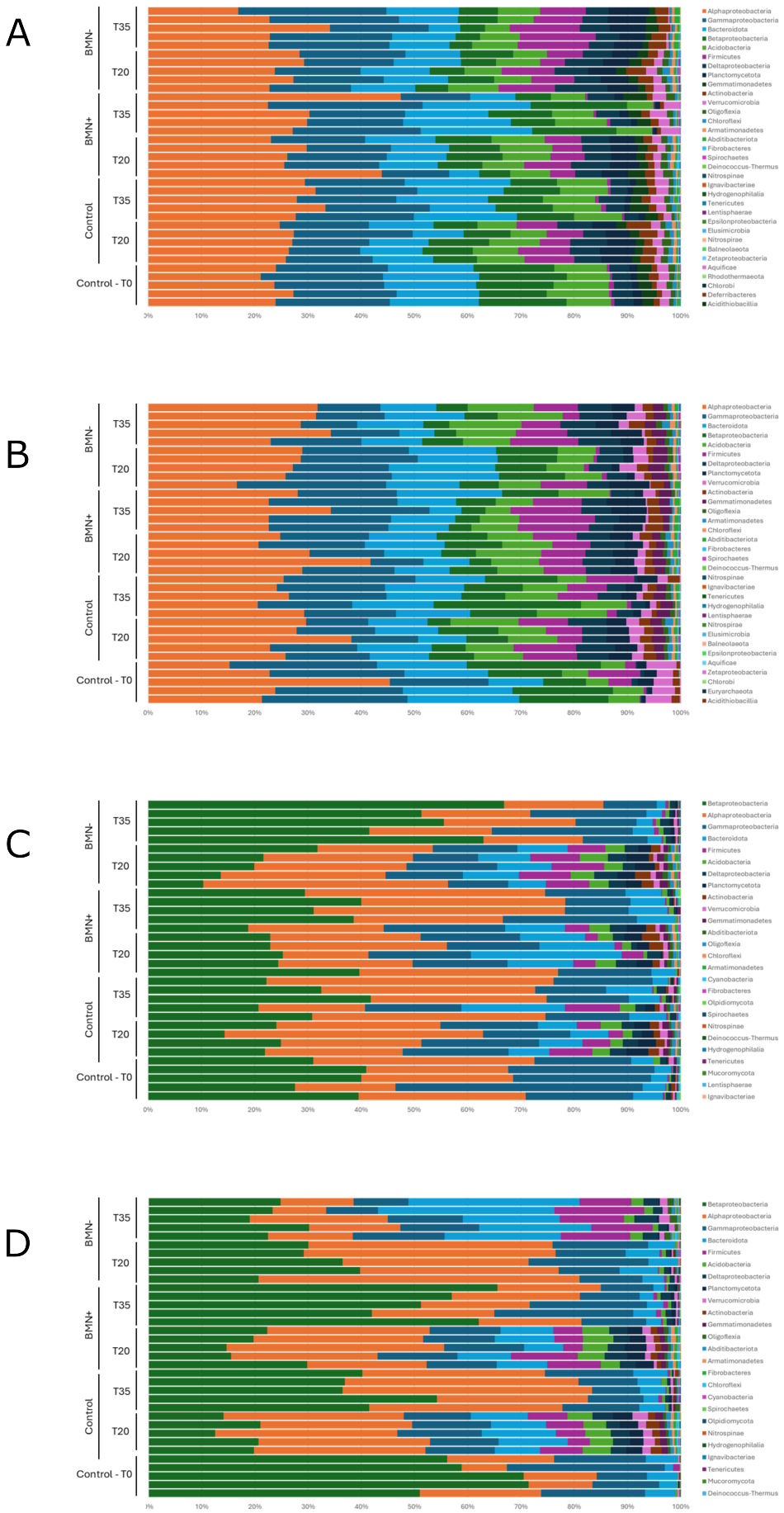

Figure S8: Phyla composition of the endospheric microbial community after amendment application (A and C) and foliar application (B and D) on samples after 0, 20 and 35 days of biostimulant application (BM N^-, BM N^+). BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days.

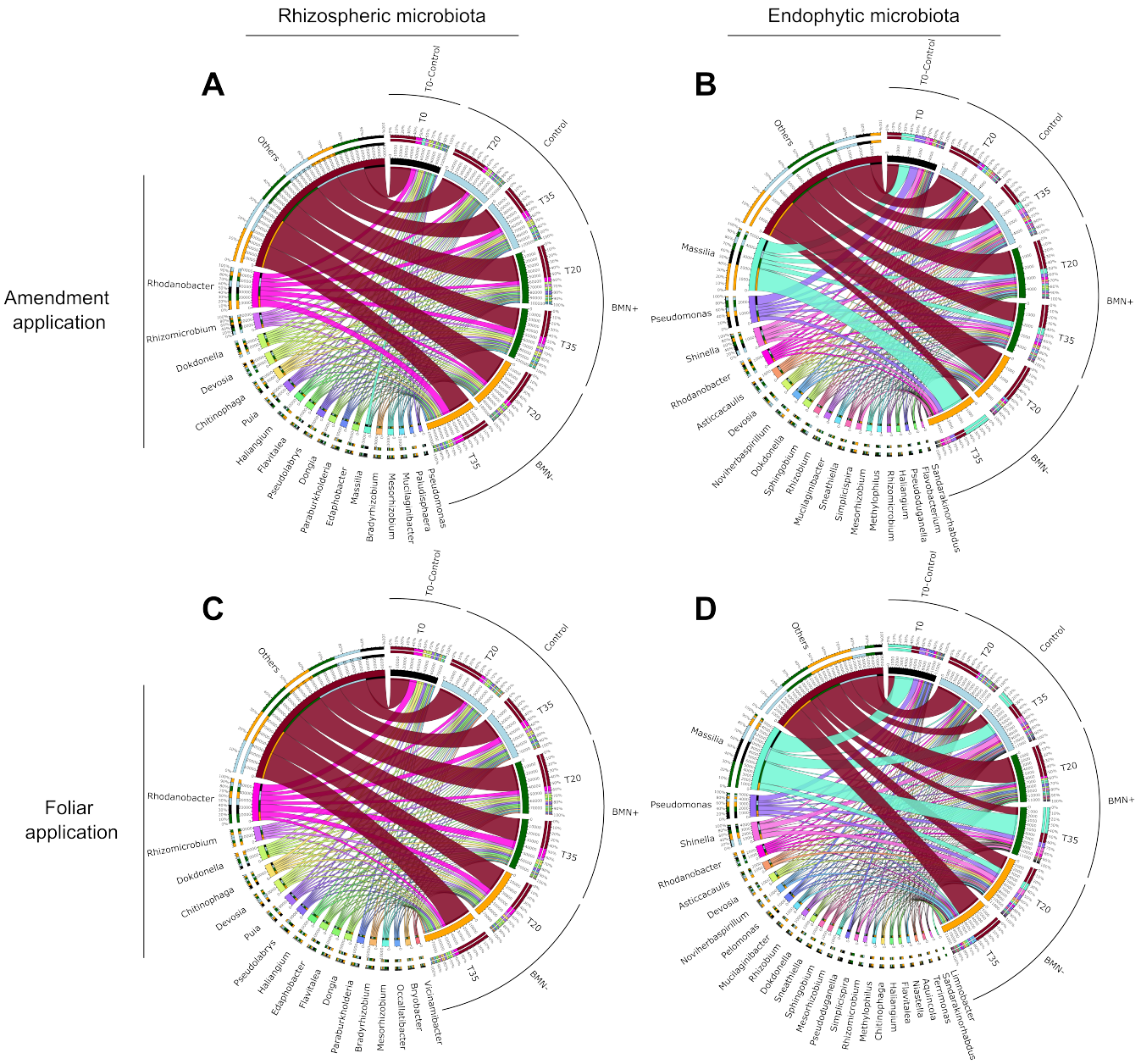

Figure S9: Circos graphs (Krzywinski et al. 2009) representing the relative abundance of rhizospheric microbiota (A and C) and endophytic microbiota (B and D) at T0, T20 and T35 following the application of *L. indica* biomass-based biostimulant via amendment (A and B) and foliar (C and D) treatment. CM = Culture media biostimulants, BM = biomass extract biostimulants, H2O = Negative control. T0 = biostimulation started, T20 = 20 days, T35 = 35 days.