Supplemental Figures and Tables

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Table S1 Monthly total precipitation and average temperature values during the 2021-2022 farming seasons at Champaign, IL (40° 3'6.61"N, 88°13'52.01"W) and the 30-year average of precipitation and temperature of the region obtained from the Illinois Water Survey.

	Precipitation (inches)			Temperature (°F)		
Month	2021	2022	30-Year Average	2021	2022	30-Year Average
April	2.1	3.2	4	53	50	53
May	3.4	3.2	5	61	66	63
June	7.6	0.8	4.7	75	75	72
July	4.3	2.4	4.4	74	76	75
August	4.1	4.9	3.5	76	73	74
September	3	4.6	3.3	70	67	67
Total/Average	24.5	19.1	24.9	68	68	67

Pre-plant soil properties (0-12” depth) and Mehlich 3-extraction-based mineral test results at Champaign, IL

Soil edaphic properties	†OM	††CEC	pH	NO_3	NH_4	P	K
Units	%	meq/100g		ppm			
	3.1	17.1	6.8	5.2	2.9	20	104

† OM=organic matter; ††CEC= cation exchange capacity

TABLE S2 Individual and interaction effects of genotype, inoculant, mineral N amendment, and GDD on soil prokaryotic richness and alpha diversity indices, evaluated by linear model. F-values are given, and significance is indicated by asterisks

Factors (2021)	**Observed**	**Chao1**	**Simpson**	**Shannon**
∞Genotype	3.02	3.02	0.63	4.10*
αInoculant	0.69	0.69	1.41	1.77
εN dosage	4.34*	4.34*	1.23	1.39
¥ Growth stage	20.70***	20.70***	1.09	15.68***
Genotype:Inoculant	0.05	0.05	0.78	0.08
Genotype:N dosage	0.10	0.10	0.29	0.05
Inoculant:N dosage	0.01	0.01	1.03	0.01
Genotype: Growth stage	0.15	0.15	0.56	0.03
Inoculants: Growth stage	1.07	1.07	0.97	0.78
N dosages: Growth stage	1.30	1.30	0.77	1.26
Genotype:Inoculant: Growth stage	0.16	0.16	1.22	0.67
Genotype:N dosages: Growth stage	0.03	0.03	1.10	0.24
Inoculant:N dosages: Growth stage	0.31	0.31	1.50	0.32

Factors (2022)	**Observed**	**Chao1**	**Simpson**	**Shannon**
Genotype	0.75	0.75	1.15	1.10
Inoculant	1.40	1.40	1.61	2.50
N dosage	2.05	2.05	2.31	3.69
Growth stage	2.57	2.57	0.36	0.38
Genotype:Inoculant	0.82	0.82	0.58	0.76
Genotype:N dosage	0.83	0.83	1.03	0.75
Inoculant:N dosage	1.39	1.39	0.09	0.32
Genotype: Growth stage	0.09	0.09	0.70	0.12
Inoculant: Growth stage	0.01	0.01	1.91	0.49
N dosage: Growth stage	3.59	3.59	0.18	1.73
Genotype:Inoculant:N dosage	2.10	2.10	2.30	2.90
Genotype:Inoculant: Growth stage	0.55	0.55	0.43	0.19
Genotype:N dosage: Growth stage	0.31	0.31	0.75	0.48
Inoculant:N dosage: Growth stage	8.21**	8.21**	2.26	5.56*
Genotype:Inoculant:N dosage: Growth stage	0.65	0.65	0.49	0.19

∞Genotype (B73, NIL 1, and NIL 2), αInoculant (Proven, None), εN dosage= (N:0 kg ha^{-1}, N:67 kg ha^{-1}), ¥ Growth stage= In 2021 maize vegetative growth stages of V5 and V12 and in 2022 the vegetative maize growth stages of V8 and VT (tasseling), were considered. NIL= near isogenic line.
Significance codes: $P < 0.05$ '*', $P < 0.01$ '**'; $P < 0.001$ '***'

TABLE S3 Individual and interaction effects of genotype, inoculant, mineral N amendment, and GDD on soil Fungi richness and alpha diversity indices, evaluated by linear model. F-values are given, and significance is indicated by asterisks

Factors (2021)	**Observed**	**Chao1**	**Simpson**	**Shannon**
∝Genotype	0.21	0.21	0.61	0.26
αInoculant	0.14	0.14	0.11	0.01
εN dosage	2.28	2.28	5.37*	6.51*
¥ Growth stage	10.64***	10.64***	1.67	5.88**
Genotype:Inoculant	0.34	0.34	0	1.16
Genotype:N dosage	5.64*	5.64*	0.45	1.89
Inoculant:N dosage	0.38	0.38	0.6	0.05
Genotype: Growth stage	0.85	0.85	0.48	0.9
Inoculants: Growth stage	1.48	1.48	0.26	0.67
N dosages: Growth stage	8.86***	8.86***	0.21	6.23***
Genotype:Inoculant: Growth stage	0.61	0.61	0.85	0.14
Genotype:N dosages: Growth stage	2.34	2.38	0.17	0.25
Inoculant:N dosages: Growth stage	0.09	0.09	1.06	0.41

Factors (2022)	**Observed**	**Chao1**	**Simpson**	**Shannon**
Genotype	0.69	0.69	1.22	0.29
Inoculant	0.1	0.1	1.36	0.2
N dosage	1.36	1.36	0.24	0.48
Growth stage	0.42**	0.42**	0.67	2.44
Genotype:Inoculant	0.3	0.3	1.31	1.26
Genotype:N dosage	1.07	1.07	0.24	0.29
Inoculant:N dosage	0.09	0.09	1.66	1.61
Genotype: Growth stage	0.05	0.05	1.7	0.79
Inoculant: Growth stage	1.57	1.57	4.07*	3.74
N dosage: Growth stage	3.59	3.59	0.5	0.8
Genotype:Inoculant:N dosage	0.45	0.45	0.17	0.05
Genotype:Inoculant: Growth stage	0.48	0.48	1.41	1.38
Genotype:N dosage: Growth stage	0.59	0.59	0.55	1.03
Inoculant:N dosage: Growth stage	1.57	1.57	0.72	0.04
Genotype:Inoculant:N dosage: Growth stage	0.02	0.02	0.3	0.23

∝Genotype (B73, NIL 1, and NIL 2), αInoculant (Proven, None), εN dosage= (N:0 kg ha^{-1}, N:67 kg ha^{-1}), ¥ Growth stage= In 2021 maize vegetative growth stages of V5 and V12 and in 2022 the vegetative maize growth stages of V8 and VT (tasseling), were considered. NIL= near isogenic line.
Significance codes: $P < 0.05$ '*', $P < 0.01$ '**'; $P < 0.001$ '***'

TABLE S4 Individual and interactive effects of genotype, inoculant, mineral N dosage, and growth stages as well as their interactions across 2021 on prokaryotic (a) and fungi community (b) structure assessed by ADONIS, applying Bray-Curtis distance matrices with number of permutations=999

Treatment (a)	**n**	**R^2**	**P**
All samples (prokaryotes 2021)	**56**		
∝Genotype		0.01	0.26
ε N dosage		0.01	0.14
α Inoculant		0.01	0.87
¥ Growth stage		0.06	0.001 ***
Genotype:N.dosages		0.01	0.14
Genotype:Inoculant		0.01	0.67
N.dosages:Inoculant		0.01	0.29
Genotype: Growth stage		0.03	0.75
N.dosages: Growth stage		0.02	1.00
Inoculant: Growth stage		0.02	0.93
Genotype:N.dosages: Growth stage		0.02	0.99
Genotype:Inoculant: Growth stage		0.02	1.00
N.dosages:Inoculant: Growth stage		0.02	0.98
Residual		0.75	0.26
Total		1.00	0.14
All samples (Fungi 2021)	**56**		
Genotype		0.01	0.32
N.dosages		0.01	0.75
Inoculant		0.01	0.84
Growth stage		0.06	0.00***
Genotype:N.dosages		0.01	0.19
Genotype:Inoculant		0.01	0.38
N.dosages:Inoculant		0.01	0.36
Genotype: Growth stage		0.03	0.05*
N.dosages: Growth stage		0.03	0.56
Inoculant: Growth stage		0.03	0.48
Genotype:N.dosages: Growth stage		0.03	0.34
Genotype:Inoculant: Growth stage		0.02	0.86
N.dosages:Inoculant: Growth stage		0.02	0.94
Residual		0.73	
Total		1.00	

∝Genotype (B73, NIL 1, and NIL 2), αInoculant (Proven, None), εN dosage= (N:0 kg ha^{-1}, N:67 kg ha^{-1}), ¥ Growth stage= In 2021 maize vegetative growth stages of V5 and V12 and in 2022 the vegetative maize growth stages of V8 and VT (tasseling), were considered. NIL= near isogenic line.
Significance codes: P < 0.05 '*', P < 0.01 '**'; P < 0.001 '***'

TABLE S5 Individual and interactive effects of Genotype, Inoculant, mineral N dosage, and growth stage as well as their interactions in 2022 on prokaryotic and fungi community structure assessed by ADONIS, applying Bray-Curtis distance matrices, with number of permutations=999

Treatment (b)	**n**	**R^2**	**P**
All samples (prokaryotes 2022)	**96**		
∞Genotype		0.02	0.38
ε N dosage		0.01	0.51
α Inoculant		0.01	0.13
¥ Growth stage		0.01	0.00**
Genotype:N.dosage		0.02	0.03*
Genotype:Inoculant		0.02	0.03*
N.dosage:Inoculant		0.01	0.54
Genotype: Growth stage		0.02	0.85
N.dosage: Growth stage		0.01	0.82
Inoculant: Growth stage		0.01	0.46
Genotype:N.dosage:Inoculant		0.02	0.98
Genotype:N.dosage: Growth stage		0.02	0.99
Genotype:Inoculant: Growth stage		0.02	0.73
N.dosage:Inoculant: Growth stage		0.01	0.98
Genotype:N.dosage:Inoculant: Growth stage		0.02	0.93
Residual		0.76	
Total		1.00	
All samples (Fungi 2022)	**96**		
Genotype		0.02	0.19
N dosage		0.01	0.30
Inoculant		0.01	0.38
Growth stage		0.02	0.00***
Genotype:N dosages		0.02	0.52
Genotype:Inoculant		0.02	0.08
N dosages:Inoculant		0.01	0.47
Genotype: Growth stage		0.02	0.35
N dosages: Growth stage		0.01	0.39
Inoculant: Growth stage		0.01	0.81
Genotype:N.dosages:Inoculant		0.02	0.97
Genotype:N dosages: Growth stage		0.02	0.75
Genotype:Inoculant: Growth stage		0.02	0.95
N dosages:Inoculant: Growth stage		0.01	0.65
Genotype:N dosages:Inoculant: Growth stage		0.02	0.73
Residual		0.76	
Total		1.00	

∞Genotype (B73, NIL 1, and NIL 2), ε N dosage= (N:0 kg ha^{-1}, N:67 kg ha^{-1}), α Inoculant (Proven, None), ¥ Growth stage= In 2021 maize vegetative growth stages of V5 and V12 and in 2022 the vegetative maize growth stages of V8 and VT (tasseling), were considered. NIL= near isogenic line.

Significance codes: P < 0.05 '*', P < 0.01 '**'; P < 0.001 '***'

Table S6 Significant Fungi taxa contributing to differential abundance between treatments

ITS 21	**N dosages**	**Enriched**	**padj**
marker1	k__Fungi|p__Ascomycota|c__Eurotiomycetes|o__Chaetothyriales|f__Herpotrichiellaceae|g__Exophiala|s__Exophiala_alcalophila	N:0	***
	Inoculant		
marker1	k__Fungi|p__Basidiomycota|c__Agaricomycetes|o__Agaricales|f__Bolbitiaceae	None	***
marker2	k__Fungi|p__Ascomycota|c__Dothideomycetes|o__Capnodiales|f__Mycosphaerellaceae|g__Septoria|g__Septoria	Proven	***
marker3	k__Fungi|p__Chytridiomycota|c__Rhizophydiomycetes|o__Rhizophydiales	Proven	***
ITS 22	**Genotype**		
marker1	k__Fungi|p__Basidiomycota|c__Tremellomycetes|o__Tremellales|f__Bulleribasidiaceae|g__Hannaella|s__Hannaella_luteola	NIL 1	***
marker2	k__Fungi|p__Ascomycota|c__Eurotiomycetes|o__Eurotiales|f__Aspergillaceae|g__Aspergillus	NIL 1	**
marker3	k__Fungi|p__Ascomycota|c__Sordariomycetes|o__Hypocreales|f__Hypocreaceae|g__Trichoderma	NIL 2	**
marker4	k__Fungi|p__Mortierellomycota|c__Mortierellomycetes|o__Mortierellales|f__Mortierellaceae|g__Mortierella	B73	**
marker5	k__Fungi|p__Ascomycota|c__Sordariomycetes|o__Hypocreales|f__Hypocreaceae	NIL 2	**
marker6	k__Fungi|p__Ascomycota|c__Sordariomycetes|o__Sordariales|f__Lasiosphaeriaceae|g__Apodus|s__Apodus_deciduus	NIL 1	*
marker7	k__Fungi|p__Ascomycota|c__Dothideomycetes|o__Pleosporales|f__Sporormiaceae|g__Preussia|s__Preussia_flanaganii	B73	*
marker8	k__Fungi|p__Ascomycota|c__Pezizomycetes|o__Pezizales|f__Ascobolaceae	NIL 1	*
marker9	k__Fungi|p__Ascomycota|c__Eurotiomycetes|o__Eurotiales|f__Aspergillaceae|g__Aspergillus|s__Aspergillus_caninus	NIL 1	*
marker10	k__Fungi|p__Basidiomycota|c__Agaricomycetes|o__Hymenochaetales	NIL 1	*
marker11	k__Fungi|p__Basidiomycota|c__Agaricomycetes|o__Hymenochaetales|f__Schizoporaceae	NIL 1	*
marker12	k__Fungi|p__Ascomycota	NIL 1	*
	Growth stage	**Enriched**	**padj**
marker1	k__Fungi|p__Basidiomycota|c__Agaricomycetes|o__Hymenochaetales|f__Schizoporaceae|g__Lyomyces|s__Lyomyces_mascarensis	V8	***
marker2	k__Fungi|p__Ascomycota|c__Eurotiomycetes|o__Chaetothyriales|f__Chaetothyriaceae	V8	***
marker3	k__Fungi|p__Ascomycota|c__Leotiomycetes|o__Helotiales|f__Myxotrichaceae|g__Oidiodendron|s__Oidiodendron_cereale	V8	***
marker4	k__Fungi|p__Ascomycota|c__Leotiomycetes|o__Helotiales|f__Helotiaceae|g__Hymenoscyphus|s__Hymenoscyphus_menthae	V8	***
marker5	k__Fungi|p__Ascomycota|c__Sordariomycetes|o__Sordariales|f__Lasiosphaeriaceae|g__Lasiosphaeris|s__Lasiosphaeris_hispida	VT	***
marker6	k__Fungi|p__Ascomycota|c__Dothideomycetes|o__Pleosporales|f__Sporormiaceae	V8	***
	N.dosages		
marker1	k__Fungi|p__Ascomycota|c__Sordariomycetes|o__Hypocreales|f__Nectriaceae	N.67	***
marker2	k__Fungi|p__Ascomycota|c__Dothideomycetes|o__Pleosporales|f__Sporormiaceae	N.0	***
marker3	k__Fungi|p__Ascomycota|c__Orbiliomycetes|o__Orbiliales|f__Orbiliaceae|g__Arthrobotrys	N.67	***

***Significant with $P < 0.001$.

Table S7 significant Prokaryotes taxa contributing to differential abundance between treatments

Prokaryotes21	Genotype	Enriched	padj
marker1	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Burkholderiales|f__Oxalobacteraceae|g__Noviherbaspirillum|s__Noviherbaspirillum_malthae	NIL.1	***
	Growth stage		
marker1	d__Bacteria|p__Acidobacteriota|c__Acidobacteriae|o__Acidobacteriales_f__uncultured_g__uncultured| s__uncultured_Acidobacteria	V12	***
marker2	d__Bacteria|p__Actinobacteriota|c__Actinobacteria|o__Frankiales|f__Acidothermaceae|g__Acidothermus|g__Acidothermus	V12	***
marker5	d__Bacteria|p__Actinobacteriota|c__Thermoleophilia| o__Gaiellales_f__uncultured_g__uncultured|s__uncultured_Conexibacteraceae	V12	***
marker6	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Enterobacterales|f__Enterobacteriaceae	V12	***
marker7	d__Bacteria|p__Acidobacteriota|c__Acidobacteriae|o__Acidobacteriales|o__Acidobacteriales	V12	***
marker8	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria_o__uncultured_f__uncultured_g__uncultured_s__uncultured_Alphaproteobacteria	V12	***
marker9	d__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales|f__Planococcaceae	V12	***
marker10	d__Bacteria|p__Acidobacteriota|c__Acidobacteriae|o__Acidobacteriales	V12	***
marker11	d__Bacteria|p__Chloroflexi|c__Ktedonobacteria|o__Ktedonobacterales|f__JG30-KF-AS9|g__JG30-KF-AS9|g__JG30-KF-AS9	V12	**
marker12	d__Bacteria|p__Chloroflexi|c__AD3|o__AD3|f__AD3|g__AD3	V12	**
marker14	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|c__Alphaproteobacteria_o__uncultured|c__Alphaproteobacteria_o__uncultured_f__uncultured	V12	***
marker15	d__Bacteria|p__Proteobacteri __Alphaproteobacteria	V12	***
marker16	d__Bacteria|p__Acidobacteriota|c__Acidobacteriae|o__Subgroup_2|f__Subgroup_2|g__Subgroup_2	V12	**
marker17	d__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales|f__Planococcaceae|g__Sporosarcina	V12	**
marker18	d__Bacteria|p__Actinobacteriota|c__Thermoleophilia|o__Gaiellales|f__Gaiellaceae|g__Gaiella|g__Gaiella	V12	**
marker19	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Burkholderiales|f__Rhodocyclaceae	V12	**
marker20	d__Bacteria|p__Chloroflexi|c__AD3|o__AD3|f__AD3|g__AD3	V12	**
marker21	d__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales|f__Planococcaceae|g__Sporosarcina|g__Sporosarcina	V12	**
marker22	d__Bacteria|p__Methylomirabilota|c__Methylomirabilia|o__Rokubacteriales|f__Rokubacteriales|g__Rokubacteriales	V12	**
marker23	d__Bacteria|p__Acidobacteriota|c__Subgroup_25|o__Subgroup_25|f__Subgroup_25|g__Subgroup_25	V12	*
marker24	d__Bacteria|p__Gemmatimonadota|c__Gemmatimonadetes|o__Gemmatimonadales|f__Gemmatimonadaceae|g__uncultured|s__uncultured_Gemmatimonas	V12	*
marker25	d__Bacteria|p__Acidobacteriota|c__Acidobacteriae|o__Acidobacteriales	V12	*
marker26	d__Bacteria|p__Latescibacterota|c__Latescibacterota|o__Latescibacterota|f__Latescibacterota|g__Latescibacterota	V12	*
marker27	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Enterobacterales|f__Enterobacteriaceae|g__Escherichia-Shigella	V12	*
marker28	d__Bacteria|p__Chloroflexi|c__AD3|o__AD3|f__AD3|g__AD3|g__AD3_s__uncultured_Thermomicrobia	V12	*
marker29	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Xanthobacteraceae|g__Xanthobacteraceae|s__uncultured_Alphaproteobacteria	V12	*
marker30	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Rhodanobacteraceae|g__Ahniella|g__Ahniella	V12	*
marker31	d__Bacteria|p__Verrucomicrobiota|c__Verrucomicrobiae|o__Opitutales|f__Opitutaceae|g__Opitutus	V5	***
marker32	d__Bacteria|p__Myxococcota|c__Polyangia|o__Polyangiales|f__BIrii41|g__BIrii41	V5	***
marker33	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae|g__Arenimonas|s__uncultured_Arenimonas	V5	***
marker34	d__Bacteria|p__Myxococcota|c__Polyangia|o__Polyangiales|f__BIrii41|g__BIrii41	V5	***
marker35	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae|g__Arenimonas	V5	***
marker36	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Pseudomonadales	V5	***
marker37	d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Cytophagales|f__Microscillaceae|f__Microscillaceae	V5	***
marker38	d__Bacteria|p__Verrucomicrobiota|c__Verrucomicrobiae|o__Pedosphaerales|f__Pedosphaeraceae|f__Pedosphaeraceae	V5	***
marker39	d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Cytophagales	V5	***
marker40	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae	V5	***

marker41	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Pseudomonadales|f__Pseudomonadaceae|g__Pseudomonas	V5	***
marker42	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae|g__MND1	V5	**
marker43	d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Flavobacteriales|f__Flavobacteriaceae|g__Flavobacterium	V5	**
marker44	d__Bacteria|p__Myxococcota|c__Polyangia|o__Polyangiales	V5	**
marker45	d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Flavobacteriales	V5	**
marker46	d__Bacteria|p__Actinobacteriota|c__Actinobacteria|o__Micrococcales|f__Microbacteriaceae	V5	**
marker48	d__Bacteria|p__Armatimonadota|c__Fimbriimonadia|o__Fimbriimonadales	V5	**
marker49	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae|	V5	**
marker50	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales	V5	**
marker51	d__Bacteria|p__Chloroflexi|c__Anaerolineae|o__SBR1031	V5	**
marker52	d__Bacteria|p__Armatimonadota|c__Fimbriimonadia|o__Fimbriimonadales|f__Fimbriimonadaceae|g__Fimbriimonadaceae	V5	*
marker53	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Dongiales|f__Dongiaceae|g__Dongia	V5	*
marker54	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Burkholderiales|f__Oxalobacteraceae|g__Massilia|s__Massilia_brevitalea	V5	*
marker55	d__Bacteria|p__Firmicutes|c__Bacilli|o__Paenibacillales|f__Paenibacillaceae|g__Ammoniphilus|g__Ammoniphilus	V5	*
marker56	d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Cytophagales|f__Microscillaceae	V5	*
marker57	d__Bacteria|p__Armatimonadota|c__Fimbriimonadia|o__Fimbriimonadales|f__Fimbriimonadaceae| |g__Fimbriimonadaceae	V5	*
marker58	d__Bacteria|p__Verrucomicrobiota|c__Verrucomicrobiae|o__Opitutales|f__Opitutaceae|g__Lacunisphaera	V5	*
marker59	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Oceanospirillales|f__Pseudohongiellaceae|g__BIyi10	V5	*
marker60	d__Bacteria|p__Chloroflexi|c__Anaerolineae	V5	*
marker61	d__Bacteria|p__Planctomycetota|c__OM190|o__OM190|f__OM190|g__OM190	V5	*
marker62	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__R7C24|f__R7C24|g__R7C24	V5	*

Significance codes: P < 0.05 '*', P < 0.01 '**'; P < 0.001 '***'

TABLE S8 Individual and interactive effects of Genotype, Inoculant, mineral N dosage, and growth stages as well as their interactions on nitrifiers community structure assessed by ADONIS, applying a Bray-Curtis distance matrix; number of permutations=999

Treatment	n	R^2	P
Nitrifiers 2021	**56**		
[∝]Genotype		0.00	0.77
[ε]N dosage		0.03	0.05
[α]Inoculant		0.00	0.71
[¥] Growth stage		0.14	0.001 ***
Genotype:N.dosages		0.00	0.75
Genotype:Inoculant		0.00	0.81
N.dosages:Inoculant		0.01	0.23
Genotype: Growth stage		0.01	0.98
N.dosages: Growth stage		0.02	0.51
Inoculant: Growth stage		0.01	0.78
Genotype:N.dosages: Growth stage		0.02	0.50
Genotype:Inoculant: Growth stage		0.01	0.89
N.dosages:Inoculant: Growth stage		0.01	0.89
Residual		0.72	
Total		1.00	

	n	R^2	P
Nitrifiers 2022	**96**		
Genotype		0.01	0.67
N.dosages		0.00	0.99
Inoculant		0.01	0.38
Growth stage		0.02	0.18
Genotype:N.dosages		0.03	0.15
Genotype:Inoculant		0.05	0.03*
N.dosages:Inoculant		0.01	0.46
Genotype: Growth stage		0.02	0.54
N.dosages: Growth stage		0.00	0.94
Inoculant: Growth stage		0.00	1.00
Genotype:N.dosages:Inoculant		0.01	0.77
Genotype:N.dosages: Growth stage		0.02	0.46
Genotype:Inoculant: Growth stage		0.02	0.48
N.dosages:Inoculant: Growth stage		0.00	0.91
Genotype:N.dosages:Inoculant: Growth stage		0.01	0.93
Residual		0.78	
Total		1.00	

[∝]Genotype (B73, NIL 1, and NIL 2), [α]Inoculant (Proven, None), [ε]N dosage= (N:0 kg ha^{-1}, N:67 kg ha^{-1}), [¥] Growth stage= In 2021 maize vegetative growth stages of V5 and V12 and in 2022 the vegetative maize growth stages of V8 and VT (tasseling), were considered. NIL= near isogenic line.
Significance codes: P < 0.05 '*', P < 0.01 '**'; P < 0.001 '***'

Table S9 significant nitrifier taxa contributing to differential abundance between treatments

Nitrifiers 2021	**N dosage**	**Enriched**	**padj**
marker1	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Burkholderiales|f__Nitrosomonadaceae|g__Nitrosospira	N:67	***
marker2	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae| g__Nitrosospira| s__Nitrosospira tenuis	N:67	***
	Growth stage		
marker1	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o_Rhizobiales|f__Xanthobacteraceae|g__Nitrobacter|s_uncultured_Nitrobacter	V5	***
marker3	d__Archaea|p__Crenarchaeota|c__Nitrososphaeria|o__Nitrososphaerales|f__Nitrososphaeraceae|g_Candidatus_Nitrososphaera|s_Thaumarchaeota_archaeon	V12	***
marker4	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Nitrosococcales|f__Nitrosococcaceae|g__wb1-P19	V5	***
marker5	d__Bacteria|p__Proteobacteria|c Betaproteobacteria | o__Nitrosomonadales f__ Nitrosomonadaceae |g__Nitrosomonas|	V5	***
marker7	d__Archaea|p__Crenarchaeota|c__Nitrososphaeria|o__Nitrosotaleales|f__Nitrosotaleaceae|g__Candidatus_Nitrosotalea|s__uncultured_archaeon	V5	***
marker8	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae	V5	***
marker10	d__Archaea|p__Crenarchaeota|c__Nitrososphaeria|o__Nitrososphaerales|f__Nitrososphaeraceae|g__Candidatus_Nitrososphaera|	V5	***
marker11	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae| g__Nitrosomonas	V12	***
marker12	d__Archaea|p__Crenarchaeota|c__Nitrososphaeria|o__Nitrosotaleales|f__Nitrosotaleaceae|g__Nitrosotaleaceae	V12	***
marker13	__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae |	V5	***
marker15	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__ Bradyrhizobiaceae |g__Nitrobacter	V5	***
Nitrifiers 2022	**Growth stage**	**Enriched**	**padj**
marker1	d__Bacteria|p__Proteobacteria|c__ Betaproteobacteria |o__ Nitrosomonadales |f__Nitrosomonadaceae |g__Nitrosospira	V8	***
marker2	d__Archaea|p__Crenarchaeota|c__Nitrososphaeria|o__Nitrososphaerales|f__Nitrososphaeraceae	VT	***

Significance codes: P < 0.001 '***'

Table S10 comparative and interactive effects of genotype and management practices on potential nitrification rate, plant N content and grain protein%. Letters show the pairwise Tukey HSD results. lsmean ± standard deviation is shown in upper part of the table. The lower part shows the fixed factors results of linear mixed-effect models. The output is summarized by anova function. The significance of each individual factor and their interactions are shown by F-values followed by asterisks as the indicators of P-values as defined in footnote.

		†Gen		ᵍGS		#Inoc		‡N (kg ha^{-1})	
	Potential	B73	NIL 1	V5	V12	None	Proven	N:0	N:67
	Nitrification rate (ngN g^{-1} soil)	1901± 110.0	1724 ± 133.0	1536 ± 137.0 a	2089 ± 137.0 b	1674 ± 147.0	1951 ± 127.0	1523 ± 133.0 a	2120 ± 110.0 b
		†Gen		#Inoc		‡N (kg ha^{-1})			
Year 2021	Plant data	B73	NIL 1	None	Proven	N:0	N:67		
	N content/V8	15.1 ± 0.7	15.0 ± 0.8	14.8 ± 0.6	15.4 ± 0.9	14.6 ± 0.8	15.6 ± 0.6		
	N content/VT	76.8 ± 4.50	78.4 ± 5.1	77.3 ± 4.3	78.0 ± 5.8	67.5 ± 5.4 a	87.7 ± 4.2 b		
	Grain protein %	7.3 ± 0.1	8.0 ± 0.2	7.7 ± 0.1	7.6 ± 0.2	7.3 ± 0.2 a	8.0 ± 0.1 b		
	ᵝGrain N conc %	45.3± 0.9 a	50.0 ± 1.0 b	48.0 ± 0.8	47.3 ± 1.2	45.3 ± 1.1 a	50.0 ±0.8 b		

		†Gen			ᵍGS		#Inoc		‡N (kg ha^{-1})	
	Potential	B73	NIL 1	NIL 2	V8	VT	None	Proven	N:0	N:67
	Nitrification rate (ngN g^{-1} soil)	1127 ± 58.8	1145 ± 59.3	1153 ± 55.3	1176 ± 46.9	1108 ± 44.5	1156 ± 45.3	1128 ± 48.5	990± 47.2 a	1294 ± 44.4 b
		†Ge			#Inoc		‡N (kg ha^{-1})			
Year 2022	Plant data	B73	NIL 1	NIL 2	None	Proven	N:0	N:67		
	N content/V8	29.0 ± 0.9 a	29.3 ± 0.9 a	33.8 ± 0.9 b	31.0 ± 0.7	30.3 ± 0.7	29.2 ± 0.7 a	32.1 ± 0.7 b		
	N content/VT	63.5 ± 2.4	65.0 ± 2.4 a	72.3 ± 2.4 b	66.2 ± 2.0	67.7 ± 2.0	62.4 ± 2.0 a	71.5 ± 2.0 b		
	Grain protein %	7.5 ± 0.1 a	8.4 ± 0.1 b	7.8 ± 0.1 a	7.8 ± 0.1	7.9 ± 0.1	7.3 ± 0.2 a	8.4 ± 0.2 b		
	Grain N conc %	47.0 ± 0.9 a	51.5 ±0.9 b	48.7 ± 0.9 ab	48.7 ± 0.8	49.4 ± 0.8	45.9 ± 0.7 a	52.3 ± 0.7 b		
	Kernel weight mg kernel^{-1}	187 ± 2.26 b	179 ± 2.23 a	190 ± 2.25 c	183 ± 1.92 a	188 ± 1.92 b	181 ± 1.86 a	190 ± 1.86 b		

2021

Main effects	Nitrification rate	Main effects	Plant N content V5 (kg ha^{-1})	Plant N content V12 %	Grain protein %	Grain N conc %
Units						
Ge	1.72	Ge	0.00	1.12	3.69	0.16
N	18.21***	N	1.21	11.82**	16.28***	0.00
GS	3.37	Inoc	0.35	0.01	0.38	0.71
Inoc	2.5	Ge: N	0.03	1.82	1.32	0.46
Ge: N	0.6					0.07
Ge: GS	0.02					
N: GS	0.81					
Ge: N: GS	0.15					

2022

Main effects	Nitrification rate ng N g^{-1} soil	Main effects	Plant N content V8 (kg ha^{-1})	Plant N content VT	Grain protein %	Grain N conc %	Kernel weight
Ge	1.83	Ge	5.4**	3.91*	4.57*	4.51*	0.73
N	31.99***	N	9.58**	12.89***	66.11***	59.09***	12.89***
Inoc	1.34	Inoc	0.15	1.25	0.18	0.17	3.93*
GS	1.64	Ge:N	1.08	0.22	3.70*	3.19*	2.91
Ge: N	2.82	Ge: Inoc	1.86	0.37	1.19	1.56	2.63
Ge: Inoc	0.72	N: Inoc	0.03	0.97	0.08	0.05	0.00
N: Inoc	0.90	Ge: N: Inoc	2.71	0.19	1.23	1.31	1.59
Ge: GS	0.87						
N: GS	0.44						
Inoc: GS	0.35						
Ge: N: Inoc	0.94						
Ge: N: GS	0.89						
Ge: Inoc: GS	7.82**						
N: Inoc: GS	9.78**						
Ge: N: Inoc: GS	0.95						

†Ge= Genotype (B73, NIL_1, and NIL_2), ᵃGS= Growth stage (2021 (vegetative growth stages V5 and V12), 2022 (vegetative growth stages V8 and VT (tasseling)), #Inoc=Inoculant (Proven, None), ‡N= N dosages (N:0 kg ha^{-1}, N:67 kg ha^{-1}), ᵝGrain N conc= Grain N concentration %.

* Significant at the 0.05 level. ** Significant at the 0.01 level. *** Significant at the 0.001 level. P values were adjusted, using the Hochberg method.

Table S11 Topological properties of microbial networks. The F-values, accompanied by asterisks in the lower table, depict the results of the generalized linear model (GLM) assessing the impact of genotype and the interaction between genotype and management on network topological properties. Topological properties Z-scale normalized, allowing comparison across networks.

Treatments	Module connectivity		Modularity	Modules No.	Weight		Edge_ betweenness	Node Betweenness	Closeness	Transitivity	Harmonic centrality	Edge density	Mean degree	Size	
	Among	Within× 10^{-11}			Negative	Positive								Nodes	Edges
Descriptions	Connectedness within a niche and among microbial niches		Network structure	No. of microbial niches	Interactions/associations the frequency of co-occurrence among the connected nodes		No. of the shortest paths that go through an edge (revealing network connectivity & resilience)	Crucial microbial taxa facilitating information flow in a community	Length of path from a node to all others (communication within the community)	Interference and resource exploitation within a community	Organization level around central nodes (highly influential microbes) within a network.	Edge proportion in a network relative to max edges (density of connections between microbes)	Avg. No. of edges/connections per node	Co-occurring ASVs	Co-occurring interactions
	(Schmidt et al., 2019; Ma et al., 2022)				(Fletcher et al., 2013; Zhang et al., 2018)		(Zamkovaya et al., 2021)			(Verdú et al., 2023)	(Freeman, 1978; Nasirian et al., 2020)	(Brisson et al., 2019; Schmidt et al., 2019; Ma et al., 2022)			
Genotype															
B73	0.74	-1.3	0.682	21	137(41.39%)	194(58.61%)	376.169	534.041	0.010	0.064	865.092	0.017	3.360	198	332
NIL 1	0.71	-2.2	0.692	20	198(50.64%)	193(49.36%)	372.422	596.582	0.013	0.100	1742.703	0.018	3.760	209	392
NIL 2	0.69	-2.1	0.651	18	201(46.42%)	232(53.58%)	330.097	561.407	0.013	0.112	1087.956	0.019	4.047	215	434
[δ]Genotype: management															
B73 : management	0.74	2.3	0.595	19	277(44.39%)	347(55.61%)	557.021	794.884	0.018	0.172	1366.105	0.026	5.558	220	625
NIL 1 : management	0.72	8.3	0.638	18	211(53.42%)	184(46.58%)	362.765	574.109	0.011	0.085	767.688	0.018	3.744	202	396
NIL 2 : management	0.75	2.3	0.668	20	204(45.03%)	249(54.97%)	341.523	596.691	0.013	0.114	1013.500	0.019	4.137	220	454

Variables	Module connectivity		Modularity	Node Betweenness	Closeness	Harmonic centrality	Degree
	Among	Within					
Treatments							
Genotype	2.7	0.0	2.7	3.4*	155.0***	4.8**	41.3***
management	0.01	0.0	1.8	24.6***	590.03***	4.2*	111.0***
Genotype: management	4.6*	0.0	4.7***	13.8***	394.2***	4.3*	103.0***

[δ] Genotype: management (interactive effect of Genotype and management with an N-fixing inoculant, with 67 kg ha^{-1} mineral N), P values were adjusted using (the "Hochberg") method.

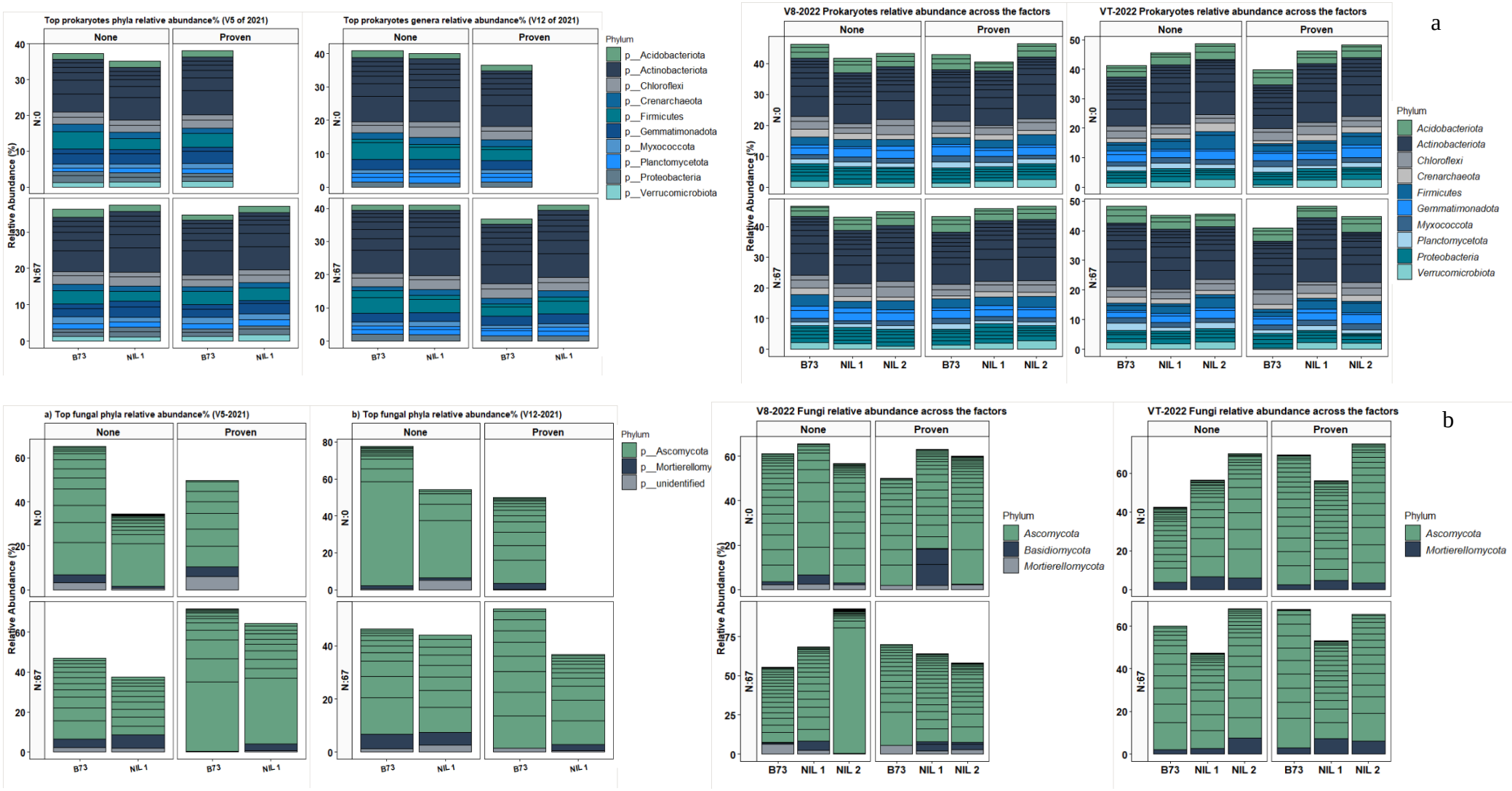


Figure S1 Taxonomic distributions of top dominant phyla among prokaryotes (a) at V8 and VT growth stages of 2022 and 2021 and fungi (b) in V5 and V12 growth stages of maize in 2021. Facets grouping the relative abundance of prokaryotes and fungi at phylum level based on treatments × management × Inoculant (Proven, None), mineral N dosages amendment (N:0 kg ha^{-1}, N:67 kg ha^{-1}).

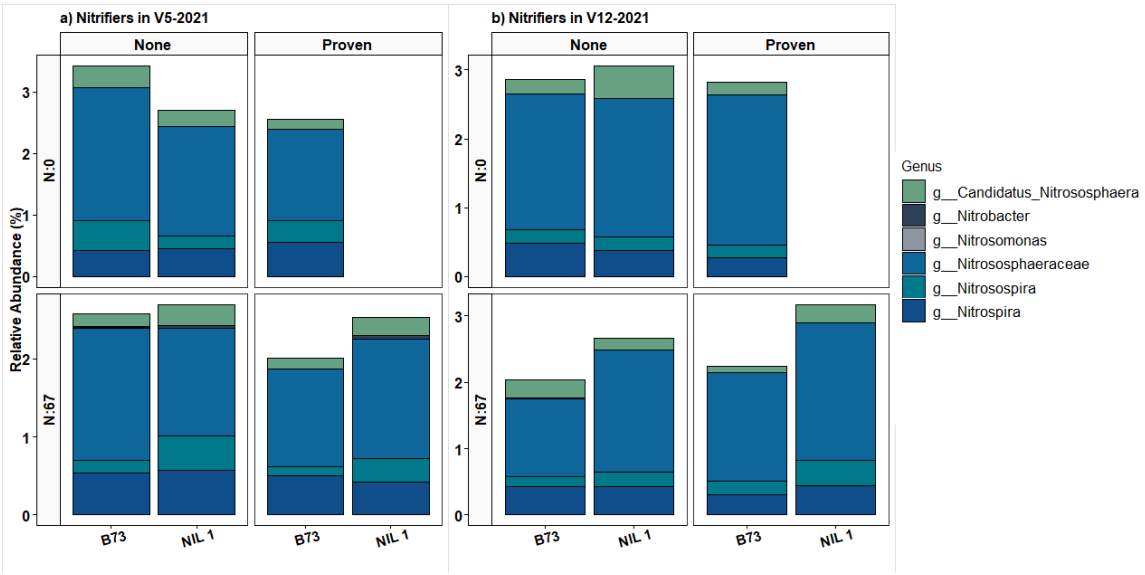
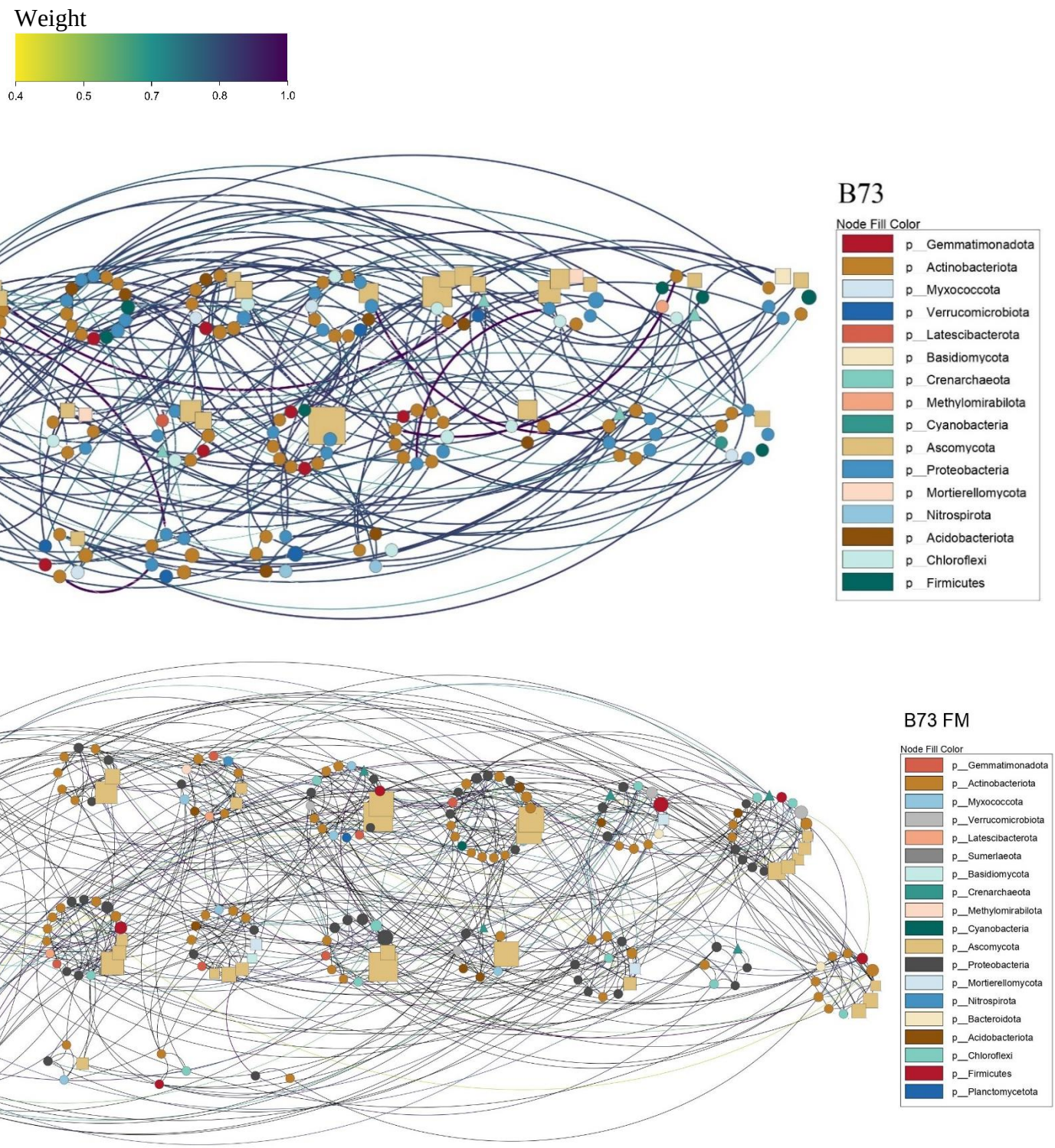


Figure S2a-b Comparing nitrifiers relative abundance across the genotypes and management with (a) and without (b) an N-fixing inoculant and N:67 kg ha^{-1} amendment in 2021 at V5 and V12 growth stages of maize. Facets grouping the relative abundance of nitrifiers based on treatments: management: Inoculant (Proven, None), mineral N dosages amendment (N:0 kg ha^{-1}, N:67 kg ha^{-1}).
NIL= near isogenic line, management (0 vs. 67 mineral N kg ha^{-1} and none vs application of an N-fixing inoculant (Proven)).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0.7
0.8
1.0
B73
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p Myxococcota
p Verrucomicrobiota
p Latescibacterota
p Basidiomycota
p Crenarchaeota
p Methylomirabilota
p Cyanobacteria
p Ascomycota
p Proteobacteria
p Mortierellomycota
p Nitrospirota
p Acidobacteriota
p Chloroflexi
p Firmicutes
B73 FM
Node Fill Color
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p__Latescibacterota
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p__Basidiomycota
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p__Methylomirabilota
p__Cyanobacteria
p__Ascomycota
p__Proteobacteria
p__Mortierellomycota
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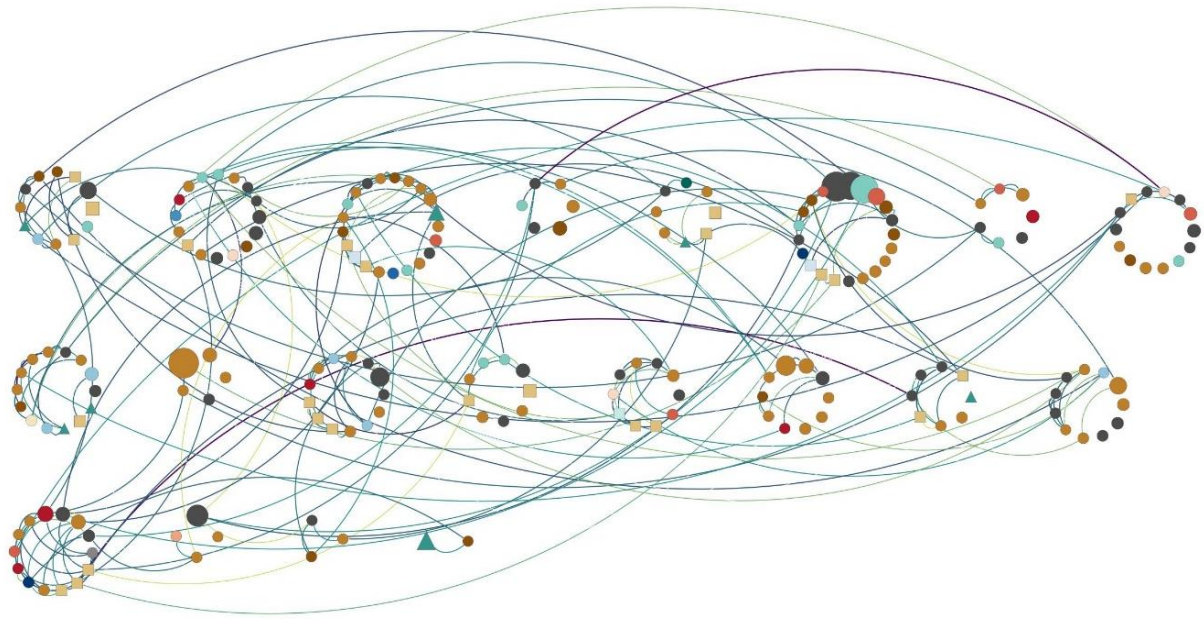
p__Acidobacteriota
p__Chloroflexi
p__Firmicutes
p__Planctomycetota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p__Methylomirabilota
p__Cyanobacteria
p__Ascomycota
p__Proteobacteria
p__Mortierellomycota
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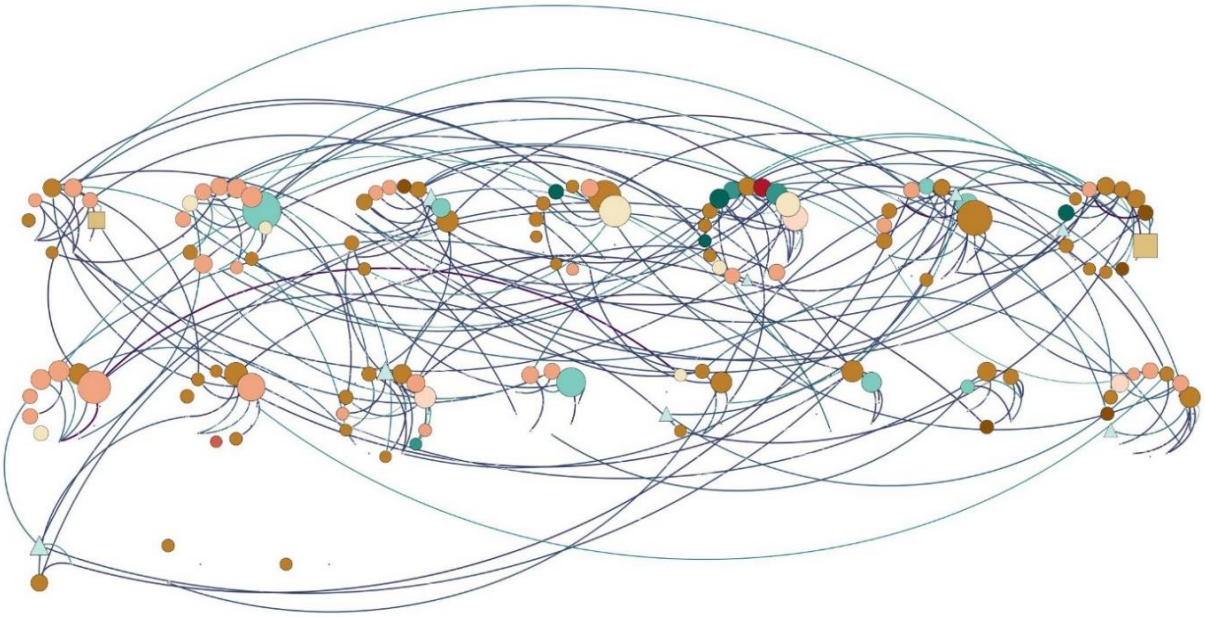
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p__Myxococcota
p__Verrucomicrobiota
p__Proteobacteria
p__Nitrospirota
p__Acidobacteriota
p__Crenarchaeota
p__Chloroflexi
p__Firmicutes
p__Planctomycetota

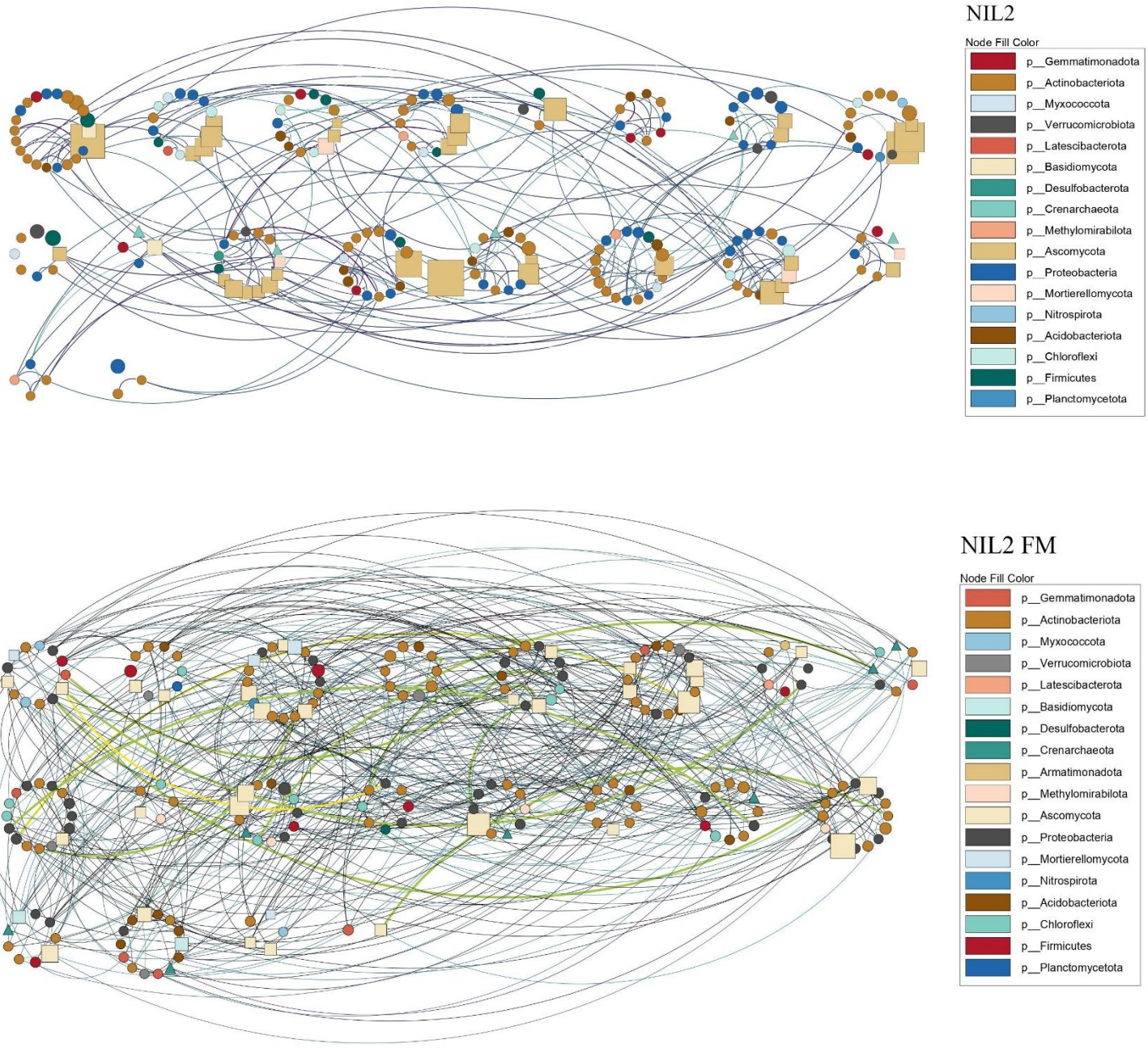

Figure S3a-f Modules and among modules connectivity under genotype (B73, NIL 1, and NIL 2) (a-c) and genotype: management (management = FM with an N-fixing inoculant (Proven) and mineral N amendment (N:67 kg ha^{-1}) (high N availability) interactions (d-f) are shown. The presence and size of edges represent among-modules-connectivity. The nodes are color-coded to indicate ASVs relevant to phyla present in the co-occurrence network. Node sizes are proportional to phyla relative abundance, and wights have been used for edge thickness. Networks' properties and details of their ecological relevance are defined in Table S11. Bacteria are shown by a circle, Archaea are shown by a triangle and Fungi are shown by a square.

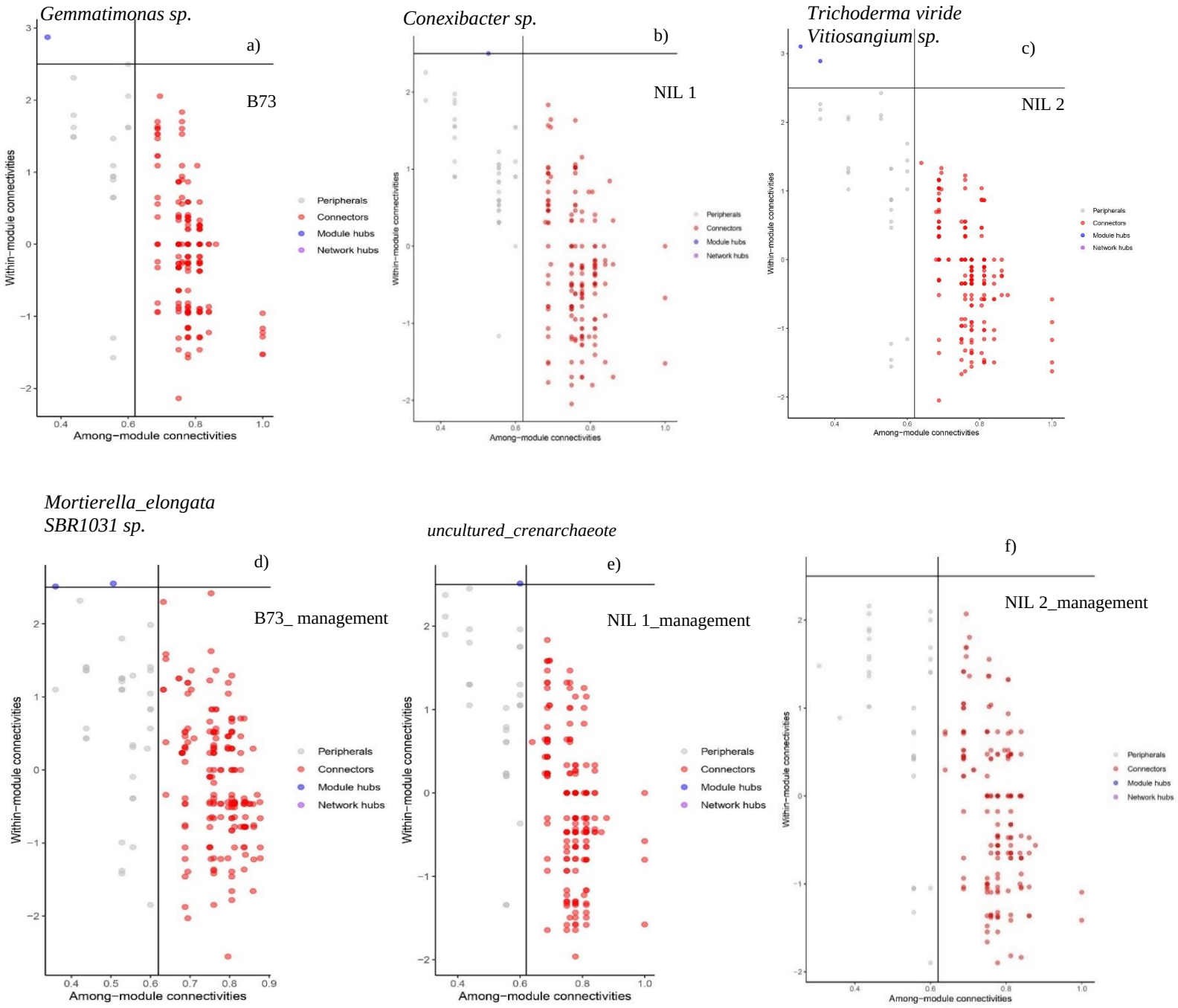

Figure S4a-F Classification of nodes to identify putative keystone species among the factors. The plots illustrate the modularity of networks constructed from predominant prokaryotic and fungal ASVs at the same depth, (2022 trial). The nodes are classified based on connectivity patterns: module hubs (blue dots display highly connected nodes within modules), network hubs (purple dots show highly connected nodes in the entire network), connectors (red dots indicate nodes connecting modules), and peripherals (gray nodes display interconnected nodes in modules with few outside connections). Figures a-c exhibit the genotype effect and figures d-f show the interactive effects of genotype and management on the connectivity pattern of cross-domain network of microbes. Genotypes (B73, NIL 1, and NIL 2) and a combination of genotype: management (Inoculant (Proven, None), mineral N dosages amendment (N:0 kg ha^{-1}, N:67 kg ha^{-1}). Network properties are defined in Table S11.