未见刊文章的部分结果展示

齐齐哈尔大学—生命科学与农林学院—微生物学—2021 级—刘淞

Impacts of continuous potato cropping on soil microbial assembly processes and spread of potato common scab

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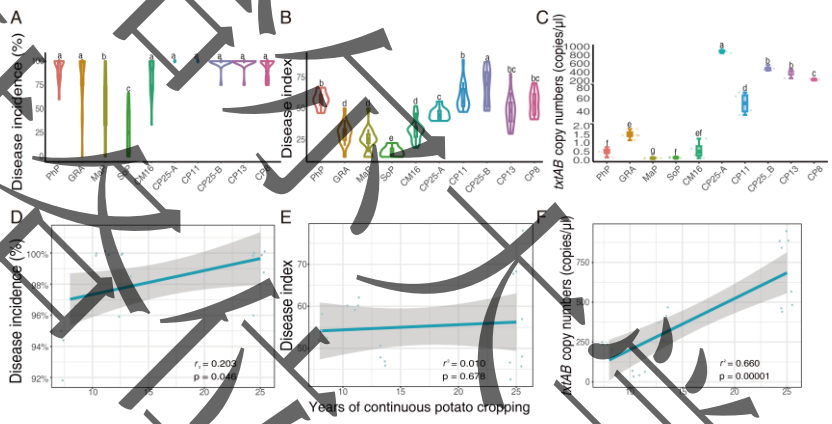
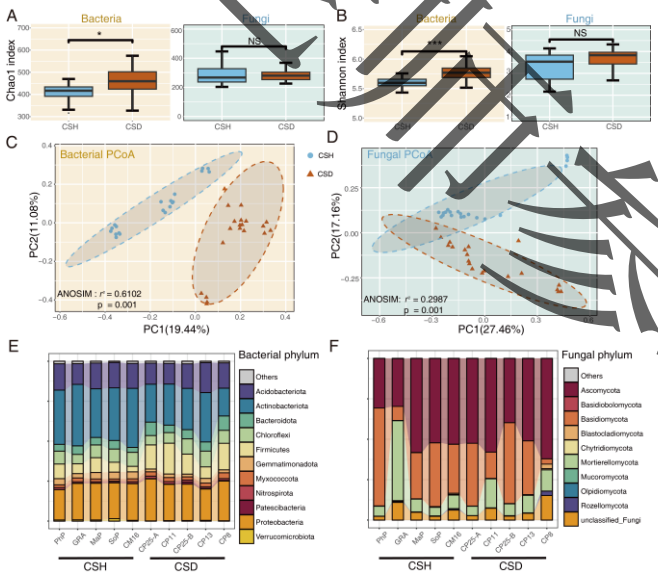
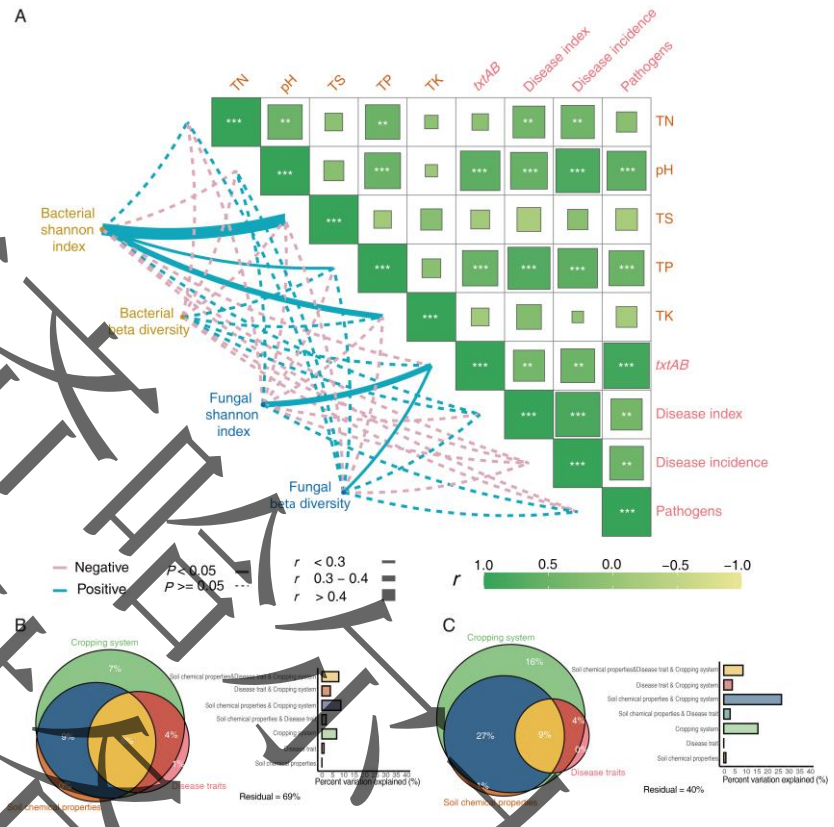


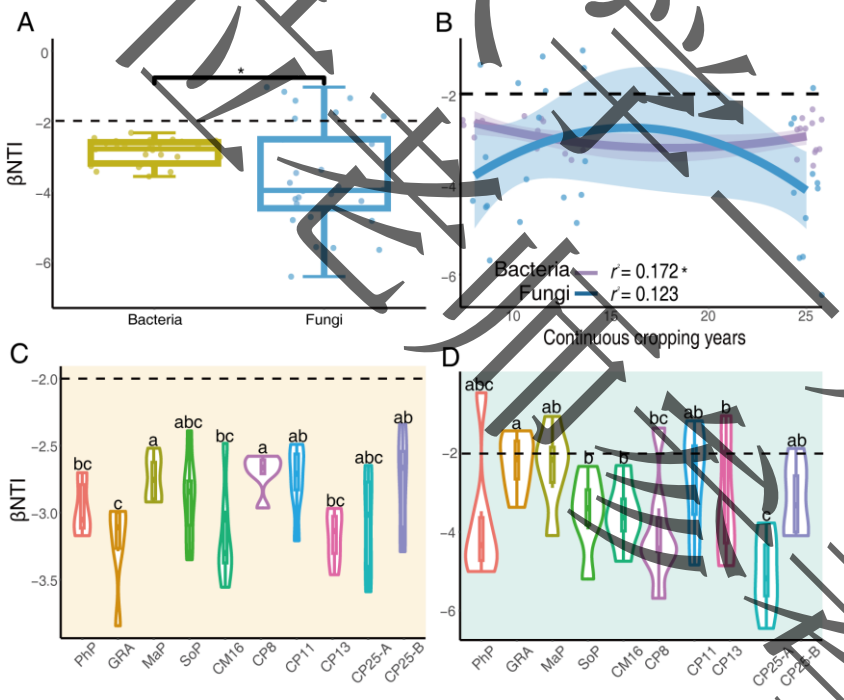
Disease traits of all ten treatments, and regression with years of continuous potato cropping.



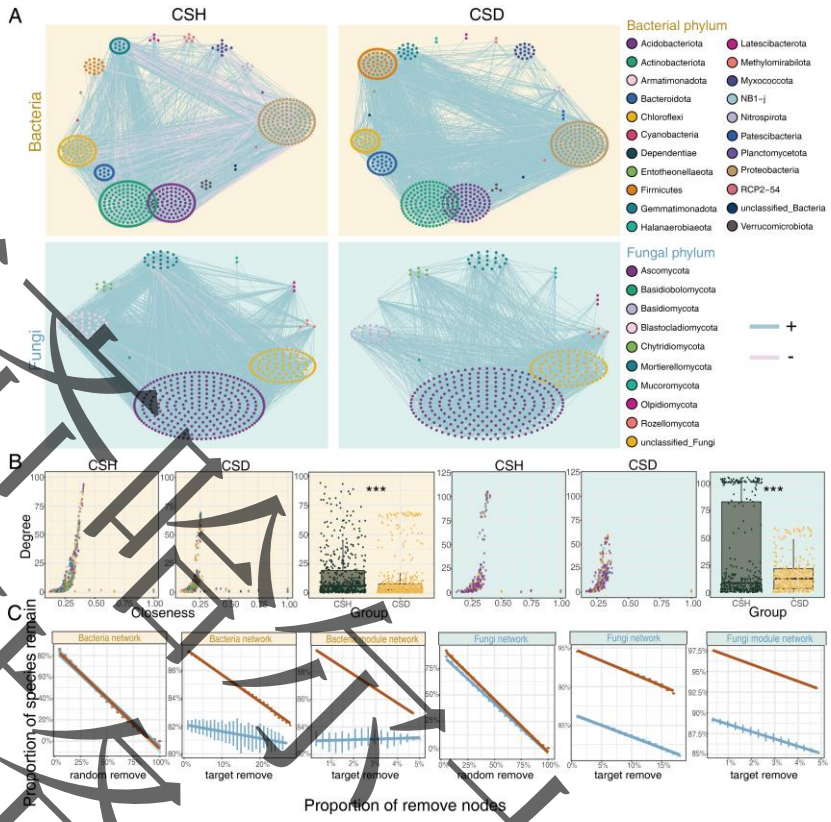
Differences in microbial community composition between CSH and CSD



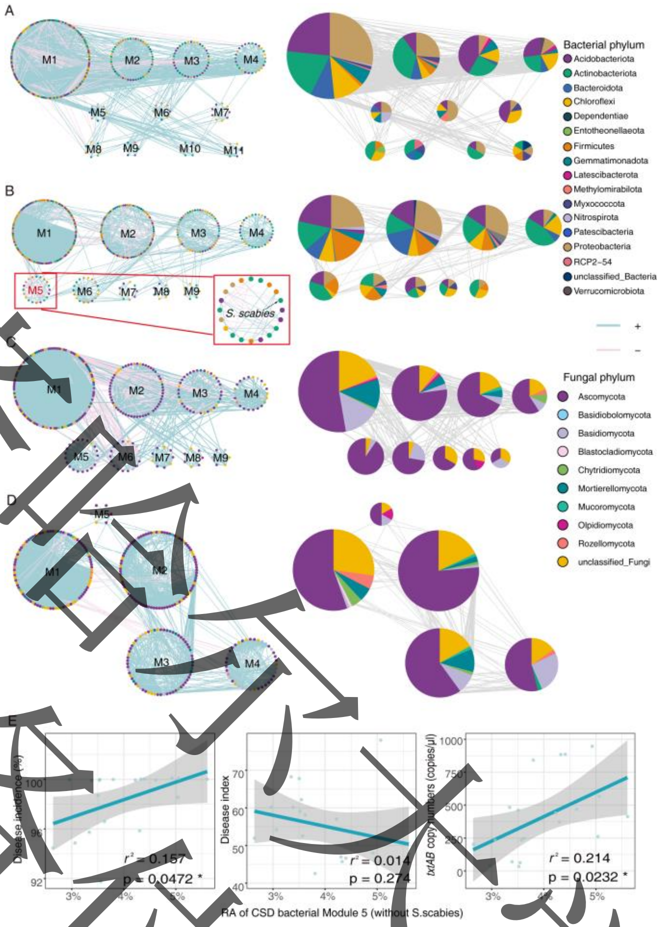
Relationship among microbial communities, chemical properties, and disease traits.



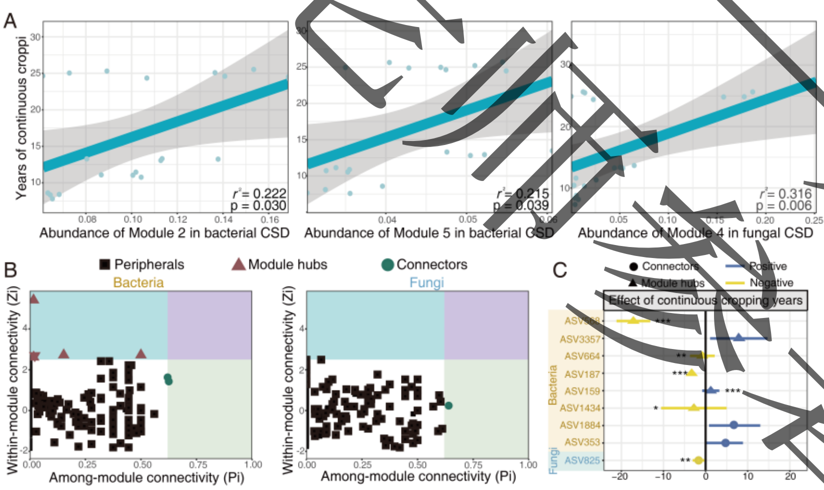
Construction process of bacterial and fungal communities. The beta nearest taxon index (βNTI) of bacterial (A) and fungal (B) communities in the ten treatments.



Bacterial and fungal intra co-occurrence networks. Co-occurrence networks (A) and comparison of node-level topological features (B) of bacterial and fungal communities in CSH and CSD sub-communities.



The relationship between the pathogen-containing network module and disease incidence, disease index, and *txtAB* gene copy numbers (E)



Relationship between continuous cropping and network modules

Effect of tomato keystone metabolites under different partitioning methods in potato-onion intercropping on rhizosphere microbial community assembly and network complexity

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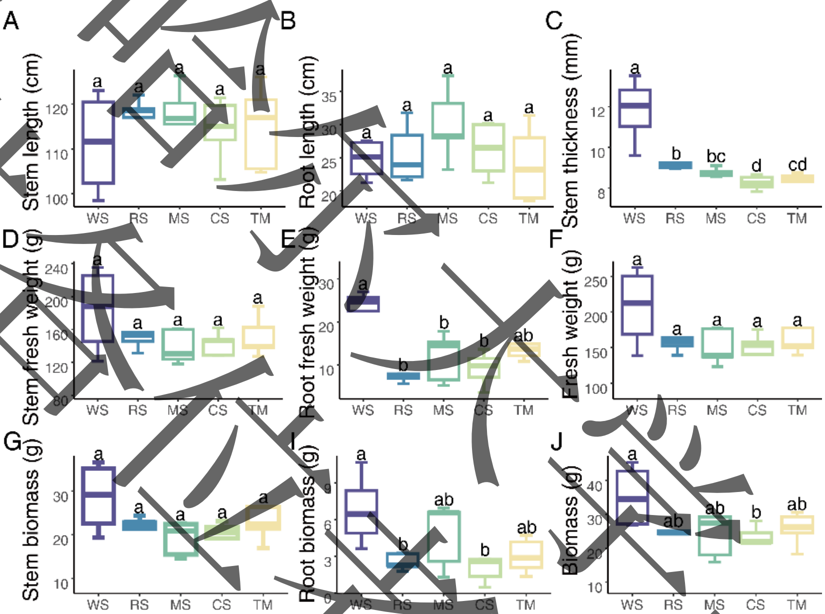
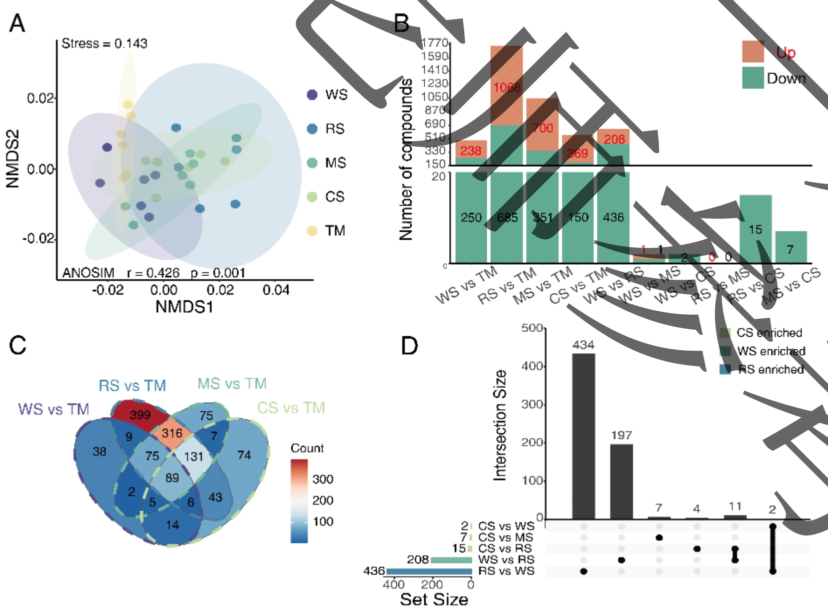
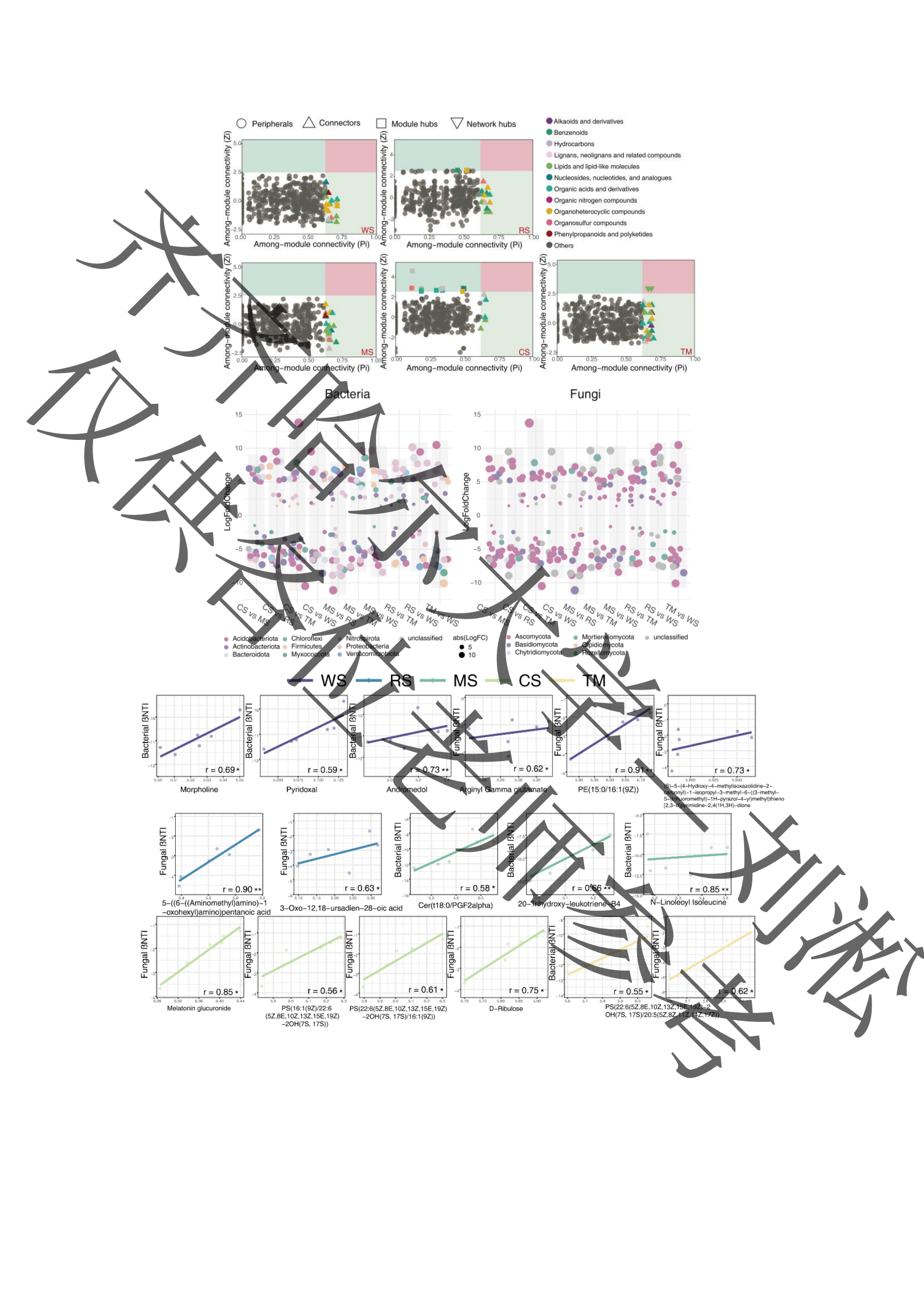
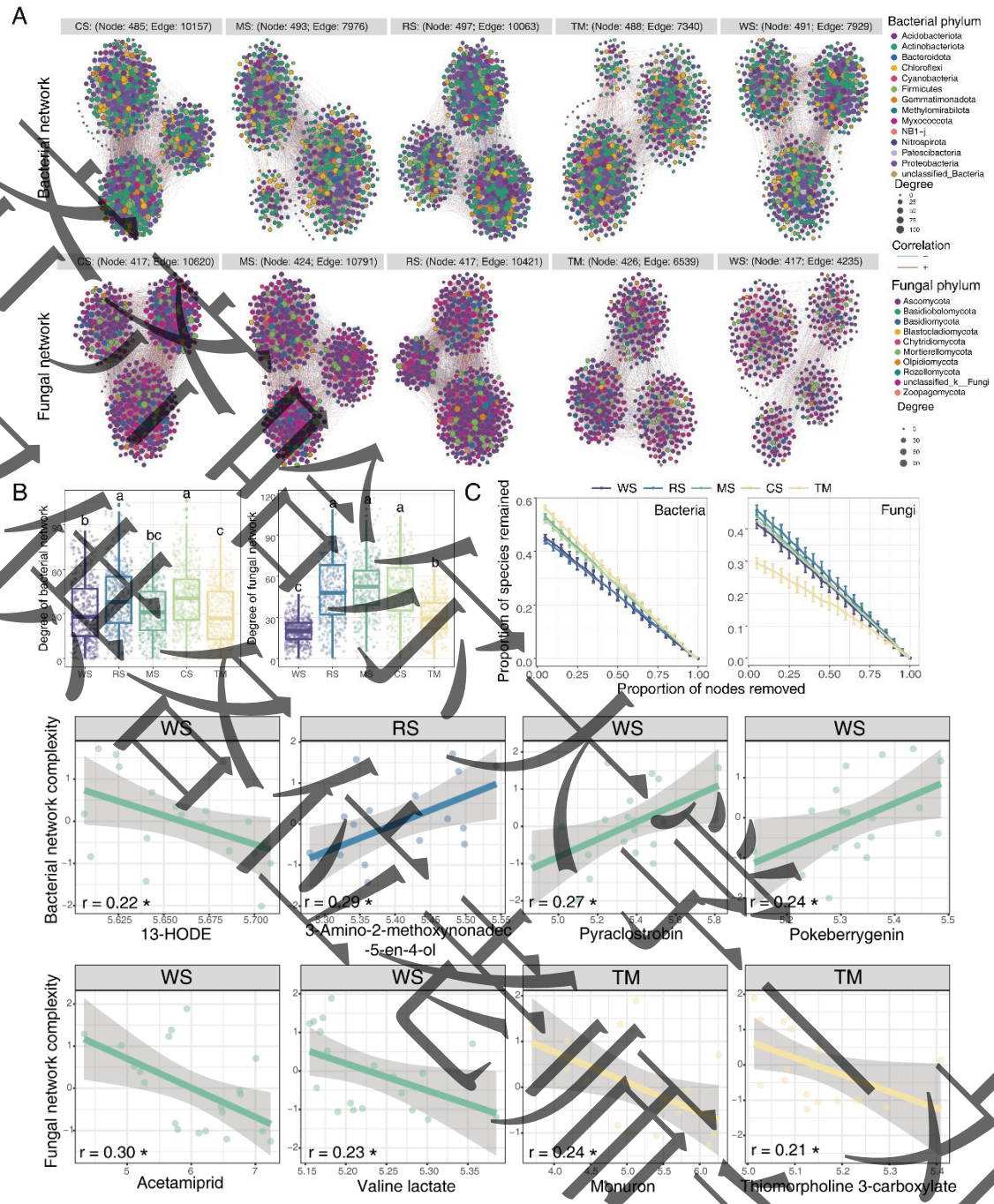





Peripherals
Connectors
Module hubs
Network hubs
Among−module connectivity (Zi)
Among−module connectivity (Pi)
WS
RS
MS
CS
TM
Alkaoids and derivatives
Benzenoids
Hydrocarbons
Lignans, neolignans and related compounds
Lipids and lipid-like molecules
Nucleosides, nucleotides, and analogues
Organic acids and derivatives
Organic nitrogen compounds
Organoheterocyclic compounds
Organosulfur compounds
Phenylpropanoids and polyketides
Others
Bacteria
Fungi
LogFoldChange
CS vs MS
CS vs RS
CS vs TM
CS vs WS
MS vs RS
MS vs TM
MS vs WS
RS vs TM
RS vs WS
TM vs WS
Acidobacteriota
Actinobacteriota
Bacteroidota
Chloroflexi
Firmicutes
Myxococcota
Nitrospirota
Proteobacteria
Verrucomicrobiota
unclassified
abs(LogFC)
Ascomycota
Basidiomycota
Chytridiomycota
Mortierellomycota
Olpidiomycota
Rozellomycota
Bacterial βNTI
Fungal βNTI
r = 0.69 *
Morpholine
r = 0.59 *
Pyridoxal
r = 0.73 **
Andromedol
r = 0.62 *
Arginyl Gamma glutamate
r = 0.91 **
PE(15:0/16:1(9Z))
r = 0.73 *
(S)−5−(4−Hydroxy−4−methylisoxazolidine−2−carbonyl)−1−isopropyl−3−methyl−6−((3−methyl−5−(trifluoromethyl)−1H−pyrazol−4−yl)methyl)thieno[2,3−d]pyrimidine−2,4(1H,3H)−dione
r = 0.90 **
5−((6−((Aminomethyl)amino)−1−oxohexyl)amino)pentanoic acid
r = 0.63 *
3−Oxo−12,18−ursadien−28−oic acid
r = 0.58 *
Cer(t18:0/PGF2alpha)
r = 0.66 **
20−Trihydroxy−leukotriene−B4
r = 0.85 **
N−Linoleoyl Isoleucine
r = 0.85 *
Melatonin glucuronide
r = 0.56 *
PS(16:1(9Z)/22:6(5Z,8E,10Z,13Z,15E,19Z)−2OH(7S, 17S))
r = 0.61 *
PS(22:6(5Z,8E,10Z,13Z,15E,19Z)−2OH(7S, 17S)/16:1(9Z))
r = 0.75 *
D−Ribulose
r = 0.55 *
PS(22:6(5Z,8E,10Z,13Z,15E,19Z)−2OH(7S, 17S)/20:5(5Z,8Z,11Z,14Z,17Z))
r = 0.62 *


A
CS: (Node: 485; Edge: 10157)
MS: (Node: 493; Edge: 7976)
RS: (Node: 497; Edge: 10063)
TM: (Node: 488; Edge: 7340)
WS: (Node: 491; Edge: 7929)
Bacterial network
Bacterial phylum
Acidobacteriota
Actinobacteriota
Bacteroidota
Chloroflexi
Cyanobacteria
Firmicutes
Gammatimonadota
Methylomirabilota
Myxococcota
NB1-j
Nitrospirota
Patescibacteria
Proteobacteria
unclassified_Bacteria
Degree
CS: (Node: 417; Edge: 10620)
MS: (Node: 424; Edge: 10791)
RS: (Node: 417; Edge: 10421)
TM: (Node: 426; Edge: 6539)
WS: (Node: 417; Edge: 4235)
Fungal network
Correlation
Fungal phylum
Ascomycota
Basidiobolomycota
Basidiomycota
Blastocladiomycota
Chytridiomycota
Mortierellomycota
Olpidiomycota
Rozellomycota
unclassified_k__Fungi
Zoopagomycota
Degree
B
Degree of bacterial network
Degree of fungal network
WS
RS
MS
CS
TM
C
Proportion of species remained
Bacteria
Fungi
Proportion of nodes removed
Bacterial network complexity
r = 0.22 *
13-HODE
r = 0.29 *
3-Amino-2-methoxynonadec-5-en-4-ol
r = 0.27 *
Pyraclostrobin
r = 0.24 *
Pokeberrygenin
Fungal network complexity
r = 0.30 *
Acetamiprid
r = 0.23 *
Valine lactate
r = 0.24 *
Monuron
r = 0.21 *
Thiomorpholine 3-carboxylate

Biological control of potato common scab by Bacillus safensis. LS01 and potential role of secondary metabolites

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本篇文章涉及核心结论，不便过多展示，望包涵