



A synthetic community promotes macadamia growth via root-microbe interactions and systemic plant responses

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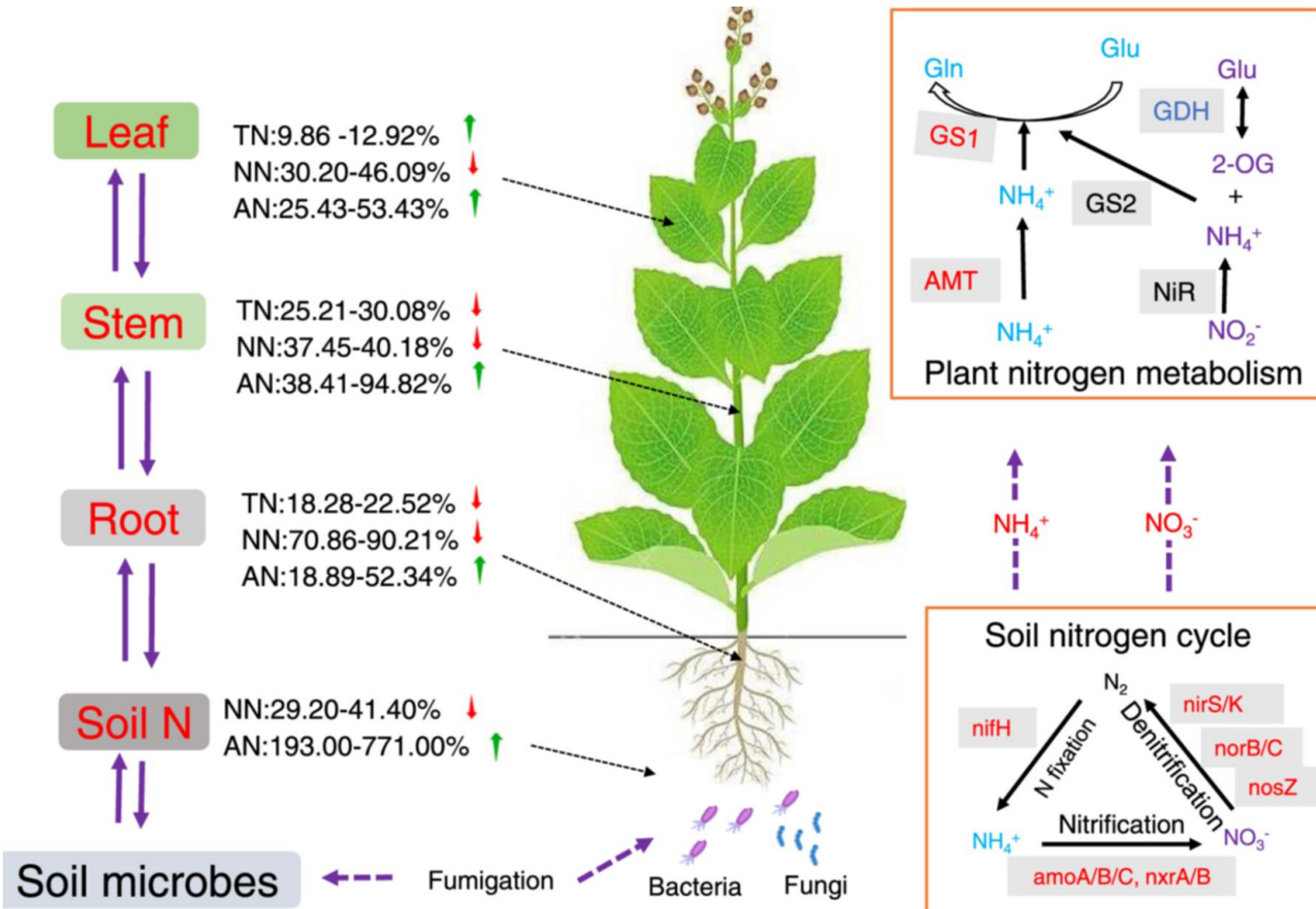
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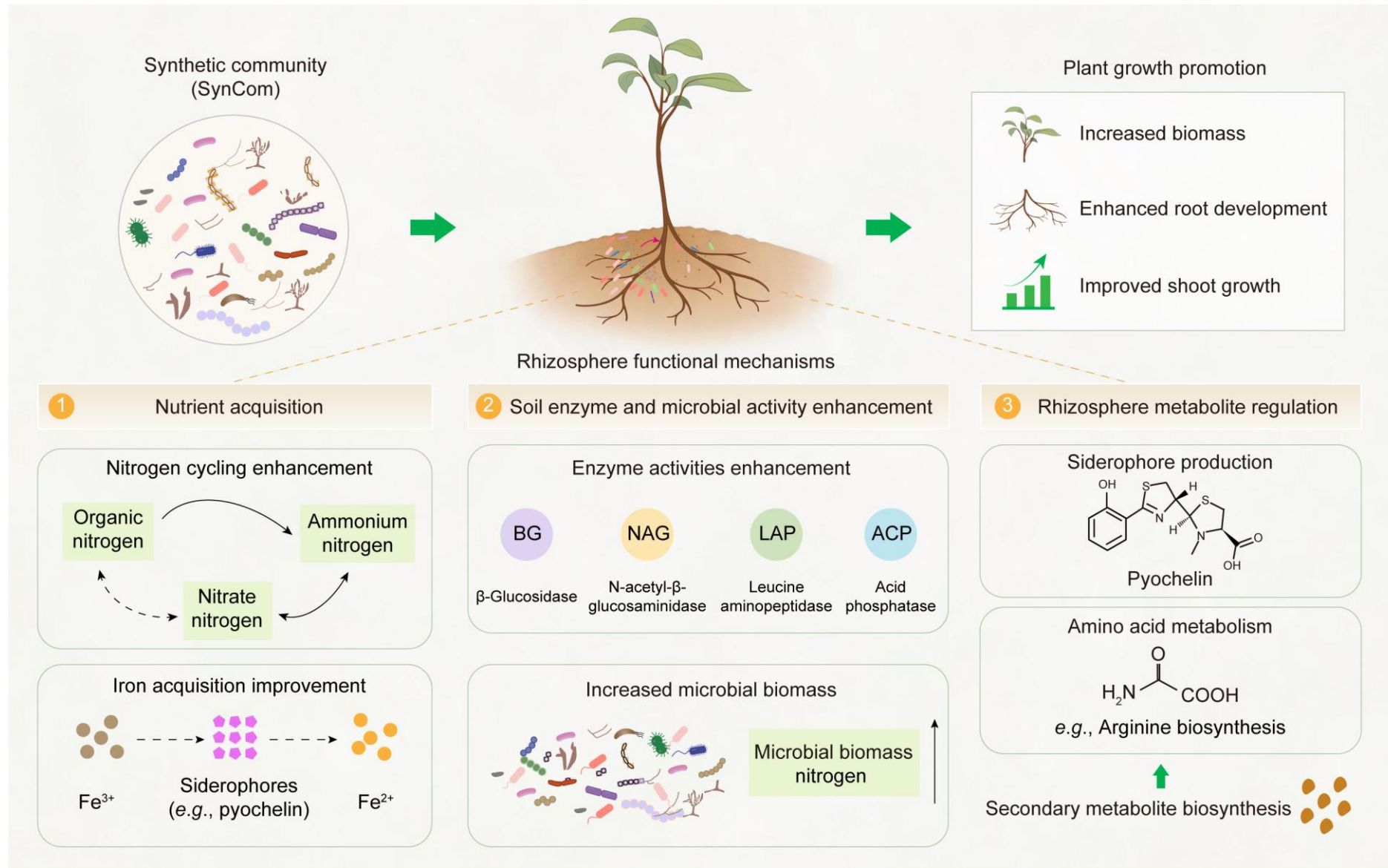
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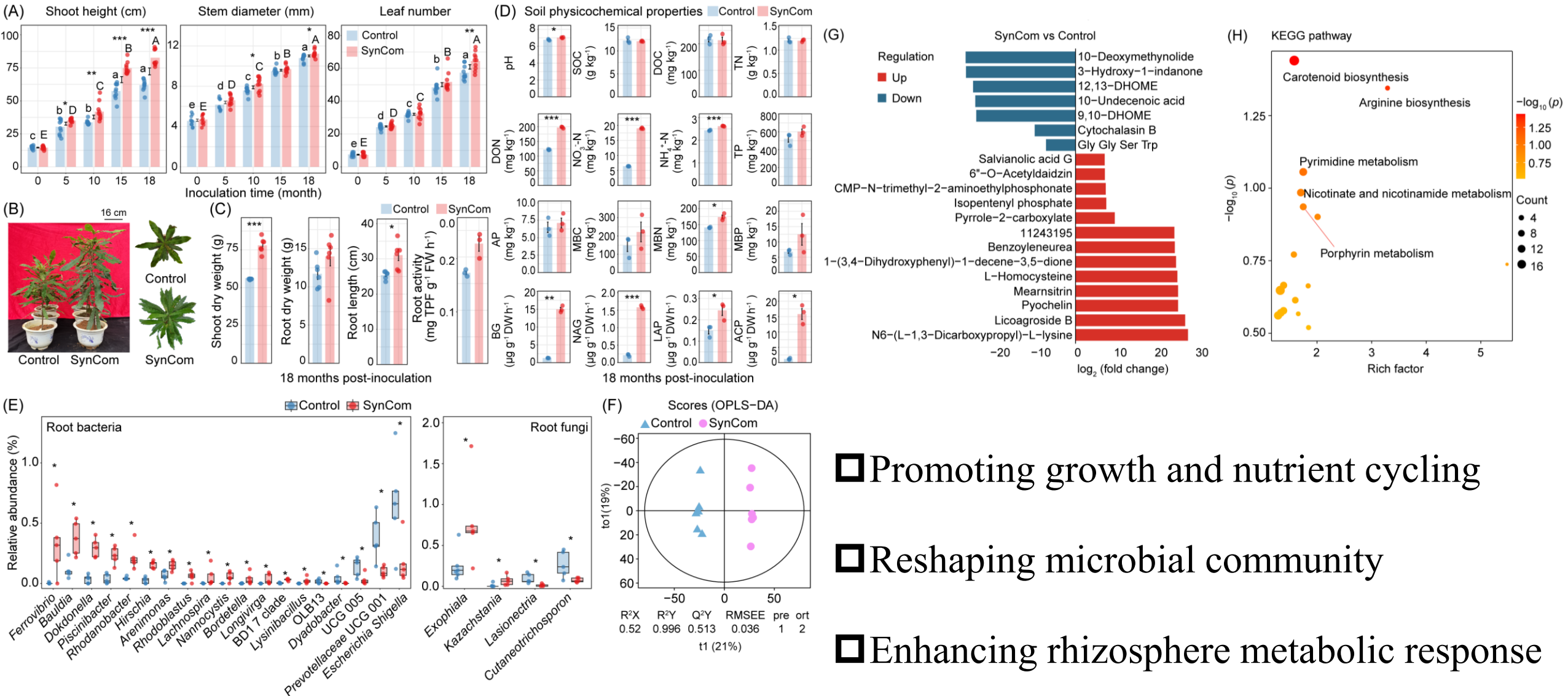
Introduction



- ❑ Plant microbiome is the second genome of plants.
- ❑ SynComs are a promising strategy for sustainable agriculture.
- ❑ However, mechanisms underlying long-term SynCom-host interactions in perennial woody crops remain poorly understood.



SynCom shapes macadamia growth, microbiome, and metabolome



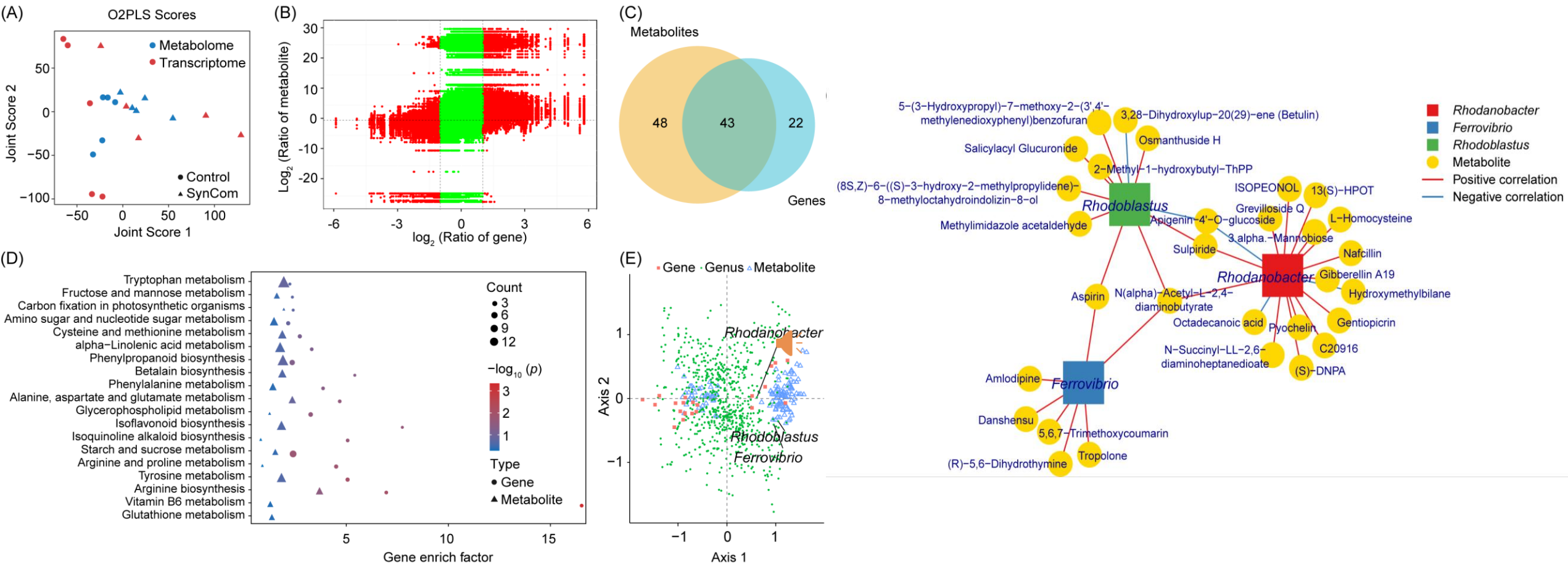
□ Promoting growth and nutrient cycling

□ Reshaping microbial community

□ Enhancing rhizosphere metabolic response



Multi-omics reveals host metabolism and transcription



Integrated metabolomic and transcriptomic analysis

Integrated microbiome, metabolomic and transcriptomic analysis



Summary

- ❑ In an 18-month pot experiment synthetic community (SynCom) enriched *Rhodanobacter*, *Ferrovibrio*, and *Rhodoblastus* in the root compartment.
- ❑ SynCom promoted the accumulation of rhizosphere metabolites such as the microbial siderophore pyochelin, and drove the co-enrichment of transcriptomic and metabolomic pathways, notably the arginine biosynthesis pathway.
- ❑ This coordinated response may have stimulated nitrogen and iron cycling in the soil and promoted the healthy growth of macadamia.

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