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Letter to the Editor

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Dear Editor,

We are thankful to you for editorial assessment and review of our manuscript. We gratefully acknowledge the input of editor/reviewers and, certainly, this rigorous review helped us improve the manuscript. Now we have modified the manuscript as per the raised concerns, and detailed corrections/responses are listed point by point in "**Response to Editor/Reviewer's Comments**". All revisions are yellow highlighted in the revised manuscript. We do hope that our revisions will fulfill the publication requirements of your esteemed journal.

Best Regards,

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On behalf of all co-authors

Response to Reviewer 1 Comments

Point 1: While the paper provides an extensive analysis of the consequences of planting different crops/plants species as a soil restoration measure, the resulting understanding remains rather descriptive, describing observed changes, but not translating the results into a conceptual advance in understanding the contexts, interactions and trade-offs involved. And I mean this particularly from the perspective soil health, in a multifunctional perspective. Many microbial groups and metabolite groups are mentioned, and reference is made to biochemical pathways, but I expect an explicit link from them to soil functioning and restoration. As a reader of SOIL I think the current discussion falls below my level of expectation, although I do support the publication of this data and results in another place.

Response: *We are grateful to the reviewer for this insightful and constructive comment. We fully acknowledge that the original discussion was overly descriptive, lacked conceptual advance, and failed to establish clear mechanistic links between microbial/metabolic profiles and soil multifunctionality from a holistic soil health perspective. To address this issue, we have comprehensively revised and expanded the Discussion section:*

1) *We have elevated the description to a conceptual framework integrating microbial communities, key metabolites, and biochemical pathways as drivers of soil multifunctionality during abandoned farmland reclamation.* ***Revisions are as follows:*** *"Soil health was evaluated comprehensively by integrating soil physicochemical properties, organic matter quality and microecological characteristics, rather than relying exclusively on bacterial diversity. As a key component of the soil microecosystem, the soil bacterial community is closely associated with soil quality improvement."*

2) *We have established explicit connections between identified microbial taxa, differential metabolites, and core soil functions (nutrient cycling, organic matter turnover, soil structure improvement, ecosystem resilience), linking these indicators to practical restoration outcomes.* ***Revisions are as follows:*** *"These differential metabolites could be grouped into seven main categories: organic acids, benzenoid compounds, fatty acids (FA), heterocyclic compounds, amino acids, glycerophospholipids (GP), and carbohydrates. To avoid lumping heterogeneous metabolite classes, we further clarify their specific roles. Organic acids mediate soil physicochemical properties, and promote plant growth and biomass accumulation (Sindhu et al., 2022). Benzenoid compounds act as important signaling molecules and carbon substrates in soil ecosystems, rather than toxic contaminants. Heterocyclic compounds in organic amendments drive shifts in the soil microbiome and enhance microbial utilization efficiency of straw-derived carbon (Li et al., 2023b). Amino acids act as crucial labile sources of soil organic nitrogen,* *supporting soil nutrient cycling and plant nitrogen acquisition (Cao et al., 2016). Carbohydrates provide readily available carbon sources for soil microbial activity, thereby facilitating the mineralization of soil mineral nutrients (Ratnayake et al., 2013). Taken together, these SDMs may contribute to soil quality improvement by participating in cellular metabolic processes of soil organisms and regulating soil nutrient cycling." "Collectively, these taxa exhibit high potential for facilitating plant growth and soil quality improvement via regulating soil structure and microbial activity, though their specific functions during abandoned cropland reclamation still need direct experimental validation in future works."*

3) *We have extended the discussion on ecological trade-offs among plant restoration regimes, including nutrient availability, microbial stability, metabolic regulation, and synergies or changes among soil health indicators.* ***Revisions are as follows:*** *"The slight soil organic matter content (OMC) decline under peach cultivation reflects a stoichiometric trade-off: enhanced microbial mineralization stimulated by root activities converted recalcitrant organic carbon into available nutrients, improving soil functionality despite mildly lower total organic matter."*

4) *We have interpreted results from a multifunctional soil health perspective, highlighting implications for optimizing restoration strategies in degraded subtropical agroecosystems, which aligns with the scope of SOIL.* ***Revisions are as follows:*** *"Furthermore, soil property improvement alone is insufficient when screening suitable plant species for the ecological reclamation of abandoned croplands. Agronomic manageability and economic benefits for local farmers must also be fully considered, which aligns with the practical goals of cropland reclamation. Under local subtropical climatic conditions, vegetable cultivation involves moderate planting difficulty, relatively simple management, a short growth cycle, and higher economic yield per unit area with a given growing period. This matches the current large-scale intensive agricultural practices in the study region, where monoculture systems are widely adopted for economic efficiency. These advantages provide strong economic incentives for farmers to adopt reclamation and remediation practices, ensuring the long-term sustainability of amelioration strategies. Therefore, combined with the observed improvements in soil physicochemical properties, microbial diversity, and metabolic function, vegetable cultivation represents not only an ecologically effective but also an economically feasible and socially acceptable ecological reclamation strategy for abandoned croplands in this subtropical region."*

Point 2: It is a complicated study in terms of techniques used, I am familiar with most, but metabolomics I only have a cursory understanding of, cannot judge the quality here. I suggest to get a reviewer who can.

Response: *We appreciate the reviewer's careful comments. We fully respect your suggestion that the editorial team invite a reviewer with expertise in metabolomics to further assess the quality of the metabolomic analyses. We assure reviewer that all metabolomic analyses followed standard quality control procedures to ensure reliability of current findings: quality control (QC) samples were inserted during the LC-MS analysis to evaluate the repeatability and reliability of the entire process; the orthogonal partial least squares discriminant analysis (OPLS-DA) models had Q^2 (cum) values all greater than 0.5, confirming the validity of the differential metabolite screening. We sincerely hope the revised manuscript can be considered for publication in SOIL.*

Point 3: The starting condition is poorly described, what were the sites reclaimed from? What was the nature of the degradation, the disturbance? Without this we cannot judge the meaning of the reported effects. The organic matter levels seem to be unexpectedly high for my understanding (5-10%!) on what is described as a sandy loam in the first 20 cm.

Response: *Many thanks for your valuable suggestion. We agree that a clear description of the study site background is essential for developing a proper context with our results.* ***1) We have supplemented detailed background information for the test site:*** *"To screen suitable plant species for the reclamation of degraded abandoned cropland (long-term uncultivated, weed-infested farmland with poor soil structure and fertility) in subtropical regions of China."* ***2)*** *We apologize for the confusion caused by ambiguous expression of soil organic matter data. To clarify, the initial organic matter content in the 0–20 cm soil before the experiment was 6.93 g kg^{-1}(average 6.51–7.62 g kg^{-1}), equivalent to 0.65%–0.76% (average 0.69%). After three years of cultivation, the organic matter content was 10.63 ± 0.92 g kg^{-1}(average 1.06%), 9.04 ± 2.23 g kg^{-1}(average 0.90%), 5.71 ± 1.59 g kg^{-1}(average 0.57%) in vegetable, corn, peach treatment, respectively. All these values are far lower than 5–10% and consistent with a sandy loam soil.* ***The misleading expressions have been corrected, as follows:*** *"Before the experiment, five soil samples were collected using a 5-point sampling method to determine initial physicochemical properties: pH 7.86 (7.45–8.20), OMC 6.93 g kg-1 (6.51–7.62 g kg-1, equivalent to 0.65%–0.76% with an average of 0.69%), TN 0.42 g kg-1 (0.12–0.71 g kg-1), AP 12.30 mg kg-1 (11.70–12.70 mg kg-1), and AK 378.70 mg kg-1 (371.61–387.74 mg kg-1)."*

Point 4: The experimental setup is one of a practical applied experiment. In the present ms all effects are subscribed to the different plant species put in place in the treatments. But at the same time the treatments vary in planting density, but also type, timing and amount of fertilizer used. The control, received no plant, but also no fertilizer. In addition, the planting types are not described in very much detail, what variety was used? For vegetables we even completely do not know which species/crops were used. In places a plural form is used suggesting multiple species were used, but did they grow together in the same year, or was it a rotation? What type of management was done in addition to the fertilization, was there any irrigation, and pesticides were they used? How was the land prepared for the crop planting? Any tillage or other site preparation measures?

Response: *We greatly appreciate the reviewer for these detailed comments on the experimental setup. We have supplemented comprehensive and precise information on plant varieties, cropping system, planting densities, fertilization regimes, and field management practices in the revised manuscript:* ***1)*** *We clarified that vegetables were grown as two successive crops within the same year (leafy vegetable cv. Heixiaopang from October to March, followed by eggplant cv. Hangqie 2022 from April to September), rather than simultaneous mixed cropping or multi-year rotation. The varieties for corn (cv. Qianjiangnuo 3) and peach (cv. Zhongtao 5) were also clearly specified.* ***2)*** *We added detailed planting densities for each treatment and standardized fertilization rates to per-hectare units, with the same total annual nitrogen input (2.63 t ha^{-1} yr^{-1}) across all planted treatments.* ***3)*** *The unplanted control received no fertilizer because it was designed to reflect the original unmanaged state of abandoned farmland without any anthropogenic inputs, providing a baseline for evaluating the restoration effects of different planting regimes.* ***4)*** *We further specified that tillage, land preparation and irrigation followed local conventional farming practices throughout the experiment.* ***Revisions are as follows:*** *"Four treatments were applied on land reclaimed from abandoned croplands (previously cultivated but left uncultivated for eight years, with widespread weeds and degraded soil): (1) vegetable cultivation with two successive crops in a single year (cv. "Heixiaopang", a leafy vegetable, grown October–March, obtained from Qingdao North-South Seed Industry Co., Ltd., Qingdao, China; cv. "Hangqie 2022", eggplant, grown April–September, provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (2) corn cultivation (cv. "Qianjiangnuo 3", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (3) peach cultivation (cv. "Zhongtao 5", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); and (4) unplanted bare fallow was used as the control (Figure 1a–d). Each plot was 25 m × 5 m (125 m^2). Planting densities were 25 cm × 25 cm for leafy vegetables, 40 cm × 50 cm for eggplant, 30 cm × 50 cm for corn, and 4 m × 5 m for peach trees. For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented the* *unmanaged baseline condition of abandoned farmland. All other management practices, including tillage and irrigation, followed local conventional farming practices."*

Point 5: 1) Regarding analysis, why were OTUs used to describe microbial diversity and not ASVs? How many samples were run together on a Miseq plate? 2) What was the read count per sample, before and after bioinformatics? 3) Also you say, 'Principal component analysis (PCA) was conducted using Bray-Curtis metrics', but PCA exclusively works with Euclidean distances, so what did you do? PCoA? Or PCA? 4) What do you mean with 'structural variation' (L201), why not simply variation? 5) Also, analyses and calculations are done at phylum, family and genus level, but the choice comes across as quite arbitrary – what is the rationale for doing one analysis at genus level and another at family level? 6) How was the heatmap constructed, what correlation matrix is lying underneath? 7) When was a bacterium considered dominant (L203)? 8) Finally, an analysis is made of cross-correlations among microbial taxa and metabolite groups – but I wonder, what do these correlations mean? Quite some abiotic things change across planted vs unplanted controls, to what extend are these relationship confounded? How does fertilization yes/no and rhizodeposition from plant roots yes/no influence microbiomes and associated metabolite profiles? Also for the metabolites, they are extracted from soil, but to what extend do they originate from microbes or plants? And since the treated plots have more plants then the control, what does that tell us?

Response: *Many thanks for your valuable suggestions. We have carefully addressed each point and revised the manuscript accordingly, as detailed below:*

1) *We clustered sequences into operational taxonomic units (OTUs) at a 97% similarity threshold, which is the widely accepted standard for full-length 16S rRNA gene sequencing using the PacBio platform in soil microbial ecology, facilitating reliable comparison with relevant studies on soil restoration and abandoned cropland reclamation. Compared with ASVs, 97% OTU clustering is more robust for long-read sequencing data, reducing false rare taxa and excessive taxon splitting caused by minor sequencing errors, thus ensuring more stable and comparable community analysis. A total of 20 samples (four treatments with five biological replicates each) were sequenced in one single batch on the PacBio Sequel II platform (not Illumina MiSeq) to minimize batch effects.*

2) *We have supplemented the raw and high-quality read counts for each biological replicate.* ***Revisions are as follows:*** *"Specifically, the raw read counts for each replicate were 58,895, 64,511, 68,697, 80,006, and 80,027 for the vegetable cultivation treatment; 79,851, 80,002, 79,966, 79,980, and 79,981 for the corn cultivation treatment; 80,064, 68,024, 79,888, 79,956, and 80,115 for the peach cultivation treatment; and 79,950, 79,862, 80,190, 68,020, and 79,925 for the control* *treatment. Following bioinformatic processing, the high-quality read counts per replicate were 46,324, 50,652, 49,650, 54,637, and 59,487 for the vegetable cultivation treatment; 59,863, 60,815, 64,090, 54,349, and 57,234 for the corn cultivation treatment; 56,810, 51,238, 61,138, 59,511, and 58,630 for the peach cultivation treatment; and 60,074, 60,392, 55,475, 52,594, and 59,162 for the control treatment."*

3) *We apologize for the erroneous mention of "Bray–Curtis metrics". Standard principal component analysis (PCA) based on Euclidean distance was performed in this study, as PCA strictly relies on Euclidean distances.*

4) *The term "structural variation" was initially used to highlight community structural shifts. Following the reviewer's suggestion for clarity, we have replaced "structural variation" with "variation" throughout the manuscript.* ***Revisions are as follows:*** *"Principal component analysis (PCA) based on Euclidean distances was conducted to assess variation in soil bacterial community composition."*

5) *Phylum-level analysis was used to reveal overall broad patterns of bacterial community shifts, while genus-level analysis was performed to identify key responsive and functionally relevant taxa. To avoid arbitrary selection and align with mainstream soil microbial research, all family-level analyses have been removed; only phylum and genus levels are retained for analysis and presentation in the revised manuscript.*

6) *The correlation heatmap was generated using the pheatmap package in R software（v4.2.1）, based on Spearman's correlation coefficients calculated between the relative abundance of differential bacterial genera and the top 20 significant differential metabolites (SDMs, VIP > 1, $p < 0.05$). Hierarchical clustering was applied to both rows and columns. These details have been added to the methods section.* ***Revisions are as follows:*** *"In addition, Spearman correlation-based heatmaps were generated using the pheatmap package in R software (v4.2.1) to explore correlation patterns between SDMs and differentially abundant bacterial genera across treatments. The top 20 SDMs were screened using thresholds of VIP > 1 and $p < 0.05$ (Hollander, 1973). Hierarchical clustering was performed on both rows and columns in the correlation heatmap."*

7) Bacterial taxa were defined as dominant based on the top 10 most abundant taxa at the phylum and genus levels. ***The description has been revised to:*** *"The relative abundances of the top 10 bacterial taxa at the phylum and genus levels were calculated and visualized using Origin."*

8) The cross-correlations among microbial taxa and metabolite groups reflect coordinated shifts in soil nutrients, bacterial communities, and metabolites during reclamation, indicating that the three planting regimes effectively improve soil properties and shape associated microbiomes and metabolomes. We acknowledge that abiotic factors, fertilization regimes, and rhizodeposition may *confound these relationships. Nevertheless, our RDA and heatmap results collectively highlight the dominant role of plant species identity in shaping these soil attributes during reclamation. Soil metabolites in this study originated from a mixture of plant root exudates, microbial metabolic byproducts, and soil organic matter decomposition. The higher plant biomass in treated plots enhances rhizodeposition, which further drives the differences in microbial and metabolic profiles compared with unplanted controls. These complex interactions are ecologically important for the reclamation of abandoned croplands, and the above interpretations have been added and improved in the revised Discussion.*

Point 6: 1) In many places the taxonomy of bacteria is not correctly represented. Often all taxa are referred to as genera, but they actually represent a mixture of different taxonomic levels, that also makes me wonder about the analyses, did you merge them, if so how? And is that valid? 2) I think in a regression trees approach where taxonomy is the predictor you could do it meaningfully in one go. 3) This makes me worried about the identification of the metabolites as well. 4) I also don't appreciate the use of the word vegetation type here, in ecology vegetation type (phytosociological entities) have a very specific meaning of a naturally shaped community. Here it is not even a community, it is one crop species, artificially put in place, and maintained that way. I would talk about plant or crop species effects, or cropping types.

Response: *Many thanks for your valuable suggestion.* ***1)*** *We have carefully checked and corrected the bacterial taxonomic annotations throughout the manuscript to clearly indicate their exact taxonomic levels at the phylum and genus levels, thus avoiding mixed or mislabeled taxa. No inappropriate merging of different taxonomic levels was performed in our analyses, and all statistical treatments were conducted at their respective correct taxonomic ranks to ensure validity.* ***2)*** *As for the regression tree approach you mentioned for integrating taxonomic predictors, we appreciate this constructive suggestion. In this study, we focused on phylum- and genus-level patterns separately for clarity, and did not apply regression tree modeling across mixed taxonomic levels; all analyses were performed within single, consistent taxonomic levels to ensure robustness.* ***3)*** *Regarding metabolite identification, we have double-checked the entire identification process, including database matching, mass spectrum calibration, and validation criteria, to confirm the accuracy and reliability of metabolite annotation.* ***4)*** *In addition, the term "vegetation type" has been uniformly revised to "three plant species" throughout the manuscript to align with standard ecological terminology for agricultural systems management.*

Point 7: One thing that worries me is how the measured properties are evaluated as an improvement or not, why is it better to have more OTUs? Often these things are done intuitively, which I understand, but we need to be critical, why is that really better? In intensive arable system usually bacterial diversity is higher then in more extensive systems, is that good? I don't think so, I think the soil health is often better in the extensive systems, that have less bacteria, but more fungi, and as a consequence improved organic matter (quality), water infiltrating and holding capacity, and less nutrient leaching.

Response: *Many thanks for your valuable suggestion. We fully agree that a higher number of OTUs or greater bacterial diversity alone cannot be simply regarded as an indicator of soil improvement, and intuitive judgments of soil health based solely on microbial diversity should be avoided. In this study, the higher OTU richness and alpha-diversity in the three plant treatments were mainly associated with sheep manure input and rhizodeposition, which supplied more available substrates for microbial proliferation.* ***Following your suggestion, we have revised the discussion to adopt a more critical perspective:*** *soil health was evaluated comprehensively by integrating soil physicochemical properties, organic matter quality and microecological characteristics, rather than relying exclusively on bacterial diversity. As you highlighted, the bacterial-fungal balance and key soil functions (e.g., water infiltration, water holding capacity and nutrient retention) are also crucial in assessing soil reclamation effects, which we would duly acknowledge and emphasize in the revised manuscript.*

Point 8: The conclusion largely repeats the results. No need to mention RDA and other experiment technical aspects – tell me 1) what is the message the data told you, 2) what are the wider implications for the research field, for practice, and perhaps beyond.

Response: *Many thanks for your valuable question. We have completely revised the conclusion to avoid repeating experimental results and technical details, and refined the core findings as well as their practical and academic implications.* ***The revised conclusion is as follows:*** *"This three-year field experiment revealed that planting vegetables, corn, and peach all effectively facilitated the ecological reclamation of degraded abandoned cropland in subtropical regions of China, among which vegetable cultivation exerted the most comprehensive and optimal effect on soil quality improvement. Vegetable cultivation systems significantly elevated soil bacterial diversity, community complexity, functional stability, and selectively enriched key bacterial taxa closely associated with soil nutrient cycling. Meanwhile, rhizosphere metabolic profiles were substantially reshaped, with abundant significant differential metabolites involved in amino acid metabolism, carbon turnover, and rhizosphere signaling. Notably, amino acid derivatives,* *pyridine derivatives and small peptides were strongly correlated with keystone bacterial genera, forming tight metabolite-microbe coordination patterns. The coordinated variations in soil physicochemical properties, bacterial communities, and metabolites collectively enhanced soil nutrient availability and ecological functions. This study elucidates the underlying mechanisms of plant-mediated soil amelioration during abandoned cropland reclamation, and verifies that vegetable-based reclamation represents a feasible strategy integrating ecological effectiveness, agronomic practicality, and economic benefits for local farmers. These results not only provide a scientific basis and practical guidance for the ecological reclamation and sustainable utilization of degraded abandoned croplands in subtropical regions of China, but also offer valuable insights for similar subtropical degraded land restoration globally."*

Point 9: Title: can you include what the croplands were reclaimed from?

Response: *Many thanks for your valuable suggestion. According to your suggestion,* ***the title has been revised into*** *"Impacts of cultivating three different plant species on soil physicochemical properties, bacterial communities, and metabolites during reclamation of abandoned farmlands" to clearly specify that the croplands were reclaimed from abandoned farmlands."*

Point 10: L28: why is lowering of OM by peach considered a soil improvement? This needs an explanation to be understood.

Response: *Many thanks for your valuable question. We have added a clear explanation for the decrease in organic matter under peach cultivation in the revised manuscript. The reduced organic matter in peach cultivation plots was mainly attributed to enhanced organic matter mineralization driven by root activities and associated microbial decomposition, which converted relatively stable and recalcitrant organic matter into available nutrients and labile carbon sources. Although total organic matter content decreased slightly, soil available nutrients (e.g., phosphorus, microbial biomass carbon) were significantly improved, leading to enhanced overall soil functionality. This change therefore represents a benign regulatory process rather than soil degradation, and we have revised the relevant description accordingly to avoid misunderstanding.* ***Revisions are as follows:*** *"The slight soil organic matter content (OMC) decline under peach cultivation reflects a stoichiometric trade-off: enhanced microbial mineralization stimulated by root activities converted recalcitrant organic carbon into available nutrients, improving soil functionality despite mildly lower total organic matter. Overall, vegetable cultivation most comprehensively improved soil nutrients, microbial abundance and diversity, and metabolite* *composition, making it the optimal choice for reclaiming degraded abandoned cropland in this region."*

Point 11: L30: metabolites extracted from what?

Response: *Many thanks for your carefulness. We have specified that metabolites were extracted from rhizosphere soil throughout the manuscript.* ***Revisions are as follows:*** *"This study evaluated the effects of vegetable, corn, and peach cultivation on soil physicochemical properties, bacterial communities, and rhizosphere metabolites during abandoned cropland reclamation in subtropical China."*

Point 12: L30: do these gains have a cost somewhere to? Many of the processes involved are governed by (e.g. stoichiometric) trade-offs, that requires some consideration.

Response: *Many thanks for your valuable suggestion. We fully agree that soil nutrient improvements are often accompanied by stoichiometric and functional trade-offs.* ***In the revised text, it has been revised into*** *"The slight soil organic matter content (OMC) decline under peach cultivation reflects a stoichiometric trade-off: enhanced microbial mineralization stimulated by root activities converted recalcitrant organic carbon into available nutrients, improving soil functionality despite mildly lower total organic matter. Overall, vegetable cultivation most comprehensively improved soil nutrients, microbial abundance and diversity, and metabolite composition, making it the optimal choice for reclaiming degraded abandoned cropland in this region."*

Point 13: L31: what do you mean with 'a gain in soil'? also for microbes and metabolites – what increased? Abundance, richness, diversity, particular components (species, compounds)?

Response: *Many thanks for your valuable suggestion. The vague expression has been revised to clearly state improvements in soil nutrients, microbial abundance and diversity, and metabolite composition.* ***Revisions are as follows:*** *"This study evaluated the effects of vegetable, corn, and peach cultivation on soil physicochemical properties, bacterial communities, and rhizosphere metabolites during abandoned cropland reclamation in subtropical regions of China. All three plant cultivation regimes increased soil available phosphorus (AP), available potassium (AK, except peach), and microbial biomass carbon (MBC), enhanced rhizosphere bacterial diversity, and significantly altered soil metabolite profiles. The slight soil organic matter content (OMC) decline under peach cultivation reflects a stoichiometric trade-off: enhanced microbial mineralization stimulated by root activities converted recalcitrant organic carbon into available* *nutrients, improving soil functionality despite mildly lower total organic matter. Overall, vegetable cultivation most comprehensively improved soil nutrients, microbial abundance and diversity, and metabolite composition, making it the optimal choice for reclaiming degraded abandoned cropland in this region."*

Point 14: L32-33 this sentence is not complete. Also, why focus on one vegetation type? Why not a mixture, or several types that is spread over the landscape in a mosaic?

Response: *Many thanks for your valuable suggestion.* ***The sentence has been revised into*** *"To screen suitable plant species for the reclamation of degraded abandoned cropland (long-term uncultivated, weed-infested farmland with poor soil structure and fertility) in subtropical regions of China, a three-year field experiment was conducted to assess the effects of vegetables, corn, and peach cultivation on soil physicochemical properties, bacterial communities, and rhizosphere metabolites".*

In addition, we focused on monoculture species mainly because most reclaimed farmlands in China are currently used for large-scale intensive agricultural production for economic benefits, wherein single crops (e.g., vegetables, corn, fruit trees) are generally cultivated in large contiguous areas rather than mixed or mosaic planting patterns. Therefore, we selected representative single plant species to better reflect actual field production conditions.

Point 15: L34-35: reclaimed from what? What were they before? What is the degradation like?

Response: *Many thanks for your valuable question.* ***We have clarified the background of the study site as*** *"To screen suitable plant species for the reclamation of degraded abandoned cropland (long-term uncultivated, weed-infested farmland with poor soil structure and fertility) in subtropical regions of China."*

Point 16: L40-42, you need to tell something before about the situation in the control so readers can put these effects in context.

Response: *Many thanks for your valuable suggestion. We have added a clear description of the control condition, which represents the original unmanaged abandoned cropland with no planting, no fertilization and no anthropogenic disturbance, serving as a realistic baseline to contextualize the effects of different planting treatments.* ***Revisions are as follows:*** *"Compared with the unplanted bare fallow control (representing the original unmanaged abandoned cropland without planting, fertilization, or anthropogenic disturbance)."*

Point 17: L45-47: you start with talking about relative abundances, but the evidence you give is about overall diversity levels. Please make consistent. And add some comma's in the right places to help your reader.

Response: *Many thanks for your valuable suggestion. We have revised the text to align descriptions of bacterial diversity and relative abundance and added appropriate commas for readability.* ***The revised sentence reads:*** *"all three plant cultivation regimes elevated soil bacterial diversity, with operational taxonomic unit (OTU) richness, Chao1 and Shannon indices increasing by 6.21–10.54%, 6.22–10.53%, and 2.30–3.11%, respectively."*

Point 18: L47: redundancy discriminant analysis (RDA), RDA in the literature stands for Redundancy Analysis, what the discriminant is doing in your term is unclear to me. You have linear discriminant analysis (LDA) or redundancy analysis (RDA) – mathematically related approaches, but with a different objective. From the figure I think you did RDA.

Response: *Many thanks for your carefulness. The term has been corrected to redundancy analysis (RDA) throughout the manuscript, and* ***the sentence has been revised to*** *"Redundancy analysis (RDA) demonstrated close linkages between soil properties and bacterial community structure."*

Point 19: L51 I don't think the 'while' is appropriate here, it suggests something else is coming. While we observed X, we also saw Y.

Response: *Many thanks for your valuable suggestion. The inappropriate conjunction has been removed, and* ***the sentence has been revised to*** *"liquid chromatography-mass spectrometry (LC-MS) analysis identified 130 significant differential metabolites (SDMs) between vegetable-cultivated soil and the control, including organic acids, amino acids, and heterocyclic compounds. The top 20 SDMs were strongly correlated with seven dominant bacterial genera."*

Point 20: L122 what do you mean with 'site' here? How many sites were there? How far apart? Differences in slope, rainfall, etc?

Response: *Many thanks for your valuable question. The term "site" refers to the experimental plots in this study. A total of 20 plots were established within a 1 ha area, including four treatments (vegetable, corn, and peach cultivation, and bare fallow control) with five replicates per treatment. All plots shared uniform slope and environmental conditions under a subtropical monsoon climate (mean annual temperature 17.8°C, mean annual precipitation 1454 mm).* ***The revised sentence reads:*** *"The site has a subtropical monsoon climate with a mean annual temperature of 17.8°C* *and mean annual precipitation of 1454 mm, with uniform slope and environmental conditions across the experimental area. A total of 20 experimental plots were established within a 1 ha area, comprising four treatments (vegetable, corn, and peach cultivation, and bare fallow control) with five replicates per treatment."*

Point 21: L123-125: I want to see what the variation is in these base variables.

Response: *Many thanks for your valuable suggestion.* ***We have added the initial variation ranges of the basic soil variables as follows:*** *"Before the experiment, five soil samples were collected using a 5-point sampling method to determine initial physicochemical properties: pH 7.86 (7.45–8.20), OMC 6.93 g kg-1 (6.51–7.62 g kg-1, equivalent to 0.65%–0.76% with an average of 0.69%), TN 0.42 g kg-1 (0.12–0.71 g kg-1), AP 12.30 mg kg-1 (11.70–12.70 mg kg-1), and AK 378.70 mg kg-1 (371.61–387.74 mg kg-1)."*

Point 22: L127: change the word restoration here to planting/sowing or so (what fits), because you don't know if the treatment will not restore anything, so while it is the goal, you cannot be sure that it does what you think until you tested it.

Response: *Many thanks for your valuable suggestion. We have removed the term "restoration" and revised the relevant description to focus on the actual planting treatments,* ***as follows****: "Four treatments were applied on land reclaimed from abandoned croplands (previously cultivated but left uncultivated for eight years, with widespread weeds and degraded soil): (1) vegetable cultivation with two successive crops in a single year (cv. "Heixiaopang", a leafy vegetable, grown October–March, obtained from Qingdao North-South Seed Industry Co., Ltd., Qingdao, China; cv. "Hangqie 2022", eggplant, grown April–September, provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (2) corn cultivation (cv. "Qianjiangnuo 3", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (3) peach cultivation (cv. "Zhongtao 5", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); and (4) unplanted bare fallow was used as the control (Figure 1a–d). Each plot was 25 m × 5 m (125 m^2). Planting densities were 25 cm × 25 cm for leafy vegetables, 40 cm × 50 cm for eggplant, 30 cm × 50 cm for corn, and 4 m × 5 m for peach trees. For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented* *the unmanaged baseline condition of abandoned farmland. All other management practices, including tillage and irrigation, followed local conventional farming practices."*

Point 23: L127-8 describe this newly reclaimed cropland.

Response: *Many thanks for your valuable suggestion.* ***A detailed description of the study land has been added****: "land reclaimed from abandoned croplands (previously cultivated but left uncultivated for eight years, with widespread weeds and degraded soil)".*

Point 24: L130-131 okay so you have a compound treatment, combining plant species and fertilizer application in one combined measure. Can you rescale the amounts of fertilizer to equivalent per hectare? Also, can you give a sense of the N-input thus realized?

Response: *Many thanks for your valuable suggestion. All fertilizer rates have been converted to per-hectare units, and the annual N input (2.63 t ha^{-1} yr^{-1}) has been added for all planted treatments.* ***As revised into*** *"For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented the unmanaged baseline condition of abandoned farmland."*

Point 25: L133 what is in the compound fertilizer? Please give NPK amouns, and micronutrients if included.

Response: *Many thanks for your valuable suggestion.* ***The compound fertilizer had an $N:P_2O_5:K_2O$ ratio of 15:15:15 with no additional micronutrients, which has been clearly stated in*** *" compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1})."*

Point 26: L136: the control was sampled to the same depth? Now it reads a bit confusing, I know in the control there is no root zone, but we need to be sure you used the same setup.

Response: *Many thanks for your carefulness. The sampling depth was consistently 5–20 cm for both planted treatments and the bare fallow control, which has been clarified in the manuscript.* ***The revised sentence as follows:*** *"approximately 1.0 kg of fresh soil per replicate was sampled from the rhizosphere of plants (5–20 cm soil layer) using a sterile shovel and packed in sterile bags; the same 5–20 cm soil depth was used for the bare fallow control".*

Point 27: L138: what do you mean with quickly? 1h, 1day, 1 week? Make precise.

Response: *Many thanks for your carefulness.* ***The vague description has been replaced with a precise timescale:*** *"all soil samples were transported to the laboratory in an ice box within two hours."*

Point 28: L165: what do you mean with 'clean read'.

Response: *Many thanks for your carefulness. The term "clean read" was an informal description of high-quality filtered sequences that may have caused ambiguity. We have removed this vague expression and replaced it with a detailed, standardized bioinformatic pipeline for PacBio SMRT sequencing data processing,* ***as shown in*** *"To ensure data quality, subreads from raw sequencing data were preprocessed using SMRT Link (v8.0) to remove low-quality reads (minPasses < 5, minPredictedAccuracy < 0.9), and then generate CCS. CCS reads were demultiplexed using lima (v1.7.0), and those lacking primer sequences or with lengths outside the range of 1200–1650 bp were removed using Cutadapt (v2.7). After removing chimeric sequences using USEARCH (v10), high-quality CCS reads were clustered into OTUs at a 97% similarity threshold using USEARCH (v10). This 97% threshold is a widely accepted standard for PacBio full-length 16S rRNA sequencing in soil microbial ecology, enabling reliable comparisons with related studies. Compared with ASV clustering, OTU clustering at 97% similarity is more robust for long-read data, minimizing false rare taxa and excessive splitting from sequencing errors. All 20 samples (four treatments with five biological replicates each) were sequenced in a single batch on the PacBio Sequel II platform to minimize batch effects. Taxonomic annotation was performed against the SILVA Release 138 database using the RDP classifier (Edgar, 2013, 2016; Quast et al., 2012)."*

Point 29: L429: also here the sentence after 'while' seems unfinished, the greater what was observed?

Response: *Many thanks for your carefulness.* ***The incomplete and unclear expression has been revised to*** *"Zheng et al. (2020) showed that vegetation restoration increased OTUs, Chao1, and Shannon indices, and the greater increase was observed during the initial seven years."*

Point 30: L431: what is ACE?

Response: *Many thanks for your carefulness. ACE stands for Abundance-based Coverage Estimator, which is a commonly used index of soil bacterial alpha diversity. The full name has* *been supplemented in the manuscript for clarity, as follows: "Zheng et al. (2022) revealed that different plant species restoration strategies (grassland, cropland, and plantation forest) on degraded land significantly increased OTU richness, Abundance-based Coverage Estimator (ACE), and Chao1 indices, resulting in shifts in bacterial phyla favoring Actinobacteriota, Proteobacteria and Acidobacteriota."*

Point 31: L447: please write out Ras here and elsewhere.

Response: *Many thanks for your carefulness. All RAs has been spelled out as relative abundances throughout the manuscript for clarity and consistency.*

Point 32: L461: "The improvement of microbes in soil quality" I don't get what you mean here. Please clarify.

Response: *Many thanks for your carefulness. The ambiguous expression has been revised for clarity.* ***The sentence is updated to:*** *"The contribution of microbes to soil quality may be mainly attributed to a total of 17 bacterial biomarkers".*

Point 33: L463-471 how likely is it that the strains you found in your plots, do the same as other members of their genus/family in another location?

Response: *Many thanks for your valuable suggestion. In microbial ecology, bacterial taxa within the same genus or family generally possess functionally conserved ecological roles across different habitats and regions. On this basis, we infer that the taxa identified in this study may perform similar functions as those reported in other areas. We have clarified this reasoning in the manuscript, and acknowledged that further functional verification is still required in future research.* ***As revised in*** *"The contribution of microbes to soil quality may be mainly attributed to the 17 bacterial biomarkers identified across all soil samples in this study. Given that bacterial taxa within the same lineage generally possess functionally conserved ecological roles across habitats and regions, the key taxa identified here may exert similar beneficial roles as those documented in other areas."; "Further experimental evidence (e.g., microbial isolation and targeted metabolite assays) would be required to confirm genuine functional interactions between soil bacteria and metabolites."*

Point 34: L498: what is FA and GP.

Response: *Many thanks for your carefulness. The abbreviations FA and GP have been spelled out as fatty acids (FA) and glycerophospholipids (GP) at their first occurrence in the manuscript for* *clarity.* ***The revised sentence reads:*** *"These differential metabolites identified in soils treated with three different plant species could be grouped into seven main categories: organic acids, benzenoid compounds, fatty acids (FA), heterocyclic compounds, amino acids, glycerophospholipids (GP), and carbohydrates."*

Point 35: L502-504: but do they have a function in the soil itself?

Response: *Many thanks for your valuable suggestion. We have supplemented detailed descriptions to clarify the functions of these differential metabolites in soil ecosystems and added relevant supporting references. We now clearly state that these metabolites are involved in regulating soil physicochemical properties, driving shifts in the soil microbiome, mediating soil nutrient cycling, and providing available carbon and nitrogen sources for soil microorganisms.* ***The corresponding revisions have been made in*** *"To avoid lumping heterogeneous metabolite classes, we further clarify their specific roles. Organic acids mediate soil physicochemical properties, and promote plant growth and biomass accumulation (Sindhu et al., 2022). Benzenoid compounds act as important signaling molecules and carbon substrates in soil ecosystems, rather than toxic contaminants. Heterocyclic compounds in organic amendments drive shifts in the soil microbiome and enhance microbial utilization efficiency of straw-derived carbon (Li et al., 2023b). Amino acids act as crucial labile sources of soil organic nitrogen, supporting soil nutrient cycling and plant nitrogen acquisition (Cao et al., 2016). Carbohydrates provide readily available carbon sources for soil microbial activity, thereby facilitating the mineralization of soil mineral nutrients (Ratnayake et al., 2013)."*

Point 36: L518: write out AK too. Okay, and is that study relevant in this case? I don't know it, but context matters hugely, so be careful with extrapolations.

Response: *Many thanks for your valuable suggestion.* ***The abbreviation AK has been spelled out as available potassium in*** *"Jiang et al. (2024) further confirmed that soil acidity, soil organic carbon, total nitrogen, moisture, available potassium, and microbial biomass carbon were key drivers of soil bacterial community dynamics during forest succession in the karst region of southwest China.".* ***Additionally, we have supplemented contextual explanations to clarify the relevance of the cited studies****: specifically, we emphasized that while these studies were conducted in geographically distinct ecosystems (e.g., southeastern Australia's large-scale transect and southwest China's karst forest), they collectively highlight that soil nutrient availability and physicochemical properties are universal drivers of bacterial community assembly. This alignment with our core findings validates the rationality of the citations and avoids excessive extrapolation.*

Point 37: L505: essential is too strong in my opinion, plants can also grow on mineral nitrogen.

Response: *Many thanks for your valuable suggestion. We agree with your point that "essential" was too strong, as plants can indeed utilize mineral nitrogen.* ***The original sentence has been revised to*** *"Amino acids act as crucial labile sources of soil organic nitrogen, supporting soil nutrient cycling and plant nitrogen acquisition."*

Point 38: L523: what do you mean by connection here, I assume correlation? Or do you infer a functional dependence? Does microbe A produce compound X? if the latter, you need stronger evidence then an RDA or heatmap.

Response: *Many thanks for your carefulness. We agree that the original term "connection" was ambiguous.* ***It has been revised to*** *"Results indicated that seven bacterial genera (unclassified_A4b, Bacillus, MND1, uncultured_Gammaproteobacterium, Subgroup_10, unclassified_Vicinamibacteraceae, and unclassified_Vicinamibacterales) exhibited significant correlations with multiple soil metabolites" to clarify that we are describing statistical associations identified via correlation heatmaps, not inferring functional dependence or causal relationships (e.g., microbial production of specific compounds).* ***We have also added a brief note in the discussion to emphasize that further experimental evidence (e.g., microbial isolation and targeted metabolite assays) would be needed to confirm functional links between soil bacteria and metabolites in*** *"We acknowledge that abiotic factors (e.g., soil texture, pH), fertilization regimes, and rhizodeposition may confound these correlations. These observed relationships represent statistical correlations rather than definitive functional links; further experimental evidence (e.g., microbial isolation and targeted metabolite assays) is required to confirm genuine functional interactions between soil bacteria and metabolites. Nevertheless, our RDA and heatmap results collectively highlight the dominant role of plant species in shaping these soil attributes during reclamation."*

Point 39: L525: what do you mean with CAR and FFA? Write out.

Response: *Many thanks for your carefulness. Actually, the abbreviations CAR and FFA have been spelled out in full in the manuscript. They are clarified as* ***constitutive androgen receptor agonists*** *and* ***free fatty acids****, respectively, to eliminate ambiguity.*

Point 40: L550: Vicinamibacterales is a family, not a genus. Check the others too and correct mistakes. Is A4b a complete name?

Response: *Many thanks for your carefulness. We have carefully checked and corrected all taxonomic classification errors throughout the manuscript. Vicinamibacterales is an order rather than a genus or family, and its taxonomic rank has been uniformly annotated correctly.* ***The corresponding bacterial taxa are revised to****: "unclassified Vicinamibacterales, uncultured Gammaproteobacterium, unclassified Vicinamibacteraceae, and unclassified A4b.". A4b is a well-recognized subordinate taxon in public microbial databases, affiliated with the class Anaerolineae. All other taxonomic names have also been verified and revised accordingly.*

Point 41: L552: identified as what?

Response: *Many thanks for your valuable suggestion. We have revised the conclusion section to clearly specify what the findings and recommended reclamation mode are identified,* ***as follows:*** *"This three-year field experiment revealed that planting vegetables, corn, and peach all effectively facilitated the ecological reclamation of degraded abandoned cropland in subtropical regions of China, among which vegetable cultivation exerted the most comprehensive and optimal effect on soil quality improvement. Vegetable cultivation systems significantly elevated soil bacterial diversity, community complexity, functional stability, and selectively enriched key bacterial taxa closely associated with soil nutrient cycling. Meanwhile, rhizosphere metabolic profiles were substantially reshaped, with abundant significant differential metabolites involved in amino acid metabolism, carbon turnover, and rhizosphere signaling. Notably, amino acid derivatives, pyridine derivatives and small peptides were strongly correlated with keystone bacterial genera, forming tight metabolite-microbe coordination patterns. The coordinated variations in soil physicochemical properties, bacterial communities, and metabolites collectively enhanced soil nutrient availability and ecological functions. This study elucidates the underlying mechanisms of plant-mediated soil amelioration during abandoned cropland reclamation, and verifies that vegetable-based reclamation represents a feasible strategy integrating ecological effectiveness, agronomic practicality, and economic benefits for local farmers. These results not only provide a scientific basis and practical guidance for the ecological reclamation and sustainable utilization of degraded abandoned croplands in subtropical regions of China, but also offer valuable insights for similar subtropical degraded land restoration globally."*

Point 42: L526: there is not one organic acid, nor one nucleotide – including derivatives these seem like large heterogenous groups to talk about, is it meaningful to lump them?

Response: *Many thanks for your valuable suggestion. To avoid grouping highly heterogeneous metabolite classes, we have refined the description and removed overly broad categories such as organic acids and nucleotides.* ***The relevant sentence has been revised to:*** *"exhibited significant* *correlations with soil metabolites including amino acid derivatives, benzene and substituted derivatives, bile acids, constitutive androgen receptor agonists, and free fatty acids."*

Point 43: Fig 1. Please add a picture of the control. When were photos taken and the data, how many years into the study is this?

Response: *Many thanks for your valuable suggestion. Photographs of all experimental plots, including the unplanted bare fallow control, were taken in September 2024, three years after the initiation of the experiment, on the same day as soil sample collection. A detailed description including the control treatment, photograph date, sampling time and experimental duration has been added to the caption of Figure 1.* ***Revisions are as follows:*** *"Figure 1. Field photographs of the three planting regimes and the unplanted bare fallow control. (a) vegetables; (b) corn; (c) peach; (d) control, and box-and-whisker plots showing the distribution of observed bacterial OTUs (e), Chao1 richness (f), and Shannon diversity (g) indices of soil bacterial communities across the four treatments during abandoned cropland reclamation. Significant differences ($p < 0.05$) are indicated by different lowercase letters above the boxes. V, vegetables; C, corn; P, peach; CK, control. All photographs were taken in September 2024, three years following the initiation of the field experiment and on the same day that soil samples were collected. No plants were cultivated and no fertilizer was applied in the control treatment."*

Point 44: Table 2. it is unclear what the values represent? Community composition quantified how, in what units? Is the post-hoc analysis done across the table, or can I only look across columns, or rows?

Response: *Many thanks for your valuable suggestion. Table 2 presents the number of soil bacterial taxa at phylum, class, order, family, and genus levels across the four treatments. Post-hoc multiple comparisons were conducted within each row (i.e., among the four treatments for the same bacterial taxonomic level), with significant differences indicated by different lowercase letters. The details regarding the meaning of the values, quantification method, and post-hoc comparison rules have been added to the caption of Table 2.* ***Revisions are as follows:*** *"Table 2. Effects of four experimental treatments on the number of soil bacterial taxa across different taxonomic levels during soil reclamation.", "Values are presented as mean ± standard error. Post-hoc multiple comparisons were conducted within each row (among the four treatments for the same bacterial taxonomic level), with significant differences indicated by different lowercase letters. Values represent the number of bacterial taxa identified at each taxonomic level (phylum, class, order, family, genus) across the four treatments."*

Point 45: Fig. 3. In b that's not only genus level, it's a mix of taxonomic levels. Please correct this.

Response: *Many thanks for your carefulness. We have checked the taxonomic annotations in Fig. 3b and corrected the mixed levels, unifying them strictly to the genus level as originally intended. The updated figure is included in the revised manuscript.* ***The corresponding figure caption has been revised to:*** *"Figure 3. Stacked bar plots showing the relative abundances of soil bacterial communities at the phylum (a) and genus (b) levels across the four treatments during soil reclamation. V, vegetables; C, corn; P, peach; CK, control."*

Point 46: Fig 4. In b the rendering is way to small to make any sense of whats in the data.

Response: *Many thanks for your valuable suggestion. The original heatmap in Fig. 4a (showing the relative abundance of dominant bacterial taxa at the family level) has been removed. The Linear discriminant analysis Effect Size (LEfSe) plot illustrating bacterial biomarker taxa has been redrawn, enlarged, and optimized in layout and font size to ensure all data elements are clearly legible. The revised high-resolution figure is included in the updated manuscript.* ***The corresponding figure caption has been revised to:*** *"Figure 4. Cladogram generated from Linear discriminant analysis Effect Size (LEfSe) showing significantly enriched soil bacterial taxa across the four treatments. Only taxa with LDA scores > 4 ($p < 0.05$) are presented. V, vegetables; C, corn; P, peach; CK, control."*

Point 47: Fig. 5. OPLS-DA is an abbreviation for orthogonal partial least squares discriminant analysis, not what you call it. Is it the same technique or not? If so, please use the common term. How do you read that donut plot? Is it a relative abundance visualization or something else? If the former, can you switch to stacked barchart, its easier to see the pattern. If the latter, more guidance on how to read the result is needed.

Response: *Many thanks for your carefulness. We have corrected the full name of OPLS-DA to the standard terminology orthogonal partial least squares discriminant analysis throughout the manuscript. In addition, since the panel represents relative abundance, the original donut plot in Fig. 5d has been replaced with a stacked bar chart to make the compositional patterns clearer and easier to interpret.* ***Revisions are as follows:*** *"Figure 5. Orthogonal partial least squares discriminant analysis (OPLS-DA) score plots of soil metabolites comparing the vegetable, corn, and peach cultivation treatments with the unplanted control, respectively (a–c). Stacked bar plot showing the relative proportion of identified soil metabolite classes (d). Volcano plots of* *significantly differentially metabolites (SDMs) in V vs control (e), C vs control (f), and P vs control (g). Each point represents a metabolite, with red indicating upregulation, green indicating downregulation, and gray indicating no significant difference. Only metabolites with variable importance in projection (VIP) > 1 and p < 0.05 were defined as SDMs. V, vegetables; C, corn; P, peach; CK, control."*

Point 48: Fig. 6. What is VIP here? The labels and plots are too small to read, Improve the readability.

Response: *Many thanks for your valuable suggestion. VIP stands for Variable Importance in Projection, and we have added this definition to the figure caption for clarity.* ***Revisions are as follows:*** *"Figure 6. Variable importance in projection (VIP) plots showing the top 20 significantly differential metabolites (SDMs) with the highest VIP scores in V vs control (a), C vs control (b), and P vs control (c). Red dots represent upregulated metabolites, and green dots represent downregulated metabolites. V, vegetables; C, corn; P, peach." In addition, the fonts, labels and overall layout of Figure 6 have been enlarged and optimized to greatly improve readability.*

Point 49: Fig. 7. Typically RDA stands for Redundancy analysis. I don't know what Redundancy discriminant analysis is, I don't think it exists, unless you mean Linear Discriminant Analysis? But the plot suggests classic RDA was used. Please fix for clarity. Please spell out the abbreviations for soil abiotic variables at first mention. What is SDM, please write out?

Response: *Many thanks for your valuable suggestion. We have corrected the terminology to Redundancy analysis (RDA) and removed the incorrect "discriminant" wording throughout the manuscript and figure caption. Additionally, the full names of all soil abiotic variables and the abbreviations SDMs (significant differential metabolites) have been spelled out at their first mention in both the text and the figure caption for clarity.* ***Revisions are as follows:*** *"Figure 8. Redundancy analysis (RDA) of genus-level soil bacterial community composition in relation to soil physicochemical properties. Red arrows indicate the direction and magnitude of soil physicochemical properties (pH, soil bulk density (SBD), organic matter content (OMC), total nitrogen (TN), available phosphorus (AP), available potassium (AK), and microbial biomass carbon (MBC)), while blue arrows represent the associated bacterial genera. Sub10: Subgroup_10; Vice: unclassified_Vicinamibacteraceae; Vics: unclassified_Vicinamibacterales; Pro: uncultured_Gammaproteobacterium; Bac: Bacillus; Gem: unclassified_Gemmatimonadaceae; unB: unclassified_Bacteria. V, vegetables; C, corn; P, peach; CK, control."*

Reviewer 2

The manuscript describes an investigation of vegetation restoration on soil physicochemical and microbial properties in newly reclaimed croplands in China. The authors applied many analytical techniques to their soil samples to identify the appropriate vegetation for the management of reclaimed soils. However, their presentation quality and the way they present the results are far from the publication standards. Moreover, their descriptions of the investigated field and experimental design are substantially insufficient for the standard. For example, the initial conditions of their soils and fields are very unclear. Their descriptions of soil physiochemical properties in L120-L125 and Table 1 are totally different. Such contradictions and insufficient description of the methodology make it difficult for us to derive meaningful insights from the manuscript and the investigation. Whereas the authors claimed the vegetable was likely the best vegetation for reclaimed croplands, the fertilization and management systems, and consequently the difficulties and economic benefits for farmers, should be fundamentally different among cultivated vegetations. This means it is substantially insufficient for comparing soil properties across different vegetative cultivation methods to find the best one.

Response: *Many thanks for your valuable and constructive comments, which are crucial for improving the quality of our manuscript. We fully agree with your suggestions and have carefully addressed all the issues raised, with detailed revisions as follows:*

1) Insufficient description of the study site and experimental design, and unclear initial soil conditions

We have substantially supplemented the descriptions of the study site and experimental design in the Methodology section (section 2). Specifically, we added the detailed initial soil physicochemical properties (including soil type, pH, soil organic matter, total nitrogen, available phosphorus, available potassium) before the experiment started, as well as the basic information of the experimental field (location, altitude, climate conditions, previous land use history, and plot size). All these details are presented clearly to ensure the reproducibility of the study, as follows: "The experiment was conducted from September 2021 to September 2024 at the Zhijiang Base of Hangzhou Academy of Agricultural Sciences in Zhejiang Province, China (30°9'12" N; 119°5'36" E; 6 m above sea level). The site has a subtropical monsoon climate with a mean annual temperature of 17.8°C and mean annual precipitation of 1454 mm, with uniform slope and environmental conditions across the experimental area. A total of 20 experimental plots were established within a 1 ha area, comprising four treatments (vegetable, corn, and peach cultivation, and bare fallow control) with five replicates per treatment. The top 0–20 cm soil was classified as *sandy loam according to the USDA soil taxonomy. Before the experiment, five soil samples were collected using a 5-point sampling method to determine initial physicochemical properties: pH 7.86 (7.45–8.20), OMC 6.93 g kg-1 (6.51–7.62 g kg-1, equivalent to 0.65%–0.76% with an average of 0.69%), TN 0.42 g kg-1 (0.12–0.71 g kg-1), AP 12.30 mg kg-1 (11.70–12.70 mg kg-1), and AK 378.70 mg kg-1 (371.61–387.74 mg kg-1).*

Four treatments were applied on land reclaimed from abandoned croplands (previously cultivated but left uncultivated for eight years, with widespread weeds and degraded soil): (1) vegetable cultivation with two successive crops in a single year (cv. "Heixiaopang", a leafy vegetable, grown October–March, obtained from Qingdao North-South Seed Industry Co., Ltd., Qingdao, China; cv. "Hangqie 2022", eggplant, grown April–September, provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (2) corn cultivation (cv. "Qianjiangnuo 3", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (3) peach cultivation (cv. "Zhongtao 5", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); and (4) unplanted bare fallow was used as the control (Figure 1a–d). Each plot was 25 m × 5 m (125 m^2). Planting densities were 25 cm × 25 cm for leafy vegetables, 40 cm × 50 cm for eggplant, 30 cm × 50 cm for corn, and 4 m × 5 m for peach trees. For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented the unmanaged baseline condition of abandoned farmland. All other management practices, including tillage and irrigation, followed local conventional farming practices.

In September 2024 (after three years of planting), approximately 1.0 kg of fresh soil per replicate was sampled from the rhizosphere of plants (5–20 cm soil layer) using a sterile shovel and packed in sterile bags; the same 5–20 cm soil depth was used for the bare fallow control. In addition, soil cores were collected from each plot using a stainless-steel cylinder (5 cm height, 100 cm3 volume). All soil samples were transported to the laboratory in an ice box within two hours for subsequent analysis."

2) Contradictions between the descriptions of soil physicochemical properties in L120-L125 and Table 1

We have carefully checked and verified the descriptions in Lines 120–125 and the data in Table 1. The values reported in Lines 120–125 represent the initial soil physicochemical properties before the experiment, whereas Table 1 shows the corresponding properties after three years of *cultivation treatments.* ***To eliminate confusion, we have added clear labels distinguishing "before the experiment" and "after three years" in the revised manuscript, as follows:*** *"Before the experiment, five soil samples were collected using a 5-point sampling method to determine initial physicochemical properties: pH 7.86 (7.45–8.20), OMC 6.93 g kg-1 (6.51–7.62 g kg-1, equivalent to 0.65%–0.76% with an average of 0.69%), TN 0.42 g kg-1 (0.12–0.71 g kg-1), AP 12.30 mg kg-1 (11.70–12.70 mg kg-1), and AK 378.70 mg kg-1 (371.61–387.74 mg kg-1)".* ***The title of Table 1 has been revised to:*** *"Table 1 Impacts of cultivating three cultivation types on soil physicochemical properties in degraded abandoned cropland after three years."*

3) Insufficient methodological descriptions affecting the interpretation of results

We have expanded the Methodology section (section 2) to supplement the detailed operation procedures of all analytical techniques (e.g., soil physicochemical property determination methods, 16S rRNA gene sequencing process, metabolomic detection protocols), as well as the specific parameters and quality control standards of each technique. We also clarified the data processing and statistical analysis methods to ensure that the research process is transparent and the results are credible. ***Revisions are as follows:*** *"2.1. Experimental design and sample collection: The experiment was conducted from September 2021 to September 2024 at the Zhijiang Base of Hangzhou Academy of Agricultural Sciences in Zhejiang Province, China (30°9'12" N; 119°5'36" E; 6 m above sea level). The site has a subtropical monsoon climate with a mean annual temperature of 17.8°C and mean annual precipitation of 1454 mm, with uniform slope and environmental conditions across the experimental area. A total of 20 experimental plots were established within a 1 ha area, comprising four treatments (vegetable, corn, and peach cultivation, and bare fallow control) with five replicates per treatment. The top 0–20 cm soil was classified as sandy loam according to the USDA soil taxonomy. Before the experiment, five soil samples were collected using a 5-point sampling method to determine initial physicochemical properties: pH 7.86 (7.45–8.20), OMC 6.93 g kg-1 (6.51–7.62 g kg-1, equivalent to 0.65%–0.76% with an average of 0.69%), TN 0.42 g kg-1 (0.12–0.71 g kg-1), AP 12.30 mg kg-1 (11.70–12.70 mg kg-1), and AK 378.70 mg kg-1 (371.61–387.74 mg kg-1).*

Four treatments were applied on land reclaimed from abandoned croplands (previously cultivated but left uncultivated for eight years, with widespread weeds and degraded soil): (1) vegetable cultivation with two successive crops in a single year (cv. "Heixiaopang", a leafy vegetable, grown October–March, obtained from Qingdao North-South Seed Industry Co., Ltd., Qingdao, China; cv. "Hangqie 2022", eggplant, grown April–September, provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (2) corn cultivation (cv. "Qianjiangnuo 3", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); (3) peach *cultivation (cv. "Zhongtao 5", provided by Hangzhou Academy of Agricultural Sciences, Hangzhou, China); and (4) unplanted bare fallow was used as the control (Figure 1a–d). Each plot was 25 m × 5 m (125 m²). Planting densities were 25 cm × 25 cm for leafy vegetables, 40 cm × 50 cm for eggplant, 30 cm × 50 cm for corn, and 4 m × 5 m for peach trees. For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented the unmanaged baseline condition of abandoned farmland. All other management practices, including tillage and irrigation, followed local conventional farming practices.*

In September 2024 (after three years of planting), approximately 1.0 kg of fresh soil per replicate was sampled from the rhizosphere of plants (5–20 cm soil layer) using a sterile shovel and packed in sterile bags; the same 5–20 cm soil depth was used for the bare fallow control. In addition, soil cores were collected from each plot using a stainless-steel cylinder (5 cm height, 100 cm3 volume). All soil samples were transported to the laboratory in an ice box within two hours for subsequent analysis.

2.2. Soil physiochemical properties measurement: To study the soil properties, about 1.0 kg of fresh soil from each plot was sampled, air-dried and passed through a 0.45-mm sieve to measure the soil pH, OMC, TN, AP, and AK. In detail, soil pH was measured in a soil suspension (soil: water = 1 g: 5 mL) using a pH meter (FE28, Mettler Toledo, Zurich, Switzerland), while the OMC, TN, AP, and AK contents were determined using the K2Cr2O7 oxidation method, Kjeldahl distillation-titration method, molybdenum-based colorimetric method, and flame photometer method, respectively (Brookes et al., 1985). Furthermore, SBD was calculated using the oven-drying method, while MBC was determined in fresh soil samples using the fumigation-extraction method (Vance et al., 1987; McLaren and Cameron, 1990).

2.3. Soil bacterial 16S rRNA high-throughput sequencing analysis: About 2 g of fresh soil from each plot was sampled for 16S rRNA gene high-throughput sequencing. In detail, DNA was extracted from soil samples using the E.Z.N.ATM Mag-Bind Soil DNA Kit (OMEGA, Norcross, GA, USA) and assessed using a NanoDrop (ND-1000) spectrophotometer (Thermo Fisher Scientific, USA). PCR amplification of the full-length bacterial 16S rRNA gene was performed using the universal primers 27F and 1492R (5′–AGAGTTTGATCMTGGCTCAG–3′; 5′–TACGGYTACCTTGTTACGACTT–3′, respectively) (Weisburg et al., 1991). The PCR components included ddH2O (12 μL), 2×Hieff® Robust PCR Master Mix (15 μL), 10 μM forward *and reverse primers (1 μL each), and DNA template (1 μL). The PCR thermal cycling protocol consisted of an initial denaturation at 94℃ for 3 min, followed by 25 cycles of denaturation at 94℃ for 30 s, annealing at 55℃ for 30 s, and extension at 72℃ for 1 min, with a final extension at 72℃ for 5 min. PCR products were purified using Hieff NGSTM DNA selection beads (Yeasen, Shanghai, China) and subjected to circular consensus sequencing (CCS) on a PacBio Sequel II platform (Tsingke Biotechnology Co., Ltd., Hangzhou, China).*

To ensure data quality, subreads from raw sequencing data were preprocessed using SMRT Link (v8.0) to remove low-quality reads (minPasses < 5, minPredictedAccuracy < 0.9), and then generate CCS. CCS reads were demultiplexed using lima (v1.7.0), and those lacking primer sequences or with lengths outside the range of 1200–1650 bp were removed using Cutadapt (v2.7). After removing chimeric sequences using USEARCH (v10), high-quality CCS reads were clustered into OTUs at a 97% similarity threshold using USEARCH (v10). This 97% threshold is a widely accepted standard for PacBio full-length 16S rRNA sequencing in soil microbial ecology, enabling reliable comparisons with related studies. Compared with ASV clustering, OTU clustering at 97% similarity is more robust for long-read data, minimizing false rare taxa and excessive splitting from sequencing errors. All 20 samples (four treatments with five biological replicates each) were sequenced in a single batch on the PacBio Sequel II platform to minimize batch effects. Taxonomic annotation was performed against the SILVA Release 138 database using the RDP classifier (Edgar, 2013, 2016; Quast et al., 2012).

2.4. Soil liquid chromatography-mass spectrometry (LC-MS) analysis: About 2 g of fresh soil from each plot was sampled for metabolomics assay. In detail, 250 mg of each soil sample was added into 500 μl extract solution (methanol: H_2O = 7: 3), vortexed at 35 Hz for 3 min, sonicated for 10 min in an ice-water bath, and incubated at -20℃ for 30 min. After centrifugation at 12,000 rpm for 10 min (4℃) and filtering using 0.22 μm PTFE filter, the supernatant was transferred into a brown glass vial for LC-MS analysis. The HPLC conditions were set as follows: chromatographic column: Waters ACQUITY Premier HSS T3 column (1.8 μm, 2.1 mm × 100 mm); mobile phase A: 0.1% formic acid in water; mobile phase B: 0.1% formic acid in acetonitrile; gradient program: 5 to 20% B in 2 min, increased to 60% B in the following 3 min, then increased to 99% B in 1 min, and held for 1.5 min, followed by returning to 5% B within 0.1 min and holding for 2.4 min; column temperature: 40℃, flow rate: 0.4 mL min $^{-1}$; injection volume: 4 μL. The ESI source conditions of Q Exactive HF-X were set as follows: ion spray voltage, 3.5 KV (positive) or 3.2 KV (negative), respectively; sheath gas, 30 Arb; aux gas, 5 Arb; ion transfer tube temperature, 320℃; vaporizer temperature, 300℃; scan range, 75–1000 Da; resolution, 35,000; collision energy, 30, 40, 50 V; signal intensity threshold, 1×10^6 cps; top N vs top speed, 10; exclusion duration, 3 s. The repeatability and reliability of the entire analysis process were evaluated by *inserting one quality control sample, which was prepared by pooling and mixing 10 μL of each sample. All treatments had five replicates. The data obtained in this study were converted into the mzXML format using ProteoWizard, processed with the XCMS program, and then compared with the in-house database (HMDB, http://hmdb.ca/) and KEGG, https://www.kegg.jp/) for metabolite annotation.*

2.5. Data analysis: One-way analysis of variance (ANOVA) was performed using SPSS software (v16.0, SPSS Inc., Chicago, IL, USA) to analyze significant differences among the four treatments. Chao1 and Shannon indices were calculated based on OTU data using the vegan package in R software (v4.2.1, R Foundation for Statistical Computing, Vienna, Austria) and visualized using Origin (v2022, Hampton, MA, USA) to evaluate soil bacterial abundance and alpha diversity. Principal component analysis (PCA) based on Euclidean distances was conducted to assess variation in soil bacterial community composition (Ramette, 2007). The relative abundances of the top 10 bacterial taxa at the phylum and genus levels were calculated and visualized using Origin. Linear discriminant analysis (LDA) effect size (LEfSe) was performed with default parameters to identify differentially abundant taxa among treatments (Segata et al., 2011). Furthermore, variations in rhizosphere soil metabolites under different plant treatments were analyzed using MetaboAnalyst 4.0, including orthogonal partial least squares discriminant analysis (OPLS-DA), volcano plots, variable importance in projection (VIP) scores, and KEGG pathway enrichment analysis. RDA was performed using the vegan package in R to examine the effects of soil physicochemical properties (pH, SBD, OMC, TN, AP, AK, and MBC) on soil bacterial community structure, and plotted using Origin. In addition, Spearman correlation-based heatmaps were generated using the pheatmap package in R to explore correlation patterns between SDMs and differentially abundant bacterial genera across treatments. The top 20 SDMs were screened using thresholds of VIP > 1 and $p < 0.05$ (Hollander, 1973). Hierarchical clustering was performed on both rows and columns in the correlation heatmap.

4) Insufficient consideration of fertilization, management systems, and economic benefits when concluding that vegetables are the optimal vegetation

We fully acknowledge this critical point. We have supplemented detailed fertilization and management regimes for the three planting systems, and added an analysis of their economic benefits and practical manageability based on local field investigations. This further supports our conclusion that vegetables are the optimal option for abandoned cropland reclamation. ***Revisions are as follows:*** *"This study evaluated the effects of vegetable, corn, and peach cultivation on soil physicochemical properties, bacterial communities, and rhizosphere metabolites during abandoned cropland reclamation in subtropical regions of China. All three plant cultivation* *regimes increased soil available phosphorus (AP), available potassium (AK, except peach), and microbial biomass carbon (MBC), enhanced rhizosphere bacterial diversity, and significantly altered soil metabolite profiles. The slight soil organic matter content (OMC) decline under peach cultivation reflects a stoichiometric trade-off: enhanced microbial mineralization stimulated by root activities converted recalcitrant organic carbon into available nutrients, improving soil functionality despite mildly lower total organic matter. Overall, vegetable cultivation most comprehensively improved soil nutrients, microbial abundance and diversity, and metabolite composition, making it the optimal choice for reclaiming degraded abandoned cropland in this region."*

"For vegetable and corn cultivation treatments, the 0–20 cm soil was amended with sheep manure (15 t ha^{-1}) and compound fertilizer ($N:P_2O_5:K_2O$ = 15:15:15, no micronutrients; 0.75 t ha^{-1}) before planting in early spring and autumn (twice yearly, corresponding to a total N input of 2.63 t ha^{-1} yr^{-1}). For peach cultivation, sheep manure (30 t ha^{-1}) and compound fertilizer (1.50 t ha^{-1}) were applied in early winter (once yearly, with an equivalent N input of 2.63 t ha^{-1} yr^{-1}). No fertilizer was added to the control, which represented the unmanaged baseline condition of abandoned farmland. All other management practices, including tillage and irrigation, followed local conventional farming practices."

"Furthermore, soil property improvement alone is insufficient when screening suitable plant species for the ecological reclamation of abandoned croplands. Agronomic manageability and economic benefits for local farmers must also be fully considered, which aligns with the practical goals of cropland reclamation. Under local subtropical climatic conditions, vegetable cultivation involves moderate planting difficulty, relatively simple management, a short growth cycle, and higher economic yield per unit area with a given growing period. This matches the current large-scale intensive agricultural practices in the study region, where monoculture systems are widely adopted for economic efficiency. These advantages provide strong economic incentives for farmers to adopt reclamation and remediation practices, ensuring the long-term sustainability of amelioration strategies. Therefore, combined with the observed improvements in soil physicochemical properties, microbial diversity, and metabolic function, vegetable cultivation represents not only an ecologically effective but also an economically feasible and socially acceptable ecological reclamation strategy for abandoned croplands in this subtropical region."

"This three-year field experiment revealed that planting vegetables, corn, and peach all effectively facilitated the ecological reclamation of degraded abandoned cropland in subtropical regions of China, among which vegetable cultivation exerted the most comprehensive and optimal effect on soil quality improvement. Vegetable cultivation systems significantly elevated soil bacterial diversity, community complexity, functional stability, and selectively enriched key

bacterial taxa closely associated with soil nutrient cycling. Meanwhile, rhizosphere metabolic profiles were substantially reshaped, with abundant significant differential metabolites involved in amino acid metabolism, carbon turnover, and rhizosphere signaling. Notably, amino acid derivatives, pyridine derivatives and small peptides were strongly correlated with keystone bacterial genera, forming tight metabolite-microbe coordination patterns. The coordinated variations in soil physicochemical properties, bacterial communities, and metabolites collectively enhanced soil nutrient availability and ecological functions. This study elucidates the underlying mechanisms of plant-mediated soil amelioration during abandoned cropland reclamation, and verifies that vegetable-based reclamation represents a feasible strategy integrating ecological effectiveness, agronomic practicality, and economic benefits for local farmers. These results not only provide a scientific basis and practical guidance for the ecological reclamation and sustainable utilization of degraded abandoned croplands in subtropical regions of China, but also offer valuable insights for similar subtropical degraded land restoration globally."

In summary, we have comprehensively revised the manuscript according to Reviewer 2's comments, focusing on improved presentation, clarified background and methodology, resolved data inconsistencies, and strengthened the rationality and context of our conclusions. We hope the revised manuscript now meets the publication standards of SOIL, and we sincerely appreciate your constructive guidance.