This manuscript assessed the microbial diversity of soils near a gold mine. It showed a very interesting conclusions on the influence of disturbance-induced permafrost thaw on microbial communities.

Thank you for your analysis, time, and comments. We have addressed your comments, and are confident that your efforts have strengthened the manuscript. Line numbers in our responses refer to those found in the updated manuscript. Our responses are found below, and can also be found in red in an attached pdf.

This research may provide valuable information on the possible environmental influence of permafrost thaw. However, data from six sites in this study seems actually not representative and more extensive environmental data is needed to confirm the findings. The close spacing of sampling stations may limit their representativeness.

We have better explained our justification for our sampling design in edits on lines 167-170 "Adjacent undisturbed areas were used as controls to minimize the impact of soil spatial heterogeneity, however, some underlying spatial variation cannot be fully removed." We agree that the close spacing of sampling sites may impact broader interpretations. To better express this caveat, we have made the following changes throughout the manuscript. To better frame our results in the abstract, we altered Lines 20-22 to read "These results suggest that active layer communities rapidly colonized thawed permafrost at our sample site…". We have altered a paragraph in the introduction to ensure that it is clear this study is site-specific: Lines 92-94 now read: "In this site-specific study, we assess the soil microbial community structure shifts and drivers at a locally disturbed site …". We have also altered a concluding sentence in lines 632 to 634 to read: "Six weeks of thaw following disturbance was sufficient to shift bacterial community composition, membership, and diversity in disturbed permafrost soils to become more similar to lower active layer soils at a single permafrost-affected site".

Given that the article's focus is on the relationship between environmental parameters and microorganisms, several environmental parameters were measured. However, the paper lacks figures/tables to visually present key environmental data.
Figure 2 in this manuscript directly addresses how environmental parameters differ between the soils studied. A model was created through the backward selection of critical micronutrients and soil chemical parameters, which was then visualized in Figure 2. While the model included only Mn, SOM, Ca, S, TC, NO_3-N, pH, NH_4-N, Na, Mg, and Fe, all soil chemical parameters which were measured are present in this figure in yellow boxes. The data used to populate this figure is found in Table S2 of the supplemental information. We have also updated the caption of Figure 2 to better explain the environmental parameters visualized.

Moreover, the mechanisms underlying the influence of environmental factors are not thoroughly analyzed—for example, the relationship between microbial communities and Zn mentioned in the abstract. It would be valuable to include key parameters in future research. More convincing conclusions could potentially be drawn by measuring more environmental parameters (such as measurements of soil redox potential) or conducting analyses over longer time scales.
The relationship between microbial community composition and Zn concentrations were established by fitting environmental parameters to the Bray-Curtis distances visualized in the NMDS in Figure 4. An underlying mechanism for the correlation of Zn to community composition is now discussed in Lines 572-574 "One exception within our study, the correlation of Zn to bacterial community composition, may be due to the site-specific mobilization of Zn during permafrost thaw or due to other underlying processes (Burn et al., 2025)."

While the paper's title and conclusions present interesting perspectives, they might benefit from additional supporting analysis or a more precisely framed title to accurately represent the study's scope. Thus, I think major revisions are needed. Additional specific comments are given below:

We have altered the title to read: "Bacterial community composition changes independently of soil edaphic parameters following localized permafrost disturbance".

L280-290 It is repetitive. The information has been given in the method.

This section has been integrated into the methods in the section 3.1 Field Site and Sampling Procedure.

What is the possible functional shift during your thaw experiment?

This study analysed bacterial community composition. Additional work investigating the functional shifts would require transcriptomic or direct activity measurements, some of which are forthcoming in future publications. Therefore, inferring functional shifts unfortunately resides outside the scope of the present study.

We have included a sentence in the discussion at lines 527-532 to partially address this: “Thermokarst formation as found in this study can induce anaerobic conditions, increasing acetogenic fermentation and methanogenesis (Coolen & Orsi et al., 2015). Future study into methane cycling, such as through the use of stable isotope probing of methanotrophic communities, may be particularly beneficial to understanding functional shifts in anthropogenically disturbed permafrost soils such as the ones studied here.”

Figure 5: Why does the accumulation of active layer bacterial indicator species and permafrost bacterial indicator species exceed 1?

Each indicator group is calculated independently. The proportion represents the fraction of indicator OTUs from either active layer or permafrost that are present within each surface soil. As an example, approximately 85% of active layer indicator OTUs are present in sample A, while the remaining 15% are absent. Likewise, approximately 5% of permafrost indicator OTUs are present in sample A, while 95% of them are absent within this sample. This is why the proportion exceeds 1.

This description has been added to lines 423-426 of the figure 5 caption.

What were the original differences between the communities of ABCDE before they thawed?

Unfortunately, samples before disturbance could not be obtained. To better understand how this disturbance impacted microbial communities and soil physicochemical parameters, we instead sampled along a chronosequence, from most to least disturbed. While we were unable to sample the sites before disturbance, we were able to include non-disturbed controls as a metric for comparison (sample A and core 1).

585 Have you measured gaseous geochemical parameters like methane?

This study does not include gas flux analysis, as this is forthcoming in a future study. This caveat is also addressed in a previous comment, where a sentence at lines 527-532 now reads: “Thermokarst formation as found in this study can induce anaerobic conditions, increasing acetogenic fermentation and methanogenesis (Coolen & Orsi et al., 2015). Future study into methane cycling, such as through the use of stable isotope probing of methanotrophic communities, may be particularly beneficial to understanding functional shifts in anthropogenically disturbed permafrost soils such as the ones studied here.”