Reviewer 1

1. L. 23: should the Hg have a charge?

The ionic forms are reduced to Hg^0. The ionic forms $Hg^{+2/+3}$ are not volatile, but the elemental Hg is volatile.

2. L. 78 and elsewhere: use correct notation for small subunit genes. The “S” is a unit of measure and always capitalized. Also, rRNA must be followed by “gene” when based on DNA.

Corrected

3. L. 103 and elsewhere: it is very hard to tell that the notation “MB1-6” is referring to 6 different samples. The way the MBS1-MBS4 samples are mentioned in line 94 is much easier to read. I’m the results it was very confusing that you were referring to multiple samples and hard to track the names to the figures.

MB1-6 changed to MB1-MB6 and the samples are grouped in () for convenience. The previous announcements and sequence submission follow the same nomenclature so at this point it is not advisable to rename/change it anymore.

4. L. 143: it really would be fine to leave the PCR details here.

Corrected

5. L. 212-224 and elsewhere: sulfate and nitrate are ions and must have their charges presented.

Corrected

6. L. 230-232: chao1 index is not shown in figure 4. Update figure 4 with an axis label for panel B and the caption for accuracy. Also correct the text so it matches the figure

Corrected

7. L. 235-248: I still find this section to be too strong. “Conclusively” and “replaced” are very definitive terms and I don’t think you can be that strong without temporal data. To be this strong you need to demonstrate selection. Toning down the language and “suggesting “ or “hypothesizing” conclusions will make your paper stronger while overstating your findings can be a red flag.

Corrected

8. Figure 4c: can any geochemical vectors be added? Also, consider using different shapes in your plots to make the figures colorblind accessible.

Actually, it is not possible because we don’t have reading for all of the samples.

9. L. 268 and elsewhere: where are the DEseq2 data? These should be presented in the SI at least.

Added

10. L. 270-271: why are Deltaproteobacteria mentioned twice?

Typo corrected.

11. L. 271: correct “are”

corrected

12. L. 272: why are 2 values presented for Actinobacteria? Also in this paragraph please reference the figures.
These are values per sample MBS1-MBS4. Actinobacteria values in MBS3 and MBS4 samples. corrected

13. L. 275: add respectively after group
corrected
14. L. 276: assumed is too strong, hypothesized is more appropriate
corrected
15. L. 295-296: move reference to figure after observed.
corrected
16. L. 299: “accounts” is too strong. Your data suggests this but you’re not sure because you didn’t measure succession.
corrected
17. L. 301-312: why keep these data here? In the previous version I suggested edits to this section and to move it for flow. The responses stated that the changes were made but they weren’t. If you disagree with the suggestion a response explaining why would be appreciated.
Your previous comment was 21. 302-313: the phylogenetic analysis was based on 350 bp amplicon sequences which doesn’t provide a lot of information for robust taxonomic affiliation or phylogenetic inference. Making definitive statements about an OTU being rare or a novel class/species is a big reach based on limited sequence read length.
Yes, we agree that the phylogenetic analysis is based on 350 bp but it raises important questions about reclassifying the C0119 taxa as another class of Chloroflexi rather than in *Ktedonobacteria* and general comparison between the abundant taxas at species level is not possible anywhere else. The language has been toned down to avoid any novel class/species claims.
18. L. 323: specific
corrected
19. L. 345 and 346: wondering if these are the best word choices? Does a MAG really mediate a process or encode it? Or does the MAG have genes mediating or encoding for processes? (Also applied elsewhere)
corrected
20. Figure 7: please correct the blurry and overlapping text. Also GO or Go terms?
corrected
21. Reminder to make sure gene names are italicized.
corrected
22. L. 411-412: put the element symbols in parentheses
corrected

23. L. 425: “generally, the habitats” is unclear / hanging thought. What habitats? How are you distinguishing which habitats are dominated by chemolithoautotrophs?
Added "Acid mine drainage habitats"

24. L. 339-440: I think you should expand on which taxa are known to be metal resistant in your amplifying dataset.

Expanded

25. The paper is still missing comparisons to other mining affected systems. It would be valuable to know how often their key organisms are found in other heavy metal contaminated sites. Especially because Ktedonobacteria are poorly represented in culture. If this is a unique habitats it could be a great place to target for future cultivation work.

Ktedonobacteria are soil inhabiting bacteria which become abundant under heavy metal stress. L. 460-479 highlight this point. We tried to find *Ktedonobacteria* in similar mines settings but in vain; probably because of artificial illumination at the sampling site and cocolonization of *Ktedonobacteria* and *Oxyphotobacteria* makes this site a unique habitat. Furthermore, I had compared *Ktedonobacteria* MAG019 with other type strains (*K.racemifer* and *T.hazakensis*) in my thesis and found that MAG019 has some unique genes related to heat shock, copper homeostasis, etc
Added in L.485

26. Did you omit Table 3? It's mentioned in the responses but no longer in the manuscript
No, the manuscript doesn't have any table, only supplementary info has tables and Table S3 is included in the URL https://doi.org/10.25625/DFFZ9R which may have caused confusion. The table S3 is changed to abundance graphs.

27. Figure S2: correct the spelling of proteobacteria and the overlapping text on the left
Corrected

28. Figure S3: pie charts are relative abundance?
Pie charts show the cumulative actual abundance of all taxes from all samples.
Corrected

29. Table S1 does not include the indices, only results of a statistical test. Please include both
Added

30. Table S2: define abbreviations especially for groups. Also recommend defining the different sub tables via a,b,c etc and including some borders
Corrected

31. PCR methods in SI are so short that it makes more sense to move them to the main pap
Corrected

Reviewer 2
The authors have addressed all the comments. I only have some technical concerns. Line 212, 223-228, It may be better to add the ordinate axis and the tick marks in Figure 3.
Added

Line 214-221, The units "mgL-1" and "ugL-1" should be "mg·L-1" and "ug·L-1". Please check the full text and revise.
Corrected

Line 283-288, What kind of bacteria is "Delta Gamma Proteobacteria" in "MBS1" in Figure 5? Is there a typo? Please check and fix.
These are subclasses of Proteobacteria: Delta relates to the blue part of the column, Gamma to the green part so they were mentioned together in figure to show relative proportion.

Line 323, Some microorganism names in the article are not italicized, such as "Ktedonobacteria" on line 323. Please check and correct any typos in the text
Corrected