

# Molecular assessment of metal-cycling microbial communities associated with critical mineral resources in historic mine waste

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New Mexico Tech

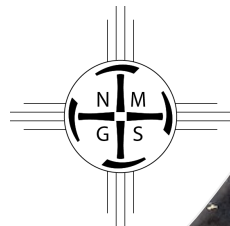
# Acknowledgements

- Zohreh Kazemi Motlagh  
Acid mine drainage and critical minerals in Black Hawk Mine waste, Grant County, NM
- Abena Serwah Acheampong-Mensah  
Geochemistry of critical minerals in mine wastes at Hillsboro and Steeple Rock Districts, NM
- Evan Owen, Stelah Cherotich, Bonnie Frey, Kyle Stafford, Bob and Jacob Newcomber, Bob Seal

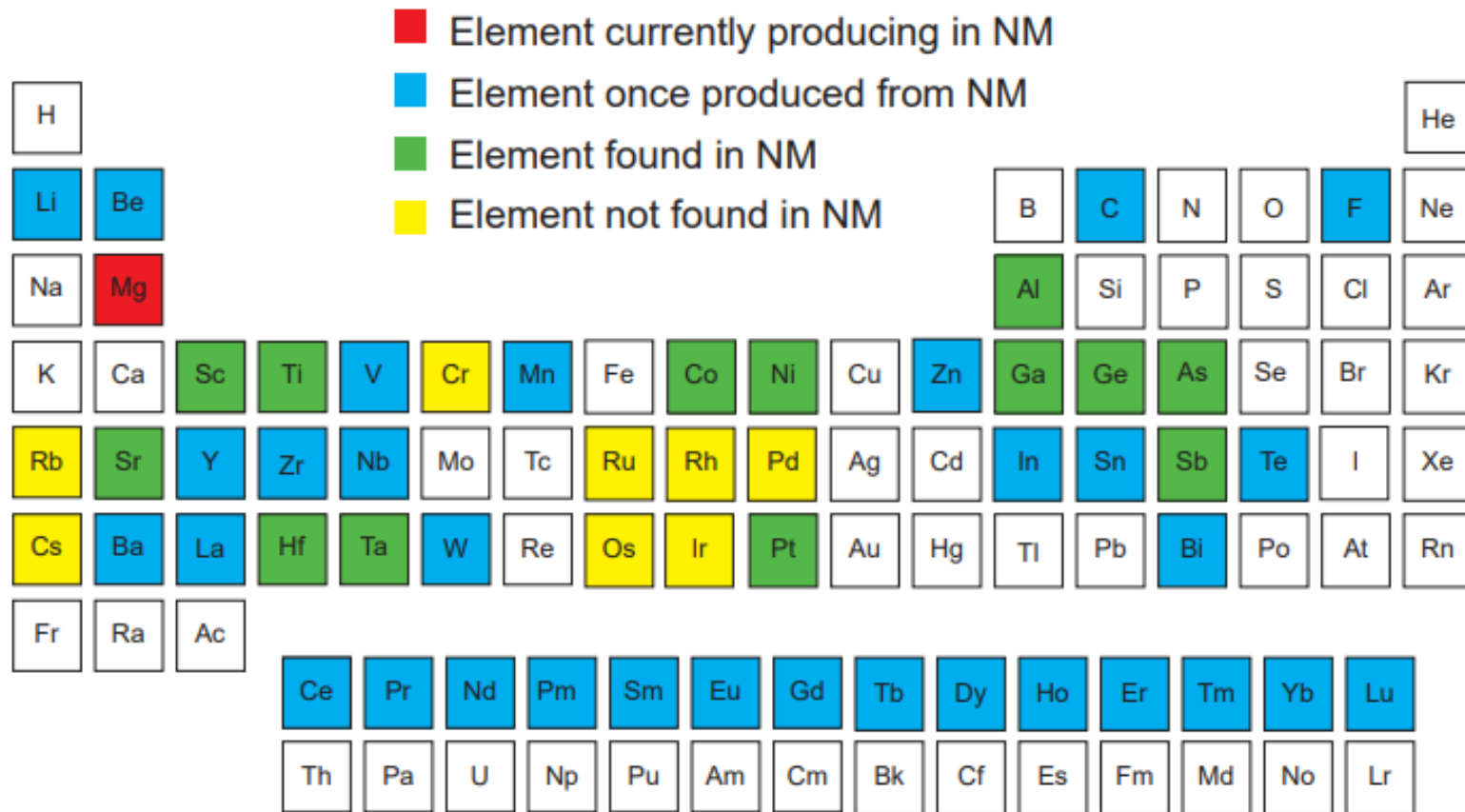
## Funding

USGS Earth MRI award #G22AC00510

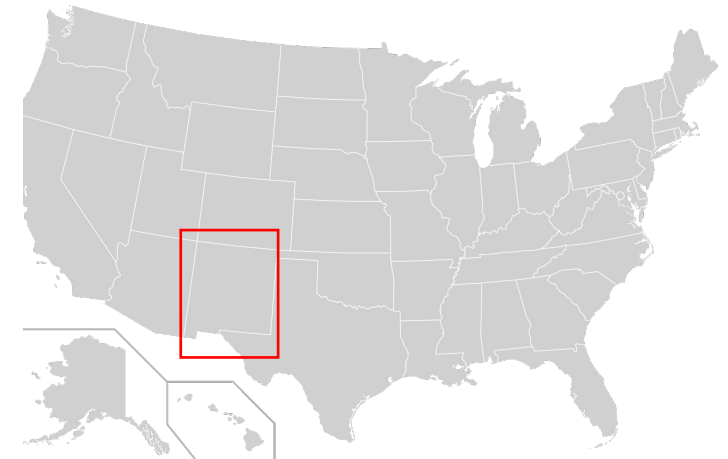
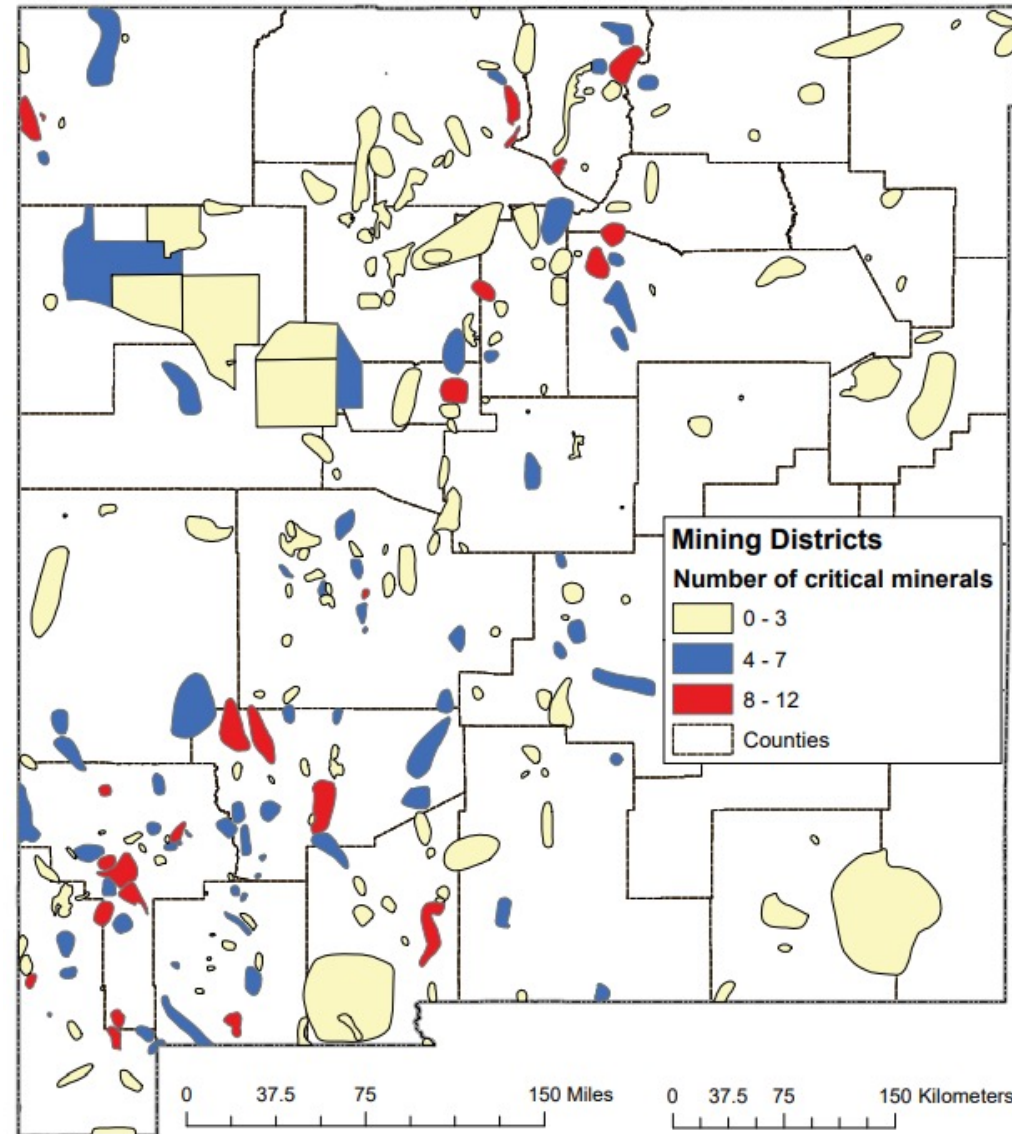
New Mexico Geological Society Graduate Grant-in-Aid



# Critical minerals contain elements that are vital to the economy

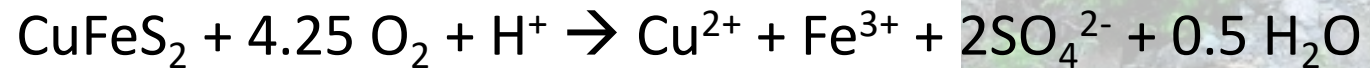


# Many of New Mexico's historic mining districts have not been actively mined in decades



# Microorganisms catalyze many important geochemical reactions that matter for mining

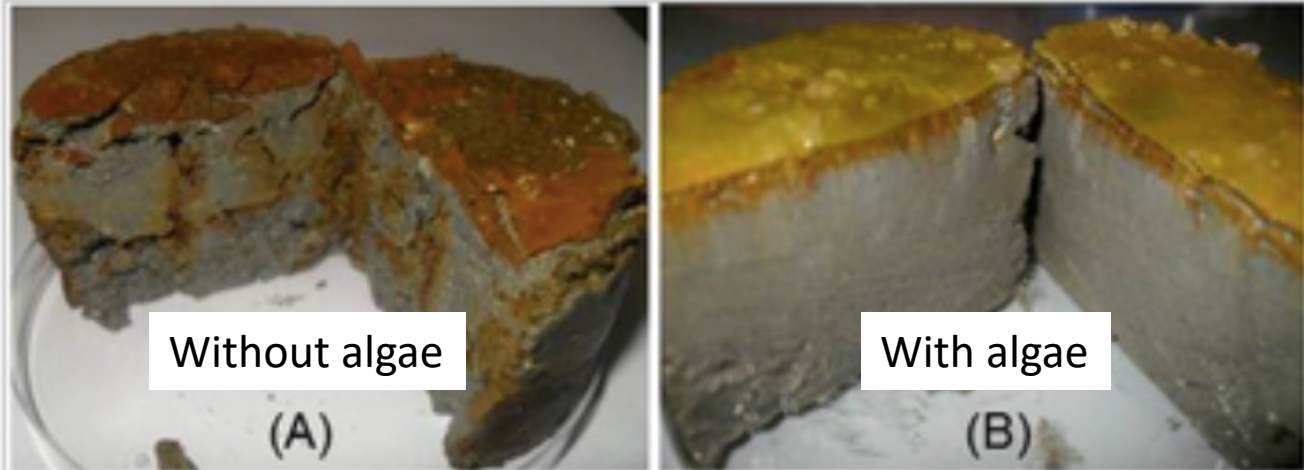
- Fe and S oxidizing microorganisms drive sulfide mineral oxidation, which can result in acidic rock drainage (ARD) generation



- Bioremediation of metal-impacted areas

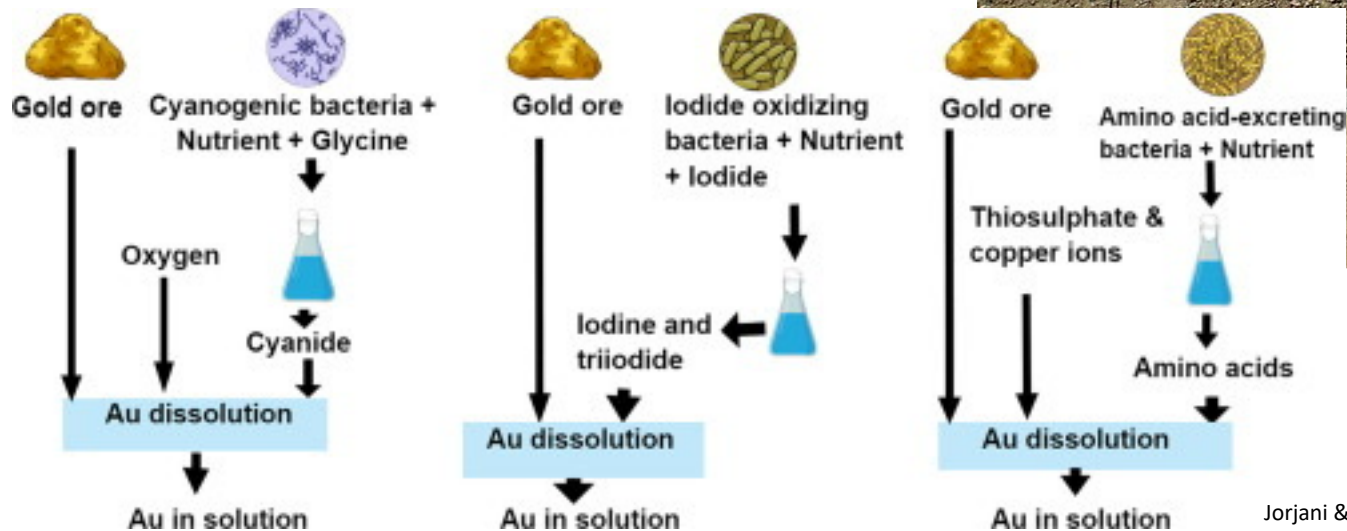
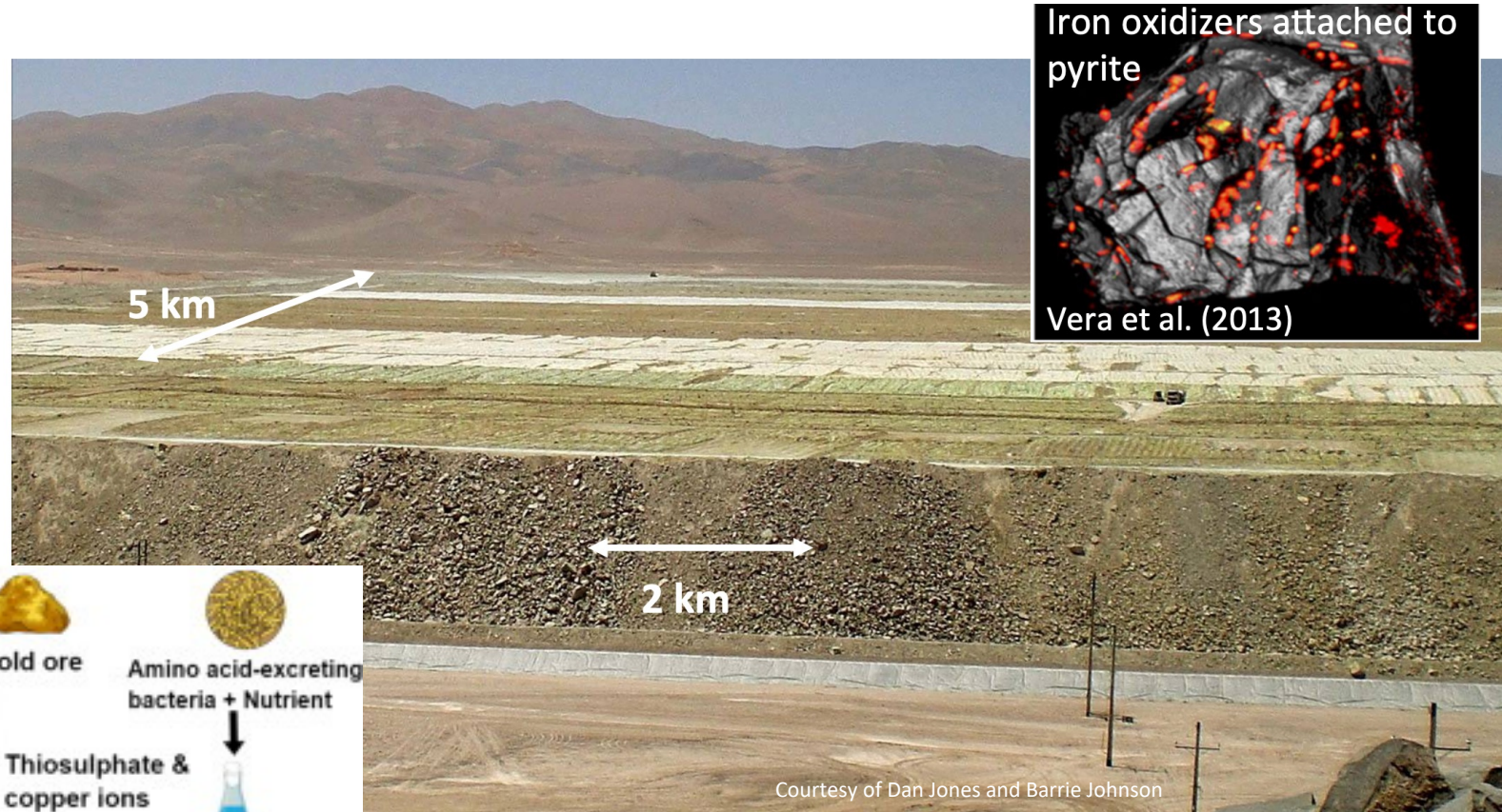


<https://www.geologyin.com/2015/02/acid-mine-drainage-reduces.html>



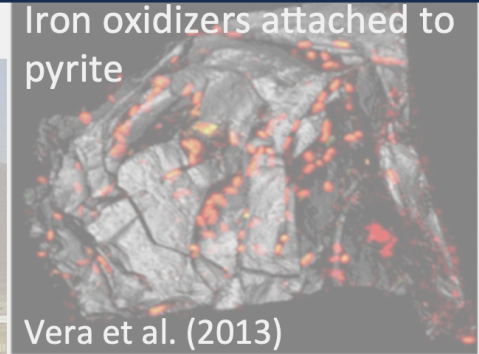
# Microorganisms catalyze many important geochemical reactions that matter for mining

- Metal-cycling microorganisms can be used for biomining and bioleaching
- Biotic Fe and S oxidation is faster than abiotic oxidation

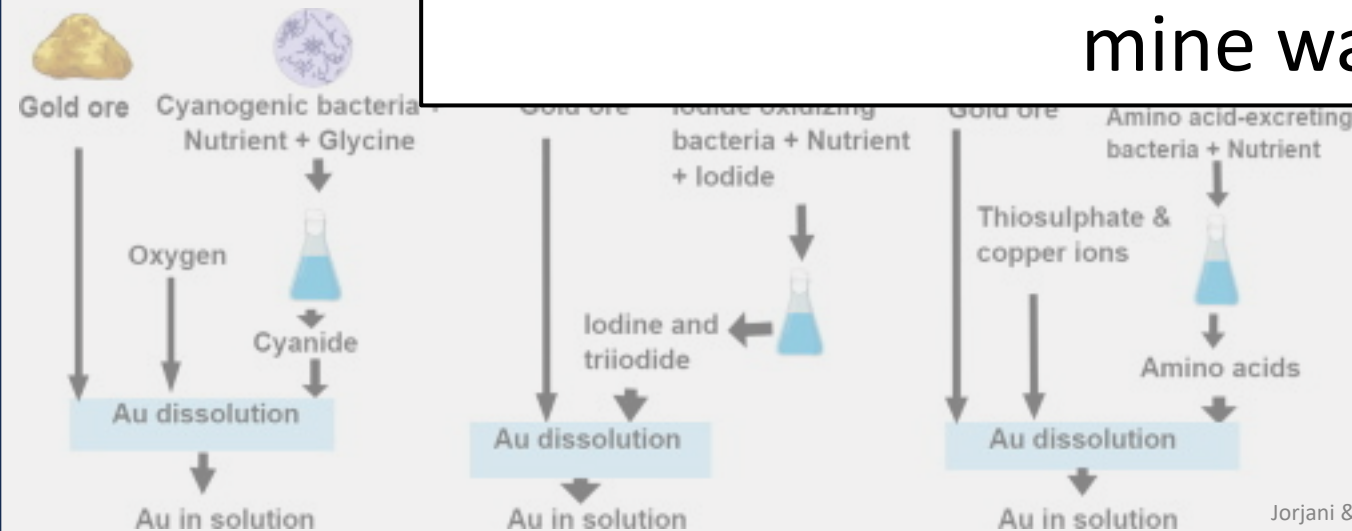


# Microorganisms catalyze many important geochemical reactions that matter for mining

- Metal-cycling microorganisms can be used for biomining and bioleaching



Despite their importance to metal cycling, we don't know that much about microorganisms in mine waste



Jorjani & Sabzkoohi (2022)

Courtesy of Dan Jones and Barrie Johnson

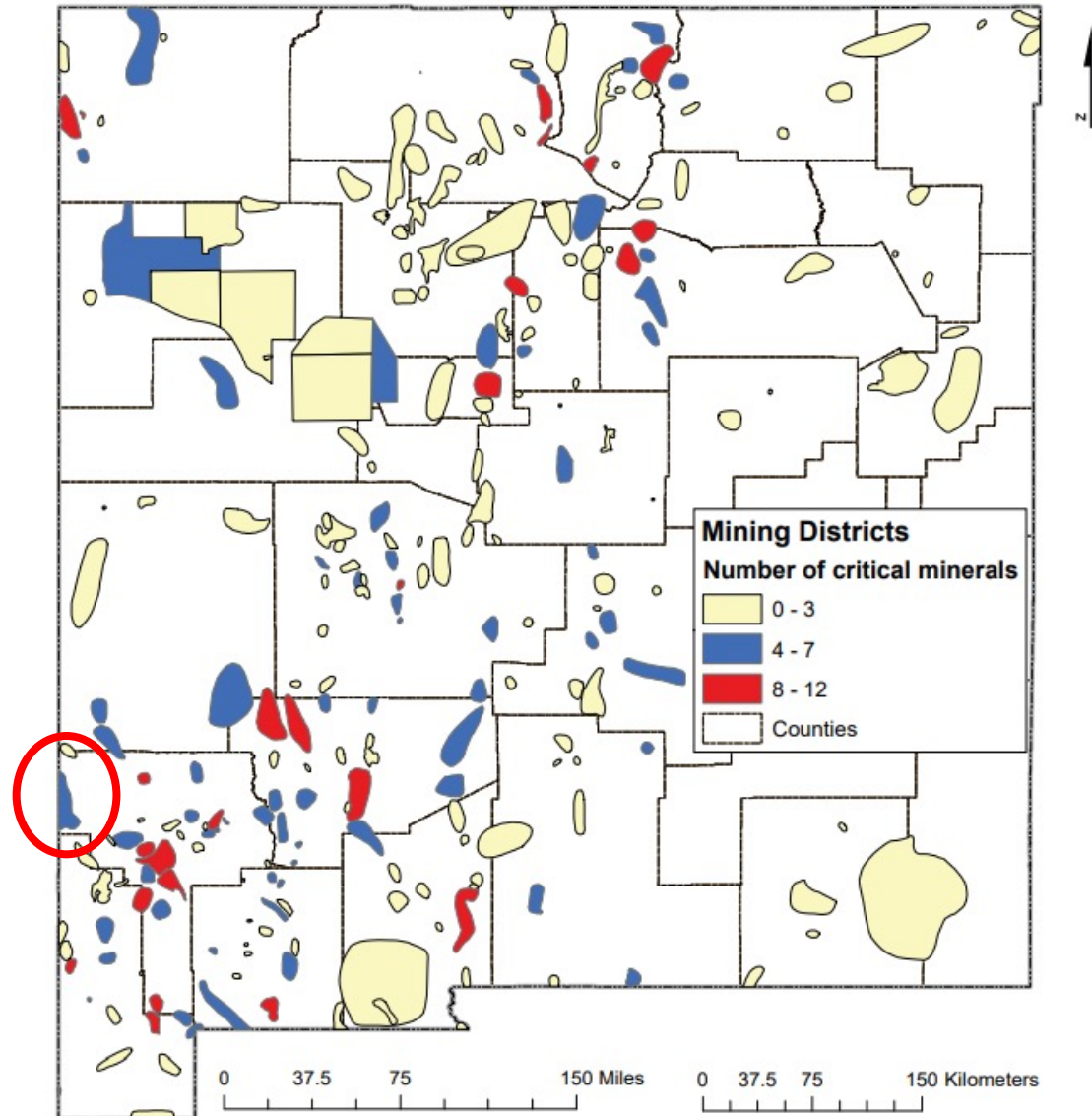
# Research motivations

- What microorganisms are associated with historic mine waste?
- How do microbial communities relate to waste type, mineralogy, and geochemistry?
- Are metal cycling microorganisms abundant? What can microbial communities tell us about biogeochemical processes occurring in historic mine waste?



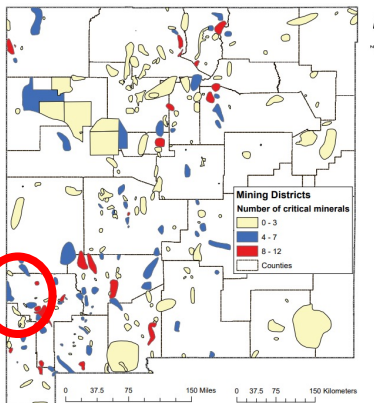


# Center and Carlisle Mines (Steeple Rock District)



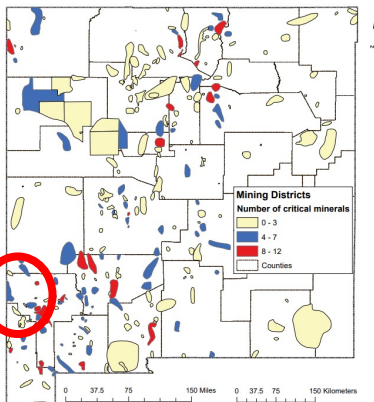
# Center Mine (Steeple Rock District)

- Active until 1994
- District produced Au, Ag, Cu, Pb, Zn
- 6 in of cover on top of mixed waste



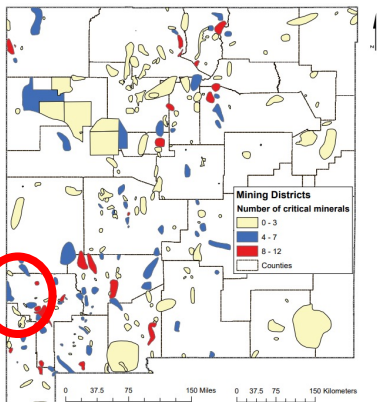
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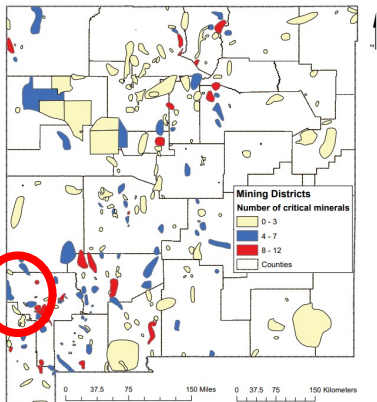
# Carlisle Mine (Steeple Rock District)

- Exploration began 1860, Production first reported 1880
- District produced Au, Ag, Cu, Pb, Zn
- Intensive exploration from 1970-1994 for Au-Ag
- Mostly bulk waste, some tailings

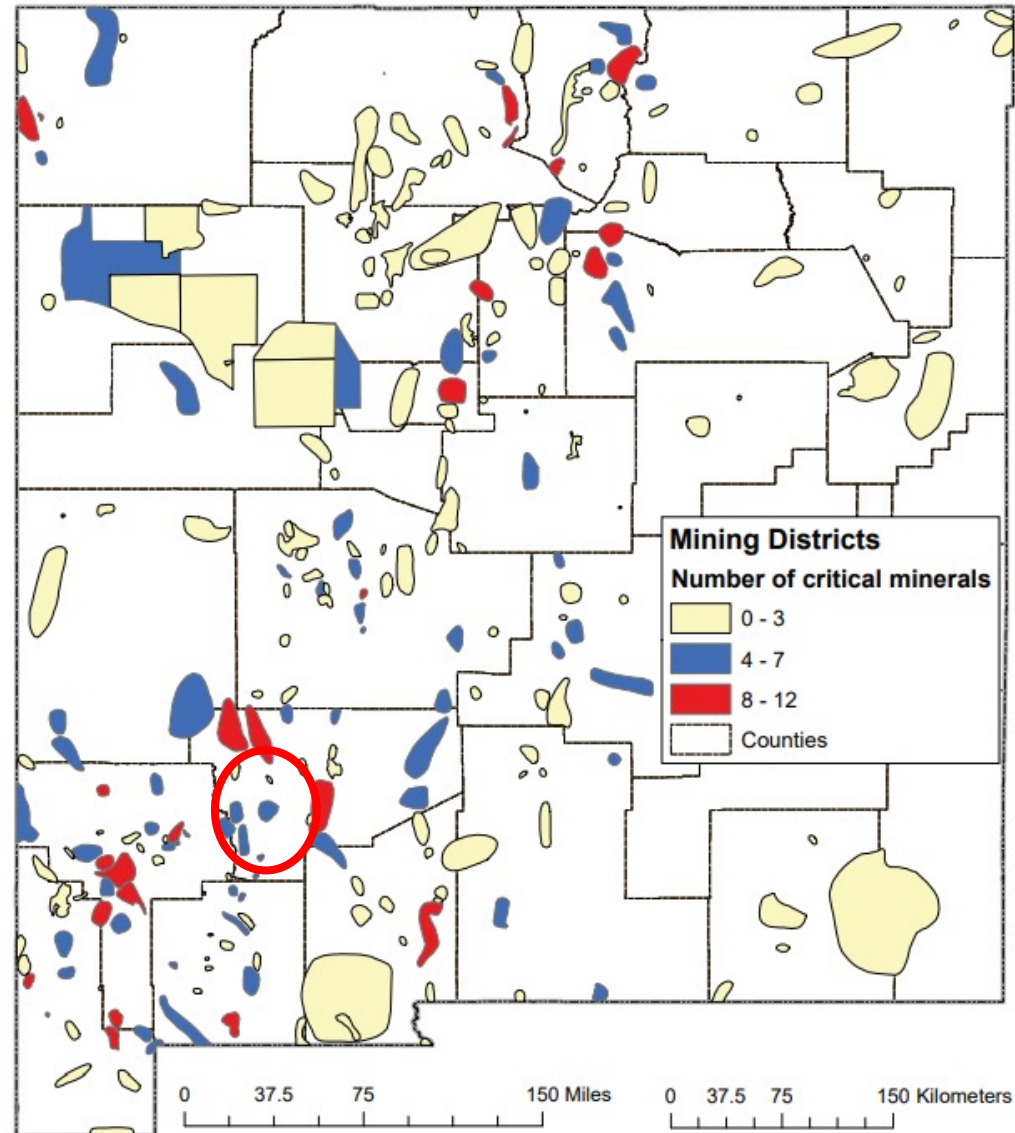


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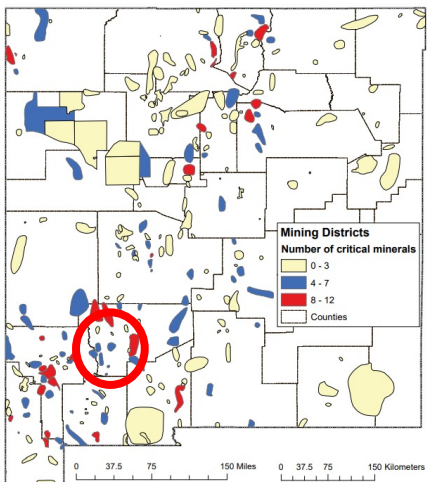


# Copper Flat (Hillsboro)



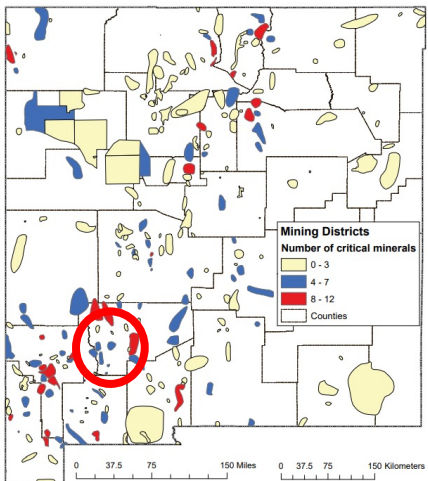
# Copper Flat (Hillsboro)

- Laramide porphyry-copper
- Sporadic production since 1982
- Seasonal acidic seep
- Bulk waste rock and tailings



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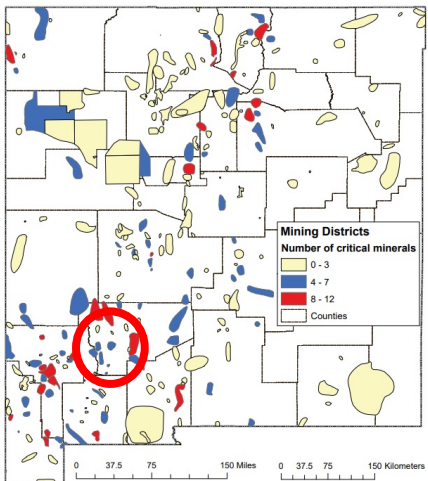
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# Copper Flat (Hillsboro)

- Laramide porphyry-copper
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# Research motivations

- What are the microbial communities associated with mine waste?
- How do these communities relate

**How do we get a representative sample?**

composition, abundance, and metabolic activity be correlated with geochemistry and mineralogy, especially with an eye towards critical minerals?



Capture heterogeneity  
while maintaining a  
balance with the overall  
community

- Consistent sampling depth
- Cover the entirety of waste pile geometry



Capture heterogeneity  
while maintaining a  
balance with the overall  
community

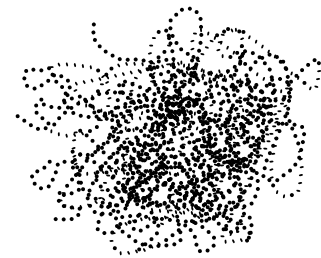
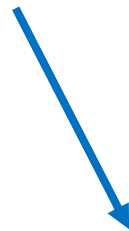
Individual geochemistry hole  
samples AND a composite for  
each waste type



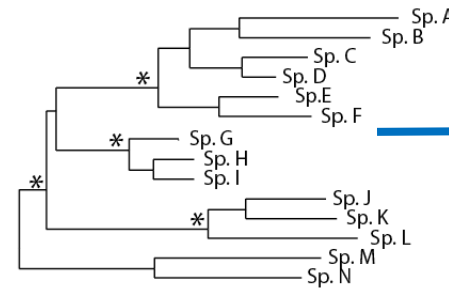
# Amplicon sequencing: Community fingerprinting with rRNA or other genes/transcripts

Sample

Extract



Amplify specific genes/transcripts



Identify/classify

	Sp. A	Sp. B	Sp. C	Sp. D	Sp. E	...
Sample 1	0	0	0	4	0	
Sample 2	23	0	0	0	0	
Sample 3	0	4	3	32	0	
Sample 4	71	8	58	4	0	
Sample 5	31	0	45	5	0	
Sample 6	1	0	2	19	1	
Sample 7	0	0	0	0	0	
Sample 8	0	0	0	0	0	
Sample 9	0	0	0	1	0	
Sample 10	0	0	2	4	0	
...						



Analyze

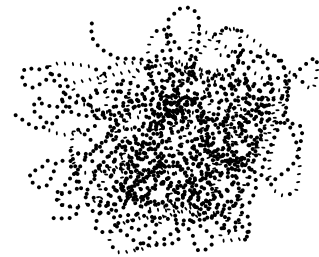
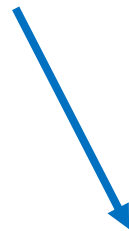


- **Who is home?** (In many samples)
- rRNA genes/transcripts, other functional genes
- Bacterial, archaeal, and eukaryotic communities

# Amplicon sequencing: Community fingerprinting with rRNA or other genes/transcripts

Sample

Extract



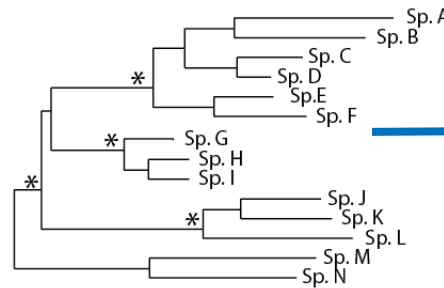
Amplify specific genes/transcripts

- V
- r
- B

At least 2 DNA extractions per sample to avoid “nugget effect”

genes  
unities

Identify/classify



Analyze

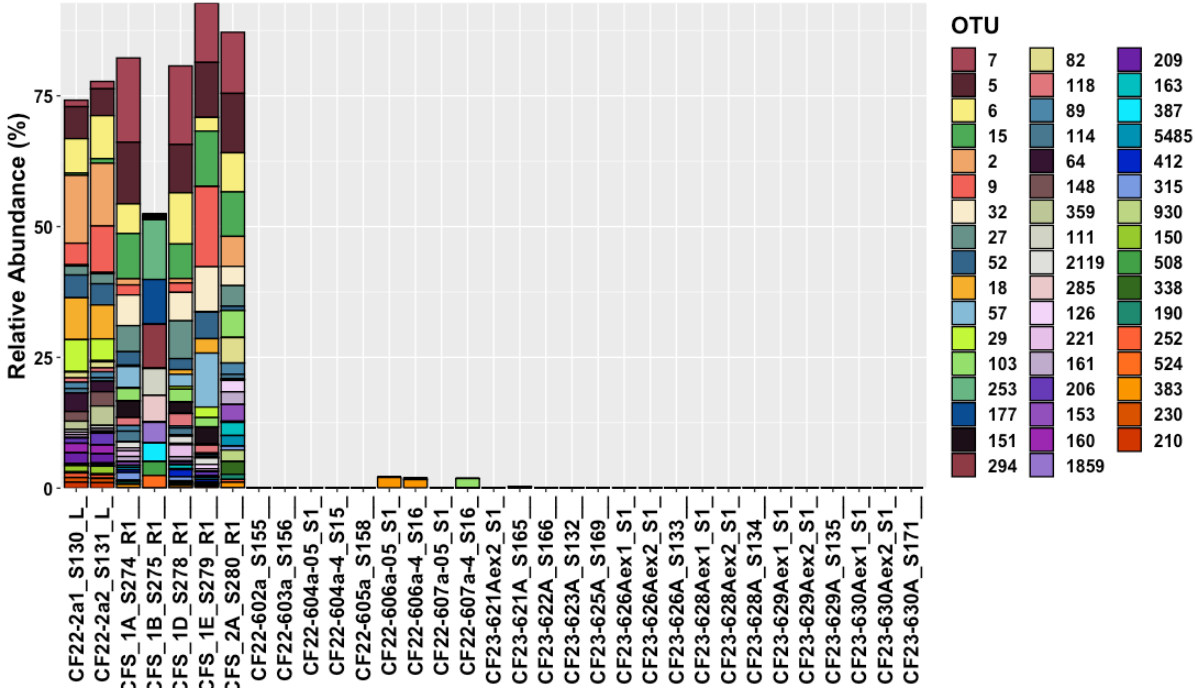
	Sp. A	Sp. B	Sp. C	Sp. D	Sp. E	...
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Sample 8	0	0	0	0	0	
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...						



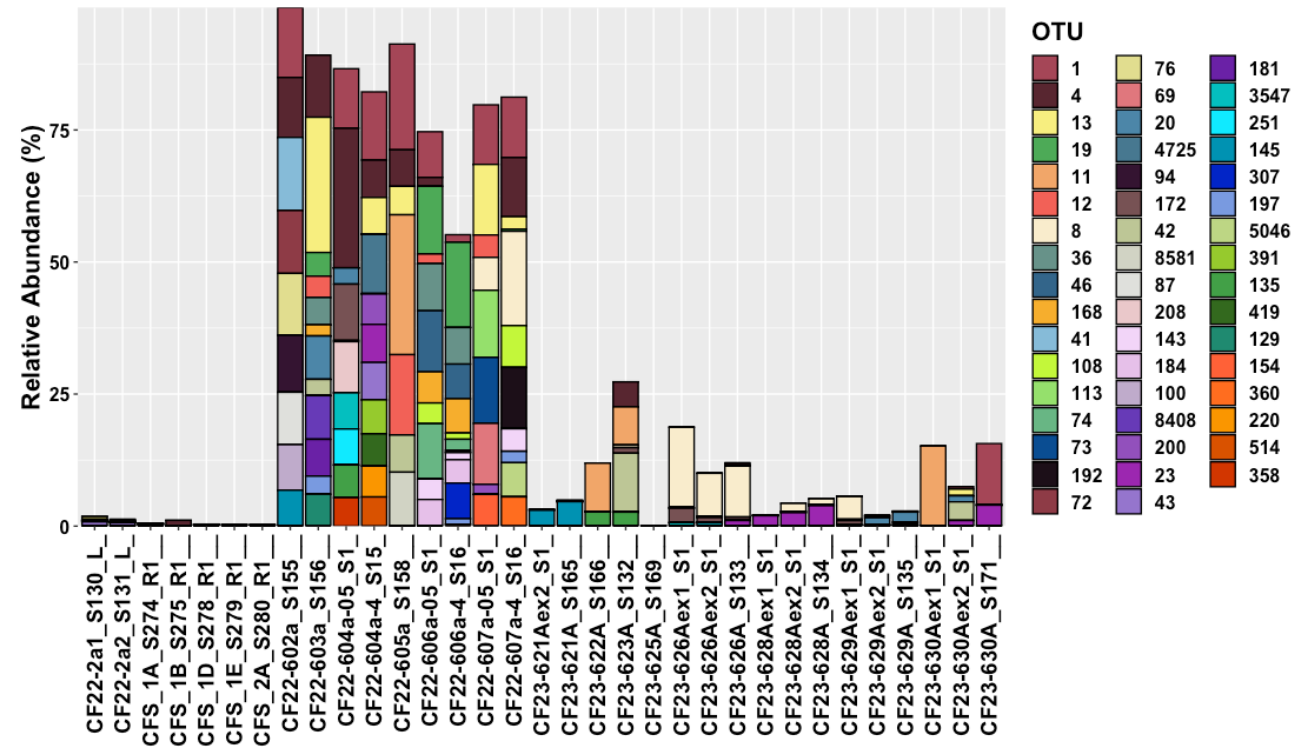
PCR optimization

# Different waste types have very different microbial communities with little to no overlap

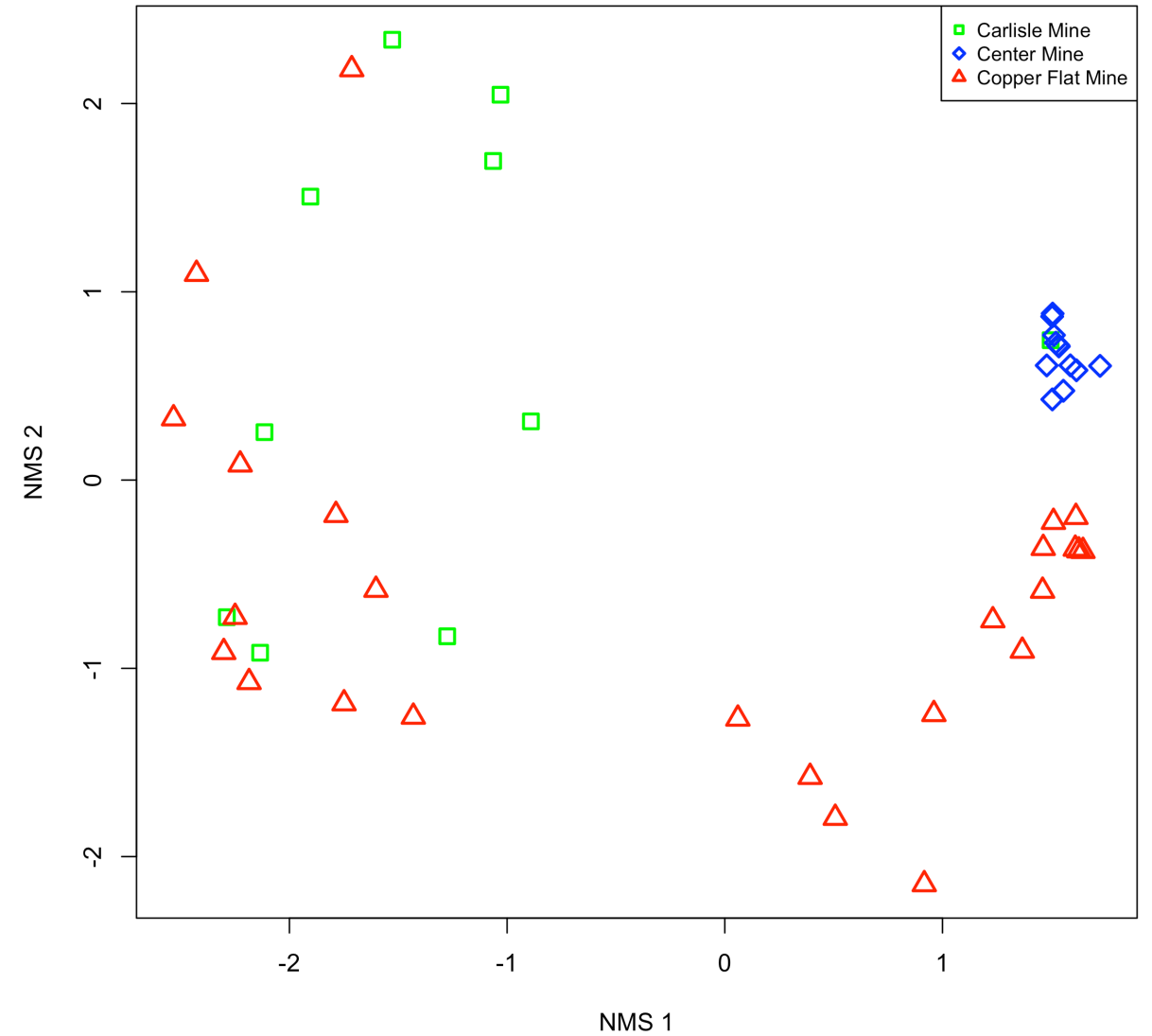
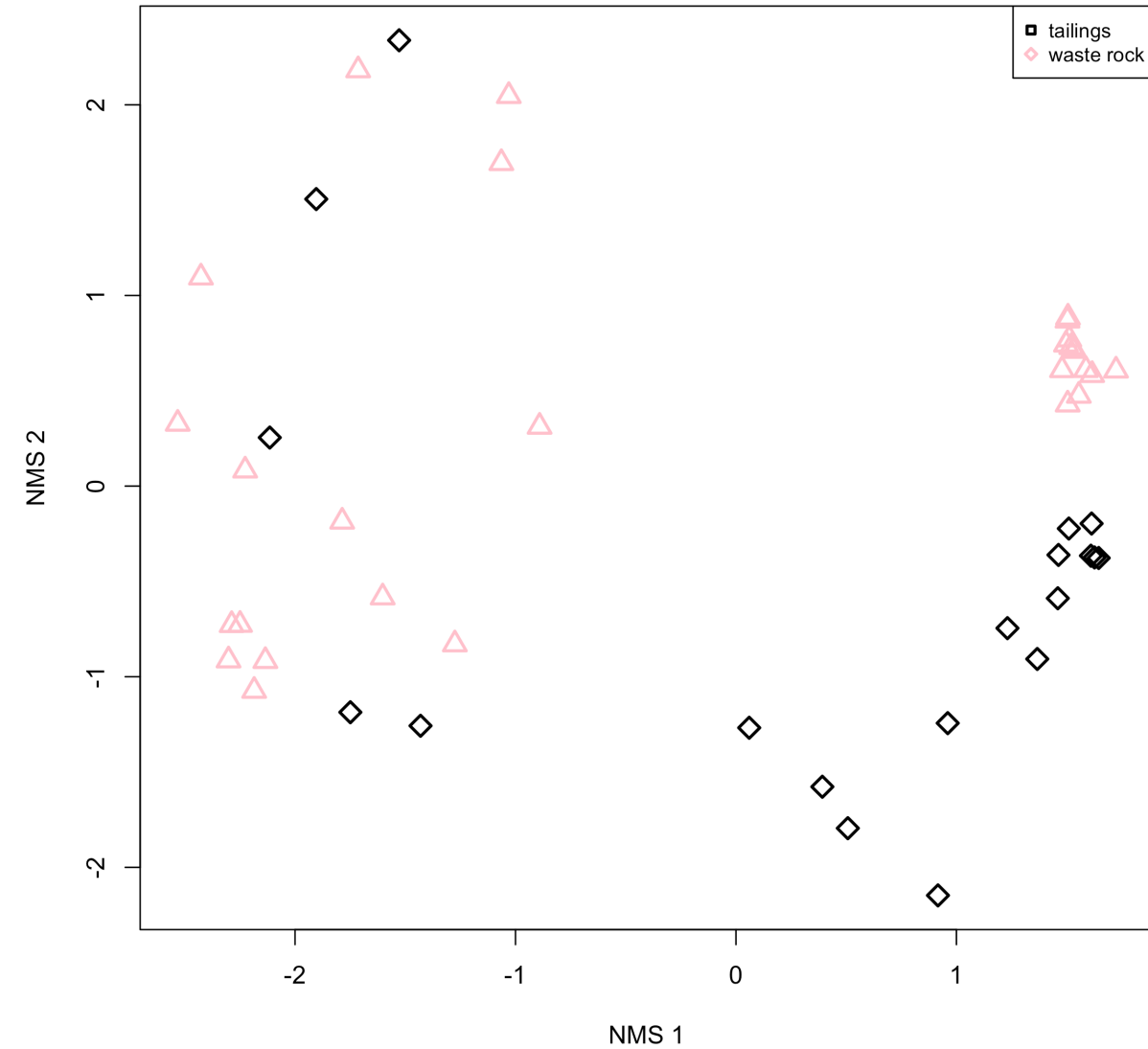
## Copper Flat Seep



## Copper Flat Waste rock

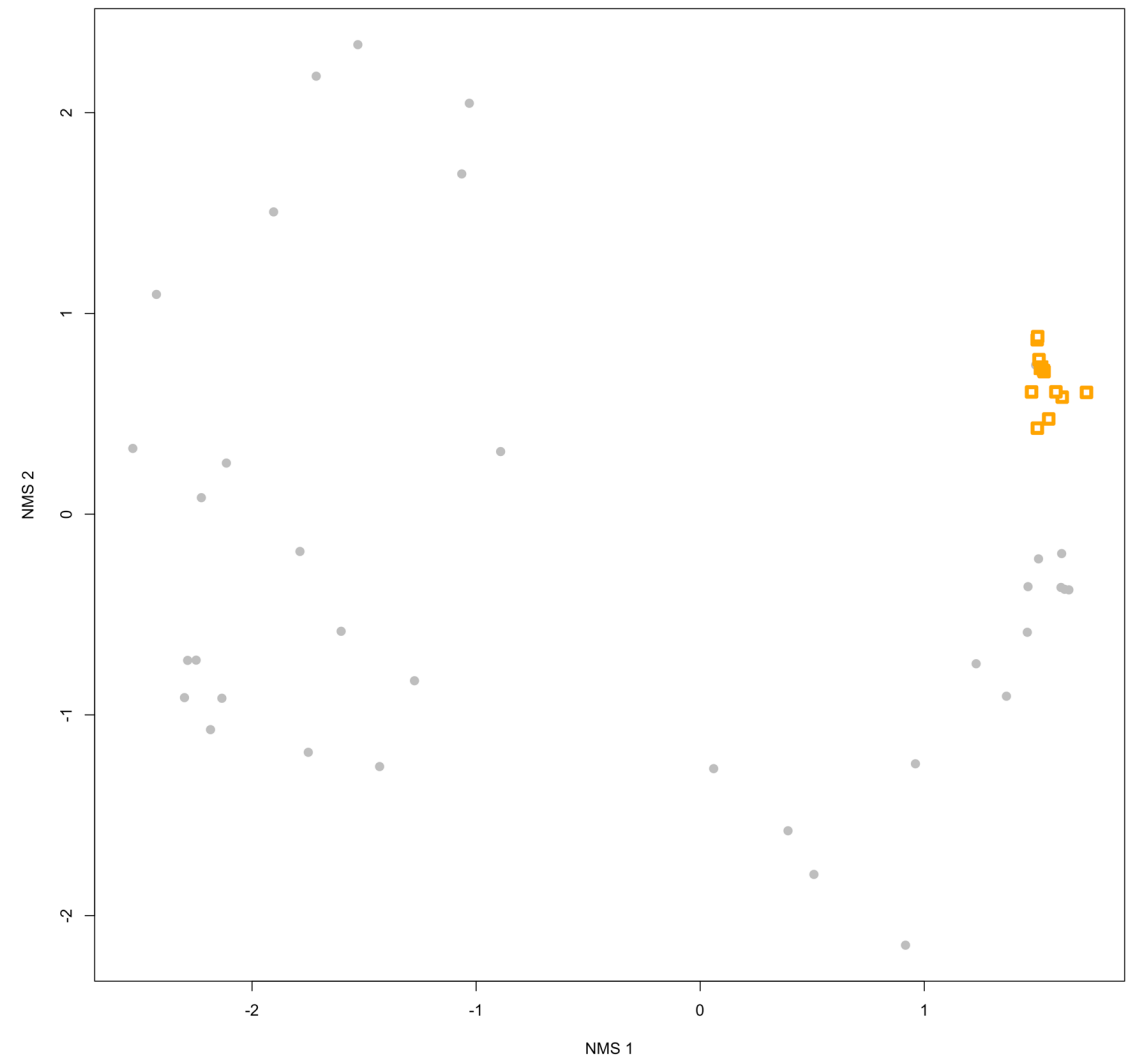
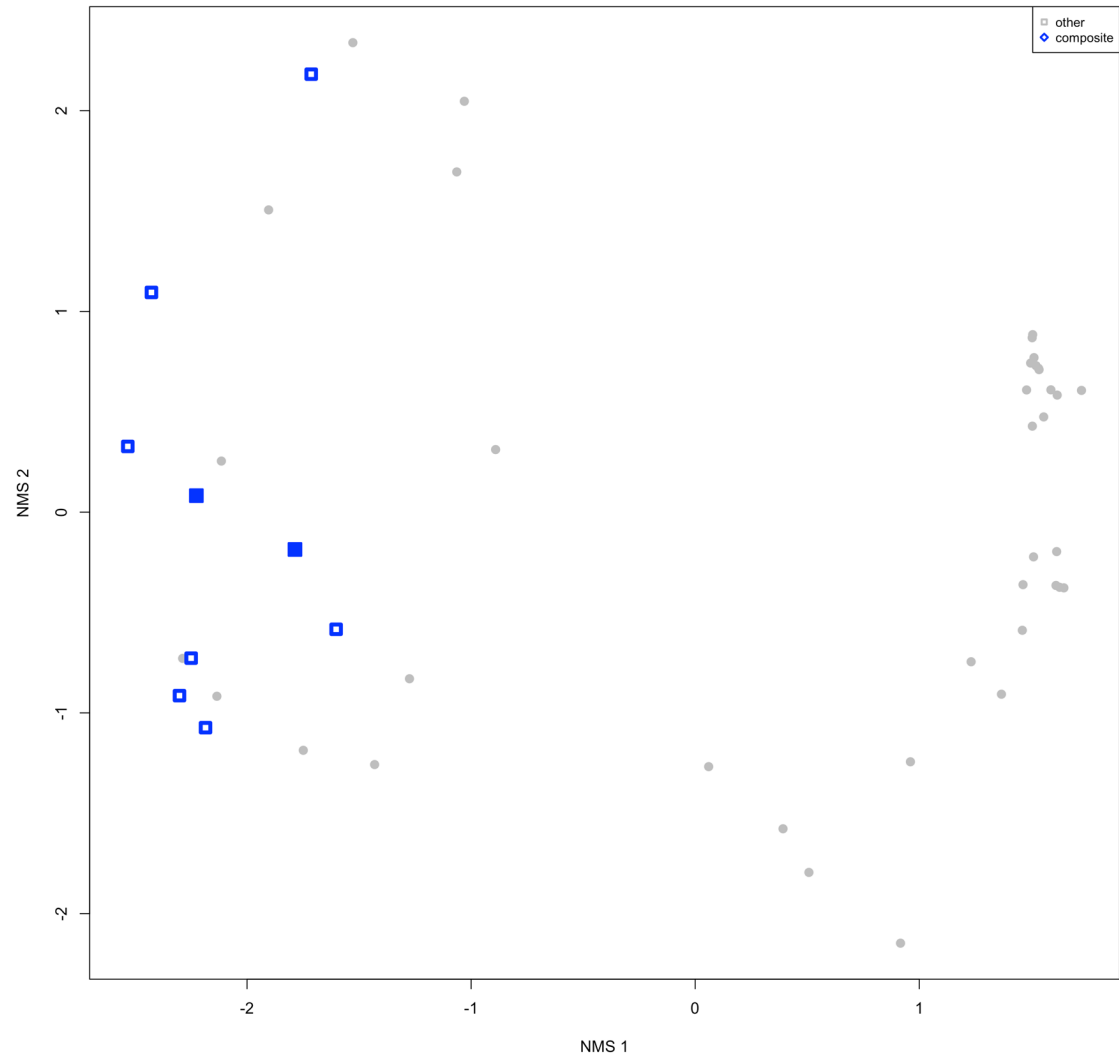


# Waste type drives community differences

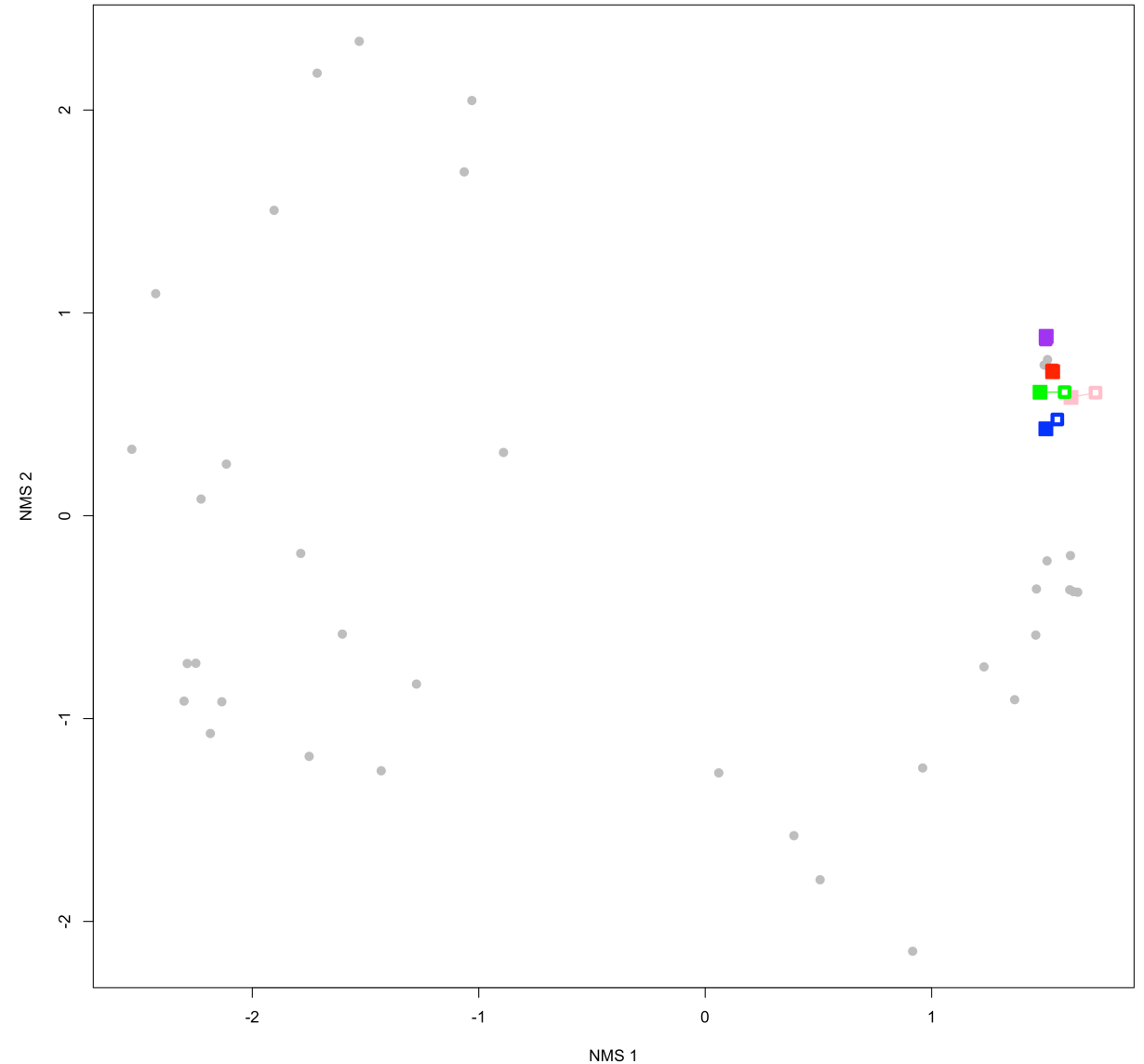
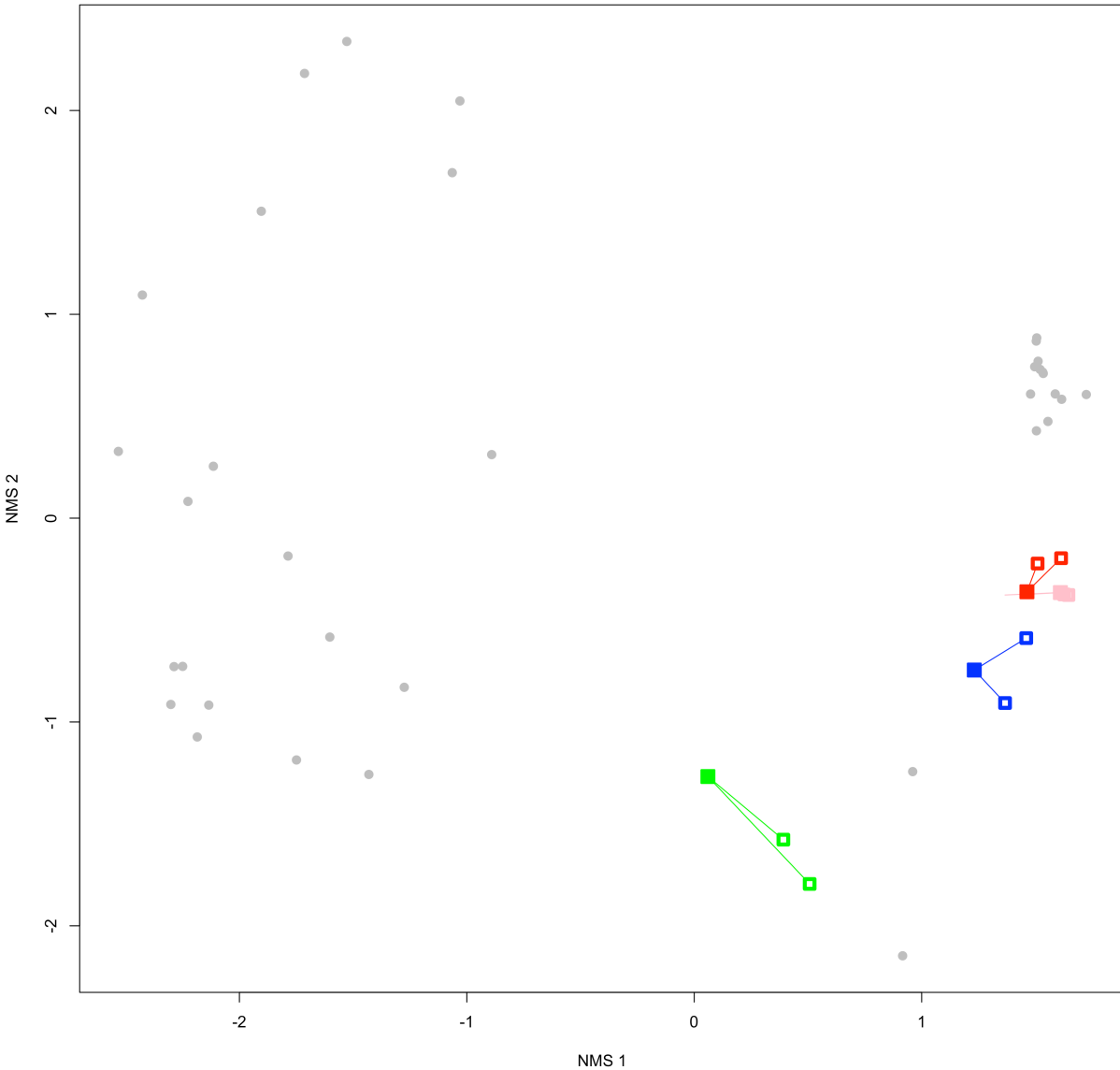




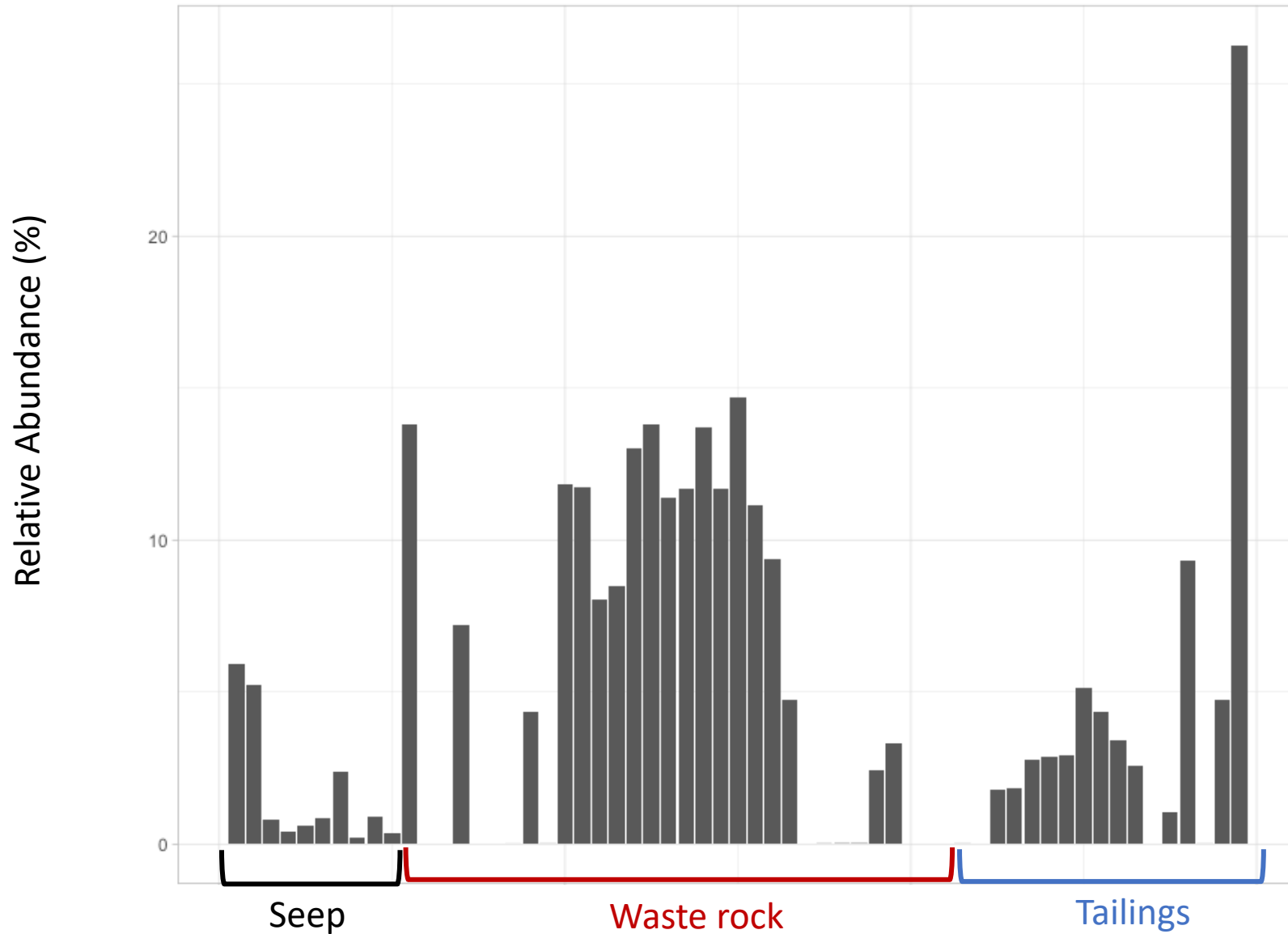
# Testing our methodology: Composite samples capture some of the heterogeneity of the individual samples without overemphasizing that heterogeneity



# Testing our methodology: Multiple DNA extractions per sample were similar

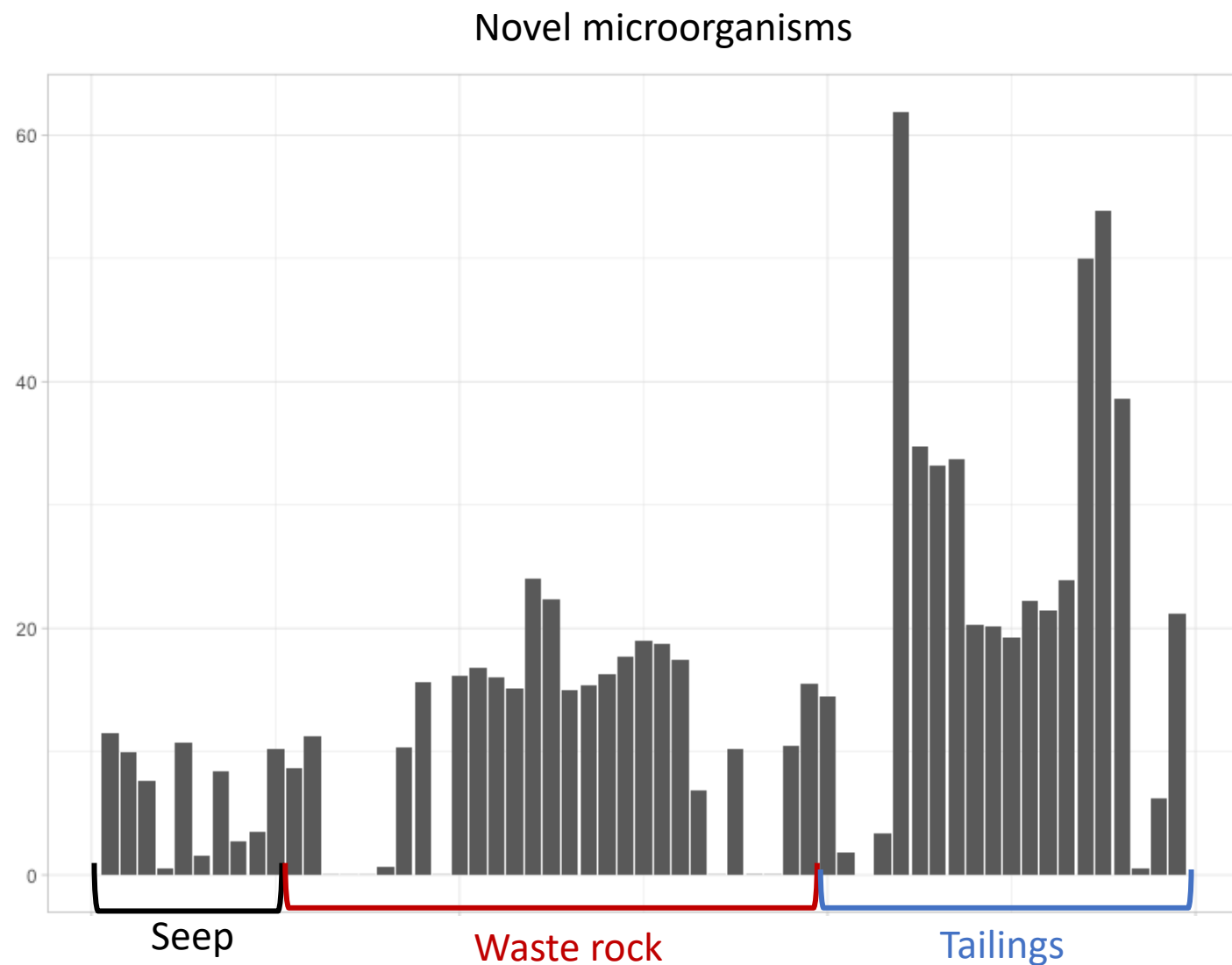
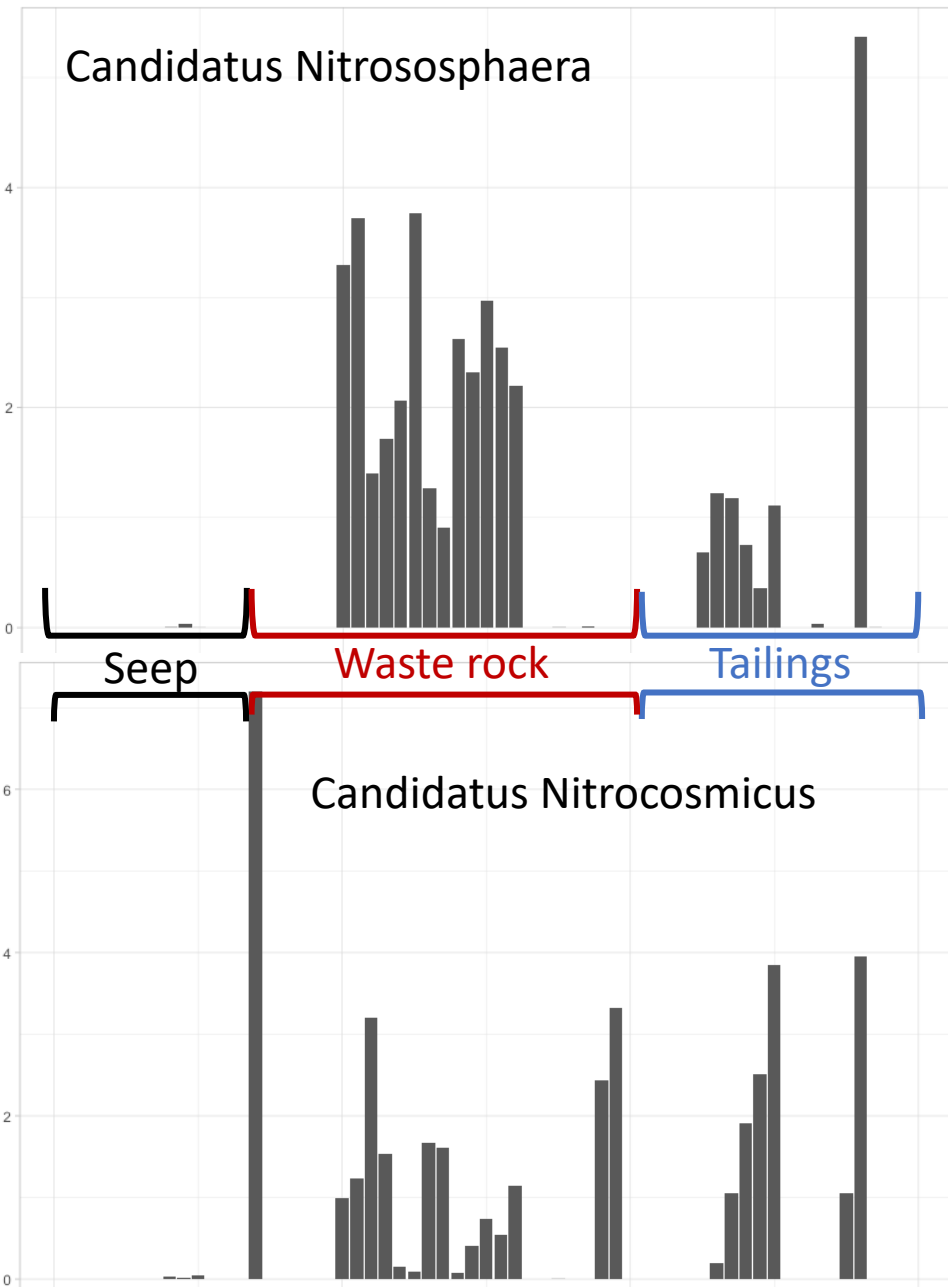


# Relative abundance of archaea is greatest in seeps and waste rock



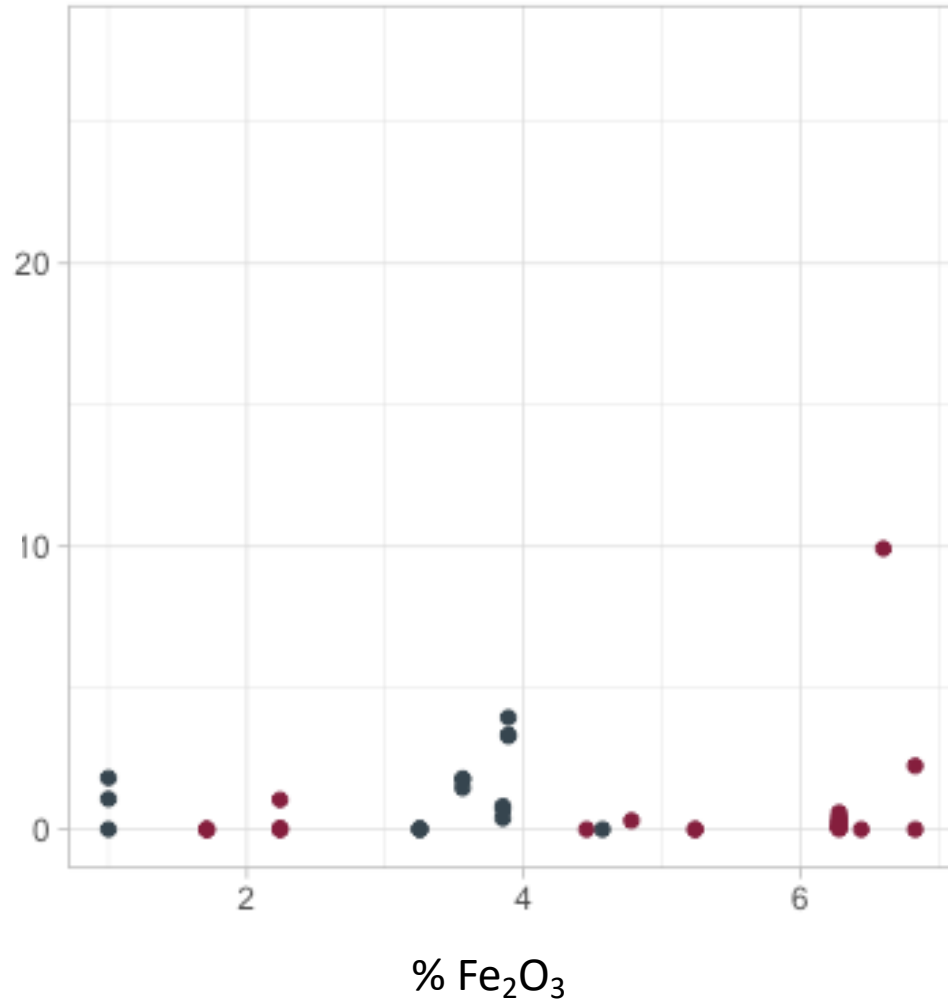


# What about the other microorganisms present?

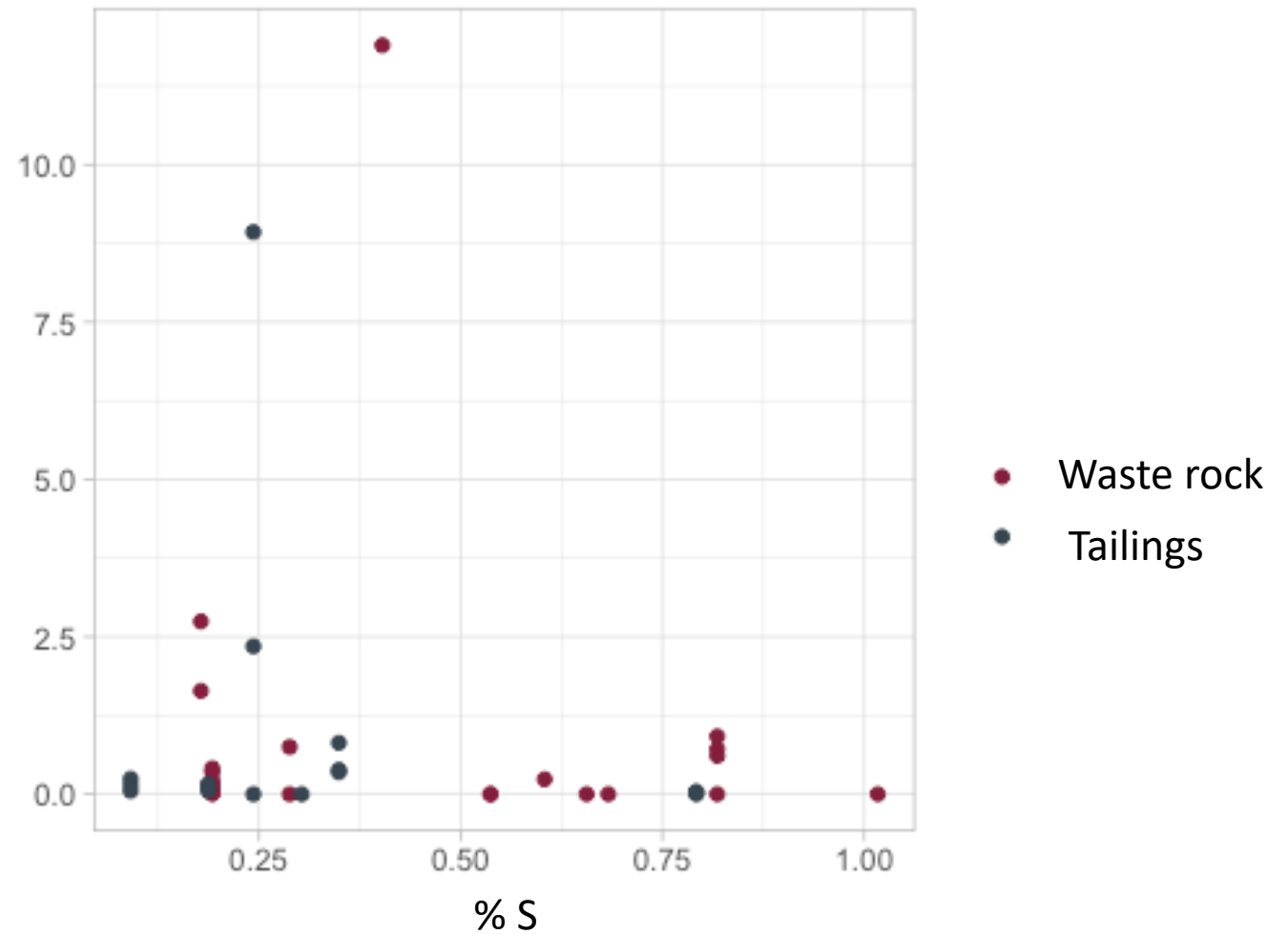


# Metal cyclers only loosely track geochemical results

Iron cyclers

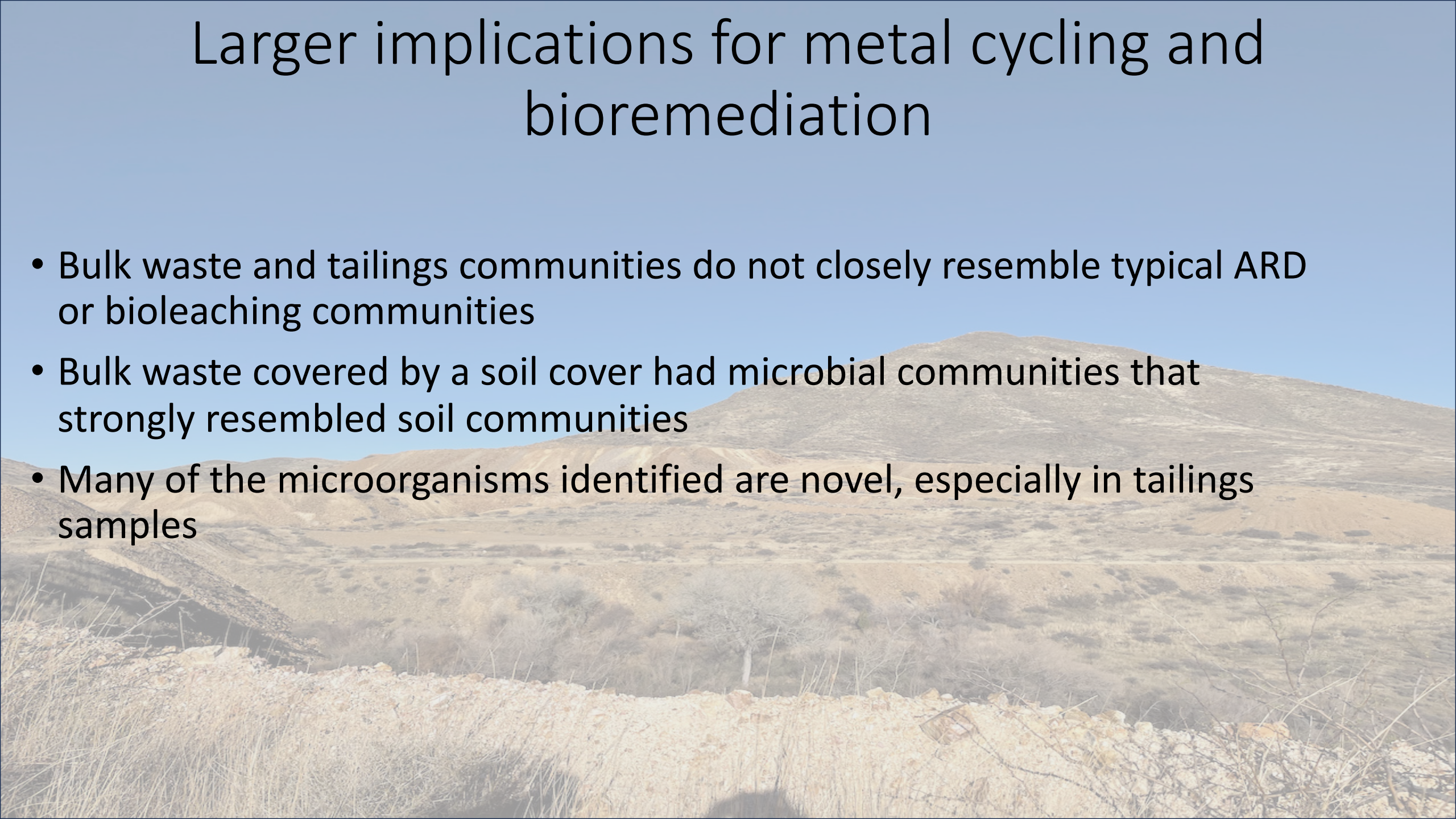


Sulfur cyclers



# Larger implications for metal cycling and bioremediation

- Bulk waste and tailings communities do not closely resemble typical ARD or bioleaching communities
- Bulk waste covered by a soil cover had microbial communities that strongly resembled soil communities
- Many of the microorganisms identified are novel, especially in tailings samples



## Future Work

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- rRNA transcripts analysis
- Cell counts
- Amplicon sequencing from Black Hawk and Alhambra Mines from the Black Hawk District
- Microbial diversity analyses

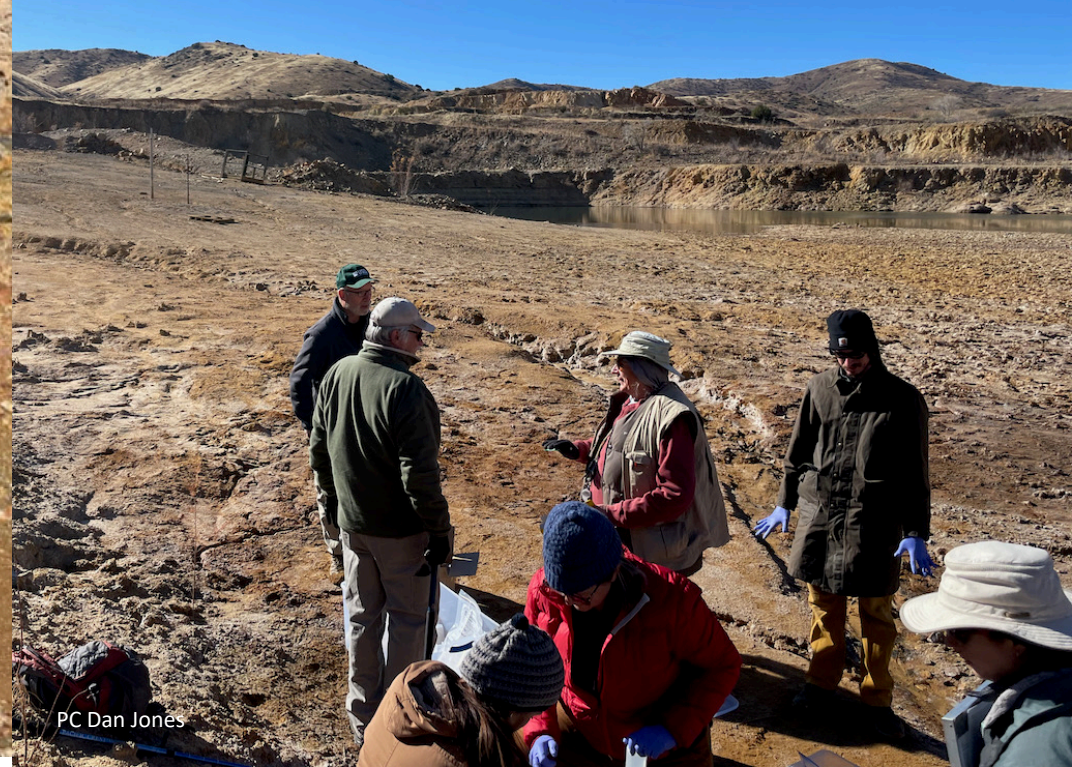




# Thank you!



PC Dan Jones

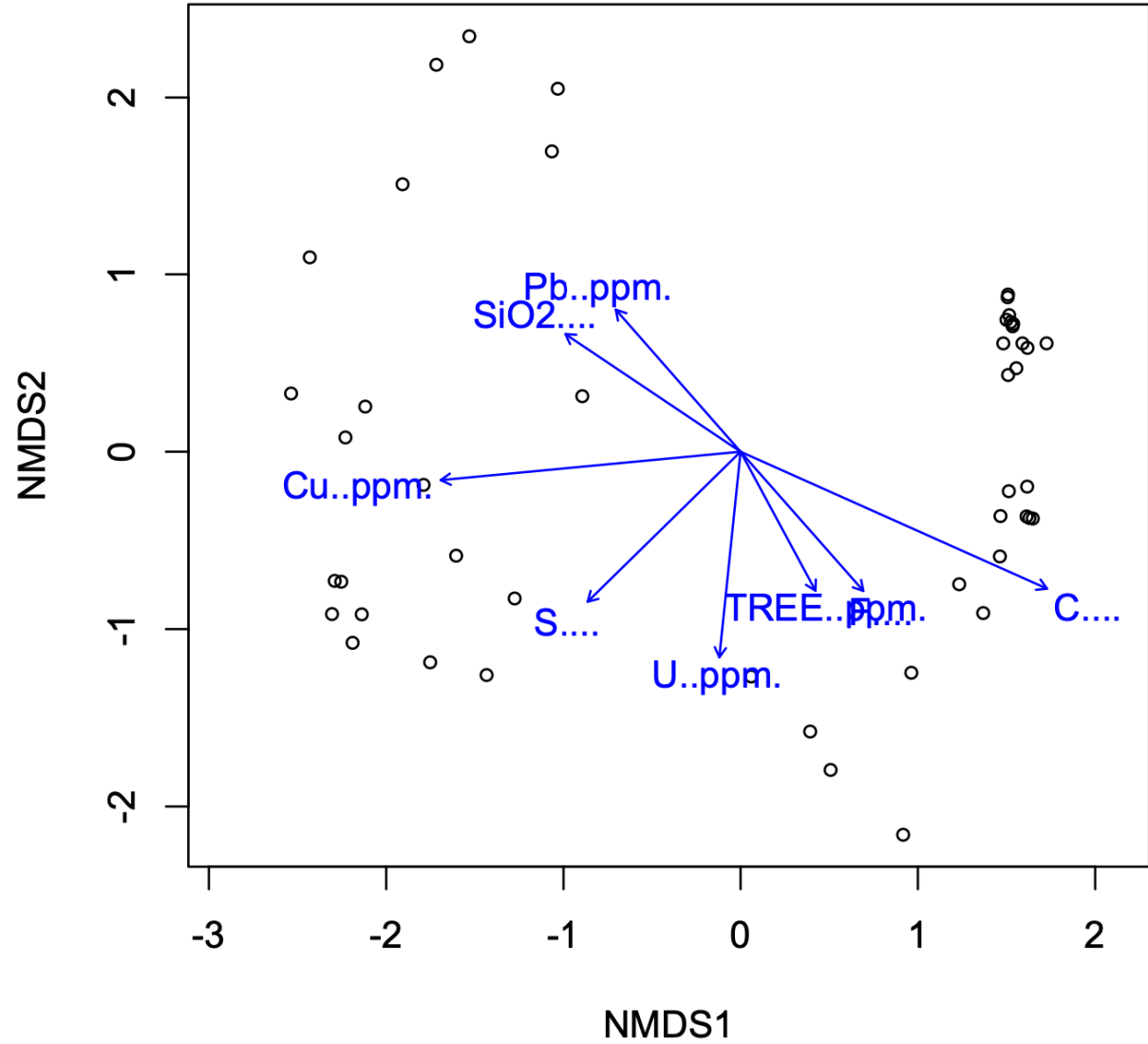
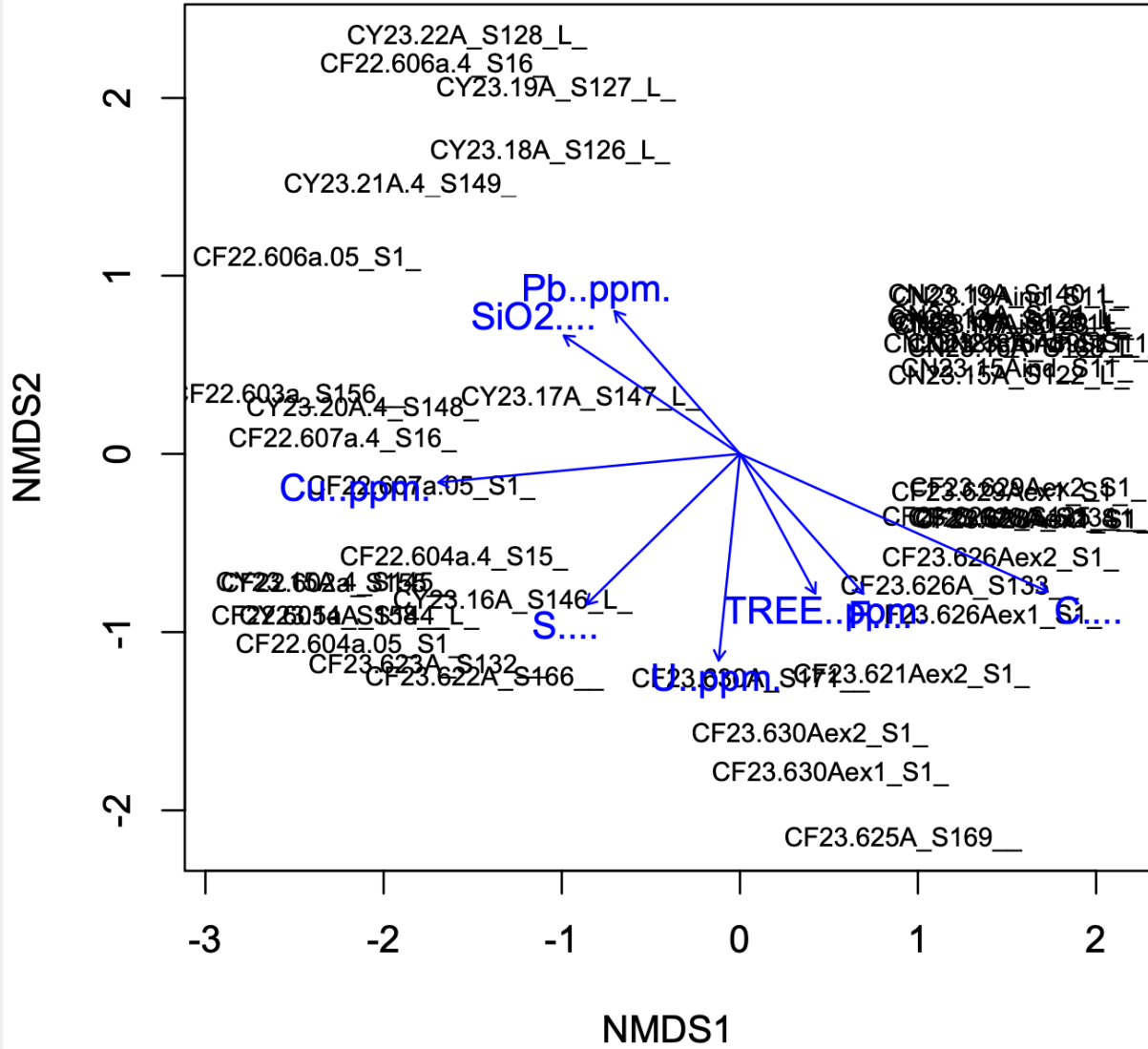


PC Dan Jones

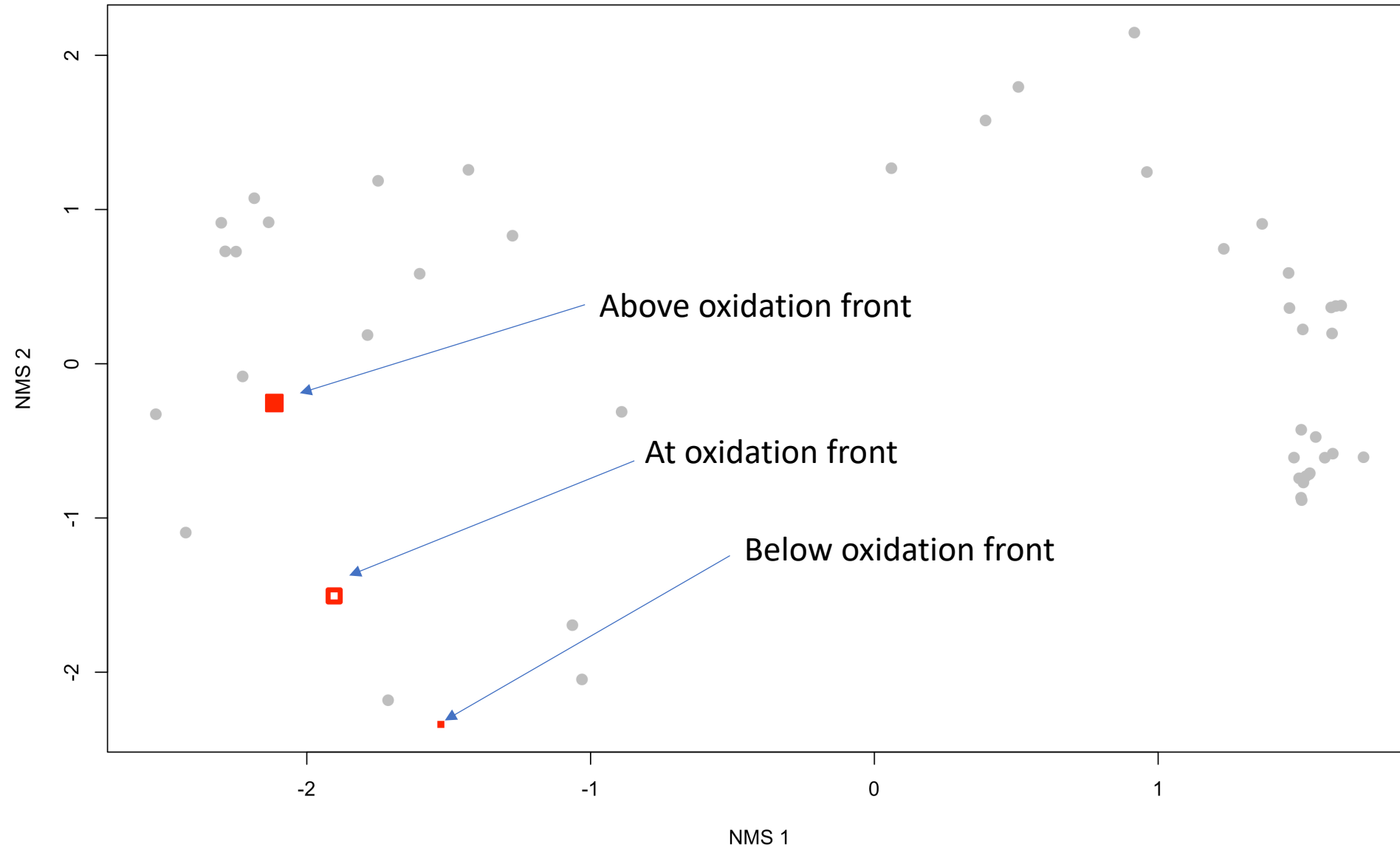
[Mackenzie.best@student.nmt.edu](mailto:Mackenzie.best@student.nmt.edu)  
<https://www.linkedin.com/in/mackenzie-best-657159142/>



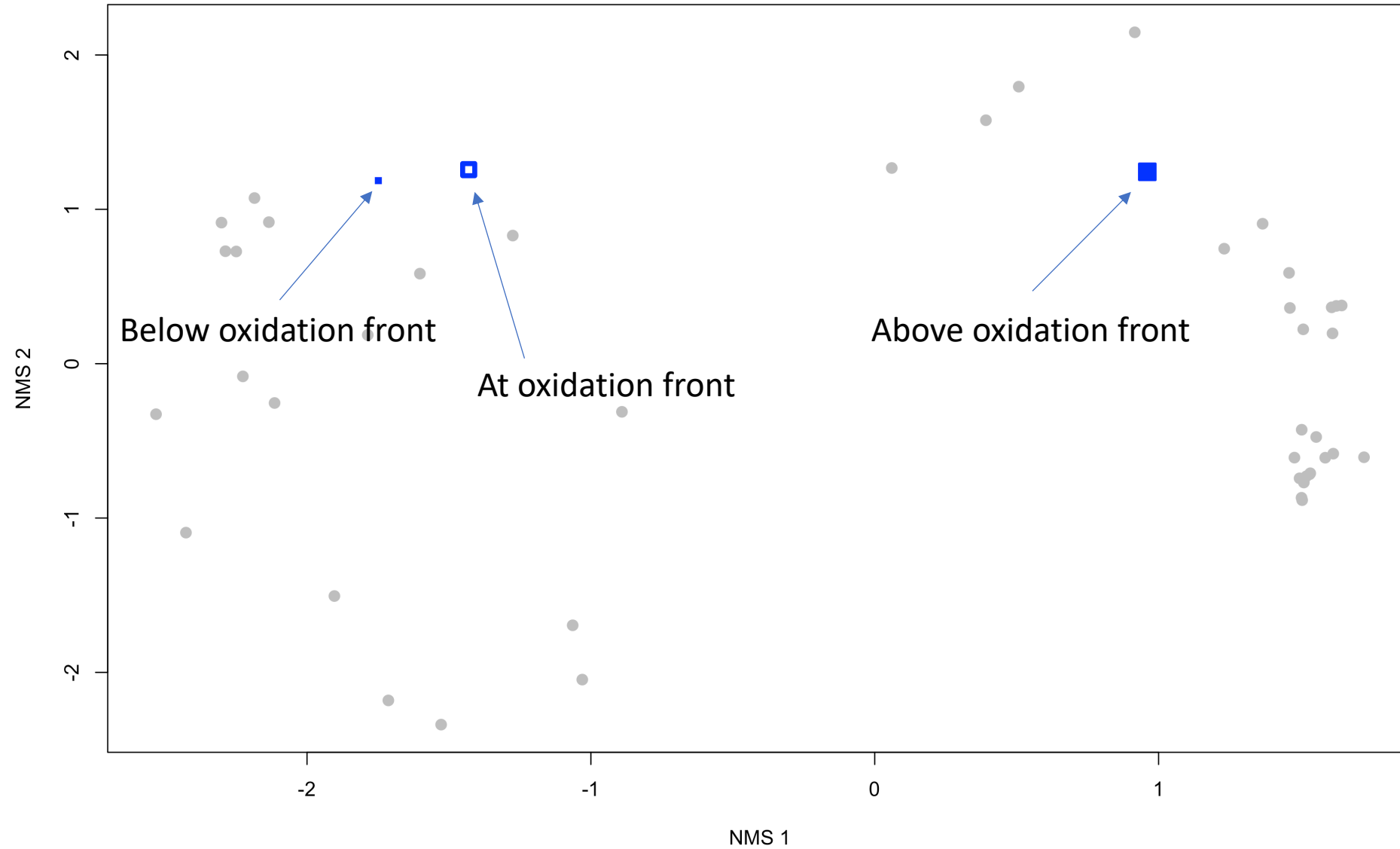




# Microbial communities vary with depth (and oxidation)



# Microbial communities vary with depth (and oxidation)



# Testing our methodology: Multiple DNA extractions per sample were similar

