

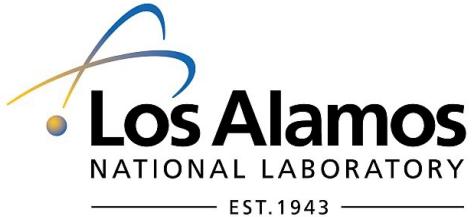


# Trait drift in the field and laboratory: Characterizing microbial community composition and genotype shifts through time

**Monica Sanchez**, Ellen Denning (LANL), Thomas Biondi (LANL), Ahlem Jebali (NMSU), Isidora Echenique (UCSD), Blake Hovde (LANL), Shawn Starkenburg, (LANL), Matt Green (LANL), Earl Middlebrook (LANL), Steve Eacker (Phase Genomics), Ivan Liachko (Phase Genomics), Alina Corcoran (NMSU)



**International Conference on Algal Biomass, Biofuels and Bioproducts 2023**  
**13<sup>th</sup> June | Waikoloa Beach, Hawaii, USA**



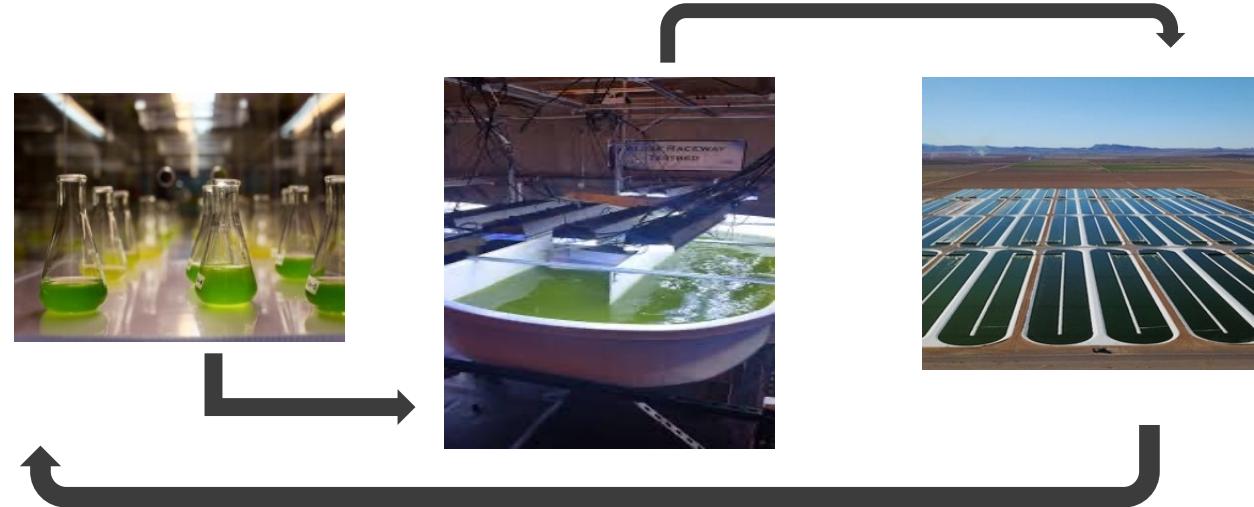


# Optimizing Selection Pressures and Pest Management to Maximize Algal Biomass Yield (OSPREY)



What drives desirable traits?

- 1) Balancing Indoor and Outdoor Selection Pressures
  - 1) Abiotic – Temperature, pH, Salinity
  - 2) Biotic- Pests/predators, Competitors
- 2) Improvement of Field Strain Performance, Resiliency, and Composition



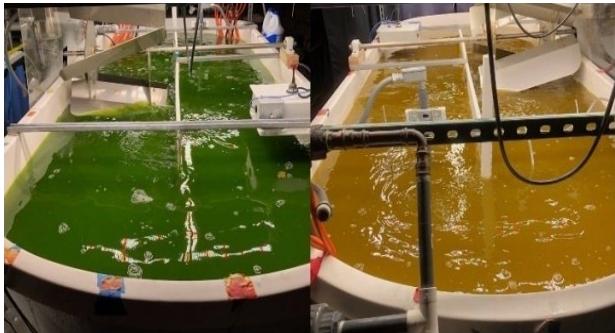
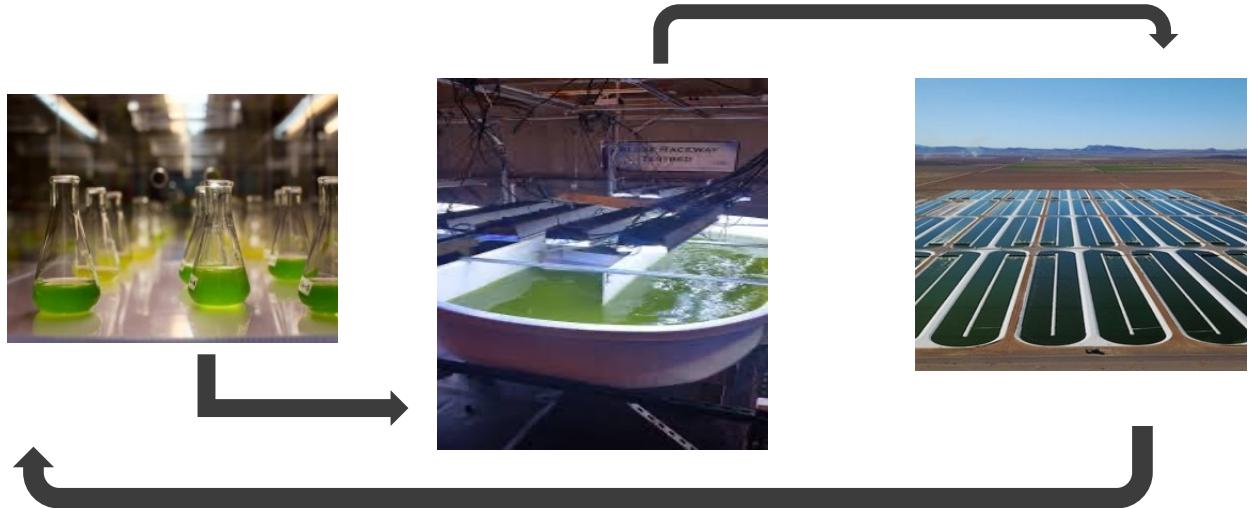


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**Healthy**                                    **Sick**



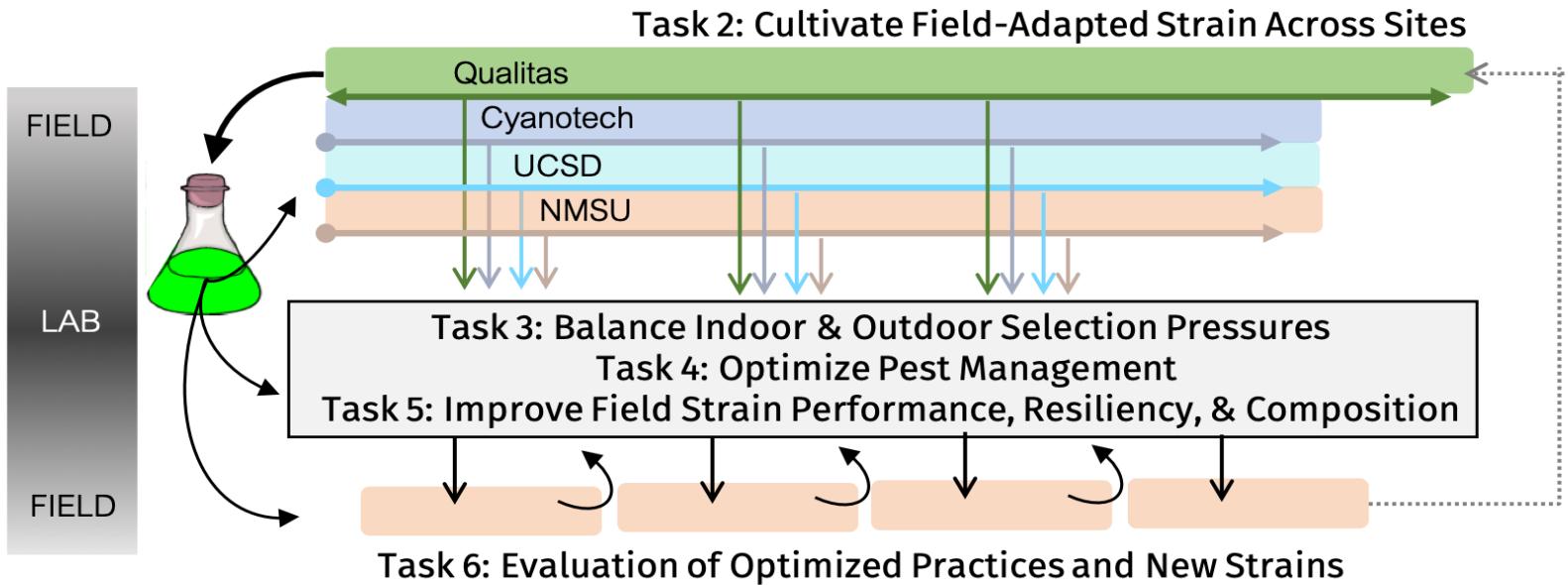
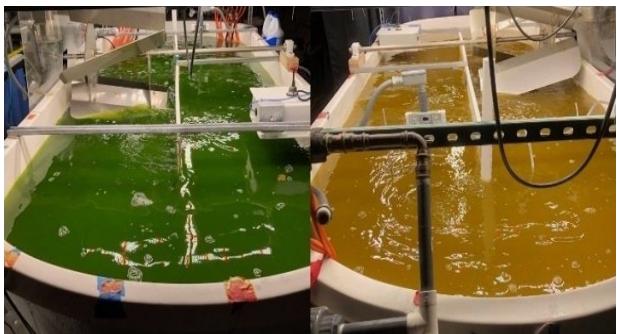


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# Tracking microbial diversity and genotypic changes



What drives changes in productivity at all scales of cultivation over time?

- 1) Maintenance in the lab – Changes in phenotype
  - 1) Plates
  - 2) Flasks
  - 3) Bioreactors
- 1) Field cultivation
  - 1) Pests
  - 2) Environmental effects
1. Acquire growth rates and phenotypically characterize over time
2. Characterize changes in microbial diversity
3. Identify algal genomic changes

# Tracking microbial diversity and genotypic changes



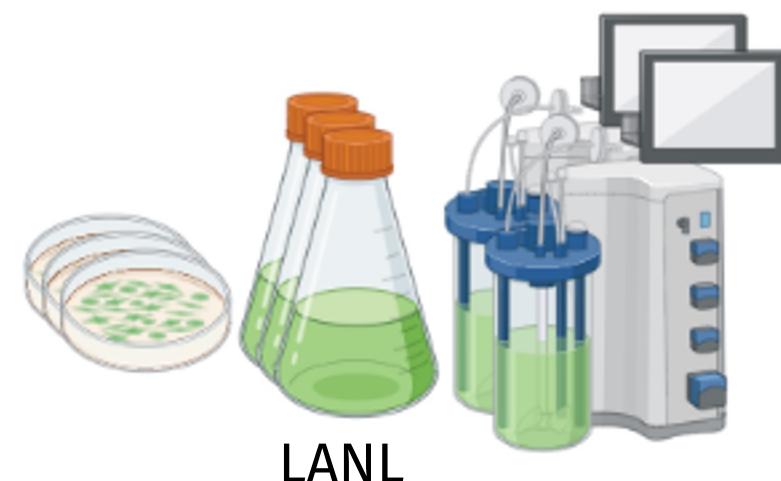
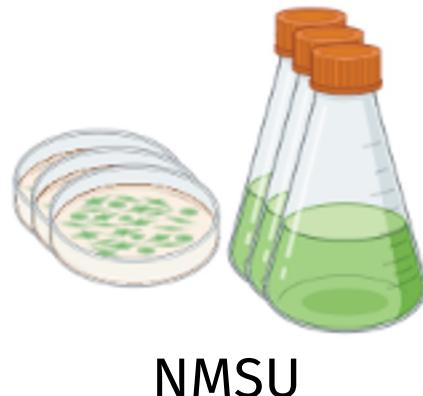
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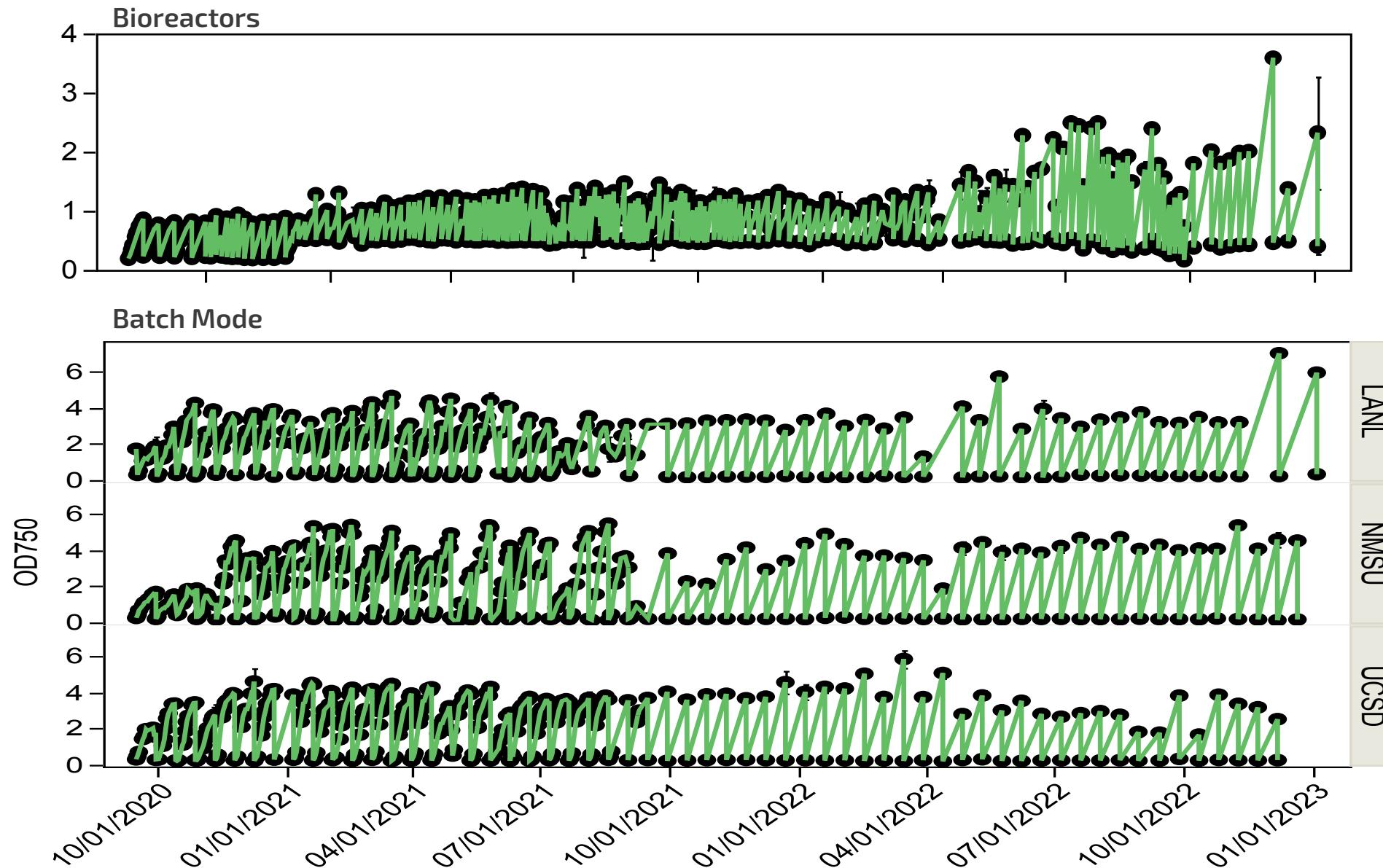
# Maintenance of field-adapted strain across three labs using three different culturing methods

## I) QT001 established under 3 different growth modes

- 1) Storage on plates (3 reps each at of 3 labs)
- 2) Batch w/ transfers every 2 weeks (3 reps at each of 3 labs)
- 3) Bioreactors to simulate Imperial, TX (2 reps at LANL)



# Cultivation across lab sites and culture modes



# Distributed test beds across four sites

*Nannochloropsis* sp. QT001 ponds in Texas, New Mexico, California and Hawaii

Different environmental pressures

Changes in microbial diversity

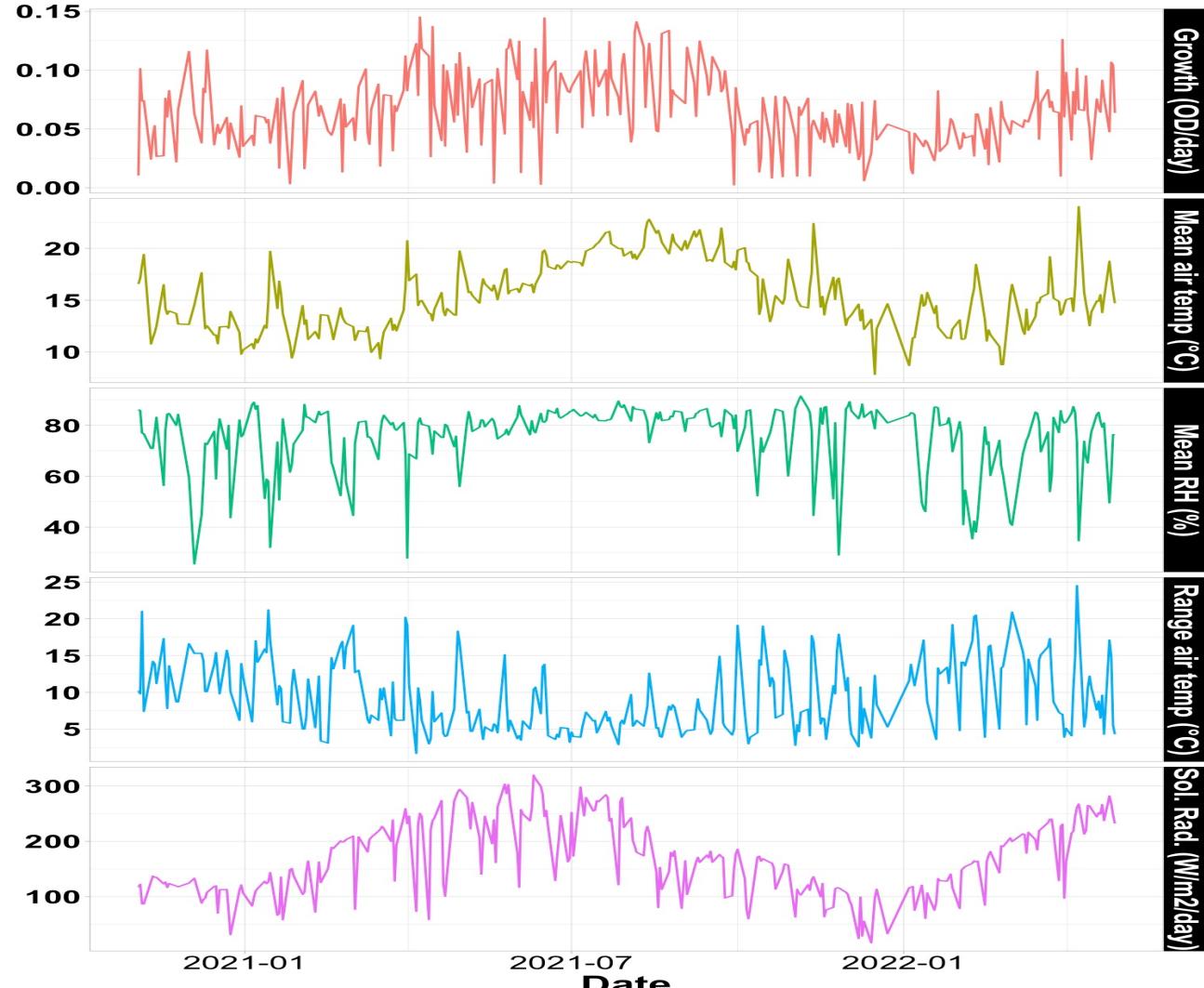


# UCSD Growth and environmental parameters

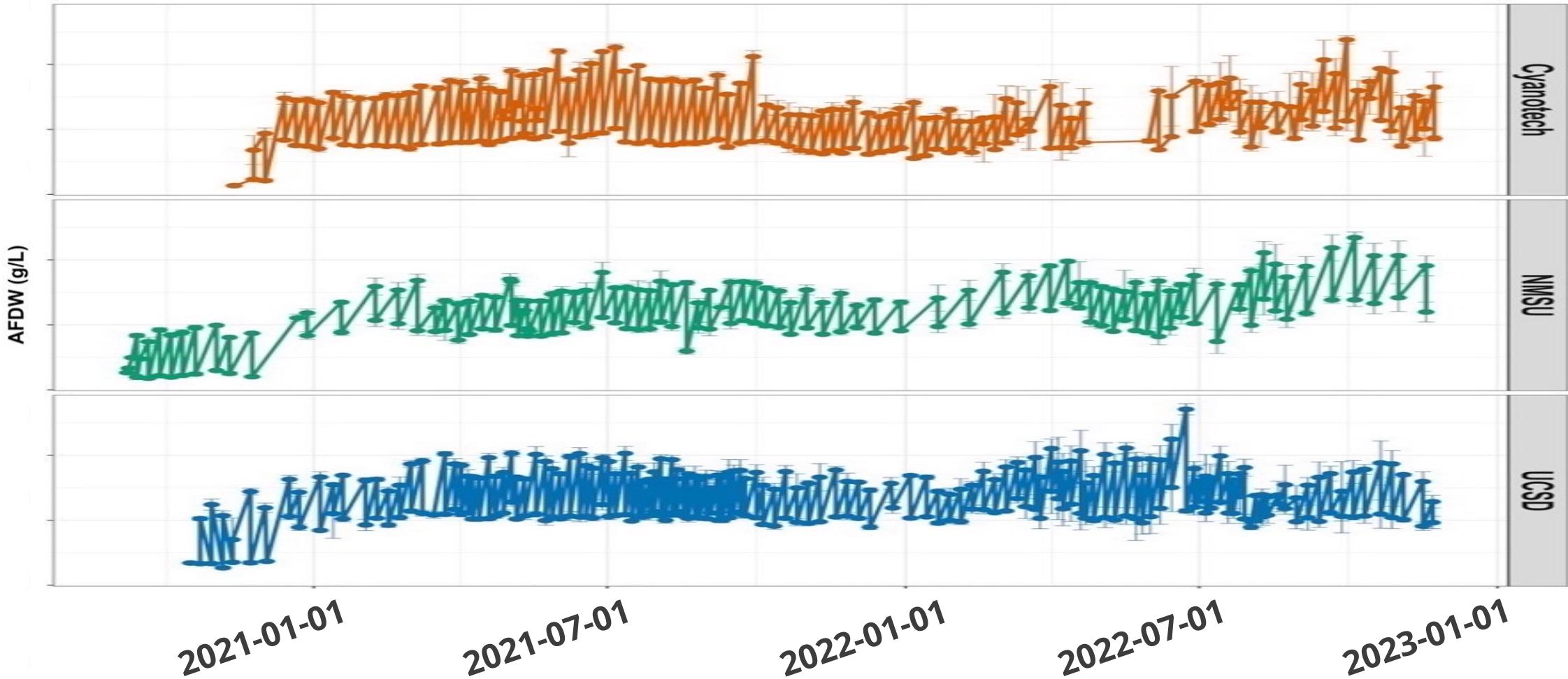


- 1) Growth monitoring over time
- 2) Environmental data
- 3) 16S sequencing
- 4) ProxiMeta Analysis
- 5) Metadata (CO<sub>2</sub>, bleach dosing, etc.,)

Correlate periods of low productivity with various factors



# Cultivation Across Sites and Culture Modes over



# Tracking microbial diversity and genotypic changes



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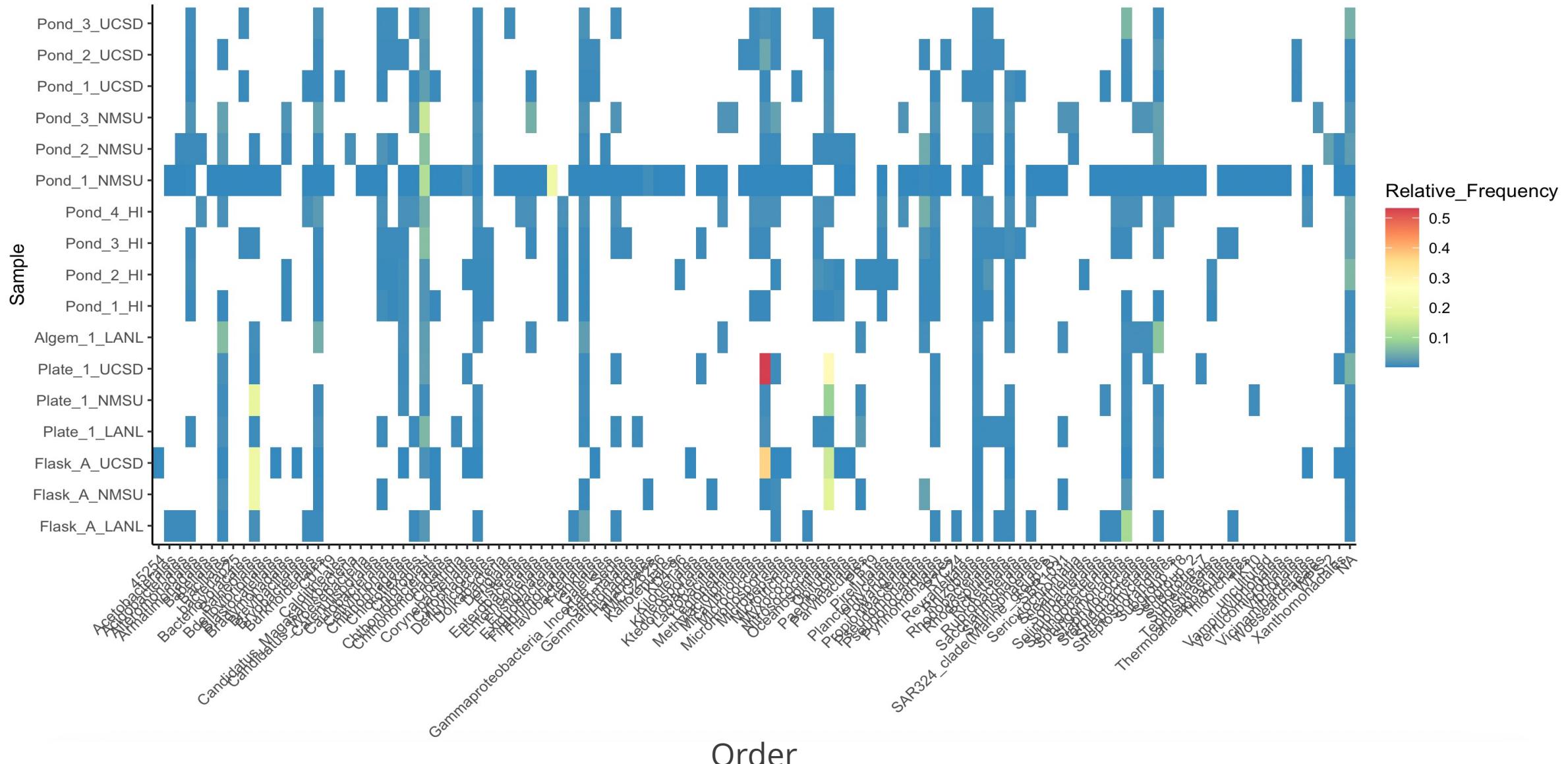
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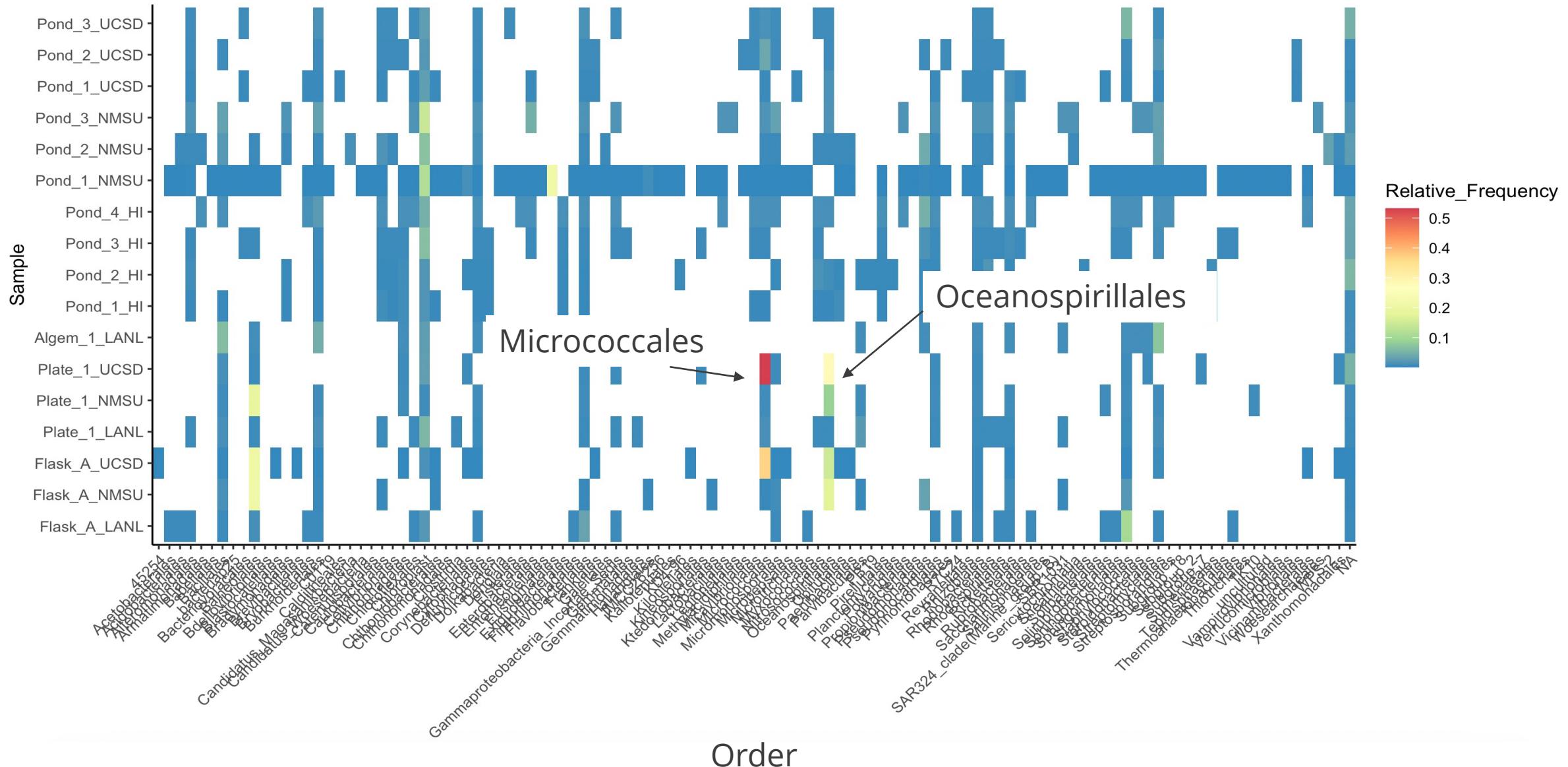
# 16S Relative abundance after three months of cultivation



15

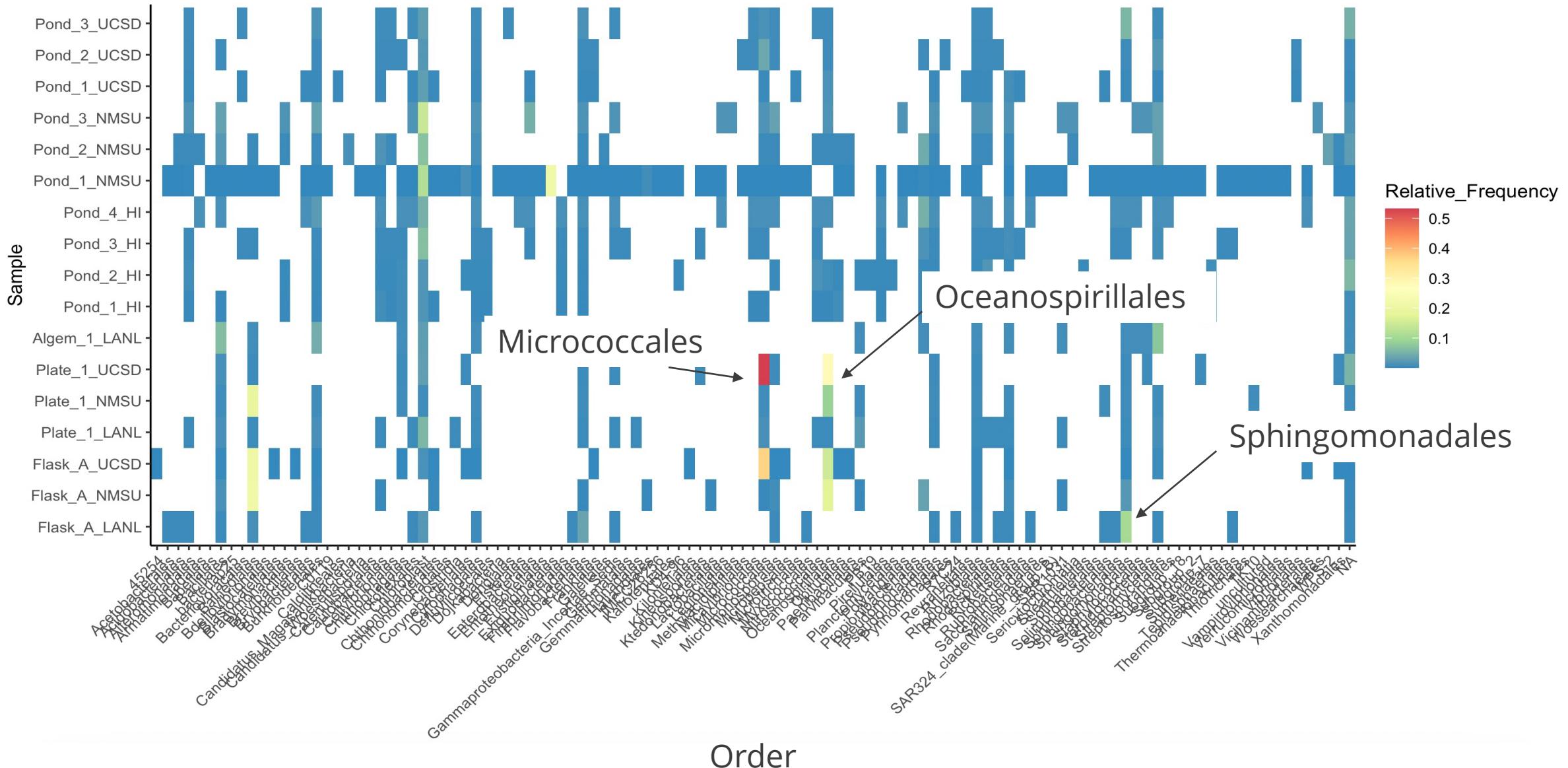


## 16S Relative abundance after three months of cultivation

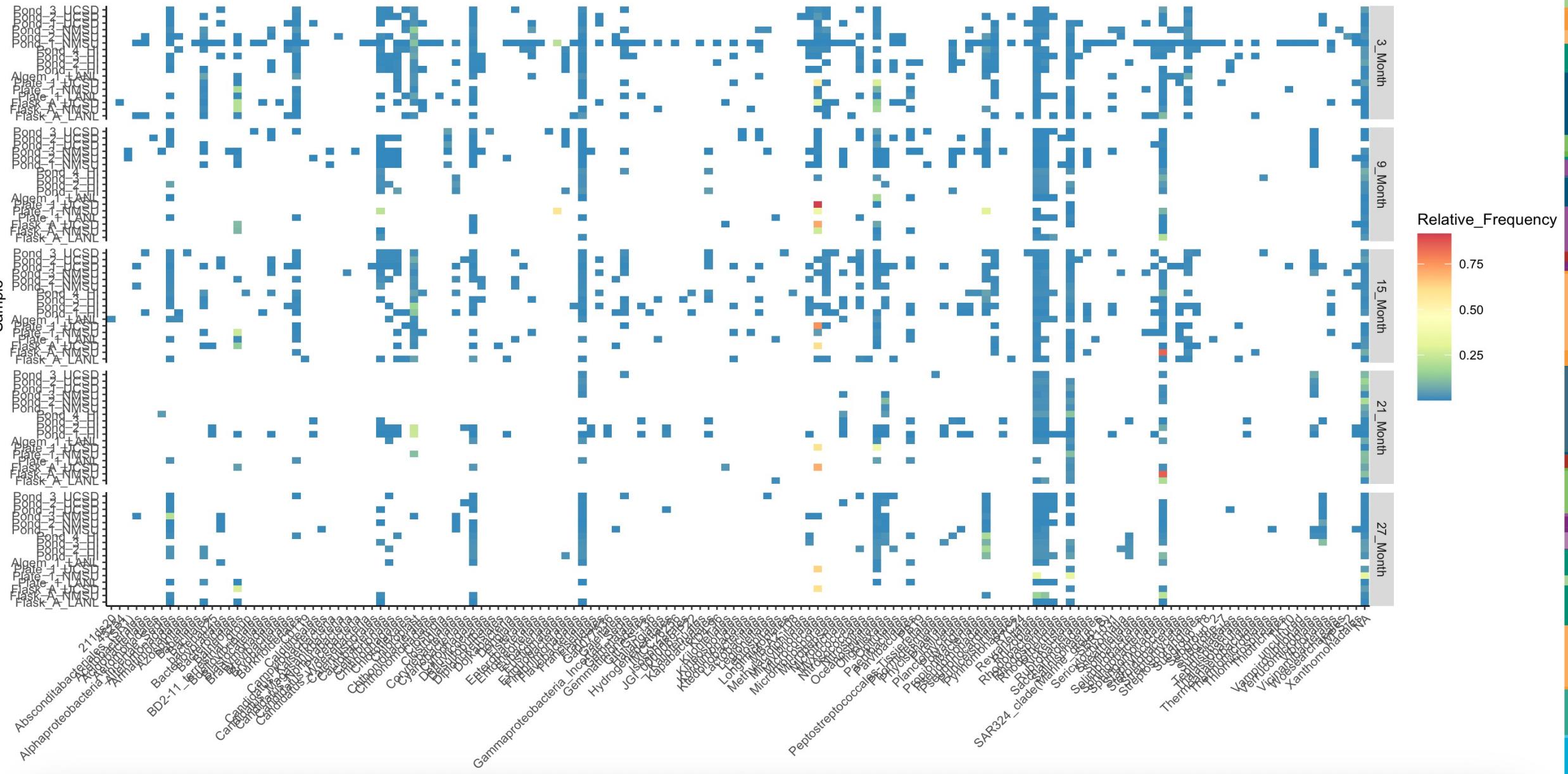


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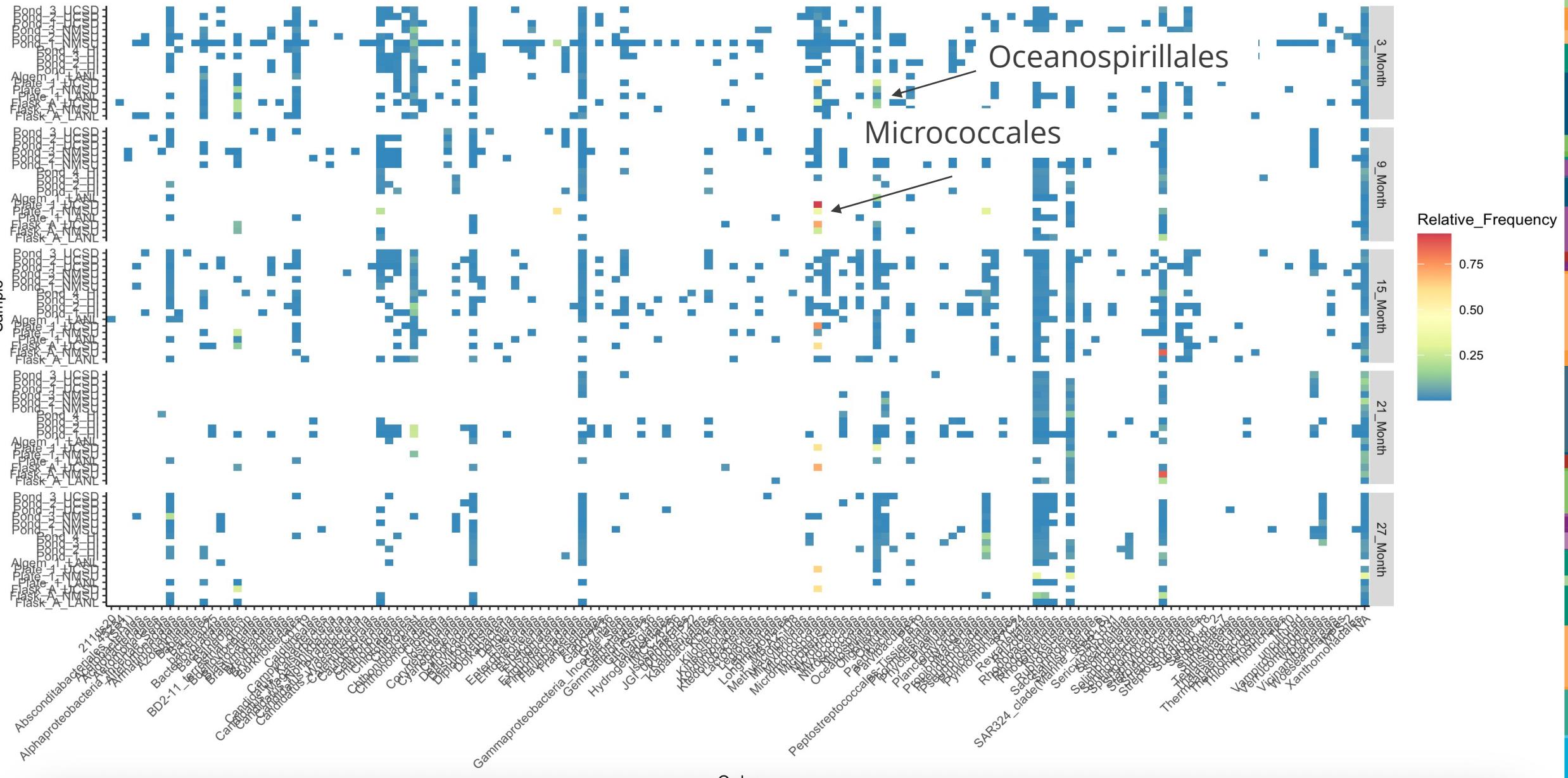
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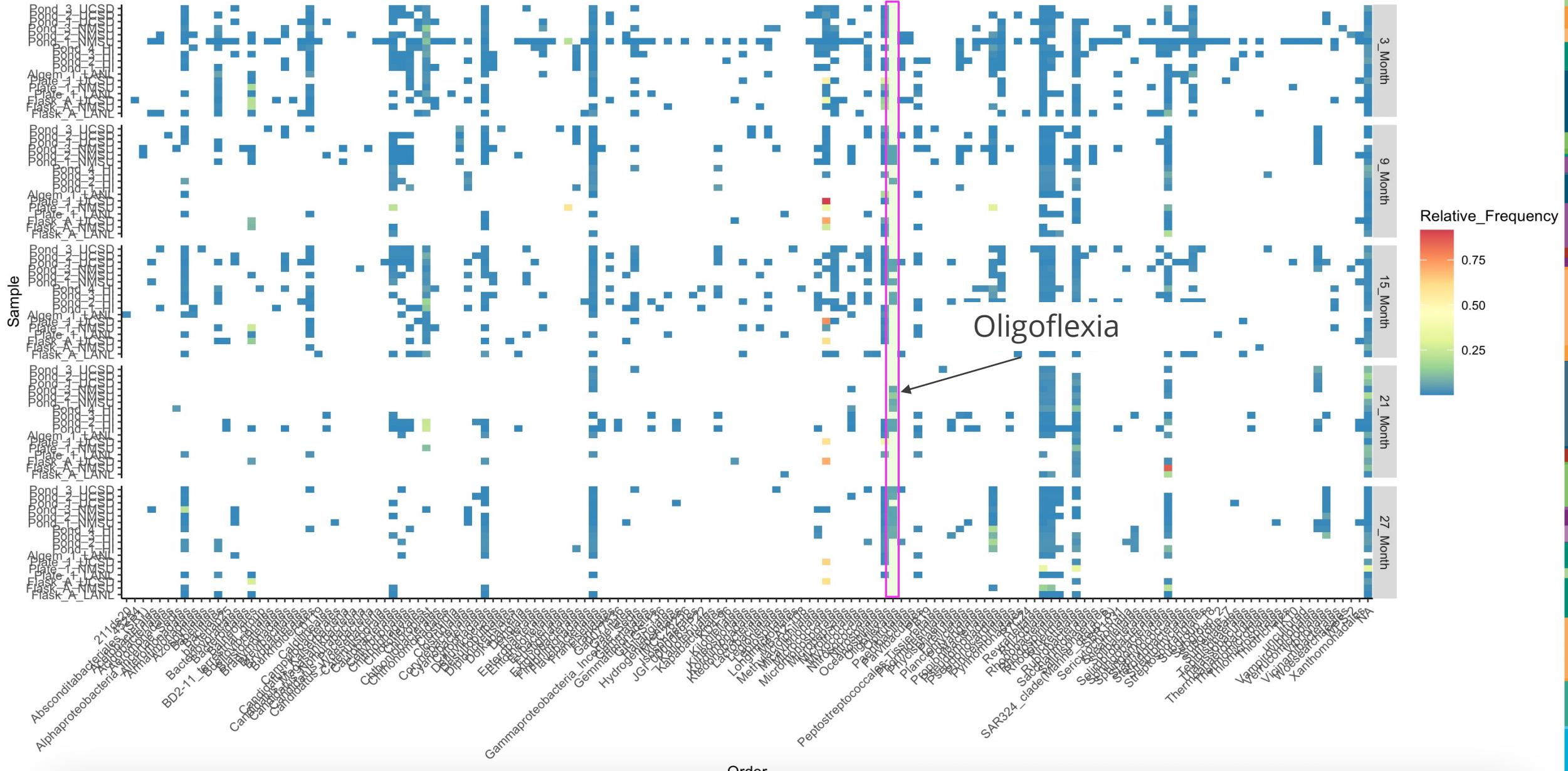
# 16S Relative abundance over twenty-seven months



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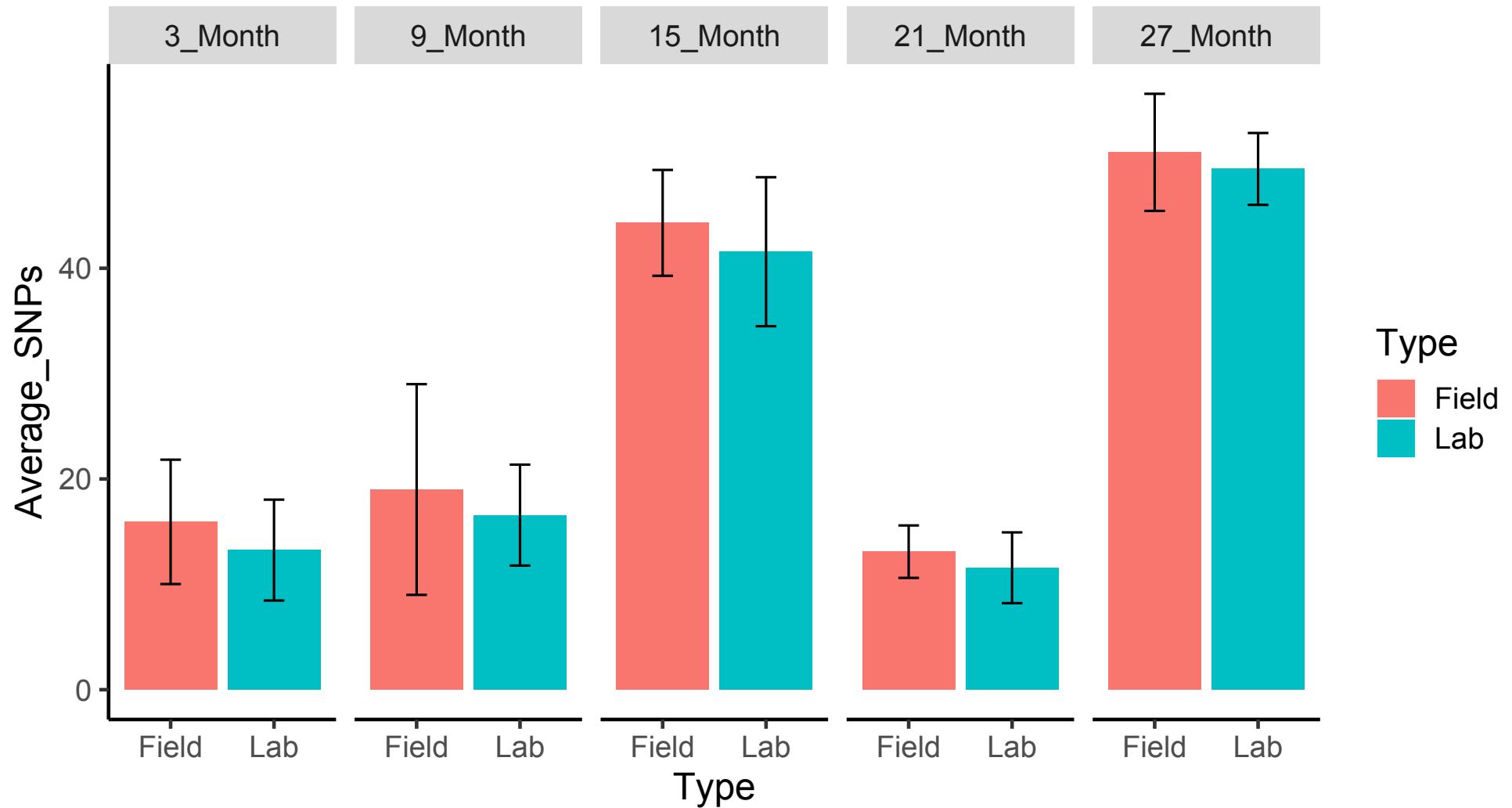
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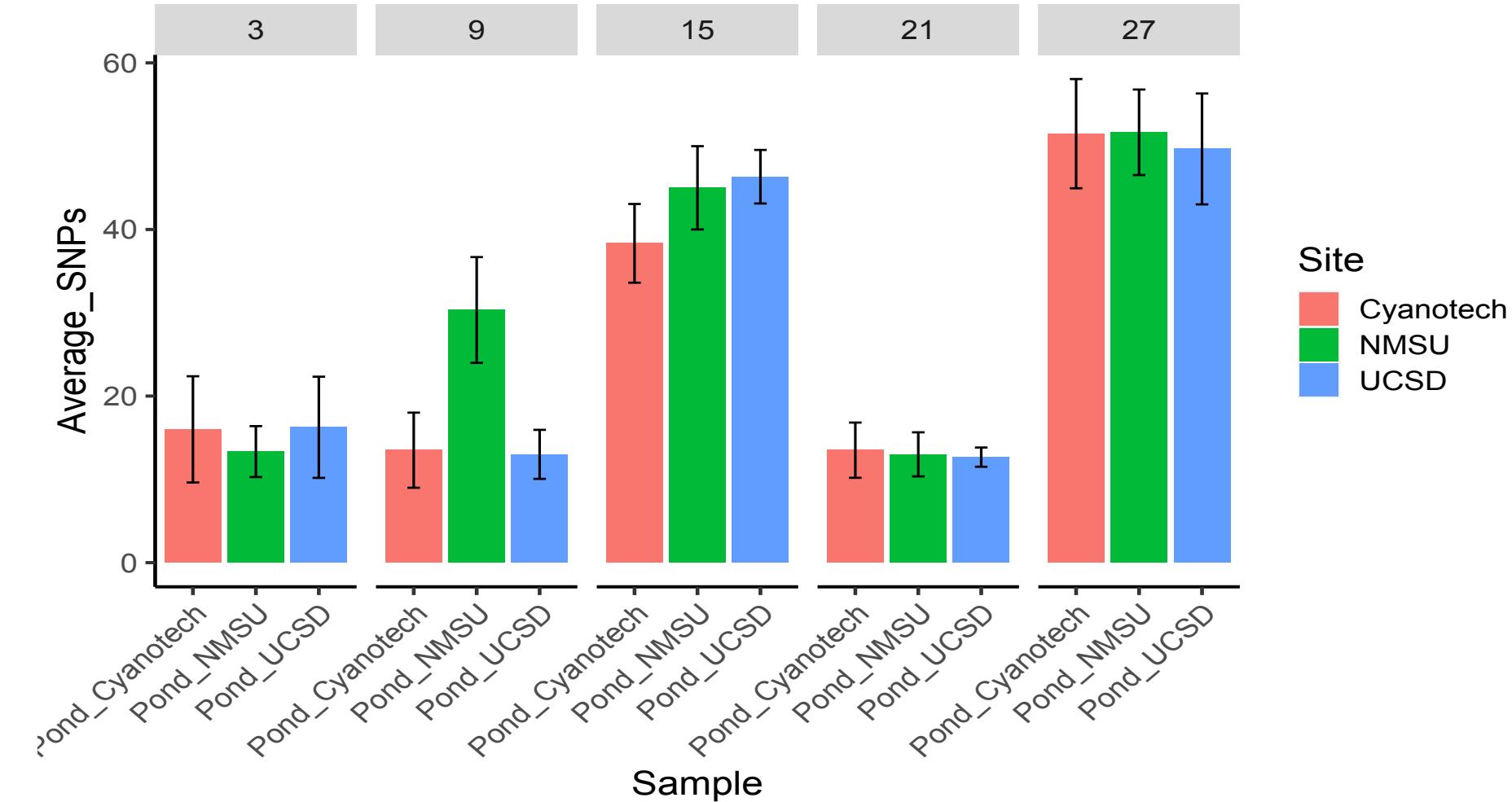
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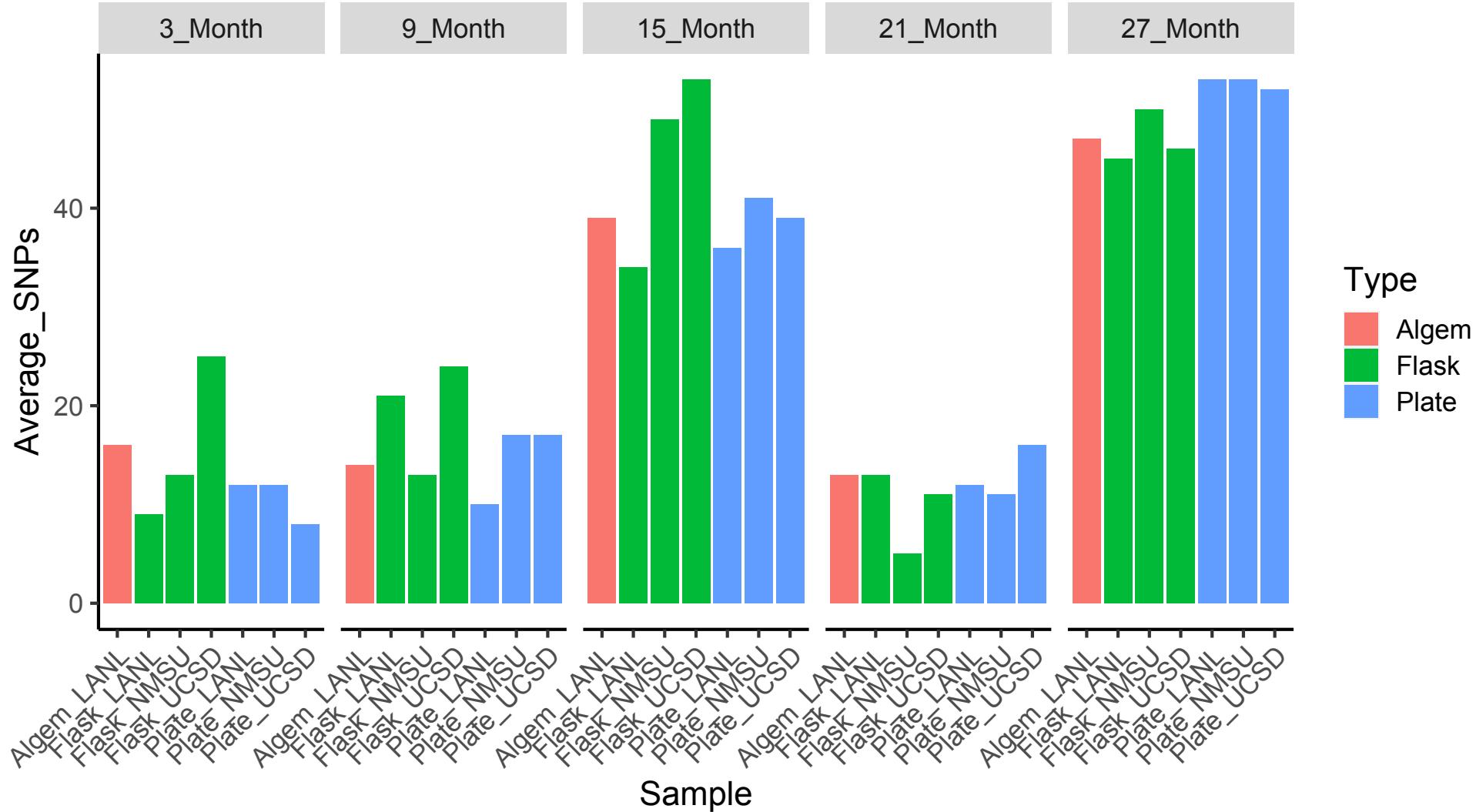
# Average number of SNPs over time: Field vs Lab



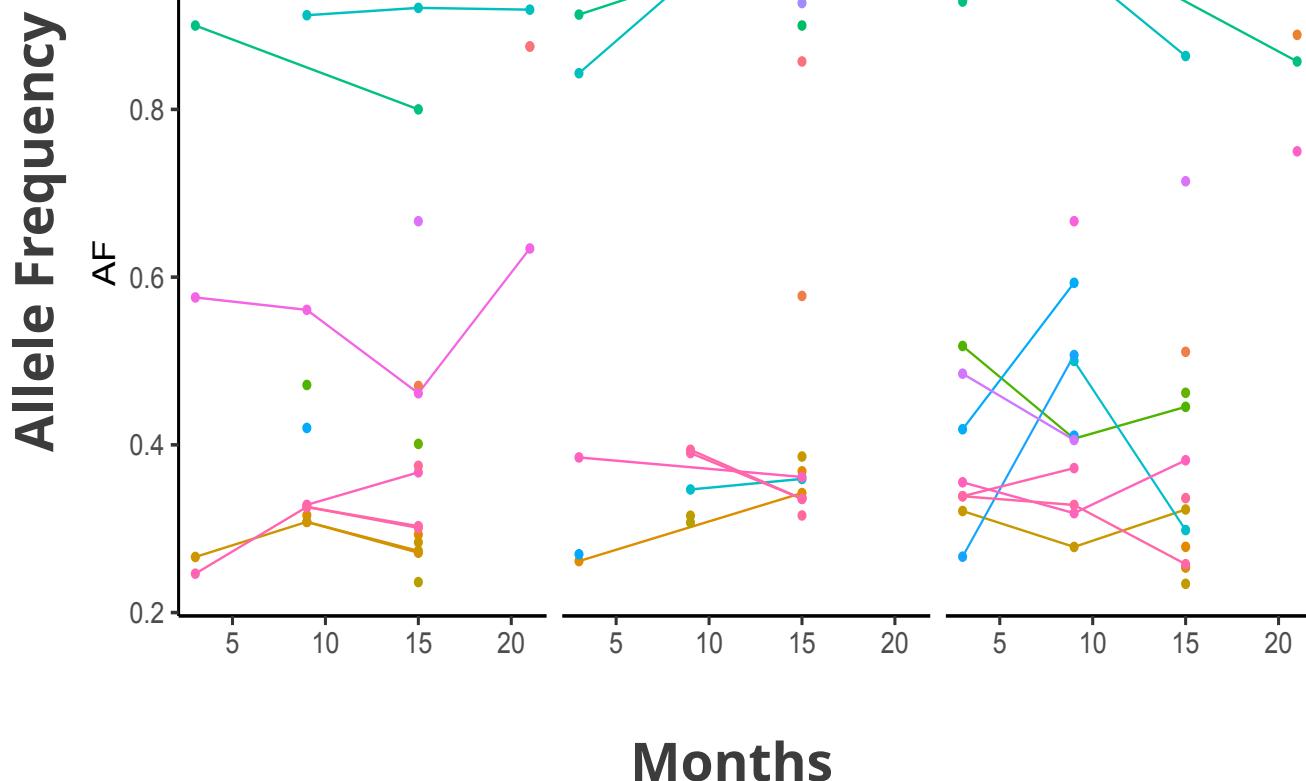
# Average number of SNPs over time: Ponds



# Average number of SNPs over time: Lab



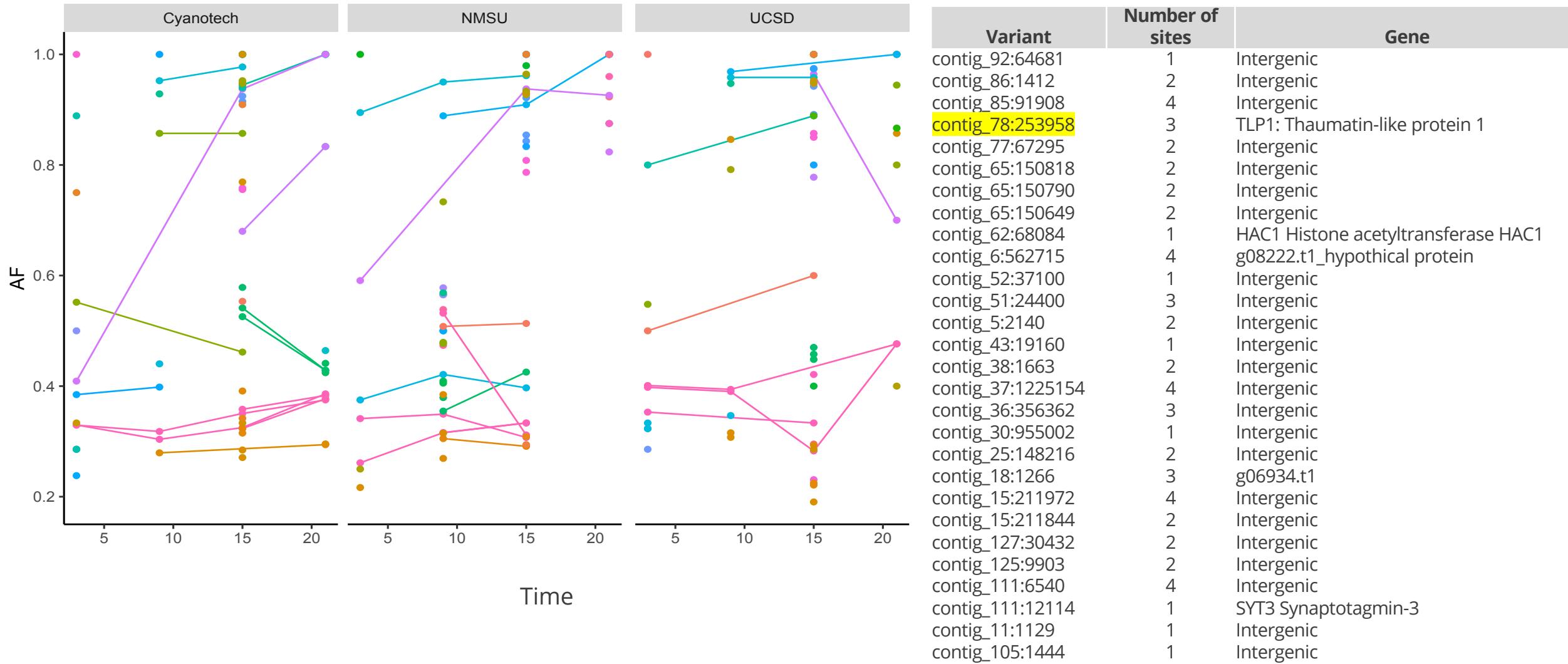
# Tracking allele frequencies of lab-maintained strains (Flasks)



Variant	Number of sites	Gene
contig_127:30432	3	Intergenic
		MNS4: Alpha-mannosidase I
contig_36:356361	3	MNS4
contig_37:1225154	3	Intergenic
contig_5:2139	3	Intergenic
contig_51:24400	3	Intergenic
contig_52:37100	3	Intergenic
contig_6:562714	3	Hypothetical protein
contig_65:150702	2	Intergenic
contig_65:150790	2	Intergenic
contig_77:68452	3	Transcription elongation factor spt6
contig_38:2084	1	ATP-dependent DNA/RNA helicase DHX36

- Some alleles started out at fixation or quickly approached fixation
- Others changed through time

# Tracking allele frequencies of field-maintained strains (Ponds)



# In Summary



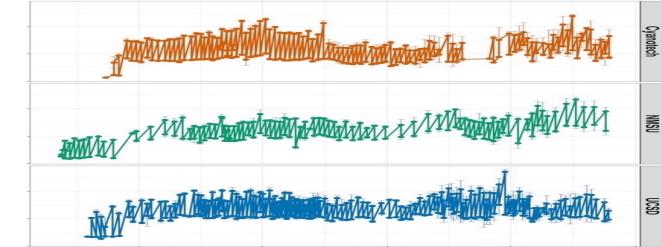
- 1) Cultivate field adapted strain across sites and cultivation type



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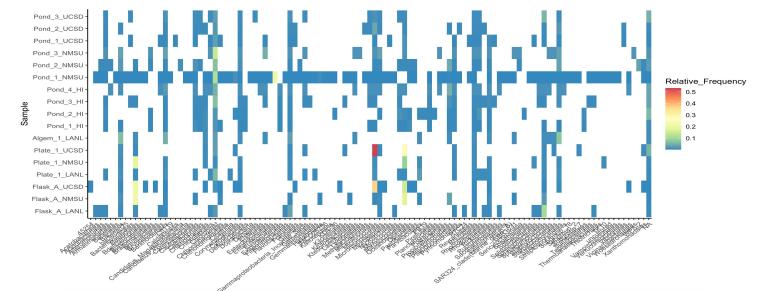
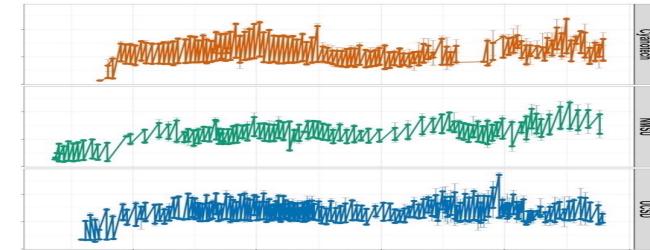
- 1) Cultivate field adapted strain across sites and cultivation type
- 2) Acquired growth and metadata across ~3 year time span



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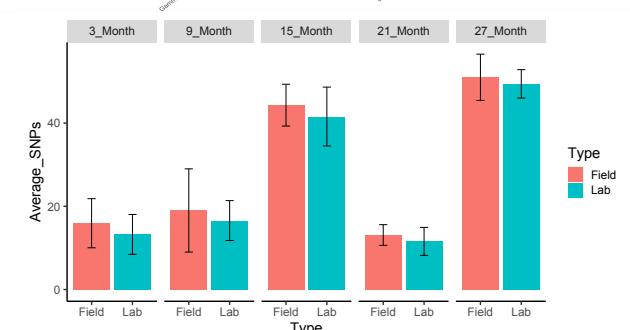
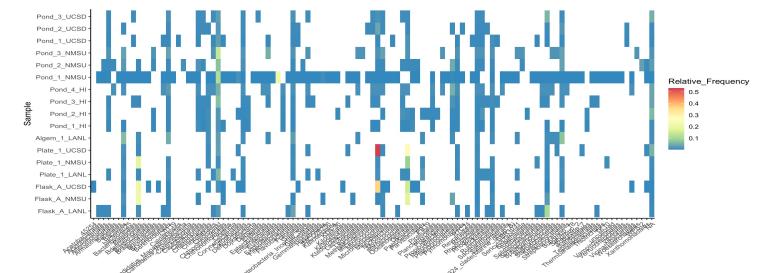
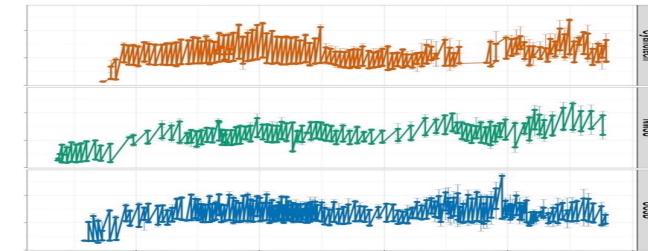
- 1) Cultivate field adapted strain across sites and cultivation type
- 2) Acquired growth and metadata across ~3 year time span
- 3) Characterize microbial dynamics in lab and field maintained cultures
  - 1) Differences in microbial diversity across labs
  - 2) Identification of potential pest



# In Summary



- 1) Cultivate field adapted strain across sites and cultivation type
- 2) Acquired growth and metadata across ~3 year time span
- 3) Characterize microbial dynamics in lab and field maintained cultures
  - 1) Differences in microbial diversity across labs
  - 2) Identification of potential pest
- 1) Track algal genotypic changes through time
  - 1) General trend of increase in mutations over time
  - 2) Associate mutations with increases in productivity





Thank  
you!

