

# Sign of the times: the lipid signature of a collapsing phytoplankton bloom

W. Kumler<sup>1</sup>, H. Fredricks<sup>2</sup>, J. Ossolinski<sup>2</sup>, A. Allen<sup>3</sup>, K. Thamatrakoln<sup>4</sup>, K. Bidle<sup>4</sup>, B. Van Mooy<sup>2</sup>, and B. R. Edwards<sup>1</sup>

<sup>1</sup>Earth and Planetary Science, UC Berkeley; <sup>2</sup>Marine Chemistry and Geochemistry, WHOI; <sup>3</sup>Biological Oceanography, SIO; <sup>4</sup>Marine and Coastal Sciences, Rutgers

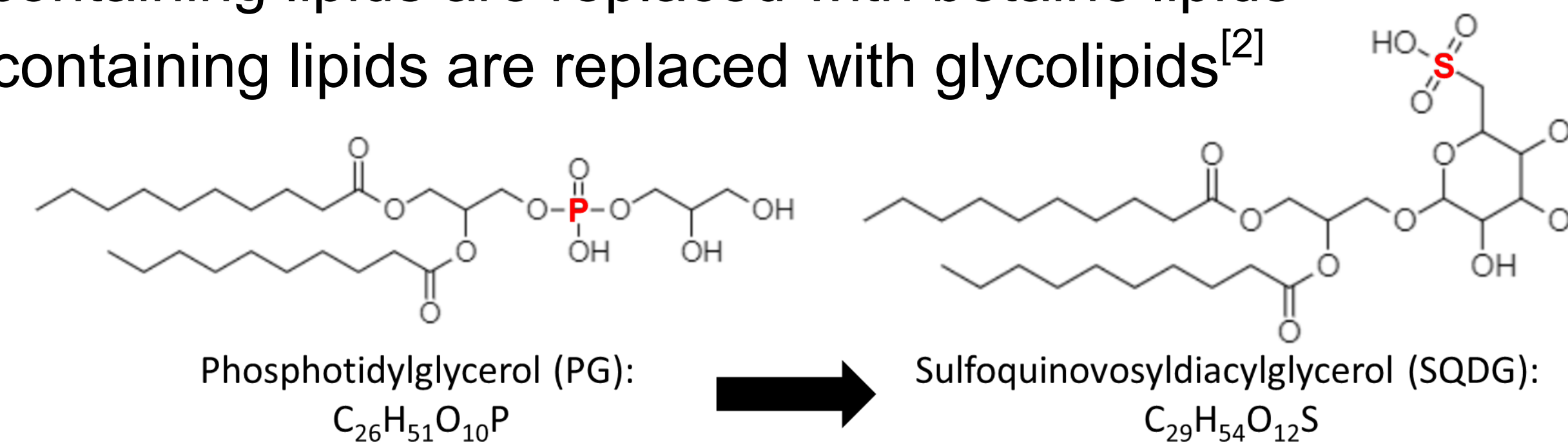
## Background

- Phytoplankton blooms are impactful, large-scale events in the ocean
- They collapse abruptly when population controls are re-established



- Traditional methods have emphasized nutrient limitation as the major decay factor

- Lipids are excellent biomarkers for environmental stresses and community composition
- In oligotrophic environments, lipid swapping has been used as a biomarker for nutrient stress
  - P-containing lipids are replaced with betaine lipids<sup>[1]</sup>
  - N-containing lipids are replaced with glycolipids<sup>[2]</sup>

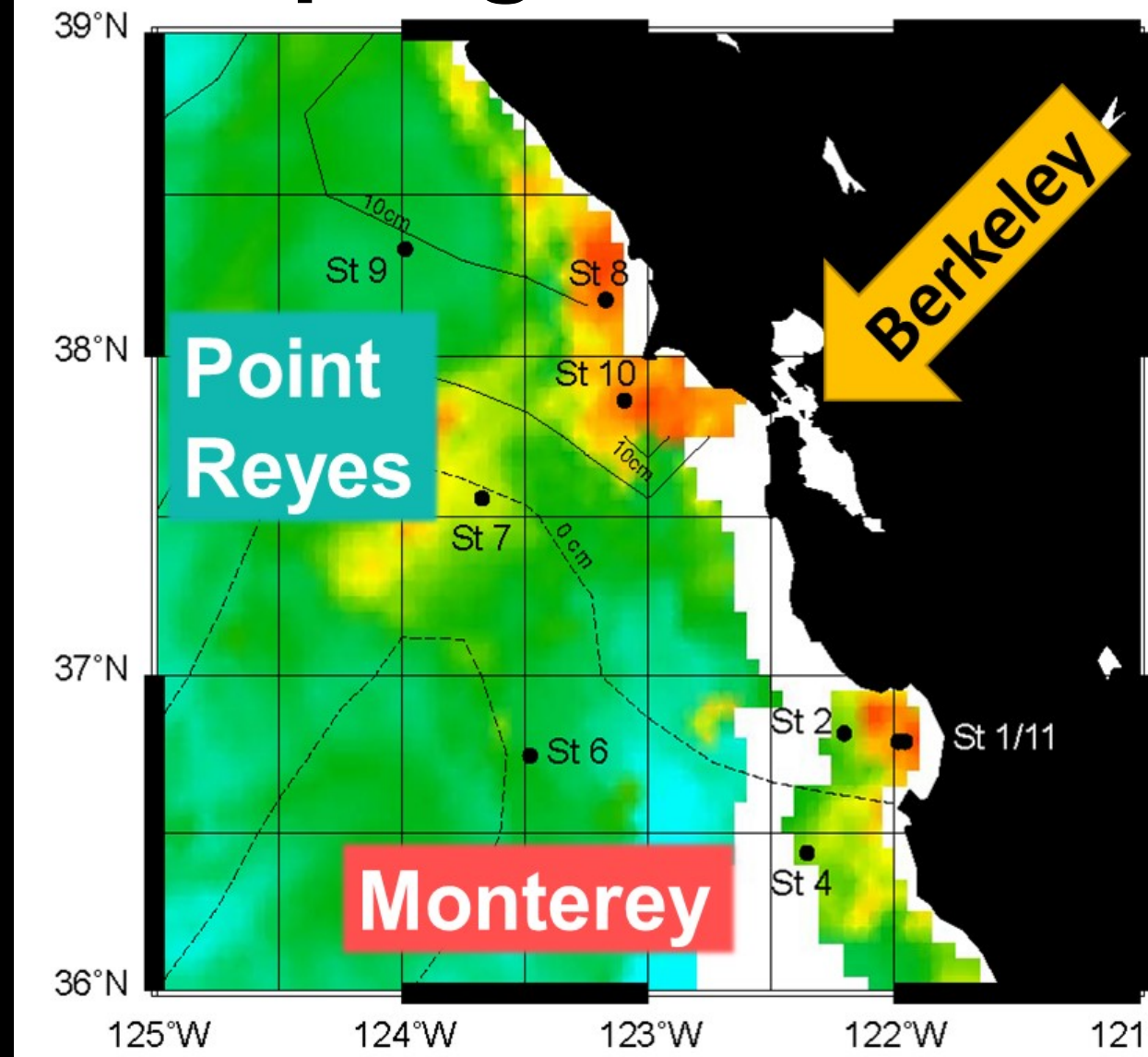


Research question:

Can we use lipids to assess bloom dynamics in eutrophic systems?

## Methods

### Sampling locations:



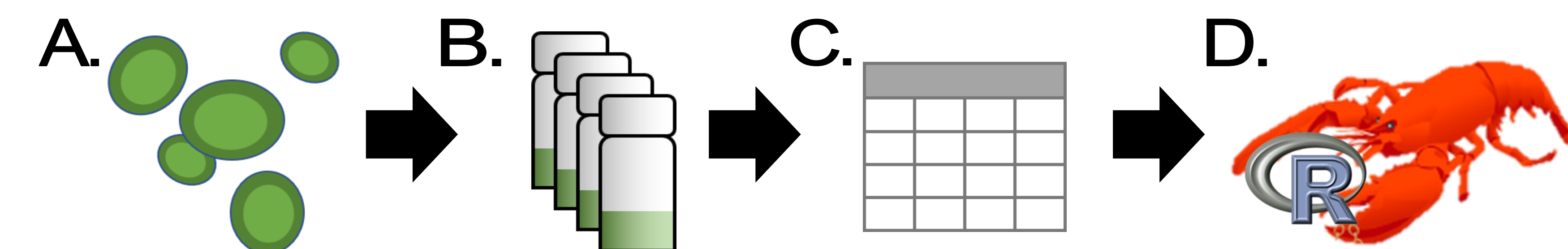
Samples were processed via lipidomics pipeline. Environmental samples were collected from 9 stations in the California Current Ecosystem then

**A.** filtered onto 0.2  $\mu$ m Durapore filters and

**B.** extracted via a modified Bligh & Dyer.<sup>[3]</sup> These extracts were then

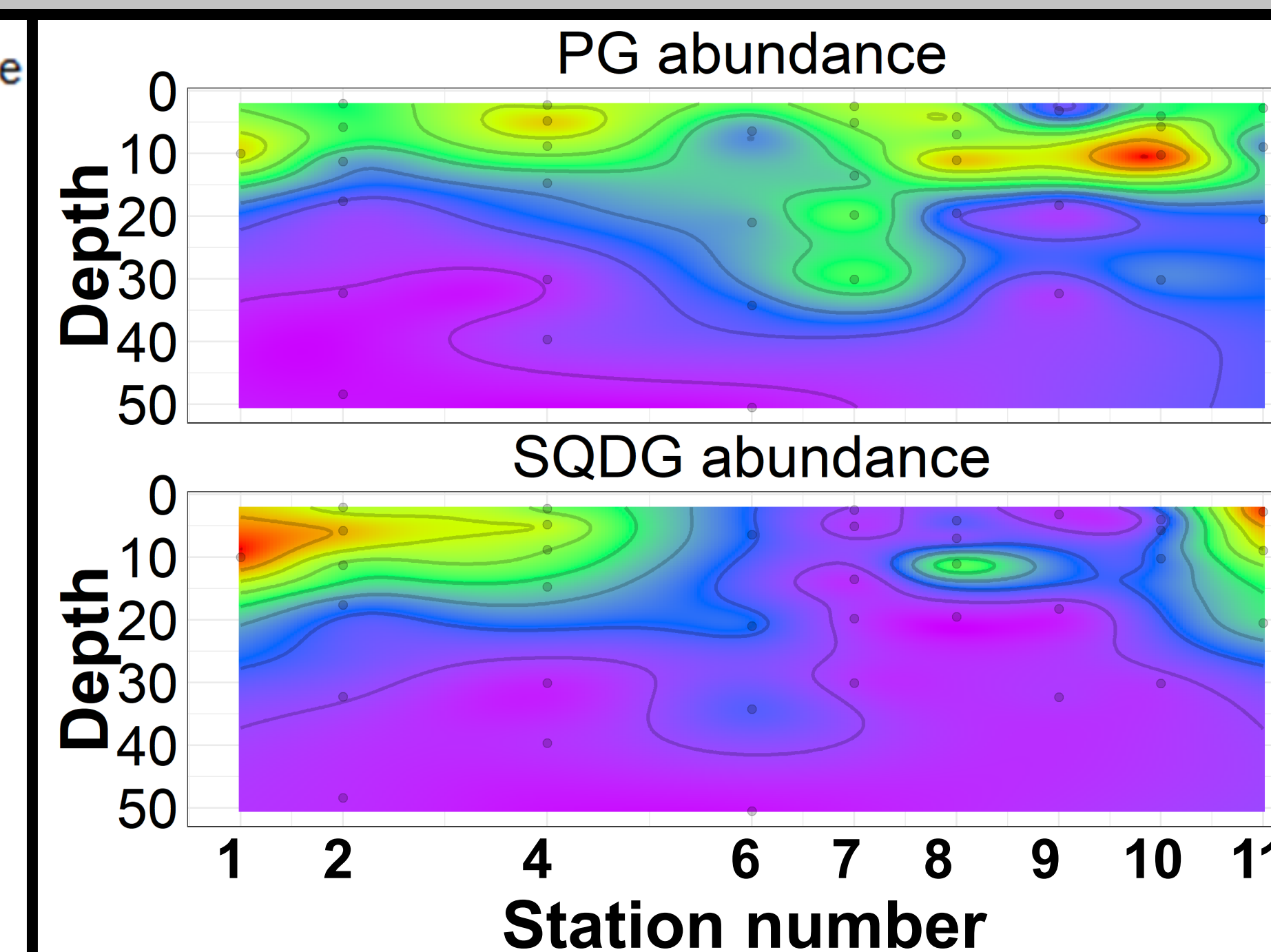
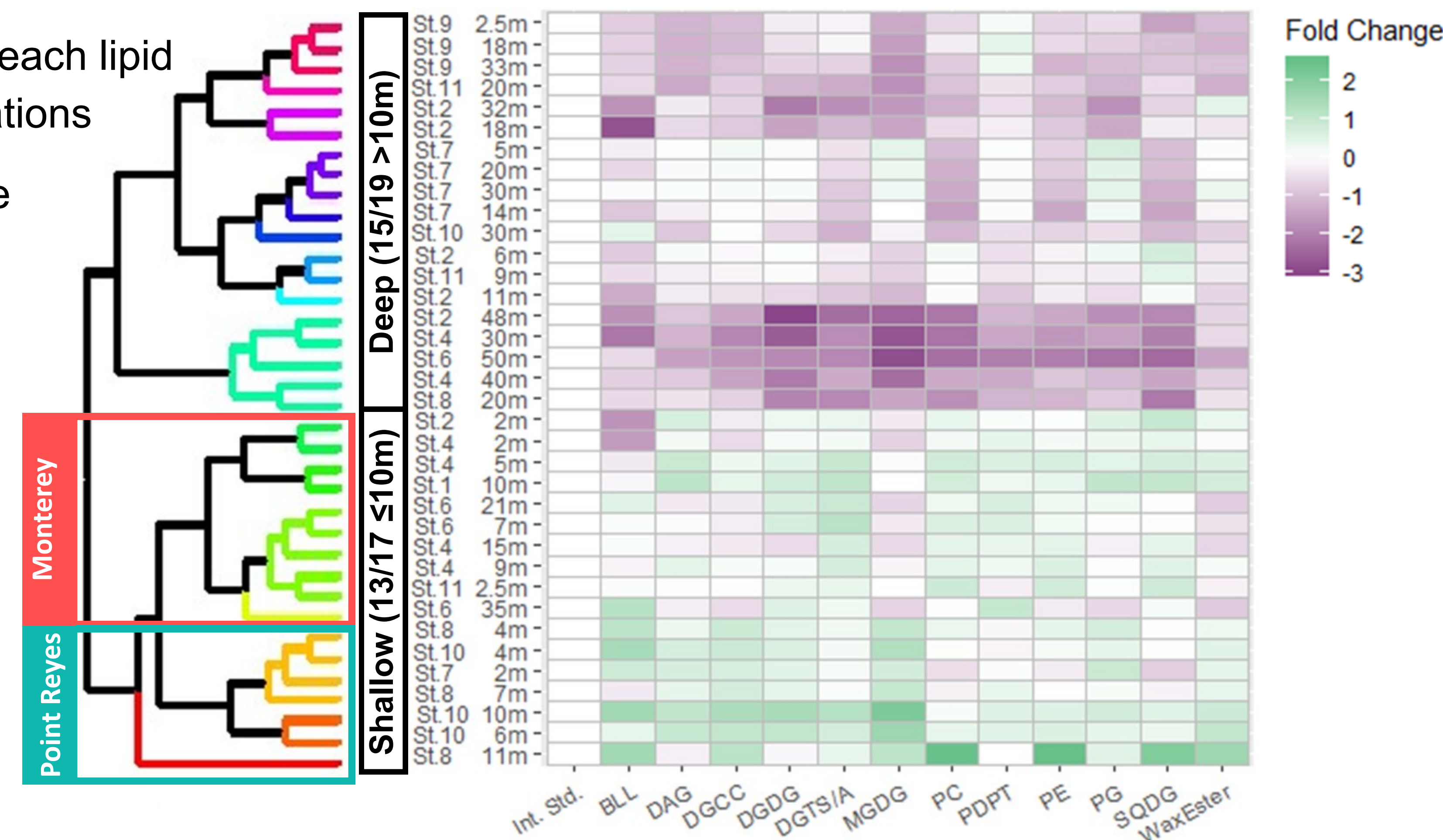
**C.** analyzed via HPLC-MS<sup>[4]</sup> and

**D.** annotated via the R packages xcms, CAMERA, and LOBSTAHS.<sup>[5]</sup>



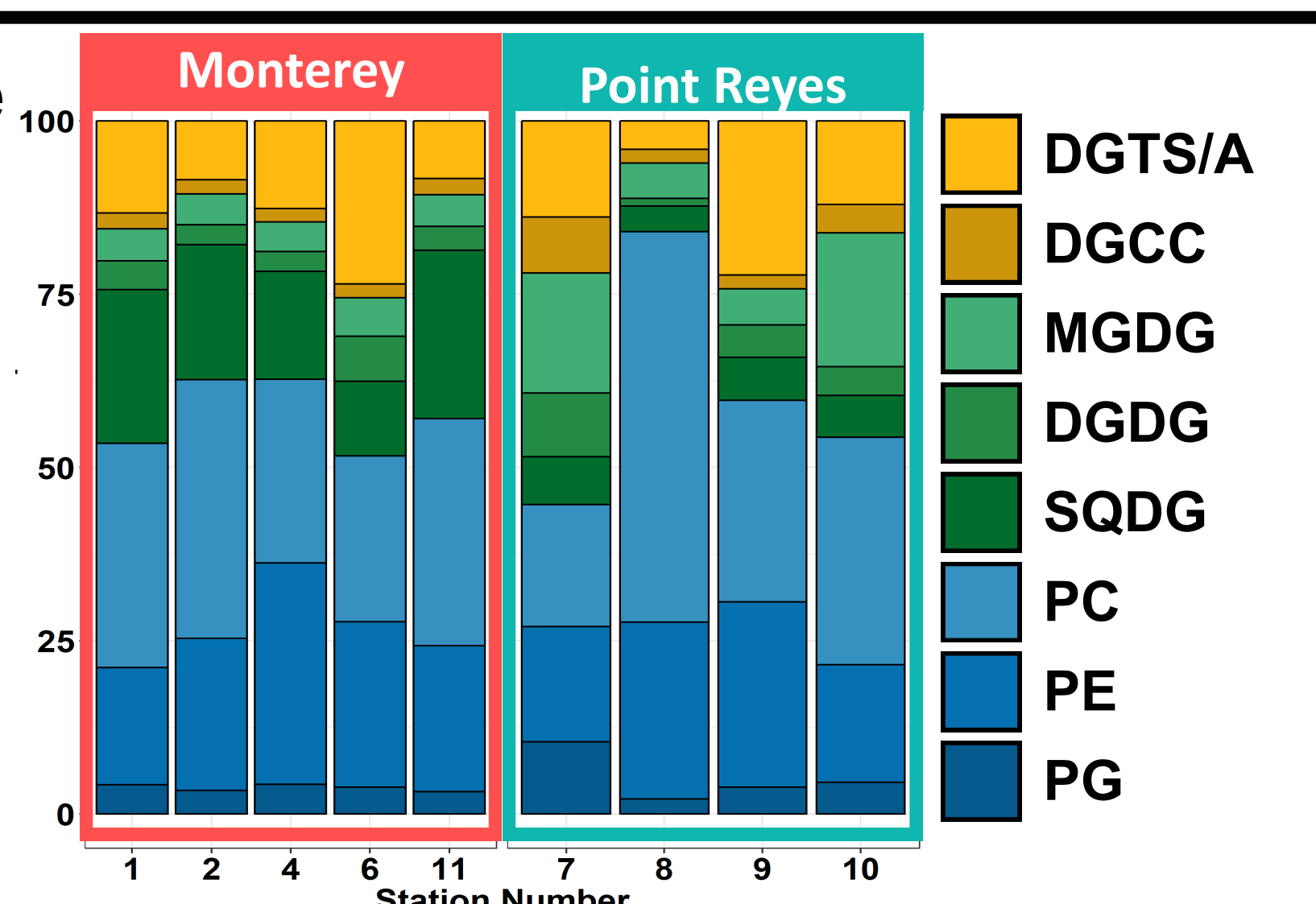
## Results

- Heatmap data shows the fold-change of each lipid sub-class relative to the mean across stations
- Dendrogram group colors denote that the lipidome structure is significantly similar between those samples<sup>[6]</sup>
- Deep samples (>10 meters) show a significant decrease in intensity, aligning with expectations based on lipid lability
- Among the shallow samples, all Point Reyes samples are significantly different from all Monterey samples



- Something about PG not changing implying that SQDG is driving biomarker changes
- ...and therefore community shift?

- Common intact membrane lipids (IP-DAGs) identified at every station
- Variation in relative abundances imply either nutrient stress induced lipid swapping or shifts in community composition



DGTS = diacylglyceroltrimethylhomoserine

DGTA = diacylglycerol hydroxymethyltrimethyl- $\beta$ -alanine

DGCC = diacylglycerol carboxyhydroxymethylcholine

MGDG = monogalactosyldiacylglycerol

DGDG = digalactosyldiacylglycerol

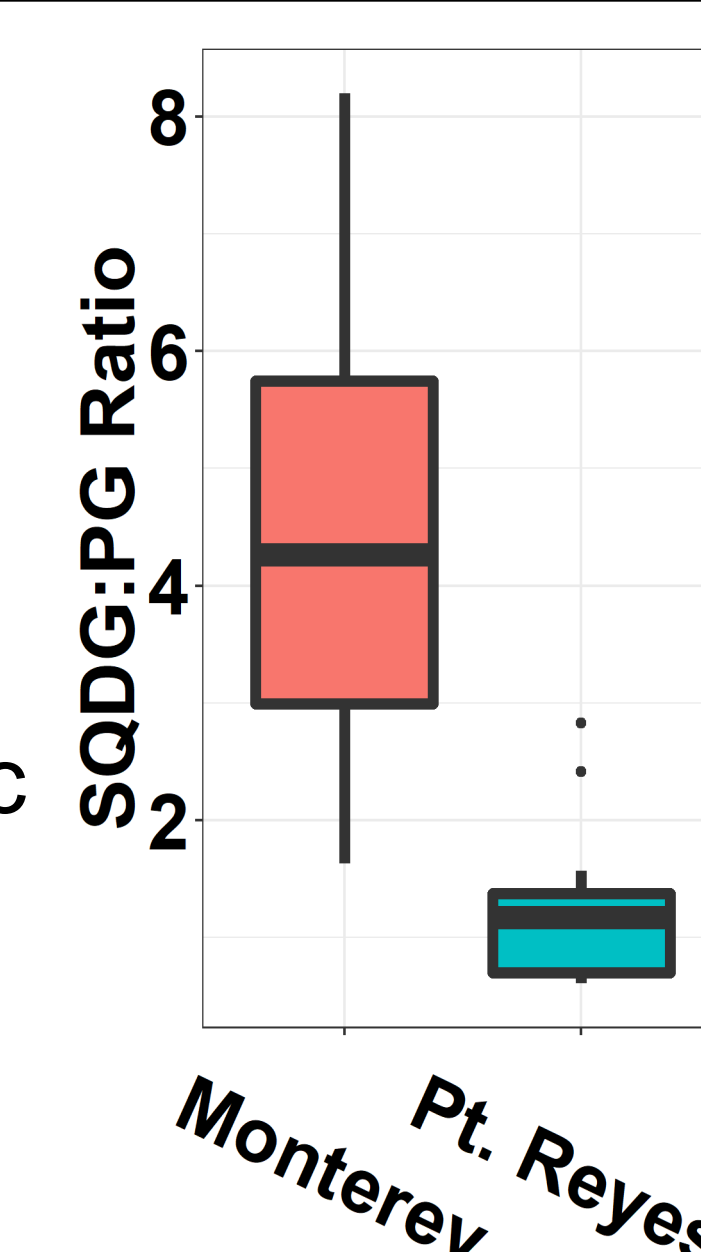
SQDG = sulfoquinovosyldiacylglycerol

PC = phosphatidylcholine

PE = phosphatidylethanolamine

PG = phosphatidylglycerol

- Monterey stations have SQDG:PG ratios statistically different from Point Reyes stations (Mann-Whitney U, p-value < 0.001, n = 36)
- SQDG:PG values for oligotrophic regions typically vary between 2 and 7<sup>[7]</sup>, implying the Monterey region is nutrient-limited



- However, SQDG:PG and phosphorus concentration are minimally correlated and other proxies for bloom health, such as chlorophyll:pheophytin, show that high SQDG:PG levels are correlated with...

## Conclusions

## Acknowledgements