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Combining eDNA and traditional surveys to study biodiversity in seamount communities

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Thanks to:



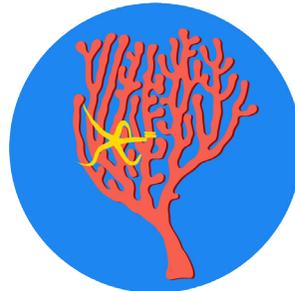
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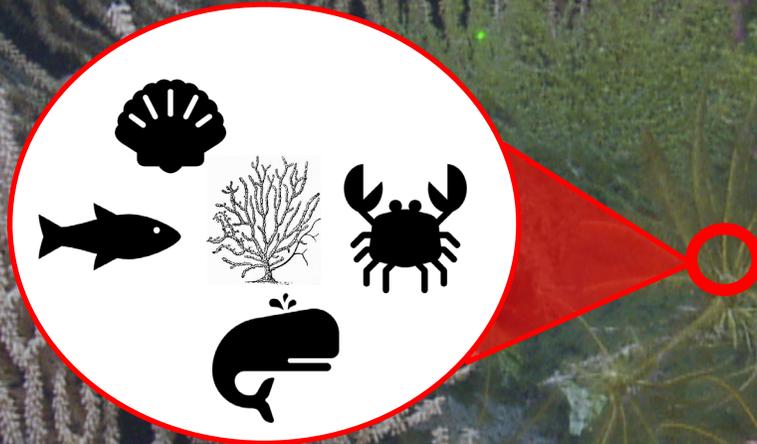


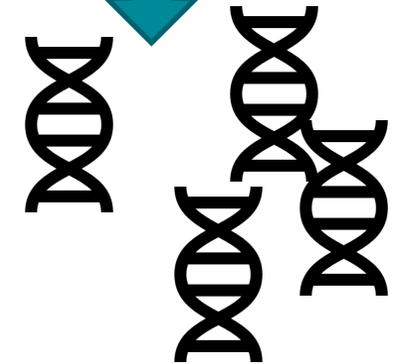
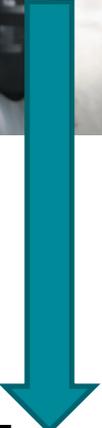
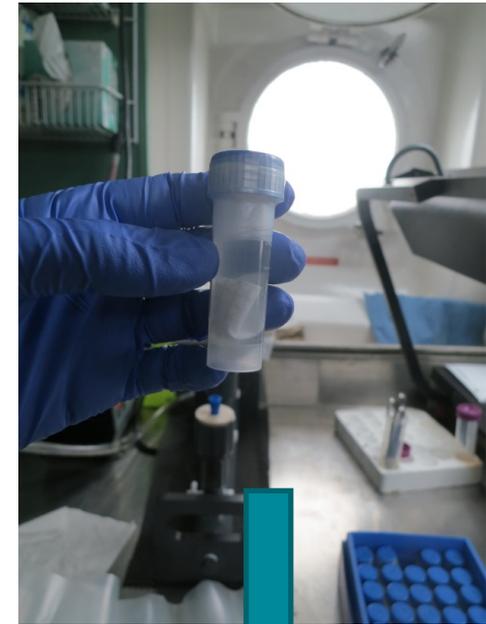
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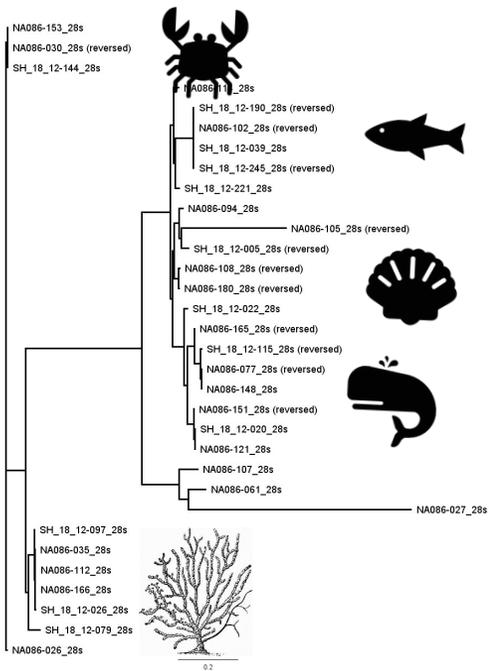
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What is eDNA?



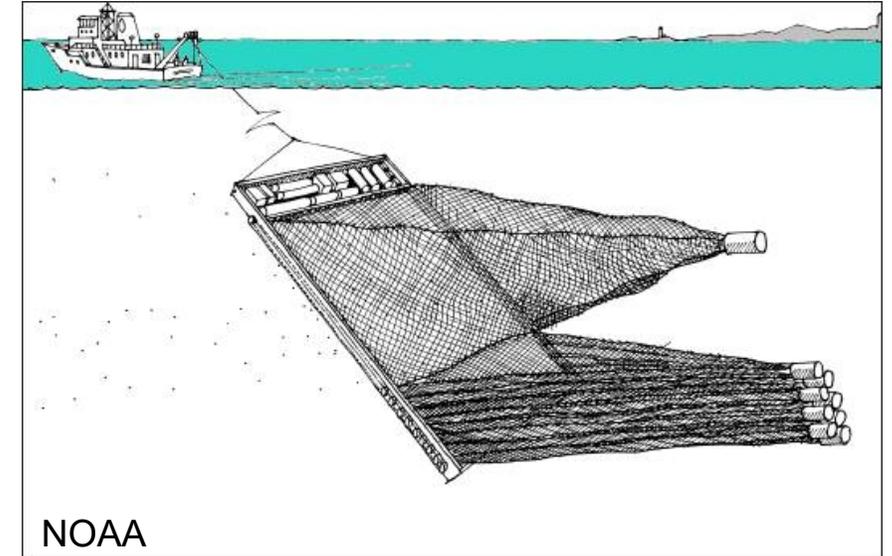


Illumina sequencing...(or other process)



eDNA is a “different type of net”

- Can have different “mesh” sizes = different levels of specificity



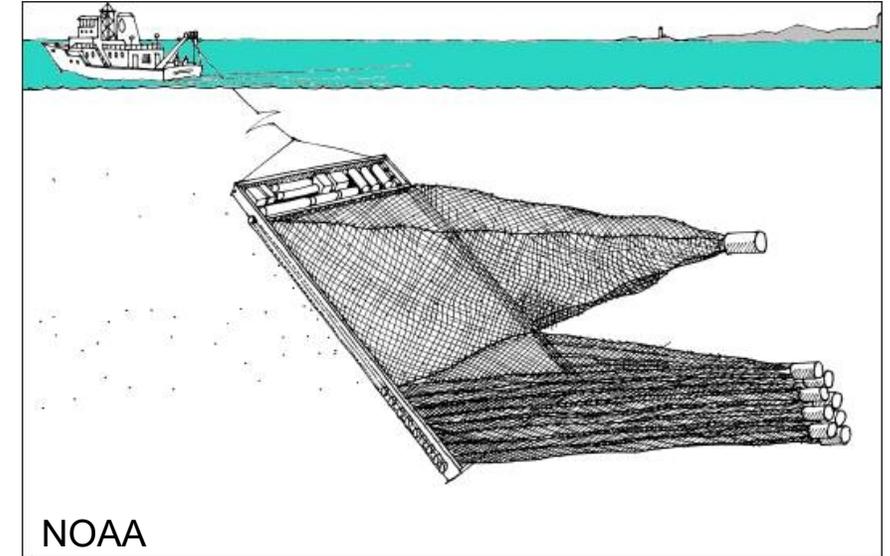
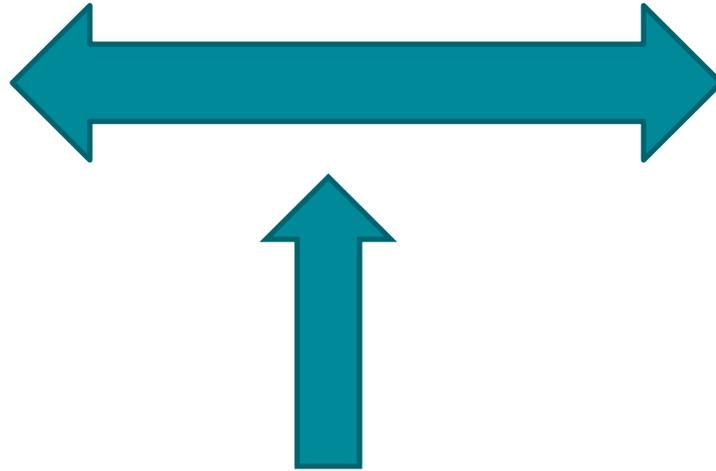
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- Detect single organisms at very high sensitivity
- qPCR or ddPCR

- Detect everything in the sample
- Illumina sequencing and broad primers
- Loose species level specificity

eDNA is a “different type of net”

- Can have different “mesh” sizes = different levels of specificity



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- Detect single organisms at very high sensitivity
- qPCR or ddPCR

Our goal is to detect a broad range of species, but trying to be as species specific as possible

- Detect everything in the sample
- Illumina sequencing and broad primers
- Loose species level specificity

eDNA in the deep-sea

- eDNA is a good tool to examine and compare biodiversity in deep-sea habitats including seamounts:
 - Only requires a water sample
 - Reduces need for individual sampling
 - Can be used when direct sampling is unfeasible
 - Can enhance traditional sampling efforts.

One habitat where eDNA can enhance sampling and community profiling is seamounts

eDNA in the deep-sea

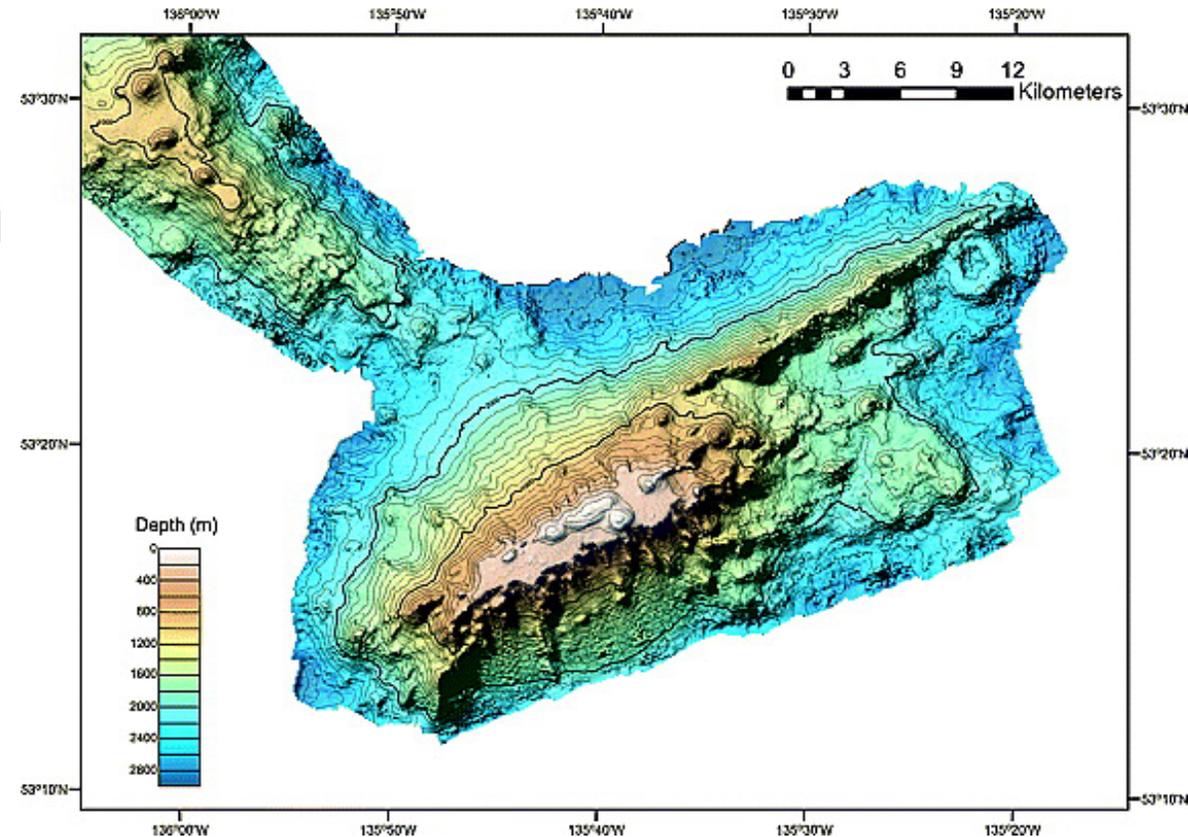
- Seamounts:
 - Hotspots of biodiversity, of interest for conservation
 - Question of endemism:
 - Who lives there?
 - What is the level of connectivity among seamounts within a region?
 - Not consistent everywhere...some regions/species have more connectivity than others

Two test cases: Canadian Pacific and Central Pacific Seamounts

- Many samples collected in both locations by teams on *E/V Nautilus* in 2018
 - Canadian Pacific: Hodgkins and SGaan Kinghla-Bowie Seamounts
 - Central Pacific: Unnamed Seamount 10 and Naifeh Seamount in Papahānaumokuākea Marine National Monument

Canadian Seamounts

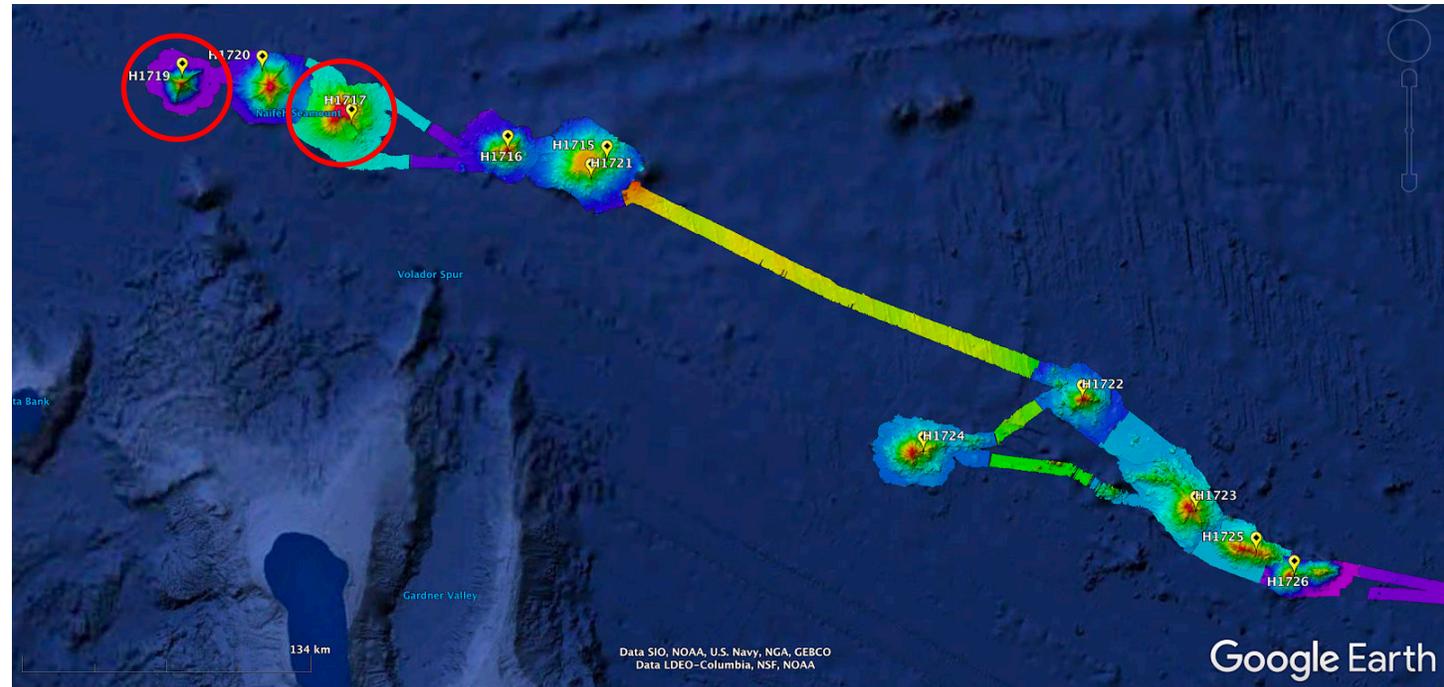
- SGaan Kinghlas-Bowie Seamount:
 - 180 km west of Haida Gwaii
 - Depth ranges from 3,000 m to 24 m
 - High productivity area
- Hodgkins Seamount:
 - Just northeast of SGaan Kinghlas-Bowie
 - Depth range 3,000m to ~600m
 - High productivity area



Chaytor et al. 2007

Central Pacific Seamounts

- Unnamed Seamount 10 and Naifeh Seamount
 - Far from mainland, 1000+ km from the Hawaiian Islands
 - Very deep: Shallowest sample ~1700m
 - Lower productivity than mainland coast



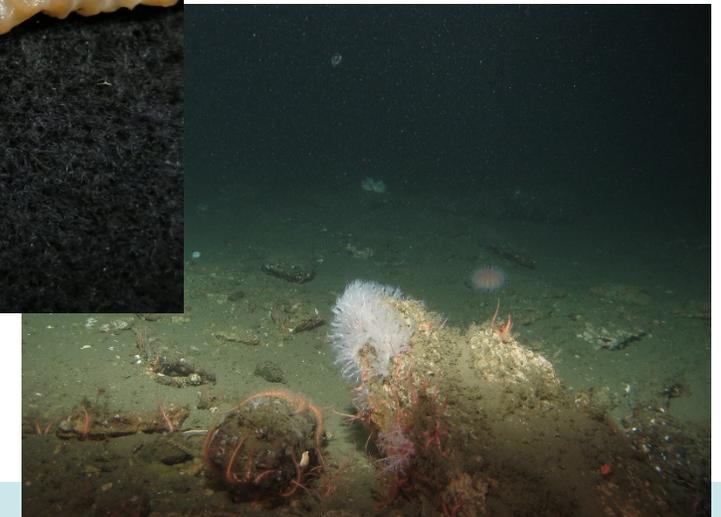
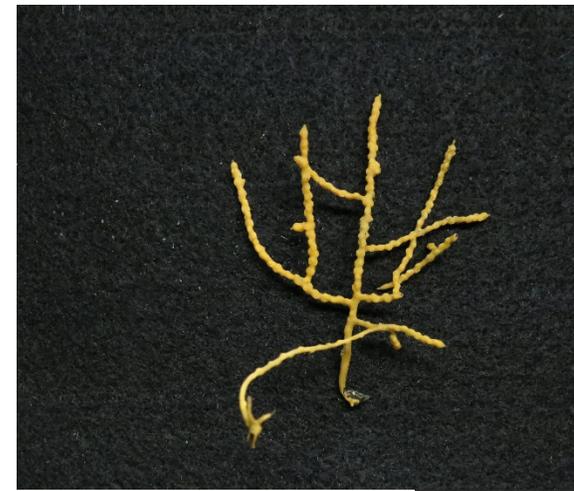
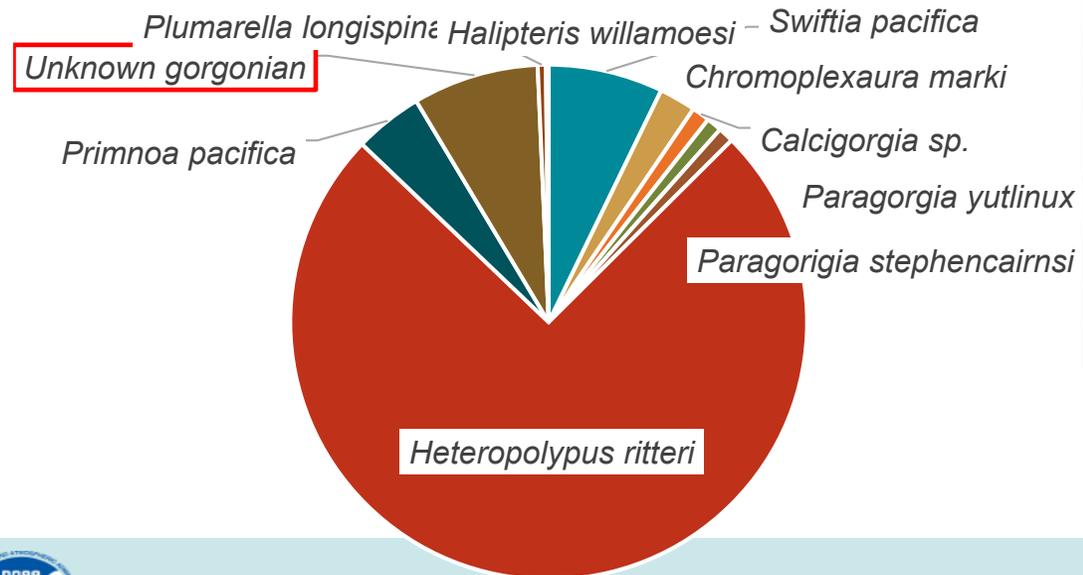
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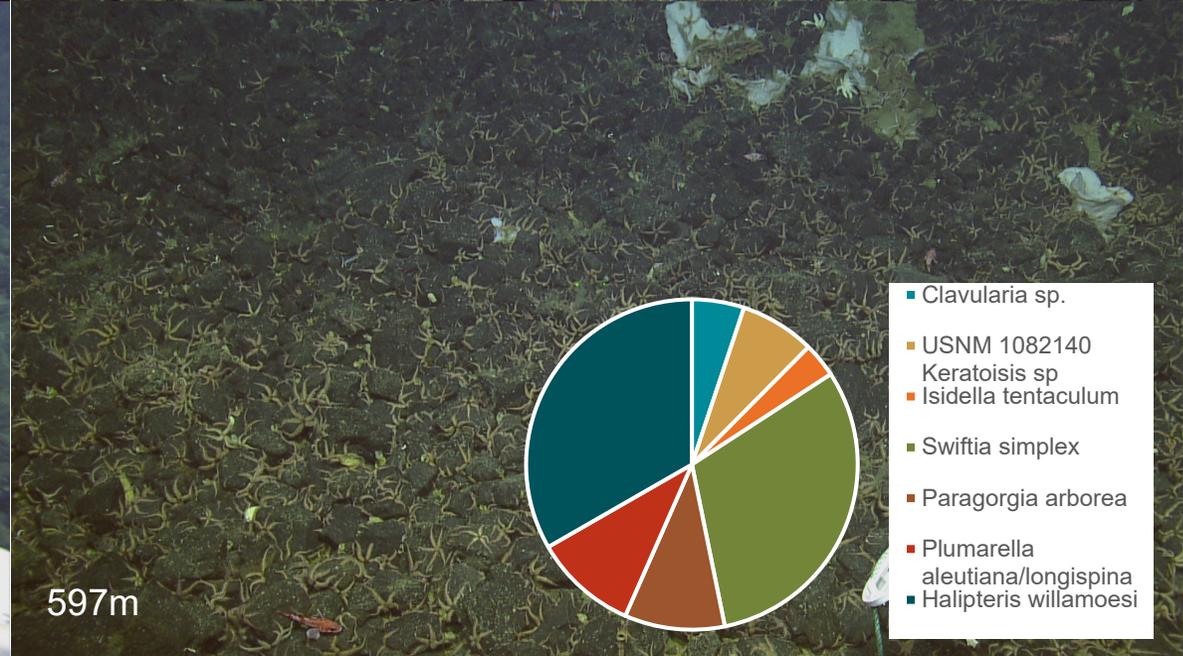
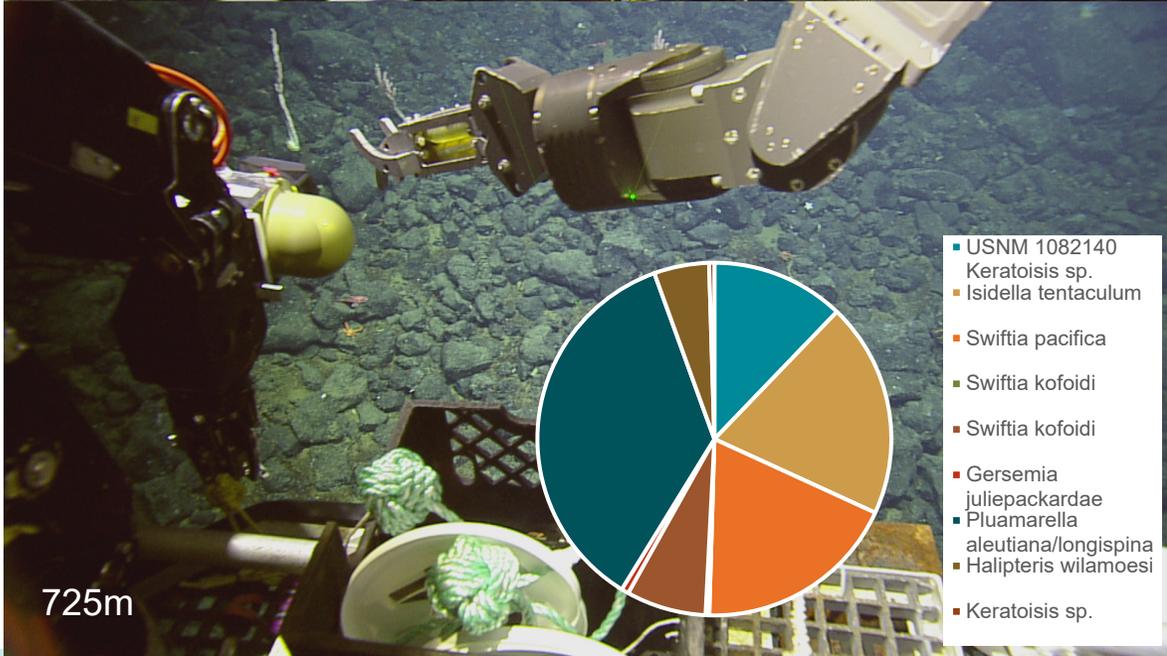
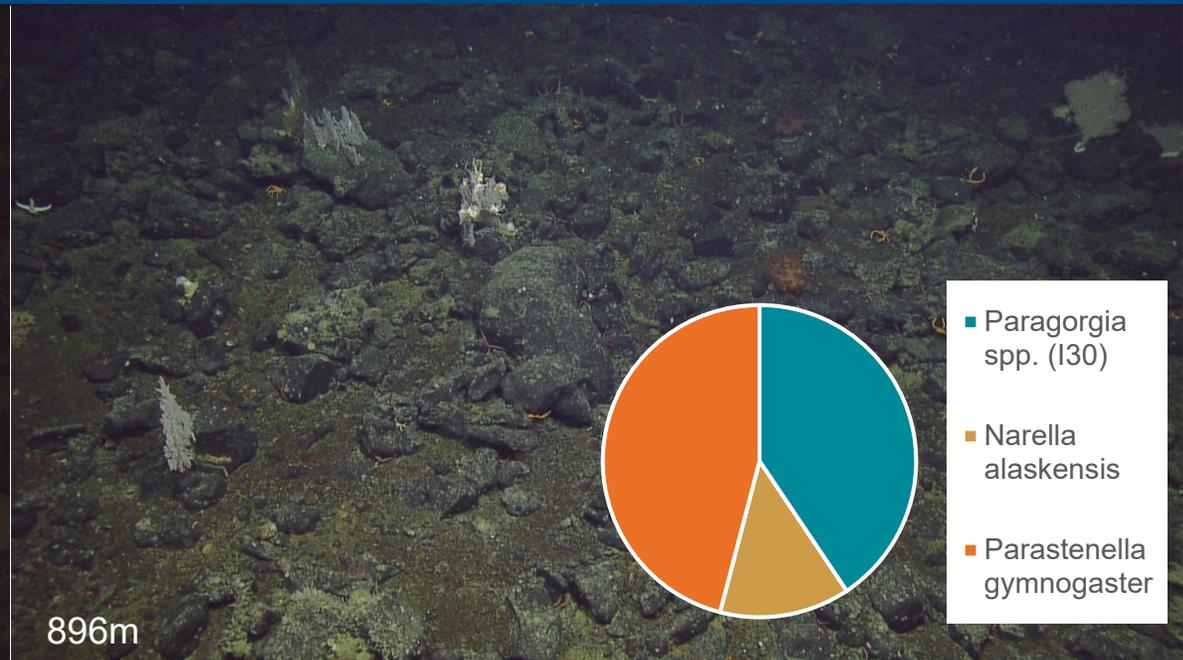
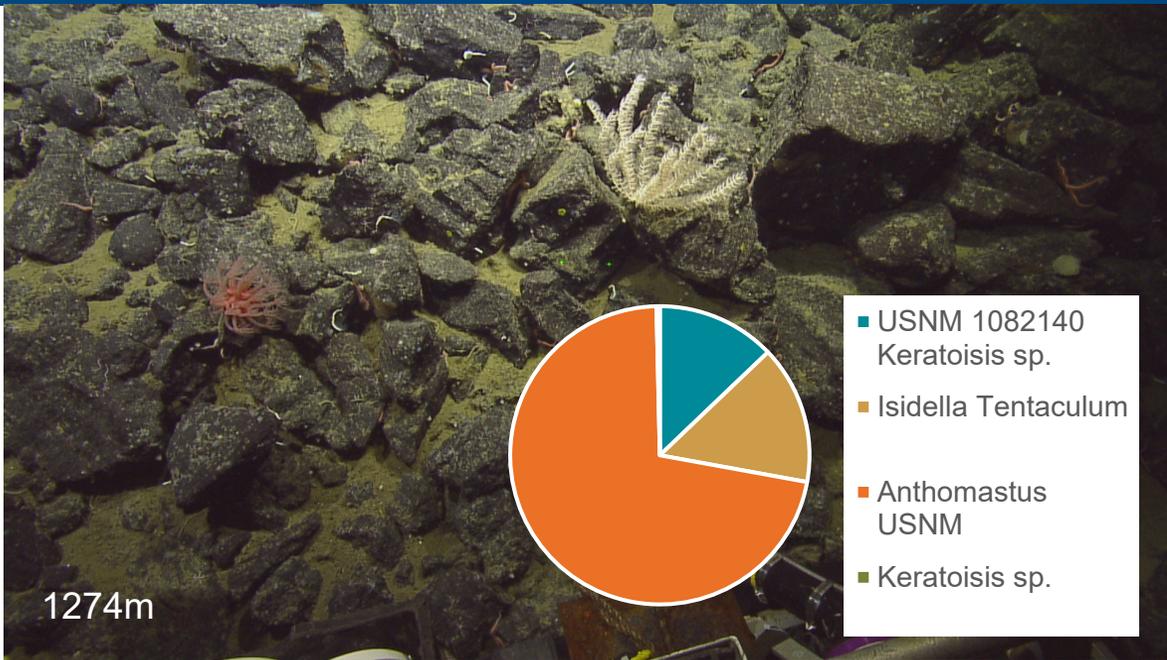
Methods

- Samples collected via Niskin bottles on ROV *Hercules* and filtered aboard E/V *Nautilus*.
- PCR amplify with octocoral specific markers (*MutS*), general fish markers (16s)
- Sequence amplicons on an Illumina MiSeq
- Use a bioinformatics pipeline to place unknown sequences on a reference phylogeny
 - Similar to methods used in microbial metagenomics
 - Reference database based on NOAA's species lists
 - Don't need a complete database of reference sequences

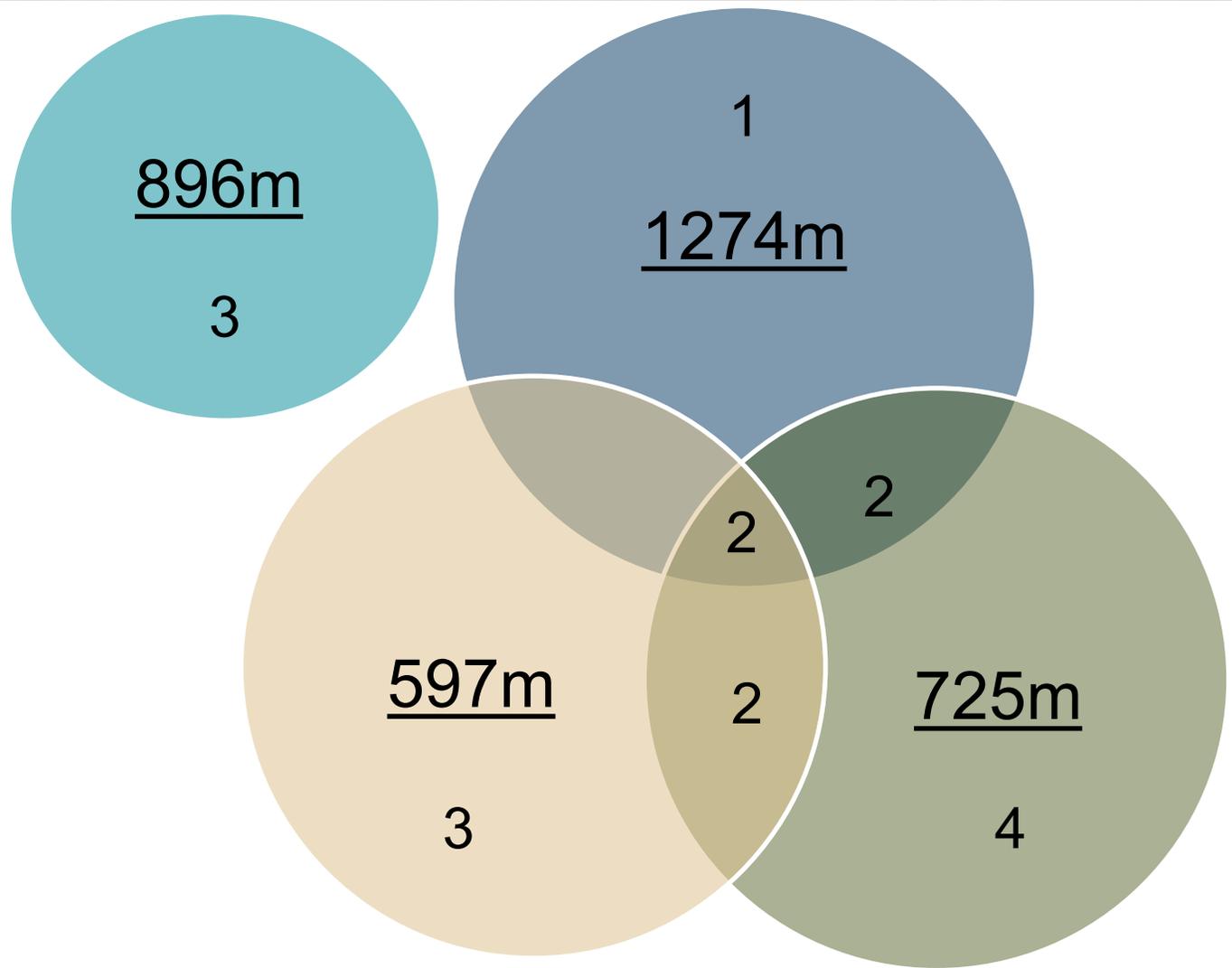
A few words on reference libraries:

- eDNA library is iterative, new sequences added from ROV collections and new unknowns give us targets to look for in future or other collections

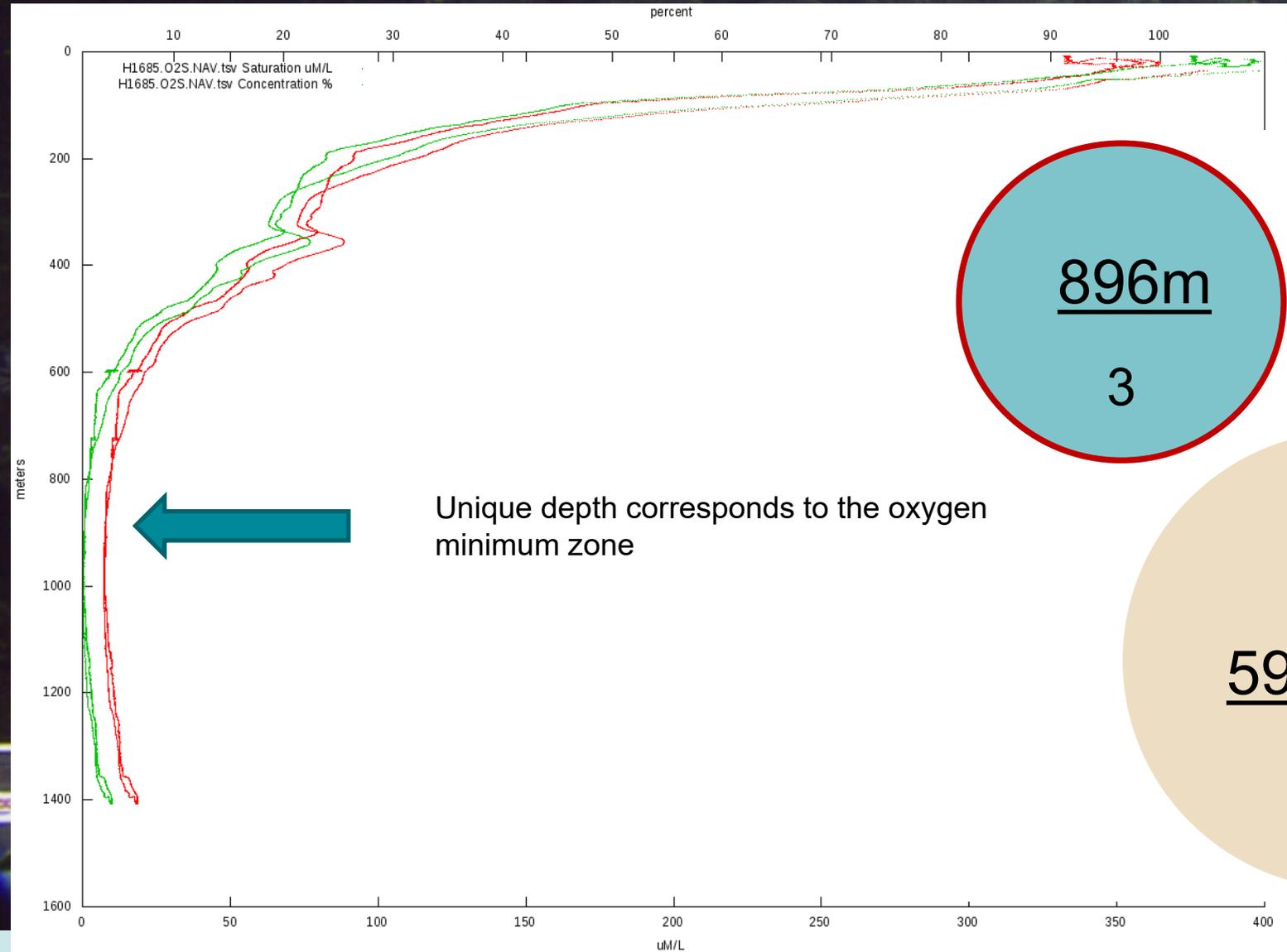




Shared species across depths



Interesting patterns with environmental factors:

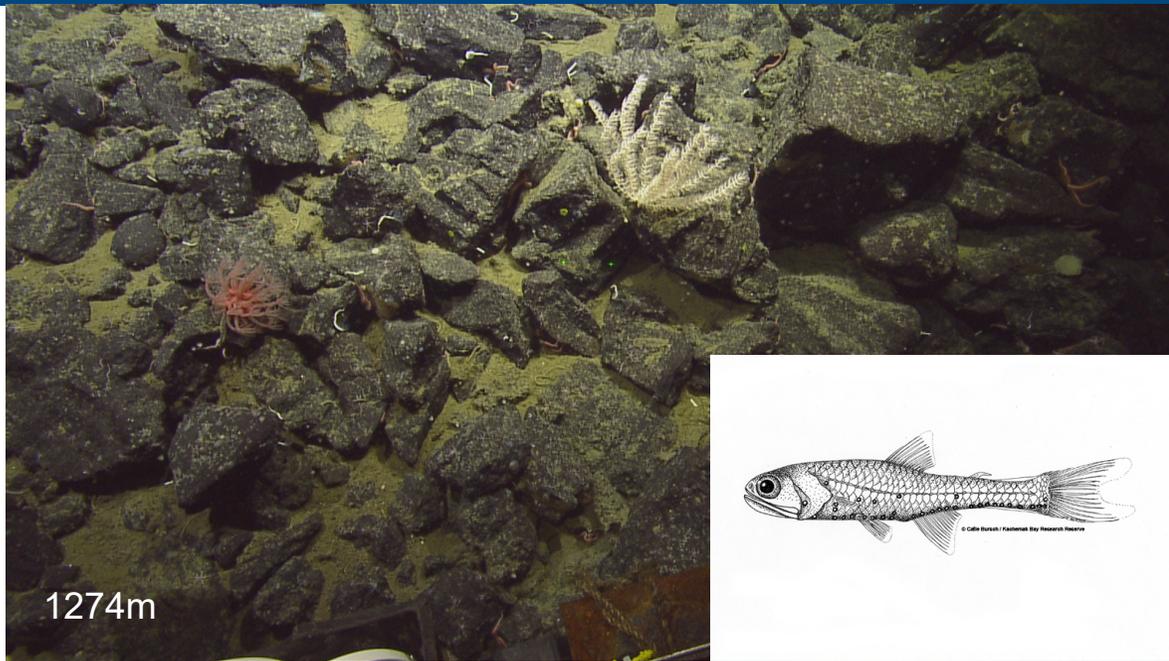


896m
3

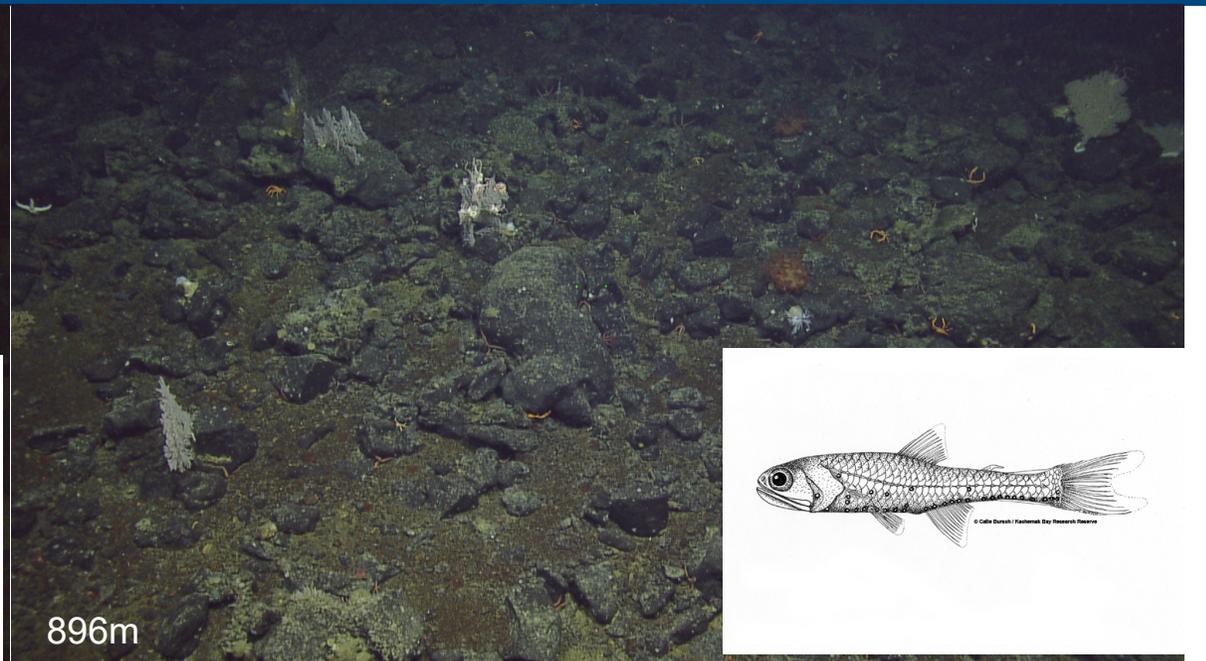
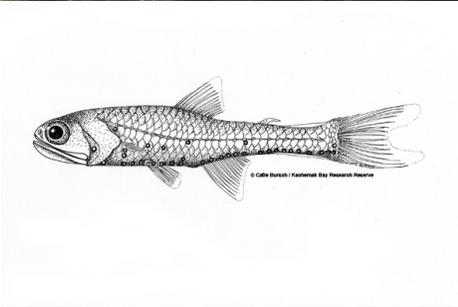
1274m
1

597m
3

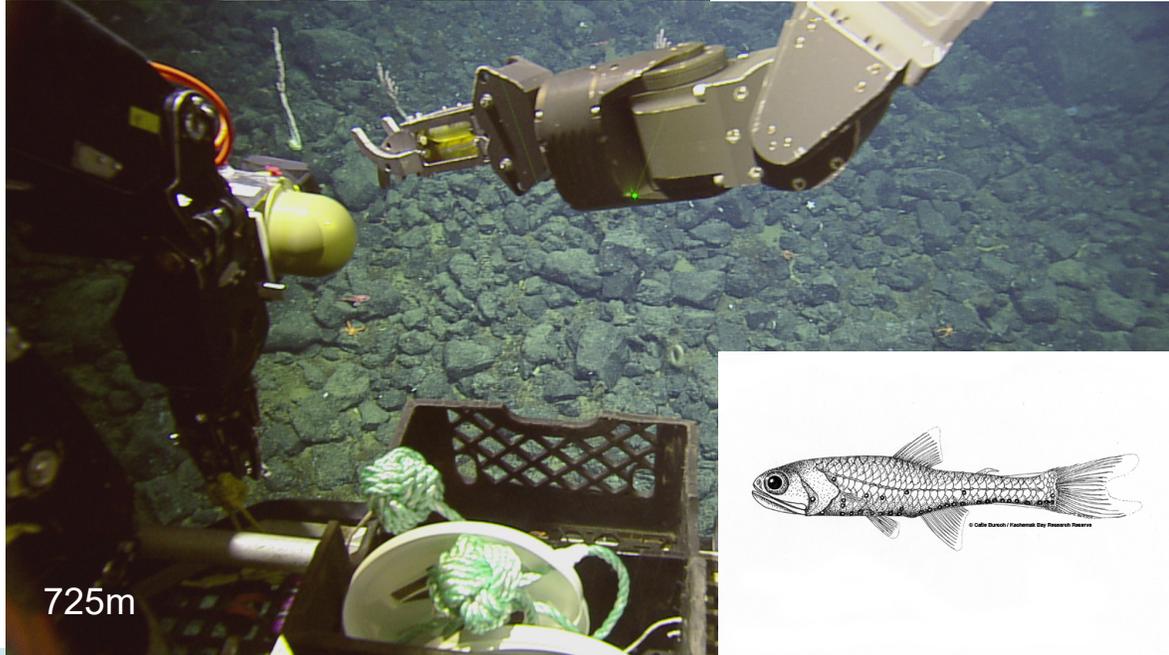
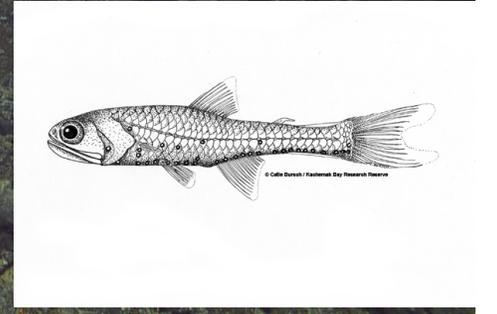
725m
4



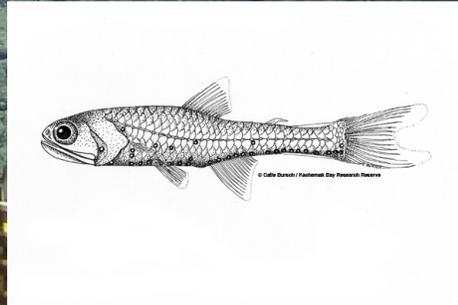
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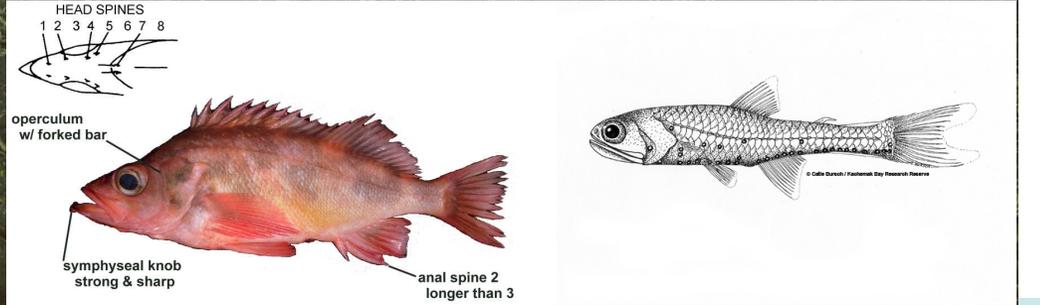
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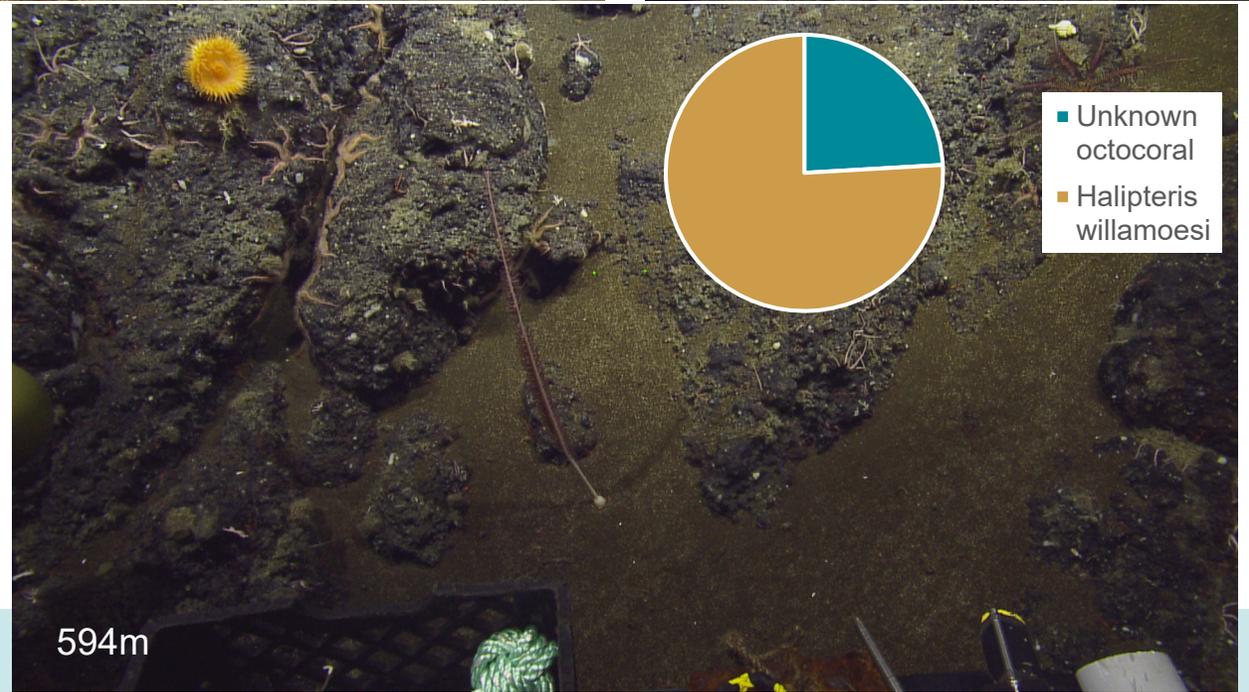
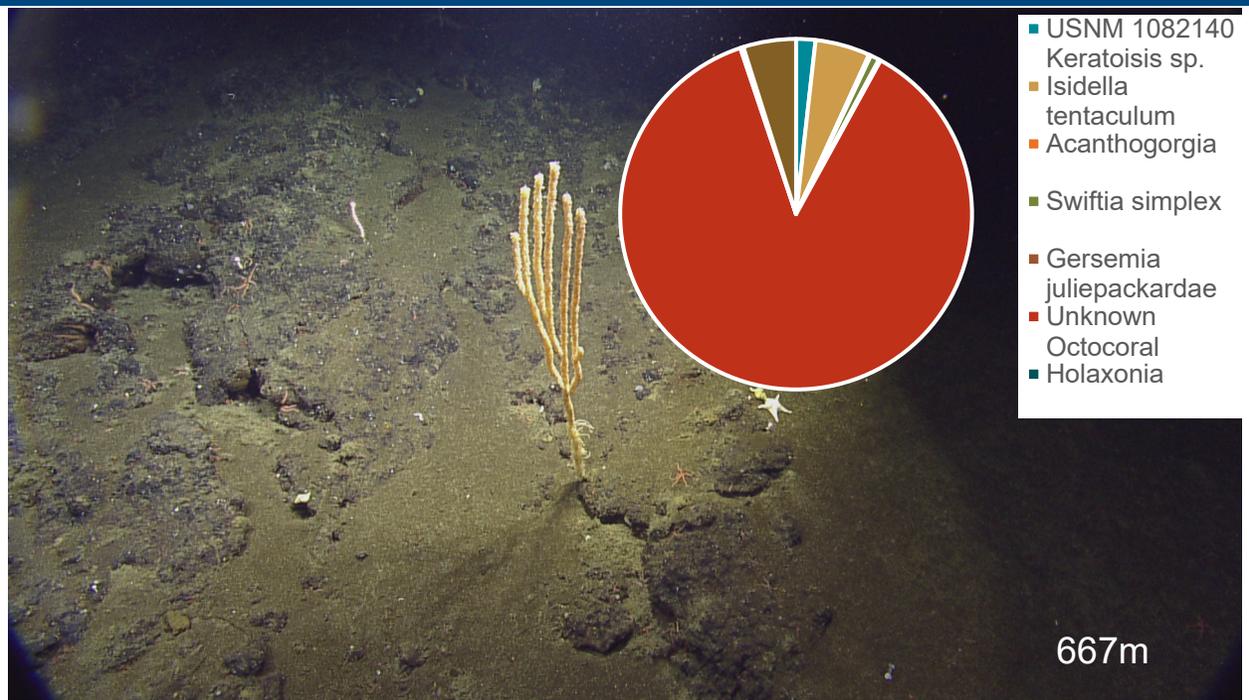
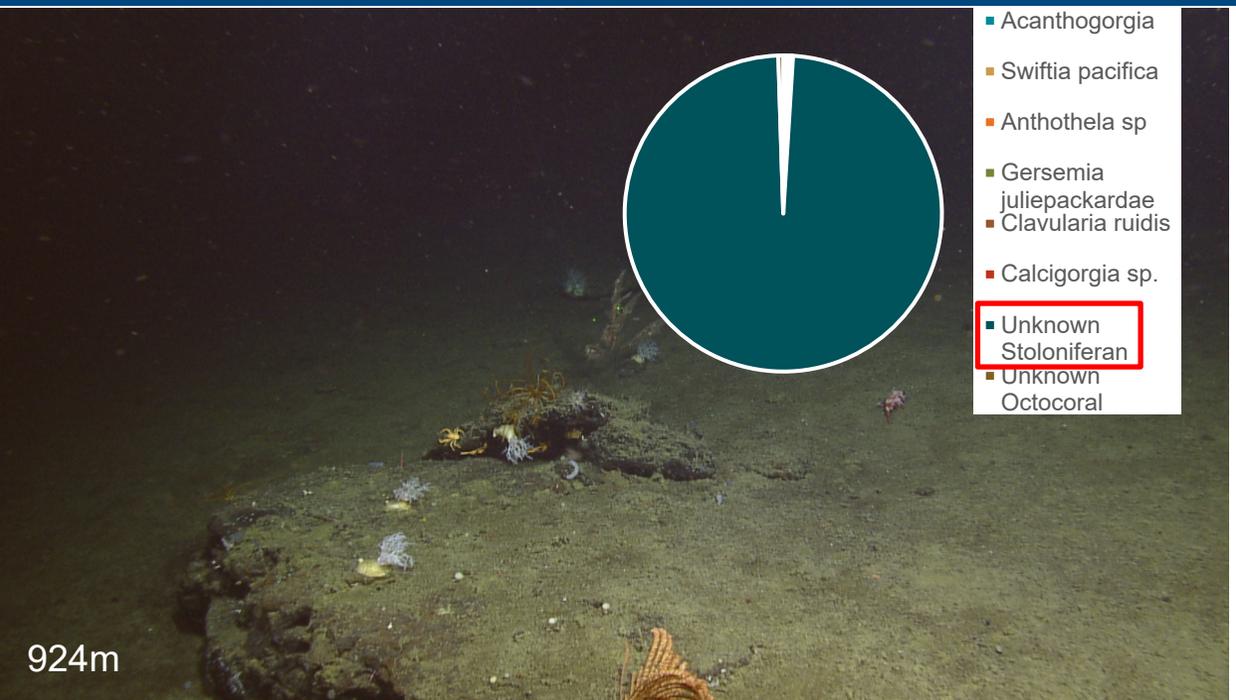


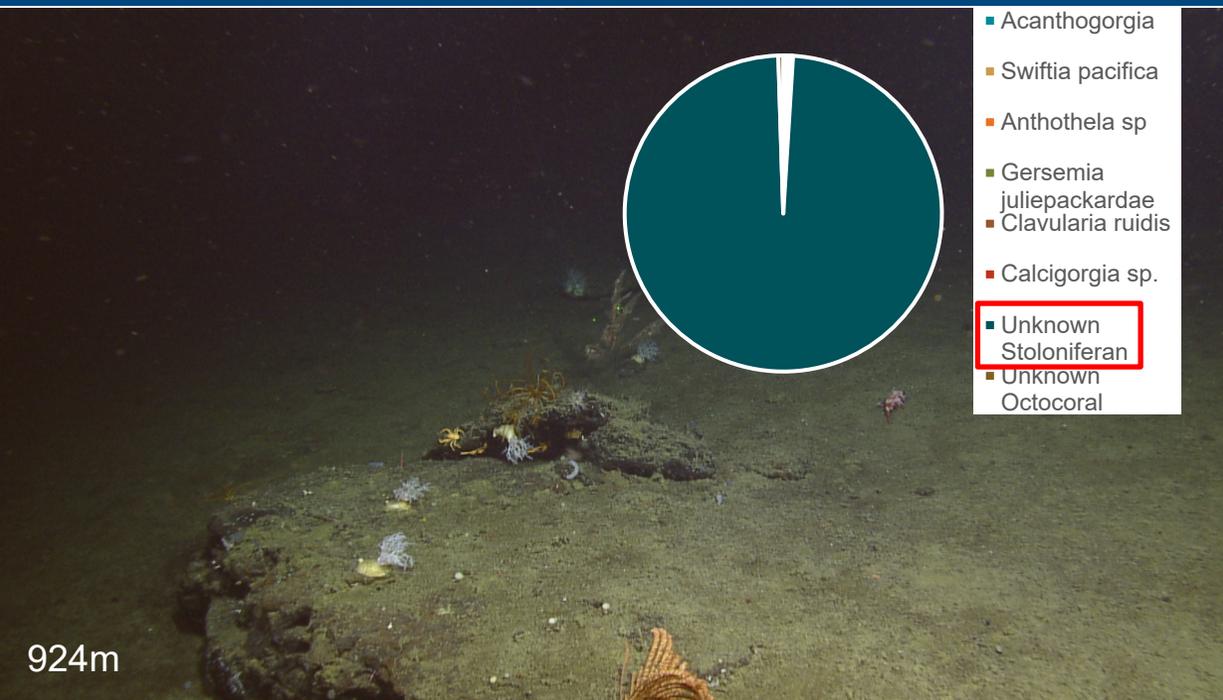
725m



597m

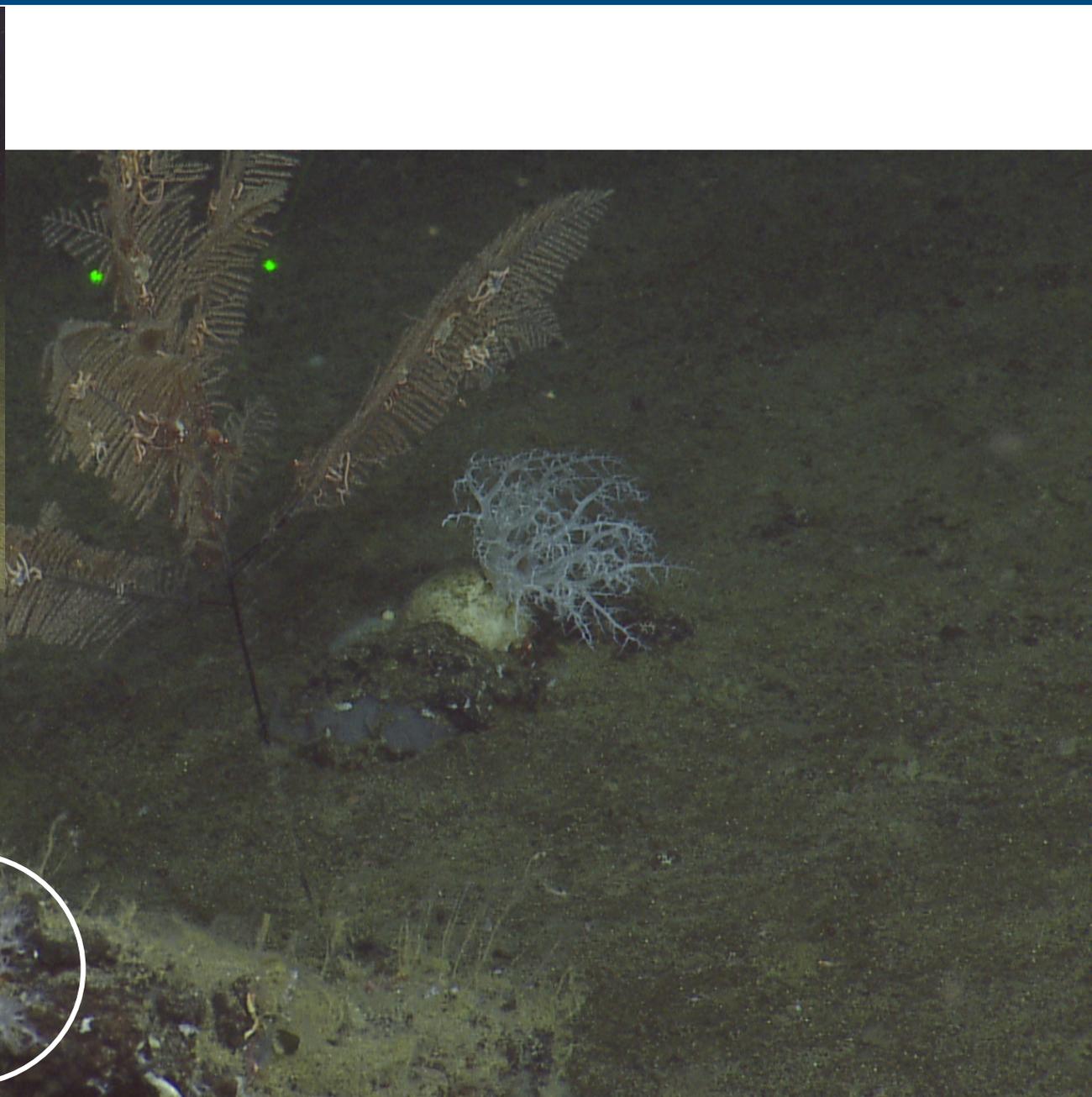




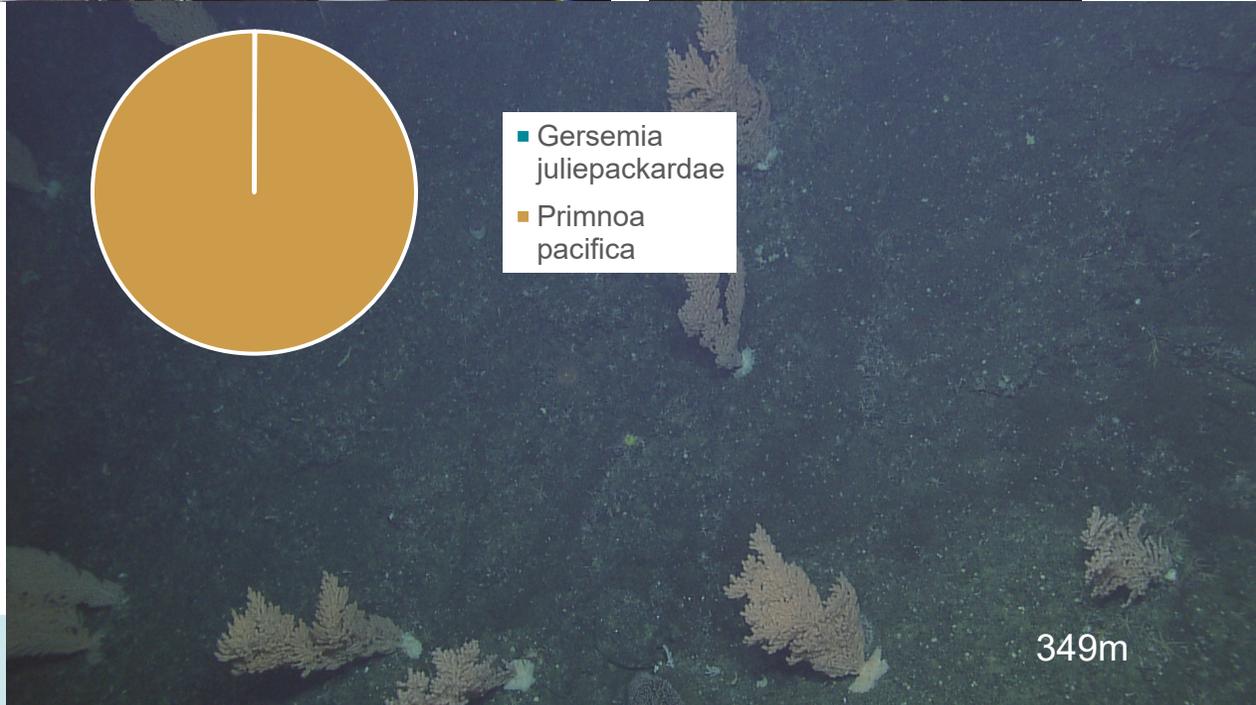
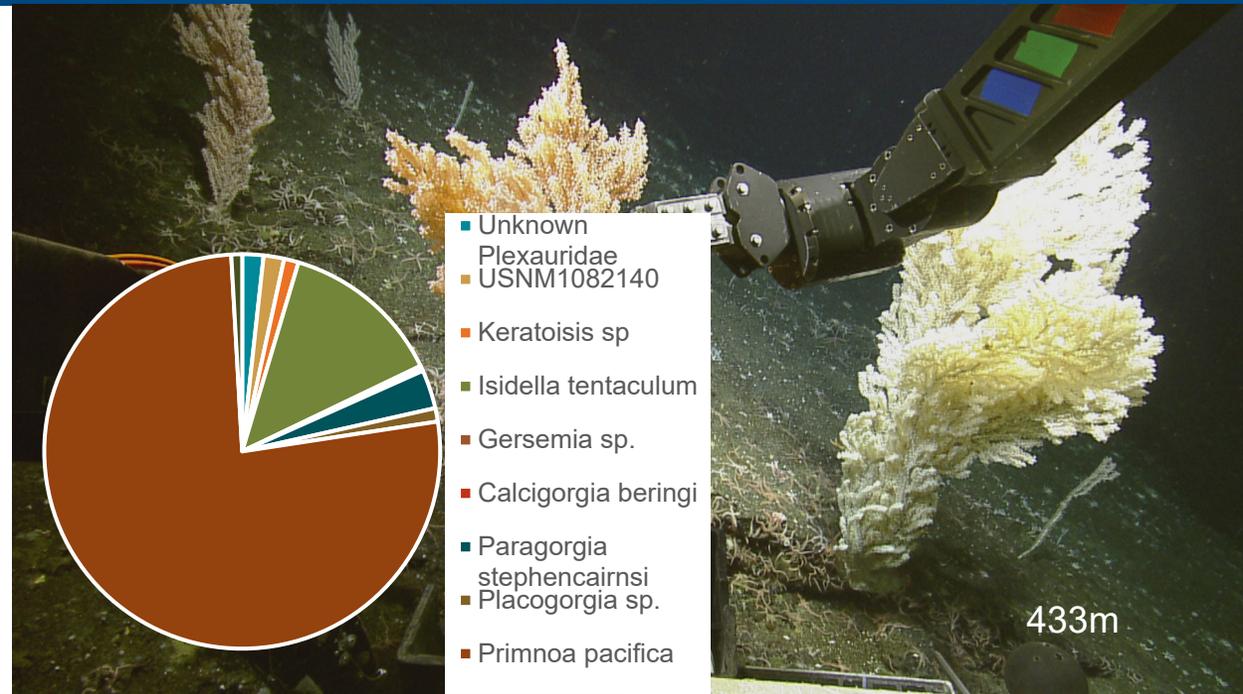
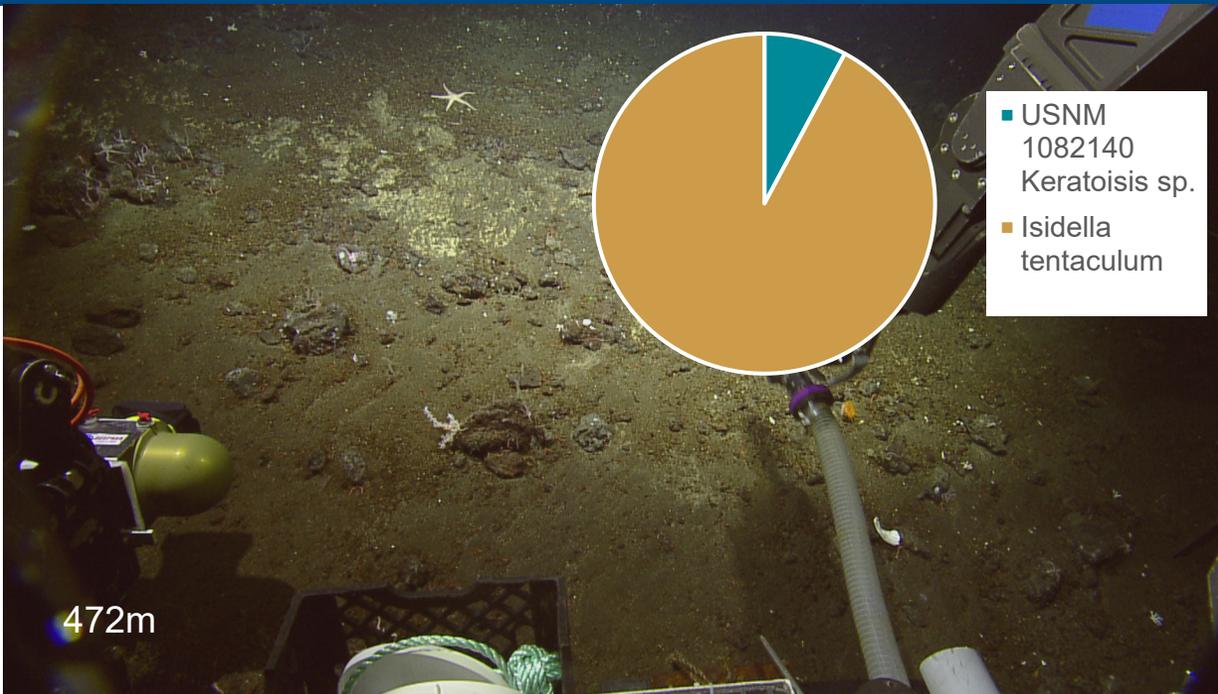


924m

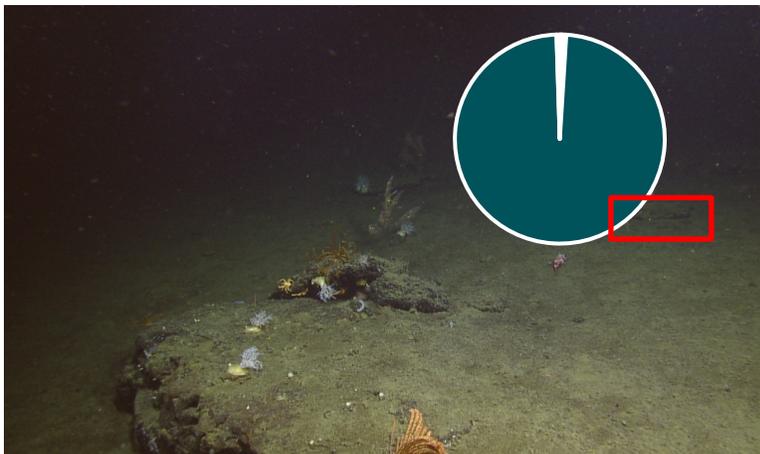
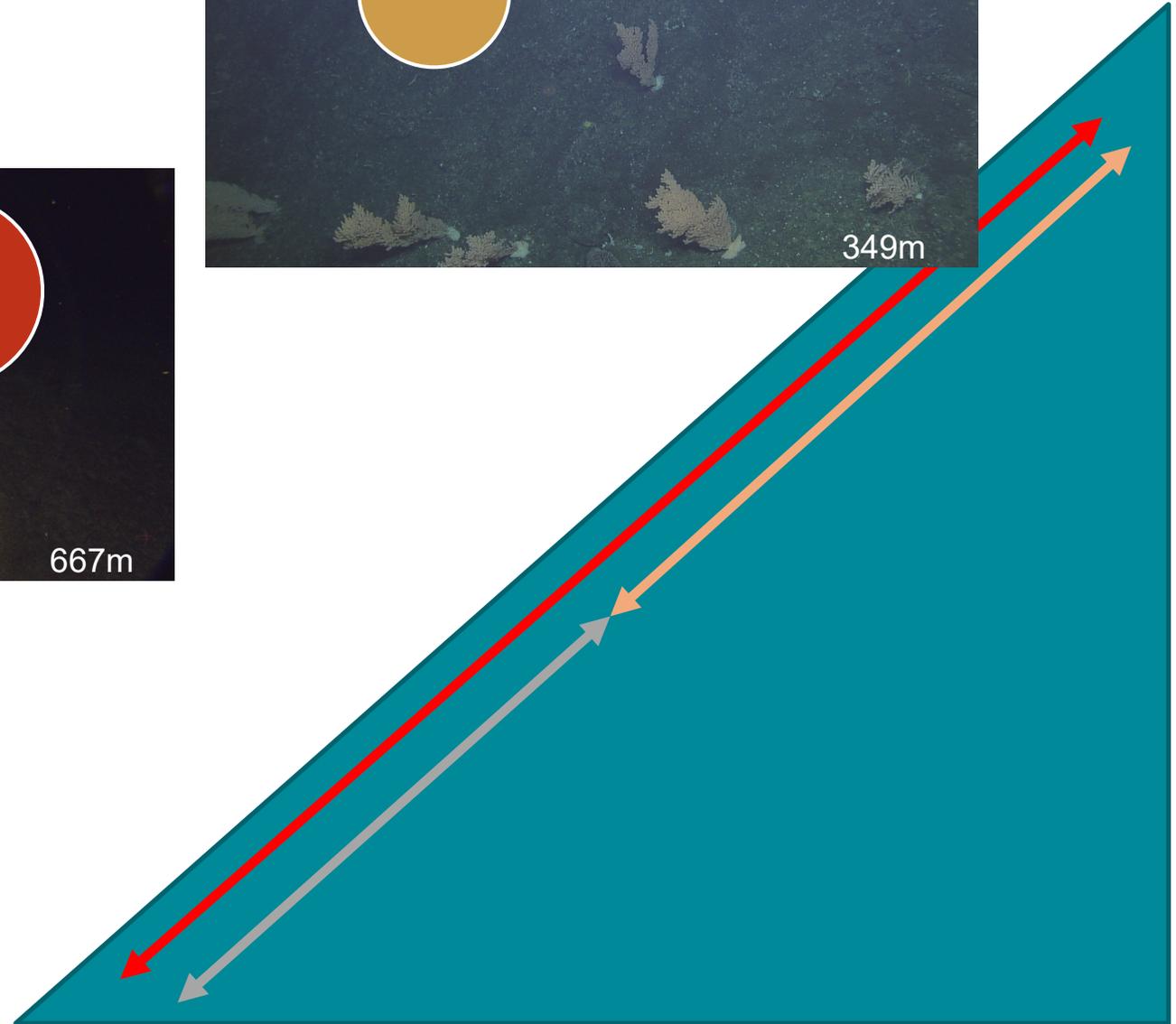
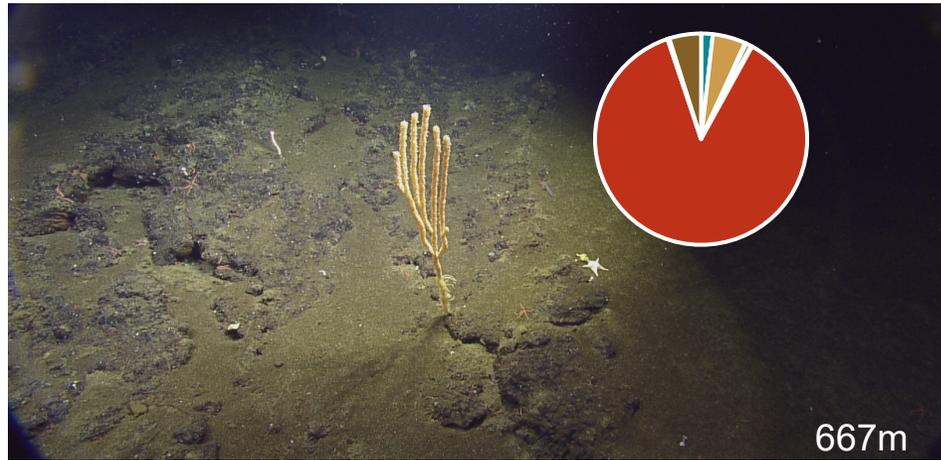
- Acanthogorgia
- Swiftia pacifica
- Anthothela sp
- Gersemia juliepackardae
- Clavularia ruidis
- Calcigorgia sp.
- Unknown Stoloniferan
- Unknown Octocoral
- Unknown

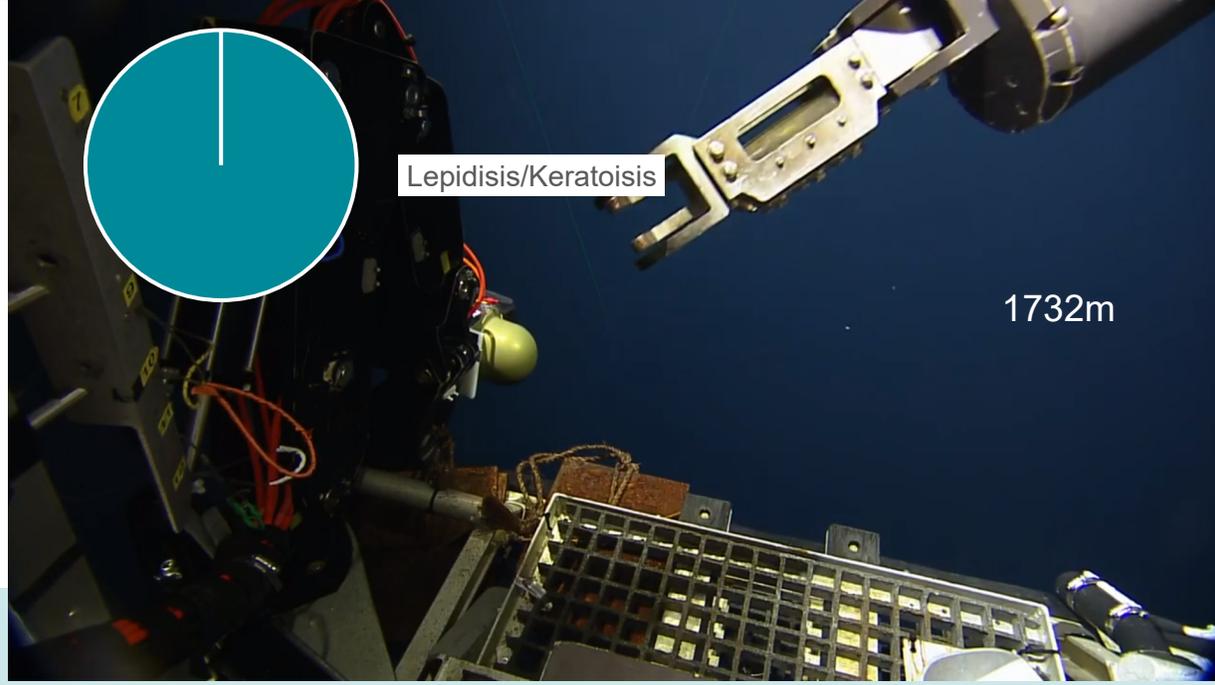
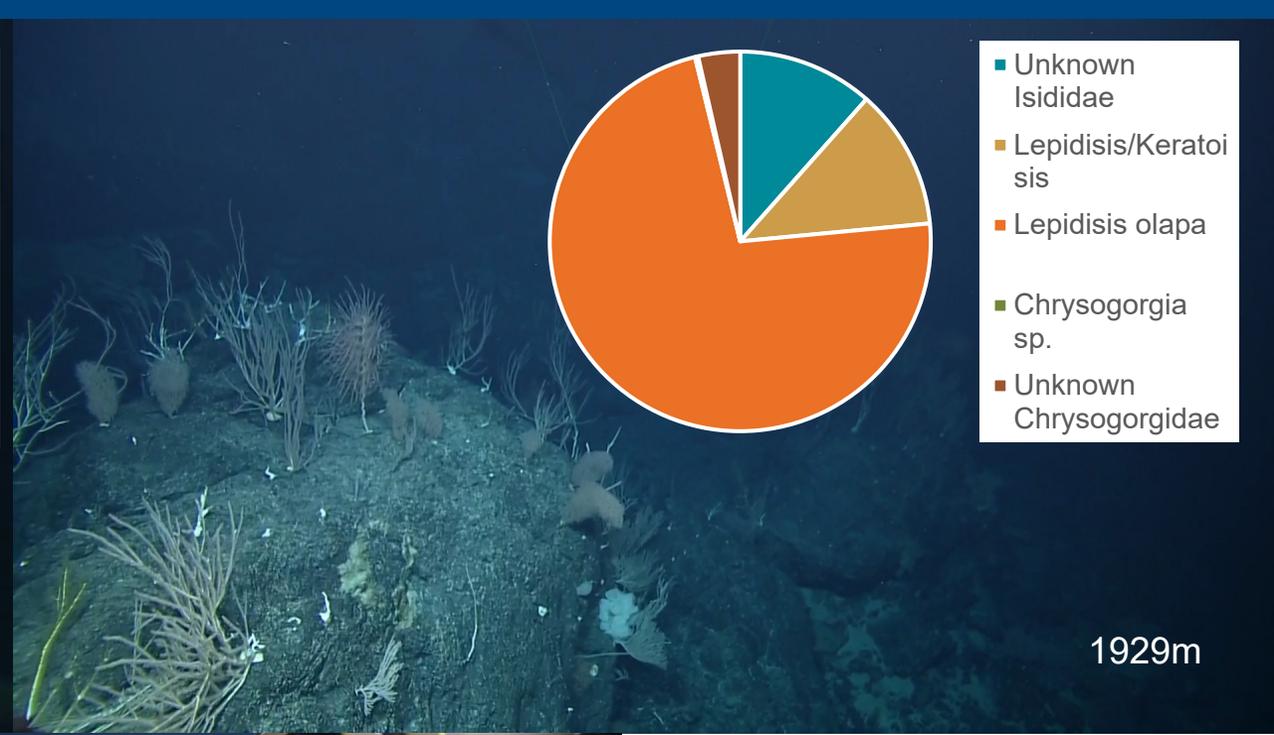
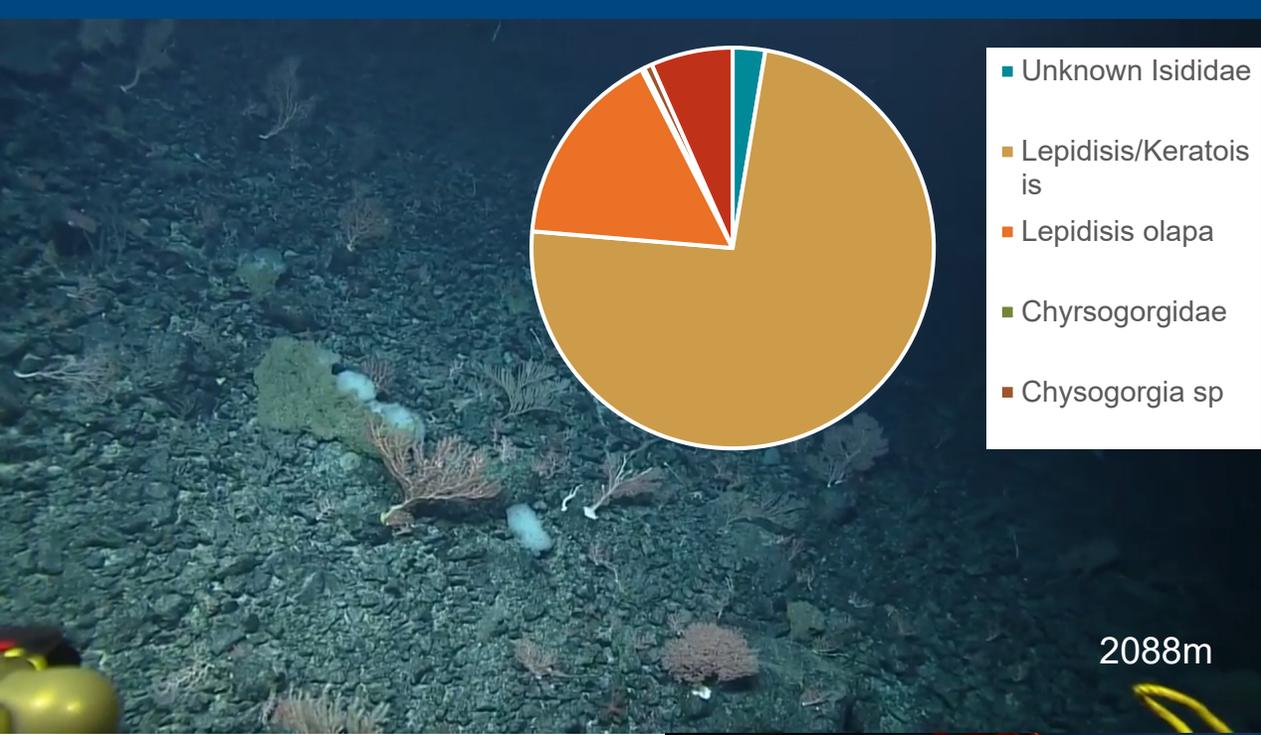


594m



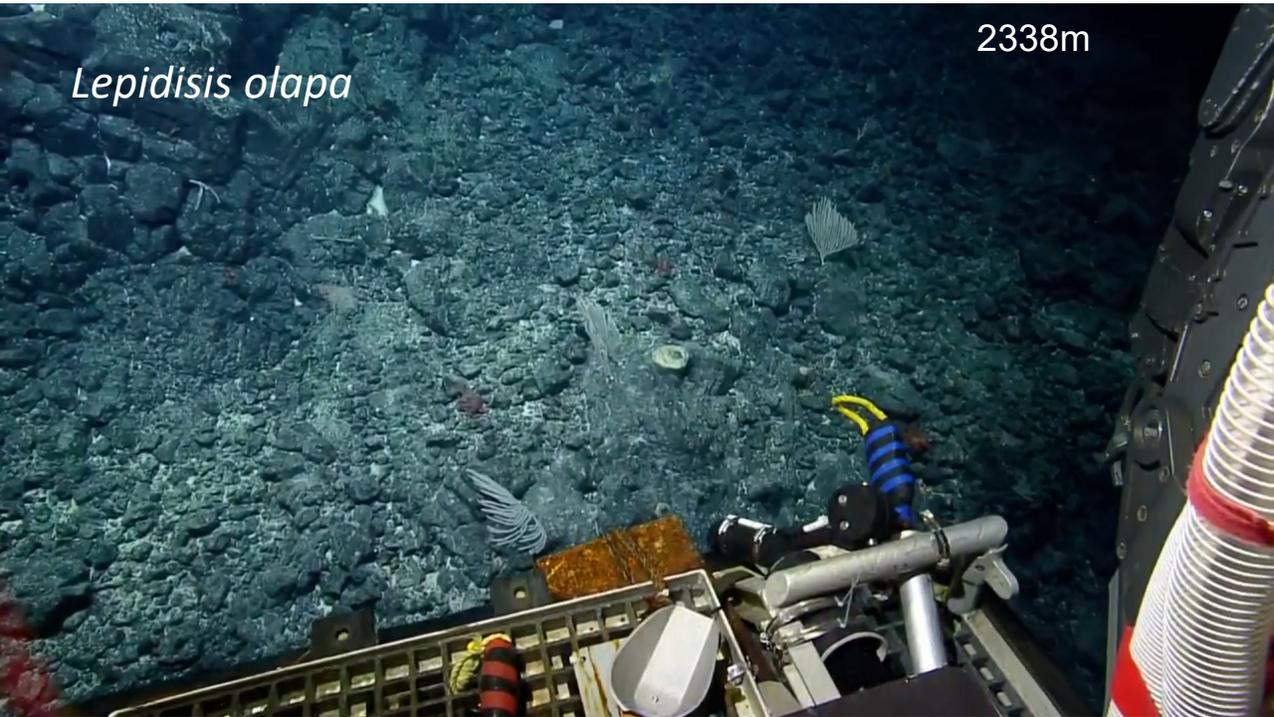
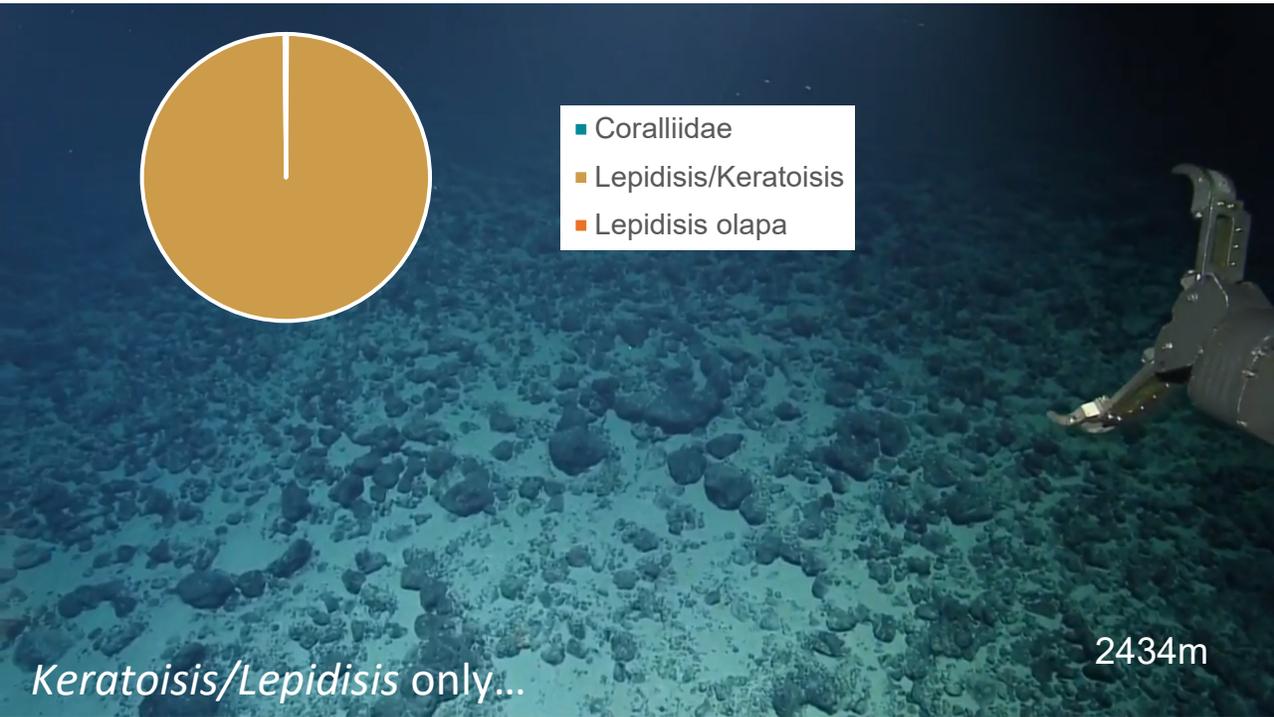
Again, can begin to look at species distribution across depth...







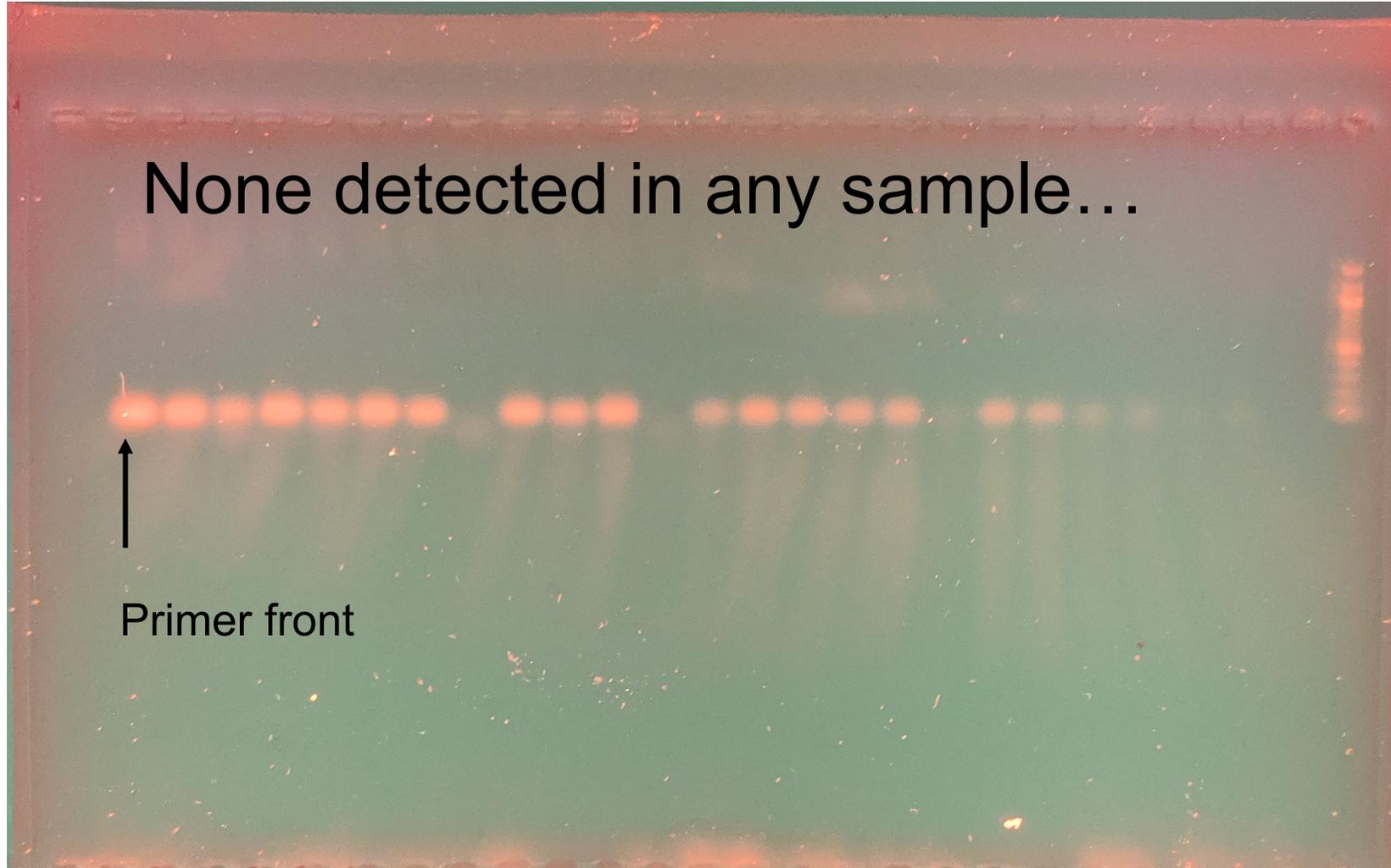
- Coralliidae
- Lepidisis/Keratoisis
- Lepidisis olapa



Keratoisis/Lepidisis only...

- Slight variation in rare species detection between duplicates...stochasticity vs. sequencing depth?
- Bamboo corals around, but morphologically different than *L. olapa*, need additional references for this region.
- Primnoidae missing from detection.

What about fish?



Summary

- eDNA can enhance identification of fauna and patterns of biodiversity in seamount communities
- eDNA can identify potential targets for future collection and research
- More work is needed to further develop reference databases based on existing samples
- Work is ongoing on these and additional samples to use this technique to characterize coral, sponge, and associate communities in the Pacific ocean

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Questions?



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