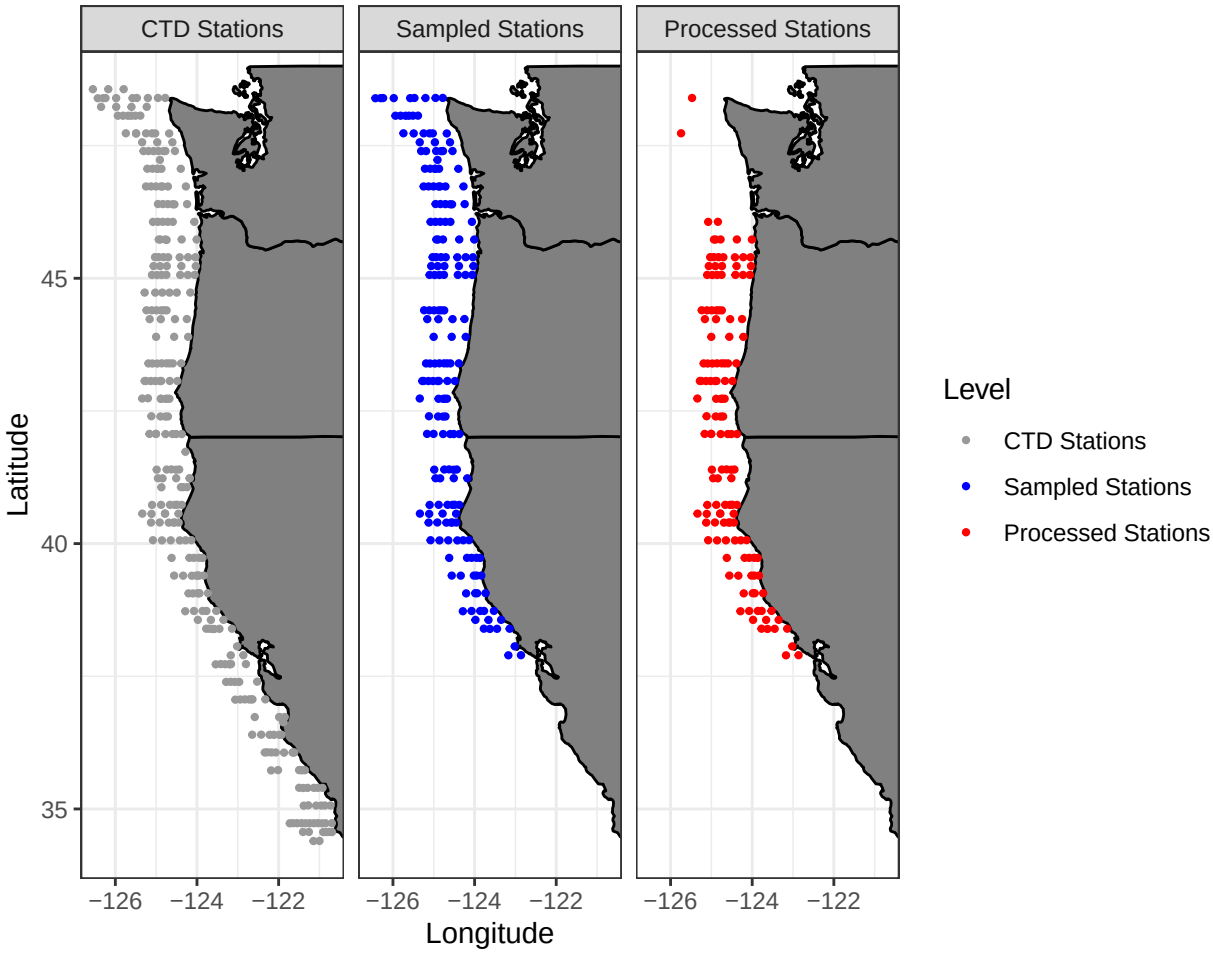
Hake 2019 Survey

eDNA from the 2019 Hake cruise

Sampling and processing to date.

In total we have processed qPCR for pacific hake, pacific lamprey, and eulachon from 134 CTD stations representing 653 station-depth combinations for 1304 individual 2.5L water samples.

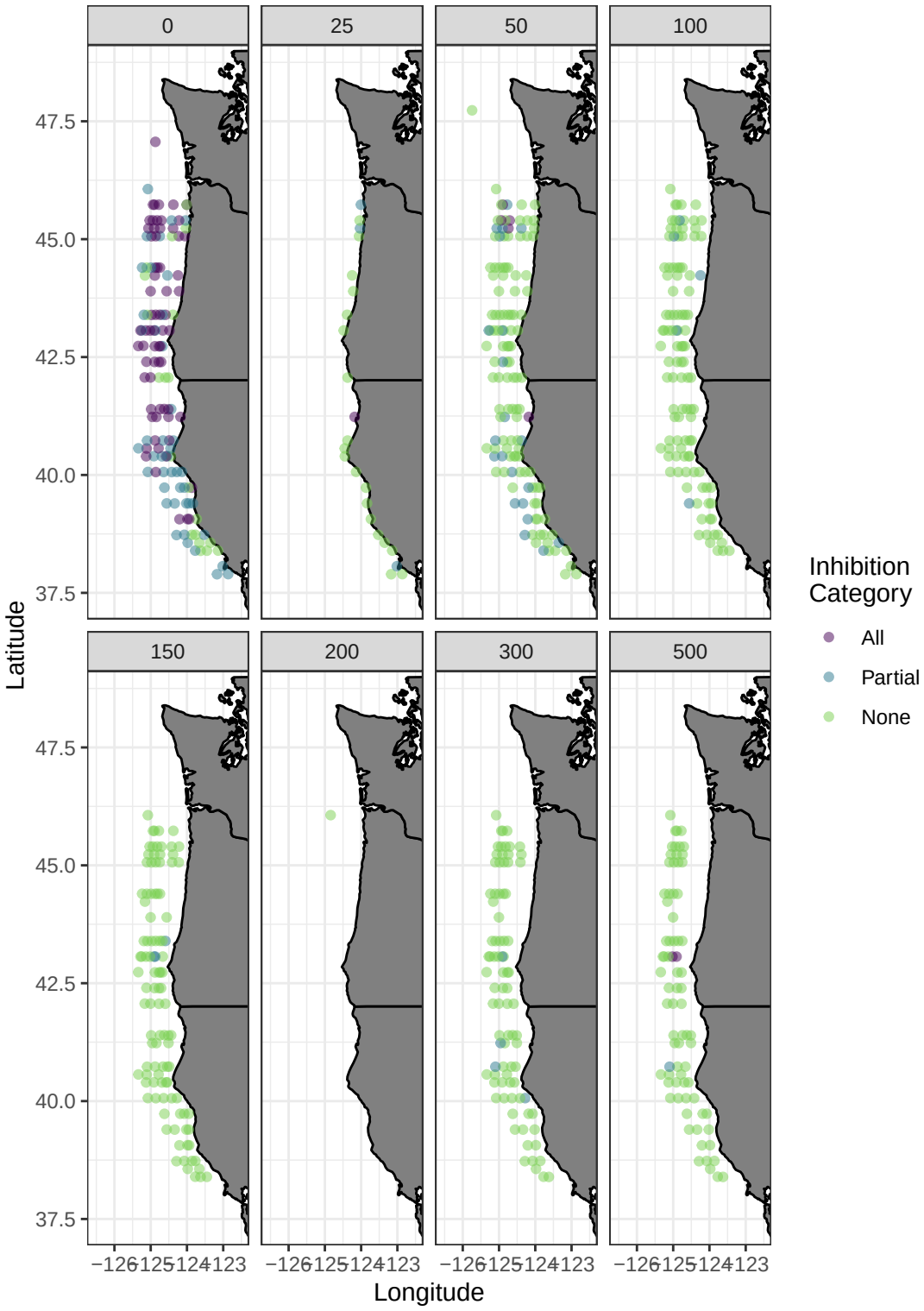


Inhibition

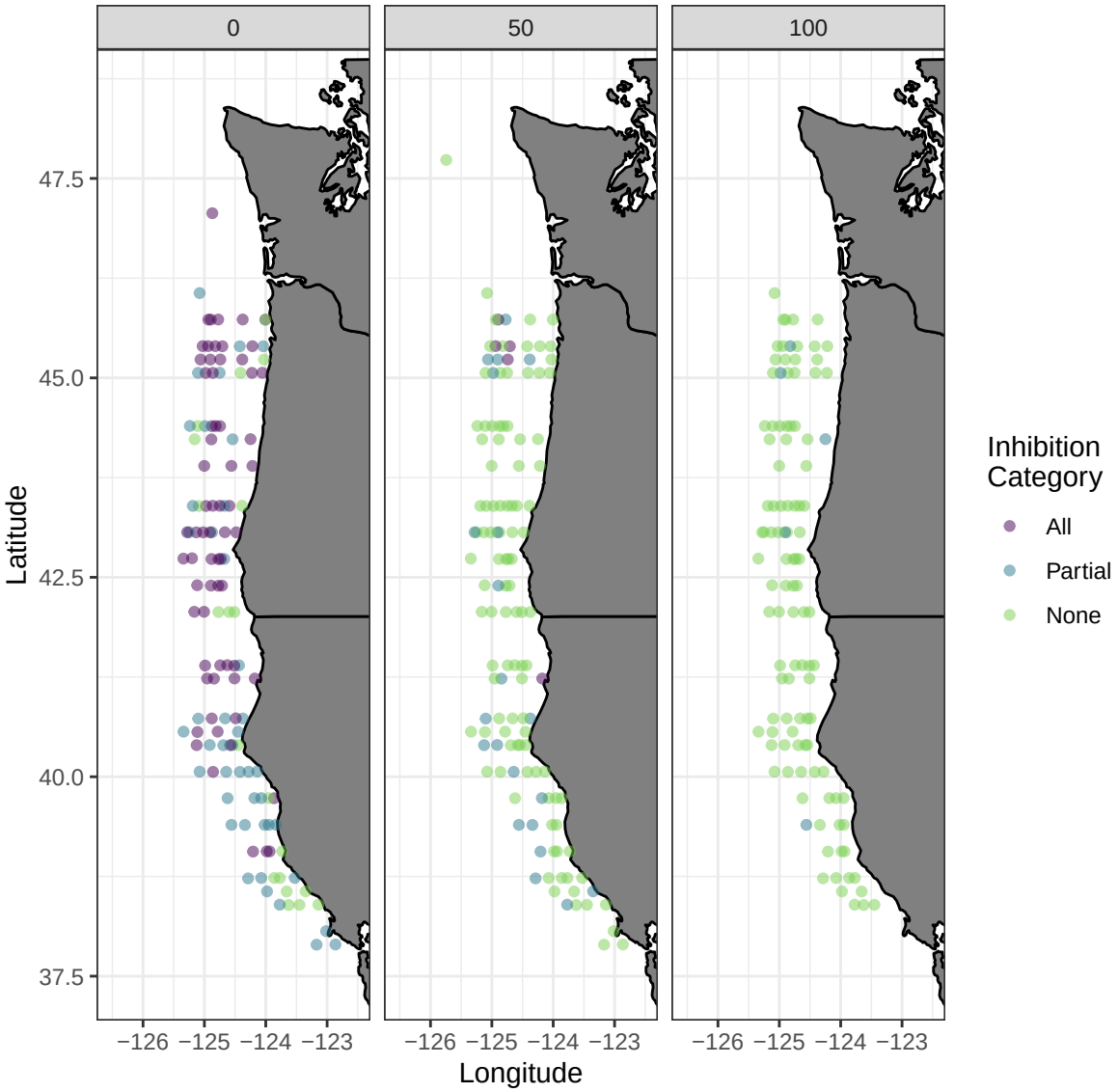
There are a lot of samples that show signs of inhibition. They are concentrated in the surface samples. Here are the inhibition by station-depths and depth categories. 'Completely inhibited' means zero PCR replicates from any water sample at that station-depth combination have amplified within the PCR parameters. 'Not inhibited' indicates that no PCR from that station-depth has evidence of inhibition. Insert language about non-template controls, how inhibition is identified.

Depth Category (m)	Total	Not_inhibited	Partially_inhibited	Completely_inhibited
0	130	20	43	67
25	23	19	3	1
50	128	102	21	5
100	107	102	5	0
150	103	100	3	0
200	1	1	0	0
300	84	80	4	0
500	75	72	1	2
TOTAL	651	496	80	75

We can look at the patterns of inhibition spatially and by depth.

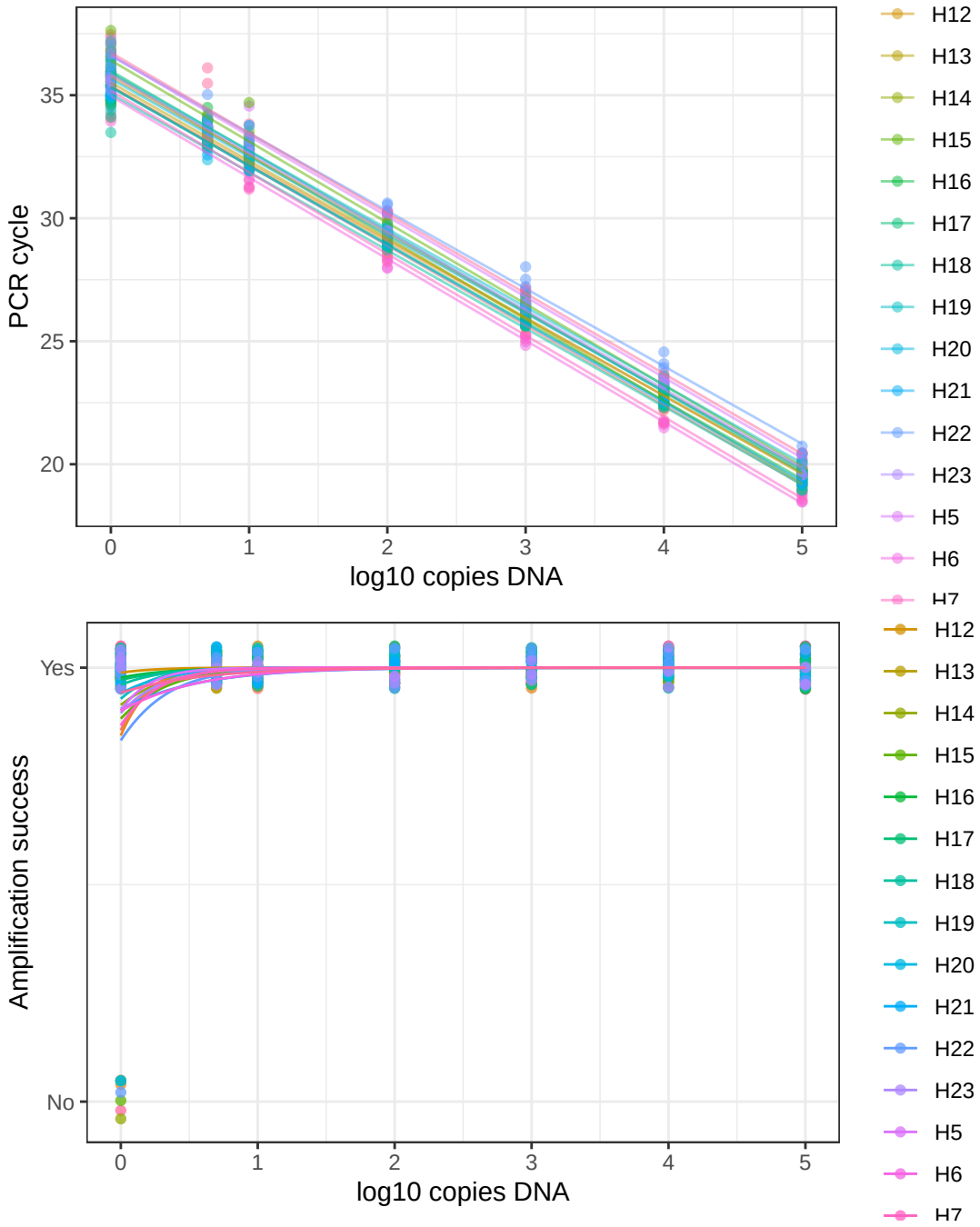

0
25
50
100
150
200
300
500
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Latitude
Longitude
Inhibition Category
All
Partial
None

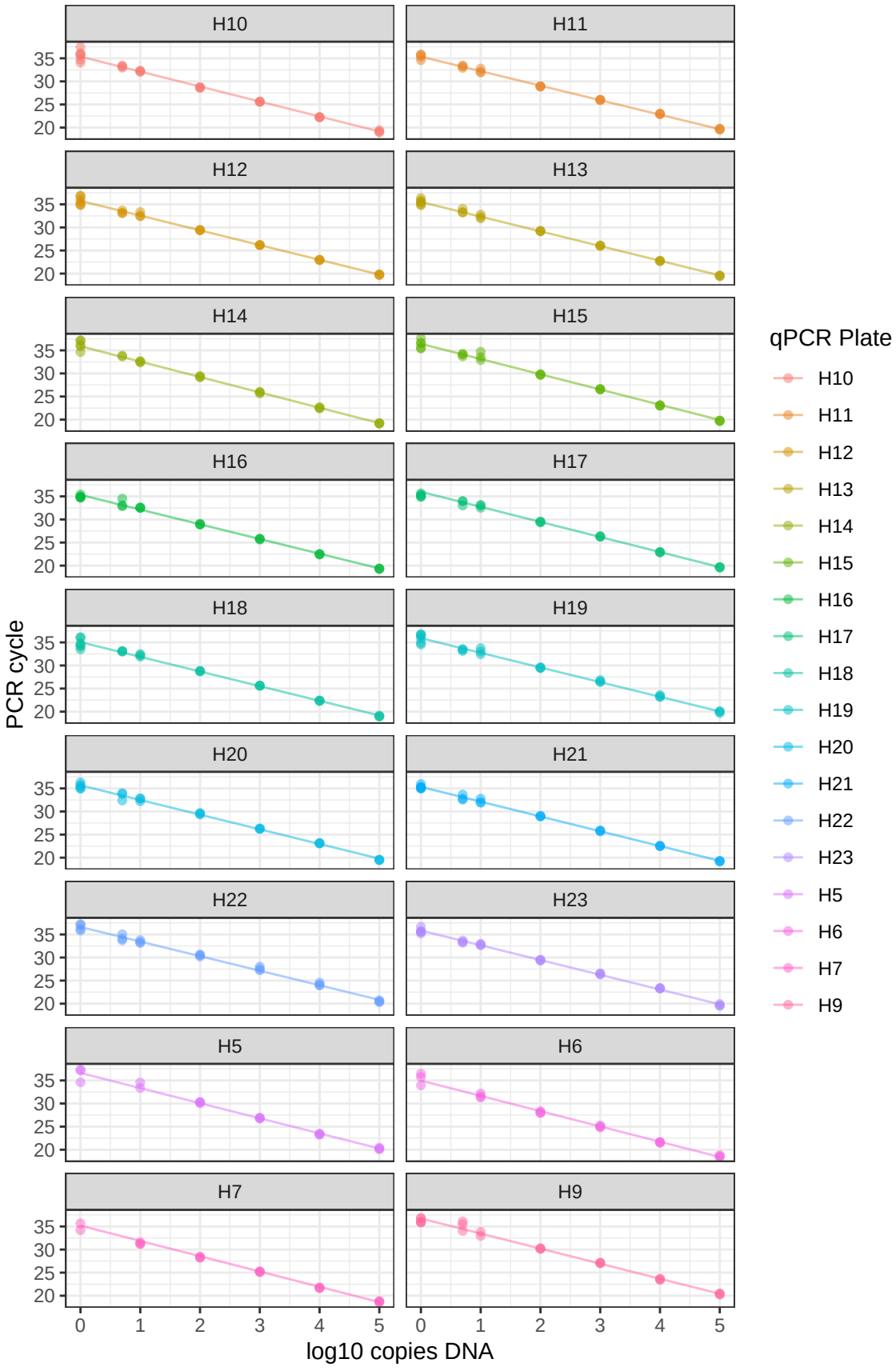
Here are some larger plot of just a few shallow depths. Inhibition is clearly strongest at the surface, but beyond depth there is no obvious pattern of inhibition among the samples. Perhaps there is a hint of inhibition in the offsore edges of the transects at the 50 and 100m depths, but it is not a strong pattern.



Standards

The standards used in the qPCR assay look pretty reasonable good. Each color represents a different PCR plate. They are pretty much on top of each other.

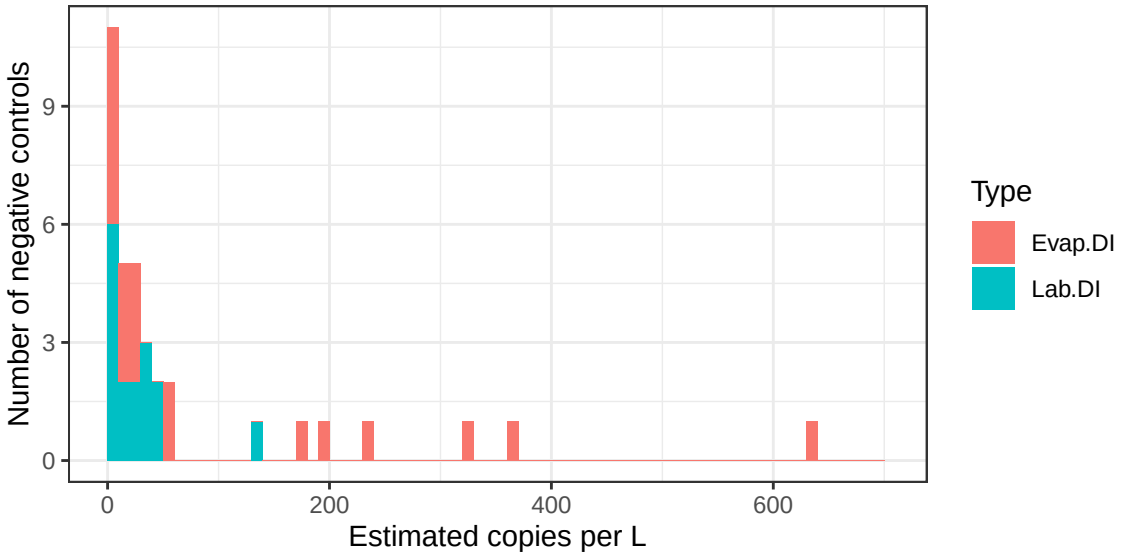



H10
H11
H12
H13
H14
H15
H16
H17
H18
H19
H20
H21
H22
H23
H5
H6
H7
H9
35
30
25
20
0
1
2
3
4
5
PCR cycle
log10 copies DNA
qPCR Plate
H10
H11
H12
H13
H14
H15
H16
H17
H18
H19
H20
H21
H22
H23
H5
H6
H7
H9

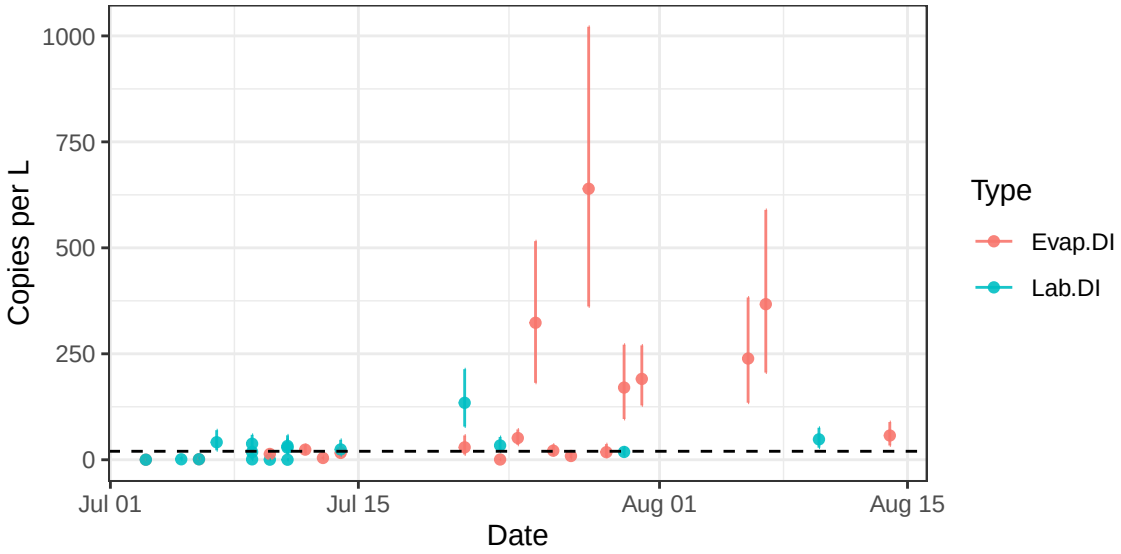
Controls

There are two main types of control: field negative control and extraction controls. The extraction controls have never produced any measurable amount of hake DNA, so we will ignore them for now.

Thus far we have analyzed 35 samples out of a total of 53 field negative samples. Out of the 35, 19 have detectable amounts (> 20 Copies L^{-1}) of hake DNA. In general the amount of detected hake DNA is low but is non-zero.

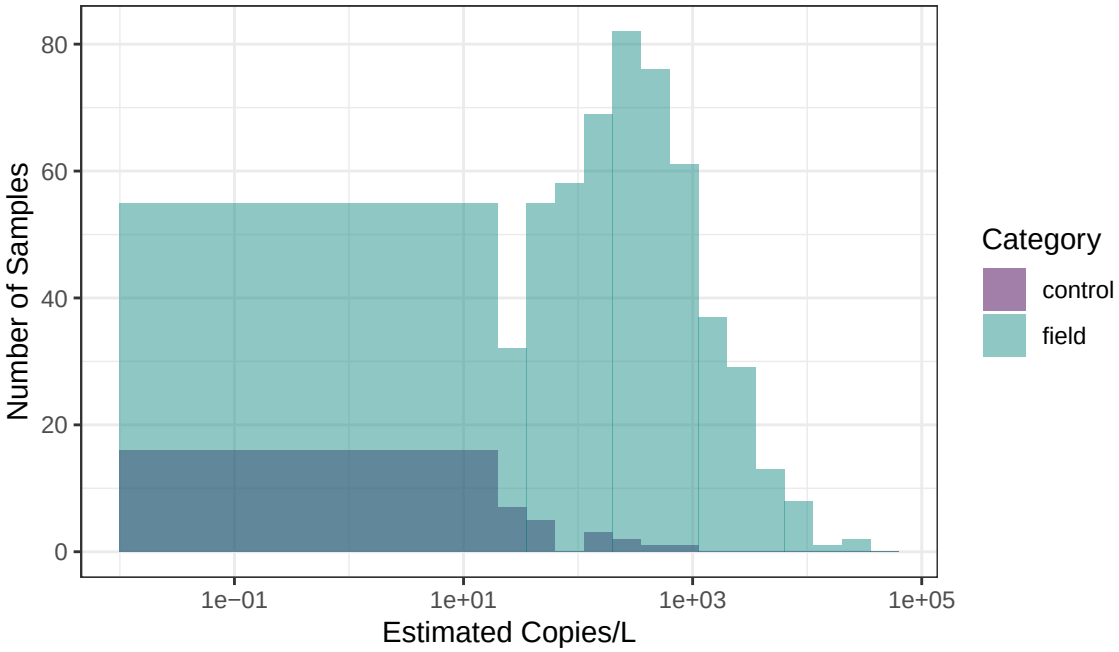


We can look at the temporal pattern of the control values too. This will be more informative when we have more samples analyzed. The highest levels of contamination seem to come from the Evaporated DI water controls... and occur later in the sampling season. These counts now also account for the amount of water filtered in each negative control.

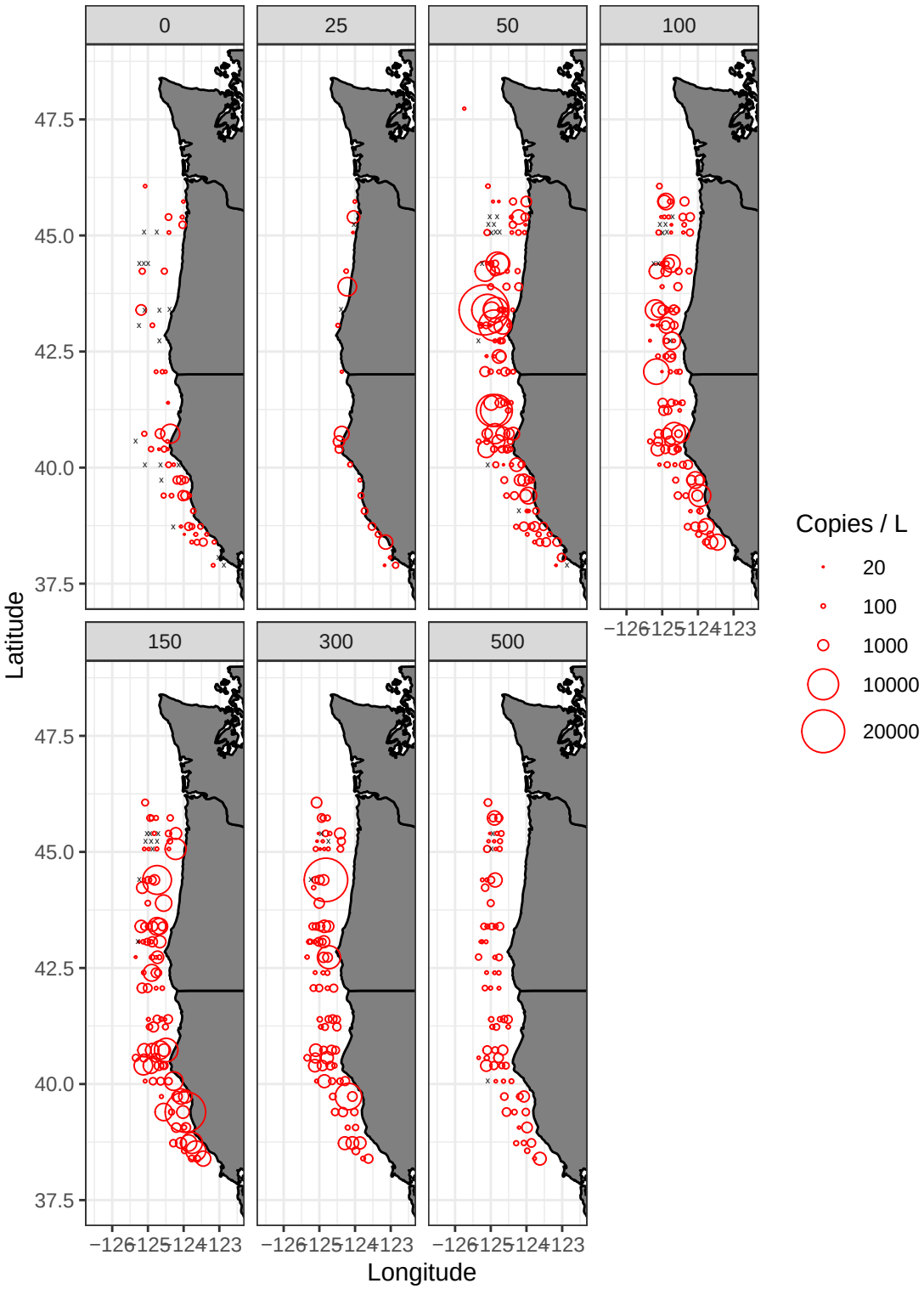


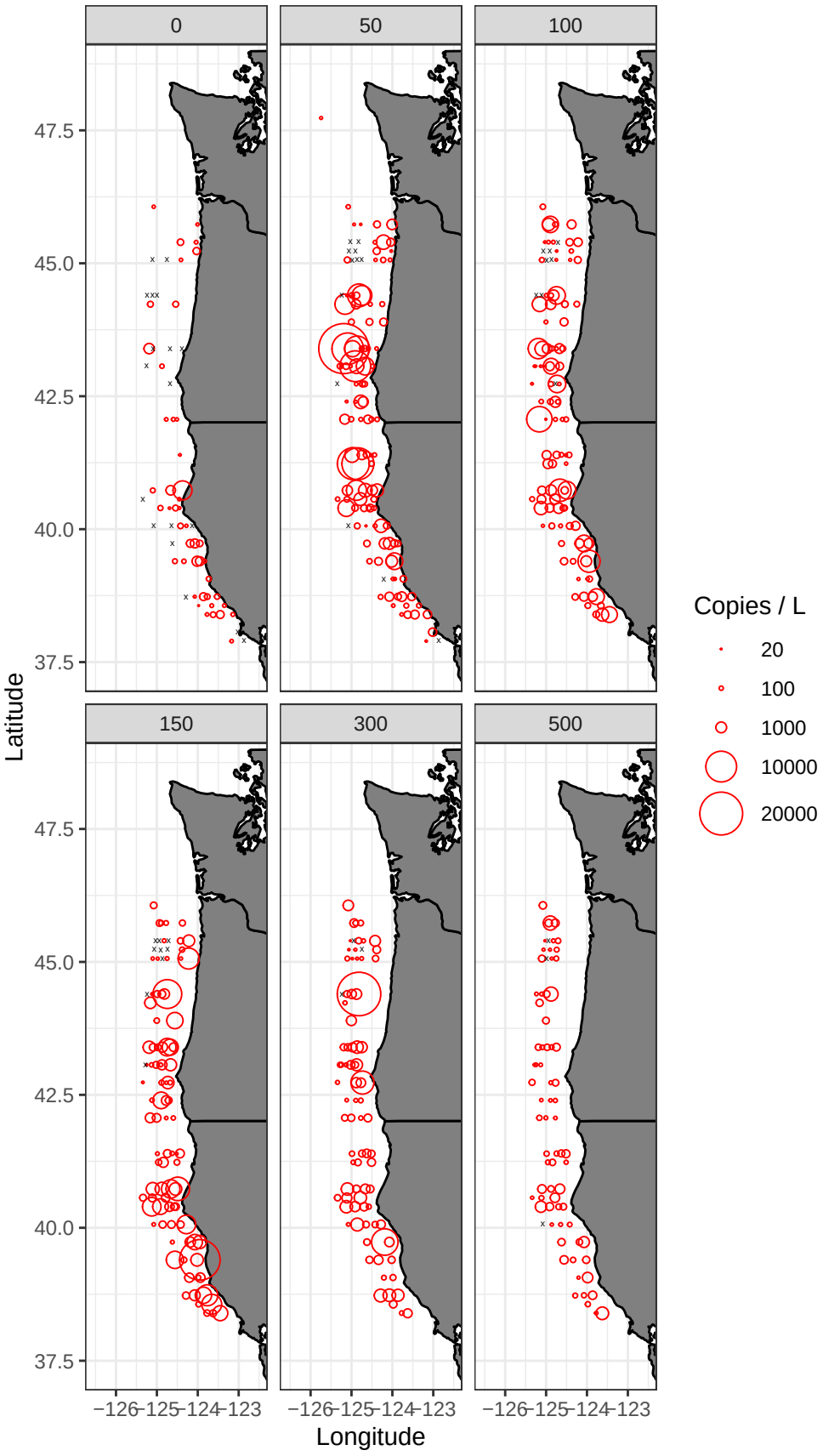
Hake eDNA

We can first ask if the distribution of estimated hake DNA compare to the values present in the field samples. The water samples are substantially larger than the controls... which is good.



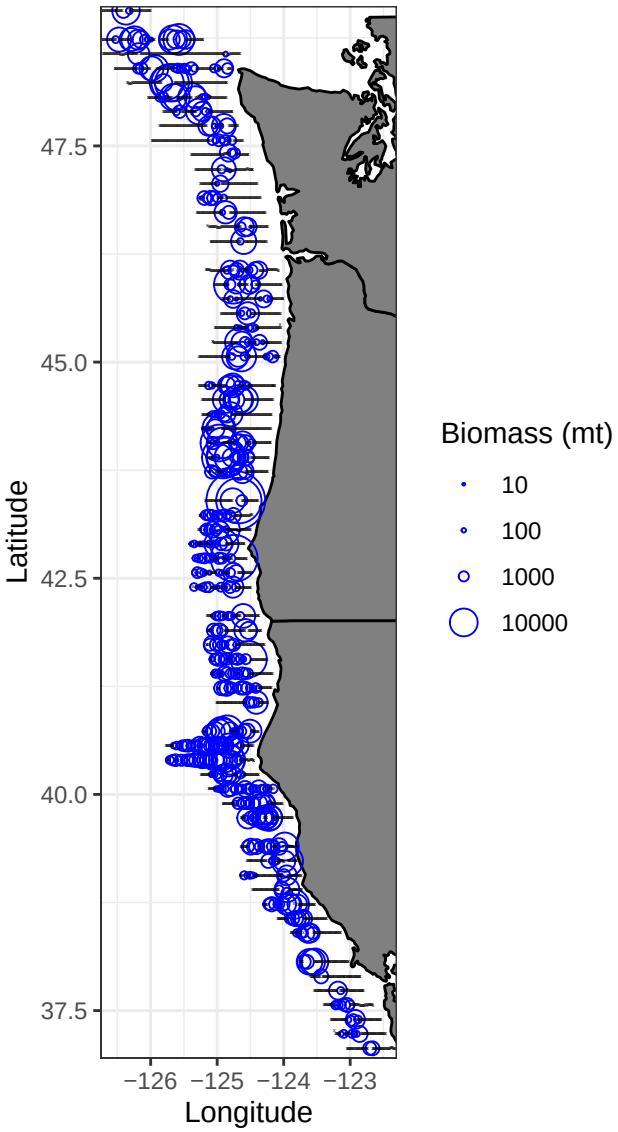
Let's make some plots of the spatial distribution of hake DNA.


0
25
50
100
150
300
500
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Latitude
Longitude
Copies / L
20
100
1000
10000
20000


0
50
100
150
300
500
47.5
45.0
42.5
40.0
37.5
Latitude
−126
−125
−124
−123
Longitude
Copies / L
20
100
1000
10000
20000

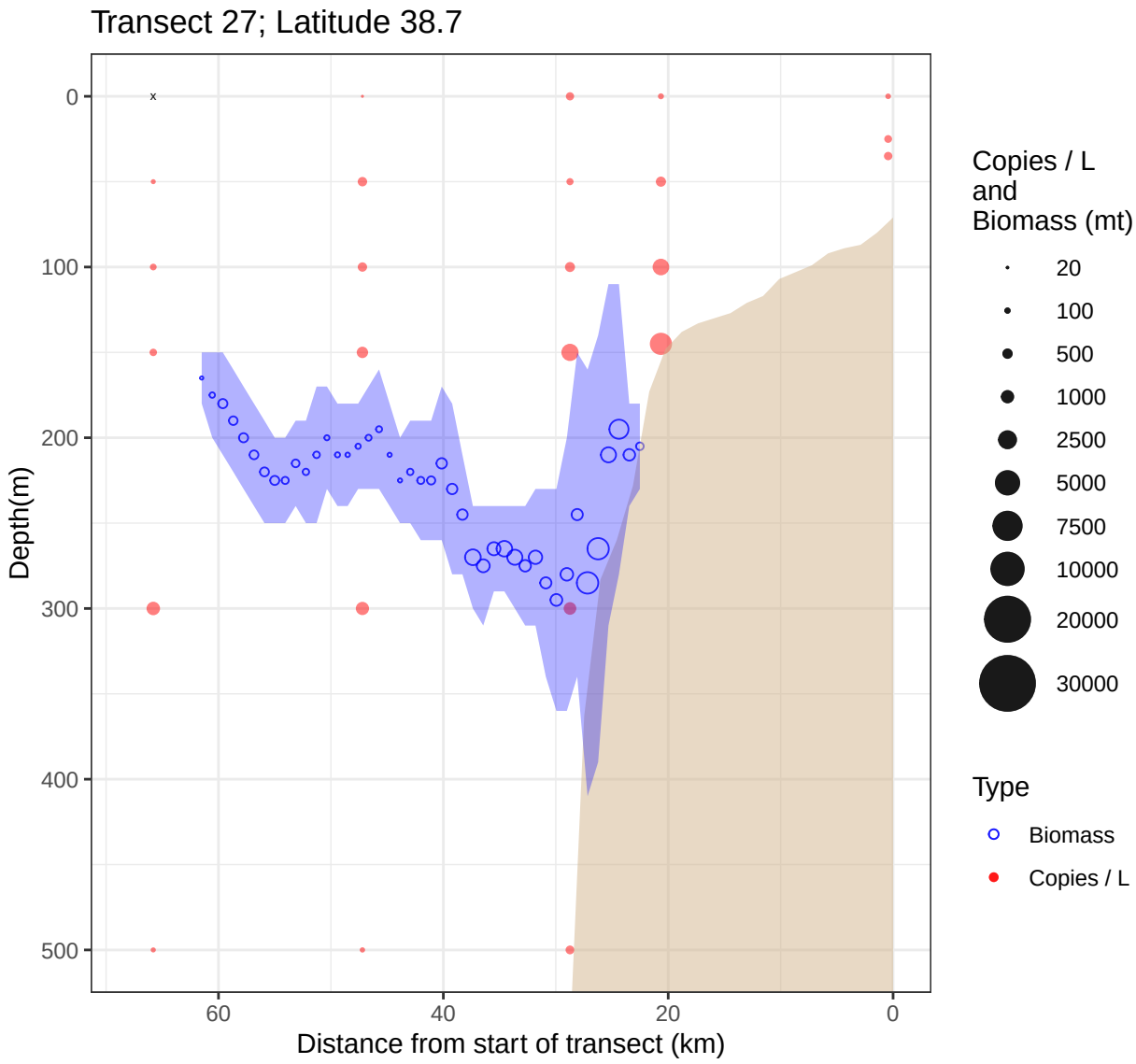
Acoustic Data.

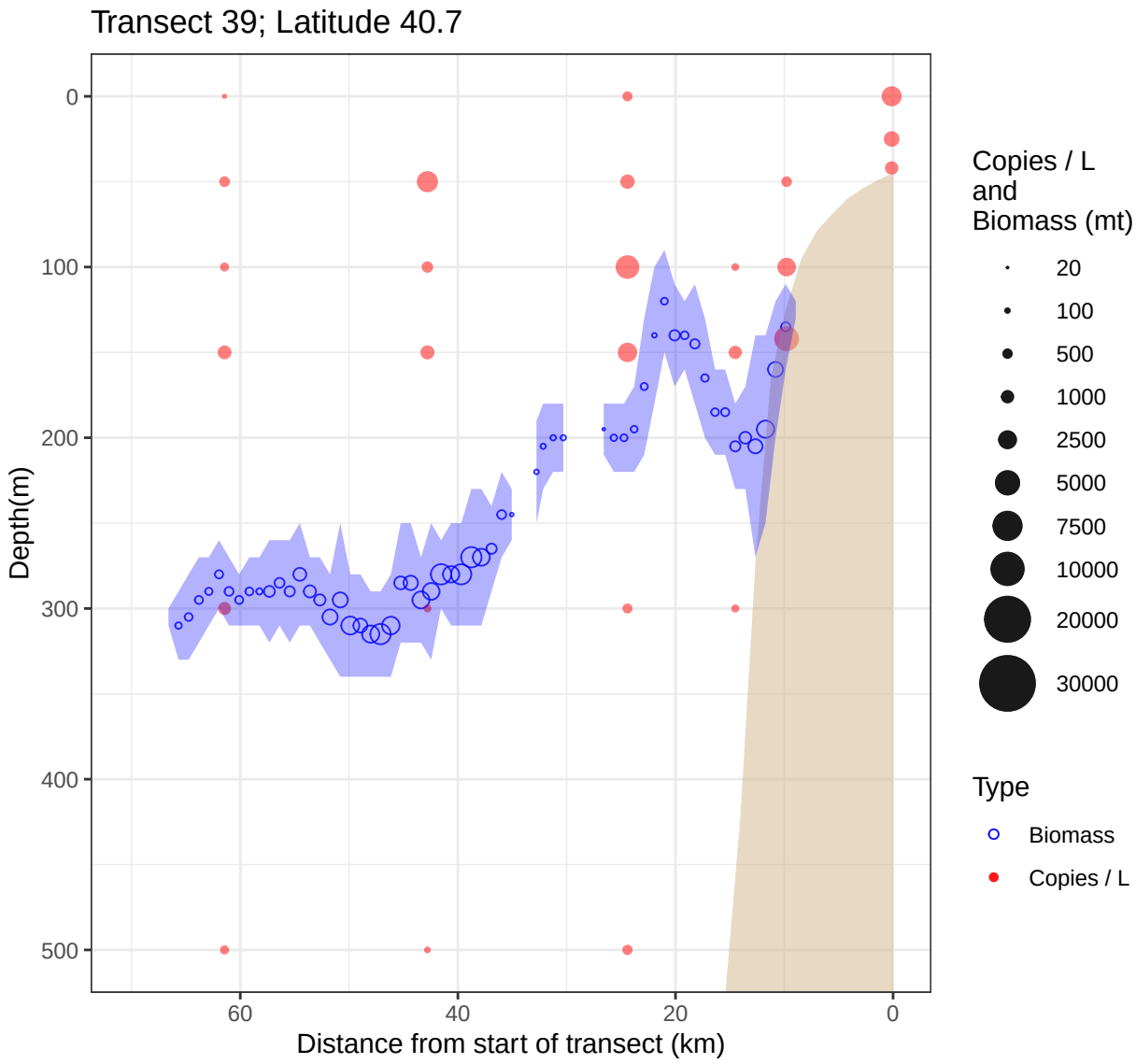
This is a spatial plot of the biomass from the acoustic surveys. The raw data is in 0.5 nm longitudinal bins. To make things prettier for plotting, I have aggregated the data into 2 nm bins. Unlike the eDNA data, the acoustic data does not currently have biomass estimated by depth strata. It does have the mean depth associated with each 0.5 nm bin and the estimated width of the hake layer, though. I make some of those plots later.

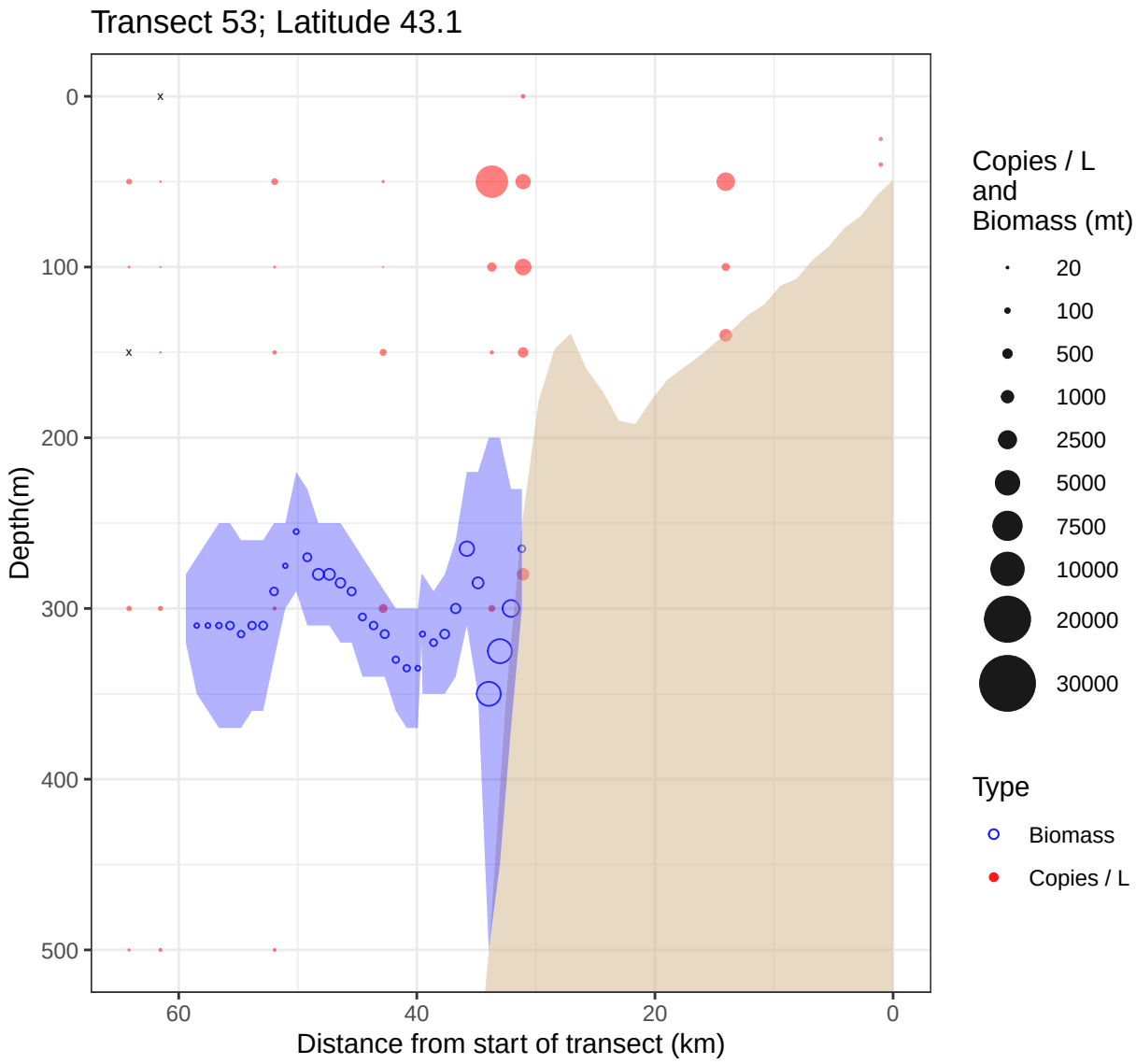


Acoustic and eDNA Data.

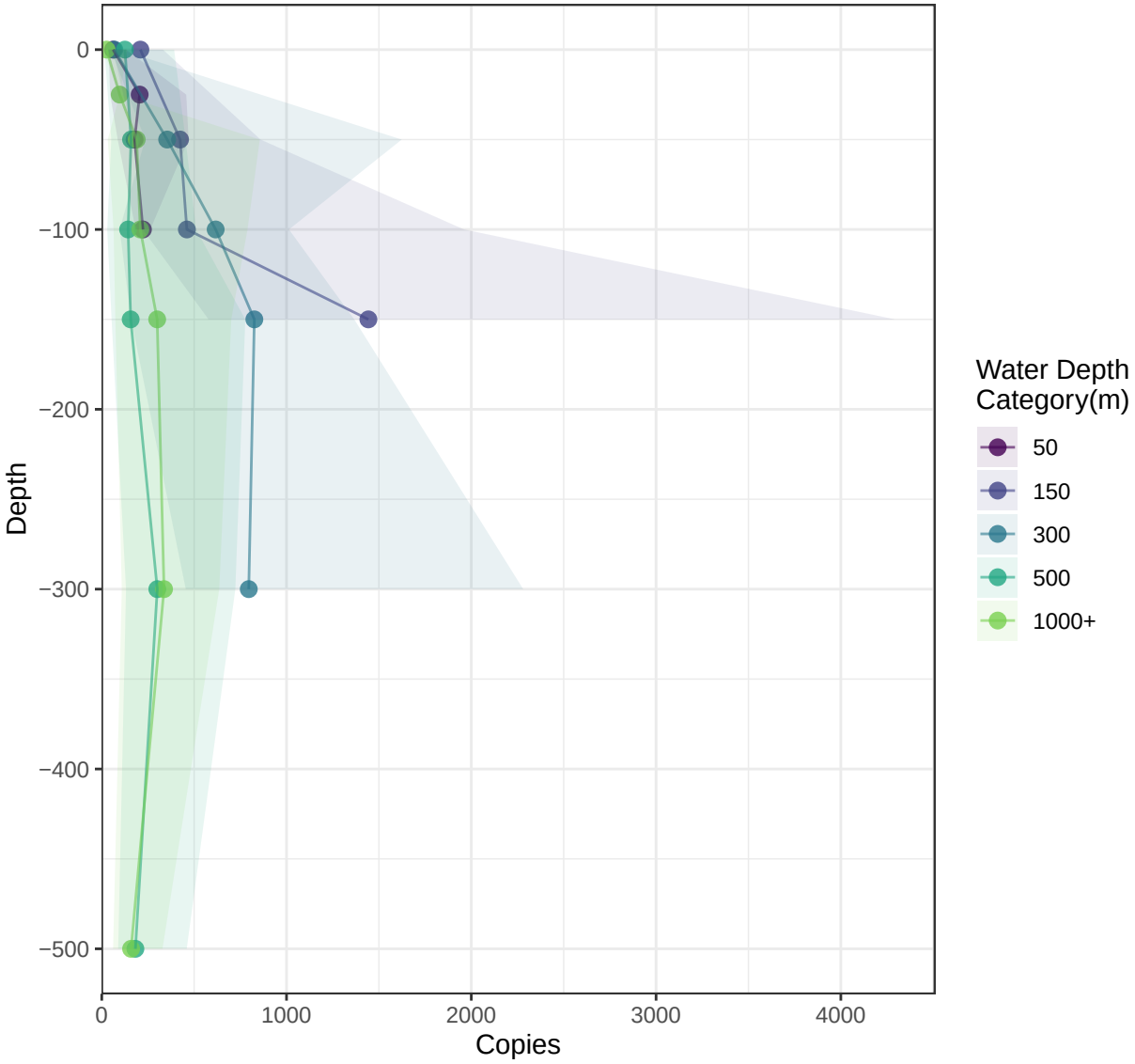
Here are a few plots from individual transects. Coast is on the right side of the graph

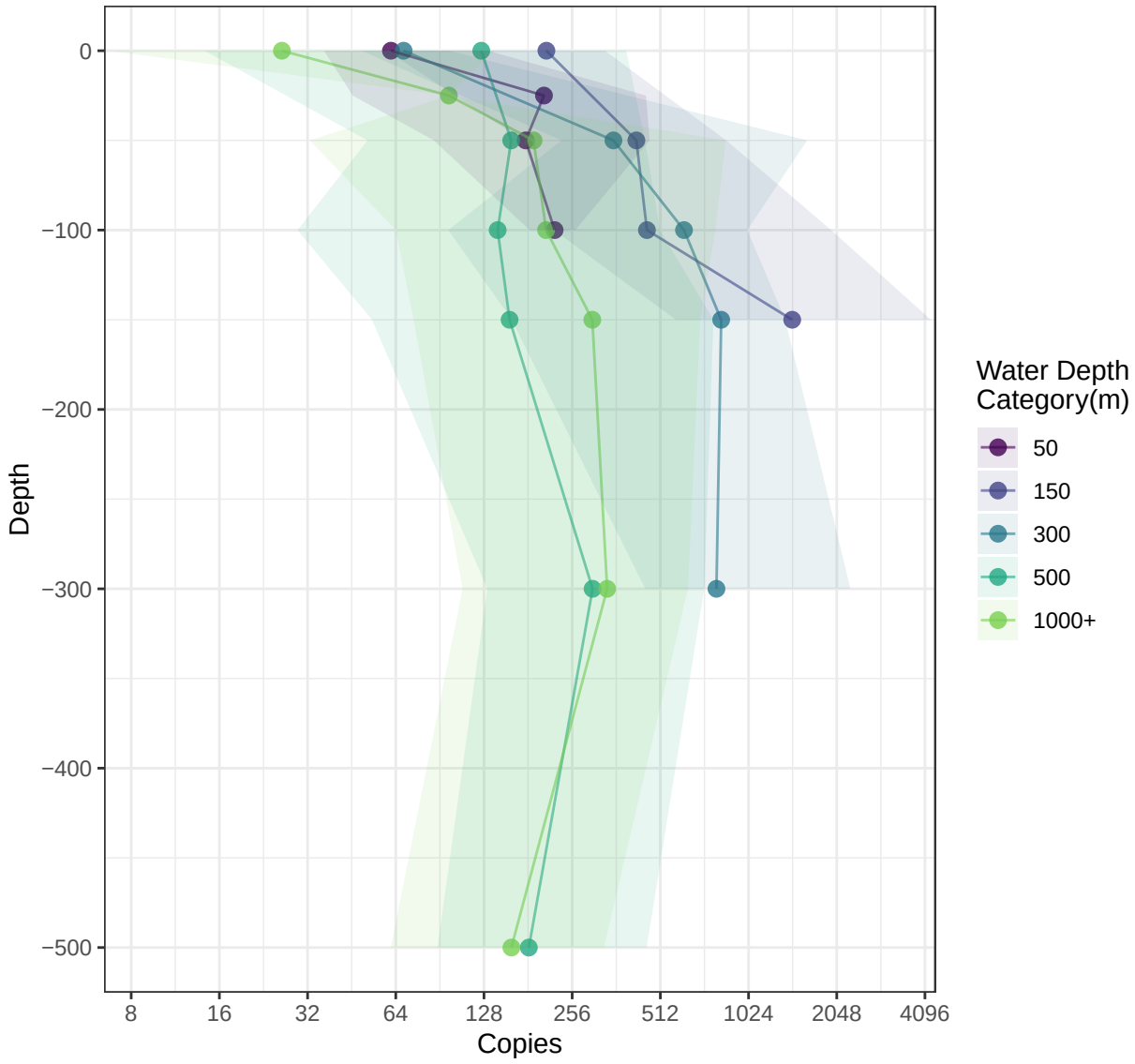

Transect 27; Latitude 38.7
Depth(m)
0
100
200
300
400
500
60
40
20
0
Distance from start of transect (km)
Copies / L and Biomass (mt)
20
100
500
1000
2500
5000
7500
10000
20000
30000
Type
Biomass
Copies / L


Transect 39; Latitude 40.7
Depth(m)
0
100
200
300
400
500
60
40
20
0
Distance from start of transect (km)
Copies / L and Biomass (mt)
20
100
500
1000
2500
5000
7500
10000
20000
30000
Type
Biomass
Copies / L


Transect 53; Latitude 43.1
Depth(m)
0
100
200
300
400
500
60
40
20
0
Distance from start of transect (km)
Copies / L and Biomass (mt)
20
100
500
1000
2500
5000
7500
10000
20000
30000
Type
Biomass
Copies / L

This is a plot of median (plus interquartile range) for hake DNA concentration by the water depth category. Shallower sites are on the shelf (same data with two different x-axes, plotted)




0
−100
−200
−300
−400
−500
Depth
8
16
32
64
128
256
512
1024
2048
4096
Copies
Water Depth Category(m)
50
150
300
500
1000+