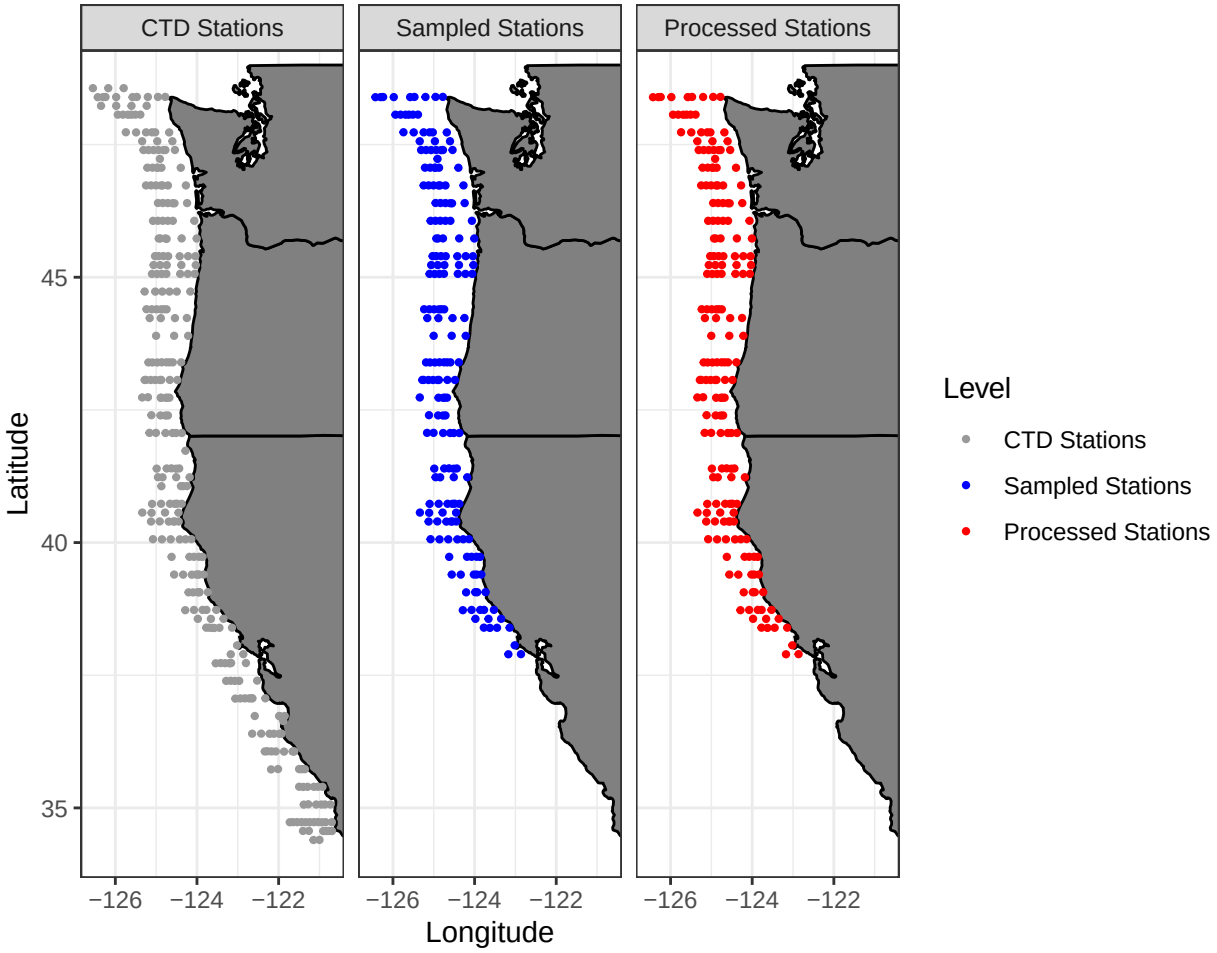
Hake 2019 Survey

eDNA from the 2019 Hake cruise, eulachon

Sampling and processing to date.

In total we have processed qPCR for pacific hake, pacific lamprey, and eulachon from 186 CTD stations representing 925 station-depth combinations for 1838 individual 2.5L water samples.

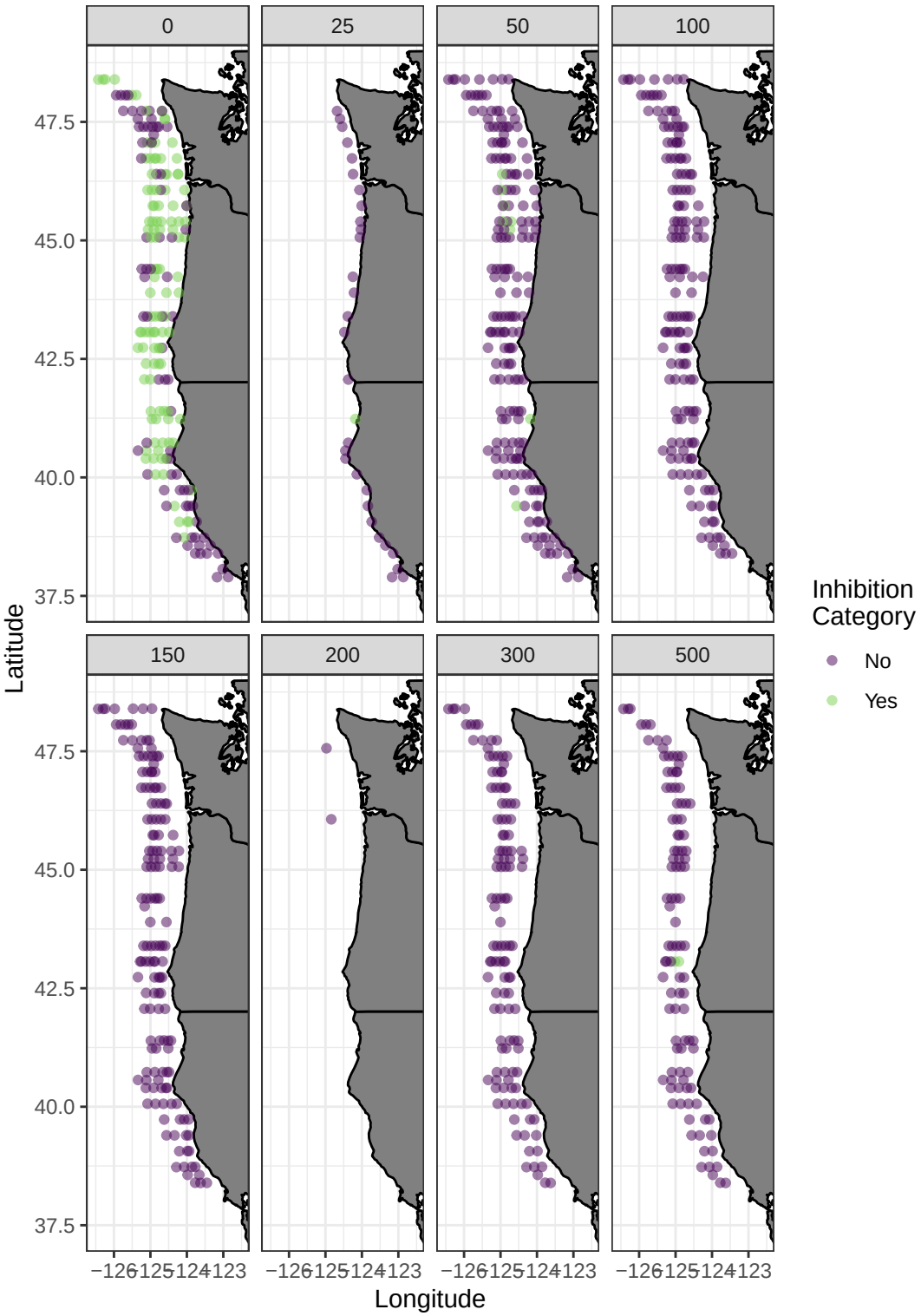


Inhibition

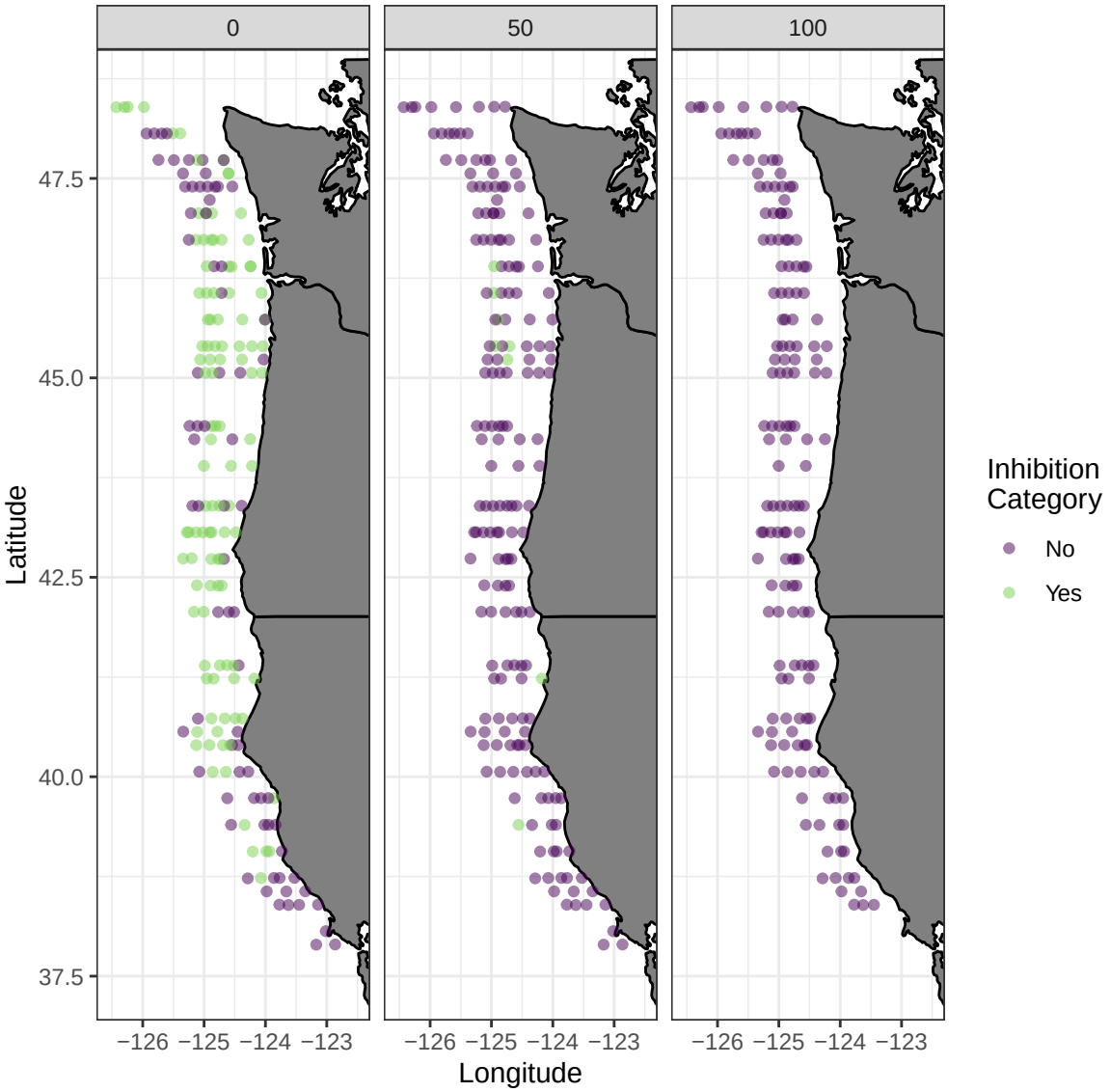
There are a lot of samples that show signs of inhibition. They are concentrated in the surface samples. Here are the inhibition by station-depths and depth categories. 'Completely inhibited' means zero PCR replicates from any water sample at that station-depth combination have amplified within the PCR 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_m	No	Yes
0	75	107
25	29	1
50	174	8
100	155	0
150	149	0
200	2	0
300	120	0
500	103	2

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

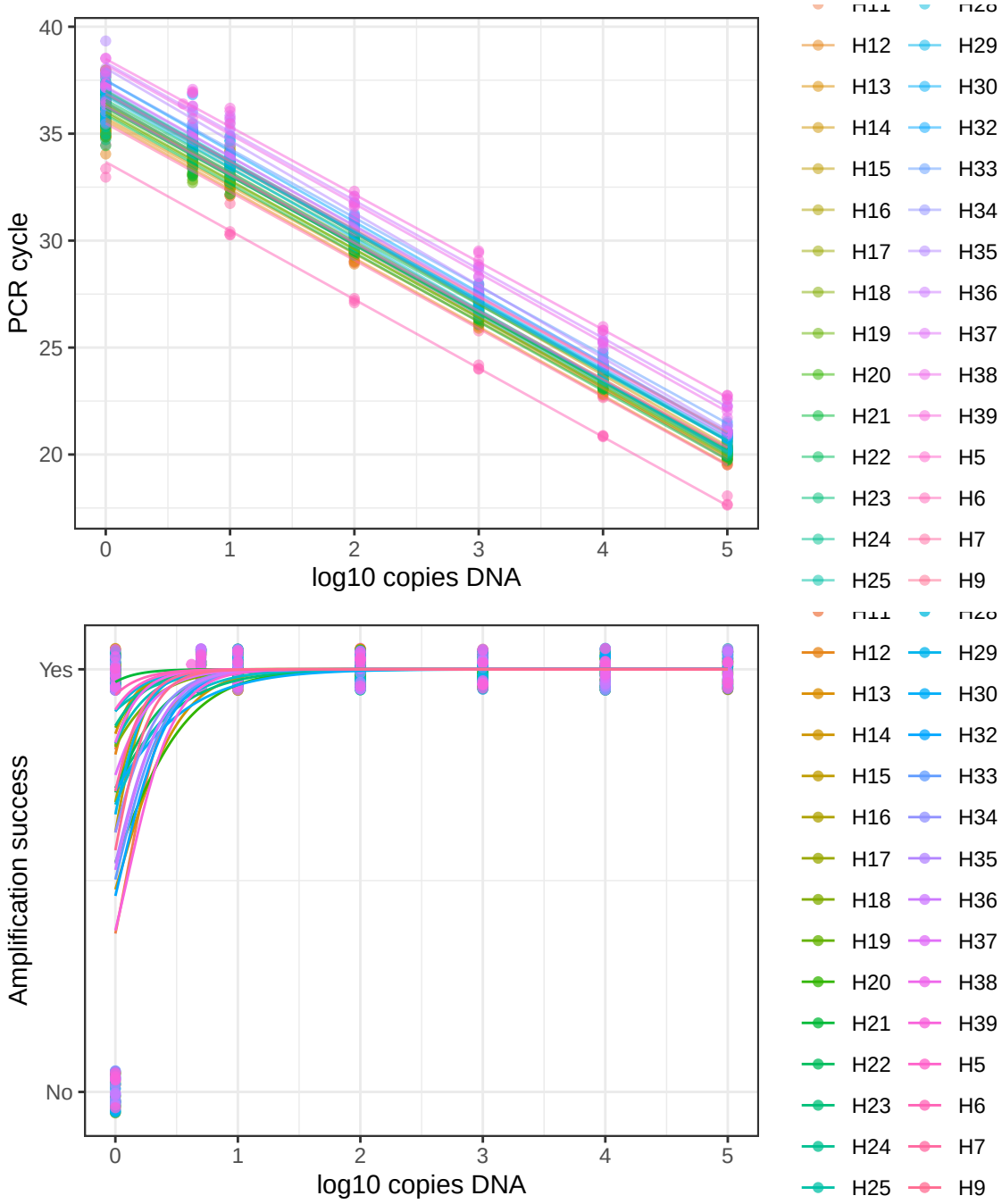

0
25
50
100
150
200
300
500
Latitude
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Longitude
Inhibition Category
No
Yes

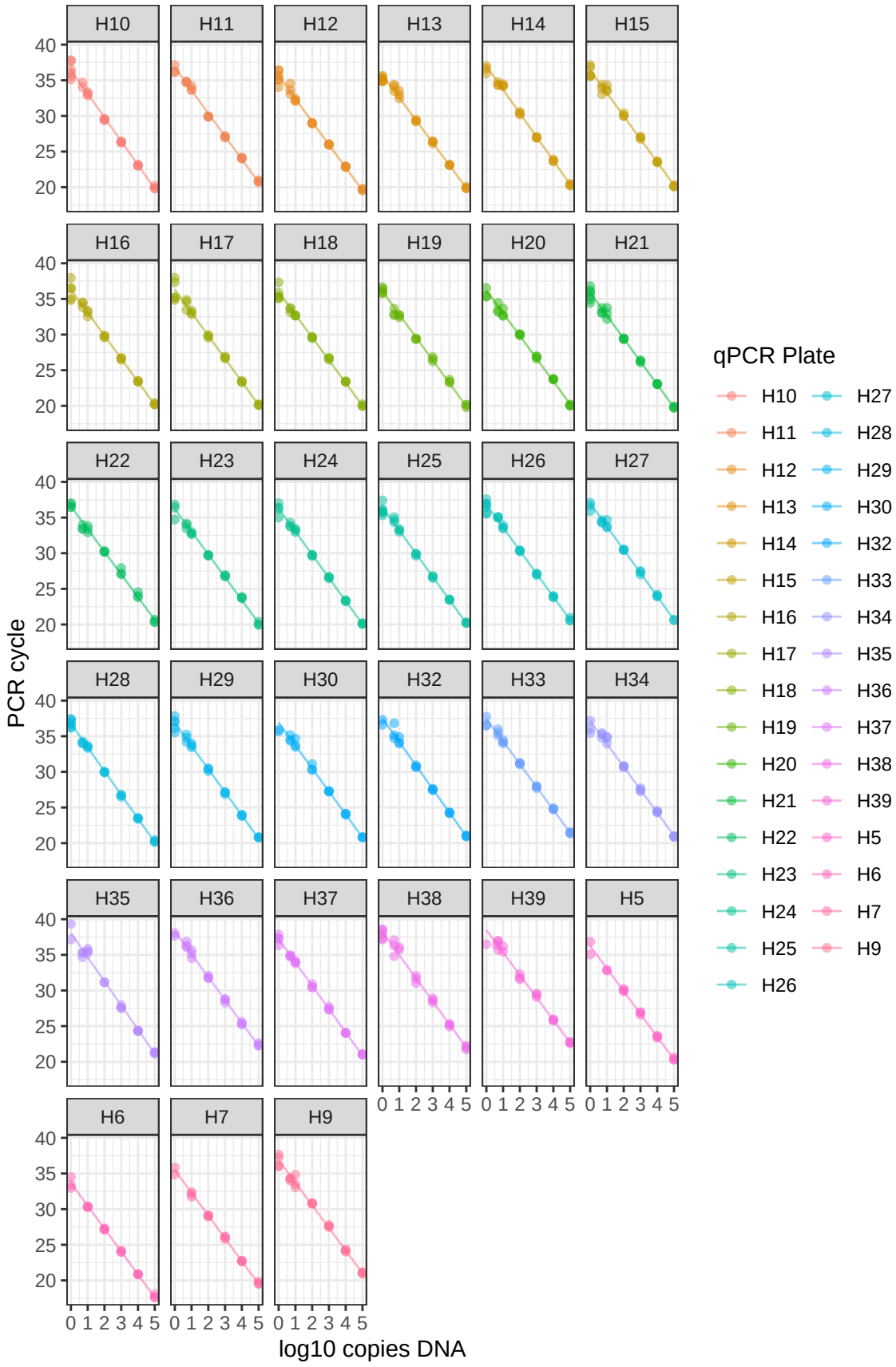
Here are some larger plot of just a few shallow depths. Inhibition is clearly strongest at the surface, but beyond depth there is no obvious pattern of inhibition among the samples. Perhaps there is a hint of inhibition in the offsore edges of the transects at the 50 and 100m depths, but it is not a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



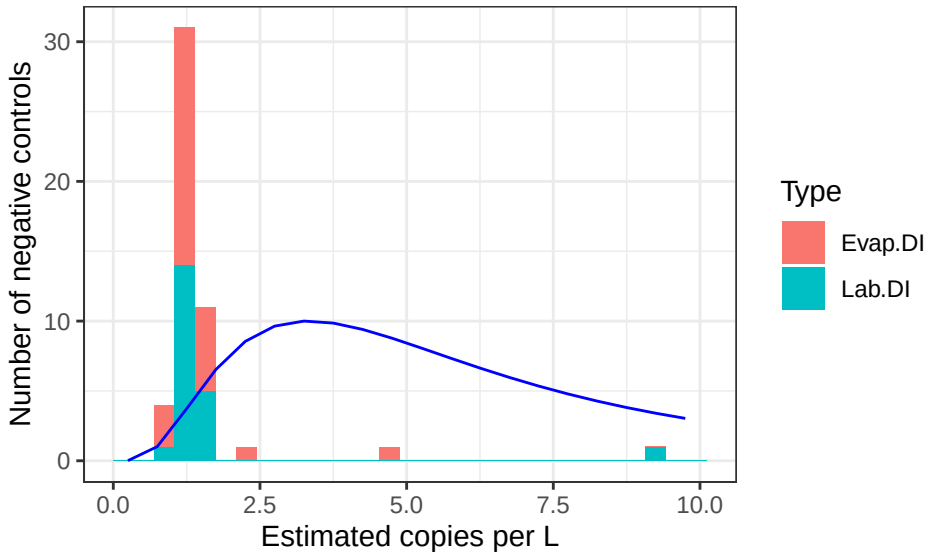

H10
H11
H12
H13
H14
H15
H16
H17
H18
H19
H20
H21
H22
H23
H24
H25
H26
H27
H28
H29
H30
H32
H33
H34
H35
H36
H37
H38
H39
H5
H6
H7
H9
PCR cycle
log10 copies DNA
qPCR Plate

Dilutions

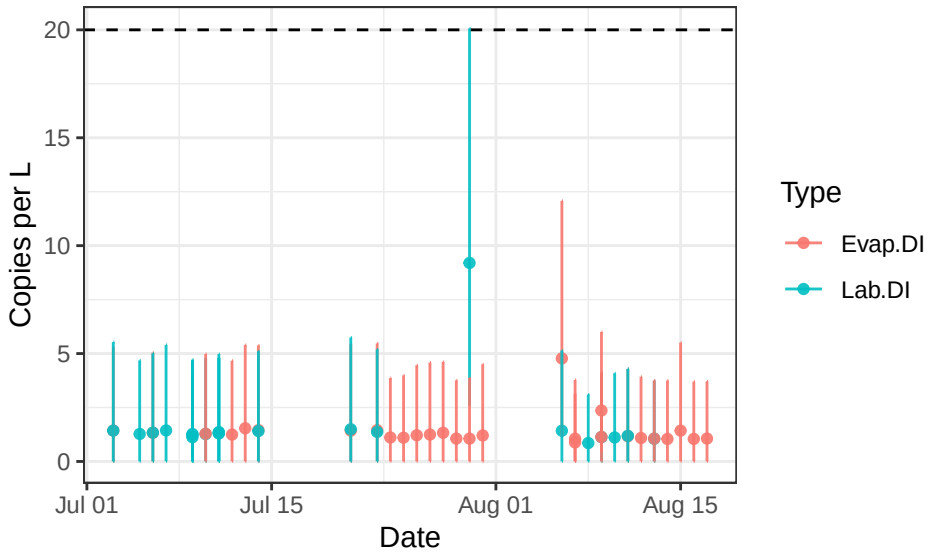
Controls

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

Thus far we have analyzed 49 samples out of a total of 53 field negative samples. Out of the 49, 0 have detectable amounts (> 20 Copies L^{-1}) of eulachon DNA. In general the amount of detected eulachon DNA is pretty much zero.



We can look at the temporal pattern of the control values too. All are below the detection limit for the assay.

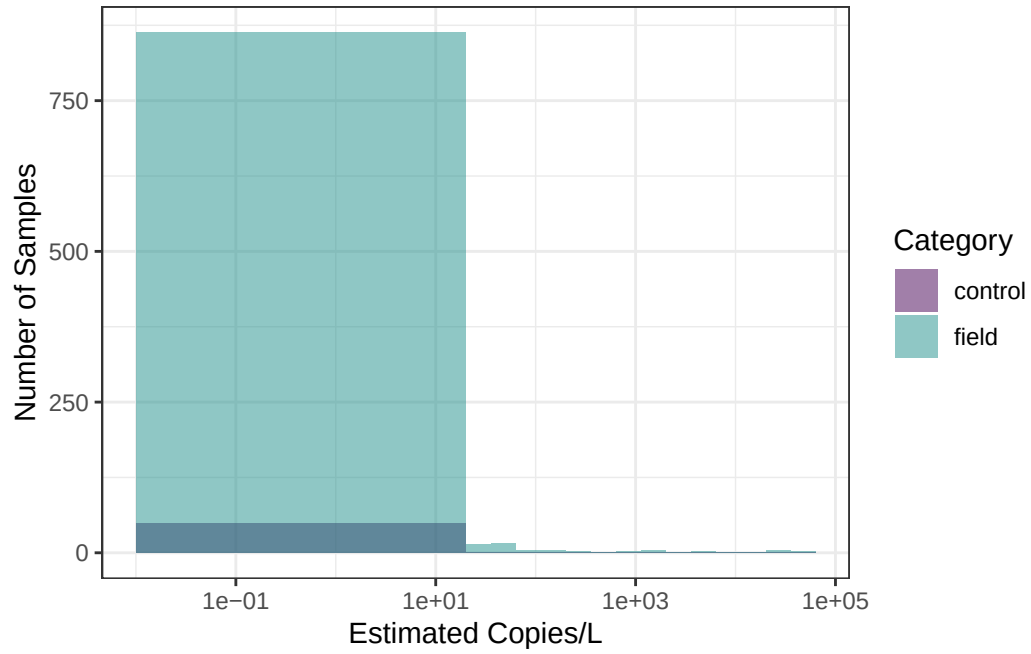


Ethanol wash samples

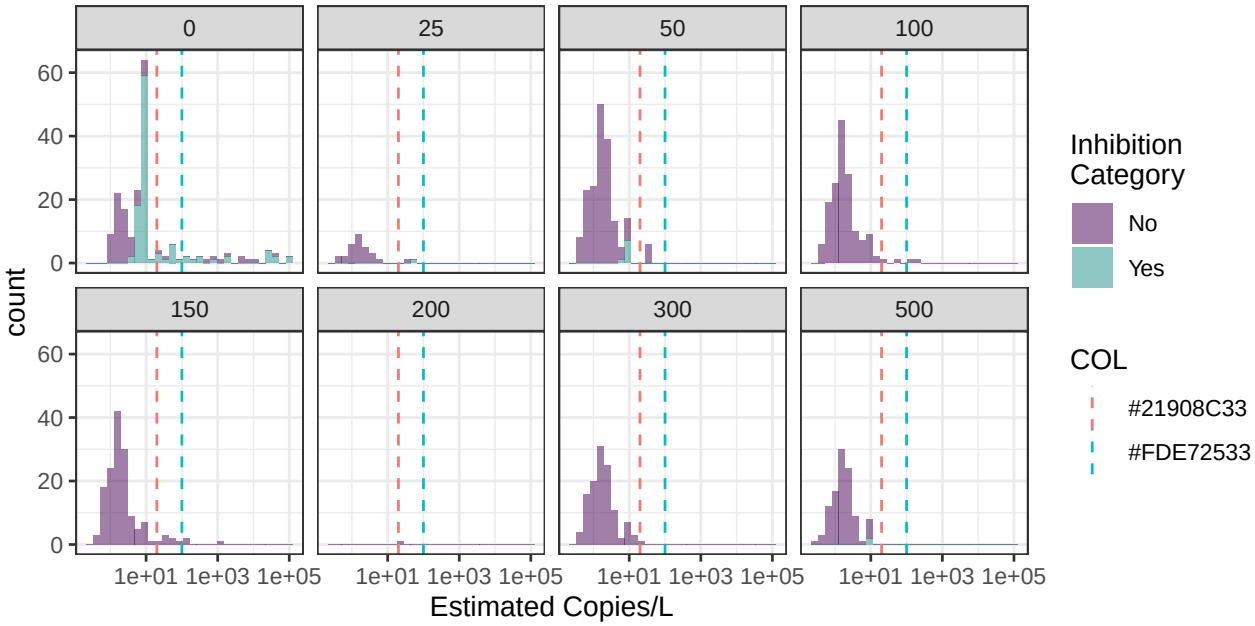
For a buch of samples, the final stage of th extraction wash was conducted using a 30% Ethanol wash as opposed to a 70% ethanol wash. This should result in some amount of DNA being lost from the samples. To examine this, we intentionally washed one of the two Niskin bottles from 23 station-depth combinations with 30% ethanol and one with 70% ethanol with the goal of detecting what the average difference in DNA concentration between the two samples washed in DNA would be.

Eulachon eDNA

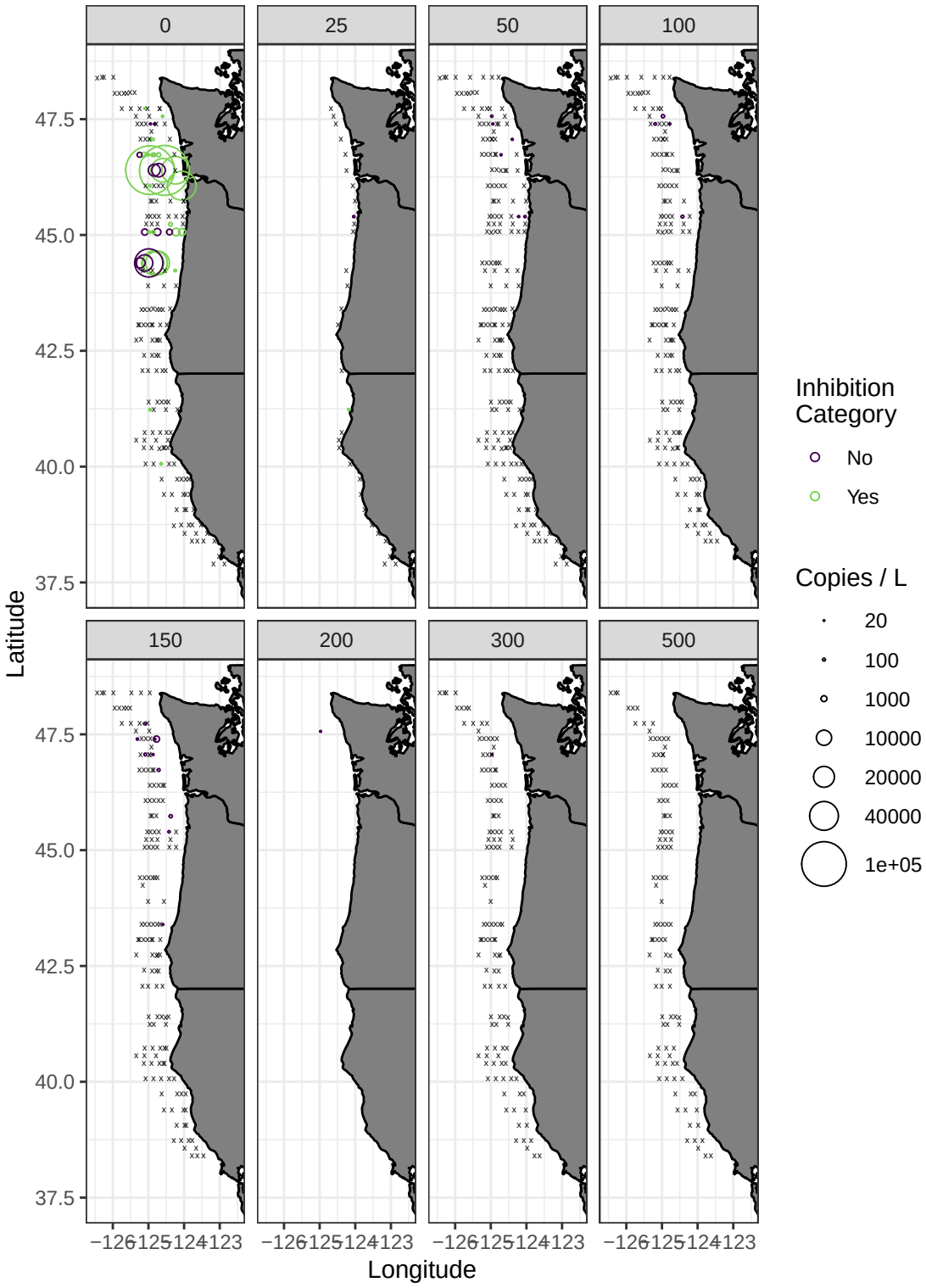
We can first ask if the distribution of estimated DNA compare to the values present in the field samples. The vast majority of samples have effectively 0 eulachon DNA.

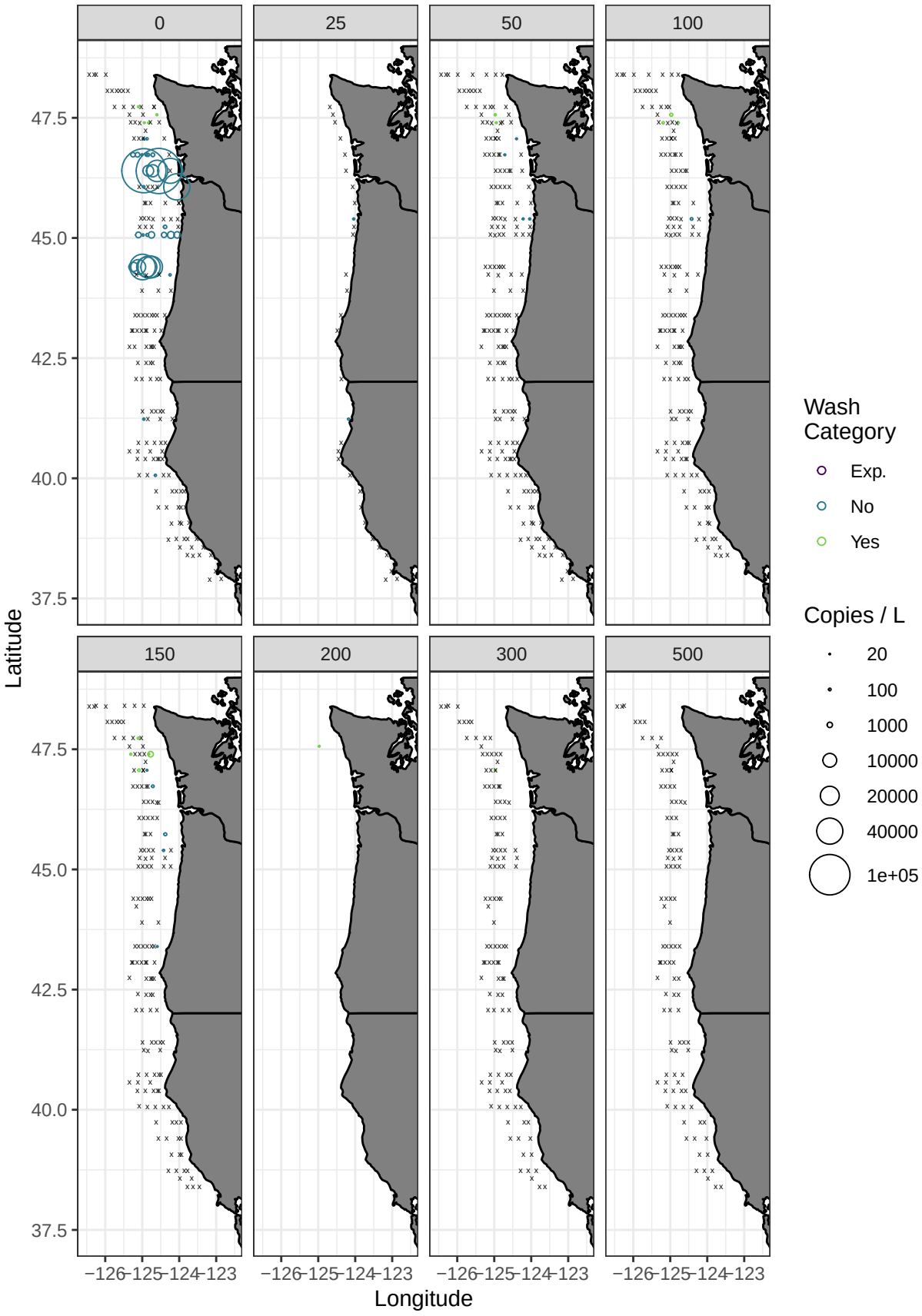


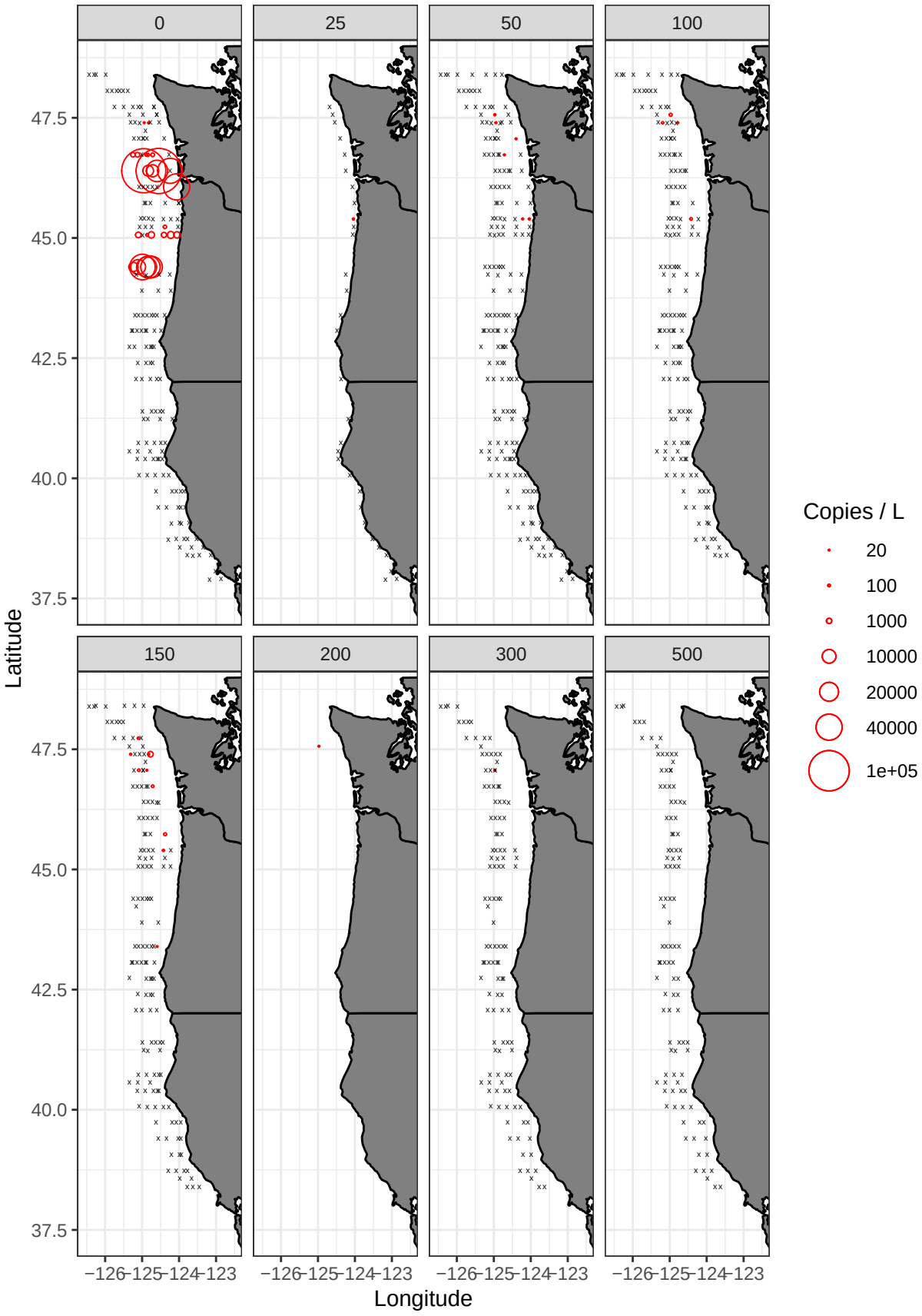

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

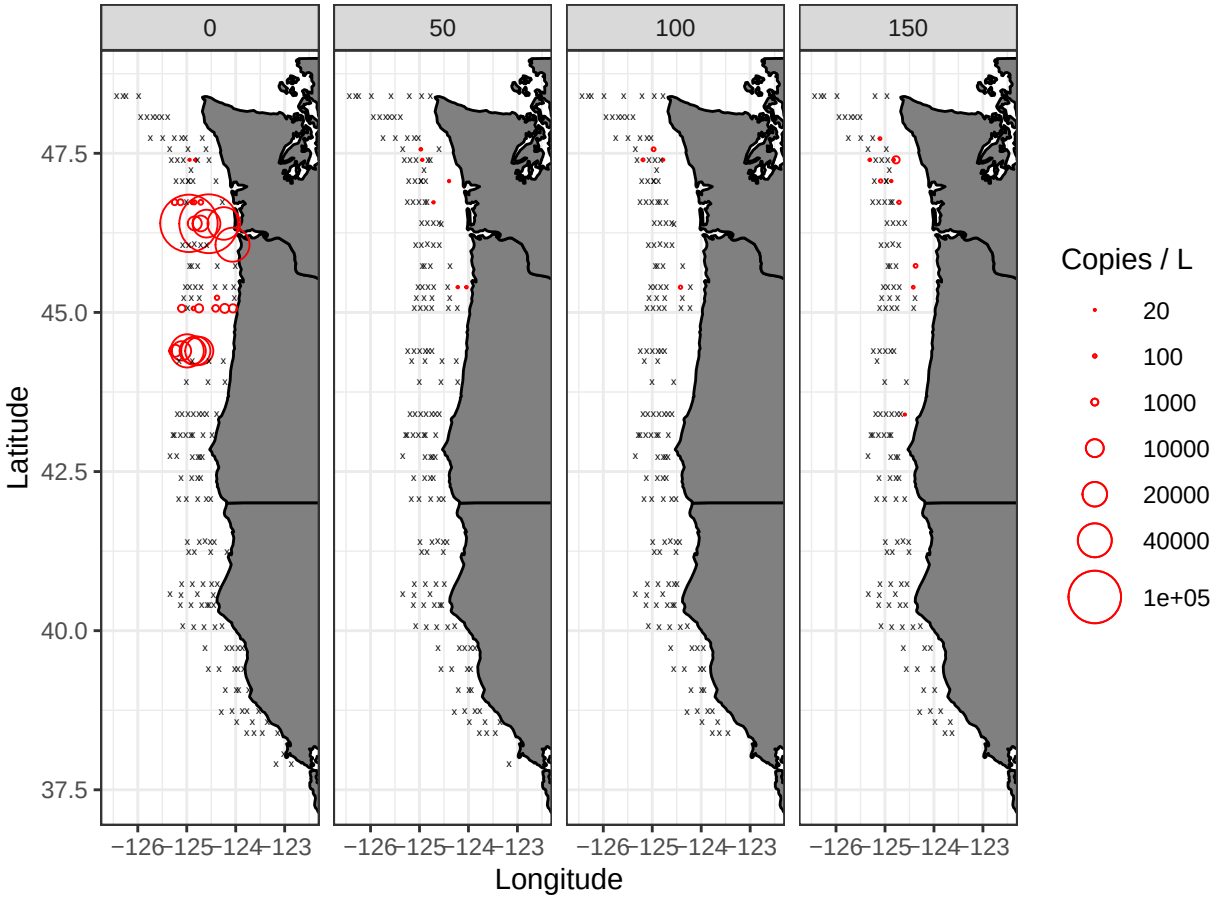


Let's make some plots of the spatial distribution of eulachon DNA. I think that it is clear that the major problem is with inhibition in the surface samples for eulachon. There are a lot of missing data points for eulachon.


0
25
50
100
150
200
300
500
Latitude
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Longitude
Inhibition Category
No
Yes
Copies / L
20
100
1000
10000
20000
40000
1e+05


0
25
50
100
150
200
300
500
Latitude
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Longitude
Wash Category
Exp.
No
Yes
Copies / L
20
100
1000
10000
20000
40000
1e+05


0
25
50
100
150
200
300
500
Latitude
47.5
45.0
42.5
40.0
37.5
−126
−125
−124
−123
Longitude
Copies / L
20
100
1000
10000
20000
40000
1e+05

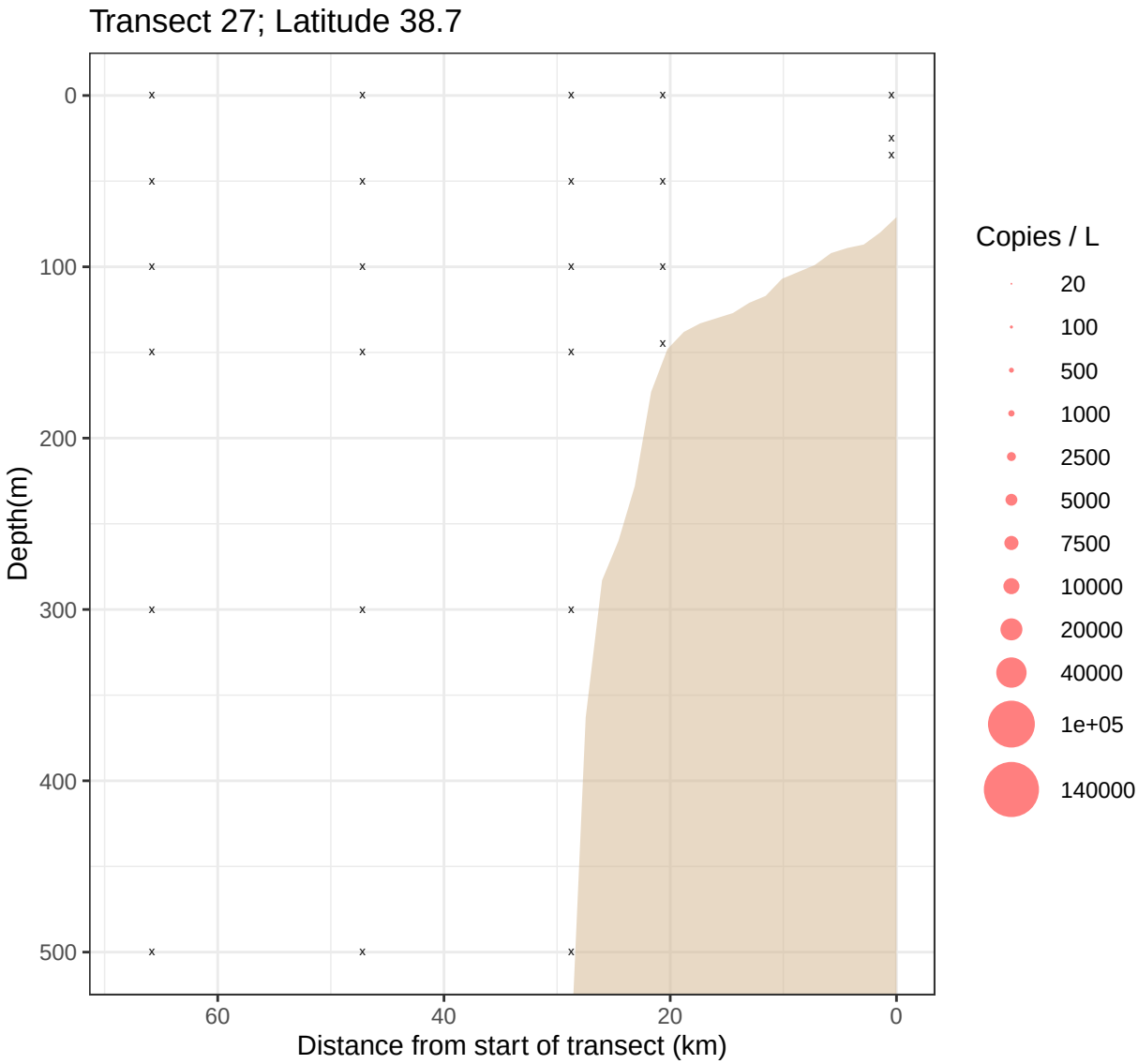

0
50
100
150
47.5
45.0
42.5
40.0
37.5
Latitude
−126
−125
−124
−123
Longitude
Copies / L
20
100
1000
10000
20000
40000
1e+05

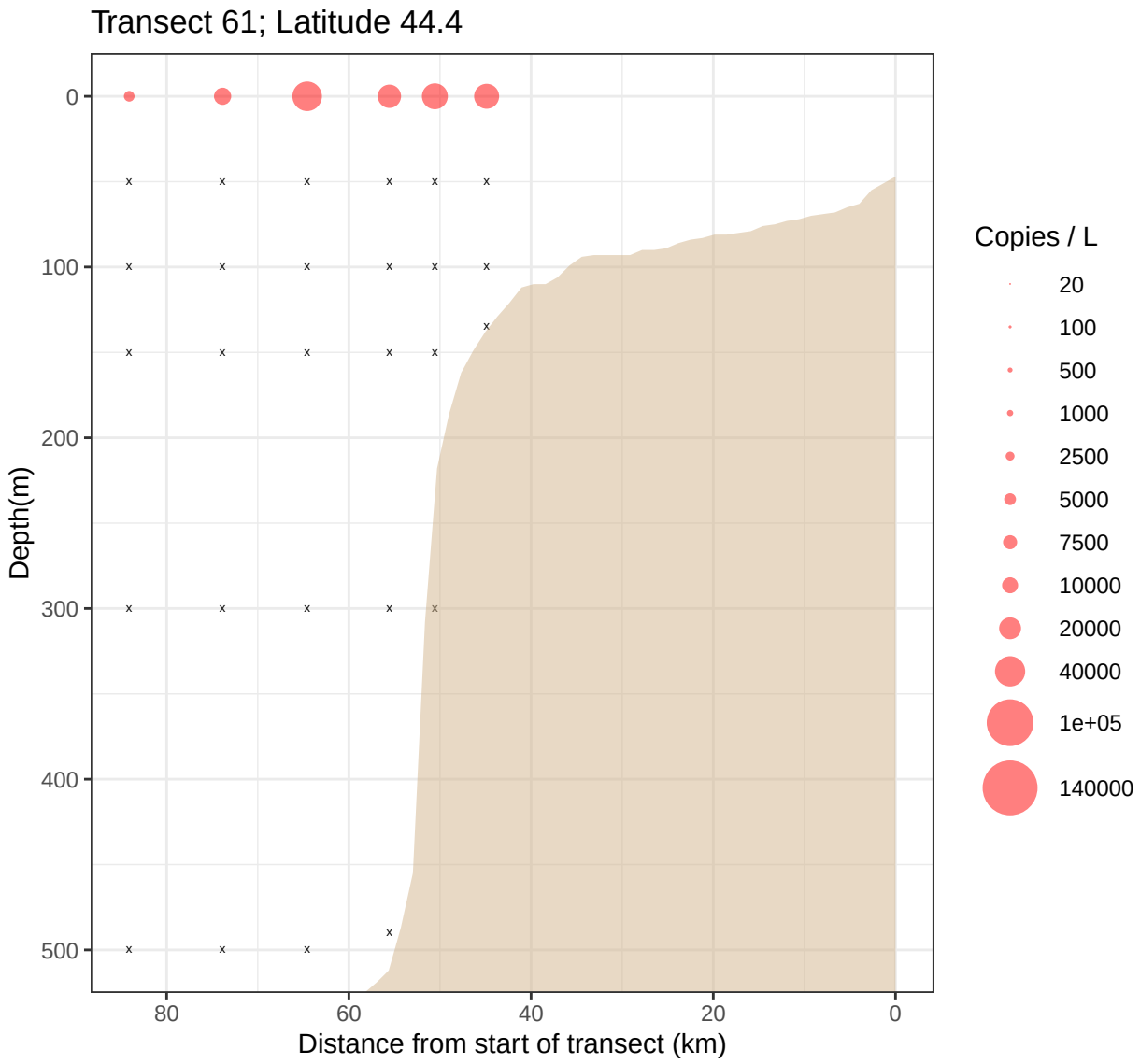
Acoustic Data.

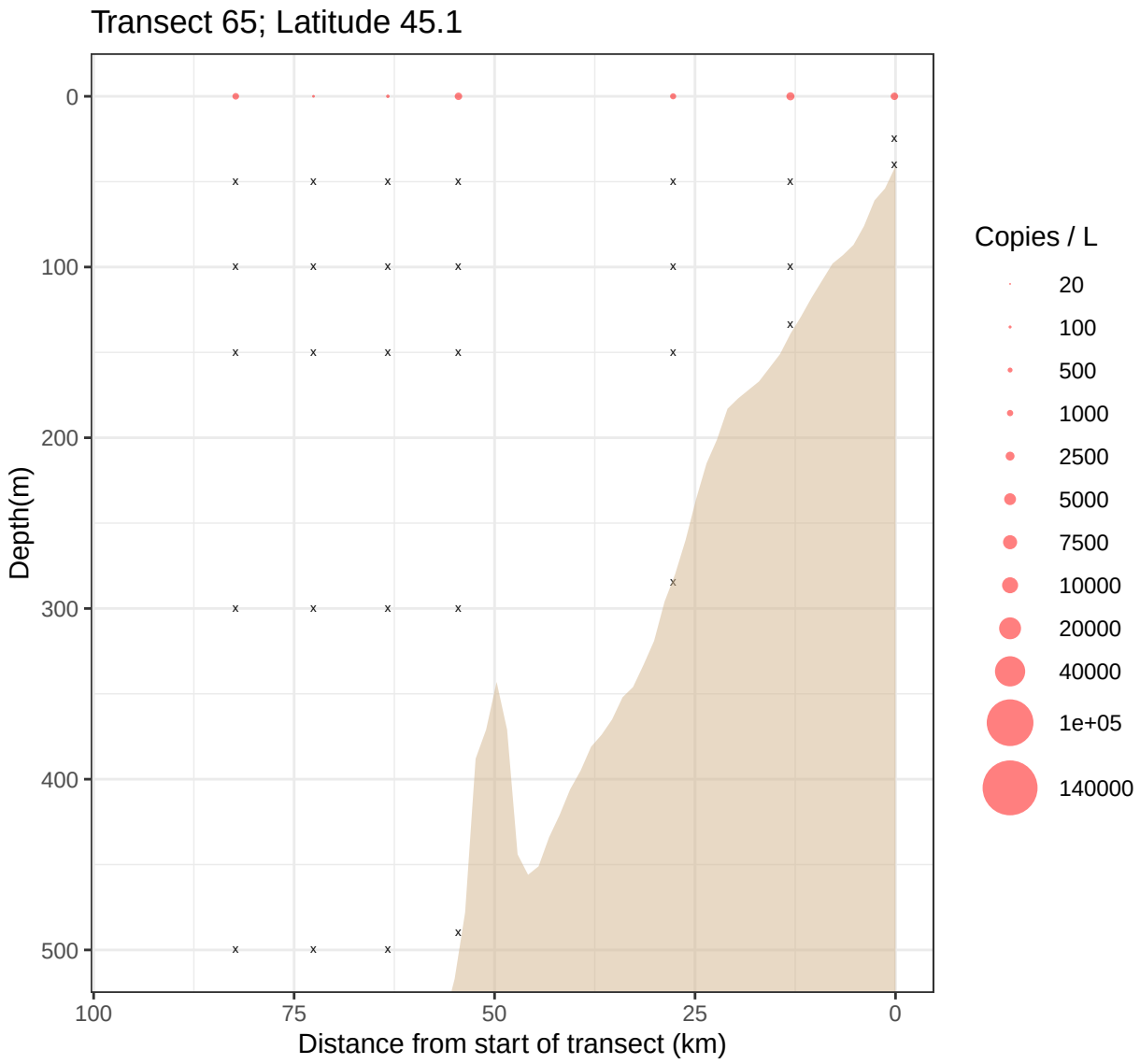
There is no acoustic information for eulachon.

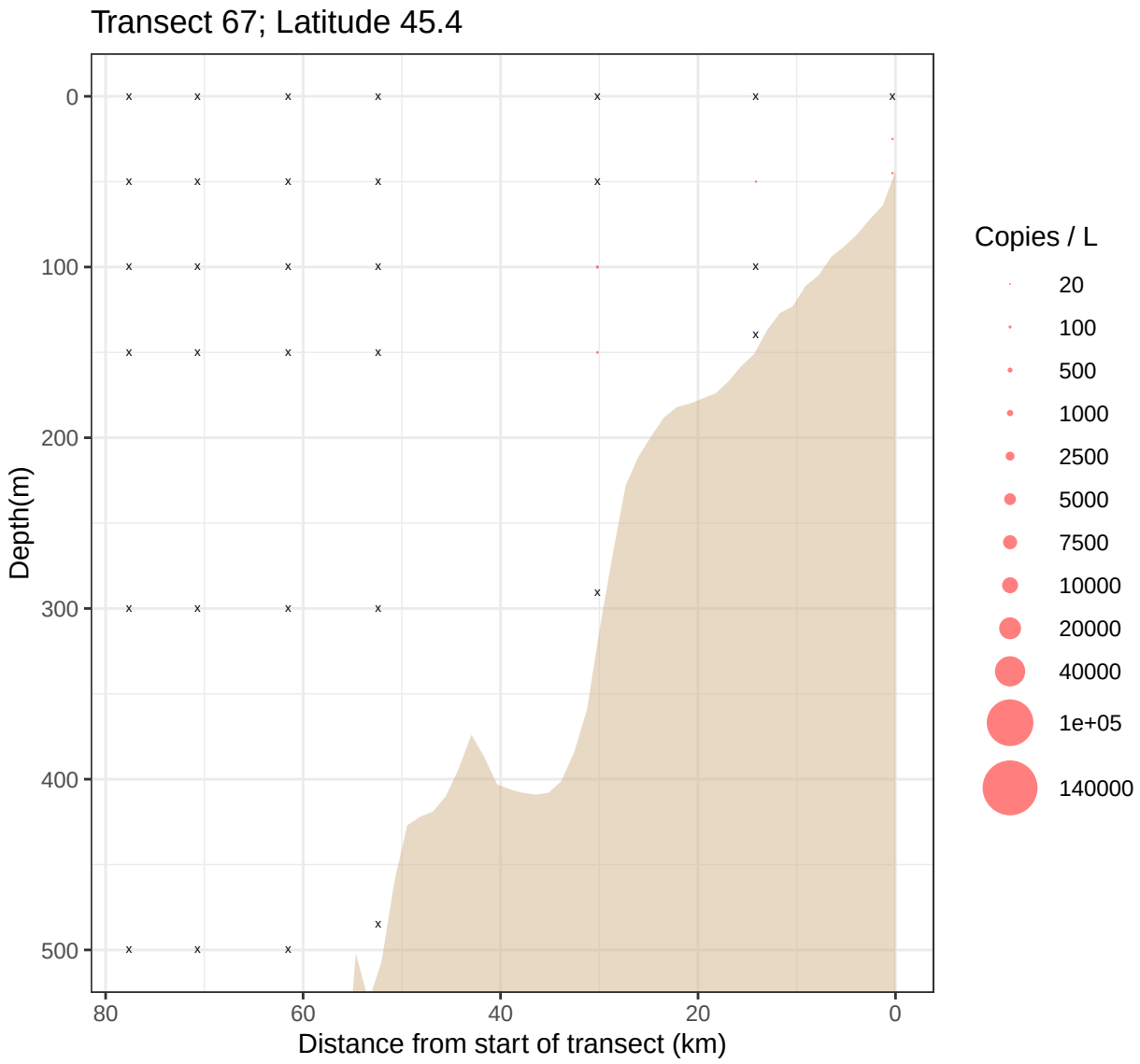
eDNA transects.

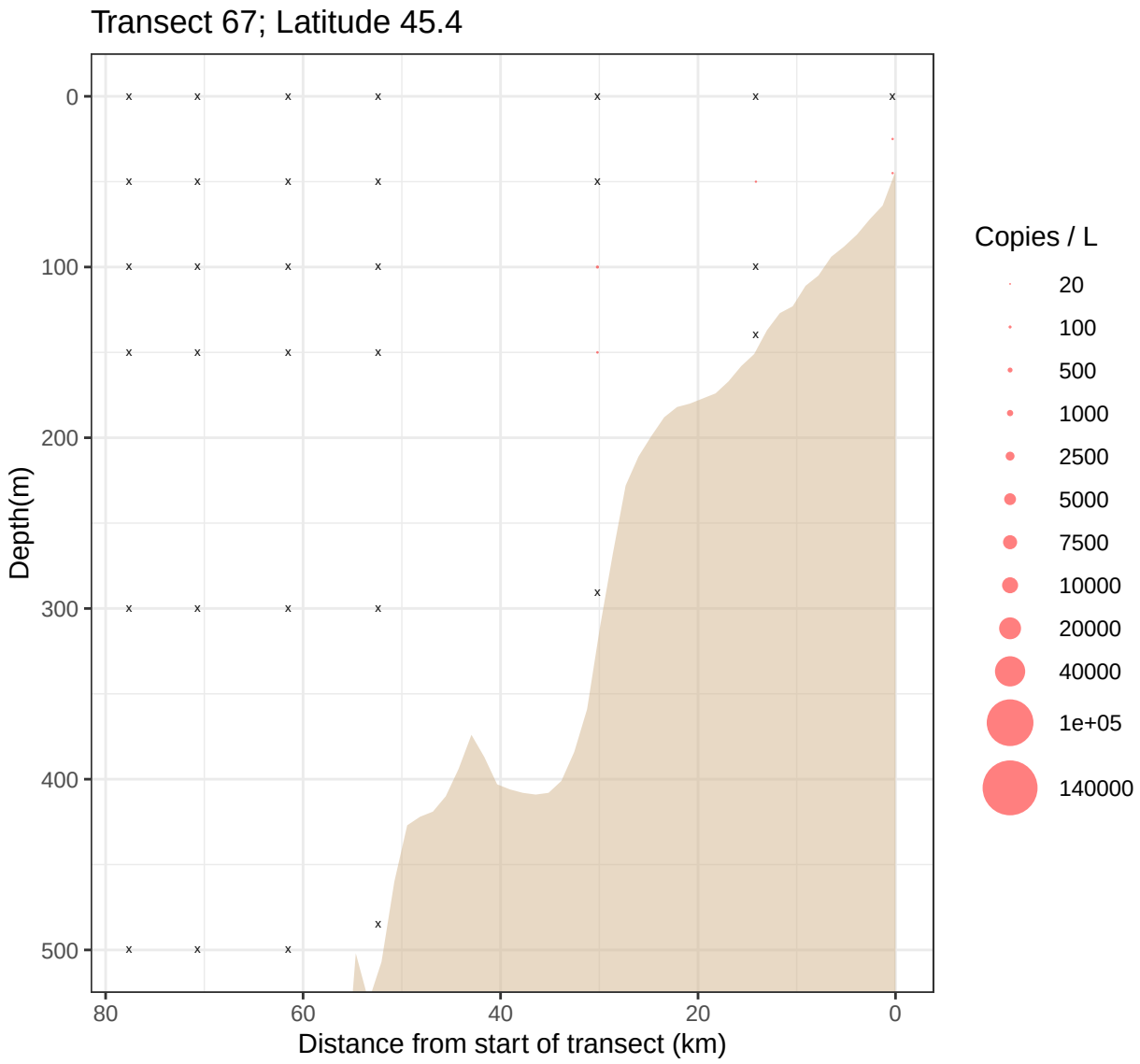
Here are a few plots from individual transects. Coast is on the right side of the graph.

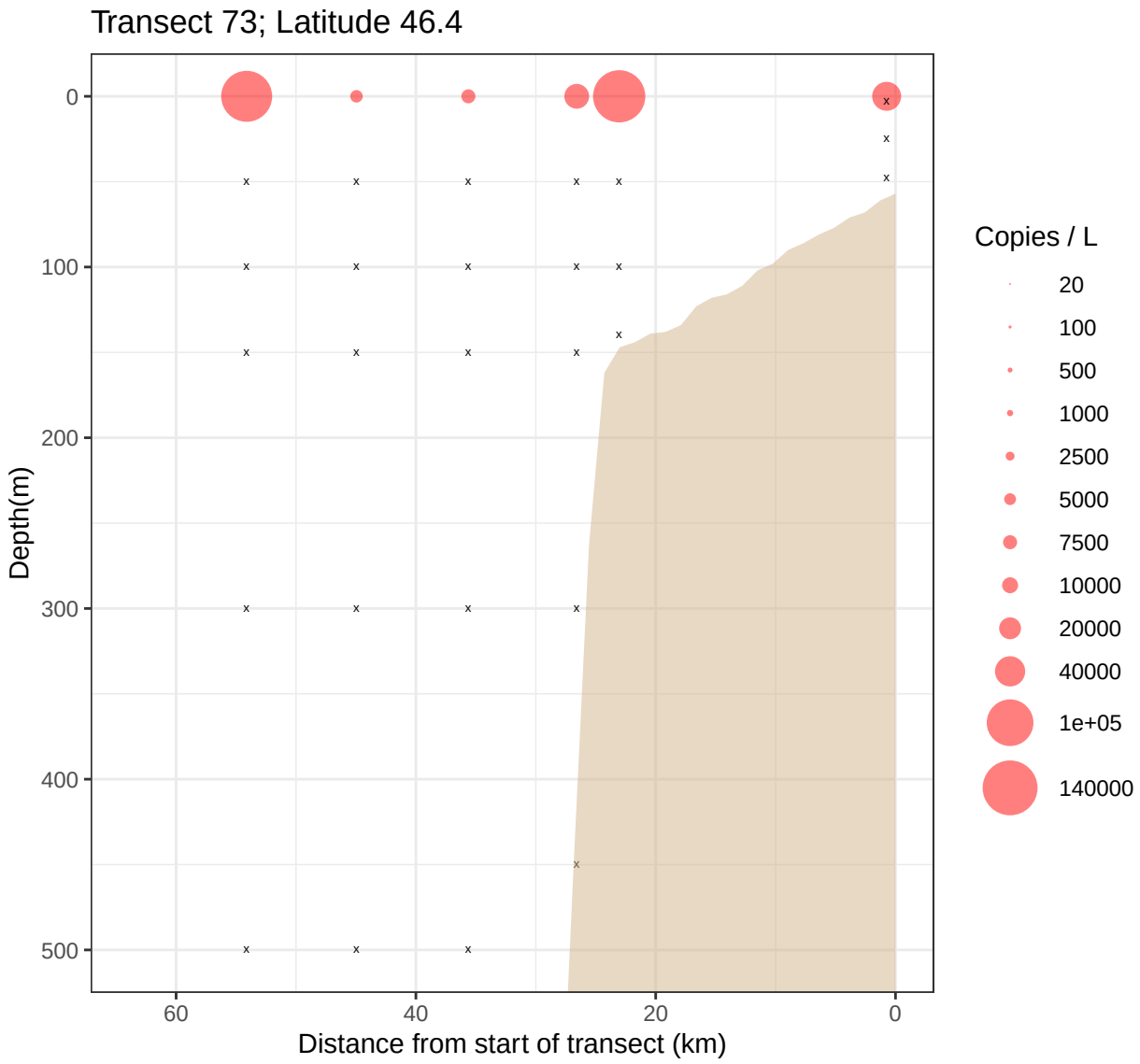


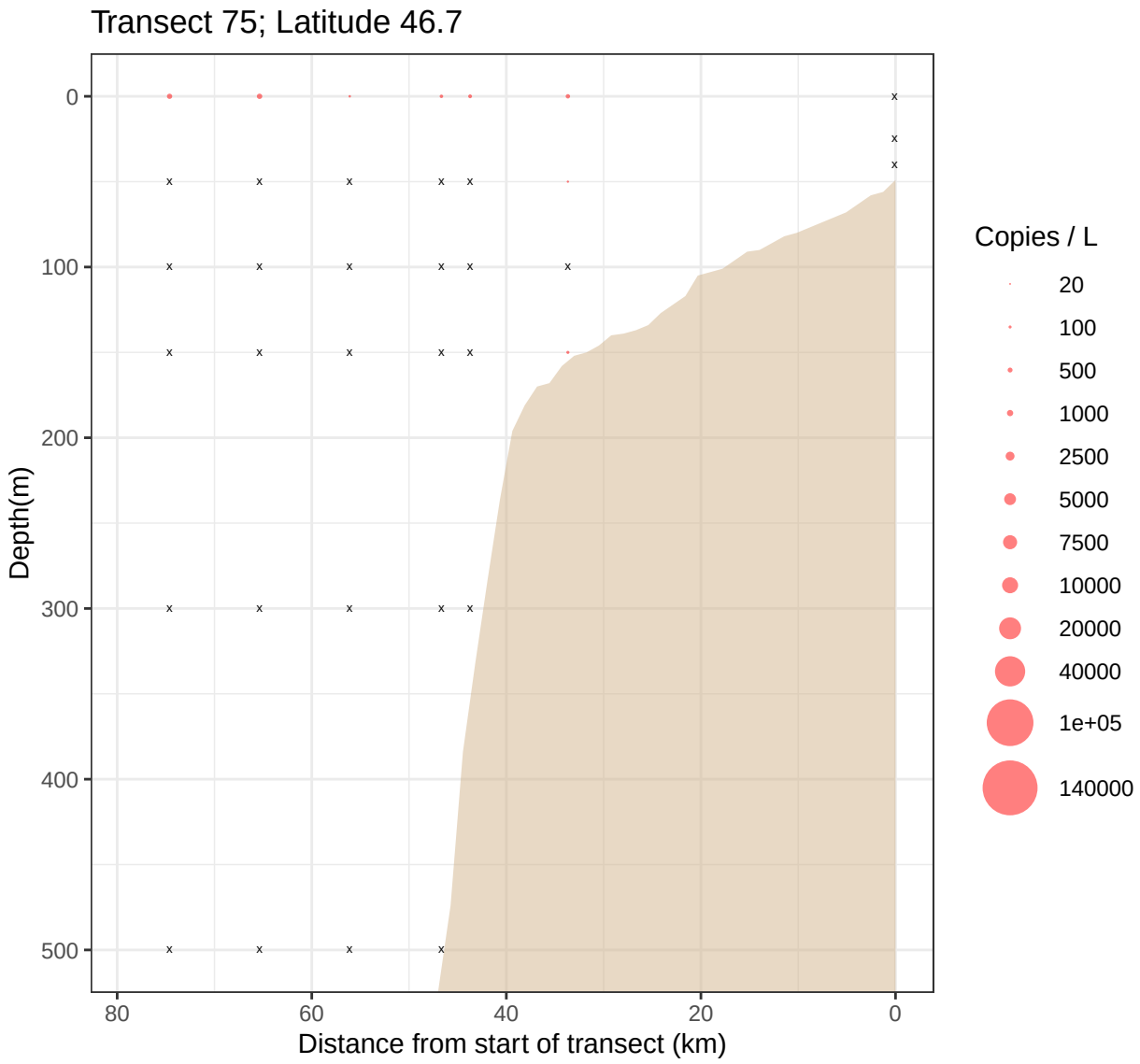

Transect 61; Latitude 44.4
Depth(m)
0
100
200
300
400
500
80
60
40
20
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000


Transect 65; Latitude 45.1
Depth(m)
0
100
200
300
400
500
100
75
50
25
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000

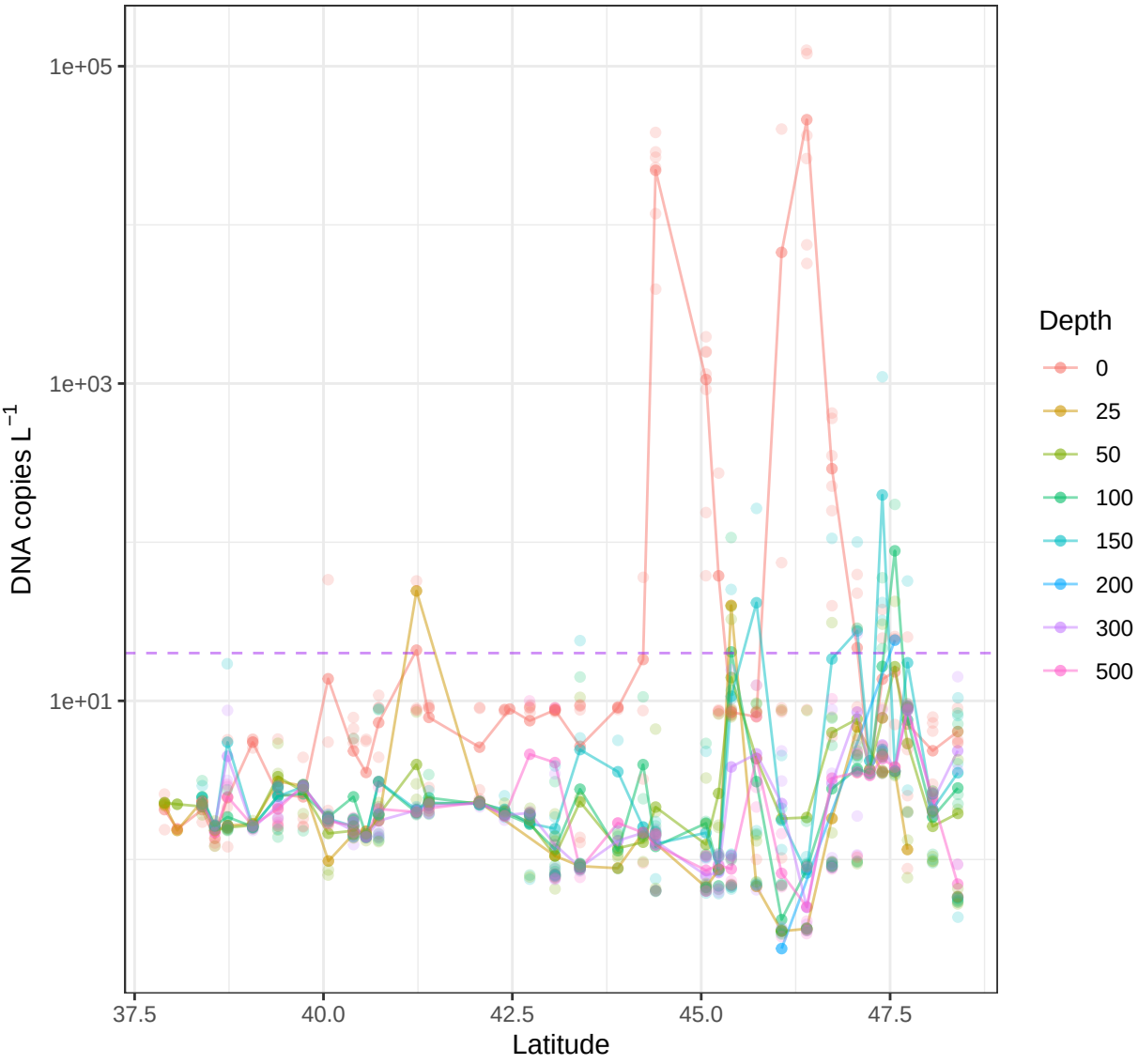

Transect 67; Latitude 45.4
Depth(m)
0
100
200
300
400
500
80
60
40
20
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000

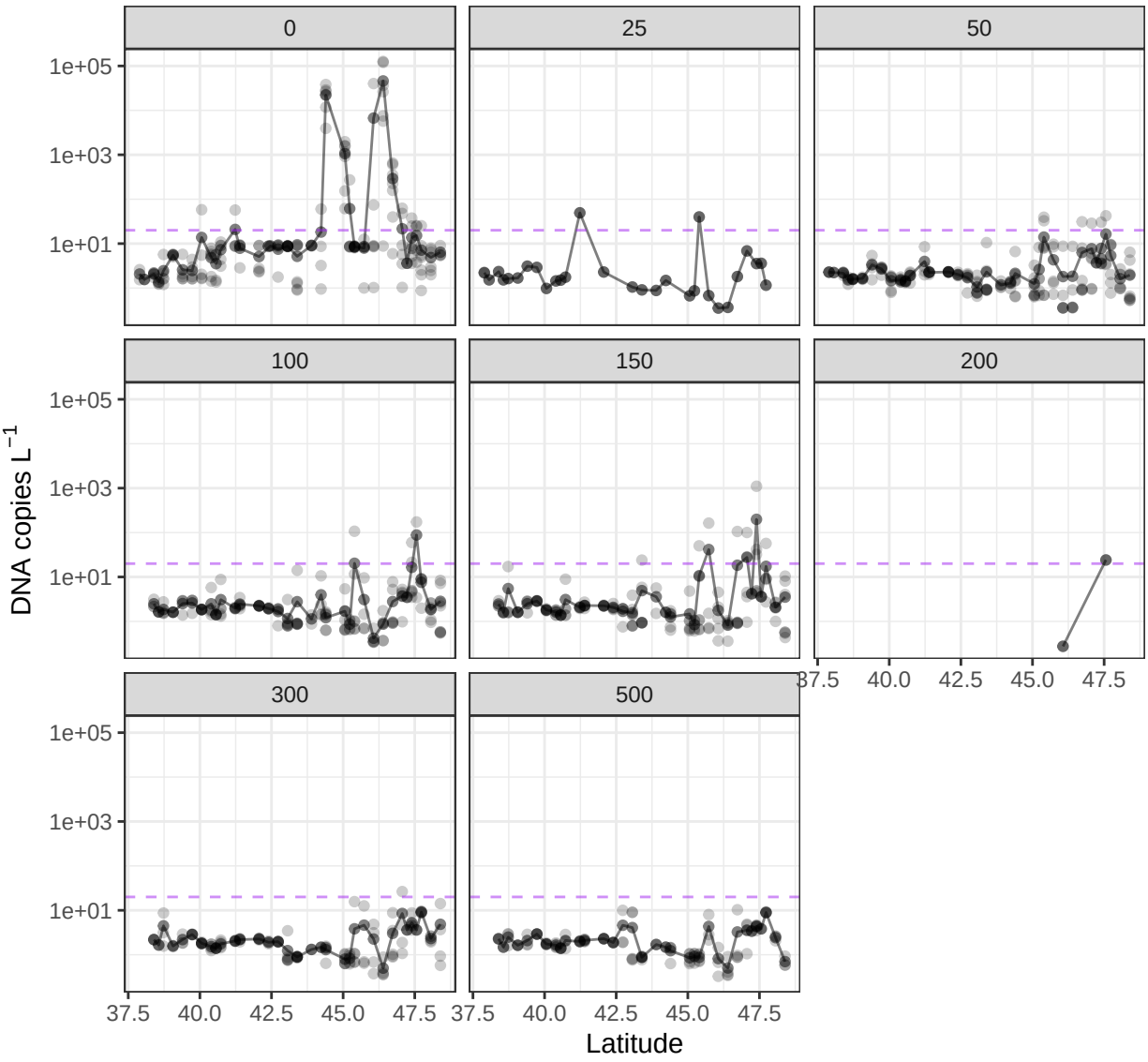

Transect 67; Latitude 45.4
Depth(m)
0
100
200
300
400
500
80
60
40
20
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000


Transect 73; Latitude 46.4
Depth(m)
0
100
200
300
400
500
60
40
20
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000


Transect 75; Latitude 46.7
Depth(m)
0
100
200
300
400
500
80
60
40
20
0
Distance from start of transect (km)
Copies / L
20
100
500
1000
2500
5000
7500
10000
20000
40000
1e+05
140000

North to south patterns by water depth categoris.




0
25
50
100
150
200
300
500
1e+05
1e+03
1e+01
DNA copies L^{-1}
37.5
40.0
42.5
45.0
47.5
Latitude