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 85 CTD stations representing 382 station-depth combinations for 769 individual 2.5L water samples.

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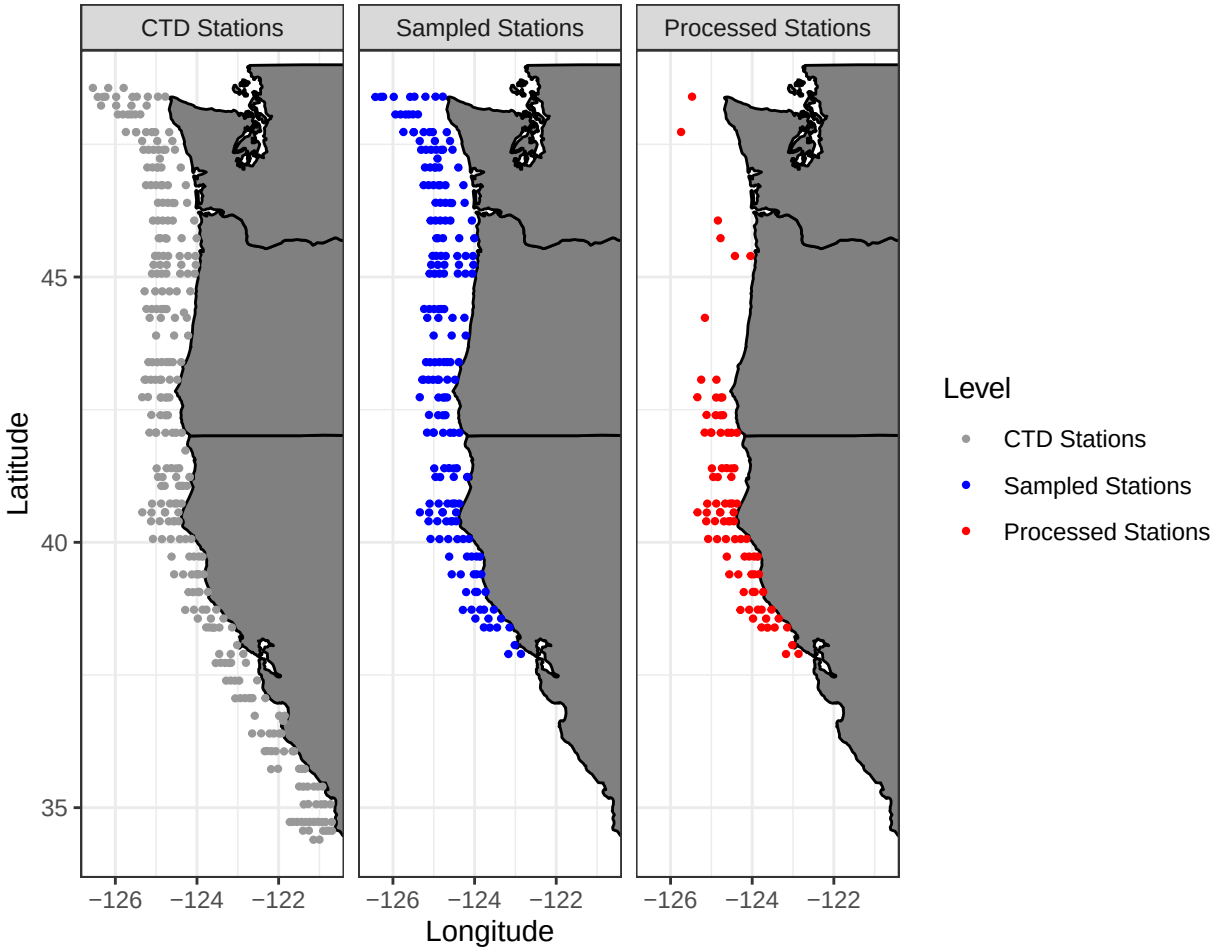
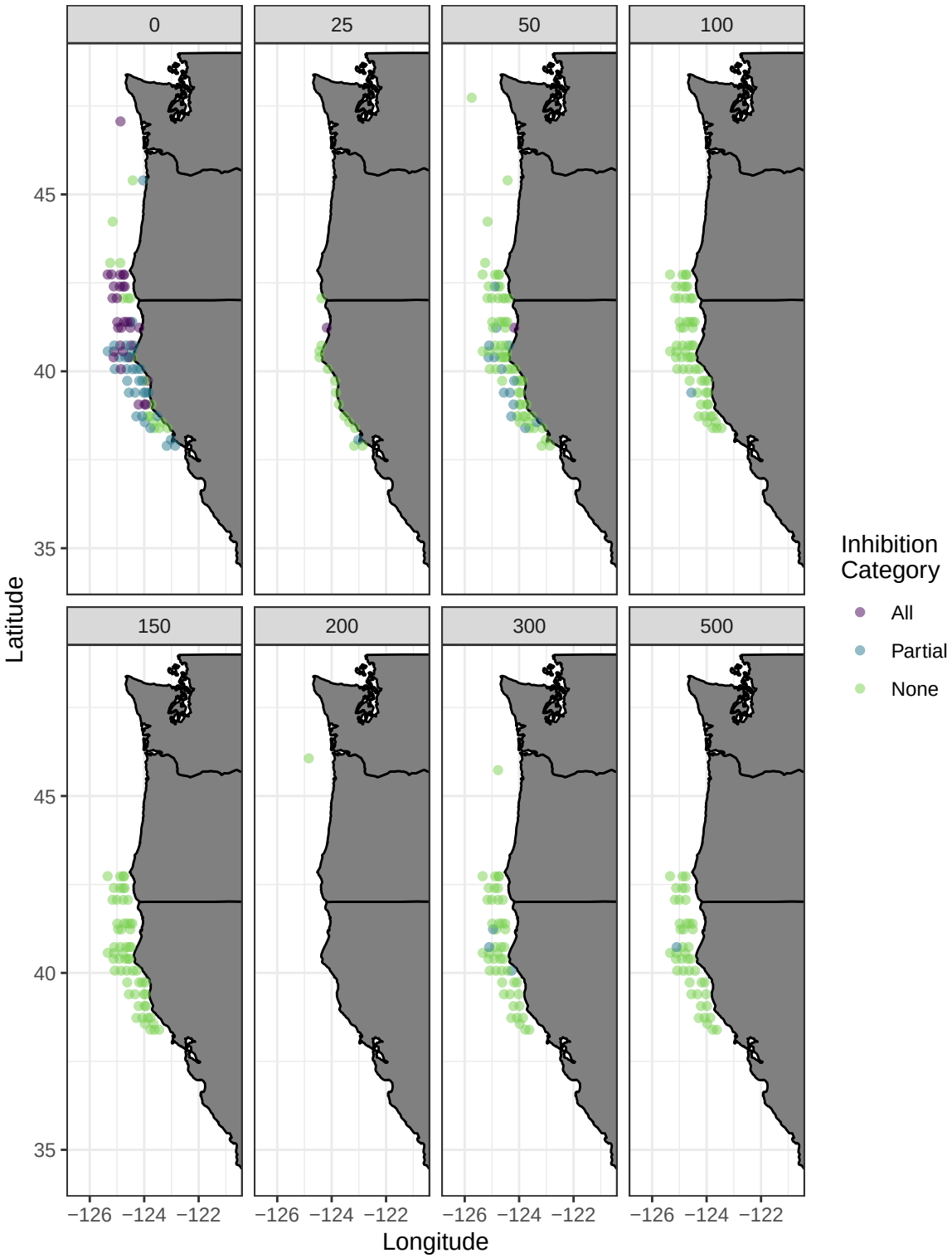


Inhibition

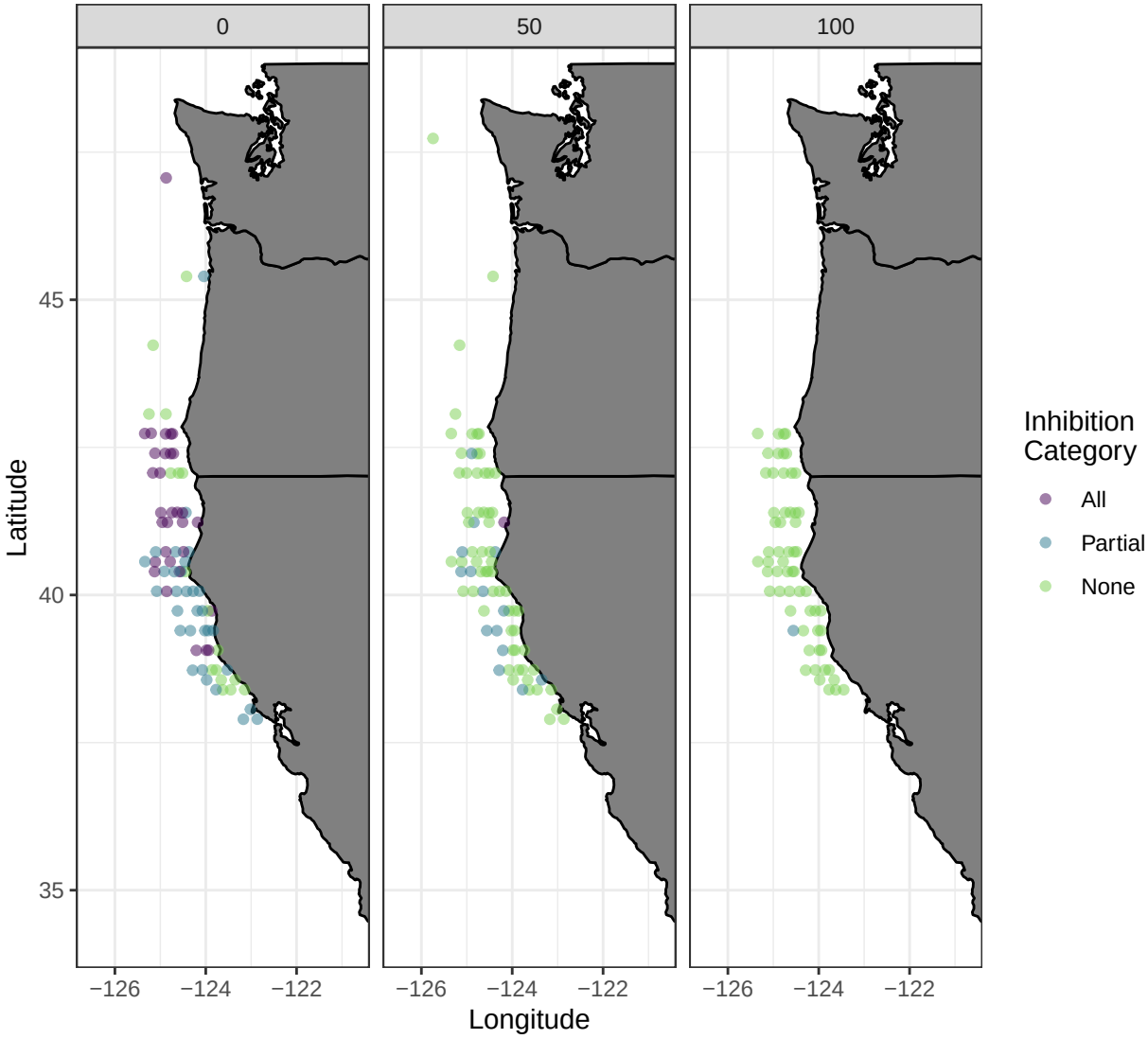
There are a lot of samples that show signs of inhibition. They are concentrated in the surface samples. Here are the inhibition by station-depths and depth categories. 'Completely inhibited' means zero PCR replicates from any water sample at that station-depth combination have amplified within the PCR 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	79	17	31	31
25	15	13	1	1
50	76	61	14	1
100	59	58	1	0
150	58	58	0	0
200	1	1	0	0
300	49	46	3	0
500	44	43	1	0
TOTAL	381	297	51	33

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

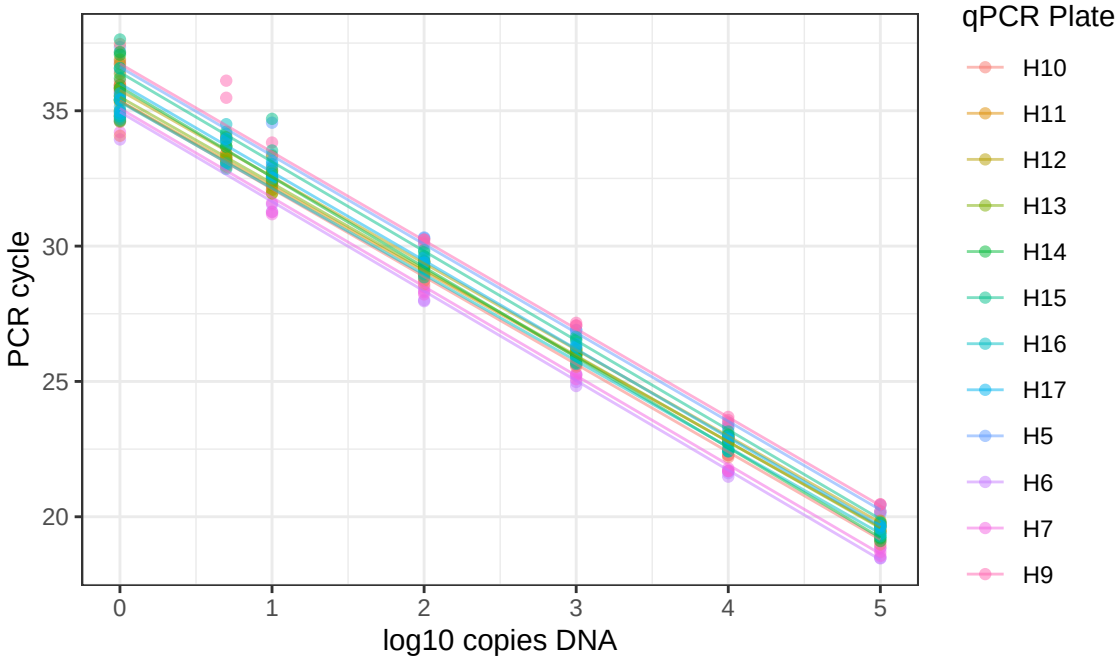

0
25
50
100
150
200
300
500
Latitude
45
40
35
−126
−124
−122
Longitude
Inhibition Category
All
Partial
None

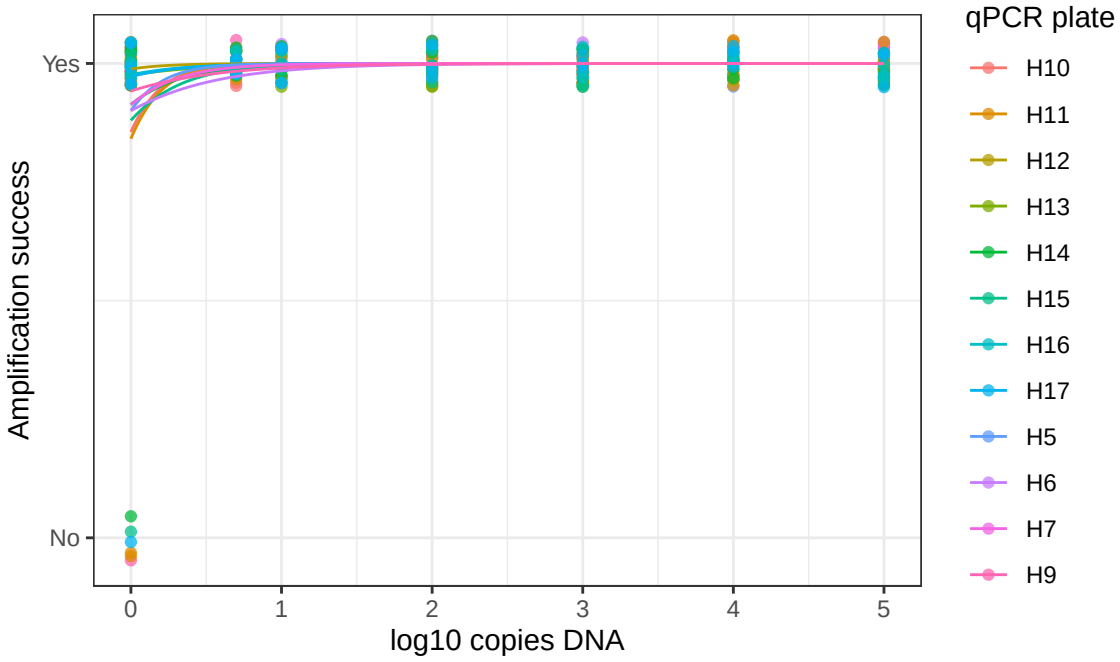
Here are some larger plot of just a few shallow depths. Inhibition is clearly strongest at the surface, but beyond depth there is no obvious pattern of inhibition among the samples. Perhaps there is a hint of inhibition in the offsore edges of the transects at the 50 and 100m depths, but it is not a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



Standards

The standards used in the qPCR assay look pretty reasonable good. Each color represents a different PCR plate.

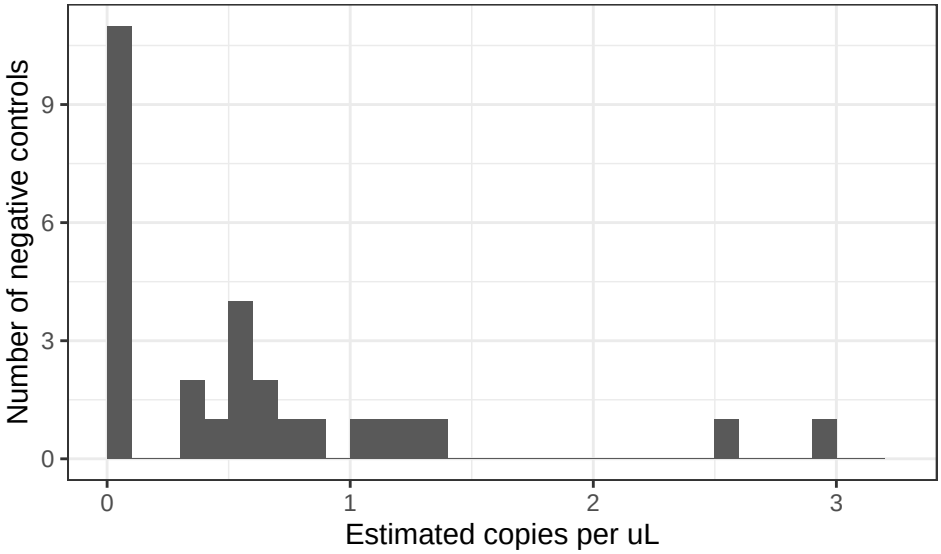




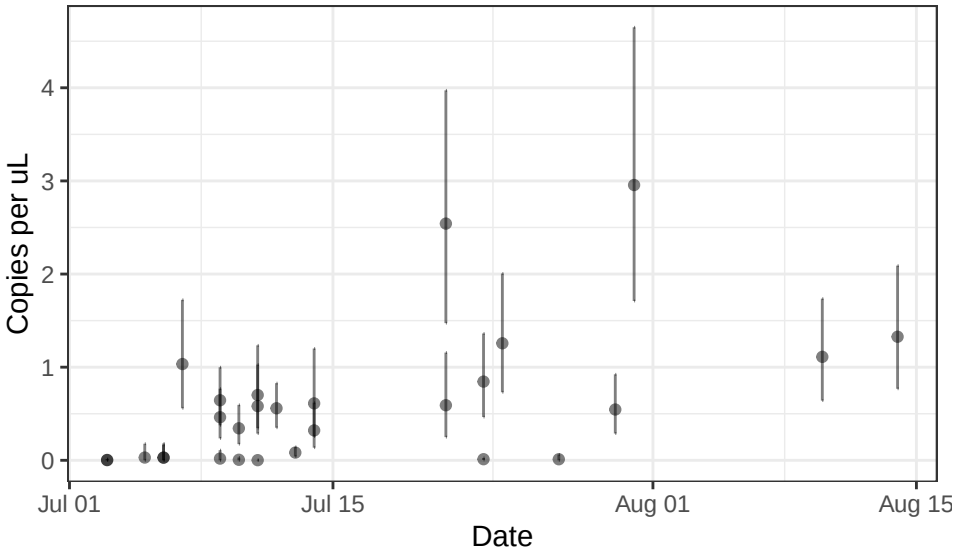
Controls

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 28 samples out of a total of 93 field negative samples. Out of the 28, 17 have detectable amounts of hake DNA. In general the amount of detected hake DNA is low but is non-zero.

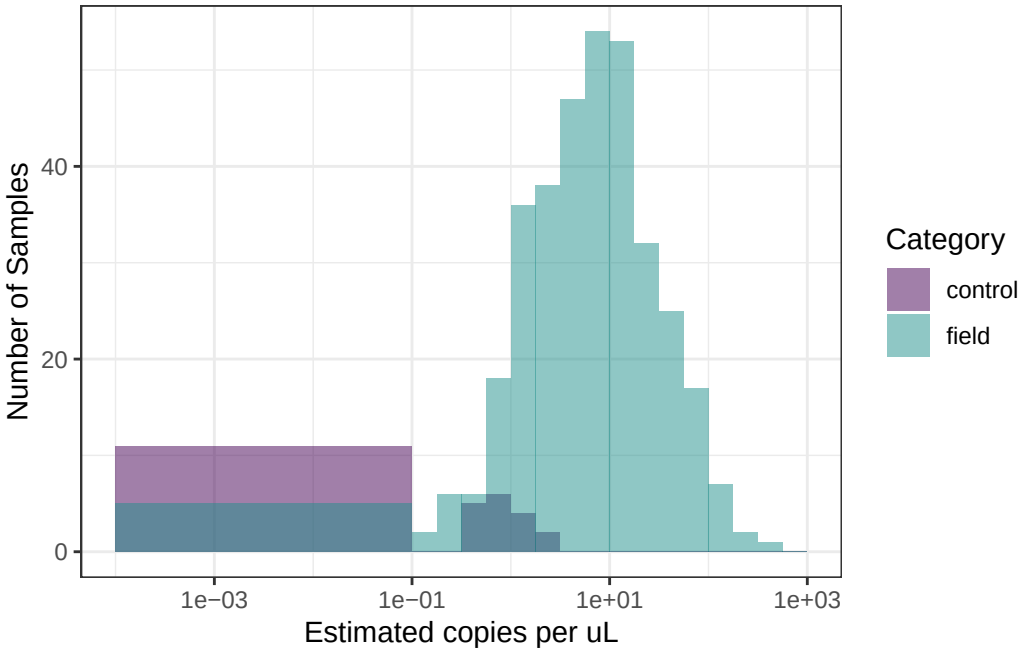


We can look at the temporal pattern of the control values too. This will be more informative when we have more samples analyzed.

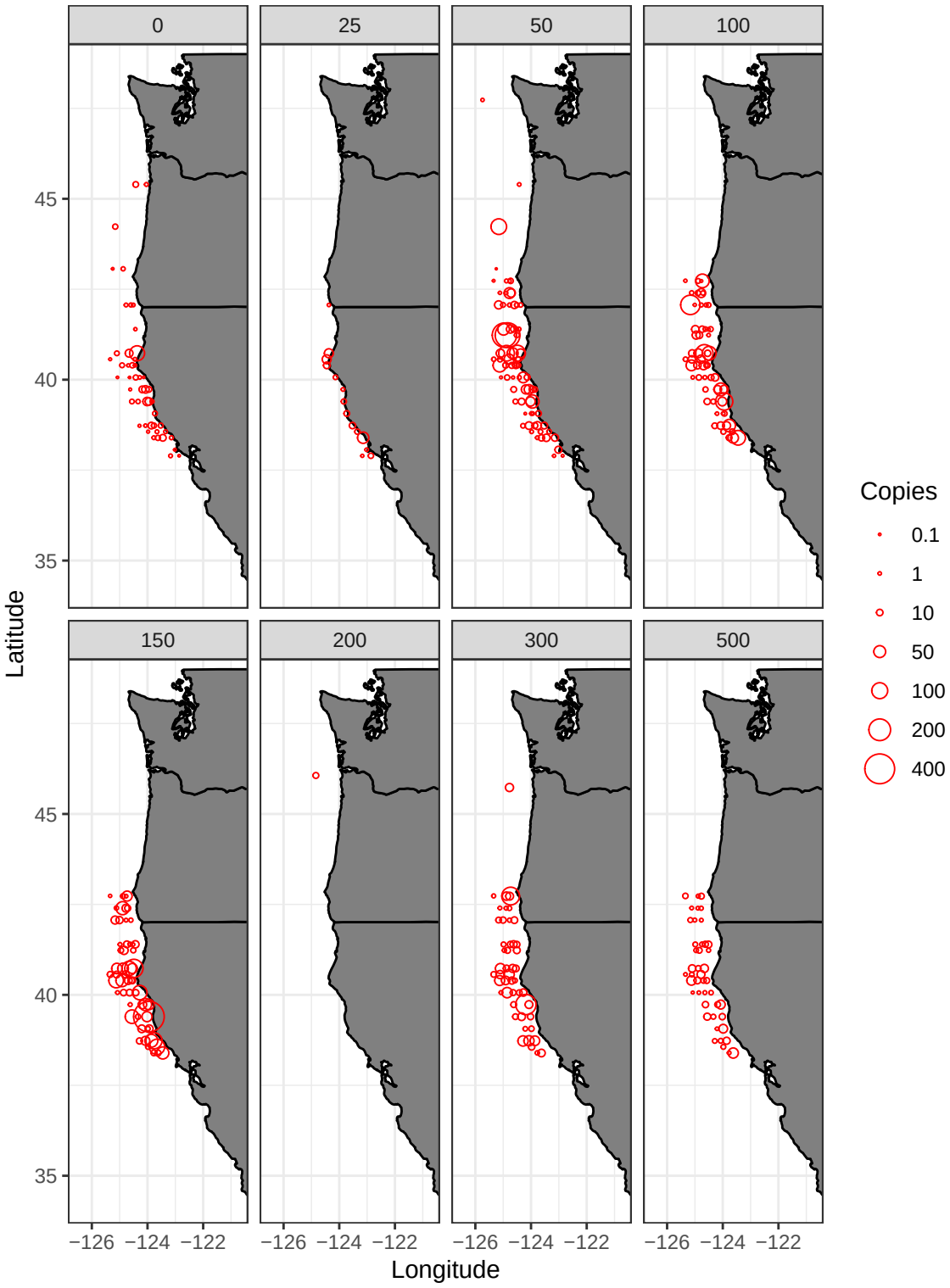


Hake eDNA

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.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25
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−122
Longitude
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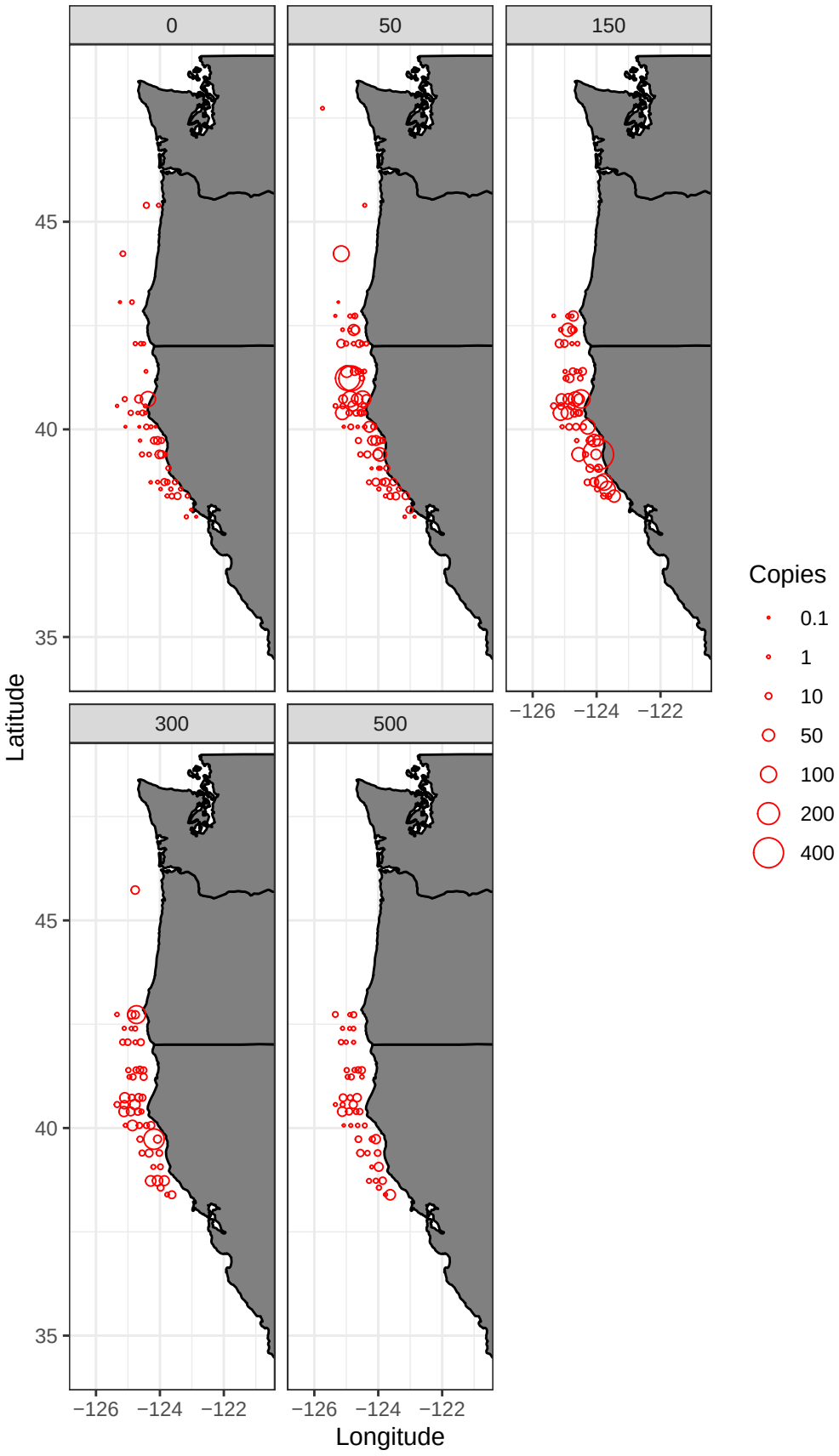
1
10
50
100
200
400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50
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Latitude
Longitude
Copies
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50
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200
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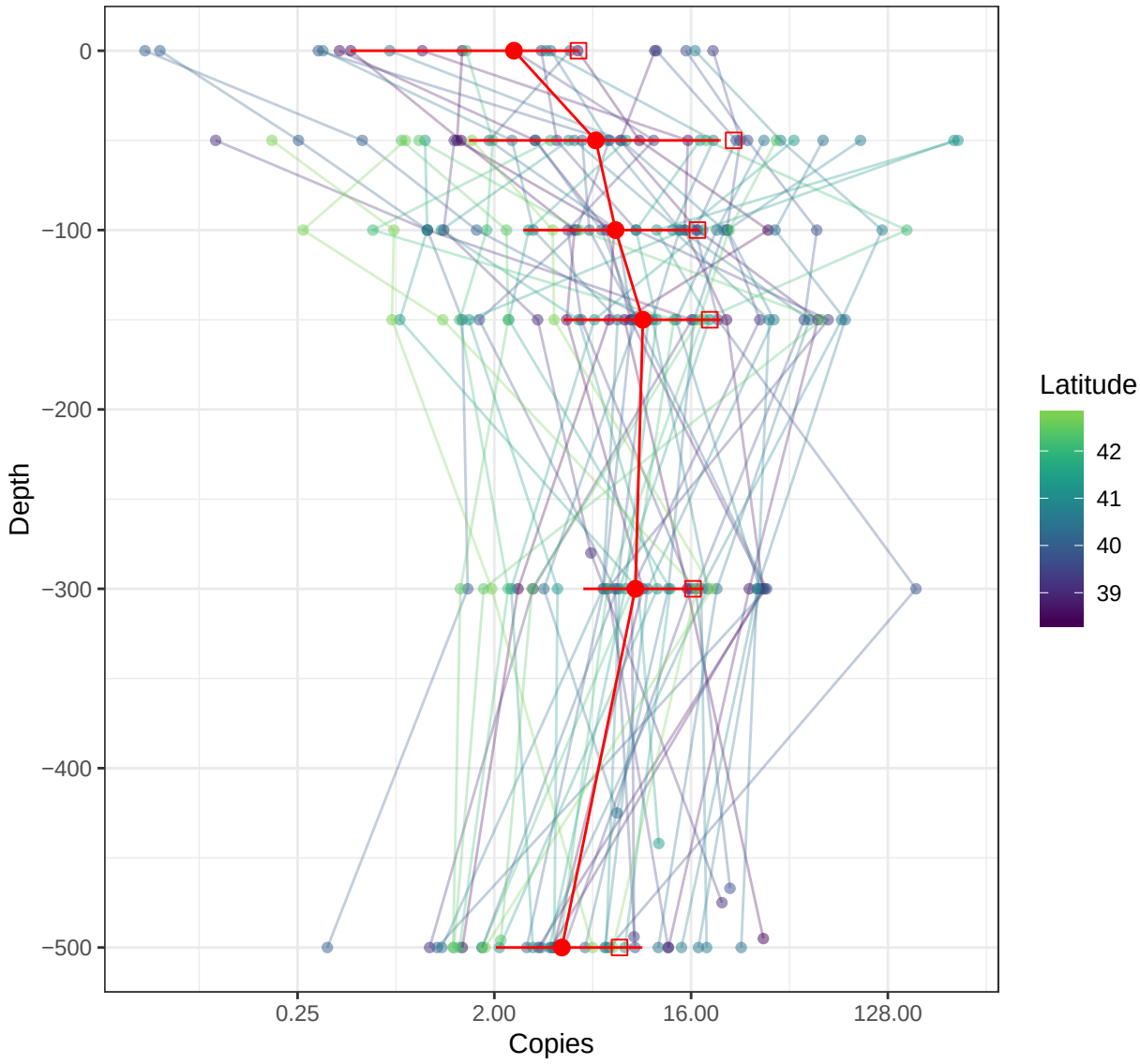
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−300
−400
−500
Depth
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2.00
16.00
128.00
Copies
Latitude
42
41
40
39