

Supplementary Materials

Supplementary Table 1: Sampling stations. Location, date, and number of salmon processed at sampling stations during the Gulf of Alaska winter expedition.

Supplementary Table 2. Novel putative viral contigs discovered through metatranscriptomic sequencing

Supplementary Table 3: Infectious agent prevalences in the Gulf of Alaska winter 2019

Supplementary Table 4. Changes in oceanographic variables experienced by salmon. Maximal and mean changes in oceanographic variables between sampling stations were calculated per km and in percent. Then, the values were multiplied by the daily net distance travel of 15.1 km of salmon in the area to derive the daily changes per variable experienced by the salmon:

$0.795 \text{ body length s}^{-1}$ (average speed) * 0.529 (gross to net distance conversion) * 415mm (mean length of salmon in study) * 24h = 15.1 km. Swim speed and conversion factor are based on Ogura and Ishida, 1992 and 1995. See Table 3 for abbreviations.

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Supplementary Figure 3: Number of infectious agents and pathogens (A) and Shannon Weaver diversity (B) of infectious agents and pathogens by species. $n(\text{chum}) = 84$, $n(\text{coho}) = 80$, $n(\text{pink}) = 27$, $n(\text{sockeye}) = 61$.

Supplementary Figure 4: Histopathology of high load individuals from the GoA for *Ichthyophonus hoferi* and *Loma* sp.. (a): Coho salmon heart: multiple granulomatous

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Supplementary Figure 5: Statistically significant covaried metadata with gene expression clusters in chum salmon. Covariance was tested with anova and differences between groups was assessed with t-test ($p < 1e-04$: "*****", $p < 0.001$: "****", $p < 0.01$: "***", $p < 0.05$: "**").

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Supplementary Figure 10: Spatial correlation of mean relative infection burden (RIB) at site of capture with temperature and primary prey of salmon species in the Gulf of Alaska during the winter 2019.

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Supplementary materials: Histopathology

Supplementary Table 1: Sampling stations. Location, date, and number of salmon processed at sampling stations during the Gulf of Alaska winter expedition.

Station	Lat	Long	Date	Sockeye	Pink	Coho	Chum
1	48.4	-128.5	19-Feb-19	0	0	0	0
2	48.4	-130	19-Feb-19	0	0	0	0
3	47.4	-137	21-Feb-19	0	1	1	0
4	47.4	-138.5	22-Feb-19	0	8	0	0
5	47.4	-140	22-Feb-19	0	0	6	2
6	47.4	-141.5	23-Feb-19	0	3	0	2
7	47.4	-143	23-Feb-19	0	0	0	0
8	47.4	-144.5	24-Feb-19	0	0	10	0
9	47.4	-146	24-Feb-19	0	0	0	1
10	47.4	-147.5	24-Feb-19	0	0	4	1
11	48.4	-147.5	25-Feb-19	6	0	2	1
12	49.4	-147.5	25-Feb-19	1	0	0	2
13	50.4	-147.5	25-Feb-19	1	0	0	1
14	51.4	-147.5	26-Feb-19	0	0	1	0
15	52.4	-147.5	26-Feb-19	0	0	1	0
16	53.4	-147.5	26-Feb-19	6	0	0	2
17	54.4	-147.5	27-Feb-19	1	0	0	2
18	55.4	-147.5	27-Feb-19	0	0	0	0
19	56.4	-147.5	28-Feb-19	0	0	0	1
20	56.4	-146	28-Feb-19	0	0	0	0
21	56.4	-144.5	28-Feb-19	0	0	0	0
22	56.4	-143	28-Feb-19	10	0	0	0
23	55.4	-143	01-Mar-19	0	0	0	1
24	55.4	-144.5	01-Mar-19	0	0	1	0
25	55.4	-146	01-Mar-19	9	0	0	1
26	54.4	-146	02-Mar-19	2	0	0	2
27	53.4	-146	02-Mar-19	4	0	0	2
28	52.4	-146	02-Mar-19	2	0	0	2
29	51.4	-146	03-Mar-19	0	0	0	4
30	50.4	-146	03-Mar-19	0	0	0	9
31	49.4	-146	03-Mar-19	0	0	4	3
32	48.4	-146	04-Mar-19	0	5	2	3
33	48.4	-144.5	04-Mar-19	0	5	5	0
34	49.4	-144.5	04-Mar-19	4	1	0	2
35	50.4	-144.5	05-Mar-19	0	1	0	9
36	51.4	-144.5	05-Mar-19	0	1	0	8
37	52.4	-144.5	05-Mar-19	6	0	1	1
38	53.4	-144.5	06-Mar-19	0	0	0	4
39	54.4	-144.5	06-Mar-19	0	0	0	1
40	54.4	-143	06-Mar-19	1	0	0	0

41	53.4	-143	07-Mar-19	0	0	0	0
42	52.4	-143	07-Mar-19	0	0	0	1
43	51.4	-143	07-Mar-19	0	0	2	4
44	50.4	-143	08-Mar-19	0	0	0	9
45	49.4	-143	08-Mar-19	0	2	7	0
46	48.4	-143	09-Mar-19	1	0	9	0
47	48.4	-141.5	09-Mar-19	0	0	3	0
48	49.4	-141.5	09-Mar-19	1	0	10	0
49	50.4	-141.5	10-Mar-19	1	0	6	0
50	51.4	-141.5	10-Mar-19	0	0	0	0
51	52.4	-141.5	10-Mar-19	0	0	2	0
52	53.4	-141.5	11-Mar-19	3	0	1	1
53	53.4	-140	11-Mar-19	0	0	0	0
54	52.4	-140	12-Mar-19	5	0	1	0
55	51.4	-140	12-Mar-19	0	0	0	0
56	50.4	-140	13-Mar-19	0	0	0	0
57	50.4	-138.5	13-Mar-19	0	0	0	0
58	49.4	-138.5	14-Mar-19	0	0	0	0
59	48.4	-138.5	14-Mar-19	0	0	0	0
60	48.4	-137	15-Mar-19	0	0	0	0

Supplementary Table 2. Novel putative viral contigs discovered through metatranscriptomic sequencing

Putative virus name	Assay name	Host of sequencing library	Contig for which assay was designed	Genbank accession of contig	Top Blast hit	Amino acid identity
Putative bafini virus	Bafini_b	Chinook	TCTTGTGTTTTGATTTCATCACTTAGAAAATGTTGAA GGATCAGTGGGTTGGTCACATTCATCGAAGAGAGATGT TCTAGTGATAATGCCGACTGAAGTTGGCATTTCACACA TGAATGAAAGAGTGGTATTTAATTAACGTAGCTTGATG GTCAATAAGGGCCAGCGACATGCCCTGTGACATGATTT CACACATTACTTTAACTGAAGGCCTGATAAGCAATGGT AGAGCTTTGAAGGATCTTGTGGGTACAGCTAAGC	MW373508	White bream virus strain DF24/00, complete genome	53%
Putative circo virus	Circo	Chinook	CGAGAAGTCCCCACCACCAAGAATAACATTGGCAGT GCATGGGCATTGTGCGAAAAACATAACTTTGAAACAA GCCATTGCGGTATTGCCAATGCACACTTGGAGCCCTC TAAATGTGAAGCCCTCGATGCCTACGTATGAAAAAAG AGACGAGGATCGAGGGCTCTACATTTGAAGTCGGAAA GAGGCCATTTAAGATGAACTAAAAACGGACTGGGCAG CAATGAGACCGACCTTGC	MW373509	Circoviridae 18 LDMD-2013, complete genome	48%
Putative hantavirus	Hantavirus	Chinook	CAGGAATTGAGGTCAGGGACTGCAAAGGAATCTCAGG GACCTCAATGGGAACAGTGTGCAGTGTACAGTGATGT GCAGCGGGCCAACTCATGCGGATGTCTCAGCCCTGT ACAAAGAGACTTGCTGTGTGGAGAAGAGACTATGATTG CATTACCCGCAACAAGCCAGGACCAAGAGGTGTTCTCG TGTGGAGAAAGGAGACAACGGCAAGCTGGACCTTG AGATCGTGATGTTGGGATCGAAACCGCTGTGATAGGA GCAGCCACAATGGGGCGGTTGAAGCCTTAACTGGGC TTAAGCCATGGGAGCTTGGCCTTGAATAGGAGGAGG CCTTGACGAGTGTCTCCTTGCCTGATTGTCATCTCTG TGGTCTATGTAAGGCTAAGCAAAAAAGAAAAAAGA GATGACTGAGAAGCCGATTAAGTCCGAAGGTTTATAA ACACCGGAAGGAACTATAAATCAAACAAG	MW373510	Wenling red spikefish hantavirus	43%
Pacific salmon nidovirus sequence variant	Nido2_a	Chinook	GATATCAACAACACTACCTCCAGAGGAGACAGTAGTAGCG ATGTCCACCATTGCCTCAATGTGCACACCCCTGCAACA ACACCCCTCCAGTCCCTTCTACGGTGTCTATCAATTCAAC ACCCCGAAAGAAACACCTACATTTTGTAGGAACACT ACCACCGCTCTACCTGAAAGCTCCAGTTCCCTCAGCTG AAGTTCGCACACCTGATGCAGTTACGGAATTCATTCTG CCTGCAATACCAGATTCCCGAG	MW373511	Pacific salmon nidovirus isolate	77%
Putative picorna virus	Picorna2	Chinook	CTATTGGTCAACCCATCTTTCAACAATTACAAGCAGTGT CTTGTGCTATGAAATCCGCACGCCATATTCGAGGT ATTGATGTGACGTTGTAGACTCAACTCAGACTCCATTT CTTGGTGACGTTTCTGACTTGTGTTTCGTTCTCAGAAATAG GACAGGGATTGGGAATACTAGCGCTCCTTCTACCTCT ATGAGGGCGCAGGCGATGATTTCAATTTCTTCTCATG GTCGGTCCACCACCTATGATGGACATCAAGAAATGTGAA GAATGTCTTCTTCCCACTGGAACGTCCCGTTCCG TGGACCTTGCTG	MW373512	Halhan virus 1 replicative protein and structural protein genes, complete cds	68%
Putative Qin-like virus	Qin	Chinook	AAAAGTGCCAAACTATTCTATCCCGTTATAGACGCCG ACAATCGTGAGTTATACAGTCTATCCATATGATCGGG CACTGGGCCTACTACCTCAGCTCAGAAAGCTAGG CTTCTCAAGTGTGTTGGATGTTACACCTTACGTTGAAGG CTATGACTTCGCAGTGCCTGAGGACATAAACTTAGATT GTCGGGACACCAGCCGGCACGGCAAAGGCCTACGTT GCTCATGCGAGTTAAAAAGGCTTATTCATAGTGGTCTC ACCGGTTTAC	MW373513	Sanxia Qinvirus-like virus 1 strain	39%
Putative rhabdo virus	Rhabdo3	Chinook	TCTTCCAATTCATCATTGTTTCTAACTGTTGTTGCTTAT AATGAGTGCATATAACTTGATTATCTCCTTGAGCTAGCA CTTTCACCACAGTATTCCTGACTGCTGATTCTCTTTTA TGACTAAAAGATTCAATATGCTCCAACCTTTTTGCTCA ATCCTTCTAATCCACCTTTCTGTCCATCCCG	MW373514	Spring Viremia of Carp complete genome	79%

Supplementary Table 3: Infectious agent prevalences in the Gulf of Alaska winter 2019

Species	Pathogen	Type	Prevalence
Chum	<i>Candidatus</i> Branchiomonas cysticola	Bacterium	56%
	<i>Candidatus</i> Synngnamydia salmonis (Sch)	Bacterium	6%
	<i>Ceratanova shasta</i>	Parasite	10%
	<i>Ichthyobodo</i> sp.	Parasite	21%
	<i>Ichthyophonus hoferi</i>	Parasite	29%
	<i>Loma</i> sp.	Parasite	50%
	<i>Myxobolus insidiosus</i>	Parasite	1%
	<i>Parvicapsula kabatai</i>	Parasite	2%
	<i>Parvicapsula pseudobranchicola</i>	Parasite	26%
	<i>Sphaerothecum destruens</i>	Parasite	1%
	Viral encephalopathy and retinopathy virus	Virus	1%
Coho	<i>Candidatus</i> Branchiomonas cysticola	Bacterium	89%
	<i>Candidatus</i> Synngnamydia salmonis (Sch)	Bacterium	10%
	<i>Ceratanova shasta</i>	Parasite	4%
	Erythrocytic necrosis virus	Virus	3%
	<i>Ichthyobodo</i> sp.	Parasite	14%
	<i>Ichthyophonus hoferi</i>	Parasite	59%
	<i>Ichthyophthirius multifiliis</i>	Parasite	1%

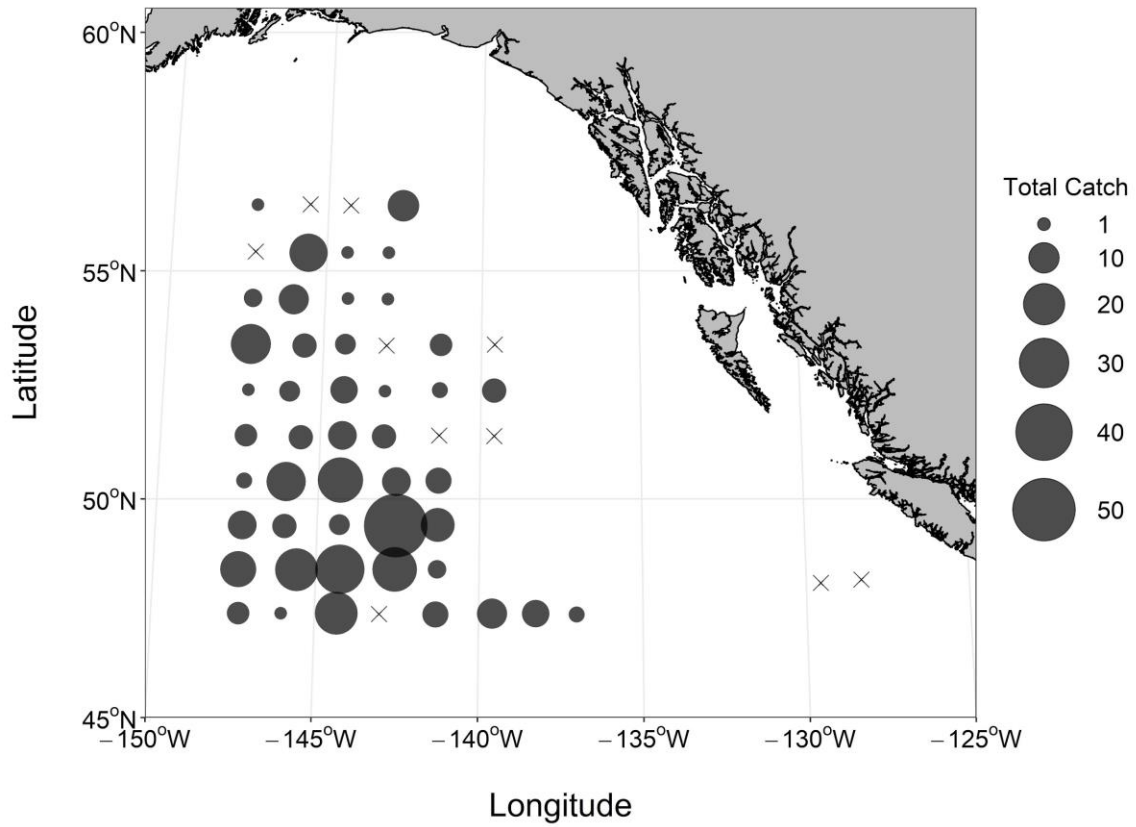
	<i>Kudoa thyrsites</i>	Parasite	1%
	<i>Loma</i> sp.	Parasite	53%
	<i>Myxobolus insidiosus</i>	Parasite	4%
	<i>Nanophyetus salmincola</i>	Parasite	1%
	<i>Paranucleospora theridion</i> / <i>Desmozoon lepeophtherii</i>	Parasite	6%
	<i>Parvicapsula kabatai</i>	Parasite	3%
	<i>Parvicapsula minibicornis</i>	Parasite	9%
	<i>Parvicapsula pseudobranchicola</i>	Parasite	18%
	Putative rhabdo virus	Virus	1%
	Salmovirus WFRC1	Virus	5%
	<i>Sphaerothecum destruens</i>	Parasite	5%
	Viral encephalopathy and retinopathy virus	Virus	36%
Pink	<i>Candidatus</i> Branchiomonas cysticola	Bacterium	89%
	<i>Candidatus</i> Synonymydia salmonis (Sch)	Bacterium	4%
	<i>Ichthyobodo</i> sp.	Parasite	30%
	<i>Ichthyophonus hoferi</i>	Parasite	37%
	<i>Kudoa thyrsites</i>	Parasite	4%
	<i>Loma</i> sp.	Parasite	19%
	<i>Parvicapsula pseudobranchicola</i>	Parasite	26%
	<i>Sphaerothecum destruens</i>	Parasite	4%

Sockeye	<i>Candidatus</i> Branchiomonas cysticola	Bacterium	59%
	<i>Candidatus</i> Syngnamydia salmonis (Sch)	Bacterium	11%
	<i>Ichthyobodo</i> sp.	Parasite	3%
	<i>Ichthyophonus hoferi</i>	Parasite	33%
	<i>Ichthyophthirius multifiliis</i>	Parasite	2%
	<i>Loma</i> sp.	Parasite	67%
	Pacific salmon parvovirus	Virus	39%
	<i>Parvicapsula minibicornis</i>	Parasite	2%
	<i>Parvicapsula pseudobranchicola</i>	Parasite	16%
	Putative -picorna virus	Virus	2%
	<i>Sphaerothecum destruens</i>	Parasite	25%
	Viral encephalopathy and retinopathy virus	Virus	2%

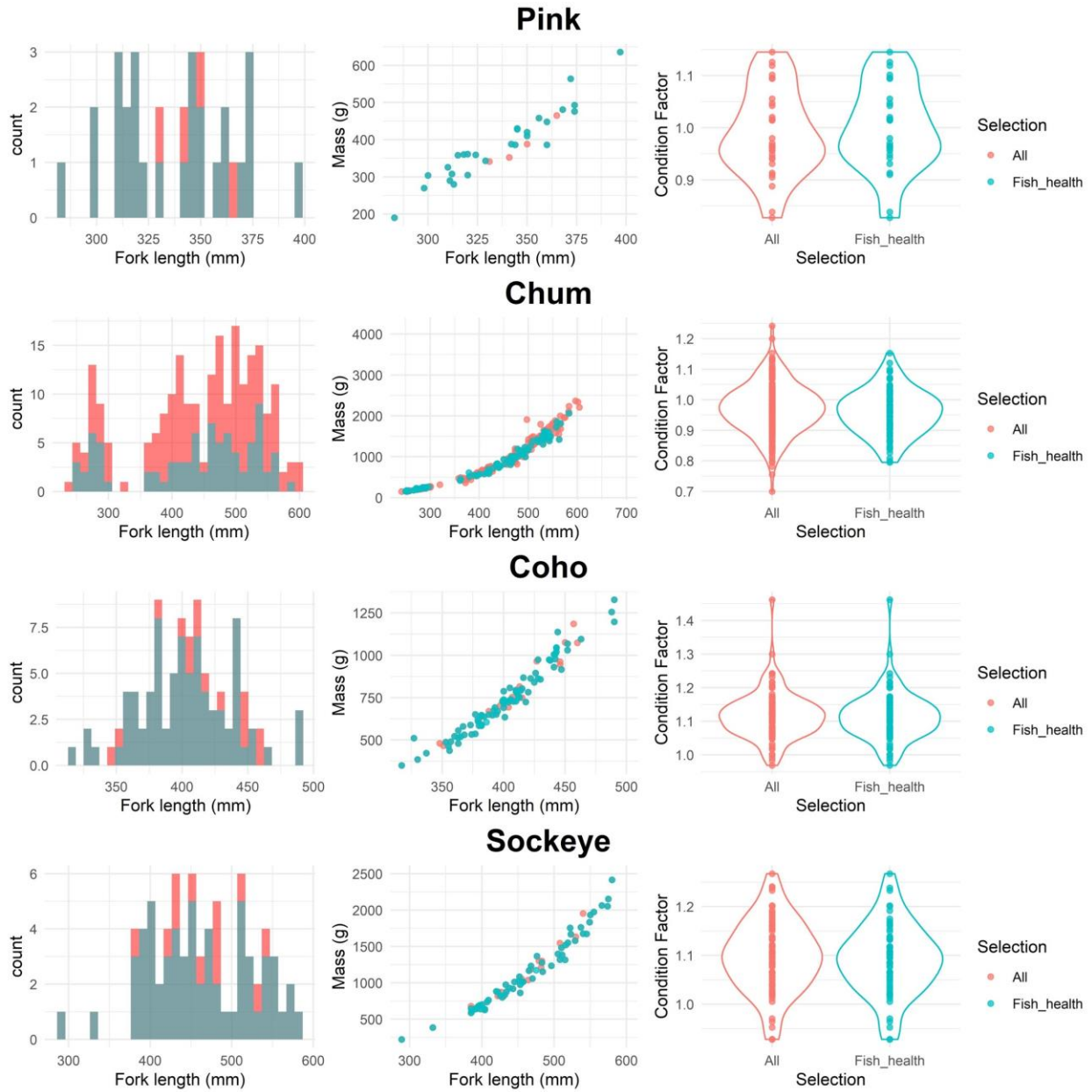
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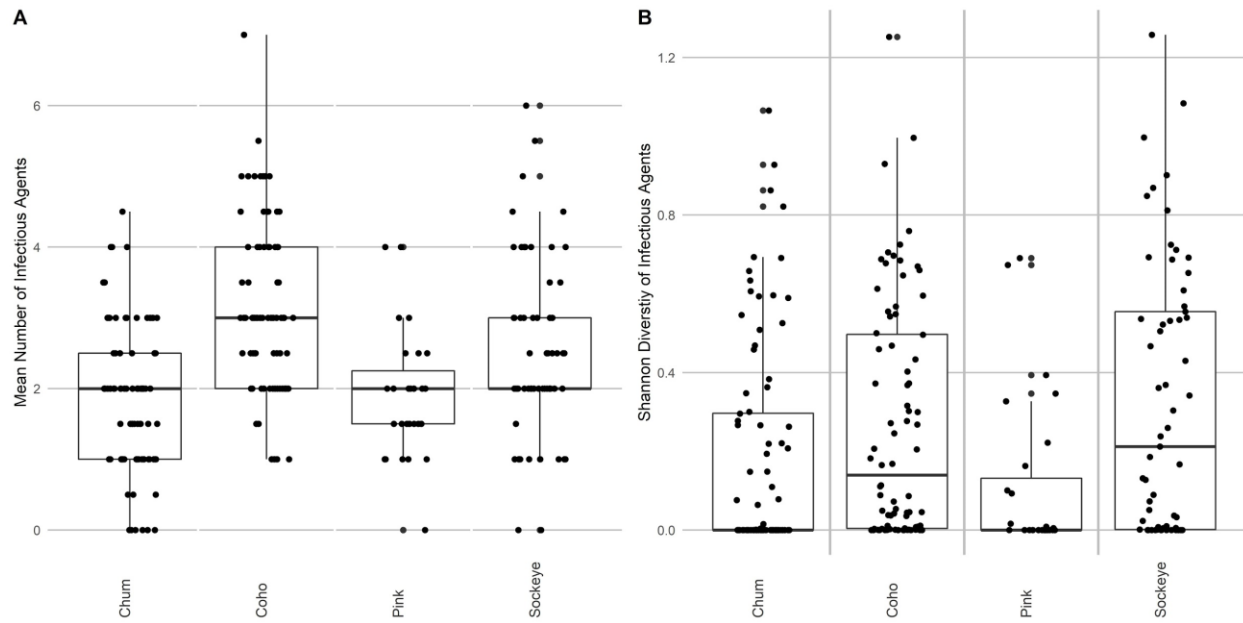
Factor	Unit	Observed		Max. change day ⁻¹		Mean change day ⁻¹	
		Max	Mean	Value	%	Value	%
TEM	°C	8.27	6.40	0.13	2%	0.03	0%
SAL	ppt	32.67	32.46	0.03	0%	0.00	0%
Chl_Flu	ppb	82.91	52.52	3.65	5%	0.41	1%
DO_p	%	97.61	95.47	0.66	1%	0.04	0%
Zoo_S	mgWW.m-3	48.09	16.72	2.86	44%	0.52	3%
Zoo_M	mgWW.m-3	44.36	3.48	4.14	532%	0.38	11%
Zoo_L	mgWW.m-3	727.02	108.09	82.16	41%	5.16	5%
Zoo_total	mgWW.m-3	767.33	137.03	83.04	36%	4.30	3%
Cope	mgWW.m-3	283.25	72.20	20.70	30%	2.63	4%
Euphaus	mgWW.m-3	38.65	0.86	5.24	5244%	0.25	28%
Ptero	mgWW.m-3	3.24	0.49	0.43	194%	0.04	9%
Medu	mgWW.m-3	29.38	1.95	3.98	3983%	0.44	23%
Chaeto	mgWW.m-3	679.70	26.95	79.24	2544%	2.74	10%



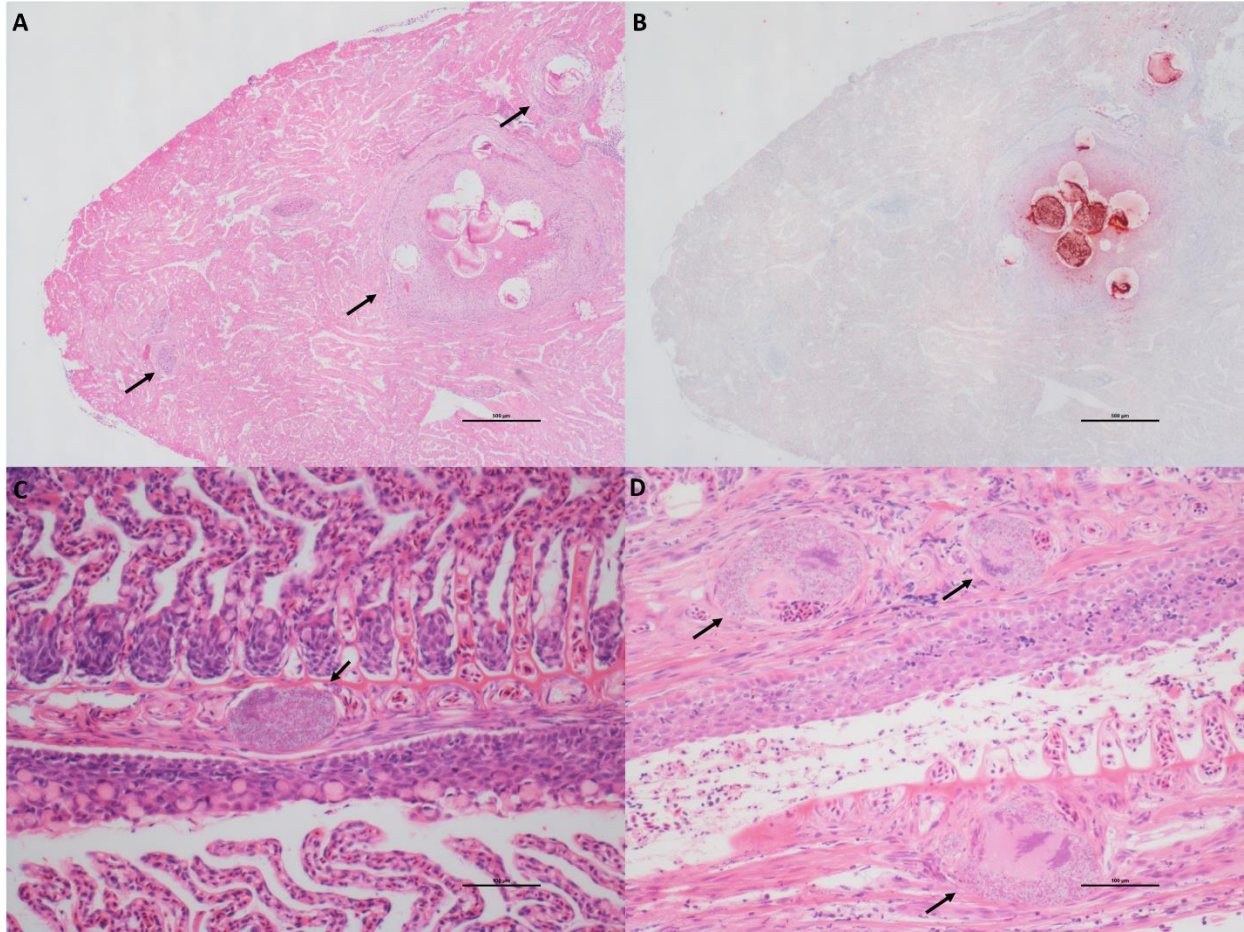
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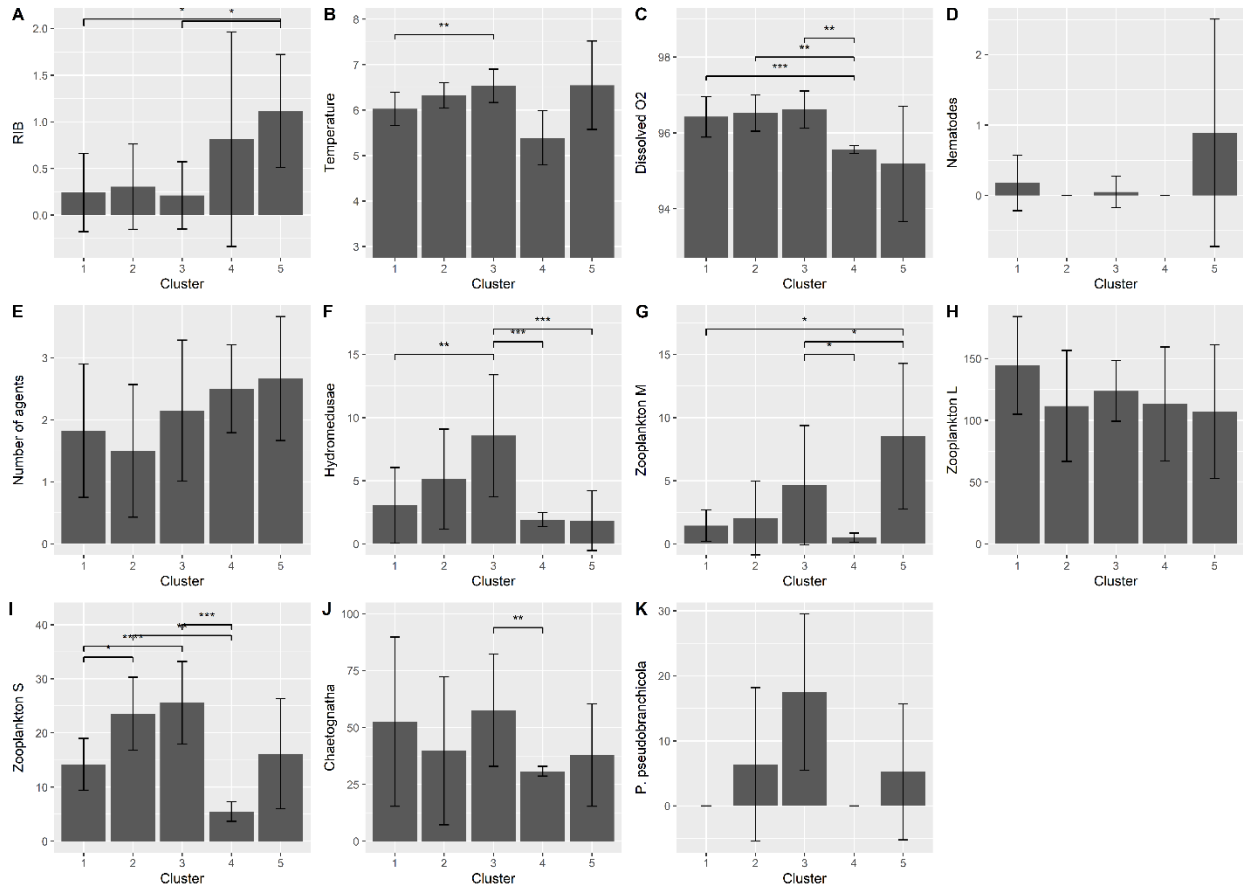
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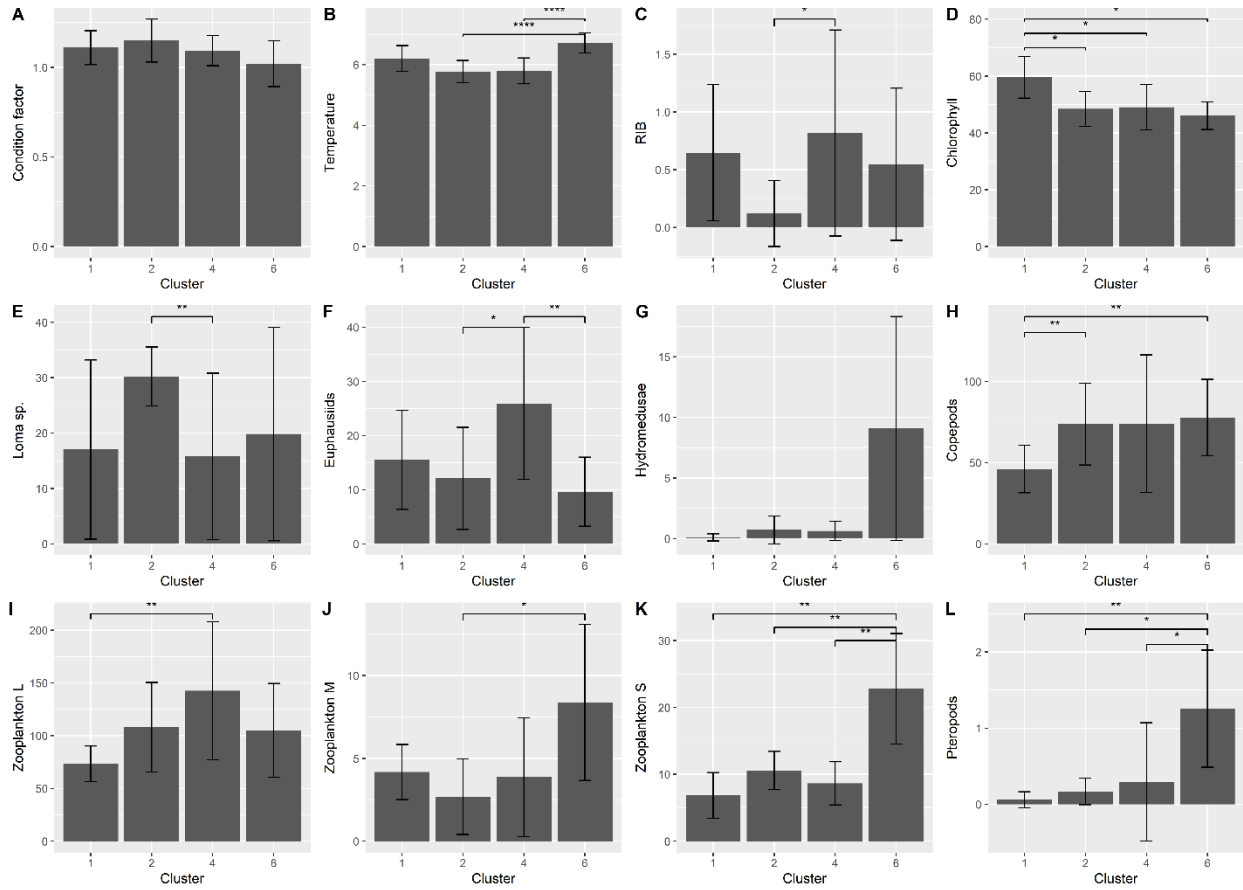
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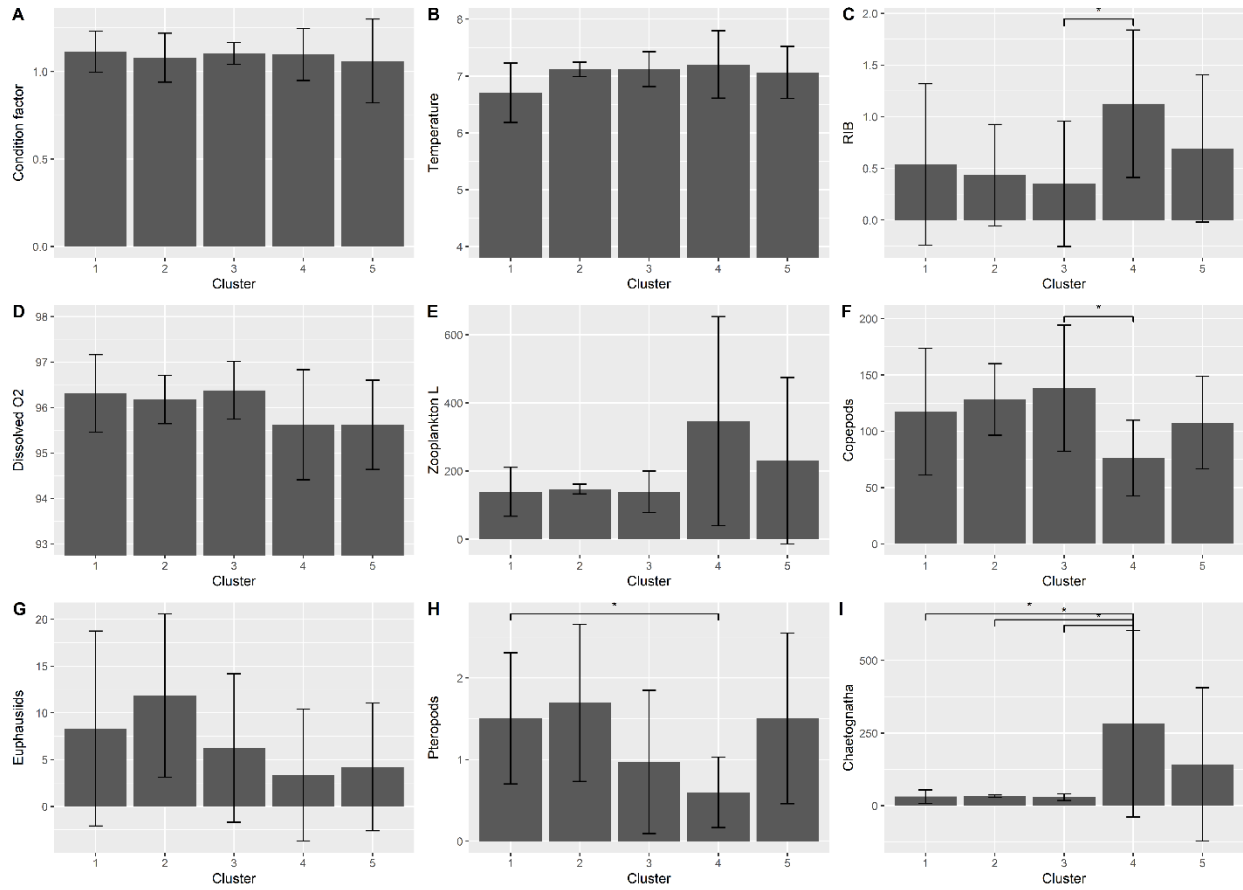
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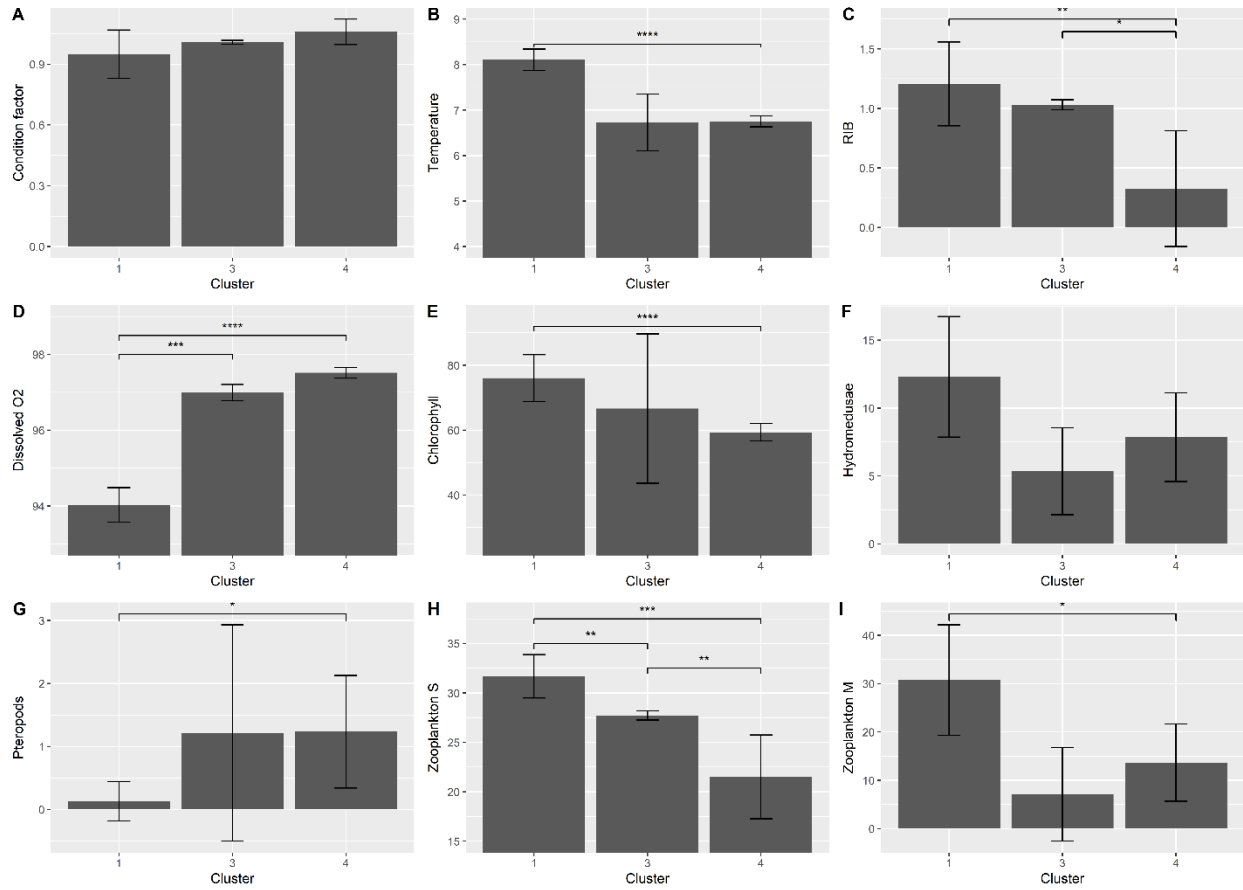
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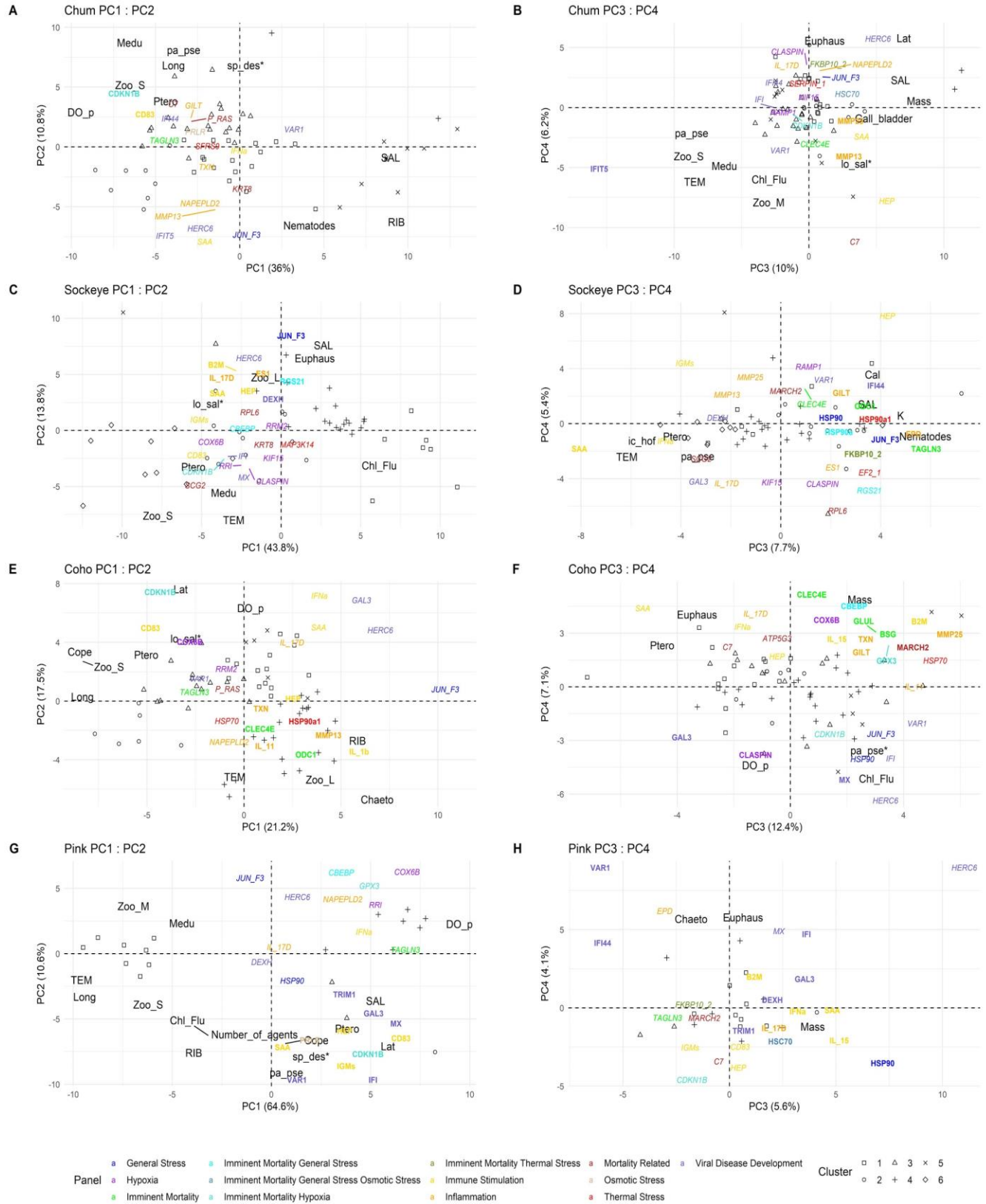
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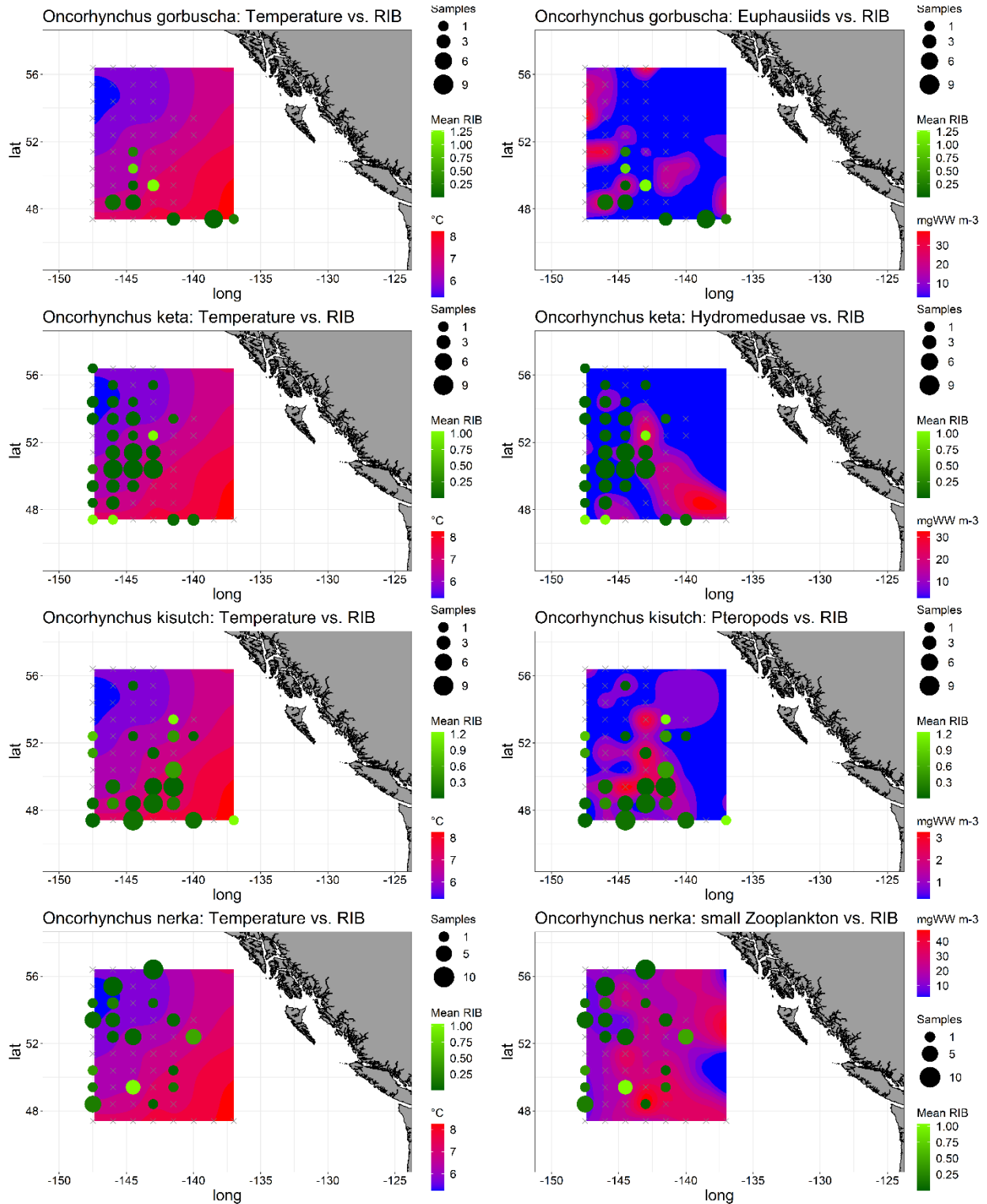
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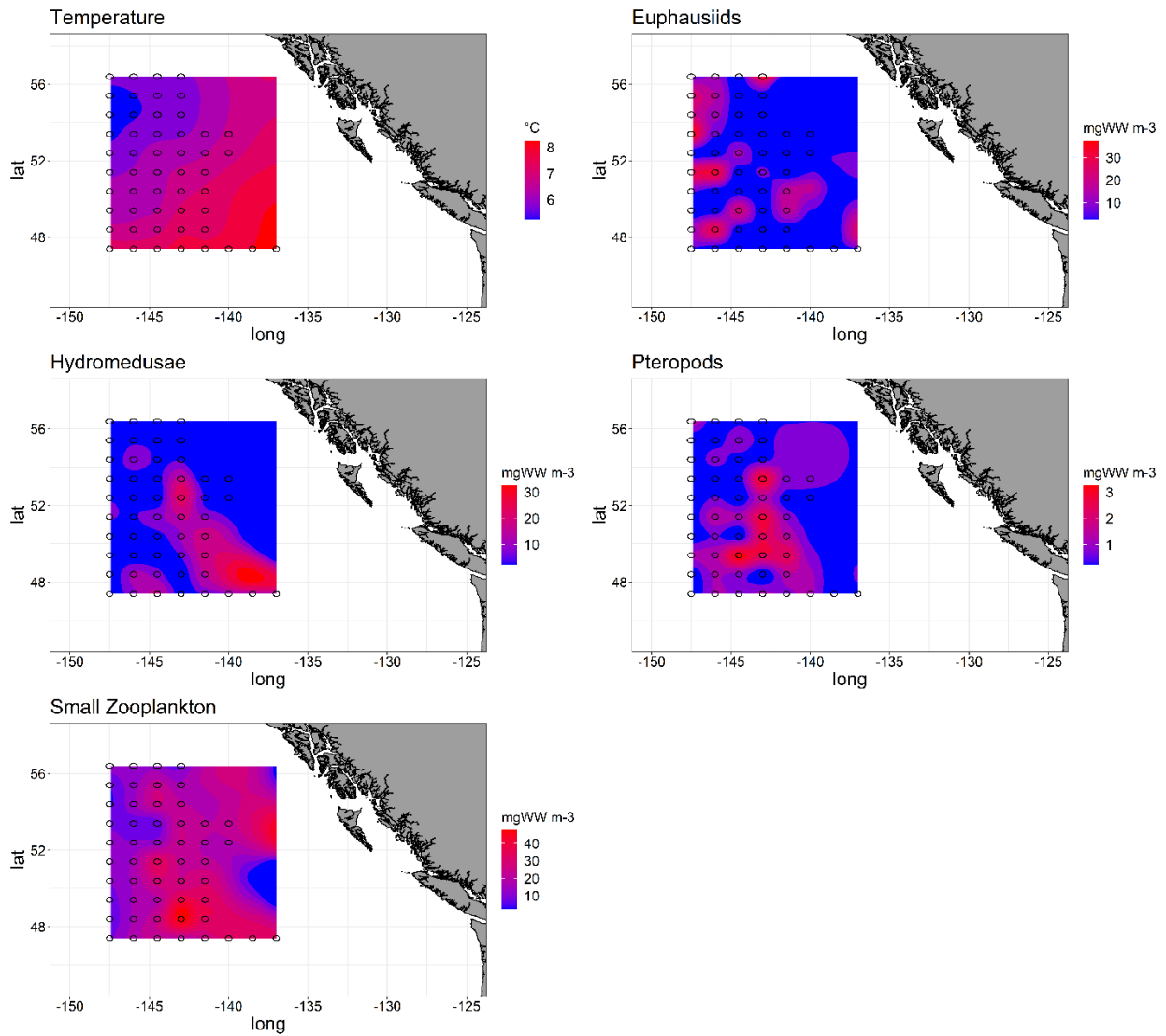
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Supplementary materials and methods:

Histopathology

Gills, skeletal muscle, spleen, liver, heart, anterior and posterior kidney, pyloric caeca, and brain were fixed in 10% neutral buffered formalin. For salmon showing infection with selected high load agents, histopathological samples were prepared to visualize and localize lesions and pathogens by *in-situ* hybridization (ISH). Samples were dehydrated through an alcohol gradient, embedded in paraffin, cut at 3.5 µm, and stained with ematoxylin and eosin (H&E) for morphological evaluation by bright field microscopy. To confirm the presence and tissue infection of *Ichthyophonus hoferi*, it was visualized using an RNAscope probe (Advanced Cell Diagnostics, Newark, California, USA - F-I.hoferi-18S-rRNA Cat No. 823981). A housekeeping gene RNAscope probe (Advanced Cell Diagnostics, Newark, California, USA - Om-ppib Cat No. 540651) was utilized as a positive control. Samples with no detectable infection from the Fluidigm screen were used as negative controls. Signal amplification was performed with RNAscope 2.5 HD assay (Advanced Cell Diagnostics, Newark, California, USA, catalog No. 322350), according to the manufacturer's instructions, and followed by counterstaining with Gill's hematoxylin.