Text S1. Detailed molecular methods

Tissue samples were screened for the presence of 59 infectious agent taxa (Table S1), using HT-qPCR on the Fluidigm Biomark Dynamic Array™ microfluidics platform (Fluidigm, San Francisco, CA, USA) at the Pacific Biological Station, Nanaimo, British Columbia, Canada. This platform has recently been analytically validated for quantitative infectious agent profiling in salmon tissue (Miller et al. 2016) and applied to multiple studies of Pacific salmon (Di Cicco et al. 2017; Miller et al. 2017; Thakur et al. 2018). Infectious agent taxa were chosen based on knowledge of their presence in Canada or evidence of their association with disease worldwide (Miller et al. 2016). Assays utilizing Taqman probes (Table S1) were designed to target both RNA and DNA. Not all of the same assays were used over the course of the qPCR runs, as some new assays were developed (Mordecai et al. 2019) (107 dynamic arrays run over the course of four years).

Total RNA and DNA were extracted using methods previously described in (Miller et al.2016; Thakur et al. 2018). Briefly, tissues were homogenized separately in TRI-reagent™ (Ambion Inc., Austin, TX, USA). Next, 1-bromo-3-chloropropane was added to the homogenate, and equal volumes of both the aqueous phase (RNA) and the organic/interphase (DNA) from each tissue type were combined for extraction. RNA extractions were carried out using MagMAX™-96 for Microarrays Total RNA Isolation Kits (Ambion Inc.) with a Biomek NXP™ automated liquid-handling instrument. RNA quantity and purity was assessed by measuring the A260/A280 ratio using a Beckman Coulter DTX 880 Multimode Spectrophotometer (Brea, CA, USA). DNA was extracted using the TNES-6U method following the Qiagen BioSprint protocol.

Normalized RNA (1µg) was reverse transcribed to cDNA using the SuperScript VILO MasterMix Kit (Invitrogen, Carlsbad, CA) following the manufacturer's instructions. DNA and cDNA were then mixed in equal proportions. The assay volume used for qPCR on the BioMark is small (7nL) and therefore a pre-amplification step is recommended by the manufacturer. Thus, 0.2µmol/L of the cDNA/DNA mix from each sample was pre-amplified with primer pairs corresponding to all assays (microbes and 3 reference genes) in a 5 µL reaction volume using 1X TaqMan Preamp Master Mix (Applied Biosystems, Foster City, California) according to the BioMark protocol. Unincorporated primers were removed using ExoSAP-IT™ (Affymetrix, Santa Clara, California), and samples were diluted 1:5 in DNA Suspension Buffer (Teknova, Hollister, California).

Artificial positive constructs (APC clones) corresponding to all assays were run in six serial dilutions on the dynamic array to construct a standard curve and calculate efficiency for each assay and estimate RNA copy number for each positive sample. The APC clones contained an additional probe labelled with NED™ reporter dye (Life Technologies) that allowed for the detection of vector contamination (see Miller et al. 2016).

A 5µL sample mix was prepared containing 1X TaqMan Universal Master-Mix (Life Technologies), 1X GE Sample Loading Reagent (Fluidigm PN 85000746), and amplified cDNA/DNA, which was added to each assay inlet of the array following the manufacturer's recommendations. All assays were run in duplicate. Five µL of assay mix was prepared containing 10µM primers (infectious agent in FAM-MGB and APC in NED-MGB) and 3µM probes for the TaqMan assays. After loading the assays and samples into the chip using an IFC controller HX (Fluidigm), PCR was performed with the following conditions: 50°C for 2 min, 95°C for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1 min.

Cycle threshold was determined using the BioMark Real-Time PCR analysis software. Reaction curves for each positive sample-assay combination were visually evaluated for abnormal curve shapes, close correspondence between duplicates, and presence of APC contamination as indicated by NED positives. Using scripts created in R statistical software (R Core Team 2019), we calculated efficiency for each assay (standard curve method (Larionov et al. 2005)), omitted results where only one duplicate was positive for a sample-assay combination, removed NED positive samples, and averaged duplicates. Limit of detection (LOD) is defined as the estimated cycle threshold (Ct) number under which true positive results are expected 95% of the time for a given assay (Miller et al. 2016). Because LOD was established

for maximum compliance with OIE standards but limits the sensitivity of the BioMark to detect low-level infection, we present data exceeding the LOD. Note that we only included detections beyond the LOD for infectious agents that were also detected within the LOD whereas infectious agents only detected beyond the LOD were considered to be false positives.

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Table S1. Taqman assays run for 59 infectious agents and 3 host reference genes (Ref) in Chinook salmon mixed-tissue samples (2008 2018) using the Fluidigm Biomark HT-qRT-PCR platform (DFO Pacific Biological Station, Nanaimo, BC). Below the limit of detection (LOD) Ct value, positive samples are detected 95% of the time.

Scientific name	Abbrev.	LOD (ct)	Forward primer sequence (5'–3')	Reverse primer sequence (5'–3')	Probe sequence (FAM-5'–3'-MGB)
Aeromonas hydrophila	ae_hyd	28.7	ACCGCTGCTCATTACTCTGATG	CCAACCCAGACGGGAAGAA	TGATGGTGAGCTGGTTG
Aeromonas salmonicida	ae_sal	25.6	TAAAGCACTGTCTGTTACC	GCTACTTCACCCTGATTGG	ACATCAGCAGGCTTCAGAGTCACTG
Candidatus Branchiomonas cysticola	c_b_cys	25.7	AATACATCGGAACGTGTCTAGTG	GCCATCAGCCGCTCATGTG	CTCGGTCCCAGGCTTTCCTCTCCCA
Flavobacterium psychrophilum	fl_psy	29.5	GATCCTTATTCTCACAGTACCGTCAA	TGTAAACTGCTTTTGCACAGGAA	AAACACTCGGTCGTGACC
Moritella viscosa	mo_vis		CGTTGCGAATGCAGAGGT	AGGCATTGCTTGCTGGTTA	TGCAGGCAAGCCAACTTCGACA
Candidatus Piscichlamydia salmonis	pch_sal	23.3	TCACCCCCAGGCTGCTT	GAATTCCATTTCCCCCTCTTG	CAAAACTGCTAGACTAGAGT
Piscirickettsia salmonis	pisck_sal	23.3	TCTGGGAAGTGTGGCGATAGA	TCCCGACCTACTCTTGTTTCATC	TGATAGCCCCGTACACGAAACGGCATA
Renibacterium salmoninarum	re_sal	25.9	CAACAGGGTGGTTATTCTGCTTTC	CTATAAGAGCCACCAGCTGCAA	CTCCAGCGCCGCAGGAGGAC
Rickettsia-like organism	rlo	25.2	GGCTCAACCCAAGAACTGCTT	GTGCAACAGCGTCAGTGACT	CCCAGATAACCGCCTTCGCCTCCG
Candidatus Syngnamydia salmonis	sch	27.9	GGGTAGCCCGATATCTTCAAAGT	CCCATGAGCCGCTCTCTCT	TCCTTCGGGACCTTAC
Tenacibaculum maritimum	te_mar		TGCCTTCTACAGAGGGATAGCC	CTATCGTTGCCATGGTAAGCCG	CACTTTGGAATGGCATCG
Vibrio anguillarum	vi_ang	26.4	CCGTCATGCTATCTAGAGATGTATTTGA	CCATACGCAGCCAAAAATCA	TCATTTCGACGAGCGTCTTGTTCAGC
Vibrio salmonicida	vi_sal	25.8	GTGTGATGACCGTTCCATATTT	GCTATTGTCATCACTCTGTTTCTT	TCGCTTCATGTTGTGTAATTAGGAGCGA
Yersinia ruckeri	ye_ruc	25.8	TGCCGCGTGTGTGAAGAA	ACGGAGTTAGCCGGTGCTT	AATAGCACTGAACATTGAC
Dermocystidium salmonis	de_sal	25.5	CAGCCAATCCTTTCGCTTCT	GACGGACGCACACCACAGT	AAGCGGCGTGTGCC
Ichthyophonus spp.	ic_hof	24.2	GTCTGTACTGGTACGGCAGTTTC	TCCCGAACTCAGTAGACACTCAA	TAAGAGCACCCACTGCCTTCGAGAAGA
Ceratonova shasta	ce_sha	28.5	CCAGCTTGAGATTAGCTCGGTAA	CCCCGGAACCCGAAAG	CGAGCCAAGTTGGTCTCTCCGTGAAAAC
Sphaerothecum destruens	sp_des	26.5	GGGTATCCTTCCTCTCGAAATTG	CCCAAACTCGACGCACACT	CGTGTGCGCTTAAT
Facilispora margolisi	fa_mar	30.6	AGGAAGGAGCACGCAAGAAC	CGCGTGCAGCCCAGTAC	TCAGTGATGCCCTCAGA

Scientific name	Abbrev.	LOD (ct)	Forward primer sequence (5'–3')	Reverse primer sequence (5'–3')	Probe sequence (FAM-5'–3'-MGB)
Loma spp.	lo_sal	25.4	GGAGTCGCAGCGAAGATAGC	CTTTTCCTCCCTTTACTCATATGCTT	TGCCTGAAATCACGAGAGTGAGACTACCC
Nucleospora salmonis	nuc_sal	26.1	GCCGCAGATCATTACTAAAAACCT	CGATCGCCGCATCTAAACA	CCCCGCGCATCCAGAAATACGC
Paranucleospora theridion (syn. *Desmozoon lepeophtherii*)	pa_ther	28.2	CGGACAGGGAGCATGGTATAG	GGTCCAGGTTGGGTCTTGAG	TTGGCGAAGAATGAAA
Kudoa thyristes	ku_thy	26.2	TGGCGGCCAAATCTAGGTT	GACCGCACACAAGAAGTTAATCC	TATCGCGAGAGCCGC
Myxobolus arcticus	my_arc	26.8	TGGTAGATACTGAATATCCGGGTTT	AACTGCGCGGTCAAAGTTG	CGTTGATTGTGAGGTTGG
Myxobolus cerebalis	my_cer	26.2	GCCATTGAATTTGACTTTGGATTA	ACCATTCATGTAAGCCCGAACT	TCGAAGCCTTGACCATCTTTTGGCC
Myxobolus insidiosus	my_ins	26.4	CCAATTTGGGAGCGTCAAA	CGATCGGCAAAGTTATCTAGATTCA	CTCTCAAGGCATTTAT
Parvicapsula kabatai	pa_kab	25.6	CGACCATCTGCACGGTACTG	ACACCACAACTCTGCCTTCCA	CTTCGGGTAGGTCCGG
Parvicapsula minibicornis	pa_min	29.6	AATAGTTGTTTGTCGTGCACTCTGT	CCGATAGGCTATCCAGTACCTAGTAAG	TGTCCACCTAGTAAGGC
Parvicapsula pseudobranchicola	pa_pse	25.2	CAGCTCCAGTAGTGTATTTCA	TTGAGCACTCTGCTTTATTCAA	CGTATTGCTGTCTTTGACATGCAGT
Tetracapsuloides bryosalmonae	te_bry	25.0	GCGAGATTTGTTGCATTTAAAAAG	GCACATGCAGTGTCCAATCG	CAAAATTGTGGAACCGTCCGACTACGA
Gyrodactylus salaris	gy_sal	26.4	CGATCGTCACTCGGAATCG	GGTGGCGCACCTATTCTACA	TCTTATTAACCAGTTCTGC
Nanophyetus salmincola	na_sal	24.3	GATCTGCATTTGGTTCTGTAACA	CCAACGCCACAATGATAGCTATAC	TGAGGCGTGTTTTATG
Cryptobia salmositica	cr_sal	24.3	TCAGTGCCTTTCAGGACATC	GAGGCATCCACTCCAATAGAC	AGGAGGACATGGCAGCCTTTGTAT
Ichthyophthirius multifiliis	ic_mul	23.7	AAATGGGCATACGTTTGCAAA	AACCTGCCTGAAACACTCTA	ACTCGGCCTTCACTGGTTCGACTTGGATTTTT
Neoparamoeba perurans	ne_per	25.4	GTTCTTTCGGGAGCTGGGAG	GAACTATCGCCGGCACAAAAG	CAATGCCATTCTTTTCGGA
Spironucleus salmonicida	sp_sal	26.1	GCAGCCGCGGTAATTCC	CGAACTTTTTAACTGCAGCAACA	ACACGGAGAGTATTCT
Atlantic salmon calicivirus virus	ascv		ACCGACTGCCCGGTTGT	CTTAGGGTTAAAGCAGTCG	CTCCGATTGCCTGTGATAATACC
Atlantic salmon paramyxovirus	Aspv	26.2	CCCATATTAGCAAATGAGCTCTATCTT	CGTTAAGGAACTCATCATTG	AGCCCTTTTGTTCTGCAGCTT
Chinook aquareovirus	Reov		AACTTTCGGCTTTCTGCTATGC	GAGGACAAGGGTCTCCATCTGA	TTAATTGCGGTACTGCTC
Cutthroat trout virus 2	ctv		CCACTTGTCGCTACGATGAAAC	ATGCCGGGCCATC	CGCCTCCTTTGCCTTTCTC
Erythrocytic necrosis virus	ven	24.9	CGTAGGGCCCCAATAGTTTCT	GGAGGAAATGCAGACAAGATTTG	TCTTGCCGTTATTTCCAGCACCCG

Scientific name	Abbrev.	LOD (ct)	Forward primer sequence (5'–3')	Reverse primer sequence (5'–3')	Probe sequence (FAM-5'–3'-MGB)
Infectious hematopoietic necrosis virus	ihnv	27.6	AGAGCCAAGGCACTGTGCG	TTCTTTGCGGCTTGGTTGA	TGAGACTGAGCGGGACA
Infectious pancreatic necrosis virus	ipnv	27.6	GCAACTTACTTGAGATCCATTATGCT	AGACCTCTAAGTTGTATGACGAGGTCTCT	CGAGAATGGGCCAGCAAGCA
Infectious salmon anemia virus 7	isa7	27.0	TGGGATCATGTGTTTCCTGCTA	GAAAATCCATGTTCTCAGATG-CAA	CACATGACCCCTCGTC
Infectious salmon anemia virus 8	isa8	26.1	TGGGCAATGGTGTATGGTATGA	GAAGTCGATGAACTGCAGCGA	CAGGATGCAGATGTATGC
Pacific salmon nidovirus	cov		GGATAATCCCAACCGAAAAGTTT	GCATGAAATGTTGTCTCGGTTTAA	CGATCCCGATTATC
Pacific salmon parvovirus	pspv	26.4	CCCTCAGGCTCCGATTTTTAT	CGAAGACAACATGGAGGTGACA	CAATTGGAGGCAACTGTA
Piscine myocarditis virus	pmcv	26.3	TTCCAAACAATTCGAGAAGCG	ACCTGCCATTTTCCCCTCTT	CCGGGTAAAGTATTTGCGTC
Piscine orthoreovirus	PRv	26.1	TGCTAACACTCCAGGAGTCATTG	TGAATCCGCTGCAGATGAGTA	CGCCGGTAGCTCT
Putative narna-like virus	pnarna		TGTCCCTGAAGATTCATTTCGA	TCCTAGGTGATGATATAAT	CTATGTAAAGCCTCGTCGGTGAT
Putative RNA virus 1	smallUK		GTACCTAATTTAACTGGAACAGTAGAC	TGCAACAGGCAAGTGATATGCTTGA	CGTTCAGTAACACAAGTATCCAAA
Putative toti-like virus	toti		TCTGCGCGCTGCACCTA	CAAGTGCTACACTGCG	ATGCGGAGGAACTCACACACT
Rainbow trout orthomyxovirus	ortho		GGAAGCAGTGGACGCTAACC	TCGCGAAGGTCTCTCAATGTC	ATTCTTCTCATCAAAGGCA
Salmon alphavirus	sav	26.3	CCGGCCCTGAACCAGTT	GTAGCCAAGTGGGAGAAAGCT	TCGAAGTGGTGGCCAG
Salmon gill pox virus	sgpx		ATCCAAAATACGGAACATAAGCAAT	CAACGACAAGGAGATCAACGC	CTCAGAAACTTCAAAGGA
Salmonid herpesvirus	shv	26.6	GCCTGGACCACAATCTCAATG	CGAGACAGTGTGGCAAGACAAC	CCAACAGGATGGTCATTA
Salmon pescarenavirus 1	arena1		CCTGCCTCTTTGCTCATTGTG	AGAAAAAGCTGTGGTACTTTAGAAAGC	ATCCGCCTAACGGTTGG
Salmon pescarenavirus 2	arena2		AACATGAAGGGCGATTCGTT	CAGCCCGCGGACTGAGT	CAAGTGATGTAAGCTTG
Viral encephalopathy and retinopathy virus	ver	26.2	TTCCAGCGATACGCTGTTGA	CACCGCCCGTGTTTGC	AAATTCAGCCAATGTGCCCC
Viral hemorrhagic septicemia virus	vhsv	26.9	ATGAGGCAGGTGTCGGAGG	TGTAGTAGGACTCTCCCAGCATCC	TACGCCATCATGATGAGT
78d16.1	Ref	NA	GTCAAGACTGGAGGCTCAGAG	GATCAAGCCCCAGAAGTGTTTG	AAGGTGATTCCCTCGCCGTCCGA
COIL-P84-2	Ref	NA	GCTCATTTGAGGAGAAGGAGGATG	CTGGCGATGCTGTTCCTGAG	TTATCAAGCAGCAAGCC
MRPL40	Ref	NA	CCCAGTATGAGGCACCTGAAGG	GTTAATGCTGCCACCCTCTCAC	ACAACAACATCACCA

Table S2: Groupings of infectious agents used in spatial models for hypothesis testing via meta-analysis (excluding distance to aquaculture, see Table S3). References are provided as evidence for groupings.

Taxa	**Transmission environment§**	**Temperature preference£**	**Transmission complexity¥**
Ca. Branchiomonas cysticola	*freshwater*[1,2]	unknown	freshwater-simple[2]
Flavobacterium psychrophilum	freshwater[3,4]	cold[5]	freshwater-simple
Ca. Syngnamydia salmonis	saltwater[1]	unknown	saltwater-simple
Piscirickettsia salmonis	saltwater[6]	cold[6]	saltwater-simple[7]
Renibacterium salmoninarum	*freshwater*	warm[8]	freshwater-simple
Rickettsia-like organism	freshwater[9]	warm[10]	freshwater-simple
Tenacibaculum maritimum	saltwater[11]	warm[11]	saltwater-simple
Ichthyophonus hoferi	*saltwater*[1,12]	warm[13]	saltwater-complex[12]
Sphaerothecum destruens	*saltwater**	warm[14]	saltwater-simple
Facilispora margolisi	saltwater[15]	unknown	saltwater-complex
Loma salmonae	*saltwater*[16]*	warm[16,17]	saltwater-simple[18]
Paranucleospora theridion	saltwater[19]	warm[19,20]	saltwater-complex[21]
Ceratonova shasta	freshwater[22]	warm[10,23]	freshwater-complex[22]
Kudoa thyrsites	saltwater	warm[10]	saltwater-complex
Myxobolus arcticus	freshwater[24]	unknown	freshwater-complex[24]
Parvicapsula kabatai	saltwater[1]	unknown	saltwater-complex
Parvicapsula minibicornis	freshwater[25]	warm[10,26]	freshwater-complex[25]
Parvicapsula pseudobranchicola	saltwater[27]	unknown	saltwater-complex
Tetracapsuloides bryosalmonae	freshwater	warm[28,29]	freshwater-complex[30]
Cryptobia salmositica	freshwater[31]	cold[31]	Freshwater-complex[31]
Nanophyetus salmincola	freshwater	unknown	freshwater-complex
Ichthyopthirius multifiliis	freshwater[32]	warm[32,33]	freshwater-simple
Pacific salmon arena virus 1	saltwater*	cold[34]	saltwater-simple
Pacific salmon nidovirus	freshwater*	cold[34]	freshwater-simple
Piscine orthoreovirus	*saltwater**	cold[34]	saltwater-simple
Erythrocytic necrosis virus	*saltwater*[35]	cold[34]	saltwater-simple
Putative RNA virus 1[36]	saltwater*	cold[34]	saltwater-complex[36]

§ Pathogens in italics can be transmitted in both environments. We chose the environment where transmission is most likely to first occur for juvenile Chinook salmon in the study area.

***** If evidence from published studies was insufficient to categorize pathogen, we relied upon unpublished observations from the SSHI dataset

£ Given that viability of most fish viruses decline as water temperature increases[34], we categorized all viruses, including those recently discovered, as cold-associated.

¥ For myxozoans where life cycle is unknown, transmission is assumed to involve an invertebrate alternate host

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Table S3. Grouping of infectious agents for the "distance to aquaculture" hypothesis meta-analysis. References are provided to support categorization rationale.

Taxa	Ranking	Rationale
Cryptobia salmositica	Moderate	Outbreaks in BC Pacific salmon in marine netpens[1] Transmission without alternate host requires physical contact[2]
Ca. Branchiomonas cysticola	Moderate	PCR detections in BC aquaculture[3,4] Frequently the most common pathogen in studies of Pacific wild salmon[5,6]
Flavobacterium psychrophilum	High	Major pathogen in FW aquaculture but little known in SW[7] PCR detections in BC aquaculture[3,4] Elevated eDNA at active BC aquaculture sites relative to inactive[8]
Ca. Syngnamydia salmonis	Moderate	Present in Norwegian and BC aquaculture[4,9]
Piscirickettsia salmonis	High	Frequent outbreaks in Chile[10] PCR detections in BC aquaculture[4] Elevated eDNA at active BC aquaculture sites relative to inactive[8]
Renibacterium salmoninarum	High	Outbreaks and transmission in SW for BC aquaculture[11]
Rickettsia-like organism	Low	No evidence of presence in BC aquaculture or evidence of SW aquaculture presence elsewhere
Tenacibaculum maritimum	High	Outbreaks in BC aquaculture[12] Potential for transmission to BC wild salmon from aquaculture[13] Elevated eDNA at active BC aquaculture sites relative to inactive[8]
Ichthyophonus hoferi	Moderate	Potential to persist in feeds that contain herring[14] Presence in first summer *S. salar* in BC marine netpens[15]
Sphaerothecum destruens	Moderate	Outbreaks in netpen Pacific salmon in WA, USA[16]
Facilispora margolisi	Moderate	PCR detections in BC aquaculture[3]
Loma salmonae	Moderate	Outbreaks in netpen Pacific salmon[17]
Paranucleospora theridion	High	High prevalence in Norwegian aquaculture[18] High prevalence in BC aquaculture[4]
Ceratonova shasta	Low	Freshwater pathogen with no evidence of presence in marine aquaculture
Kudoa thyrsites	High	Common in BC aquaculture[19] Elevated eDNA at active BC aquaculture sites relative to inactive[8]
Myxobolus arcticus	Low	Freshwater pathogen with no evidence of presence in marine aquaculture
Parvicapsula kabatai	Moderate	PCR detections in BC aquaculture[4]
Parvicapsula minibicornis	Low	Freshwater pathogen with no evidence of presence in marine aquaculture
Parvicapsula pseudobranchicola	High	High prevalence in Norwegian aquaculture[20] Elevated eDNA at active BC aquaculture sites relative to inactive[8]
Tetracapsuloides bryosalmonae	Low	Freshwater pathogen with no evidence of presence in marine aquaculture
Nanophyetus salmincola	Low	Freshwater pathogen with no evidence of presence in marine aquaculture
Ichthyophthirius multifiliis	Moderate	Outbreaks in FW salmonids[21] PCR detections in BC aquaculture[3]

Taxa	Ranking	Rationale
Pacific salmon arena virus 1	Moderate	PCR detections in Pacific salmon in BC aquaculture[22]
Pacific salmon nidovirus	Low	Little known virus with majority of detections in freshwater[23]
Piscine orthoreovirus	High	High prevalence in BC aquaculture[3,24] Association between likelihood of infection and distance to aquaculture[24]
Erythrocytic necrosis virus	Moderate	Infections in Pacific and Atlantic salmon in BC aquaculture[15] PCR detections in BC aquaculture[4]
Putative RNA virus 1	Low	No evidence of presence in marine aquaculture

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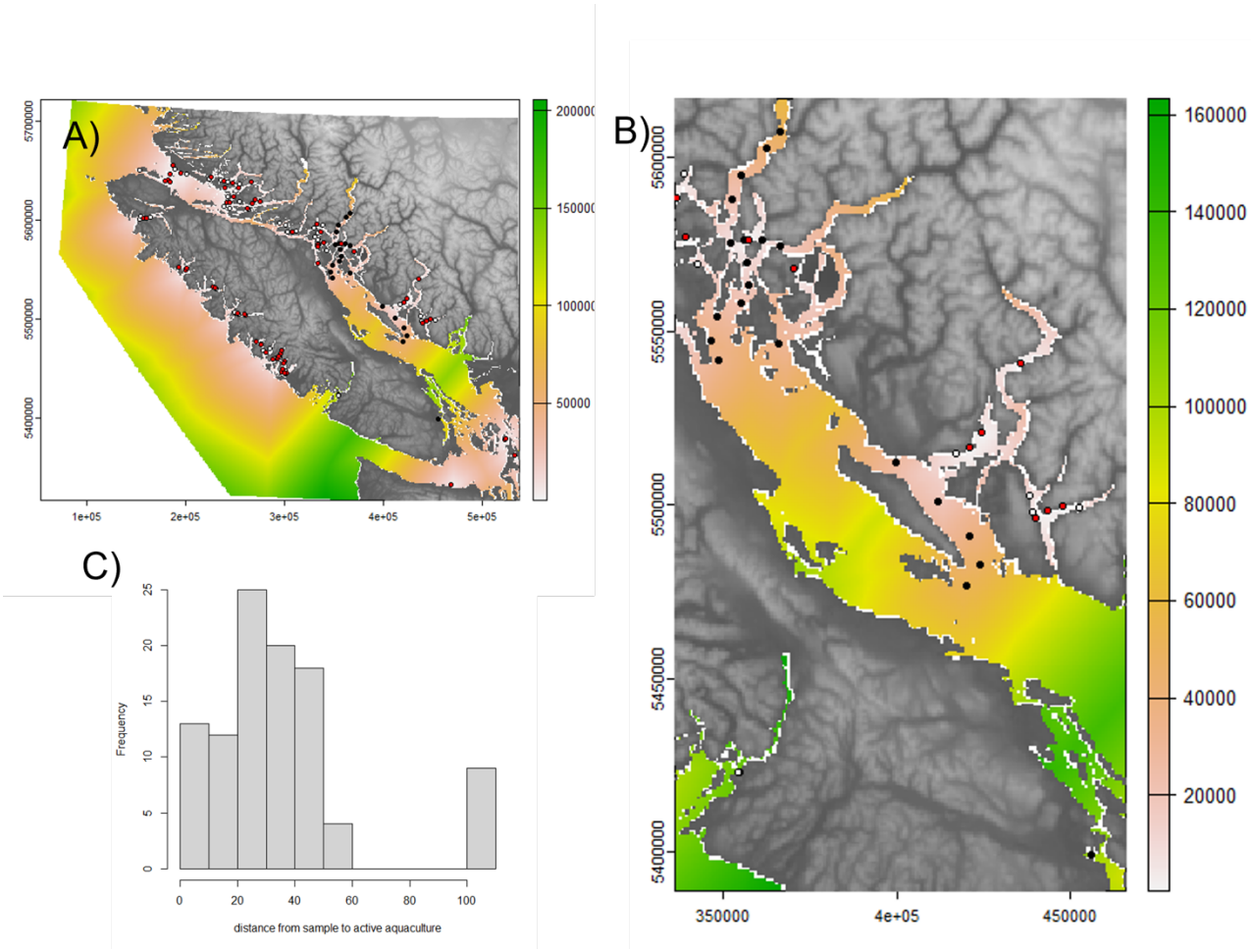

Figure S1. Example of seaway distance from active aquaculture data. Panel A shows the seaway distance raster from September, 2014. Cell color of raster over sea surface (1 km resolution) indicates distance from nearest active finfish aquaculture netpen facilities (red points) in meters. White points are aquaculture facilities that were inactive in September, 2014. Black points are locations where Chinook salmon were collected in September, 2014. Panel B is zoomed in to the extent of Chinook salmon collections in September, 2014. Panel C shows a histogram of seaway distances (km) to active aquaculture for Chinook collected in September, 2014 (corresponding to points in B).

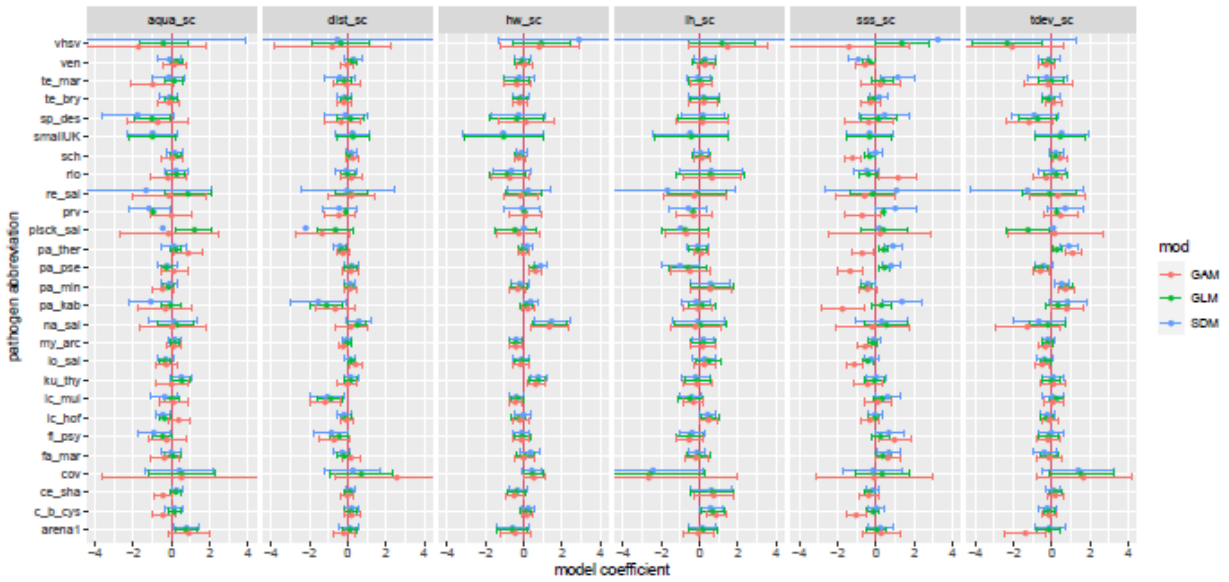

Figure S2. Plots of all Chinook model coefficients for three spatial model types demonstrating the consistency between geostatistical modeling approaches. Error bars represent 99% confidence intervals. Full names corresponding to pathogen abbreviations can be found in Table S1. Model variables at top of plots represent: distance to active aquaculture (aqua), distance to nearest shoreline (dist), finclip status (hw), age at ocean entry (lh), sea surface salinity (SSS), and sea surface temperature deviation (tdev).

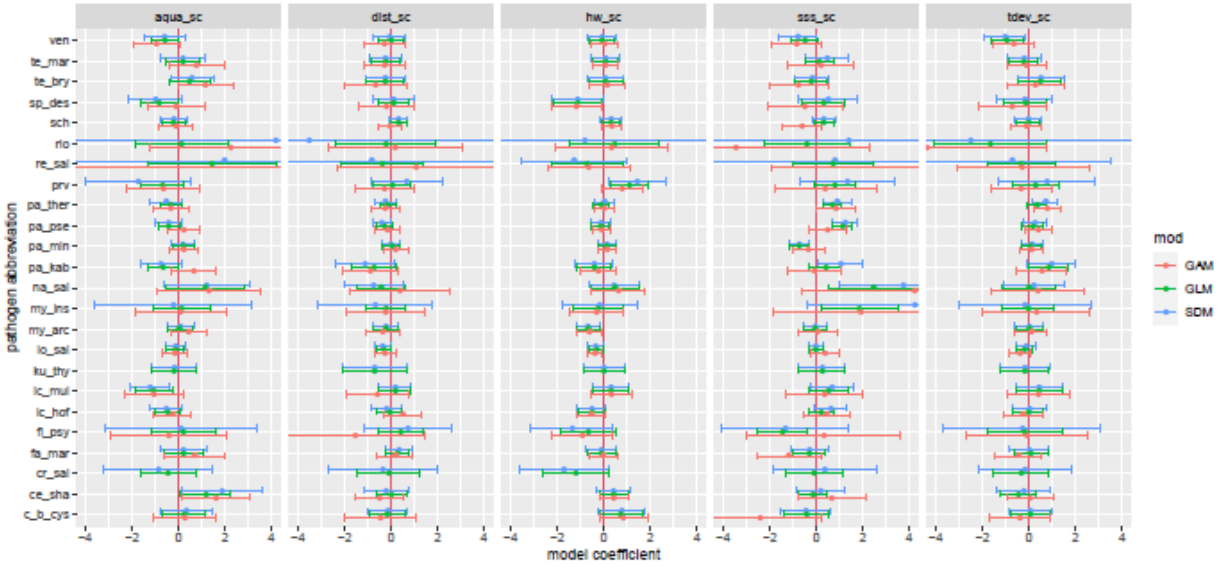

Figure S3. Plots of all Coho model coefficients for three spatial model types demonstrating the consistency between geostatistical modeling approaches. Error bars represent 99% confidence intervals. Full names corresponding to pathogen abbreviations can be found in Table S1. Model variables at top of plots represent: distance to active aquaculture (aqua), distance to nearest shoreline (dist), finclip status (hw), age at ocean entry (lh), sea surface salinity (SSS), and sea surface temperature deviation (tdev).

Figures S4–S13. Forest plots for hypothesis tests using sdmTMB model coefficients (see Tables 2 & 3). Squares are model estimates (orange = Chinook, blue = Coho) with 99% confidence intervals. Diamonds represent meta-analytical means with 95% confidence intervals. The bottom diamond and dotted red vertical line represent the mean coefficient estimate across all models. Square size is proportional to weight, which represents a given coefficient estimates relative contribution to the group and overall means.

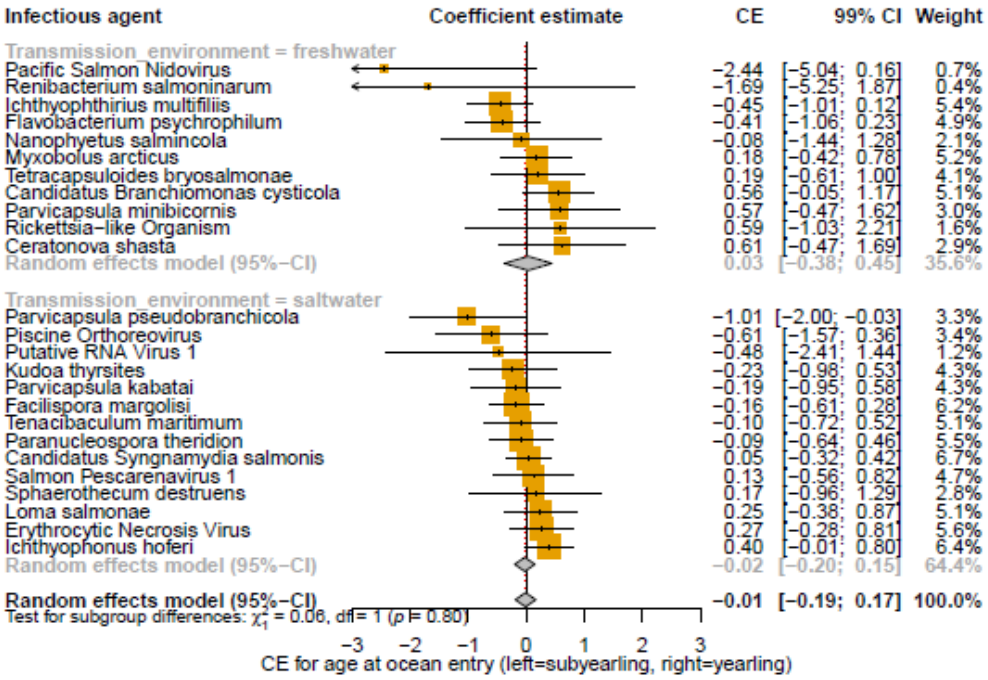

Figure S4

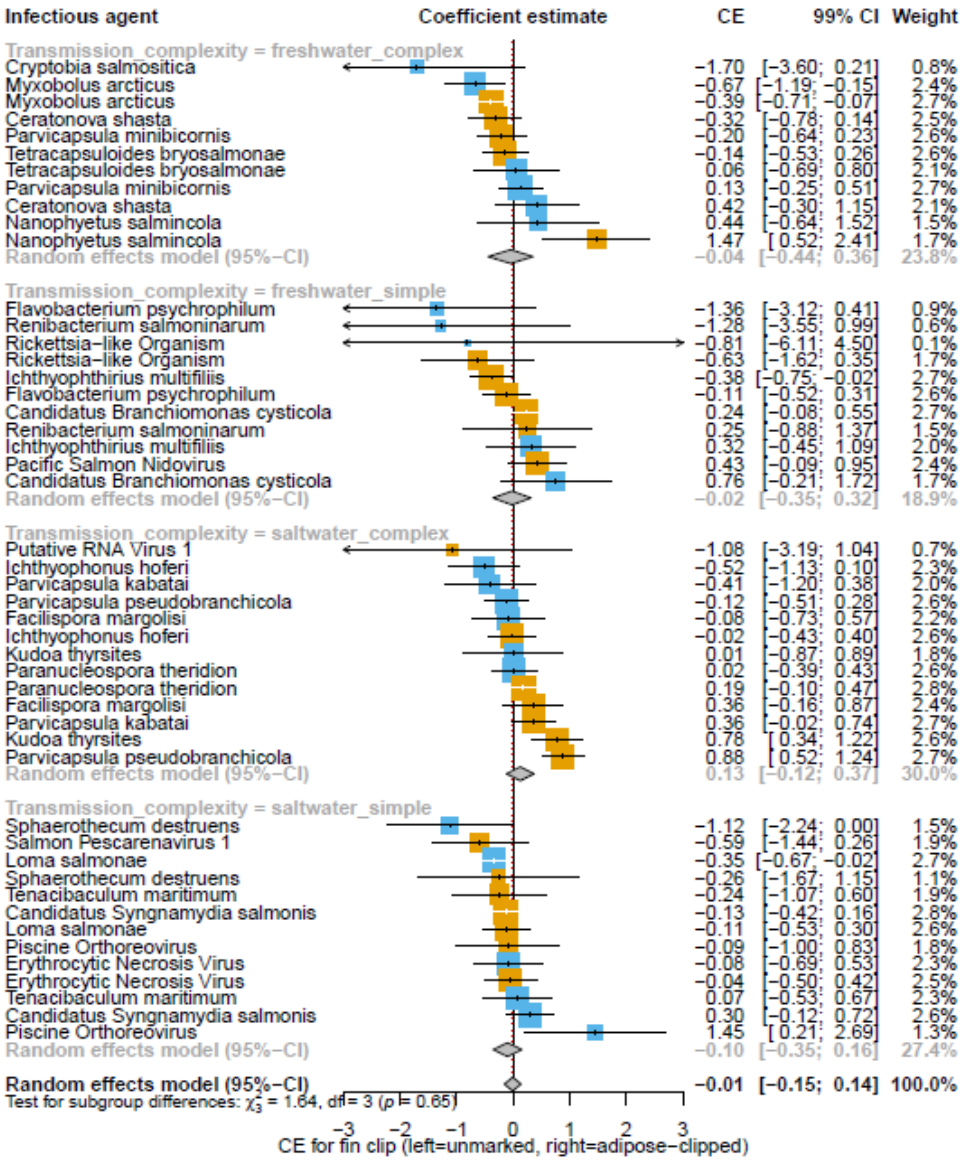
Infectious agent
Coefficient estimate
CE
99% CI
Weight
Transmission_complexity = freshwater_complex
Cryptobia salmositica −1.70 [−3.60; 0.21] 0.8%
Myxobolus arcticus −0.67 [−1.19; −0.15] 2.4%
Myxobolus arcticus −0.39 [−0.71; −0.07] 2.7%
Ceratonova shasta −0.32 [−0.78; 0.14] 2.5%
Parvicapsula minibicornis −0.20 [−0.64; 0.23] 2.6%
Tetracapsuloides bryosalmonae −0.14 [−0.53; 0.26] 2.6%
Tetracapsuloides bryosalmonae 0.06 [−0.69; 0.80] 2.1%
Parvicapsula minibicornis 0.13 [−0.25; 0.51] 2.7%
Ceratonova shasta 0.42 [−0.30; 1.15] 2.1%
Nanophyetus salmincola 0.44 [−0.64; 1.52] 1.5%
Nanophyetus salmincola 1.47 [0.52; 2.41] 1.7%
Random effects model (95%−CI) −0.04 [−0.44; 0.36] 23.8%
Transmission_complexity = freshwater_simple
Flavobacterium psychrophilum −1.36 [−3.12; 0.41] 0.9%
Renibacterium salmoninarum −1.28 [−3.55; 0.99] 0.6%
Rickettsia−like Organism −0.81 [−6.11; 4.50] 0.1%
Rickettsia−like Organism −0.63 [−1.62; 0.35] 1.7%
Ichthyophthirius multifiliis −0.38 [−0.75; −0.02] 2.7%
Flavobacterium psychrophilum −0.11 [−0.52; 0.31] 2.6%
Candidatus Branchiomonas cysticola 0.24 [−0.08; 0.55] 2.7%
Renibacterium salmoninarum 0.25 [−0.88; 1.37] 1.5%
Ichthyophthirius multifiliis 0.32 [−0.45; 1.09] 2.0%
Pacific Salmon Nidovirus 0.43 [−0.09; 0.95] 2.4%
Candidatus Branchiomonas cysticola 0.76 [−0.21; 1.72] 1.7%
Random effects model (95%−CI) −0.02 [−0.35; 0.32] 18.9%
Transmission_complexity = saltwater_complex
Putative RNA Virus 1 −1.08 [−3.19; 1.04] 0.7%
Ichthyophonus hoferi −0.52 [−1.13; 0.10] 2.3%
Parvicapsula kabatai −0.41 [−1.20; 0.38] 2.0%
Parvicapsula pseudobranchicola −0.12 [−0.51; 0.28] 2.6%
Facilispora margolisi −0.08 [−0.73; 0.57] 2.2%
Ichthyophonus hoferi −0.02 [−0.43; 0.40] 2.6%
Kudoa thyrsites 0.01 [−0.87; 0.89] 1.8%
Paranucleospora theridion 0.02 [−0.39; 0.43] 2.6%
Paranucleospora theridion 0.19 [−0.10; 0.47] 2.8%
Facilispora margolisi 0.36 [−0.16; 0.87] 2.4%
Parvicapsula kabatai 0.36 [−0.02; 0.74] 2.7%
Kudoa thyrsites 0.78 [0.34; 1.22] 2.6%
Parvicapsula pseudobranchicola 0.88 [0.52; 1.24] 2.7%
Random effects model (95%−CI) 0.13 [−0.12; 0.37] 30.0%
Transmission_complexity = saltwater_simple
Sphaerothecum destruens −1.12 [−2.24; 0.00] 1.5%
Salmon Pescarenavirus 1 −0.59 [−1.44; 0.26] 1.9%
Loma salmonae −0.35 [−0.67; −0.02] 2.7%
Sphaerothecum destruens −0.26 [−1.67; 1.15] 1.1%
Tenacibaculum maritimum −0.24 [−1.07; 0.60] 1.9%
Candidatus Syngnamydia salmonis −0.13 [−0.42; 0.16] 2.8%
Loma salmonae −0.11 [−0.53; 0.30] 2.6%
Piscine Orthoreovirus −0.09 [−1.00; 0.83] 1.8%
Erythrocytic Necrosis Virus −0.08 [−0.69; 0.53] 2.3%
Erythrocytic Necrosis Virus −0.04 [−0.50; 0.42] 2.5%
Tenacibaculum maritimum 0.07 [−0.53; 0.67] 2.3%
Candidatus Syngnamydia salmonis 0.30 [−0.12; 0.72] 2.6%
Piscine Orthoreovirus 1.45 [0.21; 2.69] 1.3%
Random effects model (95%−CI) −0.10 [−0.35; 0.16] 27.4%
Random effects model (95%−CI) −0.01 [−0.15; 0.14] 100.0%
Test for subgroup differences: χ^2_3 = 1.64, df = 3 (p = 0.65)
−3 −2 −1 0 1 2 3
CE for fin clip (left=unmarked, right=adipose−clipped)

Figure S5

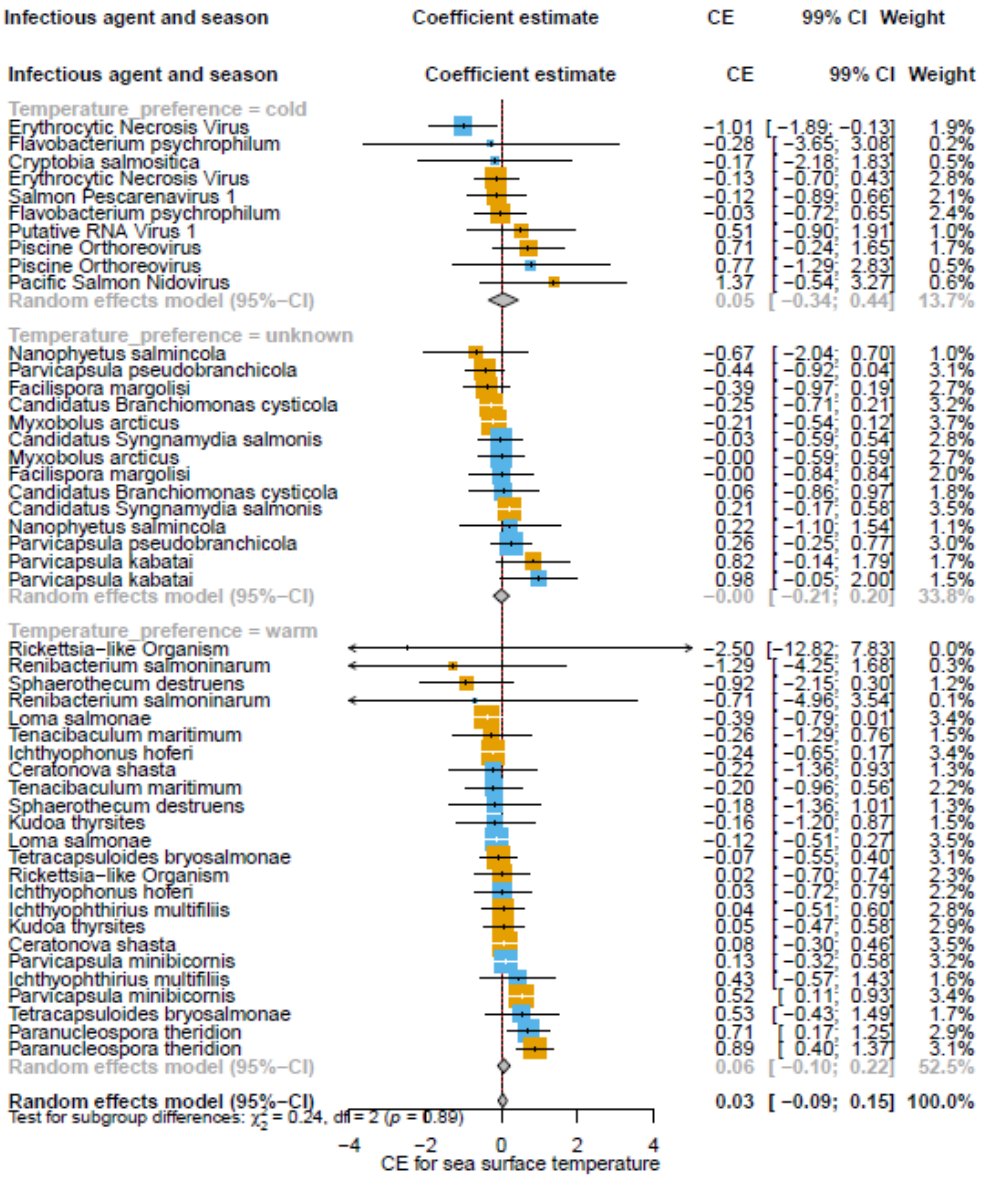
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Temperature_preference = cold
Erythrocytic Necrosis Virus −1.01 [−1.89; −0.13] 1.9%
Flavobacterium psychrophilum −0.28 [−3.65; 3.08] 0.2%
Cryptobia salmositica −0.17 [−2.18; 1.83] 0.5%
Erythrocytic Necrosis Virus −0.13 [−0.70; 0.43] 2.8%
Salmon Pescarenavirus 1 −0.12 [−0.89; 0.66] 2.1%
Flavobacterium psychrophilum −0.03 [−0.72; 0.65] 2.4%
Putative RNA Virus 1 0.51 [−0.90; 1.91] 1.0%
Piscine Orthoreovirus 0.71 [−0.24; 1.65] 1.7%
Piscine Orthoreovirus 0.77 [−1.29; 2.83] 0.5%
Pacific Salmon Nidovirus 1.37 [−0.54; 3.27] 0.6%
Random effects model (95%−CI) 0.05 [−0.34; 0.44] 13.7%
Temperature_preference = unknown
Nanophyetus salmincola −0.67 [−2.04; 0.70] 1.0%
Parvicapsula pseudobranchicola −0.44 [−0.92; 0.04] 3.1%
Facilispora margolisi −0.39 [−0.97; 0.19] 2.7%
Candidatus Branchiomonas cysticola −0.25 [−0.71; 0.21] 3.2%
Myxobolus arcticus −0.21 [−0.54; 0.12] 3.7%
Candidatus Syngnamydia salmonis −0.03 [−0.59; 0.54] 2.8%
Myxobolus arcticus −0.00 [−0.59; 0.59] 2.7%
Facilispora margolisi −0.00 [−0.84; 0.84] 2.0%
Candidatus Branchiomonas cysticola 0.06 [−0.86; 0.97] 1.8%
Candidatus Syngnamydia salmonis 0.21 [−0.17; 0.58] 3.5%
Nanophyetus salmincola 0.22 [−1.10; 1.54] 1.1%
Parvicapsula pseudobranchicola 0.26 [−0.25; 0.77] 3.0%
Parvicapsula kabatai 0.82 [−0.14; 1.79] 1.7%
Parvicapsula kabatai 0.98 [−0.05; 2.00] 1.5%
Random effects model (95%−CI) −0.00 [−0.21; 0.20] 33.8%
Temperature_preference = warm
Rickettsia−like Organism −2.50 [−12.82; 7.83] 0.0%
Renibacterium salmoninarum −1.29 [−4.25; 1.68] 0.3%
Sphaerothecum destruens −0.92 [−2.15; 0.30] 1.2%
Renibacterium salmoninarum −0.71 [−4.96; 3.54] 0.1%
Loma salmonae −0.39 [−0.79; 0.01] 3.4%
Tenacibaculum maritimum −0.26 [−1.29; 0.76] 1.5%
Ichthyophonus hoferi −0.24 [−0.65; 0.17] 3.4%
Ceratonova shasta −0.22 [−1.36; 0.93] 1.3%
Tenacibaculum maritimum −0.20 [−0.96; 0.56] 2.2%
Sphaerothecum destruens −0.18 [−1.36; 1.01] 1.3%
Kudoa thyrsites −0.16 [−1.20; 0.87] 1.5%
Loma salmonae −0.12 [−0.51; 0.27] 3.5%
Tetracapsuloides bryosalmonae −0.07 [−0.55; 0.40] 3.1%
Rickettsia−like Organism 0.02 [−0.70; 0.74] 2.3%
Ichthyophonus hoferi 0.03 [−0.72; 0.79] 2.2%
Ichthyophthirius multifiliis 0.04 [−0.51; 0.60] 2.8%
Kudoa thyrsites 0.05 [−0.47; 0.58] 2.9%
Ceratonova shasta 0.08 [−0.30; 0.46] 3.5%
Parvicapsula minibicornis 0.13 [−0.32; 0.58] 3.2%
Ichthyophthirius multifiliis 0.43 [−0.57; 1.43] 1.6%
Parvicapsula minibicornis 0.52 [0.11; 0.93] 3.4%
Tetracapsuloides bryosalmonae 0.53 [−0.43; 1.49] 1.7%
Paranucleospora theridion 0.71 [0.17; 1.25] 2.9%
Paranucleospora theridion 0.89 [0.40; 1.37] 3.1%
Random effects model (95%−CI) 0.06 [−0.10; 0.22] 52.5%
Random effects model (95%−CI) 0.03 [−0.09; 0.15] 100.0%
Test for subgroup differences: χ^2_2 = 0.24, df = 2 (p = 0.89)
−4
−2
0
2
4
CE for sea surface temperature

Figure S6

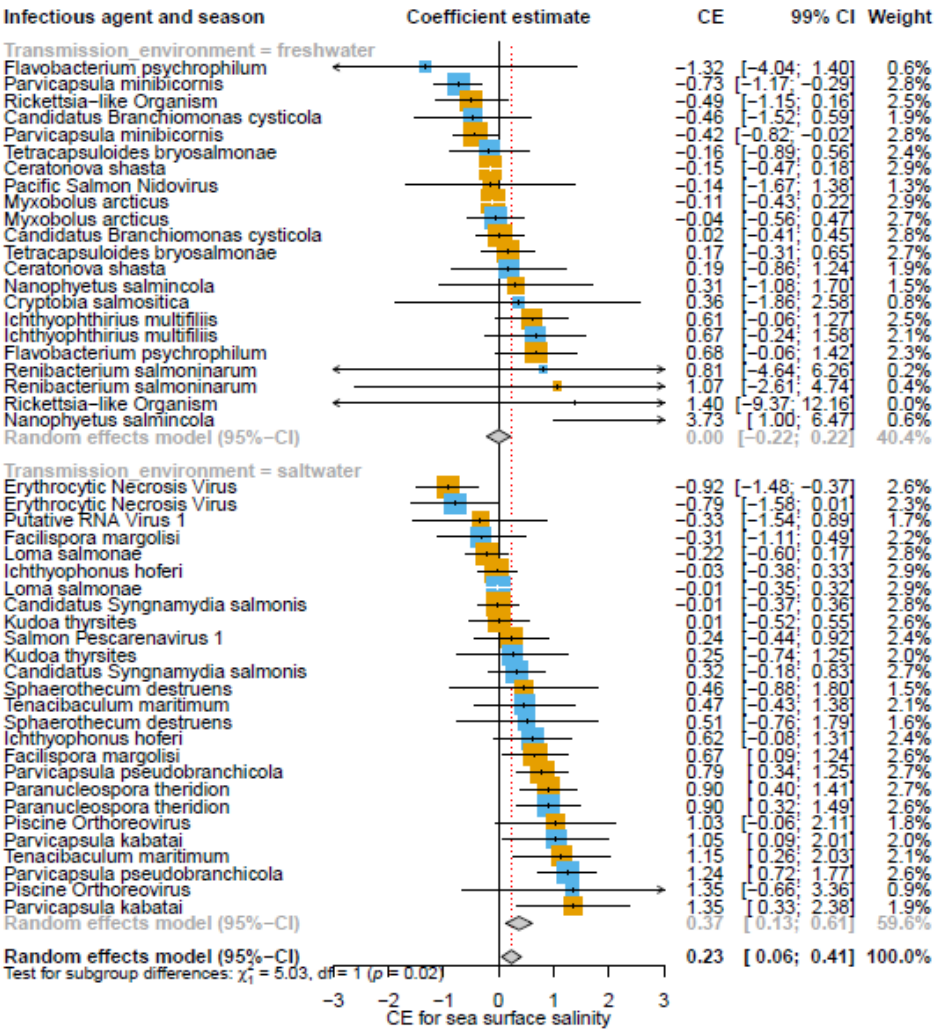
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Transmission_environment = freshwater
Flavobacterium psychrophilum −1.32 [−4.04; 1.40] 0.6%
Parvicapsula minibicornis −0.73 [−1.17; −0.29] 2.8%
Rickettsia−like Organism −0.49 [−1.15; 0.16] 2.5%
Candidatus Branchiomonas cysticola −0.46 [−1.52; 0.59] 1.9%
Parvicapsula minibicornis −0.42 [−0.82; −0.02] 2.8%
Tetracapsuloides bryosalmonae −0.16 [−0.89; 0.56] 2.4%
Ceratonova shasta −0.15 [−0.47; 0.18] 2.9%
Pacific Salmon Nidovirus −0.14 [−1.67; 1.38] 1.3%
Myxobolus arcticus −0.11 [−0.43; 0.22] 2.9%
Myxobolus arcticus −0.04 [−0.56; 0.47] 2.7%
Candidatus Branchiomonas cysticola 0.02 [−0.41; 0.45] 2.8%
Tetracapsuloides bryosalmonae 0.17 [−0.31; 0.65] 2.7%
Ceratonova shasta 0.19 [−0.86; 1.24] 1.9%
Nanophyetus salmincola 0.31 [−1.08; 1.70] 1.5%
Cryptobia salmositica 0.36 [−1.86; 2.58] 0.8%
Ichthyophthirius multifiliis 0.61 [−0.06; 1.27] 2.5%
Ichthyophthirius multifiliis 0.67 [−0.24; 1.58] 2.1%
Flavobacterium psychrophilum 0.68 [−0.06; 1.42] 2.3%
Renibacterium salmoninarum 0.81 [−4.64; 6.26] 0.2%
Renibacterium salmoninarum 1.07 [−2.61; 4.74] 0.4%
Rickettsia−like Organism 1.40 [−9.37; 12.16] 0.0%
Nanophyetus salmincola 3.73 [1.00; 6.47] 0.6%
Random effects model (95%−CI) 0.00 [−0.22; 0.22] 40.4%
Transmission_environment = saltwater
Erythrocytic Necrosis Virus −0.92 [−1.48; −0.37] 2.6%
Erythrocytic Necrosis Virus −0.79 [−1.58; 0.01] 2.3%
Putative RNA Virus 1 −0.33 [−1.54; 0.89] 1.7%
Facilispora margolisi −0.31 [−1.11; 0.49] 2.2%
Loma salmonae −0.22 [−0.60; 0.17] 2.8%
Ichthyophonus hoferi −0.03 [−0.38; 0.33] 2.9%
Loma salmonae −0.01 [−0.35; 0.32] 2.9%
Candidatus Syngnamydia salmonis −0.01 [−0.37; 0.36] 2.8%
Kudoa thyrsites 0.01 [−0.52; 0.55] 2.6%
Salmon Pescarenavirus 1 0.24 [−0.44; 0.92] 2.4%
Kudoa thyrsites 0.25 [−0.74; 1.25] 2.0%
Candidatus Syngnamydia salmonis 0.32 [−0.18; 0.83] 2.7%
Sphaerothecum destruens 0.46 [−0.88; 1.80] 1.5%
Tenacibaculum maritimum 0.47 [−0.43; 1.38] 2.1%
Sphaerothecum destruens 0.51 [−0.76; 1.79] 1.6%
Ichthyophonus hoferi 0.62 [−0.08; 1.31] 2.4%
Facilispora margolisi 0.67 [0.09; 1.24] 2.6%
Parvicapsula pseudobranchicola 0.79 [0.34; 1.25] 2.7%
Paranucleospora theridion 0.90 [0.40; 1.41] 2.7%
Paranucleospora theridion 0.90 [0.32; 1.49] 2.6%
Piscine Orthoreovirus 1.03 [−0.06; 2.11] 1.8%
Parvicapsula kabatai 1.05 [0.09; 2.01] 2.0%
Tenacibaculum maritimum 1.15 [0.26; 2.03] 2.1%
Parvicapsula pseudobranchicola 1.24 [0.72; 1.77] 2.6%
Piscine Orthoreovirus 1.35 [−0.66; 3.36] 0.9%
Parvicapsula kabatai 1.35 [0.33; 2.38] 1.9%
Random effects model (95%−CI) 0.37 [0.13; 0.61] 59.6%
Random effects model (95%−CI) 0.23 [0.06; 0.41] 100.0%
Test for subgroup differences: χ^2_1 = 5.03, df = 1 (p = 0.02)
−3
−2
−1
0
1
2
3
CE for sea surface salinity

Figure S7

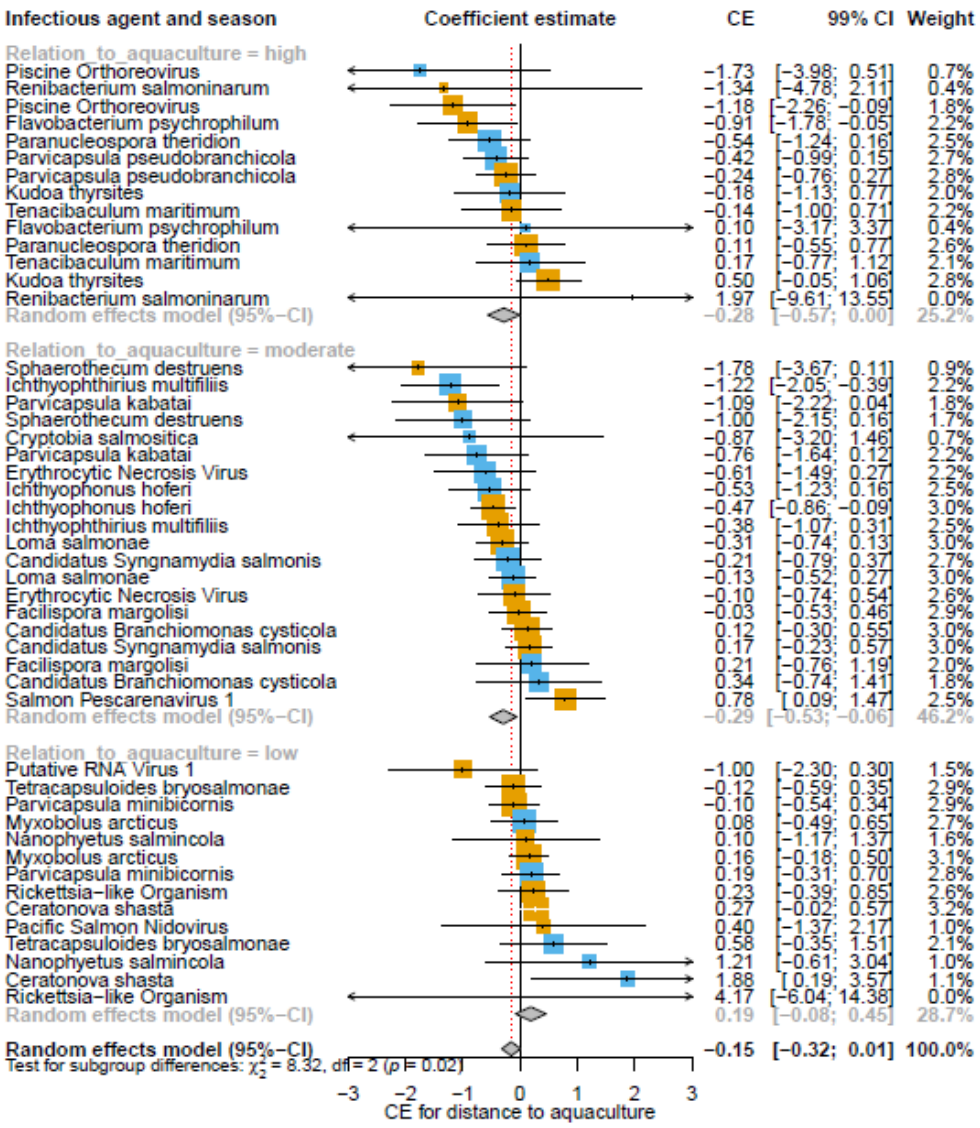
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Relation_to_aquaculture = high
Piscine Orthoreovirus −1.73 [−3.98; 0.51] 0.7%
Renibacterium salmoninarum −1.34 [−4.78; 2.11] 0.4%
Piscine Orthoreovirus −1.18 [−2.26; −0.09] 1.8%
Flavobacterium psychrophilum −0.91 [−1.78; −0.05] 2.2%
Paranucleospora theridion −0.54 [−1.24; 0.16] 2.5%
Parvicapsula pseudobranchicola −0.42 [−0.99; 0.15] 2.7%
Parvicapsula pseudobranchicola −0.24 [−0.76; 0.27] 2.8%
Kudoa thyrsites −0.18 [−1.13; 0.77] 2.0%
Tenacibaculum maritimum −0.14 [−1.00; 0.71] 2.2%
Flavobacterium psychrophilum 0.10 [−3.17; 3.37] 0.4%
Paranucleospora theridion 0.11 [−0.55; 0.77] 2.6%
Tenacibaculum maritimum 0.17 [−0.77; 1.12] 2.1%
Kudoa thyrsites 0.50 [−0.05; 1.06] 2.8%
Renibacterium salmoninarum 1.97 [−9.61; 13.55] 0.0%
Random effects model (95%−CI) −0.28 [−0.57; 0.00] 25.2%
Relation_to_aquaculture = moderate
Sphaerothecum destruens −1.78 [−3.67; 0.11] 0.9%
Ichthyophthirius multifiliis −1.22 [−2.05; −0.39] 2.2%
Parvicapsula kabatai −1.09 [−2.22; 0.04] 1.8%
Sphaerothecum destruens −1.00 [−2.15; 0.16] 1.7%
Cryptobia salmositica −0.87 [−3.20; 1.46] 0.7%
Parvicapsula kabatai −0.76 [−1.64; 0.12] 2.2%
Erythrocytic Necrosis Virus −0.61 [−1.49; 0.27] 2.2%
Ichthyophonus hoferi −0.53 [−1.23; 0.16] 2.5%
Ichthyophonus hoferi −0.47 [−0.86; −0.09] 3.0%
Ichthyophthirius multifiliis −0.38 [−1.07; 0.31] 2.5%
Loma salmonae −0.31 [−0.74; 0.13] 3.0%
Candidatus Syngnamydia salmonis −0.21 [−0.79; 0.37] 2.7%
Loma salmonae −0.13 [−0.52; 0.27] 3.0%
Erythrocytic Necrosis Virus −0.10 [−0.74; 0.54] 2.6%
Facilispora margolisi −0.03 [−0.53; 0.46] 2.9%
Candidatus Branchiomonas cysticola 0.12 [−0.30; 0.55] 3.0%
Candidatus Syngnamydia salmonis 0.17 [−0.23; 0.57] 3.0%
Facilispora margolisi 0.21 [−0.76; 1.19] 2.0%
Candidatus Branchiomonas cysticola 0.34 [−0.74; 1.41] 1.8%
Salmon Pescarenavirus 1 0.78 [0.09; 1.47] 2.5%
Random effects model (95%−CI) −0.29 [−0.53; −0.06] 46.2%
Relation_to_aquaculture = low
Putative RNA Virus 1 −1.00 [−2.30; 0.30] 1.5%
Tetracapsuloides bryosalmonae −0.12 [−0.59; 0.35] 2.9%
Parvicapsula minibicornis −0.10 [−0.54; 0.34] 2.9%
Myxobolus arcticus 0.08 [−0.49; 0.65] 2.7%
Nanophyetus salmincola 0.10 [−1.17; 1.37] 1.6%
Myxobolus arcticus 0.16 [−0.18; 0.50] 3.1%
Parvicapsula minibicornis 0.19 [−0.31; 0.70] 2.8%
Rickettsia−like Organism 0.23 [−0.39; 0.85] 2.6%
Ceratonova shasta 0.27 [−0.02; 0.57] 3.2%
Pacific Salmon Nidovirus 0.40 [−1.37; 2.17] 1.0%
Tetracapsuloides bryosalmonae 0.58 [−0.35; 1.51] 2.1%
Nanophyetus salmincola 1.21 [−0.61; 3.04] 1.0%
Ceratonova shasta 1.88 [0.19; 3.57] 1.1%
Rickettsia−like Organism 4.17 [−6.04; 14.38] 0.0%
Random effects model (95%−CI) 0.19 [−0.08; 0.45] 28.7%
Random effects model (95%−CI) −0.15 [−0.32; 0.01] 100.0%
Test for subgroup differences: χ^2_2 = 8.32, df = 2 (p = 0.02)
−3 −2 −1 0 1 2 3
CE for distance to aquaculture

Figure S8

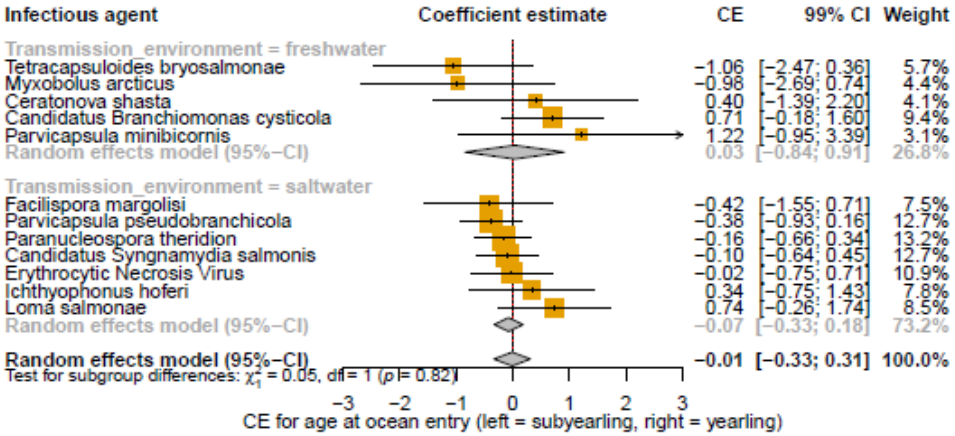
Infectious agent
Coefficient estimate
CE
99% CI
Weight
Transmission_environment = freshwater
Tetracapsuloides bryosalmonae −1.06 [−2.47; 0.36] 5.7%
Myxobolus arcticus −0.98 [−2.69; 0.74] 4.4%
Ceratonova shasta 0.40 [−1.39; 2.20] 4.1%
Candidatus Branchiomonas cysticola 0.71 [−0.18; 1.60] 9.4%
Parvicapsula minibicornis 1.22 [−0.95; 3.39] 3.1%
Random effects model (95%−CI) 0.03 [−0.84; 0.91] 26.8%
Transmission_environment = saltwater
Facilispora margolisi −0.42 [−1.55; 0.71] 7.5%
Parvicapsula pseudobranchicola −0.38 [−0.93; 0.16] 12.7%
Paranucleospora theridion −0.16 [−0.66; 0.34] 13.2%
Candidatus Syngnamydia salmonis −0.10 [−0.64; 0.45] 12.7%
Erythrocytic Necrosis Virus −0.02 [−0.75; 0.71] 10.9%
Ichthyophonus hoferi 0.34 [−0.75; 1.43] 7.8%
Loma salmonae 0.74 [−0.26; 1.74] 8.5%
Random effects model (95%−CI) −0.07 [−0.33; 0.18] 73.2%
Random effects model (95%−CI) −0.01 [−0.33; 0.31] 100.0%
Test for subgroup differences: χ^2_1 = 0.05, df = 1 (p = 0.82)
−3 −2 −1 0 1 2 3
CE for age at ocean entry (left = subyearling, right = yearling)

Figure S9

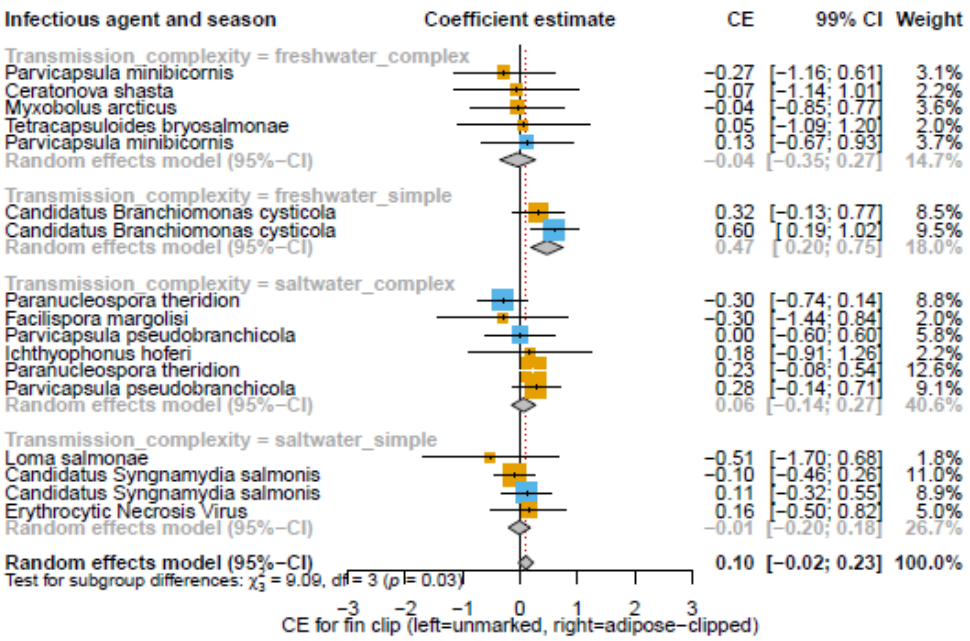
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Transmission_complexity = freshwater_complex
Parvicapsula minibicornis −0.27 [−1.16; 0.61] 3.1%
Ceratonova shasta −0.07 [−1.14; 1.01] 2.2%
Myxobolus arcticus −0.04 [−0.85; 0.77] 3.6%
Tetracapsuloides bryosalmonae 0.05 [−1.09; 1.20] 2.0%
Parvicapsula minibicornis 0.13 [−0.67; 0.93] 3.7%
Random effects model (95%−CI) −0.04 [−0.35; 0.27] 14.7%
Transmission_complexity = freshwater_simple
Candidatus Branchiomonas cysticola 0.32 [−0.13; 0.77] 8.5%
Candidatus Branchiomonas cysticola 0.60 [0.19; 1.02] 9.5%
Random effects model (95%−CI) 0.47 [0.20; 0.75] 18.0%
Transmission_complexity = saltwater_complex
Paranucleospora theridion −0.30 [−0.74; 0.14] 8.8%
Facilispora margolisi −0.30 [−1.44; 0.84] 2.0%
Parvicapsula pseudobranchicola 0.00 [−0.60; 0.60] 5.8%
Ichthyophonus hoferi 0.18 [−0.91; 1.26] 2.2%
Paranucleospora theridion 0.23 [−0.08; 0.54] 12.6%
Parvicapsula pseudobranchicola 0.28 [−0.14; 0.71] 9.1%
Random effects model (95%−CI) 0.06 [−0.14; 0.27] 40.6%
Transmission_complexity = saltwater_simple
Loma salmonae −0.51 [−1.70; 0.68] 1.8%
Candidatus Syngnamydia salmonis −0.10 [−0.46; 0.26] 11.0%
Candidatus Syngnamydia salmonis 0.11 [−0.32; 0.55] 8.9%
Erythrocytic Necrosis Virus 0.16 [−0.50; 0.82] 5.0%
Random effects model (95%−CI) −0.01 [−0.20; 0.18] 26.7%
Random effects model (95%−CI) 0.10 [−0.02; 0.23] 100.0%
Test for subgroup differences: χ^2_3 = 9.09, df = 3 (p = 0.03)
−3 −2 −1 0 1 2 3
CE for fin clip (left=unmarked, right=adipose−clipped)

Figure S10

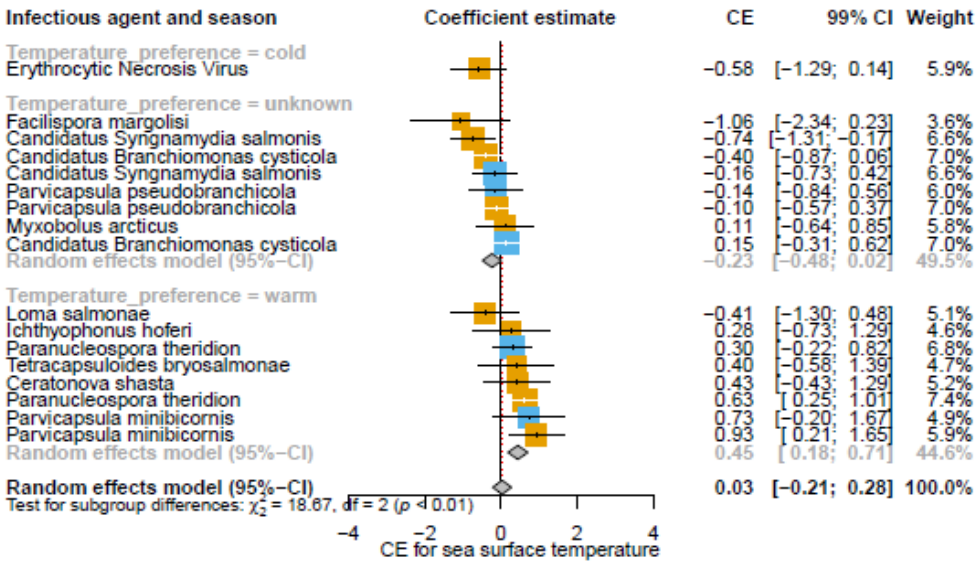
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Temperature_preference = cold
Erythrocytic Necrosis Virus −0.58 [−1.29; 0.14] 5.9%
Temperature_preference = unknown
Facilispora margolisi −1.06 [−2.34; 0.23] 3.6%
Candidatus Syngnamydia salmonis −0.74 [−1.31; −0.17] 6.6%
Candidatus Branchiomonas cysticola −0.40 [−0.87; 0.06] 7.0%
Candidatus Syngnamydia salmonis −0.16 [−0.73; 0.42] 6.6%
Parvicapsula pseudobranchicola −0.14 [−0.84; 0.56] 6.0%
Parvicapsula pseudobranchicola −0.10 [−0.57; 0.37] 7.0%
Myxobolus arcticus 0.11 [−0.64; 0.85] 5.8%
Candidatus Branchiomonas cysticola 0.15 [−0.31; 0.62] 7.0%
Random effects model (95%−CI) −0.23 [−0.48; 0.02] 49.5%
Temperature_preference = warm
Loma salmonae −0.41 [−1.30; 0.48] 5.1%
Ichthyophonus hoferi 0.28 [−0.73; 1.29] 4.6%
Paranucleospora theridion 0.30 [−0.22; 0.82] 6.8%
Tetracapsuloides bryosalmonae 0.40 [−0.58; 1.39] 4.7%
Ceratonova shasta 0.43 [−0.43; 1.29] 5.2%
Paranucleospora theridion 0.63 [0.25; 1.01] 7.4%
Parvicapsula minibicornis 0.73 [−0.20; 1.67] 4.9%
Parvicapsula minibicornis 0.93 [0.21; 1.65] 5.9%
Random effects model (95%−CI) 0.45 [0.18; 0.71] 44.6%
Random effects model (95%−CI) 0.03 [−0.21; 0.28] 100.0%
Test for subgroup differences: χ^2_2 = 18.67, df = 2 (p < 0.01)
−4
−2
0
2
4
CE for sea surface temperature

Figure S11

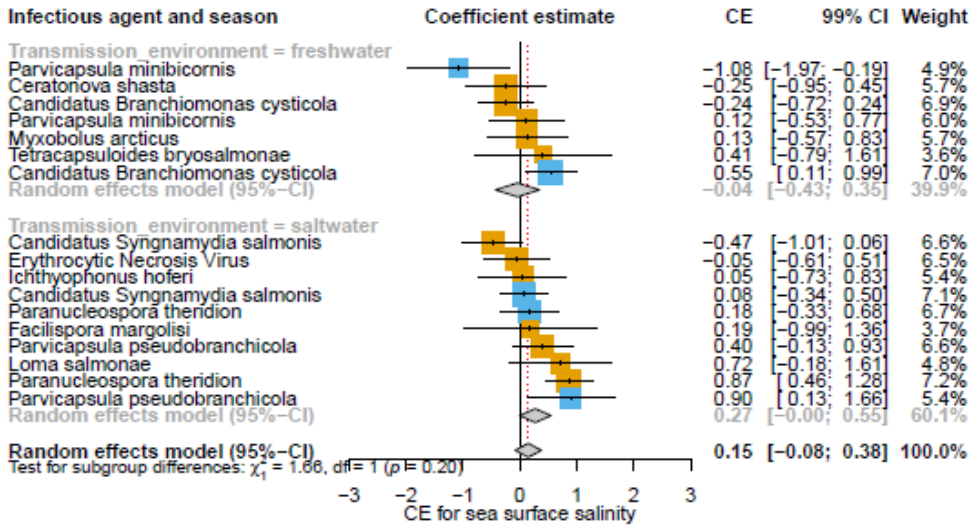
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Transmission_environment = freshwater
Parvicapsula minibicornis −1.08 [−1.97; −0.19] 4.9%
Ceratonova shasta −0.25 [−0.95; 0.45] 5.7%
Candidatus Branchiomonas cysticola −0.24 [−0.72; 0.24] 6.9%
Parvicapsula minibicornis 0.12 [−0.53; 0.77] 6.0%
Myxobolus arcticus 0.13 [−0.57; 0.83] 5.7%
Tetracapsuloides bryosalmonae 0.41 [−0.79; 1.61] 3.6%
Candidatus Branchiomonas cysticola 0.55 [0.11; 0.99] 7.0%
Random effects model (95%−CI) −0.04 [−0.43; 0.35] 39.9%
Transmission_environment = saltwater
Candidatus Syngnamydia salmonis −0.47 [−1.01; 0.06] 6.6%
Erythrocytic Necrosis Virus −0.05 [−0.61; 0.51] 6.5%
Ichthyophonus hoferi 0.05 [−0.73; 0.83] 5.4%
Candidatus Syngnamydia salmonis 0.08 [−0.34; 0.50] 7.1%
Paranucleospora theridion 0.18 [−0.33; 0.68] 6.7%
Facilispora margolisi 0.19 [−0.99; 1.36] 3.7%
Parvicapsula pseudobranchicola 0.40 [−0.13; 0.93] 6.6%
Loma salmonae 0.72 [−0.18; 1.61] 4.8%
Paranucleospora theridion 0.87 [0.46; 1.28] 7.2%
Parvicapsula pseudobranchicola 0.90 [0.13; 1.66] 5.4%
Random effects model (95%−CI) 0.27 [−0.00; 0.55] 60.1%
Random effects model (95%−CI) 0.15 [−0.08; 0.38] 100.0%
Test for subgroup differences: χ^2_1 = 1.66, df = 1 (p = 0.20)
−3 −2 −1 0 1 2 3
CE for sea surface salinity

Figure S12

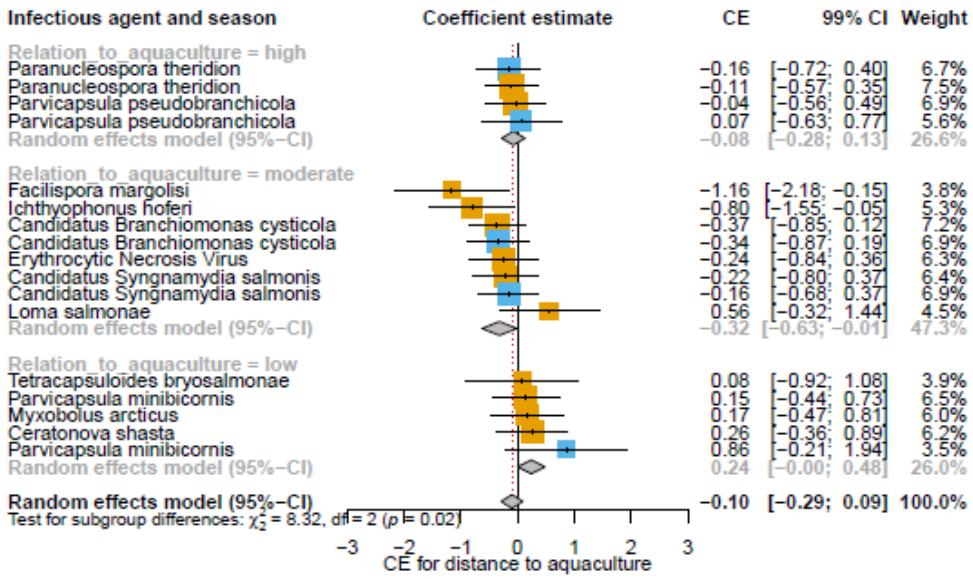
Infectious agent and season
Coefficient estimate
CE
99% CI
Weight
Relation_to_aquaculture = high
Paranucleospora theridion −0.16 [−0.72; 0.40] 6.7%
Paranucleospora theridion −0.11 [−0.57; 0.35] 7.5%
Parvicapsula pseudobranchicola −0.04 [−0.56; 0.49] 6.9%
Parvicapsula pseudobranchicola 0.07 [−0.63; 0.77] 5.6%
Random effects model (95%−CI) −0.08 [−0.28; 0.13] 26.6%
Relation_to_aquaculture = moderate
Facilispora margolisi −1.16 [−2.18; −0.15] 3.8%
Ichthyophonus hoferi −0.80 [−1.55; −0.05] 5.3%
Candidatus Branchiomonas cysticola −0.37 [−0.85; 0.12] 7.2%
Candidatus Branchiomonas cysticola −0.34 [−0.87; 0.19] 6.9%
Erythrocytic Necrosis Virus −0.24 [−0.84; 0.36] 6.3%
Candidatus Syngnamydia salmonis −0.22 [−0.80; 0.37] 6.4%
Candidatus Syngnamydia salmonis −0.16 [−0.68; 0.37] 6.9%
Loma salmonae 0.56 [−0.32; 1.44] 4.5%
Random effects model (95%−CI) −0.32 [−0.63; −0.01] 47.3%
Relation_to_aquaculture = low
Tetracapsuloides bryosalmonae 0.08 [−0.92; 1.08] 3.9%
Parvicapsula minibicornis 0.15 [−0.44; 0.73] 6.5%
Myxobolus arcticus 0.17 [−0.47; 0.81] 6.0%
Ceratonova shasta 0.26 [−0.36; 0.89] 6.2%
Parvicapsula minibicornis 0.86 [−0.21; 1.94] 3.5%
Random effects model (95%−CI) 0.24 [−0.00; 0.48] 26.0%
Random effects model (95%−CI) −0.10 [−0.29; 0.09] 100.0%
Test for subgroup differences: χ^2_2 = 8.32, df = 2 (p = 0.02)
−3
−2
−1
0
1
2
3
CE for distance to aquaculture

Figure S13