Supplementary Material 1

"Identification of infectious agents in early marine Chinook and Coho salmon associated with cohort survival"

Arthur L. Bass, Andrew W. Bateman, Brendan M. Connors, Benjamin A. Staton, Eric B. Rondeau, Gideon J. Mordecai, Amy K. Teffer, Karia H. Kaukinen, Shaorong Li, Amy M. Tabata, David A. Patterson, Scott G. Hinch, Kristina M. Miller

Detailed molecular methods

Tissue samples were screened for the presence of 59 infectious agent taxa (Table 1), using HT-qPCR on the Fluidigm Biomark Dynamic Array^{TM} 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^{TM} (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^{TM}-96 for Microarrays Total RNA Isolation Kits (Ambion Inc.) with a Biomek NXP^{TM} 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 (1 µg) 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 (7 nL) and therefore a pre-amplification step is recommended by the manufacturer. Thus, 0.2 µmol/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^{TM} (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^{TM} reporter dye (Life Technologies) that allowed for the detection of vector contamination (see Miller et al. 2016).

A 5 µL 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 10 µM primers (infectious agent in FAM-MGB and APC in NED-MGB) and 3 µM 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.

Supplementary Tables

Table S1: Taqman assays run for 59 infectious agents and 3 host reference genes 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 Ct value, positive samples are detected 95% of the time.

Scientific Name	abbreviation	Limit of Detection (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	GATCCTTATTCTCACAGTACC GTCAA	TGTAAACTGCTTTTGCACAG GAA	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	CAACAGGGTGGTTATTCTGC TTTC	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	CCGTCATGCTATCTAGAGATGTA TTTGA	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 hoferi	ic_hof	24.2	GTCTGTACTGGTACGGCAGTTTC	TCCCGAACTCAGTAGACACTCAA	TAAGAGCACCCACTGCCTTCGAGAAGA
Sphaerothecum destruens	sp_des	26.5	GGGTATCCTTCCTCTCGAAATTG	CCCAAACTCGACGCACACT	CGTGTGCGCTTAAT
Facilispora margolisi	fa_mar	30.6	AGGAAGGAGCACGCAAGAAC	CGCGTGCAGCCCAGTAC	TCAGTGATGCCCTCAGA
Loma salmonae	lo_sal	25.4	GGAGTCGCAGCGAAGATAGC	CTTTTCCTCCCTTTACTCATA TGCTT	TGCCTGAAATCACGAGAGTGAGACTACCC

Nucleospora salmonis	nuc_sal	26.1	GCCGCAGATCATTACTAAAAA CCT	CGATCGCCGCATCTAAACA	CCCCGCGCATCCAGAAATACGC
Paranucleospora theridion (syn. *Desmozoon lepeophtherii*)	pa_ther	28.2	CGGACAGGGAGCATGGTATAG	GGTCCAGGTTGGGTCTTGAG	TTGGCGAAGAATGAAA
Ceratonova shasta	ce_sha	28.5	CCAGCTTGAGATTAGCTCGGTAA	CCCCGGAACCCGAAAG	CGAGCCAAGTTGGTCTCTCCGTGA AAAC
Kudoa thyristes	ku_thy	26.2	TGGCGGCCAAATCTAGGTT	GACCGCACACAAGAAGTTAATCC	TATCGCGAGAGCCGC
Myxobolus arcticus	my_arc	26.8	TGGTAGATACTGAATATCCGG GTTT	AACTGCGCGGTCAAAGTTG	CGTTGATTGTGAGGTTGG
Myxobolus cerebalis	my_cer	26.2	GCCATTGAATTTGACTTTGG ATTA	ACCATTCATGTAAGCCCGAACT	TCGAAGCCTTGACCATCTTTTGGCC
Myxobolus insidiosus	my_ins	26.4	CCAATTTGGGAGCGTCAAA	CGATCGGCAAAGTTATCTAG ATTCA	CTCTCAAGGCATTTAT
Parvicapsula kabatai	pa_kab	25.6	CGACCATCTGCACGGTACTG	ACACCACAACTCTGCCTTCCA	CTTCGGGTAGGTCCGG
Parvicapsula minibicornis	pa_min	29.6	AATAGTTGTTTGTCGTGCAC TCTGT	CCGATAGGCTATCCAGTACCT AGTAAG	TGTCCACCTAGTAAGGC
Parvicapsula pseudobranchicola	pa_pse	25.2	CAGCTCCAGTAGTGTATTTCA	TTGAGCACTCTGCTTTATTCAA	CGTATTGCTGTCTTTGACATGCAGT
Tetracapsuloides bryosalmonae	te_bry	25.0	GCGAGATTTGTTGCATTTAA AAAG	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 ATTTTT	ACTCGGCCTTCACTGGTTCGACTTGG
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	CCCATATTAGCAAATGAGCTCT ATCTT	CGTTAAGGAACTCATCATTG AGCTT	AGCCCTTTTGTTCTGC
Chinook aquareovirus	reov		AACTTTCGGCTTTCTGCTATGC	GAGGACAAGGGTCTCCATCTGA	TTAATTGCGGTACTGCTC
Cutthroat trout virus 2	ctv		CCACTTGTCGCTACGATGAAAC	ATGCCGGGCCATC	CGCCTCCTTTGCCTTTCTC

Erythrocytic necrosis virus	ven	24.9	CGTAGGGCCCCAATAGTTTCT	GGAGGAAATGCAGACAAGATTTG	TCTTGCCGTTATTTCCAGCACCCG
Infectious hematopoietic necrosis virus	ihnv	27.6	AGAGCCAAGGCACTGTGCG	TTCTTTGCGGCTTGGTTGA	TGAGACTGAGCGGGACA
Infectious pancreatic necrosis virus	ipnv	27.6	GCAACTTACTTGAGATCCAT TATGCT	AGACCTCTAAGTTGTATGAC GAGGTCTCT	CGAGAATGGGCCAGCAAGCA
Infectious salmon anemia virus 7	isa7	27.0	TGGGATCATGTGTTTCCTGCTA	GAAAATCCATGTTCTCA GATG-CAA	CACATGACCCCTCGTC
Infectious salmon anemia virus 8	isa8	26.1	TGGGCAATGGTGTATGGTATGA	GAAGTCGATGAACTGCAGCGA	CAGGATGCAGATGTATGC
Pacific salmon nidovirus	cov		GGATAATCCCAACCGAAAAGTTT	GCATGAAATGTTGTCTCGGT TTAA	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		GTACCTAATTTAACTGGAACAG TAGAC	TGCAACAGGCAAGTGATAT GCTTGA	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	AGAAAAAGCTGTGGTACTTT AGAAAGC	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	TGTAGTAGGACTCTCCCAG CATCC	TACGCCATCATGATGAGT
78d16.1	reference gene	NA	GTCAAGACTGGAGGCTCAGAG	GATCAAGCCCCAGAAGTGTTTG	AAGGTGATTCCCTCGCCGTCCGA
COIL-P84-2	reference gene	NA	GCTCATTTGAGGAGAAGGA GGATG	CTGGCGATGCTGTTCCTGAG	TTATCAAGCAGCAAGCC

MRPL40	reference gene	NA	CCCAGTATGAGGCACCTGAAGG	GTTAATGCTGCCACCCTCTCAC	ACAACAACATCACCA

Table S2: Coded-wire tagged (CWT) stocks were matched to Conservation Units (CUs, Fisheries and Oceans Canada 2009) and their constituent populations as determined by genetic stock identification (GSI, Beacham et al. 2006, 2020). Location of CWT stocks are displayed in Figure **??**. Superscript for CUs indicate the information source for matches of CWTs to CUs ([1] = (DFO 2018), [2] = (Brown et al. 2020)). Where superscripts are not present, the authors determined which CWTs to match with CUs. An asterisk indicates that the CU was created by the authors for categorization (all in United States populations) but do not represent previously recognized CUs or other groupings. For Chinook, boldface CWT abbreviations indicate that the yearling, stream-type life history is dominant for a CWT stock.

CWT stock name	CWT Abbrev.	Conservation Unit matched	GSI Populations matched
Chinook			
Atnarko	**ATN**	Bella Coola-Bentinck[1]	Atnarko
		Homathko_SU_x.x[2]	Homathko
		Klinaklini_SU_1.3[2]	Devereux, Klinaklini
Big Qualicum	BQR	East Vancouver Island-Qualicum and Puntledge_FA_0.x[2]	Big Qualicum, L Qualicum, Puntledge
		Southern Mainland-Georgia Strai_FA_0.x[2]	Squamish, Porteau Cove, Cheakamus
Cowichan	COW	East Vancouver Island-Cowichan and Koksilah_FA_0.x[2]	Cowichan

Green	GRN	Puget Sound*	Soos Creek Hatchery, Snohomish River
Harrison	HAR	Lower Fraser River_FA_0.3[1]	Chilliwack, Harrison
Kitsumkalum	**KLM**	Kalum_late_timing[1]	Kitsumkalum R
		Lower Skeena[1]	Exchamsiks, Kasiks R, Skeena at Terrace
		Middle Skeena-large lakes[1]	Bear, Morice
		Middle Skeena-mainstem tributaries[1]	Kispiox, Kitwanga, Nangeese, Slamgeesh
		Portland Sound-Observatory Inlet-Lower Nass[1]	Ishkheenickh, Kateen, Kwinamass
		Upper Skeena[1]	Sustut
Nicola	**NIC**	Lower Thompson_SP_1.2[2]	Bonaparte, Coldwater, Deadman, L Thompson, Louis, Nicola, Spius, U Coldwater

		South Thompson-Bessette Creek_SU_1.2[2]	Bessette
Nooksack	**NSF**	Nooksack River*	Nooksack SP
Phillips	PHI	Southern Mainland-Southern Fjords_FA_0.x[2]	Bute, Phillips
Quinsam	QUI	East Vancouver Island-North_FA_0.x[2]	Nimpkish, Quinsam, Woss Lake
Robertson	RBT	West Vancouver Island-Nootka and Kyuquot_FA_0.x[2]	Conuma, Gold River, Kaouk River, Tahsis, Tlupana, Zeballos
		West Vancouver Island-North_FA_0.x[2]	Colonial Cay, Marble, Bedwell, Cypre, Kennedy, Moyeha, Nahmint, Nitinat, Robertson, San Juan, Sarita, Stamp, Thornton, Toquart, Tranquil
Samish	SAM	Boundary Bay_FA_0.3[2]	Little Campbell, Serpentine

Lower Shuswap	SHU	Shuswap River_SU_0.3[2]	Lower Shuswap, Middle Shuswap
		South Thompson_SU_0.3[2]	Lower Adams, Little River, South Thompson
Skagit	SSF	Skagit River*	Skagit, Stillaguamish
Stikine	**STI**	Stikine_early timing[1]	Andrew Creek, Little Tahltan, Shakes Creek
		Stikine_late[1]	Verrett

Coho

Bingham	BHC	Coastal Washington*	Queets, Bingham Ck, Raimie Ck

Big Qualicum	BQR	East Vancouver Island-Georgia Strait	Big Qualicum, Black, Cowichan, Goldstream, Puntledge, Quinsam, Rosewall
Inch Creek	INC	Lower Fraser	Chehalis, Chilliwack, Coquitlam, Hicks, Inch, Kanaka, Nathan, Norrish, Pitt, Stave, Widgeon
Interior Fraser	IFR	Lower Thompson	Coldwater
		North Thompson	Barriere, Birch Island, Dunn, Mann, Reg_Christie
		South Thompson	Harbour, Momich, Salmon
		Fraser Canyon	Nahatlatch
Puyallup	PUY	Southern Puget Sound*	Minter, Nisqually, Puyallup, White

Robertson	RBT	Clayoquot	Kennedy, Kootowis
		Juan de Fuca-Pachena	Dungeness, Nitinat, Pachena, San Juan
		Nahwitti Lowland	Cluxewe, Goodspeed, Marble, Stephens, Washlawlis, Waukwaas
		West Vancouver Island	Conuma, Kitsuksis, Maggie, Robertson
Skagit	SKH	North Puget Sound*	Jones, Nooksack, Skagit, Stillaguamish
Skykomish	SYH	Hood Canal*	Dewatto, Quilcene
		Mid-Puget Sound*	Grizzly, Skykomish

Table S3: Number of Chinook salmon matched to each coded wire tag (CWT) stock in each ocean entry year for the spring-summer (April through August) and fall-winter (September through following March). A minimum of 10 fish were needed in a group to estimate pathogen prevalence for use in cohort survival models (groups used indicated in boldface).

CWT stock	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
Spring-Summer										
ATN	0	**10**	**14**	6	1	0	**14**	0	0	0
BQR	0	0	**53**	**18**	**18**	1	**16**	0	5	0
COW	0	0	0	**23**	**22**	4	**452**	0	1	0
GRN	0	1	5	1	1	0	2	0	0	0
HAR	0	**10**	0	7	2	0	5	0	2	0
KLM	0	0	0	1	0	0	0	0	0	0
NIC	0	5	**52**	**15**	**30**	5	**30**	0	**12**	0
NSF	0	0	4	0	0	0	1	0	1	0
PHI	0	0	0	0	0	0	**14**	0	0	0
QUI	0	0	0	0	3	**371**	**265**	**163**	0	0
RBT	0	3	0	3	3	8	0	**19**	0	0
SAM	1	0	4	0	0	0	0	0	0	0
SHU	0	2	4	0	5	1	**17**	0	**15**	0
SSF	0	0	9	0	0	0	1	0	0	0
STI	1	0	0	0	0	0	0	0	0	0
Fall-Winter										
ATN	**27**	2	2	3	0	**14**	**12**	6	1	0
BQR	**58**	**34**	**54**	**11**	**44**	**23**	**15**	**31**	**14**	0
COW	0	**22**	0	**11**	3	2	**11**	**16**	**16**	0
GRN	**12**	**49**	**33**	4	7	3	0	**29**	0	0
HAR	3	0	0	2	**16**	0	6	**11**	5	0
KLM	**19**	**27**	**10**	4	2	0	0	0	0	0
NIC	**21**	**26**	**17**	**11**	4	**14**	**17**	**14**	**10**	0
NSF	0	1	0	0	0	1	1	4	3	1
PHI	0	0	0	0	3	0	**11**	6	0	0
QUI	3	2	0	0	5	2	5	2	1	0
RBT	**84**	**183**	**45**	**37**	**46**	**21**	**46**	**25**	**78**	0
SAM	6	2	0	0	0	0	0	0	0	0
SHU	**44**	**20**	**37**	**45**	**48**	**13**	**73**	**63**	**51**	0
SKS	0	2	0	0	0	0	0	0	0	0
SSF	3	**12**	4	0	4	0	0	0	0	0
STI	**59**	**35**	**40**	0	0	0	0	0	0	0

Table S4: Number of Coho salmon matched to each coded wire tag stock in each ocean entry year for the spring-summer (April through August) and fall-winter (September through following March). A minimum of 10 fish were needed in a group to estimate pathogen prevalence for use in cohort survival models (groups used indicated in boldface).

CWT stock	2008	2009	2010	2011	2012	2013	2014	2015	2016
Spring-Summer									
BHC	0	1	5	8	0	3	0	**15**	0
BQR	0	1	9	**20**	1	8	**31**	**18**	**15**
IFR	0	0	4	5	0	0	8	8	**12**
INC	0	0	**17**	**20**	2	3	**63**	**26**	**20**
PUY	0	0	2	1	0	4	2	3	0
RBT	0	**17**	0	0	**25**	3	3	6	0
SKH	0	0	**13**	5	1	4	**30**	9	0
SYH	0	0	2	1	3	6	5	7	0
Fall-Winter									
BHC	0	0	4	0	2	2	1	0	0
BQR	0	5	9	8	**16**	**35**	**23**	**13**	7
IFR	0	0	7	**10**	6	**13**	**12**	8	3
INC	4	6	9	**27**	**22**	**58**	**38**	**20**	9
PUY	2	5	6	2	3	6	4	1	0
RBT	0	**15**	0	0	**15**	**12**	6	3	0
SKH	1	**16**	8	8	8	**22**	**22**	**12**	0
SYH	0	4	**11**	2	7	**13**	8	4	0

Table S5: Spring-summer / fall-winter sample size by JAZ and ocean entry year for Chinook mass deviation analysis. Full names for JAZ abbreviations can be found in Fisheries and Oceans Canada (2009).

	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
BB+GStr	1/6	0/2	4/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
BCD+HStr	0/35	0/0	0/2	6/3	1/0	0/0	11/10	0/4	0/0	0/0	0/0
COWA[a]	1/0	0/2	0/3	0/0	0/0	0/0	0/0	0/0	0/1	0/0	0/0
CR-PO[a]	38/7	61/12	40/6	23/2	30/1	19/5	0/2	0/9	0/3	0/0	0/0
EVI+GStr	0/61	1/60	40/60	26/24	30/57	376/24	656/31	39/48	6/30	0/46	17/0
HK+SFj	0/0	10/2	14/0	0/0	0/0	0/14	3/2	0/2	0/1	0/0	0/0
LFR+GStr	0/10	7/5	8/2	5/3	1/17	3/0	9/6	0/13	2/6	0/19	1/0
LILL+GStr	0/0	1/0	0/0	1/0	3/0	1/0	3/0	0/0	0/0	0/0	2/0
LNR-P+NSKEst	0/14	0/10	0/8	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
LSK+NSKEst	0/0	0/0	0/2	1/4	0/1	0/0	0/0	0/0	0/0	0/0	0/0
LStk+TBFj	1/59	0/35	0/40	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
MFR+GStr	0/3	5/4	44/6	41/11	81/14	18/8	43/7	0/6	20/4	0/19	29/0
NC+HStr	1/18	0/22	1/0	0/0	0/19	0/0	33/6	0/0	0/0	0/0	0/0
NTh+GStr	0/12	16/26	64/22	17/13	51/10	9/14	52/19	0/17	22/10	0/17	31/0
ORCS[a]	0/0	0/4	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
PS[a]	0/15	1/69	18/37	2/4	3/21	0/4	8/3	0/34	1/13	0/7	1/0
RSI+HStr	0/7	0/4	0/9	0/2	0/4	0/6	1/1	0/12	0/0	0/0	0/0
SC+GStr	1/3	18/16	15/0	0/0	0/0	0/3	2/0	0/2	0/2	0/0	1/0
SC+SFj	0/11	0/0	0/0	0/0	0/3	0/0	14/0	0/2	0/2	0/0	0/0
SR-SpSu	7/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
STh+GStr	0/53	2/20	2/37	3/48	5/48	5/13	18/72	0/67	15/51	0/66	17/0
UFR+GStr	0/2	0/5	16/3	31/9	47/16	7/14	45/16	0/20	27/4	0/34	31/0
UNR+NSKEst	0/8	0/10	0/0	0/2	0/0	0/0	1/0	0/0	0/0	0/0	0/0
USK+NSKEst	0/5	0/17	0/0	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/0
Whtng+TBFj	0/23	0/14	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
WVI+WQCI	0/18	0/80	0/20	3/24	2/45	0/0	0/1	0/0	0/17	0/0	0/0
WVI+WVI	0/66	3/101	0/25	0/13	1/1	8/21	0/45	0/25	0/61	0/1	0/0

a = labels for "joint adaptive zones" created by the authors to accomodate populations originating outside British Columbia. COWA = Washington Coast, CR-PO =Columbia River, ORCS = Oregon Coast, PS = Puget Sound.

Table S6: Spring-summer / fall-winter sample size by JAZ and ocean entry year for Coho mass at length analysis. JAZ abbreviations explained in (Fisheries and Oceans Canada 2009).

	2008	2009	2010	2011	2012	2013	2014	2015	2016
BB+GStr	0/1	0/ 2	3/ 1	3/ 2	0/ 2	1/ 7	1/ 0	1/ 2	2/ 0
EVI+GStr	0/0	1/ 5	9/ 9	20/ 8	1/16	8/35	31/23	18/14	15/ 7
EVI+SFj	0/0	0/ 0	0/ 0	0/ 0	0/ 1	1/ 0	1/ 0	0/ 1	0/ 0
FRCany+GStr	0/0	0/ 0	0/ 1	1/ 1	0/ 0	0/ 3	0/ 2	0/ 0	4/ 1
HecLow+HStr	0/0	0/ 1	0/ 1	0/ 0	0/ 0	0/ 0	0/ 0	0/ 0	0/ 0
HK+SFj	0/0	0/ 0	2/ 0	2/ 0	1/ 1	0/ 3	8/ 1	2/ 0	0/ 0
LFR+GStr	0/4	0/ 6	17/ 9	20/27	2/22	3/58	63/38	26/20	20/ 9
LILL+GStr	0/2	0/ 0	1/ 0	1/ 2	0/ 0	0/ 6	3/ 3	2/ 4	5/ 1
LSK+NSKEst	0/0	0/ 0	0/ 0	0/ 0	0/ 1	0/ 0	0/ 0	0/ 0	0/ 0
LTh+GStr	0/0	0/ 0	0/ 1	1/ 4	0/ 1	0/ 4	3/ 1	2/ 0	1/ 2
MFR+GStr	0/0	0/ 1	0/ 0	1/ 0	0/ 1	0/ 4	1/ 2	1/ 2	1/ 2
NC+HStr	0/0	0/ 0	2/ 0	1/ 0	1/ 0	0/ 0	0/ 1	0/ 0	0/ 0
NTh+GStr	0/0	0/ 0	4/ 5	0/ 3	0/ 4	0/ 5	4/ 7	4/ 3	4/ 0
ORCS[a]	0/0	0/ 1	2/ 5	1/ 0	0/ 0	1/ 0	0/ 2	4/ 1	0/ 0
PS[a]	0/3	0/25	17/25	7/12	4/18	14/41	37/34	20/17	23/ 1
SC+GStr	0/3	0/ 3	13/ 9	7/ 4	2/10	3/33	31/34	16/11	15/16
SC+SFj	0/1	0/ 2	4/ 0	0/ 2	0/ 1	0/ 6	8/ 4	3/ 1	2/ 5
STh+GStr	0/0	0/ 0	0/ 0	3/ 2	0/ 1	0/ 1	1/ 2	2/ 5	3/ 0
WACO[a]	0/0	1/ 0	5/ 4	8/ 0	0/ 2	3/ 2	0/ 1	15/ 0	0/ 0
WVI+WQCI	0/3	17/ 9	7/ 4	12/ 0	20/ 7	1/ 5	1/ 1	0/ 1	0/ 0
WVI+WVI	0/2	0/ 6	6/17	7/ 0	5/ 7	1/ 7	1/ 5	6/ 1	0/ 0

a = labels for "joint adaptive zones" created by the authors to accommodate populations originating outside British Columbia. ORCS = Oregon Coast, PS = Puget Sound, WACO = Washington Coast.

Supplementary Figures

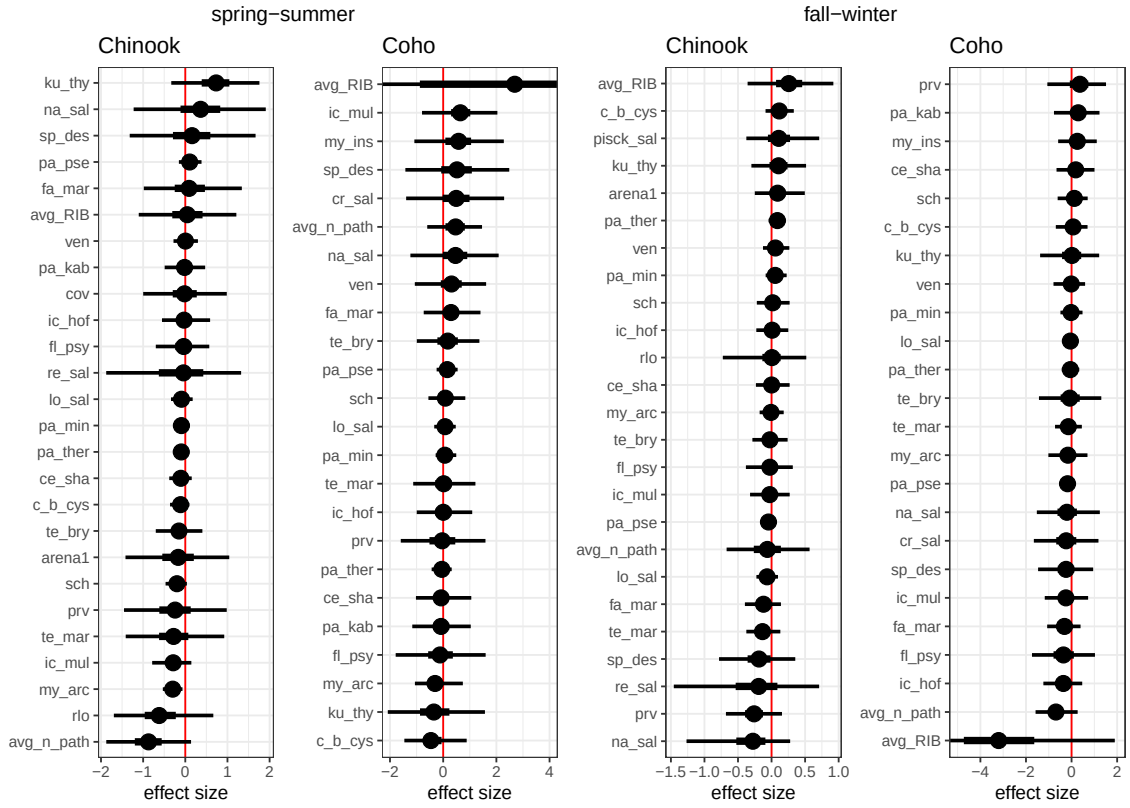

Figure S1: Dot-whisker plots depict model results from cohort survival models. Slope estimates for the association between pathogen prevalence and CWT-derived survival are presented (point = median estimate) with 50% (thick line), and 95% (thin line) credible intervals. Pathogen abbreviations can be found in Table S1.

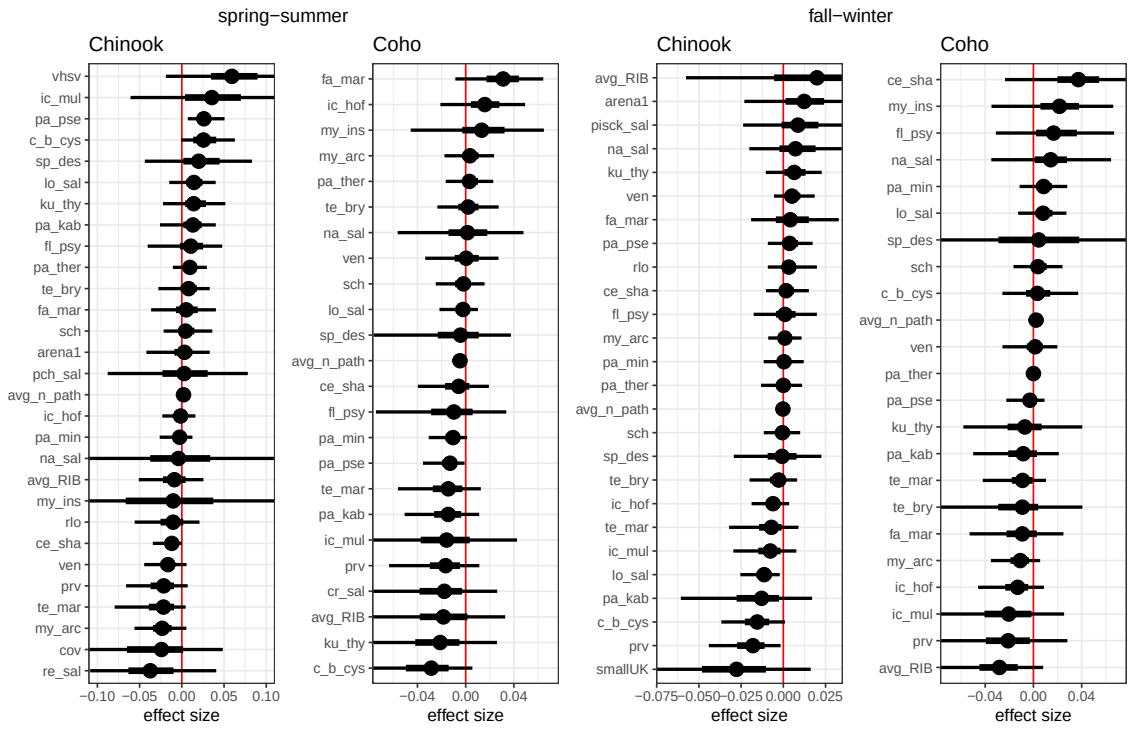

Figure S2: Dot-whisker plots depict model results from mass deviation models. Slope estimates for the association between pathogen load and mass while accounting for length are presented (point = median estimate) with 50% (thick line), and 95% (thin line) credible intervals. Pathogen abbreviations can be found in Table S1.

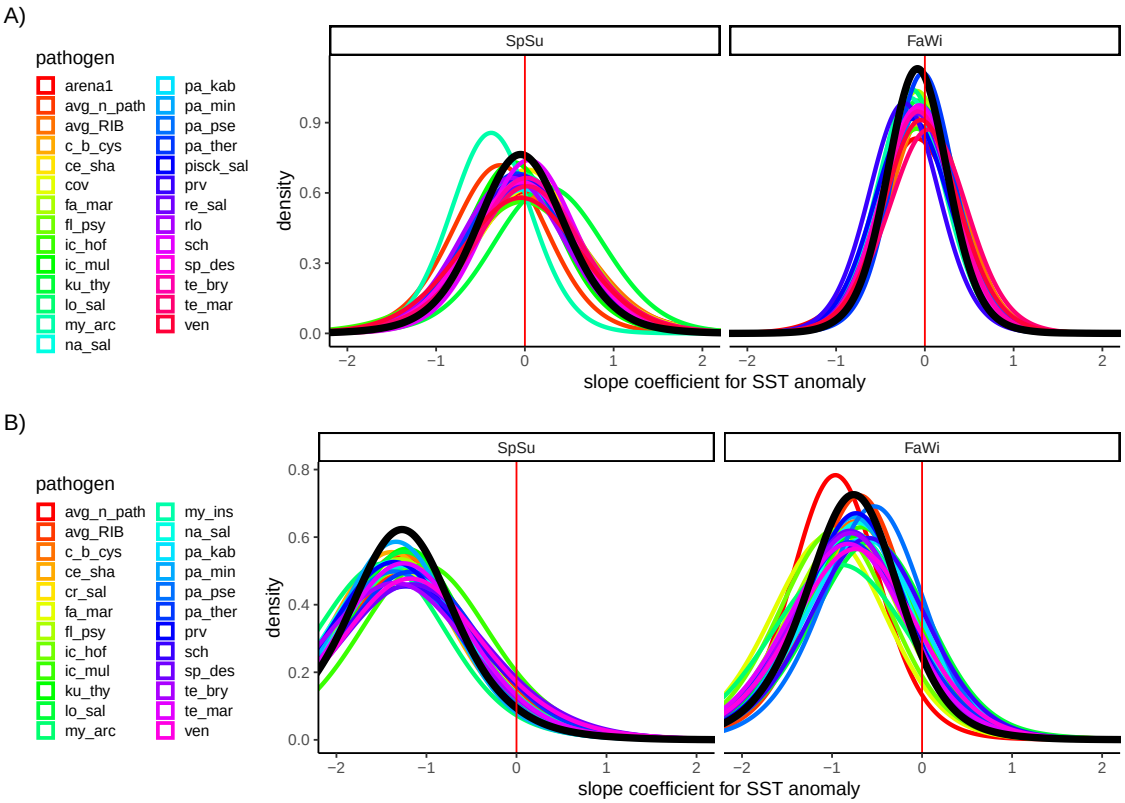

Figure S3: Posterior distributions of sea surface temperature anomaly from every cohort survival model for Chinook (A) and Coho (B) salmon. They heavy black line represents the mean of the distributions, which was created by sampling the posterior distribution from each pathogen model 5 000 times. Full names corresponding to pathogen abbreviations can be found in Table S1 (avg_n_path = average total number of pathogen taxa, avg_RIB = average relative infectious agent burden).

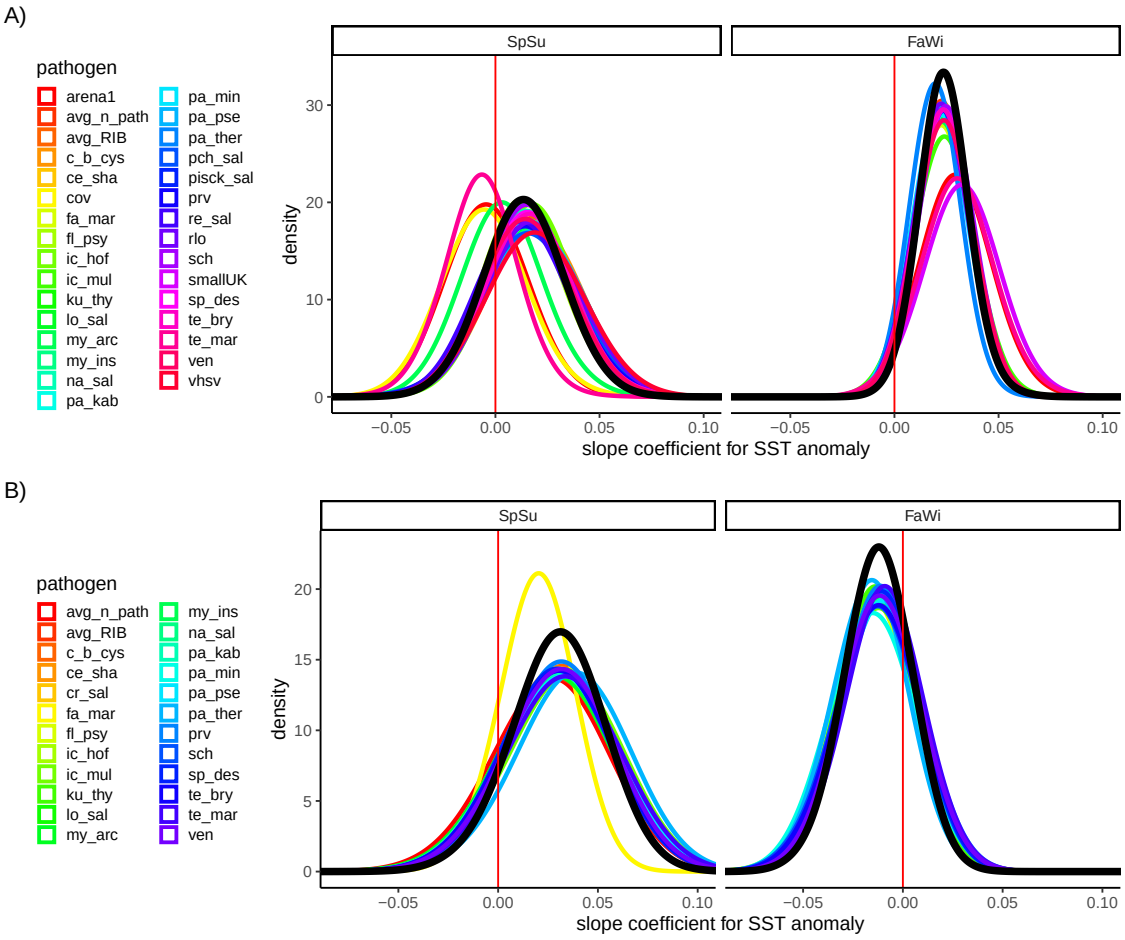

Figure S4: Posterior distributions of sea surface temperature anomaly from every mass deviation model for Chinook (A) and Coho (B) salmon. They heavy black line represents the mean of the distributions, which was created by sampling the posterior distribution from each pathogen model 5 000 times. Full names corresponding to pathogen abbreviations can be found in Table S1 (avg_n_path = average total number of pathogen taxa, avg_RIB = average relative infectious agent burden).

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