## SUPPLEMENTARY INFORMATION

## Non-stationary and interactive effects of climate and competition on pink salmon productivity

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Table S1: Multiple linear regression results. Shown are model parameter estimates, 95\% confidence intervals (lower/upper), and p-values for the main effects and interactions of the most parsimonious model.

| Coefficient Covariate effect | Estimate | Lower | Upper |  |
| :---: | :--- | :--- | :--- | :--- |
| $\alpha$ | Intercept | 0.69 | 0.45 | 0.92 |
| $\beta_{0}$ | Spawners | -1.48 | -2.05 | -0.92 |
| $\beta_{1}$ | Broodline odd | 0.59 | 0.32 | 0.86 |
| $\beta_{2}$ | Broodline odd : Spawners | 1.35 | 0.75 | 1.94 |
| $\beta_{3}$ | Regime up to 1988: | -0.38 | -0.79 | 0.04 |
|  | Broodline odd : Spawners |  |  |  |
|  | Regime up to 1988 : | 1.19 | 0.55 | 1.83 |
| $\beta_{4}$ | Temperature |  |  |  |
| $\beta_{5}$ | Temperature : Regime up to 1988 | 0.30 | 0.03 | 0.57 |
| $\beta_{6}$ | Total run (quadratic) | -0.08 | -0.14 | -0.01 |
| $\beta_{7}$ | Hatchery releases | -0.33 | -0.47 | -0.18 |
| $\beta_{8}$ | Competitor abundance (quadratic) | -0.28 | -0.40 | -0.15 |

Table S2: Model selection results. Covariates and interactions included in the top ten models were spawner abundance (S), broodline (B), temperature (T), hatchery releases (H), total pink salmon return $(\mathrm{P})$, competitor abundance (C), and regime (D).

| Model formula | AICc | delta <br> AIC | AICc <br> weight |
| :--- | :---: | :--- | :--- |
| B+C ${ }^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{R}^{2}+\mathrm{B}: \mathrm{S}+\mathrm{D}: \mathrm{T}+\mathrm{B}: \mathrm{S}: \mathrm{D}$ | 83.0 | 0 | 0.712 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{R}^{2}+\mathrm{B}: \mathrm{S}+\mathrm{B}: \mathrm{S}: \mathrm{D}$ | 85.8 | 2.8 | 0.174 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{B}: \mathrm{S}+\mathrm{D}: \mathrm{T}+\mathrm{B}: \mathrm{S}: \mathrm{D}$ | 86.9 | 3.9 | 0.1 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{B}: \mathrm{S}+\mathrm{B}: \mathrm{S}: \mathrm{D}$ | 93.5 | 10.5 | 0.004 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{B}: \mathrm{S}+\mathrm{D}: \mathrm{T}$ | 93.6 | 10.6 | 0.004 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{R}^{2}+\mathrm{B}: \mathrm{S}+\mathrm{D}: \mathrm{T}$ | 94.7 | 11.7 | 0.002 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{D}: \mathrm{T}$ | 95.3 | 12.3 | 0.002 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{R}^{2}+\mathrm{B}: \mathrm{S}$ | 95.4 | 12.4 | 0.001 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{R}^{2}$ | 96.2 | 13.2 | 0.001 |
| $\mathrm{~B}+\mathrm{C}^{2}+\mathrm{S}+\mathrm{H}+\mathrm{T}+\mathrm{B}: \mathrm{S}$ | 96.4 | 13.4 | 0.001 |



Figure S1: Comparison of $\ln ($ recruits/spawner) with Ricker residuals. Shown are estimated time series of $\ln$ (recruits/spawner) and residuals of a Ricker model that allowed for different stock-recruit relationships of each broodline. The time series had a Pearson correlation of 0.92.


Figure S2: Additional time series data used in the model selection. Shown are time series of the PDO and NPGO (top left), $\mathrm{pCO}_{2}$ in PWS and the north-eastern GoA (top right), winter SST anomaly in the eastern GoA (bottom left), and the biomass of chum and sockeye salmon in the North Pacific Ocean (bottom right, Ruggerone and Irvine 2018).


Figure S3: Predicted broodline effect on pink salmon productivity. Shown are the effects of each broodline, where thick gray line are median predictions from the model and gray polygons are $90 \%$ confidence intervals.


Figure S4: Predicted and observed $\ln$ (recruits/spawner). Shown are median predictions from the model (thick gray line) with $90 \%$ confidence intervals (gray polygons) in comparison with the observed time series (black circles and line).


Figure S5: Predicted stock-recruitment relationships from a model without covariates.
Shown is the predicted recruitment for each broodline as a function of spawner abundance for a model that contained spawner abundance, broodline as a factor, and their interaction, but no other covariates. This model explained only about $10 \%$ of the variance in $\ln$ (recruits/spawner).


Figure S6: Model diagnostics. Shown are residuals over time, residuals versus fitted values, observed versus predicted values, and sample versus theoretical quantiles.


Figure S7: Variable importance based on a random forest algorithm. Shown is the percent increase in mean squared error (MSE) when a variable is excluded from the model, based on refitting the selected model using random forests without replacement. Gray circles indicate fixed model terms and black circles indicate predictors that were selected by AICc-based model selection. Random forests were fit using the randomForest package in R, with 10,000 trees.


Figure S8: Model cross validation results. Shown are distributions of root mean squared errors (RMSE) from out of sample predictions for all sub-models that were contained in the selected covariate model. RMSEs were calculated by fitting each model to training data and subsequently comparing the predictions for the test data to the observed $\ln$ (recruits/spawner). This procedure was repeated 1000 times by randomly drawing training ( 42 years) and test datasets ( 14 years). The red filled circle indicates the selected model.


Figure S9: Probability that the top model using simulated recruits/spawner with error was the same as the top model using the observed recruits/spawner (left) and the mean absolute percent difference in parameter estimates (right) as a function of the standard deviation of the assumed observation error. This sensitivity analysis was performed by simulating observation error in recruits/spawner around the observed values using lognormal errors, running the model selection using the simulated data and comparing the resulting best model and parameter estimates to the original model (repeated for 1000 stochastic draws at each level of error variance).


Figure S10: Predicted recruits per spawner of wild pink salmon (contour) as a function of PWS pink salmon hatchery releases and wild escapements. Shown are predictions for the odd-year (top) and even-year (bottom) broodline under the previous ocean regime prior to 1989 (left) and the current ocean regime since 1989 (right). All other predictors (temperature, total return, and competitor abundance) were set to median values. Predictions do not account for uncertainty in model parameter estimates.

