

Supplementary Material

Reproductive dynamics of striped marlin (*Kajikia audax*) in the central North Pacific

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Table S1. Summary of the condition of ovarian histology slides (563 of 598 samples examined) categorised (distinct, adequate, marginal) by ease of assignment to maturity status.

Histology condition	Preservation method	Maturity status	<i>n</i>	Proportion for a given preservation method and maturity status
Distinct	Glyo-Fixx	Immature	133	0.723
Adequate	Glyo-Fixx	Immature	33	0.179
Marginal	Glyo-Fixx	Immature	18	0.098
Distinct	Formalin	Immature	24	0.118
Adequate	Formalin	Immature	81	0.397
Marginal	Formalin	Immature	99	0.485
Distinct	Glyo-Fixx	Mature	27	0.310
Adequate	Glyo-Fixx	Mature	50	0.575
Marginal	Glyo-Fixx	Mature	10	0.115
Distinct	Formalin	Mature	27	0.307
Adequate	Formalin	Mature	48	0.545
Marginal	Formalin	Mature	13	0.148

Categories are displayed by the two preservation methods (preserved at sea in Glyo-Fixx or held frozen at sea and later preserved in 10% neutrally buffered Formalin) and by maturity status (immature and mature).

Table S2. Summary of female and male maturity ogive results based on robust logistic regression analysis across all months (total) and female spawning season only (May–July) excluding regenerating (EXREG) phase female and male samples respectively.

Model name	β_1	β_1 (s. d.)	β_1 (cv)	<i>P</i> value	Test statistic	d.f.	Pr>ChiSq
♀M1.Total.EXREG	0.146	0.018	12%	<0.001	8.23	503	<0.001
♀M2.Total.EXREG	M2.Total.EXREG did not converge				na	492	na
♀M1.SS.EXREG	0.170	0.028	16%	<0.001	5.98	179	<0.001
♀M2.SS.EXREG	0.168	0.029	17%	<0.001	0.25	177	0.882
	<i>n</i>	<i>L</i> _{EF50}	<i>L</i> _{EF50} s.d.		<i>L</i> _{EF95}	<i>L</i> _{EF95} s.d.	
♀M1.Total.EXREG	505	165.2	1.1		185.4	2.9	
♀M2.Total.EXREG	505	na	na		na	na	
♀M1.SS.EXREG	181	153.6	1.9		170.9	2.7	
♀M2.SS.EXREG	181	154.4	2.4		171.9	3.0	
	β_1	β_1 (s. d.)	β_1 (cv)	<i>P</i> value	Test statistic	d.f.	Pr>ChiSq
♂M1.Total.EXREG	0.080	0.010	13%	<0.001	7.87	432	<0.001
♂M2.Total.EXREG	0.079	0.011	14%	<0.001	10.87	421	0.454
♂M1.SS.EXREG	0.060	0.018	30%	<0.001	3.36	197	<0.001
♂M2.SS.EXREG	0.061	0.019	31%	<0.001	4.03	195	0.077
	<i>n</i>	<i>L</i> _{EF50}	<i>L</i> _{EF50} s.d.		<i>L</i> _{EF95}	<i>L</i> _{EF95} s.d.	
♂M1.Total.EXREG	434	120.9	2.8		157.6	3.4	
♂M2.Total.EXREG	434	127.2	9.0		164.7	10.0	
♂M1.SS.EXREG	199	109.8	10.3		158.6	6.7	
♂M2.SS.EXREG	199	121.9	9.4		170.5	10.0	

Model names “M1” have eye-fork length (EFL) as the predictor while “M2” uses EFL and month as predictors; prefix ♀, females; ♂, males. Model names that include “SS” indicate analysis is restricted to the May–July female spawning season. All model runs exclude regenerating (EXREG) phase females and males. Other column heading abbreviations: β_1 = slope of the maturity ogive; cv, coefficient of variation; d.f., degrees of freedom; *L*_{EF50}, length at median (50%) maturity; *L*_{EF95}, length at 95% maturity; *n*, sample size; na, not applicable; s.d., standard deviation. Parameter values of best fit model for each sample category displayed in bold.

Table S3. Summary of robust logistic regression model results fitted to total females sampled and females collected during the spawning (May–July) and non-spawning (August–April) seasons.

ROBUST LOGISTIC REGRESSION ALL FEMALE SAMPLES SUMMARY							
Maturity Ogive Results							
Model Name	efl	std efl	P value	Test stat	DF	Pr(>Chisq)	AIC
m1.fem.rob	0.165	0.017	<2e-16		596		na
m2.fem.rob	0.166	0.019	<2e-16	59.683	585	1.06E-08	na
m1.fem.sp.rob	0.204	0.034	2.43E-09		225		na
m2.fem.sp.rob	0.197	0.033	3.12E-09	0.565	223	0.754	na
m1.fem.nsp.rob	0.144	0.022	1.39E-10		369		na
m2.fem.nsp.rob	0.148	0.024	6.23E-10	7.580	361	0.476	na
Model Name	n	L50	L50 std	L95	L95 std	B1	B1 CV
m1.fem.rob	598	160.995	0.798	178.890	1.936	0.165	10.2%
m2.fem.rob	598	159.008	3.980	176.716	4.602	0.166	11.3%
m1.fem.sp.rob	227	152.172	1.768	166.590	2.154	0.204	16.8%
m2.fem.sp.rob	227	153.359	2.242	168.275	2.582	0.197	16.9%
m1.fem.nsp.rob	371	167.930	1.475	188.354	4.133	0.144	15.6%
m2.fem.nsp.rob	371	159.378	4.431	179.315	5.823	0.148	16.2%

Model names with “m1” have eye-fork length as the predictor and with “m2” have eye-fork length (efl) and month (as a factor) as predictors noting that the estimated month effect parameters are not shown here for brevity. Model names with “sp” are fit to data collected during the spawning season and with “nsp” are fit to data collected during the non-spawning season. Model names without “sp” or “nsp” were analysed using total females sampled.

Table S4. Summary of robust logistic regression model results fitted to total females sampled and females collected during the spawning (May–July) and non-spawning (August–April) season but excludes regenerating phase females, signified as “nr” in the model name.

ROBUST LOGISTIC REGRESSION NO REGENERATING FEMALE SAMPLES SUMMARY							
Maturity Ogive Results							
Model Name	efl	std efl	P value	Test stat	DF	Pr(>Chisq)	AIC
m1.nr.fem.rob	0.146	0.018	<2e-16				na
m2.nr.fem.rob	Model m2.nr.fem.rob did not converge			na	na	na	na
m1.nr.fem.sp.rob	0.170	0.028	2.18E-09		179		na
m2.nr.fem.sp.rob	0.168	0.029	5.93E-09	0.251	177	0.882	na
m1.nr.fem.nsp.rob	0.097	0.030	0.001251				na
m2.nr.fem.nsp.rob	Model m2.nr.fem.nsp.rob did not converge			na	na	na	na
Model Name	n	L50	L50 std	L95	L95 std	B1	B1 CV
m1.nr.fem.rob	505	165.211	1.045	185.433	2.904	0.146	12.1%
m2.nr.fem.rob	505	na	na	na	na	na	na
m1.nr.fem.sp.rob	181	153.560	1.921	170.851	2.688	0.170	16.4%
m2.nr.fem.sp.rob	181	154.367	2.397	171.884	3.000	0.168	17.2%
m1.nr.fem.nsp.rob	324	186.484	7.519	216.764	16.501	0.097	31.0%
m2.nr.fem.nsp.rob	324	na	na	na	na	na	0.000

Model names with “m1” have eye-fork length as the predictor and with “m2” have eye-fork length (efl) and month (as a factor) as predictors noting that the estimated month effect parameters are not shown here for brevity. Model names with “sp” are fit to data collected during the spawning season and with “nsp” are collected during the non-spawning season. Model names without “sp” or “nsp” were analysed using total females sampled.

Table S5. Summary of standard logistic regression model results fitted to total females sampled and females collected during the spawning (May–July) and non-spawning (August–April) seasons.

STANDARD LOGISTIC REGRESSION ALL FEMALE SAMPLES SUMMARY									
Maturity Ogive Results									
Model Name	efl	std efl	P value	Test stat	Pr(>Chisq)	Null dev	Resid dev	Percent dev	AIC
m1.fem	0.150	0.014	<2e-16			767.58	414.39	46.0%	418.39
m2.fem	0.144	0.014	<2e-16	86.737	7.25E-14	767.58	327.65	57.3%	353.65
m1.fem.sp	0.139	0.018	1.76E-14			296.97	145.41	51.0%	149.41
m2.fem.sp	0.143	0.019	8.69E-14	6.903	0.032	296.97	138.50	53.4%	146.50
m1.fem.nsp	0.142	0.020	5.82E-13			325.04	197.51	39.2%	201.51
m2.fem.nsp	0.144	0.021	4.95E-12	8.363	0.399	325.04	189.15	41.8%	209.15
Model Name	n	L50	L50 std	L95	L95 std	B1	B1 CV		
m1.fem	598	161.982	0.814	181.647	1.979	0.150	9.0%		
m2.fem	598	160.343	4.468	180.838	5.116	0.144	9.8%		
m1.fem.sp	227	152.800	1.734	174.003	2.510	0.139	13.0%		
m2.fem.sp	227	156.523	2.073	177.086	2.881	0.143	13.4%		
m1.fem.nsp	371	168.731	1.507	189.458	3.913	0.142	13.9%		
m2.fem.nsp	371	160.322	4.489	180.737	5.785	0.144	14.5%		

Model names with “m1” have eye-fork length as the predictor and with “m2” have eye-fork length (efl) and month (as a factor) as predictors noting that the estimated month effect parameters are not shown here for brevity. Model names with “sp” are fit to data collected during the spawning season and with “nsp” are fit to data collected not during the non-spawning season. Model names without “sp” or “nsp” were analysed using total females sampled.

Table S6. Summary of standard logistic regression model results fitted to total females sampled and females collected during the spawning (May–July) and non-spawning (August–April) season but excludes regenerating phase females, signified as “nr” in the model name.

STANDARD LOGISTIC REGRESSION NO REGENERATING FEMALE SAMPLES SUMMARY									
Maturity Ogive Results									
Model Name	efl	std efl	P value	Test stat	Pr(>Chisq)	Null dev	Residual dev	Percent dev	AIC
m1.nr.fem	0.140	0.015	<2e-16			531.92	306.30	42.4%	310.30
m2.nr.fem	0.127	0.017	3.92E-14	128.600	<2.2e-16	531.92	177.69	66.6%	203.69
m1.nr.fem.sp	0.129	0.018	2.11E-12			249.32	128.35	48.5%	132.35
m2.nr.fem.sp	0.132	0.019	7.21E-12	3.284	0.1936	249.32	125.07	49.8%	133.07
m1.nr.fem.nsp	0.124	0.030	3.01E-05			102.65	71.27	30.6%	75.27
m2.nr.fem.nsp	0.107	0.036	0.00311	19.000	0.01486	102.65	52.27	49.1%	72.27
Model Name	n	L50	L50 std	L95	L95 std	B1	B1 CV		
m1.nr.fem	505	166.417	1.087	187.476	2.848	0.140	10.8%		
m2.nr.fem	505	301.535	18146.000	324.692	18146.000	0.127	13.2%		
m1.nr.fem.sp	181	155.051	1.857	177.928	3.160	0.129	14.2%		
m2.nr.fem.sp	181	157.513	2.234	179.817	3.401	0.132	14.6%		
m1.nr.fem.nsp	324	182.910	4.963	206.711	10.255	0.124	24.0%		
m2.nr.fem.nsp	324	339.897	37943.060	367.454	37943.080	0.107	33.8%		

Model names with “m1” have eye-fork length as the predictor and with “m2” have eye-fork length (efl) and month (as a factor) as predictors noting that the estimated month effect parameters are not shown here for brevity. Model names with “sp” are fit to data collected during the spawning season and with “nsp” are collected during the non-spawning season. Model names without “sp” or “nsp” were analysed using total females sampled.

Details of Robust Wald Test Results for Best Model Fit to Spawning Season Females

Model 1 (R model object code is m1.fem.sp.rob) produced the best fit to the female maturity data collected during the spawning season in comparison to Model 2 (R model object code is m2.fem.sp.rob) based on the Robust Wald test results.

```
> anova(m1.fem.sp.rob,m2.fem.sp.rob,test="Wald")
```

Robust Wald Test Table

Model 1: mature ~ efl

Model 2: mature ~ efl + month_F

Models fitted by method 'Mqle'

<u>Model</u>	<u>pseudoDf</u>	<u>Test.Stat</u>	<u>Df</u>	<u>Pr(>chisq)</u>
1	225			
<u>2</u>	<u>223</u>	<u>0.56543</u>	<u>2</u>	<u>0.7537</u>

Results for the best fitting model with all samples indicated that there was a highly significant fit to the maturity data ($P < 0.0001$). Fish length was the only significant predictor and Model 1 produced reasonable residual patterns based on the histogram and quantilequantile (Q-Q) plots of the randomised quantile residuals shown below. The estimate of the length at 50% maturity was $L_{50} = 152.2$ cm with a standard error of 1.8. The estimate of the length at 95% maturity was $L_{95} = 166.6$ cm with a standard error of 2.2. The estimate of the slope of the maturity ogive was $\beta_1 = 0.204$ with a standard error of 0.034 (Table S3). A summary of the best fitting model with all samples is listed below along with the predicted dose responses. The histogram and Q-Q plot of the quantile residuals is shown in Fig. S1 and S2 respectively.

```
> summary(m1.fem.sp.rob)
```

Call: glmrob(formula = fl, family = binomial, data = MLS.ALL, subset = female.spawn)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-31.07630	5.40086	-5.754	8.72e-09***
efl	0.20422	0.03423	5.966	2.43e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robustness weights w.r * w.x:

212 weights are ~ = 1. The remaining 15 ones are summarised as

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.02304	0.12440	0.17760	0.25510	0.31180	0.74180

Number of observations: 227

Fitted by method 'Mqle' (in 10 iterations)

(Dispersion parameter for binomial family taken to be 1)

> dose.p(m1.fem.sp.rob, p=matvec)

	Dose	SE
p = 0.010:	129.6708	4.909579
p = 0.025:	134.2324	4.189478
p = 0.050:	137.7537	3.646010
p = 0.100:	141.4126	3.099493
p = 0.250:	146.7922	2.356436
p = 0.382:	149.8161	1.996980
<u>p = 0.500:</u>	<u>152.1718</u>	<u>1.767755</u>
p = 0.618:	154.5274	1.604309
p = 0.750:	157.5514	1.524259
p = 0.900:	162.9310	1.774263
<u>p = 0.950:</u>	<u>166.5899</u>	<u>2.153618</u>
p = 0.975:	170.1112	2.604325
p = 0.990:	174.6728	3.255209

Details of Robust Wald Test Results for Best Model Fit to Spawning Season Females Excluding

Regenerating (EXREG) Phase Females

Model 1 (R model object code is m1.nr.fem.sp.rob) produced the best fit to the female maturity data collected during the spawning season in comparison to Model 2 (R model object code is m2.nr.fem.sp.rob) based on the Robust Wald test results.

```
> anova(m1.nr.fem.sp.rob,m2.nr.fem.sp.rob,test="Wald")
```

Robust Wald Test Table

Model 1: mature ~ efl

Model 2: mature ~ efl + month_F

Models fitted by method 'Mqle'

<u>Model</u>	<u>pseudoDf</u>	<u>Test.Stat</u>	<u>D.f.</u>	<u>Pr(>chisq)</u>
1	179			
2	<u>177</u>	<u>0.25113</u>	<u>2</u>	<u>0.882</u>

Results for the best fitting model with all non-regenerating spawning season samples indicated that there was a highly significant fit to the maturity data ($P < 0.0001$). Fish length was the single significant predictor and Model 1 produced adequate residual patterns based on the histogram and Q-Q plots of the randomised quantile residuals shown above (Fig. S3 and S4 respectively). The estimate of the length at 50% maturity was $L_{50} = 153.6$ cm with a standard error of 1.9. The estimate of the length at 95% maturity was $L_{95} = 170.9$ cm with a standard error of 2.7. The estimate of the slope of the maturity ogive was $\beta_1 = 0.170$ with a standard error of 0.028 (Table S4). A summary of the best fitting model with all non-regenerating spawning season samples is listed below along with the predicted dose responses. The histogram and Q-Q plot of the quantile residuals is shown in Fig. S3 and S4 respectively.

```
> summary(m1.nr.fem.sp.rob)
```

Call: glmrob(formula = fl, family = binomial, data = MLS, subset = female.spawn)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-26.14880	4.52141	-5.783	7.32e-09***
efl	0.17028	0.02846	5.984	2.18e-09***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robustness weights w.r * w.x:

166 weights are ~ = 1. The remaining 15 ones are summarised as

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.05097	0.20790	0.27980	0.36290	0.44730	0.92160

Number of observations: 181

Fitted by method 'Mqle' (in 9 iterations)

(Dispersion parameter for binomial family taken to be 1)

> dose.p(m1.nr.fem.sp.rob, p=matvec)

	Dose	SE
p=0.010:	126.5747	5.616227
p=0.025:	132.0453	4.754856
p=0.050:	136.2684	4.105580
p=0.100:	140.6564	3.454488
p=0.250:	147.1081	2.578656
p=0.382:	150.7346	2.167949
<u>p=0.500:</u>	<u>153.5597</u>	<u>1.921041</u>
p=0.618:	156.3848	1.768216
p=0.750:	160.0113	1.748220
p=0.900:	166.4630	2.178784
<u>p=0.950:</u>	<u>170.8510</u>	<u>2.688031</u>
p=0.975:	175.0741	3.259810
p=0.990:	180.5447	4.063607

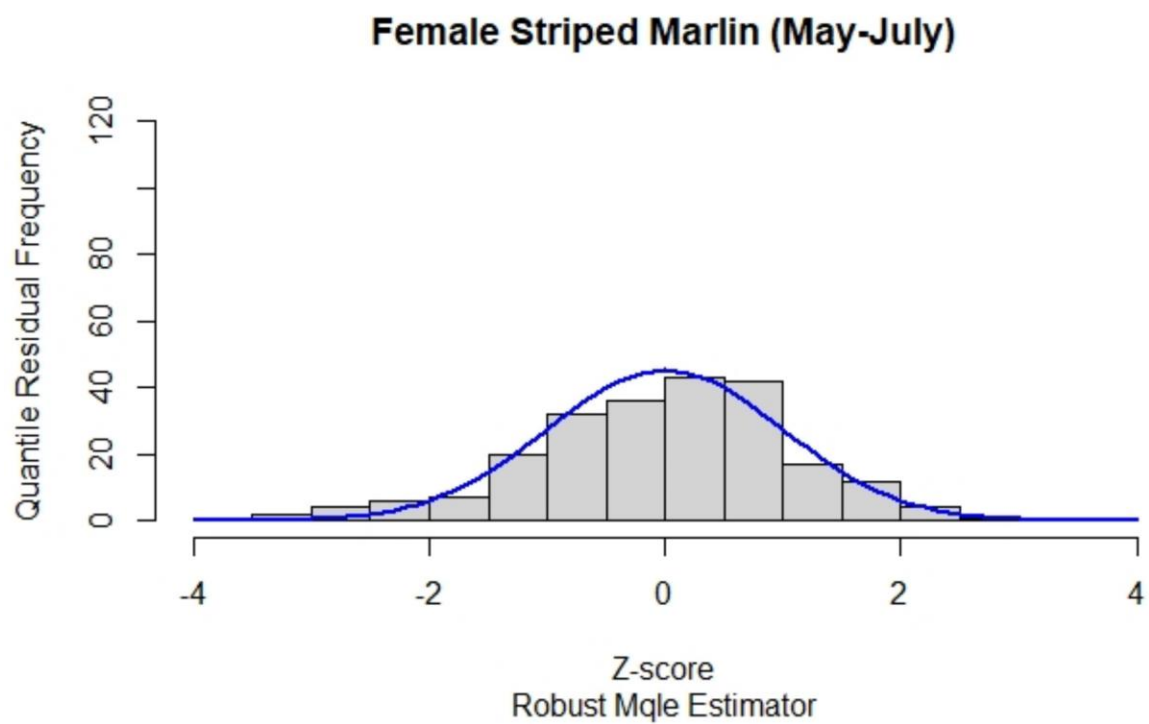


Fig. S1. Histogram of randomised quantile residuals.

Female Striped Marlin (May-July)

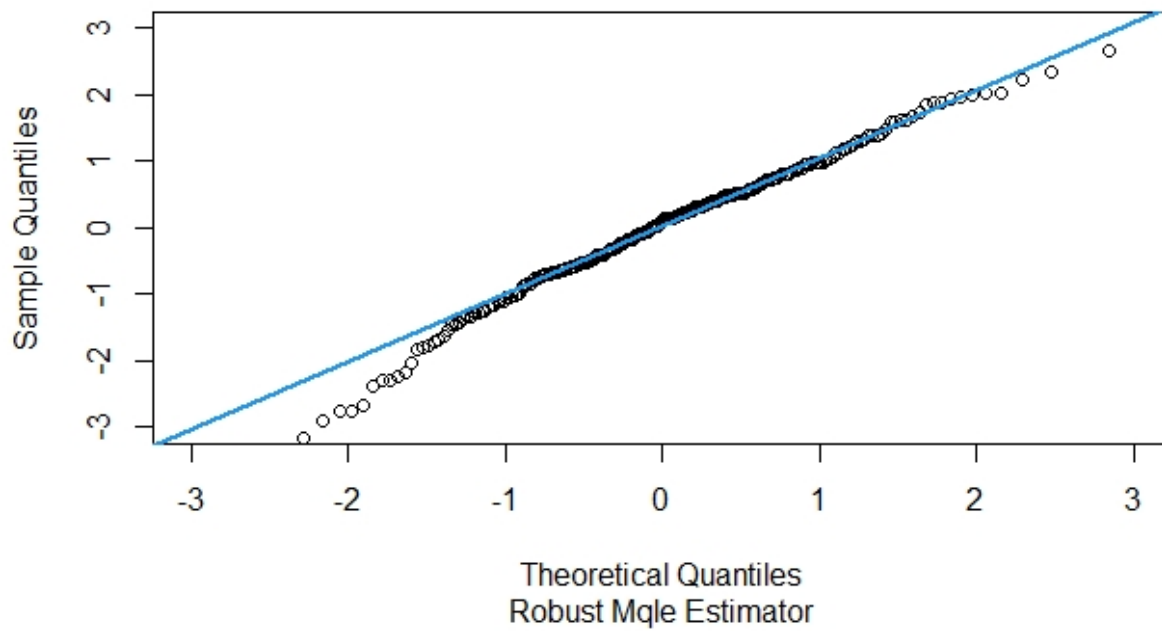


Fig. S2. Quantile–quantile (Q-Q) plot of randomised quantile residuals.

Female Striped Marlin (May-July)

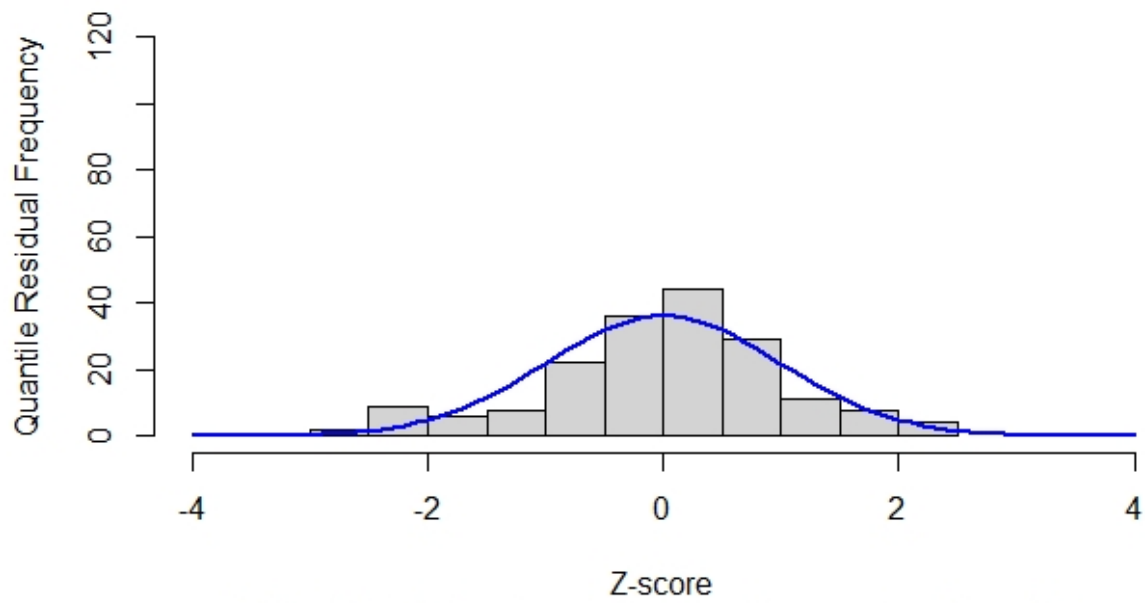


Fig. S3. Histogram of randomised quantile residuals.
Robust Mqle Estimator and Excluding Regenerating Stage Fish

Female Striped Marlin (May-July)

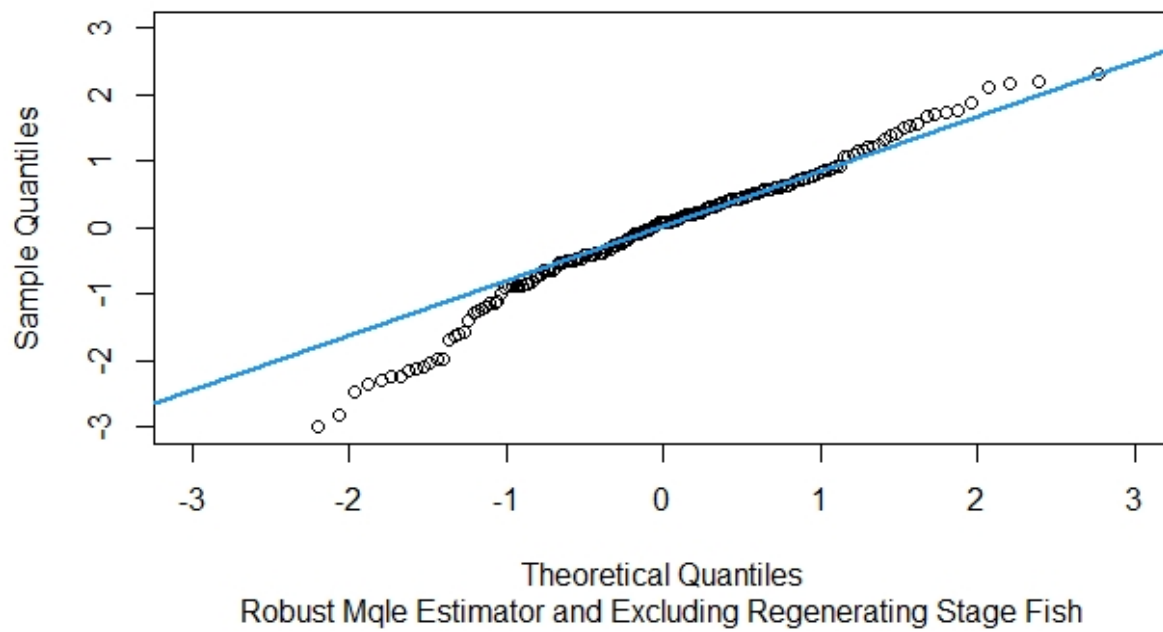


Fig. S4. Quantile–quantile (Q-Q) plot of randomised quantile residuals.

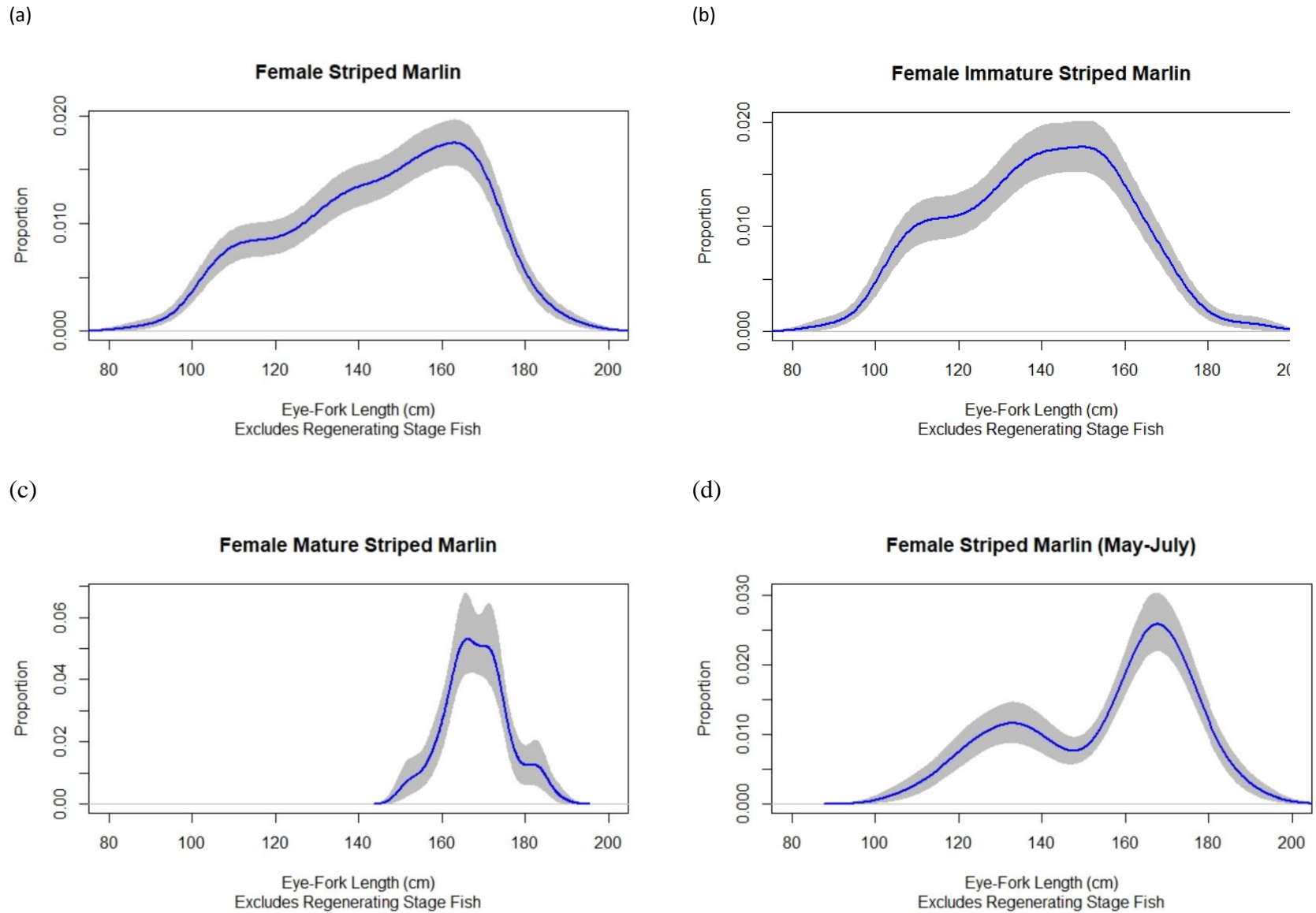
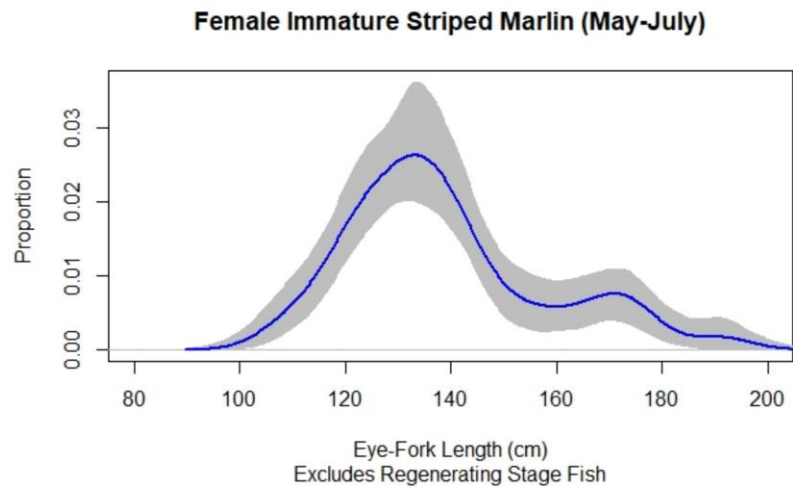
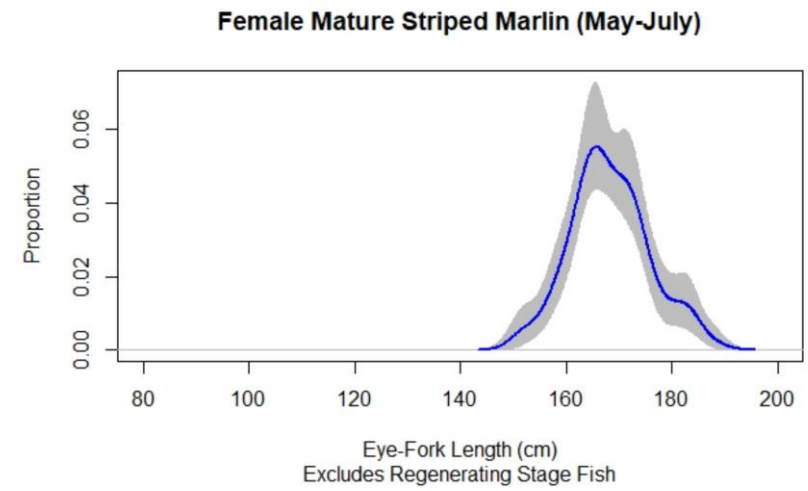


Fig. S5. Female length density distribution plots of striped marlin lengths (eye-fork length, cm) measured and sampled for subsequent gonad histology by domestic longline observers onboard vessels of the Hawaii-based pelagic longline fleet fishing in the central North Pacific. Plots displayed are based on sampled females (excluding regenerating phase females) that represent (a) total females ($n = 505$), (b) total immature females ($n = 394$), (c) total mature females ($n = 111$), (d) spawning season females ($n = 181$), (e) spawning season immature females ($n = 82$), (f) spawning season mature females ($n = 99$), (g) non-spawning season females ($n = 324$), (h) non-spawning season immature females ($n = 312$), (i) non-spawning season mature females ($n = 12$).

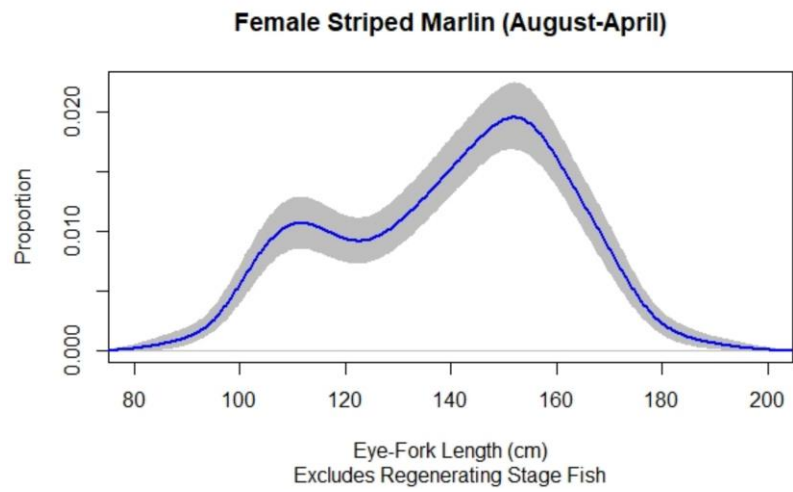
(e)



(f)



(g)



(h)

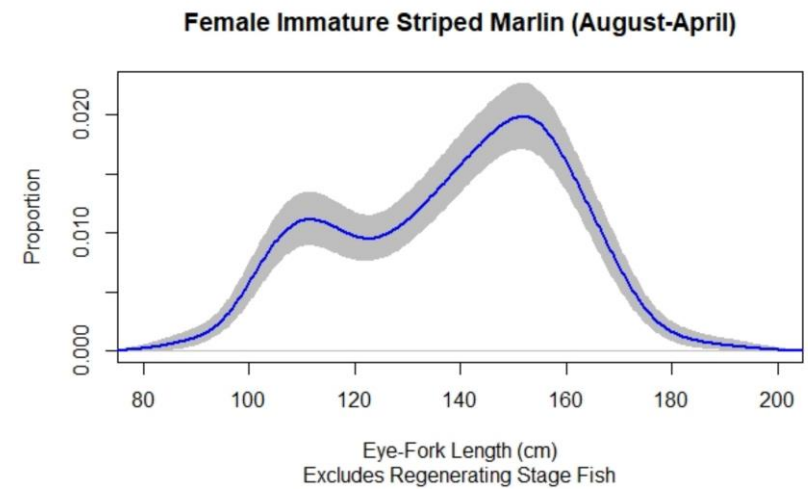


Fig. S5. (Cont.)

(i)

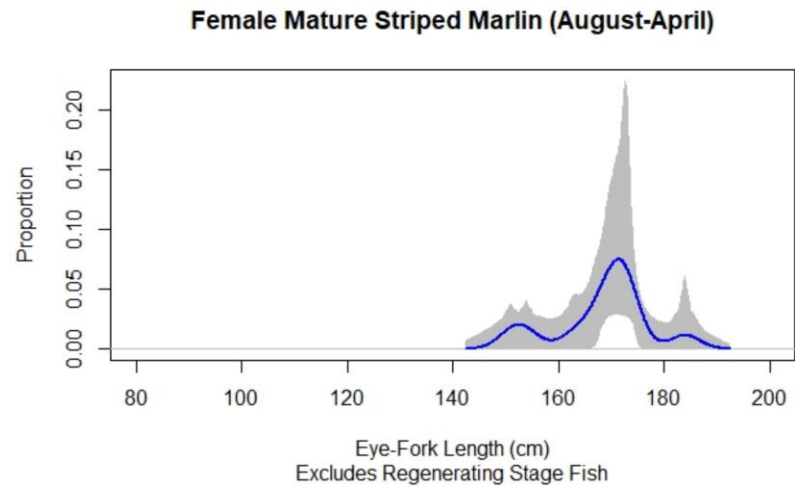


Fig. S5. *(Cont.)*

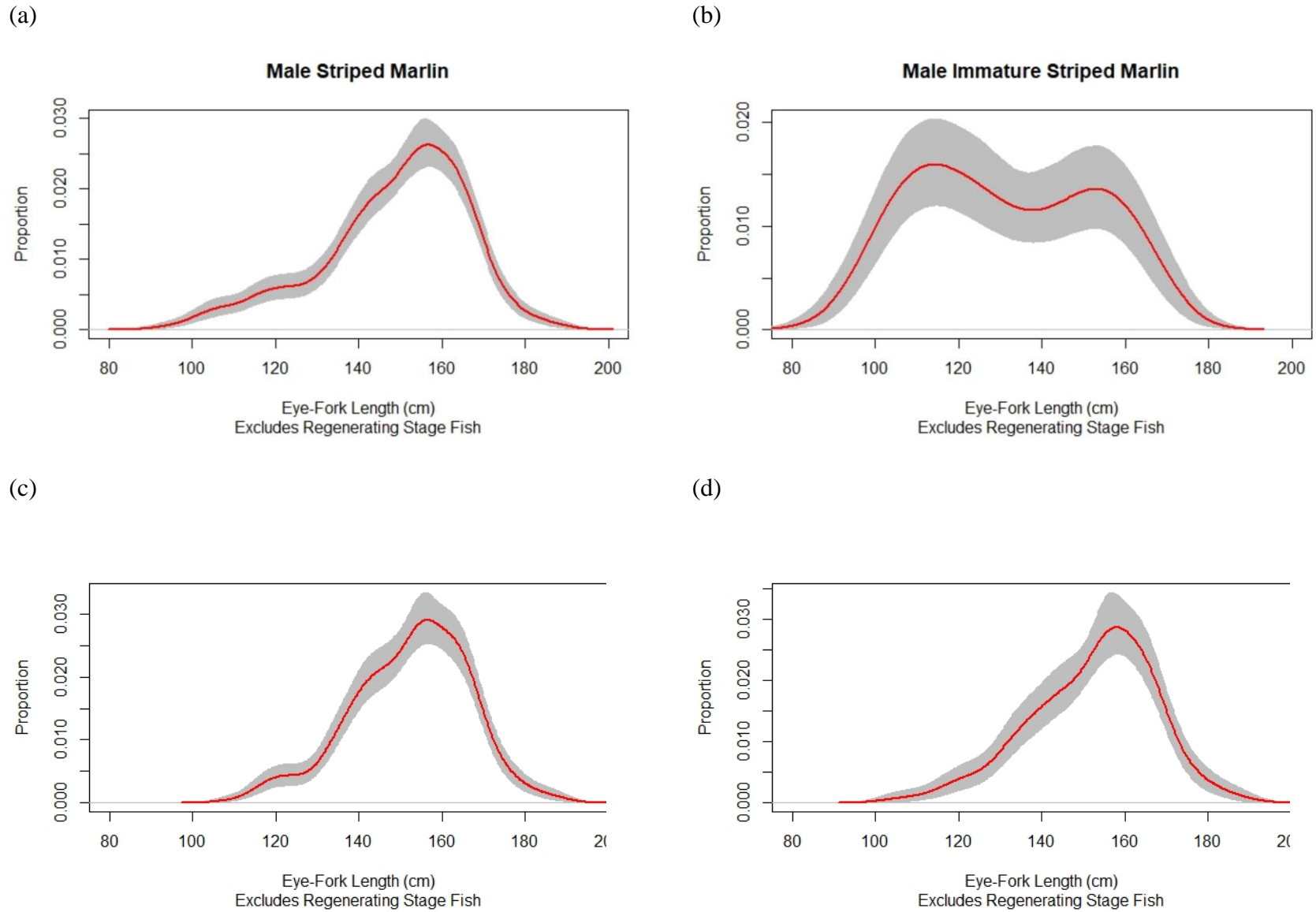
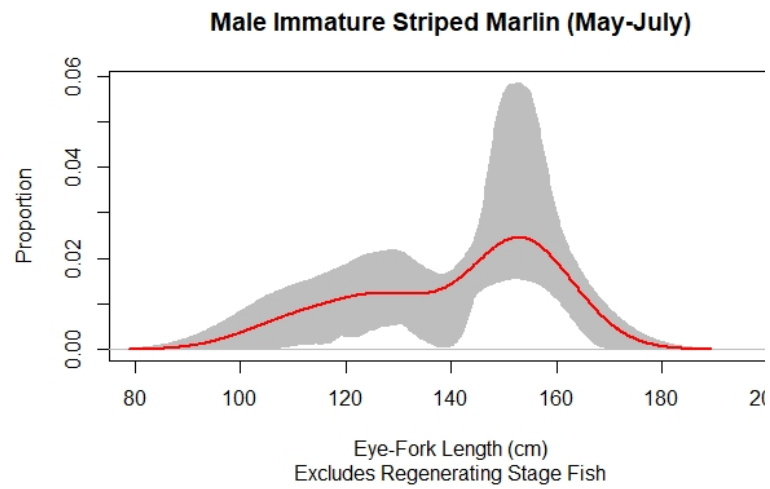
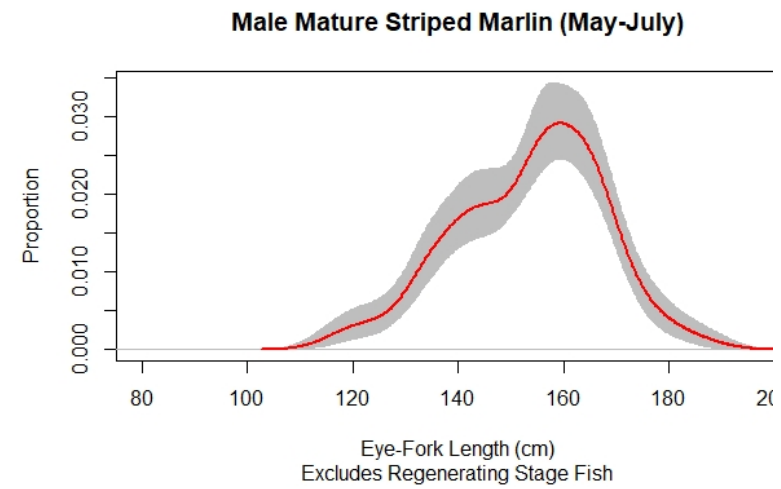


Fig. S6. Male length density distribution plots of striped marlin lengths (eye-fork length, cm) measured and sampled for subsequent gonad histology by domestic longline observers onboard vessels of the Hawaii-based pelagic longline fleet fishing in the central North Pacific. Plots displayed are based on sampled males (excluding regenerating phase males) that represent (a) total males ($n = 434$), (b) total immature males ($n = 74$), (c) total mature males ($n = 360$), (d) spawning season males ($n = 199$), (e) spawning season immature males ($n = 20$), (f) spawning season mature males ($n = 179$), (g) non-spawning season males ($n = 235$), (h) non-spawning season immature males ($n = 54$), (i) non-spawning season mature males ($n = 181$).

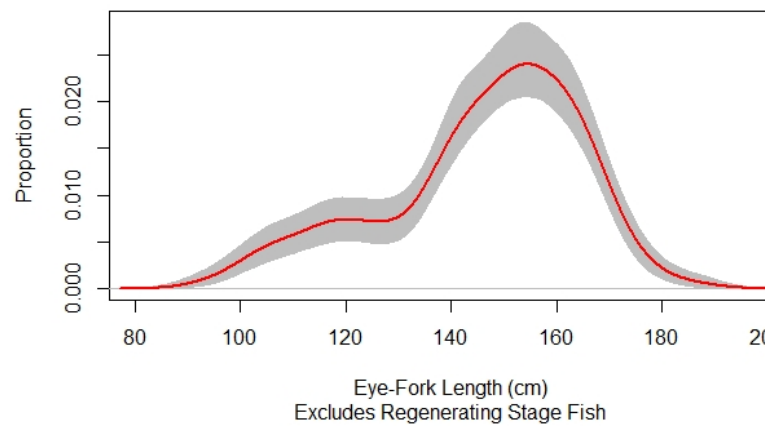
(e)



(f)



(g)



(h)

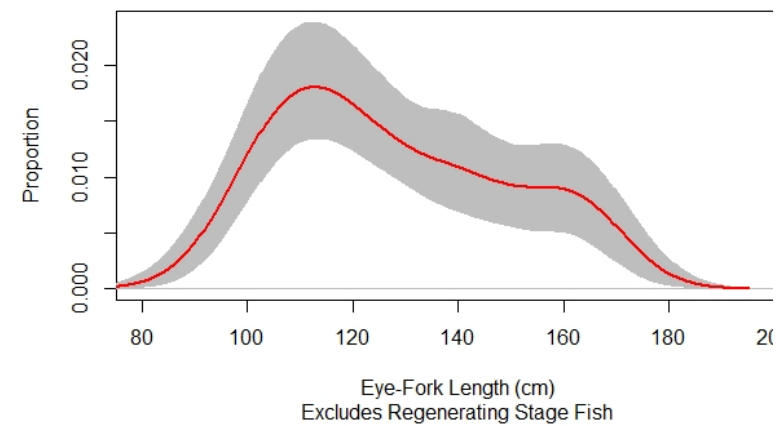


Fig. S6. (Cont.)

(i)

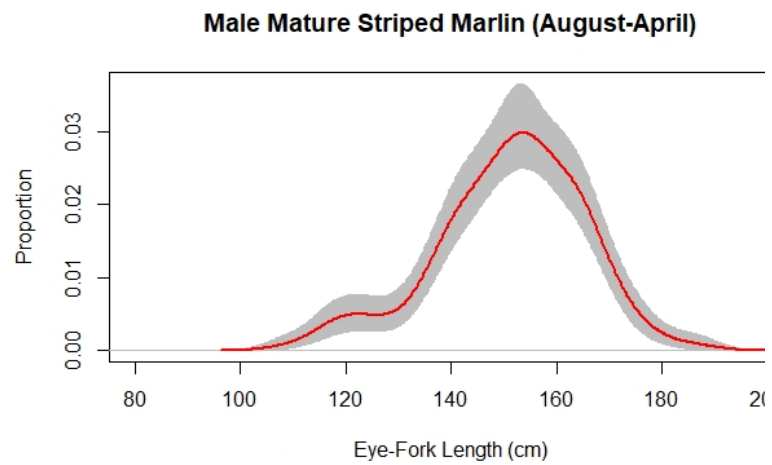


Fig. S6. *(Cont.)*