Appendix

Table A1. Covariate balance pre- and post-matching for surveys evaluating Tonga's Special Management Area program. Values over 25 suggest imbalanced covariates. Chi-squared tests using the Xbalance package were performed to determine whether at least one covariate was unbalanced pre and post matching.

Variable	***Pre-matching***	***Post-matching***
Surveyor 1	42.20	NaN
Surveyor 2	19.61	13.85
Surveyor 3	12.61	19.18
Surveyor 4	41.29	6.45
Habitat –Fringing	9.47	7.39
Habitat – Semi-exposed	6.40	6.90
Habitat - Exposed	3.03	0.15
Island group – Vava'u	91.98	16.85
Island group – Ha'apai	88.91	15.14
Island group - Tongatapu	0.00	1.08
Fishing pressure	35.35	15.99
Wave energy	2.22	21.64
Depth	36.69	13.46
Slope	24.62	17.61
Habitat rugosity	26.12	22.97
Coral cover	14.99	12.55

Table A2. Covariate values pre- and post-matching for surveys evaluating Tonga's Special Management Area program. The first column lists the covariates used to match control and treatment transects, and for each covariate match statistics are provided before and after matching, indicated in the 'unmatched' and 'matched' rows, to show how well the matching model performed. The third and fourth column present mean covariate values for treatment and control transects. The fifth column shows the mean difference between FHR and control means. The sixth and seventh column respectively show mean and maximum differences in each covariate Quantile – Quantile (QQ plot), with lower values indicating a better match. The lower table shows the total, matched and unmatched number of control and treatment transects respectively following the matching procedure.

Variable		**Treatment mean**	**Control mean**	**std. mean diff.**	**mean eQQ diff.**	**max eQQ diff.**
Depth	*unmatched*	5.46	6.34	-0.87	0.88	3
	matched	5.41	5.88	-0.48	0.58	2.30
Fishing pressure	*unmatched*	17.00	22.36	-5.36	6.09	37.41
	matched	17.12	18.24	-1.13	5.17	26.62
Habitat - Fringing	*unmatched*	0.30	0.34	-0.04	0.04	1.00
	matched	0.31	0.31	0.46	0.09	1.00
Habitat – Semi-exposed	*unmatched*	0.33	0.30	0.00	0.03	1.00
	matched	0.33	0.33	0.00	0.08	1.00
Habitat Exposed	*unmatched*	0.36	0.35	0.01	0.02	1.00
	matched	0.37	0.37	0.00	0.09	1.00
Island Ha'apai	*unmatched*	0.68	0.27	0.40	0.40	1.00
	matched	0.68	0.68	0.00	0.15	1.00
Island Tongatapu	*unmatched*	0.15	0.15	0.00	0.00	0.00
	matched	0.15	0.15	0.00	0.09	1.00
Island Vava'u	*unmatched*	0.18	0.58	-0.41	0.41	1.00
	matched	0.18	0.18	0.00	0.14	1.00
Live coral cover	*unmatched*	19.68	17.56	2.12	2.53	21.31
	matched	19.73	19.87	-0.14	0.85	5.40
Habitat rugosity	*unmatched*	2.76	3.03	-0.26	0.26	1.00
	matched	2.77	2.83	-0.06	0.20	1.00
Slope	*unmatched*	2.62	2.85	-0.24	0.24	1.00
	matched	2.62	2.74	-0.12	0.21	1.00
Surveyor 1	*unmatched*	0.00	0.08	-0.08	0.08	1.00
	matched	0.00	0.00	0.00	0.00	0.00
Surveyor 2	*unmatched*	0.06	0.11	-0.05	0.06	1.00
	matched	0.05	0.05	0.00	0.03	1.00
Surveyor 3	*unmatched*	0.13	0.17	-0.05	0.05	1.00
	matched	0.13	0.13	0.00	0.05	1.00
Surveyor 4	*unmatched*	0.82	0.64	0.18	0.18	1.00
	matched	0.82	0.82	0.00	0.01	1.00
Wave energy	*unmatched*	341.59	330.38	11.21	91.26	1450.56
	matched	337.48	285.21	52.27	85.63	951.00

	Control	Treated
All transects	1308	327
Matched transects	377	324
Unmatched transects	931	3

Table A3. Estimated regression parameters, standard error, *z*-values and *P*-values for logistic GLMs of Acanthuridae and Scarinae probability of capture.

Family		Estimate	SE	z value	*P*-value
Acanthuridae	Intercept	-1.150	0.379	3.038	< 0.01
	Size (TL)	-0.991	0.419	-2.365	< 0.05
	No-take zone	2.942	0.560	5.255	< 0.001
	PPA	1.360	0.488	2.788	< 0.01
	Size:No-take zone	0.671	0.537	1.250	0.211
	Size:PPA	0.300	0.557	0.539	0.590
Scarinae	Intercept	-2.137	0.473	-4.517	< 0.001
	Size (TL)	-0.767	0.690	-1.112	0.266
	No-take zone	2.666	0.507	5.256	< 0.001
	PPA	1.671	0.524	3.186	< 0.01
	Size:No-take zone	0.458	0.713	0.643	0.520
	Size:PPA	-0.026	0.788	-0.033	0.974

Table A4. Model outputs assessing target and total biomass and productivity impacts from no-take and restricted access areas in Tonga's Special Management Area program. CI indicates 95% confidence intervals from mixed effect models with Transect and Community included as random factors. PPA = Partially protected area

Response	*Management*	*Predictors*	*Marginal R^2*	*Conditional R^2*	*Estimates*	*CI*	*p*
Target species biomass	No-take	(Intercept)	0.186	0.396	1.81	1.55 – 2.11	**<0.001**
		Treatment [Counterfactual]			0.65	0.59 – 0.71	**<0.001**
	PPA	(Intercept)	0.030	0.641	0.57	0.33 – 0.97	**0.038**
		Treatment [Counterfactual]			0.74	0.39 – 1.40	0.356
Target species productivity	No-take	(Intercept)	0.146	0.510	1.20	0.90 – 1.61	0.218
		Treatment [Counterfactual]			0.63	0.46 – 0.88	**0.007**
	PPA	(Intercept)	0.130	0.621	1.06	0.77 – 1.46	0.712
		Treatment [Counterfactual]			0.60	0.37 – 0.97	**0.038**
Total species biomass	No-take	(Intercept)	0.231	0.629	0.96	0.67 – 1.39	0.848
		Treatment [Counterfactual]			0.50	0.29 – 0.86	**0.012**
	PPA	(Intercept)	0.048	0.613	0.71	0.44 – 1.15	0.164
		Treatment [Counterfactual]			0.72	0.41 – 1.25	0.238
Total species productivity	No-take	(Intercept)	0.208	0.558	1.75	1.41 – 2.17	**<0.001**
		Treatment [Counterfactual]			0.64	0.50 – 0.81	**<0.001**
	PPA	(Intercept)	0.159	0.623	1.53	1.12 – 2.10	**0.008**
		Treatment [Counterfactual]			0.61	0.38 – 0.98	**0.043**

Table A5. Model output of logistic binomial regression of probability of capture with fish size. SE indicates standard error of model coefficients. Mean are the results for a maximum effective range of 337 cm (the mean distance reported in Januchowski-Hartley et al. 2014), High are results for the highest estimated effective range (360 cm) while Low are results for lowest estimated range (305 cm). Statistically significant ($p < 0.05$) coefficients are indicated in bold. PPA = partially protected area

			Mean			**High**		
Taxonomic grouping	*Management*	*Parameter*	*Estimate*	*SE*	*p*	*Estimate*	*SE*	*p*
Acanthuridae	No-take	Intercept	3.820	2.181	0.080	4.432	2.478	0.074
		Total length	-0.094	0.098	0.338	-0.104	0.110	0.344
	PPA	Intercept	4.582	2.399	0.056	7.576	2.708	**0.005**
		Total length	-0.202	0.107	0.059	-0.310	0.118	**0.008**
	Fished	Intercept	5.121	2.531	**0.043**	7.894	2.573	**0.002**
		Total length	-0.290	0.123	**0.018**	-0.379	0.120	**0.002**
Scarinae	No-take	Intercept	5.387	2.013	**0.007**	8.590	2.711	**0.002**
		Total length	-0.145	0.720	**0.043**	-0.238	0.092	**0.010**
	PPA	Intercept	4.053	2.127	0.058	5.620	2.122	**0.008**
		Total length	-0.172	0.083	**0.038**	-0.216	0.082	**0.008**
	Fished	Intercept	4.292	4.751	0.366	4.152	4.063	0.307
		Total length	-0.246	0.192	0.200	-0.228	0.164	0.164

Table A6. Model output of catch vulnerability from 10 years of monitoring a community employing partially protected areas (PPA) in Solomon Islands. CI indicates 95% confidence intervals from Generalized Additive Models (GAMs).

	Vulnerability		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	44.25	43.62 – 44.88	**<0.001**
Management – PPA	-1.58	-2.58 – -0.57	**0.002**
Smooth term (Year) : Management – Open	0.97		**<0.001**
Smooth term (Year) : Management – PPA	1.90		**<0.001**
Observations	933		
Marginal R^2	0.135		

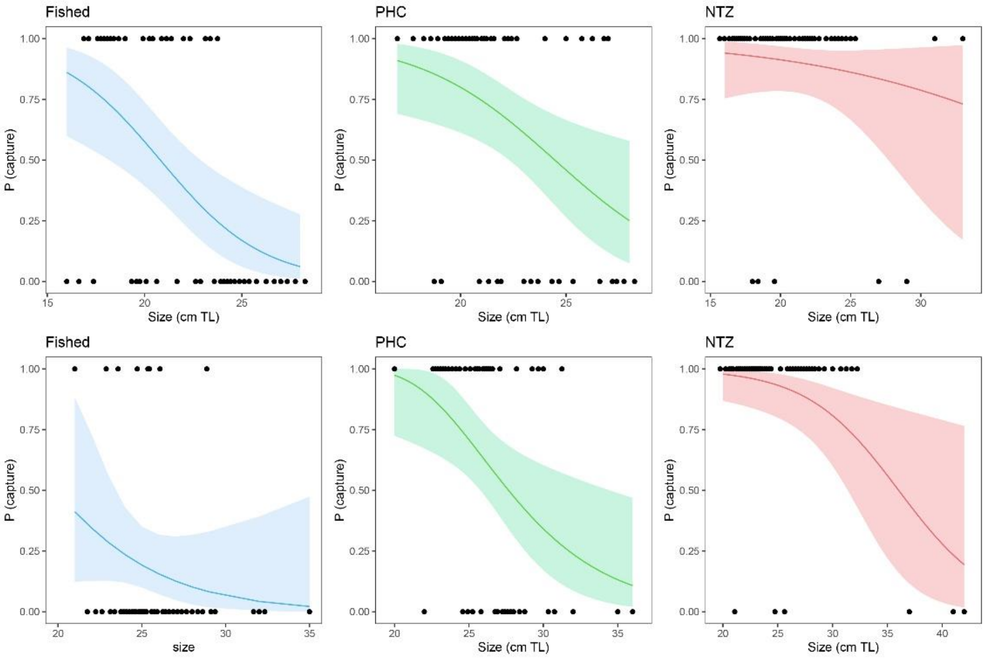

Figure A1. Differences in probability of approaching within spearing range with fish size (total length) for the family Acanthuridae and labrid subfamily Scarinae between co-management strategies. Probability of capture is defined as the likelihood of approaching to within upper spearing distance (3.6 m) of a reef fish.

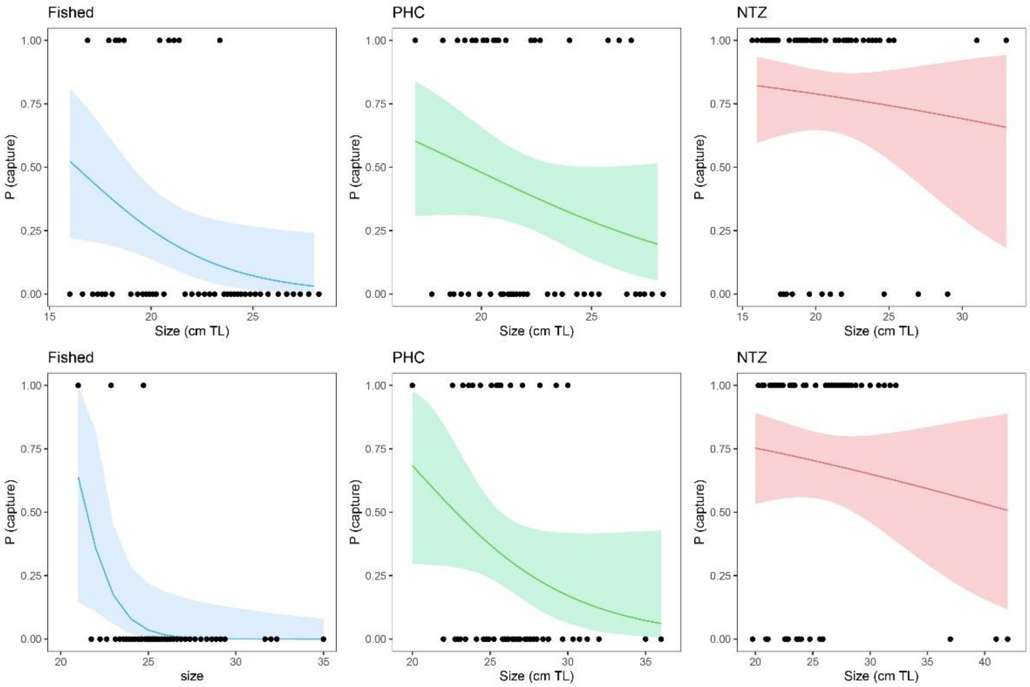

Figure A2. Differences in probability of approaching within spearing range with fish size (total length) for the family Acanthuridae and labrid subfamily Scarinae between co-management strategies. Probability of capture is defined as the likelihood of approaching to within upper spearing distance (3.05 m) of a reef fish.

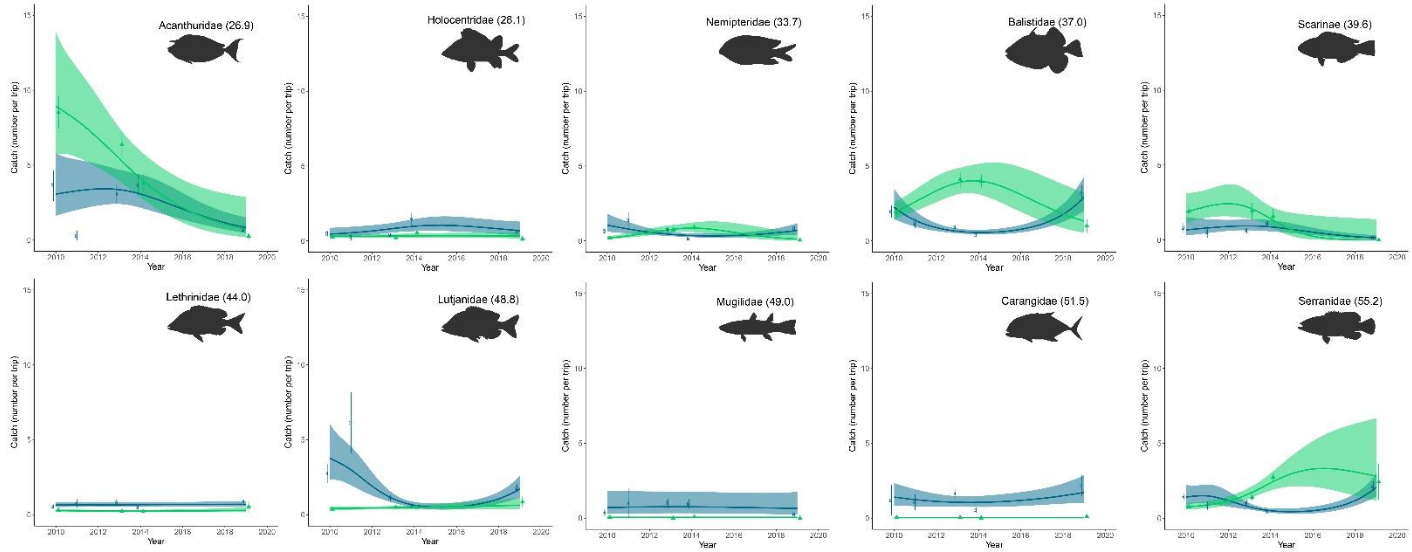

Figure A3. Temporal patterns in reef fish catch between open (Blue) and partially protected (PPA) (Green) reefs in Solomon Islands for the ten most commonly caught families. Each family comprised at least five percent of estimated total annual catch. Points represent mean ± SE values for each year on open and PPA reefs. Splines represent GAM model predictions ± 95% confidence intervals. Families are arranged according to increasing vulnerability with mean vulnerability values across species captured within each family in parenthesis.