**Table S1.** Relationship of sponge infestation (boreholes cm^{-2}) to damage to the internal surface of the left valve. Categories of damage to the internal valve surface were visually assessed as percentage cover of borehole scars in relation to shell size. None: 0%, Minimal: 1-20%, Moderate: 21-50%, High: 51-80%, Extensive: 81-100%. Because 90% of oysters used here (n= 172) only had boreholes on the left (curved) valve and borehole scars only visible on the inner surface of the left valve, additional borehole scars on the inner surface of the right valve were not considered for these categories. Model statistics are from ordinal logistic regression and wald-test.

Independent Variable: Sponge Infestation (boreholes cm^{-2}); Residual deviance: 309.232, AIC: 319.232					
Comparison: Internal Shell Damage Intensity	**Estimate**	**Std. Error**	**t**	**p**	**p adj.**
None: Minimal	1.745	0.293	5.948	< 0.001	< 0.001
Minimal: Moderate	4.022	0.474	8.480	< 0.001	< 0.001
Moderate: High	5.928	0.621	9.540	<0.001	<0.001
High: Extensive	7.555	0.742	10.180	< 0.001	< 0.001

Figure S1. a) Castrated by *Alcicornis longicornutus*. Hc = Haemocyte, Al = developing *A. longicornutus* cercariae within sporocysts. b) Reabsorption of gonad material, note the infiltration of haemocytes into the gonad follicle. Hc = Haemocyte, Fc = Follicle. c) Spawned, with collapsed follicles, note Haemocytes infiltrating Follicles. Hc = Haemocyte, Fc = Follicle. d) Developing (early) Male gonad. Sg = Spermatogonia, Sc = Spermatocytes, Sd = Spermatids. e) Ripe Male gonad. Sg = Spermatogonia, Sc = Spermatocytes, Sd = Spermatids, Sz = Spermatozoa. f) Developing (late) Female gonad. Og = Ovogonia, Oc = Ovocytes. g) Ripe Female gonad. Ov = Ova
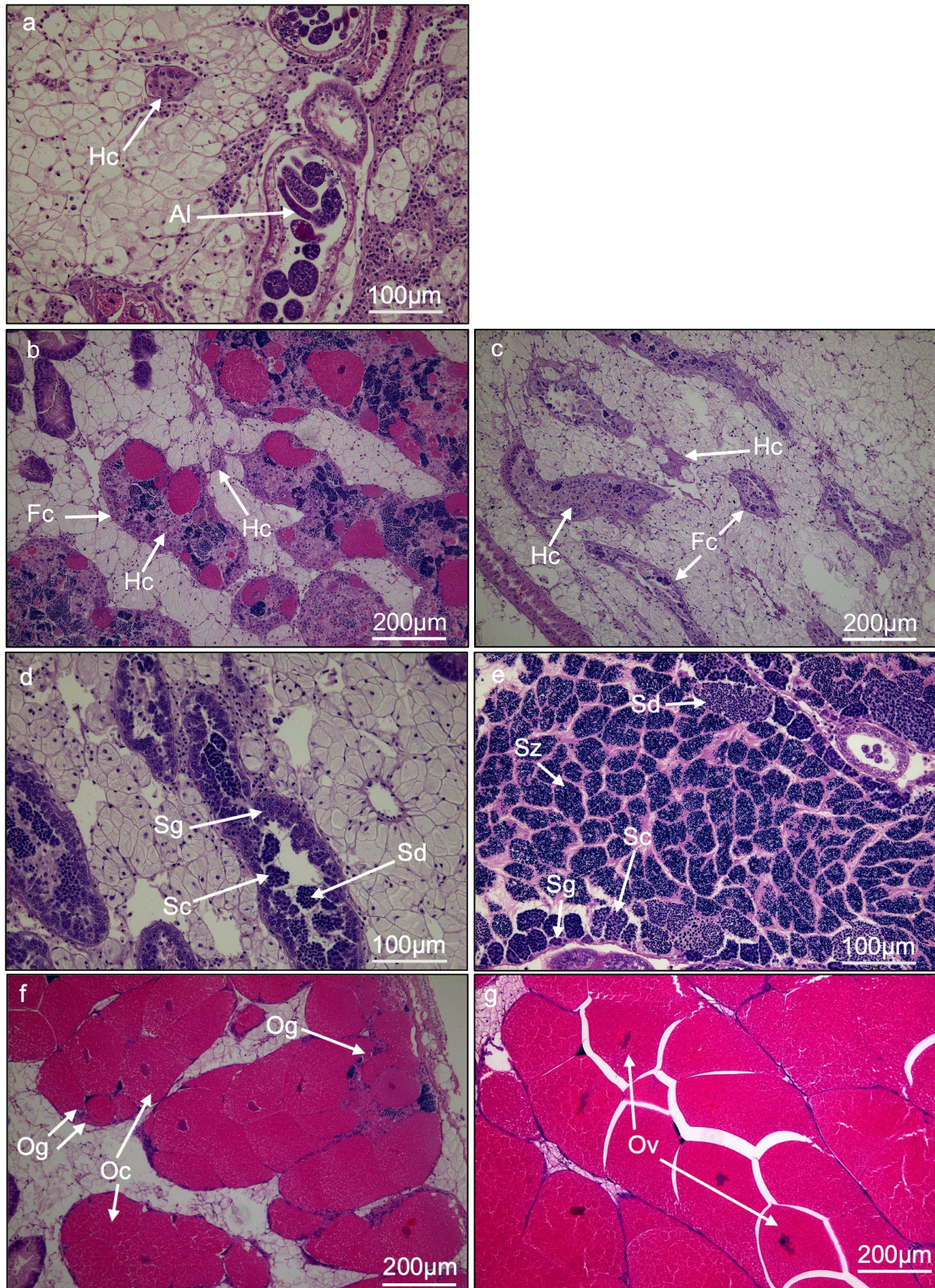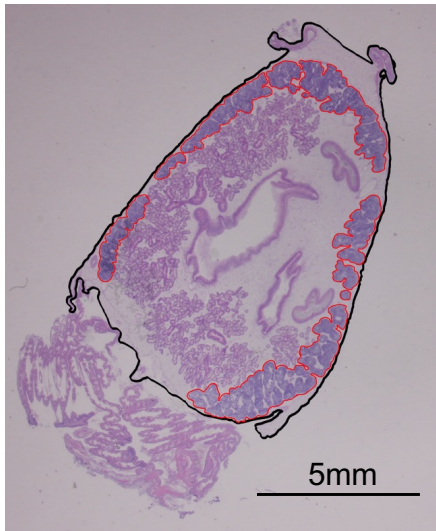
Figure S2. Oyster tissue cross section depicting areas selected to calculate Gonad Index. The black line marks the selected cross section area, and the red line marks the selected gonad area.
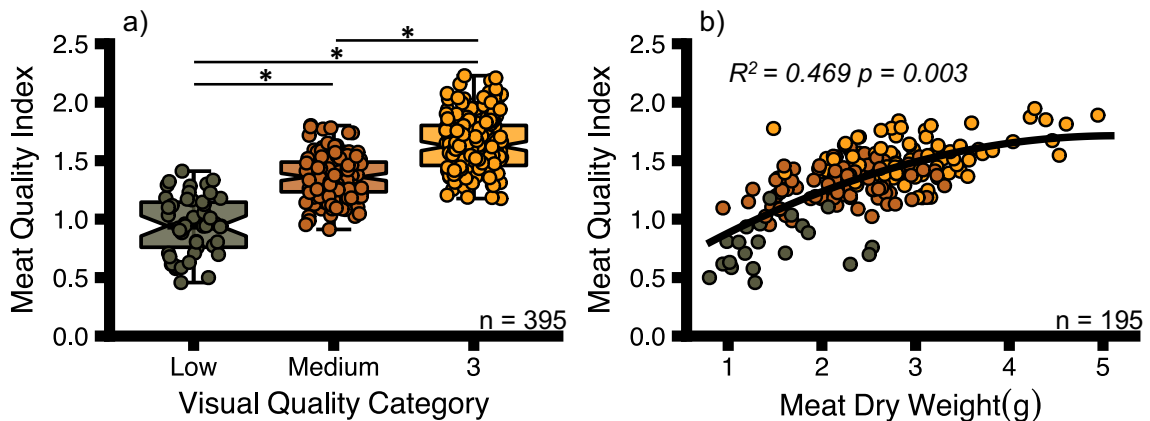
Figure S3. a) Box plot showing meat quality index in different visual meat quality categories. Bold solid line indicates the median, box shows the interquartile range (IQR), the whiskers are 1.5×IQR; **b)** meat quality index plotted against meat dry weight (g). Colours indicate visual meat quality categories (grey: low quality; bronze: medium quality; gold: good quality). Lines and asterisks indicate significance.

Table S2. Comparison of mean meat quality index in different Visual Quality categories. Model statistics are from general linear model and post-hoc Tukey comparisons.

Dependent Variable: Meat Quality Index; Residual deviance: 18.009, df: 391, AIC: -89.56				
Comparison: Visual Quality Categories	**Mean Difference**	**Std. Error**	**t**	**padj.**
Low: Medium	0.415	0.035	11.86	**< 0.001**
Low: Good	0.698	0.035	20.23	**< 0.001**
Medium: Good	0.283	0.023	12.21	**< 0.001**

Table S3. Regression of impact of meat quality index on meat dry weight (g). Model statistics are from general linear model (formula = polynomial).

Dependent Variable: Meat Quality Index							
Independent Variable	**F**	**p**	**df**	**Residual df**	**Residual SE**	**Multiple R^2**	**Adjusted R^2**
Meat Dry Weight (g)	85.830	< 0.001	21	190	0.204	0.475	0.469

Table S4. Regression of impact of sponge infestation (boreholes cm^{-2}) on meat quality index. Model statistics are from general linear model.

Dependent Variable: Sponge infestation (boreholes cm^{-2})							
Independent Variable	**F**	**p**	**df**	**Residual df**	**Residual SE**	**Multiple R^2**	**Adjusted R^2**
Meat Quality Index	2.832	0.093	1	392	0.313	0.007	0.005

Table S5. Regression of impact of sponge infestation (boreholes cm^{-2}) on the condition index. Model statistics are from general linear model.

Dependent Variable: Sponge infestation (boreholes cm^{-2})							
Independent Variable	**F**	**p**	**df**	**Residual df**	**Residual SE**	**Multiple R^2**	**Adjusted R^2**
Condition Index	0.023	0.880	1	191	1.065	< 0.001	-0.005

Table S6. Results from logistic regression testing the effect of Length (mm) on oyster sex (Male/Female) in oysters with sponge infestation and uninfested oysters. Model statistics are from generalised linear model (family = binomial).

Independent Variable: Length (mm), Infestation; Dependent Variable: Sex (Male/Female) Residual Deviance: 101.74, Residual df: 117				
Effect	**Estimate**	**Std. Error**	**z**	**p**
Length (mm)	0.103	0.041	2.535	0.011
Infestation (infested/unifested)	-2.366	4.950	-0.478	0.633
Length: Infestation (infested/uninfested)	0.041	0.078	0.522	0.602
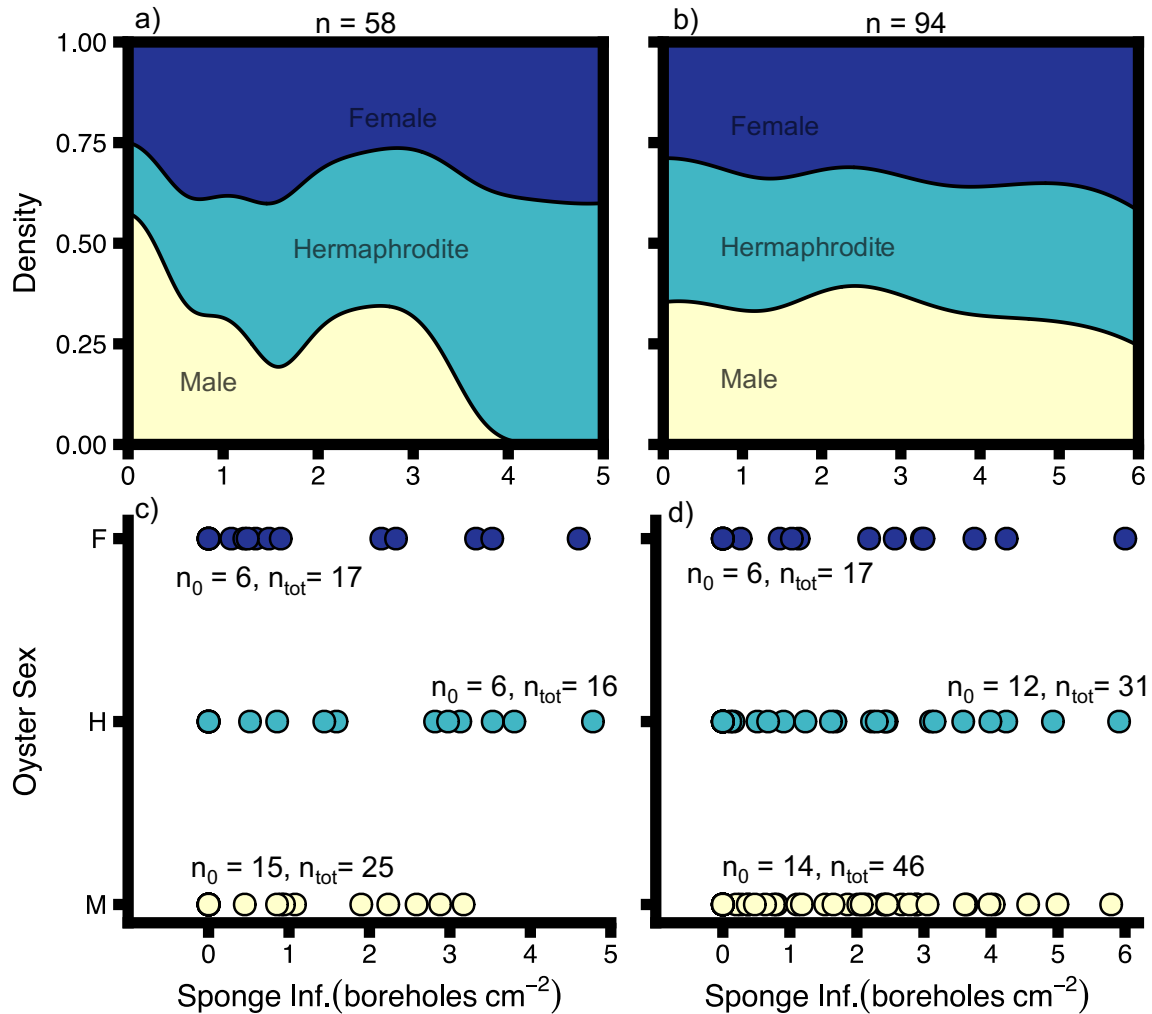
Figure S4. a)–b) Density plots illustrating kernel density estimate of the distribution of: **a)** sponge infestation within different sex categories for medium (~50–58 mm) oysters; **b)** sponge infestation within different sex categories for large (>58 mm) oysters; **c)–d)** Dot plots showing the distribution of broad sex categories (M= Male, H = Hermaphrodite, F = Female) in relation to sponge infestation (boreholes cm^{-2}) for **c)** medium (~50–58 mm) oysters and **d)** large oysters (>58 mm). Male: >60% male reproductive cells, Hermaphrodite: 60–40% male reproductive cells, Female: >60% female reproductive cells. n_0 = number of uninfested oysters (0 boreholes cm^{-2}) per category, n_{tot} = number of oysters in total per category.
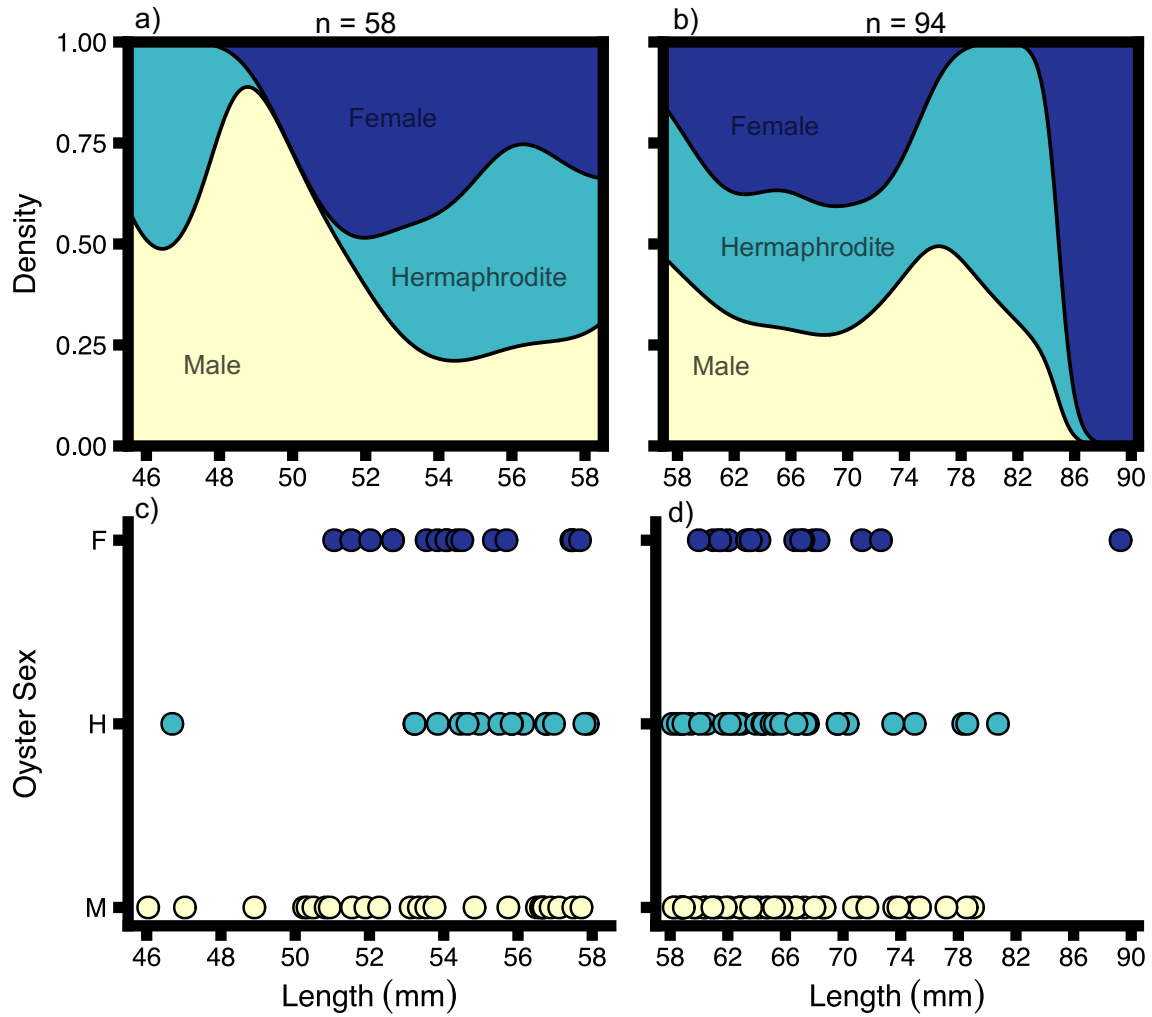
Figure S5. a)–b) Density plots illustrating kernel density estimate of the distribution of **a)** shell length (mm) within different sex categories for medium (~50–58 mm) oysters; **b)** shell length (mm) within broad sex categories (M= Male, H = Hermaphrodite, F = Female) for large (>58 mm) oysters. **c)–d)** Dot plots showing the distribution of broad sex categories in relation to shell length (mm) for **c)** medium (~50–58 mm) oysters and **d)** large oysters (>58 mm). Male: >60% male reproductive cells, Hermaphrodite: 60–40% male reproductive cells, Female: >60% female reproductive cells.

Table S7. Relationship of sponge infestation to broader sex categories in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

Independent Variable: Sponge Infestation (boreholes cm^{-2}); Medium oysters: Residual deviance 120.622, AIC: 128.622; Large oysters: Residual deviance 192.517; AIC: 200.517

Size Category	Dependent Variable: Broad Sex Categories	Estimate	Std. Error	z	p	padj.
Medium	Male: Hermaphrodite	0.497	0.250	1.991	**0.046**	0.138
	Male: Female	0.294	0.254	1.157	0.247	0.371
	Hermaphrodite: Female	-0.203	0.237	-0.857	0.392	0.392
Large	Male: Hermaphrodite	-0.038	0.142	-0.270	0.791	0.857
	Male: Female	0.030	0.167	0.181	0.857	0.857
	Hermaphrodite: Female	0.068	0.180	0.376	0.710	0.857

Table S8. Relationship of sponge infestation to detailed sex categories in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

Independent Variable: Sponge Infestation (boreholes cm^{-2}); Medium: Residual deviance 158.938, AIC: 174.938; Large: Residual deviance 278.639; AIC: 294.639

| Size Category	Dependent Variable: Detailed Sex Categories	Estimate	Std. Error	z	p	padj.
Medium	Male: Pred. Male	0.496	0.419	1.182	0.237	0.593
	Male: Equal	0.255	0.309	0.826	0.409	0.682
	Male: Pred. Female	0.643	0.287	0.954	**0.025**	0.250
	Male: Female	0.269	0.282	2.240	0.340	0.680
	Female: Pred. Male	0.227	0.429	0.528	0.597	0.746
	Female: Equal	-0.014	0.325	-0.042	0.966	0.966
	Female: Pred. Female	0.374	0.300	1.250	0.211	0.593
	Pred. Male: Equal	-0.240	0.448	-0.537	0.591	0.746
	Pred. Male: Pred. Female	0.148	0.426	-0.528	0.729	0.810
	Equal: Pred. Female	0.388	0.326	1.192	0.233	0.593
Large	Male: Pred. Male	-0.207	0.195	-1.061	0.289	0.485
	Male: Equal	-0.017	0.164	-0.101	0.920	0.920
	Male: Pred. Female	-0.286	0.222	-1.285	0.199	0.485
	Male: Female	0.187	0.216	0.864	0.388	0.485
	Female: Pred. Male	-0.394	0.256	-1.539	0.124	0.485
	Female: Equal	-0.203	0.231	-0.88	0.379	0.485
	Female: Pred. Female	-0.473	0.278	-1.701	0.089	0.485
	Pred. Male: Equal	0.191	0.211	0.902	0.367	0.485
	Pred. Male: Pred. Female	-0.078	0.257	-0.305	0.760	0.845
	Equal: Pred. Female	-0.269	0.237	-1.138	0.255	0.485

Table S9. Relationship of shell length (mm) to broader sex categories in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

| Size Category	Dependent Variables: Broad Sex Categories	Estimate	Std. Error	z	p	padj.
Independent Variable: Shell Length (mm); Medium: Residual deviance: 120.781, AIC: 128.781; Large: Residual deviance 192.123, AIC: 200.123
Medium	Male: Hermaphrodite	0.251	0.132	1.905	**0.056**	0.168
	Male: Female	0.114	0.111	1.021	0.307	0.461
	Hermaphrodite: Female	-0.092	0.140	-0.700	0.510	0.510
Large	Male: Hermaphrodite	0.017	0.038	0.447	0.655	0.751
	Male: Female	0.032	0.045	0.712	0.476	0.751
	Hermaphrodite: Female	0.015	0.047	0.317	0.751	0.751

Table S10. Relationship of shell length (mm) to detailed sex categories in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

Size Category	Dependent Variables: Sex Categories	Estimate	Std. Error	z	p	padj.
Independent Variable: Shell Length (mm); Medium: Residual deviance 159.548, AIC: 175.548; Large: Residual deviance 276.407, AIC:292.407
Medium	Male: Pred. Male	0.431	0.322	1.338	0.254	0.710
	Male: Equal	0.168	0.147	1.140	0.181	0.710
	Male: Pred. Female	0.212	0.155	1.368	0.171	0.710
	Male: Female	0.116	0.125	0.925	0.355	0.710
	Female: Pred. Male	0.332	0.337	0.985	0.324	0.710
	Female: Equal	0.064	0.169	0.376	0.707	0.846
	Female: Pred. Female	0.095	0.174	0.546	0.585	0.846
	Pred. Male: Equal	-0.109	0.293	-0.372	0.710	0.846
	Pred. Male: Pred. Female	-0.064	0.296	-0.216	0.830	0.846
	Equal: Pred. Female	0.037	0.192	0.195	0.846	0.846
Large	Male: Pred. Male	-0.084	0.062	-1.369	0.171	0.357
	Male: Equal	0.028	0.044	0.631	0.528	0.587
	Male: Pred. Female	-0.060	0.062	-0.924	0.336	0.480
	Male: Female	0.070	0.057	-1.241	0.218	0.363
	Female: Pred. Male	-0.155	0.075	-2.064	0.039	0.324
	Female: Equal	-0.043	0.059	-0.724	0.469	0.586
	Female: Pred. Female	-0.130	0.075	-1.733	0.083	0.324
	Pred. Male: Equal	0.107	0.064	1.659	0.097	0.324
	Pred. Male: Pred. Female	0.026	0.075	0.343	0.731	0.731
	Equal: Pred. Female	-0.088	0.065	-1.345	0.179	0.357
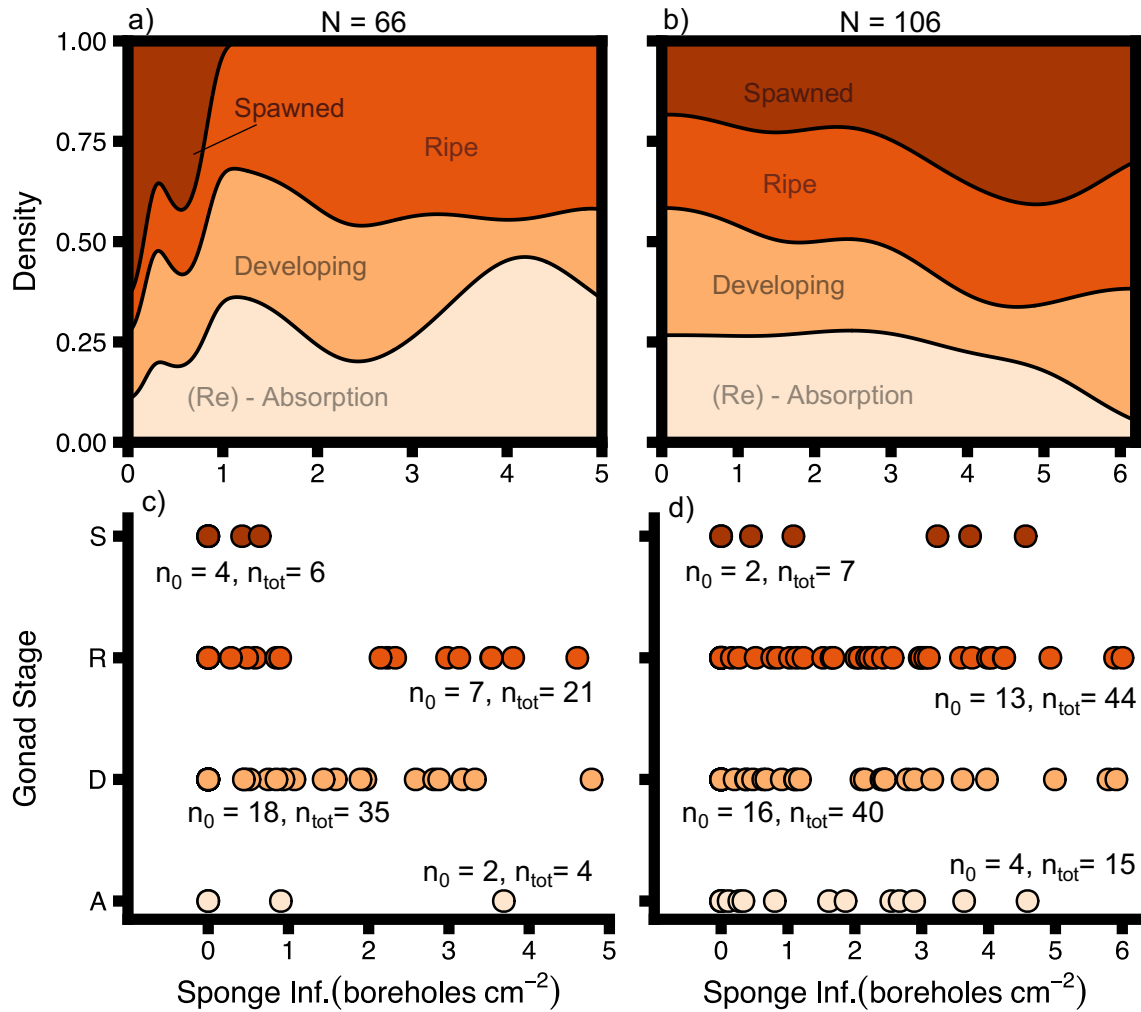
Figure S6. a)–b) Density plots illustrating kernel density estimate of the distribution of **a)** sponge infestation (boreholes cm^{-2}) within different gonad development stages for medium (~50–58 mm) oysters; **b)** sponge infestation (holes cm^{-2}) within different gonad development stages for large (>58 mm) oysters. **c)–d)** Dot plots showing the distribution of gonad development stages in relation to sponge infestation (boreholes cm^{-2}) for **c)** medium (~50–58 mm) oysters and **d)** large (>58 mm) oysters. n_0 = number of uninfested oysters (0 boreholes cm^{-2}) per category, n_{tot} = number of oysters in total per category.
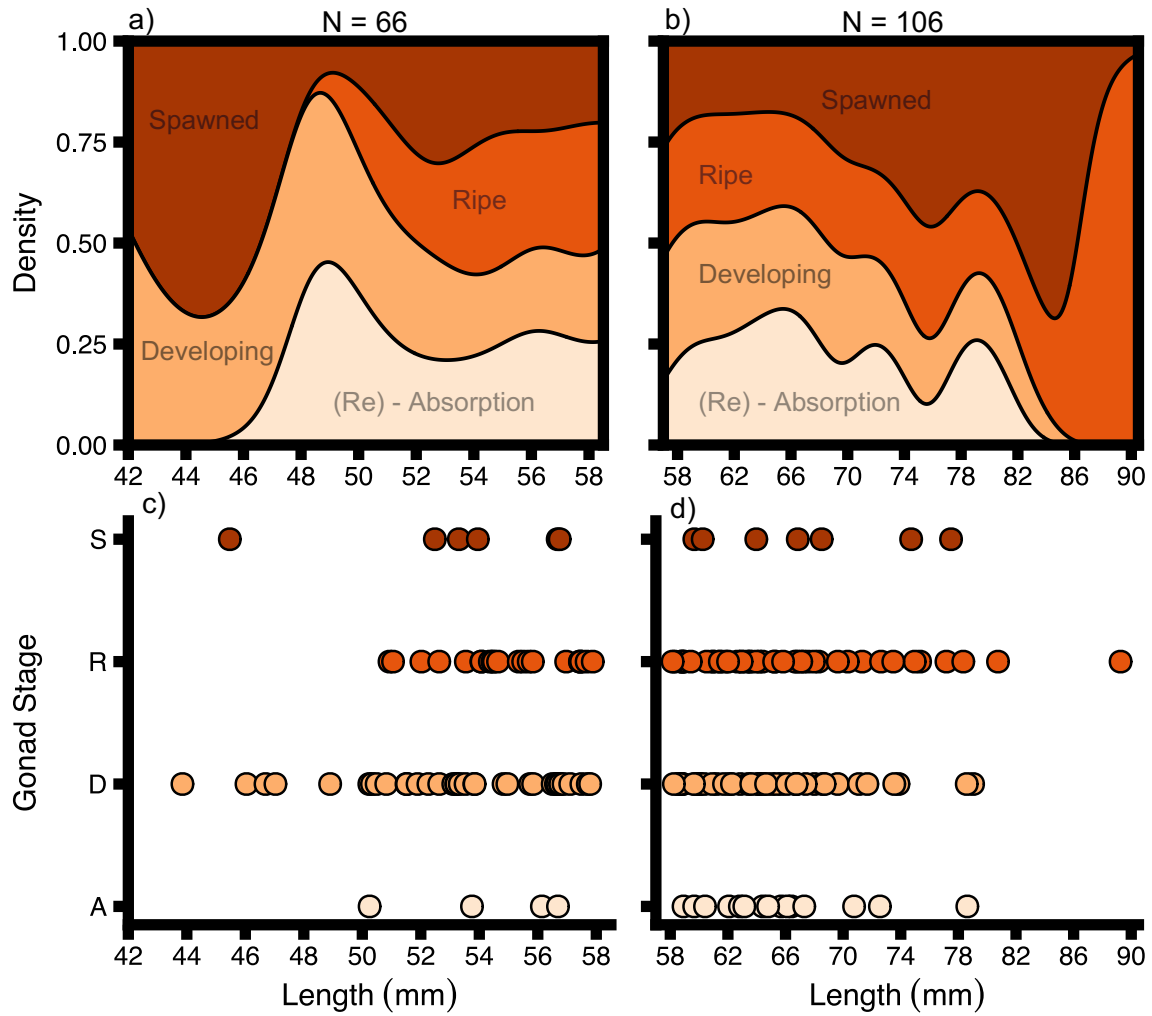
Figure S7. a)–b) Density plots illustrating kernel density estimate of the distribution of **a)** shell length (mm) within different gonad development stages for medium (~50–58 mm) oysters; **b)** shell length (mm) within different gonad development stages for large (>58 mm) oysters. **c)–d)** Dot plots showing the distribution of gonad development stages in relation to shell length (mm) for **c)** medium (~50–58 mm) oysters and **d)** large oysters (>58 mm).

Table S11. Relationship of sponge infestation to developmental stages in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

Oyster Size Category	Dependent Variable: Gonad Stage	Estimate	Std. Error	z	p	padj.
	Independent Variable: Sponge Infestation (boreholes cm^{-2}); Medium oyster: Residual deviance: 397.130, AIC: 409.130; Large oysters: Residual deviance: 397.130, AIC: 409.130					
Medium	Ripe: Absorption	-0.161	0.385	-0.416	0.677	0.713
	Ripe: Developing	-0.301	0.199	-1.516	0.130	0.375
	Ripe: Spawned	-1.400	0.960	-1.457	0.145	0.375
	Developing: Absorption	0.141	0.382	0.368	0.713	0.713
	Developing: Spawned	-1.098	0.955	-1.150	0.250	0.375
	Absorption: Spawned	-1.237	1.011	-1.223	0.221	0.375
Large	Ripe: Absorption	-0.132	0.181	-0.730	0.465	0852
	Ripe: Developing	-0.158	0.132	-1.202	0.229	0.852
	Ripe: Spawned	0.019	0.227	0.082	0.935	0.935
	Developing: Absorption	0.026	0.188	0.140	0.889	0.935
	Developing: Spawned	0.177	0.233	0.759	0.448	0.852
	Absorption: Spawned	0.151	0.264	0.570	0.568	0.852

Table S12. Relationship of shell length (mm) to gonad developmental stages in medium and large oysters. Model statistics are from multinomial logistic regression and wald-test.

Size Category	Dependent Variable: Gonad Stage	Estimate	Std. Error	z	p	padj.
	Independent Variable: Shell Length (mm); Medium: Residual deviance: 138.914, AIC: 150.914; Large: Residual deviance: 394.672, AIC: 406.672					
Medium	Ripe: Absorption	0.096	0.194	-0.496	0.620	0.810
	Ripe: Developing	-0.205	0.105	-1.939	0.052	0.312
	Ripe: Spawned	-0.208	0.151	-1.376	0.169	0.507
	Developing: Absorption	0.104	0.179	0.580	0.562	0.810
	Developing: Spawned	< 0.001	0.129	0.002	0.998	0.998
	Absorption: Spawned	-0.086	0.206	-0.419	0.675	0.810
Large	Ripe: Absorption	-0.022	0.051	-0.437	0.662	0.753
	Ripe: Developing	-0.036	0.038	-0.952	0.341	0.753
	Ripe: Spawned	0.025	0.061	0.401	0.689	0.753
	Developing: Absorption	0.017	0.053	0.315	0.753	0.753
	Developing: Spawned	0.063	0.063	0.988	0.323	0.753
	Absorption: Spawned	0.045	0.072	0.625	0.532	0.753

Table S13. Regression of impact of sponge infestation (boreholes cm^{-2}) on gonad index for developing and ripe oysters. Model statistics are from general linear model.

Gonad Stage	F	p	df	Multiple R2	Adjusted R2	Residual SE	Residual df
	Dependent Variable: Gonad Index, Independent Variable: Sponge Infestation						
Developing	1.762	0.189	1	0.025	0.012	0.062	70
Ripe	0.008	0.925	11	< 0.001	-0.016	0.063	63

Table S14. Relationship of sponge infestation to presence and absence (P/A) of different pathogens and number of pathogen types. Model statistics are from generalised linear models (P/A: family = binomial; Number of pathogen types: family = Poisson). APX = Apicomplexan X, RLO/ELO = Rickettsia-/Endozoicomonas-like organisms, *Alcicornis = Alcicornis longicornutus, M. rapuae = Microsporidium rapuae. Bonamia = Bonamia exitiosa.*

| Dependent Variable	Effect	Estimate	Std. Error	z	p	Residual deviance	AIC
Bonamia P/A	Sponge	-0.223	0.195	-1.145	0.252	256.67	264.67
	PO	-0.275	0.402	-0.683	0.495	256.67	264.67
	Sponge: PO	0.0361	0.227	0.159	0.873	256.67	264.67
APX P/A	Sponge	0.101	0.128	0.787	0.432	272.8	280.8
	PO	-0.217	0.374	-0.581	0.561	272.8	280.8
	Sponge: PO	0.028	0.181	0.155	0.876	272.8	280.8
Alcicornis	Sponge	0.155	0.267	0.582	0.561	148.90	156.9
	PO	0.587	0.726	0.809	0.419	148.90	156.9
	Sponge: PO	-0.329	0.317	-1.038	0.299	148.90	156.9
M. rapuae	Sponge	0.121	0.286	0.420	0.675	132.63	140.63
	PO	-0.665	0.7452	-0.893	0.372	132.63	140.63
	Sponge: PO	0.208	0.321	0.647	0.518	132.63	140.63
RLO/ELO	Sponge	-0.087	0.314	-0.278	0.781	124.10	132.10
	PO	-0.495	0.678	-0.730	0.465	132.63	140.63
	Sponge: PO	-0.015	0.367	-0.041	0.968	132.63	140.63

Table heading: Independent Variable: Sponge Infestation (boreholes cm^{-2}, Sponge) and Presence of other diseases (PO); Dependent Variable: Pathogens P/A. **df** =195

Table S15. Relationship of sponge infestation to number of pathogen types. Model statistics are from generalised linear models (Number of pathogen types: family = Poisson).

Table heading: Independent Variable: Sponge Infestation (boreholes cm^{-2}, Sponge) and Presence of other diseases (PO); Dependent Variable: Pathogens P/A

Dependent Variable		Estimate	Std. Error	z	p	df	Residual deviance	AIC
Number of pathogen types	PO	0.040	0.028	0.977	197	151.88	524.06	

Table S16. Relationship of sponge infestation to presence and absence of any type of pathogen. Model statistics are from generalised linear model (family = binomial).

Table heading: Independent Variable: Sponge Infestation (boreholes cm^{-2}); Residual deviance: 200.1, AIC: 204.1

Dependent Presence/Absence	Variable:	Estimate	Std. Error	z	p	df
Pathogen Presence		-0.0232	0.1081	-0.215	0.83	199
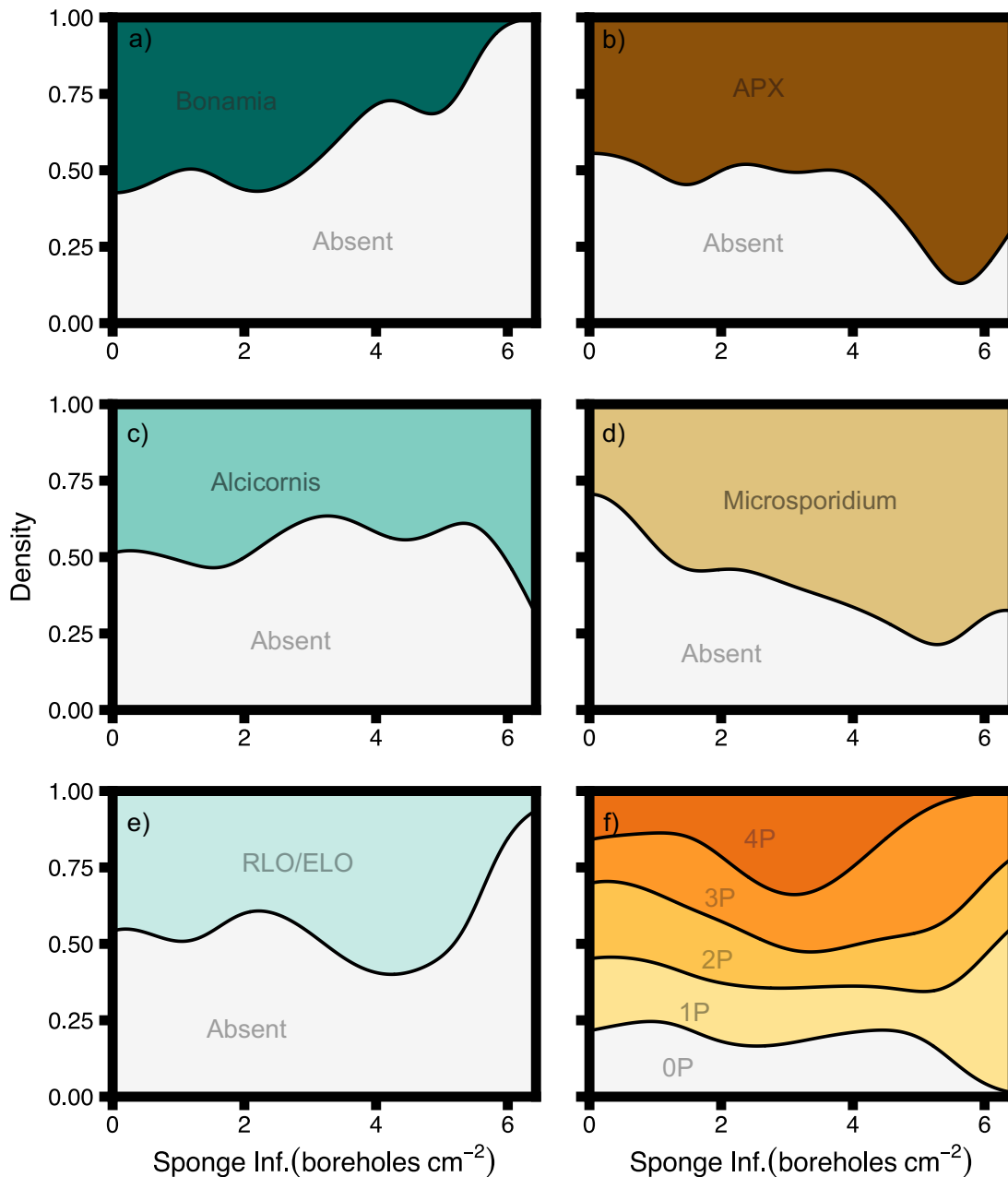
Figure S8. a)-e) Density plots illustrating kernel density estimate of the distribution of sponge infestation (holes cm^{-2}) in oysters with presence/absence of **a)** Bonamia = *Bonamia exitiosa*, **b)** APX = Apicomplexan X, **c)** Alcicornis = *Alcicornis longicornutus*, **d)** Microsporidium = *Microsporidium rapuae*, **e)** RLO/ELO = Rickettsia-/Endozoicomonas-like organism. **f)** Density plot illustrating the distribution of sponge infestation (holes cm^{-2}) in relation to number of different pathogen types detected. 0P = zero pathogens detected, 1P = one type of pathogen detected, 2P = two types of pathogens detected, 3P = three types of pathogens detected, 4P = four types of pathogens detected. Colours indicate type of pathogen present (greywhite = none, petrol = *B. exitiosa*, brown = APX, lightpetrol = *A. longicornutus*, lightbrown = *M. rapuae*, lightblue = RLO/ ELO = Rickketsia-/ Endozoicomonas-like organism).

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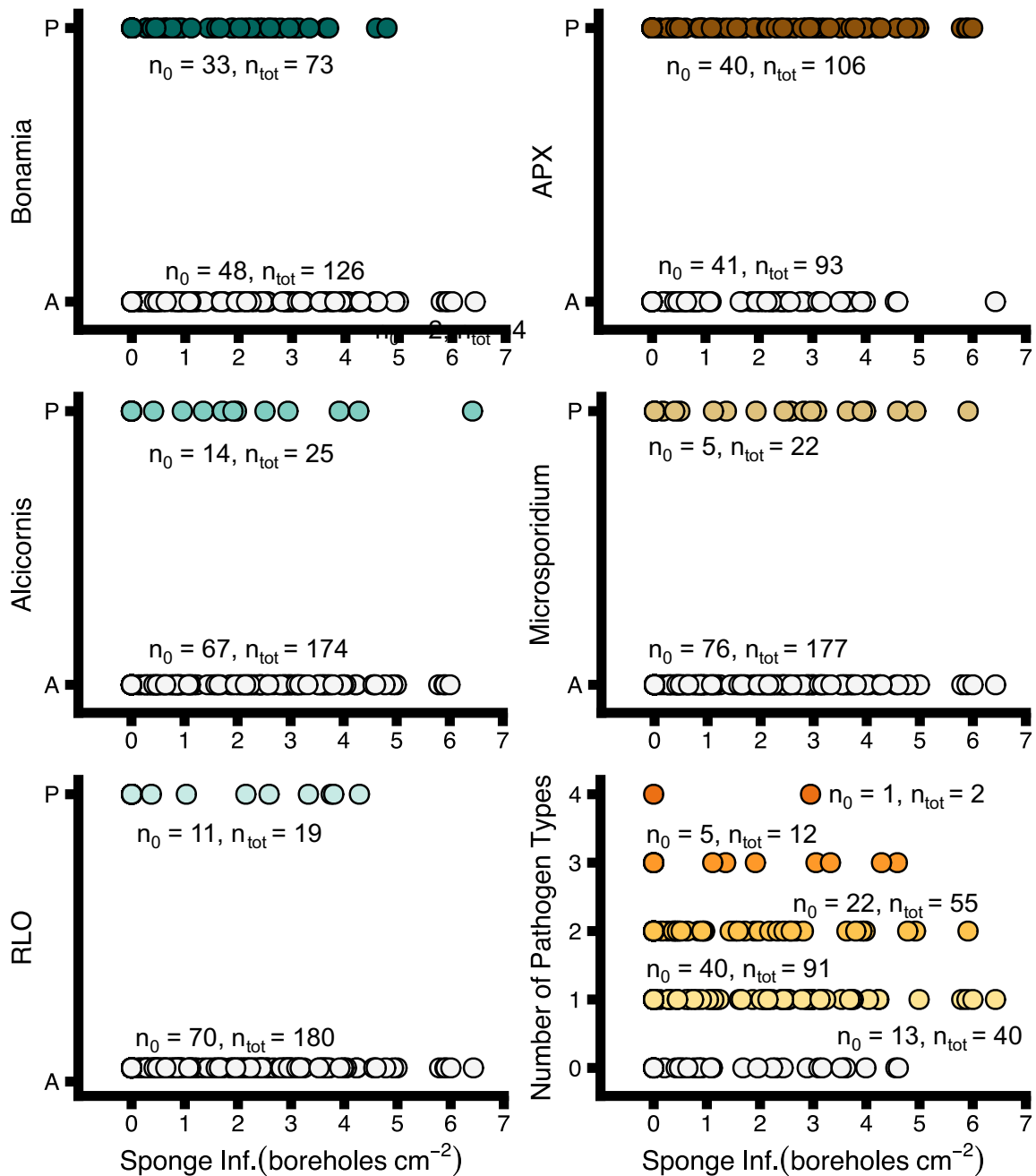
Figure S9. a)–e) Dot plots showing the distribution of pathogen presence and absence in relation to Sponge Infestation (boreholes cm^{-2}) for **a)** Bonamia = *Bonamia exitiosa*, **b)** APX = Apicomplexan X, **c)** Alcicornis = *Alcicornis longicornutus*, **d)** Microsporidium = *Microsporidium rapuae*, **e)** RLO/ELO = Rickettsia-/Endozoicomonas-like organism. **f)** Dot plots showing the distribution number of different pathogen types detected in relation to Sponge Infestation (boreholes cm^{-2}). Colours indicate type of pathogen present (greywhite = none, petrol = *B. exitiosa*, brown = APX, lightpetrol = *A. longicornutus*, lightbrown = *M. rapuae*, lightblue = RLO/ ELO = Rickketsia-/ Endozoicomonas-like organism). n_0 = number of uninfested oysters (0 boreholes cm^{-2}) per category, n_{tot} = number of oysters in total per category.