SEACAR Oyster Analysis

Last compiled on 18 June, 2025

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Important Notes

The purpose of this script is to group oyster data, create managed area statistics, perform lme analysis on density, percent live, and shell height, and create reports in pdf and Word document form for Oyster data.

All scripts and outputs can be found on the SEACAR GitHub repository:

https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses

This markdown file is designed to be compiled by Oyster_ReportRender.R (https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Oyster/Oyster_ReportRender.R).

This script is based off of code originally written by Stephen Durham.

Compiled and edited by J.E. Panzik and Tyler Hill for SEACAR.

Oyster Figures

Density

Apalachicola Bay Aquatic Preserve

Natural

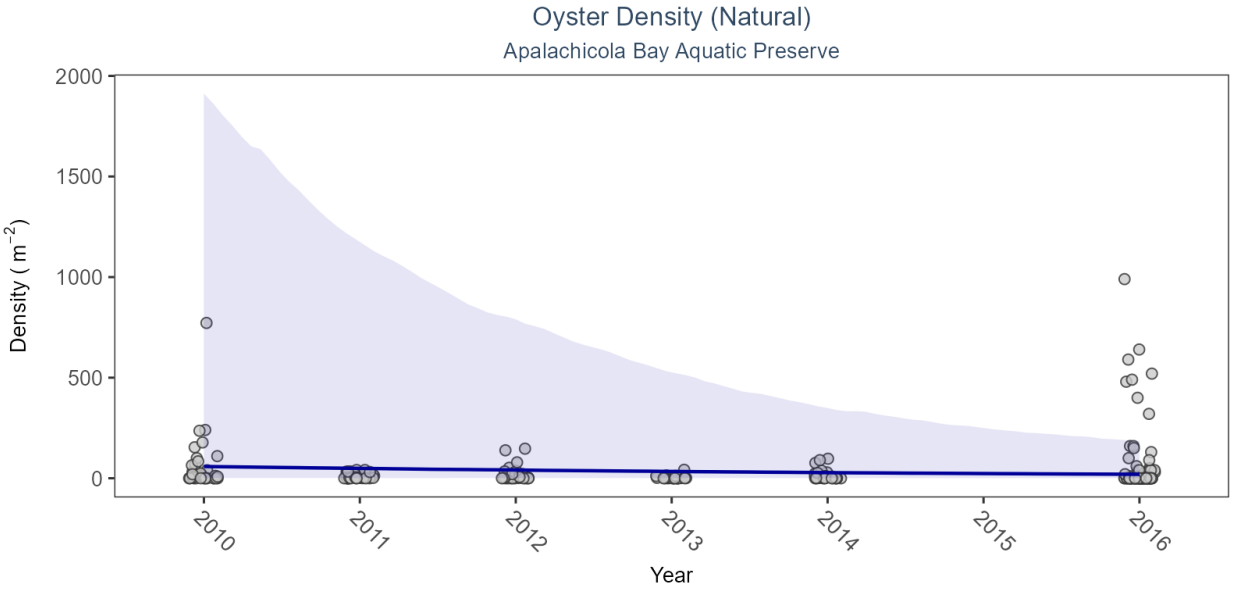


Figure 1: Figure for Oyster Density in Apalachicola Bay Aquatic Preserve

Table 1: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-7	43.4	-0.13 to -267.35

Restored

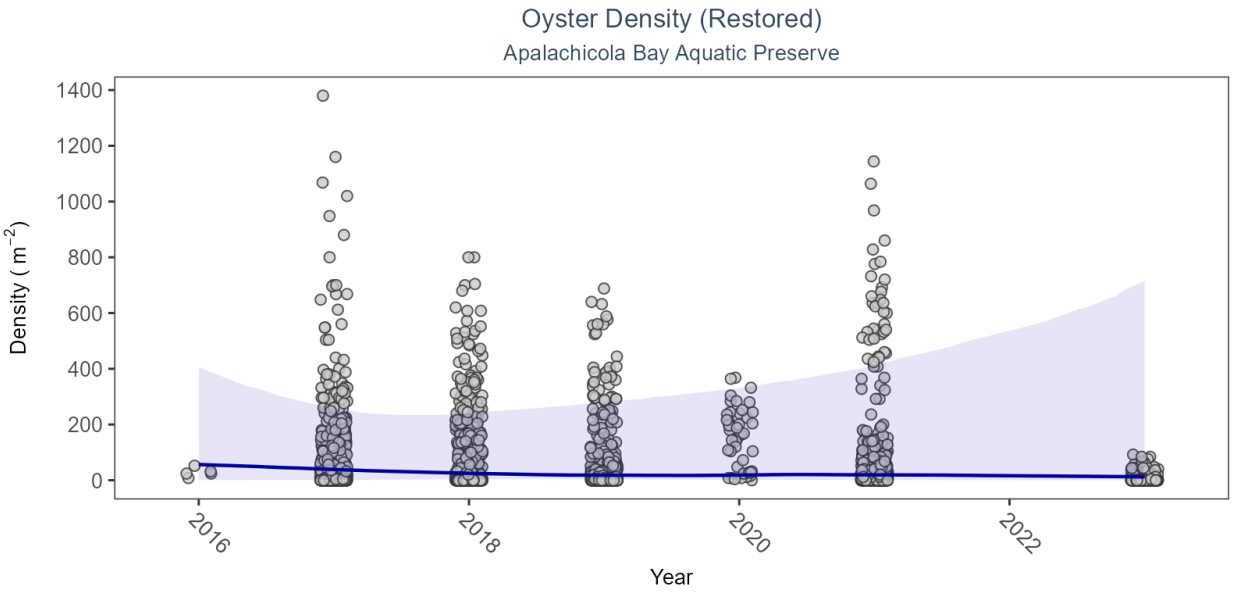
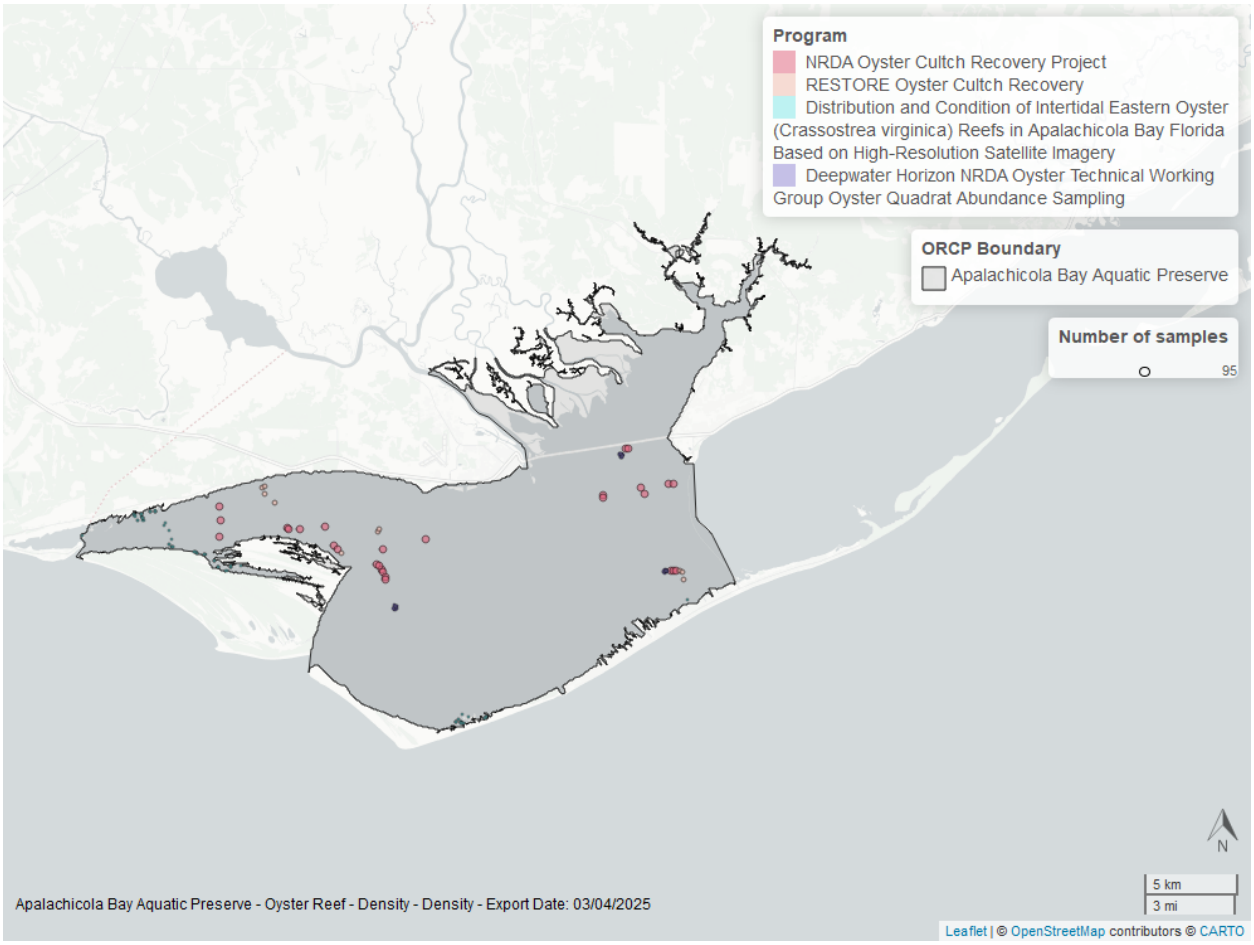


Figure 2: Figure for Oyster Density in Apalachicola Bay Aquatic Preserve

Table 2: Model results for Oyster Density - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	No significant change	-6.01	27.49	-0.05 to 33.37


Program
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Distribution and Condition of Intertidal Eastern Oyster (Crassostrea virginica) Reefs in Apalachicola Bay Florida Based on High-Resolution Satellite Imagery
Deepwater Horizon NRDA Oyster Technical Working Group Oyster Quadrat Abundance Sampling
ORCP Boundary
Apalachicola Bay Aquatic Preserve
Number of samples
95
N
5 km
3 mi
Apalachicola Bay Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Apalachicola National Estuarine Research Reserve

Natural

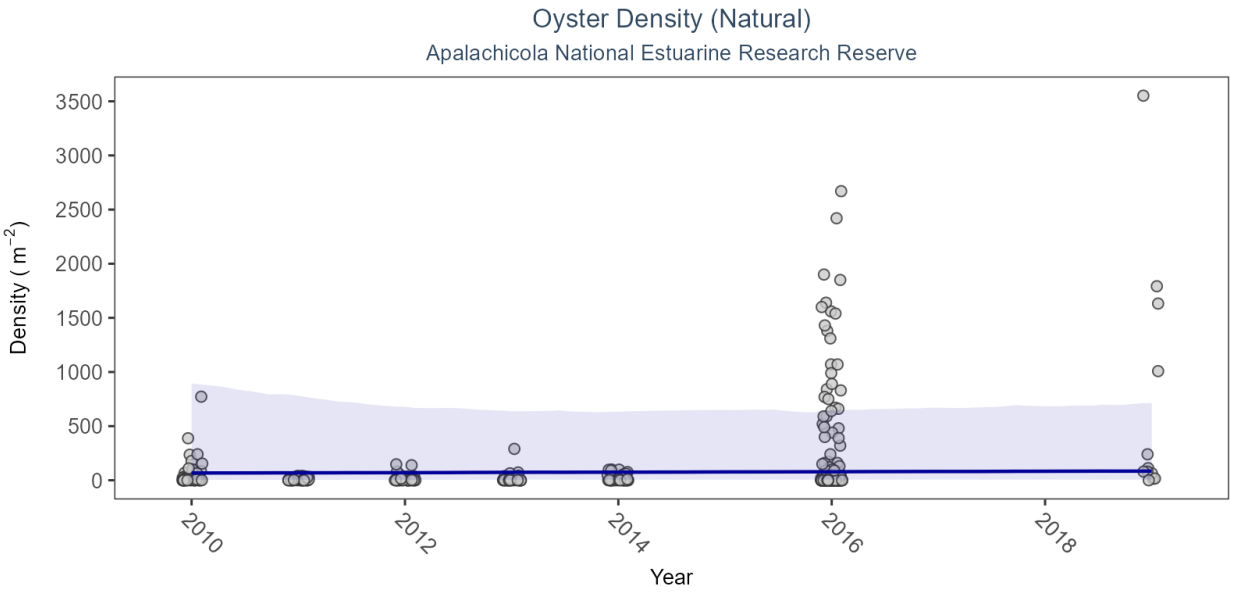


Figure 3: Figure for Oyster Density in Apalachicola National Estuarine Research Reserve

Table 3: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	No significant change	2.24	76.45	0.15 to -6.18

Restored

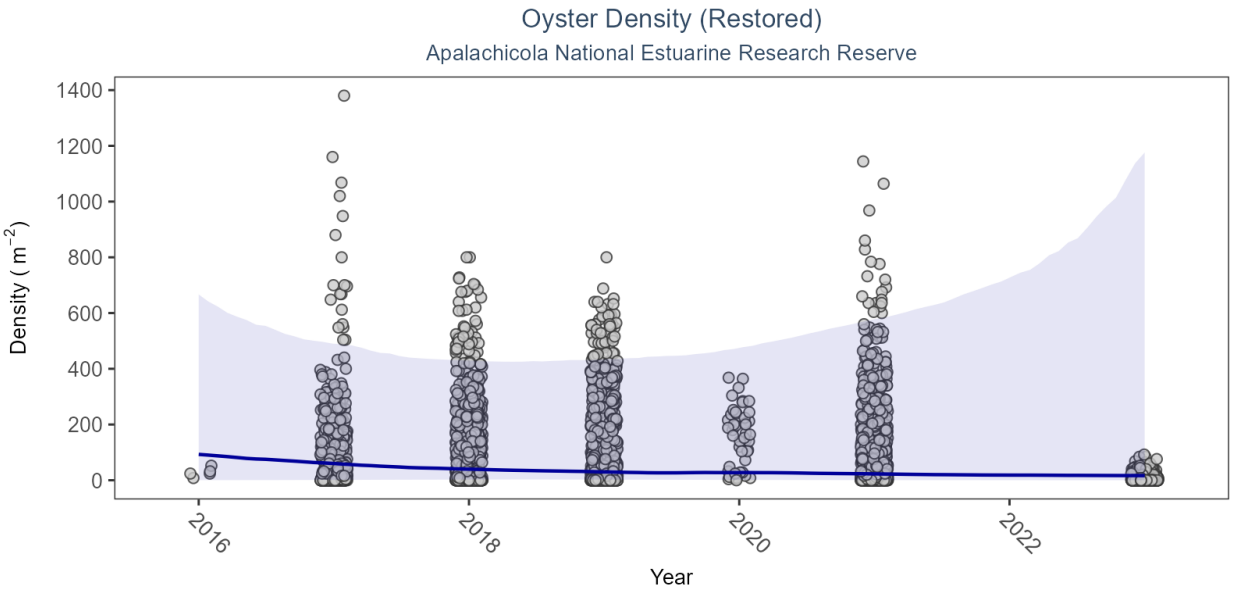
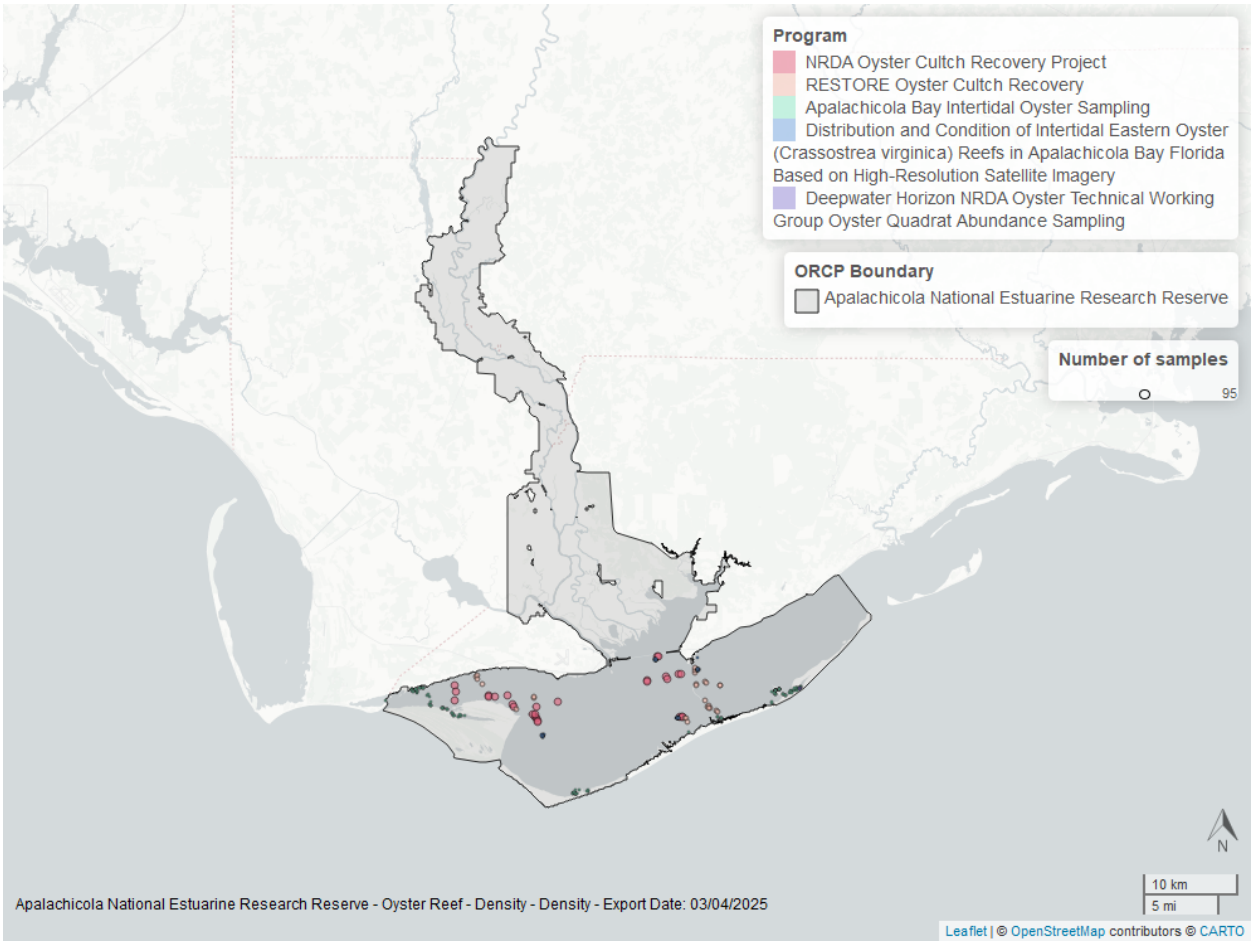


Figure 4: Figure for Oyster Density in Apalachicola National Estuarine Research Reserve

Table 4: Model results for Oyster Density - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	No significant change	-11.57	54.61	-0.03 to 72.25


Program
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Apalachicola Bay Intertidal Oyster Sampling
Distribution and Condition of Intertidal Eastern Oyster (Crassostrea virginica) Reefs in Apalachicola Bay Florida Based on High-Resolution Satellite Imagery
Deepwater Horizon NRDA Oyster Technical Working Group Oyster Quadrat Abundance Sampling
ORCP Boundary
Apalachicola National Estuarine Research Reserve
Number of samples
95
N
10 km
5 mi
Apalachicola National Estuarine Research Reserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Boca Ciega Bay Aquatic Preserve

Natural

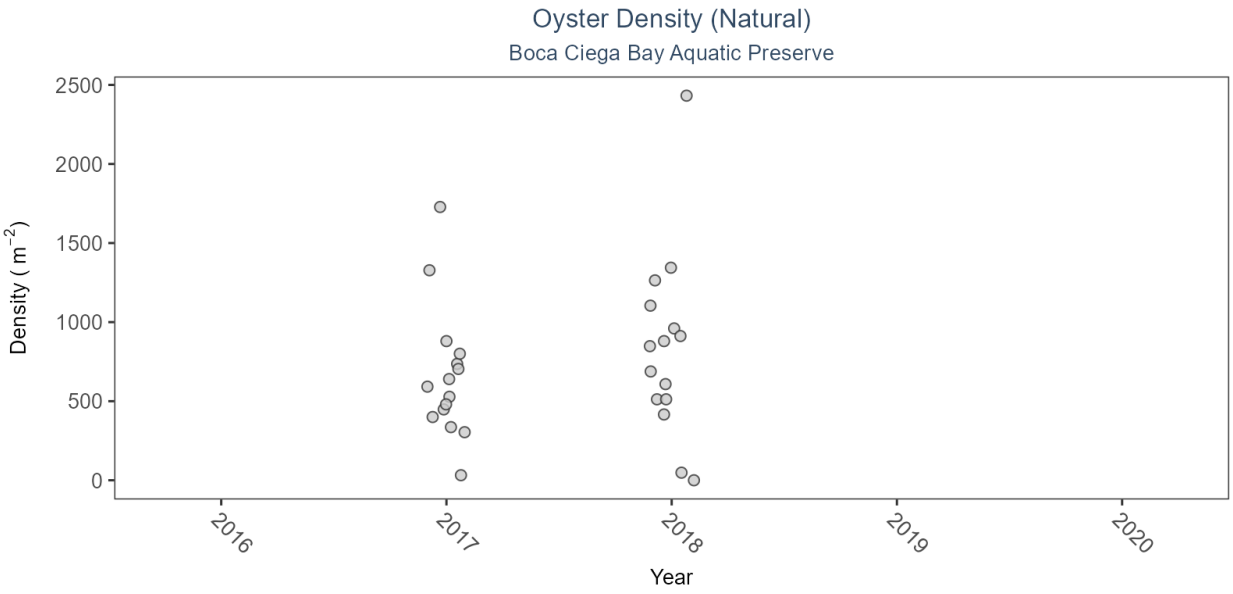
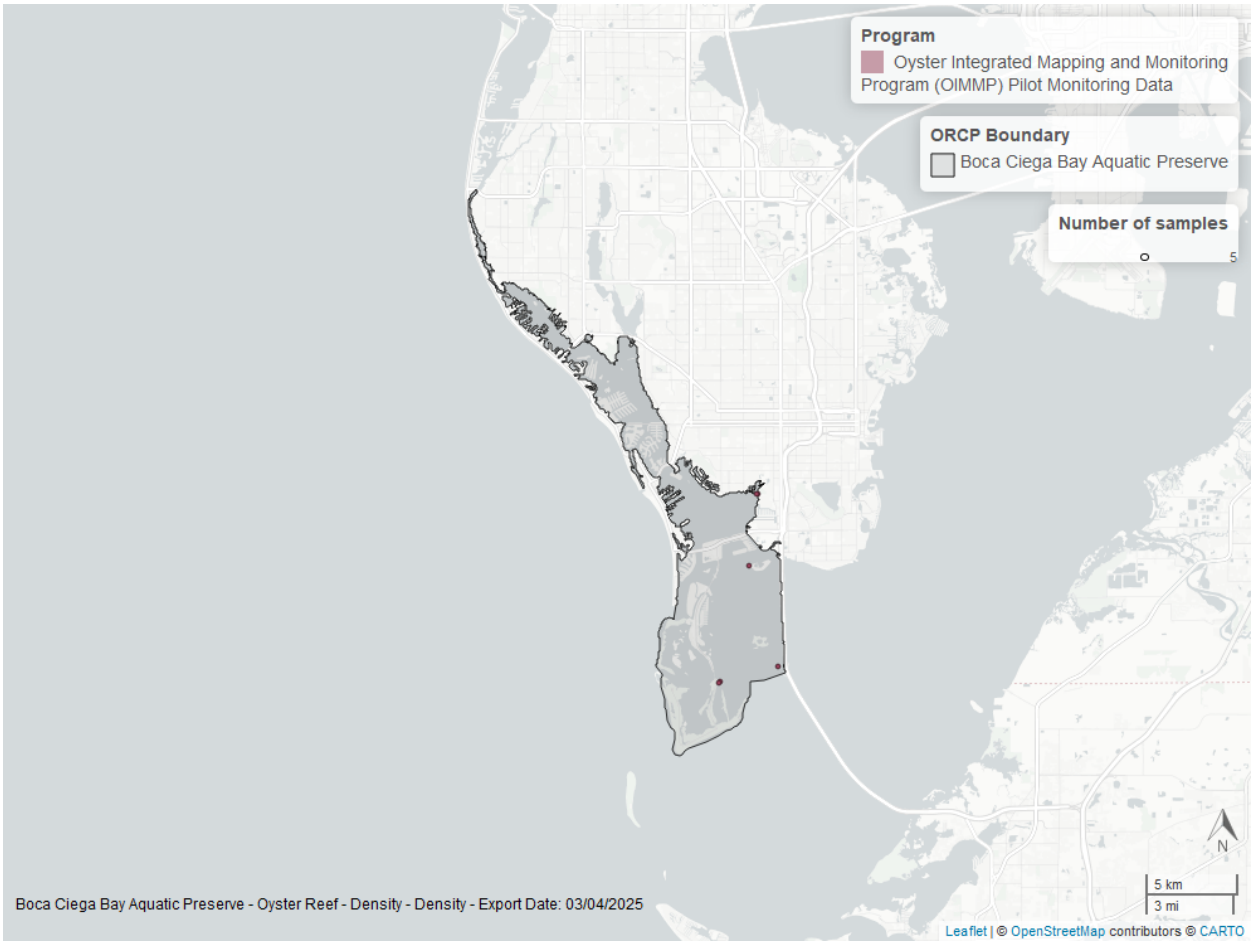


Figure 5: Figure for Oyster Density in Boca Ciega Bay Aquatic Preserve

Table 5: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Boca Ciega Bay Aquatic Preserve
Number of samples
0
5
N
5 km
3 mi
Boca Ciega Bay Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Estero Bay Aquatic Preserve

Restored

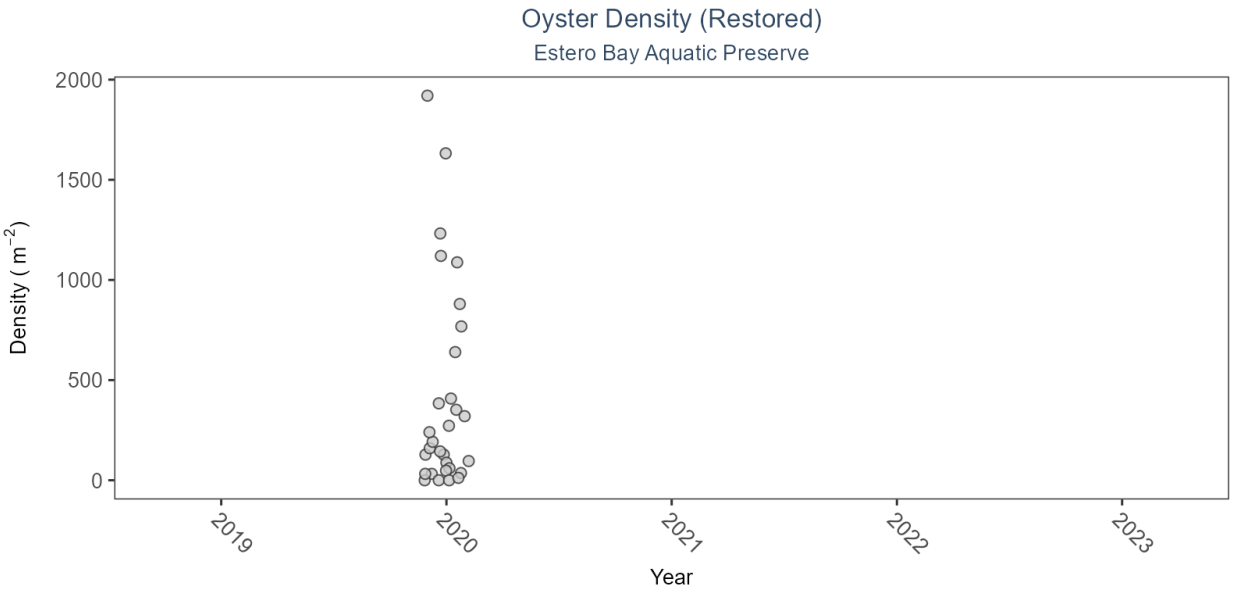


Figure 6: Figure for Oyster Density in Estero Bay Aquatic Preserve

Table 6: Model results for Oyster Density - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	-	-	-	NA to NA

Natural

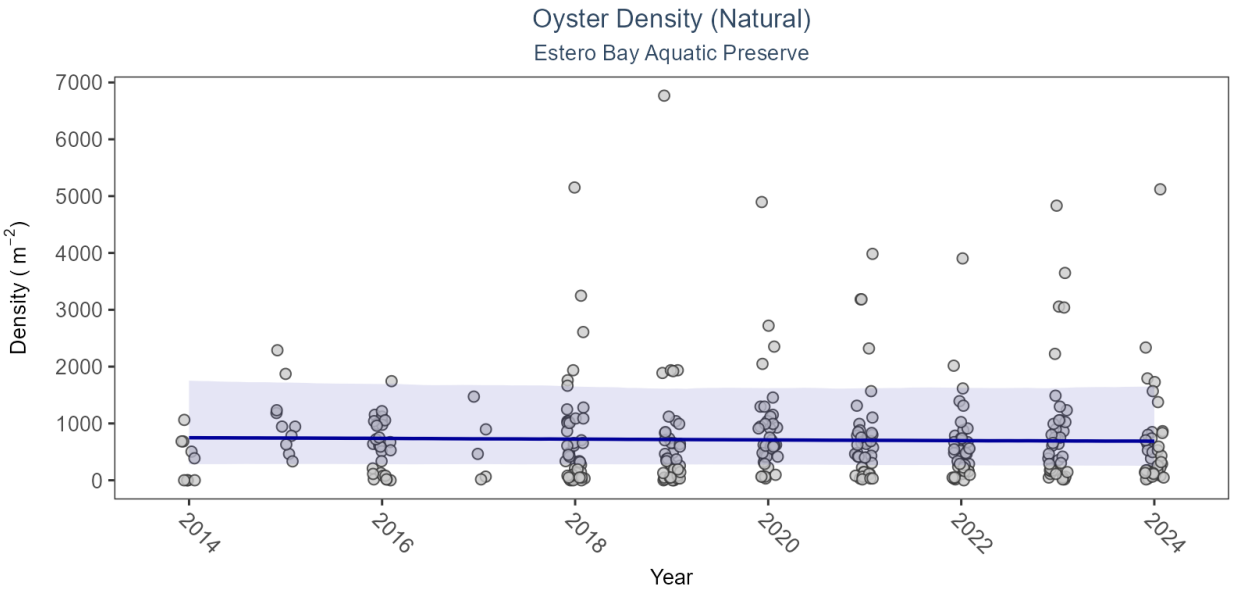
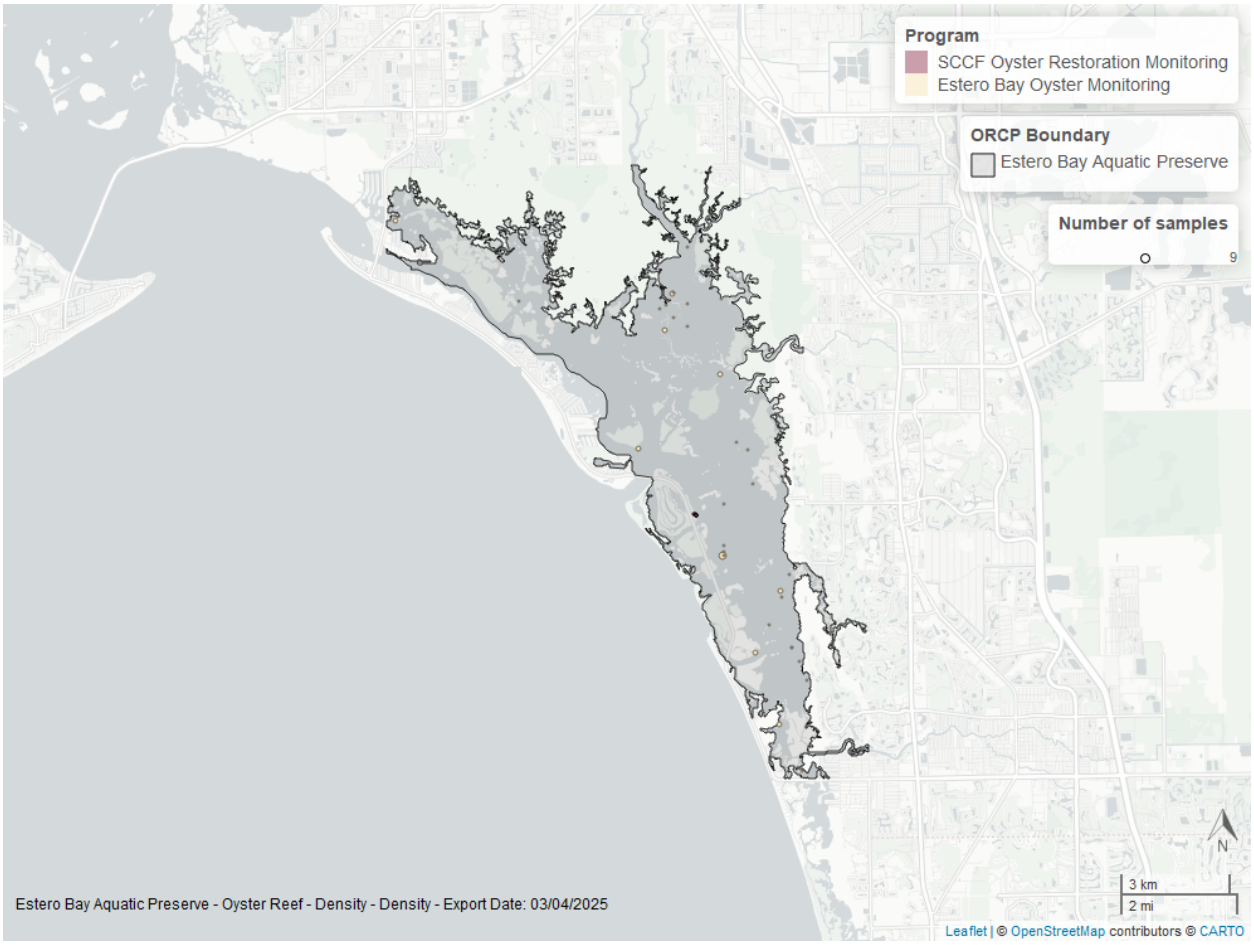


Figure 7: Figure for Oyster Density in Estero Bay Aquatic Preserve

Table 7: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-5.91	288.13	-2.84 to -9.47


Program
SCCF Oyster Restoration Monitoring
Estero Bay Oyster Monitoring
ORCP Boundary
Estero Bay Aquatic Preserve
Number of samples
9
N
3 km
2 mi
Estero Bay Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Guana River Marsh Aquatic Preserve

Natural

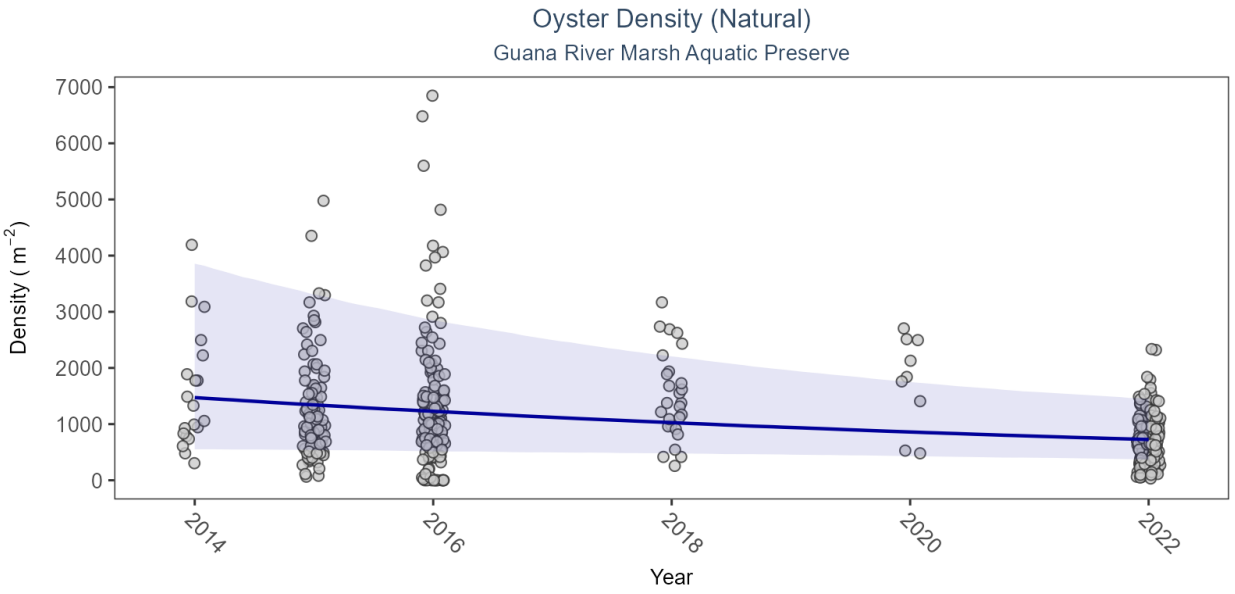


Figure 8: Figure for Oyster Density in Guana River Marsh Aquatic Preserve

Table 8: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-93.52	381.66	-24.53 to -336.43


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana River Marsh Aquatic Preserve
Number of samples
18
N
3 km
2 mi
Guana River Marsh Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Guana Tolomato Matanzas National Estuarine Research Reserve

Natural

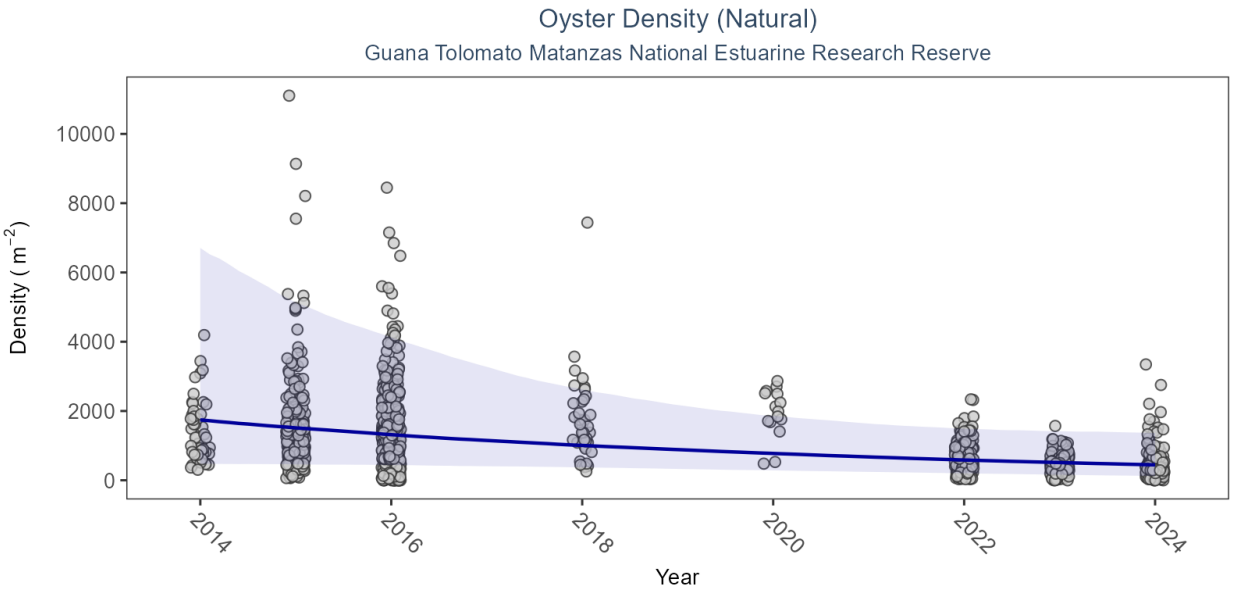
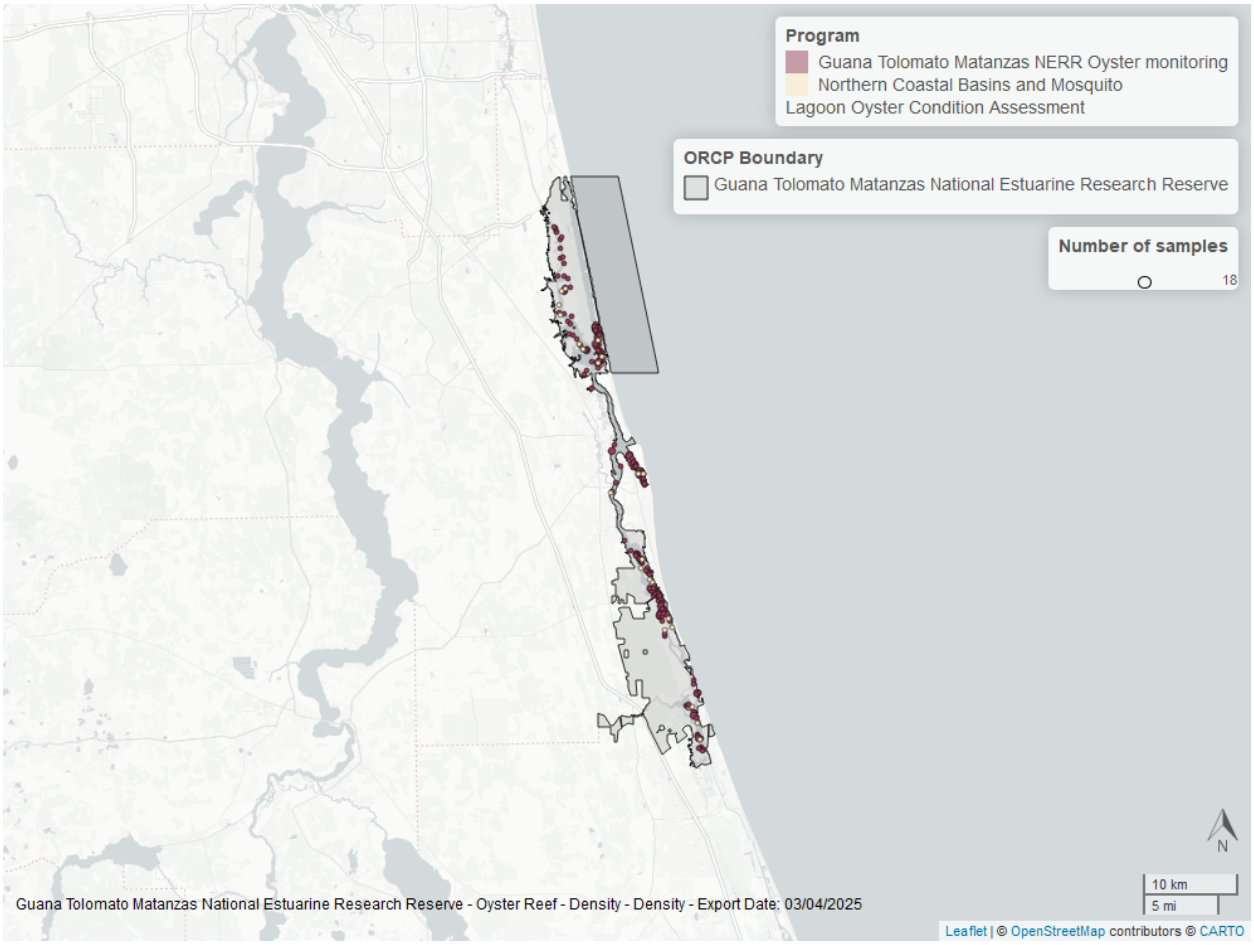


Figure 9: Figure for Oyster Density in Guana Tolomato Matanzas National Estuarine Research Reserve

Table 9: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-128.2	481.29	-32.73 to -484.82


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana Tolomato Matanzas National Estuarine Research Reserve
Number of samples
18
N
10 km
5 mi
Guana Tolomato Matanzas National Estuarine Research Reserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Indian River-Malabar to Vero Beach Aquatic Preserve

Natural

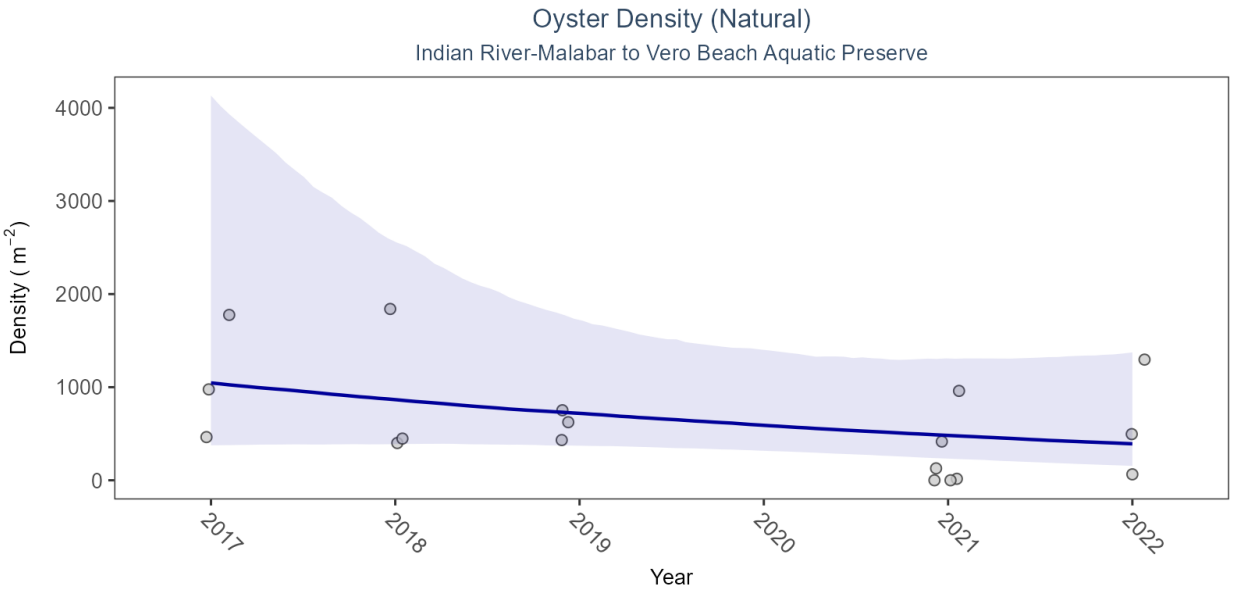
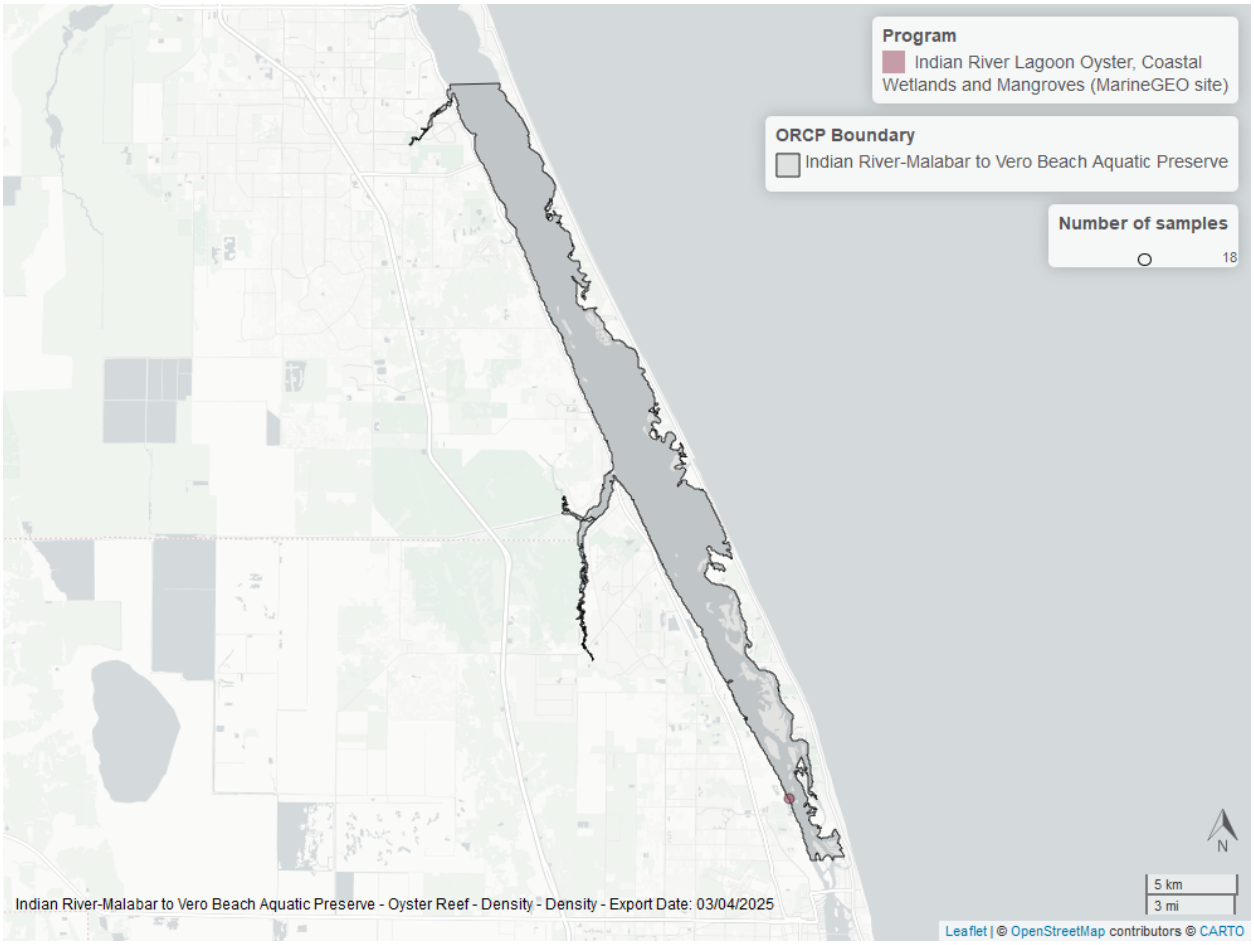


Figure 10: Figure for Oyster Density in Indian River-Malabar to Vero Beach Aquatic Preserve

Table 10: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-130.86	278.08	-44.24 to -551.55


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Malabar to Vero Beach Aquatic Preserve
Number of samples
18
N
5 km
3 mi
Indian River-Malabar to Vero Beach Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Natural

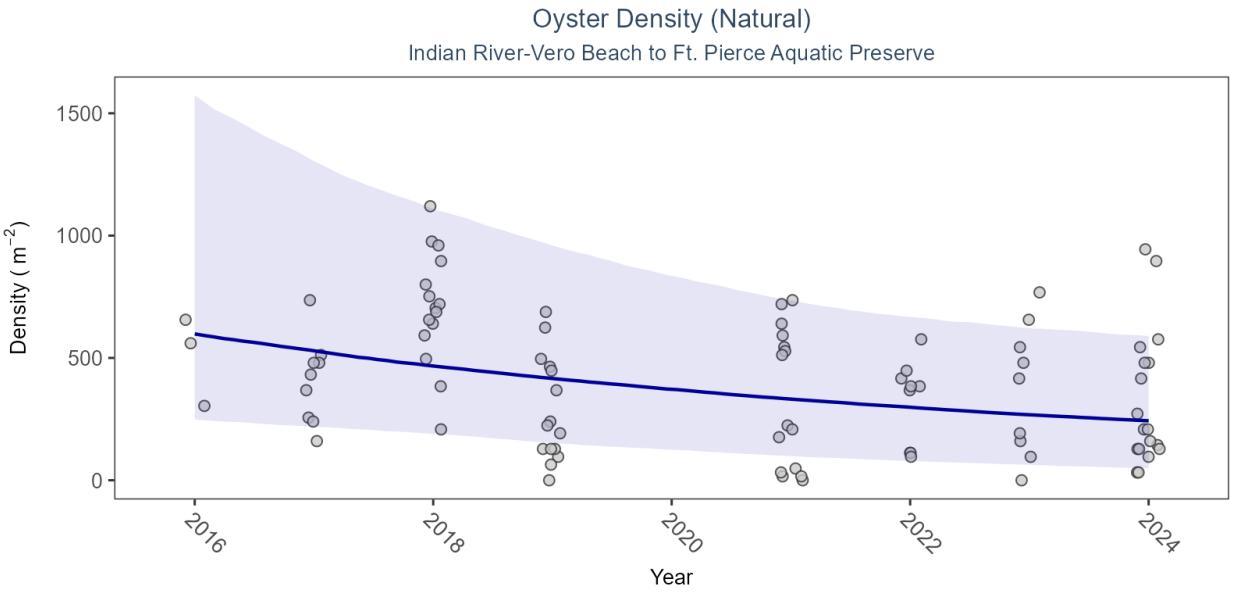
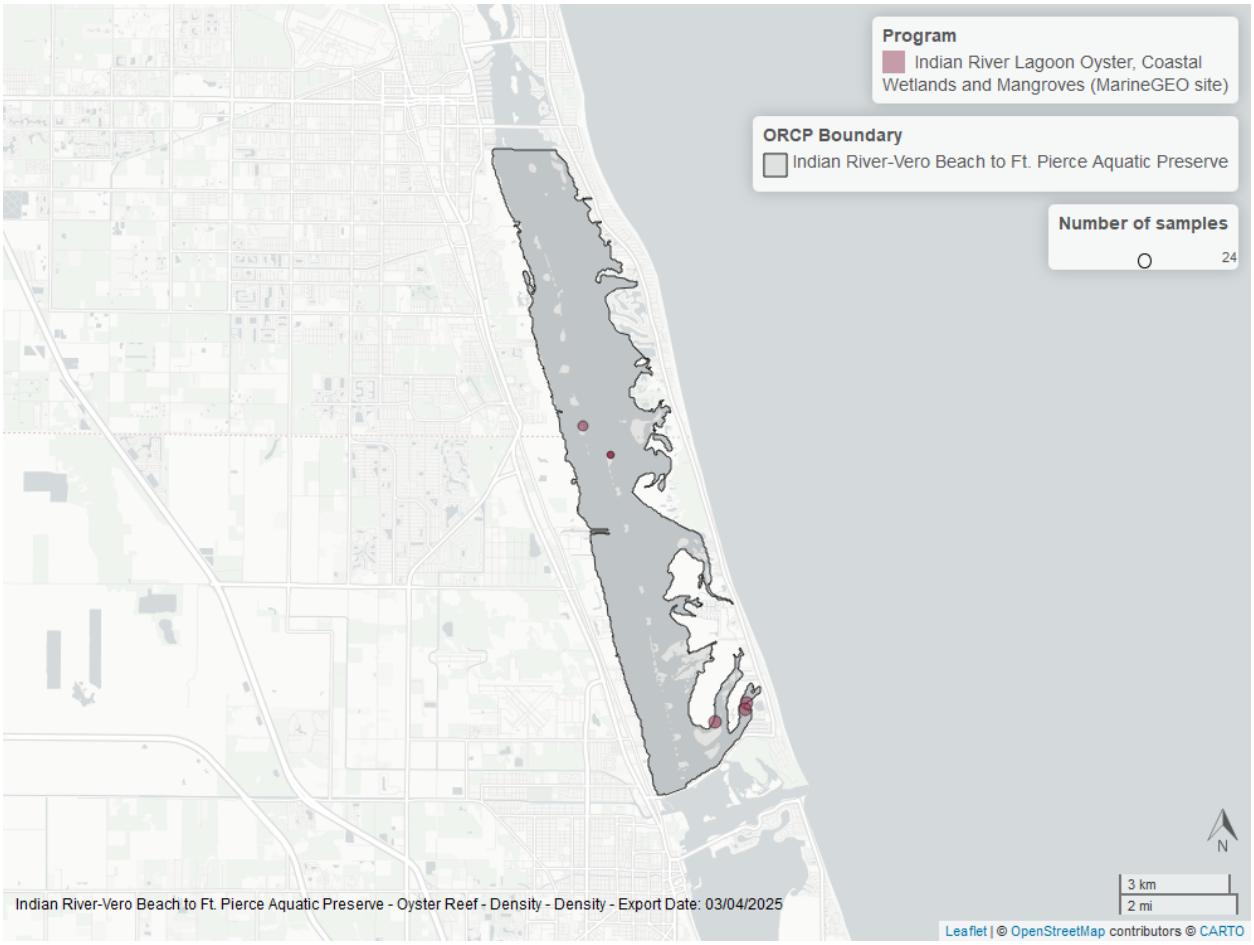


Figure 11: Figure for Oyster Density in Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Table 11: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-44.2	220.81	-23.86 to -119.22


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve
Number of samples
24
N
3 km
2 mi
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Jensen Beach to Jupiter Inlet Aquatic Preserve

Natural

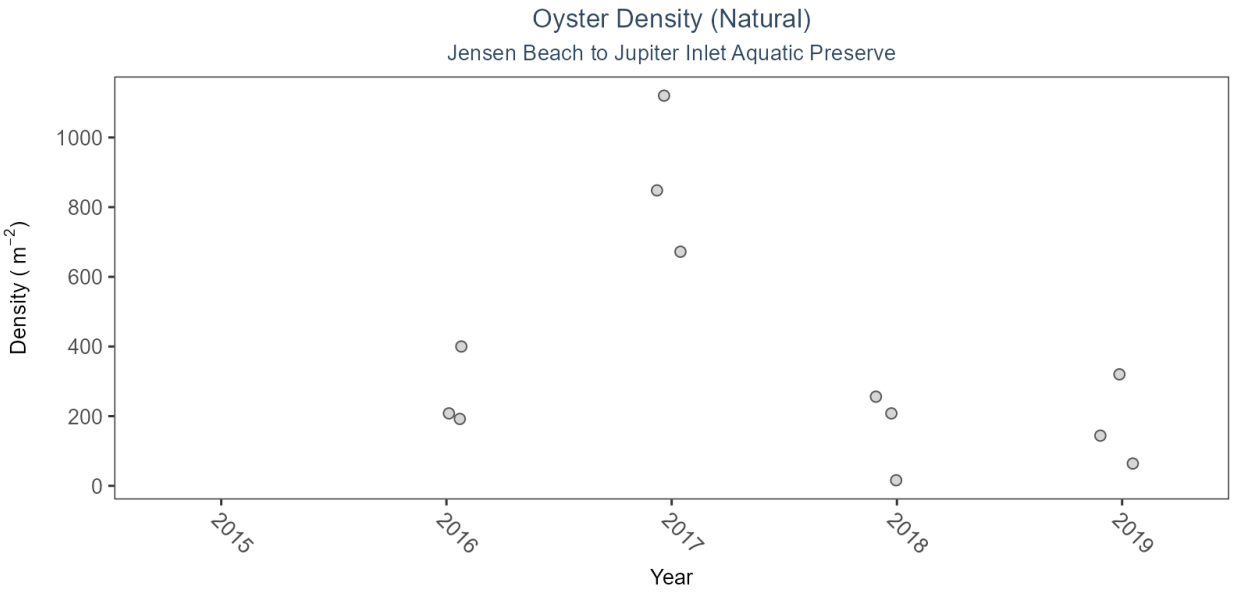
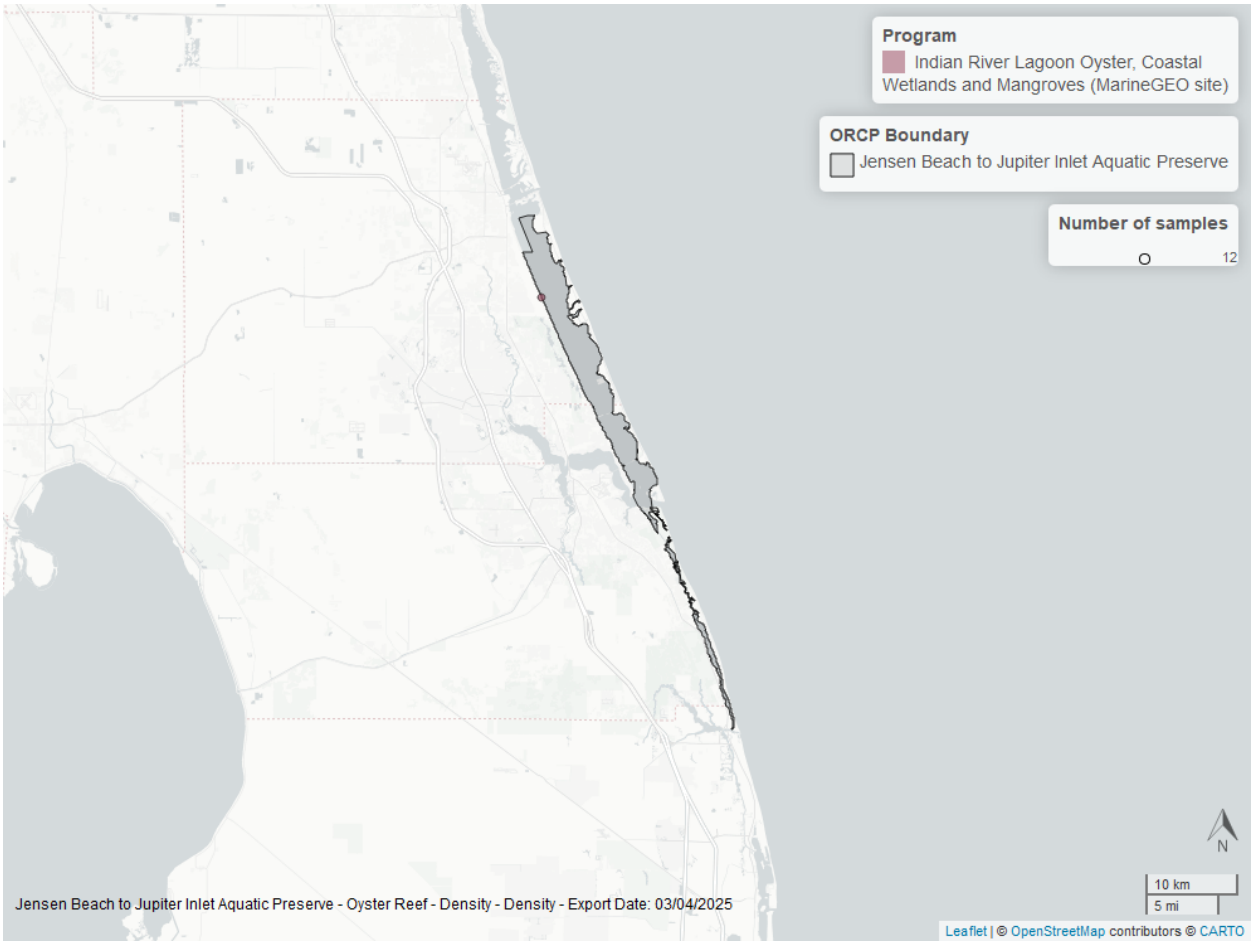


Figure 12: Figure for Oyster Density in Jensen Beach to Jupiter Inlet Aquatic Preserve

Table 12: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Jensen Beach to Jupiter Inlet Aquatic Preserve
Number of samples
12
N
10 km
5 mi
Jensen Beach to Jupiter Inlet Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
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Lemon Bay Aquatic Preserve

Natural

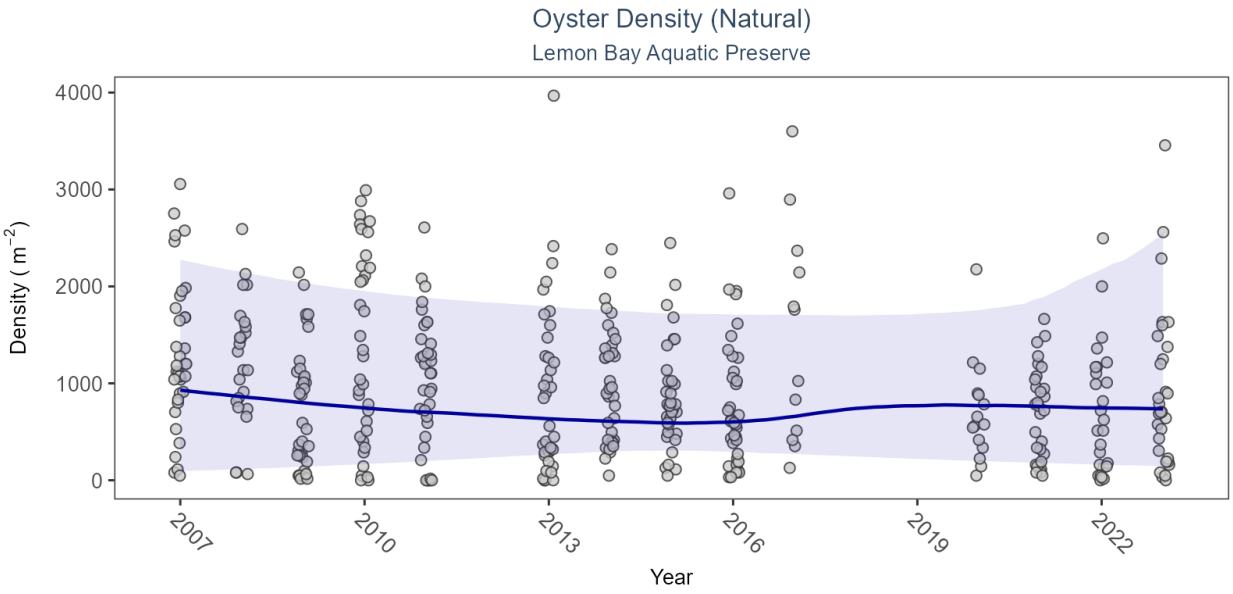
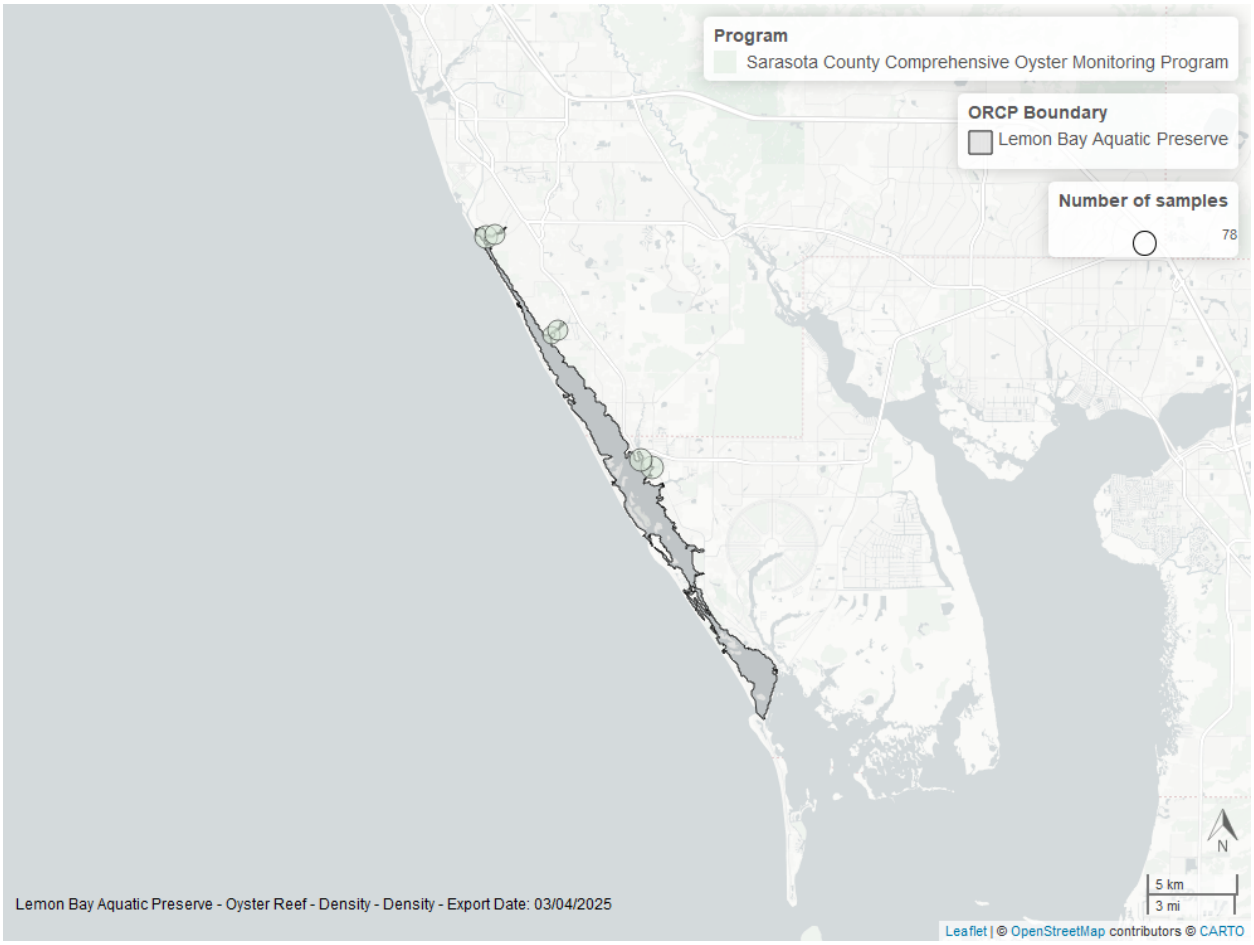


Figure 13: Figure for Oyster Density in Lemon Bay Aquatic Preserve

Table 13: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-15.52	656.16	3.57 to 17.57


Program
Sarasota County Comprehensive Oyster Monitoring Program
ORCP Boundary
Lemon Bay Aquatic Preserve
Number of samples
78
N
5 km
3 mi
Lemon Bay Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Loxahatchee River-Lake Worth Creek Aquatic Preserve

Natural

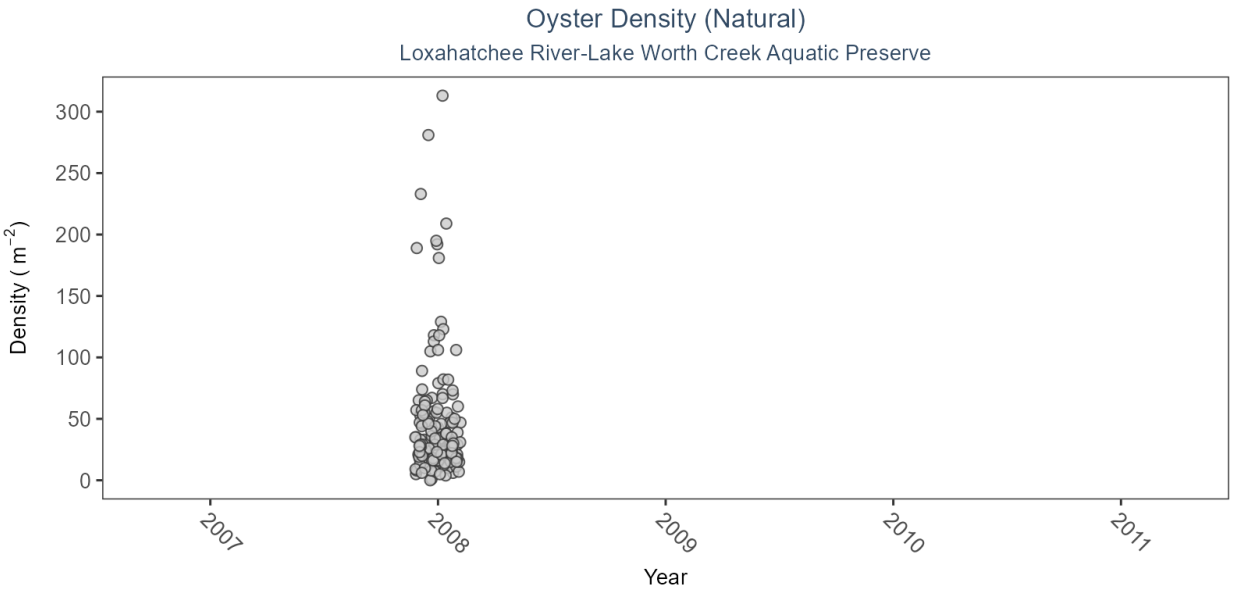
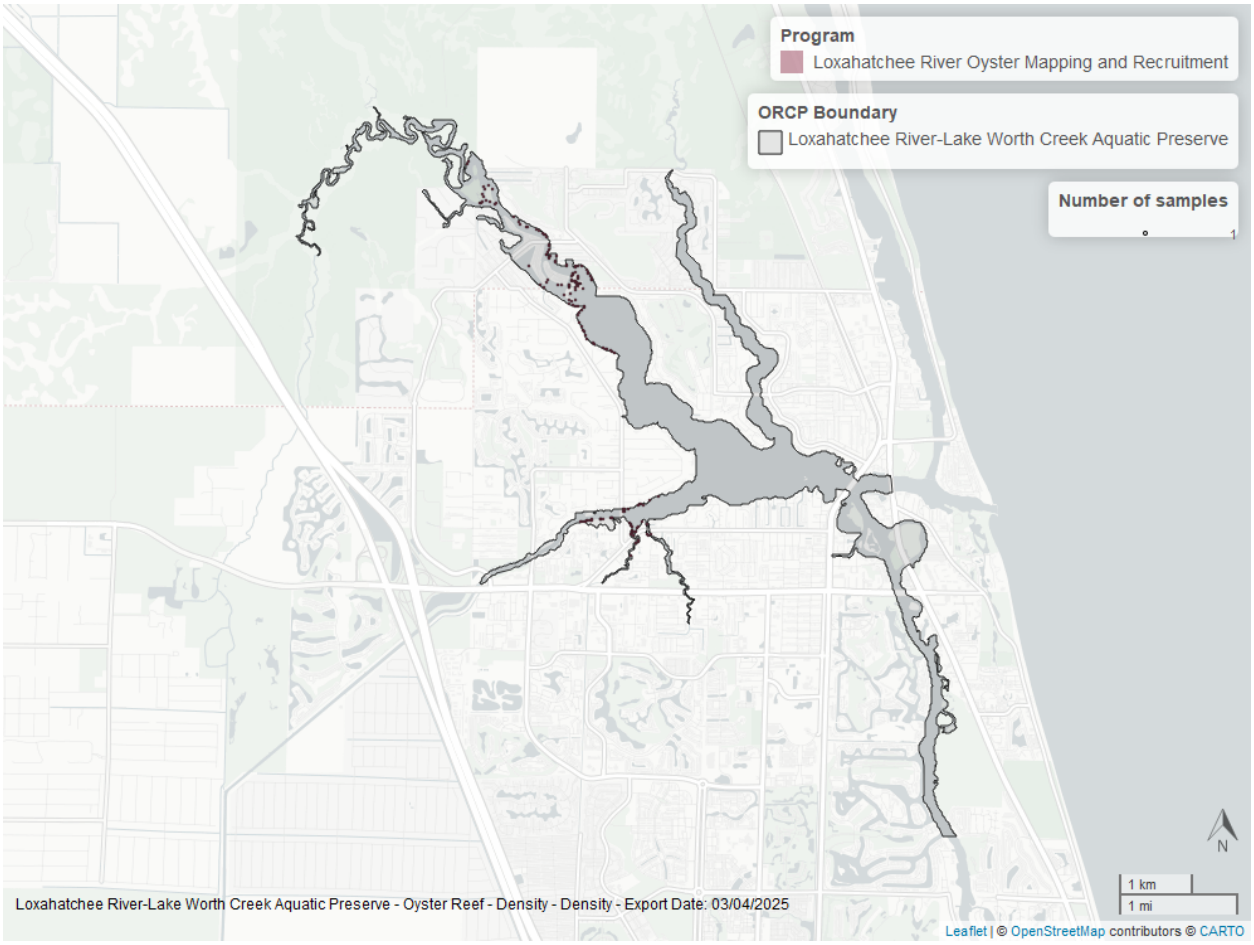


Figure 14: Figure for Oyster Density in Loxahatchee River-Lake Worth Creek Aquatic Preserve

Table 14: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Loxahatchee River Oyster Mapping and Recruitment
ORCP Boundary
Loxahatchee River-Lake Worth Creek Aquatic Preserve
Number of samples
1
N
1 km
1 mi
Loxahatchee River-Lake Worth Creek Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Mosquito Lagoon Aquatic Preserve

Natural

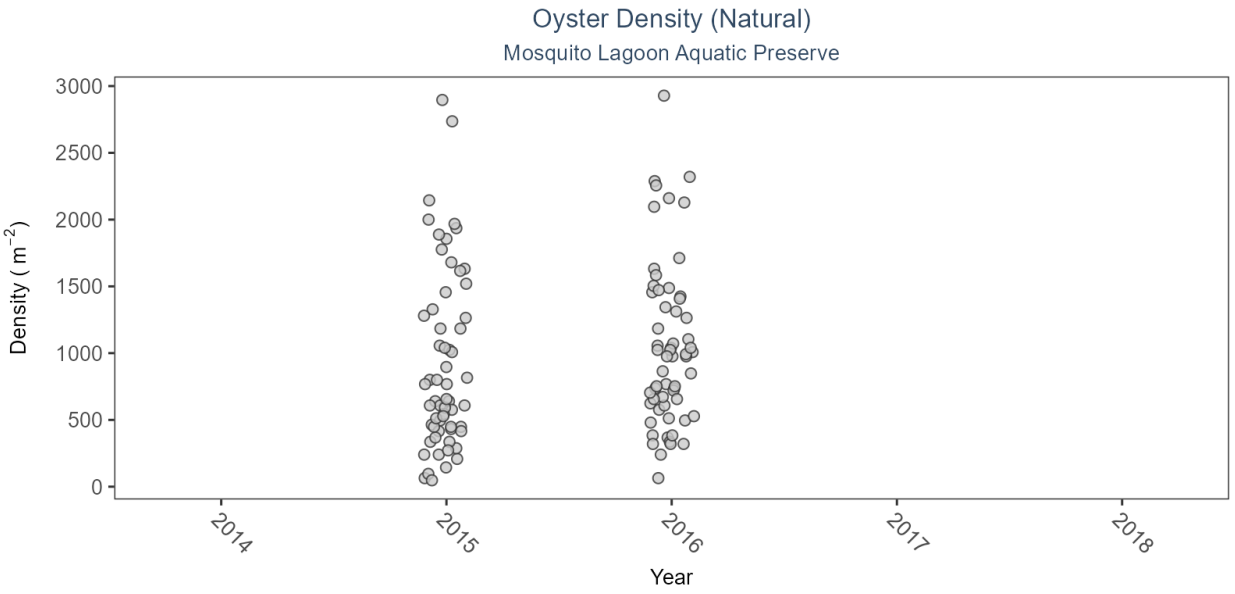
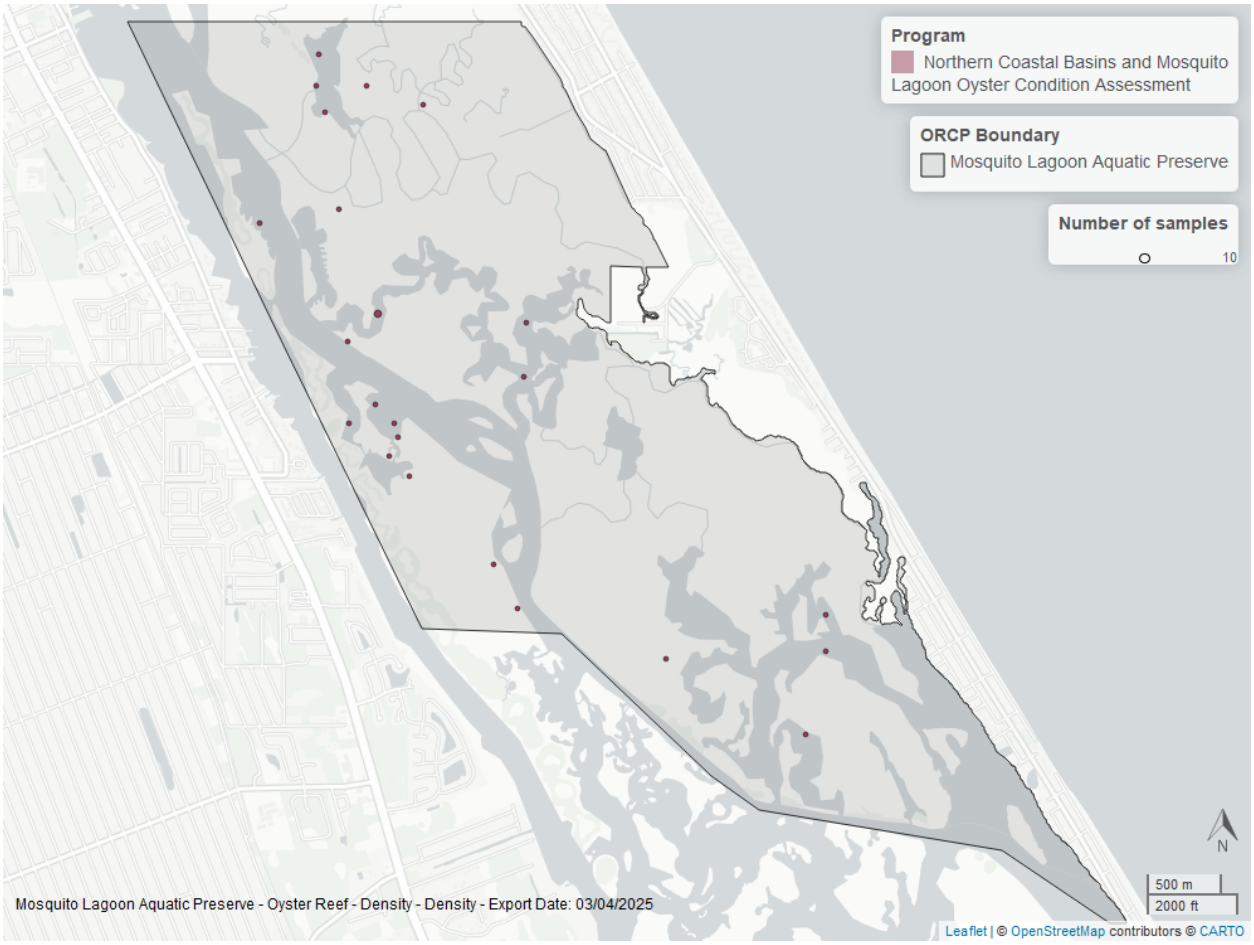


Figure 15: Figure for Oyster Density in Mosquito Lagoon Aquatic Preserve

Table 15: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Mosquito Lagoon Aquatic Preserve
Number of samples
10
N
500 m
2000 ft
Mosquito Lagoon Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Nassau River-St. Johns River Marshes Aquatic Preserve

Natural

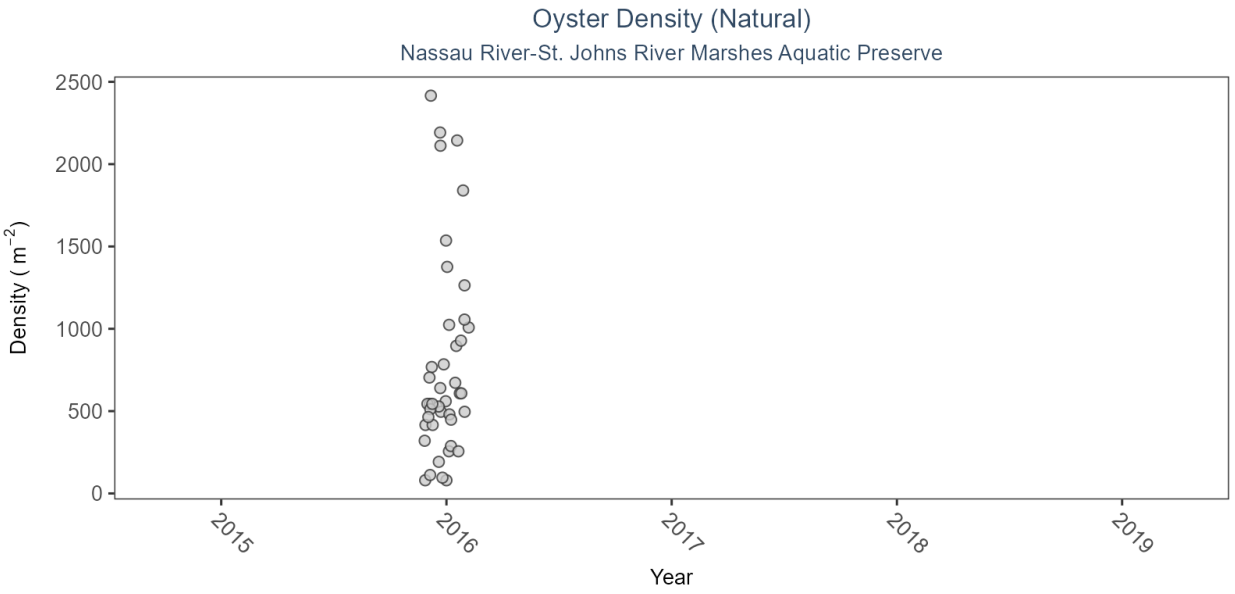
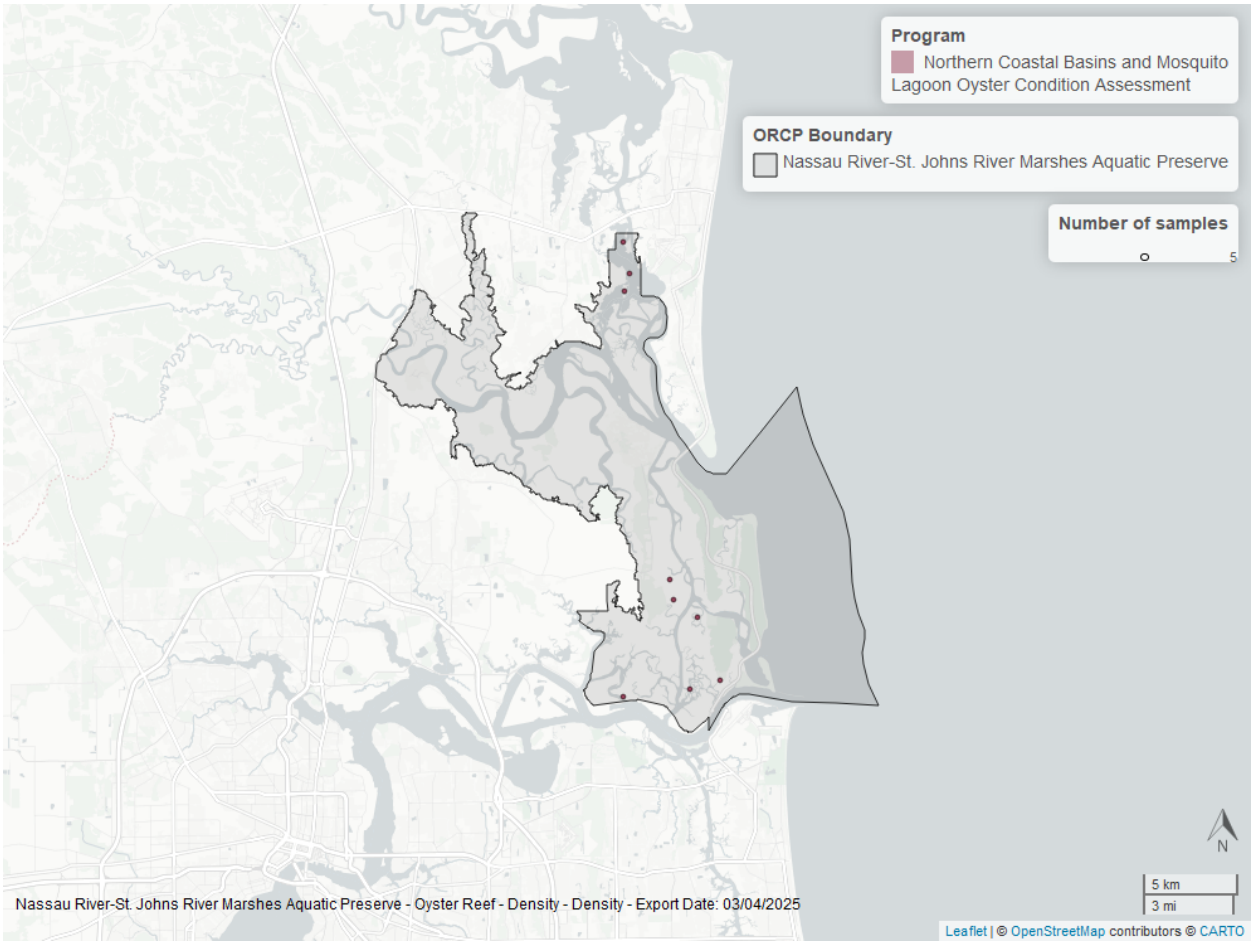


Figure 16: Figure for Oyster Density in Nassau River-St. Johns River Marshes Aquatic Preserve

Table 16: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Nassau River-St. Johns River Marshes Aquatic Preserve
Number of samples
5
N
5 km
3 mi
Nassau River-St. Johns River Marshes Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pine Island Sound Aquatic Preserve

Natural

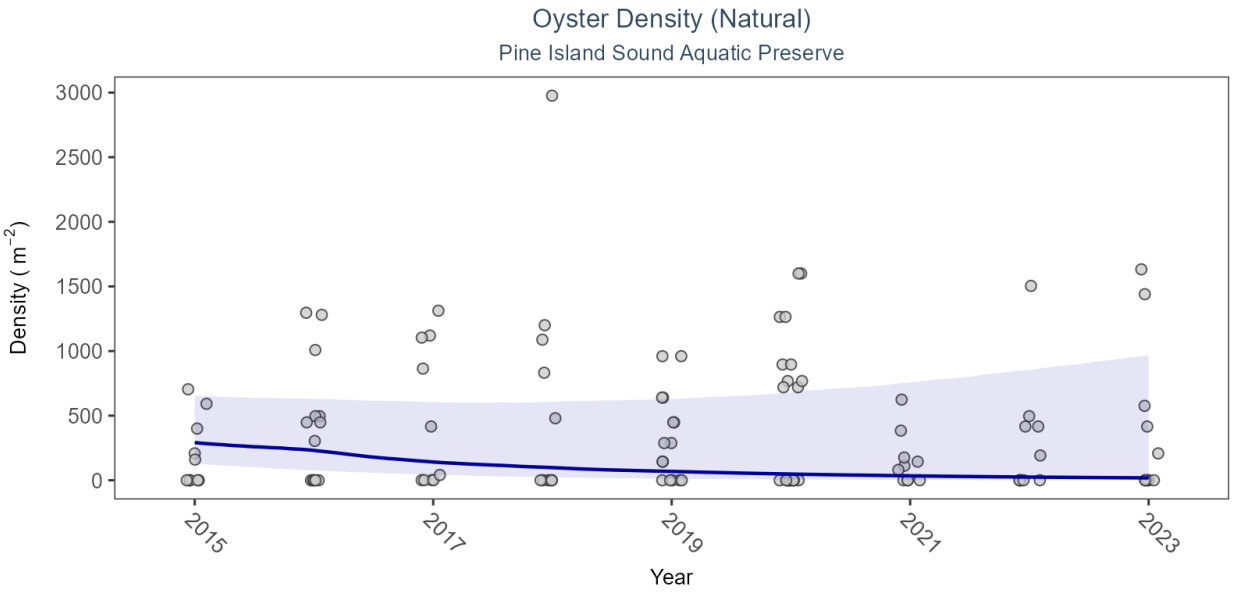


Figure 17: Figure for Oyster Density in Pine Island Sound Aquatic Preserve

Table 17: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	No significant change	-4.89	334.78	-16.24 to 43.13

Restored

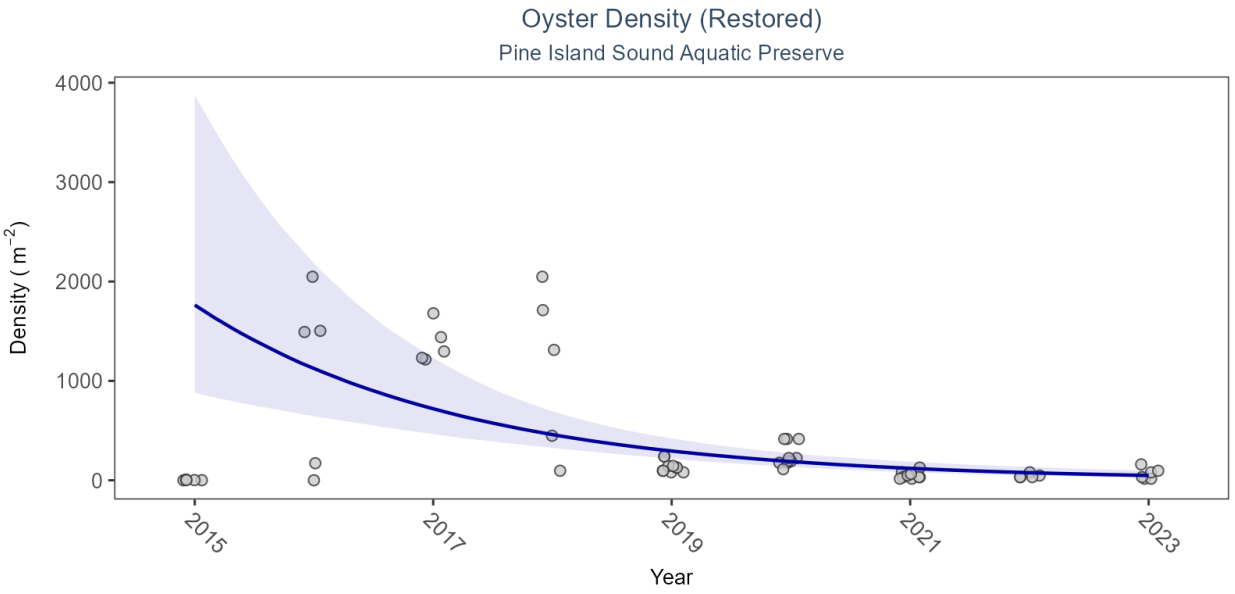
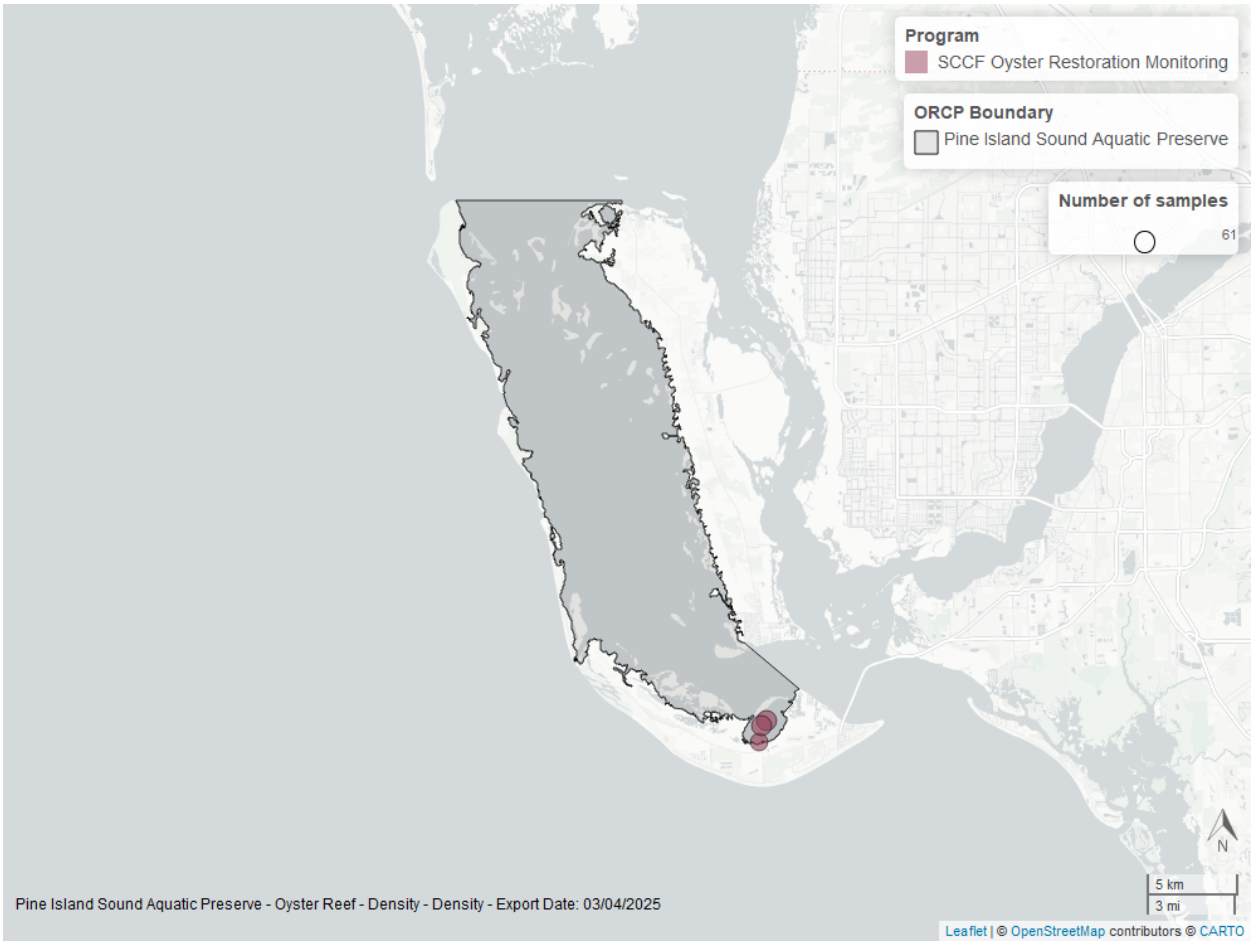


Figure 18: Figure for Oyster Density in Pine Island Sound Aquatic Preserve

Table 18: Model results for Oyster Density - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly decreasing trend	-214.22	128.39	-106.83 to -471.59


Program
SCCF Oyster Restoration Monitoring
ORCP Boundary
Pine Island Sound Aquatic Preserve
Number of samples
61
N
5 km
3 mi
Pine Island Sound Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pinellas County Aquatic Preserve

Natural

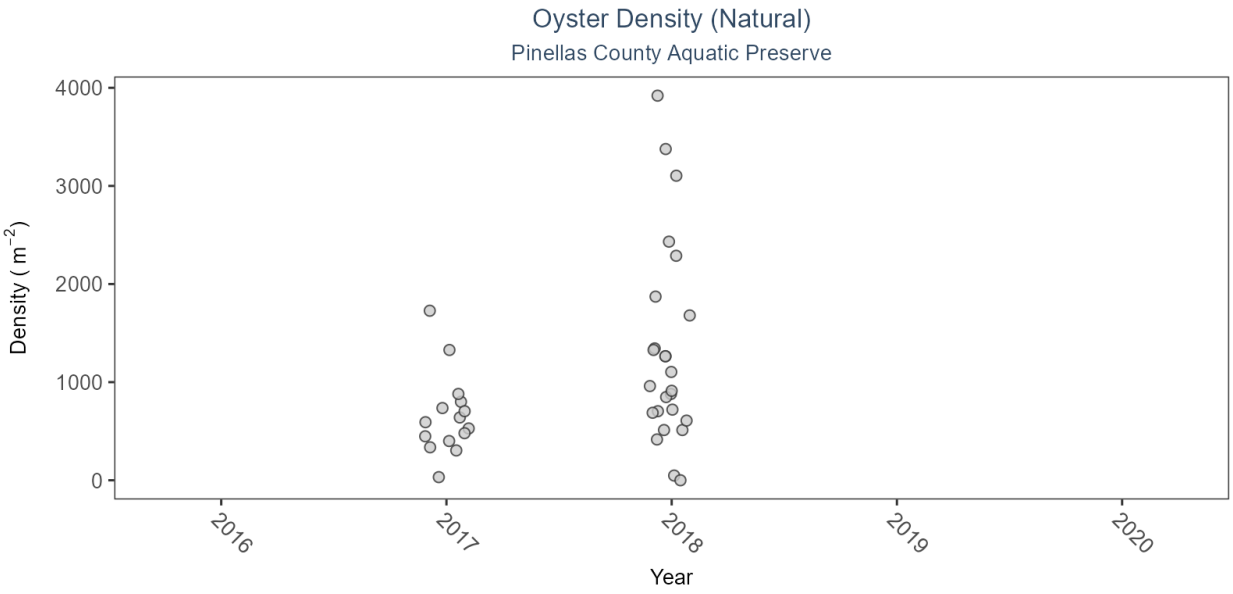
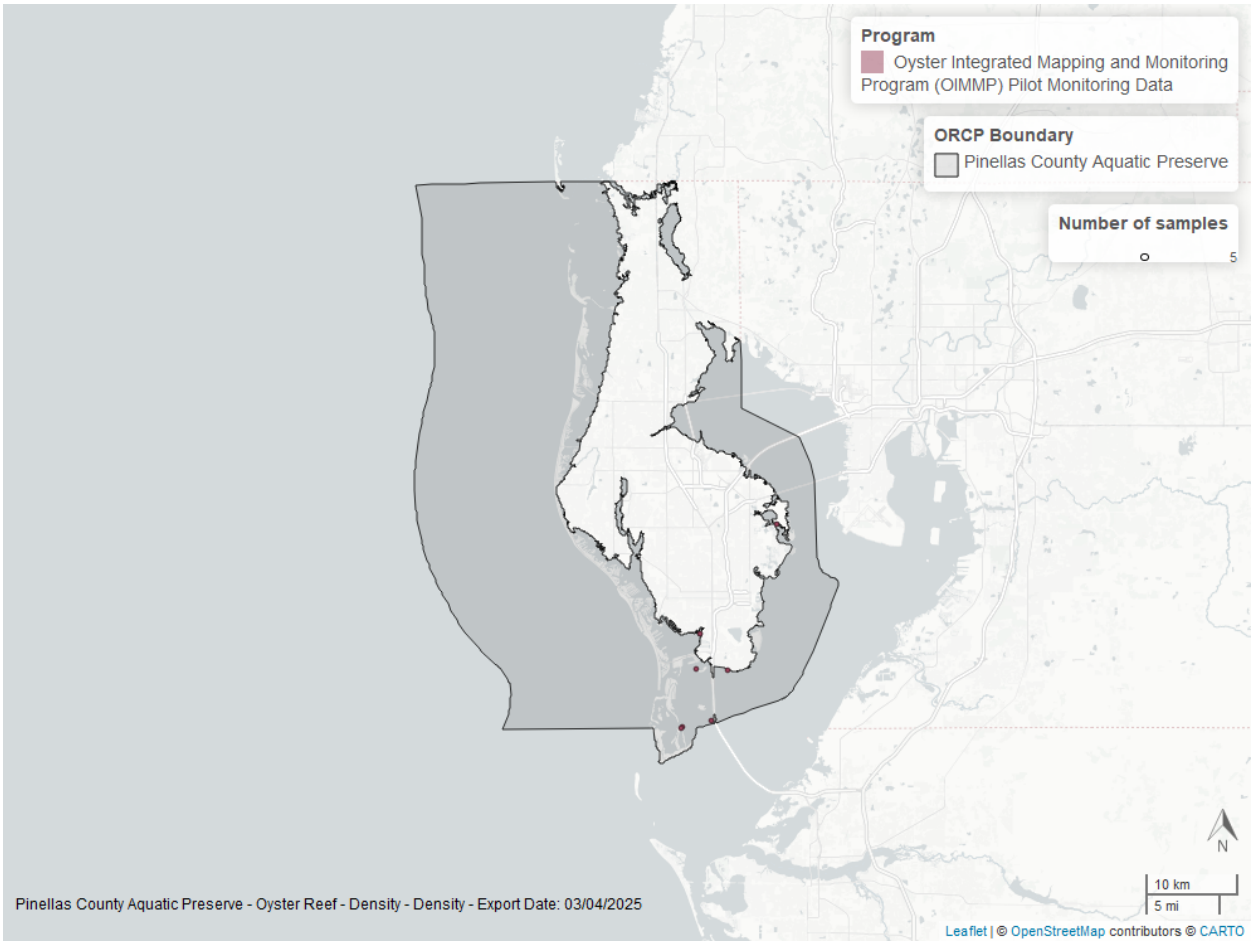


Figure 19: Figure for Oyster Density in Pinellas County Aquatic Preserve

Table 19: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Pinellas County Aquatic Preserve
Number of samples
5
N
10 km
5 mi
Pinellas County Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

St. Martins Marsh Aquatic Preserve

Natural

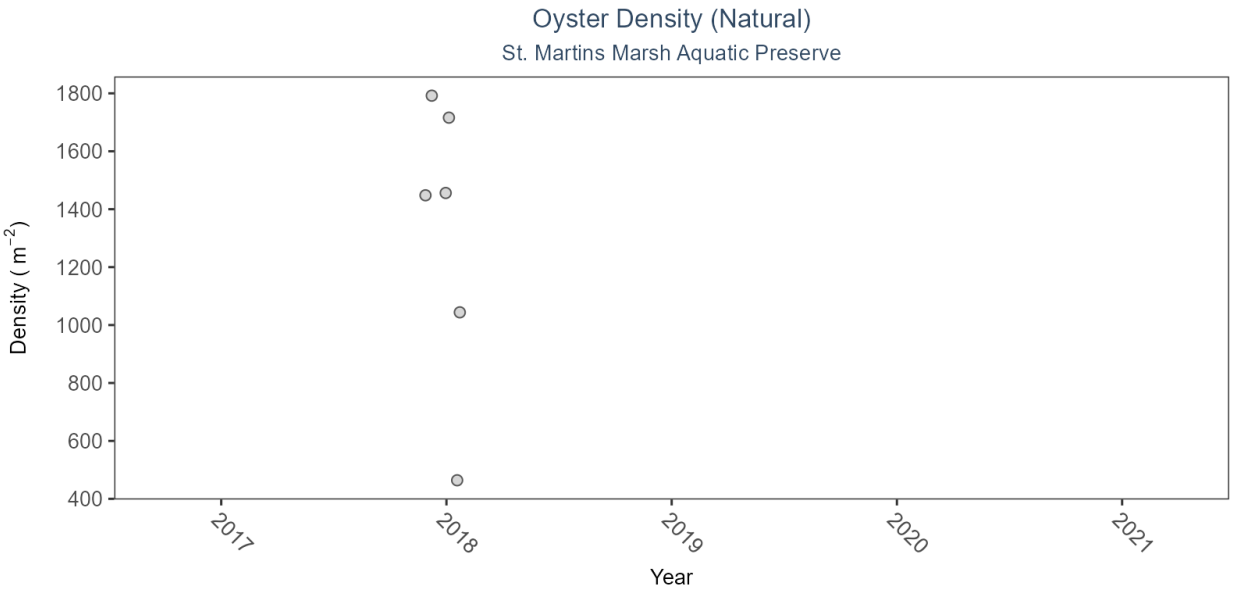
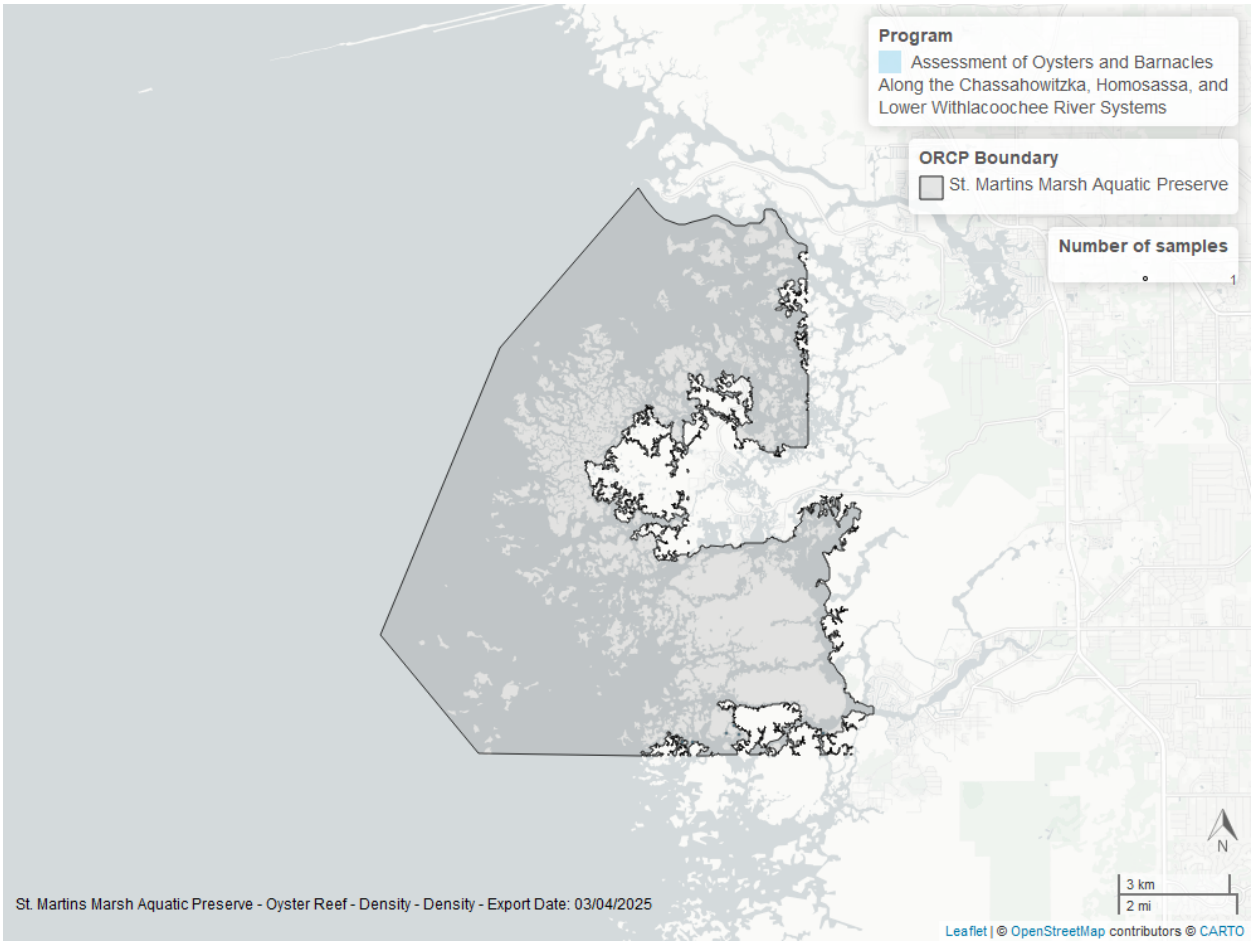


Figure 20: Figure for Oyster Density in St. Martins Marsh Aquatic Preserve

Table 20: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Assessment of Oysters and Barnacles Along the Chassahowitzka, Homosassa, and Lower Withlacoochee River Systems
ORCP Boundary
St. Martins Marsh Aquatic Preserve
Number of samples
1
N
3 km
2 mi
St. Martins Marsh Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Tomoka Marsh Aquatic Preserve

Natural

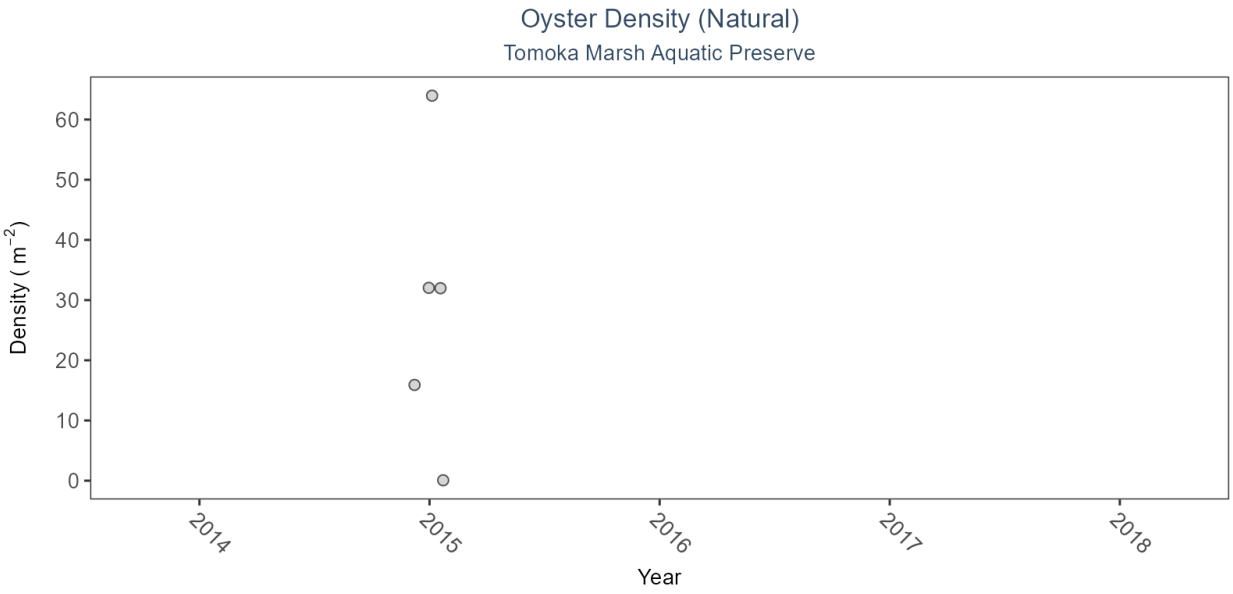


Figure 21: Figure for Oyster Density in Tomoka Marsh Aquatic Preserve

Table 21: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Tomoka Marsh Aquatic Preserve
Number of samples
0
5
N
3 km
2 mi
Tomoka Marsh Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Yellow River Marsh Aquatic Preserve

Natural

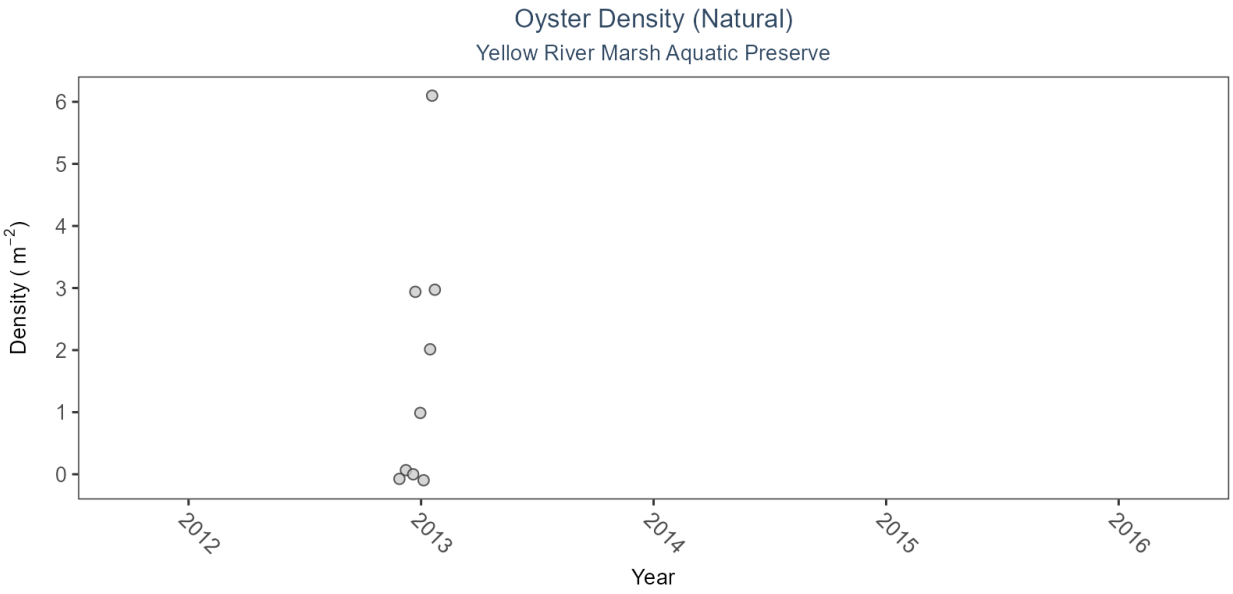


Figure 22: Figure for Oyster Density in Yellow River Marsh Aquatic Preserve

Table 22: Model results for Oyster Density - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA

Restored

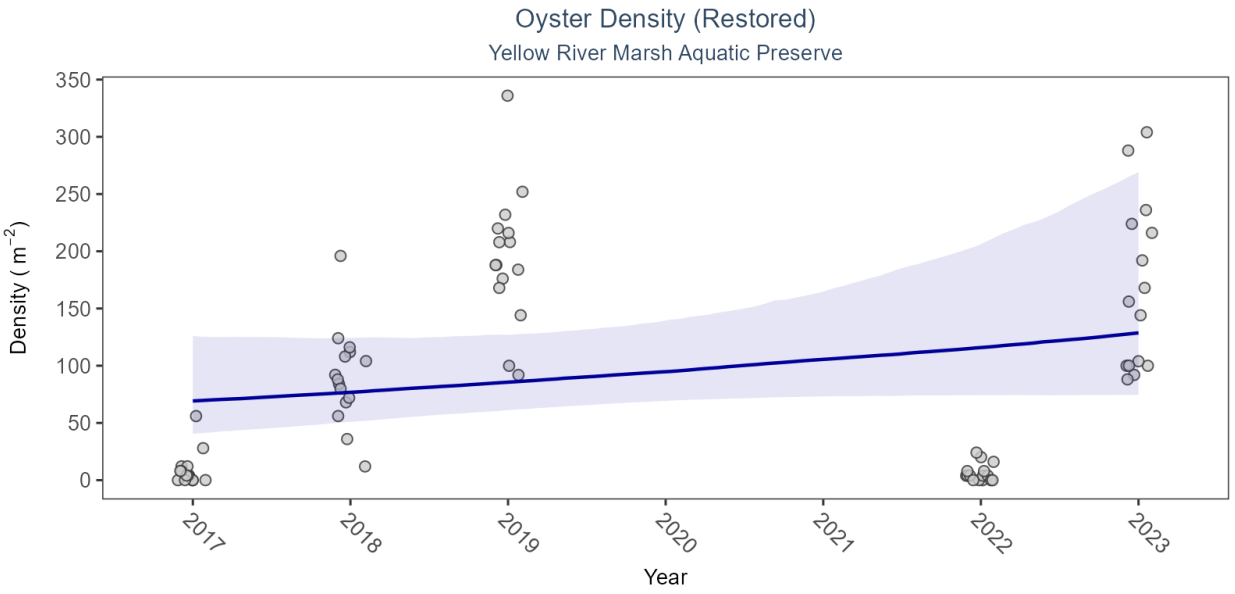
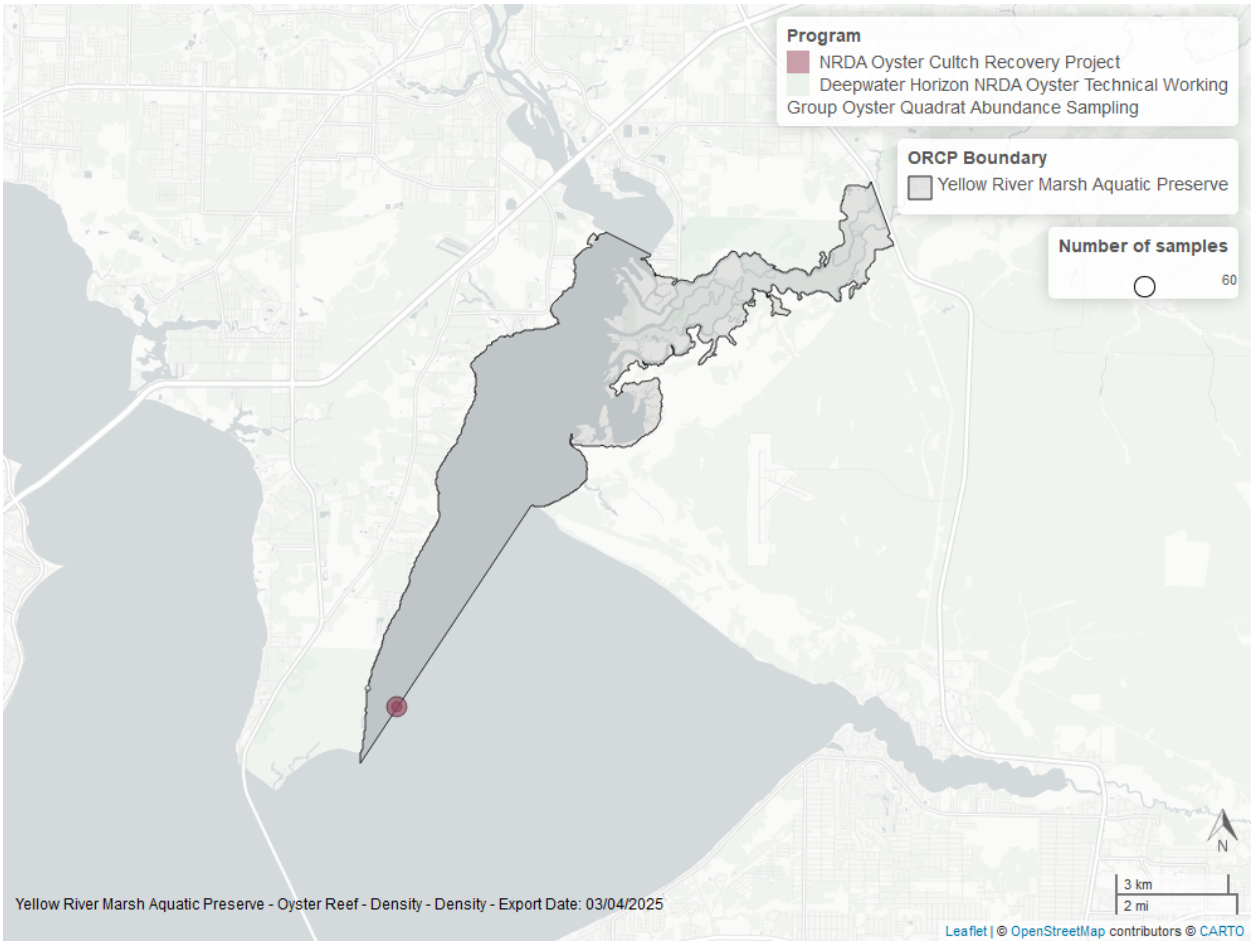


Figure 23: Figure for Oyster Density in Yellow River Marsh Aquatic Preserve

Table 23: Model results for Oyster Density - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly increasing trend	9.92	21.37	5.64 to 23.87


Program
NRDA Oyster Cultch Recovery Project
Deepwater Horizon NRDA Oyster Technical Working Group Oyster Quadrat Abundance Sampling
ORCP Boundary
Yellow River Marsh Aquatic Preserve
Number of samples
60
N
3 km
2 mi
Yellow River Marsh Aquatic Preserve - Oyster Reef - Density - Density - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Percent Live

Apalachicola Bay Aquatic Preserve

Natural

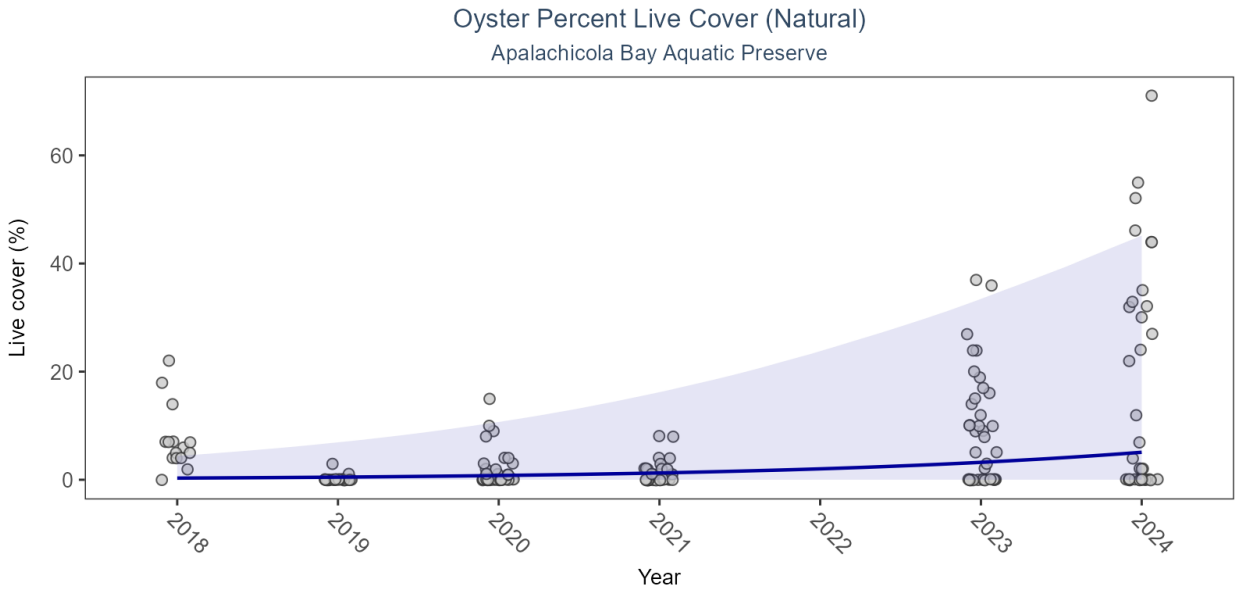


Figure 24: Figure for Oyster Percent Live in Apalachicola Bay Aquatic Preserve

Table 24: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly increasing trend	0.75	2.38	0 to 6.79

Restored

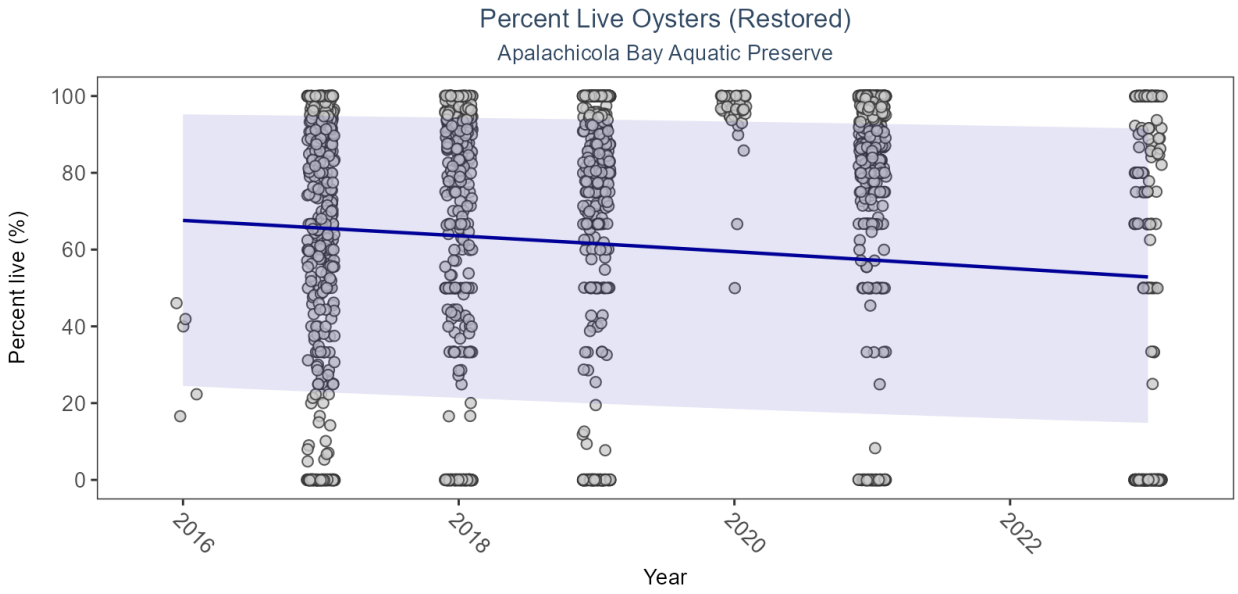
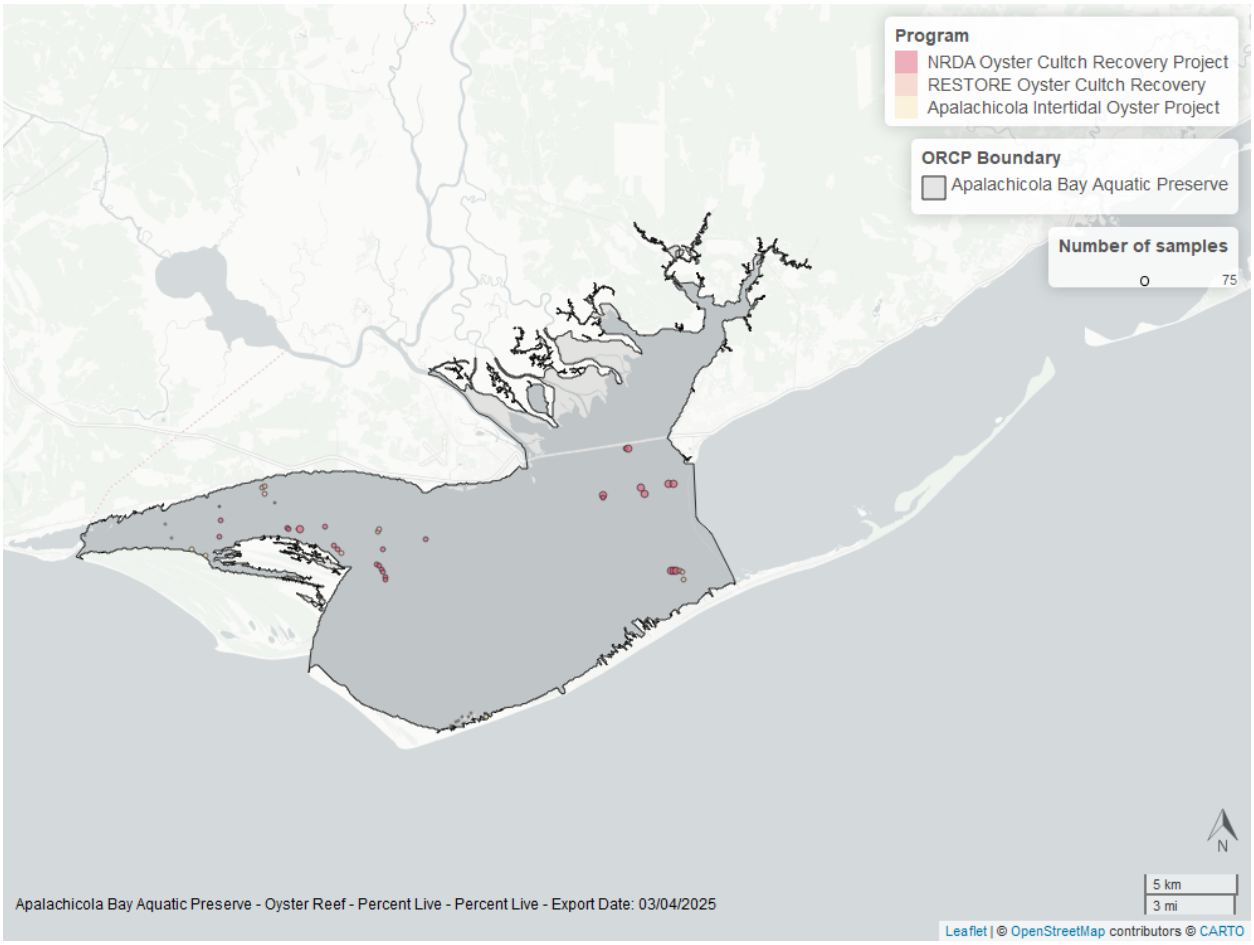


Figure 25: Figure for Oyster Percent Live in Apalachicola Bay Aquatic Preserve

Table 25: Model results for Oyster Percent Live - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly decreasing trend	-2.12	36.27	-1.39 to -0.53


Program
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Apalachicola Intertidal Oyster Project
ORCP Boundary
Apalachicola Bay Aquatic Preserve
Number of samples
0
75
N
5 km
3 mi
Apalachicola Bay Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Apalachicola National Estuarine Research Reserve

Natural

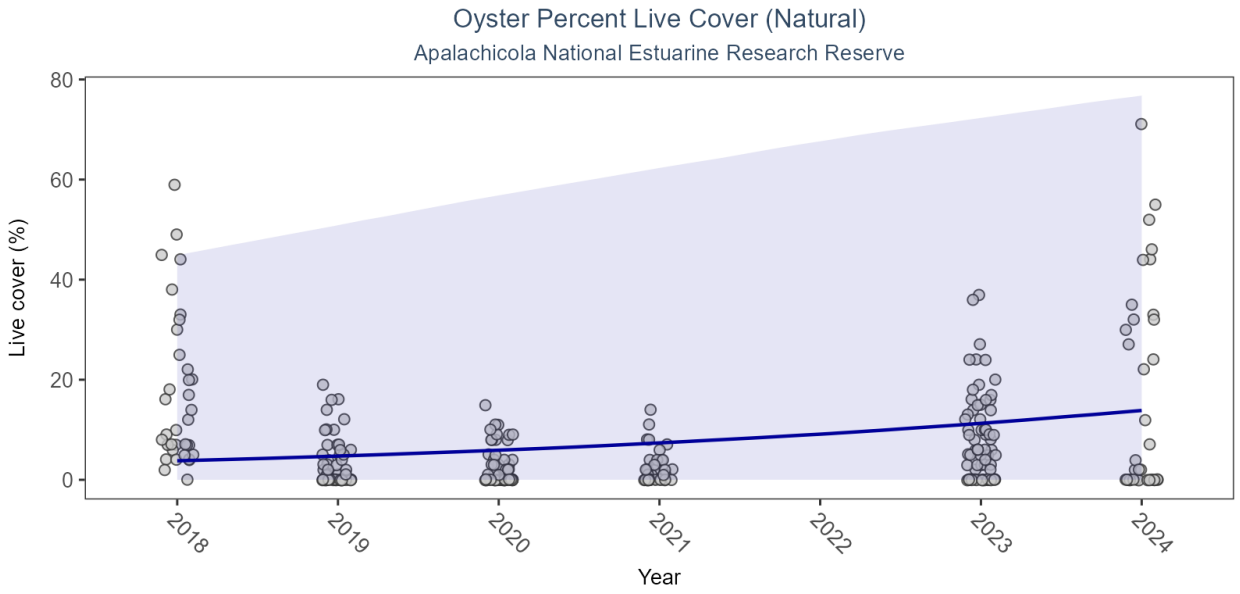


Figure 26: Figure for Oyster Percent Live in Apalachicola National Estuarine Research Reserve

Table 26: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly increasing trend	1.67	9.68	0 to 5.31

Restored

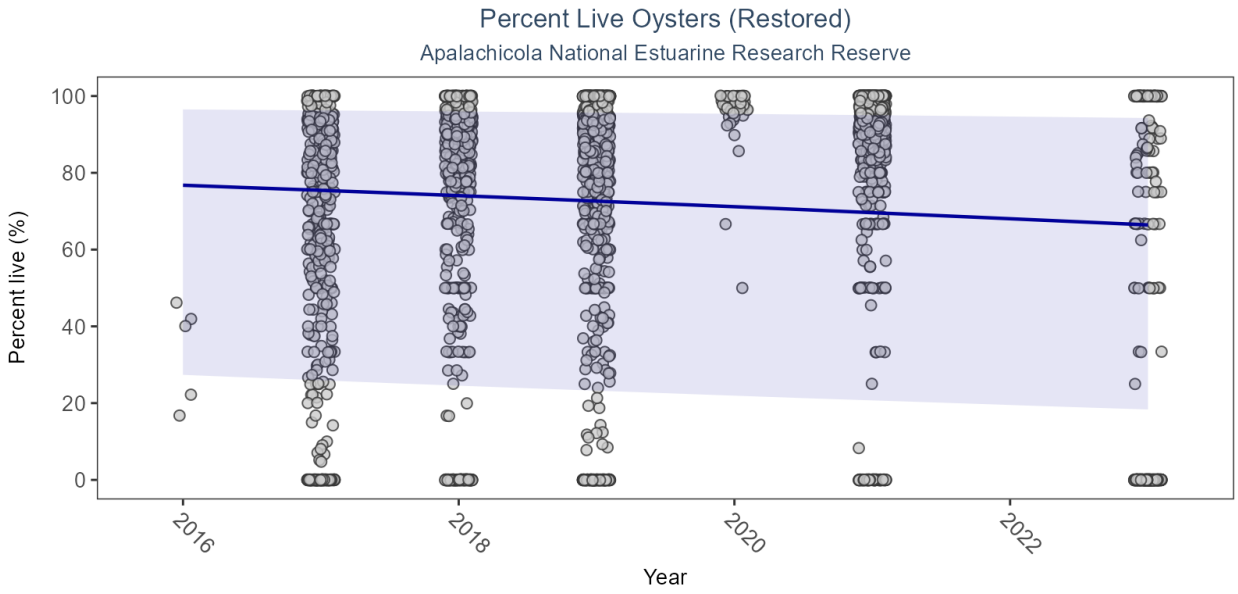
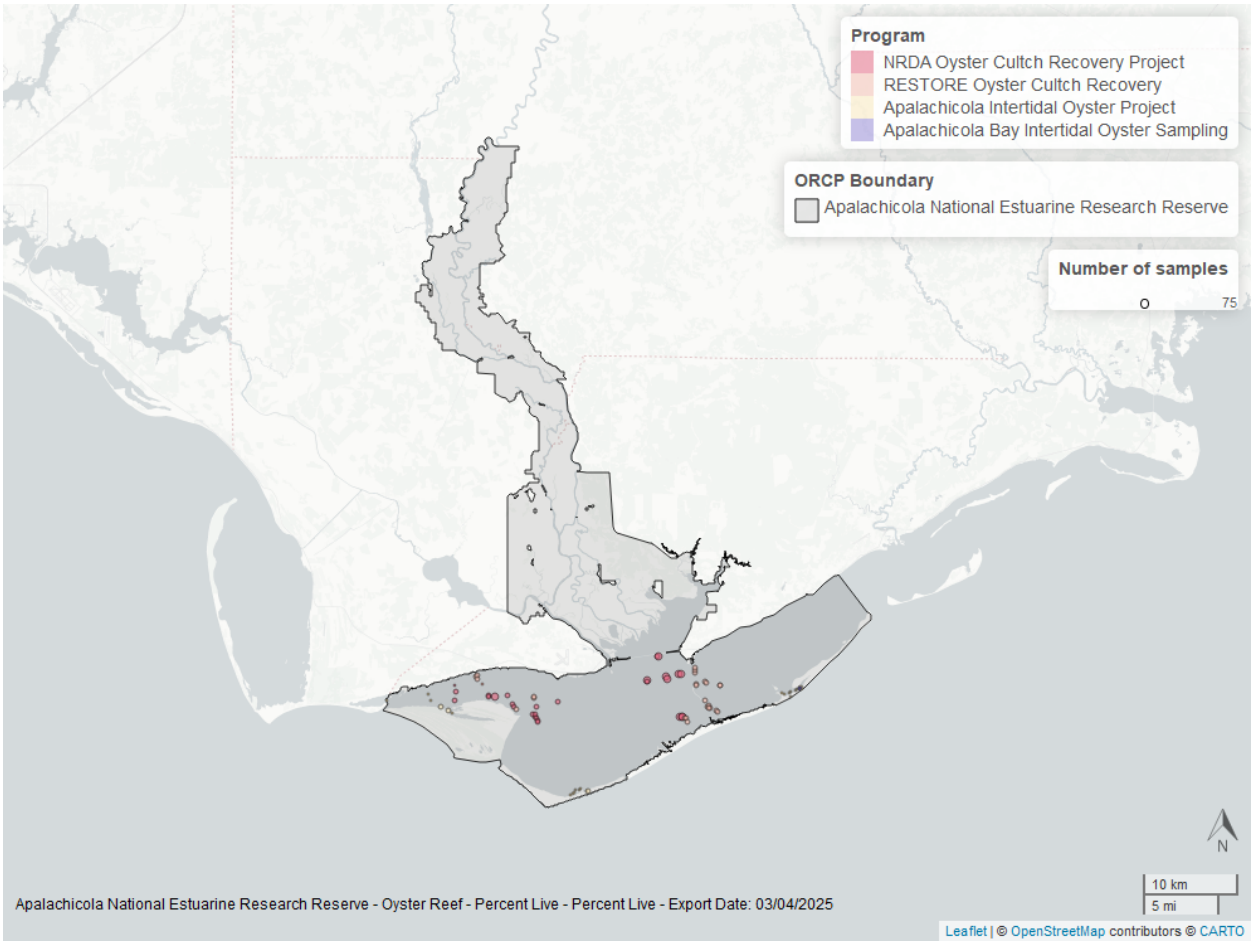


Figure 27: Figure for Oyster Percent Live in Apalachicola National Estuarine Research Reserve

Table 27: Model results for Oyster Percent Live - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly decreasing trend	-1.48	28.56	-1.26 to -0.3


Program
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Apalachicola Intertidal Oyster Project
Apalachicola Bay Intertidal Oyster Sampling
ORCP Boundary
Apalachicola National Estuarine Research Reserve
Number of samples
0
75
N
10 km
5 mi
Apalachicola National Estuarine Research Reserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Boca Ciega Bay Aquatic Preserve

Natural

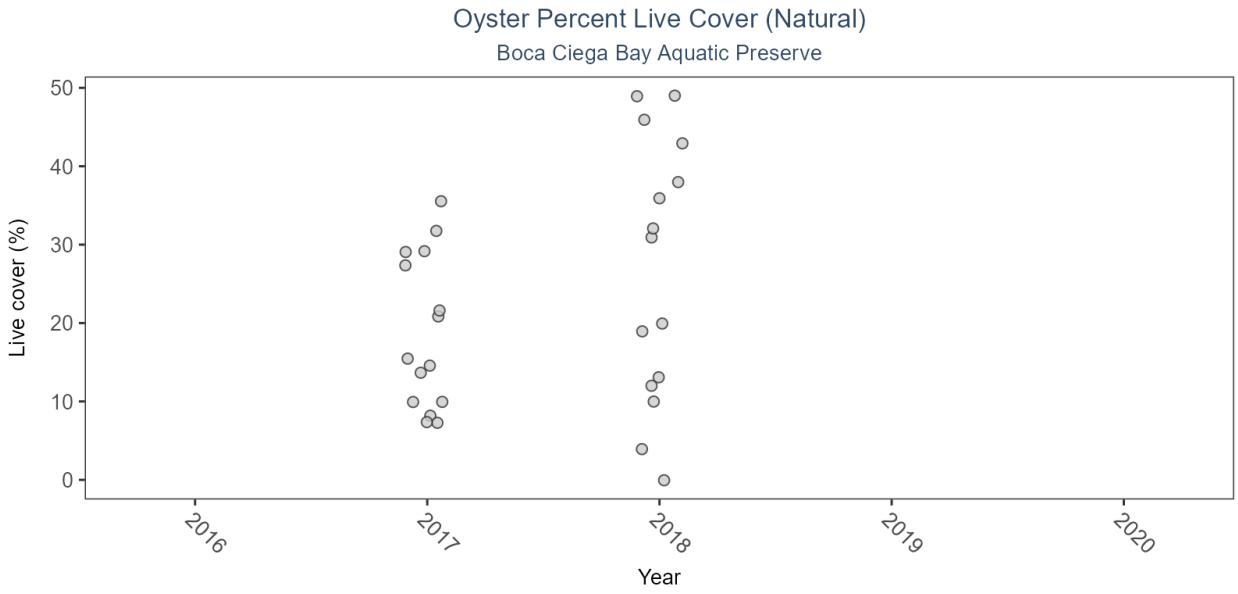
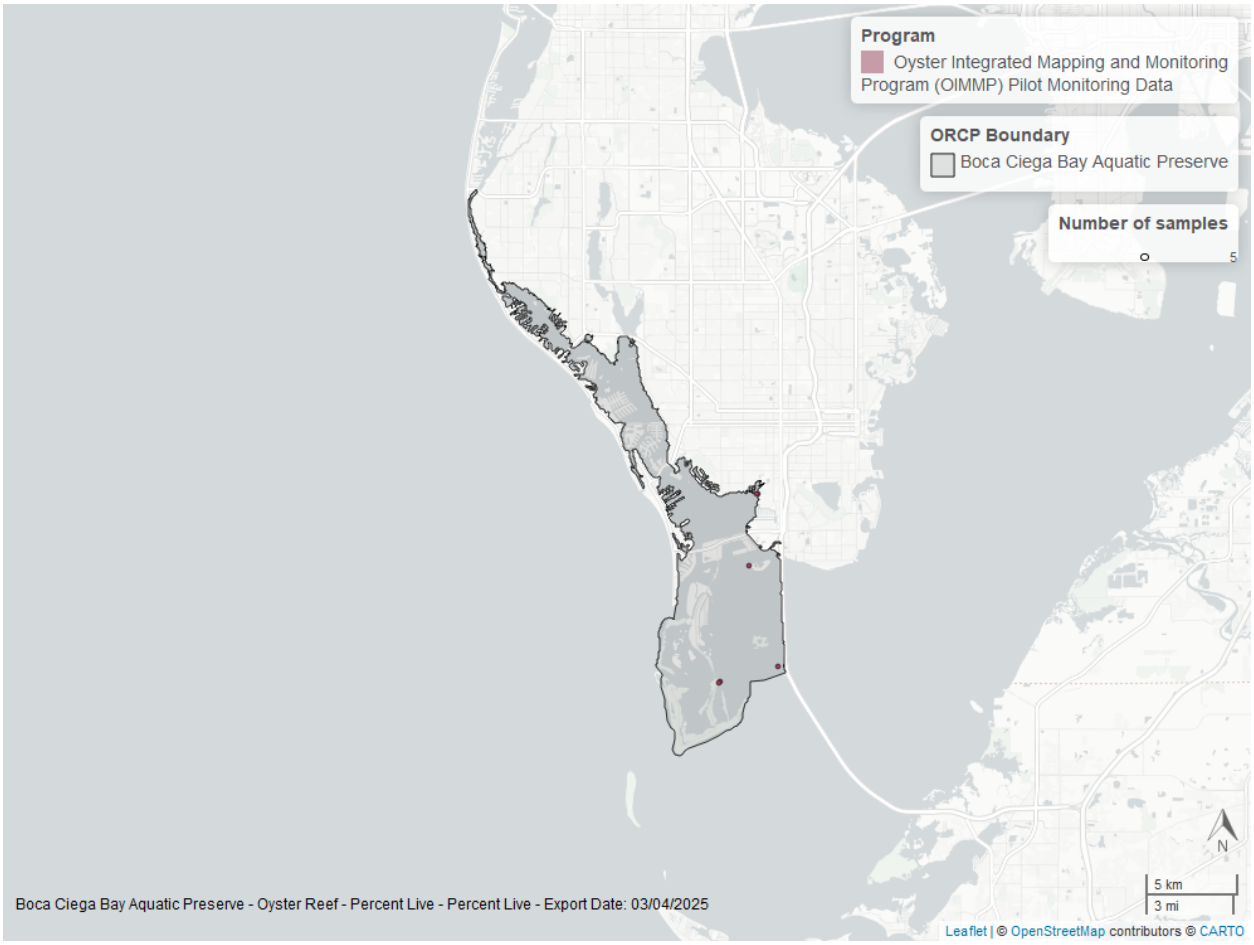


Figure 28: Figure for Oyster Percent Live in Boca Ciega Bay Aquatic Preserve

Table 28: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Boca Ciega Bay Aquatic Preserve
Number of samples
5
N
5 km
3 mi
Boca Ciega Bay Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Estero Bay Aquatic Preserve

Restored

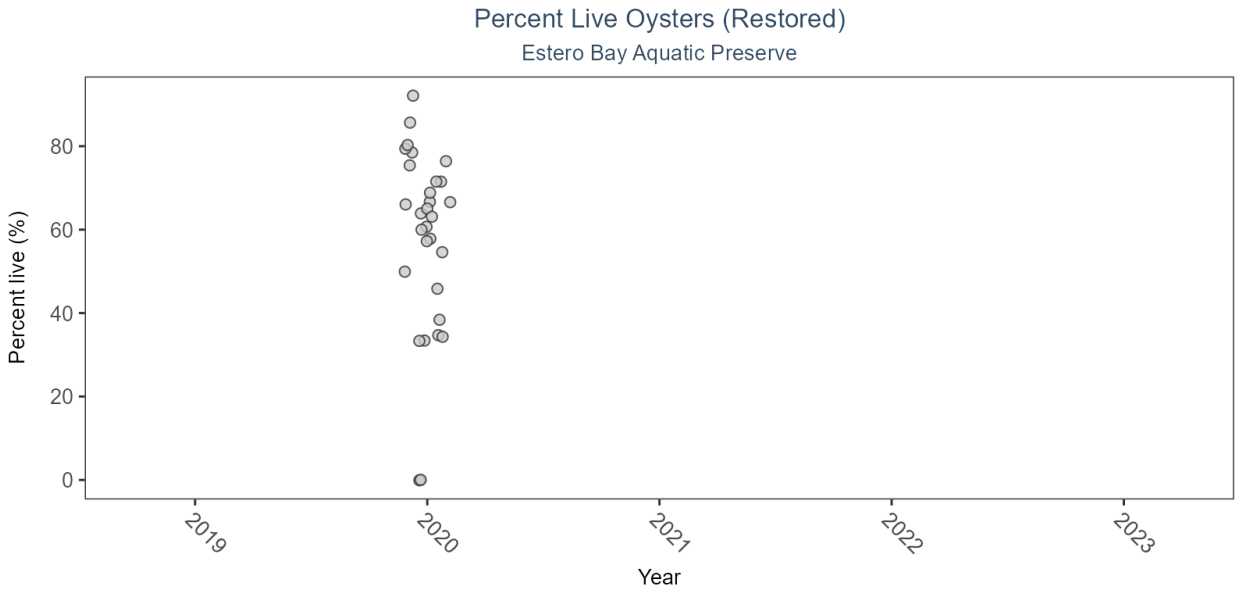


Figure 29: Figure for Oyster Percent Live in Estero Bay Aquatic Preserve

Table 29: Model results for Oyster Percent Live - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	-	-	-	NA to NA

Natural

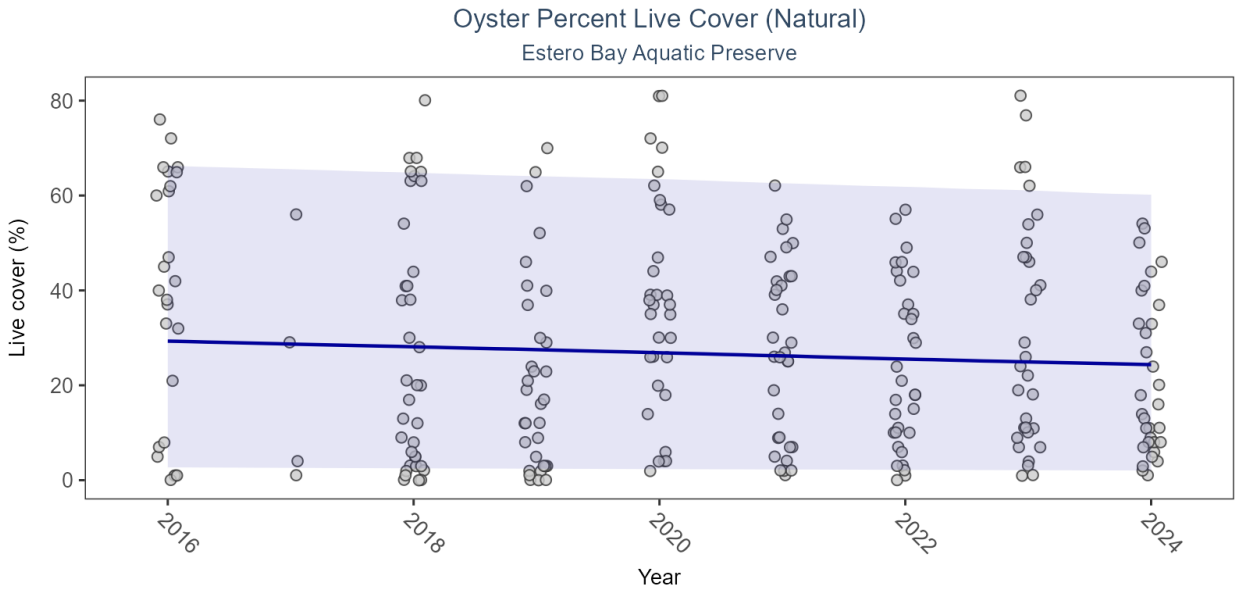
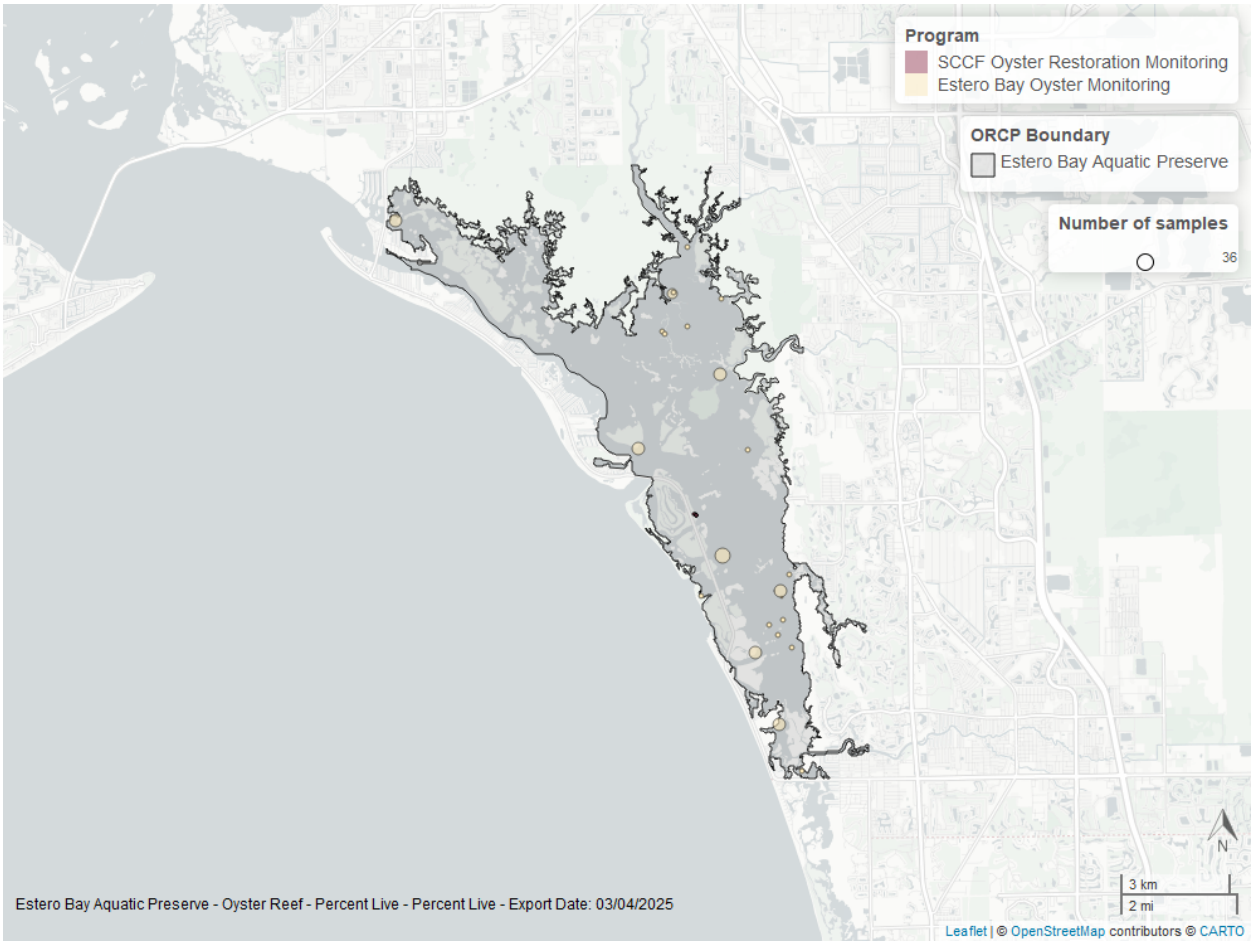


Figure 30: Figure for Oyster Percent Live in Estero Bay Aquatic Preserve

Table 30: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-0.59	18.34	-0.08 to -0.77


Program
SCCF Oyster Restoration Monitoring
Estero Bay Oyster Monitoring
ORCP Boundary
Estero Bay Aquatic Preserve
Number of samples
36
N
3 km
2 mi
Estero Bay Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Guana River Marsh Aquatic Preserve

Natural

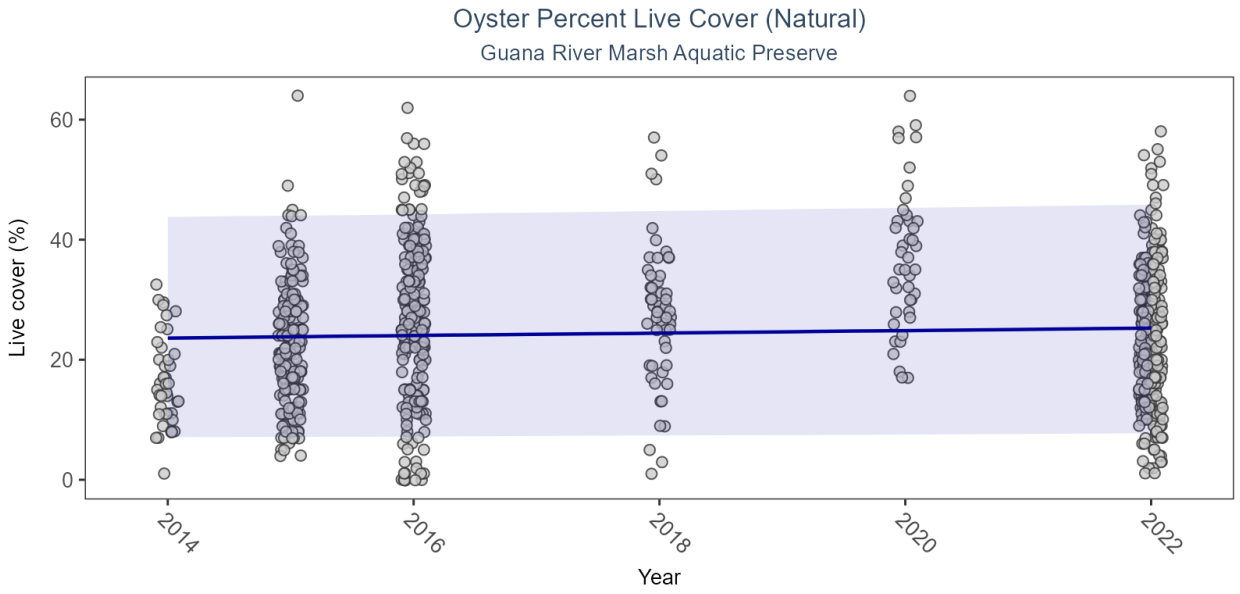


Figure 31: Figure for Oyster Percent Live in Guana River Marsh Aquatic Preserve

Table 31: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly increasing trend	0.21	9.82	0.07 to 0.31


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana River Marsh Aquatic Preserve
Number of samples
42
4
N
3 km
2 mi
Guana River Marsh Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Guana Tolomato Matanzas National Estuarine Research Reserve

Natural

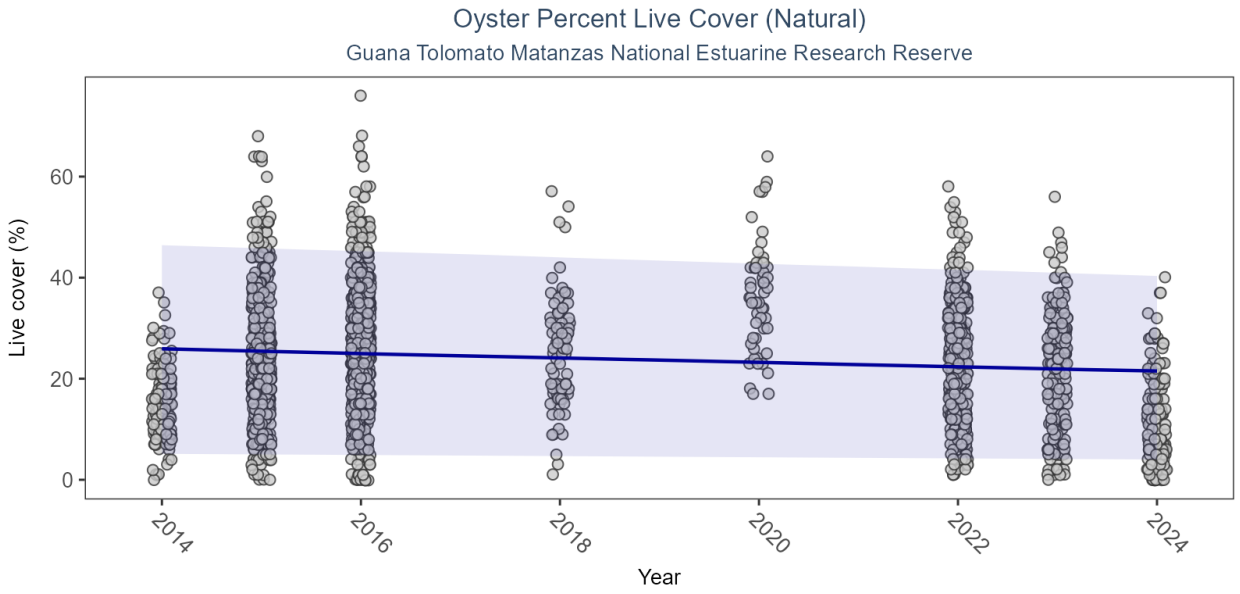
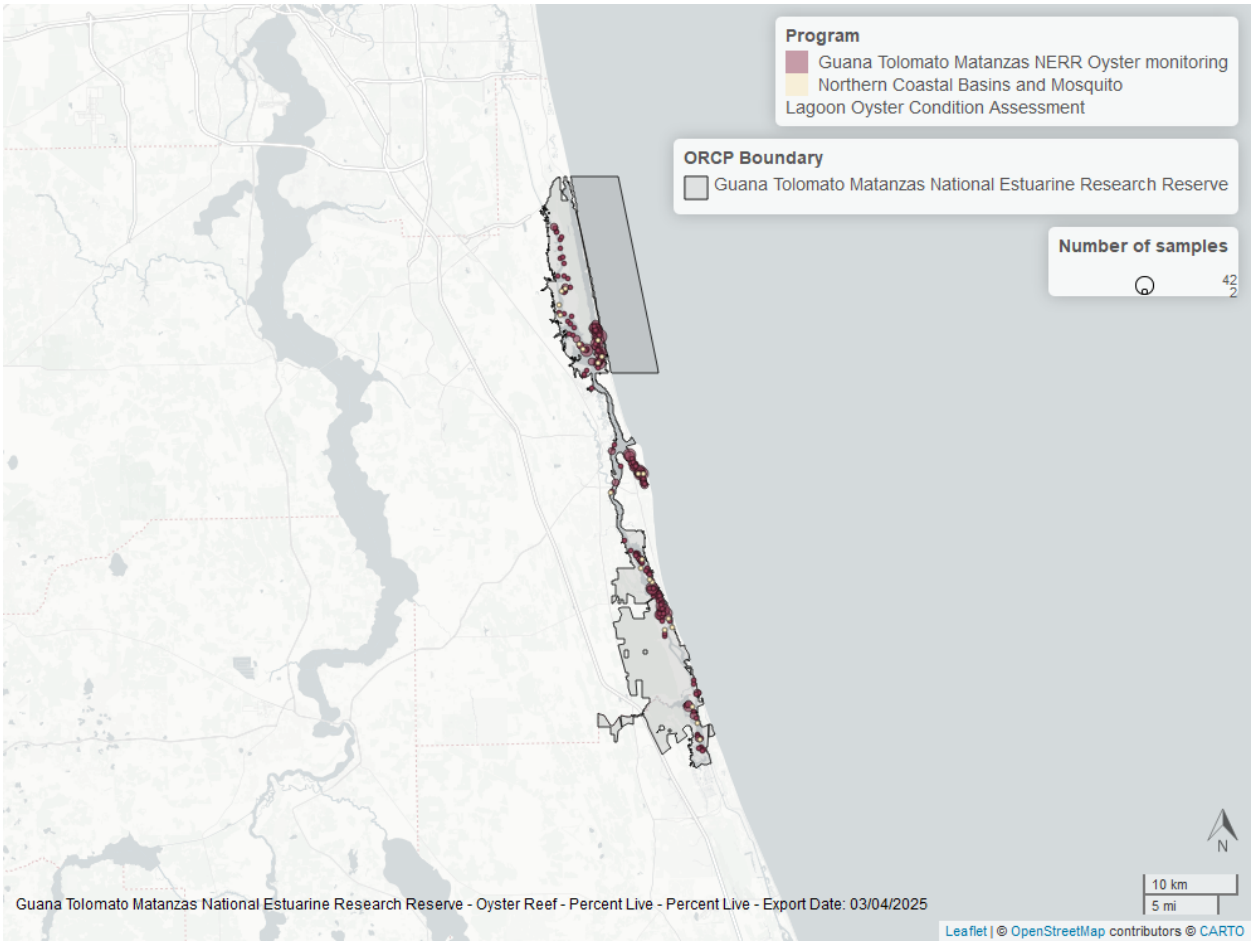


Figure 32: Figure for Oyster Percent Live in Guana Tolomato Matanzas National Estuarine Research Reserve

Table 32: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-0.44	10.12	-0.13 to -0.6


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana Tolomato Matanzas National Estuarine Research Reserve
Number of samples
42
2
N
10 km
5 mi
Guana Tolomato Matanzas National Estuarine Research Reserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Indian River-Malabar to Vero Beach Aquatic Preserve

Natural

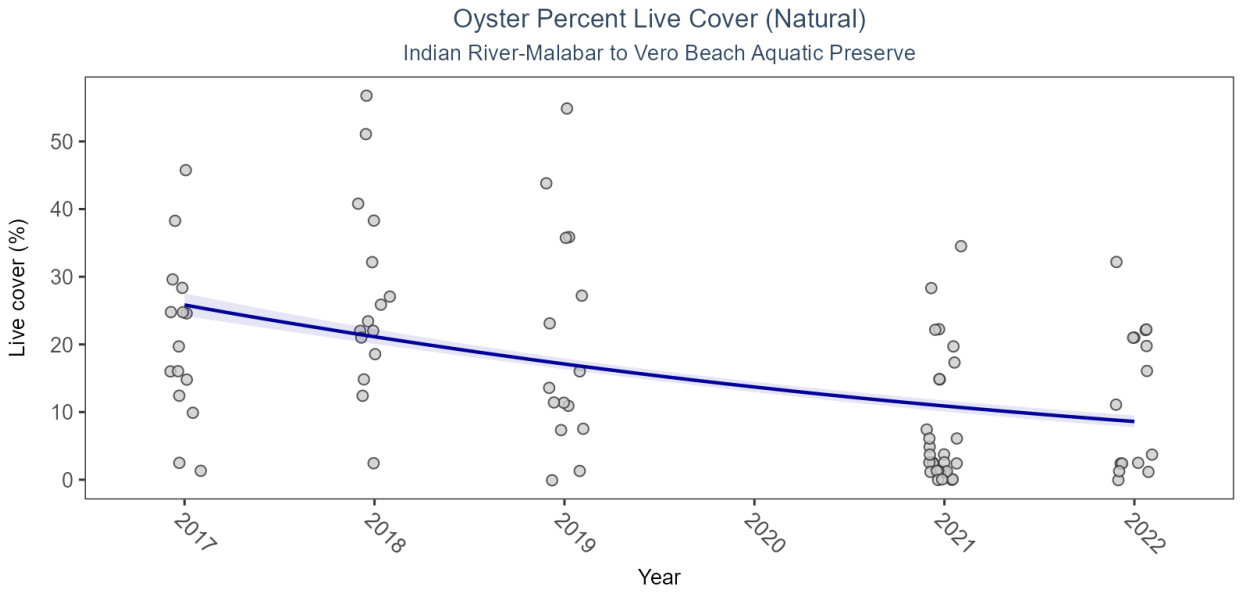
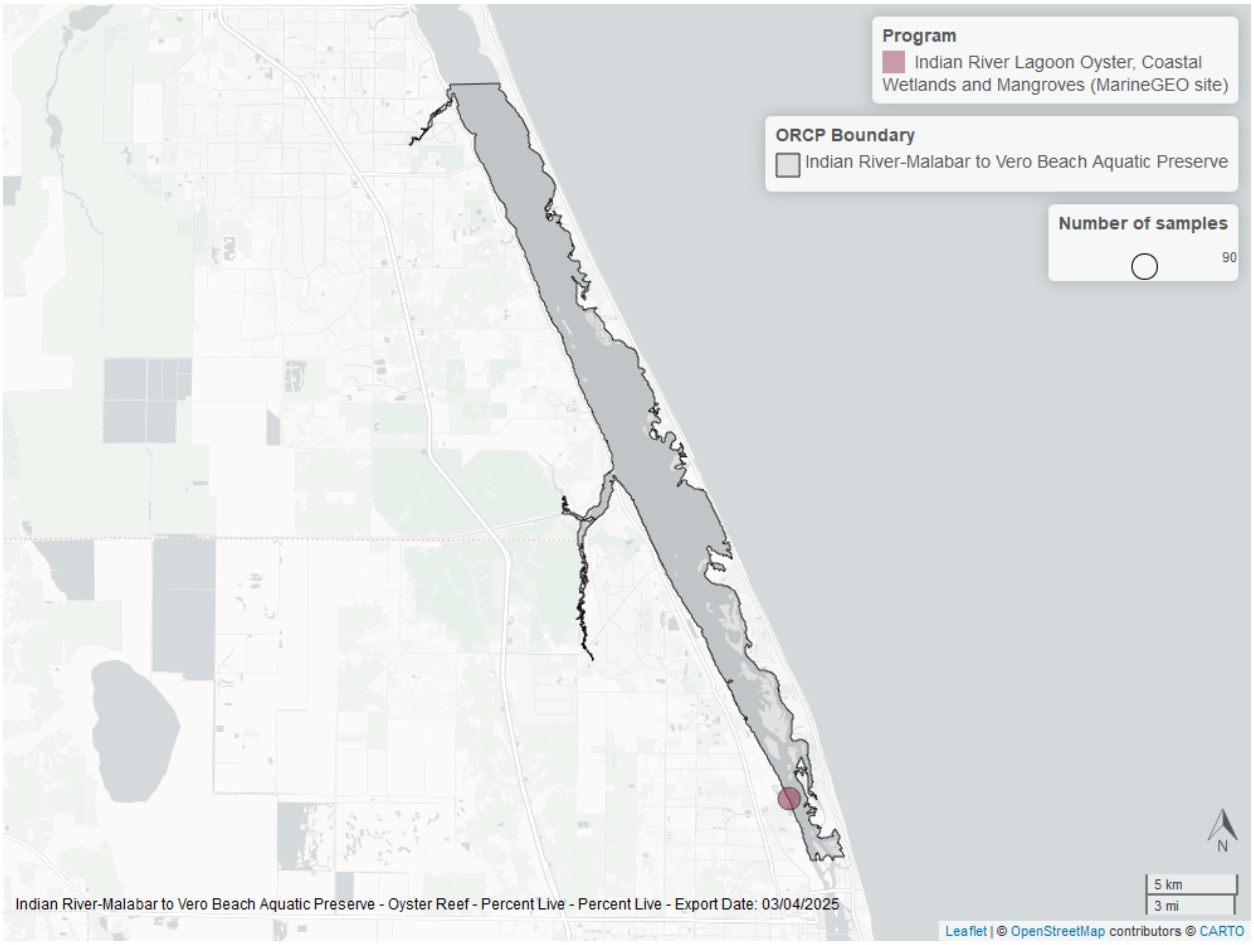


Figure 33: Figure for Oyster Percent Live in Indian River-Malabar to Vero Beach Aquatic Preserve

Table 33: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-3.45	0.48	-3.29 to -3.61


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Malabar to Vero Beach Aquatic Preserve
Number of samples
90
N
5 km
3 mi
Indian River-Malabar to Vero Beach Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Natural

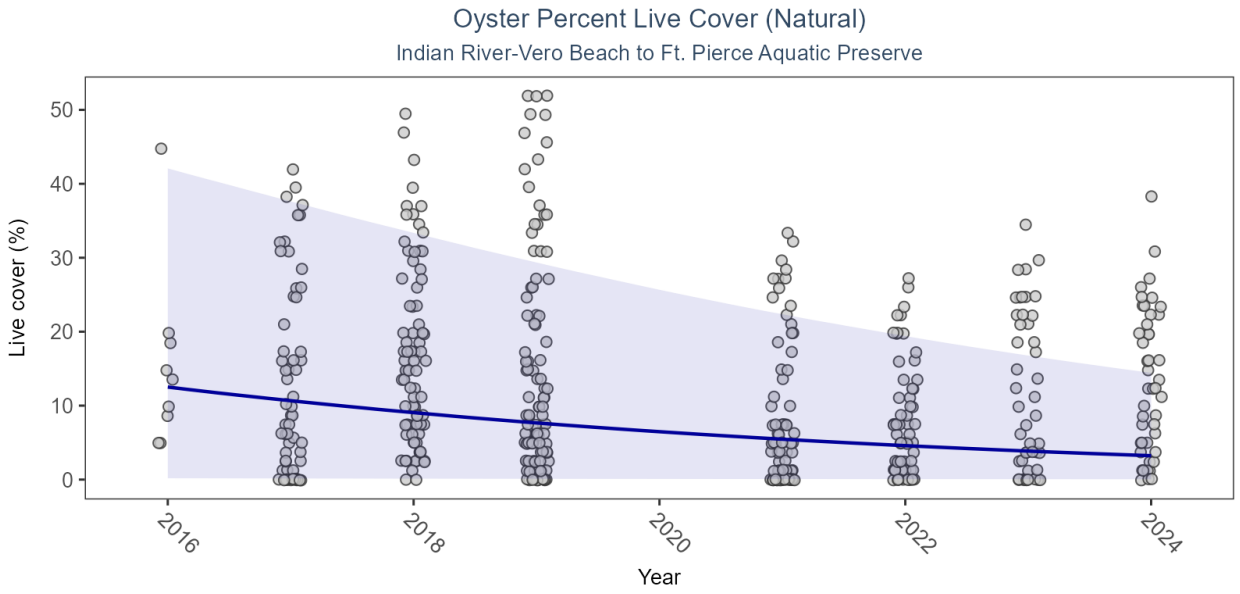
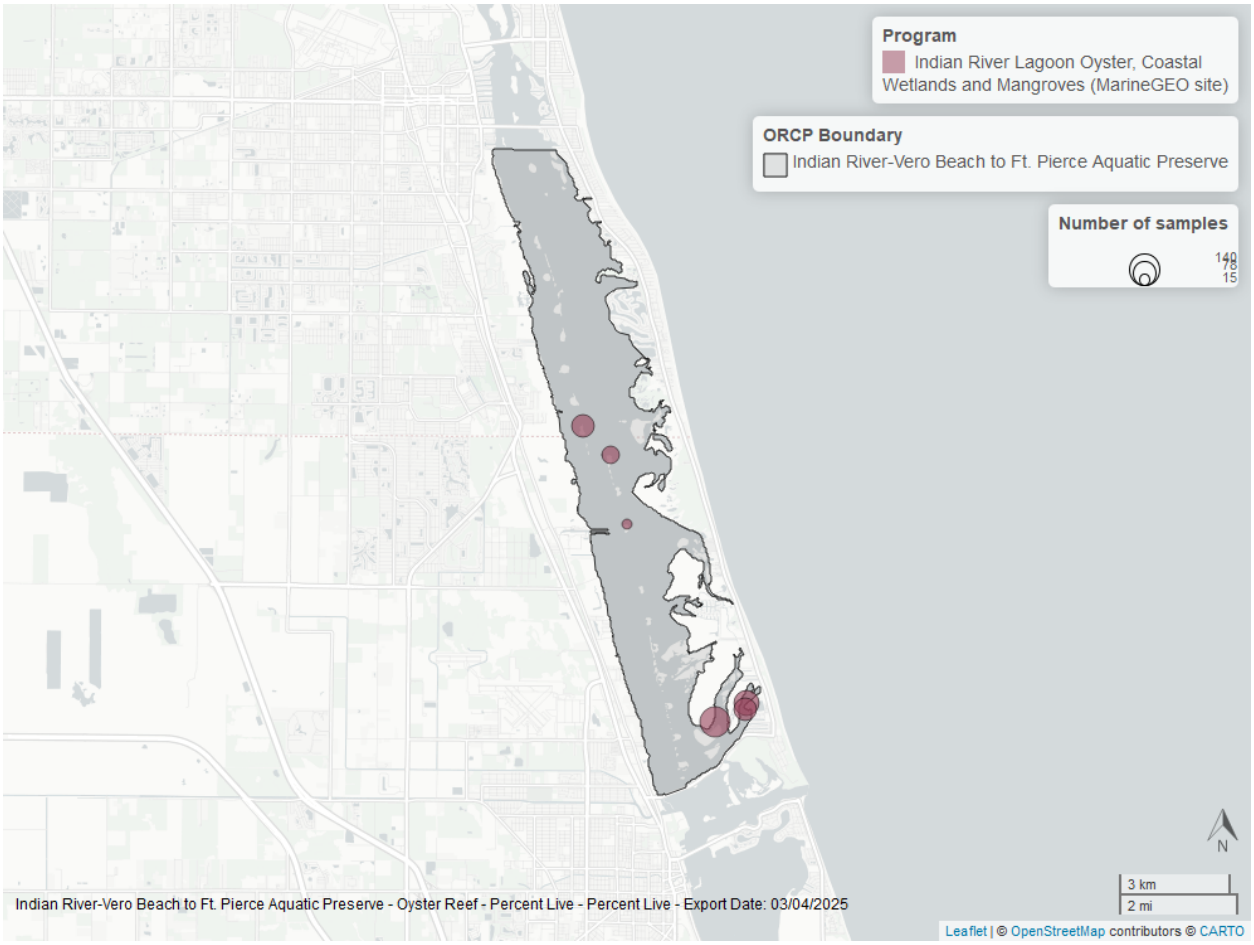


Figure 34: Figure for Oyster Percent Live in Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Table 34: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-1.17	9.86	-0.02 to -3.47


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve
Number of samples
140
78
15
N
3 km
2 mi
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Jensen Beach to Jupiter Inlet Aquatic Preserve

Natural

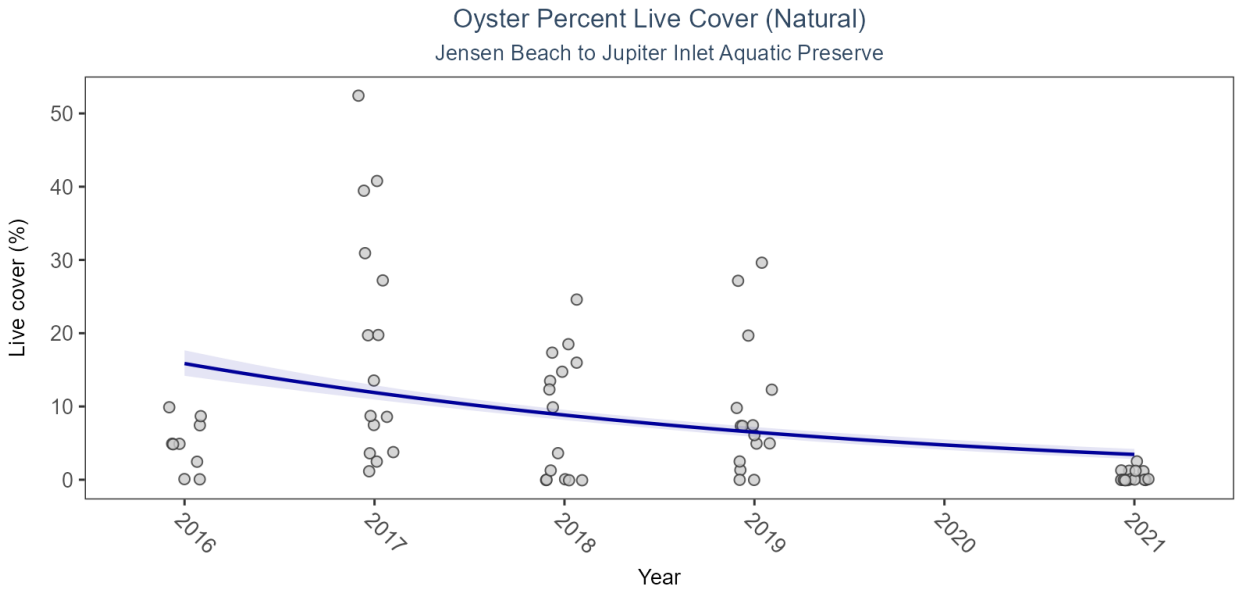
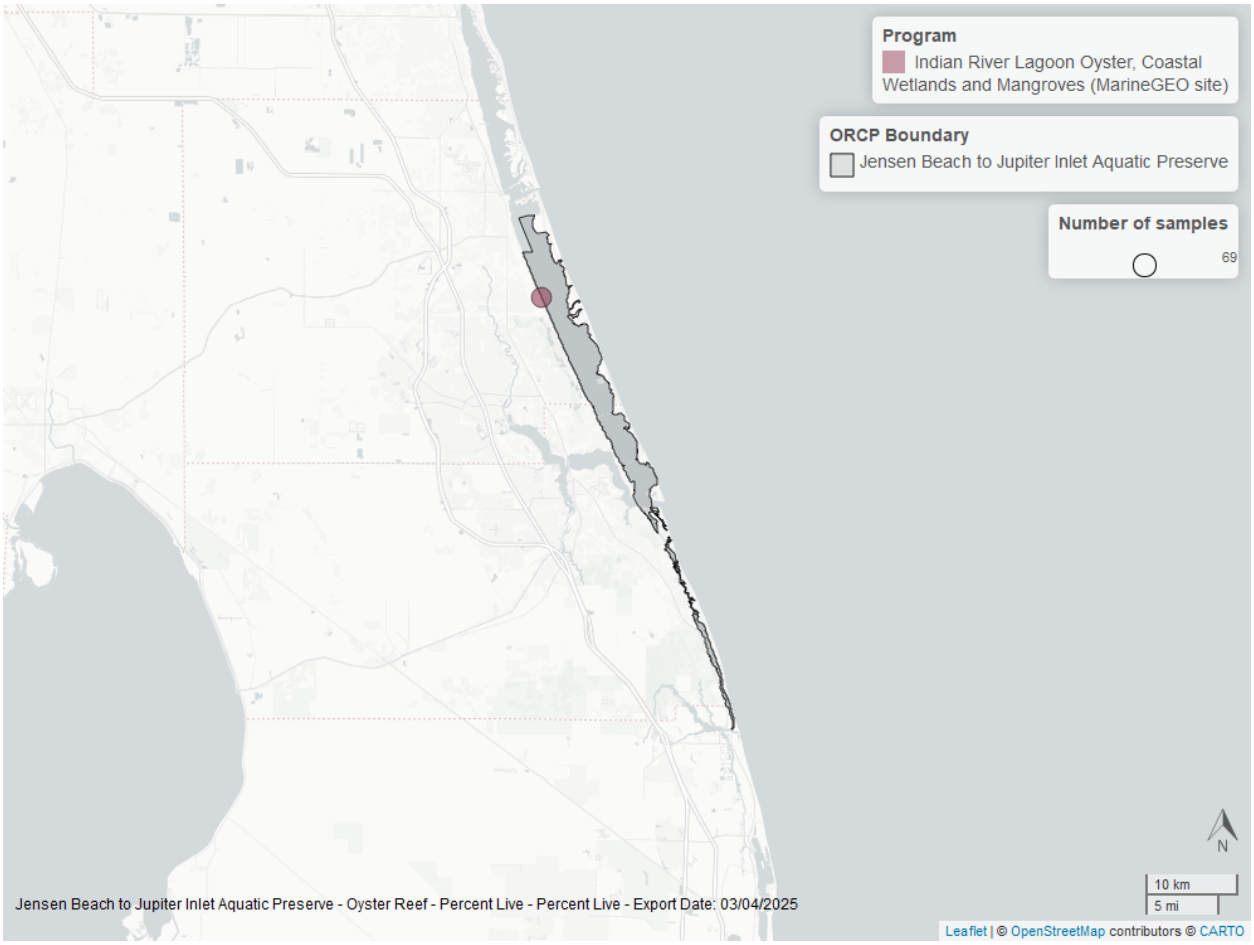


Figure 35: Figure for Oyster Percent Live in Jensen Beach to Jupiter Inlet Aquatic Preserve

Table 35: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly decreasing trend	-2.48	0.43	-2.27 to -2.69


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Jensen Beach to Jupiter Inlet Aquatic Preserve
Number of samples
69
N
10 km
5 mi
Jensen Beach to Jupiter Inlet Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Lemon Bay Aquatic Preserve

Natural

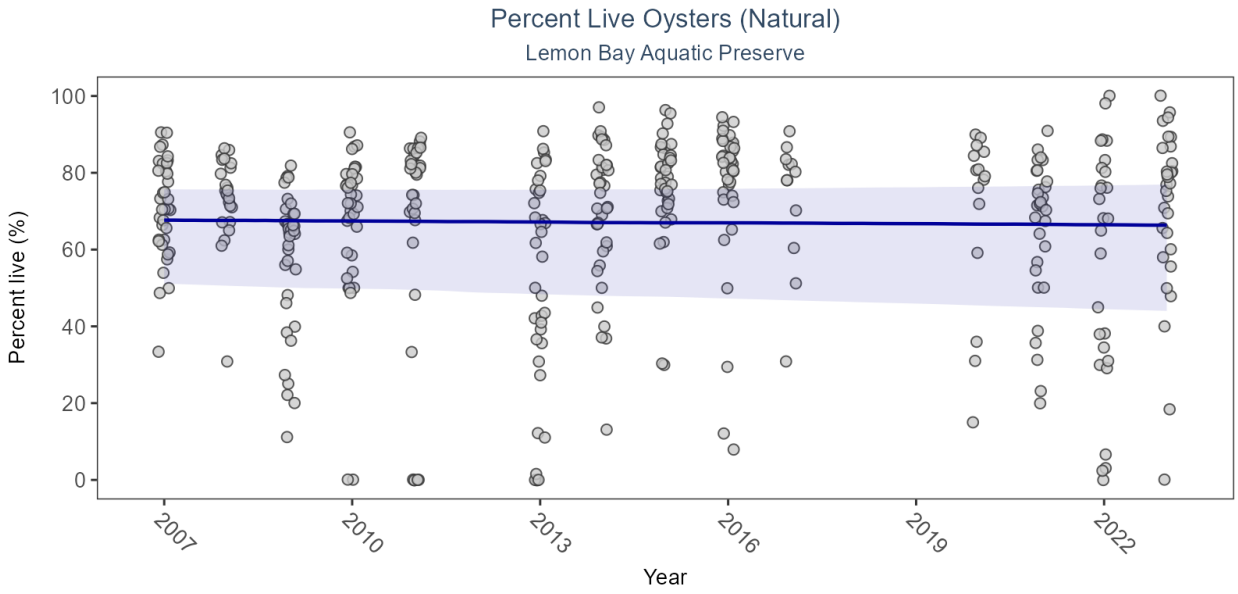
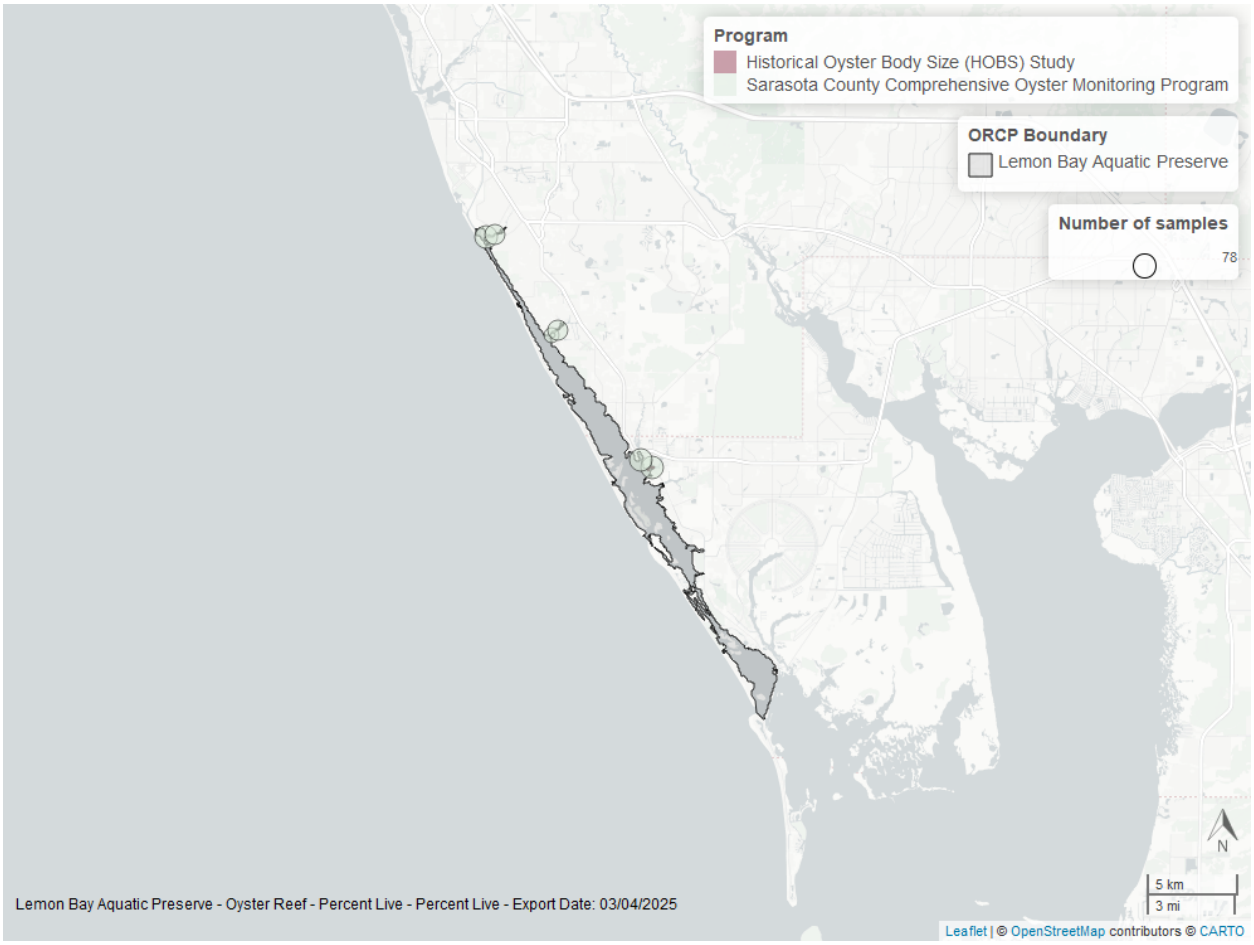


Figure 36: Figure for Oyster Percent Live in Lemon Bay Aquatic Preserve

Table 36: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	No significant change	0	0.09	0 to 0


Program
Historical Oyster Body Size (HOBS) Study
Sarasota County Comprehensive Oyster Monitoring Program
ORCP Boundary
Lemon Bay Aquatic Preserve
Number of samples
78
N
5 km
3 mi
Lemon Bay Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Loxahatchee River-Lake Worth Creek Aquatic Preserve

Natural

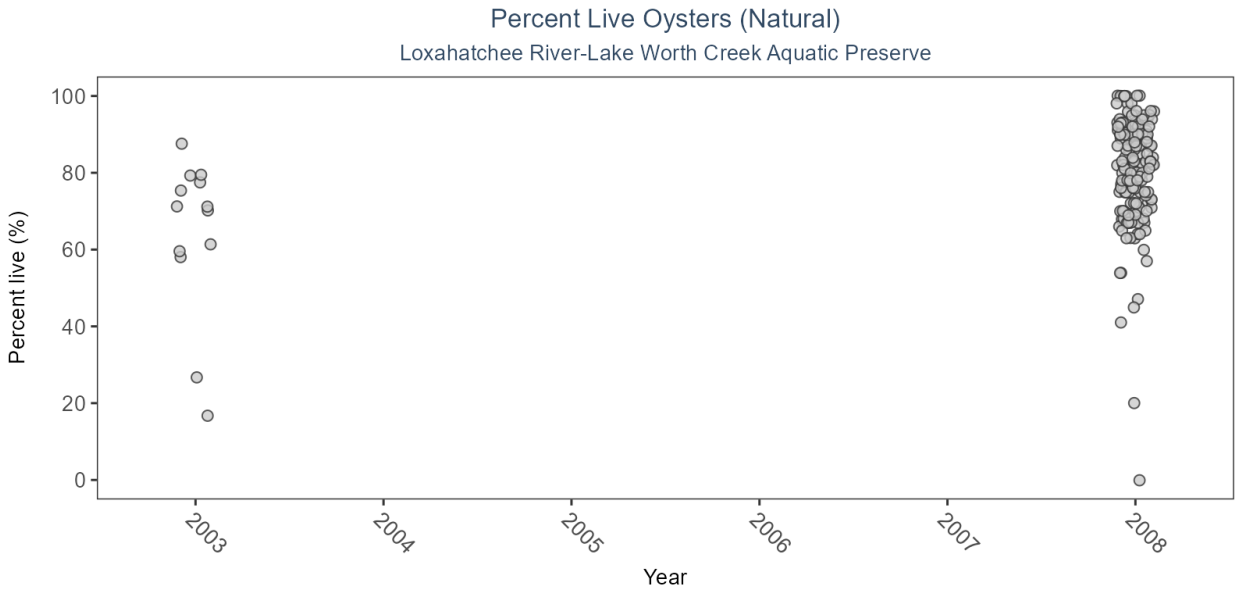
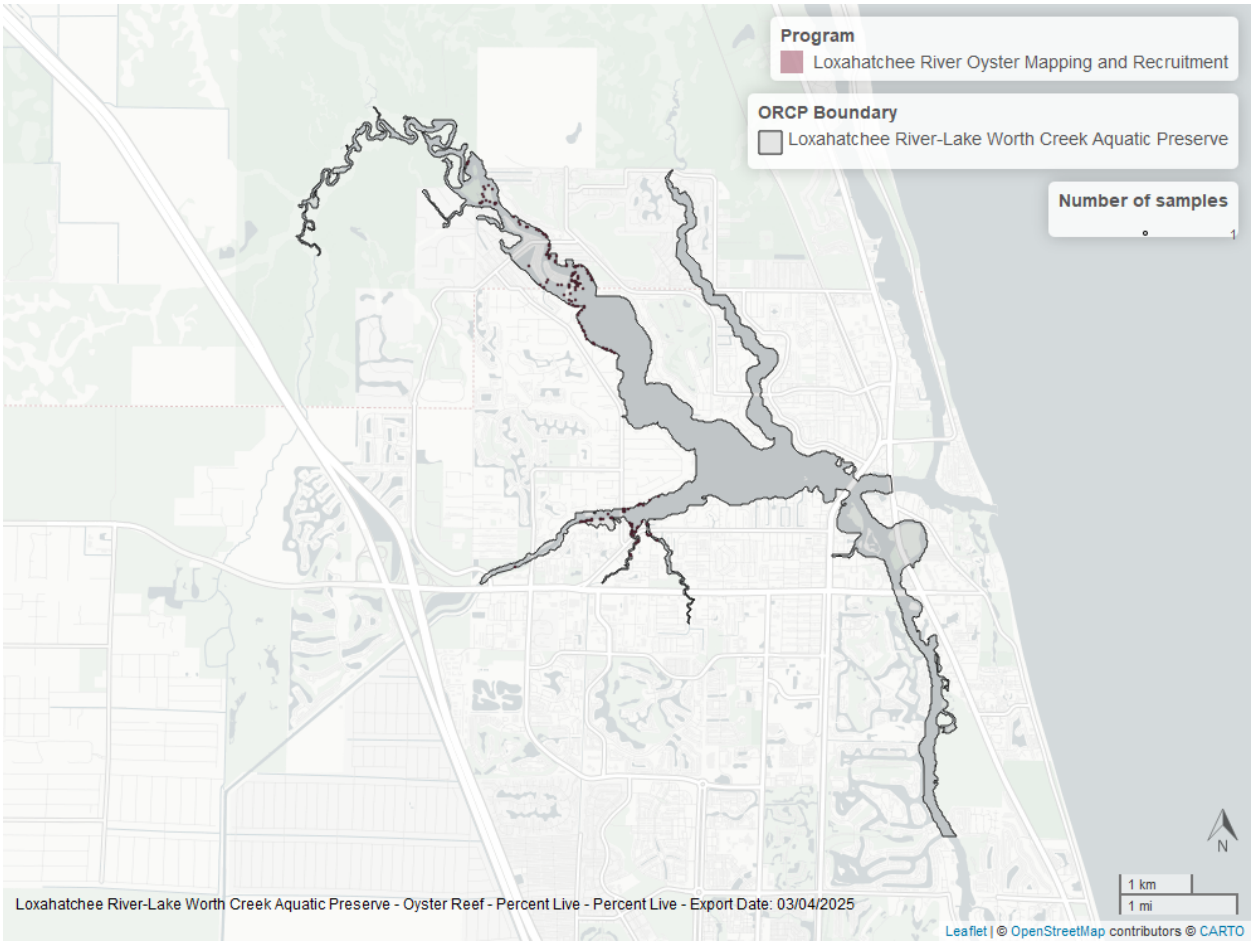


Figure 37: Figure for Oyster Percent Live in Loxahatchee River-Lake Worth Creek Aquatic Preserve

Table 37: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Loxahatchee River Oyster Mapping and Recruitment
ORCP Boundary
Loxahatchee River-Lake Worth Creek Aquatic Preserve
Number of samples
1
N
1 km
1 mi
Loxahatchee River-Lake Worth Creek Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Mosquito Lagoon Aquatic Preserve

Natural

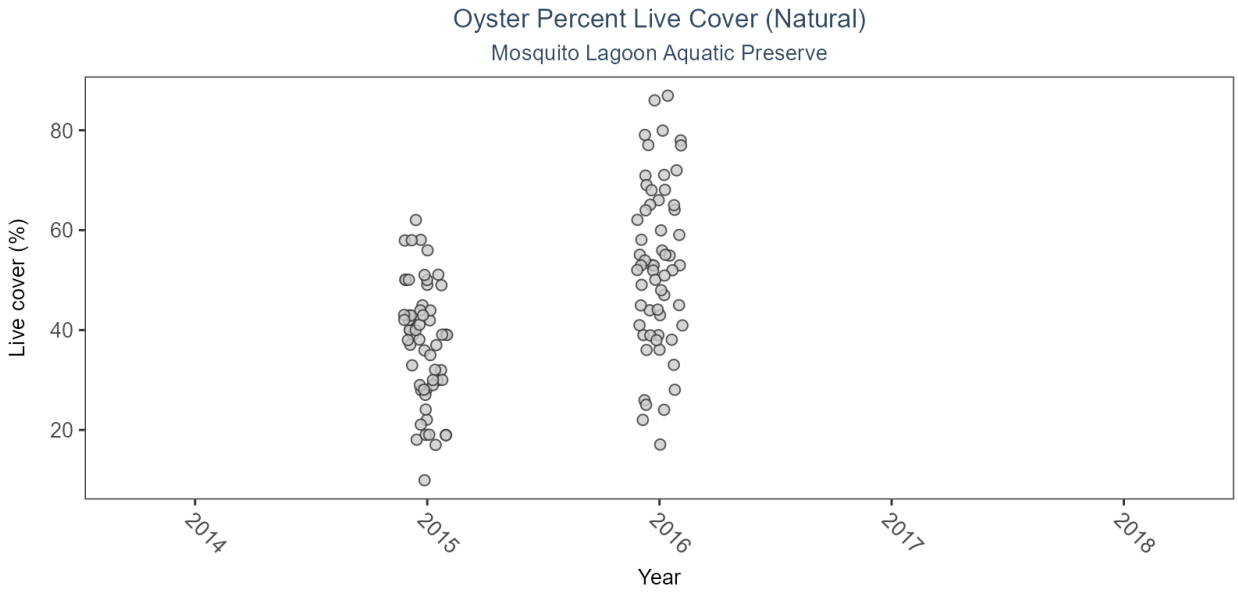
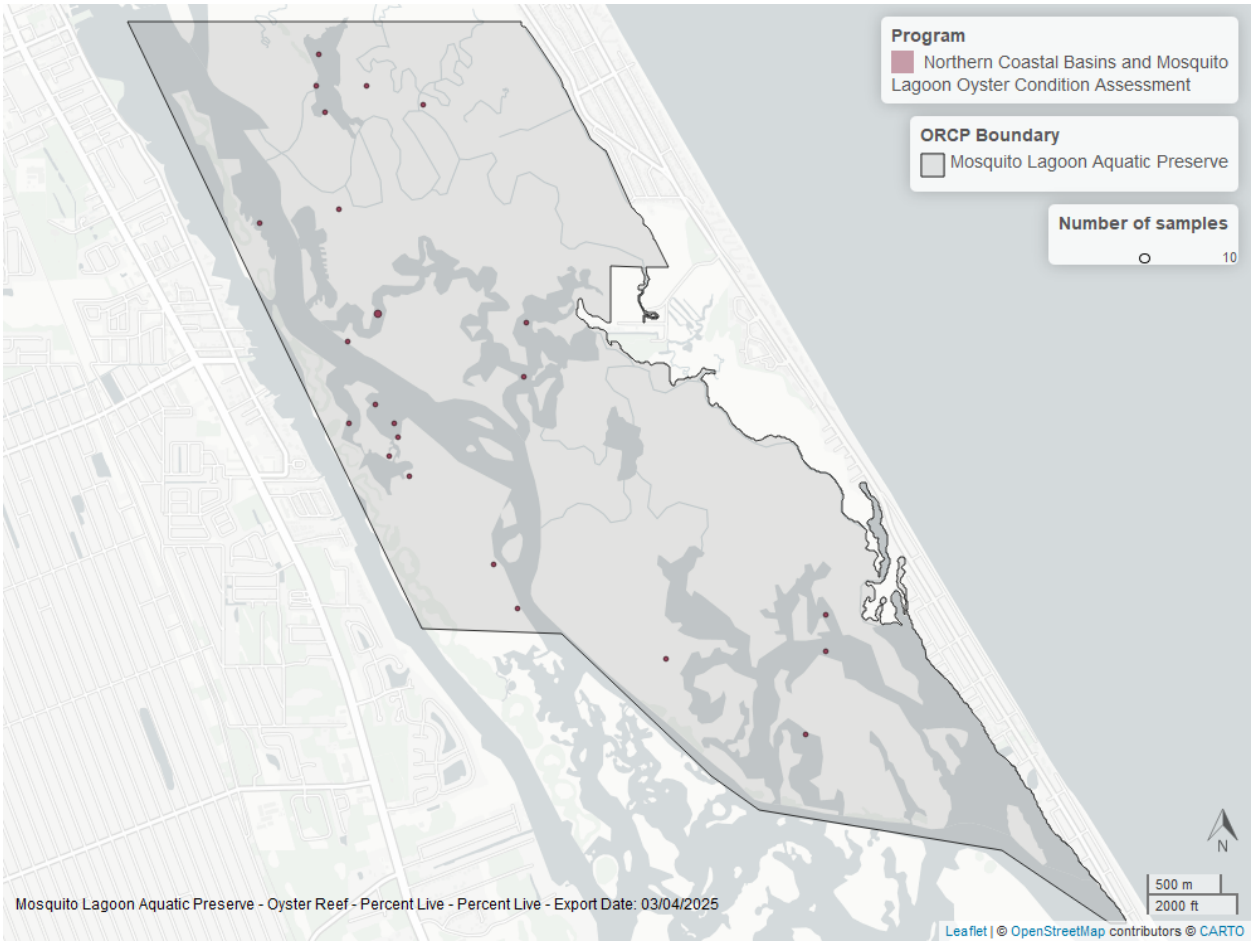


Figure 38: Figure for Oyster Percent Live in Mosquito Lagoon Aquatic Preserve

Table 38: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Mosquito Lagoon Aquatic Preserve
Number of samples
10
N
500 m
2000 ft
Mosquito Lagoon Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Nassau River-St. Johns River Marshes Aquatic Preserve

Natural

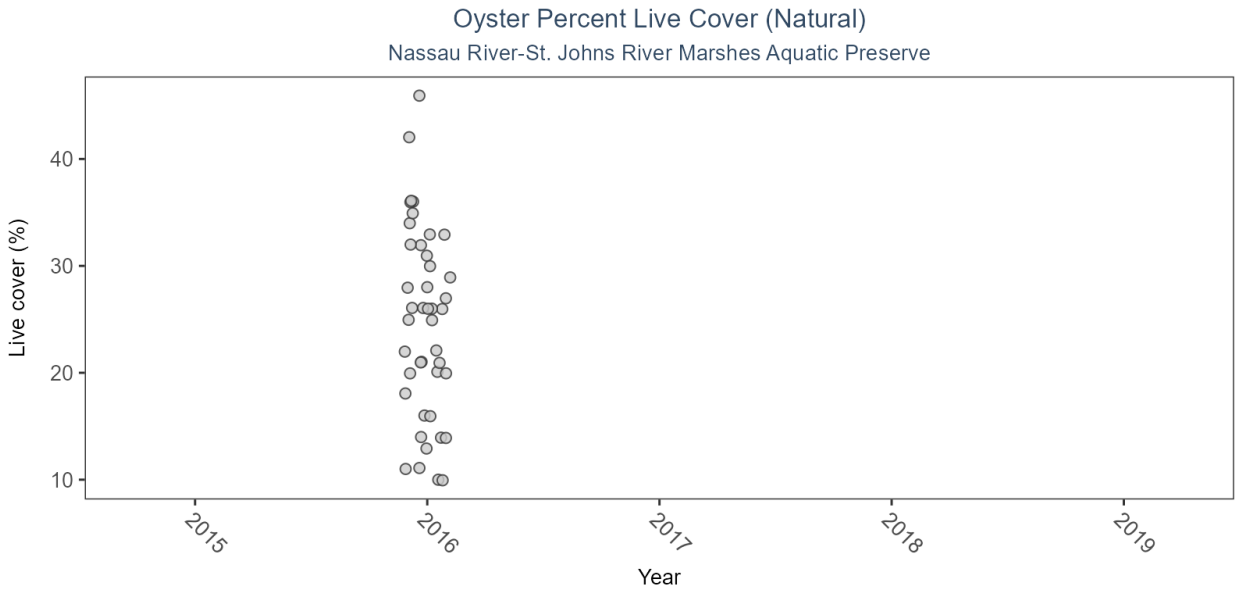
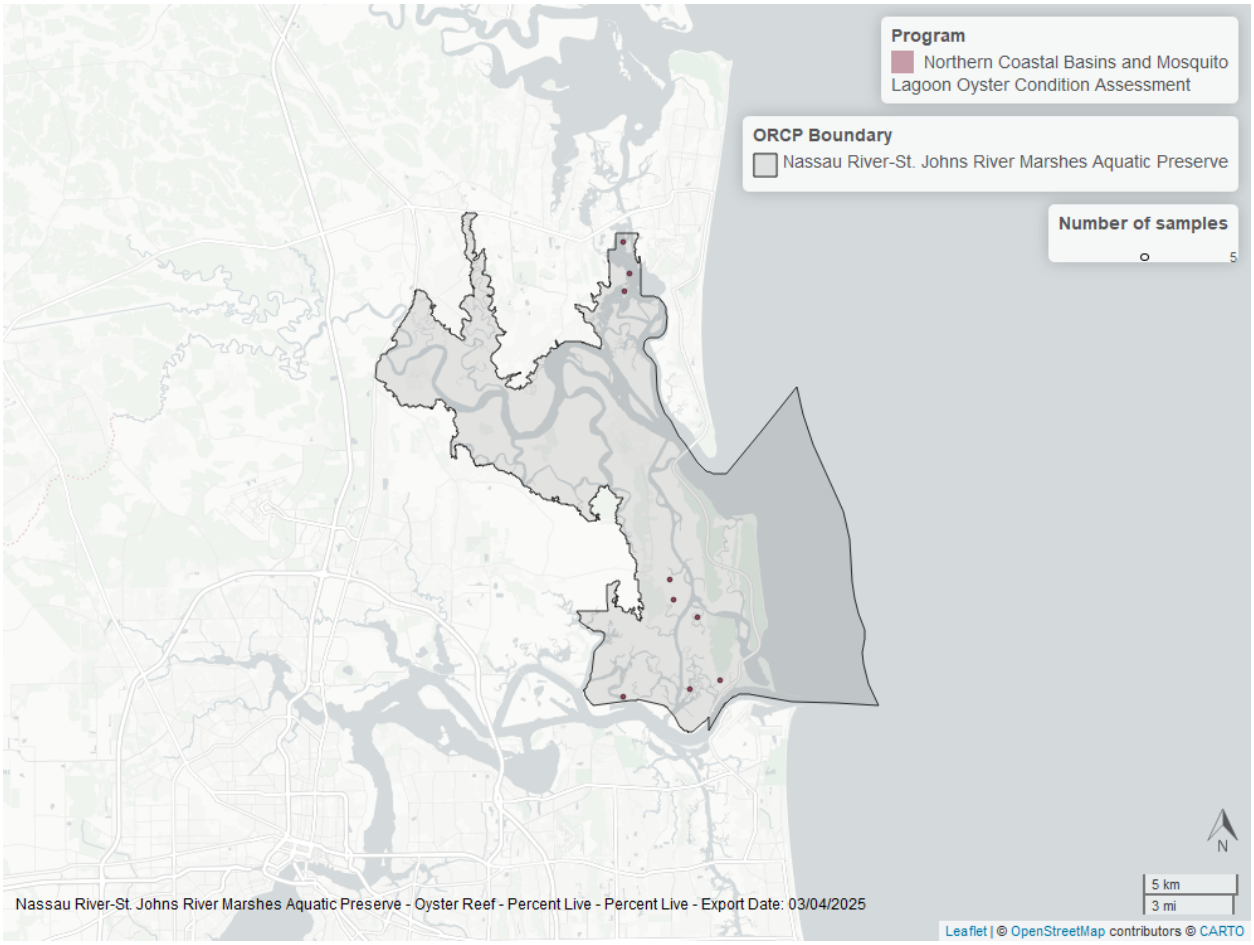


Figure 39: Figure for Oyster Percent Live in Nassau River-St. Johns River Marshes Aquatic Preserve

Table 39: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Nassau River-St. Johns River Marshes Aquatic Preserve
Number of samples
5
N
5 km
3 mi
Nassau River-St. Johns River Marshes Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pine Island Sound Aquatic Preserve

Natural

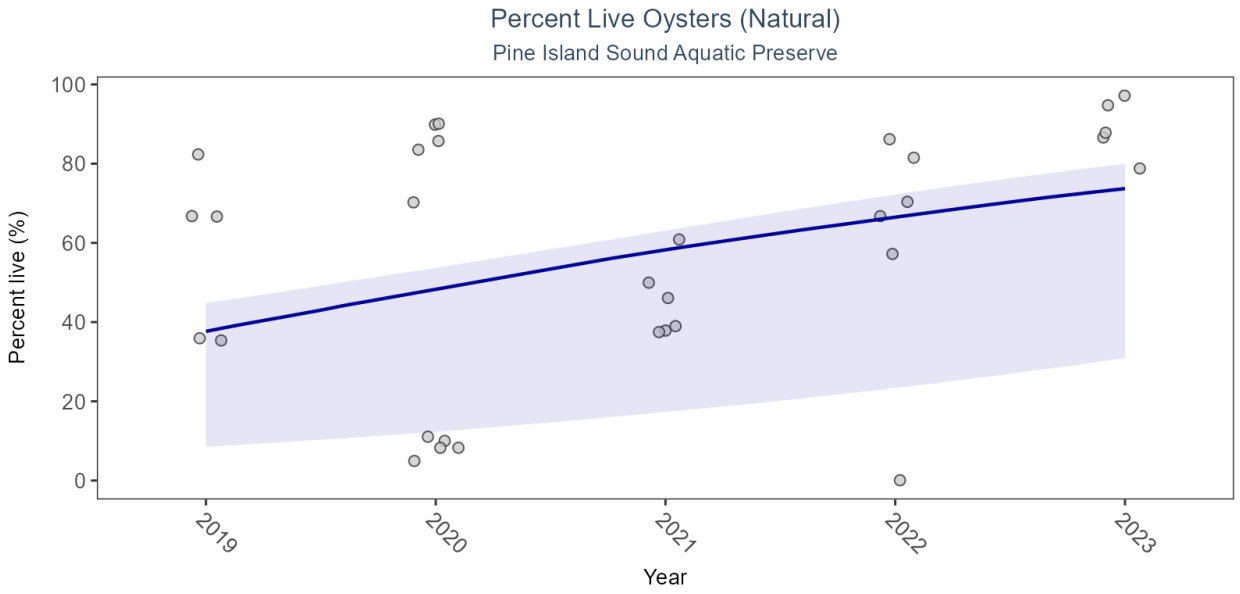


Figure 40: Figure for Oyster Percent Live in Pine Island Sound Aquatic Preserve

Table 40: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	Significantly increasing trend	8.98	6.04	5.73 to 8.78

Restored

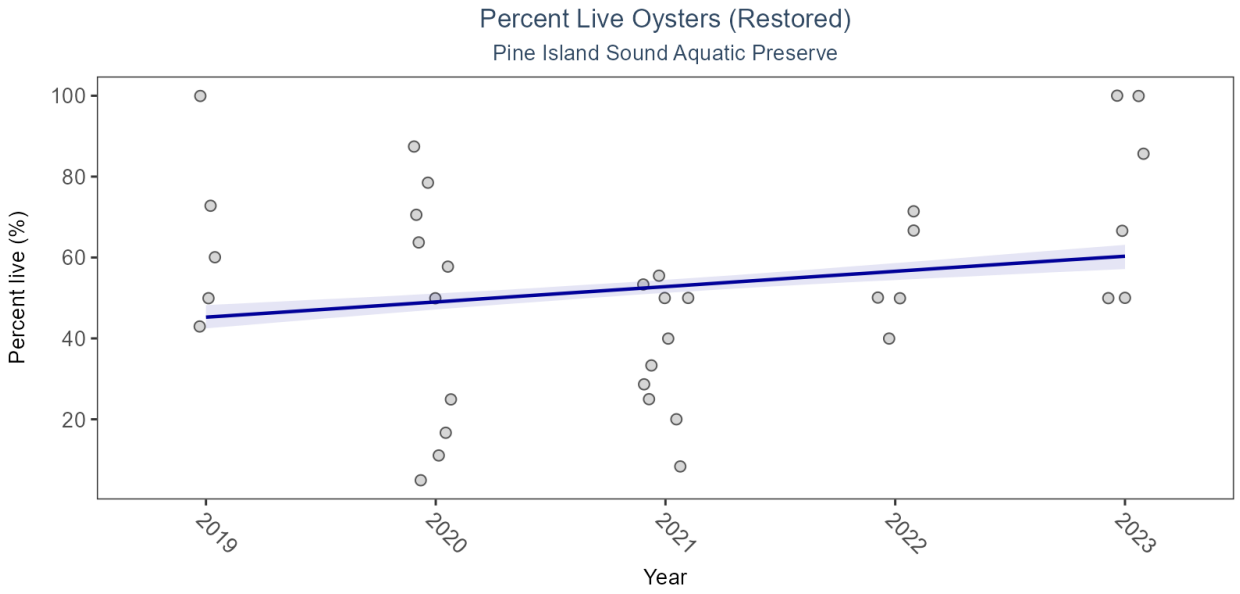
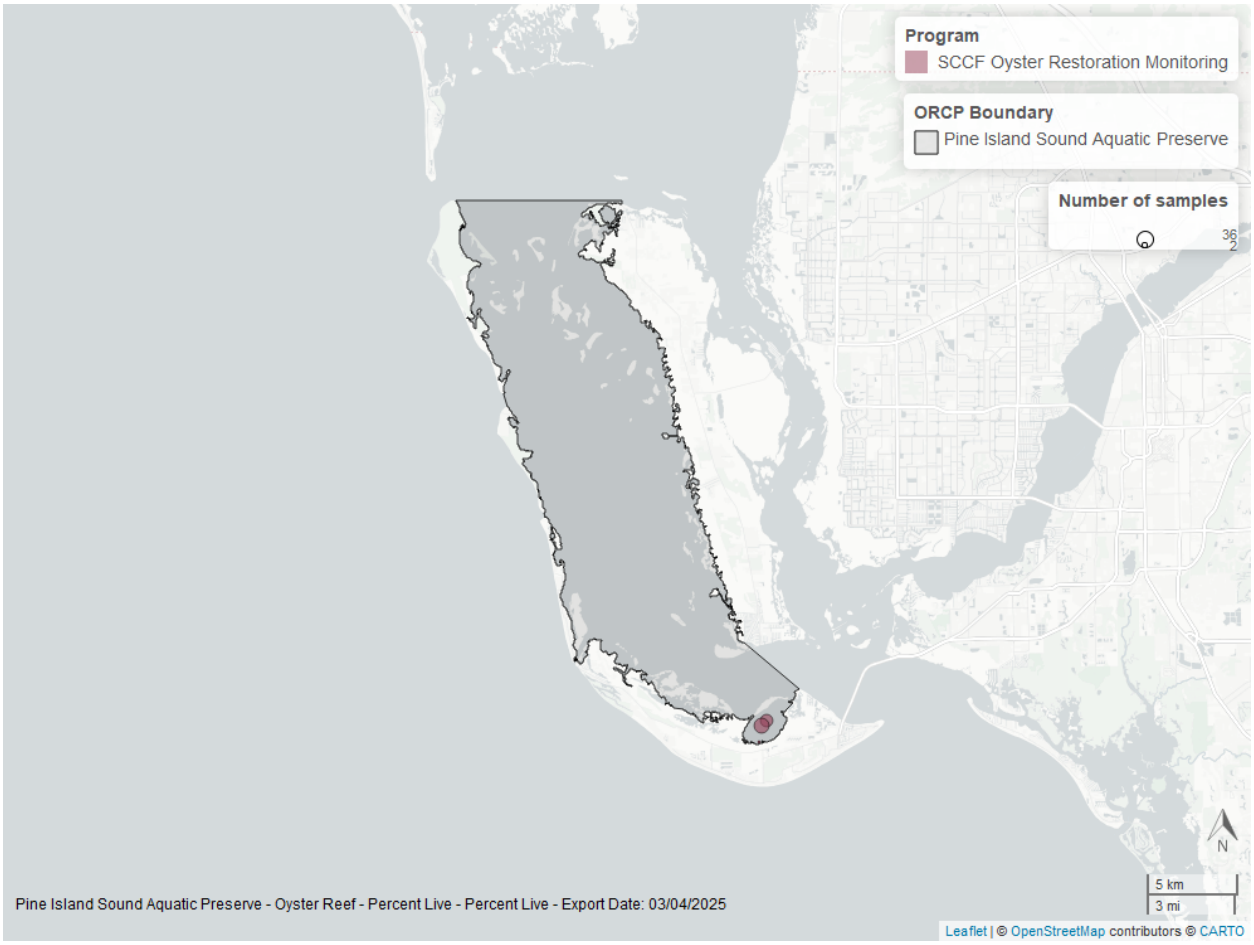


Figure 41: Figure for Oyster Percent Live in Pine Island Sound Aquatic Preserve

Table 41: Model results for Oyster Percent Live - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly increasing trend	3.77	1.1	3.67 to 3.72


Program
SCCF Oyster Restoration Monitoring
ORCP Boundary
Pine Island Sound Aquatic Preserve
Number of samples
36
2
N
5 km
3 mi
Pine Island Sound Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pinellas County Aquatic Preserve

Natural

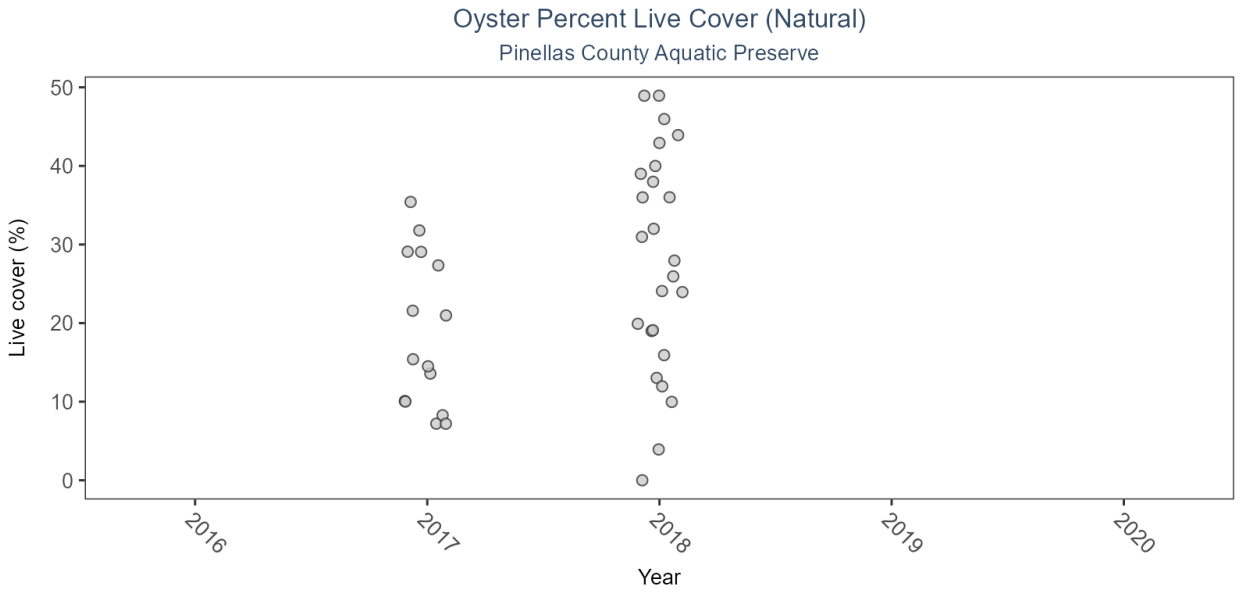
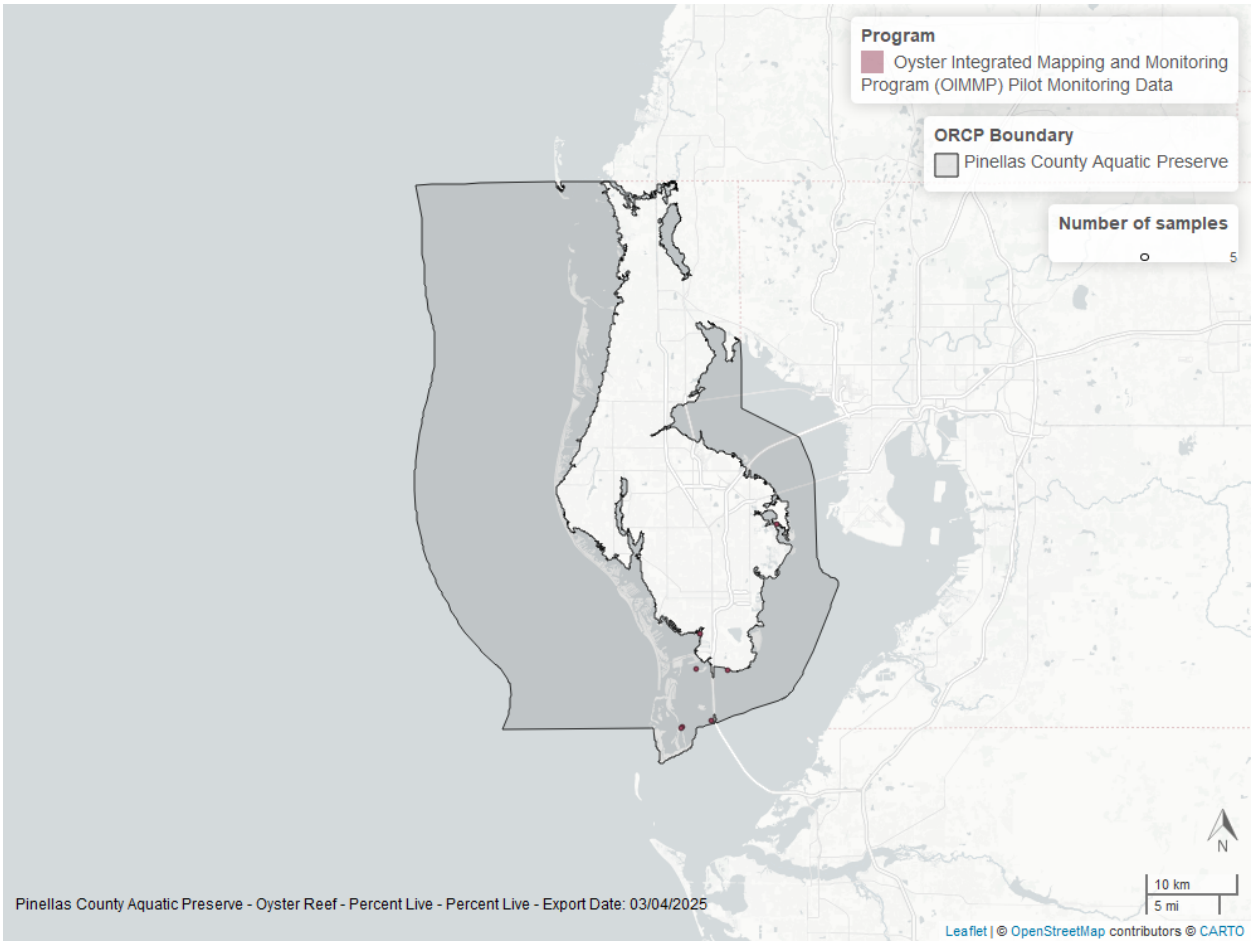


Figure 42: Figure for Oyster Percent Live in Pinellas County Aquatic Preserve

Table 42: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Pinellas County Aquatic Preserve
Number of samples
0
5
N
10 km
5 mi
Pinellas County Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

St. Martins Marsh Aquatic Preserve

Natural

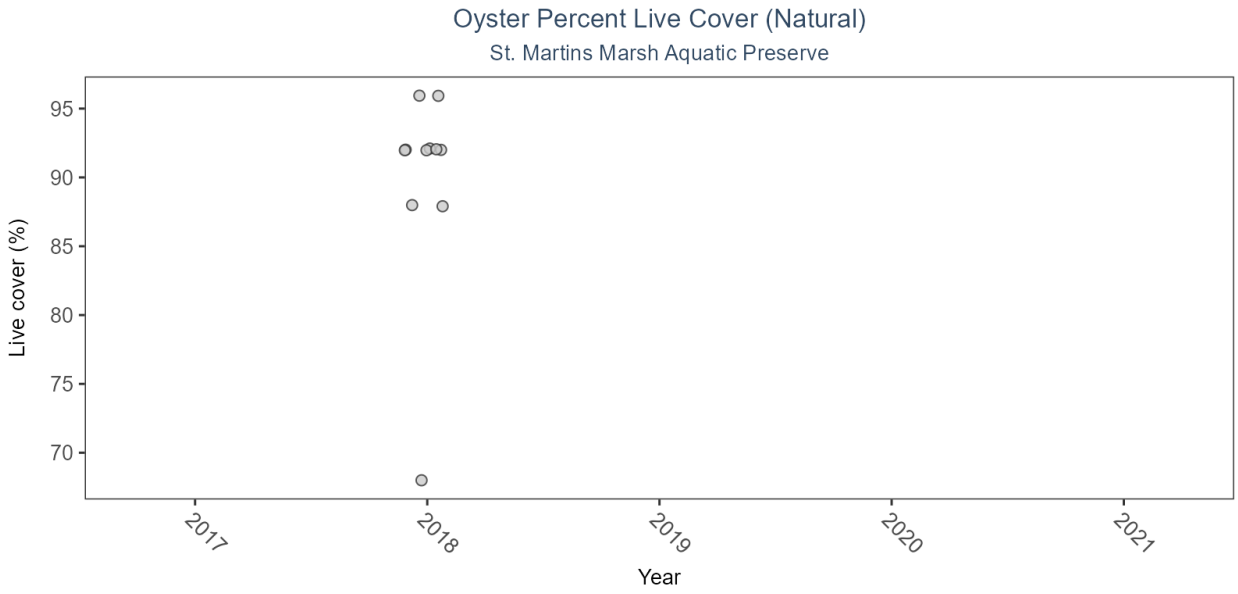
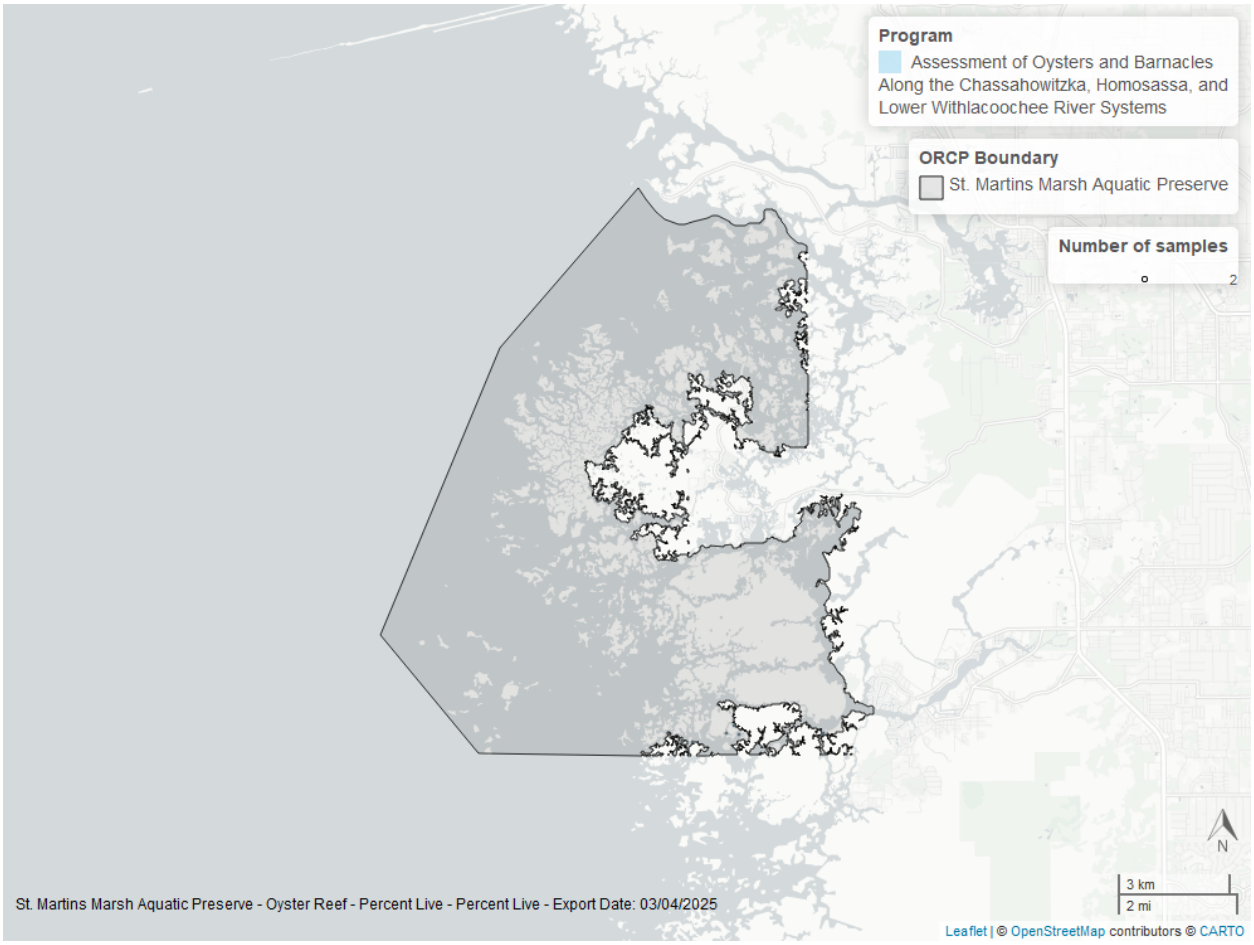


Figure 43: Figure for Oyster Percent Live in St. Martins Marsh Aquatic Preserve

Table 43: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Assessment of Oysters and Barnacles Along the Chassahowitzka, Homosassa, and Lower Withlacoochee River Systems
ORCP Boundary
St. Martins Marsh Aquatic Preserve
Number of samples
2
N
3 km
2 mi
St. Martins Marsh Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Tomoka Marsh Aquatic Preserve

Natural

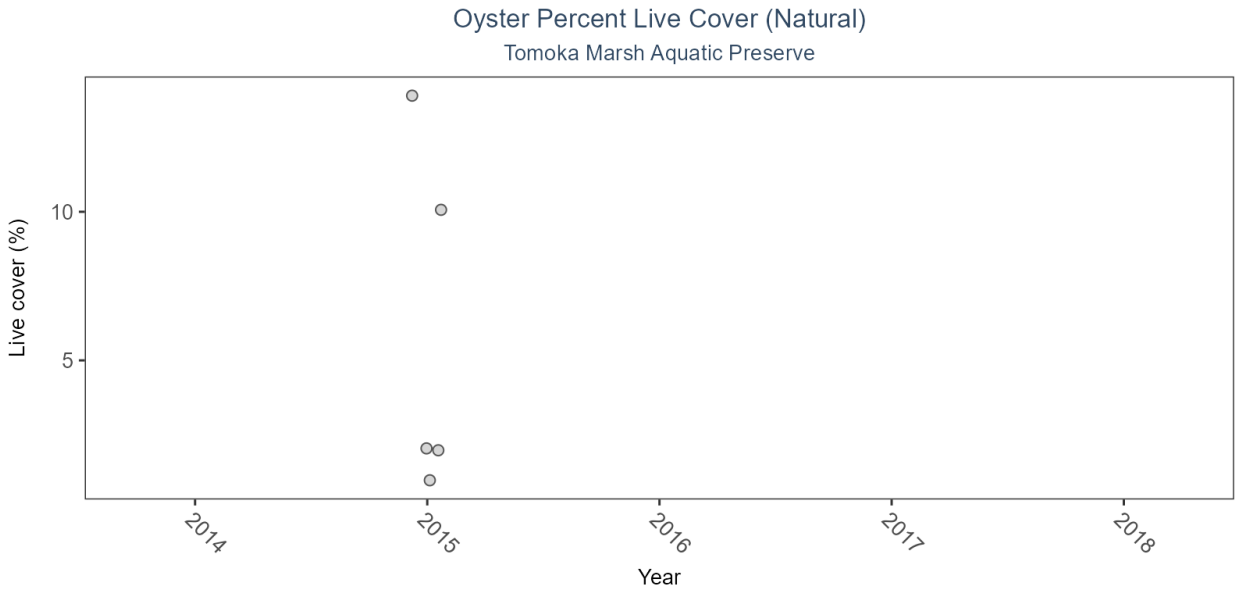


Figure 44: Figure for Oyster Percent Live in Tomoka Marsh Aquatic Preserve

Table 44: Model results for Oyster Percent Live - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Tomoka Marsh Aquatic Preserve
Number of samples
5
N
3 km
2 mi
Tomoka Marsh Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Yellow River Marsh Aquatic Preserve

Restored

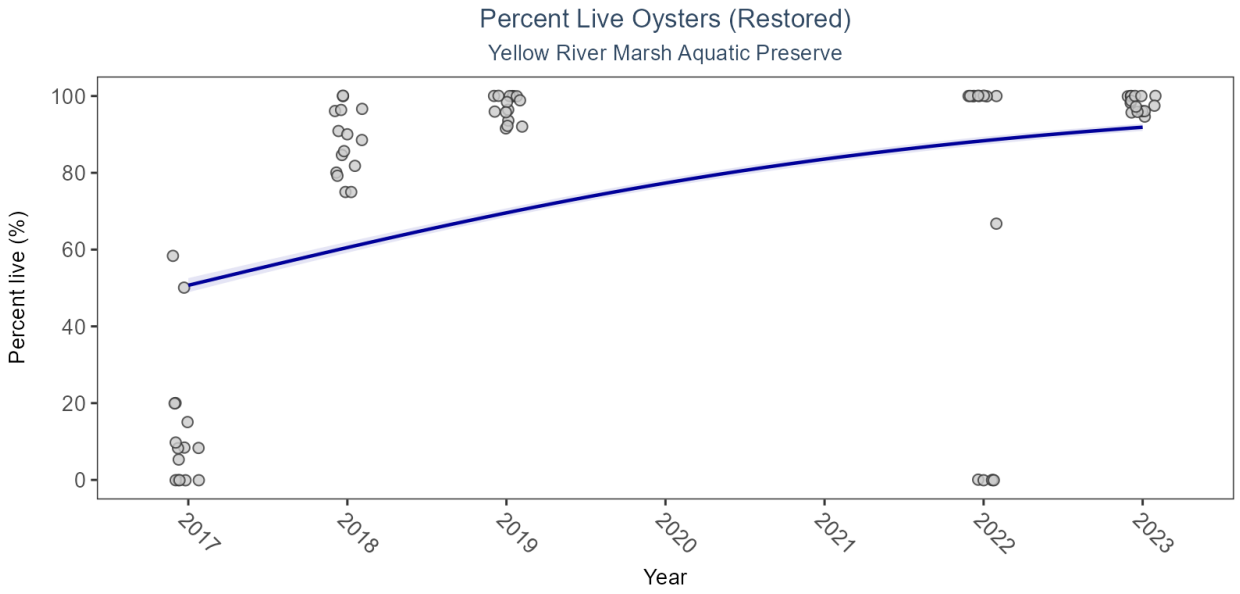
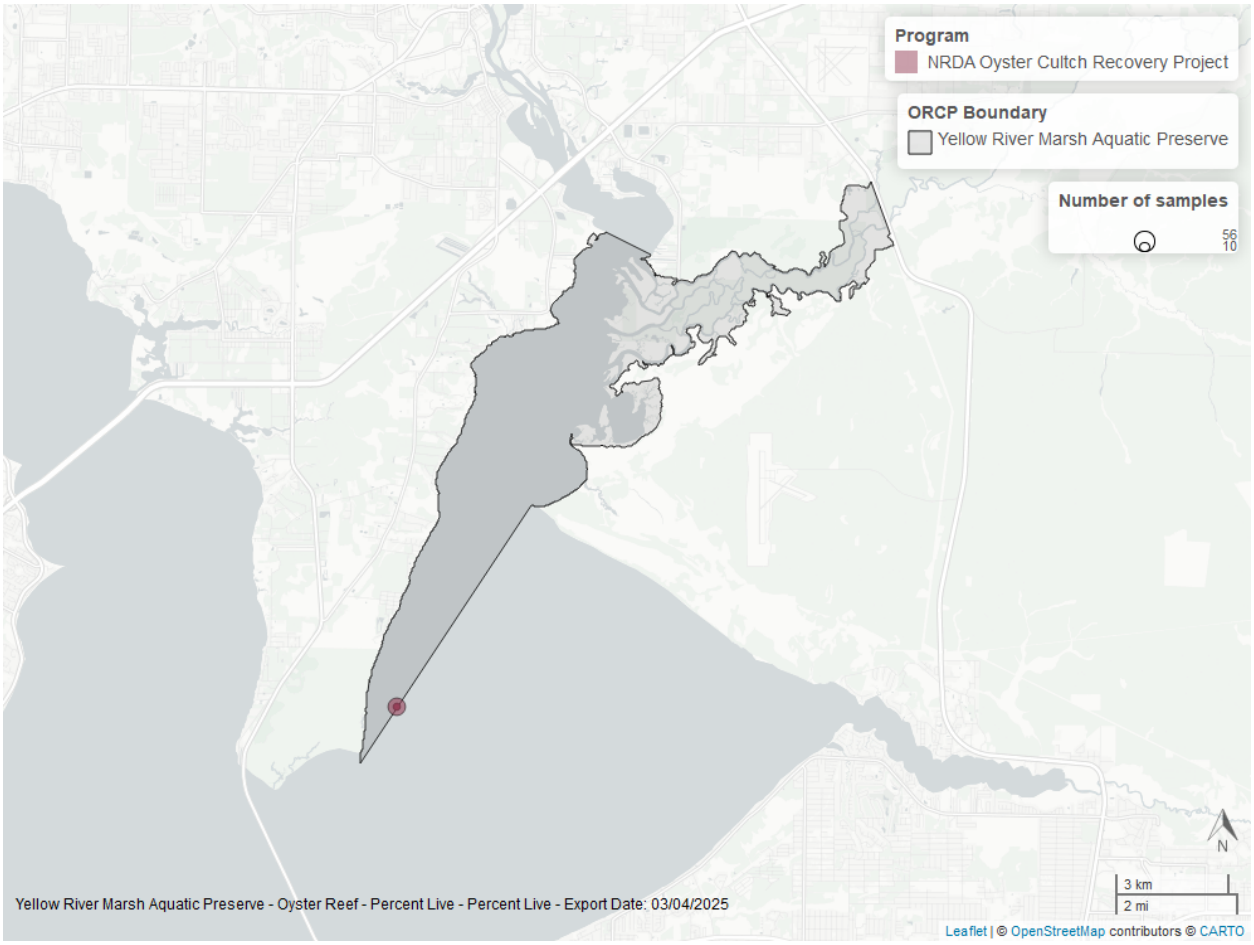


Figure 45: Figure for Oyster Percent Live in Yellow River Marsh Aquatic Preserve

Table 45: Model results for Oyster Percent Live - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly increasing trend	6.86	0.6	7 to 6.7


Program
NRDA Oyster Cultch Recovery Project
ORCP Boundary
Yellow River Marsh Aquatic Preserve
Number of samples
56
10
N
3 km
2 mi
Yellow River Marsh Aquatic Preserve - Oyster Reef - Percent Live - Percent Live - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Shell Height

Apalachicola Bay Aquatic Preserve

Natural

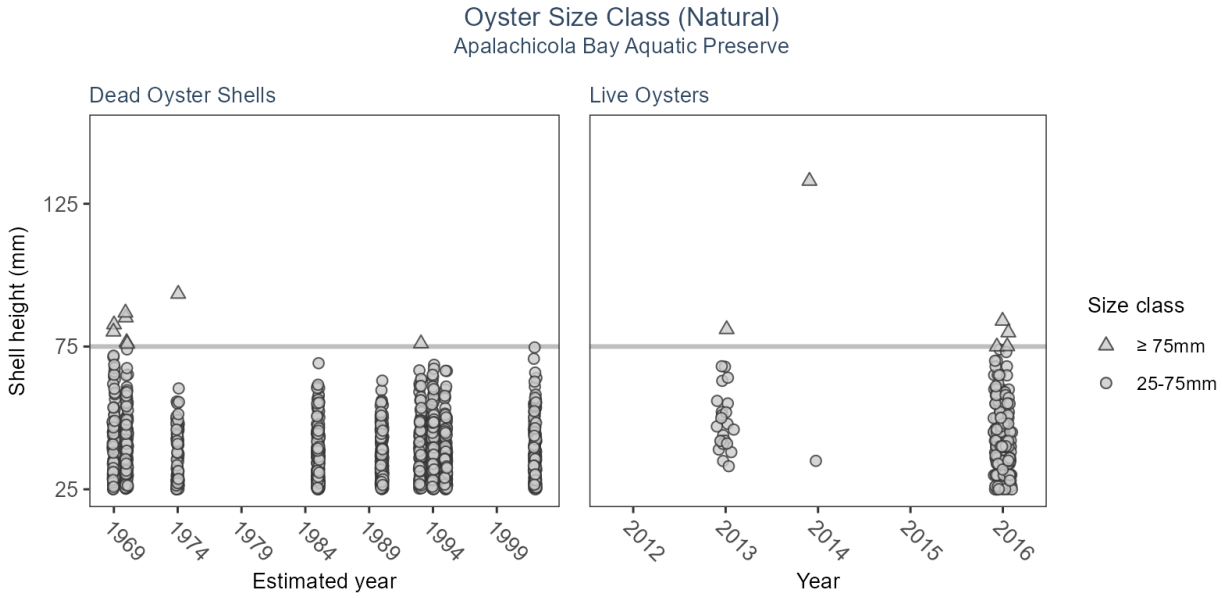
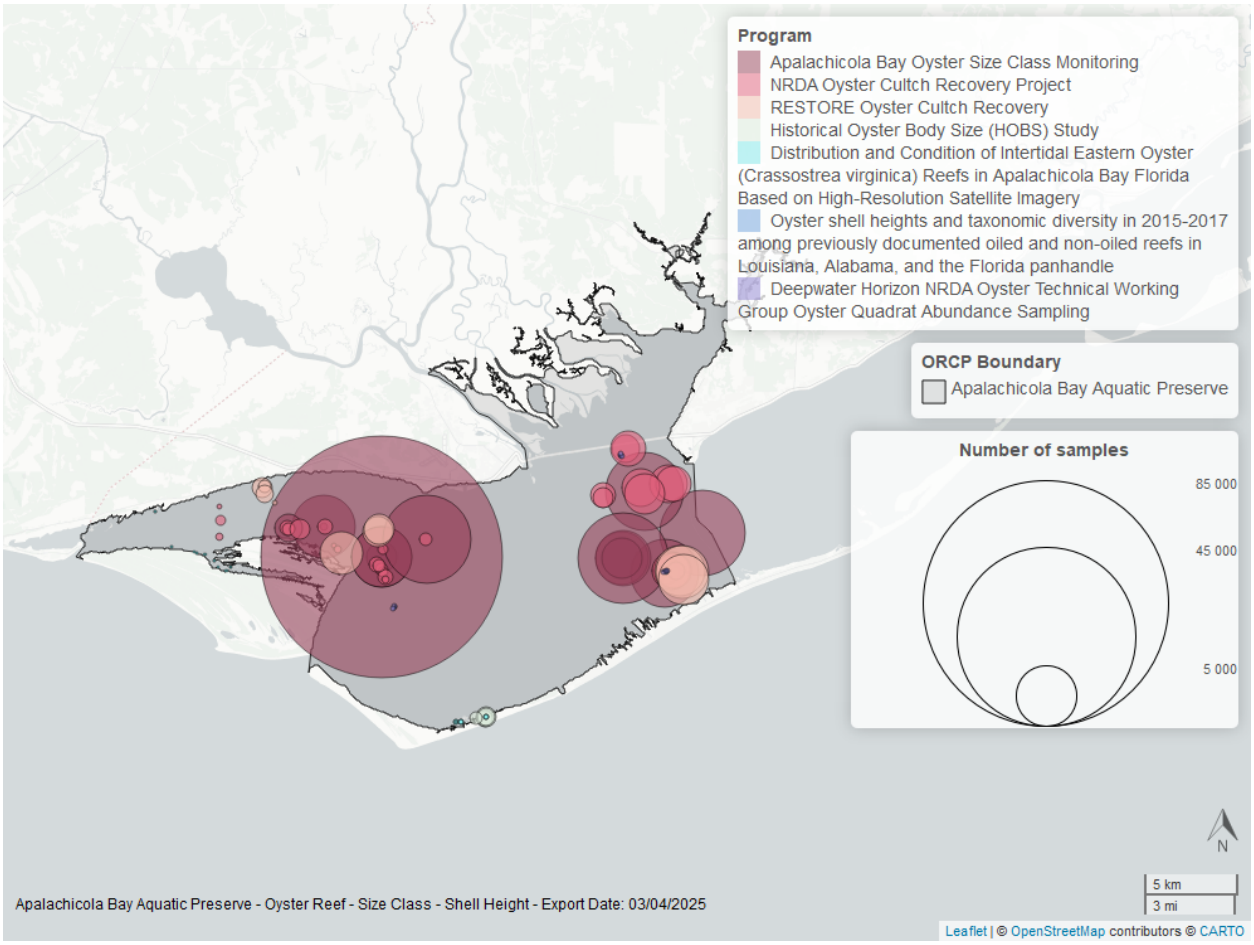


Figure 46: Figure for Oyster Shell Height in Apalachicola Bay Aquatic Preserve

Table 46: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Apalachicola Bay Oyster Size Class Monitoring
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Historical Oyster Body Size (HOBS) Study
Distribution and Condition of Intertidal Eastern Oyster (Crassostrea virginica) Reefs in Apalachicola Bay Florida Based on High-Resolution Satellite Imagery
Oyster shell heights and taxonomic diversity in 2015-2017 among previously documented oiled and non-oiled reefs in Louisiana, Alabama, and the Florida panhandle
Deepwater Horizon NRDA Oyster Technical Working Group Oyster Quadrat Abundance Sampling
ORCP Boundary
Apalachicola Bay Aquatic Preserve
Number of samples
85 000
45 000
5 000
N
5 km
3 mi
Apalachicola Bay Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Apalachicola National Estuarine Research Reserve

Natural

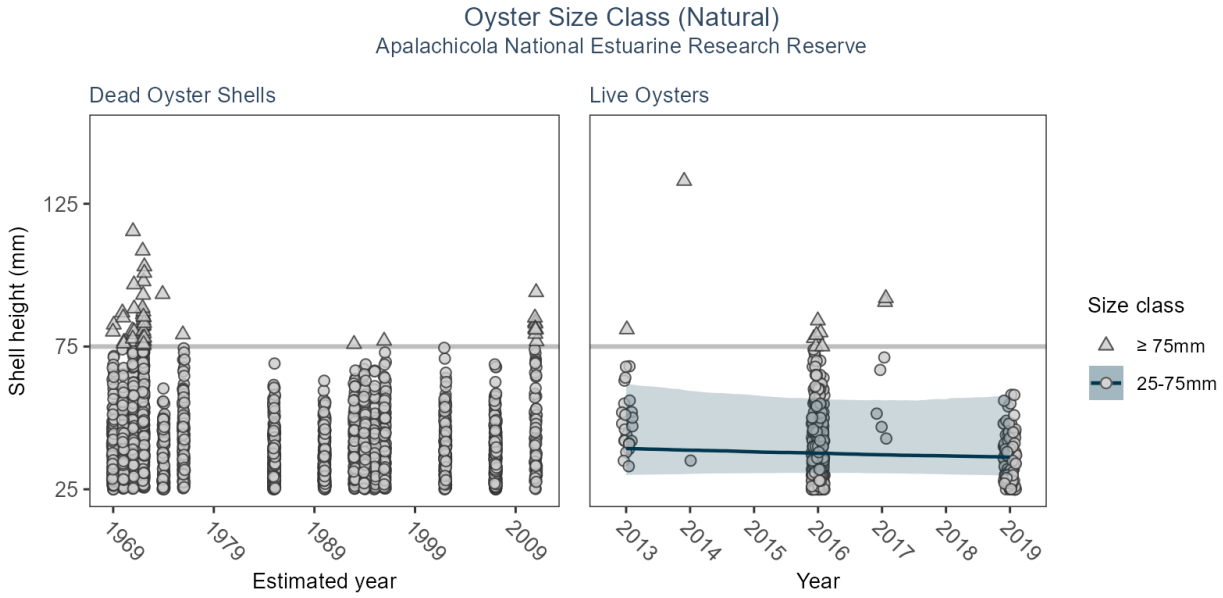
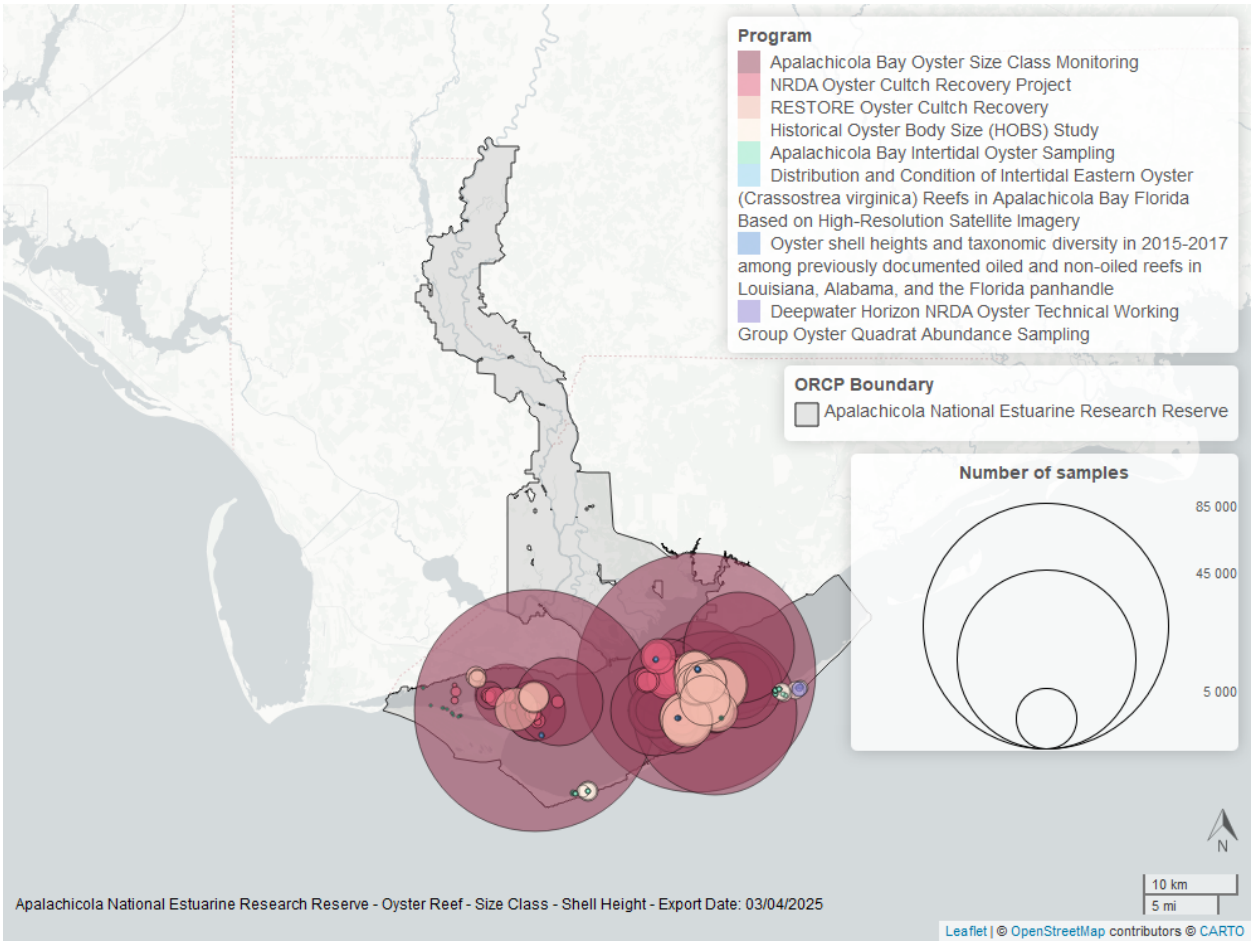


Figure 47: Figure for Oyster Shell Height in Apalachicola National Estuarine Research Reserve

Table 47: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	No significant change	-1.18	4.54	-10.28 to 7.86
Live Oysters	Natural	-	-	-	NA to NA


Program
Apalachicola Bay Oyster Size Class Monitoring
NRDA Oyster Cultch Recovery Project
RESTORE Oyster Cultch Recovery
Historical Oyster Body Size (HOBS) Study
Apalachicola Bay Intertidal Oyster Sampling
Distribution and Condition of Intertidal Eastern Oyster (Crassostrea virginica) Reefs in Apalachicola Bay Florida Based on High-Resolution Satellite Imagery
Oyster shell heights and taxonomic diversity in 2015-2017 among previously documented oiled and non-oiled reefs in Louisiana, Alabama, and the Florida panhandle
Deepwater Horizon NRDA Oyster Technical Working Group Oyster Quadrat Abundance Sampling
ORCP Boundary
Apalachicola National Estuarine Research Reserve
Number of samples
85 000
45 000
5 000
N
10 km
5 mi
Apalachicola National Estuarine Research Reserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Big Bend Seagrasses Aquatic Preserve

Natural

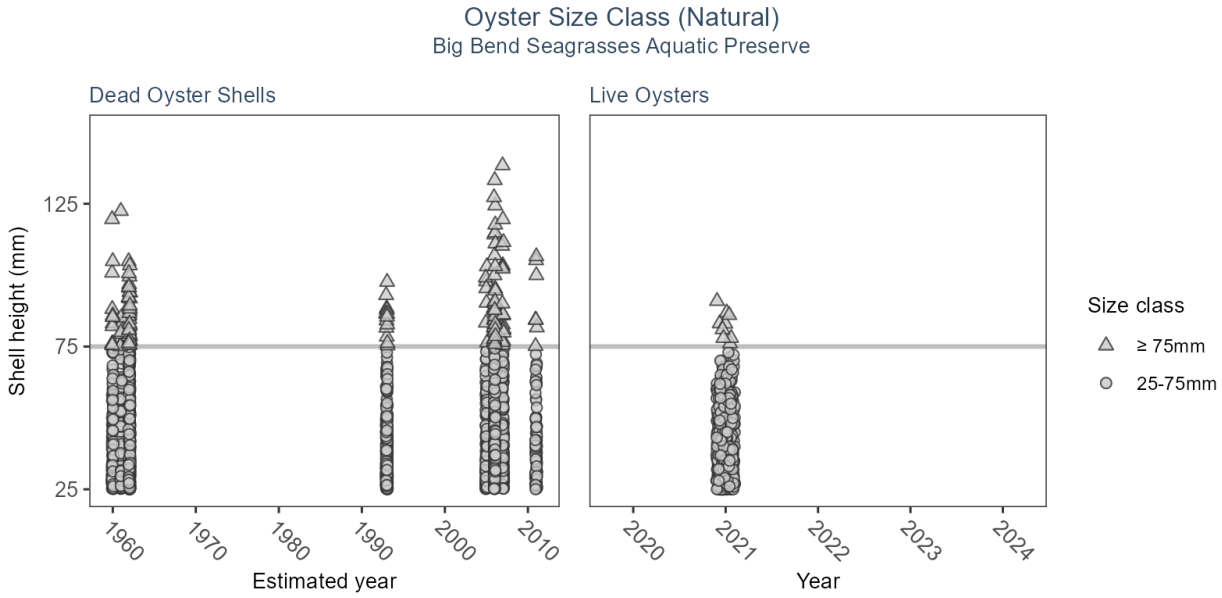
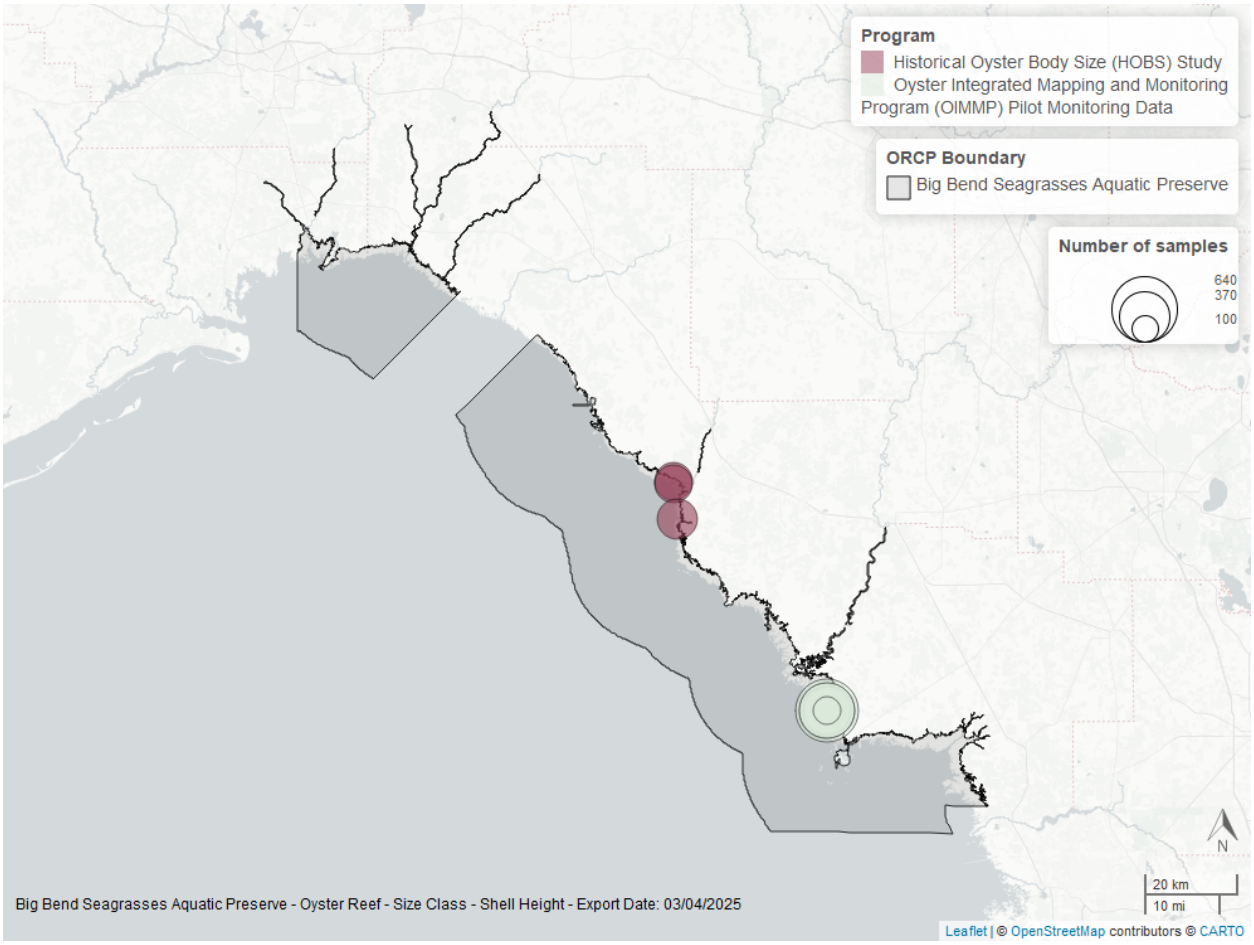


Figure 48: Figure for Oyster Shell Height in Big Bend Seagrasses Aquatic Preserve

Table 48: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Historical Oyster Body Size (HOBS) Study
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Big Bend Seagrasses Aquatic Preserve
Number of samples
640
370
100
N
20 km
10 mi
Big Bend Seagrasses Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Boca Ciega Bay Aquatic Preserve

Natural

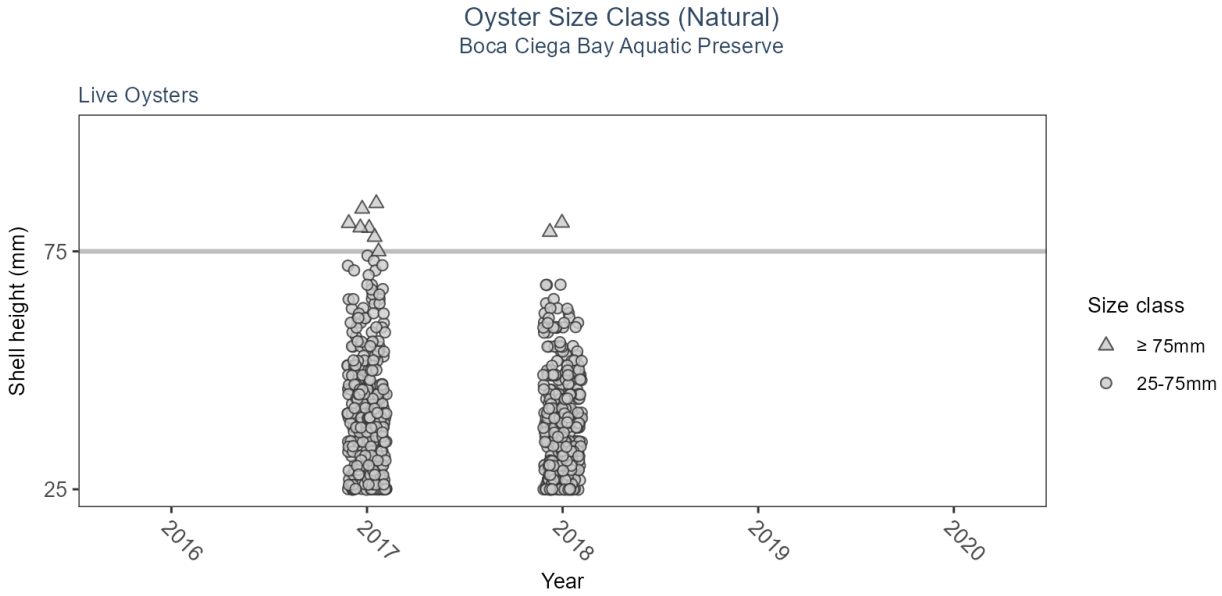
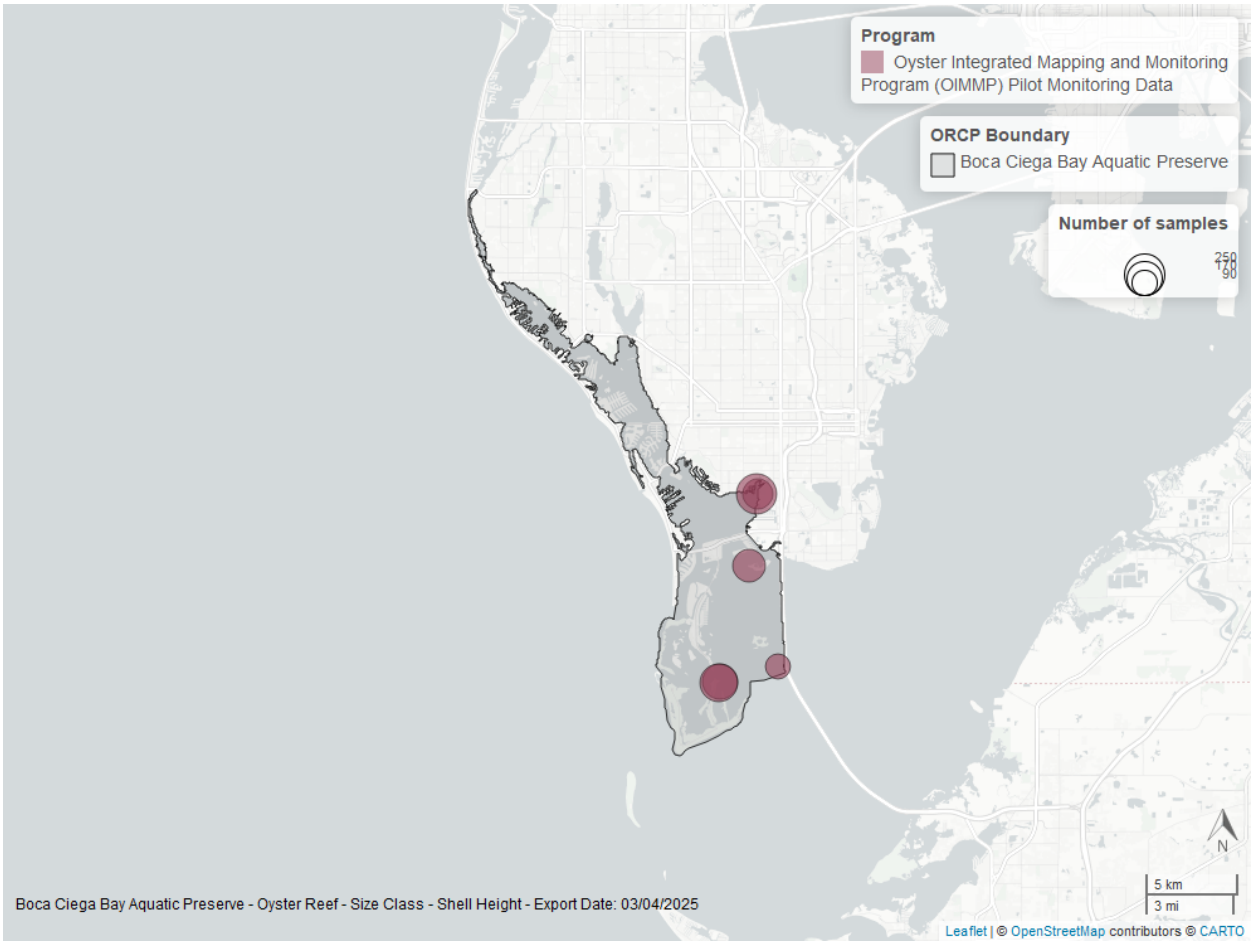


Figure 49: Figure for Oyster Shell Height in Boca Ciega Bay Aquatic Preserve

Table 49: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Boca Ciega Bay Aquatic Preserve
Number of samples
250
170
90
N
5 km
3 mi
Boca Ciega Bay Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Estero Bay Aquatic Preserve

Restored

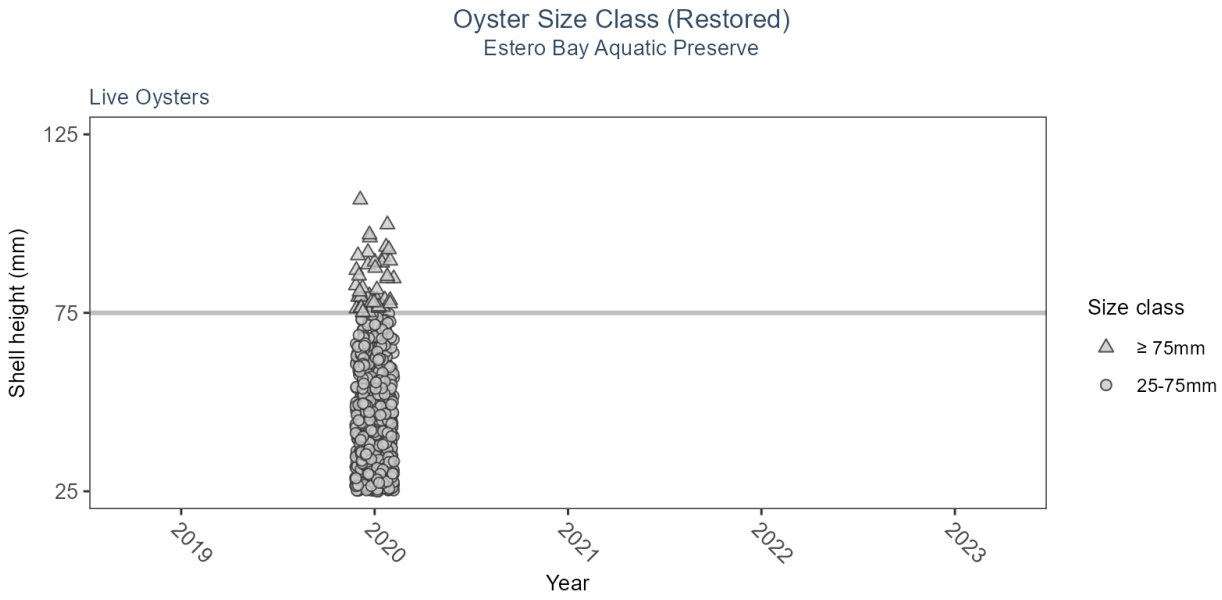


Figure 50: Figure for Oyster Shell Height in Estero Bay Aquatic Preserve

Table 50: Model results for Oyster Shell Height - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	-	-	-	NA to NA
Live Oysters	Restored	-	-	-	NA to NA
Live Oysters	Restored	-	-	-	NA to NA

Natural

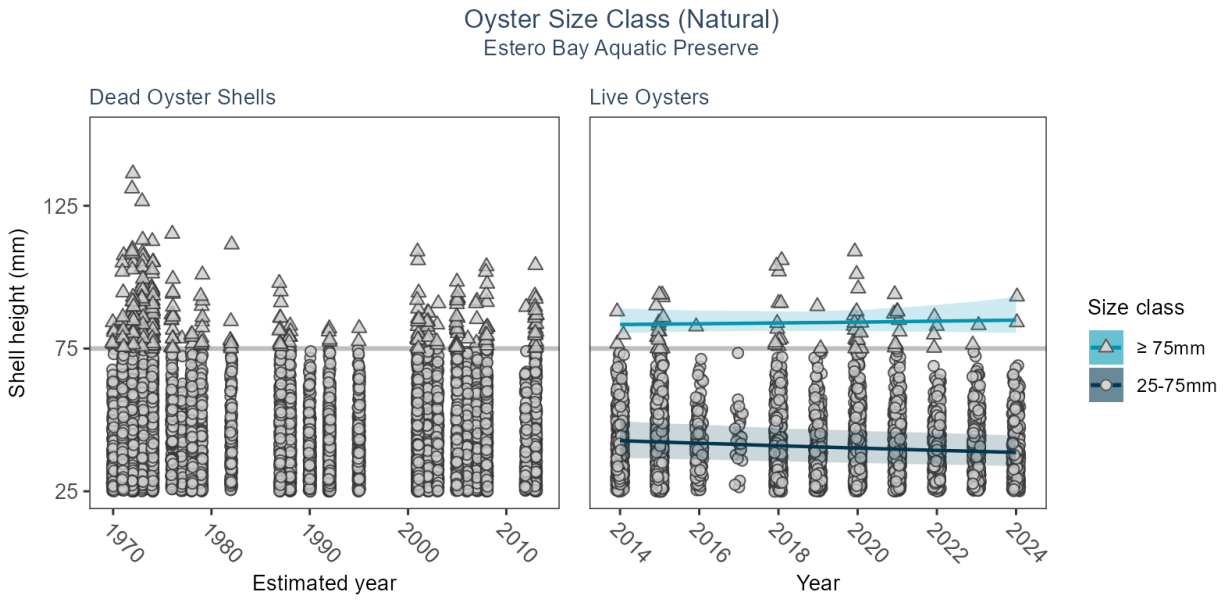
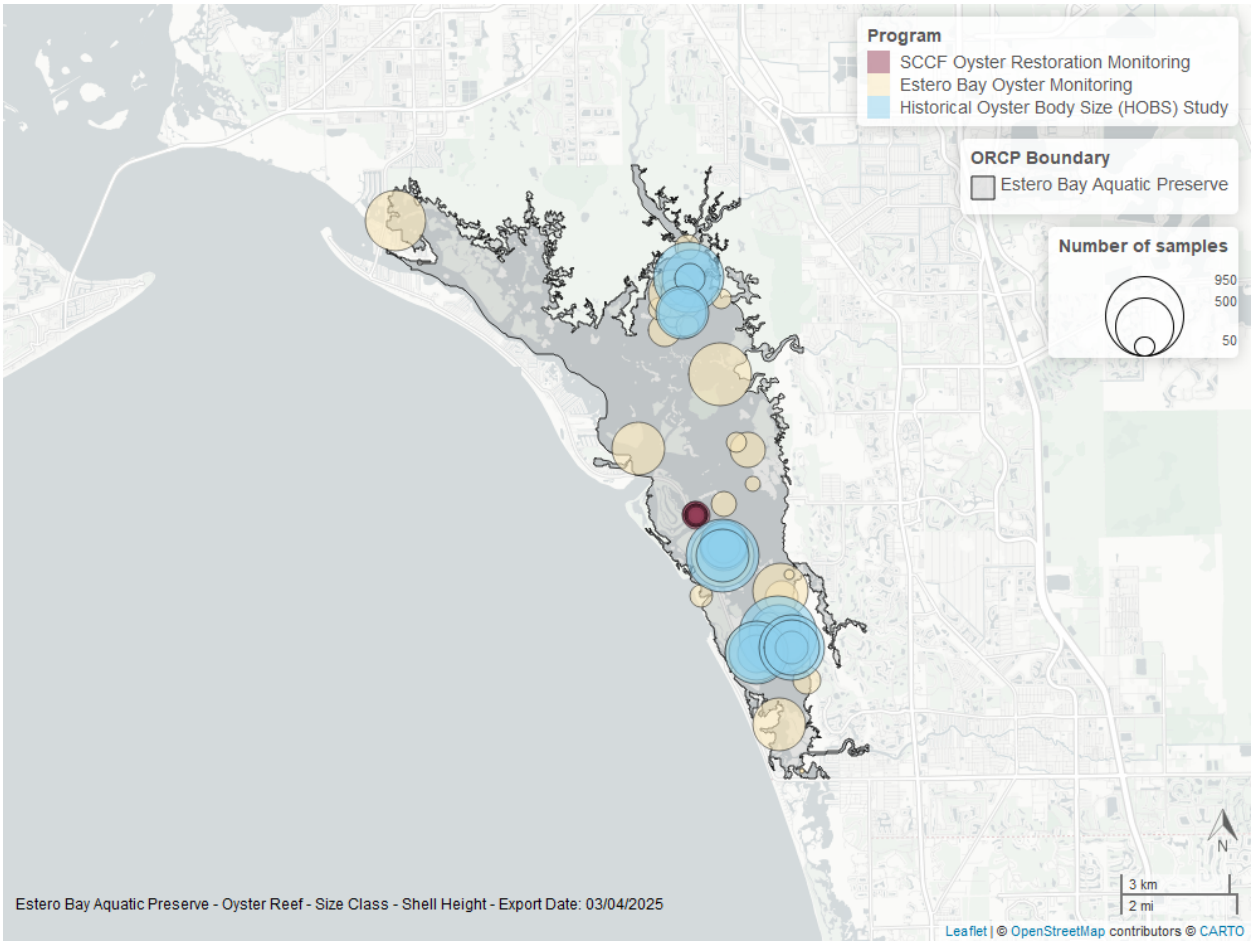


Figure 51: Figure for Oyster Shell Height in Estero Bay Aquatic Preserve

Table 51: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	No significant change	0.65	1.81	-2.76 to 4.53
Live Oysters	Natural	Significantly decreasing trend	-1.08	0.28	-1.65 to -0.55
Live Oysters	Natural	-	-	-	NA to NA


Program
SCCF Oyster Restoration Monitoring
Estero Bay Oyster Monitoring
Historical Oyster Body Size (HOBS) Study
ORCP Boundary
Estero Bay Aquatic Preserve
Number of samples
950
500
50
N
3 km
2 mi
Estero Bay Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Guana River Marsh Aquatic Preserve

Natural

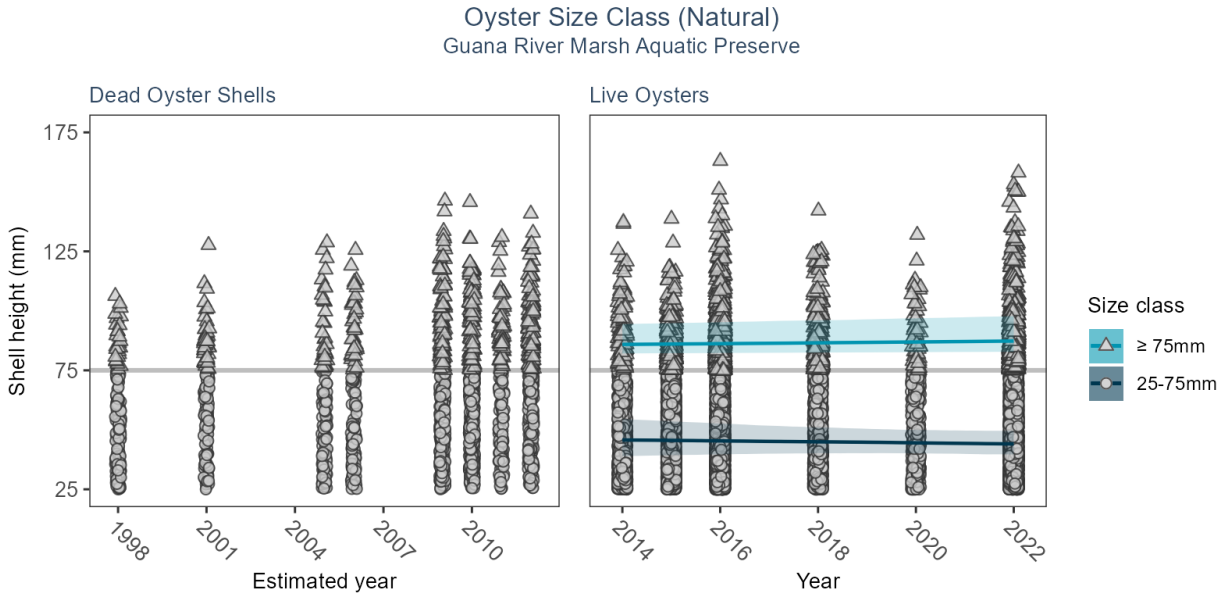
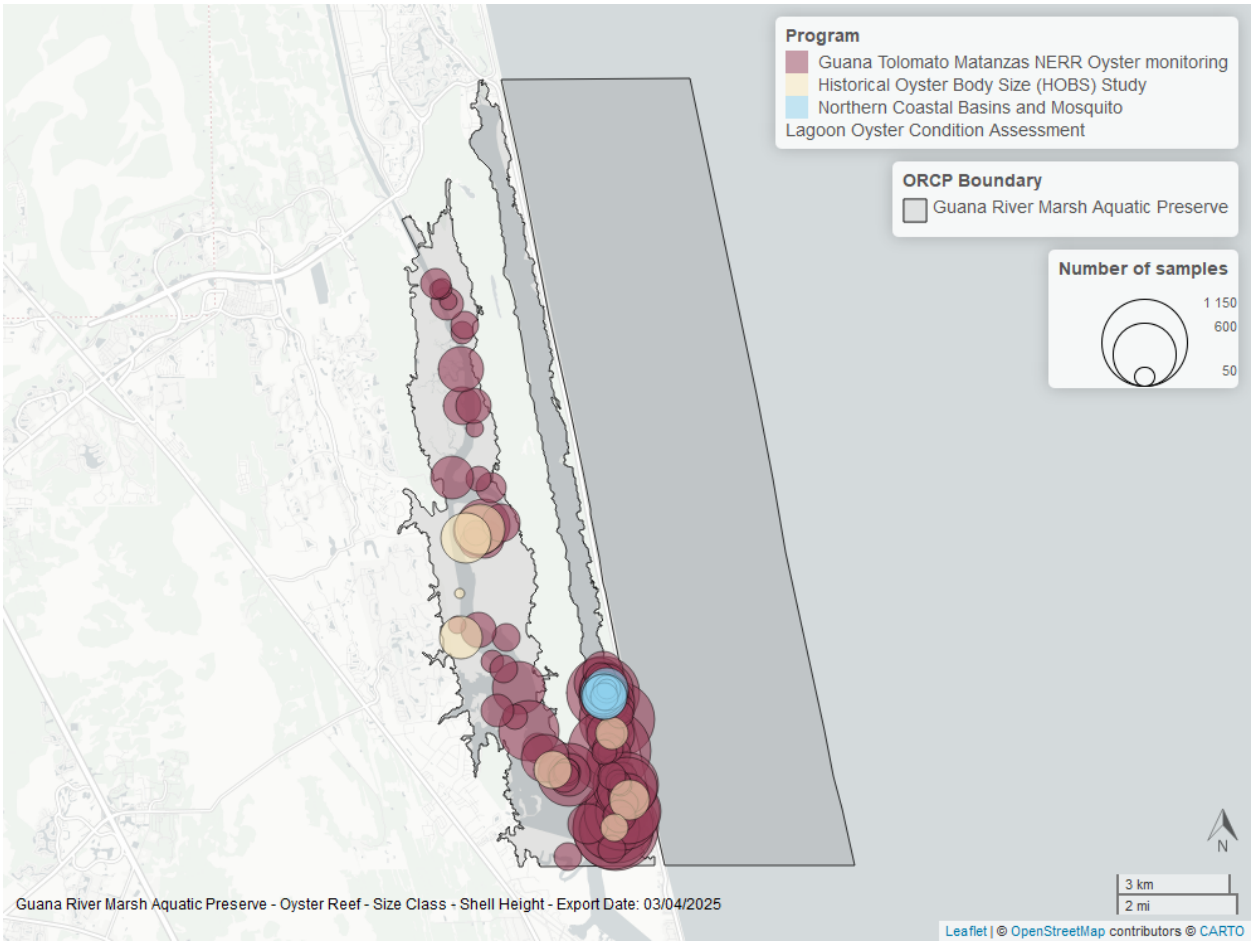


Figure 52: Figure for Oyster Shell Height in Guana River Marsh Aquatic Preserve

Table 52: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	Significantly increasing trend	1.15	0.55	0.1 to 2.28
Live Oysters	Natural	Significantly decreasing trend	-1.85	0.90	-3.77 to -0.19
Live Oysters	Natural	-	-	-	NA to NA


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Historical Oyster Body Size (HOBS) Study
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana River Marsh Aquatic Preserve
Number of samples
1 150
600
50
N
3 km
2 mi
Guana River Marsh Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Guana Tolomato Matanzas National Estuarine Research Reserve

Natural

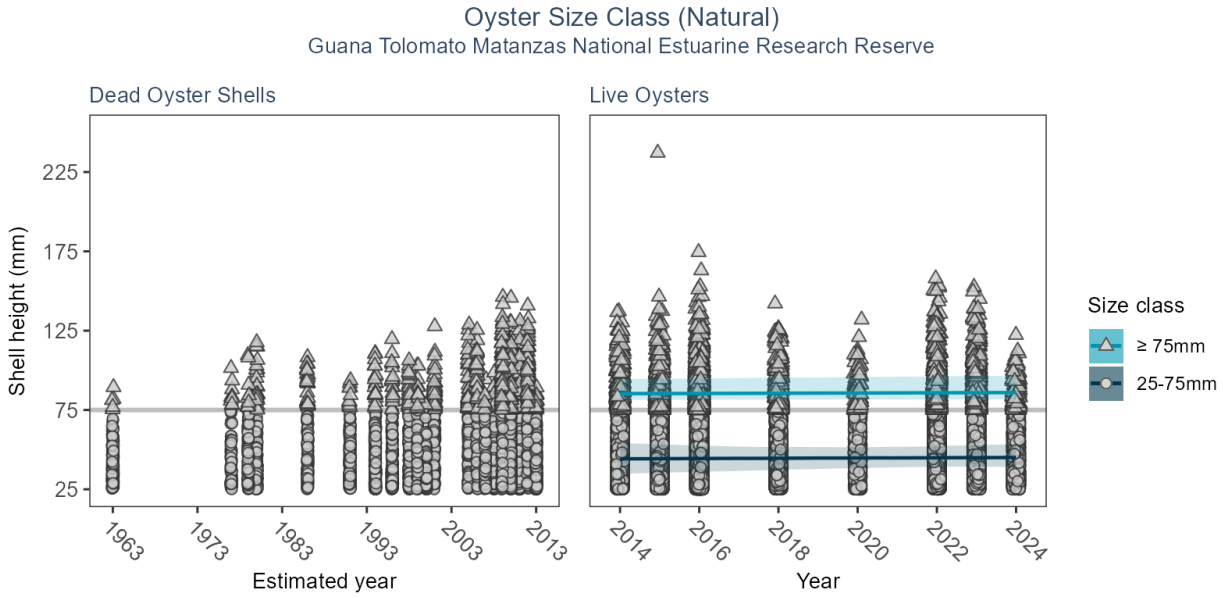
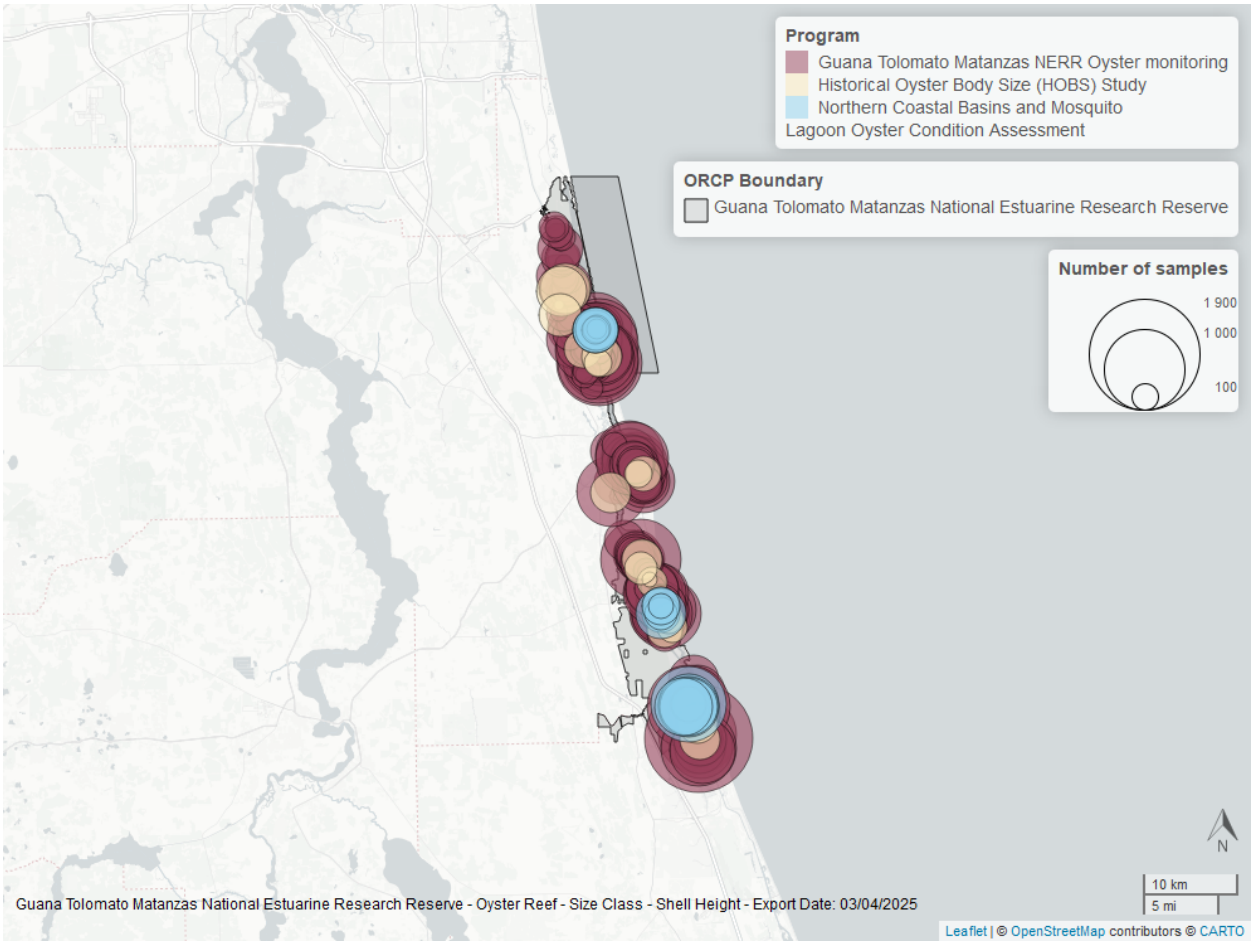


Figure 53: Figure for Oyster Shell Height in Guana Tolomato Matanzas National Estuarine Research Reserve

Table 53: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	No significant change	0.56	0.37	-0.18 to 1.3
Live Oysters	Natural	No significant change	0.84	0.44	-0.03 to 1.69
Live Oysters	Natural	-	-	-	NA to NA


Program
Guana Tolomato Matanzas NERR Oyster monitoring
Historical Oyster Body Size (HOBS) Study
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Guana Tolomato Matanzas National Estuarine Research Reserve
Number of samples
1 900
1 000
100
N
10 km
5 mi
Guana Tolomato Matanzas National Estuarine Research Reserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Indian River-Malabar to Vero Beach Aquatic Preserve

Natural

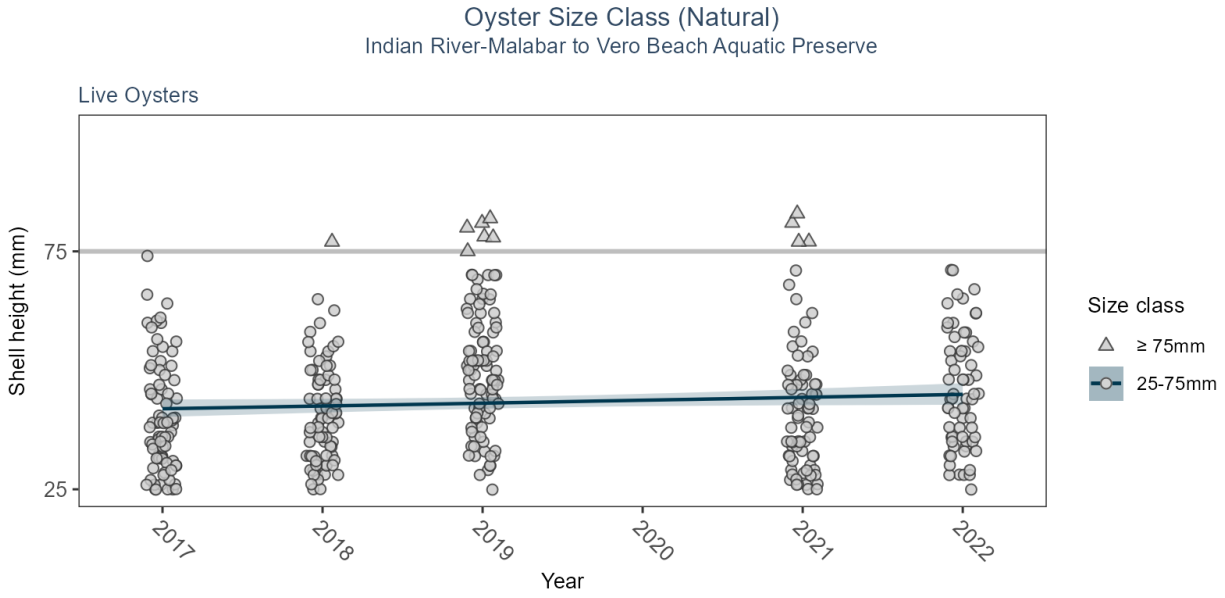
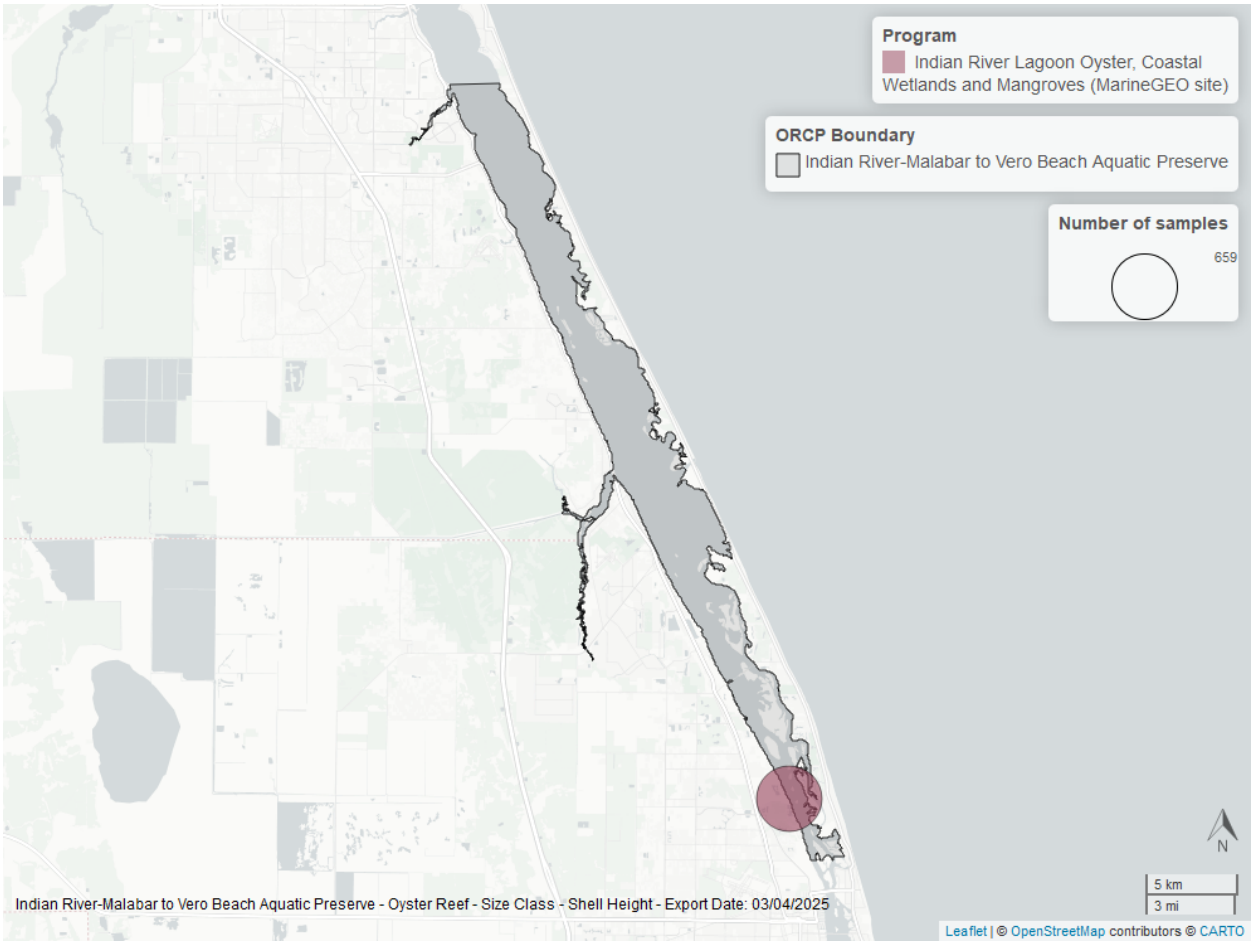


Figure 54: Figure for Oyster Shell Height in Indian River-Malabar to Vero Beach Aquatic Preserve

Table 54: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	No significant change	1.52	0.95	-0.16 to 3.54
Live Oysters	Natural	-	-	-	NA to NA


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Malabar to Vero Beach Aquatic Preserve
Number of samples
659
N
5 km
3 mi
Indian River-Malabar to Vero Beach Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Natural

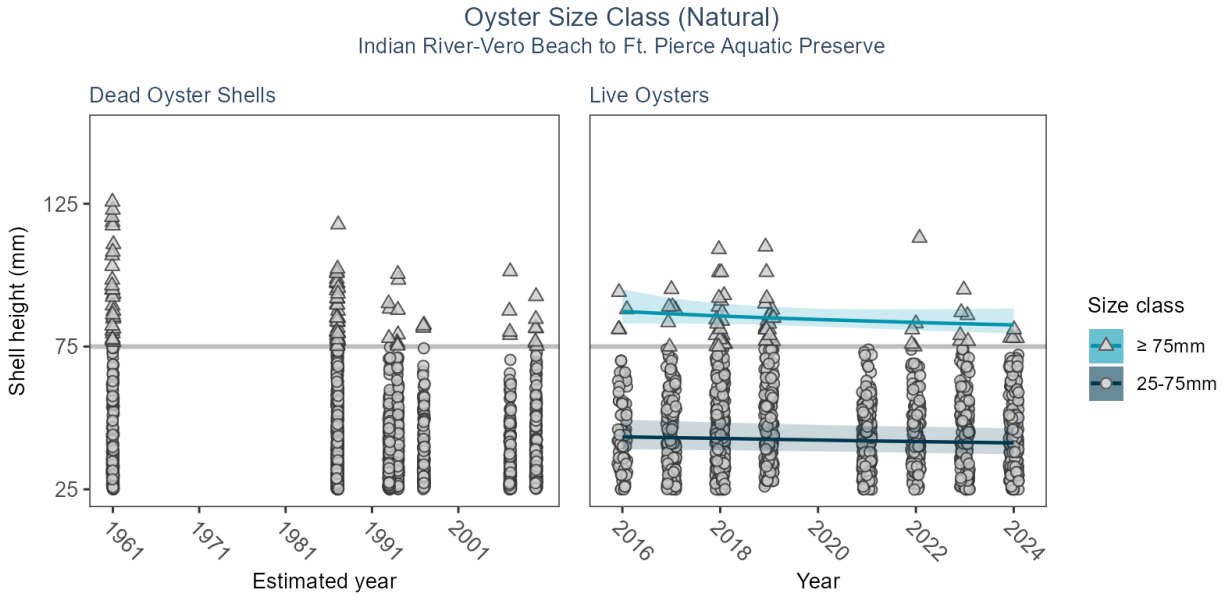
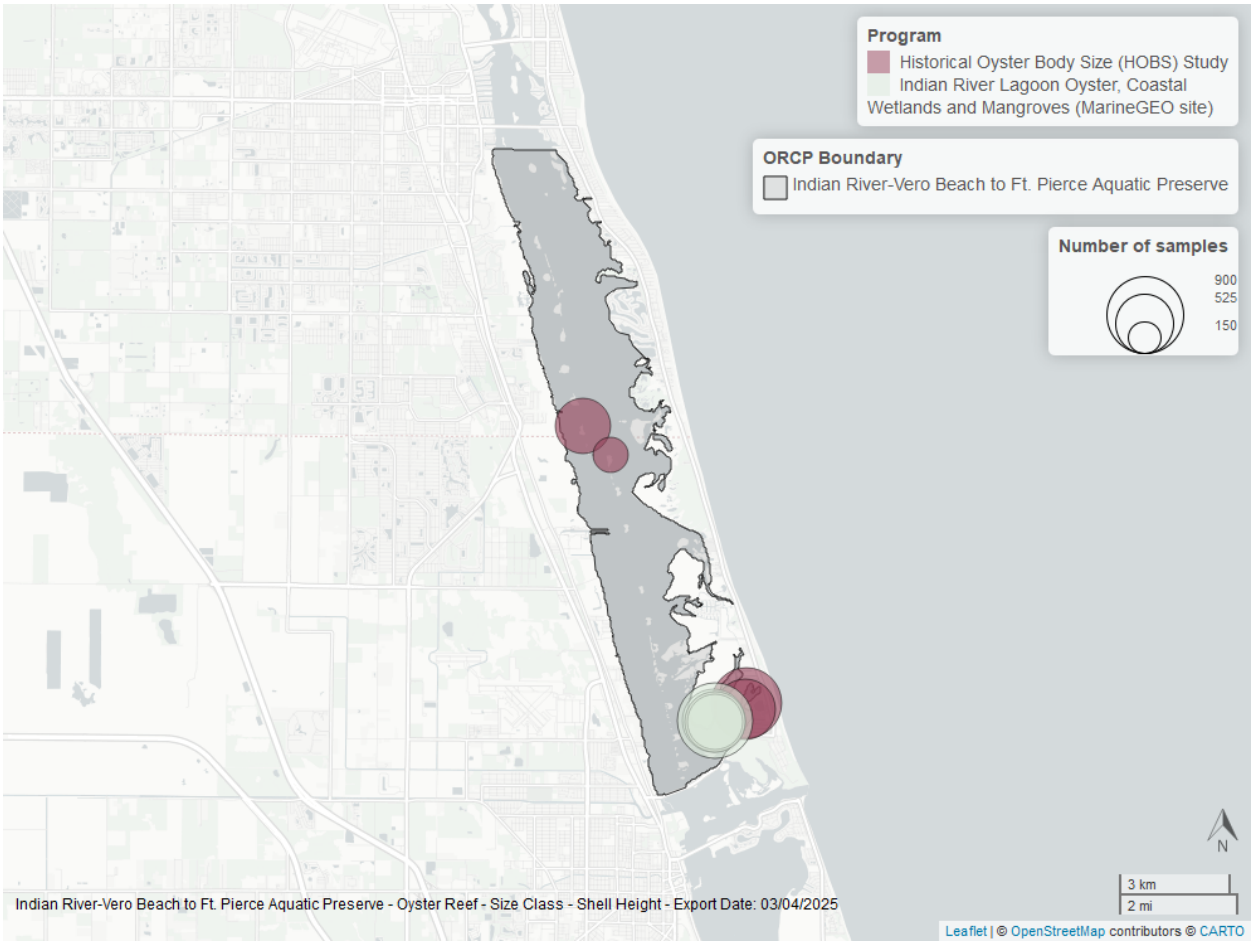


Figure 55: Figure for Oyster Shell Height in Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

Table 55: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	No significant change	-2.71	2.59	-8.62 to 1.51
Live Oysters	Natural	Significantly decreasing trend	-0.75	0.34	-1.44 to -0.07
Live Oysters	Natural	-	-	-	NA to NA


Program
Historical Oyster Body Size (HOBS) Study
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve
Number of samples
900
525
150
N
3 km
2 mi
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Jensen Beach to Jupiter Inlet Aquatic Preserve

Natural

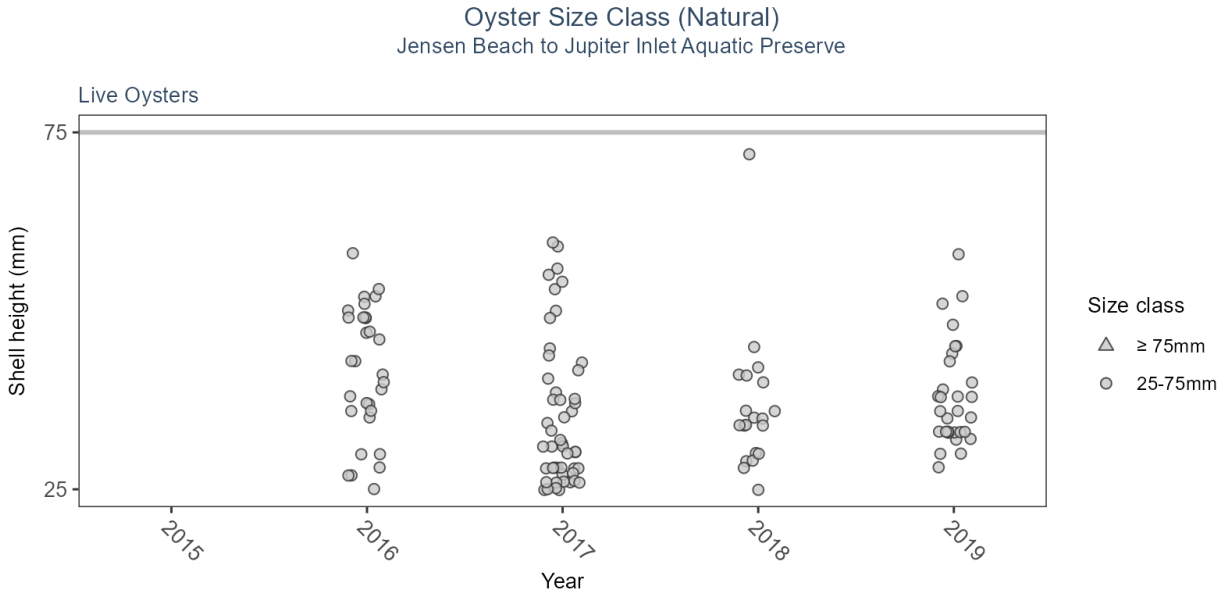
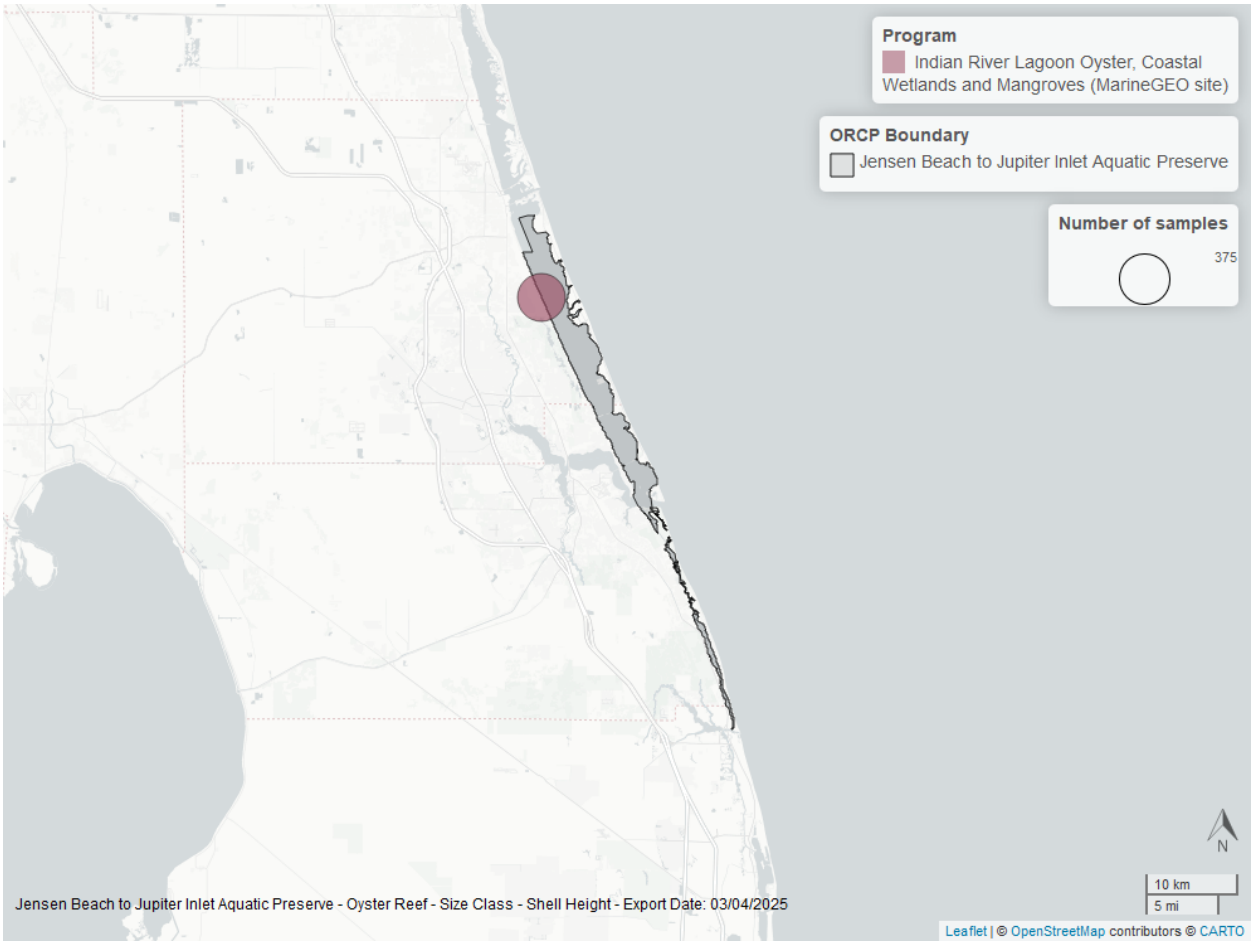


Figure 56: Figure for Oyster Shell Height in Jensen Beach to Jupiter Inlet Aquatic Preserve

Table 56: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Indian River Lagoon Oyster, Coastal Wetlands and Mangroves (MarineGEO site)
ORCP Boundary
Jensen Beach to Jupiter Inlet Aquatic Preserve
Number of samples
375
N
10 km
5 mi
Jensen Beach to Jupiter Inlet Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Lemon Bay Aquatic Preserve

Natural

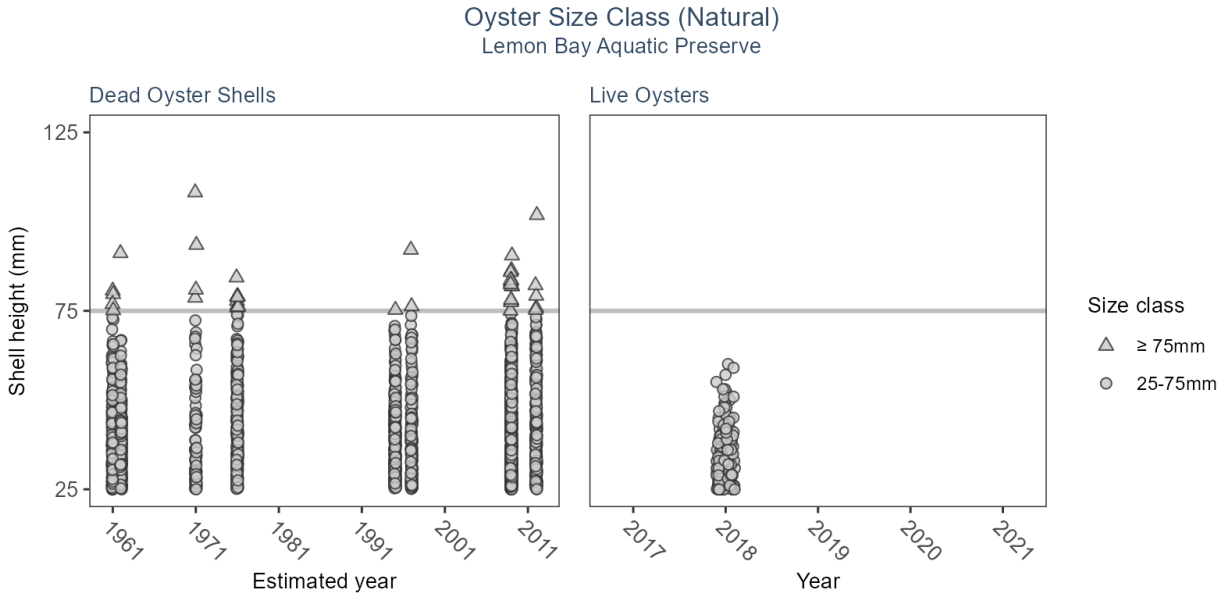
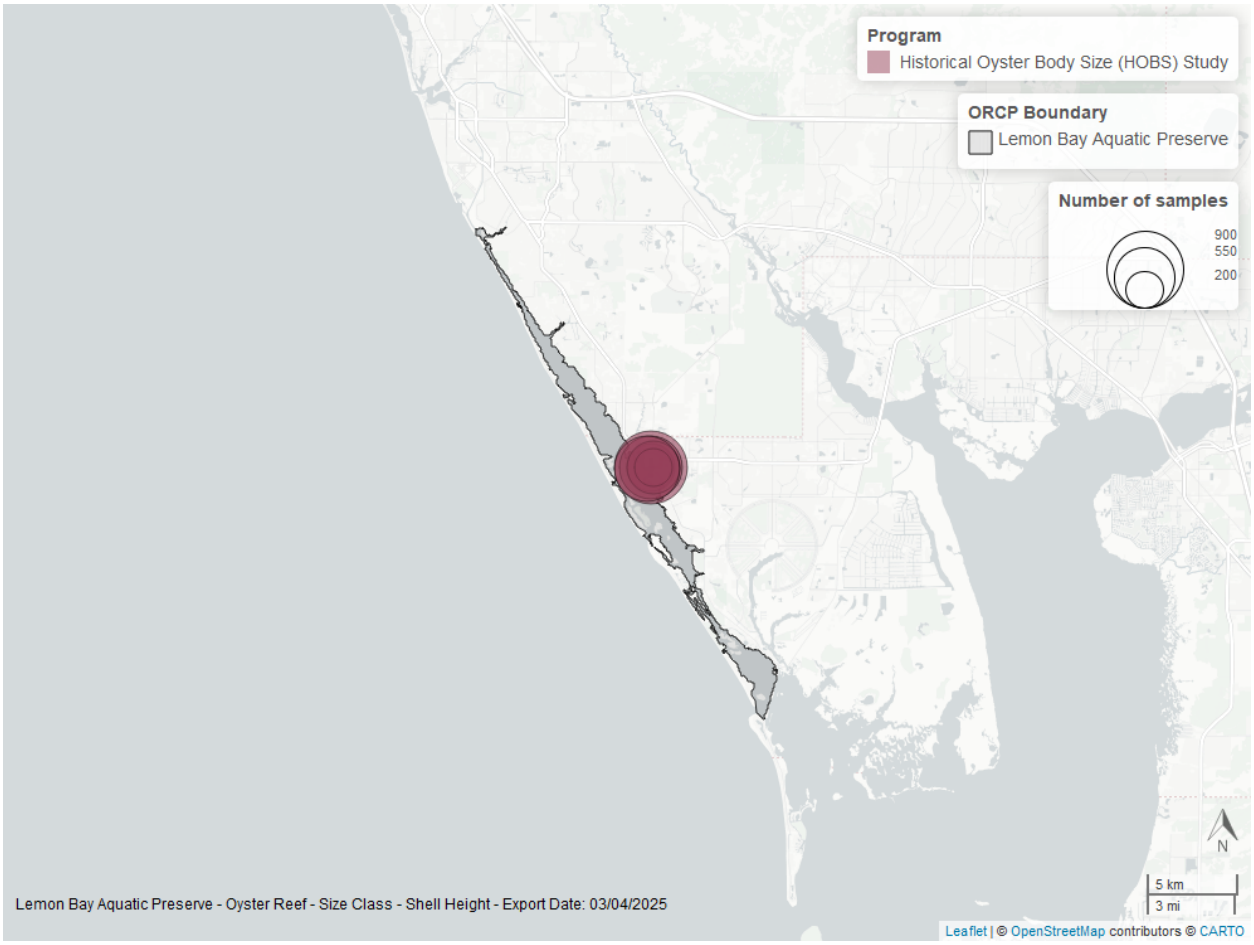


Figure 57: Figure for Oyster Shell Height in Lemon Bay Aquatic Preserve

Table 57: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Historical Oyster Body Size (HOBS) Study
ORCP Boundary
Lemon Bay Aquatic Preserve
Number of samples
900
550
200
N
5 km
3 mi
Lemon Bay Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Loxahatchee River-Lake Worth Creek Aquatic Preserve

Natural

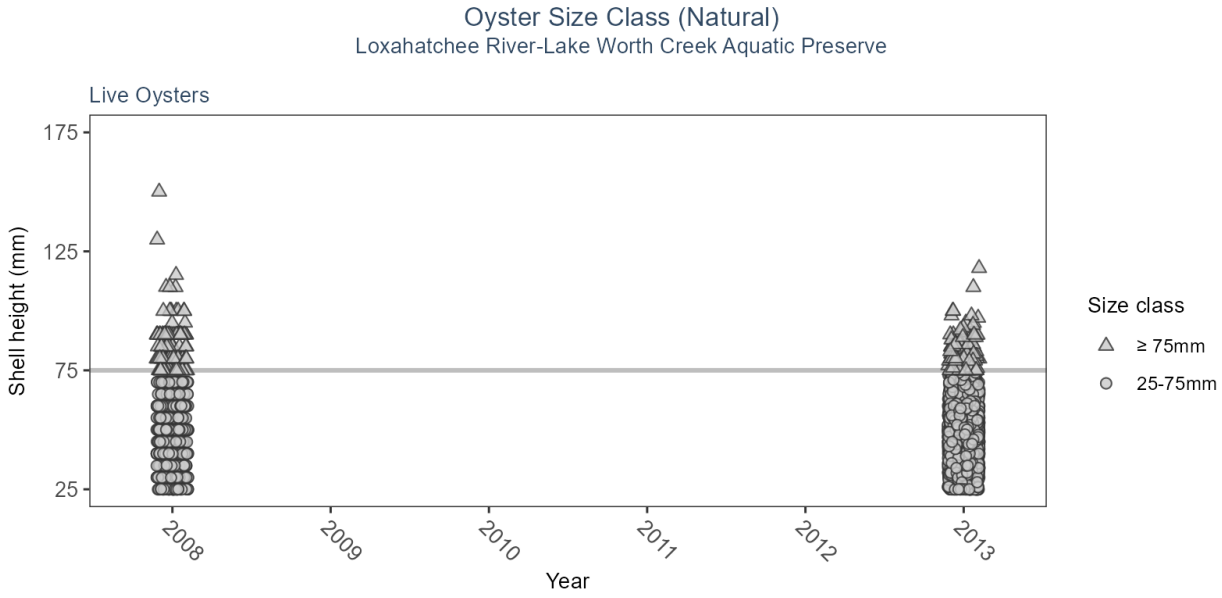
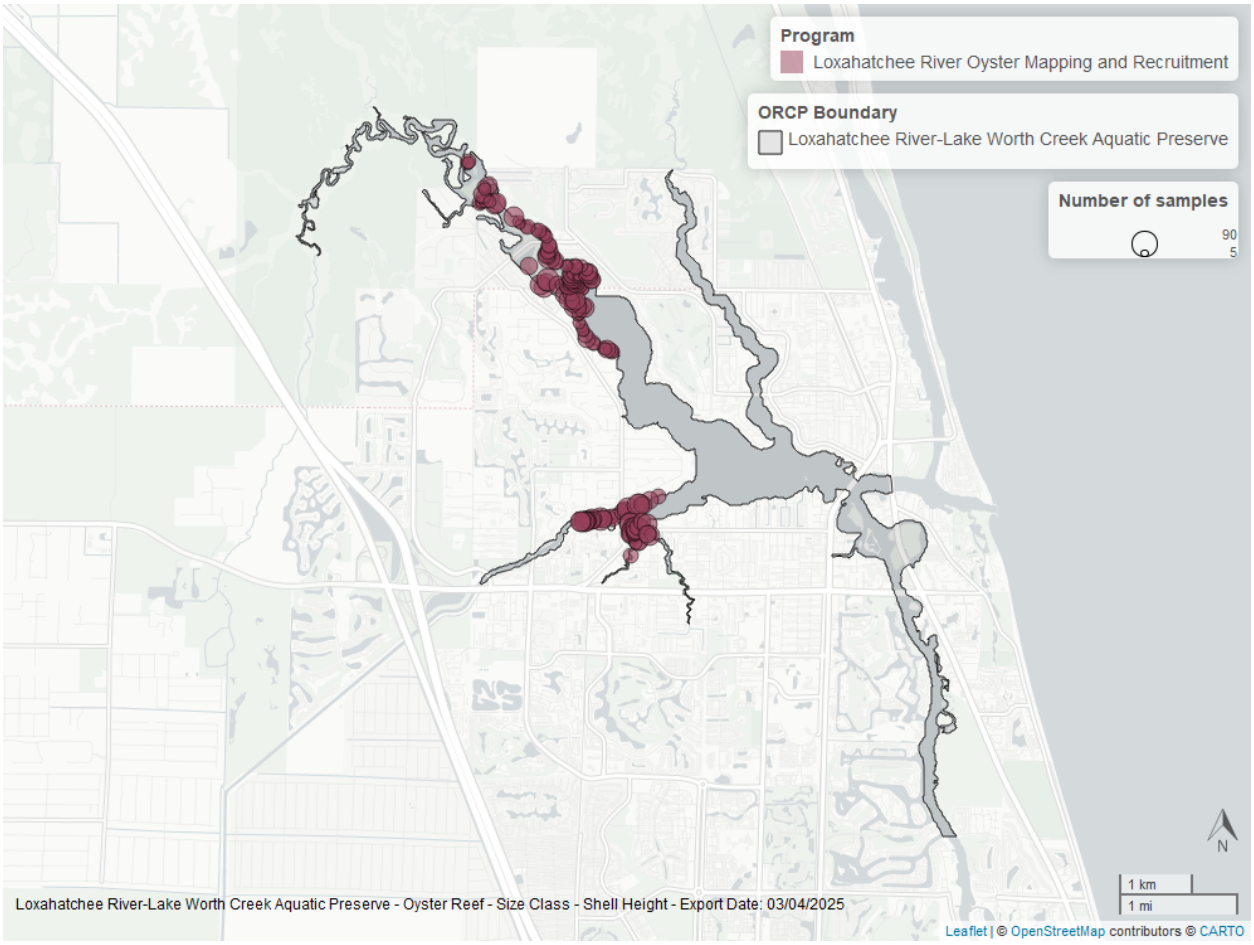


Figure 58: Figure for Oyster Shell Height in Loxahatchee River-Lake Worth Creek Aquatic Preserve

Table 58: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Loxahatchee River Oyster Mapping and Recruitment
ORCP Boundary
Loxahatchee River-Lake Worth Creek Aquatic Preserve
Number of samples
90
5
N
1 km
1 mi
Loxahatchee River-Lake Worth Creek Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Mosquito Lagoon Aquatic Preserve

Natural

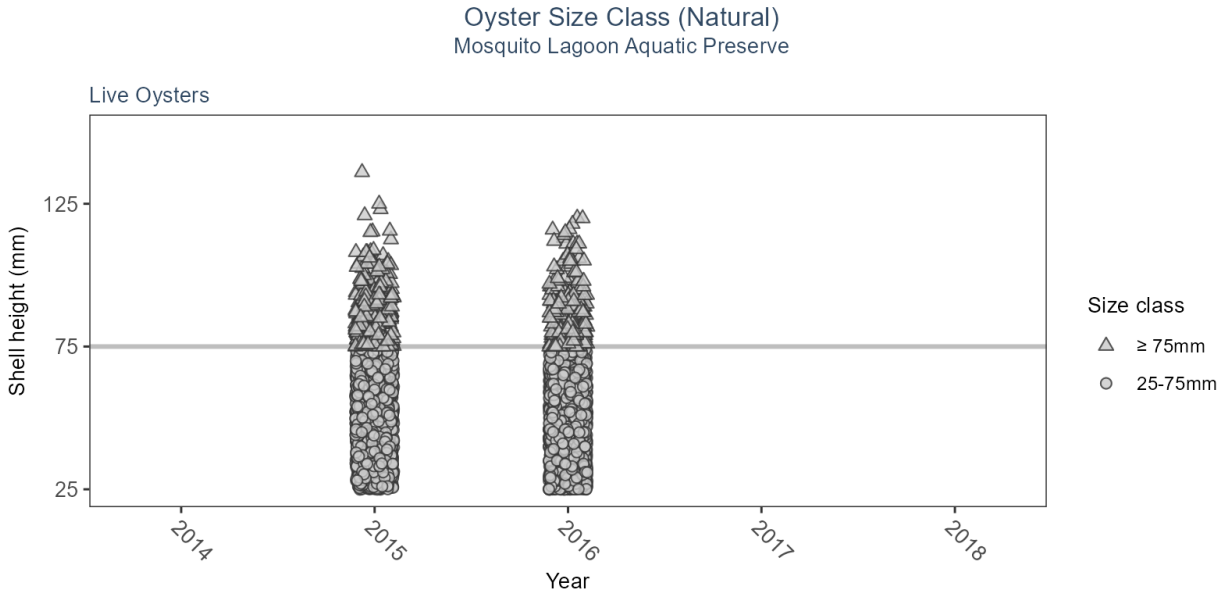
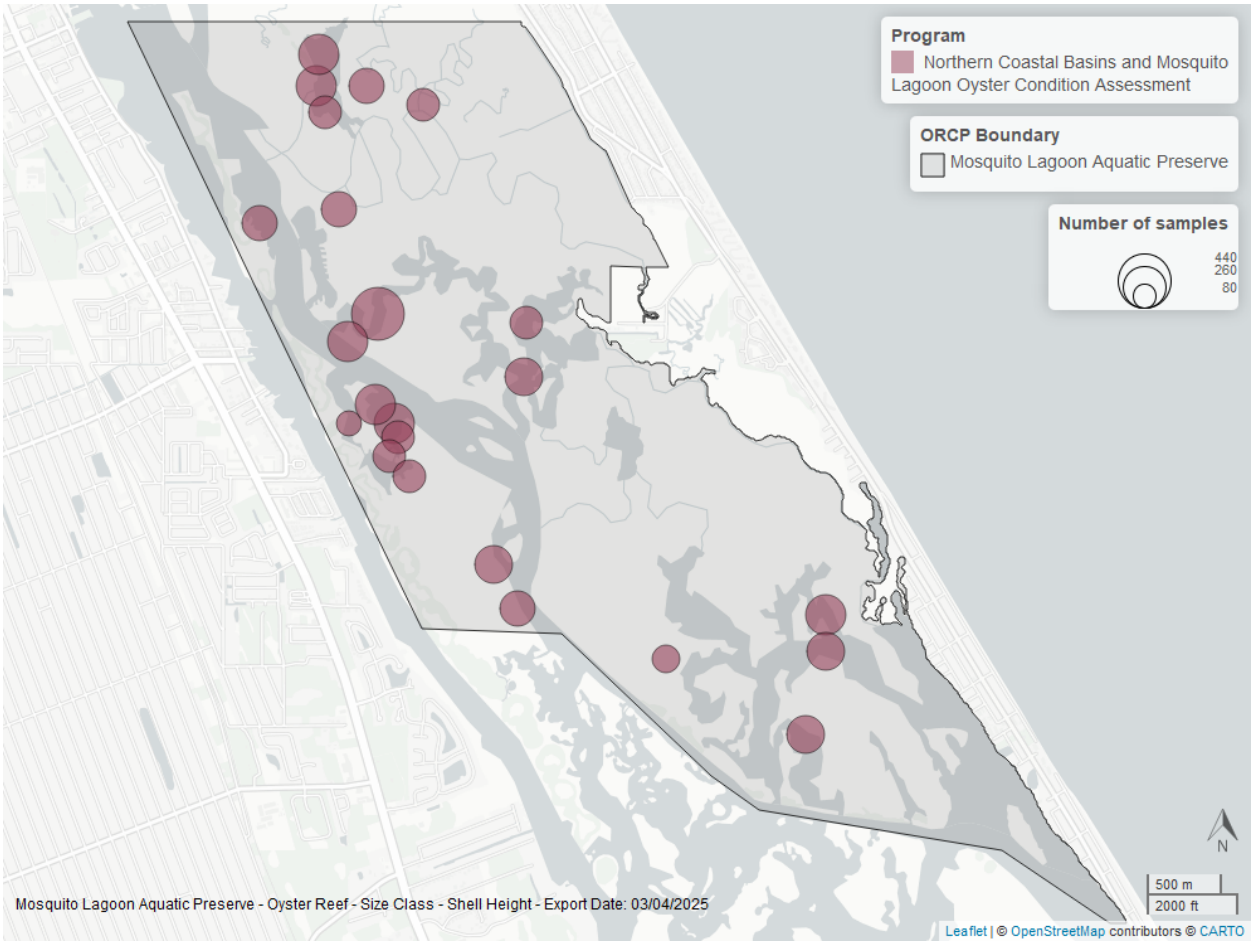


Figure 59: Figure for Oyster Shell Height in Mosquito Lagoon Aquatic Preserve

Table 59: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Mosquito Lagoon Aquatic Preserve
Number of samples
440
260
80
N
500 m
2000 ft
Mosquito Lagoon Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Nassau River-St. Johns River Marshes Aquatic Preserve

Natural

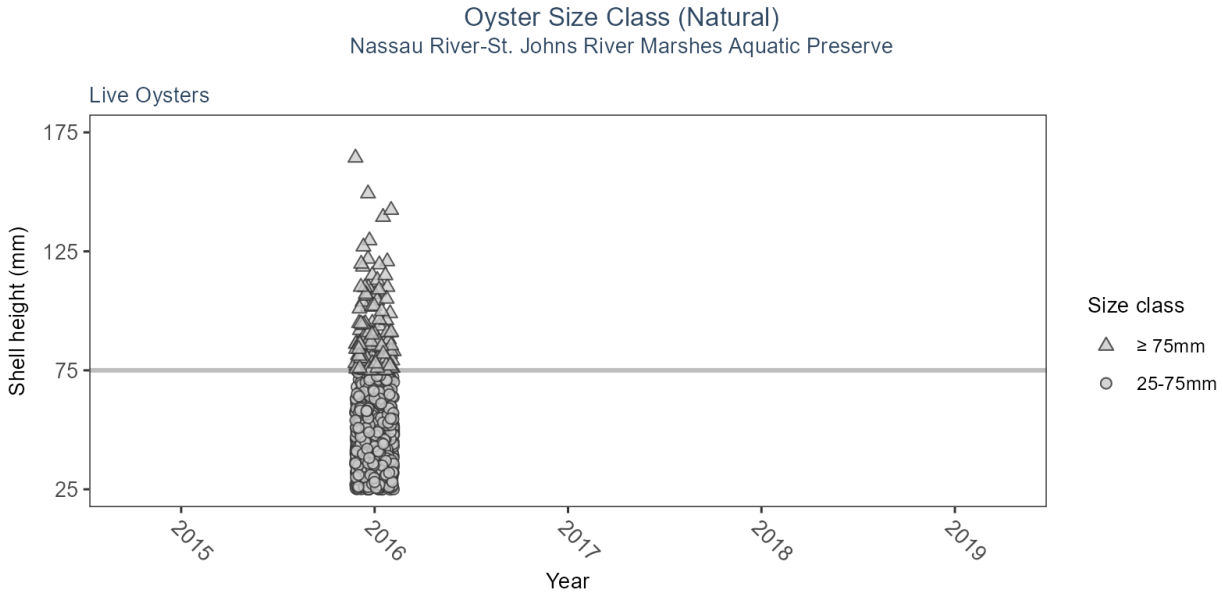
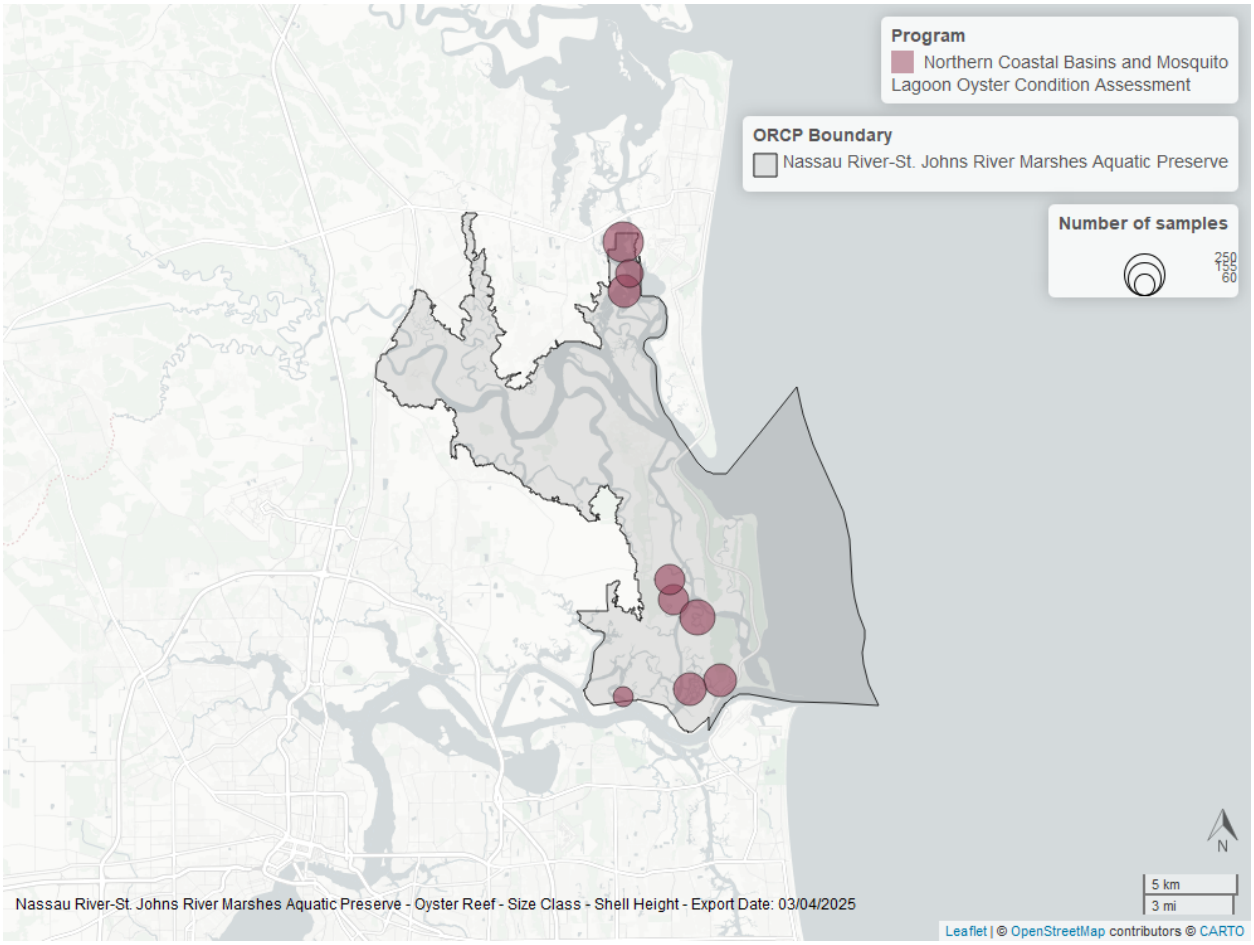


Figure 60: Figure for Oyster Shell Height in Nassau River-St. Johns River Marshes Aquatic Preserve

Table 60: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Northern Coastal Basins and Mosquito Lagoon Oyster Condition Assessment
ORCP Boundary
Nassau River-St. Johns River Marshes Aquatic Preserve
Number of samples
250
155
60
N
5 km
3 mi
Nassau River-St. Johns River Marshes Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Nature Coast Aquatic Preserve

Natural

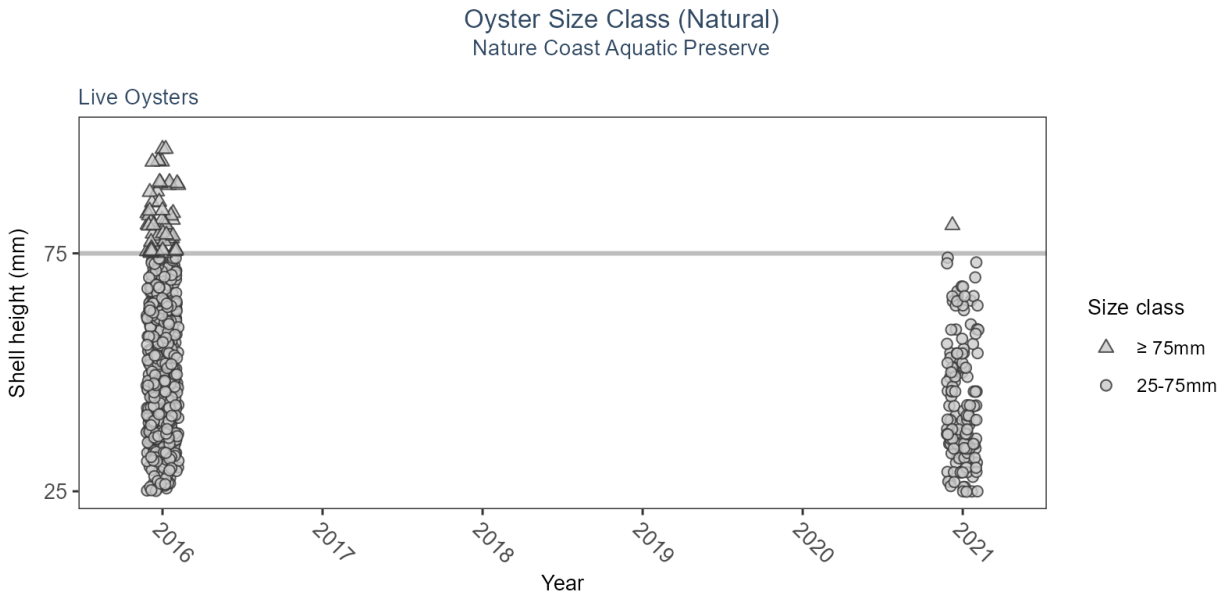
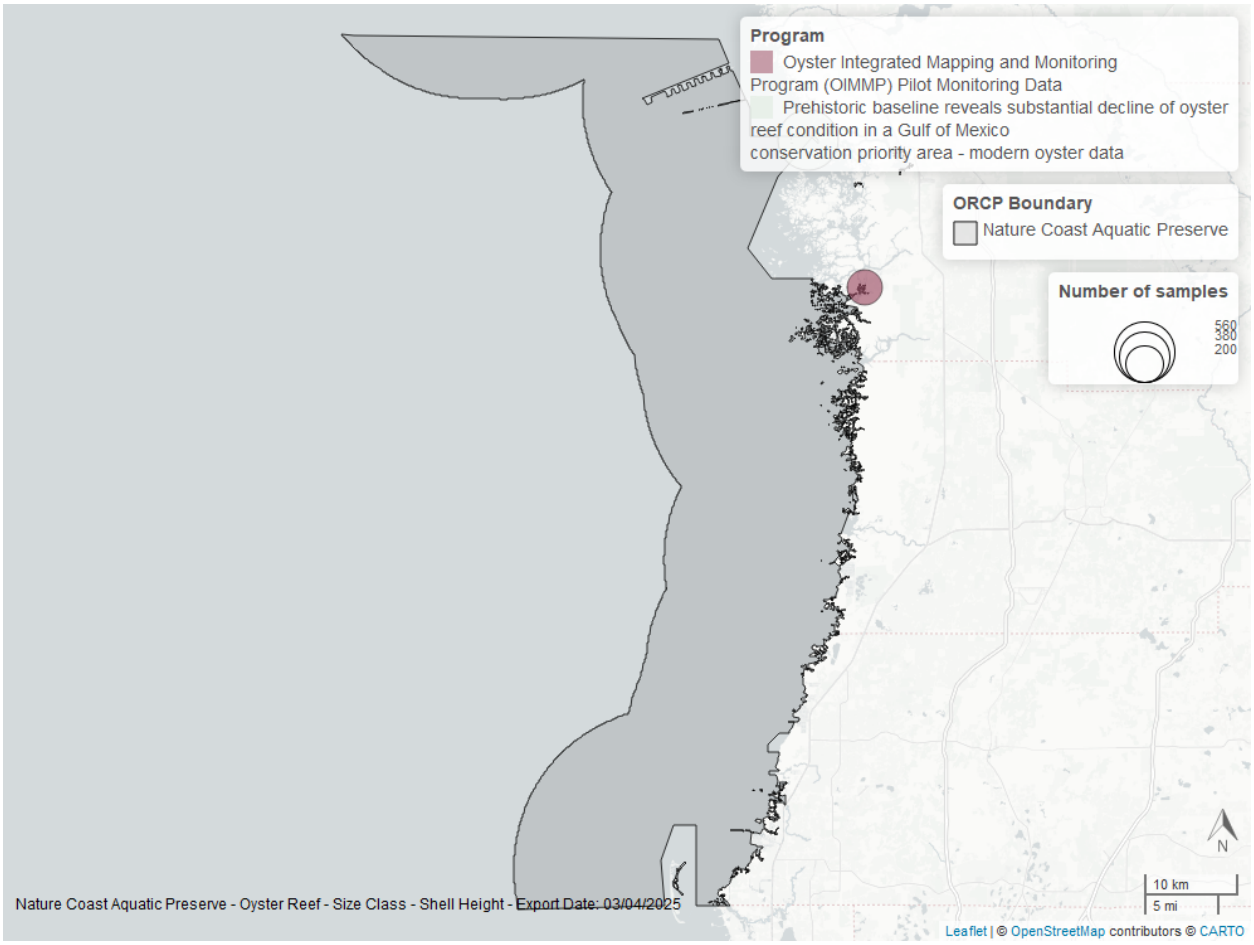


Figure 61: Figure for Oyster Shell Height in Nature Coast Aquatic Preserve

Table 61: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
Prehistoric baseline reveals substantial decline of oyster reef condition in a Gulf of Mexico conservation priority area - modern oyster data
ORCP Boundary
Nature Coast Aquatic Preserve
Number of samples
560
380
200
N
10 km
5 mi
Nature Coast Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pine Island Sound Aquatic Preserve

Natural

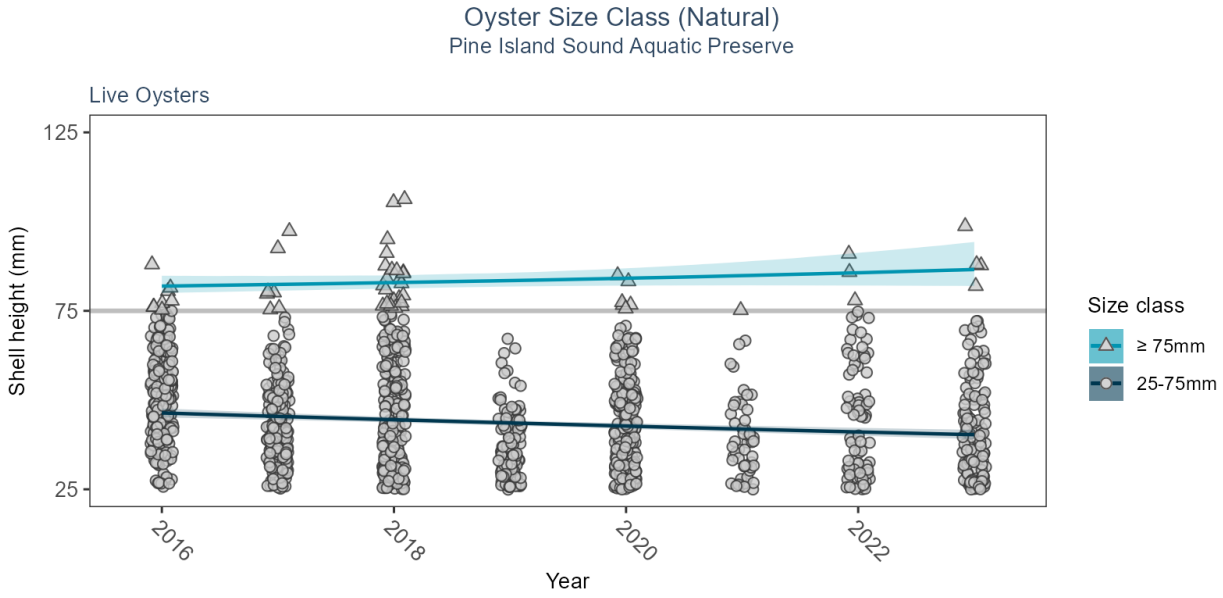


Figure 62: Figure for Oyster Shell Height in Pine Island Sound Aquatic Preserve

Table 62: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	No significant change	2.37	2.01	-1.18 to 6.83
Live Oysters	Natural	Significantly decreasing trend	-3.88	1.12	-6.54 to -2.14
Live Oysters	Natural	-	-	-	NA to NA

Restored

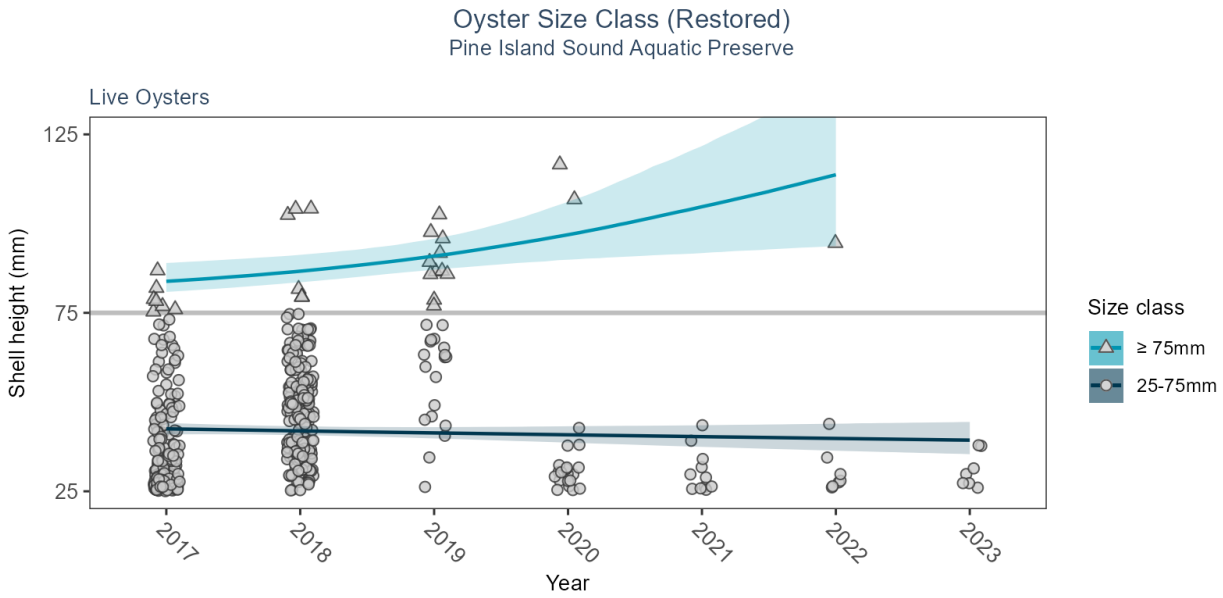
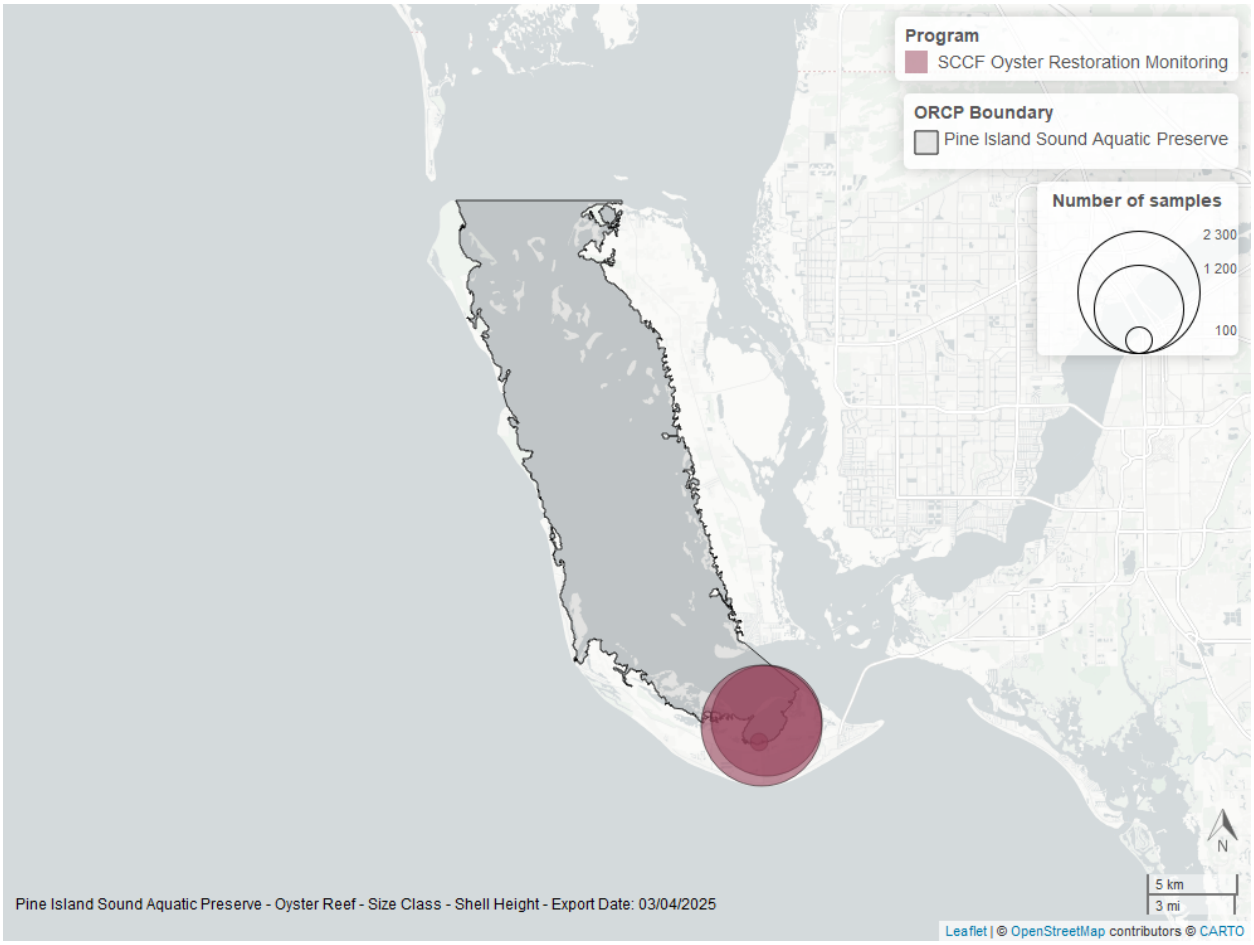


Figure 63: Figure for Oyster Shell Height in Pine Island Sound Aquatic Preserve

Table 63: Model results for Oyster Shell Height - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	Significantly increasing trend	10.38	4.62	3.05 to 21.32
Live Oysters	Restored	No significant change	-8.81	10.55	-34.64 to 6.17
Live Oysters	Restored	-	-	-	NA to NA


Program
SCCF Oyster Restoration Monitoring
ORCP Boundary
Pine Island Sound Aquatic Preserve
Number of samples
2 300
1 200
100
N
5 km
3 mi
Pine Island Sound Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Pinellas County Aquatic Preserve

Natural

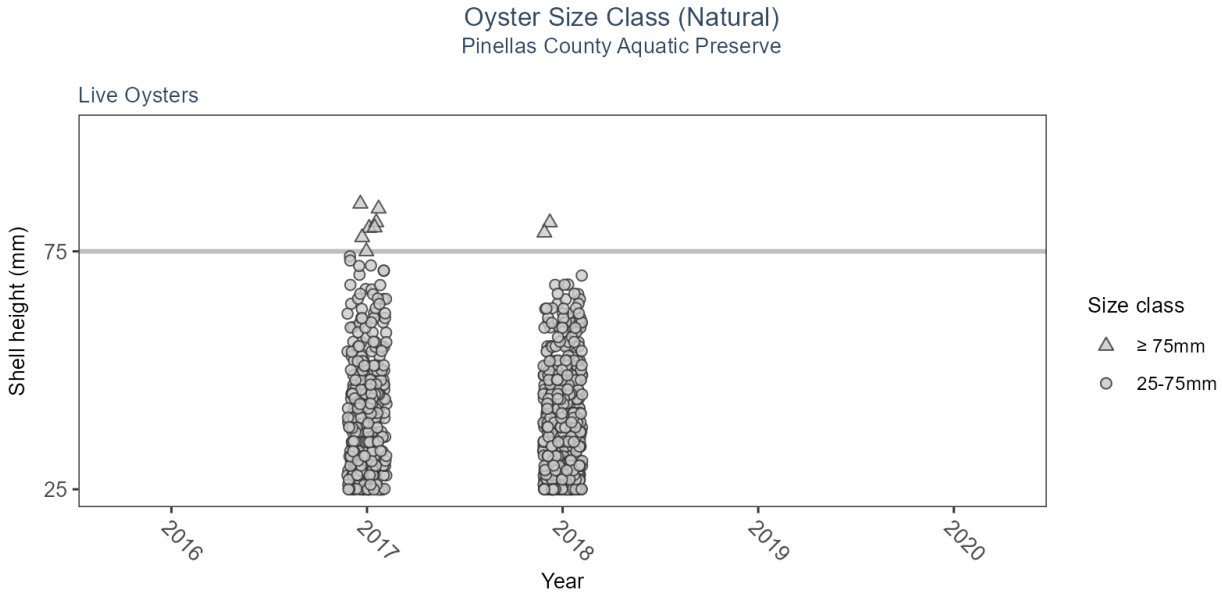
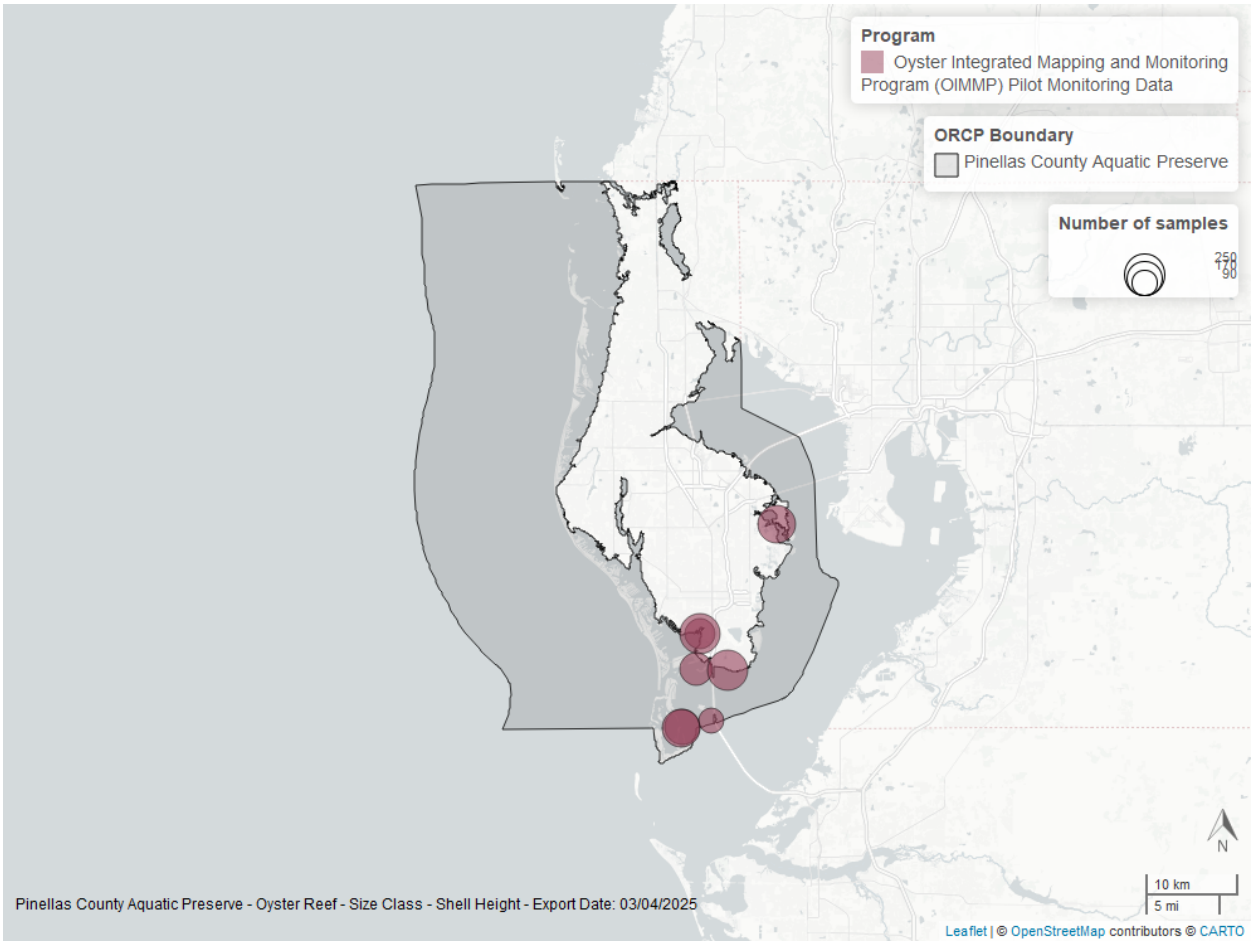


Figure 64: Figure for Oyster Shell Height in Pinellas County Aquatic Preserve

Table 64: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Oyster Integrated Mapping and Monitoring Program (OIMMP) Pilot Monitoring Data
ORCP Boundary
Pinellas County Aquatic Preserve
Number of samples
250
170
90
N
10 km
5 mi
Pinellas County Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
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St. Martins Marsh Aquatic Preserve

Natural

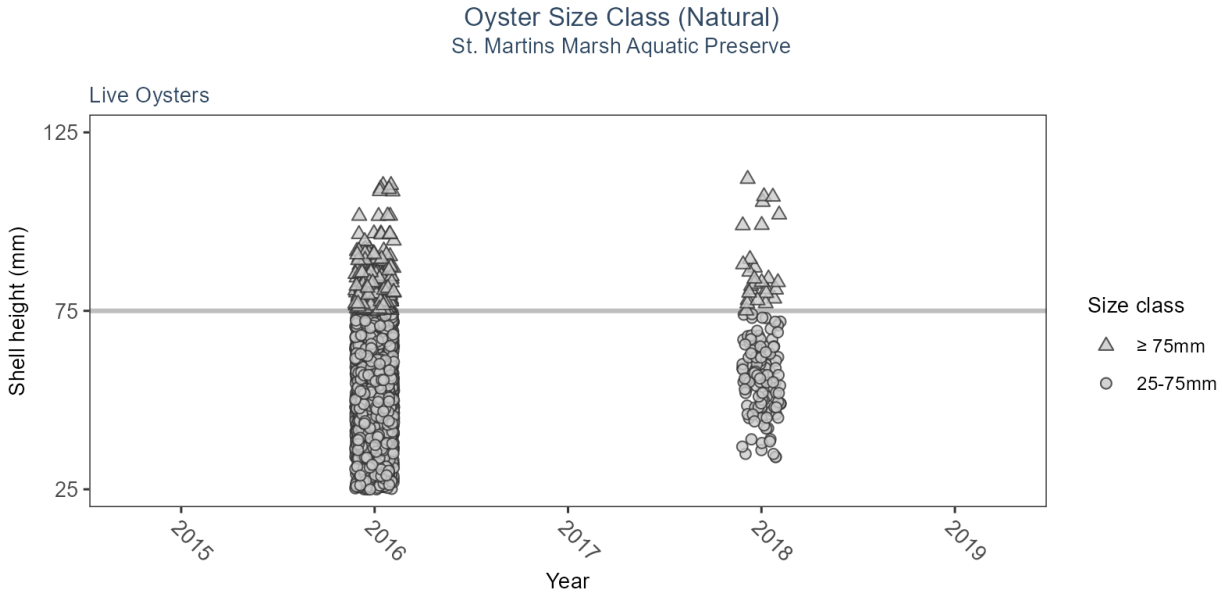
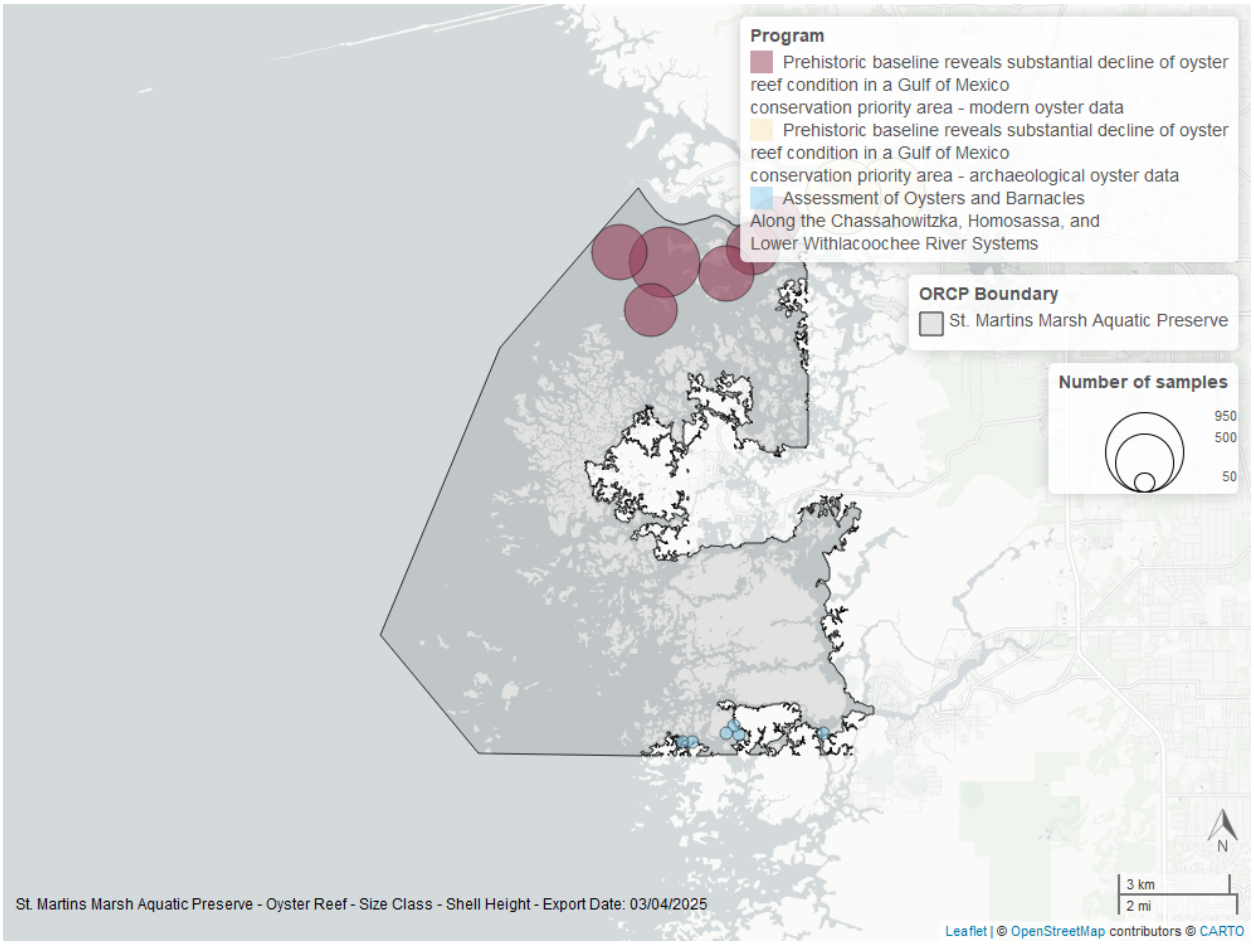


Figure 65: Figure for Oyster Shell Height in St. Martins Marsh Aquatic Preserve

Table 65: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Dead Oyster Shells	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA


Program
Prehistoric baseline reveals substantial decline of oyster reef condition in a Gulf of Mexico conservation priority area - modern oyster data
Prehistoric baseline reveals substantial decline of oyster reef condition in a Gulf of Mexico conservation priority area - archaeological oyster data
Assessment of Oysters and Barnacles Along the Chassahowitzka, Homosassa, and Lower Withlacoochee River Systems
ORCP Boundary
St. Martins Marsh Aquatic Preserve
Number of samples
950
500
50
N
3 km
2 mi
St. Martins Marsh Aquatic Preserve - Oyster Reef - Size Class - Shell Height - Export Date: 03/04/2025
Leaflet | © OpenStreetMap contributors © CARTO

Yellow River Marsh Aquatic Preserve

Natural

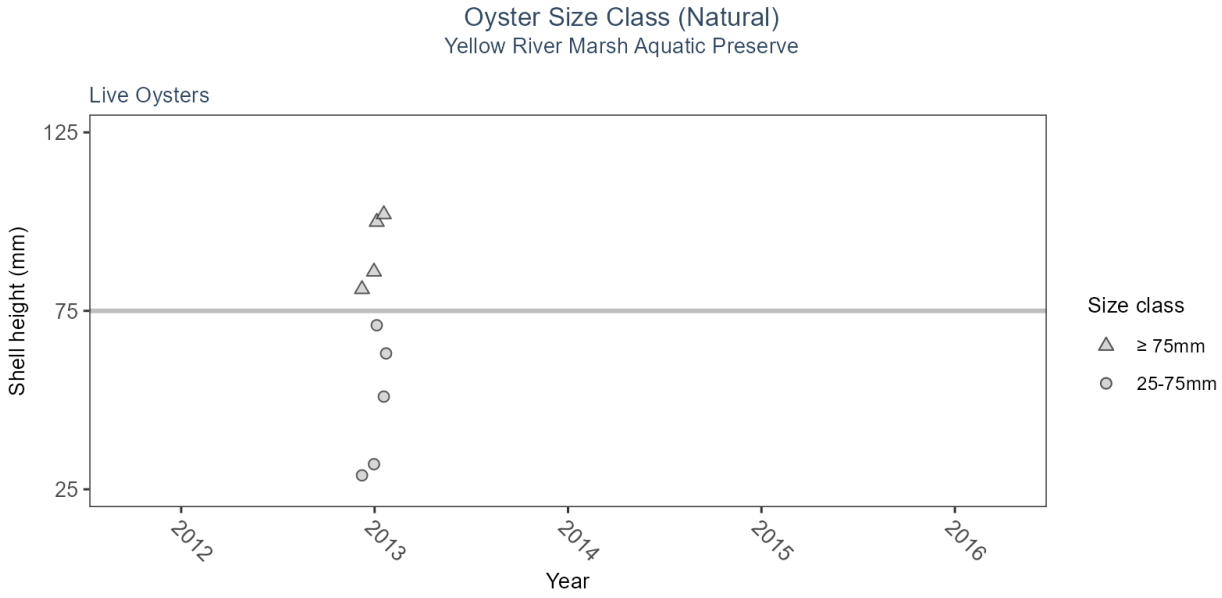


Figure 66: Figure for Oyster Shell Height in Yellow River Marsh Aquatic Preserve

Table 66: Model results for Oyster Shell Height - Natural

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA
Live Oysters	Natural	-	-	-	NA to NA

Restored

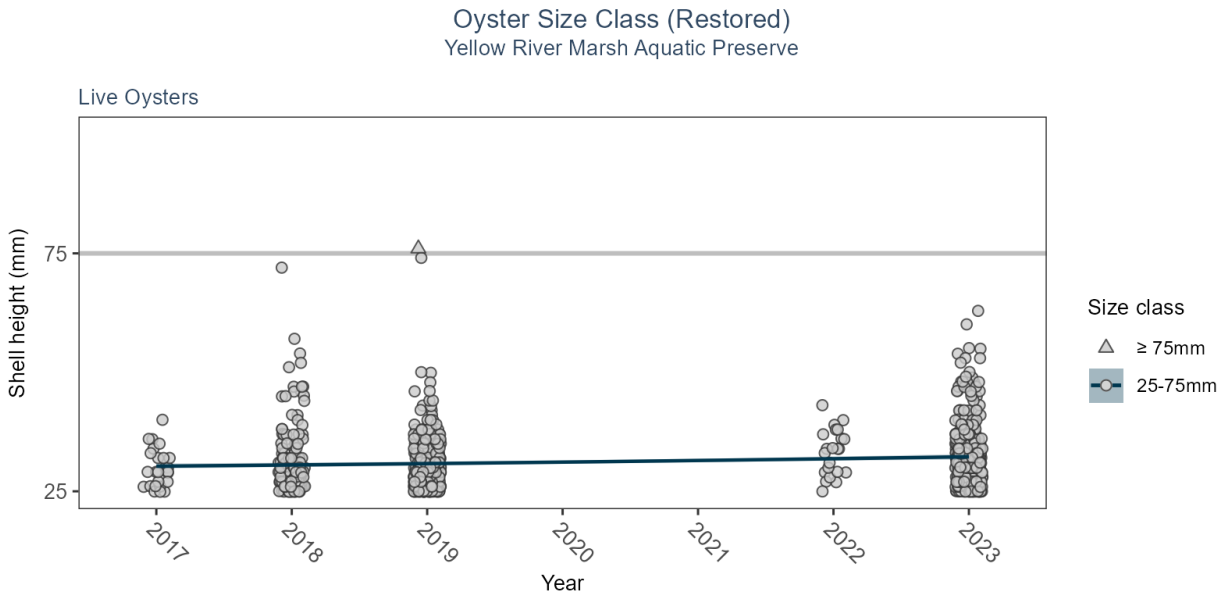
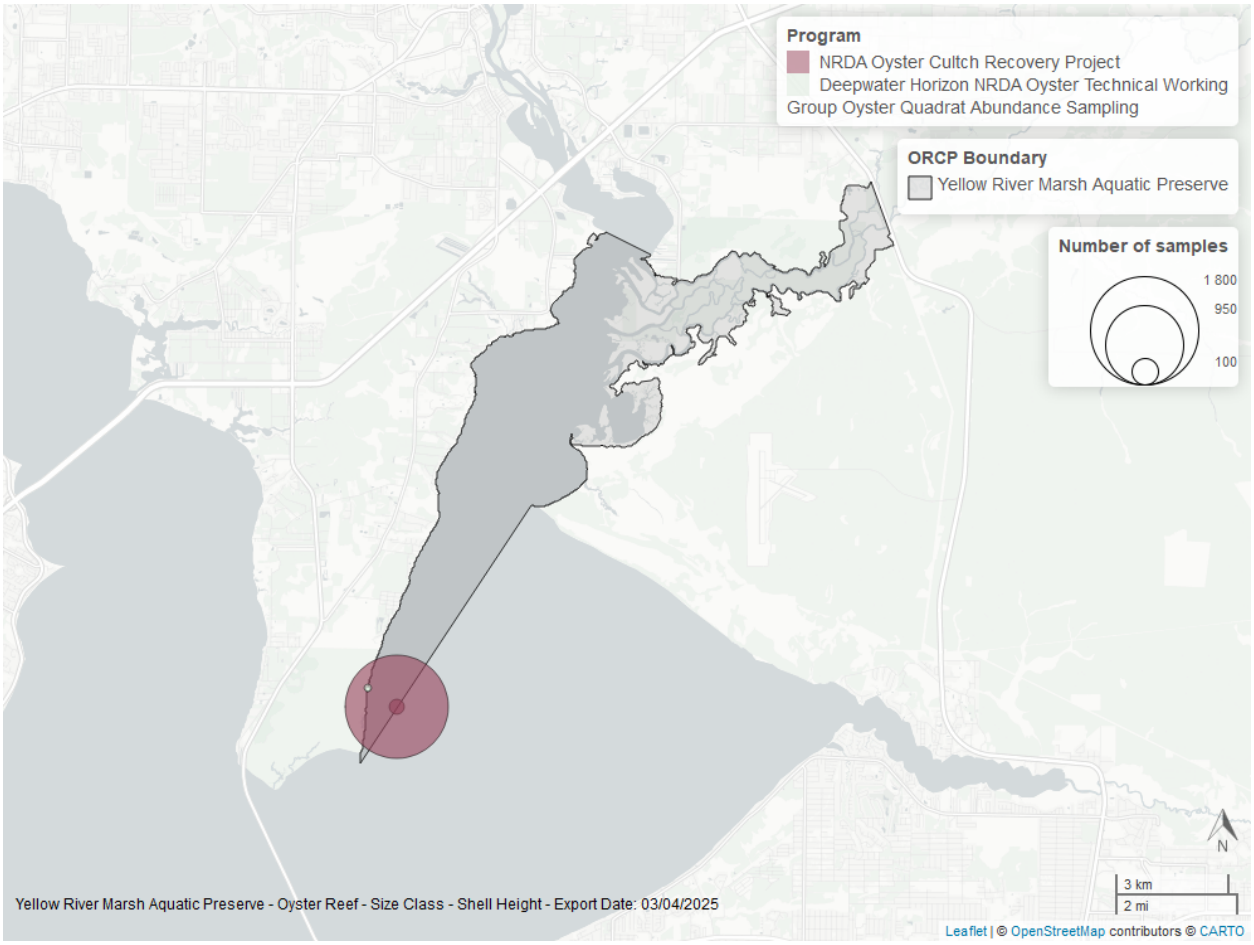


Figure 67: Figure for Oyster Shell Height in Yellow River Marsh Aquatic Preserve

Table 67: Model results for Oyster Shell Height - Restored

Shell Type	*Habitat Type*	*Trend Status*	*Estimate*	*Standard Error*	*Credible Interval*
Live Oysters	Restored	-	-	-	NA to NA
Live Oysters	Restored	Significantly increasing trend	3.19	1.22	1.47 to 6.2
Live Oysters	Restored	-	-	-	NA to NA



Libraries and Settings

Loads libraries used in the script. Loads the Segoe UI font for use in the figures. The inclusion of `scipen` option limits how frequently R defaults to scientific notation. Sets default settings for displaying warning and messages in created document, and sets figure dpi. Includes `knitr` and `kable` settings used to render this report. The code outlined below comes from `Oyster_Models_Clean_parallel.R` which performs data filtering and model fitting and can be run in parallel for more efficient results.

```
library(brms)
library(Rmisc)
library(rstan)
library(rstantools)
library(stringr)
library(data.table)
library(sf)
library(tidyverse)
library(doFuture)
library(tictoc)
library(doRNG)
library(rstudioapi)
library(ggpubr)
library(lubridate)
library(tidyverse)
```

```
library(data.table)
library(tictoc)
library(glue)
library(kableExtra)
library(future)
library(future.apply)
options(scipen=999)
knitr::opts_chunk$set(
   warning=FALSE,
   message=FALSE,
   dpi=200,
   fig.pos = 'H'
)
options(kableExtra.auto_format = FALSE)
options(knitr.kable.NA = '-')
```

File Import

Imports file that is determined in the Oyster_ReportRender.R script.

The command **fread** is used because of its improved speed while handling large data files. Updates column names.

The latest version of Oyster data is available at: https://usf.box.com/s/6dtcrcdkrtc33fqw5kl5fjo6guo0anrw

The file being used for the analysis is: **All_OYSTER_Parameters-2025-Apr-24.txt**

```
# If QAQCPlots is TRUE, plots will be created without running models
# Set to FALSE to run models
QAQCPlots <- FALSE

wd <- dirname(getActiveDocumentContext()$path)
setwd(wd)

# Set output directory
out_dir <- "output"

file_in <- str_subset(
  list.files("C:/SEACAR Data/SEACARdata/", full.names = TRUE), "OYSTER")

oysterraw <- fread(file_in, sep="|", na.strings=c("NULL"))
# New OIMMP updates include samples without MA associations, exclude for these analyses currently
oysterraw <- oysterraw[!is.na(AreaID), ]

oyster <- copy(oysterraw)
oysterraw2 <- tidyr::pivot_wider(oysterraw, names_from="ParameterName",
                           values_from="ResultValue")
setDT(oysterraw2)
setnames(oysterraw2, c("Density", "Percent Live", "Shell Height",
                       "Number of Oysters Counted - Live",
                       "Number of Oysters Counted - Dead",
                       "Number of Oysters Counted - Total", "Reef Height"),
         c("Density_m2", "PercentLive_pct", "ShellHeight_mm",
           "Number_of_Oysters_Counted_Live_Count",
           "Number_of_Oysters_Counted_Dead_Count",
```

```
           "Number_of_Oysters_Counted_Total_Count",
           "ReefHeight_mm"))
oysterraw2[, ObsIndex := seq(1:nrow(oysterraw2))]

oysterraw <- oysterraw2
rm(oysterraw2)
```

Data Setup & Filtering

Documentation on database filtering is provided here: SEACAR Documentation- Analysis Filters and Calculations.docx

Identifies and removes outliers in the data and various programs.

```
#Make sure column formats are correct-I am still getting an "NAs introduced
#by coercion" warning on the LiveDate calculation,
#but I'm not sure what is going on because when I spot-check the output,
#it does not look like it is introducing NAs...
oysterraw[, `:=` (RowID=as.integer(RowID),
                  ProgramID=as.integer(ProgramID),
                  LocationID=as.integer(LocationID),
                  ProgramName=as.character(ProgramName),
                  ProgramLocationID=as.character(ProgramLocationID),
                  QuadIdentifier=as.character(QuadIdentifier),
                  ReefIdentifier=as.character(ReefIdentifier),
                  UniversalReefID=as.factor(UniversalReefID),
                  LiveDate=as.integer(ifelse(!is.na(LiveDate_Qualifier) &
                                               str_detect(LiveDate,
                                                          "....-..-.."),
                                             paste0(str_sub(LiveDate, 1, 4)),
                                             round(as.numeric(LiveDate)))),
                  LiveDate_Qualifier=as.character(LiveDate_Qualifier),
                  LiveDate_MinEstDate=as.numeric(LiveDate_MinEstDate),
                  LiveDate_MaxEstDate=as.numeric(LiveDate_MaxEstDate),
                  SampleAge_Stdev=as.numeric(SampleAge_Stdev),
                  #GISUniqueID=as.logical(GISUniqueID),
                  Year=as.integer(Year),
                  Month=as.integer(Month),
                  ManagedAreaName=as.character(ManagedAreaName),
                  SurveyMethod=as.character(SurveyMethod),
                  PercentLiveMethod=as.character(PercentLiveMethod),
                  HabitatClassification=as.character(HabitatClassification),
                  MinimumSizeMeasured_mm=as.character(MinimumSizeMeasured_mm),
                  NumberMeasured_n=as.character(NumberMeasured_n),
                  QuadSize_m2=as.numeric(QuadSize_m2),
                  MADup=as.integer(MADup),
                  Density_m2=as.numeric(Density_m2),
                  PercentLive_pct=as.numeric(PercentLive_pct),
                  ShellHeight_mm=as.numeric(ShellHeight_mm),
                  Number_of_Oysters_Counted_Total_Count =
                    as.integer(Number_of_Oysters_Counted_Total_Count),
                  Number_of_Oysters_Counted_Live_Count =
                    as.integer(Number_of_Oysters_Counted_Live_Count),
                  Number_of_Oysters_Counted_Dead_Count =
```

```
                  as.integer(Number_of_Oysters_Counted_Dead_Count),
                ObsIndex=as.integer(ObsIndex))]

#Calculate Density_m2 values for ProgramID==4016 & 4042
oysterraw[ProgramID==4016, Density_m2 :=
            Number_of_Oysters_Counted_Live_Count/as.numeric(QuadSize_m2)]
oysterraw[ProgramID==4042 & !is.na(Number_of_Oysters_Counted_Live_Count),
          Density_m2 :=
            Number_of_Oysters_Counted_Live_Count/as.numeric(QuadSize_m2)]

#Remove "25" values from total counts column, make all "PercentLiveMethod"
#values the same, and calculate estimated live Density for ProgramID==5074 and
oysterraw <- oysterraw[RowID %in%
                         setdiff(
                           oysterraw[, RowID],
                           oysterraw[ProgramID ==5074 &
                                       Number_of_Oysters_Counted_Total_Count==25, RowID]), ]
oysterraw[ProgramID==5074, PercentLiveMethod := "Estimated percent"]
oysterraw[ProgramID==5074, SampleDate :=
            unique(oysterraw[ProgramID==5074 &
                               !is.na(Number_of_Oysters_Counted_Total_Count),
                             SampleDate])[1]]

#Some PercentLiveMethod values for ID4042 are NA
oysterraw[ProgramID==4042 | ProgramID==4016,
          PercentLiveMethod := "Point-intercept"]

#make sure quadrat identifiers are unique
oysterraw[, QuadIdentifier_old := QuadIdentifier]
oysterraw[, QuadIdentifier := paste(UniversalReefID,
                                    LocationID, Year, Month,
                                    QuadIdentifier_old, sep="_")]

oysterraw[, MA_plotlab := paste0(ManagedAreaName, "_", HabitatClassification)]
subtidal <- c(4044, 5007, 5071, 5073)
oysterraw[, Subtidal := ifelse(ProgramID %in% subtidal, 1, 0)][, Subtidal := as.logical(Subtidal)]

#Create variables for relative year and size class category for data that
#should be included in analyses and counts of live oysters measured
for(i in unique(oysterraw$ManagedAreaName)){
  oysterraw[ManagedAreaName==i & !is.na(LiveDate), `:=`
            (RelYear=(LiveDate-min(LiveDate))+1,
              YearDiff=min(LiveDate)-1,
              #adding 1 to each RelYear to avoid min(RelYear)==0,
              #because it is used later as an index for plotting years so
              #it needs to start from 1
              SizeClass=fcase(ShellHeight_mm >= 25 &
                                ShellHeight_mm < 75, "25to75mm",
                              ShellHeight_mm >= 75, "o75mm",
                              default=NA))]

  oysterraw[ManagedAreaName==i & !is.na(LiveDate),
            counts := length(ShellHeight_mm), by=c("QuadIdentifier")]
```

```
}

#Remove unrealistically high shell heights from ID_5017
oysterraw <- setdiff(oysterraw, oysterraw[ProgramID==5017 & ShellHeight_mm >= 165, ])

#Create data table to save model results
oysterresults <- data.table(indicator=character(),
                            managed_area=character(),
                            habitat_class=character(),
                            size_class=character(),
                            live_date_qual=character(),
                            n_programs=integer(),
                            programs=list(),
                            filename=character(),
                            effect=character(),
                            component=character(),
                            group=character(),
                            term=character(),
                            estimate=numeric(),
                            std.error=numeric(),
                            conf.low=numeric(),
                            conf.high=numeric())

#How many years of data for each managed area/habitat class/indicator combination?
setDT(oysterraw)
oysterraw[!is.na(Density_m2), `:=` (nyrpar="Density_m2",
                                    nyears=length(unique(Year))),
          by=MA_plotlab]
oysterraw[!is.na(PercentLive_pct), `:=` (nyrpar="PercentLive_pct",
                                         nyears=length(unique(Year))),
          by=MA_plotlab]
oysterraw[!is.na(ShellHeight_mm), `:=` (nyrpar="ShellHeight_mm",
                                        nyears=length(unique(Year))),
          by=MA_plotlab]
MAinclude <- distinct(oysterraw[, .(MA_plotlab, nyrpar, nyears)])
# View(MAinclude[!is.na(nyrpar) & nyears >= 5, ])

oysterraw[str_detect(MA_plotlab, "Pine Island Sound"),
           `:=` (MA_plotlab=ifelse(str_detect(ProgramLocationID,
                                              "Reference") |
                                   str_detect(ProgramLocationID,
                                              "Control"),
                                   "Pine Island Sound Aquatic Preserve_Natural",
                                   "Pine Island Sound Aquatic Preserve_Restored"),
                 HabitatClassification=ifelse(str_detect(ProgramLocationID,
                                                         "Reference") |
                                              str_detect(ProgramLocationID,
                                                         "Control"),
                                              "Natural", "Restored"))]
```

Managed Area Statistics

Gets summary statistics for each managed area. Uses piping from dplyr package to feed into subsequent steps. Sets of summary statistics are performed for Density, Shell Height, and Percent Living. The following steps are performed:

1. Group data that have the same `ManagedAreaName`, `Year`, `Month`, `nyrpar`, `LiveDate_Qualifier`, `SizeClass`, and `HabitatClassification`.
   - Second summary statistics do not use the `Month` grouping and are only for `ManagedAreaName`, `Year`, and the other oyster parameters.
   - Third summary statistics do not use `Year` grouping and are only for `ManagedAreaName`, `Month`, and the other oyster parameters.
   - Fourth summary statistics are only grouped based on `ManagedAreaName` and the other oyster parameters
     - Determines the years that the minimum and maximum species richness occurred
2. For each group, provide the following information: Parameter Name (ParameterName), Number of Entries (N_Data), Lowest Value (Min), Largest Value (Max), Median, Mean, Standard Deviation, and a list of all Programs included in these measurements.
3. Sort the data in ascending (A to Z and 0 to 9) order based on `ManagedAreaName` then `Year` then `Month`
4. Write summary stats to a pipe-delimited .txt file in the output directory
   - Oyster Output Files in SEACAR GitHub (https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Oyster/output)

Density

```
oysterraw$SizeClass[oysterraw$SizeClass=="25to75mm"] <- "25-75mm"
oysterraw$SizeClass[oysterraw$SizeClass=="35to75mm"] <- "35-75mm"
oysterraw$SizeClass[oysterraw$SizeClass=="o75mm"] <- ">75mm"

# Create summary statistics for each managed area based on Year and Month
# intervals.
MA_YM_Stats <- oysterraw[oysterraw$nyrpar=="Density_m2",] %>%
  group_by(AreaID, ManagedAreaName, Year, Month, nyrpar,
           LiveDate_Qualifier, SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(Density_m2[!is.na(Density_m2)]),
                   Min=min(Density_m2[!is.na(Density_m2)]),
                   Max=max(Density_m2[!is.na(Density_m2)]),
                   Median=median(Density_m2[!is.na(Density_m2)]),
                   Mean=mean(Density_m2[!is.na(Density_m2)]),
                   StandardDeviation=sd(Density_m2[!is.na(Density_m2)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_YM_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName, Year, then Month
MA_YM_Stats <- as.data.table(MA_YM_Stats[order(MA_YM_Stats$ManagedAreaName,
                                               MA_YM_Stats$Year,
                                               MA_YM_Stats$Month,
                                               MA_YM_Stats$ShellType,
```

```
                                                MA_YM_Stats$SizeClass,
                                                MA_YM_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_YM_Stats, paste0(out_dir,"/Density/Oyster_Dens_MA_MMYY_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Density"]][["MA_YM_Stats"]] <- MA_YM_Stats
# Removes variable storing data to improve computer memory
rm(MA_YM_Stats)

# Create summary statistics for each managed area based on Year intervals
MA_Y_Stats <- oysterraw[oysterraw$nyrpar=="Density_m2",] %>%
  group_by(AreaID, ManagedAreaName, Year, nyrpar, LiveDate_Qualifier,
           SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(Density_m2[!is.na(Density_m2)]),
                   Min=min(Density_m2[!is.na(Density_m2)]),
                   Max=max(Density_m2[!is.na(Density_m2)]),
                   Median=median(Density_m2[!is.na(Density_m2)]),
                   Mean=mean(Density_m2[!is.na(Density_m2)]),
                   StandardDeviation=sd(Density_m2[!is.na(Density_m2)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_Y_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName then Year
MA_Y_Stats <- as.data.table(MA_Y_Stats[order(MA_Y_Stats$ManagedAreaName,
                                             MA_Y_Stats$Year,
                                             MA_Y_Stats$ShellType,
                                             MA_Y_Stats$SizeClass,
                                             MA_Y_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_Y_Stats, paste0(out_dir,"/Density/Oyster_Dens_MA_Yr_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Density"]][["MA_Y_Stats"]] <- MA_Y_Stats
# Removes variable storing data to improve computer memory
rm(MA_Y_Stats)

# Create summary statistics for each managed area based on Month intervals.
MA_M_Stats <- oysterraw[oysterraw$nyrpar=="Density_m2",] %>%
  group_by(AreaID, ManagedAreaName, Month, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Data=length(Density_m2[!is.na(Density_m2)]),
                   Min=min(Density_m2[!is.na(Density_m2)]),
                   Max=max(Density_m2[!is.na(Density_m2)]),
                   Median=median(Density_m2[!is.na(Density_m2)]),
                   Mean=mean(Density_m2[!is.na(Density_m2)]),
```

```
                  StandardDeviation=sd(Density_m2[!is.na(Density_m2)]),
                  Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                 collapse=', '),
                  ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                   collapse=', '))
setnames(MA_M_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName then Month
MA_M_Stats <- as.data.table(MA_M_Stats[order(MA_M_Stats$ManagedAreaName,
                                             MA_M_Stats$Month,
                                             MA_M_Stats$ShellType,
                                             MA_M_Stats$SizeClass,
                                             MA_M_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_M_Stats, paste0(out_dir,"/Density/Oyster_Dens_MA_Mo_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Density"]][["MA_M_Stats"]] <- MA_M_Stats
# Removes variable storing data to improve computer memory
rm(MA_M_Stats)

# Create summary overall statistics for each managed area.
MA_Ov_Stats <- oysterraw[oysterraw$nyrpar=="Density_m2",] %>%
  group_by(AreaID, ManagedAreaName, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Years=length(unique(
    LiveDate[!is.na(LiveDate) & !is.na(Density_m2)])),
    SufficientData=ifelse(N_Years>=5, TRUE, FALSE),
    EarliestLiveDate=min(LiveDate[!is.na(Density_m2)]),
    LatestLiveDate=max(LiveDate[!is.na(Density_m2)]),
    LastSampleDate=max(SampleDate),
    N_Data=length(Density_m2[!is.na(Density_m2)]),
    Min=min(Density_m2[!is.na(Density_m2)]),
    Max=max(Density_m2[!is.na(Density_m2)]),
    Median=median(Density_m2[!is.na(Density_m2)]),
    Mean=mean(Density_m2[!is.na(Density_m2)]),
    StandardDeviation=sd(Density_m2[!is.na(Density_m2)]),
    Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                   collapse=', '),
    ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                     collapse=', '))
setnames(MA_Ov_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName
MA_Ov_Stats <- as.data.table(MA_Ov_Stats[order(MA_Ov_Stats$ManagedAreaName,
                                               MA_Ov_Stats$ShellType,
```

```
                                                MA_Ov_Stats$SizeClass,
                                                MA_Ov_Stats$HabitatType), ])

# Replaces blank ProgramIDs with NA (missing values)
MA_Ov_Stats$ProgramIDs <- replace(MA_Ov_Stats$ProgramIDs,
                                  MA_Ov_Stats$ProgramIDs=="", NA)
MA_Ov_Stats$Programs <- replace(MA_Ov_Stats$Programs,
                                MA_Ov_Stats$Programs=="", NA)
# Write overall statistics to file
fwrite(MA_Ov_Stats, paste0(out_dir,"/Density/Oyster_Dens_MA_Overall_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Density"]][["MA_Ov_Stats"]] <- MA_Ov_Stats
# Removes variable storing data to improve computer memory
rm(MA_Ov_Stats)
```

Shell Height

```
# Create summary statistics for each managed area based on Year and Month
# intervals.
MA_YM_Stats <- oysterraw[oysterraw$nyrpar=="ShellHeight_mm",] %>%
  group_by(AreaID, ManagedAreaName, Year, Month, nyrpar,
           LiveDate_Qualifier, SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Min=min(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Max=max(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Median=median(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Mean=mean(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   StandardDeviation=sd(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_YM_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName, Year, then Month
MA_YM_Stats <- as.data.table(MA_YM_Stats[order(MA_YM_Stats$ManagedAreaName,
                                               MA_YM_Stats$Year,
                                               MA_YM_Stats$Month,
                                               MA_YM_Stats$ShellType,
                                               MA_YM_Stats$SizeClass,
                                               MA_YM_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_YM_Stats, paste0(out_dir,"/Shell_Height/Oyster_SH_MA_MMYY_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Shell Height"]][["MA_YM_Stats"]] <- MA_YM_Stats
# Removes variable storing data to improve computer memory
rm(MA_YM_Stats)
```

```
# Create summary statistics for each managed area based on Year intervals
MA_Y_Stats <- oysterraw[oysterraw$nyrpar=="ShellHeight_mm",] %>%
  group_by(AreaID, ManagedAreaName, Year, nyrpar, LiveDate_Qualifier,
           SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Min=min(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Max=max(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Median=median(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Mean=mean(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   StandardDeviation=sd(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_Y_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName then Year
MA_Y_Stats <- as.data.table(MA_Y_Stats[order(MA_Y_Stats$ManagedAreaName,
                                             MA_Y_Stats$Year,
                                             MA_Y_Stats$ShellType,
                                             MA_Y_Stats$SizeClass,
                                             MA_Y_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_Y_Stats, paste0(out_dir,"/Shell_Height/Oyster_SH_MA_Yr_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Shell Height"]][["MA_Y_Stats"]] <- MA_Y_Stats
# Removes variable storing data to improve computer memory
rm(MA_Y_Stats)

# Create summary statistics for each managed area based on Month intervals.
MA_M_Stats <- oysterraw[oysterraw$nyrpar=="ShellHeight_mm",] %>%
  group_by(AreaID, ManagedAreaName, Month, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Data=length(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Min=min(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Max=max(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Median=median(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Mean=mean(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   StandardDeviation=sd(ShellHeight_mm[!is.na(ShellHeight_mm)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_M_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
```

```
# Puts the data in order based on ManagedAreaName then Month
MA_M_Stats <- as.data.table(MA_M_Stats[order(MA_M_Stats$ManagedAreaName,
                                             MA_M_Stats$Month,
                                             MA_M_Stats$ShellType,
                                             MA_M_Stats$SizeClass,
                                             MA_M_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_M_Stats, paste0(out_dir,"/Shell_Height/Oyster_SH_MA_Mo_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Shell Height"]][["MA_M_Stats"]] <- MA_M_Stats
# Removes variable storing data to improve computer memory
rm(MA_M_Stats)

# Create summary overall statistics for each managed area.
MA_Ov_Stats <- oysterraw[oysterraw$nyrpar=="ShellHeight_mm",] %>%
  group_by(AreaID, ManagedAreaName, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Years=length(unique(
    LiveDate[!is.na(LiveDate) & !is.na(ShellHeight_mm)])),
    SufficientData=ifelse(N_Years>=5, TRUE, FALSE),
    EarliestLiveDate=min(LiveDate[!is.na(ShellHeight_mm)]),
    LatestLiveDate=max(LiveDate[!is.na(ShellHeight_mm)]),
    LastSampleDate=max(SampleDate),
    N_Data=length(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    Min=min(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    Max=max(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    Median=median(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    Mean=mean(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    StandardDeviation=sd(ShellHeight_mm[!is.na(ShellHeight_mm)]),
    Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                   collapse=', '),
    ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                     collapse=', '))
setnames(MA_Ov_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName
MA_Ov_Stats <- as.data.table(MA_Ov_Stats[order(MA_Ov_Stats$ManagedAreaName,
                                               MA_Ov_Stats$ShellType,
                                               MA_Ov_Stats$SizeClass,
                                               MA_Ov_Stats$HabitatType), ])

# Replaces blank ProgramIDs with NA (missing values)
MA_Ov_Stats$ProgramIDs <- replace(MA_Ov_Stats$ProgramIDs,
                                  MA_Ov_Stats$ProgramIDs=="", NA)
MA_Ov_Stats$Programs <- replace(MA_Ov_Stats$Programs,
                                MA_Ov_Stats$Programs=="", NA)
# Write overall statistics to file
fwrite(MA_Ov_Stats, paste0(out_dir,"/Shell_Height/Oyster_SH_MA_Overall_Stats.txt"),
```

```
       sep="|")
# Save stats file to directory
ma_stats[["Shell Height"]][["MA_Ov_Stats"]] <- MA_Ov_Stats
# Removes variable storing data to improve computer memory
rm(MA_Ov_Stats)
```

Percent Live

```
# Create summary statistics for each managed area based on Year and Month
# intervals.
MA_YM_Stats <- oysterraw[oysterraw$nyrpar=="PercentLive_pct",] %>%
  group_by(AreaID, ManagedAreaName, Year, Month, nyrpar,
           LiveDate_Qualifier, SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Min=min(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Max=max(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Median=median(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Mean=mean(PercentLive_pct[!is.na(PercentLive_pct)]),
                   StandardDeviation=sd(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_YM_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_YM_Stats$ShellType[MA_YM_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName, Year, then Month
MA_YM_Stats <- as.data.table(MA_YM_Stats[order(MA_YM_Stats$ManagedAreaName,
                                               MA_YM_Stats$Year,
                                               MA_YM_Stats$Month,
                                               MA_YM_Stats$ShellType,
                                               MA_YM_Stats$SizeClass,
                                               MA_YM_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_YM_Stats, paste0(out_dir,"/Percent_Live/Oyster_PrcLive_MA_MMYY_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Percent Live"]][["MA_YM_Stats"]] <- MA_YM_Stats
# Removes variable storing data to improve computer memory
rm(MA_YM_Stats)

# Create summary statistics for each managed area based on Year intervals
MA_Y_Stats <- oysterraw[oysterraw$nyrpar=="PercentLive_pct",] %>%
  group_by(AreaID, ManagedAreaName, Year, nyrpar, LiveDate_Qualifier,
           SizeClass, HabitatClassification) %>%
  dplyr::summarize(N_Data=length(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Min=min(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Max=max(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Median=median(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Mean=mean(PercentLive_pct[!is.na(PercentLive_pct)]),
                   StandardDeviation=sd(PercentLive_pct[!is.na(PercentLive_pct)]),
```

```
                  Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                 collapse=', '),
                  ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                   collapse=', '))
setnames(MA_Y_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Y_Stats$ShellType[MA_Y_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName then Year
MA_Y_Stats <- as.data.table(MA_Y_Stats[order(MA_Y_Stats$ManagedAreaName,
                                             MA_Y_Stats$Year,
                                             MA_Y_Stats$ShellType,
                                             MA_Y_Stats$SizeClass,
                                             MA_Y_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_Y_Stats, paste0(out_dir,"/Percent_Live/Oyster_PrcLive_MA_Yr_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Percent Live"]][["MA_Y_Stats"]] <- MA_Y_Stats
# Removes variable storing data to improve computer memory
rm(MA_Y_Stats)

# Create summary statistics for each managed area based on Month intervals.
MA_M_Stats <- oysterraw[oysterraw$nyrpar=="PercentLive_pct",] %>%
  group_by(AreaID, ManagedAreaName, Month, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Data=length(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Min=min(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Max=max(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Median=median(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Mean=mean(PercentLive_pct[!is.na(PercentLive_pct)]),
                   StandardDeviation=sd(PercentLive_pct[!is.na(PercentLive_pct)]),
                   Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                                  collapse=', '),
                   ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                                    collapse=', '))
setnames(MA_M_Stats, c("nyrpar", "LiveDate_Qualifier",
                       "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_M_Stats$ShellType[MA_M_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName then Month
MA_M_Stats <- as.data.table(MA_M_Stats[order(MA_M_Stats$ManagedAreaName,
                                             MA_M_Stats$Month,
                                             MA_M_Stats$ShellType,
                                             MA_M_Stats$SizeClass,
                                             MA_M_Stats$HabitatType), ])
# Writes summary statistics to file
fwrite(MA_M_Stats, paste0(out_dir,"/Percent_Live/Oyster_PrcLive_MA_Mo_Stats.txt"),
       sep="|")
# Save stats file to directory
```

```
ma_stats[["Percent Live"]][["MA_M_Stats"]] <- MA_M_Stats
# Removes variable storing data to improve computer memory
rm(MA_M_Stats)

# Create summary overall statistics for each managed area.
MA_Ov_Stats <- oysterraw[oysterraw$nyrpar=="PercentLive_pct",] %>%
  group_by(AreaID, ManagedAreaName, nyrpar,
           LiveDate_Qualifier, SizeClass,
           HabitatClassification) %>%
  dplyr::summarize(N_Years=length(unique(
    LiveDate[!is.na(LiveDate) & !is.na(PercentLive_pct)])),
    SufficientData=ifelse(N_Years>=5, TRUE, FALSE),
    EarliestLiveDate=min(LiveDate[!is.na(PercentLive_pct)]),
    LatestLiveDate=max(LiveDate[!is.na(PercentLive_pct)]),
    LastSampleDate=max(SampleDate),
    N_Data=length(PercentLive_pct[!is.na(PercentLive_pct)]),
    Min=min(PercentLive_pct[!is.na(PercentLive_pct)]),
    Max=max(PercentLive_pct[!is.na(PercentLive_pct)]),
    Median=median(PercentLive_pct[!is.na(PercentLive_pct)]),
    Mean=mean(PercentLive_pct[!is.na(PercentLive_pct)]),
    StandardDeviation=sd(PercentLive_pct[!is.na(PercentLive_pct)]),
    Programs=paste(sort(unique(ProgramName), decreasing=FALSE),
                   collapse=', '),
    ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),
                     collapse=', '))
setnames(MA_Ov_Stats, c("nyrpar", "LiveDate_Qualifier",
                        "HabitatClassification"),
         c("ParameterName", "ShellType", "HabitatType"))
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Exact"] <- "Live Oyster Shells"
MA_Ov_Stats$ShellType[MA_Ov_Stats$ShellType=="Estimate"] <- "Dead Oyster Shells"
# Puts the data in order based on ManagedAreaName
MA_Ov_Stats <- as.data.table(MA_Ov_Stats[order(MA_Ov_Stats$ManagedAreaName,
                                               MA_Ov_Stats$ShellType,
                                               MA_Ov_Stats$SizeClass,
                                               MA_Ov_Stats$HabitatType), ])

# Replaces blank ProgramIDs with NA (missing values)
MA_Ov_Stats$ProgramIDs <- replace(MA_Ov_Stats$ProgramIDs,
                                  MA_Ov_Stats$ProgramIDs=="", NA)
MA_Ov_Stats$Programs <- replace(MA_Ov_Stats$Programs,
                                MA_Ov_Stats$Programs=="", NA)
# Write overall statistics to file
fwrite(MA_Ov_Stats, paste0(out_dir,"/Percent_Live/Oyster_PrcLive_MA_Overall_Stats.txt"),
       sep="|")
# Save stats file to directory
ma_stats[["Percent Live"]][["MA_Ov_Stats"]] <- MA_Ov_Stats
# Removes variable storing data to improve computer memory
rm(MA_Ov_Stats)
```

Plotting setup

```
# LiveDate Threshold ------------------------------------------------------
oysterraw <- oysterraw[oysterraw$LiveDate>=1960,]
for(i in unique(oysterraw$ManagedAreaName)){
  oysterraw[ManagedAreaName==i & !is.na(LiveDate), `:=`
            (RelYear=(LiveDate-min(LiveDate))+1,
              YearDiff=min(LiveDate)-1)]
}

# Plot theme and setup -----
plot_theme <- theme_bw() +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        text=element_text(family="Arial"),
        plot.title=element_text(hjust=0.5, size=12, color="#314963"),
        plot.subtitle=element_text(hjust=0.5, size=10, color="#314963"),
        legend.title=element_text(size=10),
        legend.text = element_text(hjust = 0),
        axis.title.x = element_text(size=10, margin = margin(t = 5, r = 0,
                                                             b = 10, l = 0)),
        axis.title.y = element_text(size=10, margin = margin(t = 0, r = 10,
                                                             b = 0, l = 0)),
        axis.text=element_text(size=10),
        axis.text.x=element_text(angle = -45, hjust = 0))

plot_jitter <- position_jitter(width = 0.1, height = 0.1, seed=42)
```

Oyster Shell Height Analysis

Subsets data for that which is related to shell height. The data is further subset for each managed area and shell size class. Appropriate GLMMs are called from file for each shell size class, or are created if they don't exist. `shell_height_models_par` function also creates figures and saves data.

```
# Find out which MAs should receive models for SH
sh_stats <- ma_stats[["Shell Height"]][["MA_Ov_Stats"]] %>%
  filter(!is.na(SizeClass)) %>%
  select(ManagedAreaName, ParameterName, ShellType, SizeClass, HabitatType) %>%
  as.data.table()

task_list <- sh_stats[, .(HabitatType = unique(HabitatType)), by = ManagedAreaName]
task_list <- task_list[!(ManagedAreaName %in% c("Apalachicola Bay Aquatic Preserve",
                                                "Apalachicola National Estuarine Research Reserve") & Ha
# Add MA abbreviation
task_list[, ma_abrev := MA_All[.SD, on = "ManagedAreaName", Abbreviation]]
task_list <- as.data.frame(task_list)

# Function to subset data and run models where possible
shell_height_models_par <- function(ma, ma_abrev, habitat_type, oysterraw){
  library(future)
  library(future.apply)
  library(tidyverse)
  library(data.table)
```

```
library(ggplot2)
library(brms)
library(Rmisc)
library(rstan)
library(rstantools)
library(stringr)
library(sf)
library(tictoc)
library(rstudioapi)
library(ggpubr)

# Combined MA name with habitat type
ma_plotlabel <- paste0(ma, "_", str_to_title(habitat_type))
# At least 5 years of data are required in order to run model analyses
# Function checks N years of data, returns T or F
suff_years <- function(data){length(unique(data$Year))>=5}

if(ma_abrev %in% c("ABAP", "ANERR")){
  #Exclude the five samples that don't have counts less than the "NumberMeasured"
  #value for the corresponding program (see variable exploration graphs in the
  #25to75mm section for the rationale and graphs for this step.)
  numValves <- unique(oysterraw[, c("ProgramID", "RelYear", "counts",
                                    "QuadIdentifier", "Subtidal", "QuadSize_m2",
                                    "LiveDate_Qualifier", "NumberMeasured_n")])

  exclude_samps <- subset(numValves, numValves$NumberMeasured_n=="20" &
                            numValves$counts > 19)$QuadIdentifier

  sho25 <- oysterraw[!is.na(ShellHeight_mm) & ShellHeight_mm >= 25 &
                       MA_plotlab==ma_plotlabel & QuadIdentifier %in% setdiff(
                         oysterraw[!is.na(ShellHeight_mm) & ManagedAreaName==ma, QuadIdentifier], excl
} else {
  sho25 <- oysterraw[!is.na(ShellHeight_mm) & ShellHeight_mm >= 25 & MA_plotlab==ma_plotlabel, ]
}
# Save shell height data > 25mm
saveRDS(sho25, paste0("output/model_results/data/", ma_abrev, "_sho25_", Sys.Date(), "_", habitat_type

# Subset and save for shell height data >25 & <75
sh25to75 <- sho25[ShellHeight_mm < 75, ]
saveRDS(sh25to75, paste0("output/model_results/data/", ma_abrev, "_sh25to75_", Sys.Date(), "_", habita

# Subset for model data (where LiveDate_Qualifier is "Exact" NOT "Estimate")
sh25to75_mod_data <- subset(sh25to75, sh25to75$LiveDate_Qualifier!="Estimate")

if(suff_years(sh25to75_mod_data) & !QAQCPlots){
  cat("---- Sufficient years of data for SH 25mm to 75mm. Running model. \n")
  # Set formula to account for multiple quadsizes
  if(length(unique(sh25to75_mod_data$QuadSize_m2))>1){
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=25, ub=75) ~ RelYear + QuadSize_m2 + (1 | Univers
  } else {
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=25, ub=75) ~ RelYear + (1 | UniversalReefID))
  }
  # Failed convergence in PISAP due to low number of UniversalReefID, try simpler model
```

```
  if(ma_abrev=="PISAP"){
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=25, ub=75) ~ RelYear)
  }
  sh25to75_glmm <- brm(
    # formula=ShellHeight_mm | trunc(lb=25, ub=75) ~ RelYear+QuadSize_m2+(1 | UniversalReefID),
    formula = f,
    data=sh25to75_mod_data,
    family=gaussian, cores=ncores,
    control=list(adapt_delta=0.995, max_treedepth=20),
    iter=iter, warmup=warmup, chains=nchains, thin=3, seed=5699,
    backend="rstan",
    file=paste0("output/model_results/GLMMs/", ma_abrev, "_sh25to75_glmm_", habitat_type, ".rds")
  )
  models1 <- list(sh25to75_glmm)
} else {models1 <- NULL}

# Set variables for use within plots
data1 <- sh25to75

# Subset and save for shell height data >=75
sho75 <- sho25[ShellHeight_mm >= 75, ]
saveRDS(sho75, paste0("output/model_results/data/", ma_abrev, "_sho75_", Sys.Date(), "_", habitat_typ

# Subset for model data (where LiveDate_Qualifier is "Exact" NOT "Estimate")
sho75_mod_data <- subset(sho75, sho75$LiveDate_Qualifier!="Estimate")

if(suff_years(sho75_mod_data) & !QAQCPlots){
  cat("---- Sufficient years of data for SH over 75mm. Running model. \n")
  # Set formula to account for multiple quadsizes
  if(length(unique(sh25to75_mod_data$QuadSize_m2))>1){
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=75, ub=250) ~ RelYear + QuadSize_m2 + (1 | Unive
  } else {
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=75, ub=250) ~ RelYear + (1 | UniversalReefID))
  }
  # Failed convergence in PISAP due to low number of UniversalReefID, try simpler model
  if(ma_abrev=="PISAP"){
    f <- brms::brmsformula(ShellHeight_mm | trunc(lb=75, ub=250) ~ RelYear)
  }
  sho75_glmm <- brm(
    formula = f,
    data=sho75_mod_data,
    family=gaussian, cores=ncores,
    control= list(adapt_delta=0.995, max_treedepth=20),
    iter=iter, warmup=warmup, chains=nchains, thin=3, seed=3639,
    backend="rstan",
    file=paste0("output/model_results/GLMMs/", ma_abrev, "_sho75_glmm_", habitat_type, ".rds")
  )
  models2 <- list(sho75_glmm)
} else {models2 <- NULL}
# Set variables for use within plots
data2 <- sho75

#### modresultssh_par function ####
```

```
datafile1 <- data1
datafile2 <- data2
indicator <- "Size class"
meplotzoom <- FALSE

oysterresults_temp <- data.frame()
datafile1$SizeClass[datafile1$SizeClass=="25to75mm" &
                      datafile1$MA_plotlab==
                      "St. Martins Marsh Aquatic Preserve_Natural"] <-
  "35-75mm"
sizeclass1 <- unique(datafile1$SizeClass)
for(m in seq_along(models1)){
  modelobj <- models1[[m]]
  oyres_i <- setDT(broom.mixed::tidy(modelobj))
  #tidy() does not like that parameter values have underscores
  #for some reason, so the resulting table is incomplete

  if(nrow(oyres_i[effect=="fixed", ])-nrow(summary(modelobj)$fixed)==-1){
    missingrow <- data.table(effect="fixed",
                             component="cond",
                             #not sure what "cond" means in the tidy summary.
                             group=NA,
                             term=rownames(summary(modelobj)$fixed)[2],
                             estimate=summary(modelobj)$fixed$Estimate[2],
                             std.error=summary(modelobj)$fixed$Est.Error[2],
                             conf.low=summary(modelobj)$fixed$`l-95% CI`[2],
                             conf.high=summary(modelobj)$fixed$`u-95% CI`[2])
    oyres_i <- rbind(oyres_i, missingrow) %>% arrange(effect, group)
  }

  setDT(oyres_i)
  oyres_i[, `:=` (indicator=indicator,
                  managed_area=unique(datafile1$ManagedAreaName),
                  habitat_class=unique(datafile1$HabitatClassification),
                  size_class=sizeclass1,
                  live_date_qual=ifelse(
                    str_detect(
                      modelobj$file, "_hist"), "Estimate",
                    "Exact"),
                  n_programs=if(class(
                    try(datafile1$LiveDate_Qualifier))!="try-error"){
                    length(unique(
                      datafile1[LiveDate_Qualifier==
                                  ifelse(str_detect(
                                    modelobj$file, "_hist"),
                                    "Estimate", "Exact"),
                                ProgramID]))
                  } else{length(unique(datafile1[, ProgramID]))},
                  programs=if(class(try(
                    datafile1$LiveDate_Qualifier)) != "try-error"){
                    list(unique(
                      datafile1[LiveDate_Qualifier==
                                  ifelse(
```

```
                                    str_detect(
                                      modelobj$file,
                                      "_hist"),
                                    "Estimate",
                                    "Exact"),
                                  ProgramID]))
                  } else{list(unique(datafile1[, ProgramID]))},
                  filename=modelobj$file)]

  oysterresults_temp <- rbind(oysterresults_temp, oyres_i)
}

datafile2$SizeClass[datafile2$SizeClass=="25to75mm" &
                      datafile2$MA_plotlab==
                      "St. Martins Marsh Aquatic Preserve_Natural"] <- "35-75mm"
sizeclass2 <- unique(datafile2$SizeClass)

for(m in seq_along(models2)){
  modelobj <- models2[[m]]
  oyres_i <- setDT(broom.mixed::tidy(modelobj))
  #tidy() does not like that parameter values have underscores for
  #some reason, so the resulting table is incomplete

  if(nrow(oyres_i[effect=="fixed", ])-nrow(summary(modelobj)$fixed)==-1){
    missingrow <- data.table(effect="fixed",
                             component="cond",
                             #not sure what "cond" means in the tidy summary.
                             group=NA,
                             term=rownames(summary(modelobj)$fixed)[2],
                             estimate=summary(modelobj)$fixed$Estimate[2],
                             std.error=summary(modelobj)$fixed$Est.Error[2],
                             conf.low=summary(modelobj)$fixed$`l-95% CI`[2],
                             conf.high=summary(modelobj)$fixed$`u-95% CI`[2])
    oyres_i <- rbind(oyres_i, missingrow) %>% arrange(effect, group)
  }

  oyres_i <- oyres_i %>%
    mutate(
      indicator = indicator,
      managed_area = unique(datafile2$ManagedAreaName),
      habitat_class = unique(datafile2$HabitatClassification),
      size_class = sizeclass2,
      live_date_qual = if_else(
        str_detect(modelobj$file, "_hist"), "Estimate", "Exact"
      ),
      n_programs = if (class(try(datafile2$LiveDate_Qualifier)) != "try-error") {
        datafile2 %>%
          filter(LiveDate_Qualifier == if_else(str_detect(modelobj$file, "_hist"), "Estimate", "Exact
          pull(ProgramID) %>%
          unique() %>%
          length()
      } else {
        datafile2 %>%
```

```
            pull(ProgramID) %>%
            unique() %>%
            length()
        },
        programs = if (class(try(datafile2$LiveDate_Qualifier)) != "try-error") {
          list(datafile2 %>%
                 filter(LiveDate_Qualifier == if_else(str_detect(modelobj$file, "_hist"), "Estimate", "
                 pull(ProgramID) %>%
                 unique())
        } else {
          list(datafile2 %>% pull(ProgramID) %>% unique())
        },
        filename = modelobj$file
      )
    oysterresults_temp <- rbind(oysterresults_temp, oyres_i)
}

ind <- case_when(str_detect(indicator, "ercent") ~ "Pct",
                 str_detect(indicator, "ensity") ~ "Den",
                 str_detect(indicator, "^S|^s") ~ "SH")

if(nrow(data1)>0){
  sizeclass1 <- unique(data1$SizeClass)
} else {
  sizeclass1 <- ""
}
if(nrow(data2)>0){
  sizeclass2 <- unique(data2$SizeClass)
} else {
  sizeclass2 <- ""
}

# Set size labels
if(sizeclass1 != ""){
  size1 <- case_when(
    str_detect(sizeclass1, "25") & str_detect(sizeclass1, "75") ~ "25to75",
    str_detect(sizeclass1, "35") & str_detect(sizeclass1, "75") ~ "35to75",
    str_detect(sizeclass1, "25")==FALSE & str_detect(sizeclass1, "75") ~ "o75",
    TRUE ~ "raw")
  sizelab1 <- case_when(
    str_detect(sizeclass1, "25") & str_detect(sizeclass1, "75") ~ "25-75mm",
    str_detect(sizeclass1, "35") & str_detect(sizeclass1, "75") ~ "35-75mm",
    str_detect(sizeclass1, "25")==FALSE & str_detect(sizeclass1, "75") ~ "\u2265 75mm",
    TRUE ~ "raw")
}
if(sizeclass2 != ""){
  size2 <- case_when(
    str_detect(sizeclass2, "25") & str_detect(sizeclass2, "75") ~ "25to75",
    str_detect(sizeclass2, "35") & str_detect(sizeclass2, "75") ~ "35to75",
    str_detect(sizeclass2, "25")==FALSE & str_detect(sizeclass2, "75") ~ "o75",
    TRUE ~ "raw")
  sizelab2 <- case_when(
    str_detect(sizeclass2, "25") & str_detect(sizeclass2, "75") ~ "25-75mm",
```

```
    str_detect(sizeclass2, "35") & str_detect(sizeclass2, "75") ~ "35-75mm",
    str_detect(sizeclass2, "25")==FALSE & str_detect(sizeclass2, "75") ~ "\u2265 75mm",
    TRUE ~ "raw")
} else {
  size2 <- "o75"
  sizelab2 <- "\u2265 75mm"
}

#Marginal effects plot including random effects
## Hist plot settings
if(nrow(data2)>0){
  y_max <- round(max(data2[!is.na(ShellHeight_mm), ShellHeight_mm]), -0)+1
} else {
  y_max <- round(max(data1[!is.na(ShellHeight_mm), ShellHeight_mm]), -0)+1
}
y_breaks <- seq(25, 300, 50)
y_labs <- seq(25, 300, 50)
y_minor <- seq(0, 300, 25)
ylim_upper <- ceiling(y_max/25)*25

yrdiff1 <- unique(data1$YearDiff)
yrdiff2 <- unique(data2$YearDiff)

# function to set year breaks, type == "hist" or "live"
set_breaks <- function(type, data1, data2){
  ldq <- ifelse(type=="hist", "Estimate", "Exact")

  maxyr <- max(data1[!is.na(LiveDate) & LiveDate_Qualifier==ldq, LiveDate],
               data2[!is.na(LiveDate) & LiveDate_Qualifier==ldq, LiveDate])
  minyr <- min(data1[!is.na(LiveDate) & LiveDate_Qualifier==ldq, LiveDate],
               data2[!is.na(LiveDate) & LiveDate_Qualifier==ldq, LiveDate])
  nyrs <- maxyr - minyr + 1

  current_year <- as.integer(format(Sys.Date(), "%Y"))

  # Creates break intervals for plots based on number of years of data
  if(nyrs>=40){
    # Set breaks to every 10 years if more than 40 years of data
    brk <- 10
  } else if(nyrs>=20){
    # Set breaks to every 5 years if between 40 and 20 years of data
    brk <- 5
  } else if(nyrs>=12){
    # Set breaks to every 3 years if between 20 and 12 years of data
    brk <- 3
  } else if(nyrs>=8){
    # Set breaks to every 2 years if between 12 and 8 years of data
    brk <- 2
  } else if(nyrs>=5){
    # Set breaks to every year if between 8 and 5 years of data
    brk <- 1
  } else {
    # Ensure 5 years are included on axis
```

```
    total_ticks <- 5
    extra_years <- total_ticks - nyrs
    # Always add 1 year before the first year
    years_before <- min(1, extra_years)
    years_after <- extra_years - years_before
    # Adjust min and max year, without going beyond current year
    minyr <- minyr - years_before
    maxyr <- min(maxyr + years_after, current_year)
    # Re-check if we have enough years (in case maxyr hit current year)
    minyr <- max(minyr, maxyr - (total_ticks - 1))
    brk <- 1
  }
  return(list("seq" = seq(minyr,maxyr,brk),"maxyr" = maxyr, "minyr" = minyr))
}

## Check data for Exact and Estimate
n_hist1 <- nrow(data1[data1$LiveDate_Qualifier=="Estimate" &
                        !is.na(data1$ShellHeight_mm),])
n_live1 <- nrow(data1[data1$LiveDate_Qualifier=="Exact" &
                        !is.na(data1$ShellHeight_mm),])
n_hist2 <- nrow(data2[data2$LiveDate_Qualifier=="Estimate" &
                        !is.na(data2$ShellHeight_mm),])
n_live2 <- nrow(data2[data2$LiveDate_Qualifier=="Exact" &
                        !is.na(data2$ShellHeight_mm),])

# Plot variable to record which plots to show (dead, live, or both)
available_plots <- c()
# If "Estimate" data exists, set y-axis (years)
if(n_hist1>0 | n_hist2>0){
  yrlist_hist <- set_breaks(type = "hist", data1 = data1, data2 = data2)[["seq"]]
  maxyr_hist <- set_breaks(type = "hist", data1 = data1, data2 = data2)[["maxyr"]]
  minyr_hist <- set_breaks(type = "hist", data1 = data1, data2 = data2)[["minyr"]]
  available_plots <- c(available_plots, "dead")
}
# If "Exact" data exists, set y-axis (years)
if(n_live1>0 | n_live2>0){
  yrlist_live <- set_breaks(type = "live", data1 = data1, data2 = data2)[["seq"]]
  maxyr_live <- set_breaks(type = "live", data1 = data1, data2 = data2)[["maxyr"]]
  minyr_live <- set_breaks(type = "live", data1 = data1, data2 = data2)[["minyr"]]
  available_plots <- c(available_plots, "live")
}

set.seed(987)
if(!is.null(models1) & !QAQCPlots){
  liveplot_1 <- plot(conditional_effects(models1[[1]], re_formula=NULL), plot=FALSE)
}

if(!is.null(models2) & !QAQCPlots){
  liveplot_2 <- plot(conditional_effects(models2[[1]], re_formula=NULL), plot=FALSE)
}

# Set boolean values for whether liveplot1&2 are available
liveplot1_avail <- class(try(liveplot_1, silent=TRUE)) != "try-error"
```

```
liveplot2_avail <- class(try(liveplot_2, silent=TRUE)) != "try-error"

# Set ribbon transparency value
a_ribb <- 0.2
# Set size and shapes for plots
p_shape <- c("size2"=24, "size1"=21)
sizelab <- c("size2"=sizelab2, "size1"=sizelab1)

col1 <- NA
col2 <- NA

# "transparent" allows for dummy values to be plotted. Ensures proper legend display
if(liveplot1_avail){
  col1 <- c(size1="#00374f")
} else{
  col1 <- c(size1="transparent")
}

if(liveplot2_avail){
  col2 <- c(size2="#0094b0")
} else{
  col2 <- c(size2="transparent")
}

p_color <- c(col2, col1)

# Initial plots to set legends
plot_leg <- ggplot() +
  {if(liveplot1_avail){
    list(geom_ribbon(data=liveplot_1$RelYear$data,
                     aes(x=RelYear+yrdiff1, y=ShellHeight_mm,
                         ymin=lower__, ymax=upper__,
                         fill="size1"),
                     alpha=a_ribb,
                     show.legend = TRUE),
         geom_line(data=liveplot_1$RelYear$data,
                   aes(x=RelYear+yrdiff1, y=estimate__,
                       color="size1"),
                   lwd=0.75,
                   show.legend = TRUE),
         # Dummy values
         geom_ribbon(data=liveplot_1$RelYear$data,
                     aes(x=RelYear+yrdiff1, y=ShellHeight_mm,
                         ymin=lower__, ymax=upper__,
                         fill="size2"),
                     alpha=a_ribb,
                     show.legend = TRUE),
         geom_line(data=liveplot_1$RelYear$data,
                   aes(x=RelYear+yrdiff1, y=estimate__,
                       color="size2"),
                   lwd=0.75,
                   show.legend = TRUE))
  }} +
```

```
  {if(liveplot2_avail){
    list(geom_ribbon(data=liveplot_2$RelYear$data,
                     aes(x=RelYear+yrdiff2, y=ShellHeight_mm,
                         ymin=lower__, ymax=upper__,
                         fill="size2"),
                     alpha=a_ribb,
                     show.legend = TRUE),
         geom_line(data=liveplot_2$RelYear$data,
                   aes(x=RelYear+yrdiff2, y=estimate__,
                       color="size2"),
                   lwd=0.75,
                   show.legend = TRUE),
         # Dummy values
         geom_ribbon(data=liveplot_2$RelYear$data,
                     aes(x=RelYear+yrdiff2, y=ShellHeight_mm,
                         ymin=lower__, ymax=upper__,
                         fill="size1"),
                     alpha=a_ribb,
                     show.legend = TRUE),
         geom_line(data=liveplot_2$RelYear$data,
                   aes(x=RelYear+yrdiff2, y=estimate__,
                       color="size1"),
                   lwd=0.75,
                   show.legend = TRUE))
  }} +
  # Dummy points
  geom_point(data=data1[!is.na(RelYear) & !is.na(LiveDate), ],
             aes(x=LiveDate, y=ShellHeight_mm, shape="size2"),
             position=plot_jitter, size=2, color="transparent", fill = "transparent",
             alpha=0.8, show.legend = TRUE) +
  geom_point(data=data1[!is.na(RelYear) & !is.na(LiveDate), ],
             aes(x=LiveDate, y=ShellHeight_mm, shape="size1"),
             position=plot_jitter, size=2, color="#333333", fill = "#cccccc",
             alpha=0.8, show.legend = TRUE) +
  # Dummy points
  geom_point(data=data2[!is.na(RelYear) & !is.na(LiveDate), ],
             aes(x=LiveDate, y=ShellHeight_mm, shape="size1"),
             position=plot_jitter, size=2, color="transparent", fill = "transparent",
             alpha=0.8, show.legend = TRUE) +
  geom_point(data=data2[!is.na(RelYear) & !is.na(LiveDate), ],
             aes(x=LiveDate, y=ShellHeight_mm, shape="size2"),
             position=plot_jitter, size=2, color="#333333", fill = "#cccccc",
             alpha=0.8, show.legend = TRUE) +
  plot_theme +
  theme(legend.position="right") +
  scale_shape_manual(name="Size class",
                     breaks = c("size2", "size1"),
                     values=p_shape,
                     labels=sizelab) +
  scale_color_manual(name="Size class",
                     breaks = c("size2", "size1"),
                     values=p_color,
                     labels=sizelab,
```

```
                      aesthetics = c("color", "fill"))

leg <- get_legend(plot_leg)
rm(plot_leg)

# Dead oyster shell plot
if("dead" %in% available_plots){
  plot1 <- ggplot() +
    geom_hline(yintercept=75, linewidth=1, color="grey") +
    {if(n_hist1>0){
      geom_point(data=data1[!is.na(RelYear) &
                              !is.na(LiveDate) &
                              LiveDate_Qualifier=="Estimate", ],
                 aes(x=LiveDate, y=ShellHeight_mm, shape="size1"),
                 position=plot_jitter, size=2, color="#333333", fill="#cccccc",
                 alpha=0.8, inherit.aes=FALSE)
    }} +
    {if(n_hist2>0){
      geom_point(data=data2[!is.na(RelYear) & !is.na(LiveDate) &
                              LiveDate_Qualifier=="Estimate", ],
                 aes(x=LiveDate, y=ShellHeight_mm, shape="size2"),
                 position=plot_jitter, size=2, color="#333333", fill="#cccccc",
                 alpha=0.8, inherit.aes=FALSE)
    }} +
    scale_x_continuous(limits=c(minyr_hist-0.25, maxyr_hist+0.25),
                       breaks=yrlist_hist) +
    scale_y_continuous(breaks=y_breaks,
                       labels=y_labs, minor_breaks=y_minor) +
    plot_theme +
    theme(plot.subtitle=element_text(hjust=0, size=10, color="#314963"),
          legend.position="none") +
    labs(subtitle="Dead Oyster Shells",
         x="Estimated year",
         y="Shell height (mm)") +
    scale_shape_manual(name="Shell heights",
                       values=c("size1"=21, "size2"=24),
                       labels=c(sizelab1, sizelab2)) +
    scale_color_manual(name="Shell heights",
                       values=c("size1"="#00374f", "size2"="#0094b0"),
                       labels=c(sizelab1, sizelab2)) +
    scale_fill_manual(name="Shell heights",
                      values=c("size1"="#00374f", "size2"="#0094b0"),
                      labels=c(sizelab1, sizelab2)) +
    coord_cartesian(ylim=c(25, ylim_upper))
}

# Live oyster shell plot
if("live" %in% available_plots){
  plot2 <- ggplot() +
    geom_hline(yintercept=75, size=1, color="grey") +
    {if(n_live1>0){
      geom_point(data=data1[!is.na(RelYear) & !is.na(LiveDate) &
                              LiveDate_Qualifier=="Exact", ],
```

```
                  aes(x=LiveDate, y=ShellHeight_mm, shape="size1"),
                  position=plot_jitter, size=2, color="#333333", fill="#cccccc",
                  alpha=0.8, inherit.aes=FALSE)
    }} +
    {if(n_live2>0){
      geom_point(data=data2[!is.na(RelYear) & !is.na(LiveDate) &
                              LiveDate_Qualifier=="Exact", ],
                  aes(x=LiveDate, y=ShellHeight_mm, shape="size2"),
                  position=plot_jitter, size=2, color="#333333", fill="#cccccc",
                  alpha=0.8, inherit.aes=FALSE)
    }} +
    {if(liveplot1_avail){
      list(geom_ribbon(data=liveplot_1$RelYear$data,
                       aes(x=RelYear+yrdiff1, y=ShellHeight_mm,
                           ymin=lower__, ymax=upper__, fill="size1"),
                       alpha=a_ribb),
           geom_line(data=liveplot_1$RelYear$data,
                     aes(x=RelYear+yrdiff1, y=estimate__, color="size1"),
                     lwd=0.75))
    }} +
    {if(liveplot2_avail){
      list(geom_ribbon(data=liveplot_2$RelYear$data,
                       aes(x=RelYear+yrdiff2, y=ShellHeight_mm,
                           ymin=lower__, ymax=upper__, fill="size2"),
                       alpha=a_ribb),
           geom_line(data=liveplot_2$RelYear$data,
                     aes(x=RelYear+yrdiff2, y=estimate__, color="size2"),
                     lwd=0.75))
    }} +
    scale_x_continuous(limits=c(minyr_live-0.25, maxyr_live+0.25),
                       breaks=yrlist_live) +
    scale_y_continuous(breaks=y_breaks,
                       labels=y_labs, minor_breaks=y_minor) +
    plot_theme +
    theme(plot.subtitle=element_text(hjust=0, size=10, color="#314963"),
          legend.position="none") +
    labs(subtitle="Live Oysters",
         x="Year",
         y="Shell height (mm)") +
    scale_shape_manual(name="Shell heights",
                       values=c("size1"=21, "size2"=24),
                       labels=c(sizelab1, sizelab2)) +
    scale_color_manual(name="Shell heights",
                       values=c("size1"="#00374f", "size2"="#0094b0"),
                       labels=c(sizelab1, sizelab2)) +
    scale_fill_manual(name="Shell heights",
                      values=c("size1"="#00374f", "size2"="#0094b0"),
                      labels=c(sizelab1, sizelab2)) +
    coord_cartesian(ylim=c(25, ylim_upper))
}

# Set plot title
plot_title <- ggplot() +
```

```
    labs(title=paste0("Oyster Size Class (", habitat_type, ")"), subtitle=ma) +
    plot_theme +
    theme(plot.subtitle=element_text(hjust=0.5, size=10, color="#314963"),
          panel.border=element_blank(),
          panel.grid.major=element_blank(),
          panel.grid.minor=element_blank(), axis.line=element_blank())

  if("live" %in% available_plots & "dead" %in% available_plots){
    # Remove y-axis labels, ticks, title before combining both plots
    plot2 <- plot2 +
      theme(legend.position="none",
            axis.text.y=element_blank(),  #remove y-axis labels
            axis.ticks.y=element_blank(),  #remove y-axis ticks
            axis.title.y=element_blank())   #removes y-axis title
    # Combine live and dead plots + legend
    plot_comb <- ggarrange(plot1, plot2, leg, nrow=1,
                           widths=c(0.46, 0.39, 0.15))
  } else if("live" %in% available_plots & !"dead" %in% available_plots){
    # Combine live plots with legend
    plot_comb <- ggarrange(plot2, leg, nrow=1,
                           widths=c(0.85, 0.15))
  } else if("dead" %in% available_plots & !"live" %in% available_plots){
    # Combine dead plots with legend
    plot_comb <- ggarrange(plot1, leg, nrow=1,
                           widths=c(0.85, 0.15))
  }

  plot_comb <- ggarrange(plot_title, plot_comb, ncol=1,
                         heights=c(0.125, 0.875))

  # Specify save location (QAQC Plots saved elsewhere)
  if(QAQCPlots){
    file_name <- paste0("output/QAQC/Oyster_SH_GLMM_", ma_abrev, "_", habitat_type, ".png")
  } else {
    file_name <- paste0("output/Shell_Height/Figures/Oyster_SH_GLMM_", ma_abrev, "_", habitat_type, ".p
  }

  ggsave(file_name,
         plot_comb,
         width=8,
         height=4,
         units="in",
         dpi=200,
         bg="white")

  return(oysterresults_temp)

  cat("---- Shell Height plot created for", ma, "-", habitat_type, "\n")
}

split_tasks <- split(task_list, ceiling(seq_along(1:nrow(task_list)) / 4))
oyster_sh <- oysterraw %>% filter(!is.na(ShellHeight_mm))
# Subset and save temp .rds objects for each MA (breaks up oysterraw)
```

```
for(ma in unique(oyster_sh$ManagedAreaName)){
  saveRDS(oyster_sh[oyster_sh$ManagedAreaName == ma, ],
          file = paste0("output/tmp/oystersh_", make.names(ma), ".rds"))
}

results_all <- list()
for(b in seq_along(split_tasks)){
  batch <- split_tasks[[b]]

  results_list <- future_lapply(seq_len(nrow(batch)), function(i) {
    task <- batch[i, ]
    oysterraw_path <- paste0("output/tmp/oystersh_", make.names(task$ManagedAreaName), ".rds")
    oysterraw_sub <- readRDS(oysterraw_path)
    cat("-- Analyzing ", task$ManagedAreaName, "\n")
    shell_height_models_par(
      ma = task$ManagedAreaName,
      ma_abrev = task$ma_abrev,
      habitat_type = task$HabitatType,
      oysterraw = oysterraw_sub
    )
  }, future.seed = TRUE)
  results_all[[b]] <- data.table::rbindlist(results_list, fill = TRUE)
  gc()
}

oysterresults_sh <- data.table::rbindlist(results_all, fill = TRUE)
fwrite(oysterresults_sh, "output/oyresults/oysterresults_sh.csv")
```

Density Analysis

Subsets data for that which is related to density. The data is further subset for each managed area. Appropriate GLMMs are called from file for each shell size class, or are created if they don't exist. `density_models_par` function also creates figures and saves data.

```
oysterraw$YearDiff <- oysterraw$LiveDate-oysterraw$RelYear
# #Make a collapsed version of the oysterraw table for density
oysterraw_den <- oysterraw[, c("ProgramID", "ProgramName", "LocationID",
                               "ProgramLocationID", "QuadIdentifier",
                               "ReefIdentifier", "LiveDate",
                               "LiveDate_Qualifier", "SampleDate", "Year",
                               "Month", "ManagedAreaName", "Region",
                               "SurveyMethod", "HabitatClassification",
                               "QuadSize_m2", "MADup", "Density_m2",
                               "Number_of_Oysters_Counted_Total_Count",
                               "Number_of_Oysters_Counted_Live_Count",
                               "Number_of_Oysters_Counted_Dead_Count",
                               "ObsIndex", "UniversalReefID",
                               "MA_plotlab", "Subtidal", "RelYear", "YearDiff")]
oysterraw_den[!is.na(Density_m2), DensIndex := ObsIndex]
oysterraw_den[!is.na(Number_of_Oysters_Counted_Total_Count), NTotIndex := ObsIndex]
oysterraw_den[!is.na(Number_of_Oysters_Counted_Live_Count), NLiveIndex := ObsIndex]
oysterraw_den[!is.na(Number_of_Oysters_Counted_Dead_Count), NDeadIndex := ObsIndex]
oysterraw_den[, ObsIndex := NULL]
```

```
oysterraw_den <- unique(oysterraw_den)
oysterraw_den <- oysterraw_den %>%
  dplyr::group_by(ProgramID, ProgramName, LocationID, ProgramLocationID,
                  QuadIdentifier, ReefIdentifier, LiveDate,
                  LiveDate_Qualifier, SampleDate, Year, Month,
                  ManagedAreaName, Region, SurveyMethod,
                  HabitatClassification, QuadSize_m2, MADup, UniversalReefID,
                  MA_plotlab, Subtidal) %>%
  tidyr::fill(Density_m2, Number_of_Oysters_Counted_Total_Count,
              Number_of_Oysters_Counted_Live_Count,
              Number_of_Oysters_Counted_Dead_Count,
              DensIndex, NTotIndex, NLiveIndex, NDeadIndex) %>%
  tidyr::fill(Density_m2, Number_of_Oysters_Counted_Total_Count,
              Number_of_Oysters_Counted_Live_Count,
              Number_of_Oysters_Counted_Dead_Count,
              DensIndex, NTotIndex, NLiveIndex, NDeadIndex,
              .direction='up') %>%
  dplyr::distinct()

oysterraw_den <- subset(oysterraw_den, !is.na(oysterraw_den$Density_m2) |
                          !is.na(oysterraw_den$Number_of_Oysters_Counted_Total_Count) |
                          !is.na(oysterraw_den$Number_of_Oysters_Counted_Live_Count) |
                          !is.na(oysterraw_den$Number_of_Oysters_Counted_Dead_Count) |
                          !is.na(oysterraw_den$DensIndex) |
                          !is.na(oysterraw_den$NTotIndex) |
                          !is.na(oysterraw_den$NLiveIndex) |
                          !is.na(oysterraw_den$NDeadIndex))
setDT(oysterraw_den)

#Remove NAs in Density_m2 column
oysterraw_den <- subset(oysterraw_den, !is.na(oysterraw_den$Density_m2))

#Summarize density data by managed area
den_all_sum <- summarySE(oysterraw_den, measurevar='Density_m2',
                         groupvars=c('ManagedAreaName', 'Year'))

# Find out which MAs should receive models for Density
den_stats <- ma_stats[["Density"]][["MA_Ov_Stats"]] %>%
  select(ManagedAreaName, ParameterName, HabitatType) %>%
  as.data.table()

task_list <- den_stats[, .(HabitatType = unique(HabitatType)), by = ManagedAreaName]
# Add MA abbreviation
task_list[, ma_abrev := MA_All[.SD, on = "ManagedAreaName", Abbreviation]]
task_list <- as.data.frame(task_list)

# Density modelling function
density_models_par <- function(ma, ma_abrev, habitat_type, oysterraw_den){
  library(future)
  library(future.apply)
  library(tidyverse)
  library(data.table)
  library(ggplot2)
```

```
library(brms)
library(Rmisc)
library(rstan)
library(rstantools)
library(stringr)
library(sf)
library(tictoc)
library(rstudioapi)
library(ggpubr)
cat("----", paste0("Habitat type: ", habitat_type, "\n"))
# Combined MA name with habitat type
ma_plotlabel <- paste0(ma, "_", str_to_title(habitat_type))
# At least 5 years of data are required in order to run model analyses
# Function checks N years of data, returns T or F
suff_years <- function(data){length(unique(data$Year))>=5}
# Create subset for each MA
ma_subset <- subset(oysterraw_den, oysterraw_den$MA_plotlab==ma_plotlabel)
# Ensure Density_m2 is numberic & rounded
ma_subset[, Density_m2 := as.integer(round(Density_m2))]
# Save data used in model
saveRDS(ma_subset, paste0("output/model_results/data/", ma_abrev, "_density_", Sys.Date(), "_", habita

if(suff_years(ma_subset) & !QAQCPlots){
  cat("---- Sufficient years of data for Density. Running model. \n")
  # Determine model family
  # When to use negbinomial or zero-inflated-negbinomial
  # If zeroes make up >30% of dataset, use zero-inflated
  if(mean(ma_subset$Density_m2 == 0)>0.3){
    fam <- zero_inflated_negbinomial()
  } else {
    fam <- negbinomial()
  }
  # Determine formula (if to add subtidal or quadsize factor)
  # If more than 1 values for either Subtidal or QuadSize_m2, include as fixed effect
  num_subtidals <- length(unique(ma_subset$Subtidal))
  num_quads <- length(unique(ma_subset$QuadSize_m2))
  if(num_subtidals>1 & num_quads>1){
    f <- brms::brmsformula(Density_m2 ~ RelYear + Subtidal + QuadSize_m2 + (1 + RelYear | UniversalRe
  } else if(num_subtidals>1 & !num_quads>1) {
    f <- brms::brmsformula(Density_m2 ~ RelYear + Subtidal + (1 + RelYear | UniversalReefID))
  } else if(!num_subtidals>1 & num_quads>1){
    f <- brms::brmsformula(Density_m2 ~ RelYear + QuadSize_m2 + (1 + RelYear | UniversalReefID))
  } else {
    f <- brms::brmsformula(Density_m2 ~ RelYear + (1 + RelYear | UniversalReefID))
  }
  if(ma_abrev=="PISAP"){
    f <- Density_m2 ~ RelYear + (0 + RelYear | UniversalReefID)
  }
  if(ma_abrev=="ANERR" & habitat_type=="Natural"){
    f <- Density_m2 ~ RelYear + Subtidal + QuadSize_m2 + (0 + RelYear | UniversalReefID)
  }

  cat("------ Using Formula: ", paste(f[1]), "\n")
```

```
  cat("------ Using Family: ", paste(fam[1]), "\n")

  den_glmm <- brm(formula=f, data=ma_subset,
                  family=fam, cores=ncores,
                  control= list(adapt_delta=0.995, max_treedepth=20),
                  iter=iter, warmup=warmup, chains=nchains,
                  init=0, thin=3, seed=sample.int(.Machine$integer.max, 1),
                  backend="rstan",
                  file=paste0("output/model_results/GLMMs/", ma_abrev, "_den_glmm9_", habitat_type, "
} else {
  den_glmm <- NA
}

# Create model results tables and save diagnostic plots and marginal effects plots
datafile <- ma_subset
models <- list(den_glmm)
indicator <- "Density"
meplotzoom <- FALSE
oysterresults_temp <- data.frame()
if(class(den_glmm)=="brmsfit"){
  for(m in seq_along(models)){
    modelobj <- models[[m]]
    sizeclass <- ifelse(str_detect(modelobj$file, "25to75|seed"),
                        "25-75mm",
                        ifelse(str_detect(modelobj$file, "35to75|seed"),
                               "35-75mm",
                               ifelse(str_detect(modelobj$file,
                                                 "o75|market"),
                                      ">75mm", "NA")))
    oyres_i <- setDT(broom.mixed::tidy(modelobj))
    #tidy() does not like that parameter values have underscores for
    #some reason, so the resulting table is incomplete

    if(nrow(oyres_i[effect=="fixed", ])-nrow(summary(modelobj)$fixed)==-1){
      missingrow <- data.table(effect="fixed",
                               component="cond",
                               #not sure what "cond" means in the tidy summary.
                               group=NA,
                               term=rownames(summary(modelobj)$fixed)[2],
                               estimate=summary(modelobj)$fixed$Estimate[2],
                               std.error=summary(modelobj)$fixed$Est.Error[2],
                               conf.low=summary(modelobj)$fixed$`l-95% CI`[2],
                               conf.high=summary(modelobj)$fixed$`u-95% CI`[2])
      oyres_i <- rbind(oyres_i, missingrow) %>% arrange(effect, group)
    }

    oyres_i[, `:=` (indicator=indicator,
                    managed_area=unique(datafile$ManagedAreaName),
                    habitat_class=unique(datafile$HabitatClassification),
                    size_class=sizeclass,
                    live_date_qual=ifelse(
                      str_detect(modelobj$file, "_hist"),
                      "Estimate", "Exact"),
```

```
                    n_programs=if(
                      class(try(datafile$LiveDate_Qualifier)) !=
                      "try-error"){
                      length(
                        unique(
                          datafile[LiveDate_Qualifier==
                                     ifelse(
                                       str_detect(
                                         modelobj$file,
                                         "_hist"),
                                       "Estimate",
                                       "Exact"),
                                   ProgramID]))
                    } else{length(unique(datafile[, ProgramID]))},
                    programs=if(class(try(
                      datafile$LiveDate_Qualifier)) != "try-error"){
                      list(unique(datafile[LiveDate_Qualifier==
                                             ifelse(
                                               str_detect(
                                                 modelobj$file,
                                                 "_hist"),
                                               "Estimate",
                                               "Exact"),
                                           ProgramID]))
                    } else{list(unique(datafile[, ProgramID]))},
                    filename=modelobj$file)]
    oysterresults_temp <- rbind(oysterresults_temp, oyres_i)
  }
} else {
  sizeclass <- ""
}

data <- datafile

ind <- case_when(str_detect(indicator, "ercent") ~ "Pct",
                 str_detect(indicator, "ensity") ~ "Den",
                 str_detect(indicator, "^S|^s") ~ "SH")

if(sizeclass != ""){
  size <- case_when(str_detect(sizeclass, "25") &
                      str_detect(sizeclass, "75") ~ "25to75",
                    str_detect(sizeclass, "35") &
                      str_detect(sizeclass, "75") ~ "35to75",
                    str_detect(sizeclass, "25")==FALSE &
                      str_detect(sizeclass, "75") ~ "o75", TRUE ~ "raw")
  sizelab <- case_when(str_detect(sizeclass, "25") &
                         str_detect(sizeclass, "75") ~ "25-75mm",
                       str_detect(sizeclass, "35") &
                         str_detect(sizeclass, "75") ~ "35-75mm",
                       str_detect(sizeclass, "25")==FALSE &
                         str_detect(sizeclass, "75") ~ "\u2265 75mm",
                       TRUE ~ "raw")
}
```

```r
if(ind=="Den"){
  nyrs <- max(data$LiveDate)-min(data$LiveDate)+1
  maxyr <- max(data$LiveDate)
  minyr <- min(data$LiveDate)
  yrdiff <- unique(data$YearDiff)
  current_year <- as.integer(format(Sys.Date(), "%Y"))
  # Creates break intervals for plots based on number of years of data
  # Creates break intervals for plots based on number of years of data
  if(nyrs>=40){
    # Set breaks to every 10 years if more than 40 years of data
    brk <- 10
  } else if(nyrs>=20){
    # Set breaks to every 5 years if between 40 and 20 years of data
    brk <- 5
  } else if(nyrs>=12){
    # Set breaks to every 3 years if between 20 and 12 years of data
    brk <- 3
  } else if(nyrs>=8){
    # Set breaks to every 2 years if between 12 and 8 years of data
    brk <- 2
  } else if(nyrs>=5){
    # Set breaks to every year if between 8 and 5 years of data
    brk <- 1
  } else {
    # Ensure 5 years are included on axis
    total_ticks <- 5
    extra_years <- total_ticks - nyrs
    # Always add 1 year before the first year
    years_before <- min(1, extra_years)
    years_after <- extra_years - years_before
    # Adjust min and max year, without going beyond current year
    minyr <- minyr - years_before
    maxyr <- min(maxyr + years_after, current_year)
    # Re-check if we have enough years (in case maxyr hit current year)
    minyr <- max(minyr, maxyr - (total_ticks - 1))
    brk <- 1
  }
  yrlist <- seq(minyr,maxyr,brk)

  if(class(den_glmm)=="brmsfit"){
    denplots <- plot(conditional_effects(models[[1]], re_formula=NULL), plot=FALSE)
  }

  plot1 <- ggplot() +
    {if("meanDen_int" %in% colnames(data)){
      geom_point(data=data, aes(x=LiveDate,
                                y=meanDen_int), position=plot_jitter,
                 shape=21, size=2, color="#333333", fill="#cccccc",
                 alpha=0.8, inherit.aes=FALSE)
    } else{
      geom_point(data=data, aes(x=LiveDate,
                                y=Density_m2), position=plot_jitter,
                 shape=21, size=2, color="#333333", fill="#cccccc",
```

```
                    alpha=0.8, inherit.aes=FALSE)
      }} +
      {if(class(den_glmm)=="brmsfit"){
        list(geom_ribbon(data=denplots$RelYear$data,
                         aes(x=RelYear+yrdiff, y=Density_m2,
                             ymin=lower__, ymax=upper__),
                         fill="#000099", alpha=0.1, inherit.aes=FALSE),
             geom_line(data=denplots$RelYear$data,
                       aes(x=RelYear+yrdiff,
                           y=estimate__),
                       color="#000099", lwd=0.75, inherit.aes=FALSE))
      }} +
      scale_x_continuous(limits=c(minyr-0.25, maxyr+0.25),
                         breaks=yrlist) +
      scale_y_continuous(breaks = scales::pretty_breaks(n = 6)) +
      plot_theme +
      {if("meanDen_int" %in% colnames(data)){
        labs(title=paste0("Oyster Density (", habitat_type, ")"),
             subtitle=ma,
             x="Year",
             y=bquote('Estimated density ('*~m^{-2}*')'))
      }else{
        labs(title=paste0("Oyster Density (", habitat_type, ")"),
             subtitle=ma,
             x="Year",
             y=bquote('Density ('*~m^{-2}*')'))
      }}

    ma_short <- MA_All[ManagedAreaName==ma, Abbreviation]

    # Specify save location (QAQC Plots saved elsewhere)
    if(QAQCPlots){
      file_name <- paste0("output/QAQC/Oyster_Dens_GLMM_", ma_short, "_", habitat_type,
                          ifelse(sizeclass != "", paste0("_",size), "_raw"), ".png")
    } else {
      file_name <- paste0("output/Density/Figures/Oyster_Dens_GLMM_", ma_short, "_", habitat_type,
                          ifelse(sizeclass != "", paste0("_",size), "_raw"), ".png")
    }

    ggsave(file_name,
           plot1,
           width=8,
           height=4,
           units="in",
           dpi=200)
  }

  cat("---- Density plot created for", ma, "-", habitat_type, "\n")
  return(oysterresults_temp)
}

split_tasks <- split(task_list, ceiling(seq_along(1:nrow(task_list)) / 4))
oyster_den <- oysterraw %>% filter(!is.na(Density_m2))
```

```
# Subset and save temp .rds objects for each MA (breaks up oysterraw)
for(ma in unique(oyster_den$ManagedAreaName)){
  saveRDS(oyster_den[oyster_den$ManagedAreaName == ma, ],
          file = paste0("output/tmp/oysterden_", make.names(ma), ".rds"))
}

results_all <- list()
for(b in seq_along(split_tasks)){
  batch <- split_tasks[[b]]
  results_list <- future_lapply(seq_len(nrow(batch)), function(i) {
    task <- batch[i, ]
    oysterraw_path <- paste0("output/tmp/oysterden_", make.names(task$ManagedAreaName), ".rds")
    oysterraw_sub <- readRDS(oysterraw_path)

    cat(paste0("Now starting ", task$ManagedAreaName, "\n"))

    density_models_par(
      ma = task$ManagedAreaName,
      ma_abrev = task$ma_abrev,
      habitat_type = task$HabitatType,
      oysterraw_den = oysterraw_sub
    )

  }, future.seed = TRUE)
  results_all[[b]] <- data.table::rbindlist(results_list, fill = TRUE)
  gc()
}

oysterresults_den <- data.table::rbindlist(results_all, fill = TRUE)
fwrite(oysterresults_den, "output/oyresults/oysterresults_den.csv")
```

Percent Live Analysis

Subsets data for that which is related to percent live. The data is further subset for each managed area. Appropriate GLMMs are called from file for each shell size class, or are created if they don't exist. `pctlive_models_par` function also creates figures and save data.

```
#Make a collapsed version of the oysterraw table for percent live
oysterraw_pct <- oysterraw[, c("ProgramID", "ProgramName", "ProgramLocationID",
                               "QuadIdentifier", "ReefIdentifier", "LiveDate",
                               "LiveDate_Qualifier", "SampleDate", "Year",
                               "Month", "ManagedAreaName", "Region",
                               "SurveyMethod", "PercentLiveMethod",
                               "HabitatClassification", "QuadSize_m2", "MADup",
                               "PercentLive_pct",
                               "Number_of_Oysters_Counted_Total_Count",
                               "Number_of_Oysters_Counted_Live_Count",
                               "Number_of_Oysters_Counted_Dead_Count",
                               "ObsIndex", "UniversalReefID",
                               "MA_plotlab", "Subtidal", "RelYear", "YearDiff")]
oysterraw_pct[!is.na(PercentLive_pct), PctIndex := ObsIndex]
oysterraw_pct[!is.na(Number_of_Oysters_Counted_Total_Count),
              NTotIndex := ObsIndex]
```

```
oysterraw_pct[!is.na(Number_of_Oysters_Counted_Live_Count),
              NLiveIndex := ObsIndex]
oysterraw_pct[!is.na(Number_of_Oysters_Counted_Dead_Count),
              NDeadIndex := ObsIndex]
oysterraw_pct[, ObsIndex := NULL]

oysterraw_pct <- unique(oysterraw_pct)
oysterraw_pct <- oysterraw_pct %>%
  dplyr::group_by(ProgramID, ProgramName, ProgramLocationID, QuadIdentifier,
                  ReefIdentifier, LiveDate, LiveDate_Qualifier, SampleDate,
                  Year, Month, ManagedAreaName, Region, SurveyMethod,
                  PercentLiveMethod, HabitatClassification, QuadSize_m2,
                  MADup, UniversalReefID, MA_plotlab, Subtidal,
                  RelYear) %>%
  tidyr::fill(PercentLive_pct, Number_of_Oysters_Counted_Total_Count,
              Number_of_Oysters_Counted_Live_Count,
              Number_of_Oysters_Counted_Dead_Count,
              PctIndex, NTotIndex, NLiveIndex, NDeadIndex) %>%
  tidyr::fill(PercentLive_pct, Number_of_Oysters_Counted_Total_Count,
              Number_of_Oysters_Counted_Live_Count,
              Number_of_Oysters_Counted_Dead_Count,
              PctIndex, NTotIndex, NLiveIndex, NDeadIndex,
              .direction='up') %>%
  dplyr::distinct()

oysterraw_pct <- subset(oysterraw_pct, !is.na(oysterraw_pct$PercentLive_pct) |
                          !is.na(oysterraw_pct$Number_of_Oysters_Counted_Total_Count) |
                          !is.na(oysterraw_pct$Number_of_Oysters_Counted_Live_Count) |
                          !is.na(oysterraw_pct$Number_of_Oysters_Counted_Dead_Count) |
                          !is.na(oysterraw_pct$PctIndex) |
                          !is.na(oysterraw_pct$NTotIndex) |
                          !is.na(oysterraw_pct$NLiveIndex) |
                          !is.na(oysterraw_pct$NDeadIndex))
setDT(oysterraw_pct)

#Calculate PercentLive_pct values for some ProgramIDs where it is missing.
#Couldn't include at the start of the script because need to use the counts columns
#rather than the QuadSize_m2 column which is filled for the whole combined table.
oysterraw_pct[ProgramID==972 | ProgramID==4014 | ProgramID==4044,
              PercentLive_pct :=
                (Number_of_Oysters_Counted_Live_Count/
                   (Number_of_Oysters_Counted_Live_Count+
                      Number_of_Oysters_Counted_Dead_Count) * 100)]

#Filter NAs for PercentLive_pct (these are related to 1) programs that do
#counts to measure density, but do not estimate percent live and
#2) Programs that are listed as measuring percent live by a Point-intercept
#method, which cannot be calculated from counts.
oysterraw_pct <- oysterraw_pct[!is.na(PercentLive_pct), ]

#Add column of decimal versions of percent live values
oysterraw_pct[, PercentLive_dec := PercentLive_pct/100]
```

```r
#Summarize percent live values
pct_all_sum <- summarySE(oysterraw_pct, measurevar='PercentLive_pct',
                         groupvars=c('ManagedAreaName', 'Year', 'PercentLiveMethod'))

# Find out which MAs should receive models for Percent Live
pct_stats <- ma_stats[["Percent Live"]][["MA_Ov_Stats"]] %>%
  select(ManagedAreaName, ParameterName, HabitatType) %>%
  as.data.table()

task_list <- pct_stats[, .(HabitatType = unique(HabitatType)), by = ManagedAreaName]
# Add MA abbreviation
task_list[, ma_abrev := MA_All[.SD, on = "ManagedAreaName", Abbreviation]]
task_list <- as.data.frame(task_list)

pctlive_models_par <- function(ma, ma_abrev, habitat_type, oysterraw_pct){
  library(data.table)
  # Combined MA name with habitat type
  ma_plotlabel <- paste0(ma, "_", str_to_title(habitat_type))
  # At least 5 years of data are required in order to run model analyses
  # Function checks N years of data, returns T or F
  suff_years <- function(data){length(unique(data$Year))>=5}
  # Create subset for each MA
  ma_subset <- subset(oysterraw_pct, oysterraw_pct$MA_plotlab==ma_plotlabel)
  # Exception to only run model on Percent data for LBAP (exclude 8 values from 5035 which are point-in
  if(ma_abrev=="LBAP"){ma_subset <- ma_subset[!PercentLiveMethod=="Point-intercept"]}
  # Save data used in model
  saveRDS(ma_subset, paste0("output/model_results/data/", ma_abrev, "_PrcLive_", Sys.Date(), "_", habita
  # If enough years of data, perform modelling. If not, plot data points only
  if(suff_years(ma_subset) & !QAQCPlots){
    cat("---- Sufficient years of data. \n")
    #PercentLiveMethod=="Percent" for Lemon Bay program(s) with sufficient data,
    #so cannot be modeled as binomial
    if(ma_abrev=="LBAP"){
      pct_glmm <- brm(
        formula=PercentLive_dec ~ RelYear + (0 + RelYear | ReefIdentifier),
        data=subset(ma_subset, ma_subset$PercentLive_dec > 0 & ma_subset$PercentLive_dec < 1),family=Be
        cores=ncores, control= list(adapt_delta=0.995, max_treedepth=20),
        iter=iter, warmup=warmup, chains=nchains, init=0, thin=3, seed=8465,
        backend="rstan", save_pars = save_pars(all = TRUE),
        file=paste0("output/model_results/GLMMs/", ma_abrev, "_pct_glmm_", habitat_type, ".rds")
      )
    } else {
      # Check to see if previous model already exists
      model_file <- paste0("output/model_results/GLMMs/", ma_abrev, "_pct_glmm_", habitat_type, ".rds")
      if(!file.exists(model_file)){

        ma_subset <- as.data.frame(ma_subset)
        ma_subset$LiveSuccess <- round(ma_subset$PercentLive_pct)
        ma_subset$Trials <- 100

        # ma_subset[, PercentLive_pct_rounded := round(PercentLive_pct)]
        # ma_subset[, LiveObs := lapply(PercentLive_pct_rounded, function(pct) {
        #   c(rep(1L, pct), rep(0L, 100 - pct))
```

```
      # })]
      # binom <- ma_subset[, .(LiveObs = unlist(LiveObs)),
      #                     by = .(ProgramID, ProgramLocationID, QuadIdentifier, Year,
      #                            ManagedAreaName, PercentLiveMethod, UniversalReefID,
      #                            Region, MA_plotlab, RelYear, PercentLive_pct)]

      # Save binomial data (used in model)
      saveRDS(ma_subset, paste0("output/model_results/data/", ma_abrev, "_PrcLive_binom_", Sys.Date()
      # Run model
      cat("------ Running binomial model \n")
      pct_glmm <- brm(
        formula=LiveSuccess | trials(Trials) ~ RelYear + (1 | UniversalReefID),
        data=ma_subset, family=binomial, cores=ncores,
        control= list(adapt_delta=0.995, max_treedepth=20),
        iter=iter, warmup=warmup, chains=nchains, init=0, thin=3,
        seed=4331, backend="rstan", save_pars = save_pars(all = TRUE),
        file=paste0("output/model_results/GLMMs/", ma_abrev, "_pct_glmm_", habitat_type, ".rds")
      )
    } else {
      pct_glmm <- readRDS(model_file)
    }
  }
} else {
  pct_glmm <- NA
}
# Create model results tables and save diagnostic plots and marginal effects plots
datafile <- setDT(ma_subset)
models <- list(pct_glmm)
indicator <- "Percent live"
meplotzoom <- FALSE
oysterresults_temp <- data.frame()

if(class(pct_glmm)=="brmsfit"){
  for(m in seq_along(models)){
    modelobj <- models[[m]]
    sizeclass <- ifelse(str_detect(modelobj$file, "25to75|seed"),
                        "25-75mm",
                        ifelse(str_detect(modelobj$file, "35to75|seed"),
                               "35-75mm",
                               ifelse(str_detect(modelobj$file,
                                                 "o75|market"),
                                      ">75mm", "NA")))
    oyres_i <- setDT(broom.mixed::tidy(modelobj))
    #tidy() does not like that parameter values have underscores for
    #some reason, so the resulting table is incomplete

    if(nrow(oyres_i[effect=="fixed", ])-nrow(summary(modelobj)$fixed)==-1){
      missingrow <- data.table(effect="fixed",
                               component="cond",
                               #not sure what "cond" means in the tidy summary.
                               group=NA,
                               term=rownames(summary(modelobj)$fixed)[2],
                               estimate=summary(modelobj)$fixed$Estimate[2],
```

```
                                std.error=summary(modelobj)$fixed$Est.Error[2],
                                conf.low=summary(modelobj)$fixed$`l-95% CI`[2],
                                conf.high=summary(modelobj)$fixed$`u-95% CI`[2])
      oyres_i <- rbind(oyres_i, missingrow) %>% arrange(effect, group)
    }

    oyres_i[, `:=` (indicator=indicator,
                    managed_area=unique(datafile$ManagedAreaName),
                    habitat_class=unique(datafile$HabitatClassification),
                    size_class=sizeclass,
                    live_date_qual=ifelse(
                      str_detect(modelobj$file, "_hist"),
                      "Estimate", "Exact"),
                    n_programs=if(
                      class(try(datafile$LiveDate_Qualifier)) !=
                      "try-error"){
                      length(
                        unique(
                          datafile[LiveDate_Qualifier==
                                     ifelse(
                                       str_detect(
                                         modelobj$file,
                                         "_hist"),
                                       "Estimate",
                                       "Exact"),
                                   ProgramID]))
                    } else{length(unique(datafile[, ProgramID]))},
                    programs=if(class(try(
                      datafile$LiveDate_Qualifier)) != "try-error"){
                      list(unique(datafile[LiveDate_Qualifier==
                                             ifelse(
                                               str_detect(
                                                 modelobj$file,
                                                 "_hist"),
                                               "Estimate",
                                               "Exact"),
                                           ProgramID]))
                    } else{list(unique(datafile[, ProgramID]))},
                    filename=modelobj$file)]
    oysterresults_temp <- rbind(oysterresults_temp, oyres_i)
  }
} else {
  sizeclass <- ""
}

data <- datafile

ind <- case_when(str_detect(indicator, "ercent") ~ "Pct",
                 str_detect(indicator, "ensity") ~ "Den",
                 str_detect(indicator, "^S|^s") ~ "SH")

if(sizeclass != ""){
  size <- case_when(str_detect(sizeclass, "25") &
```

```
                      str_detect(sizeclass, "75") ~ "25to75",
                    str_detect(sizeclass, "35") &
                      str_detect(sizeclass, "75") ~ "35to75",
                    str_detect(sizeclass, "25")==FALSE &
                      str_detect(sizeclass, "75") ~ "o75", TRUE ~ "raw")
  sizelab <- case_when(str_detect(sizeclass, "25") &
                         str_detect(sizeclass, "75") ~ "25-75mm",
                       str_detect(sizeclass, "35") &
                         str_detect(sizeclass, "75") ~ "35-75mm",
                       str_detect(sizeclass, "25")==FALSE &
                         str_detect(sizeclass, "75") ~ "\u2265 75mm",
                       TRUE ~ "raw")
}

if(ind=="Pct"){
  nyrs <- max(data$LiveDate)-min(data$LiveDate)+1
  maxyr <- max(data$LiveDate)
  minyr <- min(data$LiveDate)
  yrdiff <- unique(data$YearDiff)
  current_year <- as.integer(format(Sys.Date(), "%Y"))
  # Creates break intervals for plots based on number of years of data
  if(nyrs>=40){
    # Set breaks to every 10 years if more than 40 years of data
    brk <- 10
  } else if(nyrs>=20){
    # Set breaks to every 5 years if between 40 and 20 years of data
    brk <- 5
  } else if(nyrs>=12){
    # Set breaks to every 3 years if between 20 and 12 years of data
    brk <- 3
  } else if(nyrs>=8){
    # Set breaks to every 2 years if between 12 and 8 years of data
    brk <- 2
  } else if(nyrs>=5){
    # Set breaks to every year if between 8 and 5 years of data
    brk <- 1
  } else {
    # Ensure 5 years are included on axis
    total_ticks <- 5
    extra_years <- total_ticks - nyrs
    # Always add 1 year before the first year
    years_before <- min(1, extra_years)
    years_after <- extra_years - years_before
    # Adjust min and max year, without going beyond current year
    minyr <- minyr - years_before
    maxyr <- min(maxyr + years_after, current_year)
    # Re-check if we have enough years (in case maxyr hit current year)
    minyr <- max(minyr, maxyr - (total_ticks - 1))
    brk <- 1
  }
  yrlist <- seq(minyr,maxyr,brk)

  set.seed(987)
```

```
if(class(pct_glmm)=="brmsfit"){
  pctplots <- plot(conditional_effects(models[[1]], re_formula=NULL), plot=FALSE)
}

plot1 <- ggplot() +
  geom_point(data=data, aes(x=LiveDate,
                            y=100*PercentLive_dec), position=plot_jitter,
             shape=21, size=2, color="#333333", fill="#cccccc",
             alpha=0.8, inherit.aes=FALSE) +
  {if(class(pct_glmm)=="brmsfit"){
    list(
      geom_ribbon(data = pctplots$RelYear$data,
                  aes(x = RelYear + yrdiff,
                      y = 100 * estimate__,
                      ymin = 100 * lower__,
                      ymax = 100 * upper__),
                  fill = "#000099", alpha = 0.1, inherit.aes = FALSE),
      geom_line(data = pctplots$RelYear$data,
                aes(x = RelYear + yrdiff,
                    y = 100 * estimate__),
                color = "#000099", lwd = 0.75, inherit.aes = FALSE)
    )
  }} +
  scale_x_continuous(limits=c(minyr-0.25, maxyr+0.25),
                     breaks=yrlist) +
  scale_y_continuous(breaks = scales::pretty_breaks(n = 5)) +
  plot_theme +
  theme(legend.text=element_text(size=10),
        legend.title=element_text(size=10)) +
  {
    if(unique(ma_subset$PercentLiveMethod)=="Percent"){
      labs(title=paste0("Percent Live Oysters (", habitat_type, ")"),
           subtitle=ma,
           x="Year",
           y="Percent live (%)")
    } else {
      labs(title=paste0("Oyster Percent Live Cover (", habitat_type, ")"),
           subtitle=ma,
           x="Year",
           y="Live cover (%)")
    }
  }

ma_short <- MA_All[ManagedAreaName==ma, Abbreviation]

# Specify save location (QAQC Plots saved elsewhere)
if(QAQCPlots){
  file_name <- paste0("output/QAQC/Oyster_PrcLive_GLMM_",
                      ma_short, "_", habitat_type, "_raw.png")
} else {
  file_name <- paste0("output/Percent_Live/Figures/Oyster_PrcLive_GLMM_",
                      ma_short, "_", habitat_type, "_raw.png")
}
```

```
    ggsave(file_name,
           plot1,
           width=8,
           height=4,
           units="in",
           dpi=200)
  }
  cat("---- Percent Live plot created for", ma, "-", habitat_type, "\n")
  return(oysterresults_temp)
}

split_tasks <- split(task_list, ceiling(seq_along(1:nrow(task_list)) / 4))
# Subset and save temp .rds objects for each MA (breaks up oysterraw)
for(ma in unique(oysterraw_pct$ManagedAreaName)){
  saveRDS(oysterraw_pct[oysterraw_pct$ManagedAreaName == ma, ],
          file = paste0("output/tmp/oysterpct_", make.names(ma), ".rds"))
}

results_all <- list()
for(b in seq_along(split_tasks)){
  batch <- split_tasks[[b]]
  results_list <- future_lapply(seq_len(nrow(batch)), function(i) {
    task <- batch[i, ]
    oysterraw_path <- paste0("output/tmp/oysterpct_", make.names(task$ManagedAreaName), ".rds")
    oysterraw_sub <- readRDS(oysterraw_path)

    cat(paste0("Now starting ", task$ManagedAreaName, "\n"))

    pctlive_models_par(
      ma = task$ManagedAreaName,
      ma_abrev = task$ma_abrev,
      habitat_type = task$HabitatType,
      oysterraw_pct = oysterraw_sub
    )

  }, future.seed = TRUE)
  results_all[[b]] <- data.table::rbindlist(results_list, fill = TRUE)
  gc()
}

oysterresults_pct <- data.table::rbindlist(results_all, fill = TRUE)
fwrite(oysterresults_pct, "output/oyresults/oysterresults_pct.csv")
```

Save & Export Results

The compiled model results variable is saved to a csv and rds file. The model results are evaluated to see if any models need to be reconsidered based on the rhat convergence being over 1.05. rhat values are written to file. All figures are then compressed into .zip files for each respective indicator.

```
# Combine all results into a single file for processing (Oyster_ResultsCompile.R)
all_oysterresults <- bind_rows(oysterresults_sh,oysterresults_den, oysterresults_pct)

fwrite(all_oysterresults, paste0("output/GLMM_AllDates_ModelResults.csv"), sep=",")
```

```r
saveRDS(all_oysterresults, paste0("output/GLMM_AllDates_ModelResults.rds"))

#Get Rhat values for all models to check which ones may need to be reparameterized
model_list <- unique(all_oysterresults$filename)
rhats_all <- data.table(filename=character(),
                        term=character(),
                        rhat=numeric())
rhats_sum <- data.table(filename=character(),
                        rhat=numeric())
fam_overview <- data.table(filename=character(),
                           family=character())

for(mod in model_list){
  mod_i <- readRDS(mod)
  allrhat_i <- rhat(mod_i)
  sumrhat_i <- c(summary(mod_i)$fixed$Rhat, summary(mod_i)$spec_pars$Rhat)
  allrhat_model_i <- data.table(filename=mod,
                                term=names(allrhat_i),
                                rhat=allrhat_i)
  sumrhat_model_i <- data.table(filename=mod,
                                rhat=sumrhat_i)
  rhats_all <- rbind(rhats_all, allrhat_model_i)
  rhats_sum <- rbind(rhats_sum, sumrhat_model_i)
  sum <- summary(mod_i)
  familyType <- sum$formula$family$family
  fam_overview <- rbind(fam_overview, data.table(filename=mod,family=familyType))
}

# extract MA_abrev from model names
fam_overview <- fam_overview %>% rowwise() %>% mutate(
  ma_abrev = str_split_1(tail(str_split_1(filename, "/"),1), "_")[1],
  parameter = str_split_1(tail(str_split_1(filename, "/"),1), "_")[2],
  habtype = str_split_1(tail(str_split_1(tail(str_split_1(filename, "/"),1), "_"),1), ".rds")[1],
  ma = MA_All[Abbreviation==ma_abrev, ManagedAreaName],
  param = ifelse(parameter=="den", "Density", ifelse(parameter=="pct", "Percent Live", "Shell Height"))
) %>% as.data.table()

rhats_all[, rhat_r := round(rhat, 2)]
rhats_sum[, rhat_r := round(rhat, 2)]

saveRDS(rhats_all, paste0("output/rhats_all_", Sys.Date(), ".rds"))
saveRDS(rhats_sum, paste0("output/rhats_sum_", Sys.Date(), ".rds"))
saveRDS(fam_overview, paste0("output/model_family_overview", Sys.Date(), ".rds"))

models_to_check_allrhat <- unique(rhats_all[rhat_r > 1.05, filename])
models_to_check_sumrhat <- unique(rhats_sum[rhat_r > 1.05, filename])

# Zip all figures
for(p in c("Density", "Percent_Live", "Shell_Height")){
  out_dir <- paste0("output/", p)
  fig_list <- list.files(paste0(out_dir, "/Figures"), pattern=".png", full=FALSE)
  filename <- paste0("Oyster", gsub("_", "", p), "Figures")
  setwd(paste0(out_dir, "/Figures"))
```

```
  zip(filename, files=fig_list)
  setwd(wd)
}
```