APPENDIX E

Analytical Data Validation Reports for 2017 Biota Samples

Data Validation Summary
2017 Biota Sampling
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (lobsters, blue mussels, mummichogs, smelt, polychaetes and tomcods) were collected in July, August and September 2017 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 1709489, 1709490, 1709491, 1709492, 1709493, 1709612, 1709613, 1709614, 1709615, 1709616, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1709627, 1709628, 1709629, 1709630, 1709631, 1709632, 1708118, 1708240, and 1708241. Samples were analyzed by one or more of the following: Clean Water Act (CWA, 2012) or Standard Methods for the Examination of Water and Wastewater (SM, 2014):

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Mercury, Total	CWA 1631B	10% Stage III/ 90% Stage IIB
Eurofins	Methyl Mercury	CWA 1630B	10% Stage III/ 90% Stage IIB
Eurofins	Percent Solids (TS)	SM 2540B	10% Stage III/ 90% Stage IIB

A Stage IIb data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. The following qualifiers as applied during data validation or reported by the laboratory are included in the final data set:

J = The reported concentration is considered an estimated value

Validation reason codes were applied to results associated with QC measurements outside project QC goals. The validation qualification actions and associated validation reason codes applied to sample results are summarized on Table 2. The following data validation reason codes were applied to one or more sample results:

HT = Hold time exceeded
LD = Lab Duplicate limit exceeded

A complete summary of final sample results is provided in Table 3.

Data were evaluated based on the following parameters:

Data Completeness and Chain of Custody
Holding Times and Preservation
* Blanks
* Initial Calibration
* Continuing Calibration
* Laboratory Control Sample (LCS)
* Matrix Spike/Matrix Spike Duplicates (MS/MSD)
Laboratory Duplicates
* Detection Limits
* Sample Result Verification/Electronic Evaluation Verification (EDD)
* Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

With the exception of the following items discussed below, results were determined to be usable as reported by the laboratory.

2.0 Mercury – 1631

Data Completeness and Chain of Custody

SDG 1709620 – Sample MMMC-01_17MT004_092017_MUM_05_WB was submitted to the laboratory for analysis; however the laboratory lost the sample. As such there are no analytical results for sample MMMC-01_17MT004_092017_MUM_05_WB.

SDG 1709624 – Samples OB-05_17SN001_091517_RAS_01_WB and OB-05_17SN001_091517_RAS_02_WB were submitted to the laboratory for analysis. Both of these samples contained multiple fish. There was sufficient volume to perform the analysis with a single fish in sample OB-05_17SN001_091517_RAS_01_WB so the second fish was used to create a new sample identified as OB-05_17SN001_091517_RAS_03_WB. There was sufficient volume to perform the analysis with a single fish in sample OB-05_17SN001_091517_RAS_02_WB so the second and third fish were used to create two new samples identified as OB-05_17SN001_091517_RAS_04_WB and OB-05_17SN001_091517_RAS_05_WB.

SDG 1709628 – Sample ES-03_17HC001_091917_BLM_17_WB was submitted to the laboratory for analysis; however the shell was empty and no tissue was present. The analysis for ES-03_17HC001_091917_BLM_17_WB was cancelled.

SDG 1709631 - Sample ES-15_17HC001_091417_BLM_05_WB was submitted to the laboratory for analysis; however the shell was empty and no tissue was present. The analysis for ES-15_17HC001_091417_BLM_05_WB was cancelled.

Matrix Spike

SDG 1709632 – Sample L10-52_17LT007_091317_LOB_07_TA was used for MS/MSD analysis. The MS/MSD recoveries for sample L10-52_17LT007_091317_LOB_07_TA (197%/166%) were above the upper QC limit of 125%. The MS/MSD recoveries do not apply because the sample concentrations are > 4X the spike amount added. Based on professional judgement the mercury result for sample L10-52_17LT007_091317_LOB_07_TA do not require qualification.

Laboratory Duplicate

SDG 1709491 – Sample L9-45_17LT015_091317_LOB_01_TA was selected by the laboratory for duplicate analysis. The RPD (71.6) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample L9-45_17LT015_091317_LOB_01_TA was qualified estimated (J).

SDG 1709612 – Sample BO-04_17ET026_092017_TOM_05_WB was selected by the laboratory for duplicate analysis. The RPD (26.2) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample BO-04_17ET026_092017_TOM_05_WB was qualified estimated (J).

SDG 1709622 – Sample ES-13_17SN001_091417_RAS_02_WB was selected by the laboratory for duplicate analysis. The RPD (31.0) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample ES-13_17SN001_091417_RAS_02_WB was qualified estimated (J).

SDG 1709628 – Sample ES-03_17HC001_091917_BLM_15_WB was selected by the laboratory for duplicate analysis. The RPD (24.8) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample ES-03_17HC001_091917_BLM_15_WB was qualified estimated (J).

3.0 Percent Solids – 2540G

Holding Times and Preservation

1709489 – Percent total solids and percent moisture for each sample in SDG 1709489 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

1709490 – Percent total solids and percent moisture for each sample in SDG 1709490 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

1709491 – Percent total solids and percent moisture for each sample in SDG 1709491 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

1709492 – Percent total solids and percent moisture for each sample in SDG 1709492 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

1709493 – Percent total solids and percent moisture for each sample in SDG 1709493 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

1709632 – Percent total solids and percent moisture for each sample in SDG 1709632 was analyzed beyond technical hold time. The results for total solids and moisture were qualified estimated (J).

References:

Amec Foster Wheeler, 2016. “Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan”, Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA”; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use”; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review”; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures”; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta November 15, 2017

elizabeth penta

Senior Reviewer: Denise King November 16, 2017

Denise King

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709489	Lobster	FBJR_17LT024	FBJR_17LT024_091417_LOB_01_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT024	FBJR_17LT024_091417_LOB_02_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT024	FBJR_17LT024_091417_LOB_03_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT024	FBJR_17LT024_091417_LOB_04_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT025	FBJR_17LT025_091417_LOB_05_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT025	FBJR_17LT025_091417_LOB_06_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT026	FBJR_17LT026_091417_LOB_07_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT026	FBJR_17LT026_091417_LOB_08_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT026	FBJR_17LT026_091417_LOB_09_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT026	FBJR_17LT026_091417_LOB_10_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_11_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_12_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_13_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_14_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_15_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_16_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT027	FBJR_17LT027_091417_LOB_17_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT028	FBJR_17LT028_091417_LOB_18_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT028	FBJR_17LT028_091417_LOB_19_TA	9/14/2017	FS	1	1	1		1
1709489	Lobster	FBJR_17LT028	FBJR_17LT028_091417_LOB_20_TA	9/14/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT001	CJ_17LT001_091317_LOB_01_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT001	CJ_17LT001_091317_LOB_02_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT001	CJ_17LT001_091317_LOB_03_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT001	CJ_17LT001_091317_LOB_04_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT001	CJ_17LT001_091317_LOB_05_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT002	CJ_17LT002_091317_LOB_06_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT002	CJ_17LT002_091317_LOB_07_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT003	CJ_17LT003_091317_LOB_08_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT003	CJ_17LT003_091317_LOB_09_TA	9/13/2017	FS	1	1	1		1

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709490	Lobster	CJ_17LT003	CJ_17LT003_091317_LOB_10_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT004	CJ_17LT004_091317_LOB_11_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT004	CJ_17LT004_091317_LOB_12_TA	9/13/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT044	CJ_17LT044_091517_LOB_19_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT044	CJ_17LT044_091517_LOB_20_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT047	CJ_17LT047_091517_LOB_15_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT047	CJ_17LT047_091517_LOB_16_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT047	CJ_17LT047_091517_LOB_17_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT047	CJ_17LT047_091517_LOB_18_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT048	CJ_17LT048_091517_LOB_13_TA	9/15/2017	FS	1	1	1		1
1709490	Lobster	CJ_17LT048	CJ_17LT048_091517_LOB_14_TA	9/15/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_01_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_02_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_03_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_04_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_05_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_06_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_07_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT015	L9-45_17LT015_091317_LOB_08_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_09_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_10_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_11_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_12_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_13_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT016	L9-45_17LT016_091317_LOB_14_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT017	L9-45_17LT017_091317_LOB_15_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT017	L9-45_17LT017_091317_LOB_16_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT017	L9-45_17LT017_091317_LOB_17_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT017	L9-45_17LT017_091317_LOB_18_TA	9/13/2017	FS	1	1	1		1

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709491	Lobster	L9-45_17LT018	L9-45_17LT018_091317_LOB_19_TA	9/13/2017	FS	1	1	1		1
1709491	Lobster	L9-45_17LT018	L9-45_17LT018_091317_LOB_20_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_01_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_02_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_03_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_04_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_05_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_06_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_07_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT011	SVE-01_17LT011_091317_LOB_08_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT012	SVE-01_17LT012_091317_LOB_09_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT012	SVE-01_17LT012_091317_LOB_10_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT012	SVE-01_17LT012_091317_LOB_11_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT013	SVE-01_17LT013_091317_LOB_12_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT013	SVE-01_17LT013_091317_LOB_13_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT013	SVE-01_17LT013_091317_LOB_14_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT013	SVE-01_17LT013_091317_LOB_15_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT013	SVE-01_17LT013_091317_LOB_16_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT014	SVE-01_17LT014_091317_LOB_17_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT014	SVE-01_17LT014_091317_LOB_18_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT014	SVE-01_17LT014_091317_LOB_19_TA	9/13/2017	FS	1	1	1		1
1709492	Lobster	SVE-01_17LT043	SVE-01_17LT043_091517_LOB_20_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT019	HB-01_17LT019_091317_LOB_01_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT021	HB-01_17LT021_091317_LOB_02_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT022	HB-01_17LT022_091317_LOB_03_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT022	HB-01_17LT022_091317_LOB_04_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT022	HB-01_17LT022_091317_LOB_05_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT023	HB-01_17LT023_091317_LOB_06_TA	9/13/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT034	HB-01_17LT034_091517_LOB_07_TA	9/15/2017	FS	1	1	1		1

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PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	Media	Location	Field Sample ID	Sample Date	QC Code					
1709493	Lobster	HB-01_17LT034	HB-01_17LT034_091517_LOB_08_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT034	HB-01_17LT034_091517_LOB_09_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT036	HB-01_17LT036_091517_LOB_10_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT036	HB-01_17LT036_091517_LOB_11_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT036	HB-01_17LT036_091517_LOB_12_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT036	HB-01_17LT036_091517_LOB_13_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT049	HB-01_17LT049_091517_LOB_14_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT049	HB-01_17LT049_091517_LOB_15_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT050	HB-01_17LT050_091517_LOB_16_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT052	HB-01_17LT052_091517_LOB_17_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT052	HB-01_17LT052_091517_LOB_18_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT052	HB-01_17LT052_091517_LOB_19_TA	9/15/2017	FS	1	1	1		1
1709493	Lobster	HB-01_17LT052	HB-01_17LT052_091517_LOB_20_TA	9/15/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_01_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_02_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_03_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_04_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_05_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT006	L10-52_17LT006_091317_LOB_06_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT007	L10-52_17LT007_091317_LOB_07_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT007	L10-52_17LT007_091317_LOB_08_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT007	L10-52_17LT007_091317_LOB_09_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT008	L10-52_17LT008_091317_LOB_10_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT008	L10-52_17LT008_091317_LOB_11_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT008	L10-52_17LT008_091317_LOB_12_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT009	L10-52_17LT009_091317_LOB_13_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT040	L10-52_17LT040_091517_LOB_18_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT040	L10-52_17LT040_091517_LOB_19_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT040	L10-52_17LT040_091517_LOB_20_TA	9/13/2017	FS	1	1	1		1

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SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709632	Lobster	L10-52_17LT041	L10-52_17LT041_091517_LOB_14_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT041	L10-52_17LT041_091517_LOB_15_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT041	L10-52_17LT041_091517_LOB_16_TA	9/13/2017	FS	1	1	1		1
1709632	Lobster	L10-52_17LT042	L10-52_17LT042_091517_LOB_17_TA	9/13/2017	FS	1	1	1		1
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_01_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_02_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_03_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_04_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_05_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_06_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_07_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_08_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_09_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_10_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_11_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_12_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_13_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_14_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_15_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_16_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_17_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_18_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_19_WB	9/13/2017	FS			1		
1709627	Blue mussels	FRB-01_17HC001	FRB-01_17HC001_091317_BLM_20_WB	9/13/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_01_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_02_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_03_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_04_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_05_WB	9/19/2017	FS			1		

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_06_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_07_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_08_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_09_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_10_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_11_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_12_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_13_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_14_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_15_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_16_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_18_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_19_WB	9/19/2017	FS			1		
1709628	Blue mussels	ES-03_17HC001	ES-03_17HC001_091917_BLM_20_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_01_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_02_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_03_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_04_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_05_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_06_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_07_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_08_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_09_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_10_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_11_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_12_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_13_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_14_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_15_WB	9/19/2017	FS			1		

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SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	Media	Location	Field Sample ID	Sample Date	QC Code					
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_16_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_17_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_18_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_19_WB	9/19/2017	FS			1		
1709629	Blue mussels	ES-FP_17HC001	ES-FP_17HC001_091917_BLM_20_WB	9/19/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_01_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_02_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_03_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_04_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_05_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_06_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_07_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_08_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_09_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_10_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_11_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_12_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_13_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_14_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_15_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_16_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_17_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_18_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_19_WB	9/14/2017	FS			1		
1709630	Blue mussels	ES13_17HC001	ES-13_17HC001_091417_BLM_20_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_01_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_02_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_03_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_04_WB	9/14/2017	FS			1		

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_06_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_07_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_08_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_09_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_10_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_11_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_12_WB	9/14/2017	FS			1		
1709631	Blue mussels	ES-15_17HC001	ES-15_17HC001_091417_BLM_13_WB	9/14/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_01_W	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_02_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_03_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_04_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_05_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_06_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_07_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_08_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_09_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_10_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_11_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_12_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_13_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_14_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_15_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_16_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_17_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_18_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_19_WB	9/12/2017	FS			1		
1709617	Mummichog	FRB-01_17SN001	FRB-01_17SN001_091217_MUM_20_WB	9/12/2017	FS			1		
1709621	Mummichog	BO-04_17SN001	BO-04_17SN001_091717_MUM_01_WB	9/17/2017	FS			1		

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SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709621	Bait	QC	ESFP_091517_BAIT_01_QC	9/15/2017	QC			1		
1709621	Bait	QC	ESFP_091517_BAIT_02_QC	9/15/2017	QC			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091817_MUM_01_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_02_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_03_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_04_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_05_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_06_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_07_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091817_MUM_08_WB	9/18/2017	FS			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091917_MUM_09_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091917_MUM_10_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091917_MUM_11_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091917_MUM_12_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT001	OB-01_17MT001_091917_MUM_13_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091917_MUM_14_WB	9/19/2017	FS			1		
1709618	Mummichog	OB-01_17MT002	OB-01_17MT002_091917_MUM_15_WB	9/19/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_01_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_02_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_03_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_04_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_05_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_06_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_07_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_08_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_09_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_10_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_11_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_12_WB	9/15/2017	FS			1		

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SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_13_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_14_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_15_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_16_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_17_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_18_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_19_WB	9/15/2017	FS			1		
1709619	Mummichog	OB-05_17SN001	OB-05_17SN001_091517_MUM_20_WB	9/15/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT001	MMMC-01_17MT001_091817_MUM_01_WB	9/18/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT001	MMMC-01_17MT001_092017_MUM_02_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT004	MMMC-01_17MT004_092017_MUM_03_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT004	MMMC-01_17MT004_092017_MUM_04_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_06_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_07_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_08_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_09_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_10_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_11_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_12_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_13_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_14_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_15_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_16_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_17_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_18_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_19_WB	9/20/2017	FS			1		
1709620	Mummichog	MMMC-01_17MT003	MMMC-01_17MT003_092017_MUM_20_WB	9/20/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_01_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_02_WB	9/14/2017	FS			1		

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_03_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_04_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_05_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_06_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_07_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_08_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_09_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_10_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_11_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_12_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_13_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_14_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_15_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_16_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_17_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_18_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_19_WB	9/14/2017	FS			1		
1709622	Smelt	ES-13_17SN001	ES-13_17SN001_091417_RAS_20_WB	9/14/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_01_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_02_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_03_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_04_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_05_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_06_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_07_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_08_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_09_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_10_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_11_WB	9/12/2017	FS			1		

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SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_12_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_13_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_14_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_15_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_16_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_17_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_18_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_19_WB	9/12/2017	FS			1		
1709623	Smelt	FRB-01_17SN001	FRB-01_17SN001_091217_RAS_20_WB	9/12/2017	FS			1		
1709624	Smelt	OB-05_17SN001	OB-05_17SN001_091517_RAS_01_WB	9/15/2017	FS			1		
1709624	Smelt	OB-05_17SN001	OB-05_17SN001_091517_RAS_02_WB	9/15/2017	FS			1		
1709624	Smelt	OB-05_17SN001	OB-05_17SN001_091517_RAS_03_WB	9/15/2017	FS			1		
1709624	Smelt	OB-05_17SN001	OB-05_17SN001_091517_RAS_04_WB	9/15/2017	FS			1		
1709624	Smelt	OB-05_17SN001	OB-05_17SN001_091517_RAS_05_WB	9/15/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_01_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_02_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_03_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_04_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_05_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_06_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_07_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_08_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_09_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_10_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_11_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_12_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_13_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_14_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_15_WB	9/14/2017	FS			1		

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				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_16_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_17_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_18_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_19_WB	9/14/2017	FS			1		
1709625	Smelt	ES-FP_17SN001	ES-FP_17SN001_091417_RAS_20_WB	9/14/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_01_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_02_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_03_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_04_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_05_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_06_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_07_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_08_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_09_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_10_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_11_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_12_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_13_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_14_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_15_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_16_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_17_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_18_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_19_WB	9/16/2017	FS			1		
1709626	Smelt	OB-01_17SN001	OB-01_17SN001_091617_RAS_20_WB	9/16/2017	FS			1		
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_01_WB	7/25/2017	FS				1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_02_WB	7/25/2017	FS				1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_03_WB	7/25/2017	FS				1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_04_WB	7/25/2017	FS				1	

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Checked by: EP 11/14/2017

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**					
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_05_WB	7/25/2017	FS				1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_01_WB	8/1/2017	FS				1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_02_WB	8/1/2017	FS				1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_03_WB	8/1/2017	FS				1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_04_WB	8/1/2017	FS				1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_05_WB	8/1/2017	FS				1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_01_WB	8/2/2017	FS				1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_02_WB	8/2/2017	FS				1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_03_WB	8/2/2017	FS				1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_04_WB	8/2/2017	FS				1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_05_WB	8/2/2017	FS				1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_01_WB	8/2/2017	FS				1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_02_WB	8/2/2017	FS				1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_03_WB	8/2/2017	FS				1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_04_WB	8/2/2017	FS				1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_05_WB	8/2/2017	FS				1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_01_WB	7/31/2017	FS				1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_02_WB	7/31/2017	FS				1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_03_WB	7/31/2017	FS				1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_04_WB	7/31/2017	FS				1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_05_WB	7/31/2017	FS				1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_01_WB	7/31/2017	FS				1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_02_WB	7/31/2017	FS				1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_03_WB	7/31/2017	FS				1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_04_WB	7/31/2017	FS				1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_05_WB	7/31/2017	FS				1	
1709612	Tomcod	BO-04_17ET008	BO-04_17ET008_091717_TOM_01_WB	9/17/2017	FS			1		
1709612	Tomcod	BO-04_17ET010	BO-04_17ET010_091717_TOM_02_WB	9/17/2017	FS			1		
1709612	Tomcod	BO-04_17ET014	BO-04_17ET014_091717_TOM_03_WB	9/17/2017	FS			1		

Created by: BCG 10/09/2017

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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	Media	Location	Field Sample ID	Sample Date	QC Code					
1709612	Tomcod	BO-04_17ET025	BO-04_17ET025_092017_TOM_04_WB	9/20/2017	FS			1		
1709612	Tomcod	BO-04_17ET026	BO-04_17ET026_092017_TOM_05_WB	9/20/2017	FS			1		
1709612	Tomcod	BO-04_17ET030	BO-04_17ET030_092017_TOM_06_WB	9/20/2017	FS			1		
1709612	Tomcod	BO-04_17ET035	BO-04_17ET035_092017_TOM_07_WB	9/20/2017	FS			1		
1709612	Tomcod	BO-04_17ET041	BO-04_17ET041_092017_TOM_08_WB	9/20/2017	FS			1		
1709613	Tomcod	OB-05_17ET002	OB-05_17ET002_091717_TOM_01_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET002	OB-05_17ET002_091717_TOM_02_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET003	OB-05_17ET003_091717_TOM_03_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET003	OB-05_17ET003_091717_TOM_04_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET009	OB-05_17ET009_091717_TOM_05_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET010	OB-05_17ET010_091717_TOM_06_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET011	OB-05_17ET011_091717_TOM_07_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET012	OB-05_17ET012_091717_TOM_08_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET012	OB-05_17ET012_091717_TOM_09_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET013	OB-05_17ET013_091717_TOM_10_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET013	OB-05_17ET013_091717_TOM_11_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET014	OB-05_17ET014_091717_TOM_12_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET 014	OB-05_17ET 014_091717_TOM_13_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET014	OB-05_17ET014_091717_TOM_14_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET014	OB-05_17ET014_091717_TOM_15_WB	9/17/2017	FS			1		
1709613	Tomcod	OB-05_17ET002	OB-05_17ET002_091817_TOM_16_WB	9/18/2017	FS			1		
1709613	Tomcod	OB-05_17ET003	OB-05_17ET003_091817_TOM_17_WB	9/18/2017	FS			1		
1709613	Tomcod	OB-05_17ET003	OB-05_17ET003_091817_TOM_18_WB	9/18/2017	FS			1		
1709613	Tomcod	OB-05_17ET005	OB-05_17ET005_091817_TOM_19_WB	9/18/2017	FS			1		
1709613	Tomcod	OB-05_17ET008	OB-05_17ET008_091817_TOM_20_WB	9/18/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_01_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_02_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_03_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_04_WB	9/16/2017	FS			1		

TABLE 1
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2017 BIOTA SAMPLING
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PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Method Class				Mercury	Methyl Mercury	
				Analysis Method		% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	Media	Location	Field Sample ID	Sample Date	QC Code					
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_05_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_06_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_07_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_08_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET001	OB-01_17ET001_091617_TOM_09_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET002	OB-01_17ET002_091617_TOM_10_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET002	OB-01_17ET002_091617_TOM_11_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET002	OB-01_17ET002_091617_TOM_12_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET003	OB-01_17ET003_091617_TOM_13_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET004	OB-01_17ET004_091617_TOM_14_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET004	OB-01_17ET004_091617_TOM_15_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET004	OB-01_17ET004_091617_TOM_16_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET005	OB-01_17ET005_091617_TOM_17_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET006	OB-01_17ET006_091617_TOM_18_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET007	OB-01_17ET007_091617_TOM_19_WB	9/16/2017	FS			1		
1709614	Tomcod	OB-01_17ET008	OB-01_17ET008_091617_TOM_20_WB	9/16/2017	FS			1		
1709615	Tomcod	ES-13_17LT012	ES-13_17LT012_091317_TOM_01_WB	9/13/2017	FS			1		
1709615	Tomcod	ES-13_17ET718	ES-13_17ET718_091817_TOM_02_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET719	ES-13_17ET719_091817_TOM_03_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET719	ES-13_17ET719_091817_TOM_04_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET719	ES-13_17ET719_091817_TOM_05_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET719	ES-13_17ET719_091817_TOM_06_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET722	ES-13_17ET722_091817_TOM_07_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET722	ES-13_17ET722_091817_TOM_08_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET723	ES-13_17ET723_091817_TOM_09_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET723	ES-13_17ET723_091817_TOM_10_WB	9/18/2017	FS			1		
1709615	Tomcod	ES-13_17ET717	ES-13_17ET717_091817_TOM_11_WB	9/18/2017	FS			1		
1709616	Tomcod	ES-FP_17ET658	ES-FP_17ET658_091517_TOM_01_WB	9/15/2017	FS			1		

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PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

					Method Class			Mercury	Methyl Mercury	
					Analysis Method	% Moisture	% Solids	EPA 1631	EPA 1630	Mass
SDG	Media	Location	Field Sample ID	Sample Date	QC Code					

Notes:
FS = Field Sample
SDG = Sample Delivery Group
Count = # of analytes

Created by: BCG 10/09/2017
Checked by: EP 11/14/2017

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709489	% moisture	1709489-01	FBJR_17LT024_091417_LOB_01_TA	T	Percent Moisture	80.8	O-04	80.8	J	HT	% BY WT.
1709489	% Solids	1709489-01	FBJR_17LT024_091417_LOB_01_TA	T	Percent Solids	19.2	[1]	19.2	J	HT	% BY WT.
1709489	% moisture	1709489-02	FBJR_17LT024_091417_LOB_02_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709489	% Solids	1709489-02	FBJR_17LT024_091417_LOB_02_TA	T	Percent Solids	18.7	[2]	18.7	J	HT	% BY WT.
1709489	% moisture	1709489-03	FBJR_17LT024_091417_LOB_03_TA	T	Percent Moisture	79.8	O-04	79.8	J	HT	% BY WT.
1709489	% Solids	1709489-03	FBJR_17LT024_091417_LOB_03_TA	T	Percent Solids	20.2	[3]	20.2	J	HT	% BY WT.
1709489	% moisture	1709489-04	FBJR_17LT024_091417_LOB_04_TA	T	Percent Moisture	81.1	O-04	81.1	J	HT	% BY WT.
1709489	% Solids	1709489-04	FBJR_17LT024_091417_LOB_04_TA	T	Percent Solids	18.9	[4]	18.9	J	HT	% BY WT.
1709489	% moisture	1709489-05	FBJR_17LT025_091417_LOB_05_TA	T	Percent Moisture	82.1	O-04	82.1	J	HT	% BY WT.
1709489	% Solids	1709489-05	FBJR_17LT025_091417_LOB_05_TA	T	Percent Solids	17.9	[5]	17.9	J	HT	% BY WT.
1709489	% moisture	1709489-06	FBJR_17LT025_091417_LOB_06_TA	T	Percent Moisture	78.2	O-04	78.2	J	HT	% BY WT.
1709489	% Solids	1709489-06	FBJR_17LT025_091417_LOB_06_TA	T	Percent Solids	21.8	[6]	21.8	J	HT	% BY WT.
1709489	% moisture	1709489-07	FBJR_17LT026_091417_LOB_07_TA	T	Percent Moisture	80	O-04	80	J	HT	% BY WT.
1709489	% Solids	1709489-07	FBJR_17LT026_091417_LOB_07_TA	T	Percent Solids	20	[7]	20	J	HT	% BY WT.
1709489	% moisture	1709489-08	FBJR_17LT026_091417_LOB_08_TA	T	Percent Moisture	82.6	O-04	82.6	J	HT	% BY WT.
1709489	% Solids	1709489-08	FBJR_17LT026_091417_LOB_08_TA	T	Percent Solids	17.4	[8]	17.4	J	HT	% BY WT.
1709489	% moisture	1709489-09	FBJR_17LT026_091417_LOB_09_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709489	% Solids	1709489-09	FBJR_17LT026_091417_LOB_09_TA	T	Percent Solids	18.7	[9]	18.7	J	HT	% BY WT.
1709489	% moisture	1709489-10	FBJR_17LT026_091417_LOB_10_TA	T	Percent Moisture	80.9	O-04	80.9	J	HT	% BY WT.
1709489	% Solids	1709489-10	FBJR_17LT026_091417_LOB_10_TA	T	Percent Solids	19.1	[10]	19.1	J	HT	% BY WT.
1709489	% moisture	1709489-11	FBJR_17LT027_091417_LOB_11_TA	T	Percent Moisture	80.9	O-04	80.9	J	HT	% BY WT.
1709489	% Solids	1709489-11	FBJR_17LT027_091417_LOB_11_TA	T	Percent Solids	19.1	[11]	19.1	J	HT	% BY WT.
1709489	% moisture	1709489-12	FBJR_17LT027_091417_LOB_12_TA	T	Percent Moisture	82.5	O-04	82.5	J	HT	% BY WT.
1709489	% Solids	1709489-12	FBJR_17LT027_091417_LOB_12_TA	T	Percent Solids	17.5	[12]	17.5	J	HT	% BY WT.
1709489	% moisture	1709489-13	FBJR_17LT027_091417_LOB_13_TA	T	Percent Moisture	80.7	O-04	80.7	J	HT	% BY WT.
1709489	% Solids	1709489-13	FBJR_17LT027_091417_LOB_13_TA	T	Percent Solids	19.3	[13]	19.3	J	HT	% BY WT.
1709489	% moisture	1709489-14	FBJR_17LT027_091417_LOB_14_TA	T	Percent Moisture	78.3	O-04	78.3	J	HT	% BY WT.

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TABLE 2
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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709489	% Solids	1709489-14	FBJR_17LT027_091417_LOB_14_TA	T	Percent Solids	21.7	[14]	21.7	J	HT	% BY WT.
1709489	% moisture	1709489-15	FBJR_17LT027_091417_LOB_15_TA	T	Percent Moisture	79.7	O-04	79.7	J	HT	% BY WT.
1709489	% Solids	1709489-15	FBJR_17LT027_091417_LOB_15_TA	T	Percent Solids	20.3	[15]	20.3	J	HT	% BY WT.
1709489	% moisture	1709489-16	FBJR_17LT027_091417_LOB_16_TA	T	Percent Moisture	80.4	O-04	80.4	J	HT	% BY WT.
1709489	% Solids	1709489-16	FBJR_17LT027_091417_LOB_16_TA	T	Percent Solids	19.6	[16]	19.6	J	HT	% BY WT.
1709489	% moisture	1709489-17	FBJR_17LT027_091417_LOB_17_TA	T	Percent Moisture	80.7	O-04	80.7	J	HT	% BY WT.
1709489	% Solids	1709489-17	FBJR_17LT027_091417_LOB_17_TA	T	Percent Solids	19.3	[17]	19.3	J	HT	% BY WT.
1709489	% moisture	1709489-18	FBJR_17LT028_091417_LOB_18_TA	T	Percent Moisture	77.9	O-04	77.9	J	HT	% BY WT.
1709489	% Solids	1709489-18	FBJR_17LT028_091417_LOB_18_TA	T	Percent Solids	22.1	[18]	22.1	J	HT	% BY WT.
1709489	% moisture	1709489-19	FBJR_17LT028_091417_LOB_19_TA	T	Percent Moisture	80.7	O-04	80.7	J	HT	% BY WT.
1709489	% Solids	1709489-19	FBJR_17LT028_091417_LOB_19_TA	T	Percent Solids	19.3	[19]	19.3	J	HT	% BY WT.
1709489	% moisture	1709489-20	FBJR_17LT028_091417_LOB_20_TA	T	Percent Moisture	81.8	O-04	81.8	J	HT	% BY WT.
1709489	% Solids	1709489-20	FBJR_17LT028_091417_LOB_20_TA	T	Percent Solids	18.2	[20]	18.2	J	HT	% BY WT.
1709490	% moisture	1709490-01	CJ_17LT001_091317_LOB_01_TA	T	Percent Moisture	78.2	O-04	78.2	J	HT	% BY WT.
1709490	% Solids	1709490-01	CJ_17LT001_091317_LOB_01_TA	T	Percent Solids	21.8	[1]	21.8	J	HT	% BY WT.
1709490	% moisture	1709490-02	CJ_17LT001_091317_LOB_02_TA	T	Percent Moisture	83	O-04	83	J	HT	% BY WT.
1709490	% Solids	1709490-02	CJ_17LT001_091317_LOB_02_TA	T	Percent Solids	17	[2]	17	J	HT	% BY WT.
1709490	% moisture	1709490-03	CJ_17LT001_091317_LOB_03_TA	T	Percent Moisture	82.4	O-04	82.4	J	HT	% BY WT.
1709490	% Solids	1709490-03	CJ_17LT001_091317_LOB_03_TA	T	Percent Solids	17.6	[3]	17.6	J	HT	% BY WT.
1709490	% moisture	1709490-04	CJ_17LT001_091317_LOB_04_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709490	% Solids	1709490-04	CJ_17LT001_091317_LOB_04_TA	T	Percent Solids	17.8	[4]	17.8	J	HT	% BY WT.
1709490	% moisture	1709490-05	CJ_17LT001_091317_LOB_05_TA	T	Percent Moisture	80.1	O-04	80.1	J	HT	% BY WT.
1709490	% Solids	1709490-05	CJ_17LT001_091317_LOB_05_TA	T	Percent Solids	19.9	[5]	19.9	J	HT	% BY WT.
1709490	% moisture	1709490-06	CJ_17LT002_091317_LOB_06_TA	T	Percent Moisture	80.6	O-04	80.6	J	HT	% BY WT.
1709490	% Solids	1709490-06	CJ_17LT002_091317_LOB_06_TA	T	Percent Solids	19.4	[6]	19.4	J	HT	% BY WT.
1709490	% moisture	1709490-07	CJ_17LT002_091317_LOB_07_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709490	% Solids	1709490-07	CJ_17LT002_091317_LOB_07_TA	T	Percent Solids	18.7	[7]	18.7	J	HT	% BY WT.

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709490	% moisture	1709490-08	CJ_17LT003_091317_LOB_08_TA	T	Percent Moisture	83.8	O-04	83.8	J	HT	% BY WT.
1709490	% Solids	1709490-08	CJ_17LT003_091317_LOB_08_TA	T	Percent Solids	16.2	[8]	16.2	J	HT	% BY WT.
1709490	% moisture	1709490-09	CJ_17LT003_091317_LOB_09_TA	T	Percent Moisture	81.8	O-04	81.8	J	HT	% BY WT.
1709490	% Solids	1709490-09	CJ_17LT003_091317_LOB_09_TA	T	Percent Solids	18.2	[9]	18.2	J	HT	% BY WT.
1709490	% moisture	1709490-10	CJ_17LT003_091317_LOB_10_TA	T	Percent Moisture	82.1	O-04	82.1	J	HT	% BY WT.
1709490	% Solids	1709490-10	CJ_17LT003_091317_LOB_10_TA	T	Percent Solids	17.9	[10]	17.9	J	HT	% BY WT.
1709490	% moisture	1709490-11	CJ_17LT004_091317_LOB_11_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709490	% Solids	1709490-11	CJ_17LT004_091317_LOB_11_TA	T	Percent Solids	18.7	[11]	18.7	J	HT	% BY WT.
1709490	% moisture	1709490-12	CJ_17LT004_091317_LOB_12_TA	T	Percent Moisture	77.7	O-04	77.7	J	HT	% BY WT.
1709490	% Solids	1709490-12	CJ_17LT004_091317_LOB_12_TA	T	Percent Solids	22.3	[12]	22.3	J	HT	% BY WT.
1709490	% moisture	1709490-19	CJ_17LT044_091517_LOB_19_TA	T	Percent Moisture	80.8	O-04	80.8	J	HT	% BY WT.
1709490	% Solids	1709490-19	CJ_17LT044_091517_LOB_19_TA	T	Percent Solids	19.2	[19]	19.2	J	HT	% BY WT.
1709490	% moisture	1709490-20	CJ_17LT044_091517_LOB_20_TA	T	Percent Moisture	80.7	O-04	80.7	J	HT	% BY WT.
1709490	% Solids	1709490-20	CJ_17LT044_091517_LOB_20_TA	T	Percent Solids	19.3	[20]	19.3	J	HT	% BY WT.
1709490	% moisture	1709490-15	CJ_17LT047_091517_LOB_15_TA	T	Percent Moisture	82.3	O-04	82.3	J	HT	% BY WT.
1709490	% Solids	1709490-15	CJ_17LT047_091517_LOB_15_TA	T	Percent Solids	17.7	[15]	17.7	J	HT	% BY WT.
1709490	% moisture	1709490-16	CJ_17LT047_091517_LOB_16_TA	T	Percent Moisture	82.7	O-04	82.7	J	HT	% BY WT.
1709490	% Solids	1709490-16	CJ_17LT047_091517_LOB_16_TA	T	Percent Solids	17.3	[16]	17.3	J	HT	% BY WT.
1709490	% moisture	1709490-17	CJ_17LT047_091517_LOB_17_TA	T	Percent Moisture	80.8	O-04	80.8	J	HT	% BY WT.
1709490	% Solids	1709490-17	CJ_17LT047_091517_LOB_17_TA	T	Percent Solids	19.2	[17]	19.2	J	HT	% BY WT.
1709490	% moisture	1709490-18	CJ_17LT047_091517_LOB_18_TA	T	Percent Moisture	83.6	O-04	83.6	J	HT	% BY WT.
1709490	% Solids	1709490-18	CJ_17LT047_091517_LOB_18_TA	T	Percent Solids	16.4	[18]	16.4	J	HT	% BY WT.
1709490	% moisture	1709490-13	CJ_17LT048_091517_LOB_13_TA	T	Percent Moisture	80.9	O-04	80.9	J	HT	% BY WT.
1709490	% Solids	1709490-13	CJ_17LT048_091517_LOB_13_TA	T	Percent Solids	19.1	[13]	19.1	J	HT	% BY WT.
1709490	% moisture	1709490-14	CJ_17LT048_091517_LOB_14_TA	T	Percent Moisture	78.9	O-04	78.9	J	HT	% BY WT.
1709490	% Solids	1709490-14	CJ_17LT048_091517_LOB_14_TA	T	Percent Solids	21.1	[14]	21.1	J	HT	% BY WT.
1709491	E1631	1709491-01RE	L9-45_17LT015_091317_LOB_01_TA	T	Mercury	317		317	J	LD	NG/G

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709491	% moisture	1709491-01	L9-45_17LT015_091317_LOB_01_TA	T	Percent Moisture	79.6	O-04	79.6	J	HT	% BY WT.
1709491	% Solids	1709491-01	L9-45_17LT015_091317_LOB_01_TA	T	Percent Solids	20.4	O-04	20.4	J	HT	% BY WT.
1709491	% moisture	1709491-02	L9-45_17LT015_091317_LOB_02_TA	T	Percent Moisture	81.4	O-04	81.4	J	HT	% BY WT.
1709491	% Solids	1709491-02	L9-45_17LT015_091317_LOB_02_TA	T	Percent Solids	18.6	O-04	18.6	J	HT	% BY WT.
1709491	% moisture	1709491-03	L9-45_17LT015_091317_LOB_03_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709491	% Solids	1709491-03	L9-45_17LT015_091317_LOB_03_TA	T	Percent Solids	18.7	O-04	18.7	J	HT	% BY WT.
1709491	% moisture	1709491-04	L9-45_17LT015_091317_LOB_04_TA	T	Percent Moisture	81.2	O-04	81.2	J	HT	% BY WT.
1709491	% Solids	1709491-04	L9-45_17LT015_091317_LOB_04_TA	T	Percent Solids	18.8	O-04	18.8	J	HT	% BY WT.
1709491	% moisture	1709491-05	L9-45_17LT015_091317_LOB_05_TA	T	Percent Moisture	81.9	O-04	81.9	J	HT	% BY WT.
1709491	% Solids	1709491-05	L9-45_17LT015_091317_LOB_05_TA	T	Percent Solids	18.1	O-04	18.1	J	HT	% BY WT.
1709491	% moisture	1709491-06	L9-45_17LT015_091317_LOB_06_TA	T	Percent Moisture	79.9	O-04	79.9	J	HT	% BY WT.
1709491	% Solids	1709491-06	L9-45_17LT015_091317_LOB_06_TA	T	Percent Solids	20.1	O-04	20.1	J	HT	% BY WT.
1709491	% moisture	1709491-07	L9-45_17LT015_091317_LOB_07_TA	T	Percent Moisture	83.6	O-04	83.6	J	HT	% BY WT.
1709491	% Solids	1709491-07	L9-45_17LT015_091317_LOB_07_TA	T	Percent Solids	16.4	O-04	16.4	J	HT	% BY WT.
1709491	% moisture	1709491-08	L9-45_17LT015_091317_LOB_08_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709491	% Solids	1709491-08	L9-45_17LT015_091317_LOB_08_TA	T	Percent Solids	17.8	O-04	17.8	J	HT	% BY WT.
1709491	% moisture	1709491-09	L9-45_17LT016_091317_LOB_09_TA	T	Percent Moisture	80.8	O-04	80.8	J	HT	% BY WT.
1709491	% Solids	1709491-09	L9-45_17LT016_091317_LOB_09_TA	T	Percent Solids	19.2	O-04	19.2	J	HT	% BY WT.
1709491	% moisture	1709491-10	L9-45_17LT016_091317_LOB_10_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709491	% Solids	1709491-10	L9-45_17LT016_091317_LOB_10_TA	T	Percent Solids	17.8	O-04	17.8	J	HT	% BY WT.
1709491	% moisture	1709491-11	L9-45_17LT016_091317_LOB_11_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709491	% Solids	1709491-11	L9-45_17LT016_091317_LOB_11_TA	T	Percent Solids	17.8	O-04	17.8	J	HT	% BY WT.
1709491	% moisture	1709491-12	L9-45_17LT016_091317_LOB_12_TA	T	Percent Moisture	81.8	O-04	81.8	J	HT	% BY WT.
1709491	% Solids	1709491-12	L9-45_17LT016_091317_LOB_12_TA	T	Percent Solids	18.2	O-04	18.2	J	HT	% BY WT.
1709491	% moisture	1709491-13	L9-45_17LT016_091317_LOB_13_TA	T	Percent Moisture	81.4	O-04	81.4	J	HT	% BY WT.
1709491	% Solids	1709491-13	L9-45_17LT016_091317_LOB_13_TA	T	Percent Solids	18.6	O-04	18.6	J	HT	% BY WT.
1709491	% moisture	1709491-14	L9-45_17LT016_091317_LOB_14_TA	T	Percent Moisture	82	O-04	82	J	HT	% BY WT.

Created by: BCG 11/20/2017
Checked by: EP 11/21/2017

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709491	% Solids	1709491-14	L9-45_17LT016_091317_LOB_14_TA	T	Percent Solids	18	O-04	18	J	HT	% BY WT.
1709491	% moisture	1709491-15	L9-45_17LT017_091317_LOB_15_TA	T	Percent Moisture	81.1	O-04	81.1	J	HT	% BY WT.
1709491	% Solids	1709491-15	L9-45_17LT017_091317_LOB_15_TA	T	Percent Solids	18.9	O-04	18.9	J	HT	% BY WT.
1709491	% moisture	1709491-16	L9-45_17LT017_091317_LOB_16_TA	T	Percent Moisture	82.6	O-04	82.6	J	HT	% BY WT.
1709491	% Solids	1709491-16	L9-45_17LT017_091317_LOB_16_TA	T	Percent Solids	17.4	O-04	17.4	J	HT	% BY WT.
1709491	% moisture	1709491-17	L9-45_17LT017_091317_LOB_17_TA	T	Percent Moisture	81.2	O-04	81.2	J	HT	% BY WT.
1709491	% Solids	1709491-17	L9-45_17LT017_091317_LOB_17_TA	T	Percent Solids	18.8	O-04	18.8	J	HT	% BY WT.
1709491	% moisture	1709491-18	L9-45_17LT017_091317_LOB_18_TA	T	Percent Moisture	79.8	O-04	79.8	J	HT	% BY WT.
1709491	% Solids	1709491-18	L9-45_17LT017_091317_LOB_18_TA	T	Percent Solids	20.2	O-04	20.2	J	HT	% BY WT.
1709491	% moisture	1709491-19	L9-45_17LT018_091317_LOB_19_TA	T	Percent Moisture	81.4	O-04	81.4	J	HT	% BY WT.
1709491	% Solids	1709491-19	L9-45_17LT018_091317_LOB_19_TA	T	Percent Solids	18.6	O-04	18.6	J	HT	% BY WT.
1709491	% moisture	1709491-20	L9-45_17LT018_091317_LOB_20_TA	T	Percent Moisture	80.1	O-04	80.1	J	HT	% BY WT.
1709491	% Solids	1709491-20	L9-45_17LT018_091317_LOB_20_TA	T	Percent Solids	19.9	O-04	19.9	J	HT	% BY WT.
1709492	% moisture	1709492-01	SVE-01_17LT011_091317_LOB_01_TA	T	Percent Moisture	81.8	O-04	81.8	J	HT	% BY WT.
1709492	% Solids	1709492-01	SVE-01_17LT011_091317_LOB_01_TA	T	Percent Solids	18.2	O-04	18.2	J	HT	% BY WT.
1709492	% moisture	1709492-02	SVE-01_17LT011_091317_LOB_02_TA	T	Percent Moisture	77.2	O-04	77.2	J	HT	% BY WT.
1709492	% Solids	1709492-02	SVE-01_17LT011_091317_LOB_02_TA	T	Percent Solids	22.8	O-04	22.8	J	HT	% BY WT.
1709492	% moisture	1709492-03	SVE-01_17LT011_091317_LOB_03_TA	T	Percent Moisture	81.9	O-04	81.9	J	HT	% BY WT.
1709492	% Solids	1709492-03	SVE-01_17LT011_091317_LOB_03_TA	T	Percent Solids	18.1	O-04	18.1	J	HT	% BY WT.
1709492	% moisture	1709492-04	SVE-01_17LT011_091317_LOB_04_TA	T	Percent Moisture	79.7	O-04	79.7	J	HT	% BY WT.
1709492	% Solids	1709492-04	SVE-01_17LT011_091317_LOB_04_TA	T	Percent Solids	20.3	O-04	20.3	J	HT	% BY WT.
1709492	% moisture	1709492-05	SVE-01_17LT011_091317_LOB_05_TA	T	Percent Moisture	82	O-04	82	J	HT	% BY WT.
1709492	% Solids	1709492-05	SVE-01_17LT011_091317_LOB_05_TA	T	Percent Solids	18	O-04	18	J	HT	% BY WT.
1709492	% moisture	1709492-06	SVE-01_17LT011_091317_LOB_06_TA	T	Percent Moisture	81.7	O-04	81.7	J	HT	% BY WT.
1709492	% Solids	1709492-06	SVE-01_17LT011_091317_LOB_06_TA	T	Percent Solids	18.3	O-04	18.3	J	HT	% BY WT.
1709492	% moisture	1709492-07	SVE-01_17LT011_091317_LOB_07_TA	T	Percent Moisture	82.4	O-04	82.4	J	HT	% BY WT.
1709492	% Solids	1709492-07	SVE-01_17LT011_091317_LOB_07_TA	T	Percent Solids	17.6	O-04	17.6	J	HT	% BY WT.

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709492	% moisture	1709492-08	SVE-01_17LT011_091317_LOB_08_TA	T	Percent Moisture	80.2	O-04	80.2	J	HT	% BY WT.
1709492	% Solids	1709492-08	SVE-01_17LT011_091317_LOB_08_TA	T	Percent Solids	19.8	O-04	19.8	J	HT	% BY WT.
1709492	% moisture	1709492-09	SVE-01_17LT012_091317_LOB_09_TA	T	Percent Moisture	78.5	O-04	78.5	J	HT	% BY WT.
1709492	% Solids	1709492-09	SVE-01_17LT012_091317_LOB_09_TA	T	Percent Solids	21.5	O-04	21.5	J	HT	% BY WT.
1709492	% moisture	1709492-10	SVE-01_17LT012_091317_LOB_10_TA	T	Percent Moisture	78.4	O-04	78.4	J	HT	% BY WT.
1709492	% Solids	1709492-10	SVE-01_17LT012_091317_LOB_10_TA	T	Percent Solids	21.6	O-04	21.6	J	HT	% BY WT.
1709492	% moisture	1709492-11	SVE-01_17LT012_091317_LOB_11_TA	T	Percent Moisture	80.1	O-04	80.1	J	HT	% BY WT.
1709492	% Solids	1709492-11	SVE-01_17LT012_091317_LOB_11_TA	T	Percent Solids	19.9	O-04	19.9	J	HT	% BY WT.
1709492	% moisture	1709492-12	SVE-01_17LT013_091317_LOB_12_TA	T	Percent Moisture	81.5	O-04	81.5	J	HT	% BY WT.
1709492	% Solids	1709492-12	SVE-01_17LT013_091317_LOB_12_TA	T	Percent Solids	18.5	O-04	18.5	J	HT	% BY WT.
1709492	% moisture	1709492-13	SVE-01_17LT013_091317_LOB_13_TA	T	Percent Moisture	82	O-04	82	J	HT	% BY WT.
1709492	% Solids	1709492-13	SVE-01_17LT013_091317_LOB_13_TA	T	Percent Solids	18	O-04	18	J	HT	% BY WT.
1709492	% moisture	1709492-14	SVE-01_17LT013_091317_LOB_14_TA	T	Percent Moisture	80.5	O-04	80.5	J	HT	% BY WT.
1709492	% Solids	1709492-14	SVE-01_17LT013_091317_LOB_14_TA	T	Percent Solids	19.5	O-04	19.5	J	HT	% BY WT.
1709492	% moisture	1709492-15	SVE-01_17LT013_091317_LOB_15_TA	T	Percent Moisture	80.6	O-04	80.6	J	HT	% BY WT.
1709492	% Solids	1709492-15	SVE-01_17LT013_091317_LOB_15_TA	T	Percent Solids	19.4	O-04	19.4	J	HT	% BY WT.
1709492	% moisture	1709492-16	SVE-01_17LT013_091317_LOB_16_TA	T	Percent Moisture	81	O-04	81	J	HT	% BY WT.
1709492	% Solids	1709492-16	SVE-01_17LT013_091317_LOB_16_TA	T	Percent Solids	19	O-04	19	J	HT	% BY WT.
1709492	% moisture	1709492-17	SVE-01_17LT014_091317_LOB_17_TA	T	Percent Moisture	82.5	O-04	82.5	J	HT	% BY WT.
1709492	% Solids	1709492-17	SVE-01_17LT014_091317_LOB_17_TA	T	Percent Solids	17.5	O-04	17.5	J	HT	% BY WT.
1709492	% moisture	1709492-18	SVE-01_17LT014_091317_LOB_18_TA	T	Percent Moisture	81.1	O-04	81.1	J	HT	% BY WT.
1709492	% Solids	1709492-18	SVE-01_17LT014_091317_LOB_18_TA	T	Percent Solids	18.9	O-04	18.9	J	HT	% BY WT.
1709492	% moisture	1709492-19	SVE-01_17LT014_091317_LOB_19_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709492	% Solids	1709492-19	SVE-01_17LT014_091317_LOB_19_TA	T	Percent Solids	18.7	O-04	18.7	J	HT	% BY WT.
1709492	% moisture	1709492-20	SVE-01_17LT043_091517_LOB_20_TA	T	Percent Moisture	81.1	O-04	81.1	J	HT	% BY WT.
1709492	% Solids	1709492-20	SVE-01_17LT043_091517_LOB_20_TA	T	Percent Solids	18.9	O-04	18.9	J	HT	% BY WT.
1709493	% moisture	1709493-01	HB-01_17LT019_091317_LOB_01_TA	T	Percent Moisture	80.9	O-04	80.9	J	HT	% BY WT.

Created by: BCG 11/20/2017
Checked by: EP 11/21/2017

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709493	% Solids	1709493-01	HB-01_17LT019_091317_LOB_01_TA	T	Percent Solids	19.1	O-04	19.1	J	HT	% BY WT.
1709493	% moisture	1709493-02	HB-01_17LT021_091317_LOB_02_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709493	% Solids	1709493-02	HB-01_17LT021_091317_LOB_02_TA	T	Percent Solids	17.8	O-04	17.8	J	HT	% BY WT.
1709493	% moisture	1709493-03	HB-01_17LT022_091317_LOB_03_TA	T	Percent Moisture	83.7	O-04	83.7	J	HT	% BY WT.
1709493	% Solids	1709493-03	HB-01_17LT022_091317_LOB_03_TA	T	Percent Solids	16.3	O-04	16.3	J	HT	% BY WT.
1709493	% moisture	1709493-04	HB-01_17LT022_091317_LOB_04_TA	T	Percent Moisture	81.7	O-04	81.7	J	HT	% BY WT.
1709493	% Solids	1709493-04	HB-01_17LT022_091317_LOB_04_TA	T	Percent Solids	18.3	O-04	18.3	J	HT	% BY WT.
1709493	% moisture	1709493-05	HB-01_17LT022_091317_LOB_05_TA	T	Percent Moisture	81.9	O-04	81.9	J	HT	% BY WT.
1709493	% Solids	1709493-05	HB-01_17LT022_091317_LOB_05_TA	T	Percent Solids	18.1	O-04	18.1	J	HT	% BY WT.
1709493	% moisture	1709493-06	HB-01_17LT023_091317_LOB_06_TA	T	Percent Moisture	82.4	O-04	82.4	J	HT	% BY WT.
1709493	% Solids	1709493-06	HB-01_17LT023_091317_LOB_06_TA	T	Percent Solids	17.6	O-04	17.6	J	HT	% BY WT.
1709493	% moisture	1709493-07	HB-01_17LT034_091517_LOB_07_TA	T	Percent Moisture	83.4	O-04	83.4	J	HT	% BY WT.
1709493	% Solids	1709493-07	HB-01_17LT034_091517_LOB_07_TA	T	Percent Solids	16.6	O-04	16.6	J	HT	% BY WT.
1709493	% moisture	1709493-08	HB-01_17LT034_091517_LOB_08_TA	T	Percent Moisture	81.7	O-04	81.7	J	HT	% BY WT.
1709493	% Solids	1709493-08	HB-01_17LT034_091517_LOB_08_TA	T	Percent Solids	18.3	O-04	18.3	J	HT	% BY WT.
1709493	% moisture	1709493-09	HB-01_17LT034_091517_LOB_09_TA	T	Percent Moisture	84.1	O-04	84.1	J	HT	% BY WT.
1709493	% Solids	1709493-09	HB-01_17LT034_091517_LOB_09_TA	T	Percent Solids	15.9	O-04	15.9	J	HT	% BY WT.
1709493	% moisture	1709493-10	HB-01_17LT036_091517_LOB_10_TA	T	Percent Moisture	81.6	O-04	81.6	J	HT	% BY WT.
1709493	% Solids	1709493-10	HB-01_17LT036_091517_LOB_10_TA	T	Percent Solids	18.4	O-04	18.4	J	HT	% BY WT.
1709493	% moisture	1709493-11	HB-01_17LT036_091517_LOB_11_TA	T	Percent Moisture	83.8	O-04	83.8	J	HT	% BY WT.
1709493	% Solids	1709493-11	HB-01_17LT036_091517_LOB_11_TA	T	Percent Solids	16.2	O-04	16.2	J	HT	% BY WT.
1709493	% moisture	1709493-12	HB-01_17LT036_091517_LOB_12_TA	T	Percent Moisture	83	O-04	83	J	HT	% BY WT.
1709493	% Solids	1709493-12	HB-01_17LT036_091517_LOB_12_TA	T	Percent Solids	17	O-04	17	J	HT	% BY WT.
1709493	% moisture	1709493-13	HB-01_17LT036_091517_LOB_13_TA	T	Percent Moisture	83.4	O-04	83.4	J	HT	% BY WT.
1709493	% Solids	1709493-13	HB-01_17LT036_091517_LOB_13_TA	T	Percent Solids	16.6	O-04	16.6	J	HT	% BY WT.
1709493	% moisture	1709493-14	HB-01_17LT049_091517_LOB_14_TA	T	Percent Moisture	82.4	O-04	82.4	J	HT	% BY WT.
1709493	% Solids	1709493-14	HB-01_17LT049_091517_LOB_14_TA	T	Percent Solids	17.6	O-04	17.6	J	HT	% BY WT.

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709493	% moisture	1709493-15	HB-01_17LT049_091517_LOB_15_TA	T	Percent Moisture	83.4	O-04	83.4	J	HT	% BY WT.
1709493	% Solids	1709493-15	HB-01_17LT049_091517_LOB_15_TA	T	Percent Solids	16.6	O-04	16.6	J	HT	% BY WT.
1709493	% moisture	1709493-16	HB-01_17LT050_091517_LOB_16_TA	T	Percent Moisture	81.6	O-04	81.6	J	HT	% BY WT.
1709493	% Solids	1709493-16	HB-01_17LT050_091517_LOB_16_TA	T	Percent Solids	18.4	O-04	18.4	J	HT	% BY WT.
1709493	% moisture	1709493-17	HB-01_17LT052_091517_LOB_17_TA	T	Percent Moisture	82.2	O-04	82.2	J	HT	% BY WT.
1709493	% Solids	1709493-17	HB-01_17LT052_091517_LOB_17_TA	T	Percent Solids	17.8	O-04	17.8	J	HT	% BY WT.
1709493	% moisture	1709493-18	HB-01_17LT052_091517_LOB_18_TA	T	Percent Moisture	78.5	O-04	78.5	J	HT	% BY WT.
1709493	% Solids	1709493-18	HB-01_17LT052_091517_LOB_18_TA	T	Percent Solids	21.5	O-04	21.5	J	HT	% BY WT.
1709493	% moisture	1709493-19	HB-01_17LT052_091517_LOB_19_TA	T	Percent Moisture	82.4	O-04	82.4	J	HT	% BY WT.
1709493	% Solids	1709493-19	HB-01_17LT052_091517_LOB_19_TA	T	Percent Solids	17.6	O-04	17.6	J	HT	% BY WT.
1709493	% moisture	1709493-20	HB-01_17LT052_091517_LOB_20_TA	T	Percent Moisture	82.3	O-04	82.3	J	HT	% BY WT.
1709493	% Solids	1709493-20	HB-01_17LT052_091517_LOB_20_TA	T	Percent Solids	17.7	O-04	17.7	J	HT	% BY WT.
1709612	E1631	1709612-05	BO-04_17ET026_092017_TOM_05_WB	T	Mercury	199		199	J	LD	NG/G
1709622	E1631	1709622-02	ES-13_17SN001_091417_RAS_02_WB	T	Mercury	87.8		87.8	J	LD	NG/G
1709628	E1631	1709628-15	ES-03_17HC001_091917_BLM_15_WB	T	Mercury	68.9		68.9	J	LD	NG/G
1709632	% moisture	1709632-01	L10-52_17LT006_091317_LOB_01_TA	T	Percent Moisture	82.1	O-04	82.1	J	HT	% BY WT.
1709632	% Solids	1709632-01	L10-52_17LT006_091317_LOB_01_TA	T	Percent Solids	17.9	[1]	17.9	J	HT	% BY WT.
1709632	% moisture	1709632-02	L10-52_17LT006_091317_LOB_02_TA	T	Percent Moisture	82.5	O-04	82.5	J	HT	% BY WT.
1709632	% Solids	1709632-02	L10-52_17LT006_091317_LOB_02_TA	T	Percent Solids	17.5	[2]	17.5	J	HT	% BY WT.
1709632	% moisture	1709632-03	L10-52_17LT006_091317_LOB_03_TA	T	Percent Moisture	82.7	O-04	82.7	J	HT	% BY WT.
1709632	% Solids	1709632-03	L10-52_17LT006_091317_LOB_03_TA	T	Percent Solids	17.3	[3]	17.3	J	HT	% BY WT.
1709632	% moisture	1709632-04	L10-52_17LT006_091317_LOB_04_TA	T	Percent Moisture	80.5	O-04	80.5	J	HT	% BY WT.
1709632	% Solids	1709632-04	L10-52_17LT006_091317_LOB_04_TA	T	Percent Solids	19.5	[4]	19.5	J	HT	% BY WT.
1709632	% moisture	1709632-05	L10-52_17LT006_091317_LOB_05_TA	T	Percent Moisture	82.1	O-04	82.1	J	HT	% BY WT.
1709632	% Solids	1709632-05	L10-52_17LT006_091317_LOB_05_TA	T	Percent Solids	17.9	[5]	17.9	J	HT	% BY WT.
1709632	% moisture	1709632-06	L10-52_17LT006_091317_LOB_06_TA	T	Percent Moisture	82.8	O-04	82.8	J	HT	% BY WT.
1709632	% Solids	1709632-06	L10-52_17LT006_091317_LOB_06_TA	T	Percent Solids	17.2	[6]	17.2	J	HT	% BY WT.

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709632	% moisture	1709632-07	L10-52_17LT007_091317_LOB_07_TA	T	Percent Moisture	81.7	O-04	81.7	J	HT	% BY WT.
1709632	% Solids	1709632-07	L10-52_17LT007_091317_LOB_07_TA	T	Percent Solids	18.3	[7]	18.3	J	HT	% BY WT.
1709632	% moisture	1709632-08	L10-52_17LT007_091317_LOB_08_TA	T	Percent Moisture	82.5	O-04	82.5	J	HT	% BY WT.
1709632	% Solids	1709632-08	L10-52_17LT007_091317_LOB_08_TA	T	Percent Solids	17.5	[8]	17.5	J	HT	% BY WT.
1709632	% moisture	1709632-09	L10-52_17LT007_091317_LOB_09_TA	T	Percent Moisture	82.8	O-04	82.8	J	HT	% BY WT.
1709632	% Solids	1709632-09	L10-52_17LT007_091317_LOB_09_TA	T	Percent Solids	17.2	[9]	17.2	J	HT	% BY WT.
1709632	% moisture	1709632-10	L10-52_17LT008_091317_LOB_10_TA	T	Percent Moisture	81.4	O-04	81.4	J	HT	% BY WT.
1709632	% Solids	1709632-10	L10-52_17LT008_091317_LOB_10_TA	T	Percent Solids	18.6	[10]	18.6	J	HT	% BY WT.
1709632	% moisture	1709632-11	L10-52_17LT008_091317_LOB_11_TA	T	Percent Moisture	82.8	O-04	82.8	J	HT	% BY WT.
1709632	% Solids	1709632-11	L10-52_17LT008_091317_LOB_11_TA	T	Percent Solids	17.2	[11]	17.2	J	HT	% BY WT.
1709632	% moisture	1709632-12	L10-52_17LT008_091317_LOB_12_TA	T	Percent Moisture	81.3	O-04	81.3	J	HT	% BY WT.
1709632	% Solids	1709632-12	L10-52_17LT008_091317_LOB_12_TA	T	Percent Solids	18.7	[12]	18.7	J	HT	% BY WT.
1709632	% moisture	1709632-13	L10-52_17LT009_091317_LOB_13_TA	T	Percent Moisture	80	O-04	80	J	HT	% BY WT.
1709632	% Solids	1709632-13	L10-52_17LT009_091317_LOB_13_TA	T	Percent Solids	20	[13]	20	J	HT	% BY WT.
1709632	% moisture	1709632-18	L10-52_17LT040_091517_LOB_18_TA	T	Percent Moisture	81.6	O-04	81.6	J	HT	% BY WT.
1709632	% Solids	1709632-18	L10-52_17LT040_091517_LOB_18_TA	T	Percent Solids	18.4	[18]	18.4	J	HT	% BY WT.
1709632	% moisture	1709632-19	L10-52_17LT040_091517_LOB_19_TA	T	Percent Moisture	82	O-04	82	J	HT	% BY WT.
1709632	% Solids	1709632-19	L10-52_17LT040_091517_LOB_19_TA	T	Percent Solids	18	[19]	18	J	HT	% BY WT.
1709632	% moisture	1709632-20	L10-52_17LT040_091517_LOB_20_TA	T	Percent Moisture	82.8	O-04	82.8	J	HT	% BY WT.
1709632	% Solids	1709632-20	L10-52_17LT040_091517_LOB_20_TA	T	Percent Solids	17.2	[20]	17.2	J	HT	% BY WT.
1709632	% moisture	1709632-14	L10-52_17LT041_091517_LOB_14_TA	T	Percent Moisture	80.9	O-04	80.9	J	HT	% BY WT.
1709632	% Solids	1709632-14	L10-52_17LT041_091517_LOB_14_TA	T	Percent Solids	19.1	[14]	19.1	J	HT	% BY WT.
1709632	% moisture	1709632-15	L10-52_17LT041_091517_LOB_15_TA	T	Percent Moisture	82.3	O-04	82.3	J	HT	% BY WT.
1709632	% Solids	1709632-15	L10-52_17LT041_091517_LOB_15_TA	T	Percent Solids	17.7	[15]	17.7	J	HT	% BY WT.
1709632	% moisture	1709632-16	L10-52_17LT041_091517_LOB_16_TA	T	Percent Moisture	82.5	O-04	82.5	J	HT	% BY WT.
1709632	% Solids	1709632-16	L10-52_17LT041_091517_LOB_16_TA	T	Percent Solids	17.5	[16]	17.5	J	HT	% BY WT.
1709632	% moisture	1709632-17	L10-52_17LT042_091517_LOB_17_TA	T	Percent Moisture	82.6	O-04	82.6	J	HT	% BY WT.

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

SDG	Analysis Method	Lab Sample ID	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1709632	% Solids	1709632-17	L10-52_17LT042_091517_LOB_17_TA	T	Percent Solids	17.4	[17]	17.4	J	HT	% BY WT.

<u>Units</u>
NG/G = Nanogram per gram

<u>Validation Qualifier:</u>
J = Value is estimated

<u>Validation Reason Codes:</u>
LD = Lab duplicate limit exceeded
HT = Hold time exceeded

Created by: BCG 11/20/2017
Checked by: EP 11/21/2017

TABLE 3
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_01_WB	FS					30.5		9.9			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_02_WB	FS					30.6		7.5			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_03_WB	FS					32		12.7			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_04_WB	FS					35.8		10.4			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_05_WB	FS					29.5		12.3			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_01_WB	FS					53.8		7.5			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_02_WB	FS					39.9		4.1			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_03_WB	FS					37.4		5.7			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_04_WB	FS					59.2		7.7			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_05_WB	FS					54.5		6.1			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_01_WB	FS					37.1		16.9			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_02_WB	FS					45.5		5.9			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_03_WB	FS					33.2		11.6			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_04_WB	FS					21.8		4.6			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_05_WB	FS					42		16			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_01_WB	FS					28.9		12.6			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_02_WB	FS					23.9		9.7			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_03_WB	FS					24.7		8.7			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_04_WB	FS					22.1		9.3			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_05_WB	FS					25		11.1			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_01_WB	FS					17.6		9.5			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_02_WB	FS					21.2		8.7			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_03_WB	FS					14.7		8			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_04_WB	FS					12.4		3.4			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_05_WB	FS					18.3		9.5			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_01_WB	FS					10.3		6.2			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_02_WB	FS					24.6		11.8			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_03_WB	FS					29.8		11.4			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_04_WB	FS					31.5		17.7			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_05_WB	FS					38.8		10.8			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_01_WB	FS					12.9					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_02_WB	FS					12					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_03_WB	FS					9.71					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_04_WB	FS					12.9					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_05_WB	FS					8.94					
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_01_TA	FS	80.8	J	19.2	J	38.9				79.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_02_TA	FS	81.3	J	18.7	J	28.8				77.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_03_TA	FS	79.8	J	20.2	J	40.6				87.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_04_TA	FS	81.1	J	18.9	J	45.4				87.7	
1709489	FBJR_17LT025	09/14/17	FBJR_17LT025_091417_LOB_05_TA	FS	82.1	J	17.9	J	37.5				78.4	
1709489	FBJR_17LT025	09/14/17	FBJR_17LT025_091417_LOB_06_TA	FS	78.2	J	21.8	J	35.2				86.5	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_07_TA	FS	80	J	20	J	57.5				100	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_08_TA	FS	82.6	J	17.4	J	46.2				85.5	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_09_TA	FS	81.3	J	18.7	J	26.8				106	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_10_TA	FS	80.9	J	19.1	J	34.1				83.6	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_11_TA	FS	80.9	J	19.1	J	46.9				126	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_12_TA	FS	82.5	J	17.5	J	38.4				106	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_13_TA	FS	80.7	J	19.3	J	35.5				105	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_14_TA	FS	78.3	J	21.7	J	64.8				82.4	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_15_TA	FS	79.7	J	20.3	J	38.1				83.9	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_16_TA	FS	80.4	J	19.6	J	35.4				15.2	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_17_TA	FS	80.7	J	19.3	J	39.2				79.4	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_18_TA	FS	77.9	J	22.1	J	43.3				95.4	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_19_TA	FS	80.7	J	19.3	J	43.8				68.5	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_20_TA	FS	81.8	J	18.2	J	36				101	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_01_TA	FS	78.2	J	21.8	J	154				83.4	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_02_TA	FS	83	J	17	J	149				111	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_03_TA	FS	82.4	J	17.6	J	407				138	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_04_TA	FS	82.2	J	17.8	J	231				143	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_05_TA	FS	80.1	J	19.9	J	212				198	
1709490	CJ_17LT002	09/13/17	CJ_17LT002_091317_LOB_06_TA	FS	80.6	J	19.4	J	267				69.4	
1709490	CJ_17LT002	09/13/17	CJ_17LT002_091317_LOB_07_TA	FS	81.3	J	18.7	J	216				130	
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_08_TA	FS	83.8	J	16.2	J	193				106	
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_09_TA	FS	81.8	J	18.2	J	573				143	

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_10_TA	FS	82.1	J	17.9	J	386				152	
1709490	CJ_17LT004	09/13/17	CJ_17LT004_091317_LOB_11_TA	FS	81.3	J	18.7	J	229				77.9	
1709490	CJ_17LT004	09/13/17	CJ_17LT004_091317_LOB_12_TA	FS	77.7	J	22.3	J	925				141	
1709490	CJ_17LT044	09/15/17	CJ_17LT044_091517_LOB_19_TA	FS	80.8	J	19.2	J	120				104	
1709490	CJ_17LT044	09/15/17	CJ_17LT044_091517_LOB_20_TA	FS	80.7	J	19.3	J	183				95.8	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_15_TA	FS	82.3	J	17.7	J	291				152	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_16_TA	FS	82.7	J	17.3	J	358				126	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_17_TA	FS	80.8	J	19.2	J	457				132	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_18_TA	FS	83.6	J	16.4	J	114				85.9	
1709490	CJ_17LT048	09/15/17	CJ_17LT048_091517_LOB_13_TA	FS	80.9	J	19.1	J	151				105	
1709490	CJ_17LT048	09/15/17	CJ_17LT048_091517_LOB_14_TA	FS	78.9	J	21.1	J	150				101	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_01_TA	FS	79.6	J	20.4	J	317	J			124	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_02_TA	FS	81.4	J	18.6	J	549				154	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_03_TA	FS	81.3	J	18.7	J	139				103	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_04_TA	FS	81.2	J	18.8	J	359				184	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_05_TA	FS	81.9	J	18.1	J	257				103	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_06_TA	FS	79.9	J	20.1	J	263				132	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_07_TA	FS	83.6	J	16.4	J	384				141	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_08_TA	FS	82.2	J	17.8	J	591				184	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_09_TA	FS	80.8	J	19.2	J	65.6				94.9	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_10_TA	FS	82.2	J	17.8	J	272				157	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_11_TA	FS	82.2	J	17.8	J	120				111	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_12_TA	FS	81.8	J	18.2	J	247				115	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_13_TA	FS	81.4	J	18.6	J	220				110	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_14_TA	FS	82	J	18	J	286				120	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_15_TA	FS	81.1	J	18.9	J	223				76.7	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_16_TA	FS	82.6	J	17.4	J	179				160	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_17_TA	FS	81.2	J	18.8	J	114				77.1	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_18_TA	FS	79.8	J	20.2	J	177				79.4	
1709491	L9-45_17LT018	09/13/17	L9-45_17LT018_091317_LOB_19_TA	FS	81.4	J	18.6	J	117				92.5	
1709491	L9-45_17LT018	09/13/17	L9-45_17LT018_091317_LOB_20_TA	FS	80.1	J	19.9	J	240				88	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_01_TA	FS	81.8	J	18.2	J	303				134	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_02_TA	FS	77.2	J	22.8	J	290				144	

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_03_TA	FS	81.9	J	18.1	J	397				113	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_04_TA	FS	79.7	J	20.3	J	191				72.5	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_05_TA	FS	82	J	18	J	180				109	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_06_TA	FS	81.7	J	18.3	J	244				136	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_07_TA	FS	82.4	J	17.6	J	343				156	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_08_TA	FS	80.2	J	19.8	J	468				169	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_09_TA	FS	78.5	J	21.5	J	433				156	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_10_TA	FS	78.4	J	21.6	J	165				80.9	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_11_TA	FS	80.1	J	19.9	J	167				84.3	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_12_TA	FS	81.5	J	18.5	J	279				134	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_13_TA	FS	82	J	18	J	291				146	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_14_TA	FS	80.5	J	19.5	J	533				152	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_15_TA	FS	80.6	J	19.4	J	290				129	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_16_TA	FS	81	J	19	J	526				194	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_17_TA	FS	82.5	J	17.5	J	574				234	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_18_TA	FS	81.1	J	18.9	J	390				183	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_19_TA	FS	81.3	J	18.7	J	260				112	
1709492	SVE-01_17LT043	09/15/17	SVE-01_17LT043_091517_LOB_20_TA	FS	81.1	J	18.9	J	168				115	
1709493	HB-01_17LT019	09/13/17	HB-01_17LT019_091317_LOB_01_TA	FS	80.9	J	19.1	J	74.2				89	
1709493	HB-01_17LT021	09/13/17	HB-01_17LT021_091317_LOB_02_TA	FS	82.2	J	17.8	J	99.8				102	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_03_TA	FS	83.7	J	16.3	J	123				101	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_04_TA	FS	81.7	J	18.3	J	66.3				63.7	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_05_TA	FS	81.9	J	18.1	J	62.7				54.6	
1709493	HB-01_17LT023	09/13/17	HB-01_17LT023_091317_LOB_06_TA	FS	82.4	J	17.6	J	64.8				85.1	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_07_TA	FS	83.4	J	16.6	J	184				149	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_08_TA	FS	81.7	J	18.3	J	149				82	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_09_TA	FS	84.1	J	15.9	J	82.8				66.2	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_10_TA	FS	81.6	J	18.4	J	113				86.8	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_11_TA	FS	83.8	J	16.2	J	123				112	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_12_TA	FS	83	J	17	J	83.3				83.2	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_13_TA	FS	83.4	J	16.6	J	85.6				84.4	
1709493	HB-01_17LT049	09/15/17	HB-01_17LT049_091517_LOB_14_TA	FS	82.4	J	17.6	J	108				94	
1709493	HB-01_17LT049	09/15/17	HB-01_17LT049_091517_LOB_15_TA	FS	83.4	J	16.6	J	50.3				84.4	

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709493	HB-01_17LT050	09/15/17	HB-01_17LT050_091517_LOB_16_TA	FS	81.6	J	18.4	J	138				121	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_17_TA	FS	82.2	J	17.8	J	59.4				102	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_18_TA	FS	78.5	J	21.5	J	264				125	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_19_TA	FS	82.4	J	17.6	J	85.9				64.4	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_20_TA	FS	82.3	J	17.7	J	99.4				77.1	
1709612	BO-04_17ET0008	09/17/17	BO-04_17ET008_091717_TOM_01_WB	FS					104					
1709612	BO-04_17ET0010	09/17/17	BO-04_17ET010_091717_TOM_02_WB	FS					148					
1709612	BO-04_17ET0014	09/17/17	BO-04_17ET014_091717_TOM_03_WB	FS					123					
1709612	BO-04_17ET0025	09/20/17	BO-04_17ET025_092017_TOM_04_WB	FS					152					
1709612	BO-04_17ET0026	09/20/17	BO-04_17ET026_092017_TOM_05_WB	FS					199	J				
1709612	BO-04_17ET0030	09/20/17	BO-04_17ET030_092017_TOM_06_WB	FS					224					
1709612	BO-04_17ET0035	09/20/17	BO-04_17ET035_092017_TOM_07_WB	FS					173					
1709612	BO-04_17ET0041	09/20/17	BO-04_17ET041_092017_TOM_08_WB	FS					162					
1709613	OB-05_17ET002	09/17/17	OB-05_17ET002_091717_TOM_01_WB	FS					268					
1709613	OB-05_17ET002	09/17/17	OB-05_17ET002_091717_TOM_02_WB	FS					139					
1709613	OB-05_17ET002	09/18/17	OB-05_17ET002_091817_TOM_16_WB	FS					71.9					
1709613	OB-05_17ET003	09/17/17	OB-05_17ET003_091717_TOM_03_WB	FS					70.7					
1709613	OB-05_17ET003	09/17/17	OB-05_17ET003_091717_TOM_04_WB	FS					122					
1709613	OB-05_17ET003	09/18/17	OB-05_17ET003_091817_TOM_17_WB	FS					173					
1709613	OB-05_17ET003	09/18/17	OB-05_17ET003_091817_TOM_18_WB	FS					152					
1709613	OB-05_17ET005	09/18/17	OB-05_17ET005_091817_TOM_19_WB	FS					78.4					
1709613	OB-05_17ET008	09/18/17	OB-05_17ET008_091817_TOM_20_WB	FS					72.7					
1709613	OB-05_17ET009	09/17/17	OB-05_17ET009_091717_TOM_05_WB	FS					379					
1709613	OB-05_17ET010	09/17/17	OB-05_17ET010_091717_TOM_06_WB	FS					99.8					
1709613	OB-05_17ET011	09/17/17	OB-05_17ET011_091717_TOM_07_WB	FS					90.7					
1709613	OB-05_17ET012	09/17/17	OB-05_17ET012_091717_TOM_08_WB	FS					230					
1709613	OB-05_17ET012	09/17/17	OB-05_17ET012_091717_TOM_09_WB	FS					118					
1709613	OB-05_17ET013	09/17/17	OB-05_17ET013_091717_TOM_10_WB	FS					227					
1709613	OB-05_17ET013	09/17/17	OB-05_17ET013_091717_TOM_11_WB	FS					124					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_12_WB	FS					103					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_13_WB	FS					159					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_14_WB	FS					126					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_15_WB	FS					315					

TABLE 3
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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_01_WB	FS					274					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_02_WB	FS					382					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_03_WB	FS					389					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_04_WB	FS					233					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_05_WB	FS					190					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_06_WB	FS					66					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_07_WB	FS					308					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_08_WB	FS					413					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_09_WB	FS					78.7					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_10_WB	FS					205					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_11_WB	FS					70					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_12_WB	FS					49.7					
1709614	OB-01_17ET003	09/16/17	OB-01_17ET003_091617_TOM_13_WB	FS					231					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_14_WB	FS					50.1					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_15_WB	FS					81.1					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_16_WB	FS					77.3					
1709614	OB-01_17ET005	09/16/17	OB-01_17ET005_091617_TOM_17_WB	FS					65.7					
1709614	OB-01_17ET006	09/16/17	OB-01_17ET006_091617_TOM_18_WB	FS					136					
1709614	OB-01_17ET007	09/16/17	OB-01_17ET007_091617_TOM_19_WB	FS					160					
1709614	OB-01_17ET008	09/16/17	OB-01_17ET008_091617_TOM_20_WB	FS					182					
1709615	ES-13_17ET717	09/18/17	ES-13_17ET717_091817_TOM_11_WB	FS					172					
1709615	ES-13_17ET718	09/18/17	ES-13_17ET718_091817_TOM_02_WB	FS					114					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_03_WB	FS					52.8					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_04_WB	FS					36					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_05_WB	FS					45.5					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_06_WB	FS					32.7					
1709615	ES-13_17ET722	09/18/17	ES-13_17ET722_091817_TOM_07_WB	FS					52.2					
1709615	ES-13_17ET722	09/18/17	ES-13_17ET722_091817_TOM_08_WB	FS					60.2					
1709615	ES-13_17ET723	09/18/17	ES-13_17ET723_091817_TOM_09_WB	FS					239					
1709615	ES-13_17ET723	09/18/17	ES-13_17ET723_091817_TOM_10_WB	FS					209					
1709615	ES-13_17LT012	09/13/17	ES-13_17LT012_091317_TOM_01_WB	FS					226					
1709616	ES-FP_17ET658	09/15/17	ES-FP_17ET658_091517_TOM_01_WB	FS					37.2					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_01_WB	FS					5.17					

TABLE 3
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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_02_WB	FS					8.36					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_03_WB	FS					5.05					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_04_WB	FS					7.11					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_05_WB	FS					7.57					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_06_WB	FS					6.46					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_07_WB	FS					7.7					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_08_WB	FS					7.6					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_09_WB	FS					6.16					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_10_WB	FS					6.74					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_11_WB	FS					6.7					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_12_WB	FS					4.81					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_13_WB	FS					5.65					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_14_WB	FS					6.1					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_15_WB	FS					5.08					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_16_WB	FS					6.6					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_17_WB	FS					5.85					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_18_WB	FS					7.84					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_19_WB	FS					6.53					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_20_WB	FS					4.44					
1709618	OB-01_17MT001	09/18/17	OB-01_17MT001_091817_MUM_01_WB	FS					86.9					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_09_WB	FS					79.6					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_10_WB	FS					242					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_11_WB	FS					83.4					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_12_WB	FS					130					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_13_WB	FS					127					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_02_WB	FS					86.1					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_03_WB	FS					103					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_04_WB	FS					154					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_05_WB	FS					110					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_06_WB	FS					109					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_07_WB	FS					37.4					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_08_WB	FS					87.2					
1709618	OB-01_17MT002	09/19/17	OB-01_17MT002_091917_MUM_14_WB	FS					237					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709618	OB-01_17MT002	09/19/17	OB-01_17MT002_091917_MUM_15_WB	FS					118					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_01_WB	FS					150					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_02_WB	FS					114					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_03_WB	FS					121					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_04_WB	FS					117					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_05_WB	FS					65.2					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_06_WB	FS					76.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_07_WB	FS					71.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_08_WB	FS					77.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_09_WB	FS					74.1					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_10_WB	FS					74.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_11_WB	FS					77.1					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_12_WB	FS					80.8					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_13_WB	FS					76.9					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_14_WB	FS					81.3					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_15_WB	FS					77.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_16_WB	FS					65					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_17_WB	FS					66.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_18_WB	FS					69.9					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_19_WB	FS					76.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_20_WB	FS					62.6					
1709620	MMMC-01_17MT001	09/18/17	MMMC-01_17MT001_091817_MUM_01_WB	FS					51.4					
1709620	MMMC-01_17MT001	09/20/17	MMMC-01_17MT001_092017_MUM_02_WB	FS					137					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_06_WB	FS					109					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_07_WB	FS					122					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_08_WB	FS					107					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_09_WB	FS					88.2					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_10_WB	FS					207					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_11_WB	FS					94.4					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_12_WB	FS					73.2					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_13_WB	FS					104					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_14_WB	FS					150					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_15_WB	FS					145					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_16_WB	FS					72.4					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_17_WB	FS					136					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_18_WB	FS					112					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_19_WB	FS					100					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_20_WB	FS					256					
1709620	MMMC-01_17MT004	09/20/17	MMMC-01_17MT004_092017_MUM_03_WB	FS					173					
1709620	MMMC-01_17MT004	09/20/17	MMMC-01_17MT004_092017_MUM_04_WB	FS					109					
1709621	BO-04_17SN001	09/17/17	BO-04_17SN001_091717_MUM_01_WB	FS					63.4					
1709621	QC	09/15/17	ESFP_091517_BAIT_01_QC	FS					20.1					
1709621	QC	09/15/17	ESFP_091517_BAIT_02_QC	FS					0.092	J				
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_01_WB	FS					30.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_02_WB	FS					87.8	J				
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_03_WB	FS					42.2					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_04_WB	FS					35.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_05_WB	FS					29.9					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_06_WB	FS					76.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_07_WB	FS					78.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_08_WB	FS					32.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_09_WB	FS					26.4					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_10_WB	FS					37.4					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_11_WB	FS					37.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_12_WB	FS					29.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_13_WB	FS					63.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_14_WB	FS					43.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_15_WB	FS					39.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_16_WB	FS					34.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_17_WB	FS					56.6					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_18_WB	FS					40.2					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_19_WB	FS					38.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_20_WB	FS					30.1					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_01_WB	FS					18.1					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_02_WB	FS					14.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_03_WB	FS					6.88					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	Location ID	Sample Date	Sample ID	QC Code	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_04_WB	FS					22.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_05_WB	FS					10.8					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_06_WB	FS					14.5					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_07_WB	FS					26.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_08_WB	FS					24.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_09_WB	FS					8.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_10_WB	FS					10.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_11_WB	FS					10.9					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_12_WB	FS					6.57					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_13_WB	FS					9.38					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_14_WB	FS					19					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_15_WB	FS					7.29					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_16_WB	FS					15.7					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_17_WB	FS					12.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_18_WB	FS					7.36					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_19_WB	FS					7.98					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_20_WB	FS					11.8					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_01_WB	FS					72.1					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_02_WB	FS					64.4					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_03_WB	FS					83.5					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_04_WB	FS					96.5					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_05_WB	FS					83.9					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_01_WB	FS					78.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_02_WB	FS					92.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_03_WB	FS					68.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_04_WB	FS					174					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_05_WB	FS					92.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_06_WB	FS					83.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_07_WB	FS					207					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_08_WB	FS					128					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_09_WB	FS					185					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_10_WB	FS					156					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_11_WB	FS					75.7					

TABLE 3
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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_12_WB	FS					43					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_13_WB	FS					36.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_14_WB	FS					39					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_15_WB	FS					34.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_16_WB	FS					52					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_17_WB	FS					34.1					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_18_WB	FS					42.5					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_19_WB	FS					31.7					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_20_WB	FS					43.6					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_07_WB	FS					52.1					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_08_WB	FS					42.7					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_09_WB	FS					38.2					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_10_WB	FS					47.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_11_WB	FS					61.7					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_12_WB	FS					42.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_13_WB	FS					49.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_14_WB	FS					49.6					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_15_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_16_WB	FS					49.2					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_17_WB	FS					46.9					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_18_WB	FS					44.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_19_WB	FS					47.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_20_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_01_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_02_WB	FS					36					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_03_WB	FS					72					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_04_WB	FS					77.4					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_05_WB	FS					46.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_06_WB	FS					39.7					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_01_WB	FS					5.52					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_02_WB	FS					6.18					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_03_WB	FS					11.7					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_04_WB	FS					8.51					

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_05_WB	FS					7.09					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_06_WB	FS					5.46					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_07_WB	FS					11.9					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_08_WB	FS					13					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_09_WB	FS					7.19					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_10_WB	FS					7.74					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_11_WB	FS					9.2					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_12_WB	FS					7.44					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_13_WB	FS					10.5					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_14_WB	FS					6.45					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_15_WB	FS					10.3					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_16_WB	FS					7.17					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_17_WB	FS					8.36					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_18_WB	FS					6.85					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_19_WB	FS					7.68					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_20_WB	FS					7.02					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_01_WB	FS					75					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_02_WB	FS					111					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_03_WB	FS					116					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_04_WB	FS					123					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_05_WB	FS					97.6					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_06_WB	FS					63.5					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_07_WB	FS					95.6					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_08_WB	FS					104					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_09_WB	FS					103					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_10_WB	FS					89.2					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_11_WB	FS					160					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_12_WB	FS					92.3					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_13_WB	FS					72.8					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_14_WB	FS					88.7					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_15_WB	FS					68.9	J				
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_16_WB	FS					207					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_18_WB	FS					79.6					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_19_WB	FS					86.1					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_20_WB	FS					75.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_01_WB	FS					48.8					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_02_WB	FS					58.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_03_WB	FS					81.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_04_WB	FS					112					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_05_WB	FS					53					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_06_WB	FS					114					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_07_WB	FS					115					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_08_WB	FS					39.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_09_WB	FS					73.4					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_10_WB	FS					140					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_11_WB	FS					168					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_12_WB	FS					96.7					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_13_WB	FS					87					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_14_WB	FS					181					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_15_WB	FS					122					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_16_WB	FS					55.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_17_WB	FS					91.5					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_18_WB	FS					82.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_19_WB	FS					72					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_20_WB	FS					97.3					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_01_WB	FS					80.3					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_02_WB	FS					86.5					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_03_WB	FS					48.4					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_04_WB	FS					144					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_05_WB	FS					71.9					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_06_WB	FS					109					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_07_WB	FS					110					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_08_WB	FS					122					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_09_WB	FS					106					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_10_WB	FS					61.8					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_11_WB	FS					80.5					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_12_WB	FS					55.7					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_13_WB	FS					86.4					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_14_WB	FS					86.8					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_15_WB	FS					125					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_16_WB	FS					73.2					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_17_WB	FS					111					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_18_WB	FS					90.7					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_19_WB	FS					76.2					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_20_WB	FS					79.3					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_01_WB	FS					77.1					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_02_WB	FS					71.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_03_WB	FS					66.5					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_04_WB	FS					71.2					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_06_WB	FS					78.4					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_07_WB	FS					60.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_08_WB	FS					65.9					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_09_WB	FS					97.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_10_WB	FS					66.1					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_11_WB	FS					64.5					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_12_WB	FS					78.9					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_13_WB	FS					85.9					
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_01_TA	FS	82.1	J	17.9	J	194				130	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_02_TA	FS	82.5	J	17.5	J	153				122	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_03_TA	FS	82.7	J	17.3	J	321				92.4	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_04_TA	FS	80.5	J	19.5	J	309				92.1	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_05_TA	FS	82.1	J	17.9	J	128				96.9	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_06_TA	FS	82.8	J	17.2	J	178				116	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_07_TA	FS	81.7	J	18.3	J	1730				210	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_08_TA	FS	82.5	J	17.5	J	193				76	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_09_TA	FS	82.8	J	17.2	J	542				147	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_10_TA	FS	81.4	J	18.6	J	237				137	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_11_TA	FS	82.8	J	17.2	J	267				134	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_12_TA	FS	81.3	J	18.7	J	141				125	

TABLE 3
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709632	L10-52_17LT009	09/13/17	L10-52_17LT009_091317_LOB_13_TA	FS	80	J	20	J	241				126	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_18_TA	FS	81.6	J	18.4	J	519				141	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_19_TA	FS	82	J	18	J	654				194	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_20_TA	FS	82.8	J	17.2	J	278				193	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_14_TA	FS	80.9	J	19.1	J	174				46.5	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_15_TA	FS	82.3	J	17.7	J	212				88.6	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_16_TA	FS	82.5	J	17.5	J	250				94.5	
1709632	L10-52_17LT042	09/13/17	L10-52_17LT042_091517_LOB_17_TA	FS	82.6	J	17.4	J	181				144	

Notes:

NG/G = Nanogram per gram
NG/L = Nanogram per liter
FS = Field Sample
EB = Equipment Blank

J = Value is estimated
U = The target compound was not detected above the method detection limit
SDG = Sample Delivery Group

TABLE 3
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

SDGs 1709489, 1709490, 1709491, 1709492, 1709493, 1709632, 1709627, 1709628, 1709629, 1709630, 1709631, 1709617, 1709618, 1709619, 1709620, 1709621, 1709622, 1709623, 1709624, 1709625, 1709626, 1708118, 1708240, 1708241, 1709612, 1709613, 1709614, 1709615 and 1709616

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_01_WB	FS					30.5		9.9			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_02_WB	FS					30.6		7.5			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_03_WB	FS					32		12.7			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_04_WB	FS					35.8		10.4			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_05_WB	FS					29.5		12.3			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_01_WB	FS					53.8		7.5			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_02_WB	FS					39.9		4.1			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_03_WB	FS					37.4		5.7			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_04_WB	FS					59.2		7.7			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_05_WB	FS					54.5		6.1			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_01_WB	FS					37.1		16.9			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_02_WB	FS					45.5		5.9			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_03_WB	FS					33.2		11.6			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_04_WB	FS					21.8		4.6			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_05_WB	FS					42		16			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_01_WB	FS					28.9		12.6			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_02_WB	FS					23.9		9.7			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_03_WB	FS					24.7		8.7			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_04_WB	FS					22.1		9.3			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_05_WB	FS					25		11.1			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_01_WB	FS					17.6		9.5			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_02_WB	FS					21.2		8.7			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_03_WB	FS					14.7		8			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_04_WB	FS					12.4		3.4			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_05_WB	FS					18.3		9.5			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_01_WB	FS					10.3		6.2			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_02_WB	FS					24.6		11.8			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_03_WB	FS					29.8		11.4			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_04_WB	FS					31.5		17.7			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_05_WB	FS					38.8		10.8			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_01_WB	FS					12.9					

TABLE 3
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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

			Analysis Method						EPA 1631		EPA 1630			
			Parameter		% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
			Unit		PERCENT		PERCENT		NG/G		NG/G		Grams	
			Fraction		Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_02_WB	FS					12					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_03_WB	FS					9.71					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_04_WB	FS					12.9					
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_05_WB	FS					8.94					
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_01_TA	FS	80.8	J	19.2	J	38.9				79.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_02_TA	FS	81.3	J	18.7	J	28.8				77.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_03_TA	FS	79.8	J	20.2	J	40.6				87.5	
1709489	FBJR_17LT024	09/14/17	FBJR_17LT024_091417_LOB_04_TA	FS	81.1	J	18.9	J	45.4				87.7	
1709489	FBJR_17LT025	09/14/17	FBJR_17LT025_091417_LOB_05_TA	FS	82.1	J	17.9	J	37.5				78.4	
1709489	FBJR_17LT025	09/14/17	FBJR_17LT025_091417_LOB_06_TA	FS	78.2	J	21.8	J	35.2				86.5	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_07_TA	FS	80	J	20	J	57.5				100	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_08_TA	FS	82.6	J	17.4	J	46.2				85.5	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_09_TA	FS	81.3	J	18.7	J	26.8				106	
1709489	FBJR_17LT026	09/14/17	FBJR_17LT026_091417_LOB_10_TA	FS	80.9	J	19.1	J	34.1				83.6	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_11_TA	FS	80.9	J	19.1	J	46.9				126	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_12_TA	FS	82.5	J	17.5	J	38.4				106	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_13_TA	FS	80.7	J	19.3	J	35.5				105	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_14_TA	FS	78.3	J	21.7	J	64.8				82.4	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_15_TA	FS	79.7	J	20.3	J	38.1				83.9	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_16_TA	FS	80.4	J	19.6	J	35.4				15.2	
1709489	FBJR_17LT027	09/14/17	FBJR_17LT027_091417_LOB_17_TA	FS	80.7	J	19.3	J	39.2				79.4	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_18_TA	FS	77.9	J	22.1	J	43.3				95.4	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_19_TA	FS	80.7	J	19.3	J	43.8				68.5	
1709489	FBJR_17LT028	09/14/17	FBJR_17LT028_091417_LOB_20_TA	FS	81.8	J	18.2	J	36				101	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_01_TA	FS	78.2	J	21.8	J	154				83.4	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_02_TA	FS	83	J	17	J	149				111	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_03_TA	FS	82.4	J	17.6	J	407				138	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_04_TA	FS	82.2	J	17.8	J	231				143	
1709490	CJ_17LT001	09/13/17	CJ_17LT001_091317_LOB_05_TA	FS	80.1	J	19.9	J	212				198	
1709490	CJ_17LT002	09/13/17	CJ_17LT002_091317_LOB_06_TA	FS	80.6	J	19.4	J	267				69.4	
1709490	CJ_17LT002	09/13/17	CJ_17LT002_091317_LOB_07_TA	FS	81.3	J	18.7	J	216				130	
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_08_TA	FS	83.8	J	16.2	J	193				106	
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_09_TA	FS	81.8	J	18.2	J	573				143	

TABLE 3
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2017 BIOTA SAMPLING
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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709490	CJ_17LT003	09/13/17	CJ_17LT003_091317_LOB_10_TA	FS	82.1	J	17.9	J	386				152	
1709490	CJ_17LT004	09/13/17	CJ_17LT004_091317_LOB_11_TA	FS	81.3	J	18.7	J	229				77.9	
1709490	CJ_17LT004	09/13/17	CJ_17LT004_091317_LOB_12_TA	FS	77.7	J	22.3	J	925				141	
1709490	CJ_17LT044	09/15/17	CJ_17LT044_091517_LOB_19_TA	FS	80.8	J	19.2	J	120				104	
1709490	CJ_17LT044	09/15/17	CJ_17LT044_091517_LOB_20_TA	FS	80.7	J	19.3	J	183				95.8	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_15_TA	FS	82.3	J	17.7	J	291				152	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_16_TA	FS	82.7	J	17.3	J	358				126	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_17_TA	FS	80.8	J	19.2	J	457				132	
1709490	CJ_17LT047	09/15/17	CJ_17LT047_091517_LOB_18_TA	FS	83.6	J	16.4	J	114				85.9	
1709490	CJ_17LT048	09/15/17	CJ_17LT048_091517_LOB_13_TA	FS	80.9	J	19.1	J	151				105	
1709490	CJ_17LT048	09/15/17	CJ_17LT048_091517_LOB_14_TA	FS	78.9	J	21.1	J	150				101	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_01_TA	FS	79.6	J	20.4	J	317	J			124	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_02_TA	FS	81.4	J	18.6	J	549				154	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_03_TA	FS	81.3	J	18.7	J	139				103	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_04_TA	FS	81.2	J	18.8	J	359				184	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_05_TA	FS	81.9	J	18.1	J	257				103	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_06_TA	FS	79.9	J	20.1	J	263				132	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_07_TA	FS	83.6	J	16.4	J	384				141	
1709491	L9-45_17LT015	09/13/17	L9-45_17LT015_091317_LOB_08_TA	FS	82.2	J	17.8	J	591				184	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_09_TA	FS	80.8	J	19.2	J	65.6				94.9	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_10_TA	FS	82.2	J	17.8	J	272				157	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_11_TA	FS	82.2	J	17.8	J	120				111	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_12_TA	FS	81.8	J	18.2	J	247				115	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_13_TA	FS	81.4	J	18.6	J	220				110	
1709491	L9-45_17LT016	09/13/17	L9-45_17LT016_091317_LOB_14_TA	FS	82	J	18	J	286				120	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_15_TA	FS	81.1	J	18.9	J	223				76.7	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_16_TA	FS	82.6	J	17.4	J	179				160	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_17_TA	FS	81.2	J	18.8	J	114				77.1	
1709491	L9-45_17LT017	09/13/17	L9-45_17LT017_091317_LOB_18_TA	FS	79.8	J	20.2	J	177				79.4	
1709491	L9-45_17LT018	09/13/17	L9-45_17LT018_091317_LOB_19_TA	FS	81.4	J	18.6	J	117				92.5	
1709491	L9-45_17LT018	09/13/17	L9-45_17LT018_091317_LOB_20_TA	FS	80.1	J	19.9	J	240				88	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_01_TA	FS	81.8	J	18.2	J	303				134	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_02_TA	FS	77.2	J	22.8	J	290				144	

TABLE 3
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2017 BIOTA SAMPLING
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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_03_TA	FS	81.9	J	18.1	J	397				113	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_04_TA	FS	79.7	J	20.3	J	191				72.5	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_05_TA	FS	82	J	18	J	180				109	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_06_TA	FS	81.7	J	18.3	J	244				136	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_07_TA	FS	82.4	J	17.6	J	343				156	
1709492	SVE-01_17LT011	09/13/17	SVE-01_17LT011_091317_LOB_08_TA	FS	80.2	J	19.8	J	468				169	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_09_TA	FS	78.5	J	21.5	J	433				156	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_10_TA	FS	78.4	J	21.6	J	165				80.9	
1709492	SVE-01_17LT012	09/13/17	SVE-01_17LT012_091317_LOB_11_TA	FS	80.1	J	19.9	J	167				84.3	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_12_TA	FS	81.5	J	18.5	J	279				134	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_13_TA	FS	82	J	18	J	291				146	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_14_TA	FS	80.5	J	19.5	J	533				152	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_15_TA	FS	80.6	J	19.4	J	290				129	
1709492	SVE-01_17LT013	09/13/17	SVE-01_17LT013_091317_LOB_16_TA	FS	81	J	19	J	526				194	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_17_TA	FS	82.5	J	17.5	J	574				234	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_18_TA	FS	81.1	J	18.9	J	390				183	
1709492	SVE-01_17LT014	09/13/17	SVE-01_17LT014_091317_LOB_19_TA	FS	81.3	J	18.7	J	260				112	
1709492	SVE-01_17LT043	09/15/17	SVE-01_17LT043_091517_LOB_20_TA	FS	81.1	J	18.9	J	168				115	
1709493	HB-01_17LT019	09/13/17	HB-01_17LT019_091317_LOB_01_TA	FS	80.9	J	19.1	J	74.2				89	
1709493	HB-01_17LT021	09/13/17	HB-01_17LT021_091317_LOB_02_TA	FS	82.2	J	17.8	J	99.8				102	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_03_TA	FS	83.7	J	16.3	J	123				101	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_04_TA	FS	81.7	J	18.3	J	66.3				63.7	
1709493	HB-01_17LT022	09/13/17	HB-01_17LT022_091317_LOB_05_TA	FS	81.9	J	18.1	J	62.7				54.6	
1709493	HB-01_17LT023	09/13/17	HB-01_17LT023_091317_LOB_06_TA	FS	82.4	J	17.6	J	64.8				85.1	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_07_TA	FS	83.4	J	16.6	J	184				149	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_08_TA	FS	81.7	J	18.3	J	149				82	
1709493	HB-01_17LT034	09/15/17	HB-01_17LT034_091517_LOB_09_TA	FS	84.1	J	15.9	J	82.8				66.2	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_10_TA	FS	81.6	J	18.4	J	113				86.8	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_11_TA	FS	83.8	J	16.2	J	123				112	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_12_TA	FS	83	J	17	J	83.3				83.2	
1709493	HB-01_17LT036	09/15/17	HB-01_17LT036_091517_LOB_13_TA	FS	83.4	J	16.6	J	85.6				84.4	
1709493	HB-01_17LT049	09/15/17	HB-01_17LT049_091517_LOB_14_TA	FS	82.4	J	17.6	J	108				94	
1709493	HB-01_17LT049	09/15/17	HB-01_17LT049_091517_LOB_15_TA	FS	83.4	J	16.6	J	50.3				84.4	

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	Location ID	Sample Date	Sample ID	QC Code	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709493	HB-01_17LT050	09/15/17	HB-01_17LT050_091517_LOB_16_TA	FS	81.6	J	18.4	J	138				121	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_17_TA	FS	82.2	J	17.8	J	59.4				102	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_18_TA	FS	78.5	J	21.5	J	264				125	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_19_TA	FS	82.4	J	17.6	J	85.9				64.4	
1709493	HB-01_17LT052	09/15/17	HB-01_17LT052_091517_LOB_20_TA	FS	82.3	J	17.7	J	99.4				77.1	
1709612	BO-04_17ET0008	09/17/17	BO-04_17ET008_091717_TOM_01_WB	FS					104					
1709612	BO-04_17ET0010	09/17/17	BO-04_17ET010_091717_TOM_02_WB	FS					148					
1709612	BO-04_17ET0014	09/17/17	BO-04_17ET014_091717_TOM_03_WB	FS					123					
1709612	BO-04_17ET0025	09/20/17	BO-04_17ET025_092017_TOM_04_WB	FS					152					
1709612	BO-04_17ET0026	09/20/17	BO-04_17ET026_092017_TOM_05_WB	FS					199	J				
1709612	BO-04_17ET0030	09/20/17	BO-04_17ET030_092017_TOM_06_WB	FS					224					
1709612	BO-04_17ET0035	09/20/17	BO-04_17ET035_092017_TOM_07_WB	FS					173					
1709612	BO-04_17ET0041	09/20/17	BO-04_17ET041_092017_TOM_08_WB	FS					162					
1709613	OB-05_17ET002	09/17/17	OB-05_17ET002_091717_TOM_01_WB	FS					268					
1709613	OB-05_17ET002	09/17/17	OB-05_17ET002_091717_TOM_02_WB	FS					139					
1709613	OB-05_17ET002	09/18/17	OB-05_17ET002_091817_TOM_16_WB	FS					71.9					
1709613	OB-05_17ET003	09/17/17	OB-05_17ET003_091717_TOM_03_WB	FS					70.7					
1709613	OB-05_17ET003	09/17/17	OB-05_17ET003_091717_TOM_04_WB	FS					122					
1709613	OB-05_17ET003	09/18/17	OB-05_17ET003_091817_TOM_17_WB	FS					173					
1709613	OB-05_17ET003	09/18/17	OB-05_17ET003_091817_TOM_18_WB	FS					152					
1709613	OB-05_17ET005	09/18/17	OB-05_17ET005_091817_TOM_19_WB	FS					78.4					
1709613	OB-05_17ET008	09/18/17	OB-05_17ET008_091817_TOM_20_WB	FS					72.7					
1709613	OB-05_17ET009	09/17/17	OB-05_17ET009_091717_TOM_05_WB	FS					379					
1709613	OB-05_17ET010	09/17/17	OB-05_17ET010_091717_TOM_06_WB	FS					99.8					
1709613	OB-05_17ET011	09/17/17	OB-05_17ET011_091717_TOM_07_WB	FS					90.7					
1709613	OB-05_17ET012	09/17/17	OB-05_17ET012_091717_TOM_08_WB	FS					230					
1709613	OB-05_17ET012	09/17/17	OB-05_17ET012_091717_TOM_09_WB	FS					118					
1709613	OB-05_17ET013	09/17/17	OB-05_17ET013_091717_TOM_10_WB	FS					227					
1709613	OB-05_17ET013	09/17/17	OB-05_17ET013_091717_TOM_11_WB	FS					124					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_12_WB	FS					103					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_13_WB	FS					159					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_14_WB	FS					126					
1709613	OB-05_17ET014	09/17/17	OB-05_17ET014_091717_TOM_15_WB	FS					315					

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_01_WB	FS					274					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_02_WB	FS					382					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_03_WB	FS					389					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_04_WB	FS					233					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_05_WB	FS					190					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_06_WB	FS					66					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_07_WB	FS					308					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_08_WB	FS					413					
1709614	OB-01_17ET001	09/16/17	OB-01_17ET001_091617_TOM_09_WB	FS					78.7					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_10_WB	FS					205					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_11_WB	FS					70					
1709614	OB-01_17ET002	09/16/17	OB-01_17ET002_091617_TOM_12_WB	FS					49.7					
1709614	OB-01_17ET003	09/16/17	OB-01_17ET003_091617_TOM_13_WB	FS					231					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_14_WB	FS					50.1					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_15_WB	FS					81.1					
1709614	OB-01_17ET004	09/16/17	OB-01_17ET004_091617_TOM_16_WB	FS					77.3					
1709614	OB-01_17ET005	09/16/17	OB-01_17ET005_091617_TOM_17_WB	FS					65.7					
1709614	OB-01_17ET006	09/16/17	OB-01_17ET006_091617_TOM_18_WB	FS					136					
1709614	OB-01_17ET007	09/16/17	OB-01_17ET007_091617_TOM_19_WB	FS					160					
1709614	OB-01_17ET008	09/16/17	OB-01_17ET008_091617_TOM_20_WB	FS					182					
1709615	ES-13_17ET717	09/18/17	ES-13_17ET717_091817_TOM_11_WB	FS					172					
1709615	ES-13_17ET718	09/18/17	ES-13_17ET718_091817_TOM_02_WB	FS					114					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_03_WB	FS					52.8					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_04_WB	FS					36					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_05_WB	FS					45.5					
1709615	ES-13_17ET719	09/18/17	ES-13_17ET719_091817_TOM_06_WB	FS					32.7					
1709615	ES-13_17ET722	09/18/17	ES-13_17ET722_091817_TOM_07_WB	FS					52.2					
1709615	ES-13_17ET722	09/18/17	ES-13_17ET722_091817_TOM_08_WB	FS					60.2					
1709615	ES-13_17ET723	09/18/17	ES-13_17ET723_091817_TOM_09_WB	FS					239					
1709615	ES-13_17ET723	09/18/17	ES-13_17ET723_091817_TOM_10_WB	FS					209					
1709615	ES-13_17LT012	09/13/17	ES-13_17LT012_091317_TOM_01_WB	FS					226					
1709616	ES-FP_17ET658	09/15/17	ES-FP_17ET658_091517_TOM_01_WB	FS					37.2					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_01_WB	FS					5.17					

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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_02_WB	FS					8.36					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_03_WB	FS					5.05					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_04_WB	FS					7.11					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_05_WB	FS					7.57					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_06_WB	FS					6.46					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_07_WB	FS					7.7					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_08_WB	FS					7.6					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_09_WB	FS					6.16					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_10_WB	FS					6.74					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_11_WB	FS					6.7					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_12_WB	FS					4.81					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_13_WB	FS					5.65					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_14_WB	FS					6.1					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_15_WB	FS					5.08					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_16_WB	FS					6.6					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_17_WB	FS					5.85					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_18_WB	FS					7.84					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_19_WB	FS					6.53					
1709617	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_MUM_20_WB	FS					4.44					
1709618	OB-01_17MT001	09/18/17	OB-01_17MT001_091817_MUM_01_WB	FS					86.9					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_09_WB	FS					79.6					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_10_WB	FS					242					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_11_WB	FS					83.4					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_12_WB	FS					130					
1709618	OB-01_17MT001	09/19/17	OB-01_17MT001_091917_MUM_13_WB	FS					127					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_02_WB	FS					86.1					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_03_WB	FS					103					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_04_WB	FS					154					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_05_WB	FS					110					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_06_WB	FS					109					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_07_WB	FS					37.4					
1709618	OB-01_17MT002	09/18/17	OB-01_17MT002_091817_MUM_08_WB	FS					87.2					
1709618	OB-01_17MT002	09/19/17	OB-01_17MT002_091917_MUM_14_WB	FS					237					

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709618	OB-01_17MT002	09/19/17	OB-01_17MT002_091917_MUM_15_WB	FS					118					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_01_WB	FS					150					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_02_WB	FS					114					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_03_WB	FS					121					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_04_WB	FS					117					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_05_WB	FS					65.2					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_06_WB	FS					76.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_07_WB	FS					71.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_08_WB	FS					77.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_09_WB	FS					74.1					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_10_WB	FS					74.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_11_WB	FS					77.1					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_12_WB	FS					80.8					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_13_WB	FS					76.9					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_14_WB	FS					81.3					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_15_WB	FS					77.6					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_16_WB	FS					65					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_17_WB	FS					66.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_18_WB	FS					69.9					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_19_WB	FS					76.5					
1709619	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_MUM_20_WB	FS					62.6					
1709620	MMMC-01_17MT001	09/18/17	MMMC-01_17MT001_091817_MUM_01_WB	FS					51.4					
1709620	MMMC-01_17MT001	09/20/17	MMMC-01_17MT001_092017_MUM_02_WB	FS					137					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_06_WB	FS					109					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_07_WB	FS					122					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_08_WB	FS					107					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_09_WB	FS					88.2					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_10_WB	FS					207					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_11_WB	FS					94.4					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_12_WB	FS					73.2					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_13_WB	FS					104					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_14_WB	FS					150					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_15_WB	FS					145					

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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_16_WB	FS					72.4					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_17_WB	FS					136					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_18_WB	FS					112					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_19_WB	FS					100					
1709620	MMMC-01_17MT003	09/20/17	MMMC-01_17MT003_092017_MUM_20_WB	FS					256					
1709620	MMMC-01_17MT004	09/20/17	MMMC-01_17MT004_092017_MUM_03_WB	FS					173					
1709620	MMMC-01_17MT004	09/20/17	MMMC-01_17MT004_092017_MUM_04_WB	FS					109					
1709621	BO-04_17SN001	09/17/17	BO-04_17SN001_091717_MUM_01_WB	FS					63.4					
1709621	QC	09/15/17	ESFP_091517_BAIT_01_QC	FS					20.1					
1709621	QC	09/15/17	ESFP_091517_BAIT_02_QC	FS					0.092	J				
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_01_WB	FS					30.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_02_WB	FS					87.8	J				
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_03_WB	FS					42.2					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_04_WB	FS					35.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_05_WB	FS					29.9					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_06_WB	FS					76.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_07_WB	FS					78.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_08_WB	FS					32.7					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_09_WB	FS					26.4					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_10_WB	FS					37.4					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_11_WB	FS					37.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_12_WB	FS					29.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_13_WB	FS					63.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_14_WB	FS					43.5					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_15_WB	FS					39.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_16_WB	FS					34.8					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_17_WB	FS					56.6					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_18_WB	FS					40.2					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_19_WB	FS					38.1					
1709622	ES-13_17SN001	09/14/17	ES-13_17SN001_091417_RAS_20_WB	FS					30.1					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_01_WB	FS					18.1					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_02_WB	FS					14.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_03_WB	FS					6.88					

TABLE 3
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PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_04_WB	FS					22.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_05_WB	FS					10.8					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_06_WB	FS					14.5					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_07_WB	FS					26.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_08_WB	FS					24.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_09_WB	FS					8.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_10_WB	FS					10.6					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_11_WB	FS					10.9					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_12_WB	FS					6.57					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_13_WB	FS					9.38					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_14_WB	FS					19					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_15_WB	FS					7.29					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_16_WB	FS					15.7					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_17_WB	FS					12.2					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_18_WB	FS					7.36					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_19_WB	FS					7.98					
1709623	FRB-01_17SN001	09/12/17	FRB-01_17SN001_091217_RAS_20_WB	FS					11.8					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_01_WB	FS					72.1					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_02_WB	FS					64.4					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_03_WB	FS					83.5					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_04_WB	FS					96.5					
1709624	OB-05_17SN001	09/15/17	OB-05_17SN001_091517_RAS_05_WB	FS					83.9					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_01_WB	FS					78.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_02_WB	FS					92.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_03_WB	FS					68.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_04_WB	FS					174					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_05_WB	FS					92.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_06_WB	FS					83.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_07_WB	FS					207					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_08_WB	FS					128					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_09_WB	FS					185					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_10_WB	FS					156					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_11_WB	FS					75.7					

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				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_12_WB	FS					43					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_13_WB	FS					36.6					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_14_WB	FS					39					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_15_WB	FS					34.2					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_16_WB	FS					52					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_17_WB	FS					34.1					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_18_WB	FS					42.5					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_19_WB	FS					31.7					
1709625	ES-FP_17SN001	09/14/17	ES-FP_17SN001_091417_RAS_20_WB	FS					43.6					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_07_WB	FS					52.1					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_08_WB	FS					42.7					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_09_WB	FS					38.2					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_10_WB	FS					47.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_11_WB	FS					61.7					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_12_WB	FS					42.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_13_WB	FS					49.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_14_WB	FS					49.6					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_15_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_16_WB	FS					49.2					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_17_WB	FS					46.9					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_18_WB	FS					44.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_19_WB	FS					47.8					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_20_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_01_WB	FS					45.3					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_02_WB	FS					36					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_03_WB	FS					72					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_04_WB	FS					77.4					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_05_WB	FS					46.5					
1709626	OB-01_17SN001	09/16/17	OB-01_17SN001_091617_RAS_06_WB	FS					39.7					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_01_WB	FS					5.52					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_02_WB	FS					6.18					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_03_WB	FS					11.7					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_04_WB	FS					8.51					

TABLE 3
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2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_05_WB	FS					7.09					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_06_WB	FS					5.46					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_07_WB	FS					11.9					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_08_WB	FS					13					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_09_WB	FS					7.19					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_10_WB	FS					7.74					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_11_WB	FS					9.2					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_12_WB	FS					7.44					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_13_WB	FS					10.5					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_14_WB	FS					6.45					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_15_WB	FS					10.3					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_16_WB	FS					7.17					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_17_WB	FS					8.36					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_18_WB	FS					6.85					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_19_WB	FS					7.68					
1709627	FRB-01_17HC001	09/13/17	FRB-01_17HC001_091317_BLM_20_WB	FS					7.02					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_01_WB	FS					75					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_02_WB	FS					111					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_03_WB	FS					116					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_04_WB	FS					123					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_05_WB	FS					97.6					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_06_WB	FS					63.5					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_07_WB	FS					95.6					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_08_WB	FS					104					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_09_WB	FS					103					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_10_WB	FS					89.2					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_11_WB	FS					160					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_12_WB	FS					92.3					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_13_WB	FS					72.8					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_14_WB	FS					88.7					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_15_WB	FS					68.9	J				
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_16_WB	FS					207					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_18_WB	FS					79.6					

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	Location ID	Sample Date	Sample ID	QC Code	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_19_WB	FS					86.1					
1709628	ES-03_17HC001	09/19/17	ES-03_17HC001_091917_BLM_20_WB	FS					75.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_01_WB	FS					48.8					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_02_WB	FS					58.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_03_WB	FS					81.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_04_WB	FS					112					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_05_WB	FS					53					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_06_WB	FS					114					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_07_WB	FS					115					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_08_WB	FS					39.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_09_WB	FS					73.4					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_10_WB	FS					140					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_11_WB	FS					168					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_12_WB	FS					96.7					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_13_WB	FS					87					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_14_WB	FS					181					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_15_WB	FS					122					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_16_WB	FS					55.9					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_17_WB	FS					91.5					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_18_WB	FS					82.1					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_19_WB	FS					72					
1709629	ES-FP_17HC001	09/19/17	ES-FP_17HC001_091917_BLM_20_WB	FS					97.3					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_01_WB	FS					80.3					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_02_WB	FS					86.5					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_03_WB	FS					48.4					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_04_WB	FS					144					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_05_WB	FS					71.9					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_06_WB	FS					109					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_07_WB	FS					110					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_08_WB	FS					122					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_09_WB	FS					106					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_10_WB	FS					61.8					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_11_WB	FS					80.5					

TABLE 3
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_12_WB	FS					55.7					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_13_WB	FS					86.4					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_14_WB	FS					86.8					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_15_WB	FS					125					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_16_WB	FS					73.2					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_17_WB	FS					111					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_18_WB	FS					90.7					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_19_WB	FS					76.2					
1709630	ES13_17HC001	09/14/17	ES-13_17HC001_091417_BLM_20_WB	FS					79.3					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_01_WB	FS					77.1					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_02_WB	FS					71.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_03_WB	FS					66.5					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_04_WB	FS					71.2					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_06_WB	FS					78.4					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_07_WB	FS					60.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_08_WB	FS					65.9					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_09_WB	FS					97.6					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_10_WB	FS					66.1					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_11_WB	FS					64.5					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_12_WB	FS					78.9					
1709631	ES-15_17HC001	09/14/17	ES-15_17HC001_091417_BLM_13_WB	FS					85.9					
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_01_TA	FS	82.1	J	17.9	J	194				130	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_02_TA	FS	82.5	J	17.5	J	153				122	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_03_TA	FS	82.7	J	17.3	J	321				92.4	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_04_TA	FS	80.5	J	19.5	J	309				92.1	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_05_TA	FS	82.1	J	17.9	J	128				96.9	
1709632	L10-52_17LT006	09/13/17	L10-52_17LT006_091317_LOB_06_TA	FS	82.8	J	17.2	J	178				116	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_07_TA	FS	81.7	J	18.3	J	1730				210	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_08_TA	FS	82.5	J	17.5	J	193				76	
1709632	L10-52_17LT007	09/13/17	L10-52_17LT007_091317_LOB_09_TA	FS	82.8	J	17.2	J	542				147	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_10_TA	FS	81.4	J	18.6	J	237				137	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_11_TA	FS	82.8	J	17.2	J	267				134	
1709632	L10-52_17LT008	09/13/17	L10-52_17LT008_091317_LOB_12_TA	FS	81.3	J	18.7	J	141				125	

TABLE 3
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE

				Analysis Method					EPA 1631		EPA 1630			
				Parameter	% Moisture		% Solids		Mercury		Methyl Mercury		Mass	
				Unit	PERCENT		PERCENT		NG/G		NG/G		Grams	
				Fraction	Total		Total		Total		Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier	Final Result	Final Qualifier
1709632	L10-52_17LT009	09/13/17	L10-52_17LT009_091317_LOB_13_TA	FS	80	J	20	J	241				126	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_18_TA	FS	81.6	J	18.4	J	519				141	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_19_TA	FS	82	J	18	J	654				194	
1709632	L10-52_17LT040	09/13/17	L10-52_17LT040_091517_LOB_20_TA	FS	82.8	J	17.2	J	278				193	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_14_TA	FS	80.9	J	19.1	J	174				46.5	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_15_TA	FS	82.3	J	17.7	J	212				88.6	
1709632	L10-52_17LT041	09/13/17	L10-52_17LT041_091517_LOB_16_TA	FS	82.5	J	17.5	J	250				94.5	
1709632	L10-52_17LT042	09/13/17	L10-52_17LT042_091517_LOB_17_TA	FS	82.6	J	17.4	J	181				144	

Notes:

NG/G = Nanogram per gram
NG/L = Nanogram per liter
FS = Field Sample
EB = Equipment Blank
J = Value is estimated
U = The target compound was not detected above the method detection limit
SDG = Sample Delivery Group

Data Validation Summary
2017 Biota Sampling- Polychaete and Eel
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (polychaetes and eels) were collected in July and August 2017 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 1708118, 1708119, 1708120, 1708240 and 1708241. Samples were also analyzed by Eurofins Calscience (Calscience) located in Garden Grove, California and are included in the same Eurofins SDGs. Samples were analyzed by one or more of the following: Clean Water Act (CWA, 2012) and National Oceanic and Atmospheric Administration (NOAA, 1993a):

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Mercury, total	CWA 1631B	10% Stage III/ 90% Stage IIB
Calscience	% Lipids	NOAA	10% Stage III/ 90% Stage IIB

A Stage IIb data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. All QC measurements were within project QC goals and no qualifications were needed. A complete summary of final sample results is provided in Table 2.

Data were evaluated based on the following parameters:

- Data Completeness and Chain of Custody
- Holding Times and Preservation
- Blanks
- Initial Calibration
- Continuing Calibration
- Laboratory Control Sample (LCS)
- Matrix Spike/Matrix Spike Duplicates (MS/MSD)

* Laboratory Duplicates
* Detection Limits
* Sample Result Verification/Electronic Evaluation Verification (EDD)
* Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

All results were determined to be usable as reported by the laboratory.

References:

Amec Foster Wheeler, 2016. “Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan”, Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA”; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use”; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review”; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures”; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta September 06, 2017

elizabeth penta

Senior Reviewer: Denise King September 14, 2017

Denise King

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 17-08-0508, 1708118, 1708119, 1708120, 1708240, 1708241

					Method Class	Mercury	% Lipids
					Analysis Method	EPA 1631	NOAA
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**		
17-08-0508	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_02_WB	7/28/2017	FS		1
17-08-0508	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_03_WB	7/28/2017	FS		1
17-08-0508	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_04_WB	7/28/2017	FS		1
17-08-0508	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_05_WB	7/28/2017	FS		1
17-08-0508	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_06_WB	7/28/2017	FS		1
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_01_WB	7/25/2017	FS	1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_02_WB	7/25/2017	FS	1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_03_WB	7/25/2017	FS	1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_04_WB	7/25/2017	FS	1	
1708118	Polychaete	OB-01_17HC001	OB-01_17HC001_072517_POL_05_WB	7/25/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-03_17HC001_072717_POL_01_WB	7/27/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-03_17HC001_072717_POL_02_WB	7/27/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-03_17HC001_072717_POL_03_WB	7/27/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-03_17HC001_072717_POL_04_WB	7/27/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-03_17HC001_072717_POL_05_WB	7/27/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-13_17HC001_072517_POL_01_WB	7/25/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-13_17HC001_072517_POL_02_WB	7/25/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-13_17HC001_072517_POL_03_WB	7/25/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-13_17HC001_072517_POL_04_WB	7/25/2017	FS	1	
1708119	Polychaete	ES-03_17HC001	ES-13_17HC001_072517_POL_05_WB	7/25/2017	FS	1	
1708120	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_02_WB	7/28/2017	FS	1	
1708120	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_03_WB	7/28/2017	FS	1	
1708120	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_04_WB	7/28/2017	FS	1	
1708120	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_05_WB	7/28/2017	FS	1	
1708120	Eel	OV-04_17ET628	OV-04_17ET628_072817_EEL_06_WB	7/28/2017	FS	1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_01_WB	8/1/2017	FS	1	

Created by: BCG 08/30/2017

Checked by: EP 09/07/2017

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 17-08-0508, 1708118, 1708119, 1708120, 1708240, 1708241

				Method Class		Mercury	% Lipids
				Analysis Method		EPA 1631	NOAA
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**		
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_02_WB	8/1/2017	FS	1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_03_WB	8/1/2017	FS	1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_04_WB	8/1/2017	FS	1	
1708240	Polychaete	MM-MR_INT_17HC001	MM-MR_INT_17HC001_080117_POL_05_WB	8/1/2017	FS	1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_01_WB	8/2/2017	FS	1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_02_WB	8/2/2017	FS	1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_03_WB	8/2/2017	FS	1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_04_WB	8/2/2017	FS	1	
1708240	Polychaete	PI-01_17HC001	PI-01_17HC001_080217_POL_05_WB	8/2/2017	FS	1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_01_WB	8/2/2017	FS	1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_02_WB	8/2/2017	FS	1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_03_WB	8/2/2017	FS	1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_04_WB	8/2/2017	FS	1	
1708240	Polychaete	SVE-02INT_17HC001	SVE-02INT_17HC001_080217_POL_05_WB	8/2/2017	FS	1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_01_WB	7/31/2017	FS	1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_02_WB	7/31/2017	FS	1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_03_WB	7/31/2017	FS	1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_04_WB	7/31/2017	FS	1	
1708241	Polychaete	BFK_17HC001	BFK_17HC001_073117_POL_05_WB	7/31/2017	FS	1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_01_WB	7/31/2017	FS	1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_02_WB	7/31/2017	FS	1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_03_WB	7/31/2017	FS	1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_04_WB	7/31/2017	FS	1	
1708241	Polychaete	ES-02E_17HC001	ES-02E_17HC001_073117_POL_05_WB	7/31/2017	FS	1	
1708241	Polychaete	ESFP_17HC001	ESFP_17HC001_072817_POL_01_WB	7/28/2017	FS	1	
1708241	Polychaete	ESFP_17HC001	ESFP_17HC001_072817_POL_02_WB	7/28/2017	FS	1	

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Checked by: EP 09/07/2017

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 17-08-0508, 1708118, 1708119, 1708120, 1708240, 1708241

					Method Class	Mercury	% Lipids
					Analysis Method	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code		
1708241	Polychaete	ESFP_17HC001	ESFP_17HC001_072817_POL_03_WB	7/28/2017	FS	1	
1708241	Polychaete	ESFP_17HC001	ESFP_17HC001_072817_POL_04_WB	7/28/2017	FS	1	
1708241	Polychaete	ESFP_17HC001	ESFP_17HC001_072817_POL_05_WB	7/28/2017	FS	1	

Notes:

FS = Field Sample

SDG = Sample Delivery Group

Count = # of analytes

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1708118, 1708119, 1708120, 17-08-0508, 1708240, 1708241

				Analysis Method	EPA 1631		NOAALipids1993	
				Parameter	Mercury		Lipids	
				Unit	NG/G		PERCENT	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_01_WB	FS	30.5			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_02_WB	FS	30.6			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_03_WB	FS	32			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_04_WB	FS	35.8			
1708118	OB-01_17HC001	07/25/17	OB-01_17HC001_072517_POL_05_WB	FS	29.5			
1708119	ES-03_17HC001	07/25/17	ES-13_17HC001_072517_POL_01_WB	FS	46.1			
1708119	ES-03_17HC001	07/25/17	ES-13_17HC001_072517_POL_02_WB	FS	28			
1708119	ES-03_17HC001	07/25/17	ES-13_17HC001_072517_POL_03_WB	FS	19.5			
1708119	ES-03_17HC001	07/25/17	ES-13_17HC001_072517_POL_04_WB	FS	13			
1708119	ES-03_17HC001	07/25/17	ES-13_17HC001_072517_POL_05_WB	FS	13.6			
1708119	ES-03_17HC001	07/27/17	ES-03_17HC001_072717_POL_01_WB	FS	35.9			
1708119	ES-03_17HC001	07/27/17	ES-03_17HC001_072717_POL_02_WB	FS	29.7			
1708119	ES-03_17HC001	07/27/17	ES-03_17HC001_072717_POL_03_WB	FS	48			
1708119	ES-03_17HC001	07/27/17	ES-03_17HC001_072717_POL_04_WB	FS	27.8			
1708119	ES-03_17HC001	07/27/17	ES-03_17HC001_072717_POL_05_WB	FS	22.4			
17-08-0508	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_02_WB	FS			10	
17-08-0508	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_03_WB	FS			2	
17-08-0508	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_04_WB	FS			17	
17-08-0508	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_05_WB	FS			4.6	
17-08-0508	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_06_WB	FS			9.3	
1708120	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_02_WB	FS	320			
1708120	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_03_WB	FS	176			
1708120	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_04_WB	FS	161			
1708120	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_05_WB	FS	153			

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1708118, 1708119, 1708120, 17-08-0508, 1708240, 1708241

				Analysis Method	EPA 1631		NOAALipids1993	
				Parameter	Mercury		Lipids	
				Unit	NG/G		PERCENT	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1708120	OV-04_17ET628	07/28/17	OV-04_17ET628_072817_EEL_06_WB	FS	142			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_01_WB	FS	53.8			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_02_WB	FS	39.9			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_03_WB	FS	37.4			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_04_WB	FS	59.2			
1708240	MM-MR_INT_17HC001	08/01/17	MM-MR_INT_17HC001_080117_POL_05_WB	FS	54.5			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_01_WB	FS	37.1			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_02_WB	FS	45.5			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_03_WB	FS	33.2			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_04_WB	FS	21.8			
1708240	PI-01_17HC001	08/02/17	PI-01_17HC001_080217_POL_05_WB	FS	42			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_01_WB	FS	28.9			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_02_WB	FS	23.9			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_03_WB	FS	24.7			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_04_WB	FS	22.1			
1708240	SVE-02INT_17HC001	08/02/17	SVE-02INT_17HC001_080217_POL_05_WB	FS	25			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_01_WB	FS	17.6			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_02_WB	FS	21.2			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_03_WB	FS	14.7			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_04_WB	FS	12.4			
1708241	BFK_17HC001	07/31/17	BFK_17HC001_073117_POL_05_WB	FS	18.3			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_01_WB	FS	10.3			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_02_WB	FS	24.6			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_03_WB	FS	29.8			

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETE AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1708118, 1708119, 1708120, 17-08-0508, 1708240, 1708241

				Analysis Method	EPA 1631		NOAALipids1993	
				Parameter	Mercury		Lipids	
				Unit	NG/G		PERCENT	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_04_WB	FS	31.5			
1708241	ES-02E_17HC001	07/31/17	ES-02E_17HC001_073117_POL_05_WB	FS	38.8			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_01_WB	FS	12.9			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_02_WB	FS	12			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_03_WB	FS	9.71			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_04_WB	FS	12.9			
1708241	ESFP_17HC001	07/28/17	ESFP_17HC001_072817_POL_05_WB	FS	8.94			

Notes:
FS = Field Sample
SDG = Sample Delivery Group
NG/G = Nanogram per gram

Prepared by: BCG 09/18/2017
Checked by: EP 09/18/2017

Data Validation Summary
2017 Biota Sampling- Polychaetes
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (polychaetes) were collected in August and September 2017 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 1708556 and 1709391. Samples were analyzed by one or more of the Clean Water Act (CWA, 2012):

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Mercury, total	CWA 1631B	10% Stage III/ 90% Stage IIB

A Stage IIB data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. All QC measurements were within project QC goals and no qualifications were needed. A complete summary of final sample results is provided in Table 2.

Data were evaluated based on the following parameters:

- Data Completeness and Chain of Custody
- Holding Times and Preservation
- Blanks
- Initial Calibration
- Continuing Calibration
- Laboratory Control Sample (LCS)
- Matrix Spike/Matrix Spike Duplicates (MS/MSD)
- Laboratory Duplicates
- Detection Limits
- Sample Result Verification/Electronic Evaluation Verification (EDD)
- Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

All results were determined to be usable as reported by the laboratory.

References:

Amec Foster Wheeler, 2016. “Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan”, Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA”; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use”; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review”; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures”; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta October 3, 2017

elizabeth penta

Senior Reviewer: Denise King October 5, 2017

Denise King

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETES
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1708556 and 1709391

					Method Class	**Mercury**
					Analysis Method	**EPA 1631**
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**	
1708556	POLY	ES-15_17HC001	ES-15_17HC001_081617_POL_01_WB	8/16/2017	FS	1
1708556	POLY	ES-15_17HC001	ES-15_17HC001_081617_POL_02_WB	8/16/2017	FS	1
1708556	POLY	ES-15_17HC001	ES-15_17HC001_081617_POL_03_WB	8/16/2017	FS	1
1708556	POLY	ES-15_17HC001	ES-15_17HC001_081617_POL_04_WB	8/16/2017	FS	1
1708556	POLY	ES-15_17HC001	ES-15_17HC001_081617_POL_05_WB	8/16/2017	FS	1
1708556	POLY	VI-W_17HC001	VI-W_17HC001_081617_POL_01_WB	8/16/2017	FS	1
1708556	POLY	VI-W_17HC001	VI-W_17HC001_081617_POL_02_WB	8/16/2017	FS	1
1708556	POLY	VI-W_17HC001	VI-W_17HC001_081617_POL_03_WB	8/16/2017	FS	1
1708556	POLY	VI-W_17HC001	VI-W_17HC001_081617_POL_04_WB	8/16/2017	FS	1
1708556	POLY	VI-W_17HC001	VI-W_17HC001_081617_POL_05_WB	8/16/2017	FS	1
1709391	POLY	FRB-01_17HC001	FRB-01_17HD001_091217_POL_01_WB	9/12/2017	FS	1
1709391	POLY	FRB-01_17HC001	FRB-01_17HD001_091217_POL_02_WB	9/12/2017	FS	1
1709391	POLY	FRB-01_17HC001	FRB-01_17HD001_091217_POL_03_WB	9/12/2017	FS	1
1709391	POLY	FRB-01_17HC001	FRB-01_17HD001_091217_POL_04_WB	9/12/2017	FS	1
1709391	POLY	FRB-01_17HC001	FRB-01_17HD001_091217_POL_05_WB	9/12/2017	FS	1

Notes:

FS = Field Sample

SDG = Sample Delivery Group

Count = # of analytes

Created by: BCG 09/22/2017

Checked by: EP 10/03/2017

TABLE 2
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- POLYCHAETES
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1708556 and 1709391

				Analysis Method	EPA 1631	
				Parameter	Mercury	
				Unit	NG/G	
				Fraction	Total	
SDG	**Location**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier
1708556	ES-15_17HC001	8/16/2017	ES-15_17HC001_081617_POL_01_WB	FS	42.0	
1708556	ES-15_17HC001	8/16/2017	ES-15_17HC001_081617_POL_02_WB	FS	21.2	
1708556	ES-15_17HC001	8/16/2017	ES-15_17HC001_081617_POL_03_WB	FS	30.5	
1708556	ES-15_17HC001	8/16/2017	ES-15_17HC001_081617_POL_04_WB	FS	32.0	
1708556	ES-15_17HC001	8/16/2017	ES-15_17HC001_081617_POL_05_WB	FS	21.7	
1708556	VI-W_17HC001	8/16/2017	VI-W_17HC001_081617_POL_01_WB	FS	23.8	
1708556	VI-W_17HC001	8/16/2017	VI-W_17HC001_081617_POL_02_WB	FS	19.6	
1708556	VI-W_17HC001	8/16/2017	VI-W_17HC001_081617_POL_03_WB	FS	16.9	
1708556	VI-W_17HC001	8/16/2017	VI-W_17HC001_081617_POL_04_WB	FS	23.7	
1708556	VI-W_17HC001	8/16/2017	VI-W_17HC001_081617_POL_05_WB	FS	20.1	
1709391	FRB-01_17HC001	9/12/2017	FRB-01_17HD001_091217_POL_01_WB	FS	8.82	
1709391	FRB-01_17HC001	9/12/2017	FRB-01_17HD001_091217_POL_02_WB	FS	7.66	
1709391	FRB-01_17HC001	9/12/2017	FRB-01_17HD001_091217_POL_03_WB	FS	7.40	
1709391	FRB-01_17HC001	9/12/2017	FRB-01_17HD001_091217_POL_04_WB	FS	8.10	
1709391	FRB-01_17HC001	9/12/2017	FRB-01_17HD001_091217_POL_05_WB	FS	7.17	

Notes:

FS = Field Sample

SDG = Sample Delivery Group

Created by: DMK 10/03/2017

Checked by: EP 10/05/2017

Data Validation Summary
2017 Biota Sampling – Eel and Bird Blood
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (eels and bird blood) were collected in June 2017 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 1706398, 1706399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938 and 1706939. Samples were also analyzed by Eurofins Calscience (Calscience) located in Garden Grove, California and are included in the same Eurofins SDGs. Samples were analyzed by one or more of the following: Clean Water Act (CWA, 2012) and National Oceanic and Atmospheric Administration (NOAA, 1993a):

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Mercury, total	CWA 1631B	10% Stage III/ 90% Stage IIB
Calscience	% Lipids	NOAA	10% Stage III/ 90% Stage IIB

A Stage IIb data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. The following qualifiers as applied during data validation or reported by the laboratory are included in the final data set:

J = The reported concentration is considered an estimated value

Validation reason codes were applied to results associated with QC measurements outside project QC goals. The validation qualification actions and associated validation reason codes applied to sample results are summarized on Table 2. The following data validation reason codes were applied to one or more sample results:

LD = Lab Duplicate limit exceeded
MS-RPD = MS/MSD RPD limit exceeded

A complete summary of final sample results is provided in Table 3.

Data were evaluated based on the following parameters:

* Data Completeness and Chain of Custody
* Holding Times and Preservation
* Blanks
* Initial Calibration
* Continuing Calibration
* Laboratory Control Sample (LCS)
Matrix Spike/Matrix Spike Duplicates (MS/MSD)
Laboratory Duplicates
* Detection Limits
* Sample Result Verification/Electronic Evaluation Verification (EDD)
* Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

With the exception of the following items discussed below, results were determined to be usable as reported by the laboratory.

2.0 Mercury – 1631

<u>Matrix Spike</u>

SDG 1706936 – Sample MMSE-1_17MN047_062717_RWB_04_BL was used for MS/MSD analysis. The MSD RPD for mercury (39.3) was above the QC limit of 24. Sample results for MMSE-1_17MN004_062117_RWB_01_BL, MMSE-1_17MN044_062717_RWB_02_BL, MMSE-1_17MN047_062717_RWB_03_BL, MMSE-1_17MN047_062717_RWB_04_BL, MMSE-1_17MN047_062717_RWB_05_BL and MMSE-1_17MN064_062817_RWB_06_BL were qualified as estimated (J) due to the potential non-directional bias.

<u>Laboratory Duplicate</u>

SDG 1706936 – Sample MMSE-1_17MN047_062717_RWB_03_BL was selected by the laboratory for duplicate analysis. The RPD (39.9) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample MMSE-1_17MN047_062717_RWB_03_BL was qualified estimated (J).

SDG 1706938 – Sample MMSW-C_17MN022_062317_RWB_02_BL was selected by the laboratory for duplicate analysis. The RPD (154) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample MMSW-C_17MN022_062317_RWB_02_BL was qualified estimated (J).

References:

Amec Foster Wheeler, 2016. "Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan", Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA"; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use"; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review"; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures"; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta August 28, 2017

elizabeth penta

Senior Reviewer: Denise King August 29, 2017

Denise King

TABLE 1
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-Blood and Eels
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

					Method Class	Mercury	% Lipids
					Analysis Method	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code		
1706398	Eel	OV-04_17ET015	OV-04_17ET015_060917_EEL_01_WB	6/9/2017	FS	1	1
1706399	Eel	BO-04-ET0002	BO-04_17ET002_060517_EEL_01_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0002	BO-04_17ET002_060517_EEL_02_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0002	BO-04_17ET002_060517_EEL_03_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0003	BO-04_17ET003_060517_EEL_04_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0004	BO-04_17ET004_060517_EEL_05_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0005	BO-04_17ET005_060517_EEL_06_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0009	BO-04_17ET009_060517_EEL_07_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0012	BO-04_17ET012_060517_EEL_08_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_09_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_10_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_11_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_12_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_13_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_14_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0015	BO-04_17ET015_060517_EEL_15_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0016	BO-04_17ET016_060517_EEL_16_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0016	BO-04_17ET016_060517_EEL_17_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0017	BO-04_17ET017_060517_EEL_18_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0018	BO-04_17ET018_060517_EEL_19_WB	6/5/2017	FS	1	1
1706399	Eel	BO-04-ET0020	BO-04_17ET020_060517_EEL_20_WB	6/5/2017	FS	1	1
1706399	Eel Bait	QC	HORSESHOE CRAB_060717_EEL_BAIT	6/7/2017	FS	1	1
1706400	Eel	OB-05-ET0100	OB-05_17ET100_060517_EEL_01_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0100	OB-05_17ET100_060517_EEL_02_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0100	OB-05_17ET100_060517_EEL_03_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0101	OB-05_17ET101_060517_EEL_10_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0101	OB-05_17ET101_060517_EEL_11_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0104	OB-05_17ET104_060517_EEL_08_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0104	OB-05_17ET104_060517_EEL_09_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0110	OB-05_17ET110_060517_EEL_06_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0110	OB-05_17ET110_060517_EEL_07_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0111	OB-05_17ET111_060517_EEL_04_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05-ET0111	OB-05_17ET111_060517_EEL_05_WB	6/5/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_12_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_13_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_14_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_15_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_16_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_17_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_18_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_19_WB	6/6/2017	FS	1	1
1706400	Eel	OB-05_17ET141	OB-05_17ET141_060617_EEL_20_WB	6/6/2017	FS	1	1
1706933	Blood	W17-N_17MN063	W17-N_17MN063_062917_NSS_12	06/29/17	FS	1	
1706933	Blood	W17_17MN001	W17-N_17MN001_061917_NSS_01_BL	06/19/17	FS	1	
1706933	Blood	W17_17MN001	W17-N_17MN001_062017_NSS_04_BL	06/20/17	FS	1	
1706933	Blood	W17_17MN002	W17-N_17MN002_062017_NSS_05_BL	06/20/17	FS	1	
1706933	Blood	W17_17MN007	W17-N_17MN007_062017_NSS_03_BL	06/20/17	FS	1	
1706933	Blood	W17_17MN007	W17-N_17MN007_062017_NSS_06_BL	06/20/17	FS	1	
1706933	Blood	W17_17MN008	W17-N_17MN008_061917_NSS_02_BL	06/19/17	FS	1	

Created by: BCG 07/25/2017
Checked by: EP 08/02/2017

TABLE 1
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-Blood and Eels
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

					Method Class	Mercury	% Lipids
					Analysis Method	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code		
1706933	Blood	W17_17MN010	W17-N_17MN010_062017_NSS_07_BL	06/20/17	FS	1	
1706933	Blood	W17_17MN037	W17-N_17MN037_062517_NSS_08_BL	06/25/17	FS	1	
1706933	Blood	W17_17MN037	W17-N_17MN037_062517_NSS_09_BL	06/25/17	FS	1	
1706933	Blood	W17_17MN041	W17-N_17MN041_062517_NSS_10_BL	06/25/17	FS	1	
1706933	Blood	W17_17MN058	W17-N_17MN058_062617_NSS_11_BL	06/26/17	FS	1	
1706934	Blood	W17_17MN002	W17-N_17MN002_061917_RWB_01_BL	06/19/17	FS	1	
1706934	Blood	W17_17MN005	W17-N_17MN005_061917_RWB_02_BL	06/19/17	FS	1	
1706934	Blood	W17_17MN006	W17-N_17MN006_061917_RWB_03_BL	06/19/17	FS	1	
1706934	Blood	W17_17MN006	W17-N_17MN006_061917_RWB_04_BL	06/19/17	FS	1	
1706934	Blood	W17_17MN039	W17-N_17MN039_062517_RWB_05_BL	06/25/17	FS	1	
1706935	Blood	MMSE-1_17MN001	MMSE-1_17MN001_062117_NSS_06_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN002	MMSE-1_17MN002_062117_NSS_07_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN002	MMSE-1_17MN002_062117_NSS_08_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN003	MMSE-1_17MN003_062117_NSS_01_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN007	MMSE-1_17MN007_062117_NSS_03_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN008	MMSE-1_17MN008_062217_NSS_15_BL	06/22/17	FS	1	
1706935	Blood	MMSE-1_17MN009	MMSE-1_17MN009_062117_NSS_02_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN010	MMSE-1_17MN010_062117_NSS_04_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN010	MMSE-1_17MN010_062117_NSS_05_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN010	MMSE-1_17MN010_062117_NSS_09_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN010	MMSE-1_17MN010_062117_NSS_10_BL	06/21/17	FS	1	
1706935	Blood	MMSE-1_17MN011	MMSE-1_17MN011_062217_NSS_12_BL	06/22/17	FS	1	
1706935	Blood	MMSE-1_17MN011	MMSE-1_17MN011_062217_NSS_14_BL	06/22/17	FS	1	
1706935	Blood	MMSE-1_17MN018	MMSE-1_17MN018_062217_NSS_13_BL	06/22/17	FS	1	
1706935	Blood	MMSE-1_17MN019	MMSE-1_17MN019_062217_NSS_11_BL	06/22/17	FS	1	
1706936	Blood	MMSE-1_17MN004	MMSE-1_17MN004_062117_RWB_01_BL	06/21/17	FS	1	
1706936	Blood	MMSE-1_17MN044	MMSE-1_17MN044_062717_RWB_02_BL	06/27/17	FS	1	
1706936	Blood	MMSE-1_17MN045	MMSE-1_17MN045_062717_RWB_03_BL	06/27/17	FS	1	
1706936	Blood	MMSE-1_17MN047	MMSE-1_17MN047_062717_RWB_05_BL	06/27/17	FS	1	
1706936	Blood	MMSE-1_17MN064	MMSE-1_17MN064_062817_RWB_06	06/28/17	FS	1	
1706936	Blood	MMSE-1_17MN075	MMSE-1_17MN075_062717_RWB_04_BL	06/27/17	FS	1	
1706937	Blood	MMSW-C_17MN006	MMSW-C_17MN006_061917_NSS_01_BL	06/19/17	FS	1	
1706937	Blood	MMSW-C_17MN006	MMSW-C_17MN006_061917_NSS_03_BL	06/19/17	FS	1	
1706937	Blood	MMSW-C_17MN008	MMSW-C_17MN008_061917_NSS_02_BL	06/19/17	FS	1	
1706937	Blood	MMSW-C_17MN009	MMSW-C_17MN009_061917_NSS_04_BL	06/19/17	FS	1	
1706937	Blood	MMSW-C_17MN009	MMSW-C_17MN009_061917_NSS_05_BL	06/19/17	FS	1	
1706937	Blood	MMSW-C_17MN010	MMSW-C_17MN010_062017_NSS_09_BL	06/20/17	FS	1	
1706937	Blood	MMSW-C_17MN015	MMSW-C_17MN015_062017_NSS_06_BL	06/20/17	FS	1	
1706937	Blood	MMSW-C_17MN015	MMSW-C_17MN015_062017_NSS_08_BL	06/20/17	FS	1	
1706937	Blood	MMSW-C_17MN016	MMSW-C_17MN016_062017_NSS_07_BL	06/20/17	FS	1	
1706937	Blood	MMSW-C_17MN021	MMSW-C_17MN021_062317_NSS_10_BL	06/23/17	FS	1	
1706937	Blood	MMSW-C_17MN026	MMSW-C_17MN026_062317_NSS_12_BL	06/23/17	FS	1	
1706937	Blood	MMSW-C_17MN027	MMSW-C_17MN027_062317_NSS_11_BL	06/23/17	FS	1	
1706937	Blood	MMSW-C_17MN027	MMSW-C_17MN027_062317_NSS_13_BL	06/23/17	FS	1	
1706937	Blood	MMSW-C_17MN027	MMSW-C_17MN027_062517_NSS_14_BL	06/25/17	FS	1	
1706937	Blood	MMSW-C_17MN027	MMSW-C_17MN027_062517_NSS_15_BL	06/25/17	FS	1	
1706938	Blood	MMSW-C_17MN009	MMSW-C_17MN009_061917_RWB_01_BL	06/19/17	FS	1	
1706938	Blood	MMSW-C_17MN020	MMSW-C_17MN020_062317_RWB_03_BL	06/23/17	FS	1	
1706938	Blood	MMSW-C_17MN020	MMSW-C_17MN020_062317_RWB_04_BL	06/23/17	FS	1	

Created by: BCG 07/25/2017
Checked by: EP 08/02/2017

TABLE 1
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-Blood and Eels
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

SDG	Media	Location	Field Sample ID	Sample Date	Method Class Analysis Method QC Code	Mercury EPA 1631	% Lipids NOAA
1706938	Blood	MMSW-C_17MN022	MMSW-C_17MN022_062317_RWB_02_BL	06/23/17	FS	1	
1706938	Blood	MMSW-C_17MN036	MMSW-C_17MN036_062517_RWB_05_BL	06/25/17	FS	1	
1706938	Blood	MMSW-C_17MN036	MMSW-C_17MN036_062617_RWB_06_BL	06/26/17	FS	1	
1706939	Blood	ADD-01_17MN001	ADD-01_17MN001_062117_NSS_01_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN001	ADD-01_17MN001_062117_NSS_02_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN001	ADD-01_17MN001_062117_NSS_03_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN001	ADD-01_17MN001_062217_NSS_09_BL	06/22/17	FS	1	
1706939	Blood	ADD-01_17MN002	ADD-01_17MN002_062217_NSS_11_BL	06/22/17	FS	1	
1706939	Blood	ADD-01_17MN002	ADD-01_17MN002_062217_NSS_12_BL	06/22/17	FS	1	
1706939	Blood	ADD-01_17MN003	ADD-01_17MN003_062117_NSS_08_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN004	ADD-01_17MN004_062117_NSS_06_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN006	ADD-01_17MN006_062117_NSS_05_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN006	ADD-01_17MN006_062117_NSS_07_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN007	ADD-01_17MN007_062217_NSS_10_BL	06/22/17	FS	1	
1706939	Blood	ADD-01_17MN009	ADD-01_17MN009_062117_NSS_04_BL	06/21/17	FS	1	
1706939	Blood	ADD-01_17MN011	ADD-01_17MN011_062217_NSS_13_BL	06/22/17	FS	1	
1706939	Blood	ADD-01_17MN050	ADD-01_17MN050_062717_NSS_14_BL	06/27/17	FS	1	
1706939	Blood	ADD-01_17MN051	ADD-01_17MN051_062717_NSS_15_BL	06/27/17	FS	1	

Notes:
FS = Field Sample
SDG = Sample Delivery Group
Count = # of analytes

Created by: BCG 07/25/2017
Checked by: EP 08/02/2017

TABLE 2
DATA VALIDATION SUMMARY
2017 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 1706399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938 and 1706939

SDG	Analysis Method	Lab Sample Id	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1706936	EPA 1631	1706936-01	MMSE-1_17MN004_062117_RWB_01_BL	Total	Mercury	1090		1,090	J	MS-RPD	NG/G
1706936	EPA 1631	1706936-02	MMSE-1_17MN044_062717_RWB_02_BL	Total	Mercury	6260		6,260	J	MS-RPD	NG/G
1706936	EPA 1631	1706936-03RE1	MMSE-1_17MN045_062717_RWB_03_BL	Total	Mercury	6170		6,170	J	LD, MS-RPD	NG/G
1706936	EPA 1631	1706936-05	MMSE-1_17MN047_062717_RWB_05_BL	Total	Mercury	1150		1,150	J	MS-RPD	NG/G
1706936	EPA 1631	1706936-06RE1	MMSE-1_17MN064_062817_RWB_06_BL	Total	Mercury	7210		7,210	J	MS-RPD	NG/G
1706936	EPA 1631	1706936-04RE1	MMSE-1_17MN075_062717_RWB_04_BL	Total	Mercury	2680		2,680	J	MS-RPD	NG/G
1706938	EPA 1631	1706938-02RE1	MMSW-C_17MN022_062317_RWB_02_BL	Total	Mercury	6020		6,020	J	LD	NG/G

Units

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Validation Reason Codes:

MS-RPD = MS/MSD RPD limit exceeded

LD = Lab duplicate limit exceeded

Created by: BCG 08/30/2017
Checke by: EP 09/05/2017

TABLE 3
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-BLOOD AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

				Analysis Method	NOAALipids1993		EPA 1631	
				Parameter	Lipids		Mercury	
				Unit	PERCENT		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706398	OV-04_17ET015	06/09/17	OV-04_17ET015_060917_EEL_01_WB	FS	2.5		306	
1706399	BO-04-ET0002	06/05/17	BO-04_17ET002_060517_EEL_01_WB	FS	9.5		389	
1706399	BO-04-ET0002	06/05/17	BO-04_17ET002_060517_EEL_02_WB	FS	12		1320	
1706399	BO-04-ET0002	06/05/17	BO-04_17ET002_060517_EEL_03_WB	FS	8.8		732	
1706399	BO-04-ET0003	06/05/17	BO-04_17ET003_060517_EEL_04_WB	FS	1.2		430	
1706399	BO-04-ET0004	06/05/17	BO-04_17ET004_060517_EEL_05_WB	FS	4.4		391	
1706399	BO-04-ET0005	06/05/17	BO-04_17ET005_060517_EEL_06_WB	FS	3.3		422	
1706399	BO-04-ET0009	06/05/17	BO-04_17ET009_060517_EEL_07_WB	FS	3.1		643	
1706399	BO-04-ET0012	06/05/17	BO-04_17ET012_060517_EEL_08_WB	FS	6.7		488	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_09_WB	FS	0.78		485	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_10_WB	FS	2.6		540	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_11_WB	FS	1.2		483	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_12_WB	FS	9.6		589	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_13_WB	FS	0.41		519	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_14_WB	FS	8.6		648	
1706399	BO-04-ET0015	06/05/17	BO-04_17ET015_060517_EEL_15_WB	FS	3.9		489	
1706399	BO-04-ET0016	06/05/17	BO-04_17ET016_060517_EEL_16_WB	FS	7.7		604	
1706399	BO-04-ET0016	06/05/17	BO-04_17ET016_060517_EEL_17_WB	FS	4.2		493	
1706399	BO-04-ET0017	06/05/17	BO-04_17ET017_060517_EEL_18_WB	FS	1.4		294	
1706399	BO-04-ET0018	06/05/17	BO-04_17ET018_060517_EEL_19_WB	FS	0.7		294	
1706399	BO-04-ET0020	06/05/17	BO-04_17ET020_060517_EEL_20_WB	FS	2		386	
1706399	QC	06/07/17	HORSESHOE CRAB_060717_EEL_BAIT	FS	0.4		59.8	
1706400	OB-05-ET0100	06/05/17	OB-05_17ET100_060517_EEL_01_WB	FS	1.8		468	
1706400	OB-05-ET0100	06/05/17	OB-05_17ET100_060517_EEL_02_WB	FS	1.6		322	

TABLE 3
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-BLOOD AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

				Analysis Method	NOAALipids1993		EPA 1631	
				Parameter	Lipids		Mercury	
				Unit	PERCENT		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706400	OB-05-ET0100	06/05/17	OB-05_17ET100_060517_EEL_03_WB	FS	4.6		293	
1706400	OB-05-ET0101	06/05/17	OB-05_17ET101_060517_EEL_10_WB	FS	6.6		528	
1706400	OB-05-ET0101	06/05/17	OB-05_17ET101_060517_EEL_11_WB	FS	0.44		316	
1706400	OB-05-ET0104	06/05/17	OB-05_17ET104_060517_EEL_08_WB	FS	5.3		249	
1706400	OB-05-ET0104	06/05/17	OB-05_17ET104_060517_EEL_09_WB	FS	6.9		417	
1706400	OB-05-ET0110	06/05/17	OB-05_17ET110_060517_EEL_06_WB	FS	4.1		224	
1706400	OB-05-ET0110	06/05/17	OB-05_17ET110_060517_EEL_07_WB	FS	2.8		92.1	
1706400	OB-05-ET0111	06/05/17	OB-05_17ET111_060517_EEL_04_WB	FS	0.97		706	
1706400	OB-05-ET0111	06/05/17	OB-05_17ET111_060517_EEL_05_WB	FS	1		381	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_12_WB	FS	0.42		234	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_13_WB	FS	0.35		201	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_14_WB	FS	1.7		277	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_15_WB	FS	5.8		124	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_16_WB	FS	5.5		110	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_17_WB	FS	4.7		80	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_18_WB	FS	6.5		116	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_19_WB	FS	2.8		303	
1706400	OB-05_17ET141	06/06/17	OB-05_17ET141_060617_EEL_20_WB	FS	10		221	
1706933	W17_17MN001	06/19/17	W17-N_17MN001_061917_NSS_01_BL	FS			1820	
1706933	W17_17MN001	06/20/17	W17-N_17MN001_062017_NSS_04_BL	FS			3630	
1706933	W17_17MN002	06/20/17	W17-N_17MN002_062017_NSS_05_BL	FS			1410	
1706933	W17_17MN007	06/20/17	W17-N_17MN007_062017_NSS_03_BL	FS			2630	
1706933	W17_17MN007	06/20/17	W17-N_17MN007_062017_NSS_06_BL	FS			2020	
1706933	W17_17MN008	06/19/17	W17-N_17MN008_061917_NSS_02_BL	FS			1690	

TABLE 3
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-BLOOD AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

				Analysis Method	NOAALipids1993		EPA 1631	
				Parameter	Lipids		Mercury	
				Unit	PERCENT		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706933	W17_17MN010	06/20/17	W17-N_17MN010_062017_NSS_07_BL	FS			2360	
1706933	W17_17MN037	06/25/17	W17-N_17MN037_062517_NSS_08_BL	FS			3300	
1706933	W17_17MN037	06/25/17	W17-N_17MN037_062517_NSS_09_BL	FS			2350	
1706933	W17_17MN041	06/25/17	W17-N_17MN041_062517_NSS_10_BL	FS			3060	
1706933	W17_17MN058	06/26/17	W17-N_17MN058_062617_NSS_11_BL	FS			2570	
1706933	W17-N_17MN063	06/29/17	W17-N_17MN063_062917_NSS_12_BL	FS			6010	
1706934	W17_17MN002	06/19/17	W17-N_17MN002_061917_RWB_01_BL	FS			165	
1706934	W17_17MN005	06/19/17	W17-N_17MN005_061917_RWB_02_BL	FS			2450	
1706934	W17_17MN006	06/19/17	W17-N_17MN006_061917_RWB_03_BL	FS			1800	
1706934	W17_17MN006	06/19/17	W17-N_17MN006_061917_RWB_04_BL	FS			4940	
1706934	W17_17MN039	06/25/17	W17-N_17MN039_062517_RWB_05_BL	FS			4440	
1706935	MMSE-1_17MN001	06/21/17	MMSE-1_17MN001_062117_NSS_06_BL	FS			1620	
1706935	MMSE-1_17MN002	06/21/17	MMSE-1_17MN002_062117_NSS_07_BL	FS			2070	
1706935	MMSE-1_17MN002	06/21/17	MMSE-1_17MN002_062117_NSS_08_BL	FS			1570	
1706935	MMSE-1_17MN003	06/21/17	MMSE-1_17MN003_062117_NSS_01_BL	FS			2350	
1706935	MMSE-1_17MN007	06/21/17	MMSE-1_17MN007_062117_NSS_03_BL	FS			3110	
1706935	MMSE-1_17MN008	06/22/17	MMSE-1_17MN008_062217_NSS_15_BL	FS			2340	
1706935	MMSE-1_17MN009	06/21/17	MMSE-1_17MN009_062117_NSS_02_BL	FS			2810	
1706935	MMSE-1_17MN010	06/21/17	MMSE-1_17MN010_062117_NSS_04_BL	FS			2200	
1706935	MMSE-1_17MN010	06/21/17	MMSE-1_17MN010_062117_NSS_05_BL	FS			2860	
1706935	MMSE-1_17MN010	06/21/17	MMSE-1_17MN010_062117_NSS_09_BL	FS			1820	
1706935	MMSE-1_17MN010	06/21/17	MMSE-1_17MN010_062117_NSS_10_BL	FS			1290	
1706935	MMSE-1_17MN011	06/22/17	MMSE-1_17MN011_062217_NSS_12_BL	FS			1810	
1706935	MMSE-1_17MN011	06/22/17	MMSE-1_17MN011_062217_NSS_14_BL	FS			3020	

TABLE 3
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-BLOOD AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

				Analysis Method	NOAALipids1993		EPA 1631	
				Parameter	Lipids		Mercury	
				Unit	PERCENT		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706935	MMSE-1_17MN018	06/22/17	MMSE-1_17MN018_062217_NSS_13_BL	FS			2670	
1706935	MMSE-1_17MN019	06/22/17	MMSE-1_17MN019_062217_NSS_11_BL	FS			1940	
1706936	MMSE-1_17MN004	06/21/17	MMSE-1_17MN004_062117_RWB_01_BL	FS			1090	J
1706936	MMSE-1_17MN044	06/27/17	MMSE-1_17MN044_062717_RWB_02_BL	FS			6260	J
1706936	MMSE-1_17MN045	06/27/17	MMSE-1_17MN045_062717_RWB_03_BL	FS			6170	J
1706936	MMSE-1_17MN047	06/27/17	MMSE-1_17MN047_062717_RWB_05_BL	FS			1150	J
1706936	MMSE-1_17MN064	06/28/17	MMSE-1_17MN064_062817_RWB_06_BL	FS			7210	J
1706936	MMSE-1_17MN075	06/27/17	MMSE-1_17MN075_062717_RWB_04_BL	FS			2680	J
1706937	MMSW-C_17MN006	06/19/17	MMSW-C_17MN006_061917_NSS_01_BL	FS			3460	
1706937	MMSW-C_17MN006	06/19/17	MMSW-C_17MN006_061917_NSS_03_BL	FS			4200	
1706937	MMSW-C_17MN008	06/19/17	MMSW-C_17MN008_061917_NSS_02_BL	FS			2990	
1706937	MMSW-C_17MN009	06/19/17	MMSW-C_17MN009_061917_NSS_04_BL	FS			4190	
1706937	MMSW-C_17MN009	06/19/17	MMSW-C_17MN009_061917_NSS_05_BL	FS			1410	
1706937	MMSW-C_17MN010	06/20/17	MMSW-C_17MN010_062017_NSS_09_BL	FS			2400	
1706937	MMSW-C_17MN015	06/20/17	MMSW-C_17MN015_062017_NSS_06_BL	FS			2150	
1706937	MMSW-C_17MN015	06/20/17	MMSW-C_17MN015_062017_NSS_08_BL	FS			2300	
1706937	MMSW-C_17MN016	06/20/17	MMSW-C_17MN016_062017_NSS_07_BL	FS			2190	
1706937	MMSW-C_17MN021	06/23/17	MMSW-C_17MN021_062317_NSS_10_BL	FS			2140	
1706937	MMSW-C_17MN026	06/23/17	MMSW-C_17MN026_062317_NSS_12_BL	FS			5010	
1706937	MMSW-C_17MN027	06/23/17	MMSW-C_17MN027_062317_NSS_11_BL	FS			1890	
1706937	MMSW-C_17MN027	06/23/17	MMSW-C_17MN027_062317_NSS_13_BL	FS			3280	
1706937	MMSW-C_17MN027	06/25/17	MMSW-C_17MN027_062517_NSS_14_BL	FS			4410	
1706937	MMSW-C_17MN027	06/25/17	MMSW-C_17MN027_062517_NSS_15_BL	FS			3740	
1706938	MMSW-C_17MN009	06/19/17	MMSW-C_17MN009_061917_RWB_01_BL	FS			5740	

TABLE 3
DATA VALIDATION REPORT
2017 BIOTA SAMPLING-BLOOD AND EELS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706398, 17069399, 1706400, 1706933, 1706934, 1706935, 1706936, 1706937, 1706938, 1706939

				Analysis Method	NOAALipids1993		EPA 1631	
				Parameter	Lipids		Mercury	
				Unit	PERCENT		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706938	MMSW-C_17MN020	06/23/17	MMSW-C_17MN020_062317_RWB_03_BL	FS			8460	
1706938	MMSW-C_17MN020	06/23/17	MMSW-C_17MN020_062317_RWB_04_BL	FS			1030	
1706938	MMSW-C_17MN022	06/23/17	MMSW-C_17MN022_062317_RWB_02_BL	FS			6020	J
1706938	MMSW-C_17MN036	06/25/17	MMSW-C_17MN036_062517_RWB_05_BL	FS			5020	
1706938	MMSW-C_17MN036	06/26/17	MMSW-C_17MN036_062617_RWB_06_BL	FS			6720	
1706939	ADD-01_17MN001	06/21/17	ADD-01_17MN001_062117_NSS_01_BL	FS			508	
1706939	ADD-01_17MN001	06/21/17	ADD-01_17MN001_062117_NSS_02_BL	FS			520	
1706939	ADD-01_17MN001	06/21/17	ADD-01_17MN001_062117_NSS_03_BL	FS			342	
1706939	ADD-01_17MN001	06/22/17	ADD-01_17MN001_062217_NSS_09_BL	FS			343	
1706939	ADD-01_17MN002	06/22/17	ADD-01_17MN002_062217_NSS_11_BL	FS			378	
1706939	ADD-01_17MN002	06/22/17	ADD-01_17MN002_062217_NSS_12_BL	FS			373	
1706939	ADD-01_17MN003	06/21/17	ADD-01_17MN003_062117_NSS_08_BL	FS			343	
1706939	ADD-01_17MN004	06/21/17	ADD-01_17MN004_062117_NSS_06_BL	FS			375	
1706939	ADD-01_17MN006	06/21/17	ADD-01_17MN006_062117_NSS_05_BL	FS			465	
1706939	ADD-01_17MN006	06/21/17	ADD-01_17MN006_062117_NSS_07_BL	FS			339	
1706939	ADD-01_17MN007	06/22/17	ADD-01_17MN007_062217_NSS_10_BL	FS			219	
1706939	ADD-01_17MN009	06/21/17	ADD-01_17MN009_062117_NSS_04_BL	FS			280	
1706939	ADD-01_17MN011	06/22/17	ADD-01_17MN011_062217_NSS_13_BL	FS			264	
1706939	ADD-01_17MN050	06/27/17	ADD-01_17MN050_062717_NSS_14_BL	FS			460	
1706939	ADD-01_17MN051	06/27/17	ADD-01_17MN051_062717_NSS_15_BL	FS			618	

Units:

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Data Validation Summary
2017 Biota Sampling- Insects and Spiders
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (terrestrial insects and spiders) were collected in June and July 2017 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 1706929,1706930, 1706931, 1706932, 1707703 and 1707706. Samples were analyzed by Clean Water Act (CWA, 2012).

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Methyl Mercury, total	CWA 1630	10% Stage III/ 90% Stage IIB
Eurofins	Mercury, total	CWA 1631B	10% Stage III/ 90% Stage IIB

A Stage IIb data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. The following qualifiers as applied during data validation or reported by the laboratory are included in the final data set:

J = The reported concentration is considered an estimated value

Validation reason codes were applied to results associated with QC measurements outside project QC goals. The validation qualification actions and associated validation reason codes applied to sample results are summarized on Table 2. The following data validation reason codes were applied to one or more sample results:

MS-RPD = MS/MSD RPD limit exceeded
MS-H = MS and/or MSD recovery high
LD = Lab Duplicate limit exceeded
MT = Methyl mercury concentration exceeds total mercury concentration
MS-L = MS and/or MSD recovery low

A complete summary of final sample results is provided in Table 3.

Data were evaluated based on the following parameters:

- * Data Completeness and Chain of Custody
- * Holding Times and Preservation
- * Blanks
- * Initial Calibration
- * Continuing Calibration
- * Laboratory Control Sample (LCS)
  Matrix Spike/Matrix Spike Duplicates (MS/MSD)
  Laboratory Duplicates
- * Detection Limits
- * Sample Result Verification/Electronic Evaluation Verification (EDD)
- * Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

With the exception of the following items discussed below, results were determined to be usable as reported by the laboratory.

2.0 Methyl Mercury – 1630

<u>Matrix Spike</u>

SDGs 1706930 – Samples MMSE-1_17BN001_062117_TIN_01_WB and MMSE-1_17PT003_062117_SPI_01_WB were used for MS/MSD analysis. The MSD recovery of methyl mercury (230%) in sample MMSE-1_17BN001_062117_TIN_01_WB was above the upper QC limit of 130%. The MS/MSD relative percent difference (RPD) is above the acceptance criteria of (35%) at 76.7%. The methyl mercury result for sample MMSE-1_17BN001_062117_TIN_01_WB was qualified estimated (J) due to potential high bias and imprecision.

The MS/MSD recovery for methyl mercury in sample MMSE-1_17PT003_062117_SPI_01_WB (155%/230%) was above the upper QC limit of 130%. Methyl mercury result for sample MMSE-1_17PT003_062117_SPI_01_WB was qualified estimated (J) due to potential high bias.

SDG 106932 – Sample ADD-01_17BN004_062317_TIN_04_WB was used for MS/MSD analysis. The MS/MSD recoveries for methyl mercury (46%/53%) were below the lower QC limit of 65%. Sample results for ADD-01_17BN004_062317_TIN_04_WB were qualified estimated (J) due to potential bias and imprecision.

<u>Method Comparison</u>

SDGs 1706932 - In a number of the terrestrial insects and spider samples the methyl mercury concentration is higher than the total mercury concentration. The laboratory did confirm the results and attributed the higher concentration to the minimal sample size and homogenization. Based on professional judgment, any methyl mercury result that is greater than the total mercury result and has an RPD >24 will be qualified as estimated. The methyl mercury results in samples ADD-01_17HC001_062717_SPI_03_WB and were qualified as estimated (J).

SDGs 1707706 - In one of the spider samples the methyl mercury concentration is higher than the total mercury concentration. The laboratory did confirm the results and attributed the higher concentration to the minimal sample size and homogenization. Based on professional judgment, any methyl mercury result that is greater than the total mercury result and has an RPD >24 will be qualified as estimated. The methyl mercury result in sample MMSE-1_17HC005_071917_SPI_04_WB was qualified as estimated (J).

3.0 Mercury – 1631

Equipment Blank

SDG 1707703 – Mercury was detected in the equipment blank at 0.58 ng/L. An action level was established at five times the concentration reported in the blank and compared to all sample results. The mercury result for all samples was greater than the action level; no action was required.

Laboratory Duplicate

SDG 1706929 – Sample W17-N_17MN001_062517_TIN_05_WB was selected by the laboratory for duplicate analysis. The RPD (62.5) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample W17-N_17MN001_062517_TIN_05_WB was qualified estimated (J).

SDG 1706931 – Sample MMSW-C_17BN001_062317_TIN_04_WB was selected by the laboratory for duplicate analysis. The RPD (44.8) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample MMSW-C_17PT002_062317_SPI_02_WB was qualified estimated (J).

Method Comparison

SDG 1706932 - In a number of the terrestrial insects and spider samples the methyl mercury concentration is higher than the total mercury concentration. The laboratory did confirm the results and attributed the higher concentration to the minimal sample size and homogenization. Based on professional judgment, any methyl mercury result that is greater than the total mercury result and has an RPD >24 will be qualified as estimated. The methyl mercury results in samples ADD-01_17HC001_062717_SPI_03_WB and were qualified as estimated (J).

SDG 1707706 - In one of the spider samples the methyl mercury concentration is higher than the total mercury concentration. The laboratory did confirm the results and attributed the higher concentration to the minimal sample size and homogenization. Based on professional judgment, any methyl mercury result that is greater than the total mercury result and has an RPD >24 will be qualified as estimated. The methyl mercury result in sample MMSE-1_17HC005_071917_SPI_04_WB and were qualified as estimated (J).

References:

Amec Foster Wheeler, 2016. "Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan", Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA"; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use"; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review"; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures"; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta August 23, 2017

elizabeth penta

Senior Reviewer: Denise King September 1, 2017

Denise King

TABLE 1
DATA VALIDATION SUMMARY REPORT
2017 BIOTA SAMPLING- Terrestrial Insects and Spiders
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706929, 1706930, 1706931, 1706932, 1707703 and 1707706

							Methyl
					Method Class	Mercury	Mercury
					Analysis Method	EPA 1631	EPA 1630
SDG	Media	Location	Field Sample ID	Sample Date	QC Code		
1706929	Insect	W17-N_17BN005	W17-N_17BN005_062417_TIN_01_WB	6/24/2017	FS	1	1
1706929	Insect	W17-N_17BN004	W17-N_17BN004_062417_TIN_02_WB	6/24/2017	FS	1	1
1706929	Insect	W17-N_17BN001	W17-N_17BN001_062517_TIN_03_WB	6/25/2017	FS	1	1
1706929	Insect	W17-N_17BN001	W17-N_17BN001_062517_TIN_04_WB	6/25/2017	FS	1	1
1706929	Insect	W17-N_17MN001	W17-N_17MN001_062517_TIN_05_WB	6/25/2017	FS	1	1
1706929	Spider	W17-N_17PT003	W17-N_17PT003_062417_SPI_01_WB	6/24/2017	FS	1	1
1706929	Spider	W17-N_17PT003	W17-N_17PT003_062417_SPI_02_WB	6/24/2017	FS	1	1
1706929	Spider	W17-N_17PT002	W17-N_17PT002_062517_SPI_03_WB	6/25/2017	FS	1	1
1706929	Spider	W17-N_17PT004	W17-N_17PT004_062517_SPI_04_WB	6/25/2017	FS	1	1
1706929	Spider	W17-N_17PT001	W17-N_17PT001_062517_SPI_05_WB	6/25/2017	FS	1	1
1706930	Insect	MMSE-1_17BN001	MMSE-1_17BN001_062117_TIN_01_WB	6/21/2017	FS	1	1
1706930	Insect	MMSE-1_17BN001	MMSE-1_17BN001_062117_TIN_02_WB	6/21/2017	FS	1	1
1706930	Insect	MMSE-1_17BN004	MMSE-1_17BN004_062117_TIN_03_WB	6/21/2017	FS	1	1
1706930	Insect	MMSE-1_17BN001	MMSE-1_17BN001_062117_TIN_04_WB	6/21/2017	FS	1	1
1706930	Insect	MMSE-1_17BN003	MMSE-1_17BN003_062117_TIN_05_WB	6/21/2017	FS	1	1
1706930	Spider	MMSE-1_17PT003	MMSE-1_17PT003_062117_SPI_01_WB	6/21/2017	FS	1	1
1706930	Spider	MMSE-1_17PT002	MMSE-1_17PT002_062117_SPI_02_WB	6/21/2017	FS	1	1
1706931	Insect	MMSW-C_17BN003	MMSW-C_17BN003_062317_TIN_01_WB	6/23/2017	FS	1	1
1706931	Insect	MMSW-C_17BN002	MMSW-C_17BN002_062317_TIN_02_WB	6/23/2017	FS	1	1
1706931	Insect	MMSW-C_17BN002	MMSW-C_17BN002_062317_TIN_03_WB	6/23/2017	FS	1	1
1706931	Insect	MMSW-C_17BN001	MMSW-C_17BN001_062317_TIN_04_WB	6/23/2017	FS	1	1
1706931	Insect	MMSW-C_17BN004	MMSW-C_17BN004_062317_TIN_05_WB	6/23/2017	FS	1	1
1706931	Spider	MMSW-C_17PT002	MMSW-C_17PT002_062317_SPI_01_WB	6/23/2017	FS	1	1
1706931	Spider	MMSW-C_17PT002	MMSW-C_17PT002_062317_SPI_02_WB	6/23/2017	FS	1	1
1706931	Spider	MMSW-C_17PT003	MMSW-C_17PT003_062317_SPI_03_WB	6/23/2017	FS	1	1
1706931	Spider	MMSW-C_17PT001	MMSW-C_17PT001_062317_SPI_04_WB	6/23/2017	FS	1	1
1706931	Spider	MMSW-C_17PT005	MMSW-C_17PT005_062317_SPI_05_WB	6/23/2017	FS	1	1
1706932	Insect	ADD-01_17BN001	ADD-01_17BN001_062317_TIN_01_WB	6/23/2017	FS	1	1
1706932	Insect	ADD-01_17BN002	ADD-01_17BN002_062317_TIN_02_WB	6/23/2017	FS	1	1
1706932	Insect	ADD-01_17BN003	ADD-01_17BN003_062317_TIN_03_WB	6/23/2017	FS	1	1
1706932	Insect	ADD-01_17BN004	ADD-01_17BN004_062317_TIN_04_WB	6/23/2017	FS	1	1
1706932	Insect	ADD-01_17HC002	ADD-01_17HC002_062317_TIN_05_WB	6/23/2017	FS	1	1
1706932	Spider	ADD-01_17HC001	ADD-01_17HC001_062317_SPI_01_WB	6/23/2017	FS	1	1
1706932	Spider	ADD-01_17HC001	ADD-01_17HC001_062717_SPI_02_WB	6/27/2017	FS	1	1
1706932	Spider	ADD-01_17HC001	ADD-01_17HC001_062717_SPI_03_WB	6/27/2017	FS	1	1
1706932	Spider	ADD-01_17HC002	ADD-01_17HC002_062717_SPI_04_WB	6/27/2017	FS	1	1
1706932	Spider	ADD-01_17HC001	ADD-01_17HC001_062717_SPI_05_WB	6/27/2017	FS	1	1
1707706	Spider	MMSE-1_17HC005	MMSE-1_17HC005_071917_SPI_03_WB	7/19/2017	FS	1	1
1707706	Spider	MMSE-1_17HC005	MMSE-1_17HC005_071917_SPI_04_WB	7/19/2017	FS	1	1
1707706	Spider	MMSE-1_17HC005	MMSE-1_17HC005_071917_SPI_05_WB	7/19/2017	FS	1	1
1707703	BW	QC	EQ_072517_TWEEZER_QC	7/25/2017	EB	1	1

Notes:	FS = Field Sample	EB = Equipment Blank
	Count = # of analytes	BW = Blank water
	SDG = Sample Delivery Group	

Created by: BCG 08/22/2017

Checked by: EP 08/23/2017

TABLE 2
DATA VALIDATION SUMMARY
2017 BIOTA SAMPLING - INSECTS AND SPIDERS
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706929, 1706930, 1706931, 1706932 and 1707706

SDG	Analysis Method	Lab Sample Id	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
1706929	E1631	1706929-05	W17-N_17MN001_062517_TIN_05_WB	Total	Mercury	49.7		49.7	J	LD	NG/G
1706930	KOH_1630	1706930-01RE1	MMSE-1_17BN001_062117_TIN_01_WB	Total	Methyl mercury	60.2		60.2	J	MS-H, MSD-RPD	NG/G
1706930	KOH_1630	1706930-06	MMSE-1_17PT003_062117_SPI_01_WB	Total	Methyl mercury	296		296	J	MS-H	NG/G
1706931	E1631	1706931-04RE1	MMSW-C_17BN001_062317_TIN_04_WB	Total	Mercury	11.6		11.6	J	LD	NG/G
1706932	KOH_1630	1706932-04	ADD-01_17BN004_062317_TIN_04_WB	Total	Methyl mercury	26.1		26.1	J	MS-L	NG/G
1706932	E1631	1706932-08	ADD-01_17HC001_062717_SPI_03_WB	Total	Mercury	44.2		44.2	J	MT	NG/G
1706932	KOH_1630	1706932-08	ADD-01_17HC001_062717_SPI_03_WB	Total	Methyl mercury	56.7		56.7	J	MT	NG/G
1707706	E1631	1707706-02RE1	MMSE-1_17HC005_071917_SPI_04_WB	Total	Mercury	581		581	J	MT	NG/G
1707706	KOH_1630	1707706-02RE1	MMSE-1_17HC005_071917_SPI_04_WB	Total	Methyl mercury	748		748	J	MT	NG/G

Units

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Validation Reason Codes:

LD = Lab duplicate limit exceeded

MS-H = MS and/or MSD recovery high

MS-L = MS and/or MSD recovery low

MS-RPD = MS/MSD RPD limit exceeded

MT = Methyl mercury concentration exceeds total mercury concentration

Created by: BCG 09/01/2017
Checked by: EP 09/05/2017

TABLE 3
DATA VALIDATION SUMMARY REPORT
JUNE AND JULY 2017- INSECT AND SPIDER SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706929, 1706930, 1706931, 1706932, 1707706 and 1707703

				Analysis Method	EPA 1631		EPA 1630	
				Parameter	Mercury		Methyl Mercury	
				Unit	NG/G		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706929	W17-N_17BN001	06/25/17	W17-N_17BN001_062517_TIN_04_WB	FS	5.7		4.9	
1706929	W17-N_17BN001	06/25/17	W17-N_17BN001_062517_TIN_03_WB	FS	5.19		3.2	
1706929	W17-N_17BN004	06/24/17	W17-N_17BN004_062417_TIN_02_WB	FS	36.5		39.2	
1706929	W17-N_17BN005	06/24/17	W17-N_17BN005_062417_TIN_01_WB	FS	6.59		2.4	
1706929	W17-N_17MN001	06/25/17	W17-N_17MN001_062517_TIN_05_WB	FS	49.7	J	41.6	
1706929	W17-N_17PT001	06/25/17	W17-N_17PT001_062517_SPI_05_WB	FS	402		266	
1706929	W17-N_17PT002	06/25/17	W17-N_17PT002_062517_SPI_03_WB	FS	349		329	
1706929	W17-N_17PT003	06/24/17	W17-N_17PT003_062417_SPI_01_WB	FS	302		287	
1706929	W17-N_17PT003	06/24/17	W17-N_17PT003_062417_SPI_02_WB	FS	315		324	
1706929	W17-N_17PT004	06/25/17	W17-N_17PT004_062517_SPI_04_WB	FS	293		323	
1706930	MMSE-1_17BN001	06/21/17	MMSE-1_17BN001_062117_TIN_02_WB	FS	7.62		6.9	
1706930	MMSE-1_17BN001	06/21/17	MMSE-1_17BN001_062117_TIN_04_WB	FS	2.95		2.1	
1706930	MMSE-1_17BN001	06/21/17	MMSE-1_17BN001_062117_TIN_01_WB	FS	71.7		60.2	J
1706930	MMSE-1_17BN003	06/21/17	MMSE-1_17BN003_062117_TIN_05_WB	FS	22.7		21.2	
1706930	MMSE-1_17BN004	06/21/17	MMSE-1_17BN004_062117_TIN_03_WB	FS	24.6		21.5	
1706930	MMSE-1_17PT002	06/21/17	MMSE-1_17PT002_062117_SPI_02_WB	FS	526		511	
1706930	MMSE-1_17PT003	06/21/17	MMSE-1_17PT003_062117_SPI_01_WB	FS	278		296	J
1706931	MMSW-C_17BN001	06/23/17	MMSW-C_17BN001_062317_TIN_04_WB	FS	11.6	J	14.7	
1706931	MMSW-C_17BN002	06/23/17	MMSW-C_17BN002_062317_TIN_02_WB	FS	35.6		27.1	
1706931	MMSW-C_17BN002	06/23/17	MMSW-C_17BN002_062317_TIN_03_WB	FS	34.3		28.4	
1706931	MMSW-C_17BN003	06/23/17	MMSW-C_17BN003_062317_TIN_01_WB	FS	3.75		2.9	
1706931	MMSW-C_17BN004	06/23/17	MMSW-C_17BN004_062317_TIN_05_WB	FS	93.7		49.5	
1706931	MMSW-C_17PT001	06/23/17	MMSW-C_17PT001_062317_SPI_04_WB	FS	315		50.8	
1706931	MMSW-C_17PT002	06/23/17	MMSW-C_17PT002_062317_SPI_01_WB	FS	403		495	

TABLE 3
DATA VALIDATION SUMMARY REPORT
JUNE AND JULY 2017- INSECT AND SPIDER SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1706929, 1706930, 1706931, 1706932, 1707706 and 1707703

				Analysis Method	EPA 1631		EPA 1630	
				Parameter	Mercury		Methyl Mercury	
				Unit	NG/G		NG/G	
				Fraction	Total		Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	Final Result	Final Qualifier	Final Result	Final Qualifier
1706931	MMSW-C_17PT002	06/23/17	MMSW-C_17PT002_062317_SPI_02_WB	FS	305		370	
1706931	MMSW-C_17PT003	06/23/17	MMSW-C_17PT003_062317_SPI_03_WB	FS	325		330	
1706931	MMSW-C_17PT005	06/23/17	MMSW-C_17PT005_062317_SPI_05_WB	FS	279		337	
1706932	ADD-01_17BN001	06/23/17	ADD-01_17BN001_062317_TIN_01_WB	FS	1.54		1.3	J
1706932	ADD-01_17BN002	06/23/17	ADD-01_17BN002_062317_TIN_02_WB	FS	11.5		8.2	
1706932	ADD-01_17BN003	06/23/17	ADD-01_17BN003_062317_TIN_03_WB	FS	41.8		29.8	
1706932	ADD-01_17BN004	06/23/17	ADD-01_17BN004_062317_TIN_04_WB	FS	25		26.1	J
1706932	ADD-01_17HC001	06/23/17	ADD-01_17HC001_062317_SPI_01_WB	FS	67.5		73.2	
1706932	ADD-01_17HC001	06/27/17	ADD-01_17HC001_062717_SPI_02_WB	FS	51.2		59.5	
1706932	ADD-01_17HC001	06/27/17	ADD-01_17HC001_062717_SPI_03_WB	FS	44.2	J	56.7	J
1706932	ADD-01_17HC001	06/27/17	ADD-01_17HC001_062717_SPI_05_WB	FS	55		50.4	
1706932	ADD-01_17HC002	06/23/17	ADD-01_17HC002_062317_TIN_05_WB	FS	2.62		2.2	
1706932	ADD-01_17HC002	06/27/17	ADD-01_17HC002_062717_SPI_04_WB	FS	57.3		58.5	
1707706	MMSE-1_17HC005	07/19/17	MMSE-1_17HC005_071917_SPI_03_WB	FS	622		544	
1707706	MMSE-1_17HC005	07/19/17	MMSE-1_17HC005_071917_SPI_04_WB	FS	581	J	748	J
1707706	MMSE-1_17HC005	07/19/17	MMSE-1_17HC005_071917_SPI_05_WB	FS	560		564	
1707703	QC	07/25/17	EQ_072517_TWEEZER_QC	EB	0.58 (NG/L)		0.05 (NG/L)	U

Notes:

NG/G = Nanogram per gram	J = Value is estimated
NG/L = Nanogram per liter	U = The target compound was not detected above the method detection limit
FS = Field Sample	SDG = Sample Delivery Group
EB = Equipment Blank	BW = Blank water

Data Validation Summary
2018 Biota Sampling
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Black duck blood samples were collected in January 2018 from the Penobscot River located in Maine. Samples were analyzed by Eurofins Frontier Global Sciences, Inc. (Eurofins) located in Bothell, Washington and included in sample delivery groups (SDGs) 8B00079, 8B00080 and 8B00082. Samples were analyzed by the Clean Water Act (CWA, 2012):

Laboratory	Parameter	Analytical Method	Validation Level
Eurofins	Mercury, Total	CWA 1631B	10% Stage III/ 90% Stage IIB

A Stage IIb data validation was completed on all SDGs**.** A Stage III data validation was performed on ten percent of samples. Data validation was completed using National Functional Guidelines for Inorganic Superfund Data Review (USEPA, 2014) and EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (USEPA, 2013) where applicable. Data quality evaluations were completed using quality control (QC) limits specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP) [Amec Foster Wheeler, 2016]. The project laboratory reported results using a combination of two detection limits including the reporting limit (RL) and the method detection limit (MDL). Results for compounds that are not detected in samples are reported as U qualified results at the RL. Positive detections between the MDL and RL are qualified as estimated (J) by the laboratory.

Data validation review and qualification actions are discussed in the following subsections. It should be noted that only instances that result in an impact to data quality are presented in this report. There may be QC elements outside of QAPP and/or method control limits not presented in this report since there is no impact to data quality. Samples included in this data evaluation are presented in Table 1.

Data qualifications were completed if necessary in accordance with the guidelines or the professional judgment of the project chemist. The following qualifiers as applied during data validation or reported by the laboratory are included in the final data set:

J = The reported concentration is considered an estimated value

All QC measurements were within project QC goals and no qualification reason codes were applied. The validation qualification actions applied to sample results are summarized in Table 2.

A complete summary of final sample results is provided in Table 3.

Data were evaluated based on the following parameters:

- Data Completeness and Chain of Custody
- Holding Times and Preservation
- Blanks
- Initial Calibration

* Continuing Calibration
* Laboratory Control Sample (LCS)
* Matrix Spike/Matrix Spike Duplicates (MS/MSD)
* Laboratory Duplicates
* Detection Limits
* Sample Result Verification/Electronic Evaluation Verification (EDD)
* Ongoing Precision Recovery

* = indicates that criteria were met and/or no impact to data quality for this parameter

2.0 Mercury – 1631

All results were determined to be usable as reported by the laboratory.

References:

Amec Foster Wheeler, 2016. “Draft Penobscot River Estuary Phase III – Engineering Study Quality Assurance Project Plan”, Penobscot River, Maine, July 2016.

U.S. Environmental Protection Agency (USEPA), 2004. "Final Update IIIB and Method 9071B of Final Update IIIA”; Test Methods for Evaluating Solid Waste Physical/Chemical Methods SW-846; Office of Solid Waste and Emergency Response, EPA-SW-846-03-03B; November 2004.

U.S. Environmental Protection Agency (USEPA), 2009. "Guidance for Labeling Externally Validated Laboratory Analytical data for Superfund Use”; Office of Solid Waste and Emergency Response; EPA 540-R-08-005; January 13, 2009.

U.S. Environmental Protection Agency (USEPA), 2014. "National Functional Guidelines for Inorganic Superfund Data Review”; Office of Superfund Remediation and Technology Innovation; EPA-540-R-013-001; August 2014.

U.S. Environmental Protection Agency (USEPA), 2013. "EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures”; Quality Assurance Unit Staff; Office of Environmental Measurement and Evaluation; April 22, 2013.

Data Validator: Elizabeth Penta February 19, 2018

elizabeth penta

Senior Reviewer: Denise King February 20, 2018

Denise King

TABLE 1
DATA VALIDATION SUMMARY REPORT
2018 BIOTA SAMPLING- DUCK BLOOD
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 8B00079, 8B00080 and 8B00082

					Method Class	Mercury
					Analysis Method	EPA 1631
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**	
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013018_ABD_01_BL	1/30/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013018_ABD_02_BL	1/30/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013018_ABD_03_BL	1/30/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013018_ABD_04_BL	1/30/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013018_ABD_05_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_06_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_07_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_08_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_09_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_10_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_11_BL	1/30/2018	FS	1
8B00079	Blood	FRB-OCN_18WT001	FRB-OCN_18WT001_013018_ABD_12_BL	1/30/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013118_ABD_13_BL	1/31/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013118_ABD_14_BL	1/31/2018	FS	1
8B00079	Blood	FRB-01_18WT001	FRB-01_18WT001_013118_ABD_15_BL	1/31/2018	FS	1
8B00079	Duck Bait	QC	FRB-01_013118_BAIT_01_QC	1/31/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_012918_ABD_01_BL	1/29/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_02_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_03_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_04_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_05_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_06_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_07_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_08_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_09_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_10_BL	1/30/2018	FS	1

Created by: EP 02/19/2018
Checked by: DMK 02/20/2018

TABLE 1
DATA VALIDATION SUMMARY REPORT
2018 BIOTA SAMPLING- DUCK BLOOD
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 8B00079, 8B00080 and 8B00082

					Method Class	**Mercury**
					Analysis Method	**EPA 1631**
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**	
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_11_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_12_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_13_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_14_BL	1/30/2018	FS	1
8B00080	Blood	MMBKD-01_18WT001	MMBKD-01_18WT001_013018_ABD_15_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_01_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_02_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_03_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_04_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_05_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_06_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_012918_ABD_07_BL	1/29/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013018_ABD_08_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013018_ABD_09_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013018_ABD_10_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013018_ABD_11_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013018_ABD_12_BL	1/30/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES_13_18WT001_013118_ABD_13_BL	1/31/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013118_ABD_14_BL	1/31/2018	FS	1
8B00082	Blood	ES-13_18WT001	ES-13_18WT001_013118_ABD_15_BL	1/31/2018	FS	1

Notes:

Count = # of analytes

FS = Field Sample

QC = Quality Control

SDG = Sample Delivery Group

Created by: EP 02/19/2018

Checked by: DMK 02/20/2018

TABLE 2
DATA VALIDATION SUMMARY REPORT
2018 BIOTA SAMPLING- DUCK BLOOD
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 8B00079, 8B00080 and 8B00082

SDG	Analysis Method	Lab Sample Id	Field Sample Id	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Validation Reason Code	Result Units
8B00079	EPA 1631	8B00079-16RE1	FRB-01_013118_BAIT_01_QC	Total	Mercury	0.165	J	0.165	J	NA	NG/G

Units
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
NA = Not applicable

Created by: EP 02/19/2018
Checke by: DMK 02/20/2018

TABLE 3
DATA VALIDATION SUMMARY REPORT
2018 BIOTA SAMPLING- DUCK BLOOD
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 8B00079, 8B00080 and 8B00082

				Analysis Method	EPA 1631	
				Parameter	Mercury	
				Unit	NG/G	
				Fraction	Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	**Final Result**	**Final Qualifier**
8B00079	FRB-01_18WT001	1/30/2018	FRB-01_18WT001_013018_ABD_01_BL	FS	56.5	
8B00079	FRB-01_18WT001	1/30/2018	FRB-01_18WT001_013018_ABD_02_BL	FS	55.8	
8B00079	FRB-01_18WT001	1/30/2018	FRB-01_18WT001_013018_ABD_03_BL	FS	63.9	
8B00079	FRB-01_18WT001	1/30/2018	FRB-01_18WT001_013018_ABD_04_BL	FS	22.9	
8B00079	FRB-01_18WT001	1/30/2018	FRB-01_18WT001_013018_ABD_05_BL	FS	21.3	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_06_BL	FS	52.0	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_07_BL	FS	86.1	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_08_BL	FS	70.3	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_09_BL	FS	80.4	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_10_BL	FS	52.7	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_11_BL	FS	62.0	
8B00079	FRB-OCN_18WT001	1/30/2018	FRB-OCN_18WT001_013018_ABD_12_BL	FS	49.0	
8B00079	FRB-01_18WT001	1/31/2018	FRB-01_18WT001_013118_ABD_13_BL	FS	33.9	
8B00079	FRB-01_18WT001	1/31/2018	FRB-01_18WT001_013118_ABD_14_BL	FS	62.7	
8B00079	FRB-01_18WT001	1/31/2018	FRB-01_18WT001_013118_ABD_15_BL	FS	54.6	
8B00079	QC	1/31/2018	FRB-01_013118_BAIT_01_QC	FS	0.165	J
8B00080	MMBKD-01_18WT001	1/29/2018	MMBKD-01_18WT001_012918_ABD_01_BL	FS	459	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_02_BL	FS	238	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_03_BL	FS	427	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_04_BL	FS	238	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_05_BL	FS	386	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_06_BL	FS	359	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_07_BL	FS	295	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_08_BL	FS	187	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_09_BL	FS	324	

Prepared by: EP 02/19/2018
Checked by: DMK 02/20/2018

TABLE 3
DATA VALIDATION SUMMARY REPORT
2018 BIOTA SAMPLING- DUCK BLOOD
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 8B00079, 8B00080 and 8B00082

				Analysis Method	EPA 1631	
				Parameter	Mercury	
				Unit	NG/G	
				Fraction	Total	
SDG	**Location ID**	**Sample Date**	**Sample ID**	**QC Code**	**Final Result**	**Final Qualifier**
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_10_BL	FS	309	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_11_BL	FS	227	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_12_BL	FS	245	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_13_BL	FS	209	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_14_BL	FS	206	
8B00080	MMBKD-01_18WT001	1/30/2018	MMBKD-01_18WT001_013018_ABD_15_BL	FS	275	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_01_BL	FS	200	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_02_BL	FS	296	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_03_BL	FS	97.1	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_04_BL	FS	241	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_05_BL	FS	50.6	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_06_BL	FS	229	
8B00082	ES-13_18WT001	1/29/2018	ES-13_18WT001_012918_ABD_07_BL	FS	80.3	
8B00082	ES-13_18WT001	1/30/2018	ES-13_18WT001_013018_ABD_08_BL	FS	159	
8B00082	ES-13_18WT001	1/30/2018	ES-13_18WT001_013018_ABD_09_BL	FS	165	
8B00082	ES-13_18WT001	1/30/2018	ES-13_18WT001_013018_ABD_10_BL	FS	119	
8B00082	ES-13_18WT001	1/30/2018	ES-13_18WT001_013018_ABD_11_BL	FS	109	
8B00082	ES-13_18WT001	1/30/2018	ES-13_18WT001_013018_ABD_12_BL	FS	173	
8B00082	ES-13_18WT001	1/31/2018	ES_13_18WT001_013118_ABD_13_BL	FS	113	
8B00082	ES-13_18WT001	1/31/2018	ES-13_18WT001_013118_ABD_14_BL	FS	206	
8B00082	ES-13_18WT001	1/31/2018	ES-13_18WT001_013118_ABD_15_BL	FS	459	

Notes:

NG/G = Nanogram per gram

FS = Field Sample

J = Value is estimated

SDG = Sample Delivery Group

APPENDIX F

Biota Statistical Analysis Code

Appendix F-1. Terrestrial Insect Statistical Analysis Code

```
### File created for analysis of terrestrial insects data for Biota Monitoring Report (2017)
### Code edited by LSV 01/17/2018
### Code checked by NTG 01/31/2018

library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob
 $month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month
 == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


#################
### T Insects ###
#################

levels(factor(penob$PARAM_NAME[penob$LOGGED_BY == "Terrestrial Insect"]))

hg.tin = penob[penob$LOGGED_BY == "Terrestrial Insect" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples
 labeled as mercury, removes field duplicates

hg.tin$ln.resuse = log(hg.tin$resuse) #log Hg results

hg.tin = merge(hg.tin, penob[penob$LOGGED_BY == "Terrestrial Insect" & penob$PARAM_NAME == "Methyl mercury" &! penob$QC_CODE == "FD",],
 by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), by.y  = c("LOC_NAME", "ID",
 "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge Hg and Me Hg results
summary(hg.tin)
names(hg.tin)[colnames(hg.tin) == "resuse.y"] = "mehg.resuse" #rename columns to keep track of data
names(hg.tin)[colnames(hg.tin) == "resuse.x"] = "resuse" #rename columns to keep track of data

hg.tin$ln.mehg.resuse = log(hg.tin$mehg.resuse) #log Me Hg results

hg.tin$locs = as.factor(substring(hg.tin$LOC_NAME,1,5)) #location identifier
hg.tin$reach = as.factor(substring(hg.tin$LOC_NAME,1,2))

ref.tin = hg.tin[hg.tin$X_COORD > 930000 | hg.tin$Y_COORD < 22000,] #create separate dataset for reference samples
hg.tin.P = hg.tin #retaining all paired data
hg.tin = hg.tin[hg.tin$X_COORD < 930000 & hg.tin$Y_COORD > 326000,] #reducing main dataset to site, not reference samples
ref.tin = ref.tin[!is.na(ref.tin$resuse) == T,] #remove NAs
hg.tin = hg.tin[!is.na(hg.tin$resuse) == T,] #remove NAs
summary(hg.tin) #131 records
summary(ref.tin) #55 records


hg.tin.mm = hg.tin[hg.tin$Y_COORD < 342000,] #pulling out MM terr insects
hg.tin.mmse = hg.tin.mm[hg.tin.mm$X_COORD > 889600 & hg.tin.mm$Y_COORD > 335000,] #MM-SE terr insects
hg.tin.mmsw = hg.tin.mm[hg.tin.mm$X_COORD > 889600 & hg.tin.mm$Y_COORD < 335000 & hg.tin.mm$Y_COORD > 326000,] #MM-SW terr insects
 #MW-3 & 4 are w of hwy
hg.tin.w17 = hg.tin[hg.tin$Y_COORD > 347500 & hg.tin$X_COORD > 888000,] #pulling out W17 terr insects


###########################
### Terr Insect Summary ###
###########################
```

```
tin.summ = data.frame(MMSE.x = tapply(hg.tin.mmse$resuse[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)],
 hg.tin.mmse$year[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], mean))
tin.summ$MMSE.x.se = tapply(hg.tin.mmse$resuse[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], hg.tin.mmse
 $year[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.tin.mmse$resuse[(hg.tin.mmse
 $FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], hg.tin.mmse$year[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse
 $FINAL_QUAL.x) == T)], length))
tin.summ$MMSE.medn = tapply(hg.tin.mmse$resuse, hg.tin.mmse$year, median) #leave NDs in for this calc
tin.summ$MMSE.N = tapply(hg.tin.mmse$resuse, hg.tin.mmse$year, length)


tin.summ$MMSW.x = tapply(hg.tin.mmsw$resuse[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], hg.tin.mmsw
 $year[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], mean)
tin.summ$MMSW.x.se = tapply(hg.tin.mmsw$resuse[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], hg.tin.mmsw
 $year[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.tin.mmsw$resuse[(hg.tin.mmsw
 $FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], hg.tin.mmsw$year[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw
 $FINAL_QUAL.x) == T)], length))
tin.summ$MMSW.medn = tapply(hg.tin.mmsw$resuse, hg.tin.mmsw$year, median) #leave NDs in for this calc
tin.summ$MMSW.N = tapply(hg.tin.mmsw$resuse, hg.tin.mmsw$year, length)


tin.summ$w17.x = tapply(hg.tin.w17$resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], mean)
tin.summ$w17.x.se = tapply(hg.tin.w17$resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.tin.w17$resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], length))
tin.summ$w17.medn = tapply(hg.tin.w17$resuse, hg.tin.w17$year, median) #leave NDs in for this calc
tin.summ$w17.N = tapply(hg.tin.w17$resuse, hg.tin.w17$year, length)


tin.summ$ADD.x[2:3] = tapply(ref.tin$resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) ==
 T)], ref.tin$year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean)
tin.summ$ADD.x.se[2:3] = tapply(ref.tin$resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) ==
 T)], ref.tin$year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.tin$resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin
 $year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length))
tin.summ$ADD.medn[2:3] = tapply(ref.tin$resuse[ref.tin$locs == "ADD-0"], ref.tin$year[ref.tin$locs == "ADD-0"], median) #leave NDs in
 for this calc
tin.summ$ADD.N[2:3] = tapply(ref.tin$resuse[ref.tin$locs == "ADD-0"], ref.tin$year[ref.tin$locs == "ADD-0"], length)


tin.summ$BH.x = c(tapply(ref.tin$resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)],
 ref.tin$year[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean), NA, NA)
tin.summ$BH.x.se = c(tapply(ref.tin$resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)],
 ref.tin$year[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(ref.tin
 $resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin$year[ref.tin$reach == "BH"
 & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length)), NA, NA)
tin.summ$BH.medn = c(tapply(ref.tin$resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], median), NA, NA) #leave NDs in
 for this calc
tin.summ$BH.N = c(tapply(ref.tin$resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], length), NA, NA)


tin.summ$SM.x = c(tapply(ref.tin$resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)],
 ref.tin$year[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean),NA, NA)
tin.summ$SM.x.se = c(tapply(ref.tin$resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)],
 ref.tin$year[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(ref.tin
 $resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin$year[ref.tin$reach == "SM"
 & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length)),NA, NA)
tin.summ$SM.medn = c(tapply(ref.tin$resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], median), NA, NA) #leave NDs in
 for this calc
tin.summ$SM.N = c(tapply(ref.tin$resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], length), NA, NA)


# Me Hg
tin.summ$MeHgMMSE.x = tapply(hg.tin.mmse$mehg.resuse[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)],
 hg.tin.mmse$year[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], mean, na.rm = T)
tin.summ$MeHgMMSE.x.se = tapply(hg.tin.mmse$mehg.resuse[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)],
 hg.tin.mmse$year[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], sd, na.rm = T) / sqrt(tapply(hg.tin.mmse
 $mehg.resuse[(hg.tin.mmse$FINAL_QUAL.x == "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], hg.tin.mmse$year[(hg.tin.mmse$FINAL_QUAL.x ==
 "J" | is.na(hg.tin.mmse$FINAL_QUAL.x) == T)], length))
tin.summ$MeHgMMSE.medn = tapply(hg.tin.mmse$mehg.resuse, hg.tin.mmse$year, median, na.rm = T) #leave NDs in for this calc
tin.summ$MeHgMMSE.N = tapply(hg.tin.mmse$mehg.resuse, hg.tin.mmse$year, length)


tin.summ$MeHgMMSW.x = tapply(hg.tin.mmsw$mehg.resuse[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)],
 hg.tin.mmsw$year[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], mean, na.rm = T)
tin.summ$MeHgMMSW.x.se = tapply(hg.tin.mmsw$mehg.resuse[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)],
 hg.tin.mmsw$year[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], sd, na.rm = T) / sqrt(tapply(hg.tin.mmsw
 $mehg.resuse[(hg.tin.mmsw$FINAL_QUAL.x == "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], hg.tin.mmsw$year[(hg.tin.mmsw$FINAL_QUAL.x ==
```

```
 "J" | is.na(hg.tin.mmsw$FINAL_QUAL.x) == T)], length))
tin.summ$MeHgMMSW.medn = tapply(hg.tin.mmsw$mehg.resuse, hg.tin.mmsw$year, median, na.rm = T) #leave NDs in for this calc
tin.summ$MeHgMMSW.N = tapply(hg.tin.mmsw$mehg.resuse, hg.tin.mmsw$year, length)


tin.summ$MeHgw17.x = tapply(hg.tin.w17$mehg.resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], mean, na.rm = T)
tin.summ$MeHgw17.x.se = tapply(hg.tin.w17$mehg.resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], sd, na.rm = T) /
 sqrt(tapply(hg.tin.w17$mehg.resuse[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)],
 hg.tin.w17$year[(hg.tin.w17$FINAL_QUAL.x == "J" | is.na(hg.tin.w17$FINAL_QUAL.x) == T)], length))
tin.summ$MeHgw17.medn = tapply(hg.tin.w17$mehg.resuse, hg.tin.w17$year, median, na.rm = T) #leave NDs in for this calc
tin.summ$MeHgw17.N = tapply(hg.tin.w17$mehg.resuse, hg.tin.w17$year, length)


tin.summ$MeHgADD.x[2:3] = tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin
 $FINAL_QUAL.x) == T)], ref.tin$year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean)
tin.summ$MeHgADD.x.se[2:3] = tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin
 $FINAL_QUAL.x) == T)], ref.tin$year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin
 $year[ref.tin$locs == "ADD-0" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length))
tin.summ$MeHgADD.medn[2:3] = tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0"], ref.tin$year[ref.tin$locs == "ADD-0"], median) #leave
 NDs in for this calc
tin.summ$MeHgADD.N[2:3] = tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0"], ref.tin$year[ref.tin$locs == "ADD-0"], length)


tin.summ$MeHgBH.x = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) ==
 T)], ref.tin$year[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean), NA, NA)
tin.summ$MeHgBH.x.se = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x)
 == T)], ref.tin$year[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin
 $year[ref.tin$reach == "BH" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length)), NA, NA)
tin.summ$MeHgBH.medn = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], median, na.rm = T),
 NA, NA) #leave NDs in for this calc
tin.summ$MeHgBH.N = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], length), NA, NA)


tin.summ$MeHgSM.x = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) ==
 T)], ref.tin$year[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], mean), NA, NA)
tin.summ$MeHgSM.x.se = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x)
 == T)], ref.tin$year[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], ref.tin
 $year[ref.tin$reach == "SM" & (ref.tin$FINAL_QUAL.x == "J" | is.na(ref.tin$FINAL_QUAL.x) == T)], length)), NA, NA)
tin.summ$MeHgSM.medn = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], median, na.rm = T),
 NA, NA) #leave NDs in for this calc
tin.summ$MeHgSM.N = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], length), NA, NA)


write.csv(tin.summ, "Terr Insect summary.csv")


#################################
### Terrestrial Insect Figures ###
#################################

#4-1
plot(ln.resuse ~ year, data = ref.tin[ref.tin$reach == "AD",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-1\nTerrestrial
 Insect - Reference Locations\nLn Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006, max(hg.tin
 $year)), yaxs = "i", las = 1, tck = 0.015, pch = 16)
points(ln.resuse ~ year, data = ref.tin[ref.tin$reach == "SM",], pch = 18, col = 3)

points(as.numeric(levels(as.factor(ref.tin$year))), tapply(ref.tin$ln.resuse[!ref.tin$reach == "BH"], ref.tin$year[!ref.tin$reach ==
 "BH"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.tin$year))), tapply(ref.tin$ln.resuse[!ref.tin$reach == "BH"], ref.tin$year[!ref.tin$reach ==
 "BH"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Pleasant River", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,"blue","red"), pch =
 c(16,18,22,21), pt.bg = c("white","white","blue","red"), cex = 0.8)


#4-2
plot(ln.mehg.resuse ~ year, data = ref.tin[ref.tin$reach == "AD",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-2\nTerrestrial Insect - Reference Locations\nLn Methyl Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim =
 c(2006, max(hg.tin$year)), yaxs = "i", las = 1, tck = 0.015, pch = 16)
points(ln.mehg.resuse ~ year, data = ref.tin[ref.tin$reach == "SM",], pch = 18, col = 3)

points(as.numeric(levels(as.factor(ref.tin$year))), tapply(ref.tin$ln.mehg.resuse[!ref.tin$reach == "BH"], ref.tin$year[!ref.tin$reach
 == "BH"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.tin$year))), tapply(ref.tin$ln.mehg.resuse[!ref.tin$reach == "BH"], ref.tin$year[!ref.tin$reach
```

```
 == "BH"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Pleasant River", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,"blue","red"), pch =
 c(16,18,22,21), pt.bg = c("white","white","blue","red"), cex = 0.8)
title(sub = "Six samples at Spurwink River were non-detect and are included on this figure at the detection limit.", cex.sub = 0.7)


#4-3
plot(ln.resuse ~ year, data = hg.tin, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-3\nTerrestrial Insect - Whole River\nLn
 Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006, max(hg.tin$year)), yaxs = "i", las = 1, tck =
 0.015)

points(as.numeric(levels(as.factor(hg.tin$year))), tapply(hg.tin$ln.resuse, hg.tin$year, median), pch = 21, col = "red", cex = 1.3, bg
 = "red")
points(as.numeric(levels(as.factor(hg.tin$year))), tapply(hg.tin$ln.resuse, hg.tin$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Terrestrial Insects sampled at W-17-N, MM-SE, and MM-SW", cex.sub = 0.7)


#4-4
plot(ln.resuse ~ year, data = hg.tin.w17, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-4\nTerrestrial Insect - W-17-N\nLn
 Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006, max(hg.tin$year)), yaxs = "i", las = 1, tck =
 0.015)

points(as.numeric(levels(as.factor(hg.tin.w17$year))), tapply(hg.tin.w17$ln.resuse, hg.tin.w17$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.w17$year))), tapply(hg.tin.w17$ln.resuse, hg.tin.w17$year, mean), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-5
plot(ln.resuse ~ year, data = hg.tin.mmse, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-5\nTerrestrial Insect - MM-SE\nLn
 Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006, max(hg.tin$year)), yaxs = "i", las = 1, tck =
 0.015)

points(as.numeric(levels(as.factor(hg.tin.mmse$year))), tapply(hg.tin.mmse$ln.resuse, hg.tin.mmse$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.mmse$year))), tapply(hg.tin.mmse$ln.resuse, hg.tin.mmse$year, mean), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-6
plot(ln.resuse ~ year, data = hg.tin.mmsw, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-6\nTerrestrial Insect - MM-SW\nLn
 Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006, max(hg.tin$year)), yaxs = "i", las = 1, tck =
 0.015)

points(as.numeric(levels(as.factor(hg.tin.mmsw$year))), tapply(hg.tin.mmsw$ln.resuse, hg.tin.mmsw$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.mmsw$year))), tapply(hg.tin.mmsw$ln.resuse, hg.tin.mmsw$year, mean), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-7
plot(ln.mehg.resuse ~ year, data = hg.tin, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-7\nTerrestrial Insect - Whole
 River\nLn Methyl Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006,max(hg.tin$year)), yaxs = "i", las
 = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.tin$year))), tapply(hg.tin$ln.mehg.resuse, hg.tin$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin$year))), tapply(hg.tin$ln.mehg.resuse, hg.tin$year, mean, na.rm = T), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Terrestrial Insects sampled at W-17-N, MM-SE, and MM-SW", cex.sub = 0.7)
```

```
#4-8
plot(ln.mehg.resuse ~ year, data = hg.tin.w17, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-8\nTerrestrial Insect - W-17-N
 \nLn Methyl Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006,max(hg.tin$year)), yaxs = "i", las = 1,
 tck = 0.015)

points(as.numeric(levels(as.factor(hg.tin.w17$year))), tapply(hg.tin.w17$ln.mehg.resuse, hg.tin.w17$year, median, na.rm = T), pch = 21,
 col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.w17$year))), tapply(hg.tin.w17$ln.mehg.resuse, hg.tin.w17$year, mean, na.rm = T), pch = 22,
 col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "One sample collected in 2009 was non-detect and is included on this figure using the detection limit.", cex.sub = 0.7)


#4-9
plot(ln.mehg.resuse ~ year, data = hg.tin.mmse, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-9\nTerrestrial Insect - MM-SE
 \nLn Methyl Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006,max(hg.tin$year)), yaxs = "i", las = 1,
 tck = 0.015)

points(as.numeric(levels(as.factor(hg.tin.mmse$year))), tapply(hg.tin.mmse$ln.mehg.resuse, hg.tin.mmse$year, median, na.rm = T), pch =
 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.mmse$year))), tapply(hg.tin.mmse$ln.mehg.resuse, hg.tin.mmse$year, mean, na.rm = T), pch =
 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Nine samples collected in 2009 were non-detect and are included on this figure using the detection limit.", cex.sub = 0.7)


#4-10
plot(ln.mehg.resuse ~ year, data = hg.tin.mmsw, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-10\nTerrestrial Insect - MM-
 SW\nLn Methyl Mercury Concentrations", ylim = c(-2, 1.02 * max(hg.tin$ln.resuse)), xlim = c(2006,max(hg.tin$year)), yaxs = "i", las =
 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.tin.mmsw$year))), tapply(hg.tin.mmsw$ln.mehg.resuse, hg.tin.mmsw$year, median, na.rm = T), pch =
 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tin.mmsw$year))), tapply(hg.tin.mmsw$ln.mehg.resuse, hg.tin.mmsw$year, mean, na.rm = T), pch =
 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Six samples collected in 2009 were non-detect and are included on this figure using the detection limit.", cex.sub = 0.7)


hg.tin.mmse$loc2 = "MMSE" #create new location identifier
hg.tin.mmsw$loc2 = "MMSW" #create new location identifier
hg.tin.w17$loc2 = "W17" #create new location identifier
ref.tin$loc2 = ref.tin$locs #create new location identifier


bugs = rbind(hg.tin.mmse, hg.tin.mmsw, hg.tin.w17, ref.tin)
levels(bugs$MED_T.x) = c(levels(bugs$MED_T.x),"Coleoptera","Composite Sample","Diptera")
bugs$MED_T.x[bugs$MED_T.x == "Miscellaneous"] = "Composite Sample"
bugs$MED_T.x[bugs$MED_T.x == "Beetle-type bugs"] = "Coleoptera"
bugs$MED_T.x[bugs$MED_T.x == "Miscellaneous flies"] = "Diptera"
bugs$MED_T.x[bugs$MED_T.x == "Terrestrial Insect"] = "Composite Sample"
bugs$MED_T.x = factor(bugs$MED_T.x)
bugs$MED_T.x = factor(bugs$MED_T.x,levels(bugs$MED_T.x)[c(1:5,28,29,6,30,7:27)])


#3-15a
par(mfcol = c(2,2), tck = 0.015, las = 2, oma = c(0,0,3,0), mar = c(7,2.5,2,1.5), mgp = c(1.5,0.25,0), cex.axis = 0.6)
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "ADD-0",], xlab = "", ylab = "Mercury (ng/g)", main = "Addison/Pleasant River", ylim =
 c(0,1400), yaxs = "i")
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSE",], xlab = "", ylab = "Mercury (ng/g)", main = "MM-SE", ylim = c(0,1400), yaxs =
 "i")

par(mar = c(7,0,2,1.5))
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "W17",], xlab = "", ylab = "", main = "W-17-N", ylim = c(0,1400), yaxs = "i")
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSW",], xlab = "", ylab = "", main = "MM-SW", ylim = c(0,1400), yaxs = "i")
mtext(expression(bold("Figure 3-15a\n"), bold("Terrestrial Insect Mercury Concentrations by Species")), outer = T, las = 1)


#3-15b
par(mfcol = c(2,2), tck = 0.015, las = 2, oma = c(0,0,3,0), mar = c(7,2.5,2,1.5), mgp = c(1.5,0.25,0), cex.axis = 0.6)
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "ADD-0",], xlab = "", ylab = "Methyl mercury (ng/g)", main = "Addison/Pleasant
 River", ylim = c(0,1400), yaxs = "i")
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSE",], xlab = "", ylab = "Methyl mercury (ng/g)", main = "MM-SE", ylim =
```

```
 c(0,1400), yaxs = "i")

par(mar = c(7,0,2,1.5))
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "W17",], xlab = "", ylab = "", main = "W-17-N", ylim = c(0,1400), yaxs = "i")
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSW",], xlab = "", ylab = "", main = "MM-SW", ylim = c(0,1400), yaxs = "i")
mtext(expression(bold("Figure 3-15b\n"),bold("Terrestrial Insect Methyl Mercury Concentrations by Species")), outer = T, las = 1)


bugs = bugs[bugs$year == 2017,]
bugs$MED_T.x = factor(bugs$MED_T.x)

#3-16a
par(mfcol = c(2,2), tck = 0.015, las = 2, oma = c(0,0,3,0), mar = c(5,2.5,2,1.5), mgp = c(1.25,0.25,0), cex.axis = 0.6)
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "ADD-0" & bugs$year == 2017,], xlab = "", ylab = "Mercury (ng/g)", main = "Addison/
 Pleasant River", ylim = c(0,100), yaxs = "i")
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSE" & bugs$year == 2017,], xlab = "", ylab = "Mercury (ng/g)", main = "MM-SE", ylim
 = c(0,100), yaxs = "i")

par(mar = c(5,0,2,1.5))
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "W17" & bugs$year == 2017,], xlab = "", ylab = "", main = "W-17-N", ylim = c(0,100),
 yaxs = "i")
plot(resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSW" & bugs$year == 2017,], xlab = "", ylab = "", main = "MM-SW", ylim = c(0,100),
 yaxs = "i")
mtext(expression(bold("Figure 3-16a\n"), bold("Terrestrial Insect Mercury Concentrations by Species in 2017")), outer = T, las = 1)


#3-16b
par(mfcol = c(2,2), tck = 0.015, las = 2, oma = c(0,0,3,0), mar = c(5,2.5,2,1.5), mgp = c(1.25,0.25,0), cex.axis = 0.6)
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "ADD-0" & bugs$year == 2017,], xlab = "", ylab = "Methyl mercury (ng/g)", main =
 "Addison/Pleasant River", ylim = c(0,100), yaxs = "i")
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSE" & bugs$year == 2017,], xlab = "", ylab = "Methyl mercury (ng/g)", main =
 "MM-SE", ylim = c(0,100), yaxs = "i")

par(mar = c(5,0,2,1.5))
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "W17" & bugs$year == 2017,], xlab = "", ylab = "", main = "W-17-N", ylim =
 c(0,100), yaxs = "i")
plot(mehg.resuse ~ MED_T.x, data = bugs[bugs$loc2 == "MMSW" & bugs$year == 2017,], xlab = "", ylab = "", main = "MM-SW", ylim =
 c(0,100), yaxs = "i")
mtext(expression(bold("Figure 3-16b\n"), bold("Terrestrial Insect Methyl Mercury Concentrations by Species in 2017")), outer = T, las =
 1)
```

Appendix F-2. Spider Statistical Analysis Code

```
### File created for analysis of spider data for Biota Monitoring Report (2017)
### Code edited by LSV 01/02/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


###############
### SPIDERS ###
###############

levels(factor(penob$PARAM_NAME[penob$LOGGED_BY == "Spider"]))

hg.spd = penob[penob$LOGGED_BY == "Spider" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples labeled as mercury, removes field duplicates

hg.spd$ln.resuse = log(hg.spd$resuse) #log Hg results

hg.spd = merge(hg.spd, penob[penob$LOGGED_BY == "Spider" & penob$PARAM_NAME == "Methyl mercury" &! penob$QC_CODE == "FD",], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge Hg and Me Hg results
summary(hg.spd)
names(hg.spd)[colnames(hg.spd) == "resuse.y"] = "mehg.resuse" #rename columns to keep track of data
names(hg.spd)[colnames(hg.spd) == "resuse.x"] = "resuse" #rename columns to keep track of data

hg.spd$ln.mehg.resuse = log(hg.spd$mehg.resuse) #log Me Hg results

hg.spd$locs = as.factor(substring(hg.spd$LOC_NAME,1,5)) #create location identifier
hg.spd$reach = as.factor(substring(hg.spd$LOC_NAME,1,2))

ref.spd = hg.spd[hg.spd$X_COORD > 930000 | hg.spd$Y_COORD < 22000,] #pull reference samples into separate dataset
hg.spd.P = hg.spd #retain all pairings in separate dataset
hg.spd = hg.spd[hg.spd$X_COORD < 930000 & hg.spd$Y_COORD > 22000,] #reduce dataset to site spiders
ref.spd = ref.spd[!is.na(ref.spd$resuse) == T,] #remove NAs
hg.spd = hg.spd[!is.na(hg.spd$resuse) == T,] # remove NAs
summary(hg.spd) #127 records
summary(ref.spd) #35 records


hg.spd = hg.spd[!(hg.spd$locs == "SP-16" | hg.spd$locs == "SP-17" | hg.spd$locs == "SP-18" | hg.spd$locs == "SP-19"),] #reduce dataset to locations sampled in 2016

hg.spd.mm = hg.spd[hg.spd$Y_COORD < 342000,] #pulling out MM spiders
hg.spd.mmse = hg.spd.mm[hg.spd.mm$X_COORD > 889600 & hg.spd.mm$Y_COORD > 335000,] #MM-SE spiders
hg.spd.mmsw = hg.spd.mm[hg.spd.mm$X_COORD > 889600 & hg.spd.mm$Y_COORD < 335000 & hg.spd.mm$Y_COORD > 326000,] #MM-SW spiders
hg.spd.w17 = hg.spd[hg.spd$Y_COORD > 347500 & hg.spd$X_COORD > 888000,] #pulling out W17 spiders


######################
```

```
### Spider Summary ###
######################
# Hg
spd.summ = data.frame(MMSE.x = tapply(hg.spd.mmse$resuse[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)],
 hg.spd.mmse$year[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], mean))
spd.summ$MMSE.x.se = tapply(hg.spd.mmse$resuse[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], hg.spd.mmse
 $year[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.spd.mmse$resuse[(hg.spd.mmse
 $FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], hg.spd.mmse$year[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse
 $FINAL_QUAL.x) == T)], length))
spd.summ$MMSE.medn = tapply(hg.spd.mmse$resuse, hg.spd.mmse$year, median) #leave NDs in for this calc
spd.summ$MMSE.N = tapply(hg.spd.mmse$resuse, hg.spd.mmse$year, length)


spd.summ$MMSW.x = tapply(hg.spd.mmsw$resuse[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], hg.spd.mmsw
 $year[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], mean)
spd.summ$MMSW.x.se = tapply(hg.spd.mmsw$resuse[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], hg.spd.mmsw
 $year[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.spd.mmsw$resuse[(hg.spd.mmsw
 $FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], hg.spd.mmsw$year[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw
 $FINAL_QUAL.x) == T)], length))
spd.summ$MMSW.medn = tapply(hg.spd.mmsw$resuse, hg.spd.mmsw$year, median) #leave NDs in for this calc
spd.summ$MMSW.N = tapply(hg.spd.mmsw$resuse, hg.spd.mmsw$year, length)


spd.summ$w17.x[c(1,3:4)] = tapply(hg.spd.w17$resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)],
 hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], mean)
spd.summ$w17.x.se[c(1,3:4)] = tapply(hg.spd.w17$resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)],
 hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.spd.w17$resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)],
 hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], length))
spd.summ$w17.medn[c(1,3:4)] = tapply(hg.spd.w17$resuse, hg.spd.w17$year, median) #leave NDs in for this calc
spd.summ$w17.N[c(1,3:4)] = tapply(hg.spd.w17$resuse, hg.spd.w17$year, length)


spd.summ$ADD.x[3:4] = tapply(ref.spd$resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) ==
 T)], ref.spd$year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean)
spd.summ$ADD.x.se[3:4] = tapply(ref.spd$resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) ==
 T)], ref.spd$year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.spd$resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd
 $year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length))
spd.summ$ADD.medn[3:4] = tapply(ref.spd$resuse[ref.spd$locs == "ADD-0"], ref.spd$year[ref.spd$locs == "ADD-0"], median) #leave NDs in
 for this calc
spd.summ$ADD.N[3:4] = tapply(ref.spd$resuse[ref.spd$locs == "ADD-0"], ref.spd$year[ref.spd$locs == "ADD-0"], length)


spd.summ$BH.x = c(tapply(ref.spd$resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)],
 ref.spd$year[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean), NA, NA, NA)
spd.summ$BH.x.se = c(tapply(ref.spd$resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)],
 ref.spd$year[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(ref.spd
 $resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd$year[ref.spd$reach == "BH"
 & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length)), NA, NA, NA)
spd.summ$BH.medn = c(tapply(ref.spd$resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], median), NA, NA, NA) #leave NDs
 in for this calc
spd.summ$BH.N = c(tapply(ref.spd$resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], length), NA, NA, NA)


spd.summ$SM.x = c(tapply(ref.spd$resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)],
 ref.spd$year[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean), NA, NA, NA)
spd.summ$SM.x.se = c(tapply(ref.spd$resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)],
 ref.spd$year[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(ref.spd
 $resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd$year[ref.spd$reach == "SM"
 & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length)), NA, NA, NA)
spd.summ$SM.medn = c(tapply(ref.spd$resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], median), NA, NA, NA) #leave NDs
 in for this calc
spd.summ$SM.N = c(tapply(ref.spd$resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], length), NA, NA, NA)


# Me Hg
spd.summ$MeHgMMSE.x = tapply(hg.spd.mmse$mehg.resuse[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)],
 hg.spd.mmse$year[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], mean, na.rm = T)
spd.summ$MeHgMMSE.x.se = tapply(hg.spd.mmse$mehg.resuse[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)],
 hg.spd.mmse$year[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], sd, na.rm = T) / sqrt(tapply(hg.spd.mmse
 $mehg.resuse[(hg.spd.mmse$FINAL_QUAL.x == "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], hg.spd.mmse$year[(hg.spd.mmse$FINAL_QUAL.x ==
 "J" | is.na(hg.spd.mmse$FINAL_QUAL.x) == T)], length))
spd.summ$MeHgMMSE.medn = tapply(hg.spd.mmse$mehg.resuse, hg.spd.mmse$year, median, na.rm = T) #leave NDs in for this calc
spd.summ$MeHgMMSE.N = tapply(hg.spd.mmse$mehg.resuse, hg.spd.mmse$year, length)


spd.summ$MeHgMMSW.x = tapply(hg.spd.mmsw$mehg.resuse[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)],
 hg.spd.mmsw$year[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], mean, na.rm = T)
```

```
spd.summ$MeHgMMSW.x.se = tapply(hg.spd.mmsw$mehg.resuse[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)],
 hg.spd.mmsw$year[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], sd, na.rm = T) / sqrt(tapply(hg.spd.mmsw
 $mehg.resuse[(hg.spd.mmsw$FINAL_QUAL.x == "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], hg.spd.mmsw$year[(hg.spd.mmsw$FINAL_QUAL.x ==
 "J" | is.na(hg.spd.mmsw$FINAL_QUAL.x) == T)], length))
spd.summ$MeHgMMSW.medn = tapply(hg.spd.mmsw$mehg.resuse, hg.spd.mmsw$year, median, na.rm = T) #leave NDs in for this calc
spd.summ$MeHgMMSW.N = tapply(hg.spd.mmsw$mehg.resuse, hg.spd.mmsw$year, length)


spd.summ$MeHgw17.x[c(1,3:4)] = tapply(hg.spd.w17$mehg.resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)],
 hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], mean, na.rm = T)
spd.summ$MeHgw17.x.se[c(1,3:4)] = tapply(hg.spd.w17$mehg.resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) ==
 T)], hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], sd, na.rm = T) /
 sqrt(tapply(hg.spd.w17$mehg.resuse[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)],
 hg.spd.w17$year[(hg.spd.w17$FINAL_QUAL.x == "J" | is.na(hg.spd.w17$FINAL_QUAL.x) == T)], length))
spd.summ$MeHgw17.medn[c(1,3:4)] = tapply(hg.spd.w17$mehg.resuse, hg.spd.w17$year, median, na.rm = T) #leave NDs in for this calc
spd.summ$MeHgw17.N[c(1,3:4)] = tapply(hg.spd.w17$mehg.resuse, hg.spd.w17$year, length)


spd.summ$MeHgADD.x[3:4] = tapply(ref.spd$mehg.resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd
 $FINAL_QUAL.x) == T)], ref.spd$year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean)
spd.summ$MeHgADD.x.se[3:4] = tapply(ref.spd$mehg.resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd
 $FINAL_QUAL.x) == T)], ref.spd$year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(ref.spd$mehg.resuse[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd
 $year[ref.spd$locs == "ADD-0" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length))
spd.summ$MeHgADD.medn[3:4] = tapply(ref.spd$mehg.resuse[ref.spd$locs == "ADD-0"], ref.spd$year[ref.spd$locs == "ADD-0"], median) #leave
 NDs in for this calc
spd.summ$MeHgADD.N[3:4] = tapply(ref.spd$mehg.resuse[ref.spd$locs == "ADD-0"], ref.spd$year[ref.spd$locs == "ADD-0"], length)


spd.summ$MeHgBH.x = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) ==
 T)], ref.spd$year[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean, na.rm = T), NA, NA,
 NA)
spd.summ$MeHgBH.x.se = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x)
 == T)], ref.spd$year[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd, na.rm = T) /
 sqrt(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd
 $year[ref.spd$reach == "BH" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length)), NA, NA, NA)
spd.summ$MeHgBH.medn = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], median, na.rm = T),
 NA, NA, NA) #leave NDs in for this calc
spd.summ$MeHgBH.N = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], length), NA, NA, NA)


spd.summ$MeHgSM.x = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) ==
 T)], ref.spd$year[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], mean, na.rm = T), NA, NA,
 NA)
spd.summ$MeHgSM.x.se = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x)
 == T)], ref.spd$year[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], sd, na.rm = T) /
 sqrt(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], ref.spd
 $year[ref.spd$reach == "SM" & (ref.spd$FINAL_QUAL.x == "J" | is.na(ref.spd$FINAL_QUAL.x) == T)], length)), NA, NA, NA)
spd.summ$MeHgSM.medn = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], median, na.rm = T),
 NA, NA, NA) #leave NDs in for this calc
spd.summ$MeHgSM.N = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], length), NA, NA, NA)



write.csv(spd.summ, "Spider summary.csv")


######################
### SPIDER FIGURES ###
######################

#4-11
plot(ln.resuse ~ year, data = ref.spd[ref.spd$reach == "AD",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-11\nSpider -
 Reference Locations\nLn Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.resuse)), xlim = c(2006, max(hg.spd$year)), yaxs =
 "i", las = 1, tck = 0.015, pch = 16)

points(ln.resuse ~ year, data = ref.spd[ref.spd$reach == "SM",], pch = 18, col = 3)

points(as.numeric(levels(as.factor(ref.spd$year))), tapply(ref.spd$ln.resuse[!ref.spd$reach == "BH"], ref.spd$year[!ref.spd$reach ==
 "BH"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.spd$year))), tapply(ref.spd$ln.resuse[!ref.spd$reach == "BH"], ref.spd$year[!ref.spd$reach ==
 "BH"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Pleasant River", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,"blue","red"), pch =
 c(16,18,22,21), pt.bg = c("white","white","blue","red"), cex = 0.8)


#4-12
plot(ln.mehg.resuse ~ year, data = ref.spd[ref.spd$reach == "AD",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
```

```
 4-12\nSpider - Reference Locations\nLn Methyl Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.mehg.resuse, na.rm = T)), xlim
 = c(2006, max(hg.spd$year)), yaxs = "i", las = 1, tck = 0.015, pch = 16)

points(ln.mehg.resuse ~ year, data = ref.spd[ref.spd$reach == "SM",], pch = 18, col = 3)

points(as.numeric(levels(as.factor(ref.spd$year))), tapply(ref.spd$ln.mehg.resuse[!ref.spd$reach == "BH"], ref.spd$year[!ref.spd$reach
 == "BH"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.spd$year))), tapply(ref.spd$ln.mehg.resuse[!ref.spd$reach == "BH"], ref.spd$year[!ref.spd$reach
 == "BH"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Pleasant River", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,"blue","red"), pch =
 c(16,18,22,21), pt.bg = c("white","white","blue","red"), cex = 0.8)


#4-13
plot(ln.resuse ~ year, data = hg.spd, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-13\nSpider - Whole River\nLn Mercury
 Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.resuse)), xlim = c(2006, max(hg.spd$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd$year))), tapply(hg.spd$ln.resuse, hg.spd$year, median), pch = 21, col = "red", cex = 1.3, bg
 = "red")
points(as.numeric(levels(as.factor(hg.spd$year))), tapply(hg.spd$ln.resuse, hg.spd$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Spiders sampled at W-17-N, MM-SE, and MM-SW", cex.sub = 0.7)


#4-14
plot(ln.resuse ~ year, data = hg.spd.w17, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-14\nSpider - W-17-N\nLn Mercury
 Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.resuse)), xlim = c(2006, max(hg.spd$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.w17$year))), tapply(hg.spd.w17$ln.resuse, hg.spd.w17$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.w17$year))), tapply(hg.spd.w17$ln.resuse, hg.spd.w17$year, mean), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-15
plot(ln.resuse ~ year, data = hg.spd.mmse, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-15\nSpider - MM-SE\nLn Mercury
 Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.resuse)), xlim = c(2006, max(hg.spd$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.mmse$year))), tapply(hg.spd.mmse$ln.resuse, hg.spd.mmse$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.mmse$year))), tapply(hg.spd.mmse$ln.resuse, hg.spd.mmse$year, mean), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-16
plot(ln.resuse ~ year, data = hg.spd.mmsw, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-16\nSpider - MM-SW\nLn Mercury
 Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.resuse)), xlim = c(2006, max(hg.spd$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.mmsw$year))), tapply(hg.spd.mmsw$ln.resuse, hg.spd.mmsw$year, median), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.mmsw$year))), tapply(hg.spd.mmsw$ln.resuse, hg.spd.mmsw$year, mean), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-17
plot(ln.mehg.resuse ~ year, data = hg.spd, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-17\nSpider - Whole River\nLn
 Methyl Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.mehg.resuse, na.rm = T)), xlim = c(2006,max(hg.spd$year)), yaxs =
 "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd$year))), tapply(hg.spd$ln.mehg.resuse, hg.spd$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd$year))), tapply(hg.spd$ln.mehg.resuse, hg.spd$year, mean, na.rm = T), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
```

```
title(sub = "Includes Spiders sampled at W-17-N, MM-SE, and MM-SW", cex.sub = 0.7)


#4-18
plot(ln.mehg.resuse ~ year, data = hg.spd.w17, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-18\nSpider - W-17-N\nLn Methyl
 Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.mehg.resuse, na.rm = T)), xlim = c(2006,max(hg.spd$year)), yaxs = "i", las =
 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.w17$year))), tapply(hg.spd.w17$ln.mehg.resuse, hg.spd.w17$year, median, na.rm = T), pch = 21,
 col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.w17$year))), tapply(hg.spd.w17$ln.mehg.resuse, hg.spd.w17$year, mean, na.rm = T), pch = 22,
 col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-19
plot(ln.mehg.resuse ~ year, data = hg.spd.mmse, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-19\nSpider - MM-SE\nLn Methyl
 Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.mehg.resuse, na.rm = T)), xlim = c(2006,max(hg.spd$year)), yaxs = "i", las =
 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.mmse$year))), tapply(hg.spd.mmse$ln.mehg.resuse, hg.spd.mmse$year, median, na.rm = T), pch =
 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.mmse$year))), tapply(hg.spd.mmse$ln.mehg.resuse, hg.spd.mmse$year, mean, na.rm = T), pch =
 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-20
plot(ln.mehg.resuse ~ year, data = hg.spd.mmsw, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-20\nSpider - MM-SW\nLn Methyl
 Mercury Concentrations", ylim = c(0, 1.02 * max(hg.spd$ln.mehg.resuse, na.rm = T)), xlim = c(2006,max(hg.spd$year)), yaxs = "i", las =
 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.spd.mmsw$year))), tapply(hg.spd.mmsw$ln.mehg.resuse, hg.spd.mmsw$year, median, na.rm = T), pch =
 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.spd.mmsw$year))), tapply(hg.spd.mmsw$ln.mehg.resuse, hg.spd.mmsw$year, mean, na.rm = T), pch =
 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-3. Nelsons Sparrow Statistical Analysis Code

```
### File created for analysis of Nelson's sparrow data for Biota Monitoring Report (2017)
### Code edited by LSV 01/17/2018
### Code checked by NTG 01/31/2018

library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI27.DBF")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob
 $month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]

########################
### NELSON'S SPARROW ###
########################

nsp.weight = weight[weight$MED_T == "Nelson's sharp-tailed sparrow",]
nsp.weight = nsp.weight[!is.na(nsp.weight$resuse) == T,]
summary(nsp.weight) #549 records

levels(factor(penob$PARAM_NAME[penob$MED_T == "Nelson's sharp-tailed sparrow"]))

hg.nsp = penob[penob$MED_T == "Nelson's sharp-tailed sparrow" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD" & penob$MONITOR_TY == "Blood",]
 #selects samples labeled as mercury and only blood samples, removes field duplicates

hg.nsp = hg.nsp[is.na(hg.nsp$X_COORD) == F,] #removes samples without coordinates


hg.nsp$ID2[hg.nsp$year == 2006] = substring(hg.nsp$ID[hg.nsp$year == 2006],1,22)
hg.nsp$ID2[hg.nsp$year == 2007] = substring(hg.nsp$ID[hg.nsp$year == 2007],1,22)
hg.nsp$ID2[hg.nsp$year == 2008] = substring(hg.nsp$ID[hg.nsp$year == 2008],1,22)
hg.nsp$ID2[hg.nsp$year == 2009] = substring(hg.nsp$ID[hg.nsp$year == 2009],1,22)
hg.nsp$ID2[hg.nsp$year == 2010] = substring(hg.nsp$ID[hg.nsp$year == 2010],1,22)
hg.nsp$ID2[hg.nsp$year == 2012] = substring(hg.nsp$ID[hg.nsp$year == 2012],1,22)
hg.nsp$ID2[hg.nsp$year > 2014] = as.character(hg.nsp$ID[hg.nsp$year > 2014])
hg.nsp$ID = hg.nsp$ID2
summary(hg.nsp) # 562 records


nsp.weight$ID2[nsp.weight$year == 2007] = substring(nsp.weight$ID[nsp.weight$year == 2007],1,22)
nsp.weight$ID2[nsp.weight$year == 2008] = substring(nsp.weight$ID[nsp.weight$year == 2008],1,22)
nsp.weight$ID2[nsp.weight$year == 2009] = substring(nsp.weight$ID[nsp.weight$year == 2009],1,22)
nsp.weight$ID2[nsp.weight$year == 2010] = substring(nsp.weight$ID[nsp.weight$year == 2010],1,22)
nsp.weight$ID2[nsp.weight$year == 2012] = substring(nsp.weight$ID[nsp.weight$year == 2012],1,22)
nsp.weight$ID2[nsp.weight$year > 2014] = as.character(nsp.weight$ID[nsp.weight$year > 2014])
nsp.weight$ID = nsp.weight$ID2
summary(nsp.weight) #549 records


hg.nsp = merge(hg.nsp, nsp.weight[,c(2:4, 6, 7, 36, 41:46)], by.x = c("ID", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("ID", "X_COORD",
 "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge blood records with weights for each bird
names(hg.nsp)[colnames(hg.nsp) == "resuse.x"] = "resuse" #rename columns for ease of keeping track of data
names(hg.nsp)[colnames(hg.nsp) == "resuse.y"] = "weight" #rename columns for ease of keeping track of data
summary(hg.nsp) #562 records

hg.nsp$ln.resuse = log(hg.nsp$resuse) #log mercury results

hg.nsp$w.adj_resuse = hg.nsp$resuse / hg.nsp$weight * median(hg.nsp$weight,na.rm = T) #weight adjust Hg results
hg.nsp$ln.w.adj_resuse = log(hg.nsp$resuse) / hg.nsp$weight * median(hg.nsp$weight, na.rm = T) #weight adjust logged Hg results

ref.nsp = hg.nsp[hg.nsp$X_COORD < 800000 | hg.nsp$X_COORD > 950000,] #pull reference birds into separate dataset
ref.nsp$which.ref = "maine"
ref.nsp$which.ref[ref.nsp$X_COORD < 600000] = "NH"
ref.nsp$which.ref[ref.nsp$X_COORD > 950000 & ref.nsp$Y_COORD > 350000] = "Add"

hg.nsp = hg.nsp[hg.nsp$X_COORD > 800000 & hg.nsp$X_COORD < 950000,] #reduce dataset to site birds
summary(hg.nsp) #471
summary(ref.nsp) #91 records

# Addison Reference
```

```r
add.nsp = ref.nsp[ref.nsp$X_COORD > 950000 & ref.nsp$Y_COORD > 350000,]



################################################
### Dataset matching 2016 sampling locations ###
################################################

hg.nsp.mm = hg.nsp[hg.nsp$Y_COORD < 342000,] #pulling out MM sparrows
hg.nsp.mmse = hg.nsp.mm[hg.nsp.mm$X_COORD > 889600 & hg.nsp.mm$Y_COORD > 335000,] #MM-SE sparrows
hg.nsp.mmsw = hg.nsp.mm[hg.nsp.mm$X_COORD > 889600 & hg.nsp.mm$Y_COORD < 335000 & hg.nsp.mm$Y_COORD > 326000,] #MM-SW sparrows
hg.nsp.w17 = hg.nsp[hg.nsp$Y_COORD > 342000 & hg.nsp$X_COORD > 891700,] #pulling out W17 sparrows

hg.nsp.P = hg.nsp #retaining all paired data

hg.nsp = hg.nsp[(hg.nsp$X_COORD > 889600 & hg.nsp$Y_COORD > 335000 & hg.nsp$Y_COORD < 340000) | (hg.nsp$X_COORD > 889600 & hg.nsp$Y_COORD < 335000 & hg.nsp
 $Y_COORD > 326000) | (hg.nsp$Y_COORD > 342000 & hg.nsp$X_COORD > 891700),] #reducing main dataset to W-17, MM-SW, & MM-SE locations



################################
### Nelson's Sparrow Summary ###
################################

nsp.summ = data.frame(mmse_x = tapply(hg.nsp.mmse$resuse, hg.nsp.mmse$year, mean))
nsp.summ$mmse_x_se = tapply(hg.nsp.mmse$resuse, hg.nsp.mmse$year, sd) / sqrt(tapply(hg.nsp.mmse$resuse, hg.nsp.mmse$year, length))
nsp.summ$mmse_medn = tapply(hg.nsp.mmse$resuse, hg.nsp.mmse$year, median)
nsp.summ$mmse_N = tapply(hg.nsp.mmse$resuse, hg.nsp.mmse$year, length)
nsp.summ$mmse_perc = tapply(hg.nsp.mmse$resuse[hg.nsp.mmse$resuse > 2100], hg.nsp.mmse$year[hg.nsp.mmse$resuse > 2100], length) / tapply(hg.nsp.mmse$resuse,
 hg.nsp.mmse$year, length)

nsp.summ$mmsw_x = tapply(hg.nsp.mmsw$resuse, hg.nsp.mmsw$year, mean)
nsp.summ$mmsw_x_se = tapply(hg.nsp.mmsw$resuse, hg.nsp.mmsw$year, sd) / sqrt(tapply(hg.nsp.mmsw$resuse, hg.nsp.mmsw$year, length))
nsp.summ$mmsw_medn = tapply(hg.nsp.mmsw$resuse, hg.nsp.mmsw$year, median)
nsp.summ$mmsw_N = tapply(hg.nsp.mmsw$resuse, hg.nsp.mmsw$year, length)
nsp.summ$mmsw_perc = tapply(hg.nsp.mmsw$resuse[hg.nsp.mmsw$resuse > 2100], hg.nsp.mmsw$year[hg.nsp.mmsw$resuse > 2100], length) / tapply(hg.nsp.mmsw$resuse,
 hg.nsp.mmsw$year, length)

nsp.summ$w17_x[3:8] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, mean)
nsp.summ$w17_x_se[3:8] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, sd) / sqrt(tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, length))
nsp.summ$w17_medn[3:8] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, median)
nsp.summ$w17_N[3:8] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, length)
nsp.summ$w17_perc[3:8] = tapply(hg.nsp.w17$resuse[hg.nsp.w17$resuse > 2100], hg.nsp.w17$year[hg.nsp.w17$resuse > 2100], length) / tapply(hg.nsp.w17$resuse,
 hg.nsp.w17$year, length)

ref.means = rbind(NA, data.frame(x = tapply(ref.nsp$resuse, list(ref.nsp$year, ref.nsp$which.ref), mean)))
rownames(ref.means)[1] = "2006"
ref.m.se = rbind(NA, data.frame(x_se = tapply(ref.nsp$resuse, list(ref.nsp$year, ref.nsp$which.ref), sd) / sqrt(tapply(ref.nsp$resuse, list(ref.nsp$year,
 ref.nsp$which.ref), length))))
rownames(ref.m.se)[1] = "2006"
ref.medn = rbind(NA, data.frame(med.n = tapply(ref.nsp$resuse, list(ref.nsp$year, ref.nsp$which.ref), median)))
rownames(ref.medn)[1] = "2006"
ref.N = rbind(NA, data.frame(N = tapply(ref.nsp$resuse, list(ref.nsp$year, ref.nsp$which.ref), length)))
rownames(ref.N)[1] = "2006"
nsp.summ = cbind(nsp.summ,ref.means, ref.m.se, ref.medn, ref.N)

nsp.summ$Add_perc[6:8] = 0

nsp.summ$NH_perc = c(NA, rep(0,4), rep(NA, 3))

me = tapply(ref.nsp$resuse[ref.nsp$resuse > 2100 & ref.nsp$which.ref == "maine"], ref.nsp$year[ref.nsp$resuse > 2100 & ref.nsp$which.ref == "maine"],
 length) / tapply(ref.nsp$resuse[ref.nsp$which.ref == "maine" & (ref.nsp$year == 2007 | ref.nsp$year == 2012)], ref.nsp$year[ref.nsp$which.ref == "maine" &
 (ref.nsp$year == 2007 | ref.nsp$year == 2012)], length)
nsp.summ$maine_perc = c(NA, me[1], NA, 0, NA, me[2], NA, NA)

write.csv(nsp.summ, "NESP summary.csv")


##############################
### NELSONS SPARROW TRENDS ###
##############################

hg.nsp.lreg.ln = summary(lm(ln.resuse ~ year, data = hg.nsp))
hg.nsp.lnreg.mmse = summary(lm(ln.resuse ~ year, data = hg.nsp.mmse))
hg.nsp.lnreg.mmsw = summary(lm(ln.resuse ~ year, data = hg.nsp.mmsw))
hg.nsp.w17.lnreg = summary(lm(ln.resuse ~ year, data = hg.nsp.w17))


summary(lm(resuse ~ year, data = hg.nsp[hg.nsp$month == 6,]))
summary(lm(resuse ~ year, data = hg.nsp[hg.nsp$month == 7,]))
kruskal.test(resuse ~ year, data = hg.nsp[hg.nsp$month == 8,])



hg.nsp.age = read.csv("NESP in with age merge.csv")

hy.nsp = hg.nsp.age[hg.nsp.age$Age == "HY" & is.na(hg.nsp.age$Age) == F,]

ad.nsp = hg.nsp.age[!hg.nsp.age$Age == "HY" & is.na(hg.nsp.age$Age) == F,]

ref.hy.nsp = hy.nsp[hy.nsp$X_COORD < 800000 | hy.nsp$X_COORD > 950000,]
hg.hy.nsp = hy.nsp[hy.nsp$X_COORD > 800000 & hy.nsp$X_COORD < 950000,]
```

```
ref.ad.nsp = ad.nsp[ad.nsp$X_COORD < 800000 | ad.nsp$X_COORD > 950000,]
hg.ad.nsp = ad.nsp[ad.nsp$X_COORD > 800000 & ad.nsp$X_COORD < 950000,]


ref.hy.nsp$which.ref = "maine"
ref.hy.nsp$which.ref[ref.hy.nsp$X_COORD < 600000] = "NH"
ref.hy.nsp$which.ref[ref.hy.nsp$X_COORD > 950000 & ref.hy.nsp$Y_COORD > 350000] = "Add"

ref.ad.nsp$which.ref = "maine"
ref.ad.nsp$which.ref[ref.ad.nsp$X_COORD < 600000] = "NH"
ref.ad.nsp$which.ref[ref.ad.nsp$X_COORD > 950000 & ref.ad.nsp$Y_COORD > 350000] = "Add"


########################
### Hatch Year Birds ###
################################################
### Dataset matching 2016 sampling locations ###
################################################

hg.hy.nsp.mm = hg.hy.nsp[hg.hy.nsp$Y_COORD < 342000,] #pulling out MM sparrows
hg.hy.nsp.mmse = hg.hy.nsp.mm[hg.hy.nsp.mm$X_COORD > 889600 & hg.hy.nsp.mm$Y_COORD > 335000,] #MM-SE sparrows
hg.hy.nsp.mmsw = hg.hy.nsp.mm[hg.hy.nsp.mm$X_COORD > 889600 & hg.hy.nsp.mm$Y_COORD < 335000 & hg.hy.nsp.mm$Y_COORD > 326000,] #MM-SW sparrows
hg.hy.nsp.w17 = hg.hy.nsp[hg.hy.nsp$Y_COORD > 342000 & hg.hy.nsp$X_COORD > 891700,] #pulling out W17 sparrows

hg.hy.nsp.P = hg.hy.nsp #retaining all paired data

hg.hy.nsp = hg.hy.nsp[(hg.hy.nsp$X_COORD > 889600 & hg.hy.nsp$Y_COORD > 335000 & hg.hy.nsp$Y_COORD < 340000) | (hg.hy.nsp$X_COORD > 889600 & hg.hy.nsp$Y_COORD
 < 335000 & hg.hy.nsp$Y_COORD > 326000) | (hg.hy.nsp$Y_COORD > 342000 & hg.hy.nsp$X_COORD > 891700),] #reducing main dataset to W-17, MM-SW, & MM-SE locations


################################
### Nelson's Sparrow Summary ###
################################

nsp.hy.summ = data.frame(mmse_x = tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, mean))
nsp.hy.summ$mmse_x_se = tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, sd) / sqrt(tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, length))
nsp.hy.summ$mmse_medn = tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, median)
nsp.hy.summ$mmse_N = tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, length)
nsp.hy.summ$mmse_perc = c(0,tapply(hg.hy.nsp.mmse$resuse[hg.hy.nsp.mmse$resuse > 2100], hg.hy.nsp.mmse$year[hg.hy.nsp.mmse$resuse > 2100], length)) /
 tapply(hg.hy.nsp.mmse$resuse, hg.hy.nsp.mmse$year, length)

nsp.hy.summ$mmsw_x = c(tapply(hg.hy.nsp.mmsw$resuse, hg.hy.nsp.mmsw$year, mean),NA,NA)
nsp.hy.summ$mmsw_x_se = tapply(hg.hy.nsp.mmsw$resuse, hg.hy.nsp.mmsw$year, sd) / sqrt(tapply(hg.hy.nsp.mmsw$resuse, hg.hy.nsp.mmsw$year, length))
nsp.hy.summ$mmsw_medn = c(tapply(hg.hy.nsp.mmsw$resuse, hg.hy.nsp.mmsw$year, median), NA, NA)
nsp.hy.summ$mmsw_N = c(tapply(hg.hy.nsp.mmsw$resuse, hg.hy.nsp.mmsw$year, length), NA,NA)
nsp.hy.summ$mmsw_perc = c(0,NA,NA)

nsp.hy.summ$w17_x[3] = tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, mean)
nsp.hy.summ$w17_x_se[3] = tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, sd) / sqrt(tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, length))
nsp.hy.summ$w17_medn[3] = tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, median)
nsp.hy.summ$w17_N[3] = tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, length)
nsp.hy.summ$w17_perc[3] = tapply(hg.hy.nsp.w17$resuse[hg.hy.nsp.w17$resuse > 2100], hg.hy.nsp.w17$year[hg.hy.nsp.w17$resuse > 2100], length) /
 tapply(hg.hy.nsp.w17$resuse, hg.hy.nsp.w17$year, length)

ref.hy.means = data.frame(x = tapply(ref.hy.nsp$resuse, list(ref.hy.nsp$year, ref.hy.nsp$which.ref), mean))
rownames(ref.hy.means) = "2016"
colnames(ref.hy.means) = "Add.x"

ref.hy.m.se = data.frame(x_se = tapply(ref.hy.nsp$resuse, list(ref.hy.nsp$year, ref.hy.nsp$which.ref), sd) / sqrt(tapply(ref.hy.nsp$resuse, list(ref.hy.nsp
 $year, ref.hy.nsp$which.ref), length)))
rownames(ref.hy.m.se) = "2016"
colnames(ref.hy.m.se) = "Add.m.se"

ref.hy.medn = data.frame(med.n = tapply(ref.hy.nsp$resuse, list(ref.hy.nsp$year, ref.hy.nsp$which.ref), median))
rownames(ref.hy.medn) = "2016"
colnames(ref.hy.medn) = "Add.medn"

ref.hy.N = data.frame(N = tapply(ref.hy.nsp$resuse, list(ref.hy.nsp$year, ref.hy.nsp$which.ref), length))
rownames(ref.hy.N) = "2016"
colnames(ref.hy.N) = "Add.N"

ref.hy.summ = cbind(ref.hy.means, ref.hy.m.se, ref.hy.medn, ref.hy.N)
ref.hy.summ = rbind(NA,NA,ref.hy.summ)
nsp.hy.summ = cbind(nsp.hy.summ,ref.hy.summ)

nsp.hy.summ$Add_perc[3] = 0


write.csv(nsp.hy.summ, "NESP HY summary.csv")


###################
### Adult Birds ###
################################################
### Dataset matching 2016 sampling locations ###
################################################

hg.ad.nsp.mm = hg.ad.nsp[hg.ad.nsp$Y_COORD < 342000,] #pulling out MM sparrows
hg.ad.nsp.mmse = hg.ad.nsp.mm[hg.ad.nsp.mm$X_COORD > 889600 & hg.ad.nsp.mm$Y_COORD > 335000,] #MM-SE sparrows
hg.ad.nsp.mmsw = hg.ad.nsp.mm[hg.ad.nsp.mm$X_COORD > 889600 & hg.ad.nsp.mm$Y_COORD < 335000 & hg.ad.nsp.mm$Y_COORD > 326000,] #MM-SW sparrows
hg.ad.nsp.w17 = hg.ad.nsp[hg.ad.nsp$Y_COORD > 342000 & hg.ad.nsp$X_COORD > 891700,] #pulling out W17 sparrows
```

```
hg.ad.nsp.P = hg.ad.nsp #retaining all paired data

hg.ad.nsp = hg.ad.nsp[(hg.ad.nsp$X_COORD > 889600 & hg.ad.nsp$Y_COORD > 335000 & hg.ad.nsp$Y_COORD < 340000) | (hg.ad.nsp$X_COORD > 889600 & hg.ad.nsp$Y_COORD
 < 335000 & hg.ad.nsp$Y_COORD > 326000) | (hg.ad.nsp$Y_COORD > 342000 & hg.ad.nsp$X_COORD > 891700),] #reducing main dataset to W-17, MM-SW, & MM-SE locations



################################
### Nelson's Sparrow Summary ###
################################

nsp.ad.summ = data.frame(mmse_x = tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, mean))
nsp.ad.summ$mmse_x_se = tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, sd) / sqrt(tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, length))
nsp.ad.summ$mmse_medn = tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, median)
nsp.ad.summ$mmse_N = tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, length)
nsp.ad.summ$mmse_perc = tapply(hg.ad.nsp.mmse$resuse[hg.ad.nsp.mmse$resuse > 2100], hg.ad.nsp.mmse$year[hg.ad.nsp.mmse$resuse > 2100], length) /
 tapply(hg.ad.nsp.mmse$resuse, hg.ad.nsp.mmse$year, length)

nsp.ad.summ$mmsw_x = tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, mean)
nsp.ad.summ$mmsw_x_se = tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, sd) / sqrt(tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, length))
nsp.ad.summ$mmsw_medn = tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, median)
nsp.ad.summ$mmsw_N = tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, length)
nsp.ad.summ$mmsw_perc = tapply(hg.ad.nsp.mmsw$resuse[hg.ad.nsp.mmsw$resuse > 2100], hg.ad.nsp.mmsw$year[hg.ad.nsp.mmsw$resuse > 2100], length) /
 tapply(hg.ad.nsp.mmsw$resuse, hg.ad.nsp.mmsw$year, length)

nsp.ad.summ$w17_x[2:7] = tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, mean)
nsp.ad.summ$w17_x_se[2:7] = tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, sd) / sqrt(tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, length))
nsp.ad.summ$w17_medn[2:7] = tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, median)
nsp.ad.summ$w17_N[2:7] = tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, length)
nsp.ad.summ$w17_perc[2:7] = tapply(hg.ad.nsp.w17$resuse[hg.ad.nsp.w17$resuse > 2100], hg.ad.nsp.w17$year[hg.ad.nsp.w17$resuse > 2100], length) /
 tapply(hg.ad.nsp.w17$resuse, hg.ad.nsp.w17$year, length)

ref.ad.means = data.frame(x = tapply(ref.ad.nsp$resuse, list(ref.ad.nsp$year, ref.ad.nsp$which.ref), mean))
ref.ad.m.se = data.frame(x_se = tapply(ref.ad.nsp$resuse, list(ref.ad.nsp$year, ref.ad.nsp$which.ref), sd) / sqrt(tapply(ref.ad.nsp$resuse, list(ref.ad.nsp
 $year, ref.ad.nsp$which.ref), length)))
ref.ad.medn = data.frame(med.n = tapply(ref.ad.nsp$resuse, list(ref.ad.nsp$year, ref.ad.nsp$which.ref), median))
ref.ad.N = data.frame(N = tapply(ref.ad.nsp$resuse, list(ref.ad.nsp$year, ref.ad.nsp$which.ref), length))
nsp.ad.summ = cbind(nsp.ad.summ,ref.ad.means, ref.ad.m.se, ref.ad.medn, ref.ad.N)

nsp.ad.summ$Add_perc[5:7] = 0

nsp.ad.summ$NH_perc = c(rep(0,4), rep(NA, 3))

me = tapply(ref.ad.nsp$resuse[ref.ad.nsp$resuse > 2100 & ref.ad.nsp$which.ref == "maine"], ref.ad.nsp$year[ref.ad.nsp$resuse > 2100 & ref.ad.nsp$which.ref ==
 "maine"], length) / tapply(ref.ad.nsp$resuse[ref.ad.nsp$which.ref == "maine" & (ref.ad.nsp$year == 2007 | ref.ad.nsp$year == 2012)], ref.ad.nsp
 $year[ref.ad.nsp$which.ref == "maine" & (ref.ad.nsp$year == 2007 | ref.ad.nsp$year == 2012)], length)
nsp.ad.summ$maine_perc = c(me[1], NA, 0, NA, me[2], NA, NA)

write.csv(nsp.ad.summ, "NESP Adult summary.csv")



##############################
### NELSONS SPARROW TRENDS ###
##############################

# Hatch Year Birds
hg.hy.nsp.lreg.ln = summary(lm(lnresuse ~ year, data = hg.hy.nsp))
# hg.hy.nsp.lnreg.mmse = summary(lm(lnresuse ~ year, data = hg.hy.nsp.mmse))
# hg.hy.nsp.lnreg.mmsw = summary(lm(lnresuse ~ year, data = hg.hy.nsp.mmsw)) #N = 1
# hg.hy.nsp.w17.lnreg = summary(lm(lnresuse ~ year, data = hg.hy.nsp.w17)) #only 2016 birds

# Adult Birds
hg.ad.nsp.lreg.ln = summary(lm(lnresuse ~ year, data = hg.ad.nsp))
hg.ad.nsp.lnreg.mmse = summary(lm(lnresuse ~ year, data = hg.ad.nsp.mmse))
hg.ad.nsp.lnreg.mmsw = summary(lm(lnresuse ~ year, data = hg.ad.nsp.mmsw))
hg.ad.nsp.w17.lnreg = summary(lm(lnresuse ~ year, data = hg.ad.nsp.w17))


#4-21a
plot(ln.resuse ~ year, data = ref.nsp[ref.nsp$which.ref == "maine",], pch = 17, ylab = "Ln Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(ref.nsp$year)),
 las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), main = "Figure 4-21a\nNelson's Sparrow Blood - Reference Locations\nLn Mercury
 Concentrations")
points(ln.resuse ~ year, data = ref.nsp[ref.nsp$which.ref == "NH",], col = 4, pch = 18)
points(ln.resuse ~ year, data = ref.nsp[ref.nsp$which.ref == "Add",], col = 3, pch = 16)
legend("bottomright", legend = c("Pleasant River","Downeast Maine", "ME/NH/MA Coast Wetlands"), pch = 16:18, col = c(3,1,4), cex = 0.8)
title(sub = "ME/NH/MA Coast Wetlands includes: Spurwink River, Scarborough River, Moody Beach, Great Bay, and Parker River Marshes areas", cex.sub = 0.6)


#4-21b
par(mfrow = c(1,1))
plot(lnresuse ~ year, data = ref.ad.nsp[ref.ad.nsp$which.ref == "maine",], pch = 17, ylab = "Ln Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(ref.ad.nsp
 $year)), las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), main = "Figure 4-21b\nNelson's Sparrow (By Age) Blood - Reference
 Locations\nLn Mercury Concentrations")
points(lnresuse ~ year, data = ref.ad.nsp[ref.ad.nsp$which.ref == "NH",], col = 4, pch = 18)
points(lnresuse ~ year, data = ref.ad.nsp[ref.ad.nsp$which.ref == "Add",], col = 3, pch = 16)
points(lnresuse ~ year, data = ref.hy.nsp, pch = 21, col = 1, bg = 3)
legend("bottomright", legend = c("Adults - Pleasant River","Adults - Downeast Maine", "Adults - ME/NH/MA Coast Wetlands", "Hatch Year - Pleasant River"), pch
 = c(16:18,21), col = c(3,1,4,1), cex = 0.8, pt.bg = 3)
title(sub = "ME/NH/MA Coast Wetlands includes: Spurwink River, Scarborough River, Moody Beach, Great Bay, and Parker River Marshes areas", cex.sub = 0.6)
```

```
#4-22a
plot(ln.resuse ~ year, data = hg.nsp, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-22a\nNelson's Sparrow Blood - Whole River\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.nsp))

text(min(hg.nsp$year) + 1.5, max(hg.nsp$ln.resuse)*0.185, "ln(y) = -0.02979x + 68.260", cex = 0.8)
text(min(hg.nsp$year) + 1.5, max(hg.nsp$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.03", cex = 0.8)

points(as.numeric(levels(as.factor(hg.nsp$year))), tapply(hg.nsp$ln.resuse, hg.nsp$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.nsp$year))), tapply(hg.nsp$ln.resuse, hg.nsp$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)
title(sub = "Includes Nelson's Sparrows sampled at MM-SE, MM-SW, and W-17-N", cex.sub = 0.7)


#4-22b
plot(lnresuse ~ year, data = hg.hy.nsp, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-22b\nNelson's Sparrow (Hatch Year) Blood - Whole River
 \nLoglinear Regression", xlim = c(2006, 2017), ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.hy.nsp$year) + 0.5, max(hg.nsp$ln.resuse)*0.20, "ln(y) = 0.0578x - 108.67", cex = 0.8)
text(min(hg.hy.nsp$year) + 0.5, max(hg.nsp$ln.resuse)*0.17, "p = 0.19, Adj." ~R^2~ "= 0.04", cex = 0.8)

points(as.numeric(levels(as.factor(hg.hy.nsp$year))), tapply(hg.hy.nsp$lnresuse, hg.hy.nsp$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.nsp$year))), tapply(hg.hy.nsp$lnresuse, hg.hy.nsp$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)
title(sub = "Includes Nelson's Sparrows sampled at MM-SE, MM-SW, and W-17-N", cex.sub = 0.7)


#4-22c
par(mfrow = c(1,1))
plot(lnresuse ~ year, data = hg.ad.nsp, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-22c\nNelson's Sparrow (Adult) Blood - Whole River
 \nLoglinear Regression", xlim = c(2006, 2017), ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(lnresuse ~ year, data = hg.ad.nsp))

text(min(hg.ad.nsp$year) + 0.5, max(hg.nsp$ln.resuse)*0.20, "ln(y) = -0.0342x + 77.201", cex = 0.8)
text(min(hg.ad.nsp$year) + 0.5, max(hg.nsp$ln.resuse)*0.17, "p < 0.001, Adj." ~R^2~ "= 0.05", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.nsp$year))), tapply(hg.ad.nsp$lnresuse, hg.ad.nsp$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.nsp$year))), tapply(hg.ad.nsp$lnresuse, hg.ad.nsp$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)
title(sub = "Includes Nelson's Sparrows sampled at MM-SE, MM-SW, and W-17-N", cex.sub = 0.7)


#4-23a
plot(ln.resuse ~ year, data = hg.nsp.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-23a\nNelson's Sparrow Blood - MM-SE\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.nsp.mm$ln.resuse)), xlim = c(min(hg.nsp$year), max(hg.nsp$year)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.nsp$year) + 1.5, 0.185 * max(hg.nsp.mm$ln.resuse), "ln(y) = -0.01019x + 28.757", cex = 0.8)
text(min(hg.nsp$year) + 1.5, 0.15 * max(hg.nsp.mm$ln.resuse), "p = 0.44, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.nsp.mmse$year))), tapply(hg.nsp.mmse$ln.resuse, hg.nsp.mmse$year, median, na.rm = T), pch = 21, col = "red", cex = 1.3,
 bg = "red")
points(as.numeric(levels(as.factor(hg.nsp.mmse$year))), tapply(hg.nsp.mmse$ln.resuse, hg.nsp.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex = 1.3,
 bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-23b
plot(lnresuse ~ year, data = hg.hy.nsp.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-23b\nNelson's Sparrow (Hatch Year) Blood - MM-SE
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006, 2017), las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.hy.nsp.mmse$year))), tapply(hg.hy.nsp.mmse$lnresuse, hg.hy.nsp.mmse$year, median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.nsp.mmse$year))), tapply(hg.hy.nsp.mmse$lnresuse, hg.hy.nsp.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-23c
plot(lnresuse ~ year, data = hg.ad.nsp.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-23c\nNelson's Sparrow (Adult) Blood - MM-SE
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006,2017), las = 1, tck = 0.015, yaxs = "i")
abline(lm(lnresuse ~ year, data = hg.ad.nsp.mmse), lty = 2)

text(min(hg.ad.nsp$year) + 0.5, 0.20 * max(hg.nsp$ln.resuse), "ln(y) = -0.0210x + 50.620", cex = 0.8)
text(min(hg.ad.nsp$year) + 0.5, 0.17 * max(hg.nsp$ln.resuse), "p = 0.086, Adj." ~R^2~ "= 0.01", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.nsp.mmse$year))), tapply(hg.ad.nsp.mmse$lnresuse, hg.ad.nsp.mmse$year, median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.nsp.mmse$year))), tapply(hg.ad.nsp.mmse$lnresuse, hg.ad.nsp.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
```

```
 c("white","blue","red"), cex = 0.8)


#4-24a
plot(ln.resuse ~ year, data = hg.nsp.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-24a\nNelson's Sparrow Blood - MM-SW\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.nsp.mm$ln.resuse)), xlim = c(min(hg.nsp$year), max(hg.nsp$year)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.nsp.mmsw))

text(min(hg.nsp$year) + 1.5, 0.185 * max(hg.nsp.mm$ln.resuse), "ln(y) = -0.04202x + 93.00", cex = 0.8)
text(min(hg.nsp$year) + 1.5, 0.15 * max(hg.nsp.mm$ln.resuse), "p < 0.001, Adj." ~R^2~ "= 0.08", cex = 0.8)

points(as.numeric(levels(as.factor(hg.nsp.mmsw$year))), tapply(hg.nsp.mmsw$ln.resuse, hg.nsp.mmsw$year, median, na.rm = T), pch = 21, col = "red", cex = 1.3,
 bg = "red")
points(as.numeric(levels(as.factor(hg.nsp.mmsw$year))), tapply(hg.nsp.mmsw$ln.resuse, hg.nsp.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex = 1.3,
 bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-24b
plot(lnresuse ~ year, data = hg.hy.nsp.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-24b\nNelson's Sparrow (Hatch Year) Blood - MM-SW
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006, 2017), las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.hy.nsp.mmsw$year))), tapply(hg.hy.nsp.mmsw$lnresuse, hg.hy.nsp.mmsw$year, median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.nsp.mmsw$year))), tapply(hg.hy.nsp.mmsw$lnresuse, hg.hy.nsp.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-24c
plot(lnresuse ~ year, data = hg.ad.nsp.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-24c\nNelson's Sparrow (Adult) Blood - MM-SW
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006,2017), las = 1, tck = 0.015, yaxs = "i")
abline(lm(lnresuse ~ year, data = hg.ad.nsp.mmsw))

text(min(hg.ad.nsp$year) + 0.5, 0.20 * max(hg.nsp$ln.resuse), "ln(y) = -0.0538x + 116.6", cex = 0.8)
text(min(hg.ad.nsp$year) + 0.5, 0.17 * max(hg.nsp$ln.resuse), "p < 0.001, Adj." ~R^2~ "= 0.13", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.nsp.mmsw$year))), tapply(hg.ad.nsp.mmsw$lnresuse, hg.ad.nsp.mmsw$year, median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.nsp.mmsw$year))), tapply(hg.ad.nsp.mmsw$lnresuse, hg.ad.nsp.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-25a
plot(ln.resuse ~ year, data = hg.nsp.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-25a\nNelson's Sparrow Blood - W-17-N\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(min(hg.nsp$year), max(hg.nsp$year)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.nsp.w17))

text(min(hg.nsp$year) + 1.5, max(hg.nsp$ln.resuse) * 0.185, "ln(y) = -0.05053x + 109.98", cex = 0.8)
text(min(hg.nsp$year) + 1.5, max(hg.nsp$ln.resuse) * 0.15, "p = 0.009, Adj." ~R^2~ "= 0.10", cex = 0.8)

points(as.numeric(levels(as.factor(hg.nsp.w17$year))), tapply(hg.nsp.w17$ln.resuse, hg.nsp.w17$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.nsp.w17$year))), tapply(hg.nsp.w17$ln.resuse, hg.nsp.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-25b
plot(lnresuse ~ year, data = hg.hy.nsp.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-25b\nNelson's Sparrow (Hatch Year) Blood - W-17-N
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006,2017), las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.hy.nsp.w17$year))), tapply(hg.hy.nsp.w17$lnresuse, hg.hy.nsp.w17$year, median), pch = 21, col = "red", cex = 1.3, bg =
 "red")
points(as.numeric(levels(as.factor(hg.hy.nsp.w17$year))), tapply(hg.hy.nsp.w17$lnresuse, hg.hy.nsp.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-25c
plot(lnresuse ~ year, data = hg.ad.nsp.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-25c\nNelson's Sparrow (Adult) Blood - W-17-N
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.nsp$ln.resuse)), xlim = c(2006,2017), las = 1, tck = 0.015, yaxs = "i")
abline(lm(lnresuse ~ year, data = hg.ad.nsp.w17))

text(min(hg.ad.nsp$year) + 0.5, max(hg.nsp$ln.resuse) * 0.20, "ln(y) = -0.0349x + 78.52", cex = 0.8)
text(min(hg.ad.nsp$year) + 0.5, max(hg.nsp$ln.resuse) * 0.17, "p = 0.049, Adj." ~R^2~ "= 0.06", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.nsp.w17$year))), tapply(hg.ad.nsp.w17$lnresuse, hg.ad.nsp.w17$year, median), pch = 21, col = "red", cex = 1.3, bg =
 "red")
points(as.numeric(levels(as.factor(hg.ad.nsp.w17$year))), tapply(hg.ad.nsp.w17$lnresuse, hg.ad.nsp.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
```

```
 c("white","blue","red"), cex = 0.8)


#4-26a
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(resuse ~ year, data = hg.nsp[hg.nsp$month == 6,], main = "Nelson's Sparrow - June", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(min(hg.nsp$year),
 max(hg.nsp$year)), ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
#clip(2006, 2010, 0, 20000)
abline(lm(resuse ~ year, data = hg.nsp[hg.nsp$month == 6,]))
#clip(0, 20000, 0, 20000)
text(2014, max(hg.nsp$resuse)*0.97, "y = -95.19x + 194656", cex = 0.6)
text(2014, max(hg.nsp$resuse)*0.92, "p = 0.008, Adj." ~R^2~ "= 0.09", cex = 0.6)

plot(resuse ~ year, data = hg.nsp[hg.nsp$month == 7,], main = "Nelson's Sparrow - July", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(min(hg.nsp$year),
 max(hg.nsp$year)), ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2014, max(hg.nsp$resuse)*0.97, "y = -55.12x + 116617.1", cex = 0.6)
text(2014, max(hg.nsp$resuse)*0.92, "p = 0.21, Adj." ~R^2~ "= 0", cex = 0.6)

plot(resuse ~ year, data = hg.nsp[hg.nsp$month == 8,], main = "Nelson's Sparrow - August", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(min(hg.nsp$year),
 max(hg.nsp$year)), ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2014, max(hg.nsp$resuse)*0.97, "Kruskal test p = 0.074", cex = 0.6)
mtext(expression(bold("Figure 4-26a\n"),bold("Nelson's Sparrow Mercury Concentrations in each Month")), outer = T)


#4-26b
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(0,0,type = "n", axes = F, ylab = "", xlab ="")
text(0,0, "No hatch year birds collected in June", cex = 0.7)
plot(resuse ~ year, data = hg.hy.nsp[hg.hy.nsp$month == 7,], main = "Nelson's Sparrow - July", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006,2017),
 ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)

plot(resuse ~ year, data = hg.hy.nsp[hg.hy.nsp$month == 8,], main = "Nelson's Sparrow - August", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006,2017),
 ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
mtext(expression(bold("Figure 4-26b\n"),bold("Nelson's Sparrow (Hatch Year) Mercury Concentrations in each Month")), outer = T)


#4-26c
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(resuse ~ year, data = hg.ad.nsp[hg.ad.nsp$month == 6,], main = "Nelson's Sparrow - June", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006,2017),
 ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
#clip(2006, 2010, 0, 20000)
abline(lm(resuse ~ year, data = hg.ad.nsp[hg.ad.nsp$month == 6,]))
#clip(0, 20000, 0, 20000)
text(2014, max(hg.nsp$resuse)*0.97, "y = -101.12x + 206612", cex = 0.6)
text(2014, max(hg.nsp$resuse)*0.92, "p = 0.005, Adj." ~R^2~ "= 0.10", cex = 0.6)

plot(resuse ~ year, data = hg.ad.nsp[hg.ad.nsp$month == 7,], main = "Nelson's Sparrow - July", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006,2017),
 ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2014, max(hg.nsp$resuse)*0.97, "y = 4.366x - 2790.5", cex = 0.6)
text(2014, max(hg.nsp$resuse)*0.92, "p = 0.93, Adj." ~R^2~ "= 0", cex = 0.6)

plot(resuse ~ year, data = hg.ad.nsp[hg.ad.nsp$month == 8,], main = "Nelson's Sparrow - August", ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006,2017),
 ylim = c(0, max(hg.nsp$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
mtext(expression(bold("Figure 4-26c\n"),bold("Nelson's Sparrow (Adult) Mercury Concentrations in each Month")), outer = T)
```

Appendix F-4. Red-winged Blackbird Statistical Analysis Code

```r
### File created for analysis of red-winged blackbird data for Biota Monitoring Report (2017)
### Code edited by LSV 01/22/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)

penob = read.dbf("PEN_BI27.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob
 $month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


############################
### RED-WINGED BLACKBIRD ###
############################

rwb.weight = weight[weight$MED_T == "Red-Winged Blackbird",]

levels(factor(penob$PARAM_NAME[penob$MED_T == "Red-Winged Blackbird"]))

hg.rwb = penob[penob$MED_T == "Red-Winged Blackbird" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD" & penob$MONITOR_TY == "Blood",] #selects samples
 labeled as mercury and only blood samples, removes field duplicates

hg.rwb = hg.rwb[is.na(hg.rwb$X_COORD) == F,] #removes samples without coordinates


hg.rwb$ID2[hg.rwb$year < 2016] = substring(hg.rwb$ID[hg.rwb$year < 2016],1,22)
hg.rwb$ID2[hg.rwb$year >= 2016] = as.character(hg.rwb$ID[hg.rwb$year >= 2016])
hg.rwb$ID2 = factor(hg.rwb$ID2)

rwb.weight$ID2[rwb.weight$year < 2016] = substring(rwb.weight$ID[rwb.weight$year < 2016],1,22)
rwb.weight$ID2[rwb.weight$year >= 2016] = as.character(rwb.weight$ID[rwb.weight$year >= 2016])
rwb.weight$ID2 = factor(rwb.weight$ID2)
summary(rwb.weight) #236


hg.rwb = merge(hg.rwb, rwb.weight[,c(2:4, 6, 7, 37, 41:47)], by.x = c("ID2", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("ID2", "X_COORD",
 "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge blood records with weights for each bird
names(hg.rwb)[colnames(hg.rwb) == "resuse.x"] = "resuse" #rename columns for ease of keeping track of data
names(hg.rwb)[colnames(hg.rwb) == "resuse.y"] = "weight" #rename columns for ease of keeping track of data
summary(hg.rwb) #246 records


hg.rwb$ln.resuse = log(hg.rwb$resuse) #log mercury results

hg.rwb$w.adj_resuse = hg.rwb$resuse / hg.rwb$weight * median(hg.rwb$weight, na.rm = T) #weight adjust Hg results
hg.rwb$ln.w.adj_resuse = log(hg.rwb$resuse) / hg.rwb$weight * median(hg.rwb$weight, na.rm = T) #weight adjust logged Hg results

ref.rwb = hg.rwb[hg.rwb$Y_COORD < 200000 | hg.rwb$X_COORD > 915000 &! (grepl("1232-310-28_062508_RWB", hg.rwb$ID2) == T | grepl("1232-310-29_062508_RWB",
 hg.rwb$ID2) == T),] # (2 pulled out because they're on Verona Island - 1232-310-28_062508_RWB and 1232-310-29_062508_RWB)
ref.rwb$which.ref = "downeast"
ref.rwb$which.ref[ref.rwb$X_COORD < 600000] = "coast"
ref.rwb$which.ref[ref.rwb$X_COORD > 950000 & ref.rwb$Y_COORD > 350000] = "Add"

hg.rwb = hg.rwb[hg.rwb$Y_COORD > 200000 & hg.rwb$X_COORD < 915000,] #reduce dataset to site birds
summary(hg.rwb) #235 records
summary(ref.rwb) #9 records


################################################
### Dataset matching 2016 sampling locations ###
################################################

hg.rwb.mm = hg.rwb[hg.rwb$Y_COORD < 342000 & hg.rwb$X_COORD < 910000 & hg.rwb$X_COORD >889900 & hg.rwb$Y_COORD >330000,] #pulling out MM blackbirds
hg.rwb.mmse = hg.rwb.mm[hg.rwb.mm$X_COORD > 889600 & hg.rwb.mm$Y_COORD > 334800,] #MM-SE blackbirds
hg.rwb.mmsw = hg.rwb.mm[hg.rwb.mm$X_COORD > 889600 & hg.rwb.mm$Y_COORD < 334800 & hg.rwb.mm$Y_COORD > 326000,] #MM-SW blackbirds
hg.rwb.w17 = hg.rwb[hg.rwb$Y_COORD > 342000 & hg.rwb$X_COORD > 891000,] #pulling out W17 blackbirds

hg.rwb.P = hg.rwb #retaining all paired data
```

```
hg.rwb = hg.rwb[(hg.rwb$X_COORD > 889900 & hg.rwb$Y_COORD > 334800) | (hg.rwb$X_COORD > 889900 & hg.rwb$Y_COORD < 334800 & hg.rwb$Y_COORD > 326000) | (hg.rwb
 $Y_COORD > 342000 & hg.rwb$X_COORD > 891000),] #reducing main dataset to W-17, MM-SW, & MM-SE locations



####################################
### Red-winged Blackbird Summary ###
####################################


rwb.summ = data.frame(mmse.x = tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, mean))
rwb.summ$mmse_x_se = tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, sd) / sqrt(tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, length))
rwb.summ$mmse_medn = tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, median)
rwb.summ$mmse_N = tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, length)
rwb.summ$mmse_perc = tapply(hg.rwb.mmse$resuse[hg.rwb.mmse$resuse > 2100], hg.rwb.mmse$year[hg.rwb.mmse$resuse > 2100], length) / tapply(hg.rwb.mmse$resuse,
 hg.rwb.mmse$year, length)

rwb.summ$mmsw_x = tapply(hg.rwb.mmsw$resuse, hg.rwb.mmsw$year, mean)
rwb.summ$mmsw_x_se = tapply(hg.rwb.mmsw$resuse, hg.rwb.mmsw$year, sd) / sqrt(tapply(hg.rwb.mmsw$resuse, hg.rwb.mmsw$year, length))
rwb.summ$mmsw_medn = tapply(hg.rwb.mmsw$resuse, hg.rwb.mmsw$year, median)
rwb.summ$mmsw_N = tapply(hg.rwb.mmsw$resuse, hg.rwb.mmsw$year, length)
rwb.summ$mmsw_perc = tapply(hg.rwb.mmsw$resuse[hg.rwb.mmsw$resuse > 2100], hg.rwb.mmsw$year[hg.rwb.mmsw$resuse > 2100], length) / tapply(hg.rwb.mmsw$resuse,
 hg.rwb.mmsw$year, length)
rwb.summ = rbind(rwb.summ[1:5,], NA,rwb.summ[6,])
rownames(rwb.summ)[6] = "2016"

rwb.summ$w17_x[3:7] = tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, mean)
rwb.summ$w17_x_se[3:7] = tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, sd) / sqrt(tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, length))
rwb.summ$w17_medn[3:7] = tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, median)
rwb.summ$w17_N[3:7] = tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, length)
rwb.summ$w17_perc[3:7] = tapply(hg.rwb.w17$resuse[hg.rwb.w17$resuse > 2100], hg.rwb.w17$year[hg.rwb.w17$resuse > 2100], length) / tapply(hg.rwb.w17$resuse,
 hg.rwb.w17$year, length)

rwb.summ$Add_x = NA
rwb.summ$Add_x[5] = mean(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012])
rwb.summ$Add_x_se = NA
rwb.summ$Add_x_se[5] = sd(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012]) / sqrt(length(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb
 $year == 2012]))
rwb.summ$Add_medn = NA
rwb.summ$Add_medn[5] = median(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012])
rwb.summ$Add_N = NA
rwb.summ$Add_N[5] = length(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012])
rwb.summ$Add_perc = NA
rwb.summ$Add_perc[5] = length(ref.rwb$resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012 & ref.rwb$resuse > 2100]) / length(ref.rwb$resuse[ref.rwb
 $which.ref == "Add" & ref.rwb$year == 2012])

rwb.summ$me_x[c(2,4,7)] = c(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"], mean), NA)
rwb.summ$me_x_se[c(2,4,7)] = c(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"], sd), NA) /
 c(sqrt(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"],length)),NA)
rwb.summ$me_medn[c(2,4,7)] = c(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"], median), NA)
rwb.summ$me_N[c(2,4,7)] = c(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"], length), NA)
rwb.summ$me_perc[c(2,4,7)] = c(tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast" & ref.rwb$resuse > 2100], ref.rwb$year[ref.rwb$which.ref == "coast" &
 ref.rwb$resuse > 2100], length) / tapply(ref.rwb$resuse[ref.rwb$which.ref == "coast"], ref.rwb$year[ref.rwb$which.ref == "coast"], length), NA)
rwb.summ$me_perc[c(2,4,7)] = c(0,0,NA)

write.csv(rwb.summ, "RWB summary.csv")


##############################
### Log-Linear Regressions ###
##############################

summary(lm(ln.resuse ~ year, data = hg.rwb.mmse))
summary(lm(ln.resuse ~ year, data = hg.rwb.mmsw))
summary(lm(ln.resuse ~ year, data = hg.rwb.w17))



hg.rwb.age = read.csv("RWBL in with age merge.csv")
summary(hg.rwb.age)

hg.rwb.age$ln.resuse = log(hg.rwb.age$resuse)

hg.rwb.age$w.adj_resuse = hg.rwb.age$resuse / hg.rwb.age$weight * median(hg.rwb.age$weight, na.rm = T)
hg.rwb.age$ln.w.adj_resuse = log(hg.rwb.age$resuse) / hg.rwb.age$weight * median(hg.rwb.age$weight, na.rm = T)


hy.rwb = hg.rwb.age[hg.rwb.age$Age == "HY" & is.na(hg.rwb.age$Age) == F,]
summary(hy.rwb)

ad.rwb = hg.rwb.age[!(hg.rwb.age$Age == "HY" | hg.rwb.age$Age == "Local") & is.na(hg.rwb.age$Age) == F,]
summary(ad.rwb)

ref.hy.rwb = hy.rwb[hy.rwb$Y_COORD < 200000 | hy.rwb$X_COORD > 915000 &! (grepl("1232-310-28_062508_RWB", hy.rwb$ID2) == T | grepl("1232-310-29_062508_RWB",
 hy.rwb$ID2) == T),] # (2 pulled out because they're on Verona Island - 1232-310-28_062508_RWB and 1232-310-29_062508_RWB)
hg.hy.rwb = hy.rwb[hy.rwb$Y_COORD > 200000 & hy.rwb$X_COORD < 915000,]
summary(hg.hy.rwb) #93
summary(ref.hy.rwb) #3


ref.ad.rwb = ad.rwb[ad.rwb$Y_COORD < 200000 | ad.rwb$X_COORD > 915000 &! (grepl("1232-310-28_062508_RWB", ad.rwb$ID2) == T | grepl("1232-310-29_062508_RWB",
 ad.rwb$ID2) == T),] # (2 pulled out because they're on Verona Island - 1232-310-28_062508_RWB and 1232-310-29_062508_RWB)
```

```r
hg.ad.rwb = ad.rwb[ad.rwb$Y_COORD > 200000 & ad.rwb$X_COORD < 915000,]
summary(hg.ad.rwb) #141
summary(ref.ad.rwb) #6

ref.hy.rwb$which.ref = "downeast"
ref.hy.rwb$which.ref[ref.hy.rwb$X_COORD < 600000] = "coast"
ref.hy.rwb$which.ref[ref.hy.rwb$X_COORD > 950000 & ref.hy.rwb$Y_COORD > 350000] = "Add"

ref.ad.rwb$which.ref = "downeast"
ref.ad.rwb$which.ref[ref.ad.rwb$X_COORD < 600000] = "coast"
ref.ad.rwb$which.ref[ref.ad.rwb$X_COORD > 950000 & ref.ad.rwb$Y_COORD > 350000] = "Add"


########################
### Hatch Year Birds ###
################################################
### Dataset matching 2016 sampling locations ###
################################################

hg.hy.rwb.mm = hg.hy.rwb[hg.hy.rwb$Y_COORD < 342000 & hg.hy.rwb$X_COORD < 910000 & hg.hy.rwb$X_COORD >889900 & hg.hy.rwb$Y_COORD >330000,] #pulling out MM
 blackbirds
hg.hy.rwb.mmse = hg.hy.rwb.mm[hg.hy.rwb.mm$X_COORD > 889600 & hg.hy.rwb.mm$Y_COORD > 334800,] #MM-SE blackbirds
hg.hy.rwb.mmsw = hg.hy.rwb.mm[hg.hy.rwb.mm$X_COORD > 889600 & hg.hy.rwb.mm$Y_COORD < 334800 & hg.hy.rwb.mm$Y_COORD > 326000,] #MM-SW blackbirds
hg.hy.rwb.w17 = hg.hy.rwb[hg.hy.rwb$Y_COORD > 342000 & hg.hy.rwb$X_COORD > 891000,] #pulling out W17 blackbirds

hg.hy.rwb.P = hg.hy.rwb #retaining all paired data

hg.hy.rwb = hg.hy.rwb[(hg.hy.rwb$X_COORD > 889900 & hg.hy.rwb$Y_COORD > 334800) | (hg.hy.rwb$X_COORD > 889900 & hg.hy.rwb$Y_COORD < 334800 & hg.hy.rwb$Y_COORD
 > 326000) | (hg.hy.rwb$Y_COORD > 342000 & hg.hy.rwb$X_COORD > 891000),] #reducing main dataset to W-17, MM-SW, & MM-SE locations


####################################
### Red-winged Blackbird Summary ###
####################################

rwb.hy.summ = data.frame(mmse_x = tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, mean))
rwb.hy.summ$mmse_x_se = tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, sd) / sqrt(tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, length))
rwb.hy.summ$mmse_medn = tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, median)
rwb.hy.summ$mmse_N = tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, length)
rwb.hy.summ$mmse_perc = c(0,tapply(hg.hy.rwb.mmse$resuse[hg.hy.rwb.mmse$resuse > 2100], hg.hy.rwb.mmse$year[hg.hy.rwb.mmse$resuse > 2100], length)) /
 tapply(hg.hy.rwb.mmse$resuse, hg.hy.rwb.mmse$year, length)
rwb.hy.summ = rbind(NA,rwb.hy.summ,NA)
rownames(rwb.hy.summ) = c("2007","2008","2009","2010")

rwb.hy.summ$mmsw_x = tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, mean)
rwb.hy.summ$mmsw_x_se = tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, sd) / sqrt(tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, length))
rwb.hy.summ$mmsw_medn = tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, median)
rwb.hy.summ$mmsw_N = tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, length)
rwb.hy.summ$mmsw_perc = c(tapply(hg.hy.rwb.mmsw$resuse[hg.hy.rwb.mmsw$resuse > 2100], hg.hy.rwb.mmsw$year[hg.hy.rwb.mmsw$resuse > 2100], length),0,0) /
 tapply(hg.hy.rwb.mmsw$resuse, hg.hy.rwb.mmsw$year, length)
rwb.hy.summ = rbind(rwb.hy.summ,NA)
rownames(rwb.hy.summ)[5] = c("2016")

rwb.hy.summ$w17_x[3:5] = tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, mean)
rwb.hy.summ$w17_x_se[3:5] = tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, sd) / sqrt(tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, length))
rwb.hy.summ$w17_medn[3:5] = tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, median)
rwb.hy.summ$w17_N[3:5] = tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, length)
rwb.hy.summ$w17_perc[3:5] = c(tapply(hg.hy.rwb.w17$resuse[hg.hy.rwb.w17$resuse > 2100], hg.hy.rwb.w17$year[hg.hy.rwb.w17$resuse > 2100], length),0) /
 tapply(hg.hy.rwb.w17$resuse, hg.hy.rwb.w17$year, length)



ref.hy.means = data.frame(x = tapply(ref.hy.rwb$resuse, list(ref.hy.rwb$year, ref.hy.rwb$which.ref), mean))
rownames(ref.hy.means) = "2010"
colnames(ref.hy.means) = "coast.x"

ref.hy.m.se = data.frame(x_se = tapply(ref.hy.rwb$resuse, list(ref.hy.rwb$year, ref.hy.rwb$which.ref), sd) / sqrt(tapply(ref.hy.rwb$resuse, list(ref.hy.rwb
 $year, ref.hy.rwb$which.ref), length)))
rownames(ref.hy.m.se) = "2010"
colnames(ref.hy.m.se) = "coast.m.se"

ref.hy.medn = data.frame(med.n = tapply(ref.hy.rwb$resuse, list(ref.hy.rwb$year, ref.hy.rwb$which.ref), median))
rownames(ref.hy.medn) = "2010"
colnames(ref.hy.medn) = "coast.medn"

ref.hy.N = data.frame(N = tapply(ref.hy.rwb$resuse, list(ref.hy.rwb$year, ref.hy.rwb$which.ref), length))
rownames(ref.hy.N) = "2010"
colnames(ref.hy.N) = "coast.N"

ref.hy.summ = cbind(ref.hy.means, ref.hy.m.se, ref.hy.medn, ref.hy.N)
ref.hy.summ = rbind(NA,NA,NA, ref.hy.summ, NA)
rwb.hy.summ = cbind(rwb.hy.summ,ref.hy.summ)

rwb.hy.summ$coast_perc[4:5] = c(0,NA)


write.csv(rwb.hy.summ, "RWBL HY summary.csv")


###################
### Adult Birds ###
################################################
```

```r
### Dataset matching 2016 sampling locations ###
################################################

hg.ad.rwb.mm = hg.ad.rwb[hg.ad.rwb$Y_COORD < 342000 & hg.ad.rwb$X_COORD < 910000 & hg.ad.rwb$X_COORD >889900 & hg.ad.rwb$Y_COORD >330000,] #pulling out MM
 blackbirds
hg.ad.rwb.mmse = hg.ad.rwb.mm[hg.ad.rwb.mm$X_COORD > 889600 & hg.ad.rwb.mm$Y_COORD > 334800,] #MM-SE blackbirds
hg.ad.rwb.mmsw = hg.ad.rwb.mm[hg.ad.rwb.mm$X_COORD > 889600 & hg.ad.rwb.mm$Y_COORD < 334800 & hg.ad.rwb.mm$Y_COORD > 326000,] #MM-SW blackbirds
hg.ad.rwb.w17 = hg.ad.rwb[hg.ad.rwb$Y_COORD > 342000 & hg.ad.rwb$X_COORD > 891000,] #pulling out W17 blackbirds


hg.ad.rwb.P = hg.ad.rwb
hg.ad.rwb = hg.ad.rwb[(hg.ad.rwb$X_COORD > 889900 & hg.ad.rwb$Y_COORD > 334800) | (hg.ad.rwb$X_COORD > 889900 & hg.ad.rwb$Y_COORD < 334800 & hg.ad.rwb$Y_COORD
 > 326000) | (hg.ad.rwb$Y_COORD > 342000 & hg.ad.rwb$X_COORD > 891000),]


####################################
### Red-winged Blackbird Summary ###
####################################

rwb.ad.summ = data.frame(mmse_x = tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, mean))
rwb.ad.summ$mmse_x_se = tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, sd) / sqrt(tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, length))
rwb.ad.summ$mmse_medn = tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, median)
rwb.ad.summ$mmse_N = tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, length)
rwb.ad.summ$mmse_perc[c(1,3:6)] = tapply(hg.ad.rwb.mmse$resuse[hg.ad.rwb.mmse$resuse > 2100], hg.ad.rwb.mmse$year[hg.ad.rwb.mmse$resuse > 2100], length) /
 tapply(hg.ad.rwb.mmse$resuse, hg.ad.rwb.mmse$year, length)[-2]
rwb.ad.summ$mmse_perc[2] = 0

rwb.ad.summ$mmsw_x = tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, mean)
rwb.ad.summ$mmsw_x_se = tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, sd) / sqrt(tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, length))
rwb.ad.summ$mmsw_medn = tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, median)
rwb.ad.summ$mmsw_N = tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, length)
rwb.ad.summ$mmsw_perc = tapply(hg.ad.rwb.mmsw$resuse[hg.ad.rwb.mmsw$resuse > 2100], hg.ad.rwb.mmsw$year[hg.ad.rwb.mmsw$resuse > 2100], length) /
 tapply(hg.ad.rwb.mmsw$resuse, hg.ad.rwb.mmsw$year, length)

rwb.ad.summ = rbind(rwb.ad.summ[1:5,],NA, rwb.ad.summ[6,])
rownames(rwb.ad.summ)[6] = "2016"

rwb.ad.summ$w17_x[3:7] = tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, mean)
rwb.ad.summ$w17_x_se[3:7] = tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, sd) / sqrt(tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, length))
rwb.ad.summ$w17_medn[3:7] = tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, median)
rwb.ad.summ$w17_N[3:7] = tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, length)
rwb.ad.summ$w17_perc[3:7] = tapply(hg.ad.rwb.w17$resuse[hg.ad.rwb.w17$resuse > 2100], hg.ad.rwb.w17$year[hg.ad.rwb.w17$resuse > 2100], length) /
 tapply(hg.ad.rwb.w17$resuse, hg.ad.rwb.w17$year, length)

ref.ad.means = data.frame(x = tapply(ref.ad.rwb$resuse, list(ref.ad.rwb$year, ref.ad.rwb$which.ref), mean))

ref.ad.m.se = data.frame(x_se = tapply(ref.ad.rwb$resuse, list(ref.ad.rwb$year, ref.ad.rwb$which.ref), sd) / sqrt(tapply(ref.ad.rwb$resuse, list(ref.ad.rwb
 $year, ref.ad.rwb$which.ref), length)))

ref.ad.medn = data.frame(med.n = tapply(ref.ad.rwb$resuse, list(ref.ad.rwb$year, ref.ad.rwb$which.ref), median))

ref.ad.N = data.frame(N = tapply(ref.ad.rwb$resuse, list(ref.ad.rwb$year, ref.ad.rwb$which.ref), length))

ref.ad.summ = cbind(ref.ad.means, ref.ad.m.se, ref.ad.medn, ref.ad.N)
ref.ad.summ = rbind(NA, ref.ad.summ[1,], NA, ref.ad.summ[2:3,], NA,NA)
rwb.ad.summ = cbind(rwb.ad.summ,ref.ad.summ)

rwb.ad.summ$Add_perc[5:7] = c(0,NA,NA)
rwb.ad.summ$coast_perc[c(2,4,7)] = c(0,0,NA)

write.csv(rwb.ad.summ, "RWBL Adult summary.csv")


###################################
### RED-WINGED BLACKBIRD TRENDS ###
###################################

# Hatch Year Birds
hg.hy.rwb.lreg.ln = summary(lm(ln.resuse ~ year, data = hg.hy.rwb))
#hg.hy.rwb.lnreg.mmse = summary(lm(ln.resuse ~ year, data = hg.hy.rwb.mmse))
hg.hy.rwb.lnreg.mmsw = summary(lm(ln.resuse ~ year, data = hg.hy.rwb.mmsw))
hg.hy.rwb.w17.lnreg = summary(lm(ln.resuse ~ year, data = hg.hy.rwb.w17))

# Adult Birds
hg.ad.rwb.lreg.ln = summary(lm(ln.resuse ~ year, data = hg.ad.rwb))
hg.ad.rwb.lnreg.mmse = summary(lm(ln.resuse ~ year, data = hg.ad.rwb.mmse))
hg.ad.rwb.lnreg.mmsw = summary(lm(ln.resuse ~ year, data = hg.ad.rwb.mmsw))
hg.ad.rwb.w17.lnreg = summary(lm(ln.resuse ~ year, data = hg.ad.rwb.w17))


#4-27a
plot(ln.resuse ~ year, data = ref.rwb[ref.rwb$which.ref == "coast",], pch = 18, ylab = "Ln Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(hg.rwb$year)),
 las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), main = "Figure 4-27a\nRed-winged Blackbird Blood - Reference Locations\nLn
 Mercury Concentrations")
points(ln.resuse ~ year, data = ref.rwb[ref.rwb$which.ref == "Add",], col = 3, pch = 16)
legend("bottomleft", legend = c("ME Coastal Wetlands", "Pleasant River"), pch = c(18,16), col = c(1,3), cex = 0.8)
title(sub = "ME Coastal Wetlands includes: Spurwink River and Scarborough River areas", cex.sub = 0.7)


#4-27b
par(mfrow = c(1,1))
plot(ln.resuse ~ year, data = ref.hy.rwb[ref.hy.rwb$which.ref == "coast",], pch = 18, ylab = "Ln Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(hg.rwb
```

```
 $year)), las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), main = "Figure 4-27b\nRed-winged Blackbird (Hatch Year) Blood -
 Reference Locations\nLn Mercury Concentrations")
legend("bottomleft", legend = c("ME Coastal Wetlands"), pch = 18, col = 1, cex = 0.8)
title(sub = "ME Coastal Wetlands includes: Spurwink River and Scarborough River areas", cex.sub = 0.7)


#4-27c
par(mfrow = c(1,1))
plot(ln.resuse ~ year, data = ref.ad.rwb[ref.ad.rwb$which.ref == "coast",], pch = 18, ylab = "Ln Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(hg.rwb
 $year)), las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), main = "Figure 4-27c\nRed-winged Blackbird (Adult) Blood - Reference
 Locations\nLn Mercury Concentrations")
points(ln.resuse ~ year, data = ref.ad.rwb[ref.ad.rwb$which.ref == "Add",], pch = 16, col = 3)
legend("bottomleft", legend = c("Pleasant River","ME Coastal Wetlands"), pch = c(16,18), col = c(3,1), cex = 0.8)
title(sub = "ME Coastal Wetlands includes: Spurwink River and Scarborough River areas", cex.sub = 0.7)


#4-28a
plot(ln.resuse ~ year, data = hg.rwb, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-28a\nRed-winged Blackbird Blood - Whole River\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(hg.rwb$ln.resuse ~ hg.rwb$year))

text(min(hg.rwb$year) + 1.5, max(hg.rwb$ln.resuse)*0.185, "ln(y) = 0.07380x - 140.77", cex = 0.8)
text(min(hg.rwb$year) + 1.5, max(hg.rwb$ln.resuse)*0.15, "p = 0.039, Adj." ~R^2~ "= 0.02", cex = 0.8)

points(as.numeric(levels(as.factor(hg.rwb$year))), tapply(hg.rwb$ln.resuse, hg.rwb$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.rwb$year))), tapply(hg.rwb$ln.resuse, hg.rwb$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-28b
plot(ln.resuse ~ year, data = hg.hy.rwb, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-28b\nRed-winged Blackbird (Hatch Year) Blood - Whole
 River\nLoglinear Regression", xlim = c(2006, max(hg.rwb$year)), ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(hg.hy.rwb$ln.resuse ~ hg.hy.rwb$year))

text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.20, "ln(y) = -0.2503x + 509.4", cex = 0.8)
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.17, "p = 0.020, Adj." ~R^2~ "= 0.06", cex = 0.8)

points(as.numeric(levels(as.factor(hg.hy.rwb$year))), tapply(hg.hy.rwb$ln.resuse, hg.hy.rwb$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.rwb$year))), tapply(hg.hy.rwb$ln.resuse, hg.hy.rwb$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-28c
plot(ln.resuse ~ year, data = hg.ad.rwb, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-28c\nRed-winged Blackbird (Adult) Blood - Whole River
 \nLoglinear Regression", xlim = c(2006, max(hg.rwb$year)), ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.20, "ln(y) = -0.00662x - 5.029", cex = 0.8)
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.17, "p = 0.83, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.rwb$year))), tapply(hg.ad.rwb$ln.resuse, hg.ad.rwb$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.rwb$year))), tapply(hg.ad.rwb$ln.resuse, hg.ad.rwb$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)

#4-29a
plot(ln.resuse ~ year, data = hg.rwb.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-29a\nRed-winged Blackbird Blood - MM-SE\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.rwb$year)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.rwb.mmse))

text(min(hg.rwb$year) + 0.5, 0.20 * max(hg.rwb$ln.resuse), "ln(y) = 0.1521x - 298.50", cex = 0.8)
text(min(hg.rwb$year) + 0.5, 0.17 * max(hg.rwb$ln.resuse), "p = 0.032, Adj." ~R^2~ "= 0.03", cex = 0.8)

points(as.numeric(levels(as.factor(hg.rwb.mmse$year))), tapply(hg.rwb.mmse$ln.resuse, hg.rwb.mmse$year, median, na.rm = T), pch = 21, col = "red", cex = 1.3,
 bg = "red")
points(as.numeric(levels(as.factor(hg.rwb.mmse$year))), tapply(hg.rwb.mmse$ln.resuse, hg.rwb.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex = 1.3,
 bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-29b
plot(ln.resuse ~ year, data = hg.hy.rwb.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-29b\nRed-winged Blackbird (Hatch Year) Blood - MM-
 SE\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.hy.rwb$year)), las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.hy.rwb.mmse$year))), tapply(hg.hy.rwb.mmse$ln.resuse, hg.hy.rwb.mmse$year, median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.rwb.mmse$year))), tapply(hg.hy.rwb.mmse$ln.resuse, hg.hy.rwb.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-29c
plot(ln.resuse ~ year, data = hg.ad.rwb.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-29c\nRed-winged Blackbird (Adult) Blood - MM-SE
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.ad.rwb$year)), las = 1, tck = 0.015, yaxs = "i")
```

```r
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.20, "ln(y) = -0.0176x + 43.691", cex = 0.8)
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.17, "p = 0.76, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.rwb.mmse$year))), tapply(hg.ad.rwb.mmse$ln.resuse, hg.ad.rwb.mmse$year, median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.rwb.mmse$year))), tapply(hg.ad.rwb.mmse$ln.resuse, hg.ad.rwb.mmse$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-30a
plot(ln.resuse ~ year, data = hg.rwb.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-30a\nRed-winged Blackbird Blood - MM-SW\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.rwb$year)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.rwb.mmsw), lty = 2)

text(min(hg.rwb$year) + 0.5, 0.20 * max(hg.rwb$ln.resuse), "ln(y) = 0.1022x - 197.50", cex = 0.8)
text(min(hg.rwb$year) + 0.5, 0.17 * max(hg.rwb$ln.resuse), "p = 0.061, Adj." ~R^2~ "= 0.03", cex = 0.8)

points(as.numeric(levels(as.factor(hg.rwb.mmsw$year))), tapply(hg.rwb.mmsw$ln.resuse, hg.rwb.mmsw$year, median, na.rm = T), pch = 21, col = "red", cex = 1.3,
 bg = "red")
points(as.numeric(levels(as.factor(hg.rwb.mmsw$year))), tapply(hg.rwb.mmsw$ln.resuse, hg.rwb.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex = 1.3,
 bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-30b
plot(ln.resuse ~ year, data = hg.hy.rwb.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-30b\nRed-winged Blackbird (Hatch Year) Blood - MM-
 SW\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.hy.rwb$year)), las = 1, tck = 0.015, yaxs = "i")
clip(2006,2011,0,10000)
abline(lm(ln.resuse ~ year, data = hg.hy.rwb.mmsw))
clip(2000,2020,0,10000)

text(min(hg.hy.rwb$year) + 0.5, 0.20 * max(hg.rwb$ln.resuse), "ln(y) = -0.3547x + 719.2", cex = 0.8)
text(min(hg.hy.rwb$year) + 0.5, 0.17 * max(hg.rwb$ln.resuse), "p = 0.040, Adj." ~R^2~ "= 0.10", cex = 0.8)

points(as.numeric(levels(as.factor(hg.hy.rwb.mmsw$year))), tapply(hg.hy.rwb.mmsw$ln.resuse, hg.hy.rwb.mmsw$year, median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.hy.rwb.mmsw$year))), tapply(hg.hy.rwb.mmsw$ln.resuse, hg.hy.rwb.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-30c
plot(ln.resuse ~ year, data = hg.ad.rwb.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-30c\nRed-winged Blackbird (Adult) Blood - MM-SW
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.ad.rwb$year)), las = 1, tck = 0.015, yaxs = "i")
clip(2006,2018,0,10000)
abline(lm(ln.resuse ~ year, data = hg.ad.rwb.mmsw), lty = 2)
clip(2000,2020,0,10000)

text(min(hg.ad.rwb$year) + 0.5, 0.20 * max(hg.rwb$ln.resuse), "ln(y) = 0.09397x - 180.5", cex = 0.8)
text(min(hg.ad.rwb$year) + 0.5, 0.17 * max(hg.rwb$ln.resuse), "p = 0.066, Adj." ~R^2~ "= 0.04", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.rwb.mmsw$year))), tapply(hg.ad.rwb.mmsw$ln.resuse, hg.ad.rwb.mmsw$year, median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ad.rwb.mmsw$year))), tapply(hg.ad.rwb.mmsw$ln.resuse, hg.ad.rwb.mmsw$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-31a
plot(ln.resuse ~ year, data = hg.rwb.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-31a\nRed-winged Blackbird Blood - W-17-N\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.rwb$year)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse) * 0.20, "ln(y) = -0.059x + 127.36", cex = 0.8)
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse) * 0.17, "p = 0.47, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.rwb.w17$year))), tapply(hg.rwb.w17$ln.resuse, hg.rwb.w17$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.rwb.w17$year))), tapply(hg.rwb.w17$ln.resuse, hg.rwb.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-31b
plot(ln.resuse ~ year, data = hg.hy.rwb.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-31b\nRed-winged Blackbird (Hatch Year) Blood - W-17-
 N\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.hy.rwb$year)), las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.hy.rwb.w17$year))), tapply(hg.hy.rwb.w17$ln.resuse, hg.hy.rwb.w17$year, median), pch = 21, col = "red", cex = 1.3, bg =
 "red")
points(as.numeric(levels(as.factor(hg.hy.rwb.w17$year))), tapply(hg.hy.rwb.w17$ln.resuse, hg.hy.rwb.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
```

```r
 c("white","blue","red"), cex = 0.8)


#4-31c
plot(ln.resuse ~ year, data = hg.ad.rwb.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-31c\nRed-winged Blackbird (Adult) Blood - W-17-N
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb$ln.resuse)), xlim = c(2006, max(hg.ad.rwb$year)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.20, "ln(y) = -0.0957x + 200.8", cex = 0.8)
text(min(hg.rwb$year) + 0.5, max(hg.rwb$ln.resuse)*0.17, "p = 0.33, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.ad.rwb.w17$year))), tapply(hg.ad.rwb.w17$ln.resuse, hg.ad.rwb.w17$year, median), pch = 21, col = "red", cex = 1.3, bg =
 "red")
points(as.numeric(levels(as.factor(hg.ad.rwb.w17$year))), tapply(hg.ad.rwb.w17$ln.resuse, hg.ad.rwb.w17$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-32a
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(resuse ~ year, data = hg.rwb[hg.rwb$month == 6,], main = "June", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(min(hg.rwb$year), max(hg.rwb$year)), ylim =
 c(0, max(hg.rwb$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2015, max(hg.rwb$resuse)*0.97, "y = -82.36x + 170344", cex = 0.6)
text(2015, max(hg.rwb$resuse)*0.92, "p = 0.51, Adj." ~R^2~ "= 0", cex = 0.6)

plot(resuse ~ year, data = hg.rwb[hg.rwb$month == 7,], main = "July", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(min(hg.rwb$year), max(hg.rwb$year)), ylim =
 c(0, max(hg.rwb$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
abline(lm(resuse ~ year, data = hg.rwb[hg.rwb$month == 7,]))
text(2015, max(hg.rwb$resuse)*0.97, "y = 664.1x - 1330589", cex = 0.6)
text(2015, max(hg.rwb$resuse)*0.92, "p = 0.001, Adj." ~R^2~ "= 0.06", cex = 0.6)

plot(resuse ~ year, data = hg.rwb[hg.rwb$month == 8,], main = "August", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(min(hg.rwb$year), max(hg.rwb$year)), ylim
 = c(0, max(hg.rwb$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
mtext(expression(bold("Figure 4-32a\n"), bold("Red-winged Blackbird Mercury Concentrations in each Month")), outer = T)


#4-32b
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(0,0,type = "n", axes = F, ylab = "", xlab ="")
text(0,0, "No hatch year birds collected in June", cex = 0.7)

plot(resuse ~ year, data = hg.hy.rwb[hg.hy.rwb$month == 7,], main = "July", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(2006,2017), ylim = c(0, max(hg.rwb
 $resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2015, max(hg.rwb$resuse)*0.97, "y = -224.0x + 451199.5", cex = 0.6)
text(2015, max(hg.rwb$resuse)*0.88, "p = 0.13, Adj." ~R^2~ "= 0.02", cex = 0.6)

plot(resuse ~ year, data = hg.hy.rwb[hg.hy.rwb$month == 8,], main = "August", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(2006,2017), ylim = c(0,
 max(hg.hy.rwb$resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
mtext(expression(bold("Figure 4-32b\n"), bold("Red-winged Blackbird (Hatch Year) Mercury Concentrations in each Month")), outer = T)



#4-32c
par(mfrow = c(2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(resuse ~ year, data = hg.ad.rwb[hg.ad.rwb$month == 6,], main = "June", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(2006,2017), ylim = c(0, max(hg.ad.rwb
 $resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
text(2015, max(hg.rwb$resuse)*0.97, "y = -82.36x + 170344.3", cex = 0.6)
text(2015, max(hg.rwb$resuse)*0.88, "p = 0.51, Adj." ~R^2~ "= 0", cex = 0.6)

plot(resuse ~ year, data = hg.ad.rwb[hg.ad.rwb$month == 7,], main = "July", ylab = "Hg (ng/g)", xlab = "Year", xlim = c(2006,2017), ylim = c(0, max(hg.rwb
 $resuse) * 1.02), las = 1, tck = 0.015, yaxs = "i", pch = 16)
abline(lm(resuse ~ year, data = hg.ad.rwb[hg.ad.rwb$month == 7,]))
text(2015, max(hg.rwb$resuse)*0.97, "y = 616.1x - 1231857", cex = 0.6)
text(2015, max(hg.rwb$resuse)*0.88, "p = 0.015, Adj." ~R^2~ "= 0.06", cex = 0.6)
mtext(expression(bold("Figure 4-32c\n"), bold("Red-winged Blackbird (Adult) Mercury Concentrations in each Month")), outer = T)

plot(0,0,type = "n", axes = F, ylab = "", xlab ="")
text(0,0, "No hatch year birds collected in August", cex = 0.7)
```

Appendix F-5. American Black Duck Blood Statistical Analysis Code

```
### File created for analysis of black duck blood data for Biota Monitoring Report (2017)
### Code prepared by LSV 4/07/2017
### Code checked by NTG 4/20/2017


library(foreign)
library(lattice)
library(plyr)
library(stringr) #for str_sub function


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob
 $month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]

#################################
### AMERICAN BLACK DUCK BLOOD ###
#################################

abd.weight = weight[weight$MED_T == "American Black Duck",]
abd.weight$ID = str_sub(abd.weight$ID, -25, -4)
abd.weight = abd.weight[abd.weight$MONITOR_TY == "Blood" | is.na(abd.weight$MONITOR_TY) == T,]

levels(factor(penob$PARAM_NAME[penob$MED_T == "American Black Duck"]))

hg.abd = penob[penob$MED_T == "American Black Duck" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD" & penob$MONITOR_TY == "Blood",] #selects  samples
 labeled as mercury and only blood samples, removes field duplicates
summary(hg.abd) #140 records

hg.abd$ID = str_sub(hg.abd$ID, -25, -4)

hg.abd$year2[hg.abd$year == 2011 & hg.abd$month < 6] = 2011 #adjusting year to year at end of winter
hg.abd$year2[hg.abd$year == 2011 & hg.abd$month > 6] = 2012
hg.abd$year2[hg.abd$year == 2012 & hg.abd$month < 6] = 2012
hg.abd$year2[hg.abd$year == 2014 & hg.abd$month < 6] = 2014
hg.abd$year2[hg.abd$year == 2016 & hg.abd$month > 6] = 2017
hg.abd$year2[hg.abd$year == 2017 & hg.abd$month < 6] = 2017
hg.abd$year2[hg.abd$year == 2018 & hg.abd$month < 6] = 2018


hg.abd = merge(hg.abd, abd.weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("ID", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("ID",
 "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge Hg and weight
names(hg.abd)[colnames(hg.abd) == "resuse.x"] = "resuse" #rename columns
names(hg.abd)[colnames(hg.abd) == "resuse.y"] = "weight" #rename columns
summary(hg.abd) #185 records

hg.abd$ln.resuse = log(hg.abd$resuse) #log Hg results
hg.abd$w.adj_resuse = hg.abd$resuse / hg.abd$weight * median(hg.abd$weight, na.rm = T) # weight adjust Hg results
hg.abd$ln.w.adj_resuse = log(hg.abd$resuse) / hg.abd$weight * median(hg.abd$weight, na.rm = T) # weight adjust logged Hg results


ref.dub = hg.abd[hg.abd$X_COORD > 947000,] #reference dataset
hg.abd = hg.abd[hg.abd$X_COORD < 947000,] #remove reference data
summary(hg.abd) #119 records
summary(ref.dub) #66 records


hg.abd.mm = hg.abd[hg.abd$Y_COORD < 342000 & hg.abd$X_COORD < 910000,] #pulling out MM duck blood
hg.abd.SV = hg.abd[hg.abd$X_COORD > 910000,] #pulling out South Verona duck blood


#############################
### Concentration Summary ###
#############################

abd.summ = data.frame(MM_x = tapply(hg.abd.mm$resuse, hg.abd.mm$year2, mean))
abd.summ$MM_x_se = tapply(hg.abd.mm$resuse, hg.abd.mm$year2, sd) / sqrt(tapply(hg.abd.mm$resuse, hg.abd.mm$year2, length))
abd.summ$MM_medn = tapply(hg.abd.mm$resuse, hg.abd.mm$year2, median)
abd.summ$MM_N = tapply(hg.abd.mm$resuse, hg.abd.mm$year2, length)
abd.summ$MM_perc = 0 # no samples with concentrations > 2100
```

```r
abd.summ$SV_x = tapply(hg.abd.SV$resuse, hg.abd.SV$year2, mean)
abd.summ$SV_x_se = tapply(hg.abd.SV$resuse, hg.abd.SV$year2, sd) / sqrt(tapply(hg.abd.SV$resuse, hg.abd.SV$year2, length))
abd.summ$SV_medn = tapply(hg.abd.SV$resuse, hg.abd.SV$year2, median)
abd.summ$SV_N = tapply(hg.abd.SV$resuse, hg.abd.SV$year2, length)
abd.summ$SV_perc = 0 # no samples with concentrations > 2100

abd.summ$FRB_x = tapply(ref.dub$resuse, ref.dub$year2, mean)
abd.summ$FRB_x_se = tapply(ref.dub$resuse, ref.dub$year2, sd) / sqrt(tapply(ref.dub$resuse, ref.dub$year2, length))
abd.summ$FRB_medn = tapply(ref.dub$resuse, ref.dub$year2, median)
abd.summ$FRB_N = tapply(ref.dub$resuse, ref.dub$year2, length)
abd.summ$FRB_perc = 0 # no samples with concentrations > 2100

write.csv(abd.summ,"American Black Duck Blood summary.csv")



###############################
### BLACK DUCK BLOOD TRENDS ###
###############################

summary(lm(ln.resuse ~ year2, data = hg.abd))
summary(lm(ln.resuse ~ year2, data = hg.abd.mm))
summary(lm(ln.resuse ~ year2, data = hg.abd.SV))
summary(lm(ln.resuse ~ year, data = ref.dub))


#4-33
plot(ln.resuse ~ year, data = ref.dub, pch = 17, ylab = "Blood Hg (ng/g)", xlab = "Year", xlim = c(2006, max(ref.dub$year)), las = 1, tck = 0.015, yaxs = "i",
 ylim = c(0, 1.02 * max(hg.abd$ln.resuse)), main = "Figure 4-33\nAmerican Black Duck Blood - Frenchman Bay (Reference)\nLoglinear Regression")
clip(2010, 2020, 0, 5000)
abline(lm(ln.resuse ~ year, data = ref.dub))
clip(0, 2020, 0, 5000)

text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.18, "ln(y) = -0.0893x + 184.08", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.15, "p = 0.001, Adj." ~R^2~ "= 0.14", cex = 0.8)

points(as.numeric(levels(as.factor(ref.dub$year))), tapply(ref.dub$ln.resuse, ref.dub$year, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.dub$year))), tapply(ref.dub$ln.resuse, ref.dub$year, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-34
plot(ln.resuse ~ year2, data = hg.abd, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-34\nAmerican Black Duck Blood - Whole River\nLoglinear
 Regression", ylim = c(0,1.02 * max(hg.abd$ln.resuse)), las = 1, tck = 0.015, yaxs = "i", xlim = c(2006, max(hg.abd$year)))

text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.18, "ln(y) = -0.0034x + 12.437", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.15, "p = 0.91, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.abd$year2))), tapply(hg.abd$ln.resuse, hg.abd$year2, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.abd$year2))), tapply(hg.abd$ln.resuse, hg.abd$year2, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)
title(sub = "Includes American Black Ducks sampled at Mendall Marsh and South Verona", cex.sub = 0.7)


#4-35
plot(ln.resuse ~ year2, data = hg.abd.mm, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-35\nAmerican Black Duck Blood - Mendall Marsh
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.abd$ln.resuse)), las = 1, tck = 0.015, yaxs = "i", xlim = c(2006, max(hg.abd$year)))
hg.abd.mm.lnreg = summary(lm(ln.resuse ~ year2, data = hg.abd.mm))

text(max(hg.abd$year2) - 1.5, max(hg.abd.mm$ln.resuse)*0.18, "ln(y) = -0.05075x + 108.2", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd.mm$ln.resuse)*0.15, "p = 0.14, Adj." ~R^2~ "= 0.02", cex = 0.8)

points(as.numeric(levels(as.factor(hg.abd.mm$year2))), tapply(hg.abd.mm$ln.resuse, hg.abd.mm$year2, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.abd.mm$year2))), tapply(hg.abd.mm$ln.resuse, hg.abd.mm$year2, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)


#4-36
plot(ln.resuse ~ year2, data = hg.abd.SV, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-36\nAmerican Black Duck Blood - South Verona\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.abd$ln.resuse)), las = 1, tck = 0.015, yaxs = "i", xlim = c(2006, max(hg.abd$year)))
clip(2010, 2020, 0, 100)
abline(lm(ln.resuse ~ year2, data = hg.abd.SV))
clip(0, 2020, 0, 100)

text(max(hg.abd$year2) - 1.5, max(hg.abd.SV$ln.resuse)*0.19, "ln(y) = 0.0767x - 149.4", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd.SV$ln.resuse)*0.16, "p = 0.035, Adj." ~R^2~ "= 0.06", cex = 0.8)

points(as.numeric(levels(as.factor(hg.abd.SV$year2))), tapply(hg.abd.SV$ln.resuse, hg.abd.SV$year2, median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.abd.SV$year2))), tapply(hg.abd.SV$ln.resuse, hg.abd.SV$year2, mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch = c(1,22,21), pt.bg =
 c("white","blue","red"), cex = 0.8)
```

Appendix F-6. Polychaete Statistical Analysis Code

```
### File created for analysis of polychaete data for Biota Monitoring Report (2017)
### Code edited by LSV 01/17/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob
 $month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month
 == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


###################
### POLYCHAETES ###
###################

levels(factor(penob$PARAM_NAME[penob$LOGGED_BY == "Worm"]))

hg.ply = penob[penob$LOGGED_BY == "Worm" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples labeled as
 mercury, removes field duplicates

hg.ply$ln.resuse = log(hg.ply$resuse) #log Hg results

hg.ply = merge(hg.ply, penob[penob$LOGGED_BY == "Worm" & penob$PARAM_NAME == "Methyl mercury" &! penob$QC_CODE == "FD",], by.x =
 c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY",
 "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge Hg and Me Hg results
summary(hg.ply)
names(hg.ply)[colnames(hg.ply) == "resuse.y"] = "mehg.resuse" #rename columns to keep track of fields
names(hg.ply)[colnames(hg.ply) == "resuse.x"] = "resuse" #rename columns to keep track of fields

hg.ply$ln.mehg.resuse = log(hg.ply$mehg.resuse) #log Me Hg results

hg.ply$locs = as.factor(substring(hg.ply$LOC_NAME,1,5)) #create location identifier
hg.ply$locs[hg.ply$locs == "ESFP_"] = "ES-FP" #standardizing loc names
hg.ply$reach = as.factor(substring(hg.ply$LOC_NAME,1,2))

ref.ply = hg.ply[hg.ply$X_COORD > 930000,] #pull reference data into separate dataset
hg.ply.P = hg.ply #retain all pairings dataset
hg.ply = hg.ply[hg.ply$X_COORD < 930000,] #pull site data into separate dataset
ref.ply = ref.ply[!is.na(ref.ply$resuse) == T,] #remove NAs
hg.ply = hg.ply[!is.na(hg.ply$resuse) == T,] #remove NAs
summary(hg.ply) #103 records
summary(ref.ply) #15 records


hg.ply = hg.ply[hg.ply$locs == "BO-04" | hg.ply$locs == "ES-13" | hg.ply$locs == "ES-FP",] #reduce dataset to match locations sampled
 in 2016

##########################
### POLYCHAETE SUMMARY ###
##########################
# Hg
ply.summ = data.frame(BO04.x = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
```

```
 mean))
ply.summ$BO04.x.se = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$BO04.medn = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], median) #leave NDs in
 for this calc
ply.summ$BO04.N = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], length)
ply.summ = rbind(ply.summ, NA)
rownames(ply.summ)[3] = 2017

ply.summ$MM.x[2:3] = tapply(hg.ply.P$resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x == "J" |
 is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x ==
 "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$MM.x.se[2:3] = tapply(hg.ply.P$resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x == "J" |
 is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x ==
 "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.ply.P$resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") &
 (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-
 MR") & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MM.medn[2:3] = tapply(hg.ply.P$resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], hg.ply.P$year[(hg.ply.P$locs ==
 "MMPOL" | hg.ply.P$locs == "MM-MR")], median) #leave NDs in for this calc
ply.summ$MM.N[2:3] = tapply(hg.ply.P$resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], hg.ply.P$year[(hg.ply.P$locs ==
 "MMPOL" | hg.ply.P$locs == "MM-MR")], length)


ply.summ$OB05.x = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean),NA)
ply.summ$OB05.x.se = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length)),NA)
ply.summ$OB05.medn = c(NA, tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], median), NA)
 #leave NDs in for this calc
ply.summ$OB05.N = c(NA, tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], length), NA)


ply.summ$OB01.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$OB01.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$OB01.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], median) #leave NDs
 in for this calc
ply.summ$OB01.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], length)


ply.summ$BFK.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$BFK.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$BFK.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], median) #leave NDs in
 for this calc
ply.summ$BFK.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], length)


ply.summ$PI.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$PI.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$PI.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], median) #leave NDs in
 for this calc
ply.summ$PI.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], length)


ply.summ$ES02.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$ES02.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$ES02.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], median) #leave NDs
 in for this calc
ply.summ$ES02.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], length)
```

```
ply.summ$VIW.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$VIW.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$VIW.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "VI-W_"], hg.ply.P$year[hg.ply.P$locs == "VI-W_"], median) #leave NDs in
 for this calc
ply.summ$VIW.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "VI-W_"], hg.ply.P$year[hg.ply.P$locs == "VI-W_"], length)



ply.summ$ES13.x = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$ES13.x.se = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$ES13.medn = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], median) #leave NDs in
 for this calc
ply.summ$ES13.N = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], length)


ply.summ$SVE.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$SVE.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$SVE.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], median) #leave NDs in
 for this calc
ply.summ$SVE.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], length)


ply.summ$ES03.x[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$ES03.x.se[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$ES03.medn[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-03"], hg.ply.P$year[hg.ply.P$locs == "ES-03"], median) #leave NDs
 in for this calc
ply.summ$ES03.N[3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-03"], hg.ply.P$year[hg.ply.P$locs == "ES-03"], length)


ply.summ$ESFP.x = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$ESFP.x.se = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$ESFP.medn = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], median) #leave NDs in
 for this calc
ply.summ$ESFP.N = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], length)


ply.summ$FRB.x[2:3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$FRB.x.se[2:3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$FRB.medn[2:3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "FRB-0"], hg.ply.P$year[hg.ply.P$locs == "FRB-0"], median) #leave NDs
 in for this calc
ply.summ$FRB.medn[2] = "ND" #4 out of 5 are U flagged so the median is an ND
ply.summ$FRB.N[2:3] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "FRB-0"], hg.ply.P$year[hg.ply.P$locs == "FRB-0"], length)



# Me Hg

ply.summ$MeHgBO04.x = c(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean), NA)
ply.summ$MeHgBO04.x.se = c(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length)), NA)
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ply.summ$MeHgBO04.medn = c(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], median), NA)
 #leave NDs in for this calc
ply.summ$MeHgBO04.N = c(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], length), NA)


ply.summ$MeHgMM.x[2:3] = tapply(hg.ply.P$mehg.resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x ==
 "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P
 $FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$MeHgMM.x.se[2:3] = tapply(hg.ply.P$mehg.resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x
 == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P
 $FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.ply.P$mehg.resuse[(hg.ply.P$locs == "MMPOL" |
 hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[(hg.ply.P$locs ==
 "MMPOL" | hg.ply.P$locs == "MM-MR") & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgMM.medn[2:3] = tapply(hg.ply.P$mehg.resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], hg.ply.P$year[(hg.ply.P
 $locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], median) #leave NDs in for this calc
ply.summ$MeHgMM.N[2:3] = tapply(hg.ply.P$mehg.resuse[(hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], hg.ply.P$year[(hg.ply.P
 $locs == "MMPOL" | hg.ply.P$locs == "MM-MR")], length)


ply.summ$MeHgOB05.x = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean), NA)
ply.summ$MeHgOB05.x.se = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length)),NA)
ply.summ$MeHgOB05.medn = c(NA, tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], median),
 NA) #leave NDs in for this calc
ply.summ$MeHgOB05.N = c(NA, tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], length),
 NA)


ply.summ$MeHgOB01.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgOB01.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "OB-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgOB01.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], median)
 #leave NDs in for this calc
ply.summ$MeHgOB01.N[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], length)


ply.summ$MeHgBFK.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgBFK.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "BFK_1" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgBFK.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], median)
 #leave NDs in for this calc
ply.summ$MeHgBFK.N[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], length)


ply.summ$MeHgPI.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgPI.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "PI-01" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgPI.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], median)
 #leave NDs in for this calc
ply.summ$MeHgPI.N[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], length)


ply.summ$MeHgES02.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgES02.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "ES-02" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgES02.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], median)
 #leave NDs in for this calc
ply.summ$MeHgES02.N[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], length)
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ply.summ$MeHgVIW.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgVIW.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "VI-W_" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgVIW.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "VI-W_"], hg.ply.P$year[hg.ply.P$locs == "VI-W_"], median)
 #leave NDs in for this calc
ply.summ$MeHgVIW.N[3] = NA #VI-W polys not analyzed for Me Hg in 2017



ply.summ$MeHgES13.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgES13.x.se = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgES13.medn = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], median) #leave
 NDs in for this calc
ply.summ$MeHgES13.N = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], length)
ply.summ$MeHgES13.N[3] = NA #ES-13 polys not analyzed for Me Hg in 2017


ply.summ$MeHgSVE.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgSVE.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "SVE-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgSVE.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], median)
 #leave NDs in for this calc
ply.summ$MeHgSVE.N[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], length)


ply.summ$MeHgES03.x[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgES03.x.se[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "ES-03" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgES03.medn[3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-03"], hg.ply.P$year[hg.ply.P$locs == "ES-03"], median)
 #leave NDs in for this calc
ply.summ$MeHgES03.N[3] = NA #ES-03 polys not analyzed for Me Hg in 2017


ply.summ$MeHgESFP.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgESFP.x.se = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgESFP.medn = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], median) #leave
 NDs in for this calc
ply.summ$MeHgESFP.N = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], length)
ply.summ$MeHgESFP.N[3] = NA #ES-FP polys not analyzed for Me Hg in 2017


ply.summ$MeHgFRB.x[2:3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgFRB.x.se[2:3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MeHgFRB.medn[2:3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0"], hg.ply.P$year[hg.ply.P$locs == "FRB-0"], median)
 #leave NDs in for this calc
ply.summ$MeHgFRB.medn[2] = "ND" #4 out of 5 are U flagged so the median is an ND
ply.summ$MeHgFRB.N[2:3] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0"], hg.ply.P$year[hg.ply.P$locs == "FRB-0"], length)
ply.summ$MeHgFRB.N[3] = NA #FRB polys not analyzed for Me Hg in 2017


### Additional reference locs: EB and OV-04
```

```
ply.summ = rbind(NA,ply.summ)
rownames(ply.summ)[1] = 2006

ply.summ$EB.x = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean), rep(NA,3))
ply.summ$EB.x.se = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], hg.ply.P$year[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], sd) /
 sqrt(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P
 $year[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length)), rep(NA,3))
ply.summ$EB.medn = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB"], hg.ply.P$year[hg.ply.P$reach == "EB"], median), rep(NA,3)) #leave
 NDs in for this calc
ply.summ$EB.N = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB"], hg.ply.P$year[hg.ply.P$reach == "EB"], length), rep(NA,3))


ply.summ$OV04.x = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean), NA, NA)
ply.summ$OV04.x.se = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length)), NA, NA)
ply.summ$OV04.medn = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OV-04"], hg.ply.P$year[hg.ply.P$locs == "OV-04"], median), NA, NA)
 #leave NDs in for this calc
ply.summ$OV04.N = c(NA,tapply(hg.ply.P$resuse[hg.ply.P$locs == "OV-04"], hg.ply.P$year[hg.ply.P$locs == "OV-04"], length), NA, NA)


ply.summ$MeHgEB.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y)
 == T)], hg.ply.P$year[hg.ply.P$reach == "EB" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) == T)], mean)
ply.summ$MeHgEB.x.se = "NA"
ply.summ$MeHgEB.medn = "NA"
ply.summ$MeHgEB.N = "NA"


ply.summ$MeHgOV04.x = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) == T)],
 mean), NA, NA)
ply.summ$MeHgOV04.x.se = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) == T)],
 sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) == T)],
 hg.ply.P$year[hg.ply.P$locs == "OV-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) == T)], length)), NA, NA)
ply.summ$MeHgOV04.medn = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OV-04"], hg.ply.P$year[hg.ply.P$locs == "OV-04"], median),
 NA, NA) #leave NDs in for this calc
ply.summ$MeHgOV04.N = c(NA,tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OV-04"], hg.ply.P$year[hg.ply.P$locs == "OV-04"], length), NA,
 NA)



ply.summ$ES15.x[c(1:2,4)] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$ES15.x.se[c(1:2,4)] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 sd) / sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$ES15.medn[c(1:2,4)] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"], median)
 #leave NDs in for this calc
ply.summ$ES15.N[c(1:2,4)] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"], length)



ply.summ$MeHgES15.x[c(1:2,4)] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)],
 mean)
ply.summ$MeHgES15.x.se[c(1:2,4)] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" |
 is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" |
 is.na(hg.ply.P$FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-15" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], length))
ply.summ$MeHgES15.medn[c(1:2,4)] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"],
 median) #leave NDs in for this calc
ply.summ$MeHgES15.N[c(1:2,4)] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"], length)
ply.summ$MeHgES15.N[4] = NA

write.csv(ply.summ, "Polychaete summary.csv")


##########################
### POLYCHAETE FIGURES ###
##########################
```

```
#4-37
par(mfrow = c(3,5), mar = c(4,1,2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))

plot(0, 0, ylab = "", xlab = "", xlim = range(ref.ply$year), las = 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.04 * max(hg.ply.P
 $ln.resuse)), yaxt = "n", xaxt = "n", bty = "n")

legend("topleft", title = expression(bold("Site Legend")), legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"),
 col = c(1,"blue","red"), pch = c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.6, bty = "n")
legend("left", title = expression(bold("Reference Legend")), legend = c("East Branch -\nPenobscot River", "Frenchmans Bay","OV-04"),
 pch = c(15,17:18), col = c( 3,1,4), cex = 0.6, bty = "n")

axis(4,at = 2, labels = "Ln Hg (ng/g)", las = 3, tick = F)


par(mar = c(4,2,2,1))
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BO-04",], xlab = "", ylab = "", main = "BO-04", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BO-04"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "BO-04"],
 hg.ply.P$year[hg.ply.P$locs == "BO-04"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BO-04"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "BO-04"],
 hg.ply.P$year[hg.ply.P$locs == "BO-04"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-05",], xlab = "", ylab = "", main = "OB-05", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-05"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "OB-05"],
 hg.ply.P$year[hg.ply.P$locs == "OB-05"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-05"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "OB-05"],
 hg.ply.P$year[hg.ply.P$locs == "OB-05"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-01",], xlab = "", ylab = "", main = "OB-01", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-01"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "OB-01"],
 hg.ply.P$year[hg.ply.P$locs == "OB-01"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-01"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "OB-01"],
 hg.ply.P$year[hg.ply.P$locs == "OB-01"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR",], xlab = "", ylab = "", main = "Mendall
 Marsh", ylim = c(-1, 1.04 * max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis =
 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"]))), tapply(hg.ply.P
 $ln.resuse[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"], hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"],
 median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"]))), tapply(hg.ply.P
 $ln.resuse[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"], hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"],
 mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,3,2,0))
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BFK_1",], xlab = "", ylab = "", main = "BFK_1", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)
axis(2, at = 2, labels = "Ln Hg (ng/g)", tick = F, las = 3, line = 0.75)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BFK_1"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "BFK_1"],
 hg.ply.P$year[hg.ply.P$locs == "BFK_1"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BFK_1"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "BFK_1"],
 hg.ply.P$year[hg.ply.P$locs == "BFK_1"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,2,2,1))
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-02",], xlab = "", ylab = "", main = "ES-02", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-02"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-02"],
 hg.ply.P$year[hg.ply.P$locs == "ES-02"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-02"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-02"],
 hg.ply.P$year[hg.ply.P$locs == "ES-02"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "PI-01",], xlab = "", ylab = "", main = "PI-01", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "PI-01"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "PI-01"],
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 hg.ply.P$year[hg.ply.P$locs == "PI-01"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "PI-01"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "PI-01"],
 hg.ply.P$year[hg.ply.P$locs == "PI-01"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-15",], xlab = "", ylab = "", main = "ES-15", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-15"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-15"],
 hg.ply.P$year[hg.ply.P$locs == "ES-15"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-15"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-15"],
 hg.ply.P$year[hg.ply.P$locs == "ES-15"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "VI-W_",], xlab = "", ylab = "", main = "VI-W", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "VI-W_"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "VI-W_"],
 hg.ply.P$year[hg.ply.P$locs == "VI-W_"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "VI-W_"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "VI-W_"],
 hg.ply.P$year[hg.ply.P$locs == "VI-W_"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,3,2,0), mgp = c(2,0.5,0))
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-13",], xlab = "Year", ylab = "", main = "ES-13", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)
axis(2, at = 2, labels = "Ln Hg (ng/g)", tick = F, las = 3, line = 0.75)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-13"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-13"],
 hg.ply.P$year[hg.ply.P$locs == "ES-13"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-13"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-13"],
 hg.ply.P$year[hg.ply.P$locs == "ES-13"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,2,2,1), mgp = c(2,0.5,0))
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "SVE-0",], xlab = "Year", ylab = "", main = "SVE-02INT", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "SVE-0"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "SVE-0"],
 hg.ply.P$year[hg.ply.P$locs == "SVE-0"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "SVE-0"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "SVE-0"],
 hg.ply.P$year[hg.ply.P$locs == "SVE-0"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-FP",], xlab = "Year", ylab = "", main = "ES-FP", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-FP"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-FP"],
 hg.ply.P$year[hg.ply.P$locs == "ES-FP"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-FP"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-FP"],
 hg.ply.P$year[hg.ply.P$locs == "ES-FP"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-03",], xlab = "Year", ylab = "", main = "ES-03", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.resuse)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-03"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-03"],
 hg.ply.P$year[hg.ply.P$locs == "ES-03"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-03"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs == "ES-03"],
 hg.ply.P$year[hg.ply.P$locs == "ES-03"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.resuse ~ year, data = ref.ply[ref.ply$locs == "FRB-0",], pch = 17, ylab = "", xlab = "Year", xlim = range(ref.ply$year), las =
 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.04 * max(hg.ply.P$ln.resuse)), main = "Reference", cex.axis = 0.9)
points(ln.resuse ~ year, data = ref.ply[ref.ply$locs == "OV-04",], col = 4, pch = 18)
points(ln.resuse ~ year, data = ref.ply[ref.ply$reach == "EB",], col = 3, pch = 15)

mtext(expression(bold("Figure 4-37\n"),bold("Polychaete Ln Mercury Concentrations")), outer = T)


#4-38
par(mfrow = c(3,5), mar = c(4,1,2,2), mgp = c(3,0.5,0), oma = c(0,0,3,0))
plot(0, 0, ylab = "", xlab = "", xlim = range(ref.ply$year), las = 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.04 * max(hg.ply.P
 $ln.mehg.resuse, na.rm = T)), yaxt = "n", xaxt = "n", bty = "n")

legend("topleft", title = expression(bold("Site Legend")), legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"),
 col = c(1,"blue","red"), pch = c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.6, bty = "n")
legend("left", title = expression(bold("Reference Legend")), legend = c("Frenchmans Bay","OV-04"), pch = 17:18, col = c(1,4), cex =
 0.6, bty = "n")
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legend(2005, 1, legend = "Non-detect samples \n(detection limit = 0.5 ng/g) \ncollected in 2016 are \nnot shown.", cex = 0.6,bty = "n")

axis(4,at = 2, labels = "Ln MeHg (ng/g)", las = 3, tick = F)


par(mar = c(4,2,2,1))
plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BO-04",], xlab = "", ylab = "", main = "BO-04", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BO-04"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BO-04"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "BO-04"], hg.ply.P$year[hg.ply.P$locs == "BO-04"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-05",], xlab = "", ylab = "", main = "OB-05", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-05"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-05"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-01",], xlab = "", ylab = "", main = "OB-01", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-01"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "OB-01"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "OB-01"], hg.ply.P$year[hg.ply.P$locs == "OB-01"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR",], xlab = "", ylab = "", main =
 "Mendall Marsh", ylim = c(-1, 1.04 * max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las =
 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"]))), tapply(hg.ply.P
 $ln.mehg.resuse[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"], hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-
 MR"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"]))), tapply(hg.ply.P
 $ln.mehg.resuse[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-MR"], hg.ply.P$year[hg.ply.P$locs == "MMPOL" | hg.ply.P$locs == "MM-
 MR"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,3,2,0))
plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BFK_1",], xlab = "", ylab = "", main = "BFK_1", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)
axis(2, at = 2, labels = "Ln MeHg (ng/g)", tick = F, las = 3, line = 0.75)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BFK_1"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "BFK_1"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "BFK_1"], hg.ply.P$year[hg.ply.P$locs == "BFK_1"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,2,2,1))
plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-02",], xlab = "", ylab = "", main = "ES-02", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-02"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-02"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-02"], hg.ply.P$year[hg.ply.P$locs == "ES-02"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "PI-01",], xlab = "", ylab = "", main = "PI-01", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "PI-01"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "PI-01"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "PI-01"], hg.ply.P$year[hg.ply.P$locs == "PI-01"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-15",], xlab = "", ylab = "", main = "ES-15", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)
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points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-15"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-15"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-15"], hg.ply.P$year[hg.ply.P$locs == "ES-15"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-13",], xlab = "", ylab = "", main = "ES-13", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-13"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-13"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "ES-13"], hg.ply.P$year[hg.ply.P$locs == "ES-13"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,3,2,0), mgp = c(2,0.5,0))

plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "SVE-0",], xlab = "Year", ylab = "", main = "SVE-02INT", ylim = c(-1, 1.04
 * max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)
axis(2, at = 2, labels = "Ln MeHg (ng/g)", tick = F, las = 3, line = 0.75)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "SVE-0"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "SVE-0"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "SVE-0"], hg.ply.P$year[hg.ply.P$locs == "SVE-0"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


par(mar = c(4,2,2,1), mgp = c(2,0.5,0))
plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-FP",], xlab = "Year", ylab = "", main = "ES-FP", ylim = c(-1, 1.04 *
 max(hg.ply.P$ln.mehg.resuse, na.rm = T)), xlim = c(2006, max(hg.ply.P$year)), yaxs = "i", las = 1, tck = 0.015, cex.axis = 0.9)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-FP"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs == "ES-
 FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "ES-FP"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs == "ES-
 FP"], hg.ply.P$year[hg.ply.P$locs == "ES-FP"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")


plot(ln.mehg.resuse ~ year, data = ref.ply[ref.ply$locs == "FRB-0",], pch = 17, ylab = "", xlab = "Year", xlim = range(ref.ply$year),
 las = 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.04 * max(hg.ply.P$ln.mehg.resuse, na.rm = T)), main = "Reference", cex.axis = 0.9)
points(ln.mehg.resuse ~ year, data = ref.ply[ref.ply$locs == "OV-04",], col = 4, pch = 18)
points(ln.mehg.resuse ~ year, data = ref.ply[ref.ply$reach == "EB",], col = 3, pch = 15)

mtext(expression(bold("Figure 4-38\n"),bold("Polychaete Ln Methyl Mercury Concentrations")), outer = T)
```

Appendix F-7. Blue Mussel Statistical Analysis Code

```r
### File created for analysis of blue mussel data for Biota Monitoring Report (2017)
### Code edited by LSV 01/17/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob
 $month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month
 == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


###################
### BLUE MUSSEL ###
###################

hg.mus = penob[penob$MED_T == "Blue Mussel" & (penob$PARAM_NAME == "Mercury" | penob$PARAM_NAME == "Mercury - Wet Weight") &! penob
 $QC_CODE == "FD" ,] #selects ww over dw samples from 2014, and samples designated as blue mussel mercury results, removes field
 duplicates

hg.mus = merge(hg.mus, length[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE",
 "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T)
 #merge mussel tissue with length for each mussel
names(hg.mus)[colnames(hg.mus) == "resuse.y"] = "length" #rename columns for ease of keeping track of data
summary(hg.mus) #1298 records - 53 NAs

hg.mus = merge(hg.mus,weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD",
 "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x
 = T) #merge mussel tissue with length for each mussel
names(hg.mus)[colnames(hg.mus) == "resuse"] = "weight" #rename columns for ease of keeping track of data
names(hg.mus)[colnames(hg.mus) == "resuse.x"] = "resuse" #rename columns for ease of keeping track of data
summary(hg.mus) #1298 records, 787 NAs for weight

hg.mus$ln.resuse = log(hg.mus$resuse) #log mercury results
hg.mus$l.adj_resuse = hg.mus$resuse / hg.mus$length * median(hg.mus$length, na.rm = T) #length adjust Hg results
hg.mus$ln.l.adj_resuse = log(hg.mus$resuse) / hg.mus$length * median(hg.mus$length, na.rm = T) #length adjust logged Hg results

hg.mus$w.adj_resuse = hg.mus$resuse / hg.mus$weight * median(hg.mus$weight, na.rm = T) #weight adjust Hg results

hg.mus$locs = as.factor(substring(hg.mus$LOC_NAME,1,5)) #create location identifiers
hg.mus$reach = as.factor(substring(hg.mus$LOC_NAME,1,2))

ref.mus = hg.mus[(hg.mus$X_COORD > 947000 | hg.mus$X_COORD < 835000) &! is.na(hg.mus$X_COORD) == T,] #pull reference mussels into
 separate datasets
ref.mus$which.ref = "St.George"
ref.mus$which.ref[ref.mus$X_COORD > 950000] = "narragaugus"
ref.mus$which.ref[ref.mus$reach == "FR"] = "Frenchman Bay"

hg.mus = hg.mus[hg.mus$X_COORD < 947000 & hg.mus$X_COORD > 835000 &! is.na(hg.mus$X_COORD) == T,] #reduce dataset to site mussels
summary(hg.mus) #1105 records
summary(ref.mus) #180 records


hg.mus.P = hg.mus #retaining all paired data
```

```
# Reducing overall dataset to locations that have been consistently sampled over years and also in 2016 & 2017
tapply(hg.mus$resuse, list(factor(hg.mus$locs), hg.mus$year), length)

hg.mus = hg.mus[hg.mus$locs == "ES-13" | hg.mus$locs == "ES-03" | hg.mus$locs == "ES-15" | hg.mus$locs == "ES-FP",]


###########################
### Blue Mussel Summary ###
###########################

mus.summ = data.frame(ES.15_x = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"], mean))
mus.summ$ES.15_x_se = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"], sd) /
 sqrt(tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"], length))
mus.summ$ES.15_medn = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"], median)
mus.summ$ES.15_N = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"], length)
mus.summ$ES.15_perc[1] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15" & hg.mus.P$resuse > 200], hg.mus.P$year[hg.mus.P$locs ==
 "ES-15" & hg.mus.P$resuse > 200], length) / tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-15"], hg.mus.P$year[hg.mus.P$locs == "ES-15"],
 length)[2]
mus.summ$ES.15_perc[2:7] = 0

mus.summ$ES.03_x[c(1:4,6:7)] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], mean)
mus.summ$ES.03_x_se[c(1:4,6:7)] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], sd) /
 sqrt(tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], length))
mus.summ$ES.03_medn[c(1:4,6:7)] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], median)
mus.summ$ES.03_N[c(1:4,6:7)] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], length)
mus.summ$ES.03_perc[7] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03" & hg.mus.P$resuse > 200], hg.mus.P$year[hg.mus.P$locs ==
 "ES-03" & hg.mus.P$resuse > 200], length) / tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"],
 length)[6]
mus.summ$ES.03_perc[c(1:4,6)] = 0

mus.summ$ES.13_x = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"], mean)
mus.summ$ES.13_x_se = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"], sd) /
 sqrt(tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"], length))
mus.summ$ES.13_medn = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"], median)
mus.summ$ES.13_N = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"], length)
mus.summ$ES.13_perc[1] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13" & hg.mus.P$resuse > 200], hg.mus.P$year[hg.mus.P$locs ==
 "ES-13" & hg.mus.P$resuse > 200], length) / tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-13"], hg.mus.P$year[hg.mus.P$locs == "ES-13"],
 length)[1]
mus.summ$ES.13_perc[2:7] = 0

mus.summ$ES.FP_x[3:7] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], mean)
mus.summ$ES.FP_x_se[3:7] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], sd) /
 sqrt(tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], length))
mus.summ$ES.FP_medn[3:7] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], median)
mus.summ$ES.FP_N[3:7] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], length)
mus.summ$ES.FP_perc[3:7] = 0

mus.summ$NG_x[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], mean), NA)
mus.summ$NG_x_se[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], sd) /
 sqrt(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], length)), NA)
mus.summ$NG_medn[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], median), NA)
mus.summ$NG_N[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], length), NA)
mus.summ$NG_perc[c(3,7)] = c(0, NA)

mus.summ$SG_x[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], mean), NA)
mus.summ$SG_x_se[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], sd) /
 sqrt(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], length)), NA)
mus.summ$SG_medn[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], median), NA)
mus.summ$SG_N[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], length), NA)
mus.summ$SG_perc[c(3,7)] = c(0, NA)

mus.summ$SC_x[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], mean), NA)
mus.summ$SC_x_se[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], sd) /
 sqrt(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], length)), NA)
mus.summ$SC_medn[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], median), NA)
mus.summ$SC_N[c(3,7)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], length), NA)
mus.summ$SC_perc[c(3,7)] = c(0, NA)

mus.summ$FR_x[7] = tapply(ref.mus$resuse[ref.mus$reach == "FR"], ref.mus$year[ref.mus$reach == "FR"], mean)
mus.summ$FR_x_se[7] = tapply(ref.mus$resuse[ref.mus$reach == "FR"], ref.mus$year[ref.mus$reach == "FR"], sd) / sqrt(tapply(ref.mus
 $resuse[ref.mus$reach == "FR"], ref.mus$year[ref.mus$reach == "FR"], length))
mus.summ$FR_medn[7] = tapply(ref.mus$resuse[ref.mus$reach == "FR"], ref.mus$year[ref.mus$reach == "FR"], median)
mus.summ$FR_N[7] = tapply(ref.mus$resuse[ref.mus$reach == "FR"], ref.mus$year[ref.mus$reach == "FR"], length)
mus.summ$FR_perc[7] = 0

write.csv(mus.summ,"Blue Mussel summary.csv")
```

```
############################
### Reference Evaluation ###
############################

bkg.mus = read.delim("MusselWatch_EastCoast_Trace_Elements_Tissue.txt", header = T, sep = "\t")
summary(bkg.mus)

bkg.mus.percdwt = bkg.mus[(bkg.mus$General_Location == "Cape Arundel" | bkg.mus$General_Location == "Merriconeag Sound") & bkg.mus
 $Parameter == "Sample percent dry weight" & bkg.mus$Fiscal_Year >= 2006 & bkg.mus$Method == "ICP-MS",]


bkg.mus.hg = bkg.mus[(bkg.mus$General_Location == "Cape Arundel" | bkg.mus$General_Location == "Merriconeag Sound") & bkg.mus$Parameter
 == "Mercury" & bkg.mus$Fiscal_Year >= 2006,]

bkg.mus.hg = merge(bkg.mus.hg, bkg.mus.percdwt, by.x = c("General_Location", "Matrix", "Fiscal_Year", "Collection_Date", "study",
 "NST_Site", "NST_Sample_ID", "Scientific_Name", "Specific_Location"), by.y  = c("General_Location", "Matrix", "Fiscal_Year",
 "Collection_Date", "study", "NST_Site", "NST_Sample_ID", "Scientific_Name", "Specific_Location"), all.x = T)
names(bkg.mus.hg)[colnames(bkg.mus.hg) == "Result.x"] = "Hg"
names(bkg.mus.hg)[colnames(bkg.mus.hg) == "Result.y"] = "perc.dw"

summary(bkg.mus.hg)
bkg.mus.hg$resuse = (bkg.mus.hg$Hg * (bkg.mus.hg$perc.dw/100)) * 1000 #(ug/g * %) * 1000 ng/ug
bkg.mus.hg$ln.resuse = log(bkg.mus.hg$resuse)


##########################
### BLUE MUSSEL TRENDS ###
##########################

summary(lm(ln.resuse ~ year, data = hg.mus))
summary(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-03",]))
summary(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-15",]))
summary(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-13",]))
summary(lm(ln.resuse ~ year, data = hg.mus.P[hg.mus.P$locs == "ES-FP",]))


#4-39
plot(ln.resuse ~ year, data = ref.mus[ref.mus$which.ref == "St.George",], pch = 17, ylab = "Ln Hg (ng/g)", xlab = "Year", xlim =
 range(hg.mus$year), las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.mus$ln.resuse)), main = "Figure 4-39\nBlue Mussel -
 Reference Locations\nLn Mercury Concentrations")
points(ln.resuse ~ year, data = ref.mus[ref.mus$which.ref == "narragaugus",], col = 4, pch = 18)
points(ln.resuse ~ Fiscal_Year, bkg.mus.hg[bkg.mus.hg$General_Location == "Merriconeag Sound",], col = 3, pch = 15)
points(ln.resuse ~ Fiscal_Year, bkg.mus.hg[bkg.mus.hg$General_Location == "Cape Arundel",], col = "orange", pch = 19)
points(ln.resuse ~ year, data = ref.mus[ref.mus$which.ref == "Frenchman Bay",], col = 5, pch = 16)
legend("topright", legend = c("Cape Arundel", "Merriconeag Sound", "St. George River", "Narragaugus River", "Frenchman Bay"), pch =
 c(19, 15, 17, 18, 16), col = c("orange", 3, 1, 4, 5), cex = 0.8)


#4-40
plot(hg.mus$ln.resuse ~ hg.mus$year, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-40\nBlue Mussel - Whole River\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.mus$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.mus))

text(max(hg.mus$year) - 1.5, max(hg.mus$ln.resuse)*0.185, "ln(y) = -0.01020x + 24.819", cex = 0.8)
text(max(hg.mus$year) - 1.5, max(hg.mus$ln.resuse)*0.15, "p = 0.005, Adj." ~R^2~ "= 0.01", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mus$year))), tapply(hg.mus$ln.resuse, hg.mus$year, median), pch = 21, col = "red", cex = 1.3, bg
 = "red")
points(as.numeric(levels(as.factor(hg.mus$year))), tapply(hg.mus$ln.resuse, hg.mus$year, mean), pch = 22, col = "blue", cex = 1.3, bg =
 "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Blue Mussel sampled at ES-13, ES-15, ES-03, and ES-FP", cex.sub = 0.7)


#4-41
plot(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-15",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-41\nBlue Mussel -
 ES-15\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-15",]))

text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.18, "ln(y) = -0.02279x + 50.055", cex = 0.8)
text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.08", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-15"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-15"], hg.mus
 $year[hg.mus$locs == "ES-15"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-15"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-15"], hg.mus
 $year[hg.mus$locs == "ES-15"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")
```

```
legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-42
plot(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-13",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-42\nBlue Mussel -
 ES-13\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-13",]))

text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.18, "ln(y) = -0.03582x + 76.456", cex = 0.8)
text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.15", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-13"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-13"], hg.mus
 $year[hg.mus$locs == "ES-13"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-13"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-13"], hg.mus
 $year[hg.mus$locs == "ES-13"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-43
plot(ln.resuse ~ year, hg.mus[hg.mus$locs == "ES-03",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-43\nBlue Mussel -
 ES-03\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-03",]))

text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.185, "ln(y) = 0.01488x - 25.614", cex = 0.8)
text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.15, "p = 0.026, Adj." ~R^2~ "= 0.02", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-03"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-03"], hg.mus
 $year[hg.mus$locs == "ES-03"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mus$year[hg.mus$locs == "ES-03"]))), tapply(hg.mus$ln.resuse[hg.mus$locs == "ES-03"], hg.mus
 $year[hg.mus$locs == "ES-03"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch =
 c(1,22,21), pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-44
plot(ln.resuse ~ year, data = hg.mus.P[hg.mus.P$locs == "ES-FP",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-44\nBlue
 Mussel - ES-FP\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$ln.resuse)), las = 1, tck = 0.015, xlim = range(hg.mus$year),
 yaxs = "i")
clip(2008, 2018, 0, 1000)
abline(lm(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-FP",]))
clip(0, 10000, 0, 1000)

text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.18, "ln(y) = 0.04540x - 87.265", cex = 0.8)
text(max(hg.mus$year) - 1.5, max(hg.mus.P$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.23", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mus.P$year[hg.mus.P$locs == "ES-FP"]))), tapply(hg.mus.P$ln.resuse[hg.mus.P$locs == "ES-FP"],
 hg.mus.P$year[hg.mus.P$locs == "ES-FP"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mus.P$year[hg.mus.P$locs == "ES-FP"]))), tapply(hg.mus.P$ln.resuse[hg.mus.P$locs == "ES-FP"],
 hg.mus.P$year[hg.mus.P$locs == "ES-FP"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-8. Lobster Statistical Analysis Code

```r
### File created for analysis of lobster data for Biota Monitoring Report (2017)
### Code edited by LSV 01/17/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.DBF")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
summary(length)
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]
summary(weight)

###############
### LOBSTER ###
###############

hg.lob = penob[penob$MED_T == "Lobster" &! is.na(penob$MED_T) == T & (penob$PARAM_NAME == "Mercury" | penob$PARAM_NAME == "Mercury - Wet Weight") &! penob$QC_CODE == "FD" & penob$MONITOR_TY == "Tail",]  #selects ww over dw samples from 2014, plus samples designated as hg.lobsters, not NAs, not field dups, and all samples labeled as Mercury, tail tissue results

hg.lob$hold.lob[substring(hg.lob$AOC_NAME,1,1) == "H"] = 2
hg.lob$hold.lob[hg.lob$AOC_NAME == "HB"] = NA


hg.lob = hg.lob[is.na(hg.lob$hold.lob) == T,] #remove lobsters from the hold study
hg.lob = hg.lob[is.na(hg.lob$resuse) == F,] #remove any NAs in the results column

hg.lob = hg.lob[!(hg.lob$year == 2009 & is.na(hg.lob$X_COORD) == T),] #remove lobster sample with no coordinate or location information

hg.lob$AOC_NAME = factor(hg.lob$AOC_NAME)


### Lobster Areas ###
hg.lob$circle[hg.lob$AOC_NAME == "OL"] = 9
hg.lob$circle[hg.lob$AOC_NAME == "SV"] = 8
hg.lob$circle[hg.lob$AOC_NAME == "FP"] = 2
hg.lob$circle[hg.lob$AOC_NAME == "TP"] = 3
hg.lob$circle[hg.lob$AOC_NAME == "CJ"] = 4
hg.lob$circle[hg.lob$AOC_NAME == "SI"] = 5
hg.lob$circle[hg.lob$AOC_NAME == "KC"] = 6
hg.lob$circle[hg.lob$AOC_NAME == "PC"] = 7
hg.lob$circle[hg.lob$AOC_NAME == "HB"] = 7
hg.lob$circle[hg.lob$AOC_NAME == "MP"] = 5
hg.lob$circle[hg.lob$AOC_NAME == "SI" & hg.lob$X_COORD > 890000 & hg.lob$Y_COORD > 270000 & is.na(hg.lob$circle) == F] = 4
hg.lob$circle[hg.lob$AOC_NAME == "CJ" & hg.lob$X_COORD > 900000 & is.na(hg.lob$circle) == F] = 2
hg.lob$circle[hg.lob$AOC_NAME == "CJ" & hg.lob$X_COORD > 900000 & hg.lob$Y_COORD < 270000 & is.na(hg.lob$circle) == F] = 3
hg.lob$circle[hg.lob$AOC_NAME == "TP" & hg.lob$Y_COORD < 266000 & is.na(hg.lob$circle) == F] = 7
hg.lob$circle[hg.lob$AOC_NAME == "FB"] = 1

hg.lob$circle.name[hg.lob$circle == 9] = "Odom Ledge"
hg.lob$circle.name[hg.lob$circle == 8] = "South Verona"
hg.lob$circle.name[hg.lob$circle == 2] = "Fort Point"
hg.lob$circle.name[hg.lob$circle == 3] = "Turner Point"
```

```
hg.lob$circle.name[hg.lob$circle == 4] = "Cape Jellison"
hg.lob$circle.name[hg.lob$circle == 5] = "Sears Island/Marshall Point"
hg.lob$circle.name[hg.lob$circle == 6] = "Kelly's Cove"
hg.lob$circle.name[hg.lob$circle == 7] = "Harborside"
hg.lob$circle.name[hg.lob$circle == 1] = "Frenchman Bay"



#######################
### LOBSTER SUMMARY ###
#######################
lob.summ = data.frame(medn = tapply(hg.lob$resuse, list(hg.lob$year, hg.lob$circle.name), median, na.rm = T)) # Calculate medians per year
lob.summ$x = tapply(hg.lob$resuse, list(hg.lob$year, hg.lob$circle.name), mean, na.rm = T) # Calculate means per year
lob.summ$x_se = tapply(hg.lob$resuse, list(hg.lob$year, hg.lob$circle.name), sd, na.rm = T) / sqrt(tapply(hg.lob$resuse, list(hg.lob$year, hg.lob$circle.name), length))
lob.summ$N = tapply(hg.lob$resuse, list(hg.lob$year, hg.lob$circle.name), length)
lob.summ$perc = tapply(hg.lob$resuse[hg.lob$resuse > 200], list(hg.lob$year[hg.lob$resuse > 200], hg.lob$circle.name[hg.lob$resuse > 200]), length) / tapply(hg.lob$resuse[!hg.lob$circle.name == "Frenchman Bay"], list(hg.lob$year[!hg.lob$circle.name == "Frenchman Bay"], hg.lob$circle.name[!hg.lob$circle.name == "Frenchman Bay"]), length) * 100 # Calculate percent of lobsters above 200 ng/g per year
lob.summ$perc.Frenchman_Bay[9] = 0

write.csv(lob.summ, "Lobster summary.csv")



#########################################
### Length Adjusted Calc and Analysis ###
#########################################

length$MONITOR_TY[length$MED_T == "Lobster" & is.na(length$MONITOR_TY) == T] = "Fur" #way to get rid of NAs for not Tomalley on next line - have to use tissue type in field or create new factors
lob.length = length[length$MED_T == "Lobster" &! length$MONITOR_TY == "Tomalley",]
lob.length$ID2[lob.length$year == 2006] = substring(lob.length$ID[lob.length$year == 2006], 1, 21) #getting IDs into pairable state
lob.length$ID2[lob.length$year == 2008] = substring(lob.length$ID[lob.length$year == 2008], 1, 20)
lob.length$ID2[lob.length$year == 2009] = substring(lob.length$ID[lob.length$year == 2009], 1, 20)
lob.length$ID2[lob.length$year == 2009 & substring(lob.length$ID2, 20, 20) == 0] = substring(lob.length$ID[lob.length$year == 2009 & substring(lob.length$ID2, 20, 20) == 0], 1, 21)

lob.length$ID2[lob.length$year == 2010] = substring(lob.length$ID[lob.length$year == 2010], 1, 20)
lob.length$ID2[lob.length$year == 2012] = substring(lob.length$ID[lob.length$year == 2012], 1, 20)
lob.length$ID2[!lob.length$year < 2014] = as.character(lob.length$ID[!lob.length$year < 2014])
lob.length$ID = lob.length$ID2
lob.length$ID = factor(lob.length$ID)
summary(lob.length) #1430 records


hg.lob.l = hg.lob
hg.lob.l$ID2[hg.lob.l$year == 2006] = substring(hg.lob.l$ID[hg.lob.l$year == 2006], 1, 21) #getting IDs into pairable state
hg.lob.l$ID2[hg.lob.l$year == 2008] = substring(hg.lob.l$ID[hg.lob.l$year == 2008], 1, 20)
hg.lob.l$ID2[hg.lob.l$year == 2009] = substring(hg.lob.l$ID[hg.lob.l$year == 2009], 1, 20)
hg.lob.l$ID2[hg.lob.l$year == 2009 & substring(hg.lob.l$ID2, 20, 20) == 0] = substring(hg.lob.l$ID[hg.lob.l$year == 2009 & substring(hg.lob.l$ID2, 20, 20) == 0], 1, 21)

hg.lob.l$ID2[hg.lob.l$year == 2010] = substring(hg.lob.l$ID[hg.lob.l$year == 2010], 1, 20)
hg.lob.l$ID2[hg.lob.l$year == 2012] = substring(hg.lob.l$ID[hg.lob.l$year == 2012], 1, 20)
hg.lob.l$ID2[hg.lob.l$year == 2014] = substring(hg.lob.l$ID[hg.lob.l$year == 2014], 1, 17)
hg.lob.l$ID2[!hg.lob.l$year <= 2014] = as.character(hg.lob.l$ID[!hg.lob.l$year <= 2014])
hg.lob.l$ID = hg.lob.l$ID2
hg.lob.l$ID = factor(hg.lob.l$ID)
summary(hg.lob.l) #1205 records


hg.lob.l = merge(hg.lob.l, lob.length[, c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge tail tissue and length for each lobster
summary(hg.lob.l) #1205 records
names(hg.lob.l)[colnames(hg.lob.l) == "resuse.y"] = "length" #rename columns for ease of calling data
names(hg.lob.l)[colnames(hg.lob.l) == "resuse.x"] = "resuse" #rename columns for ease of calling data
summary(hg.lob.l) #expect to have 3 NAs in length - 2 in 2014 and 1 in 2009

hg.lob.l$ln.resuse = log(hg.lob.l$resuse) #log Hg results
hg.lob.l$l.adj.resuse = hg.lob.l$resuse / hg.lob.l$length * median(hg.lob.l$length, na.rm = T) #length adjusted Hg results
hg.lob.l$l.adj.lnresuse = log(hg.lob.l$resuse) / hg.lob.l$length * median(hg.lob.l$length, na.rm = T) #length adjusted logged Hg results
```

```
######################
### LOBSTER TRENDS ###
######################

hg.lob.l.16locs = hg.lob.l[hg.lob.l$circle.name == "Odom Ledge" | hg.lob.l$circle.name == "South Verona" | hg.lob.l$circle.name ==
 "Cape Jellison" | hg.lob.l$circle.name == "Turner Point" | hg.lob.l$circle.name == "Harborside",] #pulling data to match 2016
 locations

max.lob.ln = max(hg.lob.l$l.adj.lnresuse, na.rm = T)

summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l.16locs[!hg.lob.l.16locs$circle.name == "Cape Jellison",])) #estuary without CJ
summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Odom Ledge",]))
summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "South Verona",]))
summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Cape Jellison",]))
summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Harborside",]))
summary(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Turner Point",]))


#4-45
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Frenchman Bay",], xlab = "", ylab = "Length Adjusted Ln Tail Hg
 (ng/g)", main = "Figure 4-45\nLobster Tail - Frenchman Bay\nLength Adjusted Ln Mercury Concentrations", ylim = c(0, 1.02 *
 max.lob.ln), xlim = range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Frenchman Bay"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Frenchman Bay"], hg.lob.l$year[hg.lob.l$circle.name == "Frenchman Bay"], median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Frenchman Bay"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Frenchman Bay"], hg.lob.l$year[hg.lob.l$circle.name == "Frenchman Bay"], mean, na.rm = T), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-46
plot(l.adj.lnresuse ~ year, data = hg.lob.l.16locs[!hg.lob.l.16locs$circle.name == "Cape Jellison",], xlab = "", ylab = "Ln Tail Hg
 (ng/g)", main = "Figure 4-46\nLobster Tail - Penobscot Bay\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.lob.l
 $l.adj.lnresuse, na.rm = T)), yaxs = "i", las = 1, tck = 0.015)
abline(lm(l.adj.lnresuse ~ year, data = hg.lob.l.16locs[!hg.lob.l.16locs$circle.name == "Cape Jellison",]))

text(min(hg.lob.l.16locs$year) + 1.5, 0.19 * max.lob.ln, "ln(y) = -0.04208x + 89.876", cex = 0.8)
text(min(hg.lob.l.16locs$year) + 1.5, 0.16 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.03", cex = 0.8)
title(sub = "Includes lobster data from Odom Ledge, South Verona, Turner Point, and Harborside", cex.sub = 0.7)

points(as.numeric(levels(as.factor(hg.lob.l.16locs$year[!hg.lob.l.16locs$circle.name == "Cape Jellison"]))), tapply(hg.lob.l.16locs
 $l.adj.lnresuse[!hg.lob.l.16locs$circle.name == "Cape Jellison"], hg.lob.l.16locs$year[!hg.lob.l.16locs$circle.name == "Cape
 Jellison"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l.16locs$year[!hg.lob.l.16locs$circle.name == "Cape Jellison"]))), tapply(hg.lob.l.16locs
 $l.adj.lnresuse[!hg.lob.l.16locs$circle.name == "Cape Jellison"], hg.lob.l.16locs$year[!hg.lob.l.16locs$circle.name == "Cape
 Jellison"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-47
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Odom Ledge",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/
 g)", main = "Figure 4-47\nLobster Tail - Odom Ledge\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim =
 range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)

text(min(hg.lob.l$year) + 1.5, 0.18 * max.lob.ln, "ln(y) = 0.02463x + 54.955", cex = 0.8)
text(min(hg.lob.l$year) + 1.5, 0.15 * max.lob.ln, "p = 0.25, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Odom Ledge"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Odom Ledge"], hg.lob.l$year[hg.lob.l$circle.name == "Odom Ledge"], median, na.rm = T), pch = 21, col = "red", cex =
 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Odom Ledge"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Odom Ledge"], hg.lob.l$year[hg.lob.l$circle.name == "Odom Ledge"], mean, na.rm = T), pch = 22, col = "blue", cex =
 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-48
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "South Verona",], xlab = "", ylab = "Length Adjusted Ln Tail Hg
 (ng/g)", main = "Figure 4-48\nLobster Tail - South Verona\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim
 = range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)
clip(2007,2020, 0, 100)
```

```
abline(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "South Verona",]))
clip(0,2020, 0, 100)

text(min(hg.lob.l$year) + 1.5, 0.18 * max.lob.ln, "ln(y) = -0.1563x + 320.15", cex = 0.8)
text(min(hg.lob.l$year) + 1.5, 0.15 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.31", cex = 0.8)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "South Verona"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "South Verona"], hg.lob.l$year[hg.lob.l$circle.name == "South Verona"], median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "South Verona"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "South Verona"], hg.lob.l$year[hg.lob.l$circle.name == "South Verona"], mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-49
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Cape Jellison",], xlab = "", ylab = "Length Adjusted Ln Tail Hg
 (ng/g)", main = "Figure 4-49\nLobster Tail - Cape Jellison\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln),
 xlim = range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)
clip(2013,2020, 0, 100)
abline(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Cape Jellison",]))
clip(0,2020, 0, 100)

text(min(hg.lob.l$year) + 1.5, 0.18 * max.lob.ln, "ln(y) = -0.2062x + 420.66", cex = 0.8)
text(min(hg.lob.l$year) + 1.5, 0.15 * max.lob.ln, "p = 0.010, Adj." ~R^2~ "= 0.05", cex = 0.8)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Cape Jellison"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Cape Jellison"], hg.lob.l$year[hg.lob.l$circle.name == "Cape Jellison"], median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Cape Jellison"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Cape Jellison"], hg.lob.l$year[hg.lob.l$circle.name == "Cape Jellison"], mean, na.rm = T), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-50
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Turner Point",], xlab = "", ylab = "Length Adjusted Ln Tail Hg
 (ng/g)", main = "Figure 4-50\nLobster Tail - Turner Point\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim
 = range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)
abline(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Turner Point",]))

text(min(hg.lob.l$year) + 1.5, 0.18 * max.lob.ln, "ln(y) = -0.06116x + 128.19", cex = 0.8)
text(min(hg.lob.l$year) + 1.5, 0.15 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.08", cex = 0.8)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Turner Point"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Turner Point"], hg.lob.l$year[hg.lob.l$circle.name == "Turner Point"], median, na.rm = T), pch = 21, col = "red", cex
 = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Turner Point"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Turner Point"], hg.lob.l$year[hg.lob.l$circle.name == "Turner Point"], mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-51
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Harborside",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/
 g)", main = "Figure 4-51\nLobster Tail - Harborside\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim =
 range(hg.lob.l$year), yaxs = "i", las = 1, tck = 0.015)
abline(lm(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Harborside",]))

text(min(hg.lob.l$year) + 1.5, 0.18 * max.lob.ln, "ln(y) = -0.0560x + 117.54", cex = 0.8)
text(min(hg.lob.l$year) + 1.5, 0.15 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.08", cex = 0.8)

points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Harborside"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Harborside"], hg.lob.l$year[hg.lob.l$circle.name == "Harborside"], median, na.rm = T), pch = 21, col = "red", cex =
 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l$year[hg.lob.l$circle.name == "Harborside"]))), tapply(hg.lob.l$l.adj.lnresuse[hg.lob.l
 $circle.name == "Harborside"], hg.lob.l$year[hg.lob.l$circle.name == "Harborside"], mean, na.rm = T), pch = 22, col = "blue", cex =
 1.3, bg = "blue")

legend("bottomleft", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-9. Mummichog Statistical Analysis Code

```
### File created for analysis of mummichog data for Biota Monitoring Report (2017)
### Code edited by LSV 01/16/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob
 $month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month
 == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


#################
### MUMMICHOG ###
#################

levels(factor(penob$PARAM_NAME[penob$MED_T == "Mummichog"]))

hg.mum = penob[penob$MED_T == "Mummichog" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples labeled as
 mercury, removes field duplicates

hg.mum = merge(hg.mum, length[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE",
 "year", "month", "day"), by.y = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #
 merge tissue records with lengths for each fish
names(hg.mum)[colnames(hg.mum) == "resuse.y"] = "length" # rename columns for ease of keeping track of data
summary(hg.mum) #327 records

hg.mum = merge(hg.mum, weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD",
 "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID","MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x
 = T) # merge tissue records with weights for each fish
names(hg.mum)[colnames(hg.mum) == "resuse"] = "weight" # rename columns for ease of keeping track of data
names(hg.mum)[colnames(hg.mum) == "resuse.x"] = "resuse" # rename columns for ease of keeping track of data
summary(hg.mum) #327 records

hg.mum$ln.resuse = log(hg.mum$resuse) #log Hg results
hg.mum$l.adj_resuse = hg.mum$resuse / hg.mum$length * median(hg.mum$length, na.rm = T) #length adjust Hg results
hg.mum$ln.l.adj_resuse = log(hg.mum$resuse) / hg.mum$length * median(hg.mum$length, na.rm = T) #length adjust logged Hg results

hg.mum$w.adj_resuse = hg.mum$resuse/hg.mum$weight * median(hg.mum$weight, na.rm = T) #weight adjust logged Hg results


hg.mum$locs = as.factor(substring(hg.mum$LOC_NAME,1,5)) #create field of locations
hg.mum$reach = as.factor(substring(hg.mum$LOC_NAME,1,2)) #create field of reaches

ref.mum = hg.mum[hg.mum$X_COORD > 940000,] #pull reference fish into separate dataset
hg.mum = hg.mum[hg.mum$X_COORD < 940000,] #reduce dataset to site birds
summary(hg.mum) #287 records
summary(ref.mum) #40 records

hg.mum.P = hg.mum #retaining all paired data


# Reduce overall dataset to locations that have been consistently sampled over years and also in 2016
tapply(hg.mum$resuse, list(factor(hg.mum$locs), hg.mum$year), length)
```

```
hg.mum = hg.mum[hg.mum$locs == "OB-01" | hg.mum$locs == "OB-05" | hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21",]


########################################
### Mummichog Concentration Summary ###
########################################

mum.summ = data.frame(OB.05_x = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-05"], hg.mum.P$year[hg.mum.P$locs == "OB-05"], mean))
mum.summ$OB.05_x_se = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-05"], hg.mum.P$year[hg.mum.P$locs == "OB-05"], sd) /
 sqrt(tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-05"], hg.mum.P$year[hg.mum.P$locs == "OB-05"], length))
mum.summ$OB.05_medn = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-05"], hg.mum.P$year[hg.mum.P$locs == "OB-05"], median)
mum.summ$OB.05_N = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-05"], hg.mum.P$year[hg.mum.P$locs == "OB-05"], length)
mum.summ$OB.05_perc = 0

mum.summ$BO.04_x[c(1,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], mean)
mum.summ$BO.04_x_se[c(1,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], sd) /
 sqrt(tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], length))
mum.summ$BO.04_medn[c(1,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], median)
mum.summ$BO.04_N[c(1,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], length)
mum.summ$BO.04_perc[c(1,5:6)] = 0

mum.summ$OB.01_x[c(1,3,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], mean)
mum.summ$OB.01_x_se[c(1,3,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], sd) /
 sqrt(tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], length))
mum.summ$OB.01_medn[c(1,3,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], median)
mum.summ$OB.01_N[c(1,3,5:6)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], length)
mum.summ$OB.01_perc[c(1,3,5:6)] = c(tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01" & hg.mum.P$resuse > 440], hg.mum.P$year[hg.mum.P
 $locs == "OB-01" & hg.mum.P$resuse > 440], length) / tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs ==
 "OB-01"], length)[1], rep(0,3))

mum.summ = rbind(mum.summ[1:4,],NA,mum.summ[5:6,])
rownames(mum.summ)[5] = "2012"

mum.summ$MM_x[4:7] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], hg.mum.P$year[hg.mum.P$locs == "MMMC-"
 | hg.mum.P$locs == "W-21"], mean)
mum.summ$MM_x_se[4:7] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], hg.mum.P$year[hg.mum.P$locs ==
 "MMMC-" | hg.mum.P$locs == "W-21"], sd) / sqrt(tapply(hg.mum.P$resuse[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], hg.mum.P
 $year[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], length))
mum.summ$MM_medn[4:7] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], hg.mum.P$year[hg.mum.P$locs ==
 "MMMC-" | hg.mum.P$locs == "W-21"], median)
mum.summ$MM_N[4:7] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21"], hg.mum.P$year[hg.mum.P$locs == "MMMC-"
 | hg.mum.P$locs == "W-21"], length)
mum.summ$MM_perc[4:7] = c(tapply(hg.mum.P$resuse[(hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21") & hg.mum.P$resuse > 440],
 hg.mum.P$year[(hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21") & hg.mum.P$resuse > 440], length) / tapply(hg.mum.P
 $resuse[(hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21")], hg.mum.P$year[(hg.mum.P$locs == "MMMC-" | hg.mum.P$locs == "W-21")],
 length)[1], rep(0,3))

mum.summ$FRB_x[6:7] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], mean)
mum.summ$FRB_x_se[6:7] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], sd) /
 sqrt(tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], length))
mum.summ$FRB_medn[6:7] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], median)
mum.summ$FRB_N[6:7] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], length)
mum.summ$FRB_perc[6:7] = 0

write.csv(mum.summ,"Mummichog summary.csv")



########################
### MUMMICHOG TRENDS ###
########################

summary(lm(ln.l.adj_resuse ~ year, data = hg.mum))
summary(lm(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "OB-05",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21",]))


#4-52
plot(ln.l.adj_resuse ~ year, data = ref.mum, xlab = "Year", ylab = "Length Adjusted Ln Tissue Hg (ng/g)", main = "Figure
 4-52\nMummichog - Frenchman Bay (Reference)\nLength Adjusted Ln Mercury Concentrations", las = 1, tck = 0.015, ylim = c(0, 1.02 *
 max(hg.mum.P$ln.l.adj_resuse, na.rm = T)), yaxs = "i", xlim = range(hg.mum.P$year))


points(as.numeric(levels(as.factor(ref.mum$year))), tapply(ref.mum$ln.l.adj_resuse, ref.mum$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.mum$year))), tapply(ref.mum$ln.l.adj_resuse, ref.mum$year, mean, na.rm = T), pch = 22, col =
 "blue", cex = 1.3, bg = "blue")
```

```r
legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-53
plot(ln.l.adj_resuse ~ year, data = hg.mum, xlab = "Year", ylab = "Length Adjusted Ln Tissue Hg (ng/g)", main = "Figure 4-53\nMummichog
 - Whole River\nLength Adjusted Loglinear Regression", las = 1, tck = 0.015, ylim = c(0, 1.02 * max(hg.mum$ln.l.adj_resuse)), yaxs =
 "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.mum))

text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T) * 0.16, "ln(y) = -0.08124x + 168.46", cex = 0.8)
text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T) * 0.13, "p < 0.001, Adj." ~R^2~ "= 0.10", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mum$year))), tapply(hg.mum$ln.l.adj_resuse, hg.mum$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mum$year))), tapply(hg.mum$ln.l.adj_resuse, hg.mum$year, mean, na.rm = T), pch = 22, col =
 "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Mummichog sampled at OB-05, OB-01, and Mendall Marsh", cex.sub = 0.7)


#4-54
plot(ln.l.adj_resuse ~ year, hg.mum[hg.mum$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-54\nMummichog - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.mum$ln.l.adj_resuse, na.rm = T)), las = 1,
 tck = 0.015, yaxs = "i")
#abline(lm(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "OB-05",]), lty = 2)

text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.16, "ln(y) = 0.02695x - 49.203", cex = 0.8)
text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.13, "p = 0.29, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "OB-05"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum$locs == "OB-05"],
 hg.mum$year[hg.mum$locs == "OB-05"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "OB-05"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum$locs == "OB-05"],
 hg.mum$year[hg.mum$locs == "OB-05"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch =
 c(1,22,21), pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-55
plot(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21",], xlab = "Year", ylab = "Length Adjusted Ln
 Hg (ng/g)", main = "Figure 4-55\nMummichog - Mendall Marsh\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.mum
 $ln.l.adj_resuse, na.rm = T)), las = 1, tck = 0.015, yaxs = "i", xlim = range(hg.mum.P$year))
clip(2009, 2018, 0, 10000)
abline(lm(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21",]))
clip(0, 10000, 0, 10000)

text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.16, "ln(y) = -0.2972x + 603.38", cex = 0.8)
text(max(hg.mum$year) - 1.5, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.13, "p < 0.001, Adj." ~R^2~ "= 0.64", cex = 0.8)

points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum
 $locs == "MMMC-" | hg.mum$locs == "W-21"], hg.mum$year[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21"], median), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum
 $locs == "MMMC-" | hg.mum$locs == "W-21"], hg.mum$year[hg.mum$locs == "MMMC-" | hg.mum$locs == "W-21"], mean), pch = 22, col = "blue",
 cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Mummichog sampled at MMMC-01 and W-21", cex.sub = 0.7)


#4-56
plot(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-56\nMummichog - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.mum$ln.l.adj_resuse, na.rm = T)),
 las = 1, tck = 0.015, yaxs = "i")

points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "OB-01"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum$locs == "OB-01"],
 hg.mum$year[hg.mum$locs == "OB-01"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.mum$year[hg.mum$locs == "OB-01"]))), tapply(hg.mum$ln.l.adj_resuse[hg.mum$locs == "OB-01"],
 hg.mum$year[hg.mum$locs == "OB-01"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("bottomright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-10. Rainbow Smelt Statistical Analysis Code

```
### File created for analysis of smelt data for Biota Monitoring Report (2017)
### Code edited by LSV 01/16/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob
 $month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month
 == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


#####################
### RAINBOW SMELT ###
#####################

levels(factor(penob$PARAM_NAME[penob$MED_T == "Rainbow Smelt"]))

hg.sml = penob[penob$MED_T == "Rainbow Smelt" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples labeled as
 mercury, removes field duplicates

hg.sml = merge(hg.sml,length[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE",
 "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T)
 #merge tissue and lengths
names(hg.sml)[colnames(hg.sml) == "resuse.y"] = "length" #renames column
summary(hg.sml)

hg.sml = merge(hg.sml,weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD",
 "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x
 = T) #merge tissue and weight
names(hg.sml)[colnames(hg.sml) == "resuse"] = "weight" #renames columns
names(hg.sml)[colnames(hg.sml) == "resuse.x"] = "resuse" #renames columns
summary(hg.sml) #786, 21 NAs

hg.sml$ln.resuse = log(hg.sml$resuse) #log Hg results

hg.sml$l.adj_resuse = hg.sml$resuse/hg.sml$length * median(hg.sml$length, na.rm = T) #length adjust Hg results
hg.sml$ln.l.adj_resuse = log(hg.sml$resuse) / hg.sml$length * median(hg.sml$length, na.rm = T) #length adjust logged Hg results

hg.sml$w.adj_resuse = hg.sml$resuse/hg.sml$weight * median(hg.sml$weight, na.rm = T) #weight adjust Hg results


hg.sml$locs = as.factor(substring(hg.sml$LOC_NAME,1,5)) #create location identifier
hg.sml$reach = as.factor(substring(hg.sml$LOC_NAME,1,2)) #create reach identifier


ref.sml = hg.sml[hg.sml$X_COORD > 940000,] #pulls reference samples into separate dataset
hg.sml = hg.sml[hg.sml$X_COORD < 940000,] #reduce dataset to site samples
summary(hg.sml) #746 records
summary(ref.sml) #40 records

hg.sml.P = hg.sml #retain full paired dataset

# Reducing overall dataset to locations that have been consistently sampled over years and also in 2016
```

```r
tapply(hg.sml$resuse, list(factor(hg.sml$locs), hg.sml$year), length)

hg.sml = hg.sml[hg.sml$locs == "ES-13" | hg.sml$locs == "ES-15" | hg.sml$locs == "OB-05" | hg.sml$locs == "OB-01" | hg.sml$locs == "ES-
 FP" | hg.sml$locs == "OB-04" | hg.sml$locs == "Fort ",]


###################################
### Smelt concentration summary ###
###################################

sml.summ = data.frame(OB.05_x = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs == "OB-05"], mean))
sml.summ$OB.05_x_se = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs == "OB-05"], sd) /
 sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs == "OB-05"], length))
sml.summ$OB.05_medn = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs == "OB-05"], median)
sml.summ$OB.05_N = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs == "OB-05"], length)
sml.summ$OB.05_perc[c(2,4:6)] = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05" & hg.sml.P$resuse > 200], hg.sml.P$year[hg.sml.P$locs
 == "OB-05" & hg.sml.P$resuse > 200], length) / tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-05"], hg.sml.P$year[hg.sml.P$locs ==
 "OB-05"], length)[c(2,4,5)], NA)
sml.summ$OB.05_perc[c(1,3,6)] = 0

sml.summ = rbind(sml.summ[1:2,],"NA",sml.summ[3:6,])
rownames(sml.summ)[3] = "2009"


sml.summ$ES.15_x = c(NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], mean, na.rm = T)
 [1:2],rep(NA,2),tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], mean)[3],NA)
sml.summ$ES.15_x_se = c(NA, tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], sd, na.rm = T)
 [1:2] / sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], length)[1:2]), rep(NA,4))
sml.summ$ES.15_medn = c(NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], median)
 [1:2],rep(NA,2),tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], median)[3],NA)
sml.summ$ES.15_N = c(NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], length)[1:2],rep(NA,
 2),tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], length)[3],NA)
sml.summ$ES.15_perc[c(2:3,6:7)] = c(rep(0,3), NA)


sml.summ$ES.13_x[c(1:5,7)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-13"], hg.sml.P$year[hg.sml.P$locs == "ES-13"], mean)
sml.summ$ES.13_x_se[c(1:5,7)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-13"], hg.sml.P$year[hg.sml.P$locs == "ES-13"], sd) /
 sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-13"], hg.sml.P$year[hg.sml.P$locs == "ES-13"], length))
sml.summ$ES.13_medn[c(1:5,7)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-13"], hg.sml.P$year[hg.sml.P$locs == "ES-13"], median)
sml.summ$ES.13_N[c(1:5,7)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-13"], hg.sml.P$year[hg.sml.P$locs == "ES-13"], length)
sml.summ$ES.13_perc[c(1:5,7)] = 0


sml.summ$OB.04_x = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], mean)[1:4],
 NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], mean)[5], NA)
sml.summ$OB.04_x_se = c((tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], sd) /
 sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], length)))[1:4], NA, (tapply(hg.sml.P
 $resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], sd) / sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs ==
 "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], length)))[5], NA)
sml.summ$OB.04_medn = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], median)[1:4],
 NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], median)[5], NA)
sml.summ$OB.04_N = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], length)[1:4],
 NA,tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], length)[5], NA)
sml.summ$OB.04_perc[c(3,7)] = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04" & hg.sml.P$resuse > 200], hg.sml.P$year[hg.sml.P$locs
 == "OB-04" & hg.sml.P$resuse > 200], length) / tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs ==
 "OB-04"], length)[3], NA)
sml.summ$OB.04_perc[c(1:2,4,6)] = 0

sml.summ$OB.01_x = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], mean)[1], NA,
 tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], mean)[2:6])
sml.summ$OB.01_x_se = c((tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], sd) /
 sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], length)))[1], NA, (tapply(hg.sml.P
 $resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], sd) / sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs ==
 "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], length)))[2:6])
sml.summ$OB.01_medn = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], median)[1], NA,
 tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], median)[2:6])
sml.summ$OB.01_N = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], length)[1], NA,
 tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], length)[2:6])
sml.summ$OB.01_perc[c(4:5,7)] = c(tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01" & hg.sml.P$resuse > 200], hg.sml.P$year[hg.sml.P$locs
 == "OB-01" & hg.sml.P$resuse > 200], length) / tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs ==
 "OB-01"], length)[c(3:4)], 0)
sml.summ$OB.01_perc[c(1,3,6)] = 0

sml.summ$ES.FP_x[3:7] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], mean)
sml.summ$ES.FP_x_se[3:7] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], sd) /
 sqrt(tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], length))
sml.summ$ES.FP_medn[3:7] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], median)
sml.summ$ES.FP_N[3:7] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], length)
sml.summ$ES.FP_perc[7] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP" & hg.sml.P$resuse > 200], hg.sml.P$year[hg.sml.P$locs == "ES-
```

```
 FP" & hg.sml.P$resuse > 200], length) / tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"],
 length)[5]
sml.summ$ES.FP_perc[c(3:6)] = 0

sml.summ$FRB_x[6:7] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], mean)
sml.summ$FRB_x_se[6:7] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], sd) /
 sqrt(tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], length))
sml.summ$FRB_medn[6:7] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], median)
sml.summ$FRB_N[6:7] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], length)
sml.summ$FRB_perc[6:7] = 0

write.csv(sml.summ,"Smelt summary.csv")


####################
### SMELT TRENDS ###
####################

summary(lm(ln.l.adj_resuse ~ year, data = hg.sml))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-05",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-04",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-01",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml.P[hg.sml.P$locs == "ES-13",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml.P[hg.sml.P$locs == "ES-15",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.sml.P[hg.sml.P$locs == "ES-FP",]))


#4-57
plot(ln.l.adj_resuse ~ year, data = ref.sml, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-57\nRainbow Smelt - Frenchman Bay
 (Reference)\nLength Adjusted Ln Mercury Concentrations", ylim = c(0, 1.02 * max(hg.sml$ln.l.adj_resuse, na.rm = T)), las = 1, tck =
 0.015, yaxs = "i", xlim = c(2006, max(hg.sml$year)))

points(as.numeric(levels(as.factor(ref.sml$year))), tapply(ref.sml$ln.l.adj_resuse, ref.sml$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.sml$year))), tapply(ref.sml$ln.l.adj_resuse, ref.sml$year, mean, na.rm = T), pch = 22, col =
 "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-58
plot(ln.l.adj_resuse ~ year, data = hg.sml, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-58\nRainbow Smelt -
 Whole River\nLength Adjusted Loglinear Regression", las = 1, tck = 0.015, ylim = c(0, 1.02 * max(hg.sml$ln.l.adj_resuse, na.rm = T)),
 yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.sml))

text(max(hg.sml$year) - 1.5, max(hg.sml$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.1700x + 346.41", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml$ln.l.adj_resuse, na.rm = T) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.07", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml$year))), tapply(hg.sml$ln.l.adj_resuse, hg.sml$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year))), tapply(hg.sml$ln.l.adj_resuse, hg.sml$year, mean, na.rm = T), pch = 22, col =
 "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Smelt sampled at OB-05, OB-04, OB-01, ES-13, ES-15, and ES-FP", cex.sub = 0.7)


#4-59
plot(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-59\nRainbow Smelt - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las
 = 1, tck = 0.015, yaxs = "i")

text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = 0.0948x - 184.54", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.835, "p = 0.70, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-05"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-05"],
 hg.sml$year[hg.sml$locs == "OB-05"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-05"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-05"],
 hg.sml$year[hg.sml$locs == "OB-05"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch =
 c(1,22,21), pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-60
plot(ln.l.adj_resuse ~ year, data = hg.sml.P[hg.sml.P$locs == "ES-FP",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
```

```
 "Figure 4-60\nRainbow Smelt - ES-FP\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm =
 T)), las = 1, tck = 0.015, xlim = range(hg.sml$year), yaxs = "i")

text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = 0.0078x - 11.843", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.60, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml.P$year[hg.sml.P$locs == "ES-FP"]))), tapply(hg.sml.P$ln.l.adj_resuse[hg.sml.P$locs == "ES-
 FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml.P$year[hg.sml.P$locs == "ES-FP"]))), tapply(hg.sml.P$ln.l.adj_resuse[hg.sml.P$locs == "ES-
 FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-61
plot(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "ES-13",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-61\nRainbow Smelt - ES-13\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm =
 T)), las = 1, tck = 0.015, yaxs = "i", xlim = range(hg.sml$year))

text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.04866x + 102.06", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.22, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "ES-13"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "ES-13"],
 hg.sml$year[hg.sml$locs == "ES-13"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "ES-13"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "ES-13"],
 hg.sml$year[hg.sml$locs == "ES-13"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-62
plot(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-62\nRainbow Smelt - OB-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las
 = 1, tck = 0.015, yaxs = "i", xlim = range(hg.sml$year))
abline(lm(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-04",]))

text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.5109x + 1032.7", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.835, "p = 0.009, Adj." ~R^2~ "= 0.35", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-04"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-04"],
 hg.sml$year[hg.sml$locs == "OB-04"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-04"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-04"],
 hg.sml$year[hg.sml$locs == "OB-04"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch =
 c(1,22,21), pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-63
plot(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-63\nRainbow Smelt - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm =
 T)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-01",]))

text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.4605x + 931.6", cex = 0.8)
text(max(hg.sml$year) - 1.5, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.835, "p < 0.001, Adj." ~R^2~ "= 0.27", cex = 0.8)

points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-01"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-01"],
 hg.sml$year[hg.sml$locs == "OB-01"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "OB-01"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "OB-01"],
 hg.sml$year[hg.sml$locs == "OB-01"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-64
plot(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "ES-15",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-64\nRainbow Smelt - ES-15\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm =
 T)), las = 1, tck = 0.015, yaxs = "i", xlim = range(hg.sml$year))

points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "ES-15"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "ES-15"],
 hg.sml$year[hg.sml$locs == "ES-15"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.sml$year[hg.sml$locs == "ES-15"]))), tapply(hg.sml$ln.l.adj_resuse[hg.sml$locs == "ES-15"],
 hg.sml$year[hg.sml$locs == "ES-15"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
```

```
pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-11. American Eel Statistical Analysis Code

```
### File created for analysis of eel data for Biota Monitoring Report (2017)
### Code edited by LSV 01/22/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


####################
### AMERICAN EEL ###
####################

hg.eel = penob[penob$MED_T == "Eel" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD" ,] #selects all eel samples labeled as mercury, removes field duplicates

hg.eel = merge(hg.eel,length[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge tissue with length for each fish
names(hg.eel)[colnames(hg.eel) == "resuse.y"] = "length" #rename columns to ease calling data
summary(hg.eel) #713 records

hg.eel = merge(hg.eel,weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge tissue with weight for each fish
names(hg.eel)[colnames(hg.eel) == "resuse"] = "weight" #rename columns to ease calling data
names(hg.eel)[colnames(hg.eel) == "resuse.x"] = "resuse" #rename columns to ease calling data
summary(hg.eel) #713 records

hg.eel$ln.resuse = log(hg.eel$resuse) #log Hg results
hg.eel$l.adj_resuse = hg.eel$resuse / hg.eel$length * median(hg.eel$length, na.rm = T) #length adjust Hg results
hg.eel$ln.l.adj_resuse = log(hg.eel$resuse) / hg.eel$length * median(hg.eel$length, na.rm = T) #length adjust logged Hg results

hg.eel$w.adj_resuse = hg.eel$resuse/hg.eel$weight * median(hg.eel$weight,na.rm = T) #weight adjust Hg results


hg.eel$locs = as.factor(substring(hg.eel$LOC_NAME,1,5)) #creating location identifiers
hg.eel$reach = as.factor(substring(hg.eel$LOC_NAME,1,2))

ref.eel = hg.eel[hg.eel$Y_COORD > 420000,] #pull reference eel into separate account
hg.eel = hg.eel[hg.eel$Y_COORD < 420000,] #reduce dataset to site eel
summary(hg.eel) #591 records
summary(ref.eel) #122 records

hg.eel.P = hg.eel #retaining all paired data


# Reducing overall dataset to locations that have been consistently sampled over years and also in 2016
tapply(hg.eel$resuse, list(factor(hg.eel$locs), hg.eel$year), length)

hg.eel = hg.eel[hg.eel$locs == "OB-05" | hg.eel$locs == "OB-01" | hg.eel$locs == "BO-04",]
```

```
###################
### Eel Summary ###
###################

eel.summ = data.frame(OB.05_x = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], mean))
eel.summ$OB.05_x_se = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], sd) /
 sqrt(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], length))
eel.summ$OB.05_medn = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], median)
eel.summ$OB.05_N = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], length)
eel.summ$OB.05_perc = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05" & hg.eel.P$resuse > 320], hg.eel.P$year[hg.eel.P$locs == "OB-05"
 & hg.eel.P$resuse > 320], length) / tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-05"], hg.eel.P$year[hg.eel.P$locs == "OB-05"], length)

eel.summ$BO.04_x = tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], mean)
eel.summ$BO.04_x_se = tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], sd) /
 sqrt(tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], length))
eel.summ$BO.04_medn = tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], median)
eel.summ$BO.04_N = tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], length)
eel.summ$BO.04_perc = tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04" & hg.eel.P$resuse > 320], hg.eel.P$year[hg.eel.P$locs == "BO-04"
 & hg.eel.P$resuse > 320], length) / tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], length)

eel.summ$OB.01_x = c(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], mean),NA)
eel.summ$OB.01_x_se = c(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], sd) /
 sqrt(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], length)), NA)
eel.summ$OB.01_medn = c(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], median),NA)
eel.summ$OB.01_N = c(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], length),NA)
eel.summ$OB.01_perc = c(tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01" & hg.eel.P$resuse > 320], hg.eel.P$year[hg.eel.P$locs ==
 "OB-01" & hg.eel.P$resuse > 320], length) / tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"],
 length), NA)

eel.summ$Veaz_x[c(1:5,7)] = tapply(ref.eel$resuse, ref.eel$year, mean)
eel.summ$Veaz_x_se[c(1:5,7)] = tapply(ref.eel$resuse, ref.eel$year, sd) / sqrt(tapply(ref.eel$resuse, ref.eel$year, length))
eel.summ$Veaz_medn[c(1:5,7)] = tapply(ref.eel$resuse, ref.eel$year, median)
eel.summ$Veaz_N[c(1:5,7)] = tapply(ref.eel$resuse, ref.eel$year, length)
eel.summ$Veaz_perc[c(1:5,7)] = c(tapply(ref.eel$resuse[ref.eel$resuse > 320], ref.eel$year[ref.eel$resuse > 320], length), NA) /
 tapply(ref.eel$resuse, ref.eel$year, length)
eel.summ$Veaz_perc[7] = 0

write.csv(eel.summ,"Eel summary.csv")


##################
### EEL TRENDS ###
##################

summary(lm(ln.l.adj_resuse ~ year, data = hg.eel))
summary(lm(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "OB-05",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "OB-01",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "BO-04",]))


#4-65
plot(ln.l.adj_resuse ~ year, data = ref.eel, pch = 17, ylab = "Ln Hg (ng/g)", xlab = "Year", xlim = range(ref.eel$year), las = 1, tck =
 0.015, yaxs = "i", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse, hg.eel$ln.l.adj_resuse)), main = "Figure 4-65\nAmerican Eel - OV-04
 (Reference)\nLength Adjusted Loglinear Regression")

text(2016, max(ref.eel$ln.l.adj_resuse)*0.87, "y = 0.04156x - 78.625", cex = 0.8)
text(2016, max(ref.eel$ln.l.adj_resuse)*0.835, "p = 0.58, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(ref.eel$year))), tapply(ref.eel$ln.l.adj_resuse, ref.eel$year, median), pch = 21, col = "red", cex =
 1.3, bg = "red")
points(as.numeric(levels(as.factor(ref.eel$year))), tapply(ref.eel$ln.l.adj_resuse, ref.eel$year, mean), pch = 22, col = "blue", cex =
 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-66
plot(ln.l.adj_resuse ~ year, data = hg.eel, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-66\nAmerican Eel -
 Whole River\nLength Adjusted Loglinear Regression", las = 1, tck = 0.015, ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse)), yaxs =
 "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.eel))

text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.1405x + 288.65", cex = 0.8)
text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.12", cex = 0.8)

points(as.numeric(levels(as.factor(hg.eel$year))), tapply(hg.eel$ln.l.adj_resuse, hg.eel$year, median, na.rm = T), pch = 21, col =
```

```
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.eel$year))), tapply(hg.eel$ln.l.adj_resuse, hg.eel$year, mean, na.rm = T), pch = 22, col =
 "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Eel sampled at BO-04, OB-05, and OB-01", cex.sub = 0.7)


#4-67
plot(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "BO-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-67\nAmerican Eel - BO-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse)), las = 1,
 tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "BO-04",]))

text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.1786x + 365.86", cex = 0.8)
text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.13", cex = 0.8)

points(as.numeric(levels(as.factor(hg.eel$year[hg.eel$locs == "BO-04"]))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "BO-04"],
 hg.eel$year[hg.eel$locs == "BO-04"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.eel$year[hg.eel$locs == "BO-04"]))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "BO-04"],
 hg.eel$year[hg.eel$locs == "BO-04"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch =
 c(1,22,21), pt.bg = c("white","blue","red"), cex = 0.8)


#4-68
plot(ln.l.adj_resuse ~ year, hg.eel[hg.eel$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-68\nAmerican Eel - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse)), las = 1, tck =
 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, hg.eel[hg.eel$locs == "OB-05",]))

text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.1309x + 269.04", cex = 0.8)
text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.24", cex = 0.8)

points(as.numeric(levels(as.factor(hg.eel$year))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "OB-05"], hg.eel$year[hg.eel$locs ==
 "OB-05"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.eel$year))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "OB-05"], hg.eel$year[hg.eel$locs ==
 "OB-05"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch =
 c(1,22,21), pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-69
plot(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-69\nAmerican Eel - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse)), las = 1,
 tck = 0.015, yaxs = "i", xlim = range(hg.eel$year))

text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.0380x + 82.628", cex = 0.8)
text(max(hg.eel$year) - 1.5, max(ref.eel$ln.l.adj_resuse) * 0.835, "p = 0.58, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.eel$year[hg.eel$locs == "OB-01"]))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "OB-01"],
 hg.eel$year[hg.eel$locs == "OB-01"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.eel$year[hg.eel$locs == "OB-01"]))), tapply(hg.eel$ln.l.adj_resuse[hg.eel$locs == "OB-01"],
 hg.eel$year[hg.eel$locs == "OB-01"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
```

Appendix F-12. Atlantic Tomcod Statistical Analysis Code

```r
### File created for analysis of tomcod data for Biota Monitoring Report (2017)
### Code edited by LSV 01/10/2018
### Code checked by NTG 01/31/2018


library(foreign)
library(lattice)
library(plyr)


penob = read.dbf("PEN_BI26.dbf")
summary(penob)

penob$DATE=as.Date(penob$DATE,format="%m/%d/%Y")
penob$year = as.numeric(substring(penob$DATE,1,4))
penob$month = as.numeric(substring(penob$DATE,6,7))
penob$day = as.numeric(substring(penob$DATE,9,10))

penob$dec.year.date = penob$year + penob$month/12

penob$dec.month.date = penob$month + penob$day/31
penob$dec.month.date[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] = penob$month[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11] + penob$day[penob$month == 4 | penob$month == 6 | penob$month == 9 | penob$month == 11]/30
penob$dec.month.date[penob$month == 2] = penob$month[penob$month == 2] + penob$day[penob$month == 2]/28


penob$resuse = penob$PPM_RESULT
penob$resuse[is.na(penob$resuse) == T] = penob$LAB_RESULT[is.na(penob$resuse) == T]


length = penob[penob$PARAM_NAME == "Length",]
weight = penob[penob$PARAM_NAME == "Weight" | penob$PARAM_NAME == "Whole Body Weight",]


#######################
### ATLANTIC TOMCOD ###
#######################

levels(factor(penob$PARAM_NAME[penob$MED_T == "Tomcod"]))

hg.tom = penob[penob$MED_T == "Tomcod" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD",] #selects samples labeled as mercury and tomcod, removes field duplicates

hg.tom = merge(hg.tom, length[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge tomcod tissue data with length for each fish
names(hg.tom)[colnames(hg.tom) == "resuse.y"] = "length" #rename columns for ease of keeping track of data
summary(hg.tom) #765 records

hg.tom = merge(hg.tom,weight[,c(2:4, 6, 7, 36:37, 41:46)], by.x = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE","year", "month", "day"), by.y  = c("LOC_NAME", "ID", "MONITOR_TY", "X_COORD", "Y_COORD", "DATE", "year", "month", "day"), all.x = T) #merge tomcod tissue data with weight for each fish
names(hg.tom)[colnames(hg.tom) == "resuse"] = "weight" #rename columns for ease of keeping track of data
names(hg.tom)[colnames(hg.tom) == "resuse.x"] = "resuse" #rename columns for ease of keeping track of data
summary(hg.tom) #765 records

hg.tom$ln.resuse = log(hg.tom$resuse) #log mercury results
hg.tom$l.adj_resuse = hg.tom$resuse / hg.tom$length * median(hg.tom$length, na.rm = T) #length adjust Hg results
hg.tom$ln.l.adj_resuse = log(hg.tom$resuse) / hg.tom$length * median(hg.tom$length, na.rm = T) #length adjust logged Hg results

hg.tom$w.adj_resuse = hg.tom$resuse/hg.tom$weight * median(hg.tom$weight,na.rm = T) #weight adjust Hg results


hg.tom$locs = as.factor(substring(hg.tom$LOC_NAME,1,5)) #make location names for each sample
hg.tom$reach = as.factor(substring(hg.tom$LOC_NAME,1,2))

ref.tom = hg.tom[hg.tom$X_COORD > 940000,] #pull reference fish into separate dataset
hg.tom = hg.tom[hg.tom$X_COORD < 940000,] #reduce dataset to site fish
summary(hg.tom) #764 records
summary(ref.tom) #1 records

hg.tom.P = hg.tom #retain all paired data


# Reducing overall dataset to locations that have been consistently sampled over years and also in 2016
tapply(hg.tom$resuse, list(factor(hg.tom$locs), hg.tom$year), length)

hg.tom = hg.tom[hg.tom$locs == "ES-13" | hg.tom$locs == "OB-05" | hg.tom$locs == "OB-01" | hg.tom$locs == "BO-04",]
```

```
######################
### Tomcod Summary ###
######################

tom.summ = data.frame(OB.05_x = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], mean))
tom.summ$OB.05_x_se = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], sd) / sqrt(tapply(hg.tom.P
 $resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], length))
tom.summ$OB.05_medn = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], median)
tom.summ$OB.05_N = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], length)
tom.summ$OB.05_perc = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05" & hg.tom.P$resuse > 200], hg.tom.P$year[hg.tom.P$locs == "OB-05" &
 hg.tom.P$resuse > 200], length) / tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-05"], hg.tom.P$year[hg.tom.P$locs == "OB-05"], length)

tom.summ$BO.04_x[c(1,4,6:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], mean)
tom.summ$BO.04_x_se[c(1,4,6:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], sd) /
 sqrt(tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], length))
tom.summ$BO.04_medn[c(1,4,6:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], median)
tom.summ$BO.04_N[c(1,4,6:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], length)
tom.summ$BO.04_perc[c(1,4,6:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04" & hg.tom.P$resuse > 200], hg.tom.P$year[hg.tom.P$locs ==
 "BO-04" & hg.tom.P$resuse > 200], length) / tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"],
 length)

tom.summ$OB.01_x = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], mean)
tom.summ$OB.01_x_se = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], sd) / sqrt(tapply(hg.tom.P
 $resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], length))
tom.summ$OB.01_medn = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], median)
tom.summ$OB.01_N = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], length)
tom.summ$OB.01_perc = tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01" & hg.tom.P$resuse > 200], hg.tom.P$year[hg.tom.P$locs == "OB-01" &
 hg.tom.P$resuse > 200], length) / tapply(hg.tom.P$resuse[hg.tom.P$locs == "OB-01"], hg.tom.P$year[hg.tom.P$locs == "OB-01"], length)

tom.summ$ES.13_x[c(1,3,5:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], mean)
tom.summ$ES.13_x_se[c(1,3,5:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], sd) /
 sqrt(tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], length))
tom.summ$ES.13_medn[c(1,3,5:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], median)
tom.summ$ES.13_N[c(1,3,5:7)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], length)
tom.summ$ES.13_perc[6:7] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13" & hg.tom.P$resuse > 200], hg.tom.P$year[hg.tom.P$locs == "ES-13"
 & hg.tom.P$resuse > 200], length) / tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], length)[4:5]
tom.summ$ES.13_perc[c(1,3,5)] = 0

tom.summ$ES.FP_x[5:7] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], mean)
tom.summ$ES.FP_x_se[5:7] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], sd) /
 sqrt(tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], length))
tom.summ$ES.FP_medn[5:7] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], median)
tom.summ$ES.FP_N[5:7] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], length)
tom.summ$ES.FP_perc[5:7] = 0

tom.summ$FRB_x[6:7] = c(tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], mean), NA)
tom.summ$FRB_x_se[6:7] = c(tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], sd) / sqrt(tapply(ref.tom
 $resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], length)), NA)
tom.summ$FRB_medn[6:7] = c(tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], median), NA)
tom.summ$FRB_N[6:7] = c(tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], length), NA)
tom.summ$FRB_perc[6:7] = c(0,NA)

write.csv(tom.summ,"~Louise/Professional/AMEC/Penobscot/Trends/Tomcod/Tomcod summary.csv")


#####################
### TOMCOD TRENDS ###
#####################

summary(lm(ln.l.adj_resuse ~ year, data = hg.tom))
summary(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-05",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-01",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "BO-04",]))
summary(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "ES-13",]))
kruskal.test(ln.l.adj_resuse ~ year, data = hg.tom.P[hg.tom.P$locs == "ES-FP",])


#4-70
plot(ln.l.adj_resuse ~ year, data = hg.tom, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-70\nAtlantic Tomcod -
 Whole River\nLength Adjusted Loglinear Regression", las = 1, tck = 0.015, ylim = c(0, 1.02 * max(hg.tom$ln.l.adj_resuse)), yaxs = "i")
abline(lm(hg.tom$ln.l.adj_resuse ~ hg.tom$year))

text(max(hg.tom$year) - 1.5, max(hg.tom$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.0761x + 157.98", cex = 0.8)
text(max(hg.tom$year) - 1.5, max(hg.tom$ln.l.adj_resuse, na.rm = T) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.04", cex = 0.8)

points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse, hg.tom$year, median, na.rm = T), pch = 21, col = "red",
 cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse, hg.tom$year, mean, na.rm = T), pch = 22, col = "blue", cex
 = 1.3, bg = "blue")
```

```
legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
title(sub = "Includes Atlantic Tomcod sampled at BO-04, OB-05, OB-01, and ES-13", cex.sub = 0.7)


#4-71
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "BO-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-71\nAtlantic Tomcod - BO-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)), las =
 1, tck = 0.015, yaxs = "i")

text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.04112x + 88.506", cex = 0.8)
text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.29, Adj." ~R^2~ "= 0.01", cex = 0.8)

points(as.numeric(levels(as.factor(hg.tom$year[hg.tom$locs == "BO-04"]))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "BO-04"], hg.tom
 $year[hg.tom$locs == "BO-04"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom$year[hg.tom$locs == "BO-04"]))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "BO-04"], hg.tom
 $year[hg.tom$locs == "BO-04"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-72
plot(ln.l.adj_resuse ~ year, hg.tom[hg.tom$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-72\nAtlantic Tomcod - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)), las =
 1, tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-05",]))

text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.09508x + 196.8", cex = 0.8)
text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.032, Adj." ~R^2~ "= 0.04", cex = 0.8)

points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "OB-05"], hg.tom$year[hg.tom$locs ==
 "OB-05"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "OB-05"], hg.tom$year[hg.tom$locs ==
 "OB-05"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations", "Yearly Means", "Yearly Medians"), col = c(1, "blue", "red"), pch = c(1,22,21),
 pt.bg = c("white", "blue", "red"), cex = 0.8)


#4-73
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-73\nAtlantic Tomcod - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)), las =
 1, tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-01",]))

text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.08164x + 168.6", cex = 0.8)
text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p < 0.001, Adj." ~R^2~ "= 0.08", cex = 0.8)

points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "OB-01"], hg.tom$year[hg.tom$locs ==
 "OB-01"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom$year))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "OB-01"], hg.tom$year[hg.tom$locs ==
 "OB-01"], mean, na.rm = T), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-74
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "ES-13",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-74\nAtlantic Tomcod - ES-13\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)), las =
 1, tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "ES-13",]))

text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.1866x + 380.30", cex = 0.8)
text(max(hg.tom$year) - 1.5, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p < 0.001, Adj." ~R^2~ "= 0.28", cex = 0.8)

points(as.numeric(levels(as.factor(hg.tom$year[hg.tom$locs == "ES-13"]))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "ES-13"], hg.tom
 $year[hg.tom$locs == "ES-13"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom$year[hg.tom$locs == "ES-13"]))), tapply(hg.tom$ln.l.adj_resuse[hg.tom$locs == "ES-13"], hg.tom
 $year[hg.tom$locs == "ES-13"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)


#4-75
plot(ln.l.adj_resuse ~ year, data = hg.tom.P[hg.tom.P$locs == "ES-FP",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main =
 "Figure 4-75\nAtlantic Tomcod - ES-FP\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)),
 las = 1, tck = 0.015, xlim = range(hg.tom$year), yaxs = "i")
```

```
points(as.numeric(levels(as.factor(hg.tom.P$year[hg.tom.P$locs == "ES-FP"]))), tapply(hg.tom.P$ln.l.adj_resuse[hg.tom.P$locs == "ES-FP"],
 hg.tom.P$year[hg.tom.P$locs == "ES-FP"], median), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.tom.P$year[hg.tom.P$locs == "ES-FP"]))), tapply(hg.tom.P$ln.l.adj_resuse[hg.tom.P$locs == "ES-FP"],
 hg.tom.P$year[hg.tom.P$locs == "ES-FP"], mean), pch = 22, col = "blue", cex = 1.3, bg = "blue")

legend("topright", legend = c("Individual Concentrations","Yearly Means", "Yearly Medians"), col = c(1,"blue","red"), pch = c(1,22,21),
 pt.bg = c("white","blue","red"), cex = 0.8)
```

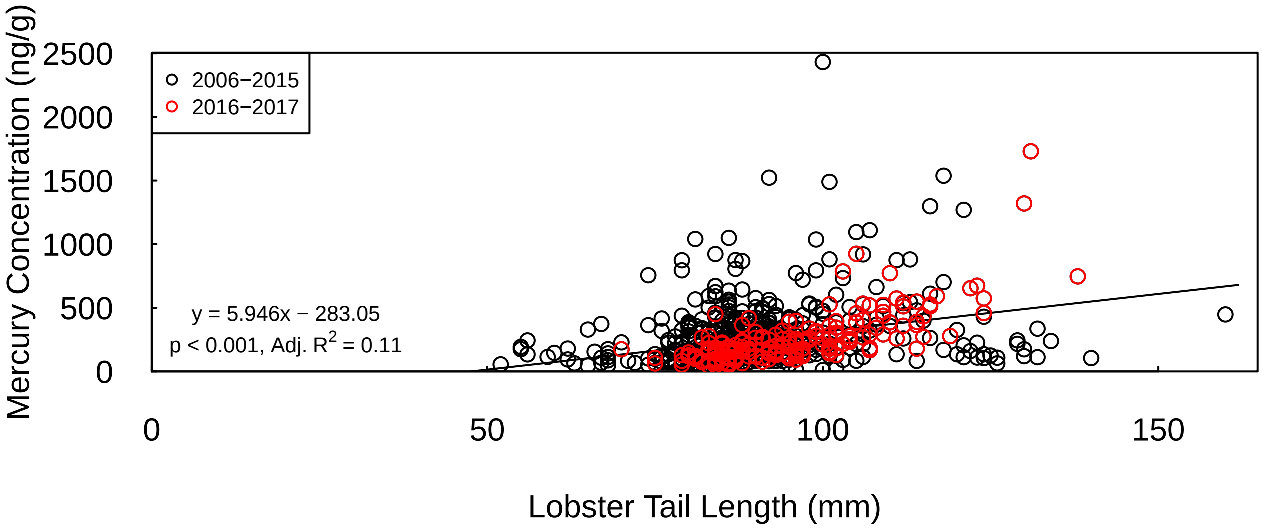
APPENDIX G

Statistical Back Up

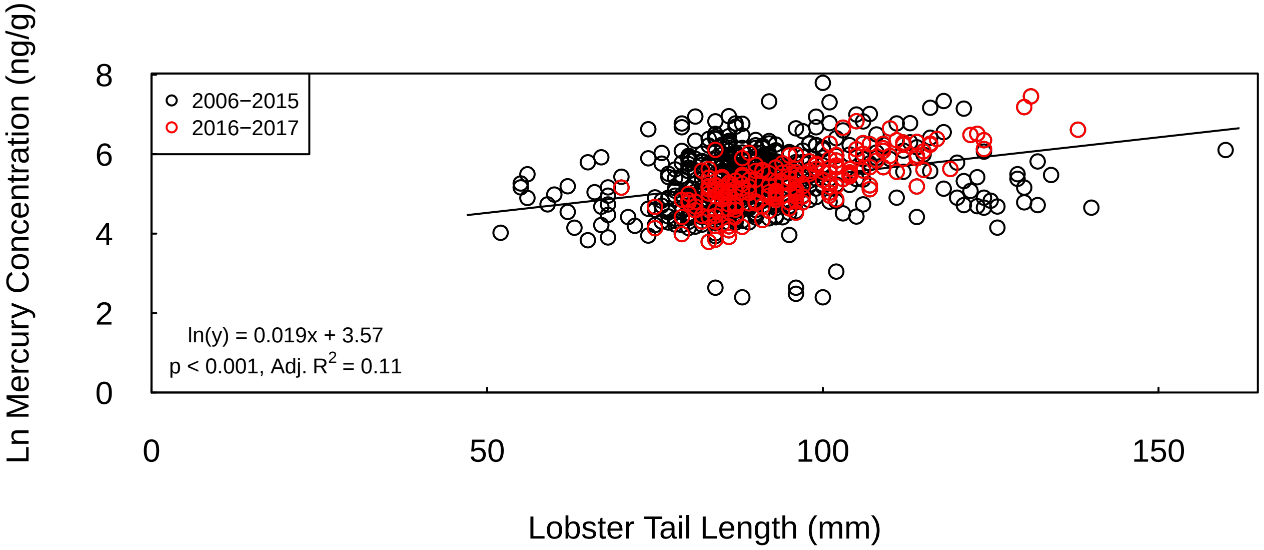
APPENDIX G-1

Length-Mercury Relationship in Fish and Lobster

Lobster Tail Length and Mercury Concentration

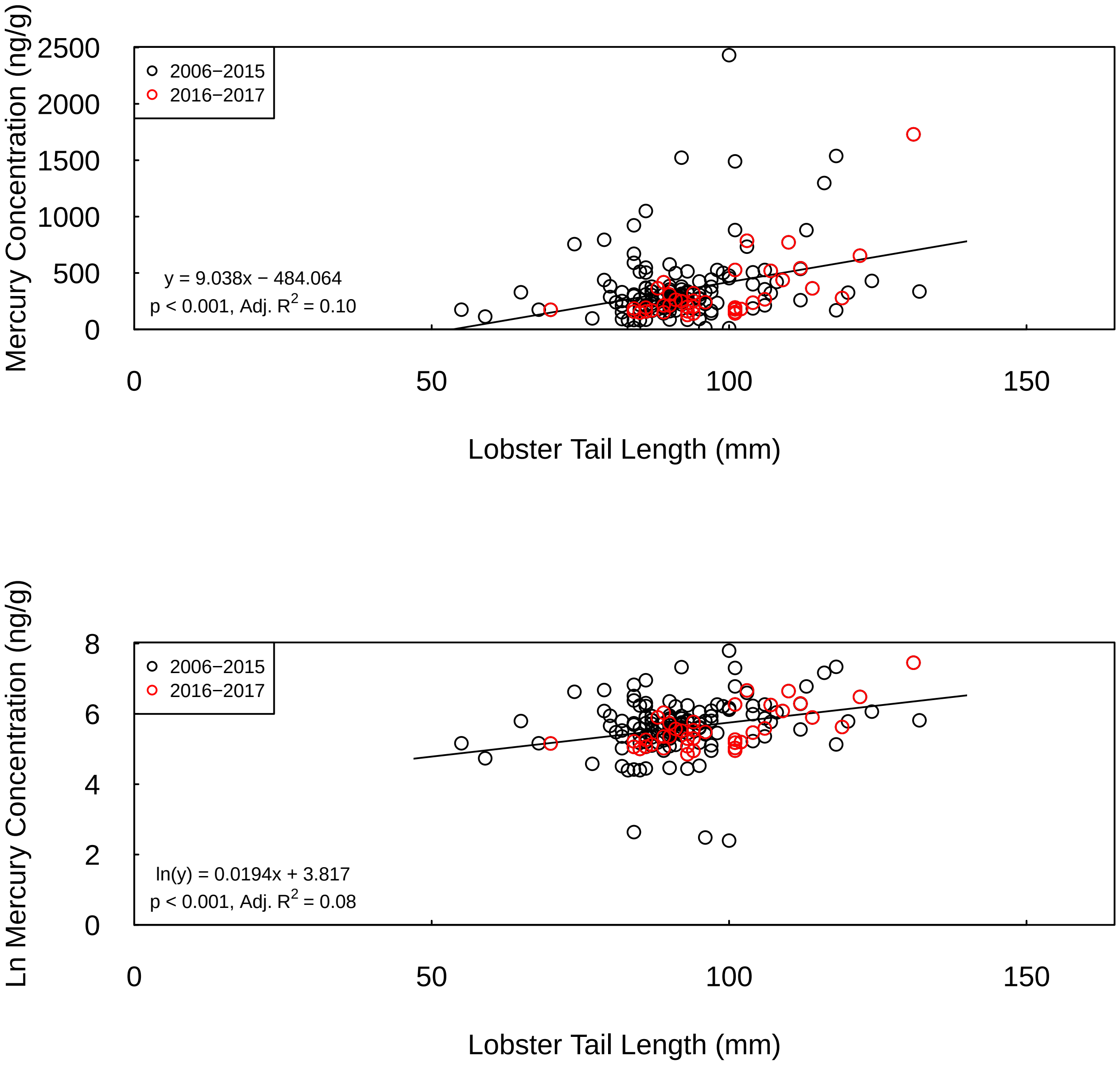


Includes lobster data from Odom Ledge, South Verona, Cape Jellison, Turner Point, and Harborside

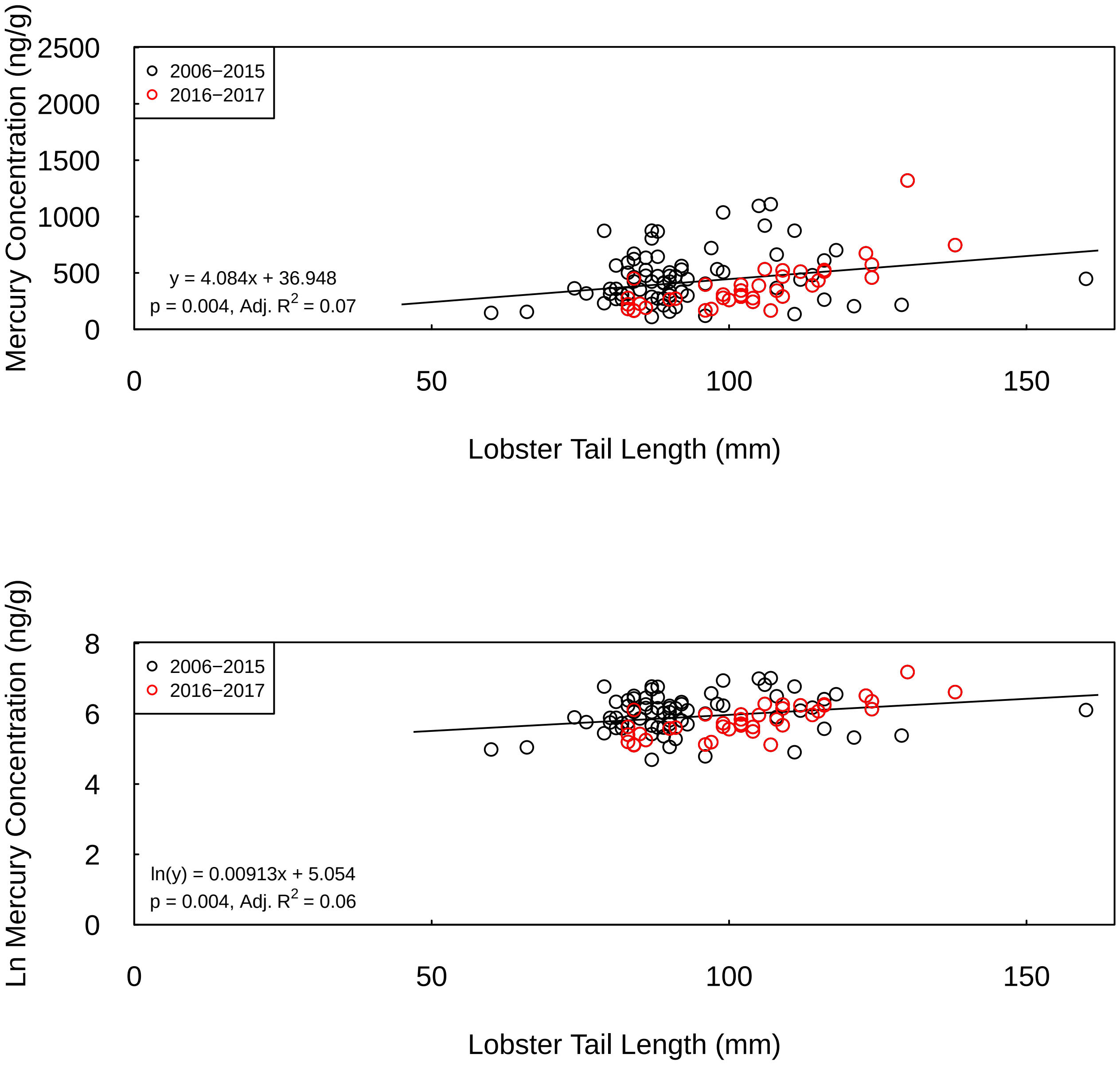


Includes lobster data from Odom Ledge, South Verona, Cape Jellison, Turner Point, and Harborside

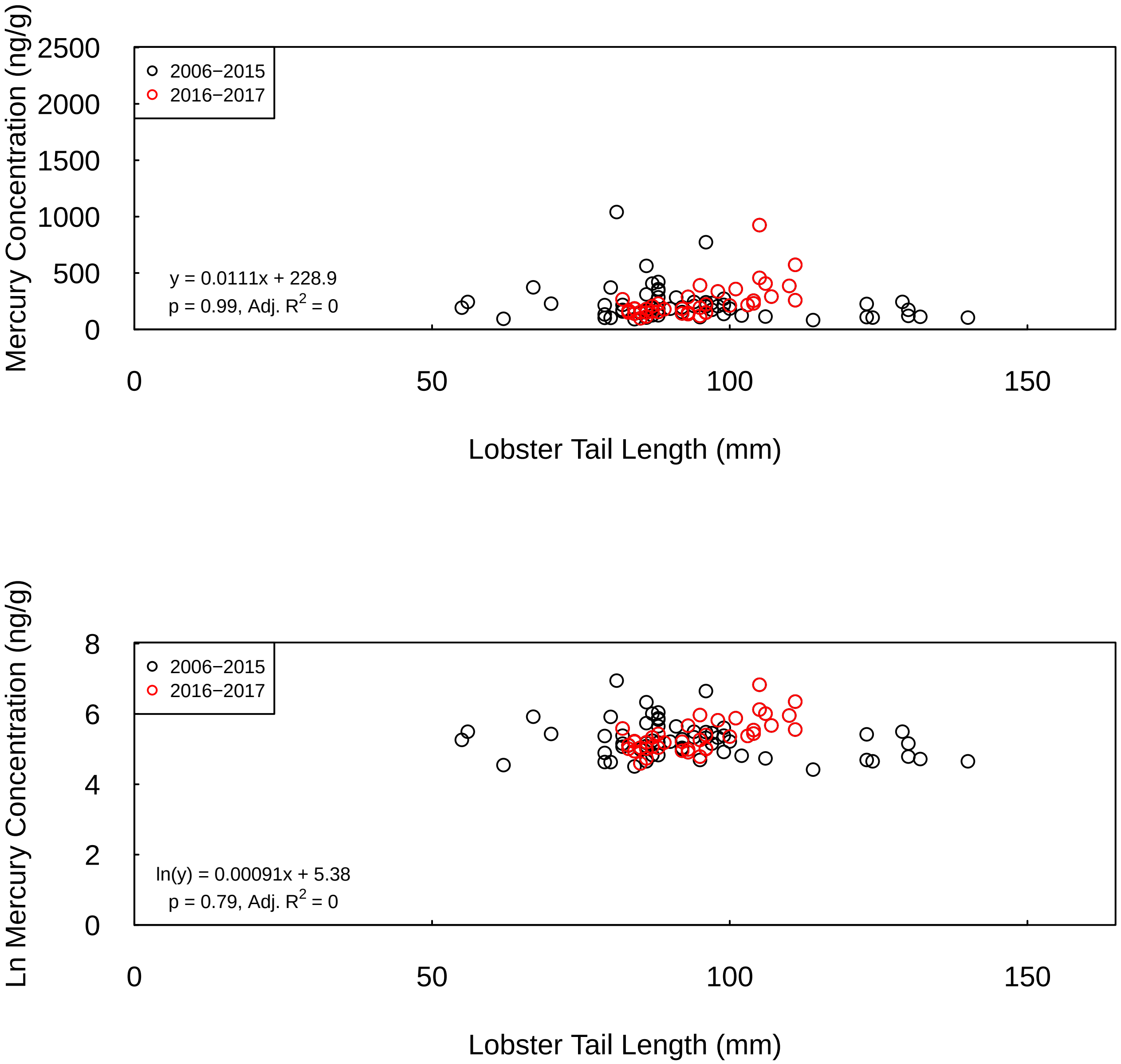
Odom Ledge Lobster Tail Length and Mercury Concentration



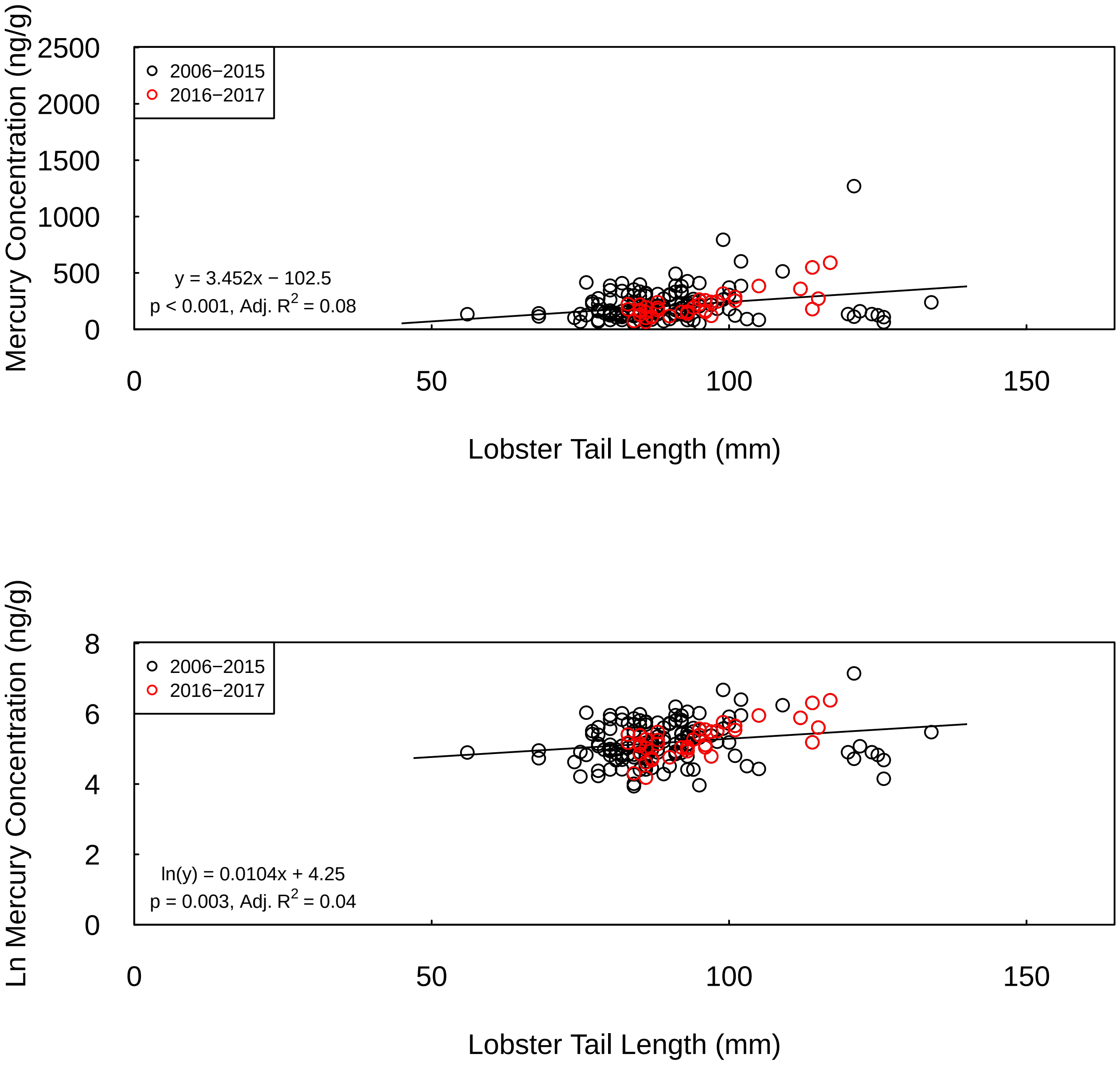
South Verona Lobster Tail Length and Mercury Concentration



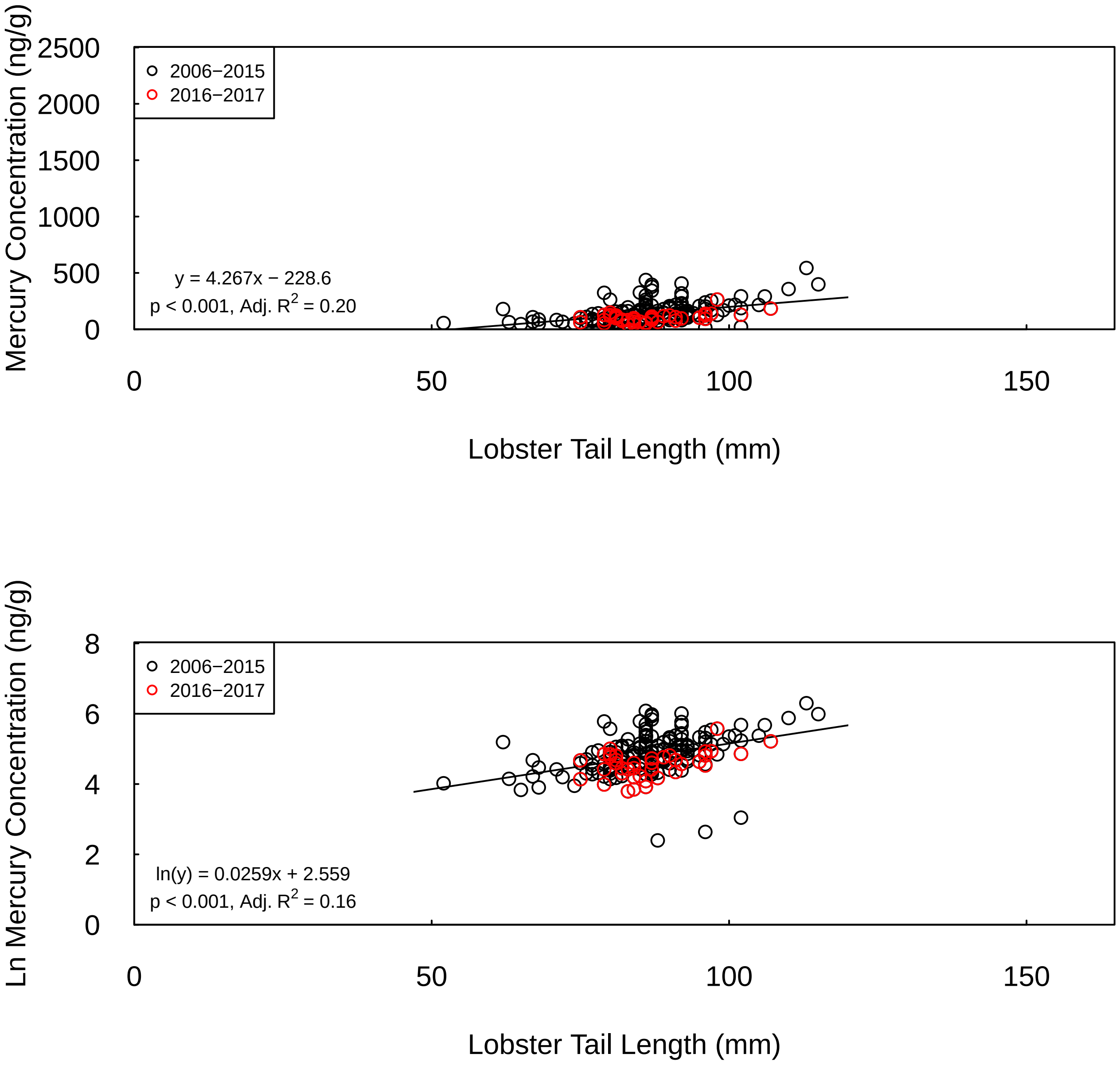
Cape Jellison Lobster Tail Length and Mercury Concentration



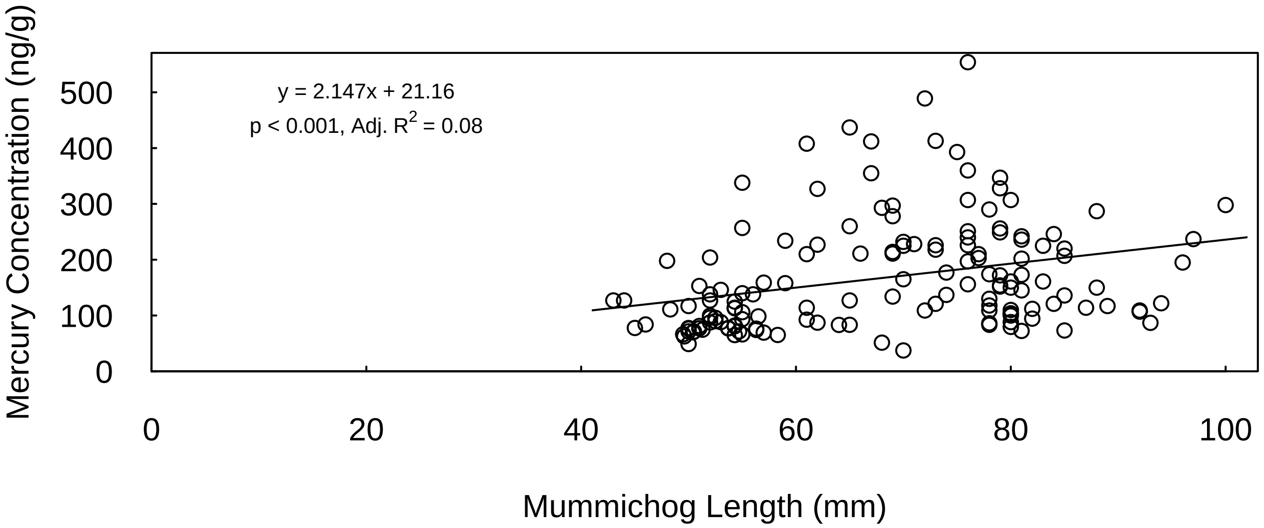
Turner Point Lobster Tail Length and Mercury Concentration



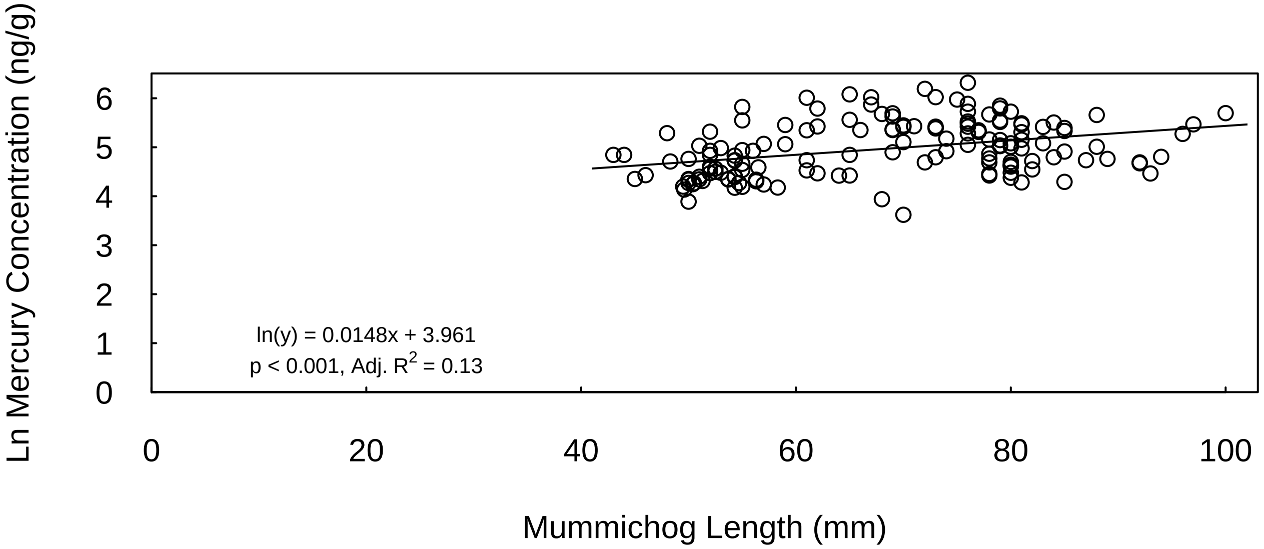
Harborside Lobster Tail Length and Mercury Concentration



Mummichog Length and Mercury Concentration

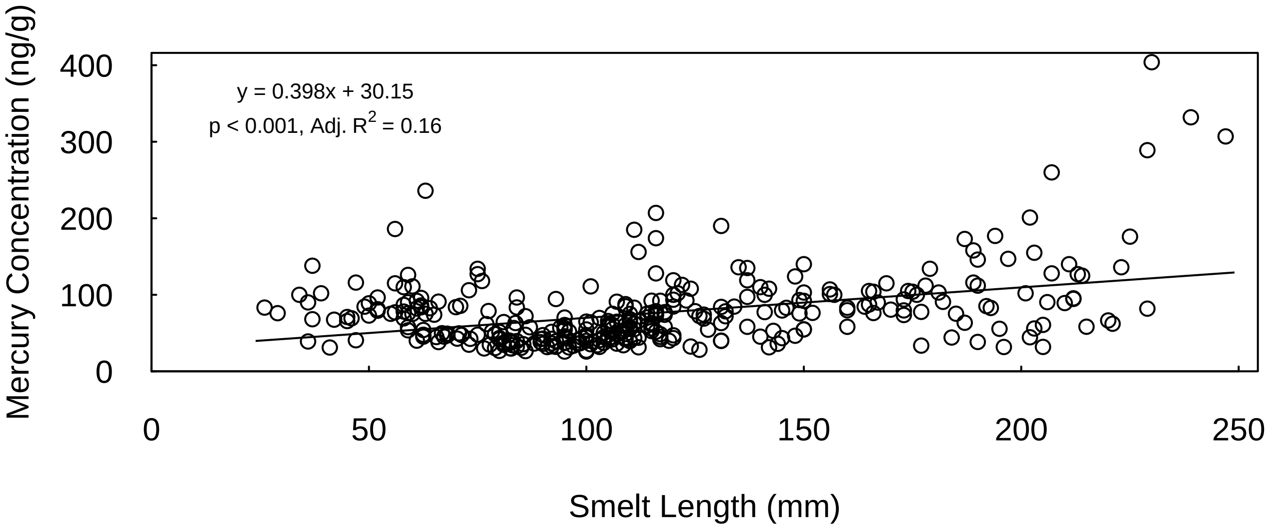


Includes Mummichog data from OB−05, OB−01, and Mendall Marsh

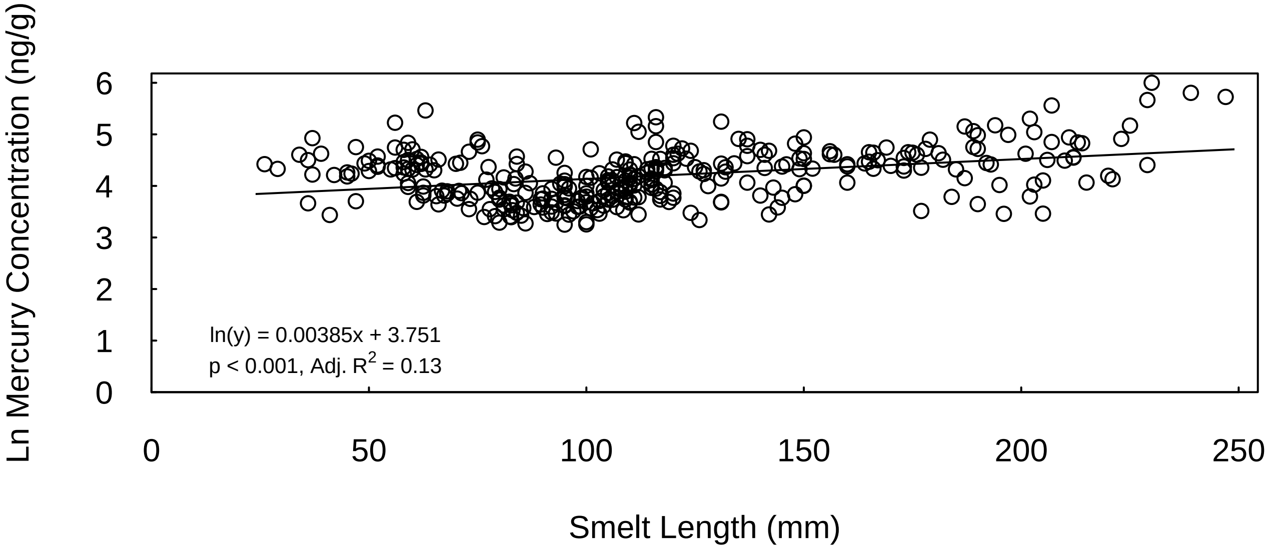


Includes Mummichog data from OB−05, OB−01, and Mendall Marsh

Smelt Length and Mercury Concentration

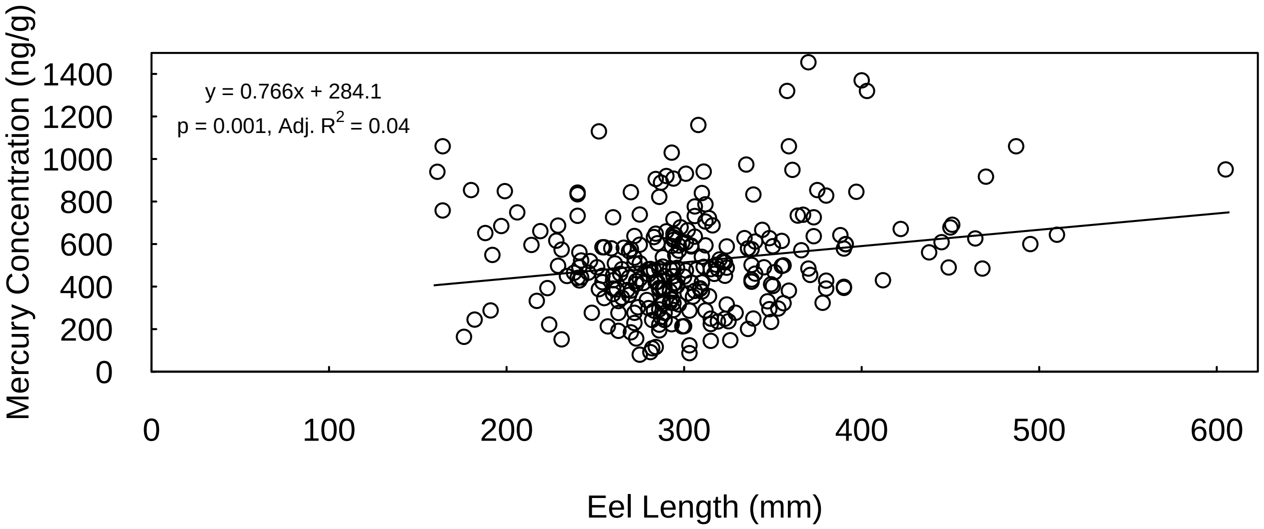


Includes Smelt data from ES−13, ES−15, OB−05, OB−01, OB−04, and Fort Point

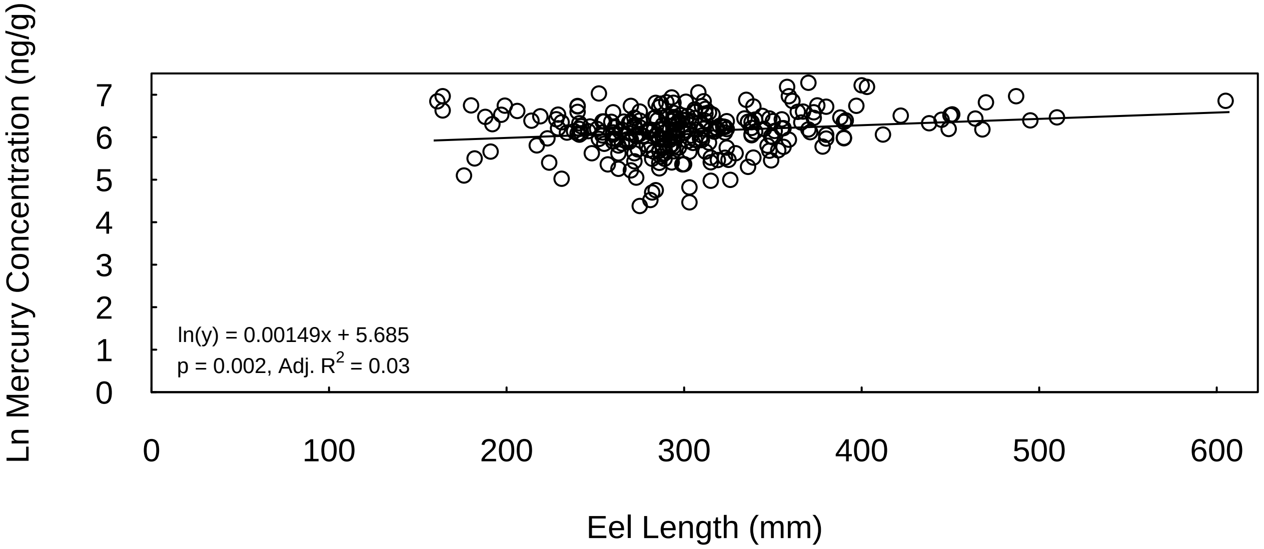


Includes Smelt data from ES−13, ES−15, OB−05, OB−01, OB−04, and Fort Point

Eel Length and Mercury Concentration

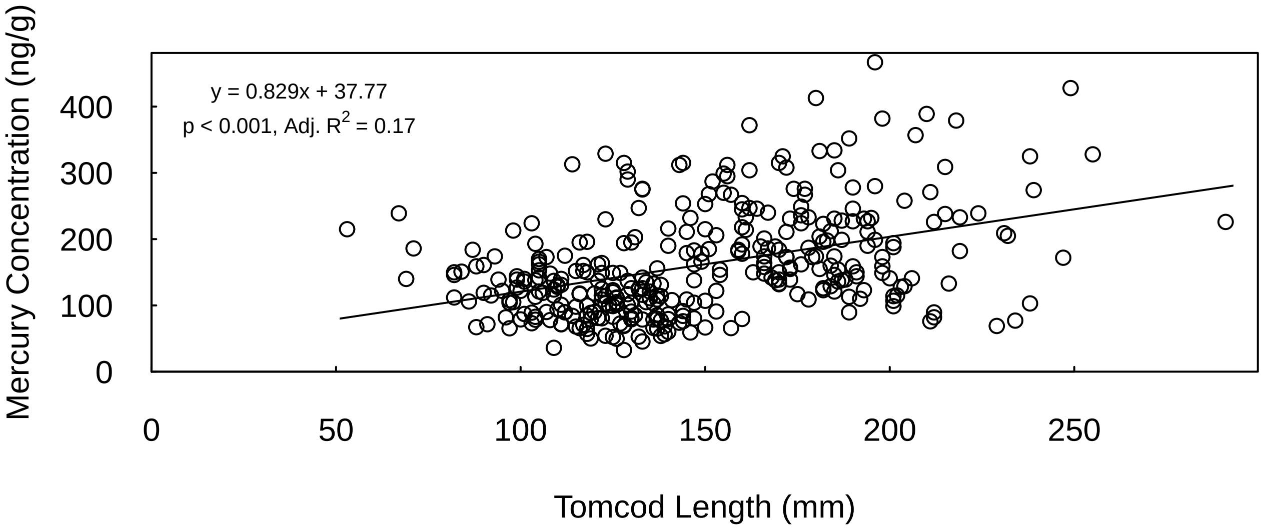


Includes Eel data from OB−05, OB−01, and BO−04

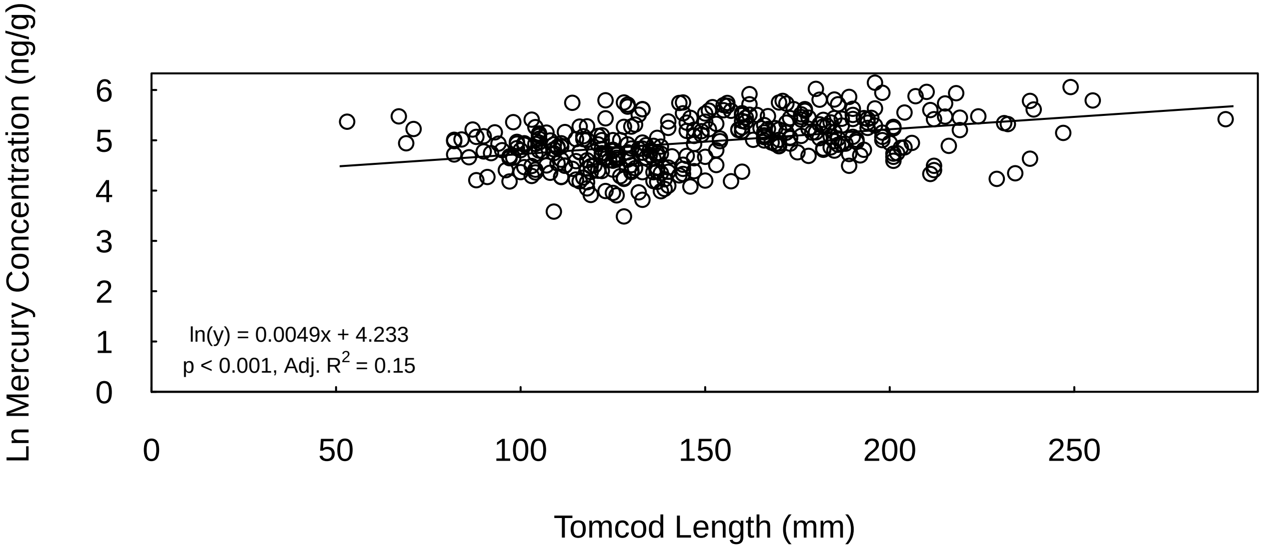


Includes Eel data from OB−05, OB−01, and BO−04

Tomcod Length and Mercury Concentration

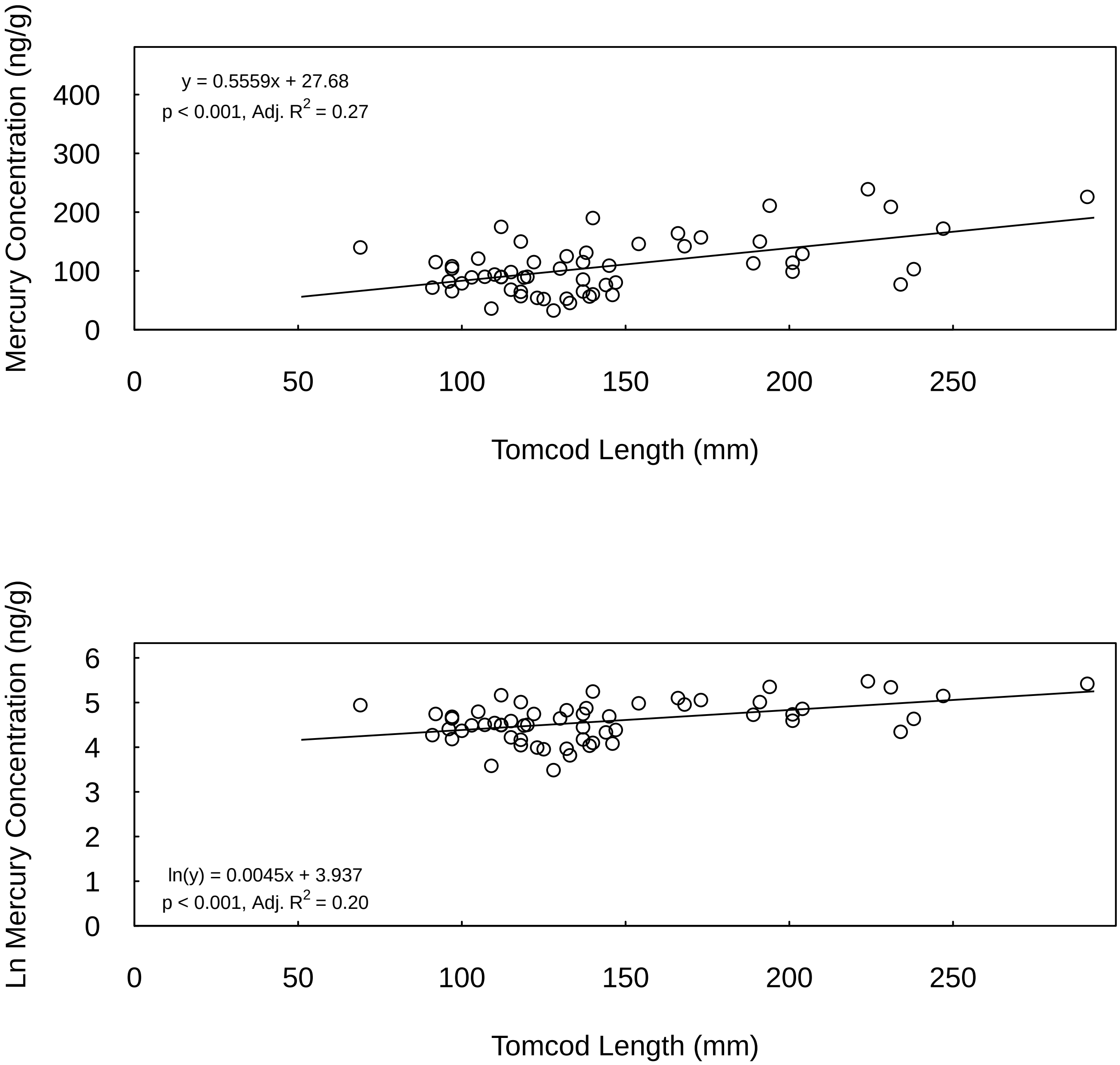


Includes Tomcod data from ES−13, OB−05, OB−01, and BO−04

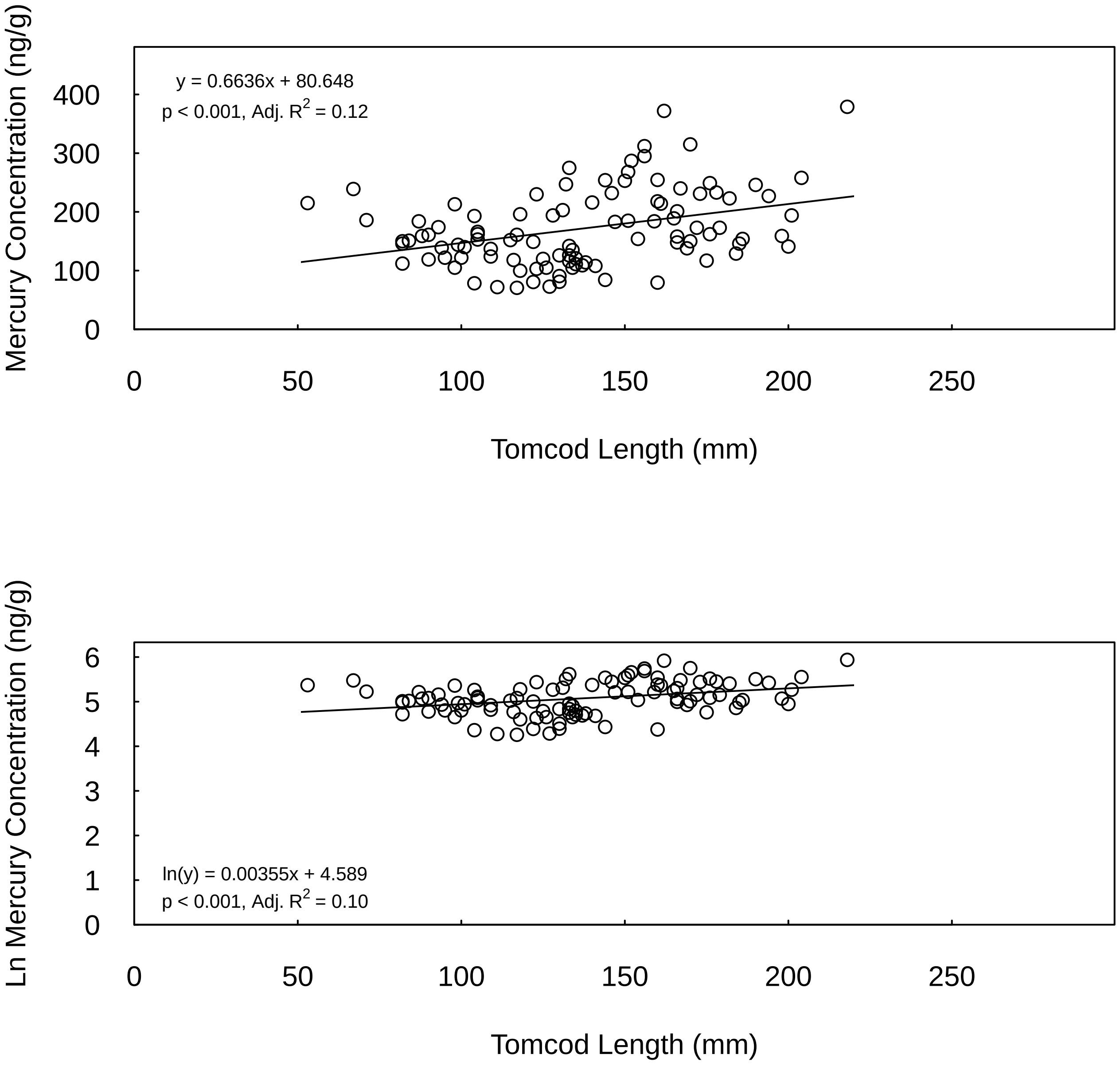


Includes Tomcod data from ES−13, OB−05, OB−01, and BO−04

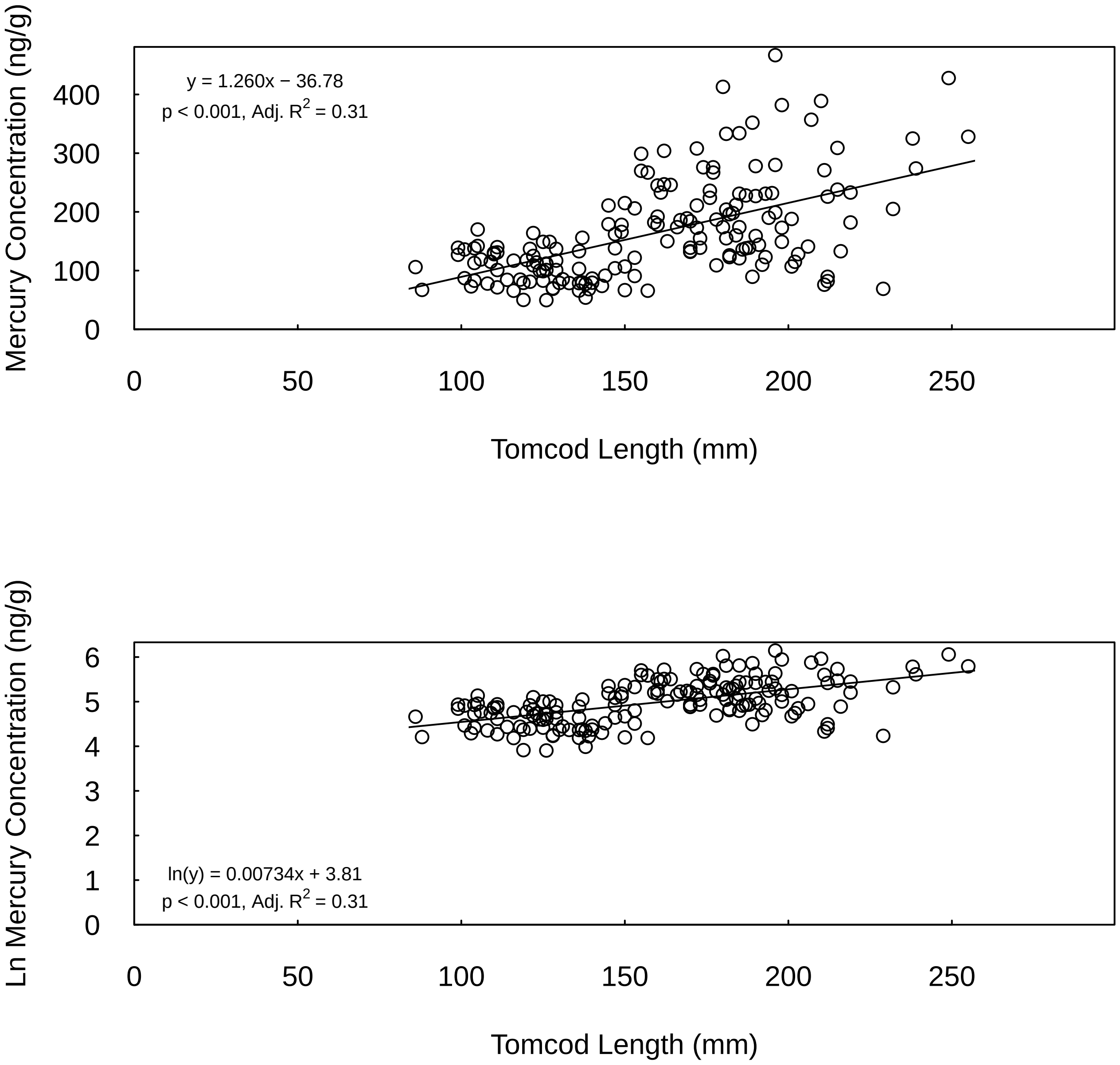
ES−13 Tomcod Length and Mercury Concentration



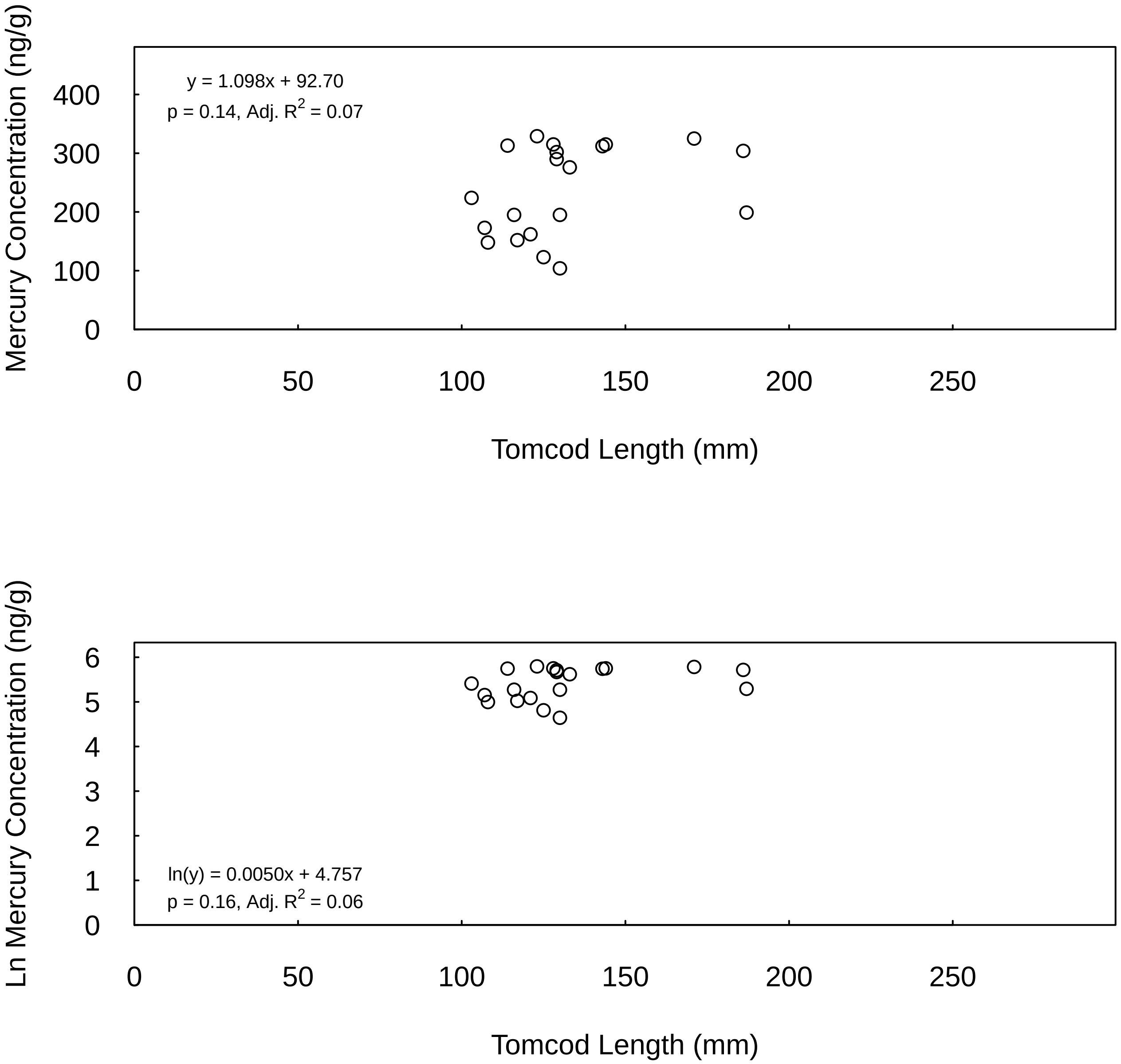
OB−05 Tomcod Length and Mercury Concentration



OB−01 Tomcod Length and Mercury Concentration

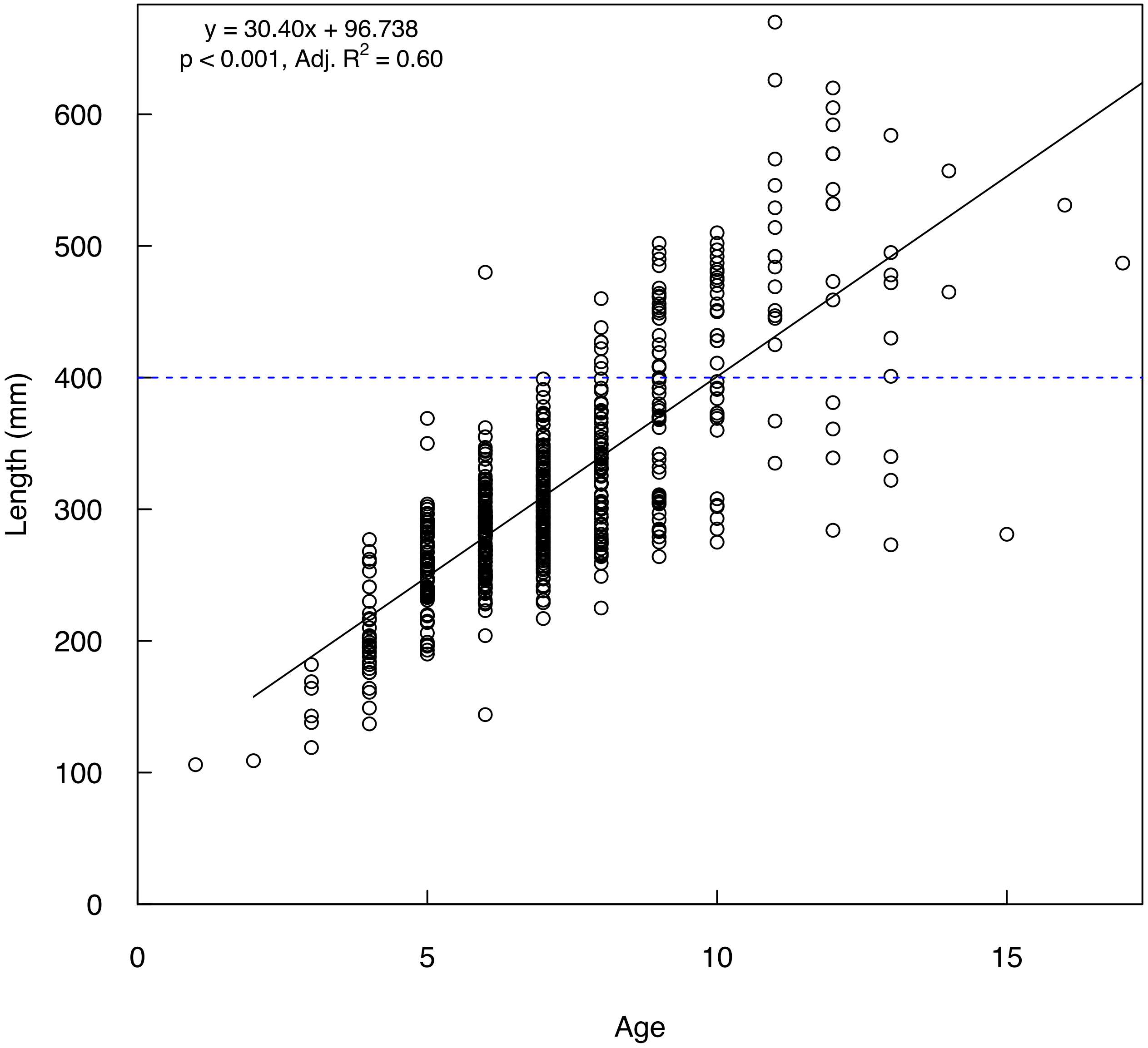


BO−04 Tomcod Length and Mercury Concentration



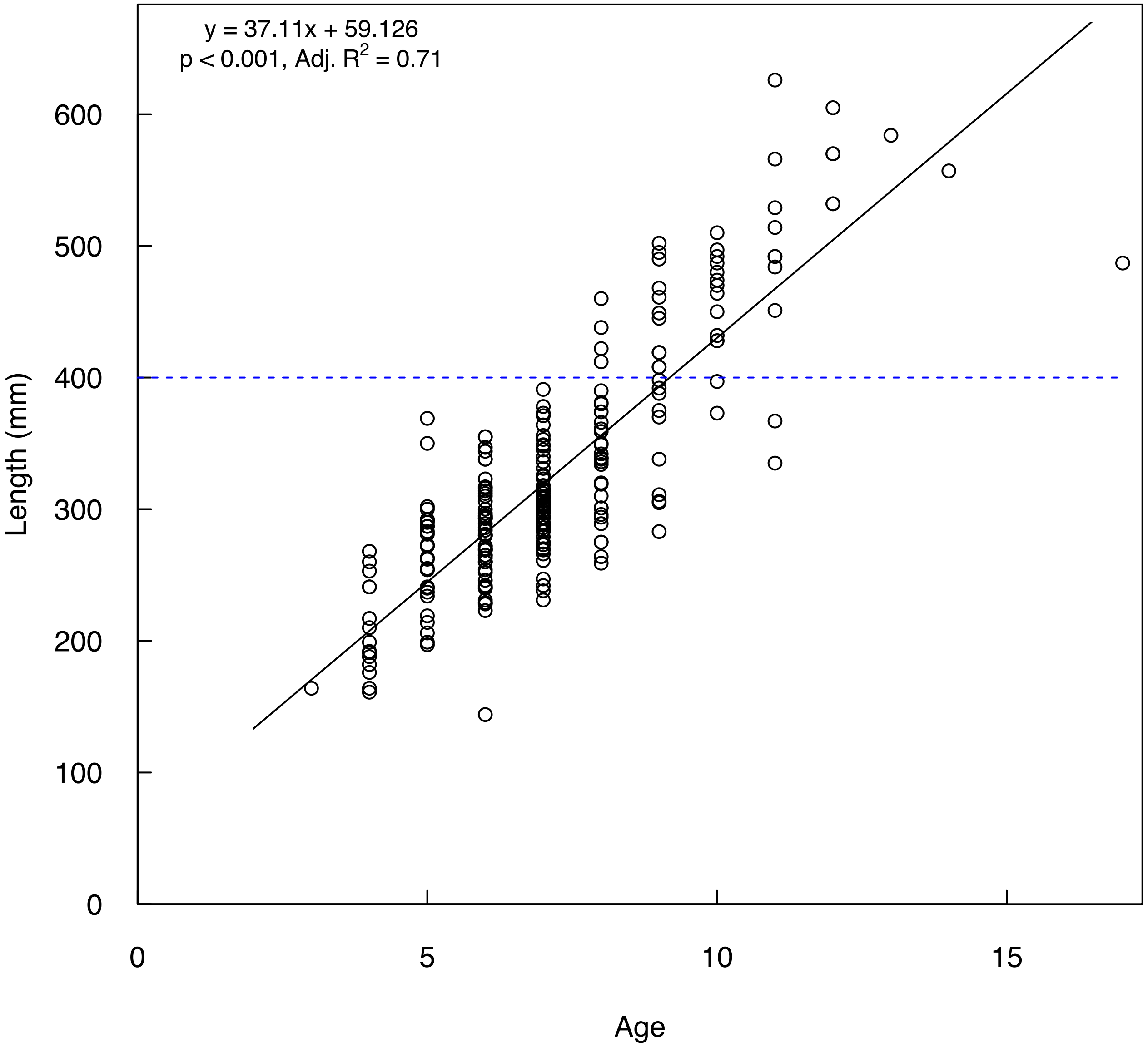
APPENDIX G-2

Age-Length Relationship in Eel

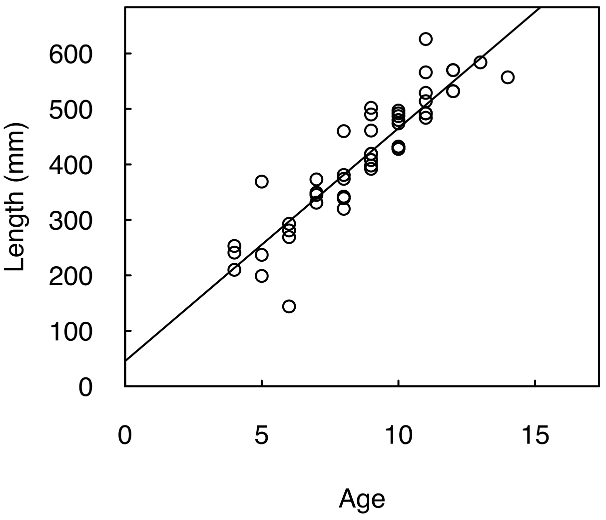


American Eel Lengths and Ages at All Sample Locations
Includes Historical and 2016 Data

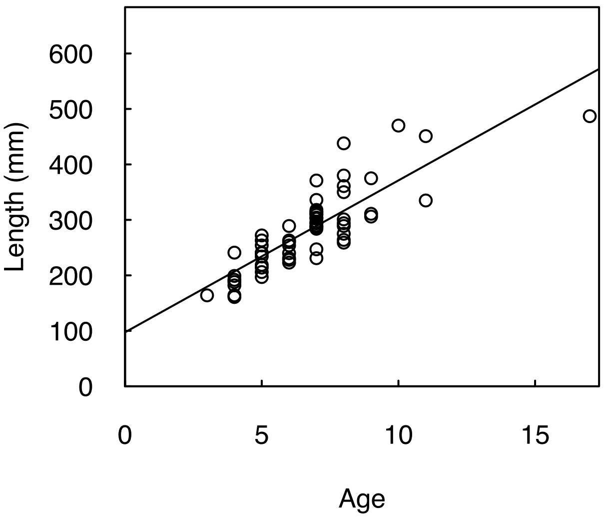
American Eel Lengths and Ages at Locations Sampled in 2016
Includes Historical Data



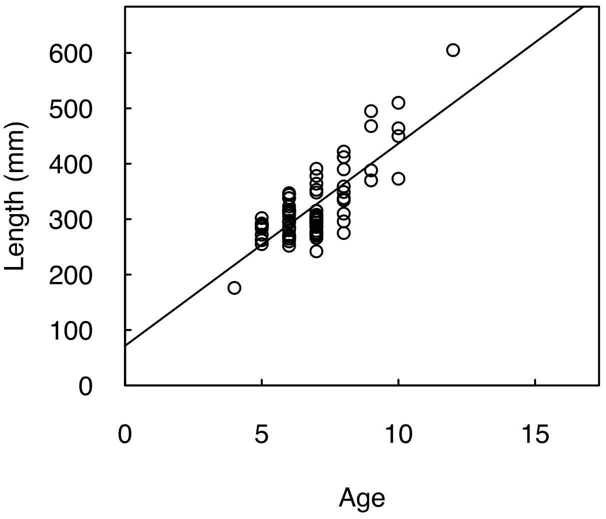
OV−04



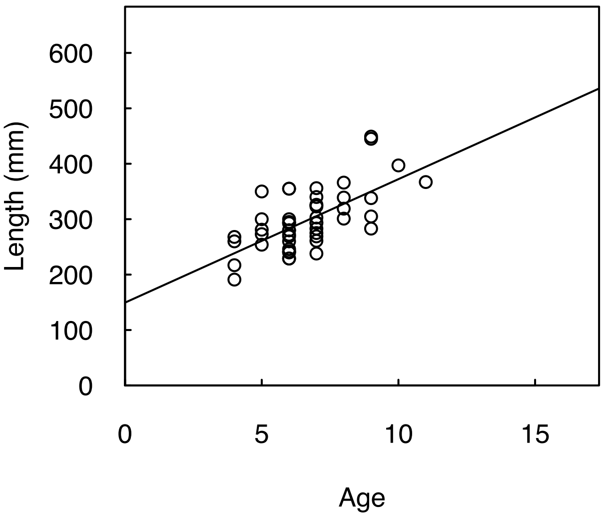
BO−04



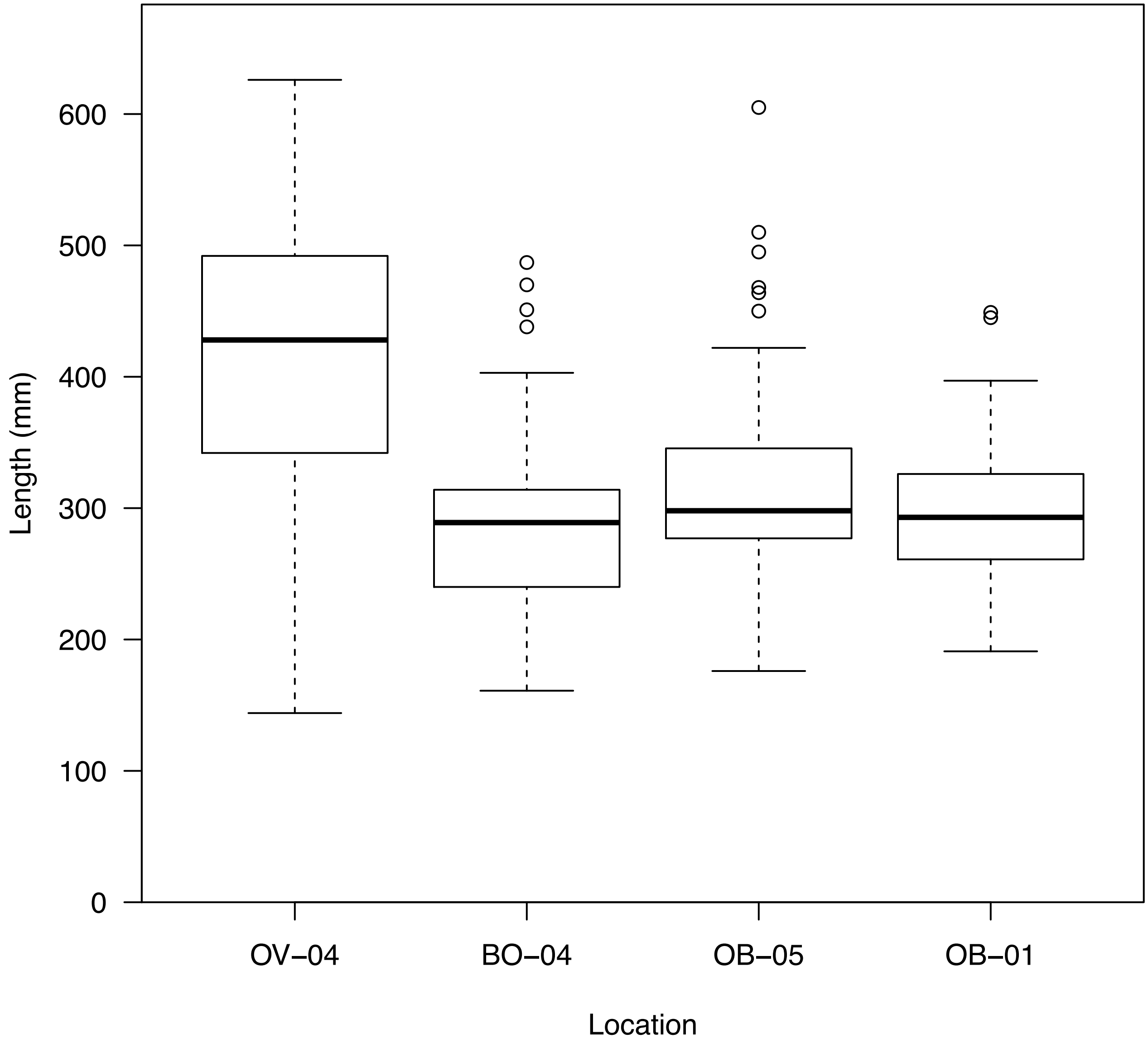
OB−05

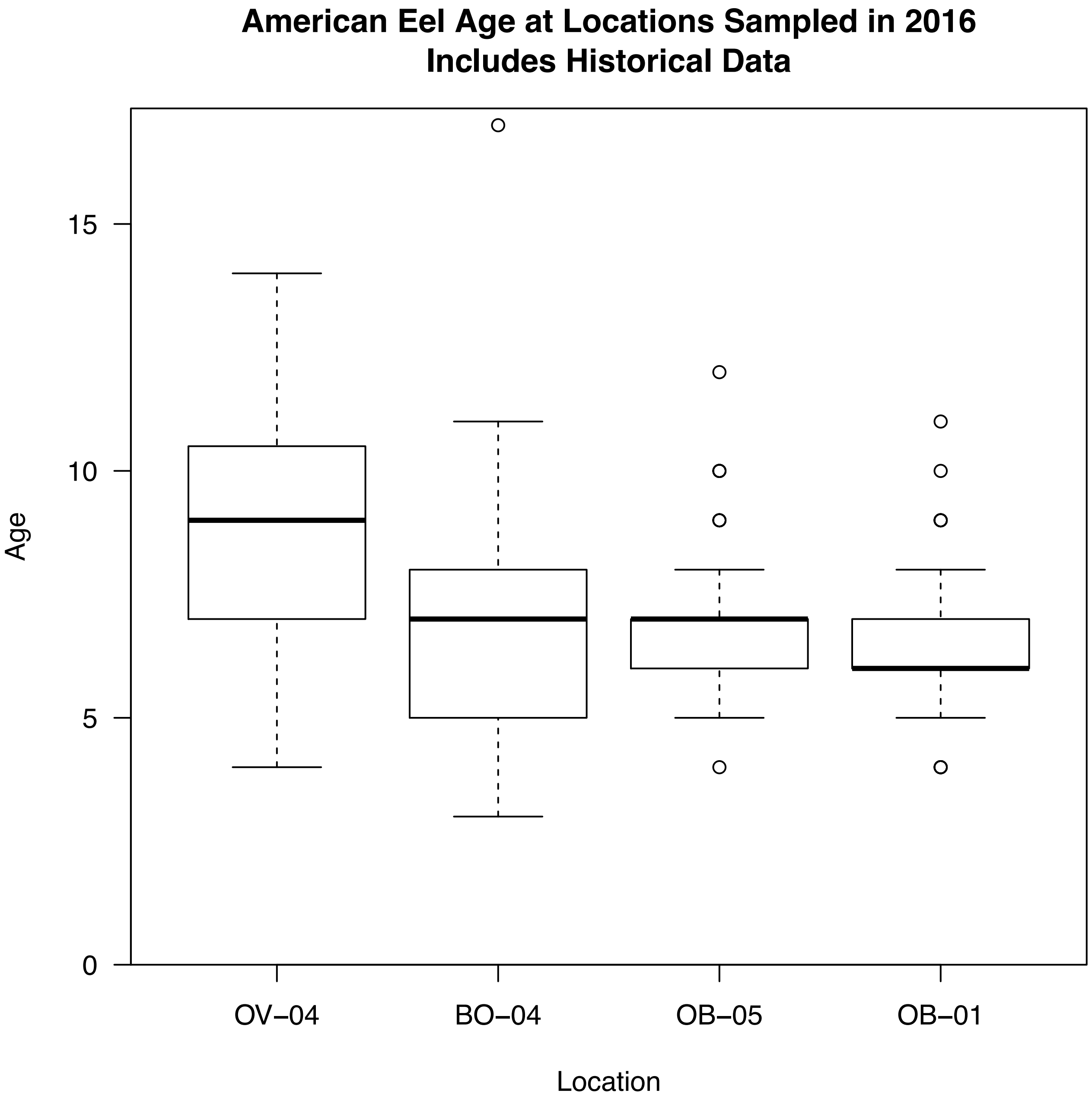


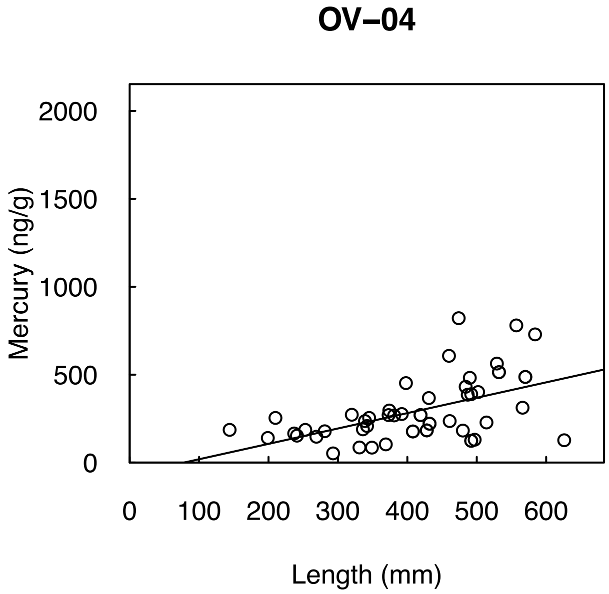
OB−01

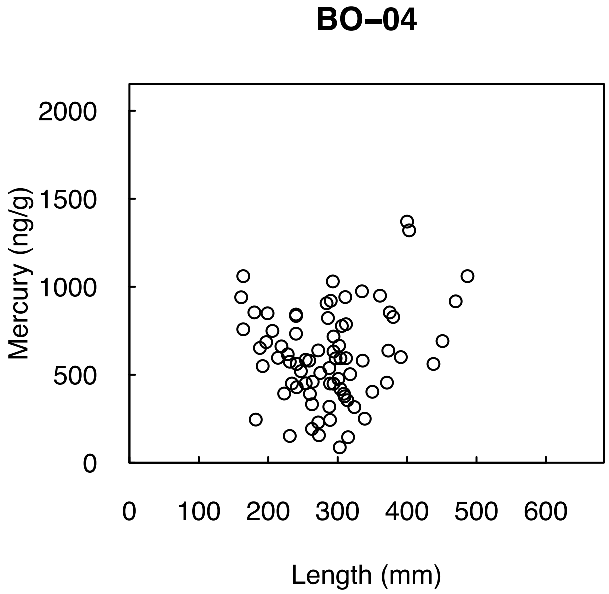


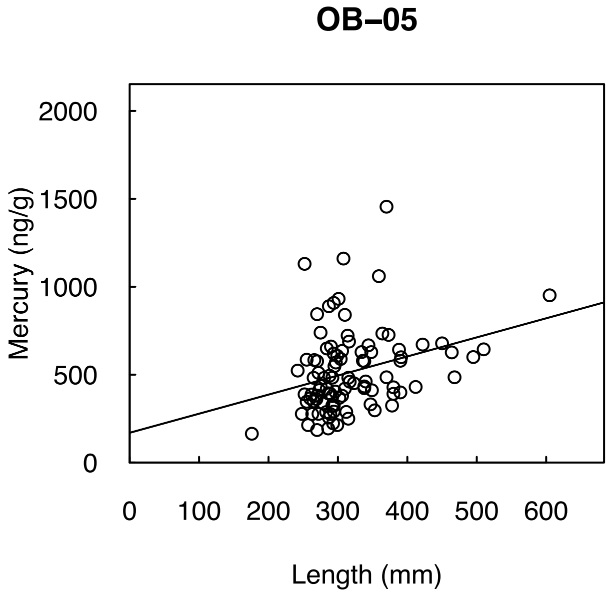
American Eel Lengths at Locations Sampled in 2016
Includes Historical and 2016 Data

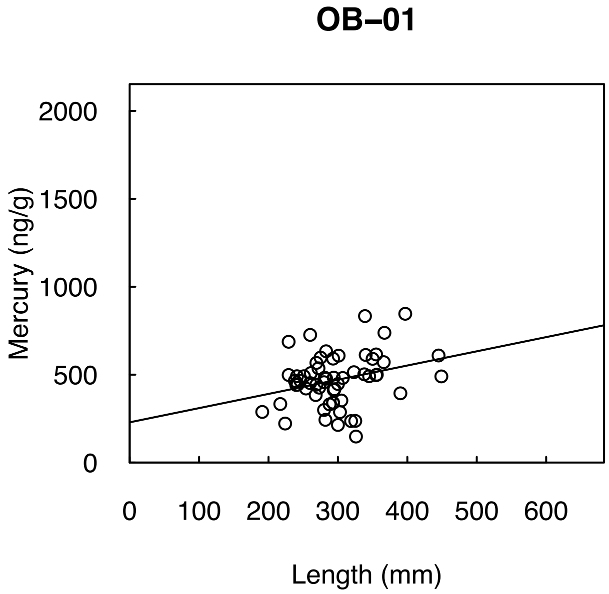


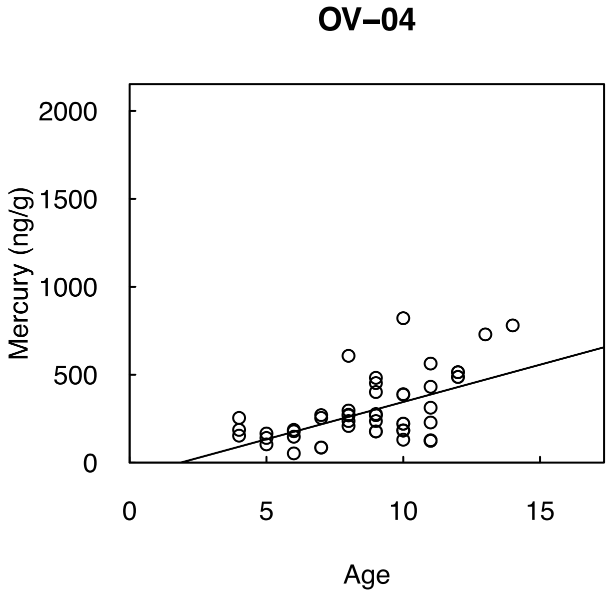

American Eel Age at Locations Sampled in 2016
Includes Historical Data
Age
0
5
10
15
OV−04
BO−04
OB−05
OB−01
Location

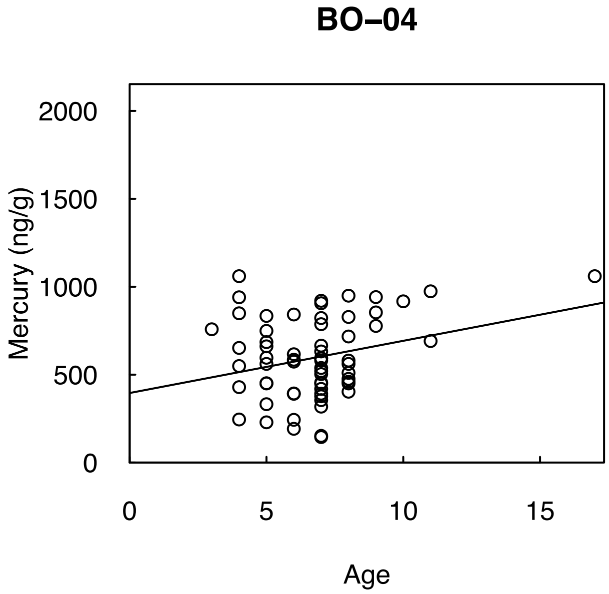

OV−04
Mercury (ng/g)
0
500
1000
1500
2000
0
100
200
300
400
500
600
Length (mm)

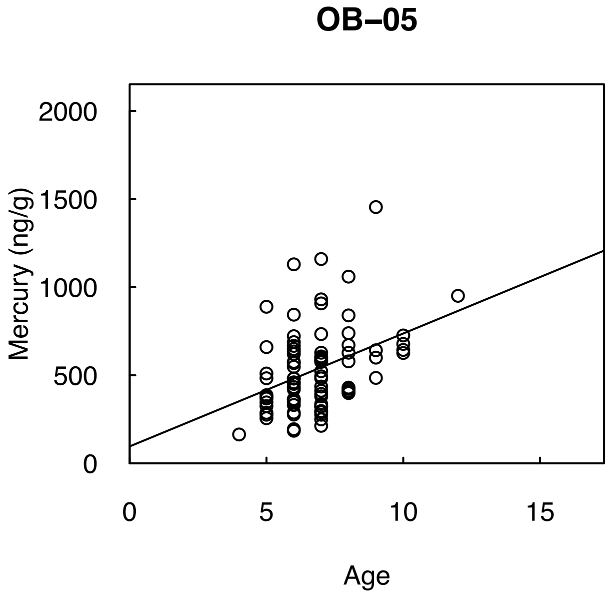

BO−04
Mercury (ng/g)
0
500
1000
1500
2000
0
100
200
300
400
500
600
Length (mm)

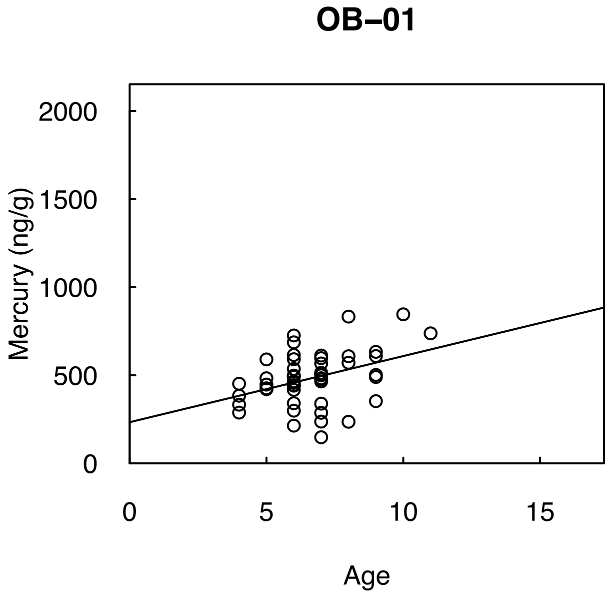

OB−05
Mercury (ng/g)
0
500
1000
1500
2000
0
100
200
300
400
500
600
Length (mm)

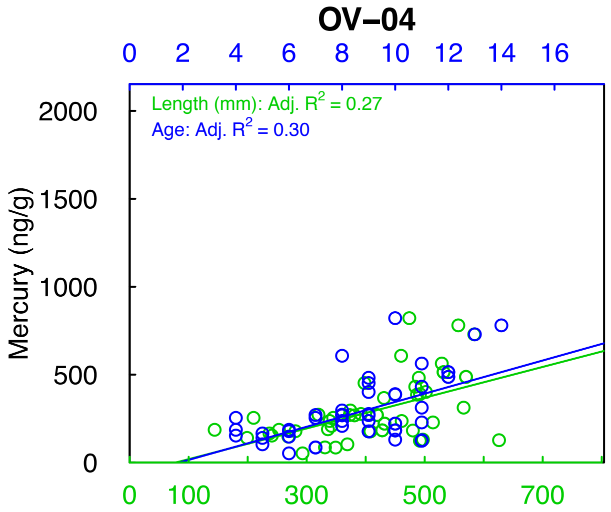

OB−01
Mercury (ng/g)
0
500
1000
1500
2000
0
100
200
300
400
500
600
Length (mm)

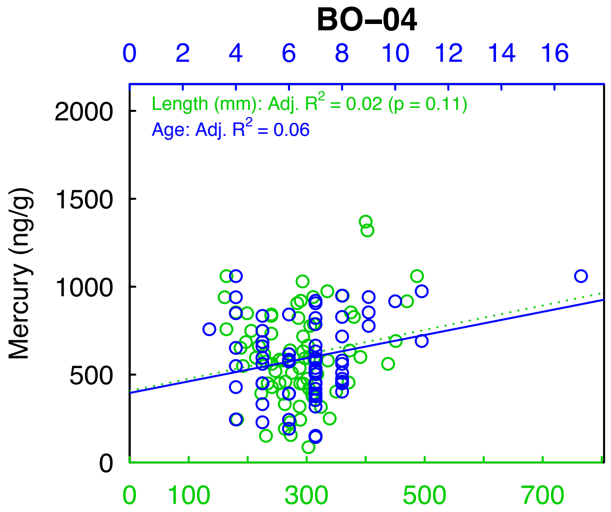

OV−04

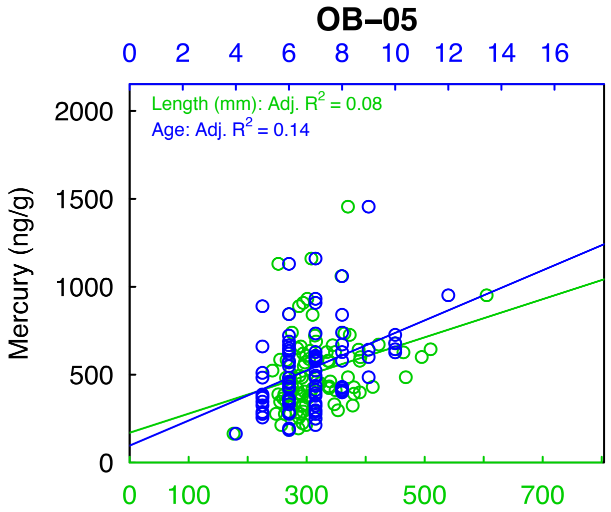

BO−04

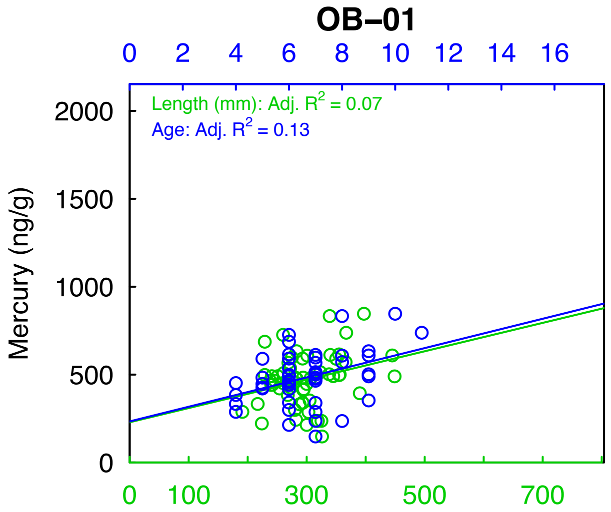

OB−05


OB−01


OV−04
0 2 4 6 8 10 12 14 16
Length (mm): Adj. R^2 = 0.27
Age: Adj. R^2 = 0.30
Mercury (ng/g)
2000
1500
1000
500
0
0 100 300 500 700


BO−04
0 2 4 6 8 10 12 14 16
Length (mm): Adj. R^2 = 0.02 (p = 0.11)
Age: Adj. R^2 = 0.06
Mercury (ng/g)
2000
1500
1000
500
0
0 100 300 500 700

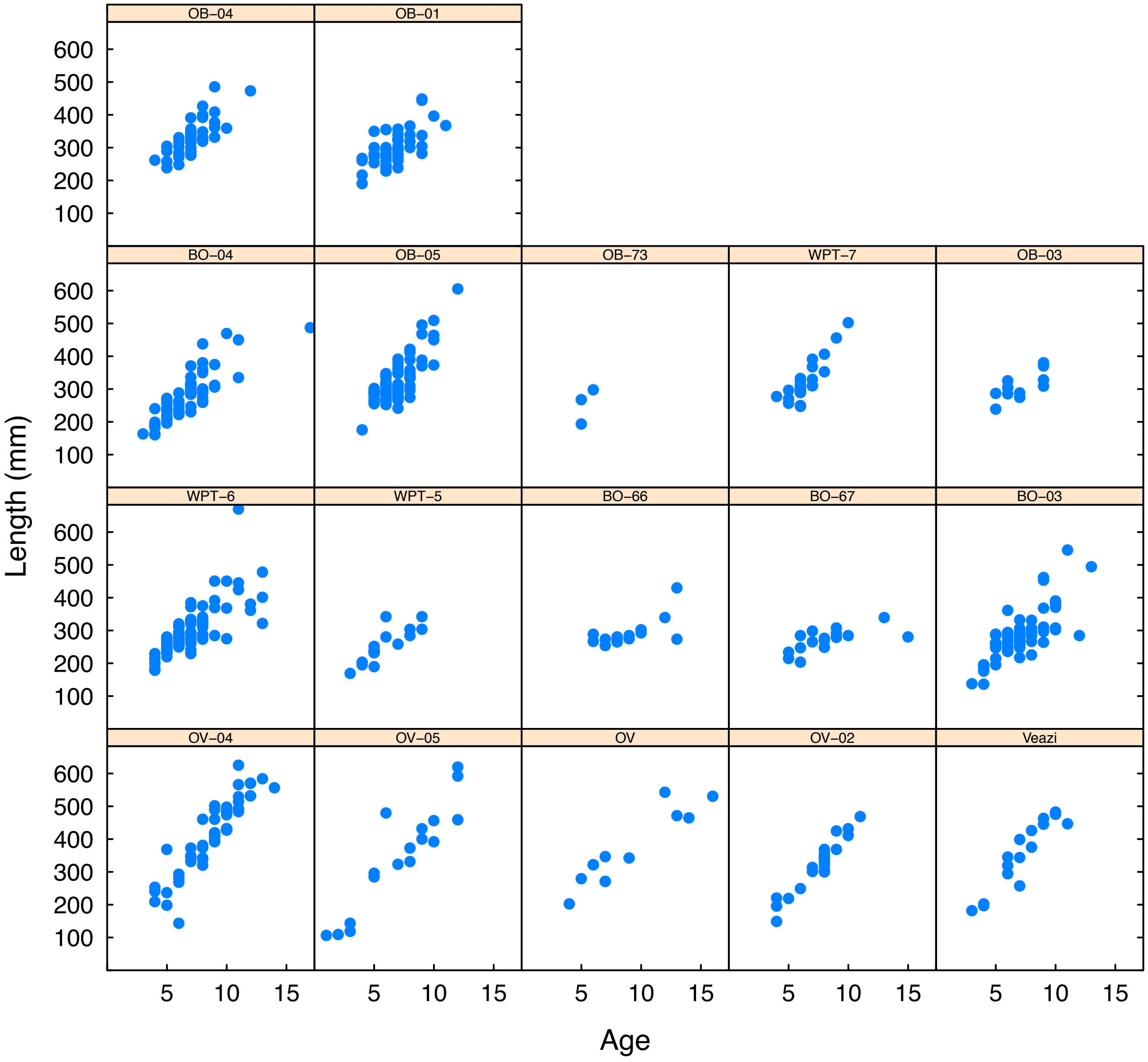

OB−05
0 2 4 6 8 10 12 14 16
Length (mm): Adj. R^2 = 0.08
Age: Adj. R^2 = 0.14
Mercury (ng/g)
2000
1500
1000
500
0
0 100 300 500 700


OB−01
0 2 4 6 8 10 12 14 16
Length (mm): Adj. R^2 = 0.07
Age: Adj. R^2 = 0.13
Mercury (ng/g)
2000
1500
1000
500
0
0 100 300 500 700

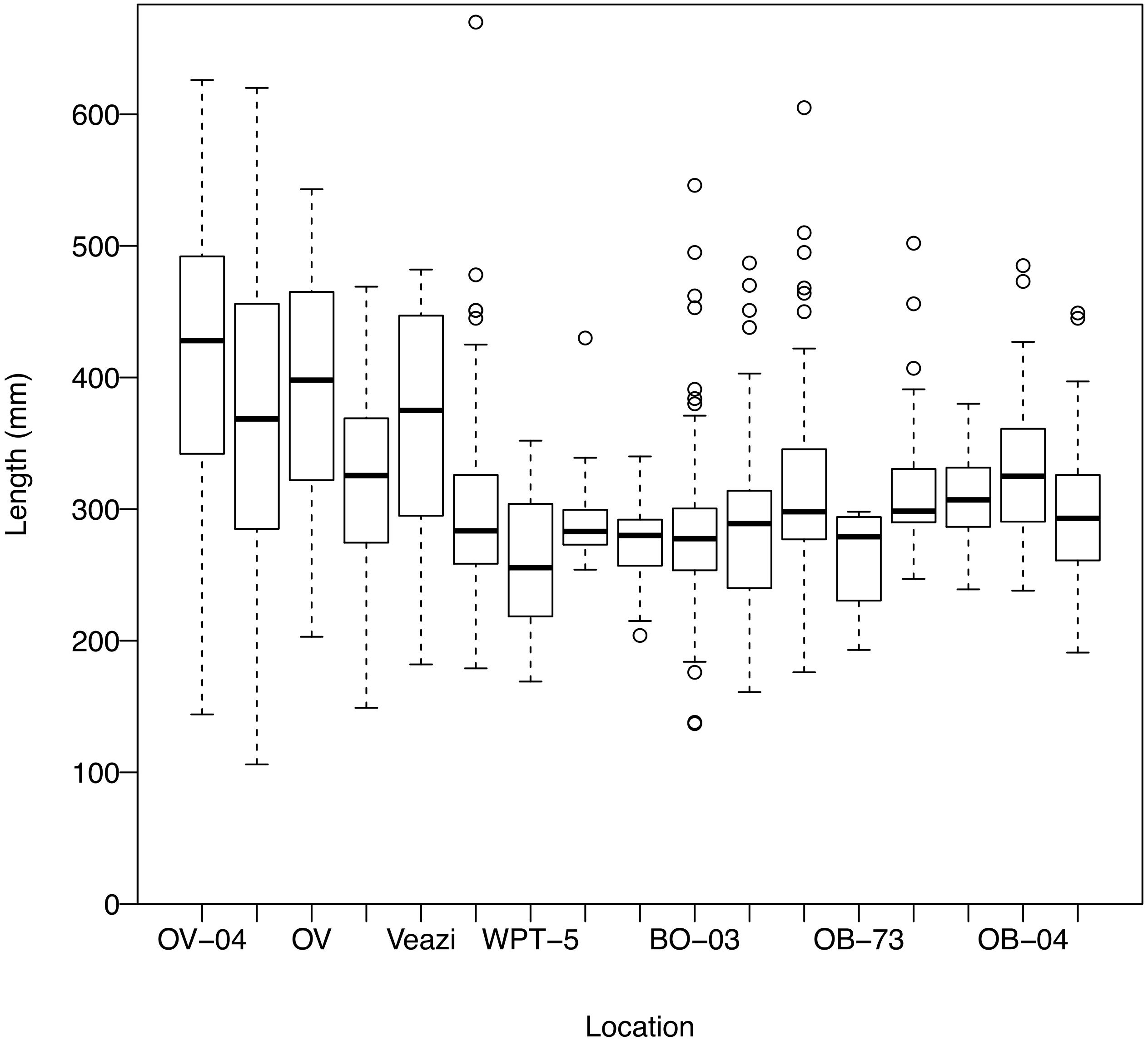
Additional Information:

The following figures show data for all locations where eel were collected

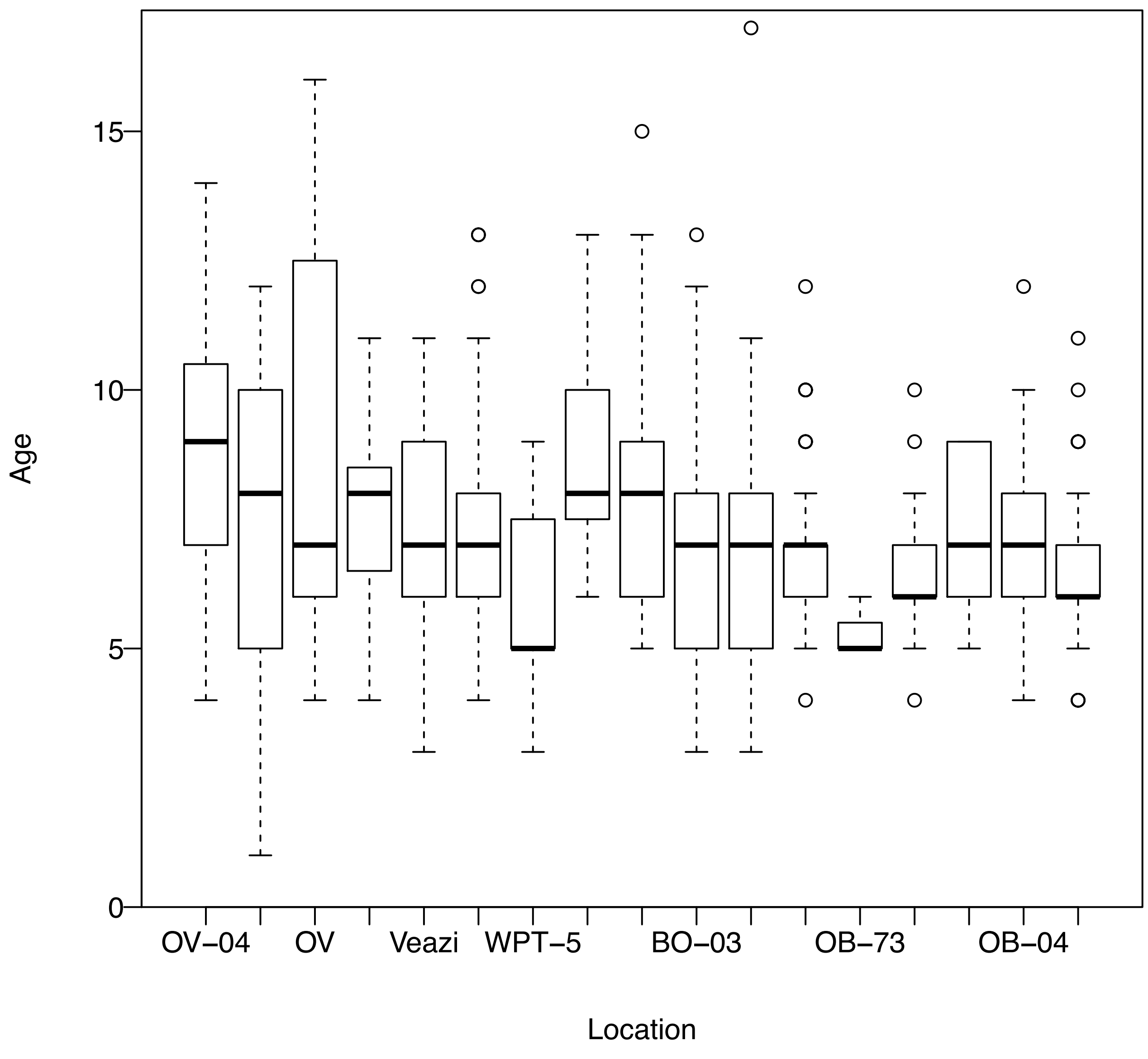
American Eel Lengths and Ages at All Sample Locations
Includes Historical Data



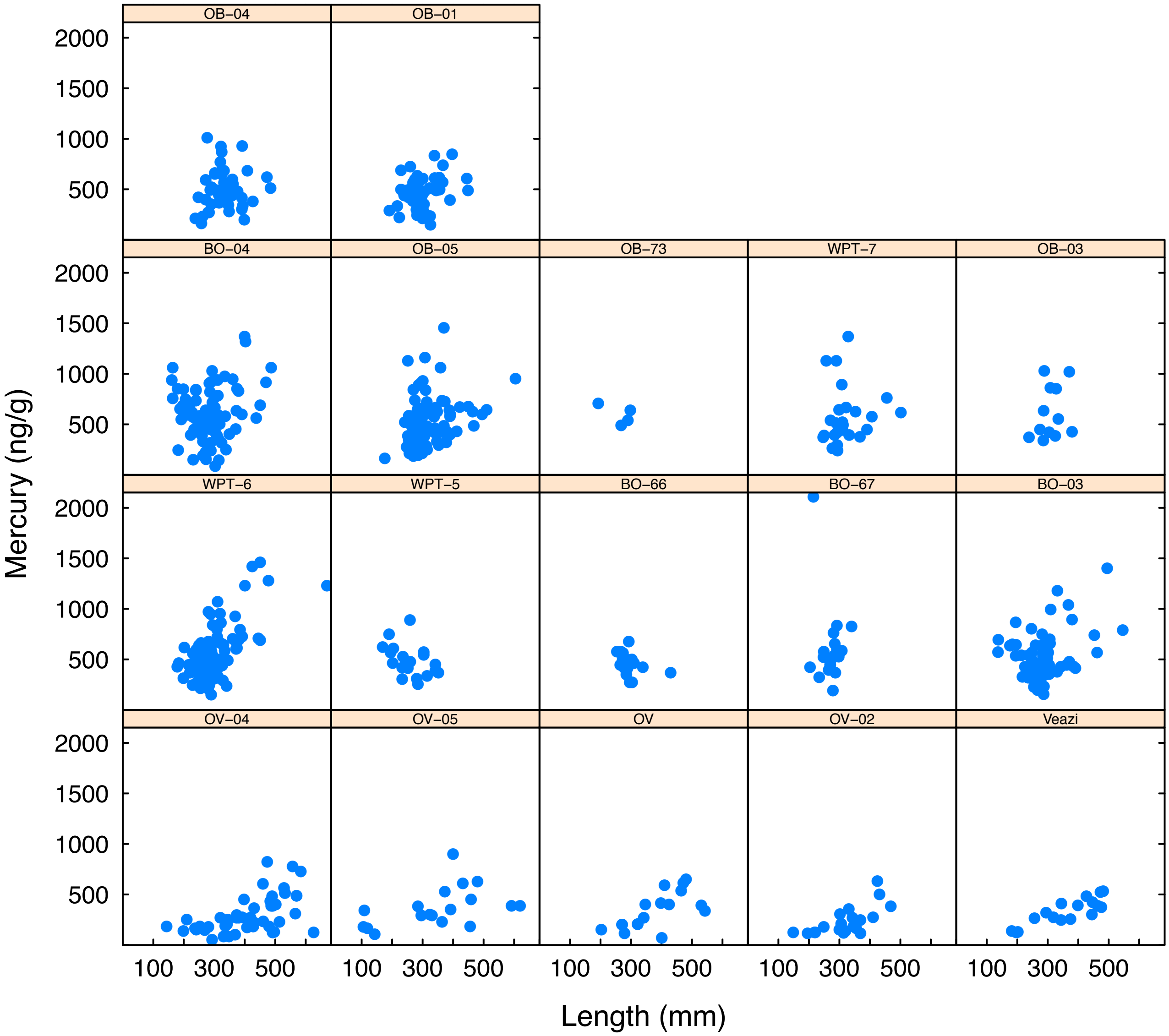
American Eel Lengths at All Sample Locations
Includes Historical and 2016 Data



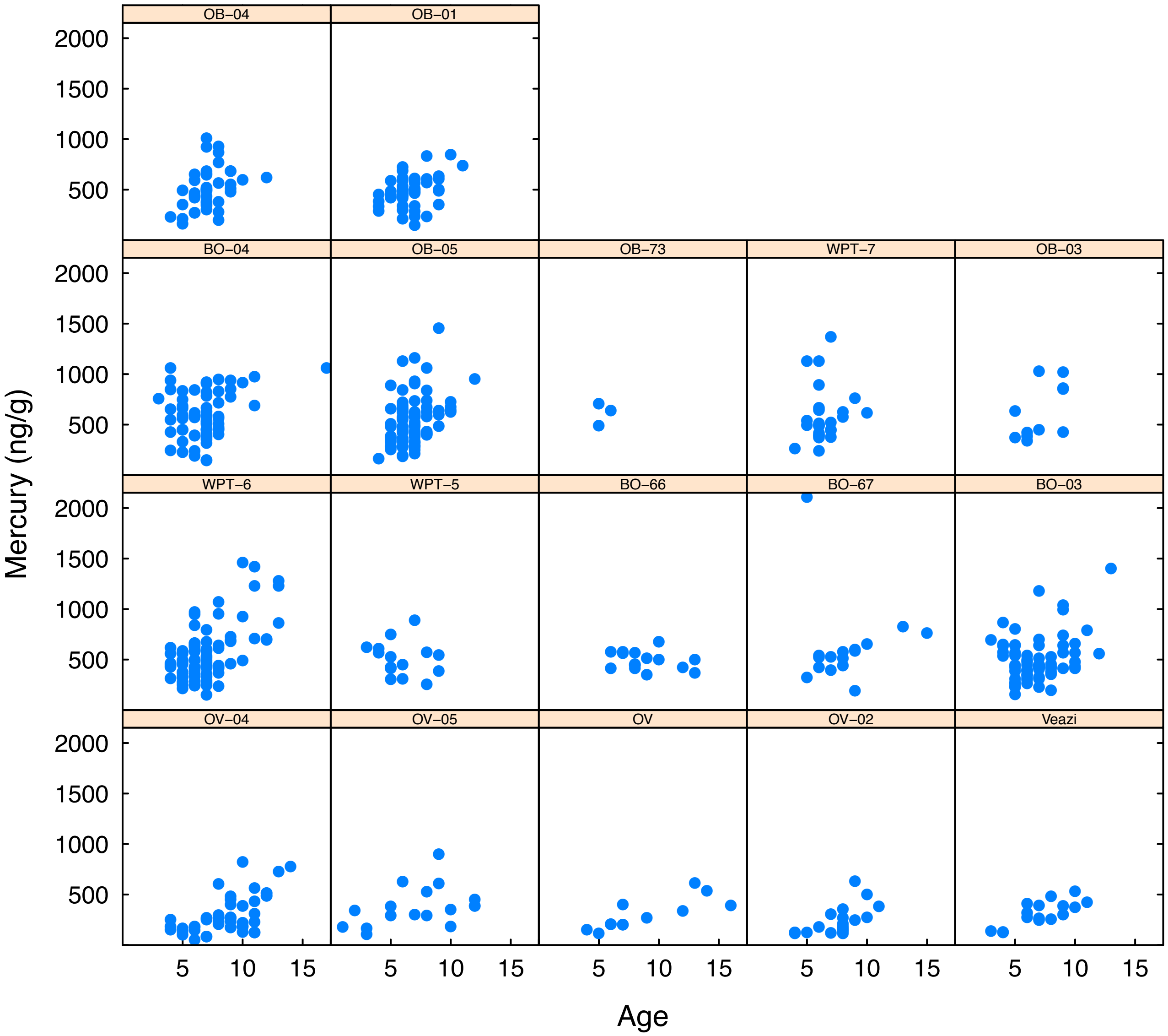
American Eel Age at All Sample Locations
Includes Historical Data



American Eel Length and Mercury Concentration
at All Sample Locations
Includes Historical and 2016 Data



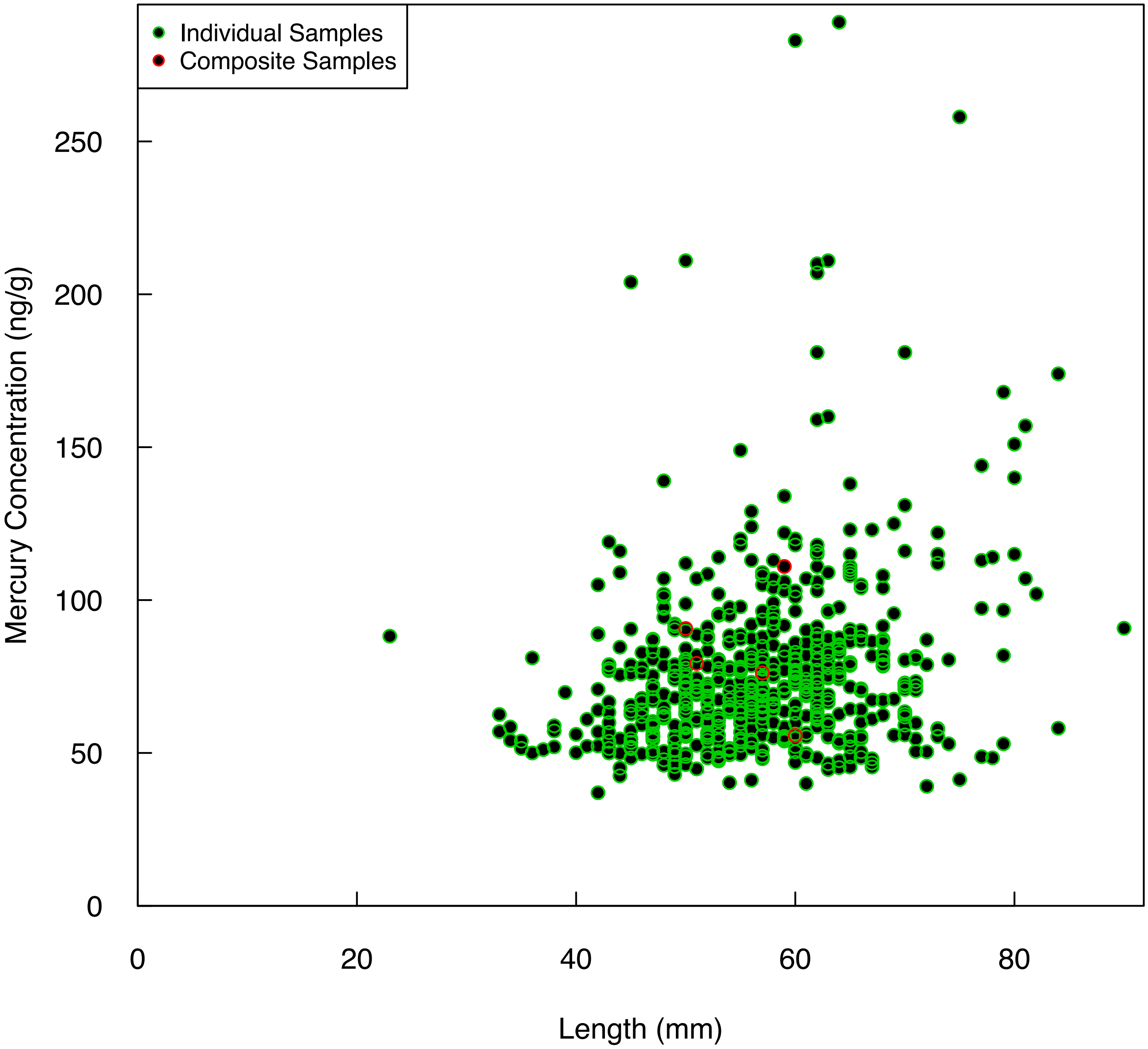
American Eel Age and Mercury Concentration
at All Sample Locations
Includes Historical Data



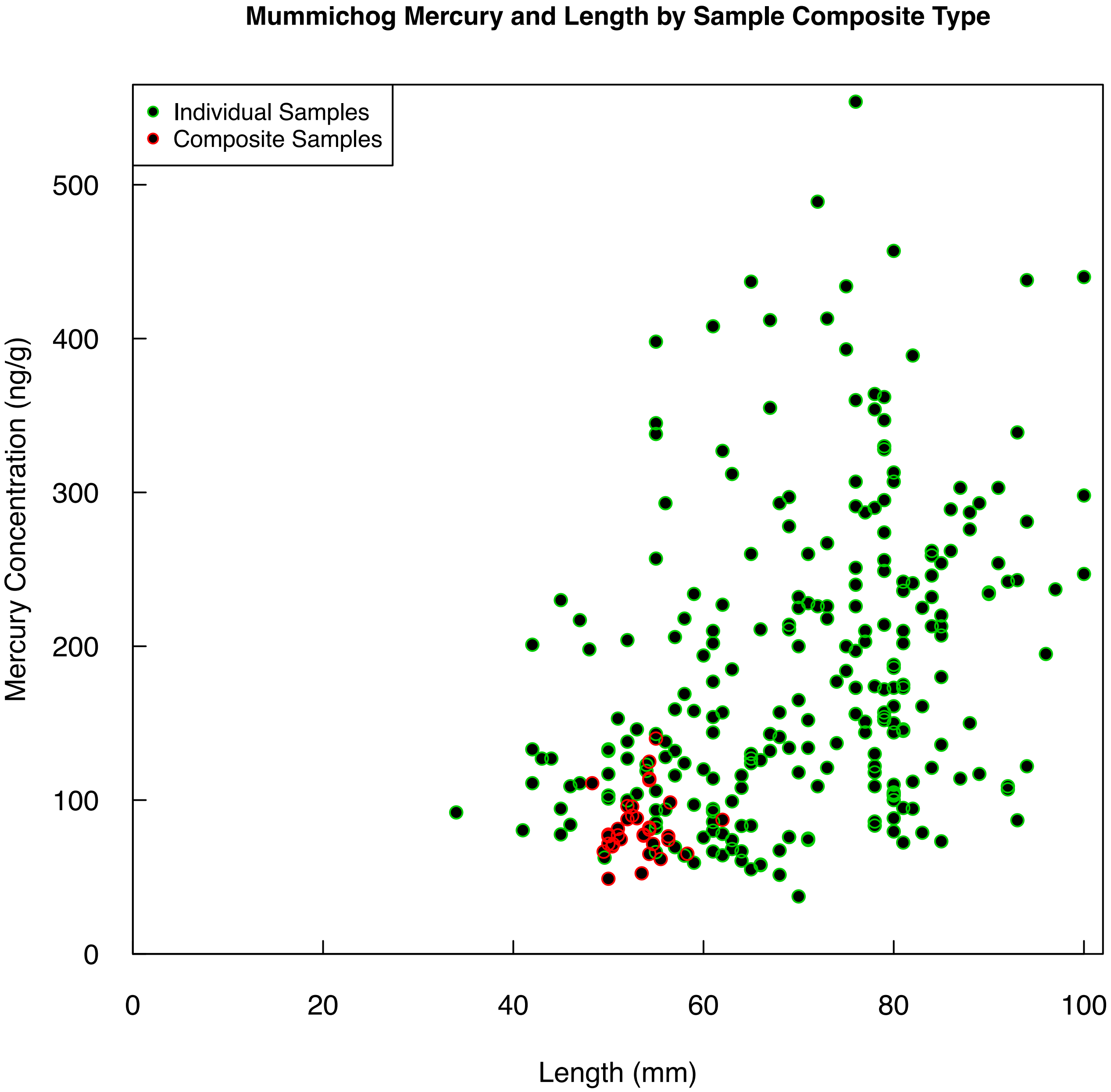
APPENDIX G-3

Length-Mercury Comparison of Individual and Composite Samples

Blue Mussel Mercury and Length by Sample Composite Type

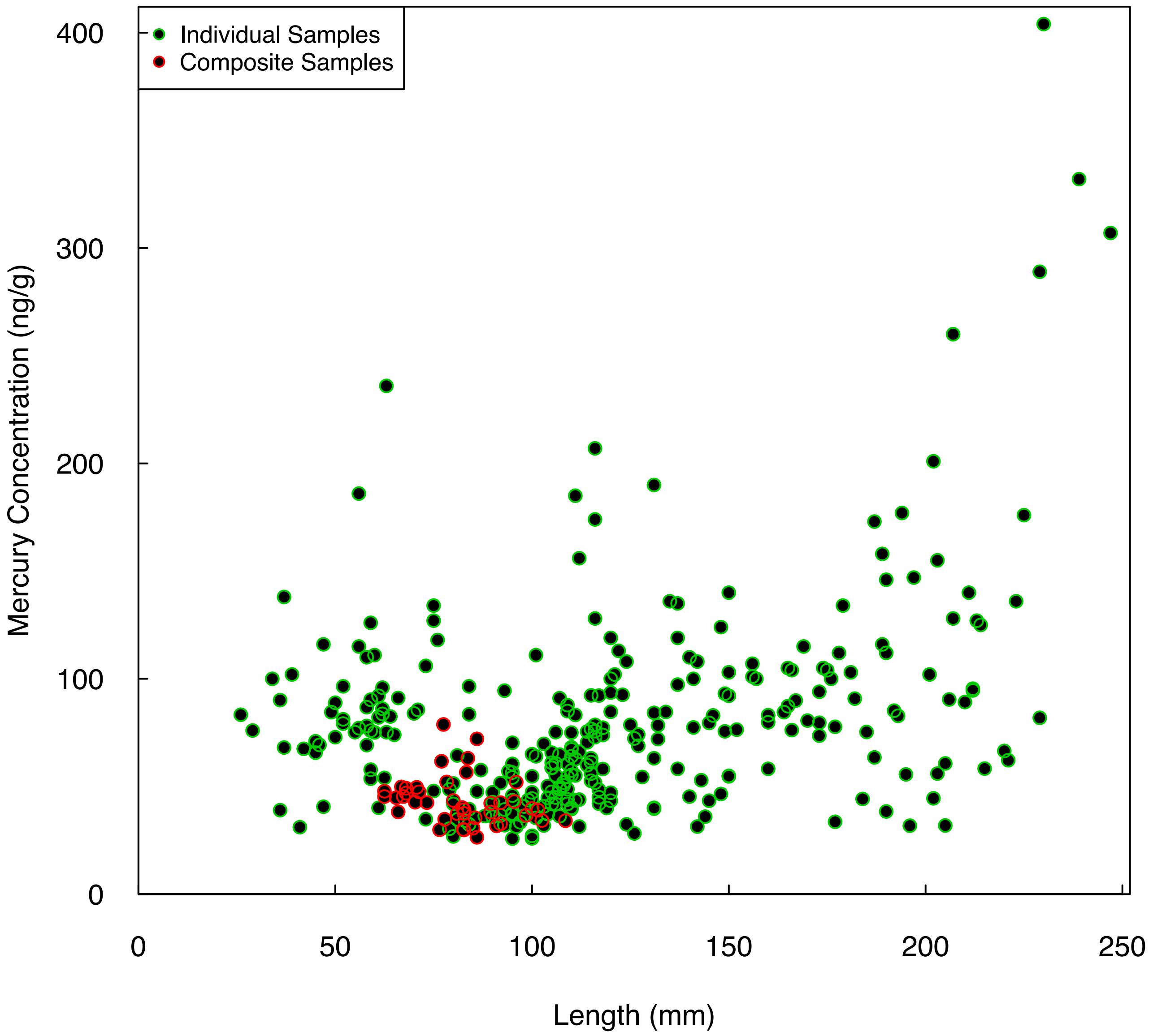


Includes Mussels sampled at ES−13, ES−15, ES−03, and ES−FP



Includes Mummichogs sampled at OB−01, OB−05, and Mendall Marsh

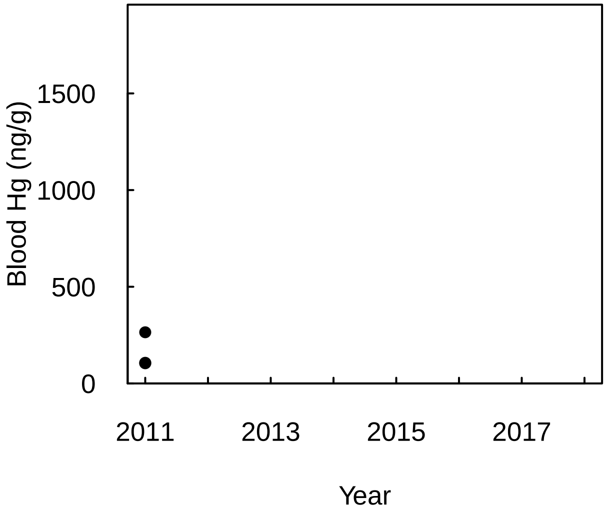
Rainbow Smelt Mercury and Length by Sample Composite Type



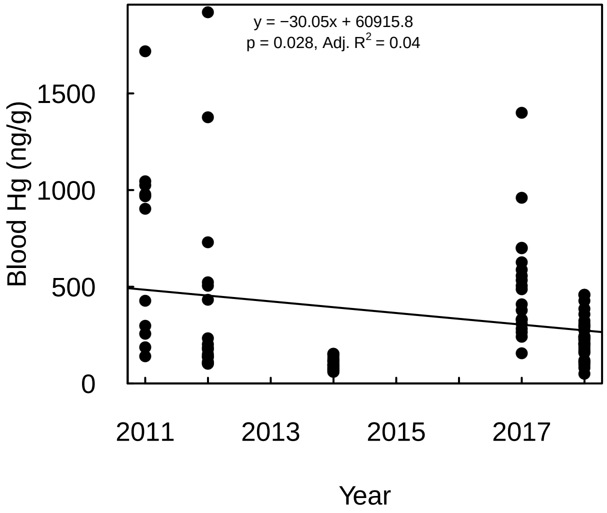
Includes Smelt sampled at OB−05, OB−04, OB−01, ES−13, ES−15, and ES−FP

APPENDIX G-4

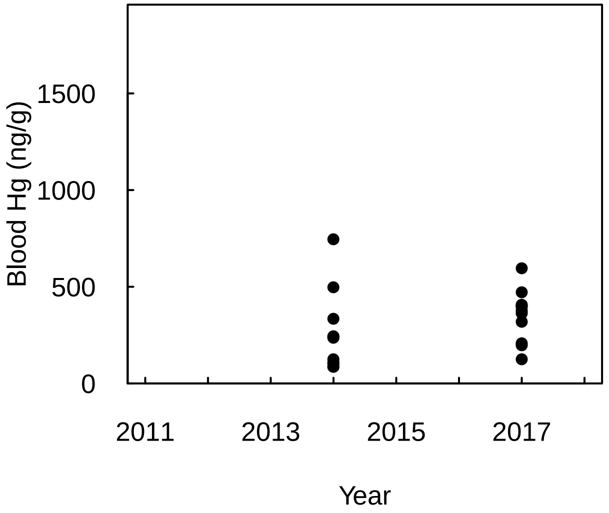
Black Duck Mercury Concentrations by Month



Black Duck Blood − October



Black Duck Blood − January



Black Duck Blood − February