APPENDIX E
Analytical Data Validation Reports for 2016 Biota Samples

Data Validation Summary
2016 Biota Sampling
Penobscot River Estuary Phase III – Engineering Evaluation
Penobscot River, Maine

1.0 INTRODUCTION

Biota samples (spiders, terrestrial insects, blood, and polychaetes) were collected in July and September 2016 for 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) 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235. Samples were also analyzed by Eurofins Calscience (Calscience) located in Garden Grove, California and 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
Eurofins	Methyl mercury, total	CWA 1630	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
U = The target compound was not detected above the method detection limit
UJ = The target compound was not detected and the reporting limit is considered to be estimated

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:

BL1 = Method blank contamination
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
TEMP = Sample temperature exceeds preservation goal

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
* Field 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

Matrix Spike

SDGs 1607740/1607741 – Sample ADD-01_072116_TIN_WB_02 was used for MS/MSD analysis. The MS recovery for methyl mercury (52.3%) was less than the lower QC limit of 65%. Sample results for ADD-01_072116_TIN_WB_01, ADD-01_072116_TIN_WB_02, ADD-01_072116_TIN_WB_03, ADD-01_072116_TIN_WB_04, and ADD-01_072116_TIN_WB_05 were qualified estimated (J) and are potentially biased low.

SDG 1607740 – Sample W17-N_071916_TIN_WB_01 was used for MS/MSD analysis. The MS/MSD recoveries for methyl mercury (470%/-10.7%) were above the upper QC limit of 130% and less than the lower QC limit of 65%. The MS/MSD relative percent difference (RPD) is above the acceptance criteria of (35%) at 209%. Sample results for W17-N_071916_TIN_WB_01, W17-N_071916_TIN_WB_02, W17-N_071916_TIN_WB_03, W17-N_071916_TIN_WB_04 and W17-N_071916_TIN_WB_05 were qualified estimated (J) due to potential bias and imprecision.

SDG 1607741 – Sample ADD-01_072116_SPI_WB_05 was used for MS/MSD analysis. The MSD recovery for methyl mercury (141%) was greater than the upper QC limit of 130%. Sample results for ADD-01_072116_SPI_WB_01, ADD-01_072116_SPI_WB_02, ADD-01_072116_SPI_WB_03, ADD-01_072116_SPI_WB_04, and ADD-01_072116_SPI_WB_05 were qualified estimated (J) and are potentially biased high.

Laboratory Duplicate

SDG 1607740 – Sample ADD-01_072116_TIN_WB_01 was selected by the laboratory for duplicate analysis. The RPD (135) between the sample and the laboratory duplicate analysis exceeded the QC limit of 35. Based on professional judgment, the methyl mercury result only for sample ADD-01_072116_TIN_WB_01 was qualified estimated (J).

SDG 1607741 – Sample ADD-01_072116_SPI_WB_01 was selected by the laboratory for duplicate analysis. The RPD (70.4) between the sample and the laboratory duplicate analysis exceeded the QC limit of 35. Based on professional judgment, the methyl mercury result only for sample ADD-01_072116_SPI_WB_01 was qualified estimated (J).

Method Comparison

SDGs 1607740, 1607741, 1607804 - 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 MMSW-C_072016_SPI_WB_01, ADD-01_072116_TIN_WB_03, ADD-01_072116_TIN_WB_04, MMSE-1_072016_TIN_WB_01, W17-N_071916_TIN_WB_02, ADD-01_072116_SPI_WB_04, W17-N_072416_SPI_WB_02, ADD-01_072116_TIN_WB_05, W17-N_072416_SPI_WB_05, MMSW-C_072616_SPI_WB_03 and W17-N_072616_SPI_WB_04 were qualified as estimated (J).

Preservation

SDG 1608069 – Samples arrived at the laboratory at the proper temperature; however the laboratory in error left the samples out overnight at ambient temperature. The samples were refrozen the following morning. Samples BO-04_072616_POL_WB_01, BO-04_072616_POL_WB_02, BO-04_072616_POL_WB_03, BO-04_072616_POL_WB_04, BO-04_072616_POL_WB_05, ES-FP_072816_POL_WB_01, ES-FP_072816_POL_WB_02, ES-FP_072816_POL_WB_03, ES-FP_072816_POL_WB_04, ES-FP_072816_POL_WB_05, MMPOLY-01_072916_POL_WB_01, MMPOLY-01_072916_POL_WB_02, MMPOLY-01_072916_POL_WB_03, MMPOLY-01_072916_POL_WB_04, MMPOLY-01_072916_POL_WB_05, OB-05_072616_POL_WB_01, OB-05_072616_POL_WB_02, OB-05_072616_POL_WB_03, OB-05_072616_POL_WB_04, and OB-05_072616_POL_WB_05 were qualified as estimated (J/UJ).

3.0 Mercury – 1631

Blanks

SDG 1610235 – Mercury was detected below the reporting limit in multiple blanks with the highest concentration of 0.508 ng/g. An action level was established at five times the highest concentration reported in the blanks and compared to sample results. The mercury result for sample FRB-01_092816_POL_WB_04 was greater than the action level; no action was required. Mercury results in samples FRB-01_092816_POL_WB_01, FRB-01_092816_POL_WB_02, FRB-01_092816_POL_WB_03 and FRB-01_092816_POL_WB_05 were less than the action level and were qualified not detected (U).

Matrix Spike

SDG 1607740 – Sample W17-N_071916_TIN_WB_01 was used for MS/MSD analysis. The MS recovery for mercury (62.9%) was less than the lower QC limit of 71%. Sample results for W17-N_071916_TIN_WB_01, W17-N_071916_TIN_WB_02, W17-N_071916_TIN_WB_03, W17-N_071916_TIN_WB_04, and W17-N_071916_TIN_WB_05 were qualified estimated (J) and are potentially biased low.

Laboratory Duplicate

SDG 1607740 – Sample MMSW-C_072016_SPI_WB_01 was selected by the laboratory for duplicate analysis. The RPD (54.9) between the sample and the laboratory duplicate analysis exceeded the QC limit of 24. Based on professional judgment, the mercury result only for sample MMSW-C_072016_SPI_WB_01 was qualified estimated (J).

Preservation

SDG 1608069 – Samples arrived at the laboratory at the proper temperature however the laboratory in error left the samples out overnight at ambient temperature. The samples were refrozen the following morning. Samples BO-04_072616_POL_WB_01, BO-04_072616_POL_WB_02, BO-04_072616_POL_WB_03, BO-04_072616_POL_WB_04, BO-04_072616_POL_WB_05, ES-FP_072816_POL_WB_01, ES-FP_072816_POL_WB_02, ES-FP_072816_POL_WB_03, ES-FP_072816_POL_WB_04, ES-FP_072816_POL_WB_05, MMPOLY-01_072916_POL_WB_01, MMPOLY-01_072916_POL_WB_02, MMPOLY-01_072916_POL_WB_03, MMPOLY-01_072916_POL_WB_04, MMPOLY-01_072916_POL_WB_05, OB-05_072616_POL_WB_01, OB-05_072616_POL_WB_02, OB-05_072616_POL_WB_03, OB-05_072616_POL_WB_04, and OB-05_072616_POL_WB_05 were qualified as estimated (J).

Method Comparison

SDGs 1607740, 1607741, 1607804 - 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 total mercury result that is less than the methyl mercury result and has an RPD >24 will be qualified as estimated. The mercury results in samples MMSW-C_072016_SPI_WB_01, ADD-01_072116_TIN_WB_03, ADD-01_072116_TIN_WB_04, MMSE-1_072016_TIN_WB_01, W17-N_071916_TIN_WB_02, ADD-01_072116_SPI_WB_04, W17-N_072416_SPI_WB_02, ADD-01_072116_TIN_WB_05, W17-N_072416_SPI_WB_05, MMSW-C_072616_SPI_WB_03 and W17-N_072616_SPI_WB_04 were qualified as estimated (J).

4.0 % Lipids

Data Completeness and Chain of Custody

SDG 1607740 – The % lipids analysis was cancelled from sample MMSW-C_072016_SPI_WB_01 in order to use sample mass to create additional spider samples MMSW-C_072016_SPI_WB_04 and MMSW-C_072016_SPI_WB_05.

SDG 1607804 – Due to insufficient sample volume % lipids analysis could not be performed for sample MMSE-1_072616_SPI_WB_04.

SDG 1608069 – Due to insufficient sample volume % lipids analysis could not be performed for samples BO-04_072616_POL_WB_01, BO-04_072616_POL_WB_02, BO-04_072616_POL_WB_03, BO-04_072616_POL_WB_04, BO-04_072616_POL_WB_05, ES-FP_072816_POL_WB_01, ES-FP_072816_POL_WB_02, ES-FP_072816_POL_WB_03, ES-FP_072816_POL_WB_05, MMPOLY-01_072916_POL_WB_01, MMPOLY-01_072916_POL_WB_02, MMPOLY-01_072916_POL_WB_03, MMPOLY-01_072916_POL_WB_04, MMPOLY-01_072916_POL_WB_05, OB-05_072616_POL_WB_01, OB-05_072616_POL_WB_02, OB-05_072616_POL_WB_03, OB-05_072616_POL_WB_04, and OB-05_072616_POL_WB_05.

SDG 1610231 – Due to insufficient sample volume % lipids analysis could not be performed for sample ES-13_072716_POL_WB_05.

SDG 1610235 – Due to insufficient sample volume % lipids analysis could not be performed for sample FRB-01_092816_POL_WB_04.

Preservation

SDG 1608069 – Samples arrived at the laboratory at the proper temperature; however the laboratory in error left the samples out overnight at ambient temperature. The samples were refrozen the following morning. Sample ES-FP_072816_POL_WB_04 was 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: Denise King January 4, 2017

Denise King

Senior Reviewer: Wolfgang Calicchio January 17, 2017

Wolfg D. Calicchio

TABLE 1
DATA VALIDATION SUMMARY REPORT
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

					Method Class	Methyl Mercury	Mercury	% Lipids
					Analysis Method	EPA 1630	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code			
1607740	Blood	ADD-01	ADD-01_072116_NSS_BL_01	07/21/16	FS		1	
1607740	Blood	ADD-01	ADD-01_072116_NSS_BL_02	07/21/16	FS		1	
1607740	Insect	ADD-01	ADD-01_072116_TIN_WB_01	07/21/16	FS	1	1	1
1607740	Insect	ADD-01	ADD-01_072116_TIN_WB_02	07/21/16	FS	1	1	1
1607740	Insect	ADD-01	ADD-01_072116_TIN_WB_03	07/21/16	FS	1	1	1
1607740	Insect	ADD-01	ADD-01_072116_TIN_WB_04	07/21/16	FS	1	1	1
1607740	Insect	MMSE-1	MMSE-1_072016_TIN_WB_01	07/20/16	FS	1	1	1
1607740	Insect	MMSE-1	MMSE-1_072016_TIN_WB_02	07/20/16	FS	1	1	1
1607740	Insect	MMSE-1	MMSE-1_072016_TIN_WB_03	07/20/16	FS	1	1	1
1607740	Insect	MMSE-1	MMSE-1_072016_TIN_WB_04	07/20/16	FS	1	1	1
1607740	Insect	MMSE-1	MMSE-1_072016_TIN_WB_05	07/20/16	FS	1	1	1
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_01	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_02	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_03	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_04	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_05	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_06	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_07	07/21/16	FS		1	
1607740	Blood	MMSE-1	MMSE-1_072116_NSS_BL_08	07/21/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_071916_NSS_BL_01	07/19/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_071916_NSS_BL_02	07/19/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_071916_NSS_BL_03	07/19/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_072016_NSS_BL_04	07/20/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_072016_NSS_BL_05	07/20/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_072016_NSS_BL_06	07/20/16	FS		1	
1607740	Blood	MMSW-C	MMSW-C_072016_NSS_BL_07	07/20/16	FS		1	
1607740	Spider	MMSW-C	MMSW-C_072016_SPI_WB_01	07/20/16	FS	1	1	

Created by: BCG 12/15/16

Checked by:DMK 01/04/17

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

SDG	Media	Location	Field Sample ID	Sample Date	Method Class Analysis Method QC Code	Methyl Mercury EPA 1630	Mercury EPA 1631	% Lipids NOAA
1607740	Spider	MMSW-C	MMSW-C_072016_SPI_WB_02	07/20/16	FS	1	1	1
1607740	Spider	MMSW-C	MMSW-C_072016_SPI_WB_04	07/20/16	FS	1	1	
1607740	Spider	MMSW-C	MMSW-C_072016_SPI_WB_05	07/20/16	FS	1	1	
1607740	Insect	MMSW-C	MMSW-C_072016_TIN_WB_02	07/20/16	FS	1	1	1
1607740	Insect	MMSW-C	MMSW-C_072016_TIN_WB_03	07/20/16	FS	1	1	1
1607740	Insect	MMSW-C	MMSW-C_072016_TIN_WB_04	07/20/16	FS	1	1	1
1607740	Insect	MMSW-C	MMSW-C_072016_TIN_WB_05	07/20/16	FS	1	1	1
1607740	Insect	MMSW-C	MMSW-C_072016_TIN_WB_06	07/20/16	FS	1	1	1
1607740	Blood	W17-N	W17-N_071916_NSS_BL_01	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_02	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_03	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_04	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_05	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_08	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_NSS_BL_11	07/19/16	FS		1	
1607740	Blood	W17-N	W17-N_071916_RWB_BL_01	07/19/16	FS		1	
1607740	Insect	W17-N	W17-N_071916_TIN_WB_01	07/19/16	FS	1	1	1
1607740	Insect	W17-N	W17-N_071916_TIN_WB_02	07/19/16	FS	1	1	1
1607740	Insect	W17-N	W17-N_071916_TIN_WB_03	07/19/16	FS	1	1	1
1607740	Insect	W17-N	W17-N_071916_TIN_WB_04	07/19/16	FS	1	1	1
1607740	Insect	W17-N	W17-N_071916_TIN_WB_05	07/19/16	FS	1	1	1
1607740	Blood	W17-N	W17-N_072016_NSS_BL_06	07/20/16	FS		1	
1607740	Blood	W17-N	W17-N_072016_NSS_BL_07	07/20/16	FS		1	
1607740	Blood	W17-N	W17-N_072016_NSS_BL_09	07/20/16	FS		1	
1607740	Blood	W17-N	W17-N_072016_NSS_BL_14	07/20/16	FS		1	
1607740	WB	W17-N	W17-N_072016_RWB_BL_02	07/20/16	FS		1	
1607740	WB	W17-N	W17-N_072016_RWB_BL_03	07/20/16	FS		1	

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Checked by:DMK 01/04/17

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

					Method Class	Methyl Mercury	Mercury	% Lipids
					Analysis Method	EPA 1630	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code			
1607741	Spider	ADD-01	ADD-01_072116_SPI_WB_01	07/21/16	FS	1	1	1
1607741	Spider	ADD-01	ADD-01_072116_SPI_WB_02	07/21/16	FS	1	1	1
1607741	Spider	ADD-01	ADD-01_072116_SPI_WB_03	07/21/16	FS	1	1	1
1607741	Spider	ADD-01	ADD-01_072116_SPI_WB_04	07/21/16	FS	1	1	1
1607741	Spider	ADD-01	ADD-01_072116_SPI_WB_05	07/21/16	FS	1	1	1
1607741	Insect	ADD-01	ADD-01_072116_TIN_WB_05	07/21/16	FS	1	1	1
1607741	Blood	ADD-01	ADD-01_072216_NSS_BL_03	07/22/16	FS		1	
1607741	Blood	ADD-01	ADD-01_072216_NSS_BL_04	07/22/16	FS		1	
1607741	Blood	ADD-01	ADD-01_072216_NSS_BL_05	07/22/16	FS		1	
1607741	Spider	MMSE-1	MMSE-01_072216_SPI_WB_01	07/22/16	FS	1	1	1
1607741	Spider	MMSE-1	MMSE-01_072216_SPI_WB_02	07/22/16	FS	1	1	1
1607741	Spider	MMSE-1	MMSE-01_072216_SPI_WB_05	07/22/16	FS	1	1	
1607741	Spider	MMSE-1	MMSE-01_072316_SPI_WB_03	07/23/16	FS	1	1	1
1607741	Blood	MMSE-1	MMSE-1_072316_NSS_BL_11	07/23/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072316_NSS_BL_12	07/23/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072316_NSS_BL_13	07/23/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072316_NSS_BL_15	07/23/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072316_NSS_BL_16	07/23/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072516_NSS_BL_17	07/25/16	FS		1	
1607741	Blood	MMSE-1	MMSE-1_072516_NSS_BL_18	07/25/16	FS		1	
1607741	Blood	MMSW-C	MMSW-C_072316_NSS_BL_08	07/23/16	FS		1	
1607741	Blood	MMSW-C	MMSW-C_072316_NSS_BL_10	07/23/16	FS		1	
1607741	Blood	MMSW-C	MMSW-C_072416_NSS_BL_09	07/24/16	FS		1	
1607741	Blood	MMSW-C	MMSW-C_072416_NSS_BL_11	07/24/16	FS		1	
1607741	Blood	W17-N	W17-N_072416_NSS_BL_12	07/24/16	FS		1	
1607741	Spider	W17-N	W17-N_072416_SPI_WB_02	07/24/16	FS	1	1	1
1607741	Spider	W17-N	W17-N_072416_SPI_WB_05	07/24/16	FS	1	1	

TABLE 1
DATA VALIDATION SUMMARY REPORT
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

					Method Class	Methyl Mercury	Mercury	% Lipids
					Analysis Method	EPA 1630	EPA 1631	NOAA
SDG	Media	Location	Field Sample ID	Sample Date	QC Code			
1607741	Blood	W17-N	W17-N_072516_NSS_BL_10	07/25/16	FS		1	
1607741	Blood	W17-N	W17-N_072516_NSS_BL_15	07/25/16	FS		1	
1607741	Blood	W17-N	W17-N_072516_NSS_BL_16	07/25/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072516_NSS_BL_06	07/25/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072516_NSS_BL_07	07/25/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072616_NSS_BL_08	07/26/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072616_NSS_BL_09	07/26/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072616_NSS_BL_10	07/26/16	FS		1	
1607804	Blood	ADD-01	ADD-01_072616_NSS_BL_11	07/26/16	FS		1	
1607804	Spider	MMSE-1	MMSE-1_072616_SPI_WB_04	07/26/16	FS	1	1	
1607804	Spider	MMSW-C	MMSW-C_072616_SPI_WB_03	07/26/16	FS	1	1	1
1607804	Spider	W17-N	W17-N_072616_SPI_WB_01	07/26/16	FS	1	1	1
1607804	Spider	W17-N	W17-N_072616_SPI_WB_03	07/26/16	FS	1	1	
1607804	Spider	W17-N	W17-N_072616_SPI_WB_04	07/26/16	FS	1	1	
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_01	07/26/16	FS	1	1	
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_02	07/26/16	FS	1	1	
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_03	07/26/16	FS	1	1	
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_04	07/26/16	FS	1		
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_04	07/26/16	FS		1	
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_05	07/26/16	FS	1		
1608069	Polychaete	BO-04	BO-04_072616_POL_WB_05	07/26/16	FS		1	
1608069	Polychaete	ES-FP	ES-FP_072816_POL_WB_01	07/28/16	FS	1	1	
1608069	Polychaete	ES-FP	ES-FP_072816_POL_WB_02	07/28/16	FS	1	1	
1608069	Polychaete	ES-FP	ES-FP_072816_POL_WB_03	07/28/16	FS	1	1	
1608069	Polychaete	ES-FP	ES-FP_072816_POL_WB_04	07/28/16	FS	1	1	1
1608069	Polychaete	ES-FP	ES-FP_072816_POL_WB_05	07/28/16	FS	1	1	
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS	1	1	

Created by: BCG 12/15/16

Checked by:DMK 01/04/17

TABLE 1
DATA VALIDATION SUMMARY REPORT
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

					Method Class	**Methyl Mercury**	**Mercury**	**% Lipids**
					Analysis Method	**EPA 1630**	**EPA 1631**	**NOAA**
SDG	**Media**	**Location**	**Field Sample ID**	**Sample Date**	**QC Code**			
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS	1		
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS		1	
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS	1		
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS		1	
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS	1	1	
1608069	Polychaete	MMPOLY	MMPOLY-01_072916_POL_WB_0	07/29/16	FS	1	1	
1608069	Polychaete	OB-05	OB-05_072616_POL_WB_01	07/26/16	FS	1	1	
1608069	Polychaete	OB-05	OB-05_072616_POL_WB_02	07/26/16	FS	1	1	
1608069	Polychaete	OB-05	OB-05_072616_POL_WB_03	07/26/16	FS	1	1	
1608069	Polychaete	OB-05	OB-05_072616_POL_WB_04	07/26/16	FS	1	1	
1608069	Polychaete	OB-05	OB-05_072616_POL_WB_05	07/26/16	FS	1	1	
1610231	Polychaete	ES-13	ES-13_072716_POL_WB_01	07/27/16	FS	1	1	1
1610231	Polychaete	ES-13	ES-13_072716_POL_WB_02	07/27/16	FS	1	1	1
1610231	Polychaete	ES-13	ES-13_072716_POL_WB_03	07/27/16	FS	1	1	1
1610231	Polychaete	ES-13	ES-13_072716_POL_WB_04	07/27/16	FS	1	1	1
1610231	Polychaete	ES-13	ES-13_072716_POL_WB_05	07/27/16	FS	1	1	
1610235	Polychaete	FRB-01	FRB-01_092816_POL_WB_01	09/28/16	FS	1	1	1
1610235	Polychaete	FRB-01	FRB-01_092816_POL_WB_02	09/28/16	FS	1	1	1
1610235	Polychaete	FRB-01	FRB-01_092816_POL_WB_03	09/28/16	FS	1	1	1
1610235	Polychaete	FRB-01	FRB-01_092816_POL_WB_04	09/28/16	FS	1	1	
1610235	Polychaete	FRB-01	FRB-01_092816_POL_WB_05	09/28/16	FS	1	1	1

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

Created by: BCG 12/15/16
Checked by:DMK 01/04/17

TABLE 2
DATA VALIDATION SUMMARY
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

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
16-11-0657	NOAALipids1993	16-11-0657-9	ES-FP_072816_POL_WB_04	Total	Lipids	1.2		1.2	J	TEMP	PERCENT
1607741	EPA 1630	1607741-16	ADD-01_072116_SPI_WB_01	Total	Methyl mercury	14.6		14.6	J	LD, MS-H	NG/G
1607741	EPA 1630	1607741-17	ADD-01_072116_SPI_WB_02	Total	Methyl mercury	24		24	J	MS-H	NG/G
1607741	EPA 1630	1607741-18	ADD-01_072116_SPI_WB_03	Total	Methyl mercury	22.9		22.9	J	MS-H	NG/G
1607741	EPA 1631	1607741-19	ADD-01_072116_SPI_WB_04	Total	Mercury	44.2		44.2	J	MT	NG/G
1607741	EPA 1630	1607741-19	ADD-01_072116_SPI_WB_04	Total	Methyl mercury	60.2		60.2	J	MT, MS-H	NG/G
1607741	EPA 1630	1607741-20	ADD-01_072116_SPI_WB_05	Total	Methyl mercury	22.9		22.9	J	MS-H	NG/G
1607740	EPA 1630	1607740-36	ADD-01_072116_TIN_WB_01	Total	Methyl mercury	24.9		24.9	J	LD, MS-L	NG/G
1607740	EPA 1630	1607740-37RE1	ADD-01_072116_TIN_WB_02	Total	Methyl mercury	2.5		2.5	J	MS-L	NG/G
1607740	EPA 1631	1607740-38RE1	ADD-01_072116_TIN_WB_03	Total	Mercury	16.8		16.8	J	MT	NG/G
1607740	EPA 1630	1607740-38	ADD-01_072116_TIN_WB_03	Total	Methyl mercury	31.2		31.2	J	MS-L, MT	NG/G
1607740	EPA 1631	1607740-39	ADD-01_072116_TIN_WB_04	Total	Mercury	7.37		7.37	J	MT	NG/G
1607740	EPA 1630	1607740-39	ADD-01_072116_TIN_WB_04	Total	Methyl mercury	12.7		12.7	J	MS-L, MT	NG/G
1607741	EPA 1631	1607741-25RE1	ADD-01_072116_TIN_WB_05	Total	Mercury	8.85		8.85	J	MT	NG/G
1607741	EPA 1630	1607741-25	ADD-01_072116_TIN_WB_05	Total	Methyl mercury	18.6		18.6	J	MS-L, MT	NG/G
1608069	EPA 1631	1608069-01	BO-04_072616_POL_WB_01	Total	Mercury	142		142	J	TEMP	NG/G
1608069	EPA 1630	1608069-01	BO-04_072616_POL_WB_01	Total	Methyl mercury	8.6		8.6	J	TEMP	NG/G
1608069	EPA 1631	1608069-02	BO-04_072616_POL_WB_02	Total	Mercury	176		176	J	TEMP	NG/G
1608069	EPA 1630	1608069-02	BO-04_072616_POL_WB_02	Total	Methyl mercury	6.9		6.9	J	TEMP	NG/G
1608069	EPA 1631	1608069-03	BO-04_072616_POL_WB_03	Total	Mercury	185		185	J	TEMP	NG/G
1608069	EPA 1630	1608069-03	BO-04_072616_POL_WB_03	Total	Methyl mercury	9.2		9.2	J	TEMP	NG/G
1608069	EPA 1631	1608069-04RE1	BO-04_072616_POL_WB_04	Total	Mercury	311		311	J	TEMP	NG/G
1608069	EPA 1630	1608069-04	BO-04_072616_POL_WB_04	Total	Methyl mercury	7.3		7.3	J	TEMP	NG/G
1608069	EPA 1631	1608069-05RE1	BO-04_072616_POL_WB_05	Total	Mercury	256		256	J	TEMP	NG/G
1608069	EPA 1630	1608069-05	BO-04_072616_POL_WB_05	Total	Methyl mercury	8.3		8.3	J	TEMP	NG/G
1608069	EPA 1631	1608069-08	ES-FP_072816_POL_WB_01	Total	Mercury	34.6		34.6	J	TEMP	NG/G
1608069	EPA 1630	1608069-08	ES-FP_072816_POL_WB_01	Total	Methyl mercury	6.2		6.2	J	TEMP	NG/G
1608069	EPA 1631	1608069-09	ES-FP_072816_POL_WB_02	Total	Mercury	24		24	J	TEMP	NG/G
1608069	EPA 1630	1608069-09	ES-FP_072816_POL_WB_02	Total	Methyl mercury	4.4		4.4	J	TEMP	NG/G
1608069	EPA 1631	1608069-10	ES-FP_072816_POL_WB_03	Total	Mercury	24.5		24.5	J	TEMP	NG/G
1608069	EPA 1630	1608069-10	ES-FP_072816_POL_WB_03	Total	Methyl mercury	0.4	U	0.4	UJ	TEMP	NG/G
1608069	EPA 1631	1608069-11	ES-FP_072816_POL_WB_04	Total	Mercury	19.4		19.4	J	TEMP	NG/G
1608069	EPA 1630	1608069-11	ES-FP_072816_POL_WB_04	Total	Methyl mercury	5.3		5.3	J	TEMP	NG/G

TABLE 2
DATA VALIDATION SUMMARY
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

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
1608069	EPA 1631	1608069-12	ES-FP_072816_POL_WB_05	Total	Mercury	46.1		46.1	J	TEMP	NG/G
1608069	EPA 1630	1608069-12	ES-FP_072816_POL_WB_05	Total	Methyl mercury	15.7		15.7	J	TEMP	NG/G
1610235	EPA 1631	1610235-01RE1	FRB-01_092816_POL_WB_01	Total	Mercury	1.9		1.9	U	BL1	NG/G
1610235	EPA 1631	1610235-02RE1	FRB-01_092816_POL_WB_02	Total	Mercury	2.46		2.46	U	BL1	NG/G
1610235	EPA 1631	1610235-03RE1	FRB-01_092816_POL_WB_03	Total	Mercury	1.15		1.15	U	BL1	NG/G
1610235	EPA 1631	1610235-05RE1	FRB-01_092816_POL_WB_05	Total	Mercury	1.82		1.82	U	BL1	NG/G
1608069	EPA 1631	1608069-13	MMPOLY-01_072916_POL_WB_01	Total	Mercury	69.9		69.9	J	TEMP	NG/G
1608069	EPA 1630	1608069-13	MMPOLY-01_072916_POL_WB_01	Total	Methyl mercury	1.4	J	1.4	J	TEMP	NG/G
1608069	EPA 1631	1608069-14RE1	MMPOLY-01_072916_POL_WB_02	Total	Mercury	321		321	J	TEMP	NG/G
1608069	EPA 1630	1608069-14	MMPOLY-01_072916_POL_WB_02	Total	Methyl mercury	11.3		11.3	J	TEMP	NG/G
1608069	EPA 1631	1608069-15RE1	MMPOLY-01_072916_POL_WB_03	Total	Mercury	190		190	J	TEMP	NG/G
1608069	EPA 1630	1608069-15	MMPOLY-01_072916_POL_WB_03	Total	Methyl mercury	11.1		11.1	J	TEMP	NG/G
1608069	EPA 1631	1608069-16	MMPOLY-01_072916_POL_WB_04	Total	Mercury	142		142	J	TEMP	NG/G
1608069	EPA 1630	1608069-16	MMPOLY-01_072916_POL_WB_04	Total	Methyl mercury	8.2		8.2	J	TEMP	NG/G
1608069	EPA 1631	1608069-17	MMPOLY-01_072916_POL_WB_05	Total	Mercury	239		239	J	TEMP	NG/G
1608069	EPA 1630	1608069-17	MMPOLY-01_072916_POL_WB_05	Total	Methyl mercury	9.9		9.9	J	TEMP	NG/G
1607740	EPA 1631	1607740-40	MMSE-1_072016_TIN_WB_01	Total	Mercury	16.5		16.5	J	MT	NG/G
1607740	EPA 1630	1607740-40	MMSE-1_072016_TIN_WB_01	Total	Methyl mercury	91.2		91.2	J	MT	NG/G
1607740	EPA 1631	1607740-34	MMSW-C_072016_SPI_WB_01	Total	Mercury	166		166	J	LD, MT	NG/G
1607740	EPA 1630	1607740-34	MMSW-C_072016_SPI_WB_01	Total	Methyl mercury	274		274	J	MT	NG/G
1607804	EPA 1631	1607804-08	MMSW-C_072616_SPI_WB_03	Total	Mercury	257		257	J	MT	NG/G
1607804	EPA 1630	1607804-08RE1	MMSW-C_072616_SPI_WB_03	Total	Methyl mercury	330		330	J	MT	NG/G
1608069	EPA 1631	1608069-18	OB-05_072616_POL_WB_01	Total	Mercury	215		215	J	TEMP	NG/G
1608069	EPA 1630	1608069-18	OB-05_072616_POL_WB_01	Total	Methyl mercury	11.7		11.7	J	TEMP	NG/G
1608069	EPA 1631	1608069-19	OB-05_072616_POL_WB_02	Total	Mercury	224		224	J	TEMP	NG/G
1608069	EPA 1630	1608069-19	OB-05_072616_POL_WB_02	Total	Methyl mercury	12.8		12.8	J	TEMP	NG/G
1608069	EPA 1631	1608069-20	OB-05_072616_POL_WB_03	Total	Mercury	205		205	J	TEMP	NG/G
1608069	EPA 1630	1608069-20	OB-05_072616_POL_WB_03	Total	Methyl mercury	11		11	J	TEMP	NG/G
1608069	EPA 1631	1608069-21	OB-05_072616_POL_WB_04	Total	Mercury	189		189	J	TEMP	NG/G
1608069	EPA 1630	1608069-21	OB-05_072616_POL_WB_04	Total	Methyl mercury	12.8		12.8	J	TEMP	NG/G
1608069	EPA 1631	1608069-22	OB-05_072616_POL_WB_05	Total	Mercury	230		230	J	TEMP	NG/G
1608069	EPA 1630	1608069-22	OB-05_072616_POL_WB_05	Total	Methyl mercury	12.7		12.7	J	TEMP	NG/G
1607740	EPA 1631	1607740-50	W17-N_071916_TIN_WB_01	Total	Mercury	254		254	J	MS-L	NG/G

TABLE 2
DATA VALIDATION SUMMARY
2016 BIOTA SAMPLING
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

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
1607740	EPA 1630	1607740-50	W17-N_071916_TIN_WB_01	Total	Methyl mercury	64.2		64.2	J	MS-L, MS-H, MS-RPD	NG/G
1607740	EPA 1631	1607740-51	W17-N_071916_TIN_WB_02	Total	Mercury	25.5		25.5	J	MS-L, MT	NG/G
1607740	EPA 1630	1607740-51	W17-N_071916_TIN_WB_02	Total	Methyl mercury	118		118	J	MS-L, MS-H, MS-RPD, MT	NG/G
1607740	EPA 1631	1607740-52	W17-N_071916_TIN_WB_03	Total	Mercury	50		50	J	MS-L	NG/G
1607740	EPA 1630	1607740-52	W17-N_071916_TIN_WB_03	Total	Methyl mercury	56.7		56.7	J	MS-L, MS-H, MS-RPD	NG/G
1607740	EPA 1631	1607740-53	W17-N_071916_TIN_WB_04	Total	Mercury	30.4		30.4	J	MS-L	NG/G
1607740	EPA 1630	1607740-53	W17-N_071916_TIN_WB_04	Total	Methyl mercury	21.7		21.7	J	MS-L, MS-H, MS-RPD	NG/G
1607740	EPA 1631	1607740-54RE1	W17-N_071916_TIN_WB_05	Total	Mercury	29.2		29.2	J	MS-L	NG/G
1607740	EPA 1630	1607740-54	W17-N_071916_TIN_WB_05	Total	Methyl mercury	28		28	J	MS-L, MS-H, MS-RPD	NG/G
1607741	EPA 1631	1607741-24	W17-N_072416_SPI_WB_02	Total	Mercury	197		197	J	MT	NG/G
1607741	EPA 1630	1607741-24	W17-N_072416_SPI_WB_02	Total	Methyl mercury	278		278	J	MT	NG/G
1607741	EPA 1631	1607741-30	W17-N_072416_SPI_WB_05	Total	Mercury	213		213	J	MT	NG/G
1607741	EPA 1630	1607741-30RE1	W17-N_072416_SPI_WB_05	Total	Methyl mercury	642		642	J	MT	NG/G
1607804	EPA 1631	1607804-11RE1	W17-N_072616_SPI_WB_04	Total	Mercury	263		263	J	MT	NG/G
1607804	EPA 1630	1607804-11RE1	W17-N_072616_SPI_WB_04	Total	Methyl mercury	480		480	J	MT	NG/G

Units

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

U = The target compound was not detected above the method detection limit

UJ = The target compound was not detected and the reporting limit is considered estimated

Validation Reason Codes:

BL1 = Method blank contamination

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

TEMP = Sample temperature exceeds preservation goal

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740/16-11-0658		1607740/16-11-0658		1607740		1607740/16-11-0658	
			Location	ADD-01		ADD-01		ADD-01		ADD-01		ADD-01	
			Sample Date	07/21/16		07/21/16		07/21/16		07/21/16		07/21/16	
			Sample ID	ADD-01_072116_NSS_BL_01		ADD-01_072116_TIN_WB_01		ADD-01_072116_TIN_WB_02		ADD-01_072116_NSS_BL_02		ADD-01_072116_TIN_WB_03	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G			24.9	J	2.5	J			31.2	J
EPA 1631	Total	Mercury	NG/G	740		63.2		49.2		566		16.8	J
NOAALipids1993	Total	Lipids	PERCENT			3.5		3.4				3.3	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated
U = The target compound was not detected above the method detection limit
UJ = The target compound was not detected and the reporting limit is considered estimated

Created by: BGP 01/05/2017
Checked by: DMK 01/12/2017

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740/16-11-0658		1607740/16-11-0658		1607740/16-11-0658		1607740/16-11-0658		1607740/16-11-0658	
			Location	ADD-01		MMSE-1		MMSE-1		MMSE-1		MMSE-1	
			Sample Date	07/21/16		07/20/16		07/20/16		07/20/16		07/20/16	
			Sample ID	ADD-01_072116_TIN_WB_04		MMSE-1_072016_TIN_WB_01		MMSE-1_072016_TIN_WB_02		MMSE-1_072016_TIN_WB_03		MMSE-1_072016_TIN_WB_04	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	12.7	J	91.2	J	68.3		241		100	
EPA 1631	Total	Mercury	NG/G	7.37	J	16.5	J	327		354		222	
NOAALipids1993	Total	Lipids	PERCENT	3.4		4.1		3.1		2.9		2.9	

Units:

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DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740/16-11-0658		1607740		1607740		1607740		1607740	
			Location	MMSE-1		MMSE-1		MMSE-1		MMSE-1		MMSE-1	
			Sample Date	07/20/16		07/21/16		07/21/16		07/21/16		07/21/16	
			Sample ID	MMSE-1_072016_TIN_WB_05		MMSE-1_072116_NSS_BL_01		MMSE-1_072116_NSS_BL_02		MMSE-1_072116_NSS_BL_05		MMSE-1_072116_NSS_BL_03	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	6.9									
EPA 1631	Total	Mercury	NG/G	56.3		7450		5730		8450		9240	
NOAALipids1993	Total	Lipids	PERCENT	3.5									

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740		1607740		1607740	
			Location	MMSE-1		MMSE-1		MMSE-1		MMSE-1		MMSW-C	
			Sample Date	07/21/16		07/21/16		07/21/16		07/21/16		07/19/16	
			Sample ID	MMSE-1_072116_NSS_BL_04		MMSE-1_072116_NSS_BL_06		MMSE-1_072116_NSS_BL_07		MMSE-1_072116_NSS_BL_08		MMSW-C_071916_NSS_BL_01	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G										
EPA 1631	Total	Mercury	NG/G	4130		4590		4330		5730		7790	
NOAALipids1993	Total	Lipids	PERCENT										

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740/16-11-0658		1607740/16-11-0658		1607740	
			Location	MMSW-C		MMSW-C		MMSW-C		MMSW-C		MMSW-C	
			Sample Date	07/19/16		07/19/16		07/20/16		07/20/16		07/20/16	
			Sample ID	MMSW-C_071916_NSS_BL_02		MMSW-C_071916_NSS_BL_03		MMSW-C_072016_TIN_WB_02		MMSW-C_072016_TIN_WB_03		MMSW-C_072016_NSS_BL_04	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G					28.3		33.5			
EPA 1631	Total	Mercury	NG/G	4230		5910		33.8		47.5		6770	
NOAALipids1993	Total	Lipids	PERCENT					3.4		3.4			

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PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740/16-11-0658		1607740		1607740		1607740		1607740/16-11-0658	
			Location	MMSW-C		MMSW-C		MMSW-C		MMSW-C		MMSW-C	
			Sample Date	07/20/16		07/20/16		07/20/16		07/20/16		07/20/16	
			Sample ID	MMSW-C_072016_TIN_WB_04		MMSW-C_072016_NSS_BL_05		MMSW-C_072016_NSS_BL_07		MMSW-C_072016_SPI_WB_01		MMSW-C_072016_SPI_WB_02	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	16.8						274	J	201	
EPA 1631	Total	Mercury	NG/G	43.8		5240		7630		166	J	200	
NOAALipids1993	Total	Lipids	PERCENT	3.5								2.7	

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740/16-11-0658		1607740		1607740	
			Location	MMSW-C		MMSW-C		MMSW-C		MMSW-C		MMSW-C	
			Sample Date	07/20/16		07/20/16		07/20/16		07/20/16		07/20/16	
			Sample ID	MMSW-C_072016_SPI_WB_04		MMSW-C_072016_SPI_WB_05		MMSW-C_072016_TIN_WB_05		MMSW-C_072016_TIN_WB_06		MMSW-C_072016_NSS_BL_06	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	151		217		26.8		7.9			
EPA 1631	Total	Mercury	NG/G	270		219		52.9		59.4		6620	
NOAALipids1993	Total	Lipids	PERCENT					3.5					

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740		1607740		1607740	
			Location	W17-N		W17-N		W17-N		W17-N		W17-N	
			Sample Date	07/19/16		07/19/16		07/19/16		07/19/16		07/19/16	
			Sample ID	W17-N_071916_NSS_BL_01		W17-N_071916_NSS_BL_02		W17-N_071916_NSS_BL_03		W17-N_071916_NSS_BL_04		W17-N_071916_NSS_BL_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G										
EPA 1631	Total	Mercury	NG/G	7570		6020		9590		734		10300	
NOAALipids1993	Total	Lipids	PERCENT										

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740		1607740/16-11-0658		1607740/16-11-0658	
			Location	W17-N		W17-N		W17-N		W17-N		W17-N	
			Sample Date	07/19/16		07/19/16		07/19/16		07/19/16		07/19/16	
			Sample ID	W17-N_071916_NSS_BL_08		W17-N_071916_RWB_BL_01		W17-N_071916_NSS_BL_11		W17-N_071916_TIN_WB_01		W17-N_071916_TIN_WB_02	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G							64.2	J	118	J
EPA 1631	Total	Mercury	NG/G	3990		5850		6680		254	J	25.5	J
NOAALipids1993	Total	Lipids	PERCENT							0.99		3.4	

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SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740/16-11-0658		1607740/16-11-0658		1607740/16-11-0658		1607740		1607740	
			Location	W17-N		W17-N		W17-N		W17-N		W17-N	
			Sample Date	07/19/16		07/19/16		07/19/16		07/20/16		07/20/16	
			Sample ID	W17-N_071916_TIN_WB_03		W17-N_071916_TIN_WB_04		W17-N_071916_TIN_WB_05		W17-N_072016_NSS_BL_06		W17-N_072016_NSS_BL_07	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	56.7	J	21.7	J	28	J				
EPA 1631	Total	Mercury	NG/G	50	J	30.4	J	29.2	J	2140		1630	
NOAALipids1993	Total	Lipids	PERCENT	3.4		2.8		3.9					

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607740		1607740		1607740		1607740		1607741/16-11-0656	
			Location	W17-N		W17-N		W17-N		W17-N		ADD-01	
			Sample Date	07/20/16		07/20/16		07/20/16		07/20/16		07/21/16	
			Sample ID	W17-N_072016_NSS_BL_14		W17-N_072016_NSS_BL_09		W17-N_072016_RWB_BL_02		W17-N_072016_RWB_BL_03		ADD-01_072116_TIN_WB_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G									18.6	J
EPA 1631	Total	Mercury	NG/G	1960		1560		99.4		2500		8.85	J
NOAALipids1993	Total	Lipids	PERCENT									5.1	

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607741/16-11-0656		1607741/16-11-0656		1607741/16-11-0656		1607741/16-11-0656		1607741/16-11-0656	
			Location	ADD-01		ADD-01		ADD-01		ADD-01		ADD-01	
			Sample Date	07/21/16		07/21/16		07/21/16		07/21/16		07/21/16	
			Sample ID	ADD-01_072116_SPI_WB_01		ADD-01_072116_SPI_WB_02		ADD-01_072116_SPI_WB_03		ADD-01_072116_SPI_WB_04		ADD-01_072116_SPI_WB_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	14.6	J	24	J	22.9	J	60.2	J	22.9	J
EPA 1631	Total	Mercury	NG/G	25.9		43.3		31.4		44.2	J	30.5	
NOAALipids1993	Total	Lipids	PERCENT	1.1		1.1		1.6		2		2.3	

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607741		1607741		1607741		1607741/16-11-0656		1607741	
			Location	ADD-01		ADD-01		ADD-01		MMSE-1		MMSE-1	
			Sample Date	07/22/16		07/22/16		07/22/16		07/22/16		07/22/16	
			Sample ID	ADD-01_072216_NSS_BL_03		ADD-01_072216_NSS_BL_04		ADD-01_072216_NSS_BL_05		MMSE-01_072216_SPI_WB_01		MMSE-01_072216_SPI_WB_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G							174		181	
EPA 1631	Total	Mercury	NG/G	317		558		382		198		208	
NOAALipids1993	Total	Lipids	PERCENT							2.6			

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SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607741/16-11-0656		1607741		1607741		1607741		1607741	
			Location	MMSE-1		MMSE-1		MMSE-1		MMSE-1		MMSE-1	
			Sample Date	07/22/16		07/23/16		07/23/16		07/23/16		07/23/16	
			Sample ID	MMSE-01_072216_SPI_WB_02		MMSE-1_072316_NSS_BL_11		MMSE-1_072316_NSS_BL_12		MMSE-1_072316_NSS_BL_13		MMSE-1_072316_NSS_BL_15	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	244									
EPA 1631	Total	Mercury	NG/G	771		6220		4880		6130		6380	
NOAALipids1993	Total	Lipids	PERCENT	4.5		4.5							

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SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607741		1607741/16-11-0656		1607741		1607741		1607741	
			Location	MMSE-1		MMSE-1		MMSE-1		MMSE-1		MMSW-C	
			Sample Date	07/23/16		07/23/16		07/25/16		07/25/16		07/23/16	
			Sample ID	MMSE-1_072316_NSS_BL_16		MMSE-01_072316_SPI_WB_03		MMSE-1_072516_NSS_BL_17		MMSE-1_072516_NSS_BL_18		MMSW-C_072316_NSS_BL_08	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G			166							
EPA 1631	Total	Mercury	NG/G	7520		205		8070		4020		5670	
NOAALipids1993	Total	Lipids	PERCENT			3.4							

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\\PLD2-FS1\USDC_Penobscot_River\3.0_Site_Data\3.4_Test_Results\2016 Validation Reports\WO005 - Biota\Polychaete, Spider, Terr Insects, Blood\Penobscot 2016 Biota Validation_Table 3.xlsx

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607741		1607741		1607741		1607741		1607741/16-11-0656	
			Location	MMSW-C		MMSW-C		MMSW-C		W17-N		W17-N	
			Sample Date	07/23/16		07/24/16		07/24/16		07/24/16		07/24/16	
			Sample ID	MMSW-C_072316_NSS_BL_10		MMSW-C_072416_NSS_BL_09		MMSW-C_072416_NSS_BL_11		W17-N_072416_NSS_BL_12		W17-N_072416_SPI_WB_02	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G									278	J
EPA 1631	Total	Mercury	NG/G	5840		3280		5310		5350		197	J
NOAALipids1993	Total	Lipids	PERCENT									2.6	

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			SDG	1607741		1607741		1607741		1607741		1607804	
			Location	W17-N		W17-N		W17-N		W17-N		ADD-01	
			Sample Date	07/24/16		07/25/16		07/25/16		07/25/16		07/25/16	
			Sample ID	W17-N_072416_SPI_WB_05		W17-N_072516_NSS_BL_10		W17-N_072516_NSS_BL_15		W17-N_072516_NSS_BL_16		ADD-01_072516_NSS_BL_06	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	642	J								
EPA 1631	Total	Mercury	NG/G	213	J	5240		5000		2920		290	
NOAALipids1993	Total	Lipids	PERCENT										

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607804		1607804		1607804		1607804		1607804	
			Location	ADD-01		ADD-01		ADD-01		ADD-01		ADD-01	
			Sample Date	07/25/16		07/25/16		07/25/16		07/25/16		07/25/16	
			Sample ID	ADD-01_072616_NSS_BL_08		ADD-01_072616_NSS_BL_10		ADD-01_072616_NSS_BL_09		ADD-01_072516_NSS_BL_07		ADD-01_072616_NSS_BL_11	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G										
EPA 1631	Total	Mercury	NG/G	434		467		296		637		469	
NOAALipids1993	Total	Lipids	PERCENT										

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DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1607804		1607804/16-11-0655		1607804/16-11-0655		1607804		1607804	
			Location	MMSE-1		MMSW-C		W17-N		W17-N		W17-N	
			Sample Date	07/25/16		07/25/16		07/25/16		07/25/16		07/25/16	
			Sample ID	MMSE-1_072616_SPI_WB_04		MMSW-C_072616_SPI_WB_03		W17-N_072616_SPI_WB_01		W17-N_072616_SPI_WB_03		W17-N_072616_SPI_WB_04	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	136		330	J	210		282		480	J
EPA 1631	Total	Mercury	NG/G	200		257	J	431		420		263	J
NOAALipids1993	Total	Lipids	PERCENT			3		2.1					

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated
U = The target compound was not detected above the meth
UJ = The target compound was not detected and the reporti

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1608069		1608069		1608069		1608069		1608069	
			Location	BO-04		BO-04		BO-04		BO-04		BO-04	
			Sample Date	07/26/16		07/26/16		07/26/16		07/26/16		07/26/16	
			Sample ID	BO-04_072616_POL_WB_01		BO-04_072616_POL_WB_02		BO-04_072616_POL_WB_03		BO-04_072616_POL_WB_04		BO-04_072616_POL_WB_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	8.6	J	6.9	J	9.2	J	7.3	J	8.3	J
EPA 1631	Total	Mercury	NG/G	142	J	176	J	185	J	311	J	256	J
NOAALipids1993	Total	Lipids	PERCENT										

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Created by: BGP 01/05/2017
Checked by: DMK 01/12/2017

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PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1608069		1608069		1608069		1608069/16-11-0657		1608069	
			Location	ES-FP		ES-FP		ES-FP		ES-FP		ES-FP	
			Sample Date	07/28/16		07/28/16		07/28/16		07/28/16		07/28/16	
			Sample ID	ES-FP_072816_POL_WB_01		ES-FP_072816_POL_WB_02		ES-FP_072816_POL_WB_03		ES-FP_072816_POL_WB_04		ES-FP_072816_POL_WB_05	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	6.2	J	4.4	J	0.4	UJ	5.3	J	15.7	J
EPA 1631	Total	Mercury	NG/G	34.6	J	24	J	24.5	J	19.4	J	46.1	J
NOAALipids1993	Total	Lipids	PERCENT							1.2	J		

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1608069		1608069		1608069		1608069	
			Location	MMPOLY		MMPOLY		MMPOLY		MMPOLY	
			Sample Date	07/29/16		07/29/16		07/29/16		07/29/16	
			Sample ID	MMPOLY-01_072916_POL_WB_01		MMPOLY-01_072916_POL_WB_02		MMPOLY-01_072916_POL_WB_03		MMPOLY-01_072916_POL_WB_04	
			QC Code	FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	1.4	J	11.3	J	11.1	J	8.2	J
EPA 1631	Total	Mercury	NG/G	69.9	J	321	J	190	J	142	J
NOAALipids1993	Total	Lipids	PERCENT								

Units:

NG/G = Nanogram per gram

Validation Qualifier:

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PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1608069		1608069		1608069		1608069		1608069	
			Location	MMPOLY		OB-05		OB-05		OB-05		OB-05	
			Sample Date	07/29/16		07/26/16		07/26/16		07/26/16		07/26/16	
			Sample ID	MMPOLY-01_072916_POL_WB_05		OB-05_072616_POL_WB_01		OB-05_072616_POL_WB_02		OB-05_072616_POL_WB_03		OB-05_072616_POL_WB_04	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	9.9	J	11.7	J	12.8	J	11	J	12.8	J
EPA 1631	Total	Mercury	NG/G	239	J	215	J	224	J	205	J	189	J
NOAALipids1993	Total	Lipids	PERCENT										

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1608069		1610231/16-11-2442		1610231/16-11-2442		1610231/16-11-2442	
			Location	OB-05		ES-13		ES-13		ES-13	
			Sample Date	07/26/16		07/27/16		07/27/16		07/27/16	
			Sample ID	OB-05_072616_POL_WB_05		ES-13_072716_POL_WB_01		ES-13_072716_POL_WB_02		ES-13_072716_POL_WB_03	
			QC Code	FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	12.7	J	3.3		1.5	J	0.4	U
EPA 1631	Total	Mercury	NG/G	230	J	20.8		45.2		12.8	
NOAALipids1993	Total	Lipids	PERCENT			1.8		3.3		3.4	

Units:
NG/G = Nanogram per gram

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

SDG				1610231/16-11-2442		1610231/16-11-2442		1610235/16-11-2553		1610235/16-11-2553	
Location				ES-13		ES-13		FRB-01		FRB-01	
Sample Date				07/27/16		07/27/16		09/28/16		09/28/16	
Sample ID				ES-13_072716_POL_WB_04		ES-13_072716_POL_WB_05		FRB-01_092816_POL_WB_01		FRB-01_092816_POL_WB_02	
QC Code				FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	1.1	J	4.1		0.4	U	0.4	U
EPA 1631	Total	Mercury	NG/G	24.7		71.3		1.9	U	2.46	U
NOAALipids1993	Total	Lipids	PERCENT	4.3				2		1.5	

Units:

NG/G = Nanogram per gram

Validation Qualifier:

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PENOBSCOT RIVER, MAINE
SDGs 1607740, 1607741, 1607804, 1608069, 1610231, and 1610235

			SDG	1610235/16-11-2553		1610235		1610235/16-11-2553	
			Location	FRB-01		FRB-01		FRB-01	
			Sample Date	09/28/16		09/28/16		09/28/16	
			Sample ID	FRB-01_092816_POL_WB_03		FRB-01_092816_POL_WB_04		FRB-01_092816_POL_WB_05	
			QC Code	FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1630	Total	Methyl mercury	NG/G	0.5	U	0.5	U	0.4	U
EPA 1631	Total	Mercury	NG/G	1.15	U	3.18		1.82	U
NOAALipids1993	Total	Lipids	PERCENT	1.4				1.4	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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DATA VALIDATION REPORT

Penobscot River Estuary Phase III - Engineering Evaluation

Penobscot River, Maine

2016 Biota Monitoring - Lobster

Prepared for:

United States District Court
District of Maine

Prepared by:

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(503) 639-3400

January 2017

Project No. 3616166052.04.05

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Table 1	Field Samples Submitted to Eurofins
Table 2	Data Validation Summary

ACRONYMS AND ABBREVIATIONS

°C	degrees Celsius
%	percent
Amec Foster Wheeler	Amec Foster Wheeler Environment & Infrastructure, Inc.
Calscience	Eurofins Calscience, Inc.
CCB	continuing calibration blank
CCV	continuing calibration verification
CLP	EPA Contract Laboratory Program
COC	chain of custody
DCM	dichloromethane
EPA	United States Environmental Protection Agency
Eurofins	Eurofins Frontier Global Sciences, Inc.
ICAL	initial calibration
ICB	initial calibration blank
ICV	initial calibration verification
ID	sample identification
LCS	laboratory control sample
LCSD	laboratory control sample duplicate
ng/g	nanograms per gram
MDL	method detection limit

MS	matrix spike
MSD	matrix spike duplicate
NOAA	National Oceanic and Atmospheric Administration
QAPP	Quality Assurance Project Plan
QC	quality control
RL	reporting limit
RPD	relative percent difference
RSD	relative standard deviation
SDG	sample delivery group
SM	standard method

DATA QUALITY REVIEW AND VALIDATION REPORT
Penobscot River Estuary Phase III - Engineering Study
Biota Monitoring - Lobster
Penobscot River, Maine

1.0 INTRODUCTION

Amec Foster Wheeler Environment & Infrastructure, Inc. (Amec Foster Wheeler) collected 100 lobster samples from September 24 through 26, 2016, from the Penobscot River and Estuary site in Penobscot, Maine. The samples were submitted to Eurofins Frontier Global Sciences, Inc. (Eurofins) in Bothell, Washington, where they were received on October 28, 2016, and assigned to sample delivery groups (SDGs) 1611255, 1611256, 1611257, 1611258, and 1611259. Eurofins analyzed the samples for mercury by United States Environmental Protection Agency (EPA) Method 1631B and percent solids and moisture by Standard Method (SM) 2540B. Eurofins in Bothell subcontracted the samples to Eurofins Calscience, Inc. (Calscience) in Garden Grove, California, where they were received on December 16, 2016, and assigned to SDGs 16121553, 16121552, 16121551, 16121554, and 16121613. Calscience analyzed the samples for percent (%) lipids by dichloromethane (DCM) extraction and gravimetric determination, as described in National Oceanic and Atmospheric Administration (NOAA) Technical Memorandum NOS ORCA 130.

A list of these samples by field sample identification (ID), sample collection date, matrix, and Eurofins sample ID is presented in Table 1.

2.0 DATA VALIDATION AND DATA QUALITY REVIEW METHODOLOGY

This data validation and data quality review has been performed by Amec Foster Wheeler with reference to the EPA Contract Laboratory Program (CLP) National Functional Guidelines for Inorganic Superfund Data Review (EPA, 2014), EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (EPA 2013), EPA Method 1631, revision B (EPA, 2001), and NOAA Technical Memorandum NOS ORCA 130. The EPA CLP guidelines were written specifically for the CLP, and have been modified for the purposes of this data validation where they differ from method-specific quality control (QC) requirements.

Amec Foster Wheeler's data validation and review methodology complied with the validation procedures specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality

Assurance Project Plan (QAPP), dated July 20, 2016 (Amec Foster Wheeler, 2016). The laboratory's analytical data packages were reviewed to assess the following criteria:

- Chain of custody (COC) compliance;
- Holding time compliance;
- Initial calibration (ICAL), initial calibration verification (ICV), and continuing calibration verification (CCV) compliance with method-specified criteria;
- Presence or absence of laboratory contamination as demonstrated by laboratory blanks, instrument blanks, initial calibration blanks (ICBs), and continuing calibration blanks (CCBs);
- Accuracy and bias as demonstrated by recovery of surrogate spikes, laboratory control sample (LCS), and matrix spike (MS) samples;
- Analytical precision as relative percent difference (RPD) of analyte concentration between laboratory duplicates, LCS and LCS duplicates (LCSDs), or MS and MS duplicates (MSDs);
- Detection limits;
- Analyte calculation verification (Stage 3 validation only); and
- Insofar as possible, the degree of conformance to method requirements and good laboratory practices.

In general, it is important to recognize that no analytical data are guaranteed to be correct, even if all QC audits are passed. Strict QC serves to increase confidence in data, but any reported value may potentially contain error.

In accordance with the specifications of QAPP Worksheet #36, the data review and validation process comprised 10% Stage 3 full validation of the raw analytical data from primary field samples and 90% Stage 2B data validation based on information provided by the laboratory as summary reporting forms. Amec Foster Wheeler performed full validation on ten samples from SDGs 1611255 and 16121554.

3.0 DEFINITIONS OF QUALIFIERS THAT MAY BE ADDED DURING DATA QUALITY REVIEW AND VALIDATION

U The analyte was analyzed for, but was not detected above the reported sample quantitation limit.

J The analyte was positively identified; the associated numerical value is the approximate concentration of the analyte in the sample.

UJ The analyte was not detected above the reported sample quantitation limit. However, the reported quantitation limit is approximate and may or may not represent the actual limit of quantitation necessary to accurately and precisely measure the analyte in the sample.

R The sample result is rejected due to serious deficiencies in the ability to analyze the sample and meet quality control criteria. The presence or absence of the analyte cannot be verified.

4.0 VALIDATION REASON CODES

No data was qualified and no reason codes were applied to the data during validation.

5.0 EXPLANATION OF DATA QUALITY INDICATORS

Data quality indicators of the review and validation process are defined below.

5.1 LABORATORY CONTROL SAMPLE RECOVERIES

LCSs and LCS duplicates are aliquots of analyte-free matrix that are spiked with the analytes of interest for an analytical method or a representative subset of those analytes. The spiked matrix is then processed through the same extraction, concentration, cleanup, and analytical procedures as the samples they accompany. LCS recovery and precision are an indication of a laboratory's ability to successfully perform an analytical method in an interference-free matrix.

5.2 MATRIX SPIKE RECOVERIES

MSs and MSDs are prepared by adding known amounts of the analytes of interest for an analytical method, or a representative subset of those analytes, to an aliquot of sample. The spiked sample is then processed through the same extraction, concentration, cleanup, and analytical procedures as the unspiked samples in an analytical batch.

MS recovery and precision are an indication of a laboratory's ability to successfully recover an analyte in the matrix of a specific sample or closely related sample matrices. It is important not to apply MS results for any specific sample to other samples without understanding how the sample matrices are related.

5.3 BLANK SAMPLES

Blank samples are aliquots of analyte-free matrix that are used as negative controls to verify that the sample collection, storage, preparation, and analysis system does not produce false positive results. Three types of blanks were employed for this project.

- Calibration blanks are aliquots of analyte-free matrix that are evaluated after calibration and every 10 samples immediately after CCVs. ICB and CCB results may not exceed one half of the practical quantitation limit.
- Instrument blanks are aliquots of analyte-free matrix that are used to evaluate instrument drift. Instrument blanks results may not exceed 0.5 nanograms per liter, and average instrument blank peak areas are used to correct peak areas of QC and field samples.
- Laboratory or preparation blanks are aliquots of analyte-free matrix that are processed by the laboratory using exactly the same procedures as the field samples. Laboratory blanks are used to monitor for contamination introduced by the laboratory during sample preparation and analysis.

Target analytes should not be found in blank samples. When target analytes are detected in laboratory blanks, analyte concentrations in associated samples greater than the RL but less than five times the concentration detected in the blank will be U qualified by Amec Foster Wheeler. Analyte concentrations between the matrix detection limit and the RL, and less than five times the concentration detected in the blank will be U qualified at the RL. Negative results in a blank may indicate a low instrument bias, if the absolute concentration detected in the blank is greater than the RL, concentrations in associated samples greater than the RL but less than ten times the absolute concentration detected in the blank are J qualified and non-detect results are UJ qualified.

6.0 CHAIN OF CUSTODY AND SAMPLE RECEIPT CONDITION DOCUMENTATION

All samples were received by Eurofins under proper COC, intact, properly preserved, and at temperatures less than the QAPP-specified maximum of 4 degrees Celsius (°C).

7.0 SPECIFIC DATA VALIDATION FINDINGS

This section contains narrative descriptions of data quality review and data validation findings and data quality limitations.

7.1 LOW LEVEL MERCURY EPA METHOD 1631B

Low level mercury results generated by Eurofins may be considered usable without qualification.

7.1.1 Holding Times

Samples were collected by Amec Foster Wheeler from September 24 through 26, 2016. This data validation assumes that all samples were properly preserved by freezing at or below -18°C within 48 hours of collection. Samples arrived at Eurofins under proper COC, intact, and properly preserved. Samples were analyzed within the method-specified hold time of 1 year from collection.

7.1.2 Initial Calibration

ICAL standard recoveries were included in the laboratory's QC summary forms, but relative standard deviations (RSDs) were only included in raw data. For samples that underwent Stage 3 validation, RSDs were less than or equal to 15%. For samples that underwent Stage 2B validation, ICAL standard recoveries were within QAPP-specified limits established for ICVs and CCVs, 77 to 123%.

7.1.3 Initial and Continuing Calibration Verification

ICVs and CCVs met the QAPP-specified 77 to 123% recovery criteria for unqualified data.

7.1.4 Laboratory, Instrument, and Calibration Blanks

Target analytes were not detected above the reporting limit in the laboratory blanks, instrument blanks, ICBs, or CCBs associated with the mercury analysis of these samples.

When mercury was detected in laboratory blanks at concentrations between the method detection limit (MDL) and the reporting limit (RL), results in the associated field samples were greater than five times the detections in the blanks, and data usability is not adversely affected.

7.1.5 Laboratory Control Sample Recovery and Precision

LCS recoveries were within the QAPP-specified 80 to 120% limits, and RPDs between LCS and LCSD results did not exceed the QAPP-specified maximum of 24%.

7.1.6 Matrix Spike Recovery and Precision

Eurofins performed MS and MSD analyses on samples CPJL-092416_LOB_TA_01, CPJL-092416_LOB_TA_10, HBI-01_092416_LOB_TA_01, HBI-01_092616_LOB_TA_20, L9-45_092416_LOB_TA_05, L9-45_092416_LOB_TA_06, L10-52_092416_LOB_TA_01, L10-52_092416_LOB_TA_02, SVE-01_092416_LOB_TA_09, and SVE-01_092416_LOB_TA_20.

MS/MSD recoveries were within the QAPP-specified 71 to 125% limits, and RPDs did not exceed the QAPP-specified maximum of 24%, with the following exception:

- Mercury recovery was low at 53.7% in the MSD performed on sample SVE-01_092416_LOB_TA_20, and the RPD between results was high at 49.0%. The spike concentration, at 366.97 nanograms per gram (ng/g), was less than the concentration of the native unspiked sample at 1,321 ng/g. The laboratory performed a subsequent MS/MSD on this sample with higher spike concentrations (3,683.8 ng/g), and recoveries and RPDs were within QAPP-specified limits. In Amec Foster Wheeler's professional opinion, data usability is not adversely affected by the low recovery in the initial MS/MSD performed on sample SVE-01_092416_LOB_TA_20.

7.1.7 Laboratory Duplicates

Eurofins performed duplicate analysis on CPJL-092416_LOB_TA_01, HBI-01_092416_LOB_TA_01, HBI-01_092616_LOB_TA_20, L9-45_092416_LOB_TA_05, L10-52_092416_LOB_TA_01, SVE-01_092416_LOB_TA_09, and SVE-01_092416_LOB_TA_20. RPDs between duplicate results did not exceed the QAPP-specified maximum of 24% for results that were greater than or equal to 5 times the RL.

7.1.8 Calculation Verification

Amec Foster Wheeler performed Stage 3 validation on 10 samples from Eurofins SDG 1611255. Stage 3 validation included recalculation of all calibrations, blanks, QC samples, and field samples. No errors in calculation were identified during Stage 3 validation.

7.1.9 Data Reporting and Analytical Procedures

There were no data anomalies associated with the solids and moisture determinations performed on these samples.

7.2 PERCENT SOLIDS BY STANDARD METHOD SM2540B

Moisture and solids results generated by Eurofins may be considered usable without qualification.

7.2.1 Holding Times

Eurofins performed percent moisture and percent solids analyses concurrent with sample preparation for mercury analysis. The laboratory qualified these results as being determined outside of method-specified hold times. However, in Amec Foster Wheeler's professional opinion, the concurrent analysis provides the most accurate results and data usability is not adversely affected by missed analytical hold times.

7.2.2 Percent Solids and Moisture Laboratory Duplicate Precision

The laboratory performed duplicate solids and moisture analysis on samples CPJL-092416_LOB_TA_01, CPJL-092416_LOB_TA_02, HBI-01_092416_LOB_TA_01, HBI-01_092616_LOB_TA_20, L9-45_092416_LOB_TA_05, L9-45_092416_LOB_TA_06, L10-52_092416_LOB_TA_01, L10-52_092416_LOB_TA_02, SVE-01_092416_LOB_TA_09, and SVE-01_092416_LOB_TA_10. RPDs between duplicate results were less than the laboratory-specified 25% limit.

7.2.3 Data Reporting and Analytical Procedures

There were no data anomalies associated with the solids and moisture determinations performed on these samples.

7.3 PERCENT LIPIDS BY DICHLOROMETHANE EXTRACTION

Percent lipid results generated by Calscience may be considered usable without qualification.

7.3.1 Holding Times

Holding times are not applicable to % lipid determination by DCM extraction.

7.3.2 Laboratory Blanks

Lipids were not detected above the reporting limit in laboratory blanks associated with the % lipids determinations of these samples.

7.3.3 Percent Lipids Laboratory Duplicate Precision

The laboratory performed duplicate % lipids analysis on samples CPJL-092416_LOB_TA_01, HBI-01_092416_LOB_TA_01, L10_52_092416_LOB_TA_01, and SVE-01_092416_LOB_TA_09. RPDs between duplicate results were less than the laboratory-specified 25% limit.

7.3.4 Calculation Verification

Amec Foster Wheeler performed Stage 3 validation on 10 samples from Calscience SDG 16121554. These are the same samples that underwent Stage 3 validation of mercury results under Eurofins SDG 1611255. Stage 3 validation included recalculation of all laboratory blanks, QC samples, and field samples. No errors in calculation were identified during Stage 3 validation.

7.3.5 Data Reporting and Analytical Procedures

There were no data anomalies associated with the % lipids determinations performed on these samples.

8.0 FIELD DUPLICATES

Field duplicates were not collected by Amec Foster Wheeler.

9.0 SUMMARY AND CONCLUSIONS

Amec Foster Wheeler reviewed 400 data records from field samples during the data validation and data quality review. No data records were qualified, and 100% of the data should be considered valid as reported.

REFERENCES

Amec Foster Wheeler, 2016. Draft Penobscot Estuary Phase III Engineering Evaluation Quality Assurance Project Plan.

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NOAA, 1998. NOAA Technical Memorandum NOS ORCA 130: Sampling and Analytical Methods of the National Status and Trends Program Mussel watch Project: 1993-1996 Update.

LIMITATIONS

This report was prepared exclusively for the United States District Court, District of Maine by Amec Foster Wheeler Environment & Infrastructure, Inc. The quality of information, conclusions, and estimates contained herein is consistent with the level of effort involved in Amec Foster Wheeler services and based on: i) information available at the time of preparation, ii) data supplied by outside sources, and iii) the assumptions, conditions, and qualifications set forth in this report. This data quality review and validation report is intended to be used by the United States District Court District of Maine for the Penobscot River Estuary Phase III Engineering Study only, subject to the terms and conditions of its contract with Amec Foster Wheeler. Any other use of, or reliance on, this report by any third party is at that party's sole risk.

TABLES

Table 1
Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Lobster Samples

Sample ID	Collection Date	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Mercury by Method 1631	% Lipids by NOAA Method	Notes
SVE-01_092416_LOB_TA_01	9/24/2016	1611255	1611255-01	16121554	16121554-01	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_02	9/24/2016	1611255	1611255-02	16121554	16121554-02	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_03	9/24/2016	1611255	1611255-03	16121554	16121554-03	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_04	9/24/2016	1611255	1611255-04	16121554	16121554-04	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_05	9/24/2016	1611255	1611255-05	16121554	16121554-05	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_06	9/24/2016	1611255	1611255-06	16121554	16121554-06	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_07	9/24/2016	1611255	1611255-07	16121554	16121554-07	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_08	9/24/2016	1611255	1611255-08	16121554	16121554-08	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_09	9/24/2016	1611255	1611255-09	16121554	16121554-09	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_10	9/24/2016	1611255	1611255-10	16121554	16121554-10	X	X	Stage 3 Validation
SVE-01_092416_LOB_TA_11	9/24/2016	1611255	1611255-11	16121554	16121554-11	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_12	9/24/2016	1611255	1611255-12	16121554	16121554-12	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_13	9/24/2016	1611255	1611255-13	16121554	16121554-13	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_14	9/24/2016	1611255	1611255-14	16121554	16121554-14	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_15	9/24/2016	1611255	1611255-15	16121554	16121554-15	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_16	9/24/2016	1611255	1611255-16	16121554	16121554-16	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_17	9/24/2016	1611255	1611255-17	16121554	16121554-17	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_18	9/24/2016	1611255	1611255-18	16121554	16121554-18	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_19	9/24/2016	1611255	1611255-19	16121554	16121554-19	X	X	Stage 2b Validation
SVE-01_092416_LOB_TA_20	9/24/2016	1611255	1611255-20	16121554	16121554-20	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_01	9/24/2016	1611256	1611256-01	16121613	16121613-01	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_02	9/24/2016	1611256	1611256-02	16121613	16121613-02	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_03	9/24/2016	1611256	1611256-03	16121613	16121613-03	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_04	9/24/2016	1611256	1611256-04	16121613	16121613-04	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_05	9/24/2016	1611256	1611256-05	16121613	16121613-05	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_06	9/24/2016	1611256	1611256-06	16121613	16121613-06	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_07	9/24/2016	1611256	1611256-07	16121613	16121613-07	X	X	Stage 2b Validation
HBI-01_092416_LOB_TA_08	9/24/2016	1611256	1611256-08	16121613	16121613-08	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_09	9/26/2016	1611256	1611256-09	16121613	16121613-09	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_10	9/26/2016	1611256	1611256-10	16121613	16121613-10	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_11	9/26/2016	1611256	1611256-11	16121613	16121613-11	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_12	9/26/2016	1611256	1611256-12	16121613	16121613-12	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_13	9/26/2016	1611256	1611256-13	16121613	16121613-13	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_14	9/26/2016	1611256	1611256-14	16121613	16121613-14	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_15	9/26/2016	1611256	1611256-15	16121613	16121613-15	X	X	Stage 2b Validation

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Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Lobster Samples

Sample ID	Collection Date	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Mercury by Method 1631	% Lipids by NOAA Method	Notes
HBI-01_092616_LOB_TA_16	9/26/2016	1611256	1611256-16	16121613	16121613-16	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_17	9/26/2016	1611256	1611256-17	16121613	16121613-17	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_18	9/26/2016	1611256	1611256-18	16121613	16121613-18	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_19	9/26/2016	1611256	1611256-19	16121613	16121613-19	X	X	Stage 2b Validation
HBI-01_092616_LOB_TA_20	9/26/2016	1611256	1611256-20	16121613	16121613-20	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_01	9/24/2016	1611257	1611257-01	16121553	16121553-01	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_02	9/24/2016	1611257	1611257-02	16121553	16121553-02	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_03	9/24/2016	1611257	1611257-03	16121553	16121553-03	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_04	9/24/2016	1611257	1611257-04	16121553	16121553-04	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_05	9/24/2016	1611257	1611257-05	16121553	16121553-05	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_06	9/24/2016	1611257	1611257-06	16121553	16121553-06	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_07	9/24/2016	1611257	1611257-07	16121553	16121553-07	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_08	9/24/2016	1611257	1611257-08	16121553	16121553-08	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_09	9/24/2016	1611257	1611257-09	16121553	16121553-09	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_10	9/24/2016	1611257	1611257-10	16121553	16121553-10	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_11	9/24/2016	1611257	1611257-11	16121553	16121553-11	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_12	9/24/2016	1611257	1611257-12	16121553	16121553-12	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_13	9/24/2016	1611257	1611257-13	16121553	16121553-13	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_14	9/24/2016	1611257	1611257-14	16121553	16121553-14	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_15	9/24/2016	1611257	1611257-15	16121553	16121553-15	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_16	9/24/2016	1611257	1611257-16	16121553	16121553-16	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_17	9/24/2016	1611257	1611257-17	16121553	16121553-17	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_18	9/24/2016	1611257	1611257-18	16121553	16121553-18	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_19	9/24/2016	1611257	1611257-19	16121553	16121553-19	X	X	Stage 2b Validation
CPJL-092416_LOB_TA_20	9/24/2016	1611257	1611257-20	16121553	16121553-20	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_01	9/24/2016	1611258	1611258-01	16121551	16121551-01	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_02	9/24/2016	1611258	1611258-02	16121551	16121551-02	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_03	9/24/2016	1611258	1611258-03	16121551	16121551-03	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_04	9/24/2016	1611258	1611258-04	16121551	16121551-04	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_05	9/24/2016	1611258	1611258-05	16121551	16121551-05	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_06	9/24/2016	1611258	1611258-06	16121551	16121551-06	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_07	9/24/2016	1611258	1611258-07	16121551	16121551-07	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_08	9/24/2016	1611258	1611258-08	16121551	16121551-08	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_09	9/24/2016	1611258	1611258-09	16121551	16121551-09	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_10	9/24/2016	1611258	1611258-10	16121551	16121551-10	X	X	Stage 2b Validation

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Checked by:DMK 02/02/17

Table 1
Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Lobster Samples

Sample ID	Collection Date	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Mercury by Method 1631	% Lipids by NOAA Method	Notes
L10-52_092416_LOB_TA_11	9/24/2016	1611258	1611258-11	16121551	16121551-11	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_12	9/24/2016	1611258	1611258-12	16121551	16121551-12	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_13	9/24/2016	1611258	1611258-13	16121551	16121551-13	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_14	9/24/2016	1611258	1611258-14	16121551	16121551-14	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_15	9/24/2016	1611258	1611258-15	16121551	16121551-15	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_16	9/24/2016	1611258	1611258-16	16121551	16121551-16	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_17	9/24/2016	1611258	1611258-17	16121551	16121551-17	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_18	9/24/2016	1611258	1611258-18	16121551	16121551-18	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_19	9/24/2016	1611258	1611258-19	16121551	16121551-19	X	X	Stage 2b Validation
L10-52_092416_LOB_TA_20	9/24/2016	1611258	1611258-20	16121551	16121551-20	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_01	9/24/2016	1611259	1611259-01	16121552	16121552-01	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_02	9/24/2016	1611259	1611259-02	16121552	16121552-02	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_03	9/24/2016	1611259	1611259-03	16121552	16121552-03	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_04	9/24/2016	1611259	1611259-04	16121552	16121552-04	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_05	9/24/2016	1611259	1611259-05	16121552	16121552-05	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_06	9/24/2016	1611259	1611259-06	16121552	16121552-06	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_07	9/24/2016	1611259	1611259-07	16121552	16121552-07	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_08	9/24/2016	1611259	1611259-08	16121552	16121552-08	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_09	9/24/2016	1611259	1611259-09	16121552	16121552-09	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_10	9/24/2016	1611259	1611259-10	16121552	16121552-10	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_11	9/24/2016	1611259	1611259-11	16121552	16121552-11	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_12	9/24/2016	1611259	1611259-12	16121552	16121552-12	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_13	9/24/2016	1611259	1611259-13	16121552	16121552-13	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_14	9/24/2016	1611259	1611259-14	16121552	16121552-14	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_15	9/24/2016	1611259	1611259-15	16121552	16121552-15	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_16	9/24/2016	1611259	1611259-16	16121552	16121552-16	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_17	9/24/2016	1611259	1611259-17	16121552	16121552-17	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_18	9/24/2016	1611259	1611259-18	16121552	16121552-18	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_19	9/24/2016	1611259	1611259-19	16121552	16121552-19	X	X	Stage 2b Validation
L9-45_092416_LOB_TA_20	9/24/2016	1611259	1611259-20	16121552	16121552-20	X	X	Stage 2b Validation

Notes:

ID = identification
Eurofins = Eurofins Frontier Global Sciences, Inc.
SDG = Sample Delivery Group

Created by: CL 01/17/17
Checked by:DMK 02/02/17

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554	
			Location	SVE-01		SVE-01		SVE-01		SVE-01		SVE-01		SVE-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	SVE-01_092416_LOB_TA_01		SVE-01_092416_LOB_TA_02		SVE-01_092416_LOB_TA_03		SVE-01_092416_LOB_TA_04		SVE-01_092416_LOB_TA_05		SVE-01_092416_LOB_TA_06	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	80.8		77		82.1		79		80.2		83.2	
Solids	Total	Percent Solids	% BY WT.	19.2		23		17.9		21		19.8		16.8	
EPA 1631	Total	Mercury	NG/G	344		265		277		222		512		523	
NOAALipids1993	Total	Lipids	Percent	0.47		0.47		0.47		0.73		0.59		0.28	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554	
			Location	SVE-01		SVE-01		SVE-01		SVE-01		SVE-01		SVE-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	SVE-01_092416_LOB_TA_07		SVE-01_092416_LOB_TA_08		SVE-01_092416_LOB_TA_09		SVE-01_092416_LOB_TA_10		SVE-01_092416_LOB_TA_11		SVE-01_092416_LOB_TA_12	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	78.9		77.3		79.7		79.7		81		78.7	
Solids	Total	Percent Solids	% BY WT.	21.1		22.7		20.3		20.3		19		21.3	
EPA 1631	Total	Mercury	NG/G	181		278		512		167		450		227	
NOAALipids1993	Total	Lipids	Percent	0.51		0.64		0.52		0.62		0.57		0.64	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554		1611255 & 16-12-1554	
			Location	SVE-01		SVE-01		SVE-01		SVE-01		SVE-01		SVE-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	SVE-01_092416_LOB_TA_13		SVE-01_092416_LOB_TA_14		SVE-01_092416_LOB_TA_15		SVE-01_092416_LOB_TA_16		SVE-01_092416_LOB_TA_17		SVE-01_092416_LOB_TA_18	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	80.3		79.3		82.4		81.9		80.3		81.9	
Solids	Total	Percent Solids	% BY WT.	19.7		20.7		17.6		18.1		19.7		18.1	
EPA 1631	Total	Mercury	NG/G	272		388		674		459		308		395	
NOAALipids1993	Total	Lipids	Percent	0.45		0.64		0.39		0.52		0.51		0.49	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611255 & 16-12-1554		1611255 & 16-12-1554		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613	
			Location	SVE-01		SVE-01		HB-01		HB-01		HB-01		HB-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	SVE-01_092416_LOB_TA_19		SVE-01_092416_LOB_TA_20		HBI-01_092416_LOB_TA_01		HBI-01_092416_LOB_TA_02		HBI-01_092416_LOB_TA_03		HBI-01_092416_LOB_TA_04	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	82.6		79.2		82.6		82.1		81.9		81.2	
Solids	Total	Percent Solids	% BY WT.	17.4		20.8		17.4		17.9		18.1		18.8	
EPA 1631	Total	Mercury	NG/G	747		1320		139		76.9		46.9		68.7	
NOAALipids1993	Total	Lipids	Percent	0.41		0.66		0.72		0.91		0.83		1	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613	
			Location	HB-01		HB-01		HB-01		HB-01		HB-01		HB-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/26/16		09/26/16	
			Sample ID	HBI-01_092416_LOB_TA_05		HBI-01_092416_LOB_TA_06		HBI-01_092416_LOB_TA_07		HBI-01_092416_LOB_TA_08		HBI-01_092616_LOB_TA_09		HBI-01_092616_LOB_TA_13	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79.8		79.9		81.7		80.7		82.9		78.6	
Solids	Total	Percent Solids	% BY WT.	20.2		20.1		18.3		19.3		17.1		21.4	
EPA 1631	Total	Mercury	NG/G	100		92.7		103		82.9		44.4		98.4	
NOAALipids1993	Total	Lipids	Percent	0.94		1		0.81		0.99		0.73		1.1	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613	
			Location	HB-01		HB-01		HB-01		HB-01		HB-01		HB-01	
			Sample Date	09/26/16		09/26/16		09/26/16		09/26/16		09/26/16		09/26/16	
			Sample ID	HBI-01_092616_LOB_TA_10		HBI-01_092616_LOB_TA_14		HBI-01_092616_LOB_TA_15		HBI-01_092616_LOB_TA_16		HBI-01_092616_LOB_TA_11		HBI-01_092616_LOB_TA_17	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	84.2		78.5		79.6		81.3		80.6		78.1	
Solids	Total	Percent Solids	% BY WT.	15.8		21.5		20.4		18.7		19.4		21.9	
EPA 1631	Total	Mercury	NG/G	117		128		119		54		129		127	
NOAALipids1993	Total	Lipids	Percent	0.64		0.85		0.93		0.94		1		0.97	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611256 & 16-12-1613		1611257 & 16-12-1553		1611257 & 16-12-1553	
			Location	HB-01		HB-01		HB-01		HB-01		CPJL		CPJL	
			Sample Date	09/26/16		09/26/16		09/26/16		09/26/16		09/24/16		09/24/16	
			Sample ID	HBI-01_092616_LOB_TA_12		HBI-01_092616_LOB_TA_18		HBI-01_092616_LOB_TA_19		HBI-01_092616_LOB_TA_20		CPJL-092416_LOB_TA_01		CPJL-092416_LOB_TA_02	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	81		77.3		79		80.3		80.1		78	
Solids	Total	Percent Solids	% BY WT.	19		22.7		21		19.7		19.9		22	
EPA 1631	Total	Mercury	NG/G	96.7		108		122		107		142		186	
NOAALipids1993	Total	Lipids	Percent	0.76		0.6		0.95		1.2		0.88		1	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553	
			Location	CPJL		CPJL		CPJL		CPJL		CPJL		CPJL	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	CPJL-092416_LOB_TA_03		CPJL-092416_LOB_TA_04		CPJL-092416_LOB_TA_05		CPJL-092416_LOB_TA_06		CPJL-092416_LOB_TA_07		CPJL-092416_LOB_TA_08	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79.8		82.5		84.2		80.4		79.5		82.1	
Solids	Total	Percent Solids	% BY WT.	20.2		17.5		15.8		19.6		20.5		17.9	
EPA 1631	Total	Mercury	NG/G	183		98.8		155		289		140		179	
NOAALipids1993	Total	Lipids	Percent	0.73		0.66		0.63		0.77		0.9		0.89	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553	
			Location	CPJL		CPJL		CPJL		CPJL		CPJL		CPJL	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	CPJL-092416_LOB_TA_09		CPJL-092416_LOB_TA_10		CPJL-092416_LOB_TA_11		CPJL-092416_LOB_TA_12		CPJL-092416_LOB_TA_13		CPJL-092416_LOB_TA_14	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	81.9		78.8		80.1		79.4		83.2		83.2	
Solids	Total	Percent Solids	% BY WT.	18.1		21.2		19.9		20.6		16.8		16.8	
EPA 1631	Total	Mercury	NG/G	147		166		159		207		136		259	
NOAALipids1993	Total	Lipids	Percent	0.86		0.82		0.91		0.98		0.95		0.81	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553		1611257 & 16-12-1553	
			Location	CPJL		CPJL		CPJL		CPJL		CPJL		CPJL	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	CPJL-092416_LOB_TA_15		CPJL-092416_LOB_TA_16		CPJL-092416_LOB_TA_17		CPJL-092416_LOB_TA_18		CPJL-092416_LOB_TA_19		CPJL-092416_LOB_TA_20	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	81.9		78.3		79.4		77.8		78.4		78.3	
Solids	Total	Percent Solids	% BY WT.	18.1		21.7		20.6		22.2		21.6		21.7	
EPA 1631	Total	Mercury	NG/G	337		255		180		150		222		391	
NOAALipids1993	Total	Lipids	Percent	0.65		0.84		0.83		0.88		0.96		0.99	

Units:

% by WT = percent by weight

NG/G = Nanogram per gram

FS = Field sample

SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551	
			Location	L10-52		L10-52		L10-52		L10-52		L10-52		L10-52	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L10-52_092416_LOB_TA_01		L10-52_092416_LOB_TA_02		L10-52_092416_LOB_TA_03		L10-52_092416_LOB_TA_04		L10-52_092416_LOB_TA_05		L10-52_092416_LOB_TA_06	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79.1		76.7		78.4		78.5		78		75.4	
Solids	Total	Percent Solids	% BY WT.	20.9		23.3		21.6		21.5		22		24.6	
EPA 1631	Total	Mercury	NG/G	169		152		149		527		159		185	
NOAALipids1993	Total	Lipids	Percent	0.41		0.48		0.29		0.5		1.4		0.84	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551	
			Location	L10-52		L10-52		L10-52		L10-52		L10-52		L10-52	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L10-52_092416_LOB_TA_07		L10-52_092416_LOB_TA_08		L10-52_092416_LOB_TA_09		L10-52_092416_LOB_TA_10		L10-52_092416_LOB_TA_11		L10-52_092416_LOB_TA_12	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	78.2		81.4		79.3		77.6		80.5		79.6	
Solids	Total	Percent Solids	% BY WT.	21.8		18.6		20.7		22.4		19.5		20.4	
EPA 1631	Total	Mercury	NG/G	158		364		365		263		161		772	
NOAALipids1993	Total	Lipids	Percent	0.47		1.4		0.51		0.73		0.7		0.66	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551		1611258 & 16-12-1551	
			Location	L10-52		L10-52		L10-52		L10-52		L10-52		L10-52	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L10-52_092416_LOB_TA_13		L10-52_092416_LOB_TA_14		L10-52_092416_LOB_TA_15		L10-52_092416_LOB_TA_16		L10-52_092416_LOB_TA_17		L10-52_092416_LOB_TA_18	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	78.3		81.4		77.6		77.6		79.8		80.4	
Solids	Total	Percent Solids	% BY WT.	21.7		18.6		22.4		22.4		20.2		19.6	
EPA 1631	Total	Mercury	NG/G	254		438		418		201		200		142	
NOAALipids1993	Total	Lipids	Percent	0.91		0.68		1		0.33		0.53		0.56	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611258 & 16-12-1551		1611258 & 16-12-1551		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552	
			Location	L10-52		L10-52		L9-45		L9-45		L9-45		L9-45	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L10-52_092416_LOB_TA_19		L10-52_092416_LOB_TA_20		L9-45_092416_LOB_TA_01		L9-45_092416_LOB_TA_02		L9-45_092416_LOB_TA_03		L9-45_092416_LOB_TA_04	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79.5		80.5		82.8		81.7		79.2		80.6	
Solids	Total	Percent Solids	% BY WT.	20.5		19.5		17.2		18.3		20.8		19.4	
EPA 1631	Total	Mercury	NG/G	212		786		108		191		254		101	
NOAALipids1993	Total	Lipids	Percent	0.61		0.57		0.65		0.58		0.62		1.1	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552	
			Location	L9-45		L9-45		L9-45		L9-45		L9-45		L9-45	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L9-45_092416_LOB_TA_05		L9-45_092416_LOB_TA_06		L9-45_092416_LOB_TA_07		L9-45_092416_LOB_TA_08		L9-45_092416_LOB_TA_09		L9-45_092416_LOB_TA_10	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79		80.2		78		80.6		80.1		81.1	
Solids	Total	Percent Solids	% BY WT.	21		19.8		22		19.4		19.9		18.9	
EPA 1631	Total	Mercury	NG/G	152		194		162		242		155		74	
NOAALipids1993	Total	Lipids	Percent	0.57		0.99		1		0.7		0.52		0.7	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552	
			Location	L9-45		L9-45		L9-45		L9-45		L9-45		L9-45	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L9-45_092416_LOB_TA_11		L9-45_092416_LOB_TA_12		L9-45_092416_LOB_TA_13		L9-45_092416_LOB_TA_14		L9-45_092416_LOB_TA_15		L9-45_092416_LOB_TA_16	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	78.3		79.5		78.9		80.9		80.8		78.9	
Solids	Total	Percent Solids	% BY WT.	21.7		20.5		21.1		19.1		19.2		21.1	
EPA 1631	Total	Mercury	NG/G	219		171		157		155		129		150	
NOAALipids1993	Total	Lipids	Percent	0.77		0.78		0.73		1.1		0.83		0.98	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

Created by: BGP 01/17/2017
Checked by: DMK 02/02/2017

TABLE 2
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1611255, 1611256, 1611257, 1611258, and 1611259

			SDG	1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552		1611259 & 16-12-1552	
			Location	L9-45		L9-45		L9-45		L9-45	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	L9-45_092416_LOB_TA_17		L9-45_092416_LOB_TA_18		L9-45_092416_LOB_TA_19		L9-45_092416_LOB_TA_20	
			QC Code	FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
Moisture	Total	Percent Moisture	% BY WT.	79.8		81.2		78.8		78.3	
Solids	Total	Percent Solids	% BY WT.	20.2		18.8		21.2		21.7	
EPA 1631	Total	Mercury	NG/G	218		166		173		195	
NOAALipids1993	Total	Lipids	Percent	0.66		0.7		0.75		0.77	

Units:
% by WT = percent by weight
NG/G = Nanogram per gram

FS = Field sample
SDG = Sample delivery group

DATA VALIDATION REPORT

Penobscot River Estuary Phase III - Engineering Evaluation

Penobscot River, Maine

2016 Biota Monitoring - Select Fish Species

Prepared for:

United States District Court
District of Maine

Prepared by:

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Project No. 3616166052.04.05

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ACRONYMS AND ABBREVIATIONS

°C	degrees Celsius
%	percent
Amec Foster Wheeler	Amec Foster Wheeler Environment & Infrastructure, Inc.
Calscience	Eurofins Calscience, Inc.
CCB	continuing calibration blank
CCV	continuing calibration verification
CLP	EPA Contract Laboratory Program
COC	chain of custody
DCM	dichloromethane
EPA	United States Environmental Protection Agency
Eurofins	Eurofins Frontier Global Sciences, Inc.
ICAL	initial calibration
ICB	initial calibration blank
ICV	initial calibration verification
ID	sample identification
LCS	laboratory control sample
LCSD	laboratory control sample duplicate
ng/g	nanograms per gram
MDL	method detection limit

MS	matrix spike
MSD	matrix spike duplicate
NOAA	National Oceanic and Atmospheric Administration
QAPP	Quality Assurance Project Plan
QC	quality control
RL	reporting limit
RPD	relative percent difference
RSD	relative standard deviation
SDG	sample delivery group

DATA QUALITY REVIEW AND VALIDATION REPORT

Penobscot River Estuary Phase III - Engineering Study
Biota Monitoring - Select Fish Species
Penobscot River, Maine

1.0 INTRODUCTION

Amec Foster Wheeler Environment & Infrastructure, Inc. (Amec Foster Wheeler) collected 183 samples from select fish species, 80 samples of mussels, 6 eels, and 5 fish bait samples from August 2 through October 4, 2016, from the Penobscot River and Estuary site in Penobscot, Maine. The samples were submitted to Eurofins Frontier Global Sciences, Inc. (Eurofins) in Bothell, Washington, where they were received on October 5, 2016, and assigned to sample delivery groups (SDGs) 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238. Eurofins analyzed the samples for mercury by United States Environmental Protection Agency (EPA) Method 1631B. Eurofins in Bothell subcontracted the samples to Eurofins Calscience, In. (Calscience) in Garden Grove, California, where they were received between November 9 and November 30, 2016, and assigned to SDGs 16110740, 16111263, 16112443, 16112444, 16112445, 16112554, 16112555, and 16112556. Calscience analyzed the samples for percent (%) lipids by dichloromethane (DCM) extraction and gravimetric determination, as described in National Oceanic and Atmospheric Administration (NOAA) Technical Memorandum NOS ORCA 130.

A list of these samples by field sample identification (ID), sample collection date, matrix, and Eurofins sample ID is presented in Table 1.

2.0 DATA VALIDATION AND DATA QUALITY REVIEW METHODOLOGY

This data validation and data quality review has been performed by Amec Foster Wheeler with reference to the EPA Contract Laboratory Program (CLP) National Functional Guidelines for Inorganic Superfund Data Review (EPA, 2014), EPA New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures (EPA 2013), EPA Method 1631, revision B (EPA, 2001), and NOAA Technical Memorandum NOS ORCA 130. The EPA CLP guidelines were written specifically for the CLP, and have been modified for the purposes of this data validation where they differ from method-specific quality control (QC) requirements.

Amec Foster Wheeler's data validation and review methodology complied with the validation procedures specified in the draft Penobscot River Estuary Phase III Engineering Evaluation Quality Assurance Project Plan (QAPP), dated July 20, 2016 (Amec Foster Wheeler, 2016). The laboratory's analytical data packages were reviewed to assess the following criteria:

- Chain of custody (COC) compliance;
- Holding time compliance;
- Initial calibration (ICAL), initial calibration verification (ICV), and continuing calibration verification (CCV) compliance with method-specified criteria;
- Presence or absence of laboratory contamination as demonstrated by laboratory blanks, instrument blanks, initial calibration blanks (ICBs), and continuing calibration blanks (CCBs);
- Accuracy and bias as demonstrated by recovery of surrogate spikes, laboratory control sample (LCS), and matrix spike (MS) samples;
- Analytical precision as relative percent difference (RPD) of analyte concentration between laboratory duplicates, LCS and LCS duplicates (LCSDs), or MS and MS duplicates (MSDs);
- Detection limits;
- Analyte calculation verification (Stage 3 validation only); and
- Insofar as possible, the degree of conformance to method requirements and good laboratory practices.

In general, it is important to recognize that no analytical data are guaranteed to be correct, even if all QC audits are passed. Strict QC serves to increase confidence in data, but any reported value may potentially contain error.

In accordance with the specifications of QAPP Worksheet #36, the data review and validation process comprised 10% Stage 3 full validation of the raw analytical data from primary field samples and 90% Stage 2B data validation based on information provided by the laboratory as summary reporting forms. Amec Foster Wheeler performed full validation on the samples from SDGs 1610138 and 1610238.

3.0 DEFINITIONS OF QUALIFIERS THAT MAY BE ADDED DURING DATA QUALITY REVIEW AND VALIDATION

U The analyte was analyzed for, but was not detected above the reported sample quantitation limit.

J	The analyte was positively identified; the associated numerical value is the approximate concentration of the analyte in the sample.
UJ	The analyte was not detected above the reported sample quantitation limit. However, the reported quantitation limit is approximate and may or may not represent the actual limit of quantitation necessary to accurately and precisely measure the analyte in the sample.
R	The sample result is rejected due to serious deficiencies in the ability to analyze the sample and meet quality control criteria. The presence or absence of the analyte cannot be verified.

4.0 VALIDATION REASON CODES

The following reason codes were applied to the data during validation:

MS-H	High MS and/or MSD % recovery. Potential high bias.
MS-RPD	High RPD between MS/MSD results. Potential analytical imprecision.
Q	The analyte concentration is between the method detection limit (MDL) and the reporting limit (RL). The result is an estimated concentration.

5.0 EXPLANATION OF DATA QUALITY INDICATORS

Data quality indicators of the review and validation process are defined below.

5.1 LABORATORY CONTROL SAMPLE RECOVERIES

LCSs and LCS duplicates are aliquots of analyte-free matrix that are spiked with the analytes of interest for an analytical method or a representative subset of those analytes. The spiked matrix is then processed through the same extraction, concentration, cleanup, and analytical procedures as the samples they accompany. LCS recovery and precision are an indication of a laboratory's ability to successfully perform an analytical method in an interference-free matrix.

5.2 MATRIX SPIKE RECOVERIES

MSs and MSDs are prepared by adding known amounts of the analytes of interest for an analytical method, or a representative subset of those analytes, to an aliquot of sample. The spiked sample is then processed through the same extraction, concentration, cleanup, and analytical procedures as the unspiked samples in an analytical batch.

MS recovery and precision are an indication of a laboratory's ability to successfully recover an analyte in the matrix of a specific sample or closely related sample matrices. It is important not to apply MS results for any specific sample to other samples without understanding how the sample matrices are related.

5.3 BLANK SAMPLES

Blank samples are aliquots of analyte-free matrix that are used as negative controls to verify that the sample collection, storage, preparation, and analysis system does not produce false positive results. Three types of blanks were employed for this project.

- Calibration blanks are aliquots of analyte-free matrix that are evaluated after calibration and every 10 samples immediately after CCVs. ICB and CCB results may not exceed one half of the practical quantitation limit.
- Instrument blanks are aliquots of analyte-free matrix that are used to evaluate instrument drift. Instrument blanks results may not exceed 0.5 nanograms per liter, and average instrument blank peak areas are used to correct peak areas of QC and field samples.
- Laboratory or preparation blanks are aliquots of analyte-free matrix that are processed by the laboratory using exactly the same procedures as the field samples. Laboratory blanks are used to monitor for contamination introduced by the laboratory during sample preparation and analysis.

Target analytes should not be found in blank samples. When target analytes are detected in laboratory blanks, analyte concentrations in associated samples greater than the RL but less than five times the concentration detected in the blank will be U qualified by Amec Foster Wheeler. Analyte concentrations between the matrix detection limit and the RL, and less than five times the concentration detected in the blank will be U qualified at the RL. Negative results in a blank may indicate a low instrument bias, if the absolute concentration detected in the blank is greater than the RL, concentrations in associated samples greater than the RL but less than ten times the absolute concentration detected in the blank are J qualified and non-detect results are UJ qualified.

6.0 CHAIN OF CUSTODY AND SAMPLE RECEIPT CONDITION DOCUMENTATION

All samples were received by Eurofins under proper COC, intact, properly preserved, and at temperatures less than the QAPP-specified maximum of 4 degrees Celsius (°C).

There was insufficient sample to perform a lipid determination on 71 of the mussel samples from Eurofins SDG 1610144.

7.0 SPECIFIC DATA VALIDATION FINDINGS

This section contains narrative descriptions of data quality review and data validation findings and data quality limitations.

7.1 LOW LEVEL MERCURY EPA METHOD 1631B

Low level mercury results generated by Eurofins may be considered usable with the addition of qualifiers from sections 7.1.1 through 7.1.9.

7.1.1 Holding Times

Samples were collected by Amec Foster Wheeler from August 2 through October 4, 2016. This data validation assumes that all samples were properly preserved by freezing at or below -18°C within 48 hours of collection. Samples arrived at Eurofins under proper COC, intact, and properly preserved. Samples were analyzed within the method-specified hold time of 1 year from collection.

7.1.2 Initial Calibration

ICAL standard recoveries were included in the laboratory’s QC summary forms, but relative standard deviations (RSDs) were only included in raw data. For samples that underwent Stage 3 validation, RSDs were less than or equal to 15%. For samples that underwent Stage 2B validation, ICAL standard recoveries were within QAPP-specified limits established for ICVs and CCVs, 77 to 123%.

7.1.3 Initial and Continuing Calibration Verification

ICVs and CCVs met the QAPP-specified 77 to 123% recovery criteria for unqualified data.

7.1.4 Laboratory, Instrument, and Calibration Blanks

Target analytes were not detected above the reporting limit in the laboratory blanks, instrument blanks, ICBs, or CCBs associated with the mercury analysis of these samples.

When mercury was detected in laboratory blanks at concentrations between the MDL and the RL, results in the associated field samples were greater than five times the detections in the blanks, and data usability is not adversely affected.

7.1.5 Laboratory Control Sample Recovery and Precision

LCS recoveries were within the QAPP-specified 80 to 120% limits, and RPDs between LCS and LCSD results did not exceed the QAPP-specified maximum of 24%.

7.1.6 Matrix Spike Recovery and Precision

Eurofins performed MS and MSD analyses on samples BO-04_080516_EEL_WB_01, BO-04_092516_TOM_WB_01, BO-04_100316_MUM_WB_01, BO-04_100316_MUM_WB_16, ES-03_092716_BLM_WB_01, ES-03_092716_BLM_WB_09, ES-13_092716_TOM_WB_04, ES-13_092916_TOM_WB_07, ES-13_093016_BLM_WB_01, ES-13_093016_BLM_WB_11, ES-15_092716_BLM_WB_01, ES-15_092716_BLM_WB_11, ES-FP_092616_BLM_WB_01, ES-FP_092616_BLM_WB_10, ES-FP_092716_RAS_WB_01, ES-FP_092716_TOM_WB_01, FRB-01_092816_MUM_WB_01, FRB-01_092816_MUM_WB_16, FRB-01_092816_RAS_WB_03, FRB-01_092816_RAS_WB_20, FRB-01_092916_TOM_WB_01, MMMC-01_092316_MUM_WB_01, OB-01_080216_EEL_WB_01, OB-01_092116_RAS_WB_01, OB-01_092116_RAS_WB_05, OB-01_092416_TOM_WB_04, OB-05_092516_MUM_WB_05, OB-05_092516_TOM_WB_06, OB-05_100316_MUM_WB_20,

MS/MSD recoveries were within the QAPP-specified 71 to 125% limits, and RPDs did not exceed the QAPP-specified maximum of 24%, with the following exception:

- Mercury recoveries were high at 129% and 178%, respectively, in the MS and MSD performed on sample BO-04_080516_EEL_WB_01, and the RPD between results was high at 32.0%. Amec Foster Wheeler J qualified the detected mercury result from sample BO-04_080516_EEL_WB_01 because of potential high analytical bias and potential analytical imprecision. (J-MS-H, MS-RPD)

7.1.7 Laboratory Duplicates

Eurofins performed duplicate analysis on samples BO-04_080516_EEL_WB_01, BO-04_092516_TOM_WB_03, BO-04_100316_MUM_WB_01, ES-03_092716_BLM_WB_09, ES-03_092716_BLM_WB_18, ES-13_093016_BLM_WB_17, ES-FP_092616_BLM_WB_01, ES-FP_092716_RAS_WB_01, ES-FP_092716_TOM_WB_01, FRB-01_092816_MUM_WB_16, FRB-01_092916_TOM_WB_01, MMMC-01_092316_MUM_WB_01, OB-01_092116_RAS_WB_05, OB-01_092416_TOM_WB_04, and OB-05_100316_MUM_WB_19. RPDs between duplicate results did not exceed the QAPP-specified maximum of 24% for results that were greater than or equal to 5 times the RL.

7.1.8 Calculation Verification

Amec Foster Wheeler performed Stage 3 validation on 8 samples from Eurofins SDG 1610138 and 20 samples from Eurofins SDG 1610236. Stage 3 validation included recalculation of all calibrations, blanks, QC samples, and field samples. No errors in calculation were identified during Stage 3 validation.

7.1.9 Data Reporting and Analytical Procedures

Eurofins J qualified results between the MDL and the RL. Amec Foster Wheeler agrees that these results are quantitatively uncertain and has maintained Eurofin's J qualifiers. (J-Q)

7.2 PERCENT LIPIDS BY DICHLOROMETHANE EXTRACTION

Percent lipid results generated by Calscience may be considered usable without qualification.

7.2.1 Holding Times

Holding times are not applicable to % lipid determination by DCM extraction.

7.2.2 Laboratory Blanks

Lipids were not detected above the reporting limit in laboratory blanks associated with the % lipids determinations of these samples.

7.2.3 Percent Lipids Laboratory Duplicate Precision

The laboratory performed duplicate % lipids analysis on samples BO-04_080516_EEL_WB_01, BO-04-100316_MUM_WB_01, ES-13_092116_RAS_WB_01, ES-13_093016_TOM_WB_09, FRB-01_092816_MUM_WB_01, FRB-01_092816_RAS_WB_08, FRB-01_092916_TOM_WB_01, MMMC-01_092316_MUM_WB_02, OB-01_092116_RAS_WB_01, OB-01_092116_RAS_WB_20, OB-05_092516_TOM_WB_04, and OB-05_092516_TOM_WB_06. RPDs between duplicate results were less than the laboratory-specified 25% limit.

7.2.4 Calculation Verification

Amec Foster Wheeler performed Stage 3 validation on 7 samples from Calscience SDG 16112443 and 20 samples from Calscience SDG 16112555. These are the same samples that underwent Stage 3 validation of mercury results under Eurofins SDGs 1610138 and 1610236. Stage 3 validation included recalculation of all laboratory blanks, QC samples, and field samples. No errors in calculation were identified during Stage 3 validation

7.2.5 Data Reporting and Analytical Procedures

There were no data anomalies associated with the % lipids determinations performed on these samples.

8.0 FIELD DUPLICATES

Field duplicates were not collected by Amec Foster Wheeler.

9.0 SUMMARY AND CONCLUSIONS

Amec Foster Wheeler reviewed 473 data records from field samples during the data validation and data quality review. Three records were J qualified as quantitatively uncertain, due to high MS/MSD recoveries and RPDs, or values between the RL and the MDL. No data were rejected, and 100% of the data should be considered valid as reported.

REFERENCES

Amec Foster Wheeler, 2016. Draft Penobscot Estuary Phase III Engineering Evaluation Quality Assurance Project Plan.

EPA, 2014. EPA Contract Laboratory Program National Functional Guidelines for Inorganic Superfund Data Review, USEPA 540-R-013-001.

EPA, 2013. New England Environmental Data Review Supplement for Regional Data Review Elements and Superfund Specific Guidance/Procedures.

EPA, 2001. Appendix to method 1631, Total Mercury in Tissue, Sludge, Sediment, and Soil by Acid Digestion and BrCl Oxidation, EPA-821-R-01-013

NOAA, 1998. NOAA Technical Memorandum NOS ORCA 130: Sampling and Analytical Methods of the National Status and Trends Program Mussel watch Project: 1993-1996 Update.

LIMITATIONS

This report was prepared exclusively for the United States District Court, District of Maine by Amec Foster Wheeler Environment & Infrastructure, Inc. The quality of information, conclusions, and estimates contained herein is consistent with the level of effort involved in Amec Foster Wheeler services and based on: i) information available at the time of preparation, ii) data supplied by outside sources, and iii) the assumptions, conditions, and qualifications set forth in this report. This data quality review and validation report is intended to be used by the United States District Court District of Maine for the Penobscot River Estuary Phase III Engineering Study only, subject to the terms and conditions of its contract with Amec Foster Wheeler. Any other use of, or reliance on, this report by any third party is at that party's sole risk.

TABLES

Table 1
Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Select Fish Species

Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
BO-04_080516_EEL_WB_01	8/5/2016	Eel	1610138	1610138-01RE1	16112443	16112443-1	Stage 3 Validation
OB-01_080216_EEL_WB_01	8/2/2016	Eel	1610138	1610138-02	16112443	16112443-2	Stage 3 Validation
OB-05_080316_EEL_WB_01	8/3/2016	Eel	1610138	1610138-03	16112443	16112443-3	Stage 3 Validation
OB-05_080316_EEL_WB_02	8/3/2016	Eel	1610138	1610138-04	16112443	16112443-4	Stage 3 Validation
OB-05_080316_EEL_WB_04	8/3/2016	Eel	1610138	1610138-05	16112443	16112443-5	Stage 3 Validation
OB-05_080516_EEL_WB_05	8/5/2016	Eel	1610138	1610138-06	16112443	16112443-6	Stage 3 Validation
HORSESHOE_080316_FISH_BAIT	8/3/2016	Fish Bait	1610138	1610138-07	--	--	Stage 3 Validation
OB-05_080316_EEL_WB_03	8/3/2016	Eel	1610138	1610138-08	16112443	16112443-7	Stage 3 Validation
BO-04_092516_TOM_WB_01	9/25/2016	Tomcod	1610141	1610141-01	16110740	16110740-1	Stage 2B Validation
BO-04_092516_TOM_WB_02	9/25/2016	Tomcod	1610141	1610141-02	16110740	16110740-2	Stage 2B Validation
BO-04_092516_TOM_WB_03	9/25/2016	Tomcod	1610141	1610141-03	16110740	16110740-3	Stage 2B Validation
BO-04_092516_TOM_WB_04	9/25/2016	Tomcod	1610141	1610141-04	16110740	16110740-4	Stage 2B Validation
ES-13_092716_TOM_WB_01	9/27/2016	Tomcod	1610141	1610141-05	16110740	16110740-5	Stage 2B Validation
ES-13_092716_TOM_WB_02	9/27/2016	Tomcod	1610141	1610141-06	16110740	16110740-6	Stage 2B Validation
ES-13_092716_TOM_WB_03	9/27/2016	Tomcod	1610141	1610141-07	16110740	16110740-7	Stage 2B Validation
ES-13_092716_TOM_WB_04	9/27/2016	Tomcod	1610141	1610141-08	16110740	16110740-8	Stage 2B Validation
ES-13_092716_TOM_WB_05	9/27/2016	Tomcod	1610141	1610141-09	16110740	16110740-9	Stage 2B Validation
ES-13_092916_TOM_WB_06	9/29/2016	Tomcod	1610141	1610141-10	16110740	16110740-10	Stage 2B Validation
ES-13_092916_TOM_WB_07	9/29/2016	Tomcod	1610141	1610141-11	16110740	16110740-11	Stage 2B Validation
ES-13_092916_TOM_WB_08	9/29/2016	Tomcod	1610141	1610141-12	16110740	16110740-12	Stage 2B Validation
ES-13_093016_TOM_WB_09	9/30/2016	Tomcod	1610141	1610141-13	16110740	16110740-13	Stage 2B Validation
ES-13_093016_TOM_WB_10	9/30/2016	Tomcod	1610141	1610141-14	16110740	16110740-14	Stage 2B Validation
ES-13_093016_TOM_WB_11	9/30/2016	Tomcod	1610141	1610141-15	16110740	16110740-15	Stage 2B Validation
ES-FP_092716_TOM_WB_01	9/27/2016	Tomcod	1610141	1610141-16	16110740	16110740-16	Stage 2B Validation
ES-FP_100116_TOM_WB_02	10/1/2016	Tomcod	1610141	1610141-17	16110740	16110740-17	Stage 2B Validation
OB-01_092416_TOM_WB_01	9/24/2016	Tomcod	1610141	1610141-18	16110740	16110740-18	Stage 2B Validation
OB-01_092416_TOM_WB_02	9/24/2016	Tomcod	1610141	1610141-19	16110740	16110740-19	Stage 2B Validation
OB-01_092416_TOM_WB_03	9/24/2016	Tomcod	1610141	1610141-20	16110740	16110740-20	Stage 2B Validation
OB-01_092416_TOM_WB_04	9/24/2016	Tomcod	1610141	1610141-21	16110740	16110740-21	Stage 2B Validation
OB-01_092416_TOM_WB_05	9/24/2016	Tomcod	1610141	1610141-22	16110740	16110740-22	Stage 2B Validation
OB-01_092416_TOM_WB_06	9/24/2016	Tomcod	1610141	1610141-23	16110740	16110740-23	Stage 2B Validation
OB-01_092416_TOM_WB_07	9/24/2016	Tomcod	1610141	1610141-24	16110740	16110740-24	Stage 2B Validation
OB-01_092416_TOM_WB_08	9/24/2016	Tomcod	1610141	1610141-25	16110740	16110740-25	Stage 2B Validation
OB-01_092416_TOM_WB_09	9/24/2016	Tomcod	1610141	1610141-26	16110740	16110740-26	Stage 2B Validation
OB-01_092416_TOM_WB_10	9/24/2016	Tomcod	1610141	1610141-27	16110740	16110740-27	Stage 2B Validation
OB-01_092416_TOM_WB_11	9/24/2016	Tomcod	1610141	1610141-28	16110740	16110740-28	Stage 2B Validation

Table 1
Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Select Fish Species

Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
OB-01_092416_TOM_WB_12	9/24/2016	Tomcod	1610141	1610141-29	16110740	16110740-29	Stage 2B Validation
OB-01_092416_TOM_WB_13	9/24/2016	Tomcod	1610141	1610141-30	16110740	16110740-30	Stage 2B Validation
OB-01_092416_TOM_WB_14	9/24/2016	Tomcod	1610141	1610141-31	16110740	16110740-31	Stage 2B Validation
OB-01_092416_TOM_WB_15	9/24/2016	Tomcod	1610141	1610141-32	16110740	16110740-32	Stage 2B Validation
OB-01_092416_TOM_WB_16	9/24/2016	Tomcod	1610141	1610141-33	16110740	16110740-33	Stage 2B Validation
OB-01_092416_TOM_WB_17	9/24/2016	Tomcod	1610141	1610141-34	16110740	16110740-34	Stage 2B Validation
OB-01_092416_TOM_WB_18	9/24/2016	Tomcod	1610141	1610141-35	16110740	16110740-35	Stage 2B Validation
OB-01_092416_TOM_WB_19	9/24/2016	Tomcod	1610141	1610141-36	16110740	16110740-36	Stage 2B Validation
OB-05_092516_TOM_WB_01	9/25/2016	Tomcod	1610141	1610141-37	16110740	16110740-37	Stage 2B Validation
OB-05_092516_TOM_WB_02	9/25/2016	Tomcod	1610141	1610141-38	16110740	16110740-38	Stage 2B Validation
OB-05_092516_TOM_WB_03	9/25/2016	Tomcod	1610141	1610141-39	16110740	16110740-39	Stage 2B Validation
OB-05_092516_TOM_WB_04	9/25/2016	Tomcod	1610141	1610141-40	16110740	16110740-40	Stage 2B Validation
OB-05_092516_TOM_WB_05	9/25/2016	Tomcod	1610141	1610141-41	16110740	16110740-41	Stage 2B Validation
OB-05_092516_TOM_WB_06	9/25/2016	Tomcod	1610141	1610141-42	16110740	16110740-42	Stage 2B Validation
OB-05_092516_TOM_WB_07	9/25/2016	Tomcod	1610141	1610141-43	16110740	16110740-43	Stage 2B Validation
OB-05_092516_TOM_WB_08	9/25/2016	Tomcod	1610141	1610141-44	16110740	16110740-44	Stage 2B Validation
OB-05_092516_TOM_WB_09	9/25/2016	Tomcod	1610141	1610141-45	16110740	16110740-45	Stage 2B Validation
OB-05_092516_TOM_WB_10	9/25/2016	Tomcod	1610141	1610141-46	16110740	16110740-46	Stage 2B Validation
OB-05_092516_TOM_WB_11	9/25/2016	Tomcod	1610141	1610141-47	16110740	16110740-47	Stage 2B Validation
OB-05_092516_TOM_WB_12	9/25/2016	Tomcod	1610141	1610141-48	16110740	16110740-48	Stage 2B Validation
OB-05_092516_TOM_WB_13	9/25/2016	Tomcod	1610141	1610141-49	16110740	16110740-49	Stage 2B Validation
OB-05_092516_TOM_WB_14	9/25/2016	Tomcod	1610141	1610141-50	16110740	16110740-50	Stage 2B Validation
OB-05_092516_TOM_WB_15	9/25/2016	Tomcod	1610141	1610141-51	16110740	16110740-51	Stage 2B Validation
OB-05_092516_TOM_WB_16	9/25/2016	Tomcod	1610141	1610141-52	16110740	16110740-52	Stage 2B Validation
OB-05_092516_TOM_WB_17	9/25/2016	Tomcod	1610141	1610141-53	16110740	16110740-53	Stage 2B Validation
OB-05_092516_TOM_WB_18	9/25/2016	Tomcod	1610141	1610141-54	16110740	16110740-54	Stage 2B Validation
ES-03_092716_BLM_WB_01	9/27/2016	Mussel	1610144	1610144-01	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_02	9/27/2016	Mussel	1610144	1610144-02	16112445	16112445-2	Stage 2B Validation
ES-03_092716_BLM_WB_03	9/27/2016	Mussel	1610144	1610144-03	16112445	16112445-3	Stage 2B Validation
ES-03_092716_BLM_WB_04	9/27/2016	Mussel	1610144	1610144-04	16112445	16112445-4	Stage 2B Validation
ES-03_092716_BLM_WB_05	9/27/2016	Mussel	1610144	1610144-05	16112445	16112445-5	Stage 2B Validation
ES-03_092716_BLM_WB_06	9/27/2016	Mussel	1610144	1610144-06	16112445	16112445-6	Stage 2B Validation
ES-03_092716_BLM_WB_07	9/27/2016	Mussel	1610144	1610144-07	16112445	16112445-7	Stage 2B Validation
ES-03_092716_BLM_WB_08	9/27/2016	Mussel	1610144	1610144-08	16112445	16112445-8	Stage 2B Validation
ES-03_092716_BLM_WB_09	9/27/2016	Mussel	1610144	1610144-09	16112445	16112445-9	Stage 2B Validation
ES-03_092716_BLM_WB_10	9/27/2016	Mussel	1610144	1610144-10	16112445	16112445-10	Stage 2B Validation

Table 1
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Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
ES-03_092716_BLM_WB_11	9/27/2016	Mussel	1610144	1610144-11	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_12	9/27/2016	Mussel	1610144	1610144-12	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_13	9/27/2016	Mussel	1610144	1610144-13	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_14	9/27/2016	Mussel	1610144	1610144-14	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_15	9/27/2016	Mussel	1610144	1610144-15	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_16	9/27/2016	Mussel	1610144	1610144-16	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_17	9/27/2016	Mussel	1610144	1610144-17	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_18	9/27/2016	Mussel	1610144	1610144-18	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_19	9/27/2016	Mussel	1610144	1610144-19	--	--	Stage 2B Validation
ES-03_092716_BLM_WB_20	9/27/2016	Mussel	1610144	1610144-20	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_01	9/30/2016	Mussel	1610144	1610144-21	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_02	9/30/2016	Mussel	1610144	1610144-22	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_03	9/30/2016	Mussel	1610144	1610144-23	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_04	9/30/2016	Mussel	1610144	1610144-24	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_05	9/30/2016	Mussel	1610144	1610144-25	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_06	9/30/2016	Mussel	1610144	1610144-26	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_07	9/30/2016	Mussel	1610144	1610144-27	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_08	9/30/2016	Mussel	1610144	1610144-28	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_09	9/30/2016	Mussel	1610144	1610144-29	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_10	9/30/2016	Mussel	1610144	1610144-30	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_11	9/30/2016	Mussel	1610144	1610144-31	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_12	9/30/2016	Mussel	1610144	1610144-32	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_13	9/30/2016	Mussel	1610144	1610144-33	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_14	9/30/2016	Mussel	1610144	1610144-34	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_15	9/30/2016	Mussel	1610144	1610144-35	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_16	9/30/2016	Mussel	1610144	1610144-36	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_17	9/30/2016	Mussel	1610144	1610144-37	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_18	9/30/2016	Mussel	1610144	1610144-38	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_19	9/30/2016	Mussel	1610144	1610144-39	--	--	Stage 2B Validation
ES-13_093016_BLM_WB_20	9/30/2016	Mussel	1610144	1610144-40	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_01	9/27/2016	Mussel	1610144	1610144-41	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_02	9/27/2016	Mussel	1610144	1610144-42	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_03	9/27/2016	Mussel	1610144	1610144-43	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_04	9/27/2016	Mussel	1610144	1610144-44	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_05	9/27/2016	Mussel	1610144	1610144-45	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_06	9/27/2016	Mussel	1610144	1610144-46	--	--	Stage 2B Validation

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Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
ES-15_092716_BLM_WB_07	9/27/2016	Mussel	1610144	1610144-47	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_08	9/27/2016	Mussel	1610144	1610144-48	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_09	9/27/2016	Mussel	1610144	1610144-49	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_10	9/27/2016	Mussel	1610144	1610144-50	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_11	9/27/2016	Mussel	1610144	1610144-51	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_12	9/27/2016	Mussel	1610144	1610144-52	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_13	9/27/2016	Mussel	1610144	1610144-53	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_14	9/27/2016	Mussel	1610144	1610144-54	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_15	9/27/2016	Mussel	1610144	1610144-55	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_16	9/27/2016	Mussel	1610144	1610144-56	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_17	9/27/2016	Mussel	1610144	1610144-57	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_18	9/27/2016	Mussel	1610144	1610144-58	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_19	9/27/2016	Mussel	1610144	1610144-59	--	--	Stage 2B Validation
ES-15_092716_BLM_WB_20	9/27/2016	Mussel	1610144	1610144-60	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_01	9/26/2016	Mussel	1610144	1610144-61	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_02	9/26/2016	Mussel	1610144	1610144-62	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_03	9/26/2016	Mussel	1610144	1610144-63	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_04	9/26/2016	Mussel	1610144	1610144-64	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_05	9/26/2016	Mussel	1610144	1610144-65	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_06	9/26/2016	Mussel	1610144	1610144-66	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_07	9/26/2016	Mussel	1610144	1610144-67	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_08	9/26/2016	Mussel	1610144	1610144-68	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_09	9/26/2016	Mussel	1610144	1610144-69	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_10	9/26/2016	Mussel	1610144	1610144-70	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_11	9/26/2016	Mussel	1610144	1610144-71	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_12	9/26/2016	Mussel	1610144	1610144-72	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_13	9/26/2016	Mussel	1610144	1610144-73	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_14	9/26/2016	Mussel	1610144	1610144-74	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_15	9/26/2016	Mussel	1610144	1610144-75	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_16	9/26/2016	Mussel	1610144	1610144-76	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_17	9/26/2016	Mussel	1610144	1610144-77	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_18	9/26/2016	Mussel	1610144	1610144-78	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_19	9/26/2016	Mussel	1610144	1610144-79	--	--	Stage 2B Validation
ES-FP_092616_BLM_WB_20	9/26/2016	Mussel	1610144	1610144-80	--	--	Stage 2B Validation
BO-04_100316_MUM_WB_01	10/3/2016	Mummichog	1610145	1610145-01	16112444	16112444-1	Stage 2B Validation
BO-04_100316_MUM_WB_02	10/3/2016	Mummichog	1610145	1610145-02	16112444	16112444-2	Stage 2B Validation

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Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
BO-04_100316_MUM_WB_03	10/3/2016	Mummichog	1610145	1610145-03	16112444	16112444-3	Stage 2B Validation
BO-04_100316_MUM_WB_04	10/3/2016	Mummichog	1610145	1610145-04	16112444	16112444-4	Stage 2B Validation
BO-04_100316_MUM_WB_05	10/3/2016	Mummichog	1610145	1610145-05	16112444	16112444-5	Stage 2B Validation
BO-04_100316_MUM_WB_06	10/3/2016	Mummichog	1610145	1610145-06	16112444	16112444-6	Stage 2B Validation
BO-04_100316_MUM_WB_07	10/3/2016	Mummichog	1610145	1610145-07	16112444	16112444-7	Stage 2B Validation
BO-04_100316_MUM_WB_08	10/3/2016	Mummichog	1610145	1610145-08	16112444	16112444-8	Stage 2B Validation
BO-04_100316_MUM_WB_09	10/3/2016	Mummichog	1610145	1610145-09	16112444	16112444-9	Stage 2B Validation
BO-04_100316_MUM_WB_10	10/3/2016	Mummichog	1610145	1610145-10	16112444	16112444-10	Stage 2B Validation
BO-04_100316_MUM_WB_11	10/3/2016	Mummichog	1610145	1610145-11	16112444	16112444-11	Stage 2B Validation
BO-04_100316_MUM_WB_12	10/3/2016	Mummichog	1610145	1610145-12	16112444	16112444-12	Stage 2B Validation
BO-04_100316_MUM_WB_13	10/3/2016	Mummichog	1610145	1610145-13	16112444	16112444-13	Stage 2B Validation
BO-04_100316_MUM_WB_14	10/3/2016	Mummichog	1610145	1610145-14	16112444	16112444-14	Stage 2B Validation
BO-04_100316_MUM_WB_15	10/3/2016	Mummichog	1610145	1610145-15	16112444	16112444-15	Stage 2B Validation
BO-04_100316_MUM_WB_16	10/3/2016	Mummichog	1610145	1610145-16	16112444	16112444-16	Stage 2B Validation
BO-04_100316_MUM_WB_17	10/3/2016	Mummichog	1610145	1610145-17	16112444	16112444-17	Stage 2B Validation
BO-04_100316_MUM_WB_18	10/3/2016	Mummichog	1610145	1610145-18	16112444	16112444-18	Stage 2B Validation
BO-04_100316_MUM_WB_19	10/3/2016	Mummichog	1610145	1610145-19	16112444	16112444-19	Stage 2B Validation
BO-04_100316_MUM_WB_20	10/3/2016	Mummichog	1610145	1610145-20	16112444	16112444-20	Stage 2B Validation
MMMC-01_092316_MUM_WB_01	9/23/2016	Mummichog	1610145	1610145-21	16112444	16112444-21	Stage 2B Validation
MMMC-01_092316_MUM_WB_02	9/23/2016	Mummichog	1610145	1610145-22	16112444	16112444-22	Stage 2B Validation
MMMC-01_092316_MUM_WB_03	9/23/2016	Mummichog	1610145	1610145-23	16112444	16112444-23	Stage 2B Validation
MMMC-01_092316_MUM_WB_04	9/23/2016	Mummichog	1610145	1610145-24	16112444	16112444-24	Stage 2B Validation
OB-01_092516_MUM_WB_01	9/25/2016	Mummichog	1610145	1610145-25	16112444	16112444-25	Stage 2B Validation
OB-05_092516_MUM_WB_01	9/25/2016	Mummichog	1610145	1610145-26	16112444	16112444-26	Stage 2B Validation
OB-05_092516_MUM_WB_02	9/25/2016	Mummichog	1610145	1610145-27	16112444	16112444-27	Stage 2B Validation
OB-05_092516_MUM_WB_03	9/25/2016	Mummichog	1610145	1610145-28	16112444	16112444-28	Stage 2B Validation
OB-05_092516_MUM_WB_04	9/25/2016	Mummichog	1610145	1610145-29	16112444	16112444-29	Stage 2B Validation
OB-05_092516_MUM_WB_05	9/25/2016	Mummichog	1610145	1610145-30	16112444	16112444-30	Stage 2B Validation
OB-05_092516_MUM_WB_06	9/25/2016	Mummichog	1610145	1610145-31	16112444	16112444-31	Stage 2B Validation
OB-05_100316_MUM_WB_07	10/3/2016	Mummichog	1610145	1610145-32	16112444	16112444-32	Stage 2B Validation
OB-05_100316_MUM_WB_08	10/3/2016	Mummichog	1610145	1610145-33	16112444	16112444-33	Stage 2B Validation
OB-05_100316_MUM_WB_09	10/3/2016	Mummichog	1610145	1610145-34	16112444	16112444-34	Stage 2B Validation
OB-05_100316_MUM_WB_10	10/3/2016	Mummichog	1610145	1610145-35	16112444	16112444-35	Stage 2B Validation
OB-05_100316_MUM_WB_11	10/3/2016	Mummichog	1610145	1610145-36	16112444	16112444-36	Stage 2B Validation
OB-05_100316_MUM_WB_12	10/3/2016	Mummichog	1610145	1610145-37	16112444	16112444-37	Stage 2B Validation
OB-05_100316_MUM_WB_13	10/3/2016	Mummichog	1610145	1610145-38	16112444	16112444-38	Stage 2B Validation

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Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
OB-05_100316_MUM_WB_14	10/3/2016	Mummichog	1610145	1610145-39	16112444	16112444-39	Stage 2B Validation
OB-05_100316_MUM_WB_15	10/3/2016	Mummichog	1610145	1610145-40	16112444	16112444-40	Stage 2B Validation
OB-05_100316_MUM_WB_16	10/3/2016	Mummichog	1610145	1610145-41	16112444	16112444-41	Stage 2B Validation
OB-05_100316_MUM_WB_17	10/3/2016	Mummichog	1610145	1610145-42	16112444	16112444-42	Stage 2B Validation
OB-05_100316_MUM_WB_18	10/3/2016	Mummichog	1610145	1610145-43	16112444	16112444-43	Stage 2B Validation
OB-05_100316_MUM_WB_19	10/3/2016	Mummichog	1610145	1610145-44	16112444	16112444-44	Stage 2B Validation
OB-05_100316_MUM_WB_20	10/3/2016	Mummichog	1610145	1610145-45	16112444	16112444-45	Stage 2B Validation
ES-13_092116_RAS_WB_01	9/21/2016	Smelt	1610232	1610232-01	16112556	16112556-1	Stage 2B Validation
ES-FP_092716_RAS_WB_01	9/27/2016	Smelt	1610232	1610232-02	16112556	16112556-2	Stage 2B Validation
ES-FP_092716_RAS_WB_02	9/27/2016	Smelt	1610232	1610232-03	16112556	16112556-3	Stage 2B Validation
ES-FP_092716_RAS_WB_03	9/27/2016	Smelt	1610232	1610232-04	16112556	16112556-4	Stage 2B Validation
ES-FP_092716_RAS_WB_04	9/27/2016	Smelt	1610232	1610232-05	16112556	16112556-5	Stage 2B Validation
ES-FP_092716_RAS_WB_05	9/27/2016	Smelt	1610232	1610232-06	16112556	16112556-6	Stage 2B Validation
ES-FP_092716_RAS_WB_06	9/27/2016	Smelt	1610232	1610232-07	16112556	16112556-7	Stage 2B Validation
ES-FP_092716_RAS_WB_07	9/27/2016	Smelt	1610232	1610232-08RE1	16112556	16112556-8	Stage 2B Validation
ES-FP_092716_RAS_WB_08	9/27/2016	Smelt	1610232	1610232-09	16112556	16112556-9	Stage 2B Validation
ES-FP_092716_RAS_WB_09	9/27/2016	Smelt	1610232	1610232-10	16112556	16112556-10	Stage 2B Validation
ES-FP_092716_RAS_WB_10	9/27/2016	Smelt	1610232	1610232-11	16112556	16112556-11	Stage 2B Validation
ES-FP_092716_RAS_WB_11	9/27/2016	Smelt	1610232	1610232-12	16112556	16112556-12	Stage 2B Validation
ES-FP_092716_RAS_WB_12	9/27/2016	Smelt	1610232	1610232-13	16112556	16112556-13	Stage 2B Validation
ES-FP_092716_RAS_WB_13	9/27/2016	Smelt	1610232	1610232-14	16112556	16112556-14	Stage 2B Validation
ES-FP_092716_RAS_WB_14	9/27/2016	Smelt	1610232	1610232-15	16112556	16112556-15	Stage 2B Validation
ES-FP_092716_RAS_WB_15	9/27/2016	Smelt	1610232	1610232-16	16112556	16112556-16	Stage 2B Validation
ES-FP_092716_RAS_WB_16	9/27/2016	Smelt	1610232	1610232-17	16112556	16112556-17	Stage 2B Validation
ES-FP_092716_RAS_WB_17	9/27/2016	Smelt	1610232	1610232-18	16112556	16112556-18	Stage 2B Validation
ES-FP_092716_RAS_WB_18	9/27/2016	Smelt	1610232	1610232-19	16112556	16112556-19	Stage 2B Validation
ES-FP_092716_RAS_WB_19	9/27/2016	Smelt	1610232	1610232-20	16112556	16112556-20	Stage 2B Validation
ES-FP_092716_RAS_WB_20	9/27/2016	Smelt	1610232	1610232-21	16112556	16112556-21	Stage 2B Validation
OB-01_092116_RAS_WB_01	9/21/2016	Smelt	1610232	1610232-22	16112556	16112556-22	Stage 2B Validation
OB-01_092116_RAS_WB_02	9/21/2016	Smelt	1610232	1610232-23	16112556	16112556-23	Stage 2B Validation
OB-01_092116_RAS_WB_03	9/21/2016	Smelt	1610232	1610232-24	16112556	16112556-24	Stage 2B Validation
OB-01_092116_RAS_WB_04	9/21/2016	Smelt	1610232	1610232-25	16112556	16112556-25	Stage 2B Validation
OB-01_092116_RAS_WB_05	9/21/2016	Smelt	1610232	1610232-26RE1	16112556	16112556-26	Stage 2B Validation
OB-01_092116_RAS_WB_06	9/21/2016	Smelt	1610232	1610232-27	16112556	16112556-27	Stage 2B Validation
OB-01_092116_RAS_WB_07	9/21/2016	Smelt	1610232	1610232-28	16112556	16112556-28	Stage 2B Validation
OB-01_092116_RAS_WB_08	9/21/2016	Smelt	1610232	1610232-29	16112556	16112556-29	Stage 2B Validation

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Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
OB-01_092116_RAS_WB_09	9/21/2016	Smelt	1610232	1610232-30	16112556	16112556-30	Stage 2B Validation
OB-01_092116_RAS_WB_10	9/21/2016	Smelt	1610232	1610232-31	16112556	16112556-31	Stage 2B Validation
OB-01_092116_RAS_WB_11	9/21/2016	Smelt	1610232	1610232-32	16112556	16112556-32	Stage 2B Validation
OB-01_092116_RAS_WB_12	9/21/2016	Smelt	1610232	1610232-33	16112556	16112556-33	Stage 2B Validation
OB-01_092116_RAS_WB_13	9/21/2016	Smelt	1610232	1610232-34	16112556	16112556-34	Stage 2B Validation
OB-01_092116_RAS_WB_14	9/21/2016	Smelt	1610232	1610232-35RE1	16112556	16112556-35	Stage 2B Validation
OB-01_092116_RAS_WB_15	9/21/2016	Smelt	1610232	1610232-36RE1	16112556	16112556-36	Stage 2B Validation
OB-01_092116_RAS_WB_16	9/21/2016	Smelt	1610232	1610232-37	16112556	16112556-37	Stage 2B Validation
OB-01_092116_RAS_WB_17	9/21/2016	Smelt	1610232	1610232-38	16112556	16112556-38	Stage 2B Validation
OB-01_092116_RAS_WB_18	9/21/2016	Smelt	1610232	1610232-39	16112556	16112556-39	Stage 2B Validation
OB-01_092116_RAS_WB_19	9/21/2016	Smelt	1610232	1610232-40	16112556	16112556-40	Stage 2B Validation
OB-01_092116_RAS_WB_20	9/21/2016	Smelt	1610232	1610232-41	16112556	16112556-41	Stage 2B Validation
OB-05_092116_RAS_WB_01	9/21/2016	Smelt	1610232	1610232-42	16112556	16112556-42	Stage 2B Validation
FRB-01_092916_TOM_WB_01	9/29/2016	Tomcod	1610233	1610233-01RE1	16111263	16111263-1	Stage 2B Validation
FRB-01_092816_MUM_WB_01	9/28/2016	Mummichog	1610234	1610234-01RE1	16112554	16112554-1	Stage 2B Validation
FRB-01_092816_MUM_WB_02	9/28/2016	Mummichog	1610234	1610234-02RE1	16112554	16112554-2	Stage 2B Validation
FRB-01_092816_MUM_WB_03	9/28/2016	Mummichog	1610234	1610234-03RE1	16112554	16112554-3	Stage 2B Validation
FRB-01_092816_MUM_WB_04	9/28/2016	Mummichog	1610234	1610234-04	16112554	16112554-4	Stage 2B Validation
FRB-01_092816_MUM_WB_05	9/28/2016	Mummichog	1610234	1610234-05	16112554	16112554-5	Stage 2B Validation
FRB-01_092816_MUM_WB_06	9/28/2016	Mummichog	1610234	1610234-06	16112554	16112554-6	Stage 2B Validation
FRB-01_092816_MUM_WB_07	9/28/2016	Mummichog	1610234	1610234-07	16112554	16112554-7	Stage 2B Validation
FRB-01_092816_MUM_WB_08	9/28/2016	Mummichog	1610234	1610234-08	16112554	16112554-8	Stage 2B Validation
FRB-01_092816_MUM_WB_09	9/28/2016	Mummichog	1610234	1610234-09	16112554	16112554-9	Stage 2B Validation
FRB-01_092816_MUM_WB_10	9/28/2016	Mummichog	1610234	1610234-10	16112554	16112554-10	Stage 2B Validation
FRB-01_092816_MUM_WB_11	9/28/2016	Mummichog	1610234	1610234-11	16112554	16112554-11	Stage 2B Validation
FRB-01_092816_MUM_WB_12	9/28/2016	Mummichog	1610234	1610234-12	16112554	16112554-12	Stage 2B Validation
FRB-01_092816_MUM_WB_13	9/28/2016	Mummichog	1610234	1610234-13	16112554	16112554-13	Stage 2B Validation
FRB-01_092816_MUM_WB_14	9/28/2016	Mummichog	1610234	1610234-14	16112554	16112554-14	Stage 2B Validation
FRB-01_092816_MUM_WB_15	9/28/2016	Mummichog	1610234	1610234-15	16112554	16112554-15	Stage 2B Validation
FRB-01_092816_MUM_WB_16	9/28/2016	Mummichog	1610234	1610234-16	16112554	16112554-16	Stage 2B Validation
FRB-01_092816_MUM_WB_17	9/28/2016	Mummichog	1610234	1610234-17	16112554	16112554-17	Stage 2B Validation
FRB-01_092816_MUM_WB_18	9/28/2016	Mummichog	1610234	1610234-18	16112554	16112554-18	Stage 2B Validation
FRB-01_092816_MUM_WB_19	9/28/2016	Mummichog	1610234	1610234-19RE1	16112554	16112554-19	Stage 2B Validation
FRB-01_092816_MUM_WB_20	9/28/2016	Mummichog	1610234	1610234-20	16112554	16112554-20	Stage 2B Validation
FRB-01_092816_RAS_WB_01	9/28/2016	Smelt	1610236	1610236-01RE1	16112555	16112555-1	Stage 3 Validation
FRB-01_092816_RAS_WB_02	9/28/2016	Smelt	1610236	1610236-02RE1	16112555	16112555-2	Stage 3 Validation

Table 1
Field Samples Submitted to Eurofins
US District Court - District of Maine
Penobscot River Phase III - Engineering Study
Data Validation Report - Select Fish Species

Sample ID	Collection Date	Media	Eurofins SDG	Eurofins ID	Calscience SDG	Calscience ID	Notes
FRB-01_092816_RAS_WB_03	9/28/2016	Smelt	1610236	1610236-03	16112555	16112555-3	Stage 3 Validation
FRB-01_092816_RAS_WB_04	9/28/2016	Smelt	1610236	1610236-04	16112555	16112555-4	Stage 3 Validation
FRB-01_092816_RAS_WB_05	9/28/2016	Smelt	1610236	1610236-05	16112555	16112555-5	Stage 3 Validation
FRB-01_092816_RAS_WB_06	9/28/2016	Smelt	1610236	1610236-06	16112555	16112555-6	Stage 3 Validation
FRB-01_092816_RAS_WB_07	9/28/2016	Smelt	1610236	1610236-07	16112555	16112555-7	Stage 3 Validation
FRB-01_092816_RAS_WB_08	9/28/2016	Smelt	1610236	1610236-08	16112555	16112555-8	Stage 3 Validation
FRB-01_092816_RAS_WB_09	9/28/2016	Smelt	1610236	1610236-09	16112555	16112555-9	Stage 3 Validation
FRB-01_092816_RAS_WB_10	9/28/2016	Smelt	1610236	1610236-10	16112555	16112555-10	Stage 3 Validation
FRB-01_092816_RAS_WB_11	9/28/2016	Smelt	1610236	1610236-11	16112555	16112555-11	Stage 3 Validation
FRB-01_092816_RAS_WB_12	9/28/2016	Smelt	1610236	1610236-12	16112555	16112555-12	Stage 3 Validation
FRB-01_092816_RAS_WB_13	9/28/2016	Smelt	1610236	1610236-13	16112555	16112555-13	Stage 3 Validation
FRB-01_092816_RAS_WB_14	9/28/2016	Smelt	1610236	1610236-14	16112555	16112555-14	Stage 3 Validation
FRB-01_092816_RAS_WB_15	9/28/2016	Smelt	1610236	1610236-15	16112555	16112555-15	Stage 3 Validation
FRB-01_092816_RAS_WB_16	9/28/2016	Smelt	1610236	1610236-16	16112555	16112555-16	Stage 3 Validation
FRB-01_092816_RAS_WB_17	9/28/2016	Smelt	1610236	1610236-17	16112555	16112555-17	Stage 3 Validation
FRB-01_092816_RAS_WB_18	9/28/2016	Smelt	1610236	1610236-18	16112555	16112555-18	Stage 3 Validation
FRB-01_092816_RAS_WB_19	9/28/2016	Smelt	1610236	1610236-19	16112555	16112555-19	Stage 3 Validation
FRB-01_092816_RAS_WB_20	9/28/2016	Smelt	1610236	1610236-20	16112555	16112555-20	Stage 3 Validation
OB-05_092316_BAIT_01	9/23/2016	Fish Bait	1610238	1610238-01	--	--	Stage 2B Validation. Mercury analysis only
9LIVES_100416_FISH_BAIT	10/4/2016	Fish Bait	1610238	1610238-02	--	--	Stage 2B Validation. Mercury analysis only
PURINA_100416_FISH_BAIT	10/4/2016	Fish Bait	1610238	1610238-03	--	--	Stage 2B Validation. Mercury analysis only
FANCYF_100416_FISH_BAIT	10/4/2016	Fish Bait	1610238	1610238-04	--	--	Stage 2B Validation. Mercury analysis only

Notes:
ID = identification
Eurofins = Eurofins Frontier Global Sciences, Inc.
SDG = Sample Delivery Group

Created by: CL 12/21/16
Checked by: DMK 01/09/17

TABLE 2
DATA VALIDATION SUMMARY
2016 BIOTA - FISH SPECIES
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

SDG	Analysis Method	Lab Sample ID	Field Sample ID	Fraction	Parameter Name	Lab Result	Lab Qualifier	Validated Result	Validated Qualifier	Val Reason Code	Result Units
1610138	EPA 1631	1610138-01RE1	BO-04_080516_EEL_WB_01	Total	Mercury	1370		1,370	J	MS-H, MS-RPD	NG/G
1610238	EPA 1631	1610238-04	FANCYF_100416_FISH_BAIT	Total	Mercury	0.197	J	0.197	J	Q	NG/G
1610238	EPA 1631	1610238-03	PURINA_100416_FISH_BAIT	Total	Mercury	0.13	J	0.13	J	Q	NG/G

Units:
NG/G = nanogram per gram

Validation Qualifier:
J = Value is estimated

Validation Reason Codes:
MS-H = High MS and/or MSD % recovery. Potential high bias.
MS-RPD = High RPD between MS/MSD results. Potential analytical imprecision.
Q = The analyte concentration is between the method detection limit (MDL) and the reporting limit (RL). The result is an estimated concentration.

Created by: BCG 01/10/2017
Checked by: DMK 01/10/2017

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610138 / 16-11-2443		1610138 / 16-11-2443		1610138 / 16-11-2443		1610138 / 16-11-2443		1610138 / 16-11-2443		1610138 / 16-11-2443	
			Location	BO-04		OB-01		OB-05		OB-05		OB-05		OB-05	
			Sample Date	08/05/16		08/02/16		08/03/16		08/03/16		08/03/16		08/03/16	
			Sample ID	BO-04_080516_EEL_WB_01		OB-01_080216_EEL_WB_01		OB-05_080316_EEL_WB_01		OB-05_080316_EEL_WB_02		OB-05_080316_EEL_WB_03		OB-05_080316_EEL_WB_04	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	1370	J	394		391		579		485		461	
NOAALipids1993	Total	Lipids	PERCENT	7.30		2.30		2.90		17.00		1.80		1.20	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610138 / 16-11-2443		1610138		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-05		QC		BO-04		BO-04		BO-04		BO-04	
			Sample Date	08/05/16		08/03/16		09/25/16		09/25/16		09/25/16		09/25/16	
			Sample ID	OB-05_080516_EEL_WB_05		HORSESHOE_080316_FISH_BAIT		BO-04_092516_TOM_WB_04		BO-04_092516_TOM_WB_01		BO-04_092516_TOM_WB_02		BO-04_092516_TOM_WB_03	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractio**	**Paramete**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	428		71		312		304		315		195	
NOAALipids1993	Total	Lipids	PERCENT	1.60				0.18		0.15		0.27		0.17	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	ES-13		ES-13		ES-13		ES-13		ES-13		ES-13		ES-13	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/29/16		09/29/16	
			Sample ID	ES-13_092716_TOM_WB_01		ES-13_092716_TOM_WB_02		ES-13_092716_TOM_WB_03		ES-13_092716_TOM_WB_04		ES-13_092716_TOM_WB_05		ES-13_092916_TOM_WB_06		ES-13_092916_TOM_WB_07	
			QC Code	FS		FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	59.2		76.1		65		164		80.4		142		129	
NOAALipids1993	Total	Lipids	PERCENT	0.61		0.27		0.14		0.29		0.11		0.19		0.13	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	ES-13		ES-13		ES-13		ES-13		ES-FP		ES-FP	
			Sample Date	09/29/16		09/30/16		09/30/16		09/30/16		09/27/16		10/01/16	
			Sample ID	ES-13_092916_TOM_WB_08		ES-13_093016_TOM_WB_09		ES-13_093016_TOM_WB_10		ES-13_093016_TOM_WB_11		ES-FP_092716_TOM_WB_01		ES-FP_100116_TOM_WB_02	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	211		103		113		56.5		55.5		74.3	
NOAALipids1993	Total	Lipids	PERCENT	0.38		0.34		0.17		0.36		0.35		0.48	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-01		OB-01		OB-01		OB-01		OB-01		OB-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	OB-01_092416_TOM_WB_01		OB-01_092416_TOM_WB_02		OB-01_092416_TOM_WB_03		OB-01_092416_TOM_WB_05		OB-01_092416_TOM_WB_06		OB-01_092416_TOM_WB_07	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parametei**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	115		215		232		69		159		76	
NOAALipids1993	Total	Lipids	PERCENT	0.26		0.33		0.40		0.46		0.32		0.29	

Units:
NG/G = Nanogram per gram

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TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-01		OB-01		OB-01		OB-01		OB-01		OB-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	OB-01_092416_TOM_WB_08		OB-01_092416_TOM_WB_09		OB-01_092416_TOM_WB_10		OB-01_092416_TOM_WB_11		OB-01_092416_TOM_WB_12		OB-01_092416_TOM_WB_13	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	174		196		82.1		89.5		89.5		179	
NOAALipids1993	Total	Lipids	PERCENT	0.34		0.48		0.32		0.60		0.35		0.22	

Units:

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Notes:

FS = Field Sample

QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-01		OB-01		OB-01		OB-01		OB-01		OB-01	
			Sample Date	09/24/16		09/24/16		09/24/16		09/24/16		09/24/16		09/24/16	
			Sample ID	OB-01_092416_TOM_WB_15		OB-01_092416_TOM_WB_16		OB-01_092416_TOM_WB_17		OB-01_092416_TOM_WB_18		OB-01_092416_TOM_WB_19		OB-01_092416_TOM_WB_04	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	276		188		155		212		245		170	
NOAALipids1993	Total	Lipids	PERCENT	0.28		0.34		0.19		0.37		0.42		0.34	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Notes:
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QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-01		OB-05		OB-05		OB-05		OB-05		OB-05	
			Sample Date	09/24/16		09/25/16		09/25/16		09/25/16		09/25/16		09/25/16	
			Sample ID	OB-01_092416_TOM_WB_14		OB-05_092516_TOM_WB_01		OB-05_092516_TOM_WB_02		OB-05_092516_TOM_WB_03		OB-05_092516_TOM_WB_04		OB-05_092516_TOM_WB_05	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	280		158		105		80.6		142		109	
NOAALipids1993	Total	Lipids	PERCENT	0.18		0.18		0.10		0.42		0.12		0.11	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
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QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-05		OB-05		OB-05		OB-05		OB-05		OB-05	
			Sample Date	09/25/16		09/25/16		09/25/16		09/25/16		09/25/16		09/25/16	
			Sample ID	OB-05_092516_TOM_WB_06		OB-05_092516_TOM_WB_07		OB-05_092516_TOM_WB_08		OB-05_092516_TOM_WB_09		OB-05_092516_TOM_WB_10		OB-05_092516_TOM_WB_11	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parametei**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	154		194		146		246		135		117	
NOAALipids1993	Total	Lipids	PERCENT	0.15		0.17		0.16		0.13		0.26		0.24	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740		1610141/16-11-0740	
			Location	OB-05		OB-05		OB-05		OB-05		OB-05		OB-05	
			Sample Date	09/25/16		09/25/16		09/25/16		09/25/16		09/25/16		09/25/16	
			Sample ID	OB-05_092516_TOM_WB_12		OB-05_092516_TOM_WB_13		OB-05_092516_TOM_WB_17		OB-05_092516_TOM_WB_18		OB-05_092516_TOM_WB_16		OB-05_092516_TOM_WB_14	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	253		105		275		161		149		201	
NOAALipids1993	Total	Lipids	PERCENT	0.11		0.29		0.26		0.18		0.35		0.22	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Notes:
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TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610141/16-11-0740		1610144		1610144/16-11-2445		1610144/16-11-2445		1610144/16-11-2445		1610144/16-11-2445	
			Location	OB-05		ES-03		ES-03		ES-03		ES-03		ES-03	
			Sample Date	09/25/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	OB-05_092516_TOM_WB_15		ES-03_092716_BLM_WB_01		ES-03_092716_BLM_WB_02		ES-03_092716_BLM_WB_03		ES-03_092716_BLM_WB_04		ES-03_092716_BLM_WB_05	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parametei**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	213		80.4		57.8		60.4		77.7		81.9	
NOAALipids1993	Total	Lipids	PERCENT	0.26				2.40		1.50		2.30		2.10	

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Notes:
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TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144/16-11-2445		1610144/16-11-2445		1610144/16-11-2445		1610144/16-11-2445		1610144/16-11-2445		1610144	
			Location	ES-03		ES-03		ES-03		ES-03		ES-03		ES-03	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	ES-03_092716_BLM_WB_06		ES-03_092716_BLM_WB_07		ES-03_092716_BLM_WB_08		ES-03_092716_BLM_WB_09		ES-03_092716_BLM_WB_10		ES-03_092716_BLM_WB_11	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	118		71.4		69		107		71		61.1	
NOAALipids1993	Total	Lipids	PERCENT	1.50		2.70		0.64		1.40		1.60			

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Notes:
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QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-03		ES-03		ES-03		ES-03		ES-03		ES-03	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	ES-03_092716_BLM_WB_12		ES-03_092716_BLM_WB_13		ES-03_092716_BLM_WB_14		ES-03_092716_BLM_WB_15		ES-03_092716_BLM_WB_16		ES-03_092716_BLM_WB_17	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	77.3		81.4		51		116		138		76	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
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Notes:
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QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-03		ES-03		ES-03		ES-13		ES-13		ES-13	
			Sample Date	09/27/16		09/27/16		09/27/16		09/30/16		09/30/16		09/30/16	
			Sample ID	ES-03_092716_BLM_WB_18		ES-03_092716_BLM_WB_19		ES-03_092716_BLM_WB_20		ES-13_093016_BLM_WB_01		ES-13_093016_BLM_WB_02		ES-13_093016_BLM_WB_03	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	88.9		87.5		68.6		63		53.9		106	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-13		ES-13		ES-13		ES-13		ES-13		ES-13	
			Sample Date	09/30/16		09/30/16		09/30/16		09/30/16		09/30/16		09/30/16	
			Sample ID	ES-13_093016_BLM_WB_04		ES-13_093016_BLM_WB_05		ES-13_093016_BLM_WB_06		ES-13_093016_BLM_WB_07		ES-13_093016_BLM_WB_08		ES-13_093016_BLM_WB_09	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	48.9		76.9		70.8		48.4		54.8		73.5	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-13		ES-13		ES-13		ES-13		ES-13		ES-13	
			Sample Date	09/30/16		09/30/16		09/30/16		09/30/16		09/30/16		09/30/16	
			Sample ID	ES-13_093016_BLM_WB_10		ES-13_093016_BLM_WB_11		ES-13_093016_BLM_WB_12		ES-13_093016_BLM_WB_13		ES-13_093016_BLM_WB_14		ES-13_093016_BLM_WB_15	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	63.5		59.2		66.4		59.6		58.5		69	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-13		ES-13		ES-13		ES-13		ES-13		ES-15	
			Sample Date	09/30/16		09/30/16		09/30/16		09/30/16		09/30/16		09/27/16	
			Sample ID	ES-13_093016_BLM_WB_16		ES-13_093016_BLM_WB_17		ES-13_093016_BLM_WB_18		ES-13_093016_BLM_WB_19		ES-13_093016_BLM_WB_20		ES-15_092716_BLM_WB_01	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	48.9		56.5		56.7		75.2		62.1		46.9	
NOAALipids1993	Total	Lipids	PERCENT												

Units:

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Notes:

FS = Field Sample

QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-15		ES-15		ES-15		ES-15		ES-15		ES-15	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	ES-15_092716_BLM_WB_02		ES-15_092716_BLM_WB_03		ES-15_092716_BLM_WB_04		ES-15_092716_BLM_WB_05		ES-15_092716_BLM_WB_06		ES-15_092716_BLM_WB_07	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	77		55.3		55.5		65.6		65		96	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-15		ES-15		ES-15		ES-15		ES-15		ES-15	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	ES-15_092716_BLM_WB_08		ES-15_092716_BLM_WB_09		ES-15_092716_BLM_WB_10		ES-15_092716_BLM_WB_11		ES-15_092716_BLM_WB_12		ES-15_092716_BLM_WB_13	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fractior**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	67.4		58.2		68		48.1		55.4		44.8	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144		1610144	
			Location	ES-15		ES-15		ES-15		ES-15		ES-15		ES-15	
			Sample Date	09/27/16		09/27/16		09/27/16		09/27/16		09/27/16		09/27/16	
			Sample ID	ES-15_092716_BLM_WB_14		ES-15_092716_BLM_WB_15		ES-15_092716_BLM_WB_16		ES-15_092716_BLM_WB_17		ES-15_092716_BLM_WB_18		ES-15_092716_BLM_WB_19	
			QC Code	FS		FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	64.8		45.6		49.7		49.8		62.7		64.1	
NOAALipids1993	Total	Lipids	PERCENT												

Units:
NG/G = Nanogram per gram

Validation Qualifier:
J = Value is estimated

Notes:
FS = Field Sample
QC = Quality Control Sample

TABLE 3
DATA VALIDATION SUMMARY
PENOBSCOT RIVER ESTUARY PHASE III - ENGINEERING EVALUATION
PENOBSCOT RIVER, MAINE
SDGs 1610138, 1610141, 1610144, 1610145, 1610232, 1610233, 1610234, 1610236, and 1610238

			SDG	1610144		1610144		1610144		1610144		1610144	
			Location	ES-15		ES-FP		ES-FP		ES-FP		ES-FP	
			Sample Date	09/27/16		09/26/16		09/26/16		09/26/16		09/26/16	
			Sample ID	ES-15_092716_BLM_WB_20		ES-FP_092616_BLM_WB_01		ES-FP_092616_BLM_WB_02		ES-FP_092616_BLM_WB_03		ES-FP_092616_BLM_WB_04	
			QC Code	FS		FS		FS		FS		FS	
Method	**Fraction**	**Parameter**	**Units**	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier	Result	Qualifier
EPA 1631	Total	Mercury	NG/G	51.1		55.4		86		48.5		62.4	
NOAALipids1993	Total	Lipids	PERCENT										

Units:

NG/G = Nanogram per gram

Validation Qualifier:

J = Value is estimated

Notes:

FS = Field Sample

QC = Quality Control Sample

APPENDIX F
Biota Statistical Analysis Code

Appendix F-1. Terrestrial Insect Statistical Analysis Code

```r
### File created for analysis of terrestrial insects data for Biota Monitoring Report (2017)
### Code prepared by LSV 5/03/2017
### Code checked by NTG 5/12/2017

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


penob = read.dbf("PEN_BI13.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

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) #116 records
summary(ref.tin) #50 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 ###
###########################

# Hg
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$ADD.x[2] = tapply(ref.tin$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$ADD.x.se[2] = tapply(ref.tin$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$ADD.medn[2] = tapply(ref.tin$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] = 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)
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)
tin.summ$BH.medn = c(tapply(ref.tin$resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], median), NA) #leave NDs in for this calc
tin.summ$BH.N = c(tapply(ref.tin$resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], length), NA)


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)
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)
tin.summ$SM.medn = c(tapply(ref.tin$resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], median), NA) #leave NDs in for this calc
tin.summ$SM.N = c(tapply(ref.tin$resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], length), NA)


# 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$MeHgADD.x[2] = tapply(ref.tin$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] = 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$MeHgADD.medn[2] = tapply(ref.tin$mehg.resuse[ref.tin$locs == "ADD-0"], ref.tin$year[ref.tin$locs == "ADD-0"], median) #leave NDs in for this
```

```
 calc
tin.summ$MeHgADD.N[2] = tapply(ref.tin$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)
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)
tin.summ$MeHgBH.medn = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], median, na.rm = T), NA) #leave NDs
 in for this calc
tin.summ$MeHgBH.N = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "BH"], ref.tin$year[ref.tin$reach == "BH"], length), NA)


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)
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)
tin.summ$MeHgSM.medn = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], median, na.rm = T), NA) #leave NDs
 in for this calc
tin.summ$MeHgSM.N = c(tapply(ref.tin$mehg.resuse[ref.tin$reach == "SM"], ref.tin$year[ref.tin$reach == "SM"], length), NA)


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 == "BH",], pch = 17, col = 3)
points(ln.resuse ~ year, data = ref.tin[ref.tin$reach == "SM",], pch = 18, col = 6)

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

legend("topright", legend = c("Pleasant River", "Bass Harbor", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,6,"blue","red"), pch =
 c(16,17,18,22,21), pt.bg = c("white","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 == "BH",], pch = 17, col = 3)
points(ln.mehg.resuse ~ year, data = ref.tin[ref.tin$reach == "SM",], pch = 18, col = 6)

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

legend("topright", legend = c("Pleasant River", "Bass Harbor", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,6,"blue","red"), pch =
 c(16,17,18,22,21), pt.bg = c("white","white","white","blue","red"), cex = 0.8)
title(sub = "Two samples at Bass Harbor and 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 - Mendall Marsh 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 - Mendall Marsh 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 - Mendall Marsh 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 - Mendall Marsh 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)
```

```
Appendix F-2. Spider Statistical Analysis Code

### File created for analysis of spider data for Biota Monitoring Report (2017)
### Code prepared by LSV 5/03/2017
### Code checked by NTG 5/12/2017


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


penob = read.dbf("PEN_BI13.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

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) #112 records
summary(ref.spd) #30 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$w17.x[c(1,3)] = tapply(hg.spd.w17$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)] = 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$w17.medn[c(1,3)] = tapply(hg.spd.w17$resuse, hg.spd.w17$year, median) #leave NDs in for this calc
spd.summ$w17.N[c(1,3)] = tapply(hg.spd.w17$resuse, hg.spd.w17$year, length)


spd.summ$ADD.x[3] = tapply(ref.spd$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$ADD.x.se[3] = tapply(ref.spd$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$ADD.medn[3] = tapply(ref.spd$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] = 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)
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)
spd.summ$BH.medn = c(tapply(ref.spd$resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], median), NA, NA) #leave NDs in for this calc
spd.summ$BH.N = c(tapply(ref.spd$resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], length), NA, NA)


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)
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)
spd.summ$SM.medn = c(tapply(ref.spd$resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], median), NA, NA) #leave NDs in for this calc
spd.summ$SM.N = c(tapply(ref.spd$resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], length), NA, NA)


# 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$MeHgw17.x[c(1,3)] = tapply(hg.spd.w17$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)] = 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$MeHgw17.medn[c(1,3)] = tapply(hg.spd.w17$mehg.resuse, hg.spd.w17$year, median, na.rm = T) #leave NDs in for this calc
spd.summ$MeHgw17.N[c(1,3)] = tapply(hg.spd.w17$mehg.resuse, hg.spd.w17$year, length)


spd.summ$MeHgADD.x[3] = tapply(ref.spd$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] = 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$MeHgADD.medn[3] = tapply(ref.spd$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] = 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)
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)
spd.summ$MeHgBH.medn = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], median, na.rm = T), NA, NA) #leave
 NDs in for this calc
spd.summ$MeHgBH.N = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "BH"], ref.spd$year[ref.spd$reach == "BH"], length), NA, NA)


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)
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)
spd.summ$MeHgSM.medn = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], median, na.rm = T), NA, NA) #leave
 NDs in for this calc
spd.summ$MeHgSM.N = c(tapply(ref.spd$mehg.resuse[ref.spd$reach == "SM"], ref.spd$year[ref.spd$reach == "SM"], length), NA, NA)


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$reach == "BH",], pch = 17, col = 3)
points(ln.resuse ~ year, data = ref.spd[ref.spd$reach == "SM",], pch = 18, col = 6)

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

legend("topright", legend = c("Pleasant River", "Bass Harbor", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,6,"blue","red"), pch =
 c(16,17,18,22,21), pt.bg = c("white","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$reach == "BH",], pch = 17, col = 3)
points(ln.mehg.resuse ~ year, data = ref.spd[ref.spd$reach == "SM",], pch = 18, col = 6)

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

legend("topright", legend = c("Pleasant River", "Bass Harbor", "Spurwink River","Yearly Means", "Yearly Medians"), col = c(1,3,6,"blue","red"), pch =
 c(16,17,18,22,21), pt.bg = c("white","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 - Mendall Marsh 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 - Mendall Marsh 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 - Mendall Marsh 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 - Mendall Marsh 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 prepared by LSV 4/05/2017
### Code checked by NTG 4/10/2017

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


penob = read.dbf("PEN_BI13.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) #493 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) # 505 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) #493 records


hg.nsp = merge(hg.nsp, nsp.weight[,c(2:4, 6, 7, 36, 40:45)], 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) #505 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) #429
summary(ref.nsp) #76 records

# Addison Reference
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 > 891800,] #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 > 891800),] #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 > 3000], hg.nsp.mmse$year[hg.nsp.mmse$resuse > 3000], 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$resuse > 3000], hg.nsp.mmsw$year[hg.nsp.mmsw$resuse > 3000], length) / tapply(hg.nsp.mmsw
 $resuse, hg.nsp.mmsw$year, length)

nsp.summ$w17_x[3:7] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, mean)
nsp.summ$w17_x_se[3:7] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, sd) / sqrt(tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, length))
nsp.summ$w17_medn[3:7] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, median)
nsp.summ$w17_N[3:7] = tapply(hg.nsp.w17$resuse, hg.nsp.w17$year, length)
nsp.summ$w17_perc[3:7] = tapply(hg.nsp.w17$resuse[hg.nsp.w17$resuse > 3000], hg.nsp.w17$year[hg.nsp.w17$resuse > 3000], length) /
 tapply(hg.nsp.w17$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$Add_perc[6:7] = 0
nsp.summ$NH_perc = c(NA, rep(0,4), NA, NA)

me = tapply(ref.nsp$resuse[ref.nsp$resuse > 3000 & ref.nsp$which.ref == "maine"], ref.nsp$year[ref.nsp$resuse > 3000 & ref.nsp$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)

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))



#4-21
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 4-21\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)


#4-22
plot(ln.resuse ~ year, data = hg.nsp, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-22\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")

text(min(hg.nsp$year) + 1.1, max(hg.nsp$ln.resuse)*0.185, "ln(y) = 0.0105x - 12.566", cex = 0.8)
text(min(hg.nsp$year) + 1.1, max(hg.nsp$ln.resuse)*0.15, "p = 0.31, Adj." ~R^2~ "= 0", 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)


#4-23
plot(ln.resuse ~ year, data = hg.nsp.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-23\nNelson's Sparrow Blood - Mendall Marsh 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")

abline(lm(ln.resuse ~ year, data = hg.nsp.mmse))
text(min(hg.nsp$year) + 1.3, 0.185 * max(hg.nsp.mm$ln.resuse), "ln(y) = 0.05086x - 93.841", cex = 0.8)
text(min(hg.nsp$year) + 1.3, 0.15 * max(hg.nsp.mm$ln.resuse), "p = 0.004, Adj." ~R^2~ "= 0.04", 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)


#4-24
plot(ln.resuse ~ year, data = hg.nsp.mmsw, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-24\nNelson's Sparrow Blood - Mendall Marsh 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")

text(min(hg.nsp$year) + 1.3, 0.185 * max(hg.nsp.mm$ln.resuse), "ln(y) = -0.002929x + 14.504", cex = 0.8)
text(min(hg.nsp$year) + 1.3, 0.15 * max(hg.nsp.mm$ln.resuse), "p = 0.85, Adj." ~R^2~ "= 0", 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)


#4-25
plot(ln.resuse ~ year, data = hg.nsp.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-25\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")

text(min(hg.nsp$year) + 1.3, max(hg.nsp$ln.resuse) * 0.185, "ln(y) = -0.0204x + 49.347", cex = 0.8)
text(min(hg.nsp$year) + 1.3, max(hg.nsp$ln.resuse) * 0.15, "p = 0.41, Adj." ~R^2~ "= 0", 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)
```

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 prepared by LSV 4/05/2017
### Code checked by NTG 4/13/2017


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

penob = read.dbf("PEN_BI13.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$MED_T == "Red-Winged Blackbird",]
rwb.weight$ID = factor(substring(rwb.weight$ID,1,22))

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$ID = factor(substring(hg.rwb$ID,1,22))

hg.rwb = merge(hg.rwb, rwb.weight[,c(2:4, 6, 7, 36, 40:45)], 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.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) #229 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 &! hg.rwb$Y_COORD == 323186,]
ref.rwb$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) #218 records
summary(ref.rwb) #11 records


# Addison Reference
add.rwb = ref.rwb[ref.rwb$X_COORD > 950000 & ref.rwb$Y_COORD > 350000,]

################################################
### 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[c(1,3:5)] = tapply(hg.rwb.mmse$resuse[hg.rwb.mmse$resuse > 3000], hg.rwb.mmse$year[hg.rwb.mmse$resuse > 3000], length) /
 tapply(hg.rwb.mmse$resuse, hg.rwb.mmse$year, length)[c(1,3:5)]

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$resuse > 3000], hg.rwb.mmsw$year[hg.rwb.mmsw$resuse > 3000], length) / tapply(hg.rwb.mmsw
 $resuse, hg.rwb.mmsw$year, length)
rwb.summ = rbind(rwb.summ, NA)
rownames(rwb.summ)[6] = "2016"

rwb.summ$w17_x = c(NA, NA, tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, mean))
rwb.summ$w17_x_se = c(NA, NA, tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, sd) / sqrt(tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, length)))
rwb.summ$w17_medn = c(NA, NA, tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, median))
rwb.summ$w17_N = c(NA, NA, tapply(hg.rwb.w17$resuse, hg.rwb.w17$year, length))
rwb.summ$w17_perc = c(NA, NA, tapply(hg.rwb.w17$resuse[hg.rwb.w17$resuse > 3000], hg.rwb.w17$year[hg.rwb.w17$resuse > 3000], length) /
 tapply(hg.rwb.w17$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 > 3000]) / length(ref.rwb
 $resuse[ref.rwb$which.ref == "Add" & ref.rwb$year == 2012])

rwb.summ$me_x = NA
rwb.summ$me_x[2] = mean(ref.rwb$resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008])
rwb.summ$me_x_se = NA
rwb.summ$me_x_se[2] = sd(ref.rwb$resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008]) / sqrt(length(ref.rwb$resuse[ref.rwb$which.ref ==
 "downeast" & ref.rwb$year == 2008]))
rwb.summ$me_medn = NA
rwb.summ$me_medn[2] = median(ref.rwb$resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008])
rwb.summ$me_N = NA
rwb.summ$me_N[2] = length(ref.rwb$resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008])
rwb.summ$me_perc = NA
rwb.summ$me_perc[2] = length(ref.rwb$resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008 & ref.rwb$resuse > 3000]) / length(ref.rwb
 $resuse[ref.rwb$which.ref == "downeast" & ref.rwb$year == 2008])


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))



#4-26
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 4-26\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)


#4-27
plot(ln.resuse ~ year, data = hg.rwb.mmse, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-27\nRed-winged Blackbird Blood - Mendall
 Marsh SE\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.rwb.mm$ln.resuse)), xlim = c(2006, max(hg.rwb$year)), las = 1, tck = 0.015, yaxs = "i")

text(min(hg.rwb$year) + .3, 0.185 * max(hg.rwb.mm$ln.resuse), "ln(y) = 0.3455x - 687.02", cex = 0.8)
text(min(hg.rwb$year) + .3, 0.15 * max(hg.rwb.mm$ln.resuse), "p = 0.12, 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)


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

text(min(hg.rwb$year) + .3, 0.185 * max(hg.rwb.mm$ln.resuse), "ln(y) = 0.1509x - 295.43", cex = 0.8)
text(min(hg.rwb$year) + .3, 0.15 * max(hg.rwb.mm$ln.resuse), "p = 0.19, Adj." ~R^2~ "= 0.01", 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)


#4-29
plot(ln.resuse ~ year, data = hg.rwb.w17, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-29\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$year) + .3, max(hg.rwb$ln.resuse) * 0.185, "ln(y) = -0.050x + 108.40", cex = 0.8)
text(min(hg.rwb$year) + .3, max(hg.rwb$ln.resuse) * 0.15, "p = 0.69, 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)
```

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_BI13.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 = merge(hg.abd,abd.weight[,c(2:4, 6, 7, 36:37, 40:45)], 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) #140 records, 3 NAs (2017 ducks, known missing data)

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) #89 records
summary(ref.dub) #51 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))
```

```r
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 > 3000

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 > 3000

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 > 3000

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))

#4-30
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 4-30\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) = -0.1099x + 225.484", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.15, "p = 0.004, 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)


#4-31
plot(ln.resuse ~ year2, data = hg.abd, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-31\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) = 0.0353x - 65.520", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd$ln.resuse)*0.15, "p = 0.39, 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)


#4-32
plot(ln.resuse ~ year2, data = hg.abd.mm, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-32\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) = -0.0174x + 41.1615", cex = 0.8)
text(max(hg.abd$year2) - 1.5, max(hg.abd.mm$ln.resuse)*0.15, "p = 0.73, Adj." ~R^2~ "= 0.01", 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)


#4-33
plot(ln.resuse ~ year2, data = hg.abd.SV, xlab = "Year", ylab = "Ln Blood Hg (ng/g)", main = "Figure 4-33\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$year) - 1.5, max(hg.abd.SV$ln.resuse)*0.19, "ln(y) = 0.1556x - 308.29", cex = 0.8)
```

```
text(max(hg.abd$year) - 1.5, max(hg.abd.SV$ln.resuse)*0.16, "p = 0.002, Adj." ~R^2~ "= 0.18", 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. American Black Duck Muscle Statistical Analysis Code

```
### File created for analysis of black duck muscle data for Biota Monitoring Report (2017); has correlation of blood and muscle at end
### 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_BI13.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 MUSCLE ###
##################################

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

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

hg.bdm = penob[penob$MED_T == "American Black Duck" & penob$PARAM_NAME == "Mercury" &! penob$QC_CODE == "FD" & penob$MONITOR_TY == "Muscle",]
 #selects samples labeled as mercury and only duck muscle samples, removes field duplicates

hg.bdm$ID = str_sub(hg.bdm$ID, -25, -4) #create sample IDs without last three characters

hg.bdm$year2[hg.bdm$year == 2010 & hg.bdm$month > 6] = 2011 #adjusting year to year at end of winter
hg.bdm$year2[hg.bdm$year == 2011 & hg.bdm$month < 6] = 2011
hg.bdm$year2[hg.bdm$year == 2011 & hg.bdm$month > 6] = 2012
hg.bdm$year2[hg.bdm$year == 2013 & hg.bdm$month > 6] = 2014
hg.bdm$year2[hg.bdm$year == 2014 & hg.bdm$month < 6] = 2014
hg.bdm$year2[hg.bdm$year == 2014 & hg.bdm$month > 6] = 2015
hg.bdm$year2[hg.bdm$year == 2016 & hg.bdm$month > 6] = 2017
hg.bdm$year2[hg.bdm$year == 2017 & hg.bdm$month < 6] = 2017


hg.bdm = merge(hg.bdm, bdm.weight[,c(2:4, 6, 7, 36:37, 40:45)], 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 Hg and weight
names(hg.bdm)[colnames(hg.bdm) == "resuse.x"] = "resuse" #rename columns
names(hg.bdm)[colnames(hg.bdm) == "resuse.y"] = "weight" #rename columns
summary(hg.bdm) #44 records

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


ref.dum = hg.bdm[hg.bdm$X_COORD > 950000,] #pull data for separate reference dataset
hg.bdm = hg.bdm[hg.bdm$X_COORD < 950000,] #reduce dataset to site birds
summary(hg.bdm) #38 records
summary(ref.dum) #6 records

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


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

bdm.summ = data.frame(MM_x = tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, mean))
bdm.summ$MM_x_se = tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, sd) / sqrt(tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, length))
```

```r
bdm.summ$MM_medn = tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, median)
bdm.summ$MM_N = tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, length)
bdm.summ$MM_perc = tapply(hg.bdm.mm$resuse[hg.bdm.mm$resuse > 200], hg.bdm.mm$year2[hg.bdm.mm$resuse > 200], length) / tapply(hg.bdm.mm$resuse, hg.bdm.mm$year2, length)

bdm.summ$SV_x[4] = tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, mean)
bdm.summ$SV_x_se[4] = tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, sd) / sqrt(tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, length))
bdm.summ$SV_medn[4] = tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, median)
bdm.summ$SV_N[4] = tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, length)
bdm.summ$SV_perc[4] = tapply(hg.bdm.SV$resuse[hg.bdm.SV$resuse > 200], hg.bdm.SV$year2[hg.bdm.SV$resuse > 200], length) / tapply(hg.bdm.SV$resuse, hg.bdm.SV$year2, length)

bdm.summ$FRB_x[3:4] = tapply(ref.dum$resuse, ref.dum$year2, mean)
bdm.summ$FRB_x_se[3:4] = tapply(ref.dum$resuse, ref.dum$year2, sd) / sqrt(tapply(ref.dum$resuse, ref.dum$year2, length))
bdm.summ$FRB_medn[3:4] = tapply(ref.dum$resuse, ref.dum$year2, median)
bdm.summ$FRB_N[3:4] = tapply(ref.dum$resuse, ref.dum$year2, length)
bdm.summ$FRB_perc[3:4] = 0 #tapply(ref.dum$resuse[ref.dum$resuse > 200], ref.dum$year2[ref.dum$resuse > 200], length) / tapply(ref.dum$resuse, ref.dum$year2, length) # no samples with concentrations > 200

write.csv(bdm.summ,"American Black Duck Muscle summary.csv")


################################
### BLACK DUCK MUSCLE TRENDS ###
################################

summary(lm(ln.resuse ~ year2, data = hg.bdm.mm))


#4-34
plot(ln.resuse ~ year, data = ref.dum, pch = 17, ylab = "Muscle Ln Hg (ng/g)", xlab = "Year", xlim = c(2006, max(ref.dum$year)), las = 1, tck = 0.015, yaxs = "i", ylim = c(0, 1.02 * max(hg.bdm$ln.resuse)), main = "Figure 4-34\nAmerican Black Duck Muscle - Frenchman Bay (Reference)\nLn Mercury Concentrations")

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

legend("topleft", 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)


#4-35
plot(ln.resuse ~ year2, data = hg.bdm.mm, xlab = "Year", ylab = "Ln Muscle Hg (ng/g)", main = "Figure 4-35\nAmerican Black Duck Muscle - Mendall Marsh\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.bdm$ln.resuse)), las = 1, tck = 0.015, yaxs = "i", xlim = c(2006, max(hg.bdm$year)))
clip(2010, 2020, 0, 100)
abline(lm(ln.resuse ~ year2, data = hg.bdm.mm), lty = 2)
clip(0, 2020, 0, 100)

text(2008, max(hg.bdm.mm$ln.resuse)*0.18, "ln(y) = -0.1282x + 264.03", cex = 0.8)
text(2008, max(hg.bdm.mm$ln.resuse)*0.15, "p = 0.082, Adj." ~R^2~ "= 0.07", cex = 0.8)

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


#4-36
plot(ln.resuse ~ year2, data = hg.bdm.SV, xlab = "Year", ylab = "Ln Muscle Hg (ng/g)", main = "Figure 4-36\nAmerican Black Duck Muscle - South Verona\nLn Mercury Concentrations", ylim = c(0, 1.02 * max(hg.bdm$ln.resuse)), las = 1, tck = 0.015, yaxs = "i", xlim = c(2006, max(hg.bdm$year)))

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

legend("topleft", 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)



########################
### CORRELATION TEST ###
########################


hg.duk = merge(hg.bdm[,c(1:8,19,21,42,46,51,45,52)], hg.abd[,c(15,1:7,9,19,21,42,46,52,45,53)], by.x = c("ID", "LOC_NAME", "X_COORD", "Y_COORD", "year", "month", "LOGGED_BY"), by.y  = c("ID", "LOC_NAME.x", "X_COORD", "Y_COORD", "year", "month", "LOGGED_BY"), all.x = T) #merge duck blood and duck muscle datasets from above
names(hg.duk)[colnames(hg.duk) == "resuse.y"] = "bl.resuse" #rename columns to keep track of data
names(hg.duk)[colnames(hg.duk) == "resuse.x"] = "mu.resuse" #rename columns to keep track of data
names(hg.duk)[colnames(hg.duk) == "ln.resuse.y"] = "ln.bl.resuse" #rename columns to keep track of data
names(hg.duk)[colnames(hg.duk) == "ln.resuse.x"] = "ln.mu.resuse" #rename columns to keep track of data
summary(hg.duk)
```

```
hg.duk = hg.duk[is.na(hg.duk$bl.resuse) == F,] #remove samples without blood results


ref.duk = merge(ref.dum[,c(1:8,19,21,42,46,51,45,52)], ref.dub[,c(15,1:7,9,19,21,42,46,52,45,53)], by.x = c("ID", "LOC_NAME", "X_COORD", "Y_COORD",
 "year", "month", "LOGGED_BY"), by.y  = c("ID", "LOC_NAME.x", "X_COORD", "Y_COORD", "year", "month", "LOGGED_BY"), all.x = T) #merge duck blood and
 duck muscle datasets from above
names(ref.duk)[colnames(ref.duk) == "resuse.y"] = "bl.resuse" #rename columns to keep track of data
names(ref.duk)[colnames(ref.duk) == "resuse.x"] = "mu.resuse" #rename columns to keep track of data
names(ref.duk)[colnames(ref.duk) == "ln.resuse.y"] = "ln.bl.resuse" #rename columns to keep track of data
names(ref.duk)[colnames(ref.duk) == "ln.resuse.x"] = "ln.mu.resuse" #rename columns to keep track of data

tot.duk = rbind(hg.duk,ref.duk) #put site and reference merged datasets together
summary(tot.duk)

cor.test(tot.duk$mu.resuse, tot.duk$bl.resuse, method = "spearman") #test of correlation


#4-37
plot(mu.resuse ~ bl.resuse, data = tot.duk, xlab = "Blood Hg (ng/g)", ylab = "Breast Muscle Hg (ng/g)", main = "Figure 4-37\nComparison of American
 Black Duck Blood\nand Breast Muscle Mercury Results", las = 1, tck = 0.015, ylim = c(0, 1650), xlim = c(0, 1750), yaxs = "i", xaxs = "i", pch = 16)
abline(lm(mu.resuse ~ bl.resuse, data = tot.duk), col = "blue")

text(300, 1600, "y = 0.7956x + 25.0515", cex = 0.8)
text(300, 1600 * 0.96, "rho = 0.94, p < 0.001", cex = 0.8)
```

Appendix F-7. Polychaete Statistical Analysis Code

```
### File created for analysis of polychaete data for Biota Monitoring Report (2017)
### Code prepared by LSV 5/04/2017
### Code checked by NTG 5/12/2017


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


penob = read.dbf("PEN_BI13.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

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) #48 records
summary(ref.ply) #10 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$MM.x[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], mean)
ply.summ$MM.x.se[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P
 $FINAL_QUAL.x) == T)], hg.ply.P$year[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) ==
 T)], sd) / sqrt(tapply(hg.ply.P$resuse[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x)
 == T)], hg.ply.P$year[hg.ply.P$locs == "MMPOL" & (hg.ply.P$FINAL_QUAL.x == "J" | is.na(hg.ply.P$FINAL_QUAL.x) == T)], length))
ply.summ$MM.medn[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], median) #leave
 NDs in for this calc
ply.summ$MM.N[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], length)


ply.summ$OB05.x[2] = tapply(hg.ply.P$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$FINAL_QUAL.x) ==
 T)], mean)
ply.summ$OB05.x.se[2] = 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$FINAL_QUAL.x) == T)], length))
ply.summ$OB05.medn[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], median) #leave
 NDs in for this calc
ply.summ$OB05.N[2] = tapply(hg.ply.P$resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], 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$ESFP.x = tapply(hg.ply.P$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$FRB.x[2] = tapply(hg.ply.P$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] = 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] = 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] = 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$MeHgBO04.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "BO-04" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], mean)
```

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


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


ply.summ$MeHgOB05.x[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], mean)
ply.summ$MeHgOB05.x.se[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "OB-05" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], length))
ply.summ$MeHgOB05.medn[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"],
 median) #leave NDs in for this calc
ply.summ$MeHgOB05.N[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "OB-05"], hg.ply.P$year[hg.ply.P$locs == "OB-05"], length)


ply.summ$MeHgES13.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], mean)
ply.summ$MeHgES13.x.se = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-13" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], length))
ply.summ$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$MeHgESFP.x = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], mean)
ply.summ$MeHgESFP.x.se = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], sd) / sqrt(tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "ES-FP" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], length))
ply.summ$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$MeHgFRB.x[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P
 $FINAL_QUAL.y) == T)], hg.ply.P$year[hg.ply.P$locs == "FRB-0" & (hg.ply.P$FINAL_QUAL.y == "J" | is.na(hg.ply.P$FINAL_QUAL.y) ==
 T)], mean)
ply.summ$MeHgFRB.x[2] = "ND"
ply.summ$MeHgFRB.x.se[2] = "NA"
ply.summ$MeHgFRB.medn[2] = 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$MeHgFRB.medn[2] = "ND"
ply.summ$MeHgFRB.N[2] = tapply(hg.ply.P$mehg.resuse[hg.ply.P$locs == "FRB-0"], hg.ply.P$year[hg.ply.P$locs == "FRB-0"], length)


### 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$FINAL_QUAL.x) == T)], mean),NA,NA)
ply.summ$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)),NA,NA)
ply.summ$EB.medn = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB"], hg.ply.P$year[hg.ply.P$reach == "EB"], median),NA,NA) #leave
 NDs in for this calc
ply.summ$EB.N = c(tapply(hg.ply.P$resuse[hg.ply.P$reach == "EB"], hg.ply.P$year[hg.ply.P$reach == "EB"], length),NA,NA)


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$FINAL_QUAL.x) ==
 T)], mean),NA)
ply.summ$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$FINAL_QUAL.x) == T)],
 length)),NA)
ply.summ$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)
 #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)


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$FINAL_QUAL.y) ==
 T)], mean),NA)
ply.summ$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
 $FINAL_QUAL.y) == T)], length)),NA)
ply.summ$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) #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)


write.csv(ply.summ, "Polychaete summary.csv")


##########################
### POLYCHAETE FIGURES ###
##########################

#4-38
plot(ln.resuse ~ year, data = ref.ply[ref.ply$locs == "FRB-0",], pch = 17, ylab = "Ln Hg (ng/g)", xlab = "Year", xlim =
 range(ref.ply$year), las = 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), main = "Figure
 4-38\nPolychaetes - Reference Locations\nLn Mercury Concentrations")
points(ln.resuse ~ year, data = ref.ply[ref.ply$locs == "OV-04",], col = 4, pch = 18)
points(ln.resuse ~ year, data = ref.ply[ref.ply$reach == "EB",], col = 3, pch = 15)
legend("topright", legend = c("East Branch - Penobscot River", "Frenchman Bay","OV-04"), pch = c(15,17:18), col = c(3,1,4), cex =
 0.8)


#4-39
plot(ln.mehg.resuse ~ year, data = ref.ply[ref.ply$locs == "FRB-0",], pch = 17, ylab = "Ln Me Hg (ng/g)", xlab = "Year", xlim =
 range(ref.ply$year), las = 1, tck = 0.015, yaxs = "i", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), main = "Figure
 4-39\nPolychaetes - Reference Locations\nLn Methyl Mercury Concentrations")
points(ln.mehg.resuse ~ year, data = ref.ply[ref.ply$locs == "OV-04",], col = 4, pch = 18)
legend("bottomleft", legend = c("Frenchman Bay","OV-04"), pch = 17:18, col = c(1,4), cex = 0.8)
title(sub = "Samples collected in 2016 were non-detect.", cex.sub = 0.7)


#4-40
```

```
plot(ln.resuse ~ year, data = hg.ply, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-40\nPolychaetes - Whole River\nLn
 Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply$year)), yaxs = "i", las = 1, tck
 = 0.015)

points(as.numeric(levels(as.factor(hg.ply$year))), tapply(hg.ply$ln.resuse, hg.ply$year, median), pch = 21, col = "red", cex =
 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply$year))), tapply(hg.ply$ln.resuse, hg.ply$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 Polychaetes sampled at BO-04, ES-13, and ES-FP", cex.sub = 0.7)


#4-41
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BO-04",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure
 4-41\nPolychaetes - BO-04\nLn Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply
 $year)), yaxs = "i", las = 1, tck = 0.015)

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")

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)


#4-42
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-05",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure
 4-42\nPolychaetes - OB-05\nLn Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply
 $year)), yaxs = "i", las = 1, tck = 0.015)

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")

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)


#4-43
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "MMPOL",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure
 4-43\nPolychaetes - Mendall Marsh\nLn Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs ==
 "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], 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"]))), tapply(hg.ply.P$ln.resuse[hg.ply.P$locs ==
 "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], 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)


#4-44
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-13",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure
 4-44\nPolychaetes - ES-13\nLn Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply
 $year)), yaxs = "i", las = 1, tck = 0.015)

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")

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)


#4-45
plot(ln.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-FP",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure
 4-45\nPolychaetes - ES-FP\nLn Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply
 $year)), yaxs = "i", las = 1, tck = 0.015)
```

```
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")

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(ln.mehg.resuse ~ year, data = hg.ply, xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure 4-46\nPolychaetes - Whole
 River\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006, max(hg.ply$year)), yaxs =
 "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.ply$year))), tapply(hg.ply$ln.mehg.resuse, hg.ply$year, median, na.rm = T), pch = 21, col =
 "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply$year))), tapply(hg.ply$ln.mehg.resuse, hg.ply$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)
title(sub = "Includes Polychaetes sampled at BO-04, ES-13, and ES-FP", cex.sub = 0.7)


#4-47
plot(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "BO-04",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-47\nPolychaetes - BO-04\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

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, na.rm = T), 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, 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(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "OB-05",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-48\nPolychaetes - OB-05\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

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, na.rm = T), 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, 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(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "MMPOL",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-49\nPolychaetes - Mendall Marsh\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], median, na.rm = T), pch = 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.ply.P$year[hg.ply.P$locs == "MMPOL"]))), tapply(hg.ply.P$ln.mehg.resuse[hg.ply.P$locs ==
 "MMPOL"], hg.ply.P$year[hg.ply.P$locs == "MMPOL"], 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(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-13",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-50\nPolychaetes - ES-13\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

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, na.rm = T), 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, 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(ln.mehg.resuse ~ year, data = hg.ply.P[hg.ply.P$locs == "ES-FP",], xlab = "Year", ylab = "Ln Me Hg (ng/g)", main = "Figure
 4-51\nPolychaetes - ES-FP\nLn Methyl Mercury Concentrations", ylim = c(-1, 1.02 * max(hg.ply$ln.resuse)), xlim = c(2006,
 max(hg.ply$year)), yaxs = "i", las = 1, tck = 0.015)

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, na.rm = T), 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, 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-8. Blue Mussel Statistical Analysis Code

```
### File created for analysis of blue mussel data for Biota Monitoring Report (2017)
### Code prepared by LSV 4/07/2017
### Code checked by NTG 4/19/2017


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


penob = read.dbf("PEN_BI13.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, 40:45)], 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) #1207 records - 53 NAs

hg.mus = merge(hg.mus,weight[,c(2:4, 6, 7, 36:37, 40:45)], 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) #1207 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

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"

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) #1034 records
summary(ref.mus) #160 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
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$ES.03_x[c(1:4,6)] = tapply(hg.mus.P$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)] = 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$ES.03_medn[c(1:4,6)] = tapply(hg.mus.P$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)] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-03"], hg.mus.P$year[hg.mus.P$locs == "ES-03"], length)

mus.summ$ES.13_x = tapply(hg.mus.P$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$ES.FP_x[3:6] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], mean)
mus.summ$ES.FP_x_se[3:6] = 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$ES.FP_medn[3:6] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], median)
mus.summ$ES.FP_N[3:6] = tapply(hg.mus.P$resuse[hg.mus.P$locs == "ES-FP"], hg.mus.P$year[hg.mus.P$locs == "ES-FP"], length)

mus.summ$NG_x[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], mean), NA)
mus.summ$NG_x_se[c(3,6)] = 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$NG_medn[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], median), NA)
mus.summ$NG_N[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "NG"], ref.mus$year[ref.mus$reach == "NG"], length), NA)

mus.summ$SG_x[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], mean), NA)
mus.summ$SG_x_se[c(3,6)] = 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$SG_medn[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], median), NA)
mus.summ$SG_N[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SG"], ref.mus$year[ref.mus$reach == "SG"], length), NA)

mus.summ$SC_x[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], mean), NA)
mus.summ$SC_x_se[c(3,6)] = 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$SC_medn[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], median), NA)
mus.summ$SC_N[c(3,6)] = c(tapply(ref.mus$resuse[ref.mus$reach == "SC"], ref.mus$year[ref.mus$reach == "SC"], length), NA)

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",]))


#4-52
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$ln.resuse)), main = "Figure 4-52\nBlue Mussel - Reference Locations\nLn Mercury
 Concentrations")
points(ln.resuse ~ year, data = ref.mus[ref.mus$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)
legend("topright", legend = c("St. George River","Narragaugus River", "Merriconeag Sound", "Cape Arundel"), pch = c(17:18, 15, 19), col =
```

```
 c(1,4,3,"orange"), cex = 0.8)


#4-53
plot(hg.mus$ln.resuse ~ hg.mus$year, xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-53\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$year) - 1.3, max(hg.mus$ln.resuse)*0.185, "ln(y) = -0.03453x + 73.677", cex = 0.8)
text(max(hg.mus$year) - 1.3, max(hg.mus$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.10", 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)


#4-54
plot(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-15",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-54\nBlue Mussel -
 ES-15\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$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) = -0.03679x + 78.170", 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-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)


#4-55
plot(ln.resuse ~ year, data = hg.mus[hg.mus$locs == "ES-13",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-55\nBlue Mussel -
 ES-13\nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$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$year) - 1.3, max(hg.mus.P$ln.resuse)*0.18, "ln(y) = -0.06239x + 129.84", cex = 0.8)
text(max(hg.mus$year) - 1.3, max(hg.mus.P$ln.resuse)*0.15, "p < 0.001, Adj." ~R^2~ "= 0.29", 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)


#4-56
plot(ln.resuse ~ year, hg.mus[hg.mus$locs == "ES-03",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-56\nBlue Mussel - ES-03\nLoglinear
 Regression", ylim = c(0, 1.02 * max(hg.mus.P$ln.resuse)), las = 1, tck = 0.015, yaxs = "i")

text(max(hg.mus$year) - 1.3, max(hg.mus.P$ln.resuse)*0.185, "ln(y) = -0.00571x + 15.736", cex = 0.8)
text(max(hg.mus$year) - 1.3, max(hg.mus.P$ln.resuse)*0.15, "p = 0.51, Adj." ~R^2~ "= 0", 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)


#4-57
plot(ln.resuse ~ year, data = hg.mus.P[hg.mus.P$locs == "ES-FP",], xlab = "Year", ylab = "Ln Hg (ng/g)", main = "Figure 4-57\nBlue Mussel - ES-FP
 \nLoglinear Regression", ylim = c(0, 1.02 * max(hg.mus.P$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$year) - 1.3, max(hg.mus.P$ln.resuse)*0.18, "ln(y) = 0.01475x - 25.648", cex = 0.8)
text(max(hg.mus$year) - 1.3, max(hg.mus.P$ln.resuse)*0.15, "p = 0.046, Adj." ~R^2~ "= 0.04", 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-9. Lobster Statistical Analysis Code

```
### File created for analysis of lobster data for Biota Monitoring Report (2017); has correlation of tail and claw at end
### Code prepared by LSV 4/18/2017
### Code checked by NTG 4/21/2017


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


penob = read.dbf("PEN_BI13.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$circle.name[hg.lob$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"



#######################
### 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$resuse, list(hg.lob$year, hg.lob$circle.name), length) * 100 # Calculate percent of lobsters above 200 ng/g per year

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) #1310 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) #1085 records


hg.lob.l = merge(hg.lob.l, lob.length[, c(2:4, 6, 7, 36:37, 40:45)], 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) #1085 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",]))

#4-58
plot(l.adj.lnresuse ~ year, data = hg.lob.l.16locs[!hg.lob.l.16locs$circle.name == "Cape Jellison",], xlab = "", ylab = "Ln Tail Hg (ng/g)", main =
 "Figure 4-58\nLobster Tail - Penobscot Bay\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.lob.l$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$year) + 1.2, 0.19 * max.lob.lnresuse, "ln(y) = -0.02849x + 62.484", cex = 0.8)
text(min(hg.lob.l.16locs$year) + 1.2, 0.16 * max.lob.lnresuse, "p = 0.009, Adj." ~R^2~ "= 0.01", 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$year))), tapply(hg.lob.l.16locs$l.adj.lnresuse, hg.lob.l.16locs$year, median, na.rm = T), pch =
 21, col = "red", cex = 1.3, bg = "red")
points(as.numeric(levels(as.factor(hg.lob.l.16locs$year))), tapply(hg.lob.l.16locs$l.adj.lnresuse, hg.lob.l.16locs$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)


#4-59
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Odom Ledge",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/g)", main =
 "Figure 4-59\nLobster Tail - Odom Ledge\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim = range(hg.lob.l$year), yaxs =
 "i", las = 1, tck = 0.015)

text(min(hg.lob.l$year) + 1.3, 0.18 * max.lob.ln, "ln(y) = 0.000774x + 3.806", cex = 0.8)
text(min(hg.lob.l$year) + 1.3, 0.15 * max.lob.ln, "p = 0.98, 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)


#4-60
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "South Verona",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/g)", main =
 "Figure 4-60\nLobster Tail - South Verona\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim = range(hg.lob.l$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$year) + 1.3, 0.18 * max.lob.ln, "ln(y) = -0.1449x + 297.2", cex = 0.8)
text(min(hg.lob.l$year) + 1.3, 0.15 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.23", 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)


#4-61
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Cape Jellison",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/g)", main =
 "Figure 4-61\nLobster Tail - Cape Jellison\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim = range(hg.lob.l$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$year) + 1.3, 0.18 * max.lob.ln, "ln(y) = -0.4055x + 822.14", cex = 0.8)
text(min(hg.lob.l$year) + 1.3, 0.15 * max.lob.ln, "p = 0.003, Adj." ~R^2~ "= 0.10", 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)


#4-62
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Turner Point",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/g)", main =
 "Figure 4-62\nLobster Tail - Turner Point\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim = range(hg.lob.l$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$year) + 1.3, 0.18 * max.lob.ln, "ln(y) = -0.0629x + 131.61", cex = 0.8)
text(min(hg.lob.l$year) + 1.3, 0.15 * max.lob.ln, "p < 0.001, Adj." ~R^2~ "= 0.07", 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)


#4-63
```

```
plot(l.adj.lnresuse ~ year, data = hg.lob.l[hg.lob.l$circle.name == "Harborside",], xlab = "", ylab = "Length Adjusted Ln Tail Hg (ng/g)", main =
 "Figure 4-63\nLobster Tail - Harborside\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max.lob.ln), xlim = range(hg.lob.l$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$year) + 1.3, 0.18 * max.lob.ln, "ln(y) = -0.0585x + 122.43", cex = 0.8)
text(min(hg.lob.l$year) + 1.3, 0.15 * max.lob.ln, "p = 0.001, Adj." ~R^2~ "= 0.06", 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)


###########################
### LOBSTER CORRELATION ###
###########################

lob = penob[(penob$PARAM_NAME == "Mercury" | penob$PARAM_NAME == "Mercury - Wet Weight") & penob$MED_T == "Lobster" &! is.na(penob$MED_T) == T &
 penob$MEDIA == "TIS" &! penob$QC_CODE == "FD",] #pull lobster tissue mercury results, remove field duplicates

lob$sample.num = str_sub(lob$ID,-2)
lob$sample.num[lob$sample.num == "TA"] = "" #create tail tissue identifier
lob$sample.num[lob$sample.num == "CL"] = "" #create claw tissue identifier

lob$unique = paste(lob$LOC_NAME,lob$sample.num, sep = "")


claw = lob[lob$MONITOR_TY == "Claw",] #pull claw tissue results into separate dataset
summary(claw)

tail = lob[lob$MONITOR_TY == "Tail",] #pull tail tissue results into separate dataset
summary(tail)

lob.cl.ta.hg = merge(claw, tail[,c(2:4,6,7,40:42,45:46)], by.x = c("unique", "LOC_NAME", "X_COORD", "Y_COORD", "DATE", "year", "month"), by.y =
 c("unique", "LOC_NAME", "X_COORD", "Y_COORD", "DATE", "year", "month")) #pulling Loc name, sample ID, date, resuse, units, year, sample number, and
 unique ID from "tail" in merge with all fields from "claw"
summary(lob.cl.ta.hg)
names(lob.cl.ta.hg)[colnames(lob.cl.ta.hg) == "resuse.y"] = "tl.resuse" #rename column to track tissue results
names(lob.cl.ta.hg)[colnames(lob.cl.ta.hg) == "resuse.x"] = "cl.resuse" #rename column to track tissue results


########################
### Correlation Test ###
########################

cor.test(lob.cl.ta.hg$cl.resuse, lob.cl.ta.hg$tl.resuse, method = "spearman")
summary(lm(cl.resuse ~ tl.resuse -1, data = lob.cl.ta.hg))


#4-64
plot(cl.resuse ~ tl.resuse, data = lob.cl.ta.hg, ylab = "Claw Hg (ng/g)", xlab = "Tail Hg (ng/g)", main = "Figure 4-64\nComparison of Lobster Claw
 and Tail Mercury Results", las = 1, tck = 0.015, xlim = c(0,2500), ylim = c(0,1050), yaxs = "i", xaxs = "i", pch = 16)
abline(lm(cl.resuse ~ tl.resuse -1, data = lob.cl.ta.hg), col = "blue")

text(300, 1000, "y = 0.433x", cex = 0.8)
text(300, 1000 * 0.97, "rho = 0.68, p < 0.001", cex = 0.8)
```

Appendix F-10. Mummichog Statistical Analysis Code

```r
### File created for analysis of mummichog data for Biota Monitoring Report (2017)
### Code prepared by LSV 4/17/2017
### Code checked by NTG 4/21/2017


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


penob = read.dbf("PEN_BI13.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, 40:45)], 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) #252 records

hg.mum = merge(hg.mum, weight[,c(2:4, 6, 7, 36:37, 40:45)], 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) #252 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

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) #232 records
summary(ref.mum) #20 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$BO.04_x[c(1,5)] = tapply(hg.mum.P$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)] = 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$BO.04_medn[c(1,5)] = tapply(hg.mum.P$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)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "BO-04"], hg.mum.P$year[hg.mum.P$locs == "BO-04"], length)

mum.summ$OB.01_x[c(1,3,5)] = tapply(hg.mum.P$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)] = 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$OB.01_medn[c(1,3,5)] = tapply(hg.mum.P$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)] = tapply(hg.mum.P$resuse[hg.mum.P$locs == "OB-01"], hg.mum.P$year[hg.mum.P$locs == "OB-01"], length)

mum.summ = rbind(mum.summ[1:4,],NA,mum.summ[5,])
rownames(mum.summ)[5] = "2012"

mum.summ$MM_x[4:6] = tapply(hg.mum.P$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[4:6] = 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[4:6] = 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[4:6] = 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$FRB_x[6] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], mean)
mum.summ$FRB_x_se[6] = 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$FRB_medn[6] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], median)
mum.summ$FRB_N[6] = tapply(ref.mum$resuse[ref.mum$locs == "FRB-0"], ref.mum$year[ref.mum$locs == "FRB-0"], length)

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",]))


#4-65
plot(ln.l.adj_resuse ~ year, data = hg.mum, xlab = "Year", ylab = "Length Adjusted Ln Tissue Hg (ng/g)", main = "Figure 4-65\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")

text(max(hg.mum$year) - 1.1, max(hg.mum$ln.l.adj_resuse, na.rm = T) * 0.19, "ln(y) = 0.0385x - 72.204", cex = 0.8)
text(max(hg.mum$year) - 1.1, max(hg.mum$ln.l.adj_resuse, na.rm = T) * 0.16, "p = 0.16, Adj." ~R^2~ "= 0.01", 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)


#4-66
plot(ln.l.adj_resuse ~ year, hg.mum[hg.mum$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-66\nMummichog -
 OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.mum$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$year) - 1.1, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.18, "ln(y) = 0.06039x - 116.40", cex = 0.8)
#text(max(hg.mum$year) - 1.1, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.15, "p = 0.064, Adj." ~R^2~ "= 0.05", 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)


#4-67
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 4-67\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, 2017, 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$year) - 1.1, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.18, "ln(y) = -0.138x + 283.44", cex = 0.8)
text(max(hg.mum$year) - 1.1, max(hg.mum.P$ln.l.adj_resuse, na.rm = T)*0.15, "p = 0.046, Adj." ~R^2~ "= 0.09", 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)


#4-68
plot(ln.l.adj_resuse ~ year, data = hg.mum[hg.mum$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-68\nMummichog - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.mum$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-11. Rainbow Smelt Statistical Analysis Code

### File created for analysis of smelt data for Biota Monitoring Report (2017)
### Code prepared by LSV 4/07/2017
### Code checked by NTG 4/21/2017


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


penob = read.dbf("PEN_BI13.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, 40:45)], 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, 40:45)], 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) #701, 18 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


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) #681 records
summary(ref.sml) #20 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
tapply(hg.sml$resuse, list(factor(hg.sml$locs), hg.sml$year), length)

hg.sml = hg.sml[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 = rbind(sml.summ[1:2,],"NA",sml.summ[3:5,])
rownames(sml.summ)[3] = "2009"

sml.summ$ES.15_x[c(2:3,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], mean)
sml.summ$ES.15_x_se[c(2:3,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], sd) / sqrt(tapply(hg.sml.P
 $resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], length))
sml.summ$ES.15_medn[c(2:3,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], median)
sml.summ$ES.15_N[c(2:3,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-15"], hg.sml.P$year[hg.sml.P$locs == "ES-15"], length)

sml.summ$OB.04_x[c(1:4,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], mean)
sml.summ$OB.04_x_se[c(1:4,6)] = 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))
sml.summ$OB.04_medn[c(1:4,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], median)
sml.summ$OB.04_N[c(1:4,6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-04"], hg.sml.P$year[hg.sml.P$locs == "OB-04"], length)

sml.summ$OB.01_x[c(1,3:6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], mean)
sml.summ$OB.01_x_se[c(1,3:6)] = 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))
sml.summ$OB.01_medn[c(1,3:6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], median)
sml.summ$OB.01_N[c(1,3:6)] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "OB-01"], hg.sml.P$year[hg.sml.P$locs == "OB-01"], length)

sml.summ$ES.FP_x[3:6] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], mean)
sml.summ$ES.FP_x_se[3:6] = 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$ES.FP_medn[3:6] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], median)
sml.summ$ES.FP_N[3:6] = tapply(hg.sml.P$resuse[hg.sml.P$locs == "ES-FP"], hg.sml.P$year[hg.sml.P$locs == "ES-FP"], length)

sml.summ$FRB_x[6] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], mean)
sml.summ$FRB_x_se[6] = 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$FRB_medn[6] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], median)
sml.summ$FRB_N[6] = tapply(ref.sml$resuse[ref.sml$locs == "FRB-0"], ref.sml$year[ref.sml$locs == "FRB-0"], length)

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-FP",]))


#4-69
plot(ln.l.adj_resuse ~ year, data = ref.sml, xlab = "Year", ylab = "Hg (ng/g)", main = "Figure 4-69\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, 2016))

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)


#4-70
plot(ln.l.adj_resuse ~ year, data = hg.sml, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-70\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$year) - 1.3, max(hg.sml$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.3926x + 794.03", cex = 0.8)
text(max(hg.sml$year) - 1.3, max(hg.sml$ln.l.adj_resuse, na.rm = T) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.18", 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-15, and ES-FP", cex.sub = 0.7)


#4-71
plot(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-71\nRainbow
 Smelt - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las = 1, tck = 0.015, yaxs =
 "i")
```

```
text(max(hg.sml$year) - 1.2, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = 0.311x - 618.3", cex = 0.8)
text(max(hg.sml$year) - 1.2, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.835, "p = 0.41, 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)


#4-72
plot(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-72\nRainbow Smelt - OB-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las = 1, tck = 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, hg.sml[hg.sml$locs == "OB-04",]))

text(max(hg.sml$year) - 1.2, max(hg.sml.P$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.516x + 1042.8", cex = 0.8)
text(max(hg.sml$year) - 1.2, max(hg.sml.P$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)


#4-73
plot(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-73\nRainbow Smelt - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$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$year) - 1.1, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.8299x + 1673.8", cex = 0.8)
text(max(hg.sml$year) - 1.1, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.835, "p < 0.001, Adj." ~R^2~ "= 0.49", 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)


#4-74
plot(ln.l.adj_resuse ~ year, data = hg.sml[hg.sml$locs == "ES-15",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-74\nRainbow Smelt - ES-15\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las = 1, tck = 0.015, yaxs = "i")

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)


#4-75
plot(ln.l.adj_resuse ~ year, data = hg.sml.P[hg.sml.P$locs == "ES-FP",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-75\nRainbow Smelt - ES-FP\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.sml.P$ln.l.adj_resuse, na.rm = T)), las = 1, tck = 0.015, xlim = range(hg.sml$year), yaxs = "i")

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")

text(max(hg.sml$year) - 1.3, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.01759x + 39.241", cex = 0.8)
text(max(hg.sml$year) - 1.3, max(hg.sml.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.38, Adj." ~R^2~ "= 0", cex = 0.8)

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. American Eel Statistical Analysis Code

```r
### File created for analysis of eel 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)


penob = read.dbf("PEN_BI13.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, 40:45)], 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) #667 records

hg.eel = merge(hg.eel,weight[,c(2:4, 6, 7, 36:37, 40:45)], 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) #667 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

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) #551 records
summary(ref.eel) #116 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$resuse > 330], hg.eel.P$year[hg.eel.P$locs == "OB-05" & hg.eel.P
 $resuse > 330], length) / tapply(hg.eel.P$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 > 330], hg.eel.P$year[hg.eel.P$locs == "BO-04" & hg.eel.P
 $resuse > 330], length) / tapply(hg.eel.P$resuse[hg.eel.P$locs == "BO-04"], hg.eel.P$year[hg.eel.P$locs == "BO-04"], length)

eel.summ$OB.01_x = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], mean)
eel.summ$OB.01_x_se = 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))
eel.summ$OB.01_medn = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], median)
eel.summ$OB.01_N = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], length)
eel.summ$OB.01_perc = tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01" & hg.eel.P$resuse > 330], hg.eel.P$year[hg.eel.P$locs == "OB-01" & hg.eel.P
 $resuse > 330], length) / tapply(hg.eel.P$resuse[hg.eel.P$locs == "OB-01"], hg.eel.P$year[hg.eel.P$locs == "OB-01"], length)

eel.summ$Veaz_x = c(tapply(ref.eel$resuse, ref.eel$year, mean), NA)
eel.summ$Veaz_x_se = c(tapply(ref.eel$resuse, ref.eel$year, sd) / sqrt(tapply(ref.eel$resuse, ref.eel$year, length)), NA)
eel.summ$Veaz_medn = c(tapply(ref.eel$resuse, ref.eel$year, median), NA)
eel.summ$Veaz_N = c(tapply(ref.eel$resuse, ref.eel$year, length), NA)
eel.summ$Veaz_perc = c(tapply(ref.eel$resuse[ref.eel$resuse > 330], ref.eel$year[ref.eel$resuse > 330], length) / tapply(ref.eel$resuse, ref.eel
 $year, length), NA)


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",]))


#4-76
plot(ln.l.adj_resuse ~ year, data = ref.eel, pch = 17, ylab = "Ln Hg (ng/g)", xlab = "Year", xlim = c(min(ref.eel$year), 2016), las = 1, tck = 0.015,
 yaxs = "i", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse, hg.eel$ln.l.adj_resuse)), main = "Figure 4-76\nAmerican Eel - OV-04 (Reference)\nLength
 Adjusted Loglinear Regression")

text(2015, max(ref.eel$ln.l.adj_resuse)*0.87, "y = 0.1072x - 210.5", cex = 0.8)
text(2015, max(ref.eel$ln.l.adj_resuse)*0.835, "p = 0.28, 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)


#4-77
plot(ln.l.adj_resuse ~ year, data = hg.eel, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-77\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$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.2420x + 492.62", cex = 0.8)
text(max(hg.eel$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.14", 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)


#4-78
plot(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "BO-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-78\nAmerican Eel - BO-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$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$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.4046x + 819.68", cex = 0.8)
text(max(hg.eel$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.19", 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")
```

```r
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)


#4-79
plot(ln.l.adj_resuse ~ year, hg.eel[hg.eel$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-79\nAmerican Eel
 - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$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$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.2133x + 434.56", cex = 0.8)
text(max(hg.eel$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.835, "p < 0.001, Adj." ~R^2~ "= 0.27", 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)


#4-80
plot(ln.l.adj_resuse ~ year, data = hg.eel[hg.eel$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-80\nAmerican Eel - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(ref.eel$ln.l.adj_resuse)), las = 1, tck = 0.015, yaxs =
 "i")

text(max(hg.eel$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.87, "ln(y) = -0.0379x + 82.348", cex = 0.8)
text(max(hg.eel$year) - 1, max(ref.eel$ln.l.adj_resuse) * 0.835, "p = 0.58, Adj." ~R^2~ "= 0", cex = 0.8)

points(as.numeric(levels(as.factor(hg.eel$year))), tapply(hg.eel$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))), 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-13. Atlantic Tomcod Statistical Analysis Code

### File created for analysis of tomcod 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)


penob = read.dbf("PEN_BI13.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, 40:45)], 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) #705 records

hg.tom = merge(hg.tom,weight[,c(2:4, 6, 7, 36:37, 40:45)], 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)

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

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) #704 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$BO.04_x[c(1,4,6)] = tapply(hg.tom.P$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)] = 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$BO.04_medn[c(1,4,6)] = tapply(hg.tom.P$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)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "BO-04"], hg.tom.P$year[hg.tom.P$locs == "BO-04"], length)
tom.summ$BO.04_perc[c(1,4,6)] = tapply(hg.tom.P$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$ES.13_x[c(1,3,5:6)] = tapply(hg.tom.P$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(1,3,5:6)] = 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$ES.13_medn[c(1,3,5:6)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], median)
tom.summ$ES.13_N[c(1,3,5:6)] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-13"], hg.tom.P$year[hg.tom.P$locs == "ES-13"], length)
tom.summ$ES.13_perc[6] = tapply(hg.tom.P$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]

tom.summ$ES.FP_x[5:6] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], mean)
tom.summ$ES.FP_x_se[5:6] = 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$ES.FP_medn[5:6] = tapply(hg.tom.P$resuse[hg.tom.P$locs == "ES-FP"], hg.tom.P$year[hg.tom.P$locs == "ES-FP"], median)
tom.summ$ES.FP_N[5:6] = 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[5:6] = 0

tom.summ$FRB_x[6] = tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], mean)
tom.summ$FRB_x_se[6] = 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))
tom.summ$FRB_medn[6] = tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], median)
tom.summ$FRB_N[6] = tapply(ref.tom$resuse[ref.tom$locs == "FRB-0"], ref.tom$year[ref.tom$locs == "FRB-0"], length)
tom.summ$FRB_perc[6] = 0

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",])


#4-81
plot(ln.l.adj_resuse ~ year, data = hg.tom, xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-81\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$year) - 1.3, max(hg.tom$ln.l.adj_resuse, na.rm = T) * 0.87, "ln(y) = -0.0936x + 193.15", cex = 0.8)
text(max(hg.tom$year) - 1.3, max(hg.tom$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)


#4-82
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "BO-04",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-82\nAtlantic Tomcod - BO-04\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$ln.l.adj_resuse, na.rm = T)), las = 1, tck =
 0.015, yaxs = "i")
abline(lm(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "BO-04",]), lty = 2)

text(max(hg.tom$year) - 1.2, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.0798x + 166.12", cex = 0.8)
text(max(hg.tom$year) - 1.2, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.089, Adj." ~R^2~ "= 0.19", 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)


#4-83
plot(ln.l.adj_resuse ~ year, hg.tom[hg.tom$locs == "OB-05",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure 4-83\nAtlantic
 Tomcod - OB-05\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$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",]), lty = 2)

text(max(hg.tom$year) - 1.1, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.1210x + 248.8", cex = 0.8)
text(max(hg.tom$year) - 1.1, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.055, Adj." ~R^2~ "= 0.03", 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)


#4-84
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "OB-01",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-84\nAtlantic Tomcod - OB-01\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$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$year) - 1.1, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.09496x + 195.4", cex = 0.8)
text(max(hg.tom$year) - 1.1, max(hg.tom.P$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.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)


#4-85
plot(ln.l.adj_resuse ~ year, data = hg.tom[hg.tom$locs == "ES-13",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-85\nAtlantic Tomcod - ES-13\nLength Adjusted Loglinear Regression", ylim = c(0, 1.02 * max(hg.tom.P$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$year) - 1.1, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.87, "ln(y) = -0.1588x + 324.43", cex = 0.8)
text(max(hg.tom$year) - 1.1, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.835, "p = 0.004, Adj." ~R^2~ "= 0.15", 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)


#4-86
plot(ln.l.adj_resuse ~ year, data = hg.tom.P[hg.tom.P$locs == "ES-FP",], xlab = "Year", ylab = "Length Adjusted Ln Hg (ng/g)", main = "Figure
 4-86\nAtlantic Tomcod - ES-FP\nLength Adjusted Kruskal Wallis Test", ylim = c(0, 1.02 * max(hg.tom.P$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")

text(min(hg.tom$year) + 2, max(hg.tom.P$ln.l.adj_resuse, na.rm = T)*0.95, "Kruskal Wallis rank sum test\np = 0.025", cex = 0.8)

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)
```