Exhibit "A"

Scope of Work
(SOW)

This SOW does not include the collection of any samples.

SRRTTF-ACE will send approximately 161 water samples over approximately 4 events for PCB congeners by High Resolution Mass Spectrometer (HRMS) analysis, EPA Method 1668C. The successful laboratory must follow the quality control criteria in EPA Method 1668C with the following exception. The labeled compound percent recovery for Sample and Method Blank Standard Recovery must be within the range of 25% to 150% (15% - 150% for the monochlorobiphenyls should be observed). Samples may be collected in various volumes or types such as 1 liter, 2.36 liters, 4.0 liters or CLAM Cartridges. A lab duplicate, matrix spike, and matrix spike duplicate will be requested for each sample event. The following tables provide sampling time frames and sample count details:

May 2014 Sampling Event	
Sample Count	Sample Details
8	Riverine samples from 2 locations (3 days and 5 days)
5	Trip Blanks (1 per sampling day)
5	Replicates (1 per sampling day)
1	3 samples collected for composite
1	5 samples collected for composite

August 2014 Sampling Event	
Sample	Sample Details
56	Riverine samples from 8 locations (7 days)
24	Point source samples from 8 locations (3 days)
8	7 samples collected for composites from each of 8 riverine locations
8	3 samples collected for composites from each of 8 point source locations
7	Trip Blanks (1 per sampling day)
7	Riverine Replicates (1 per sampling day)
3	Point Source Replicates (1 per sampling day)

December 2014 / February 2015 Sampling Event	
5	Riverine samples from 1 location
1	5 samples collected for composite
5	Replicate (1 per sampling day)
5	Trip Blanks (1 per sampling day)

May 2015 Sampling Event	
5	Riverine samples from 1 location
1	5 samples collected for composite
5	Replicate (1 per sampling day)
5	Trip Blank (1 per sampling day)

(TSS levels in riverine samples are expected to be as follows: minimum – 1 mg/L; maximum – 79 mg/L; median – 2 mg/L; mean – 3 mg/l)

Laboratories must provide a copy of the extraction methods as performed.

Laboratories must analyze and provide data for an independent source standard (different vendor than the calibration standards).

The estimated cost of ground shipping sample containers, field blank water, coolers, and blue ice are to be included in the price quote.

The laboratory must document which preparation and extraction procedures are performed – and how - for the samples from this project. The laboratory must also document in a logbook, and in a case narrative, any deviations from their Standard Operating Procedures (SOP) performed for this project.

The final data package is to include:

a) All raw data (EPA “Tier IV” or “Level 4” deliverables) in a fully bookmarked PDF file; and
b) All results in an electronic data deliverable (EDD) format as shown in Section 13 of **Reporting of Results** below. The EDD format is needed for loading results to Ecology’s Information Management (EIM) database.

Other items may be included as needed to help understand the data package.

Data Turnaround Time

45 days from sample receipt for May 2014 samples.
60 days from sample receipt for all other sample events.

Analytical Details

1. Section 9.5.1 in all versions of EPA Method 1668 state: “Analyze the blank immediately after analysis of the ongoing precision and recovery standards (OPR) (Section 15.5) to demonstrate freedom from contamination.” However, as mentioned in EPA Method 1668, Revision C, if congeners will be carried from the OPR into the Method Blank, analyze one or more aliquots of solvent between the OPR and the Method Blank.
2. Perform all result calculations using the initial calibration as per the method. In other words, do not use a single point calibration standard. Also, do not average in additional standards analyzed on a different day, or analyzed after the samples have been analyzed.
3. PCB congeners: Use the combined 209 congener standard solution for calibration verification. (Including the labeled and native toxics/Level of Chlorination (LOC)/window-defining congeners in the calibration verification allows a check against the Initial Calibration (ICAL) for those congeners.)

   Alternatively, a separate solution may be analyzed for each, but both solutions must be analyzed on the method schedule for calibration verification. SRRTTF-ACE must be able to evaluate the daily 209 standard against the initial analysis of this standard.
4. All congeners and labeled compounds in the low level Calibration Standard (CS-0.2 standard) must be within the method QC limits for their respective ion abundance ratios; otherwise, the mass spectrometer must be adjusted and this test repeated until the m/z ratios fall within the limits specified. (If the adjustment alters the resolution of the mass spectrometer, resolution must be verified prior to repeat of the test.)
5. Because of the low reporting limits requested, it is recommended the lab add in an extra standard to the initial calibration curve. This will account for increased sensitivity potentially causing analyte saturation at the high end of the curve, and allow a minimum of 5 points to be used in calculating analyte concentration. This will be accomplished by use of the CS-0.2 standard specified in the method.
6. HRMS instrument resolution must be 10,000 or better. Proof (in the form of an instrument printout) must be submitted with the data.

Reporting of Results

1. Report all results in pg/L for water.
2. Include a copy of the “Request for Laboratory Services” with signed and dated Chain of Custody section; this form will be provided by the SRRTTF-ACE Sampling Contractor. Proof of Clean Certification must be provided for project sample containers with a frequency of at least 1 in every 20 containers as well as the last 10 results.
3. Include Case Narratives and corrective action reports.
4. Provide description of: analytical method used; any modifications to the method, Quality Assurance/Quality Control (QA/QC) performed and results; definitions of all data flags and qualifiers used; and any other information that helps client understand the data package.

5. Provide fully validatable deliverables package: Deliverables shall include copies of all raw data necessary to perform an independent evaluation of the results, including, but not limited to initial calibration and verification standards, sample and QC chromatograms and spectra, analytical sequence (run) logs, bench sheets, standard logs and Certificates of Analysis for standards, etc.
   A. Include a fully paginated and bookmarked Adobe Acrobat (PDF) file on compact disk (CD).
   B. Bookmark *each individual sample and each standard chromatogram* for ease of review.
   C. Rotate landscape pages as needed so that all information is viewable left to right in the electronic file.
   D. Clearly identify all field and QC samples with the sample number or QC name in the raw data and report.
   E. All initial calibration (ICAL) standards and Calibration Verification Standard (VER), and the single point 209 PCB standard, shall be clearly identified in the raw data and separately bookmarked in the electronic file. (For example: CS-0.2, CS-1, etc., for the ICAL.)
   F. An Independent Calibration Verification (ICV) standard must be analyzed from a separate source in order to verify the initial calibration standards. The ICV must be analyzed each time a new standard curve is prepared. Provide the results of the most recent ICV with the data. This is equivalent to the Quality Control Check Sample in the method.
   G. Provide before and after printouts of any and all manual integrations.
   H. Provide analytical sequence logs that include the date, time, and filename for the initial and continuing calibrations, all field and QC samples, check standards, etc., associated with the project.

6. Reporting Limits (RL), Quantitation Limit (QL), Method Detection Limit (MDL), Estimated Detection Limit (EDL).
   A. Maximum RLs are defined in the table below.

Analytical Methods and Reporting Limits			
Analysis	**Analyte**	**Water**	**Sediment**
EPA 1668C	PCB congeners	1-20 pg/L (depending on congener)	NA

   B. If any of these limits cannot be met for individual samples due to interference or other issues, contact the client to discuss action to take.
   C. Provide the QL for each result in the electronic results file. (The QL is based on the

lowest validated standard in calibration curve; and equivalent to "Minimum Level or ML" in 1668C).

D. Provide the most recent MDL results for each analyte and include the date performed.

E. Report down to the (EDL) - aka Instrument Detection Limits (IDL) or Sample Detection Limits (SDL) - based on 2.5 times the signal-to-noise ratio. Provide this value for each target analyte in the electronic results file.

F. Dilutions

   a. Any results above the range of the calibration curve must be diluted to be within the range of the calibration curve.

   b. All results reported from dilution analyses must be within the range of the calibration curve.

G. For non-detect values, record the EDL in the "Result Reported Value" column and a "UJ" the "Result Data Qualifier" column.

H. Qualify detected values that are below the QL as estimates ("J").

I. Do not report below the EDL. Where the EDL is above the QL due to interference, raise any values below the EDL to the value of the EDL and qualify "UJ".

J. Report total homologs when not detected as "U" without a value.

K. Calculate and report the Estimated Maximum Possible Concentration (EMPC) value for results that do not meet ion abundance ratio criteria. Qualify these results with "NJ". Provide an example calculation if the result value is adjusted.

7. The qualifiers used above are defined as:

   A. "J" – The analyte was positively identified. The associated numerical result is an estimate.

   B. "U" – The analyte was not detected above the reporting limit. (This qualifier will likely be used only for total homologs, since all analytes are to be reported down to the level of the EDL.)

   C. "UJ" – The analyte was not detected at or above the estimated reporting limit.

   D. "NJ" – The analysis indicates the presence of an analyte that has been "tentatively identified" and the associated numerical value represents its approximate concentration. (See 6. K., above.)

8. Perform all QC samples as specified in the method.

   A. Report results of Laboratory Control Samples (On-going Precision and Recovery standards), labeled compounds, (including cleanup standards and extraction internal standard/surrogates) as % recoveries in the EDD.

9. Method Blanks.
   A. Clearly identify samples associated with each laboratory Method Blank.
   B. If sample results are less than three times the concentration in the associated method blank, flag sample results with "B" – even if the sample result has already been qualified "NJ"; but not when the blank result is qualified "NJ". Discuss in the Case Narrative whether these qualified results are included in the summing of total homolog results and Total PCBs; where applicable.
   C. Total PCBs in the Method Blank, at a maximum, must not exceed 50 pg/L. Method Blanks for Total PCBs in the range of 10pg/L to 1 pg/L are desired. If the 50 pg/L or other established limit is exceeded, contact SRRTTF-ACE to discuss actions to take. Most likely, any blanks with individual results greater than half the EQL should be re-extracted along with any associated samples.
   D. Concentrations of congeners in a minimum of 10 blanks must be significantly below the ML {QL}. "Significant" means that the ML for the congener is no less than 2 standard deviations above the mean (average) level in the minimum of 10 blanks. The blanks must be analyzed during the same period that samples are analyzed, ideally over an approximately 1-month period.

10. Treatment of result qualifiers for and summing of homologs.
   A. Describe in the case narrative how totals were derived for PCB homolog groups and Total PCBs (e.g. what rules are used for rounding values, dealing with non-detects, blank detects, qualifier definitions, etc.).
   B. Report Total PCB results for each homolog group in the EDD. However, do not report a QL or an EDL (leave these columns blank for summed values).
   C. Do not include EMPC results in the calculations of the total homologs.

11. Sample identification.
   A. Provide the client sample ID (field ID) associated with all sample results.
   B. Provide the lab's internal sample ID associated with all results OR a table that cross-references field ID with the lab's internal sample ID.
   C. Clearly identify QA/QC samples and results: blanks, matrix spikes, Standard Reference Materials (SRM), lab duplicates. If samples are reanalyzed, these results need be clearly identified as such.
   D. Label all analyte peaks on chromatograms with either the congener name or the retention time and scale chromatograms such that peaks are visible above the baseline.

12. Analyte identification.
   A. Provide the Chemistry Abstract Service Registry Number (CAS RN) for individual congeners/each analyte.

B. PCB Congener Numbering.

a. Name PCB congeners using the naming convention given by Guitart, et al. (Guitart R., Puig P., Gomez-Catalan J., Chemosphere 27 1451-1459, 1993).

See http://www.epa.gov/osw/hazard/tsd/pcbs/pubs/congeners.htm

b. Modify to a 7-character format that uses leading zeroes for congener numbers below 100 (e.g. PCB-008). (Conversely, the value "PCB-001" appears to have 7 characters yet actually has 11 since there are 4 spaces after the 001. This complicates export into databases and statistical packages.)

c. Records for co-eluting congeners must have no CAS number.

C. Co-eluting congeners for PCBs should be numbered in ascending order (e.g.: PCB-040/041/071), and records for co-eluting congeners must have no CAS number.

13. Electronic results must be in Excel-compatible format as in table below:

Required Fields for Electronic Data Deliverables		
Preferred Order	**Field Name**	**Example**
1	MEL (Client) Sample ID	1311021-03
2	Field ID (sample name on tag)	COLRIV034
3	Result Congener Name	2,3'-DiCB
4	Result Parameter Name	PCB-006
5	Result Parameter CAS Number	25569-80-6
6	Sample Extraction Date	11/14/2013**(format as numerical date)**
7	Sample Analysis Date	11/15/2013 **(format as numerical date)**
8	Lab Duplicate Flag	"Y" if lab duplicate, leave blank or "N" if not
9	Re-analysis Flag	"Y" if a re-analysis, leave blank or "N" if not
10	Result Reported Value	7.9 (format as number)
11	Result Data Qualifier	J
12	Result Value Units of Measure	pg/L
13	Result Value QL *	10 (format as number)
14	Result Value EDL**	3.42 (format as number)
15	Result Method Code	EPA 1668C
16	Result Lab Name	Laboratory Name
17	Contract Lab Sample ID	PR137954
18	Others as needed by contract lab or MEL.	If used, clearly identify field and content
	* = Estimated Quantitation Limit (Based on the lowest validated standard in the calibration curve and adjusted for weight, volume, % solids, etc., as applicable).	
	** = Estimated Sample Detection Limit; calculated from signal for each sample)	